



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 10:32 PM UTC

PDB ID : 9LY8 / pdb_00009ly8
EMDB ID : EMD-62530
Title : Cryo-EM structure of carboxysomal midi-shell: T=9 shell under C1 symmetry
Authors : Li, J.X.; Li, T.P.; Wang, S.M.; Zhang, Y.Z.; Liu, L.N.; Wang, P.
Deposited on : 2025-02-19
Resolution : 2.77 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

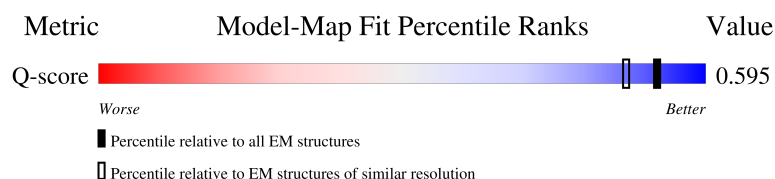
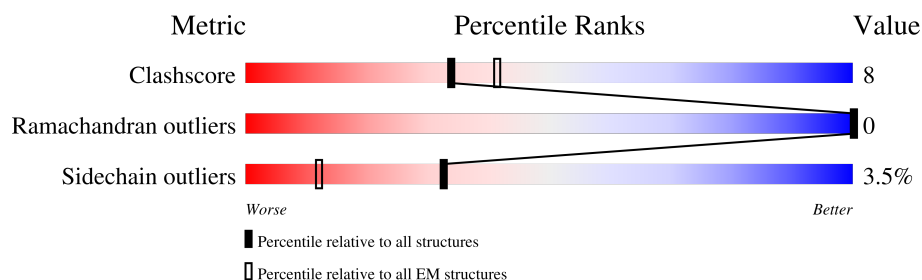
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.77 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



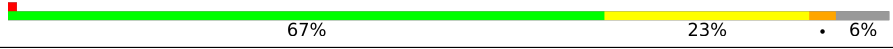
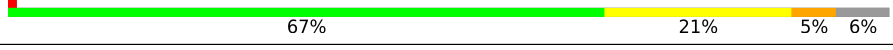
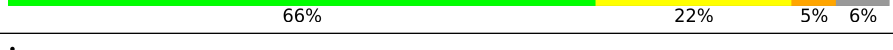
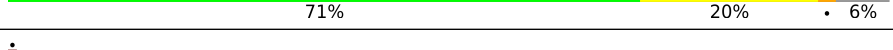
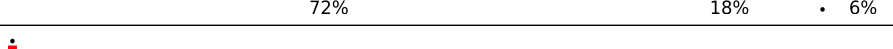
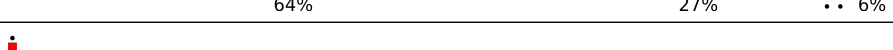
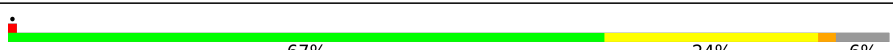
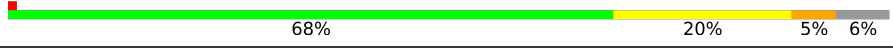
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10695 (2.27 - 3.27)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A0	98	 64% 26% • • 6%
1	A1	98	 65% 26% • 6%
1	A2	98	 67% 21% 5% 6% 6%
1	A3	98	 72% 19% • 6%

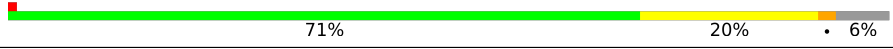
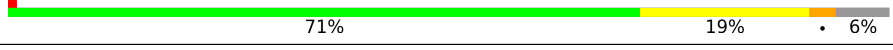
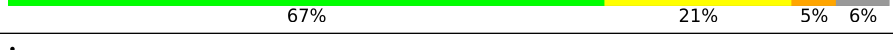
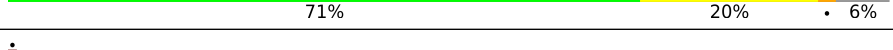
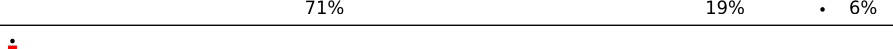
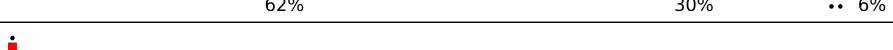
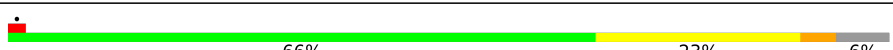
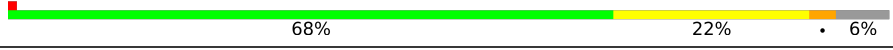
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Mol	Chain	Length	Quality of chain
1	A4	98	
1	A5	98	
1	A6	98	
1	A7	98	
1	A8	98	
1	A9	98	
1	AA	98	
1	AB	98	
1	AC	98	
1	AD	98	
1	AE	98	
1	AF	98	
1	AG	98	
1	AH	98	
1	AI	98	
1	AJ	98	
1	AK	98	
1	AL	98	
1	AM	98	
1	AN	98	
1	AO	98	
1	AP	98	
1	AQ	98	
1	AR	98	
1	AS	98	

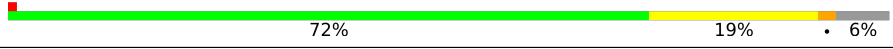
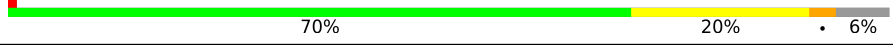
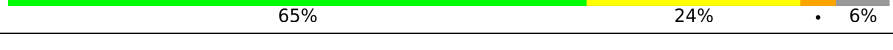
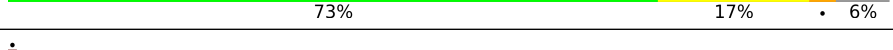
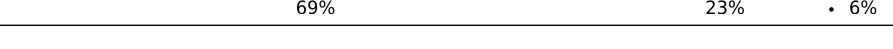
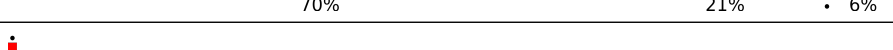
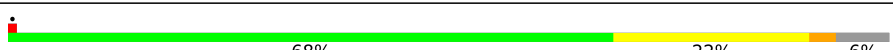
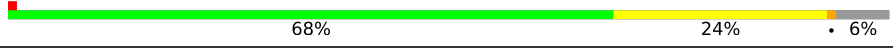
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Mol	Chain	Length	Quality of chain
1	AT	98	
1	AU	98	
1	AV	98	
1	AW	98	
1	AX	98	
1	Aa	98	
1	Ab	98	
1	Ac	98	
1	Ad	98	
1	Ae	98	
1	Af	98	
1	Ag	98	
1	Ah	98	
1	Ai	98	
1	Aj	98	
1	Ak	98	
1	Al	98	
1	Am	98	
1	An	98	
1	Ao	98	
1	Ap	98	
1	Aq	98	
1	Ar	98	
1	As	98	
1	At	98	

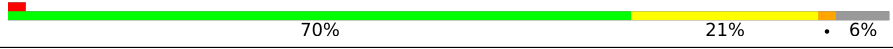
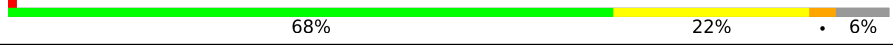
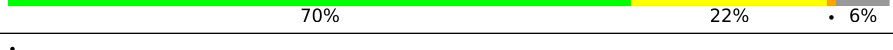
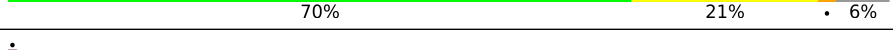
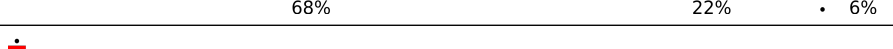
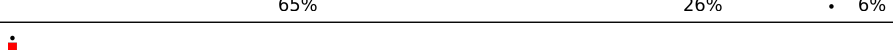
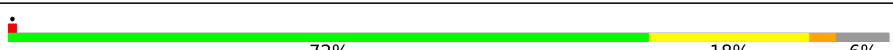
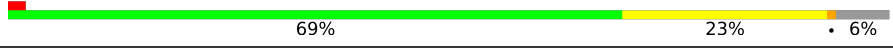
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Mol	Chain	Length	Quality of chain
1	Au	98	
1	Av	98	
1	Aw	98	
1	Ax	98	
1	Ay	98	
1	Az	98	
1	B0	98	
1	B1	98	
1	B2	98	
1	B3	98	
1	B4	98	
1	B5	98	
1	B6	98	
1	B7	98	
1	B8	98	
1	B9	98	
1	BA	98	
1	BB	98	
1	BC	98	
1	BD	98	
1	BE	98	
1	BF	98	
1	BG	98	
1	BH	98	
1	BI	98	

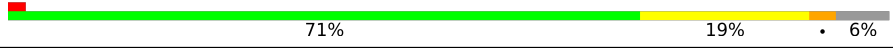
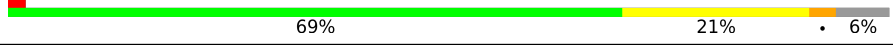
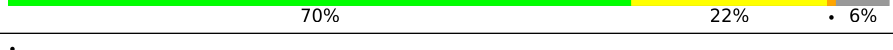
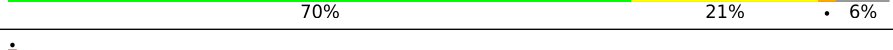
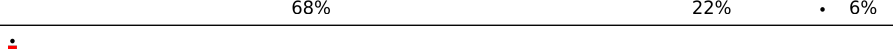
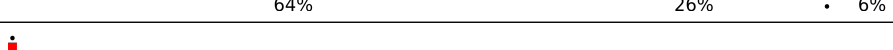
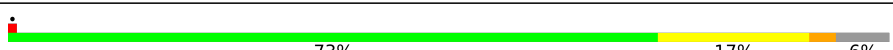
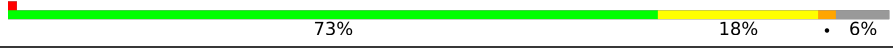
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Mol	Chain	Length	Quality of chain
1	BJ	98	
1	BK	98	
1	BL	98	
1	BM	98	
1	BN	98	
1	BO	98	
1	BP	98	
1	BQ	98	
1	BR	98	
1	BS	98	
1	BT	98	
1	BU	98	
1	BV	98	
1	BW	98	
1	BX	98	
1	Ba	98	
1	Bb	98	
1	Bc	98	
1	Bd	98	
1	Be	98	
1	Bf	98	
1	Bg	98	
1	Bh	98	
1	Bi	98	
1	Bj	98	

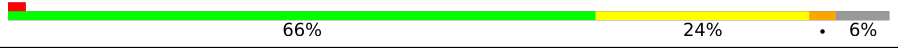
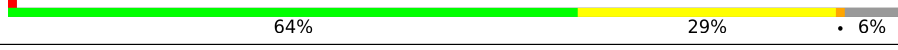
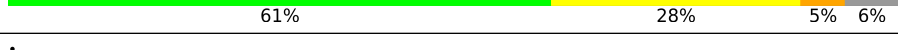
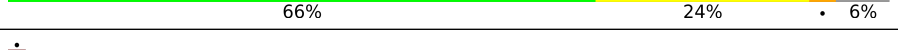
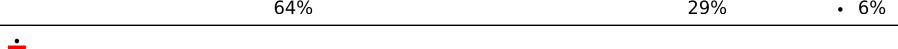
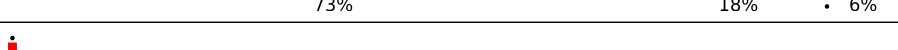
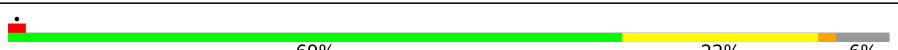
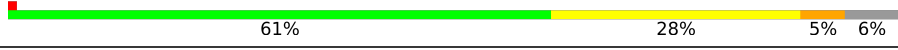
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Mol	Chain	Length	Quality of chain
1	Bk	98	
1	Bl	98	
1	Bm	98	
1	Bn	98	
1	Bo	98	
1	Bp	98	
1	Bq	98	
1	Br	98	
1	Bs	98	
1	Bt	98	
1	Bu	98	
1	Bv	98	
1	Bw	98	
1	Bx	98	
1	By	98	
1	Bz	98	
1	C0	98	
1	C1	98	
1	C2	98	
1	C3	98	
1	C4	98	
1	C5	98	
1	C6	98	
1	C7	98	
1	C8	98	

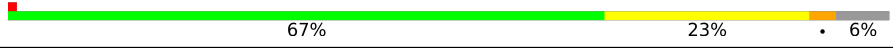
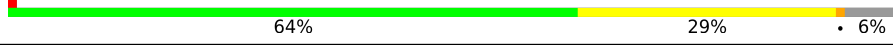
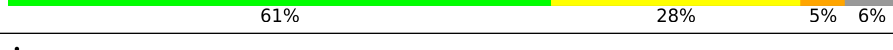
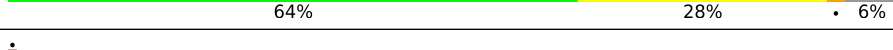
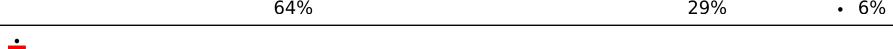
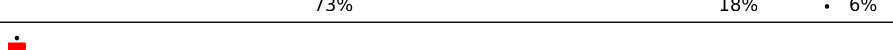
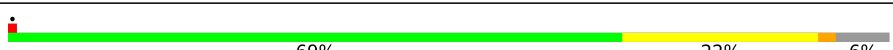
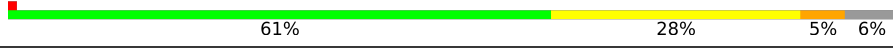
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Mol	Chain	Length	Quality of chain
1	C9	98	
1	CA	98	
1	CB	98	
1	CC	98	
1	CD	98	
1	CE	98	
1	CF	98	
1	CG	98	
1	CH	98	
1	CI	98	
1	CJ	98	
1	CK	98	
1	CL	98	
1	CM	98	
1	CN	98	
1	CO	98	
1	CP	98	
1	CQ	98	
1	CR	98	
1	CS	98	
1	CT	98	
1	CU	98	
1	CV	98	
1	CW	98	
1	CX	98	

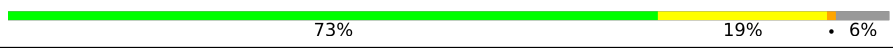
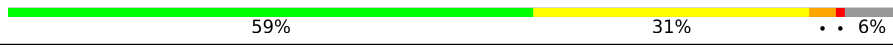
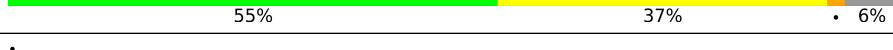
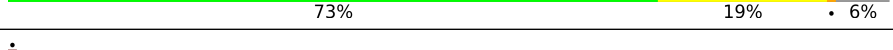
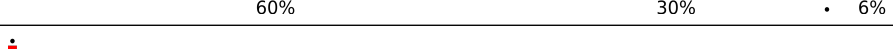
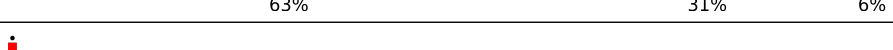
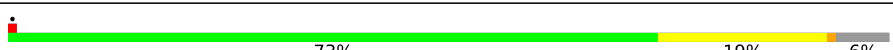
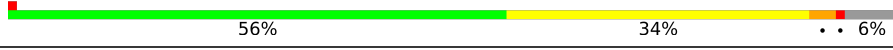
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Mol	Chain	Length	Quality of chain
1	Ca	98	
1	Cb	98	
1	Cc	98	
1	Cd	98	
1	Ce	98	
1	Cf	98	
1	Cg	98	
1	Ch	98	
1	Ci	98	
1	Cj	98	
1	Ck	98	
1	Cl	98	
1	Cm	98	
1	Cn	98	
1	Co	98	
1	Cp	98	
1	Cq	98	
1	Cr	98	
1	Cs	98	
1	Ct	98	
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1	Cv	98	
1	Cw	98	
1	Cx	98	
1	Cy	98	

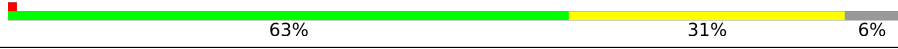
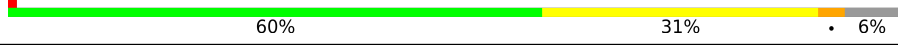
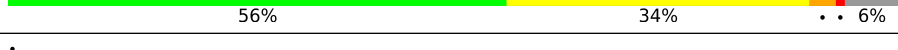
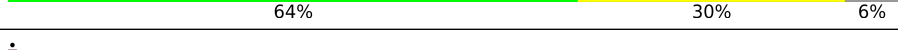
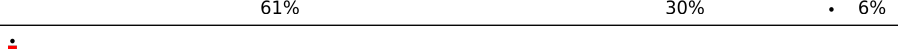
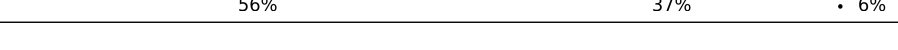
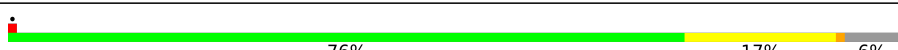
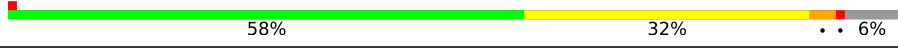
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Mol	Chain	Length	Quality of chain
1	Cz	98	
1	D0	98	
1	D1	98	
1	D2	98	
1	D3	98	
1	D4	98	
1	D5	98	
1	D6	98	
1	D7	98	
1	D8	98	
1	D9	98	
1	DA	98	
1	DB	98	
1	DC	98	
1	DD	98	
1	DE	98	
1	DF	98	
1	DG	98	
1	DH	98	
1	DI	98	
1	DJ	98	
1	DK	98	
1	DL	98	
1	DM	98	
1	DN	98	

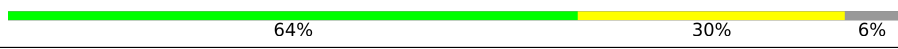
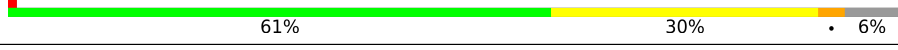
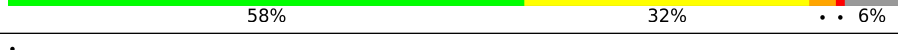
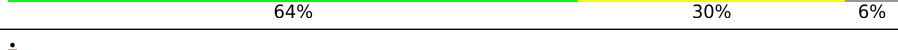
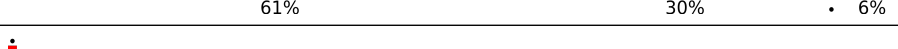
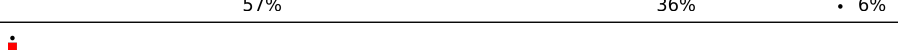
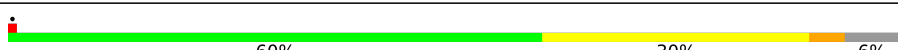
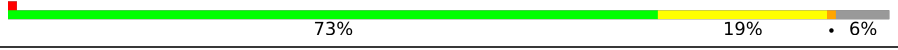
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Mol	Chain	Length	Quality of chain
1	DO	98	
1	DP	98	
1	DQ	98	
1	DR	98	
1	DS	98	
1	DT	98	
1	DU	98	
1	DV	98	
1	DW	98	
1	DX	98	
1	Da	98	
1	Db	98	
1	Dc	98	
1	Dd	98	
1	De	98	
1	Df	98	
1	Dg	98	
1	Dh	98	
1	Di	98	
1	Dj	98	
1	Dk	98	
1	Dl	98	
1	Dm	98	
1	Dn	98	
1	Do	98	

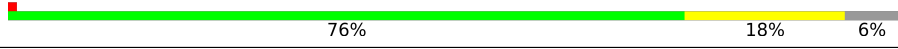
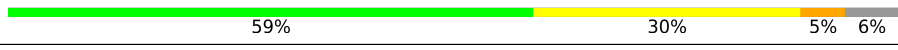
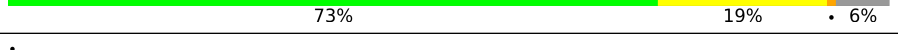
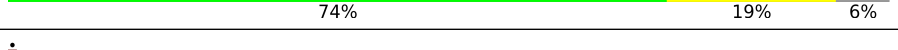
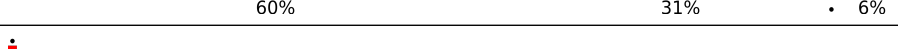
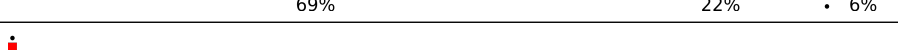
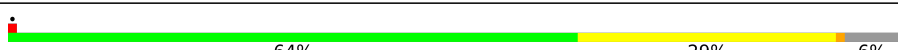
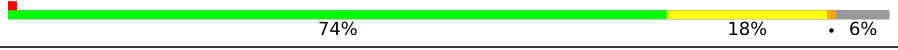
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Mol	Chain	Length	Quality of chain
1	Dp	98	
1	Dq	98	
1	Dr	98	
1	Ds	98	
1	Dt	98	
1	Du	98	
1	Dv	98	
1	Dw	98	
1	Dx	98	
1	Dy	98	
1	Dz	98	
1	E0	98	
1	E1	98	
1	E2	98	
1	E3	98	
1	E4	98	
1	E5	98	
1	E6	98	
1	E7	98	
1	E8	98	
1	E9	98	
1	EA	98	
1	EB	98	
1	EC	98	
1	ED	98	

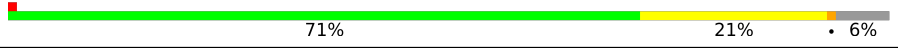
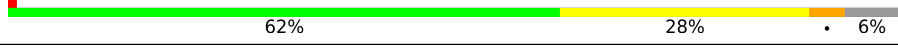
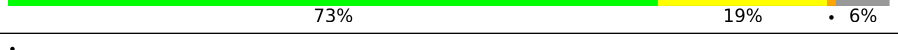
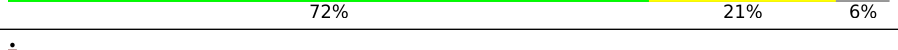
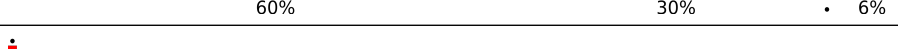
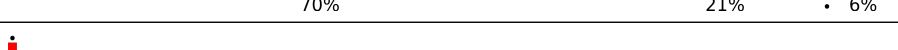
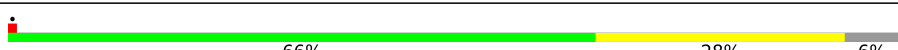
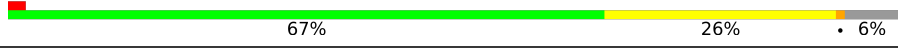
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Mol	Chain	Length	Quality of chain
1	EE	98	
1	EF	98	
1	EG	98	
1	EH	98	
1	EI	98	
1	EJ	98	
1	EK	98	
1	EL	98	
1	EM	98	
1	EN	98	
1	EO	98	
1	EP	98	
1	EQ	98	
1	ER	98	
1	ES	98	
1	ET	98	
1	EU	98	
1	EV	98	
1	EW	98	
1	EX	98	
1	Ea	98	
1	Eb	98	
1	Ec	98	
1	Ed	98	
1	Ee	98	

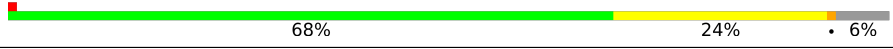
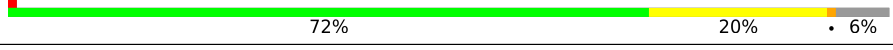
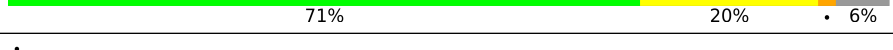
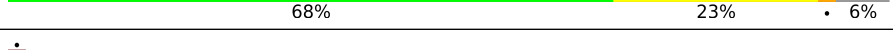
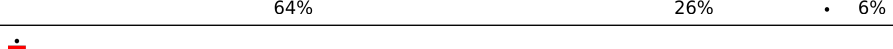
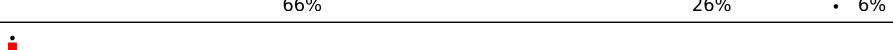
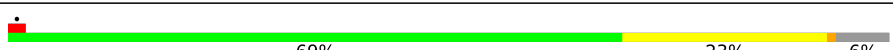
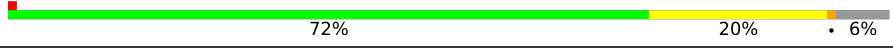
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Mol	Chain	Length	Quality of chain
1	Ef	98	
1	Eg	98	
1	Eh	98	
1	Ei	98	
1	Ej	98	
1	Ek	98	
1	El	98	
1	Em	98	
1	En	98	
1	Eo	98	
1	Ep	98	
1	Eq	98	
1	Er	98	
1	Es	98	
1	Et	98	
1	Eu	98	
1	Ev	98	
1	Ew	98	
1	Ex	98	
1	Ey	98	
1	Ez	98	
1	F0	98	
1	F1	98	
1	F2	98	
1	F3	98	

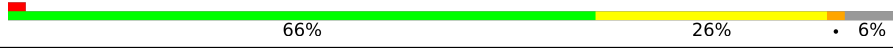
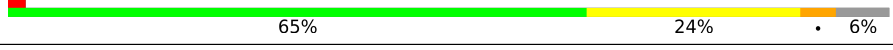
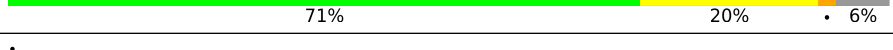
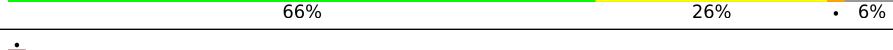
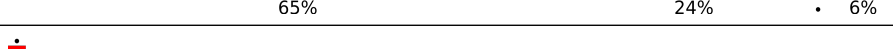
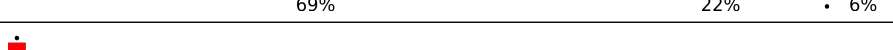
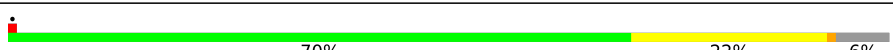
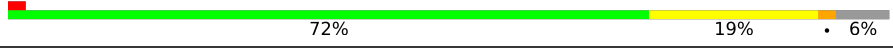
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Mol	Chain	Length	Quality of chain
1	F4	98	
1	F5	98	
1	F6	98	
1	F7	98	
1	F8	98	
1	F9	98	
1	FA	98	
1	FB	98	
1	FC	98	
1	FD	98	
1	FE	98	
1	FF	98	
1	FG	98	
1	FH	98	
1	FI	98	
1	FJ	98	
1	FK	98	
1	FL	98	
1	FM	98	
1	FN	98	
1	FO	98	
1	FP	98	
1	FQ	98	
1	FR	98	
1	FS	98	

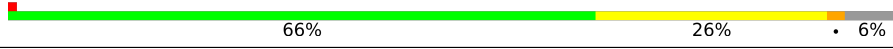
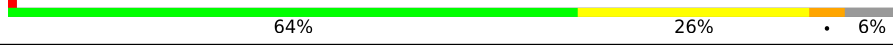
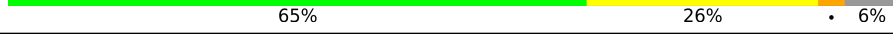
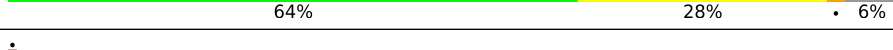
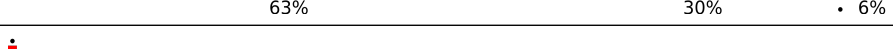
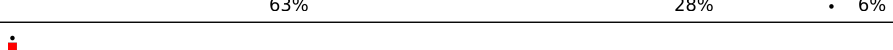
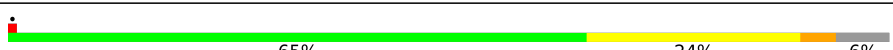
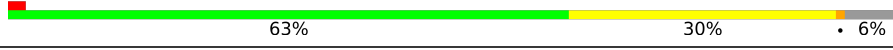
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Mol	Chain	Length	Quality of chain
1	FT	98	
1	FU	98	
1	FV	98	
1	FW	98	
1	FX	98	
1	Fa	98	
1	Fb	98	
1	Fc	98	
1	Fd	98	
1	Fe	98	
1	Ff	98	
1	Fg	98	
1	Fh	98	
1	Fi	98	
1	Fj	98	
1	Fk	98	
1	Fl	98	
1	Fm	98	
1	Fn	98	
1	Fo	98	
1	Fp	98	
1	Fq	98	
1	Fr	98	
1	Fs	98	
1	Ft	98	

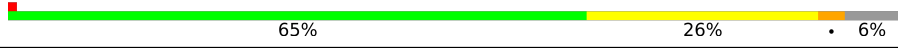
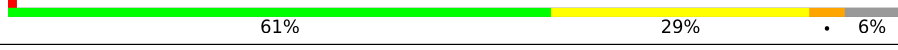
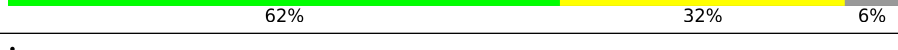
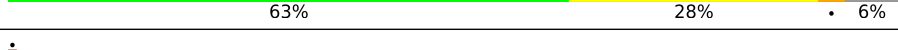
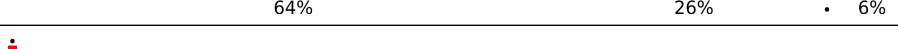
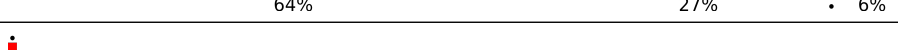
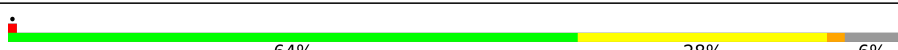
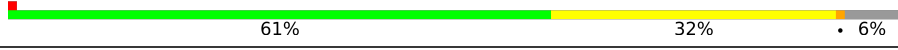
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Mol	Chain	Length	Quality of chain
1	Fu	98	
1	Fv	98	
1	Fw	98	
1	Fx	98	
1	Fy	98	
1	Fz	98	
1	G0	98	
1	G1	98	
1	G2	98	
1	G3	98	
1	G4	98	
1	G5	98	
1	G6	98	
1	G7	98	
1	G8	98	
1	G9	98	
1	GA	98	
1	GB	98	
1	GC	98	
1	GD	98	
1	GE	98	
1	GF	98	
1	GG	98	
1	GH	98	
1	GI	98	

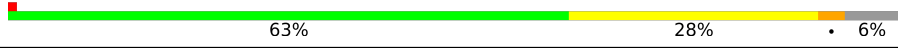
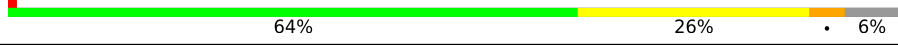
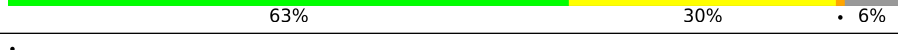
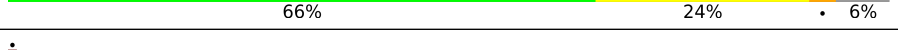
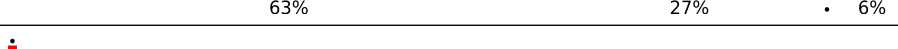
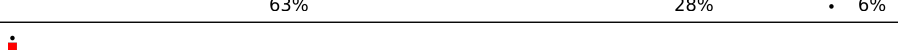
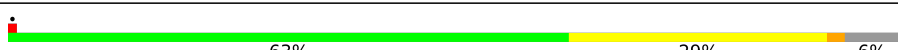
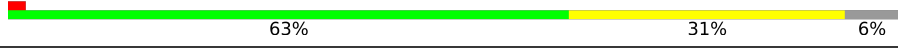
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Mol	Chain	Length	Quality of chain
1	GJ	98	
1	GK	98	
1	GL	98	
1	GM	98	
1	GN	98	
1	GO	98	
1	GP	98	
1	GQ	98	
1	GR	98	
1	GS	98	
1	GT	98	
1	GU	98	
1	GV	98	
1	GW	98	
1	GX	98	
1	Ga	98	
1	Gb	98	
1	Gc	98	
1	Gd	98	
1	Ge	98	
1	Gf	98	
1	Gg	98	
1	Gh	98	
1	Gi	98	
1	Gj	98	

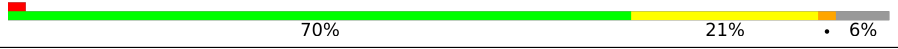
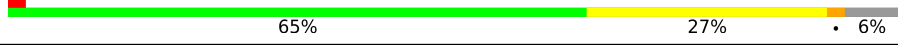
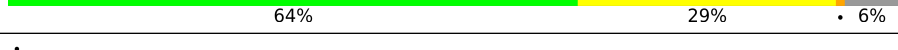
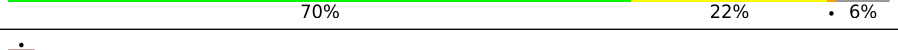
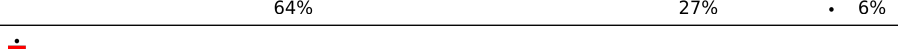
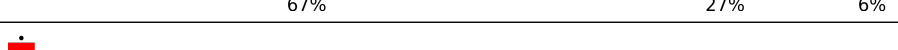
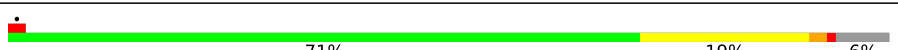
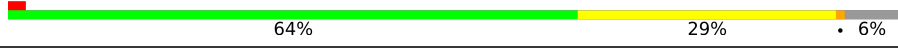
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Mol	Chain	Length	Quality of chain
1	Gk	98	
1	Gl	98	
1	Gm	98	
1	Gn	98	
1	Go	98	
1	Gp	98	
1	Gq	98	
1	Gr	98	
1	Gs	98	
1	Gt	98	
1	Gu	98	
1	Gv	98	
1	Gw	98	
1	Gx	98	
1	Gy	98	
1	Gz	98	
1	H0	98	
1	H1	98	
1	H2	98	
1	H3	98	
1	H4	98	
1	H5	98	
1	H6	98	
1	H7	98	
1	H8	98	

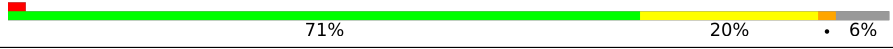
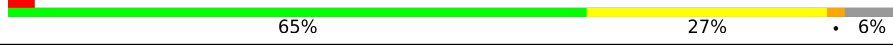
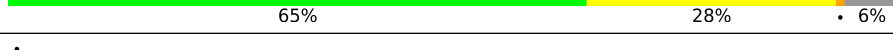
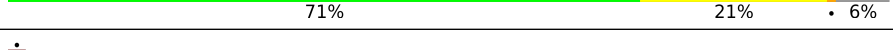
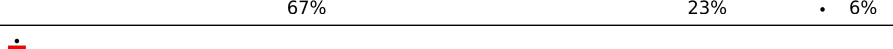
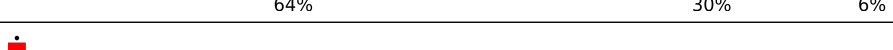
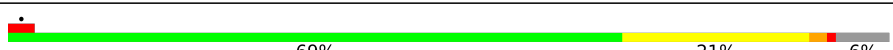
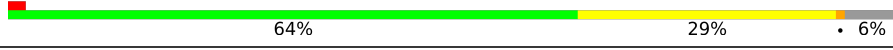
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Mol	Chain	Length	Quality of chain
1	H9	98	
1	HA	98	
1	HB	98	
1	HC	98	
1	HD	98	
1	HE	98	
1	HF	98	
1	HG	98	
1	HH	98	
1	HI	98	
1	HJ	98	
1	HK	98	
1	HL	98	
1	HM	98	
1	HN	98	
1	HO	98	
1	HP	98	
1	HQ	98	
1	HR	98	
1	HS	98	
1	HT	98	
1	HU	98	
1	HV	98	
1	HW	98	
1	HX	98	

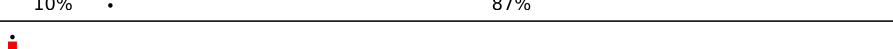
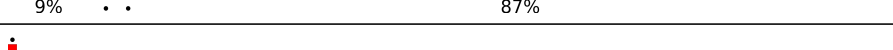
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Mol	Chain	Length	Quality of chain
1	Ha	98	
1	Hb	98	
1	Hc	98	
1	Hd	98	
1	He	98	
1	Hf	98	
1	Hg	98	
1	Hh	98	
1	Hi	98	
1	Hj	98	
1	Hk	98	
1	Hl	98	
1	Hm	98	
1	Hn	98	
1	Ho	98	
1	Hp	98	
1	Hq	98	
1	Hr	98	
1	Hs	98	
1	Ht	98	
1	Hu	98	
1	Hv	98	
1	Hw	98	
1	Hx	98	
1	Hy	98	

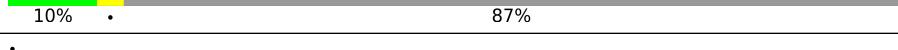
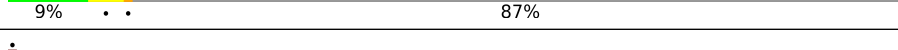
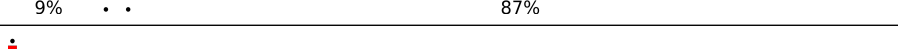
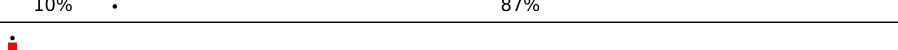
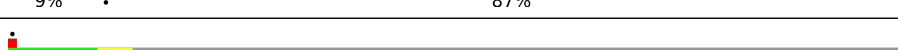
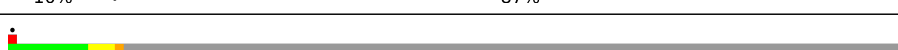
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Mol	Chain	Length	Quality of chain
1	Hz	98	
2	X0	869	
2	X1	869	
2	X2	869	
2	X3	869	
2	X4	869	
2	X5	869	
2	X6	869	
2	X7	869	
2	X8	869	
2	X9	869	
2	XA	869	
2	XB	869	
2	XC	869	
2	XD	869	
2	XE	869	
2	XF	869	
2	XG	869	
2	XH	869	
2	XI	869	
2	XJ	869	
2	XK	869	
2	XL	869	
2	XM	869	
2	XN	869	

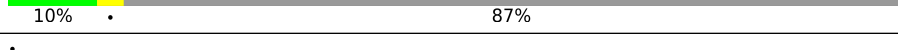
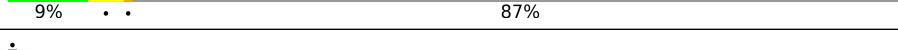
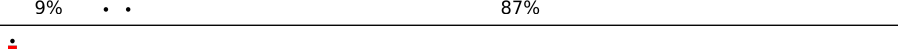
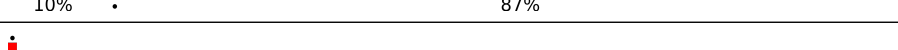
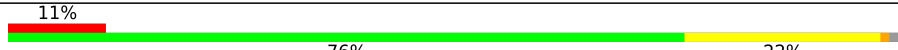
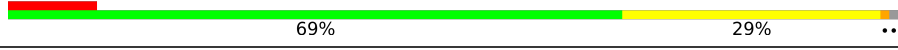
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Mol	Chain	Length	Quality of chain
2	XO	869	 9% 87%
2	XP	869	 10% 87%
2	XQ	869	 9% 87%
2	XR	869	 9% 87%
2	XS	869	 10% 87%
2	XT	869	 9% 87%
2	XU	869	 10% 87%
2	XV	869	 9% 87%
2	XW	869	 9% 87%
2	XX	869	 10% 87%
2	Xa	869	 9% 87%
2	Xb	869	 10% 87%
2	Xc	869	 9% 87%
2	Xd	869	 9% 87%
2	Xe	869	 10% 87%
2	Xf	869	 9% 87%
2	Xg	869	 10% 87%
2	Xh	869	 9% 87%
2	Xi	869	 9% 87%
2	Xj	869	 9% 87%
2	Xk	869	 10% 87%
2	Xl	869	 10% 87%
2	Xm	869	 9% 87%
2	Xn	869	 9% 87%
2	Xo	869	 10% 87%

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Mol	Chain	Length	Quality of chain
2	Xp	869	
2	Xq	869	
2	Xr	869	
2	Xs	869	
2	Xt	869	
2	Xu	869	
2	Xv	869	
2	Xw	869	
2	Xx	869	
2	Xy	869	
2	Xz	869	
3	P0	83	
3	P1	83	
3	P2	83	
3	P3	83	
3	P4	83	
3	P5	83	
3	P6	83	
3	P7	83	
3	P8	83	
3	P9	83	
3	PA	83	
3	PB	83	
3	PC	83	
3	PD	83	

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Mol	Chain	Length	Quality of chain
3	PE	83	
3	PF	83	
3	PG	83	
3	PH	83	
3	PI	83	
3	PJ	83	
3	PK	83	
3	PL	83	
3	PM	83	
3	PN	83	
3	PO	83	
3	PP	83	
3	PQ	83	
3	PR	83	
3	PS	83	
3	PT	83	
3	PU	83	
3	PV	83	
3	PW	83	
3	PX	83	
3	Pa	83	
3	Pb	83	
3	Pc	83	
3	Pd	83	
3	Pe	83	

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Mol	Chain	Length	Quality of chain
3	Pf	83	
3	Pg	83	
3	Ph	83	
3	Pi	83	
3	Pj	83	
3	Pk	83	
3	Pl	83	
3	Pm	83	
3	Pn	83	
3	Po	83	
3	Pp	83	
3	Pq	83	
3	Pr	83	
3	Ps	83	
3	Pt	83	
3	Pu	83	
3	Pv	83	
3	Pw	83	
3	Px	83	
3	Py	83	
3	Pz	83	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 403140 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Major carboxysome shell protein CsoS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A2	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	B2	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	C2	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	D2	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	E2	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	F2	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	G2	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	H2	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	A1	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	B1	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	C1	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	D1	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	E1	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	F1	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	G1	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	A5	92	Total	C	N	O	S	0	0
			656	408	123	122	3		
1	B5	92	Total	C	N	O	S	0	0
			656	408	123	122	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	C5	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	D5	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	E5	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	F5	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	G5	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	H5	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	A3	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	B3	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	C3	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	D3	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	E3	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	F3	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	G3	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	H3	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	A4	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	B4	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	C4	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	D4	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	E4	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	F4	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	G4	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	H4	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	A7	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	B7	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	C7	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	D7	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	E7	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	F7	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	G7	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	H7	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	A6	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	B6	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	C6	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	D6	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	E6	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	F6	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	G6	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	A0	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	B0	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	C0	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	D0	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	E0	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	F0	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	G0	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	H0	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	A8	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	B8	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	C8	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	D8	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	E8	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	F8	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	G8	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	H8	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	A9	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	B9	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	C9	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	D9	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	E9	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	F9	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	G9	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	H9	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ab	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bb	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Cb	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Db	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Eb	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fb	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gb	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hb	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Aa	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ba	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ca	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Da	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ea	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fa	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ga	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ha	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ae	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Be	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ce	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	De	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ee	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fe	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ge	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	He	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ac	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bc	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cc	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dc	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ec	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fc	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gc	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hc	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ad	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bd	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cd	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dd	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ed	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fd	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gd	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hd	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ag	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bg	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cg	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dg	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Eg	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fg	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gg	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hg	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Af	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bf	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cf	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Df	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ef	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ff	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gf	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Aj	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bj	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cj	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dj	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ej	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fj	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gj	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hj	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ah	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bh	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ch	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dh	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Eh	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fh	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gh	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hh	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ai	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bi	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ci	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Di	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ei	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fi	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gi	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hi	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Al	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bl	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cl	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dl	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	El	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fl	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gl	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Hl	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ak	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bk	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ck	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dk	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ek	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fk	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gk	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ao	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bo	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Co	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Do	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Eo	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fo	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Go	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ho	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Am	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bm	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cm	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dm	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Em	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Fm	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gm	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hm	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	An	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bn	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cn	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dn	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	En	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fn	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gn	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hn	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Aq	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bq	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cq	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dq	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Eq	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fq	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gq	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hq	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ap	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bp	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Cp	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dp	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ep	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fp	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gp	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hp	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	At	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bt	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ct	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dt	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Et	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ft	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gt	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ht	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ar	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Br	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cr	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dr	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Er	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fr	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gr	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Hr	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	As	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bs	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cs	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ds	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Es	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fs	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gs	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hs	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Av	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bv	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cv	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dv	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ev	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fv	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gv	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hv	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Au	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bu	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cu	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Du	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Eu	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fu	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gu	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ay	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	By	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cy	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dy	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ey	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fy	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gy	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hy	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Aw	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bw	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cw	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dw	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ew	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fw	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gw	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hw	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ax	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bx	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Cx	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dx	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ex	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fx	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gx	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hx	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AA	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BA	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CA	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DA	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EA	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FA	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GA	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HA	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Az	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Bz	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Cz	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Dz	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Ez	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Fz	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Gz	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AD	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BD	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CD	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DD	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	ED	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FD	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GD	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HD	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AB	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BB	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CB	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DB	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EB	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FB	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GB	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HB	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AC	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BC	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CC	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DC	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EC	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	FC	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GC	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HC	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AF	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BF	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CF	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DF	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EF	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FF	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GF	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HF	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AE	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BE	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CE	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DE	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EE	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FE	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GE	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HE	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AI	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BI	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CI	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DI	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EI	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FI	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GI	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HI	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AG	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BG	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CG	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DG	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EG	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FG	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GG	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HG	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AH	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BH	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CH	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DH	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EH	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FH	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GH	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HH	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AK	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BK	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CK	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DK	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EK	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FK	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GK	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HK	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AJ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BJ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CJ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DJ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EJ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FJ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GJ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HJ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AN	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BN	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CN	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DN	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	EN	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FN	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GN	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HN	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AL	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BL	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CL	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DL	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EL	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FL	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GL	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HL	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AM	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BM	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CM	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DM	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EM	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FM	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GM	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HM	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AP	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BP	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CP	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DP	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EP	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FP	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GP	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HP	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AO	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BO	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CO	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DO	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EO	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FO	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GO	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AS	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BS	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CS	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DS	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	ES	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FS	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GS	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HS	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AQ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BQ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CQ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DQ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EQ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FQ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GQ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HQ	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AR	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BR	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CR	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DR	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	ER	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FR	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GR	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HR	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AU	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BU	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CU	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DU	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	EU	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FU	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GU	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HU	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AT	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BT	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CT	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DT	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	ET	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FT	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GT	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HT	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AX	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BX	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CX	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DX	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EX	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FX	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GX	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HX	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AV	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BV	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CV	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DV	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EV	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FV	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GV	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HV	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	AW	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	BW	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	CW	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	DW	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	EW	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	FW	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	GW	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	HW	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	H1	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	H6	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hf	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hk	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hu	92	Total 656	C 408	N 123	O 122	S 3	0	0
1	Hz	92	Total 656	C 408	N 123	O 122	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HO	92	Total	C	N	O	S	0	0
			656	408	123	122	3		

- Molecule 2 is a protein called Carboxysome assembly protein CsoS2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X2	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	X1	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	X5	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	X3	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	X4	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	X7	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	X6	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	X0	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	X9	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xb	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xa	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xe	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xd	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xg	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xf	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xj	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xh	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xi	117	Total	C	N	O	S	0	0
			859	518	167	169	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Xl	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xk	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xo	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xn	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xq	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xp	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xt	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xs	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xv	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xu	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xy	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xw	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xx	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	XA	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	Xz	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	XD	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	XC	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	XF	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	XE	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	XI	117	Total	C	N	O	S	0	0
			859	518	167	169	5		
2	XH	117	Total	C	N	O	S	0	0
			859	518	167	169	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	XK	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XJ	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XN	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XL	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XM	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XP	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XO	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XS	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XQ	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XR	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XU	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XT	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XX	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XW	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	X8	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	Xc	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	Xm	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	Xr	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XB	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XG	117	Total 859	C 518	N 167	O 169	S 5	0	0
2	XV	117	Total 859	C 518	N 167	O 169	S 5	0	0

- Molecule 3 is a protein called Carboxysome shell vertex protein CsoS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P2	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P1	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P5	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P3	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P4	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P7	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P6	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P0	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P8	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	P9	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pb	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pa	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pe	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pc	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pd	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pg	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pf	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pj	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Ph	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pi	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pl	82	Total 612	C 388	N 106	O 113	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Pk	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Po	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pm	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pn	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pq	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pp	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pt	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pr	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Ps	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pv	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pu	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Py	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pw	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Px	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PA	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	Pz	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PD	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PB	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PC	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PF	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PE	82	Total 612	C 388	N 106	O 113	S 5	0	0

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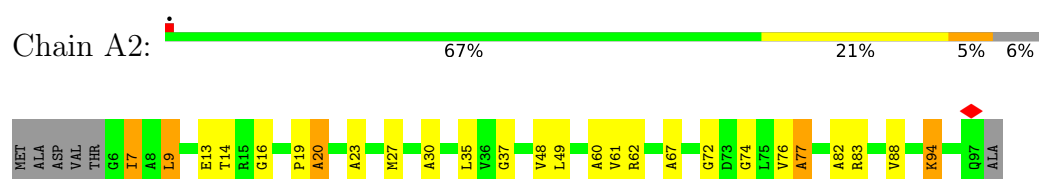
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	PI	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PG	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PH	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PK	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PJ	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PN	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PL	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PM	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PP	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PO	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PS	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PQ	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PR	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PU	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PT	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PX	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PV	82	Total 612	C 388	N 106	O 113	S 5	0	0
3	PW	82	Total 612	C 388	N 106	O 113	S 5	0	0

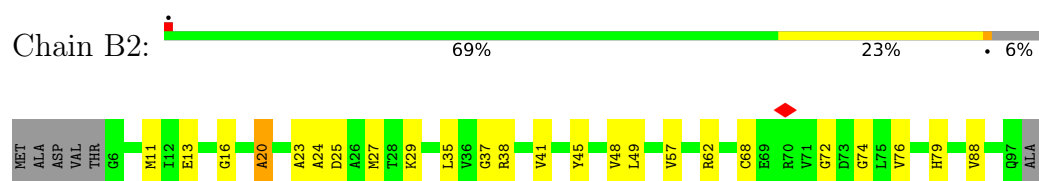
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

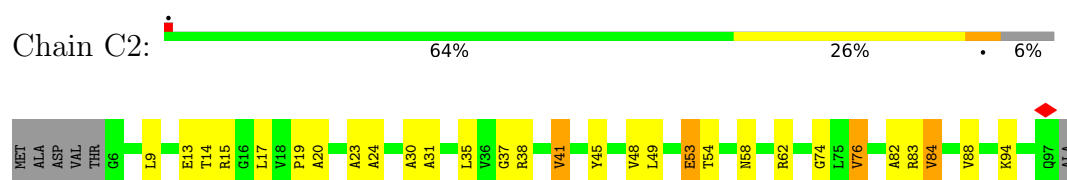
- Molecule 1: Major carboxysome shell protein CsoS1A



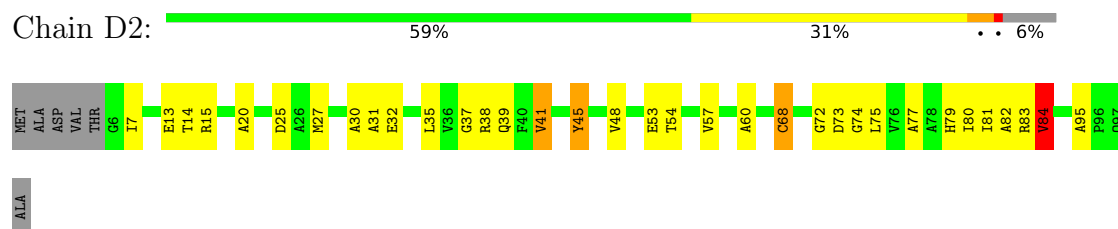
- Molecule 1: Major carboxysome shell protein CsoS1A



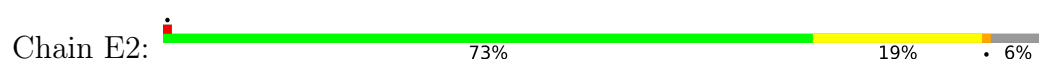
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A





- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



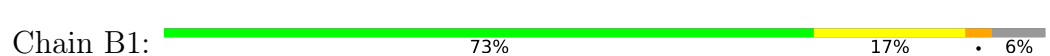
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain D1:  73% 19% 6%



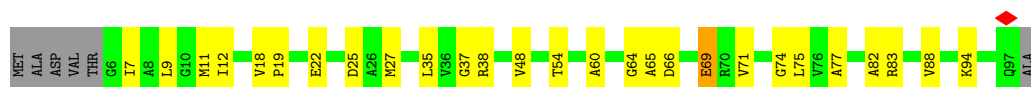
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain E1:  64% 30% 6%



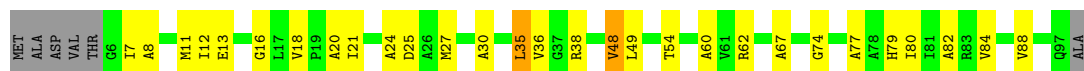
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain F1:  66% 27% 6%



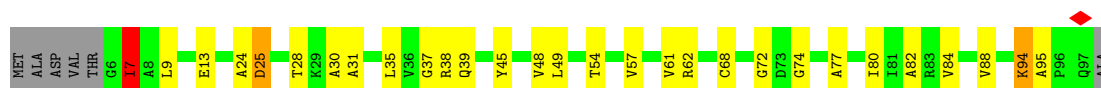
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain G1:  64% 28% 6%



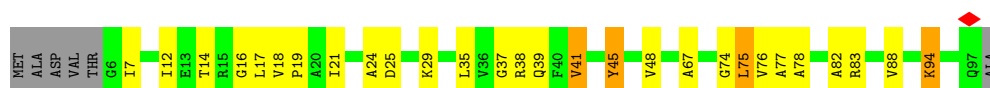
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain A5:  64% 27% 6%



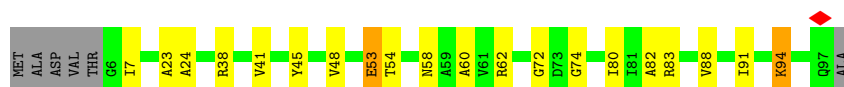
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain B5:  65% 24% 6%



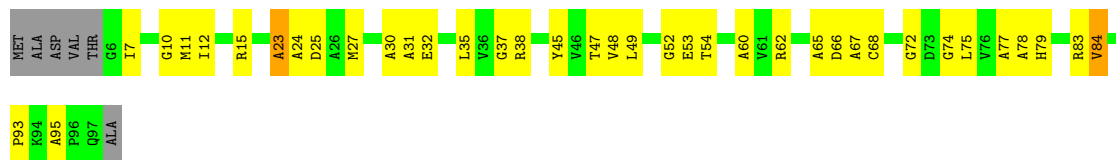
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain C5:  73% 18% 6%



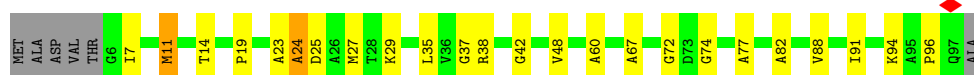
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain D5:  55% 37% 6%



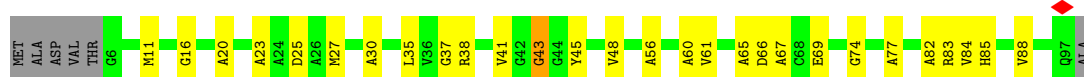
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain E5:  69% 22% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain F5:  65% 28% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain G5:  65% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain H5:  63% 31% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain A3:  72% 19% 6%



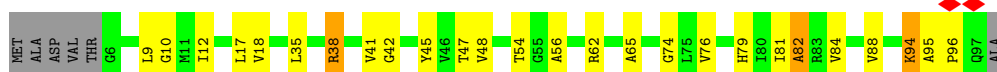
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain B3:  70% 21% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain C3:  67% 23% 6%



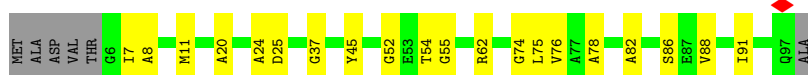
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain D3:  63% 31% 6%



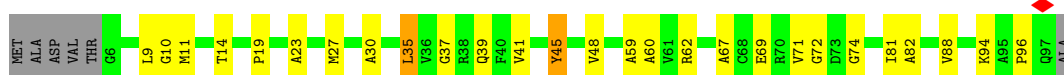
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain E3:  73% 20% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain F3:  66% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain G3:  63% 28% 6%

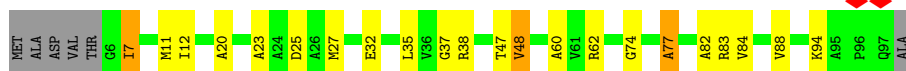
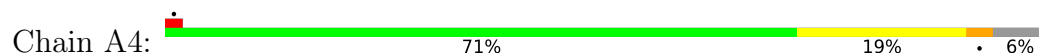


- Molecule 1: Major carboxysome shell protein CsoS1A

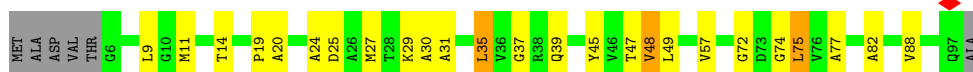
Chain H3:  70% 21% 6%



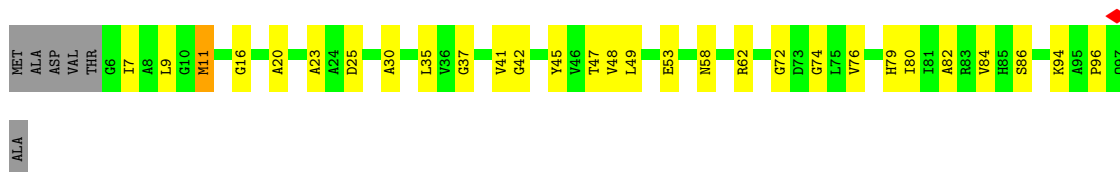
- Molecule 1: Major carboxysome shell protein CsoS1A



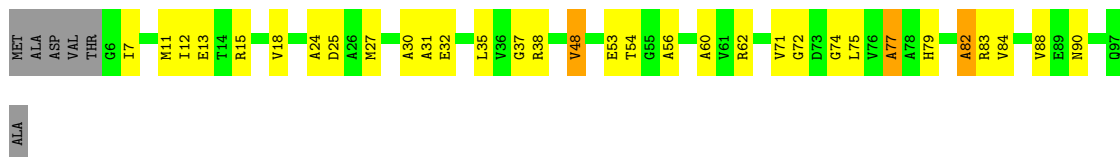
- Molecule 1: Major carboxysome shell protein CsoS1A



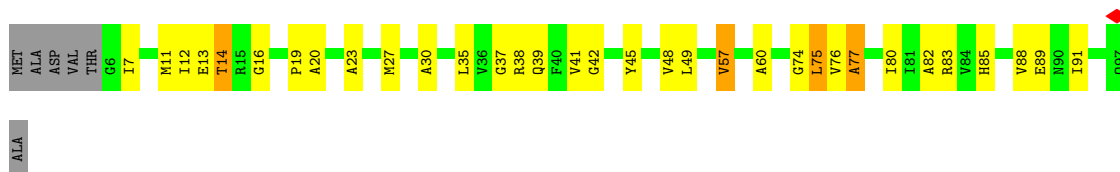
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

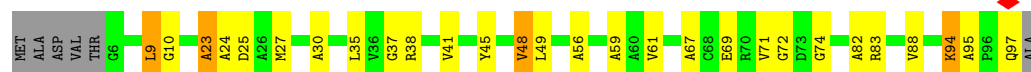


- Molecule 1: Major carboxysome shell protein CsoS1A



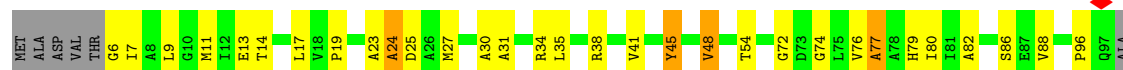
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain F4: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain G4: 



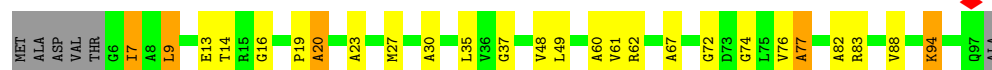
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Chain H4: 



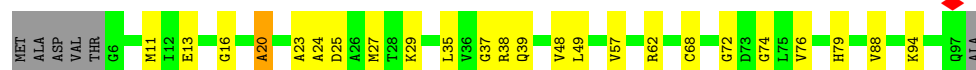
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain A7: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain B7: 



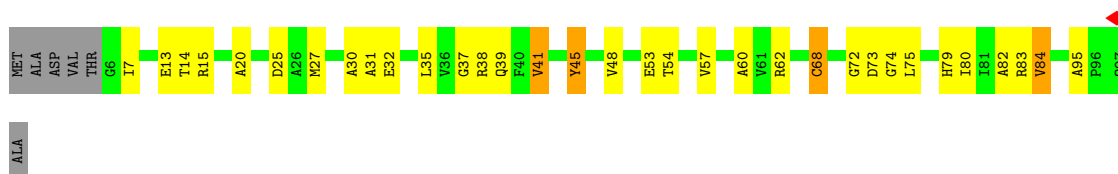
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain C7: 

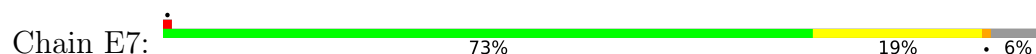


- Molecule 1: Major carboxysome shell protein CsoS1A

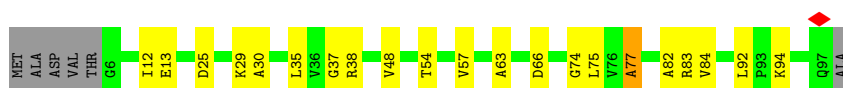
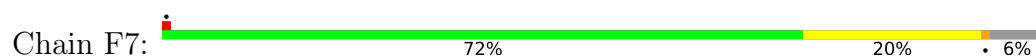
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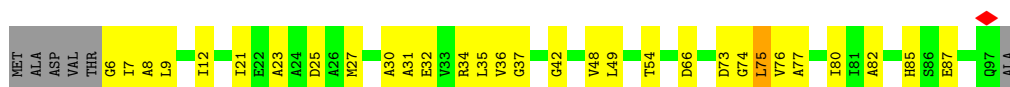
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

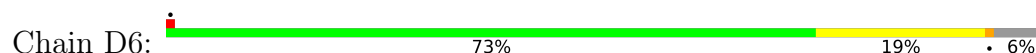




- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



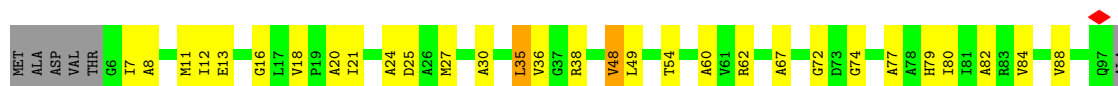
- Molecule 1: Major carboxysome shell protein CsoS1A



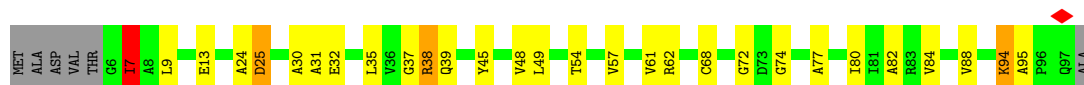
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



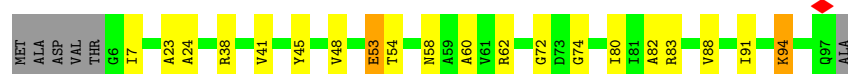
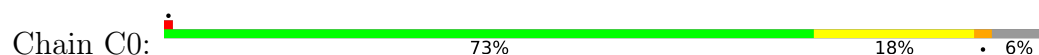
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



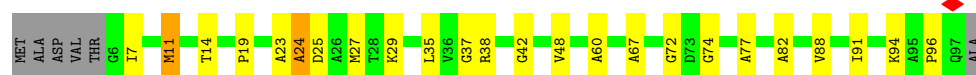
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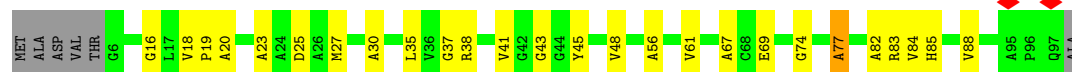
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- Molecule 1: Major carboxysome shell protein CsoS1A

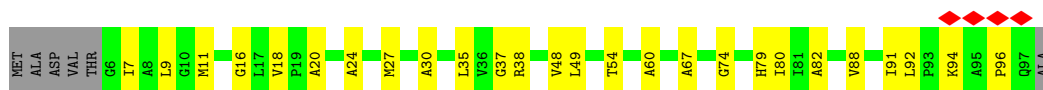


- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A





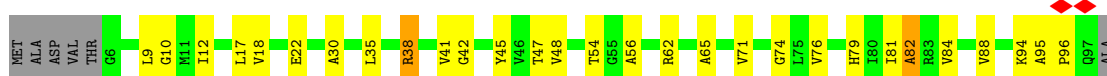
- Molecule 1: Major carboxysome shell protein CsoS1A



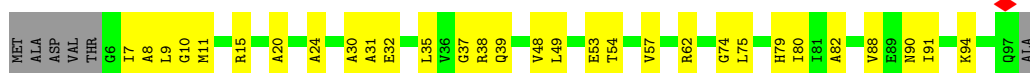
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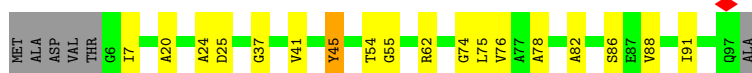
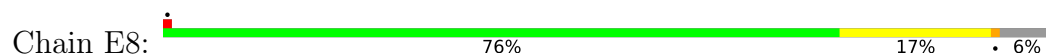
- Molecule 1: Major carboxysome shell protein CsoS1A



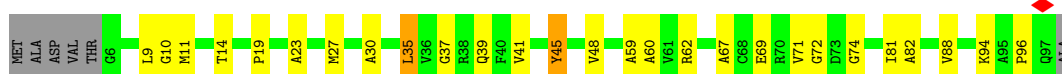
- Molecule 1: Major carboxysome shell protein CsoS1A



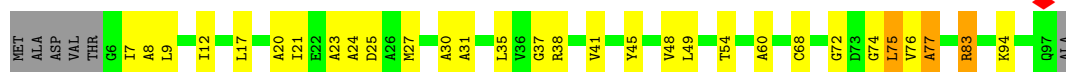
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



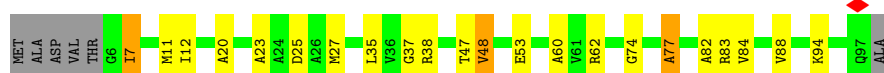
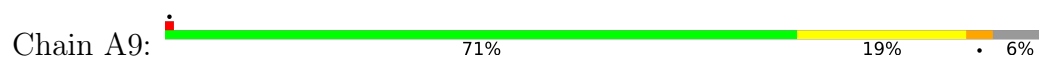
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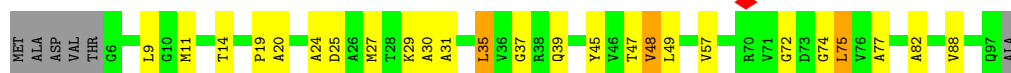
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- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



ALA

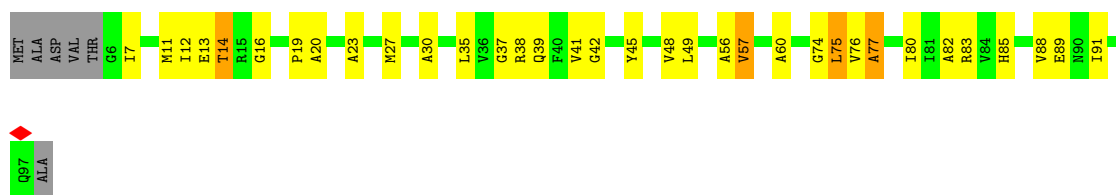
- Molecule 1: Major carboxysome shell protein CsoS1A



ALA

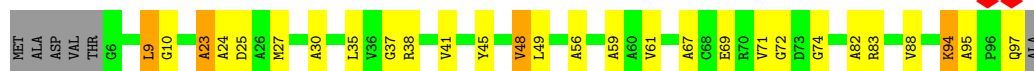
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain E9: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain F9: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain G9: 



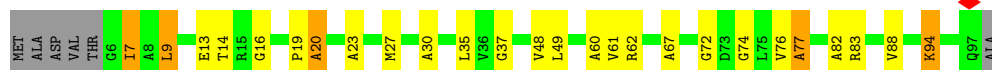
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain H9: 



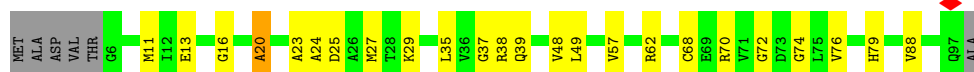
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ab: 



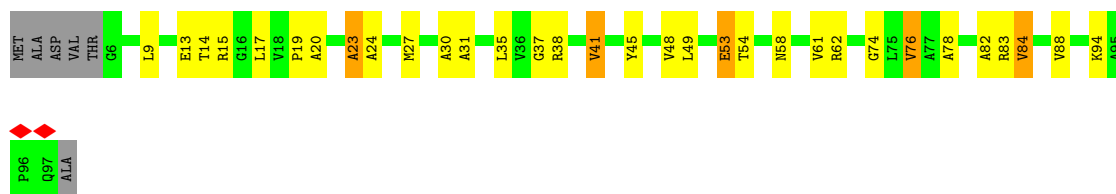
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bb: 

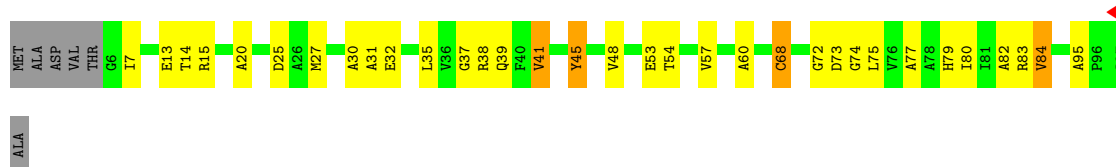


- Molecule 1: Major carboxysome shell protein CsoS1A

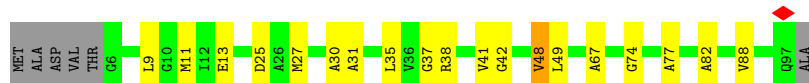
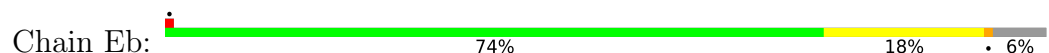
Chain Cb: 



- Molecule 1: Major carboxysome shell protein CsoS1A



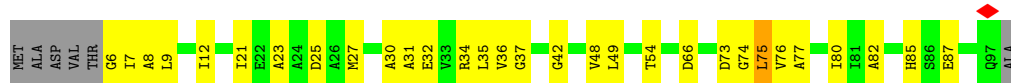
- Molecule 1: Major carboxysome shell protein CsoS1A



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- Molecule 1: Major carboxysome shell protein CsoS1A

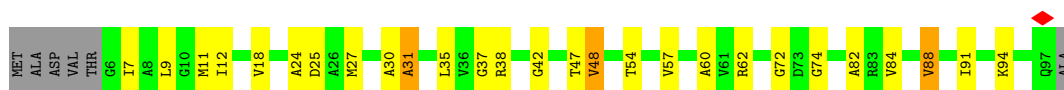


- Molecule 1: Major carboxysome shell protein CsoS1A

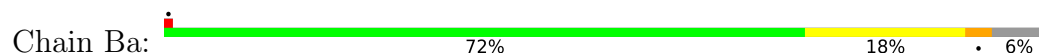


- Molecule 1: Major carboxysome shell protein CsoS1A





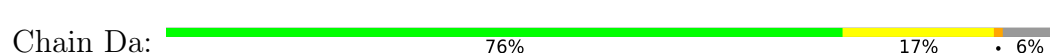
- Molecule 1: Major carboxysome shell protein CsoS1A



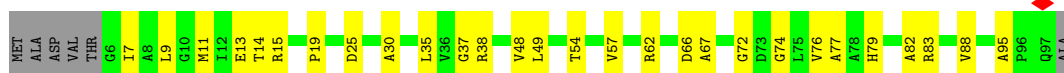
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- Molecule 1: Major carboxysome shell protein CsoS1A



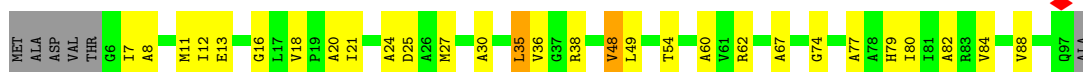
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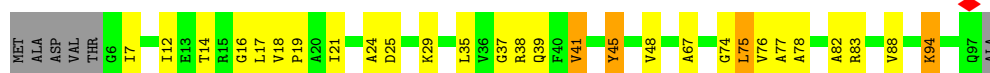
- Molecule 1: Major carboxysome shell protein CsoS1A



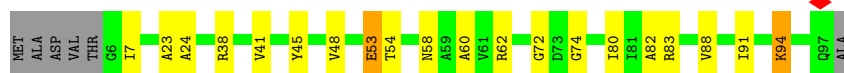
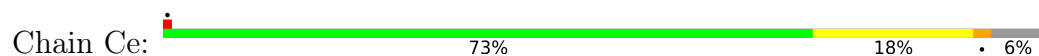
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



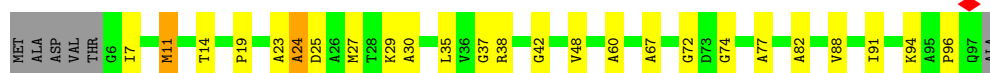
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

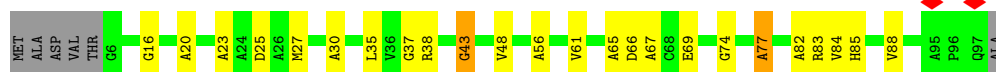


- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fe:  69% 22% 6%



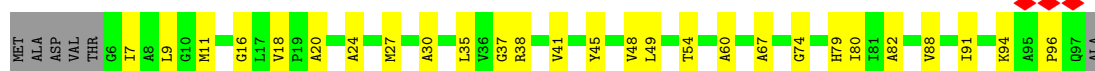
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ge:  63% 28% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain He:  66% 28% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ac:  71% 20% 6%



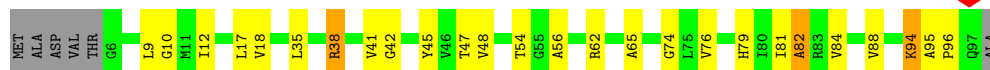
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bc:  70% 21% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Cc:  67% 23% 6%



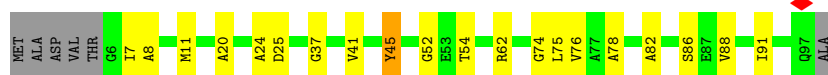
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dc:  66% 28% 6%



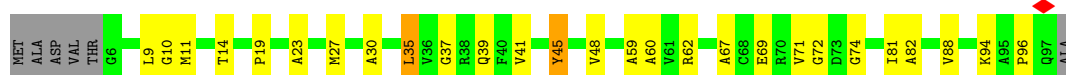
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ec:  73% 19% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fc:  66% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gc:  64% 27% 6%



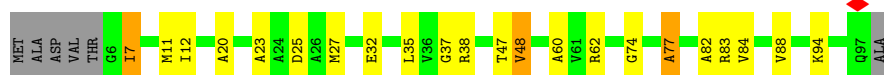
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Hc:  71% 20% 6%



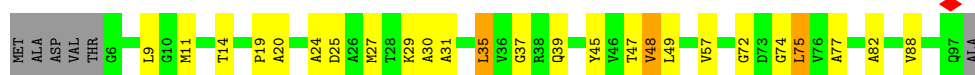
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ad:  71% 19% 6%



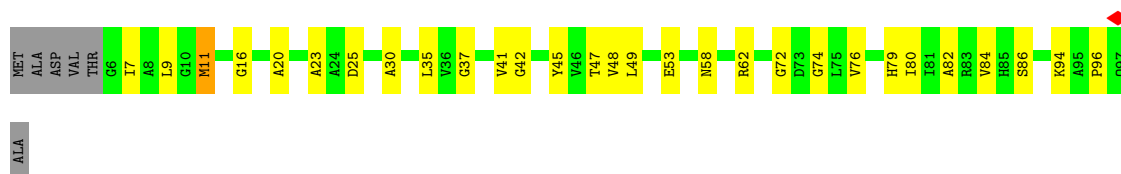
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bd:  68% 22% 6%

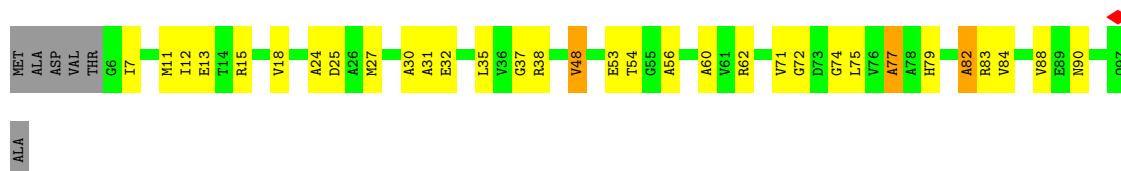


- Molecule 1: Major carboxysome shell protein CsoS1A

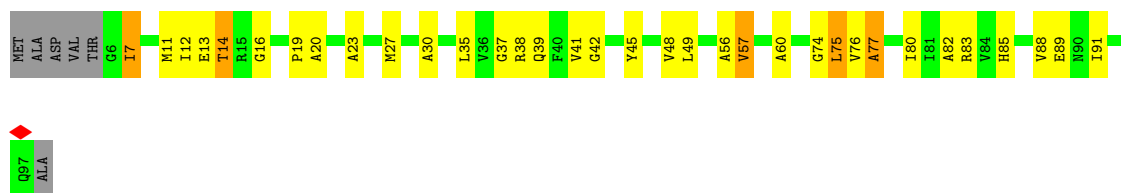
Chain Cd:  64% 29% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



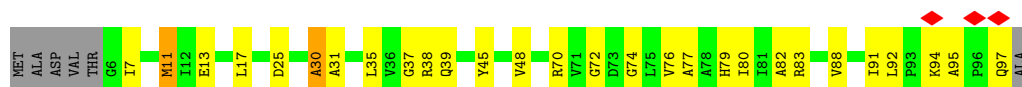
- Molecule 1: Major carboxysome shell protein CsoS1A



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- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ag:  67% 22% 6%



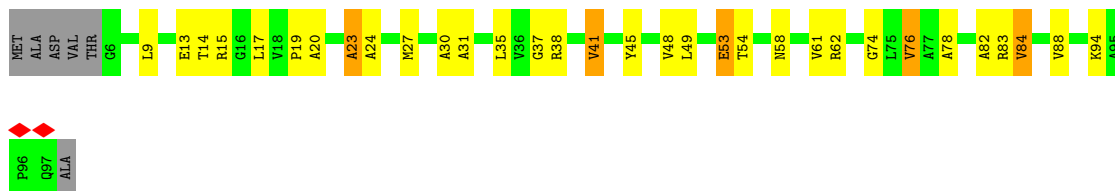
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bg:  69% 23% 6%



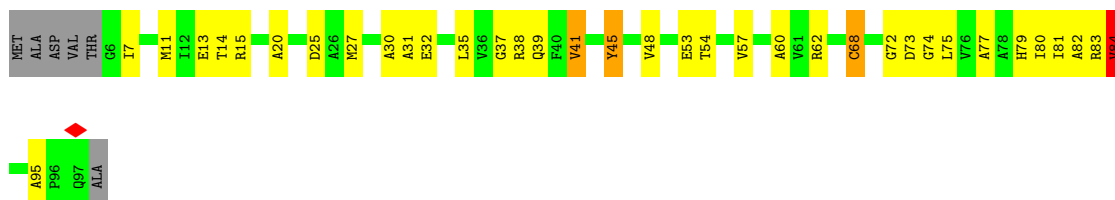
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Cg:  61% 28% 5% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dg:  57% 33% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Eg:  73% 19% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fg:  70% 22% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gg: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Hg: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Af: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bf: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Cf: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Df: 



- Molecule 1: Major carboxysome shell protein CsoS1A

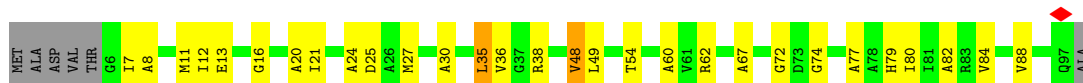
Chain Ef: 



- Molecule 1: Major carboxysome shell protein CsoS1A



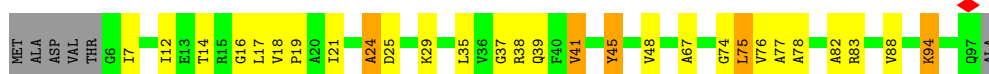
- Molecule 1: Major carboxysome shell protein CsoS1A



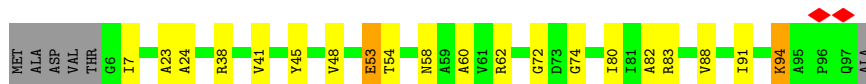
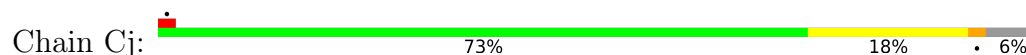
- Molecule 1: Major carboxysome shell protein CsoS1A



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- Molecule 1: Major carboxysome shell protein CsoS1A

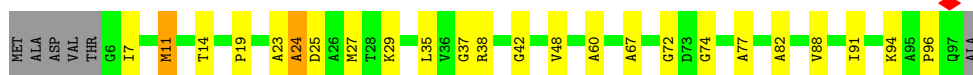


- Molecule 1: Major carboxysome shell protein CsoS1A

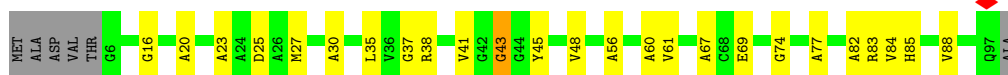




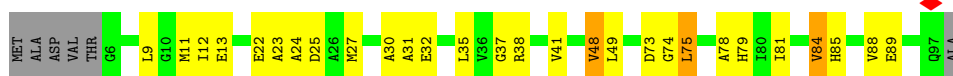
- Molecule 1: Major carboxysome shell protein CsoS1A



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- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ch: 



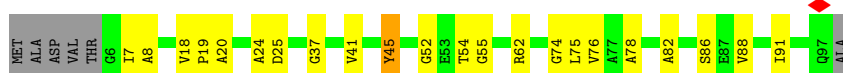
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dh: 



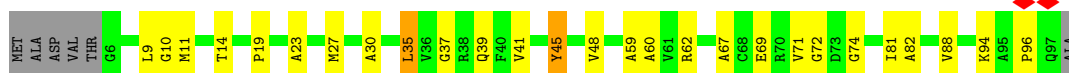
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Eh: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fh: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gh: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Hh: 



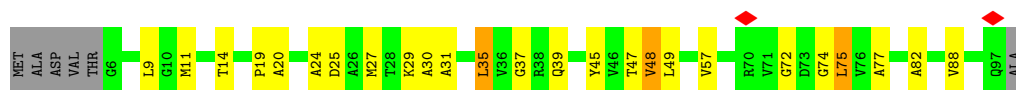
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ai: 



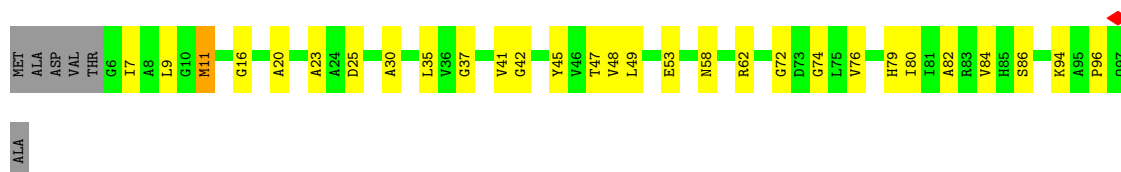
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bi: 



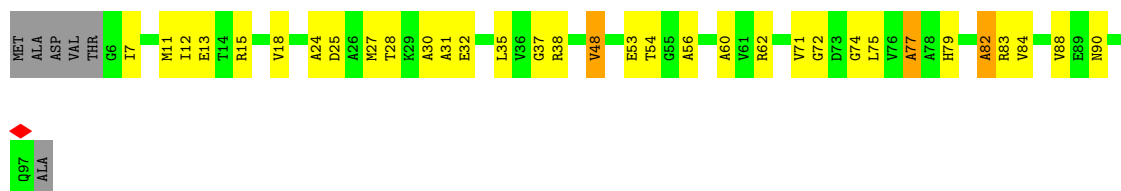
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ci: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Di: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ei: 



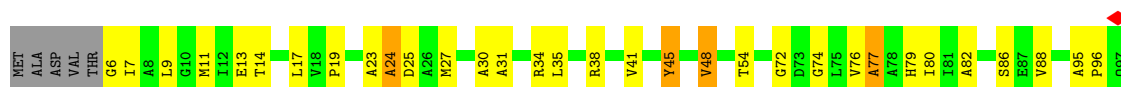
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fi: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gi: 



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Hi:  67% 23% 6%



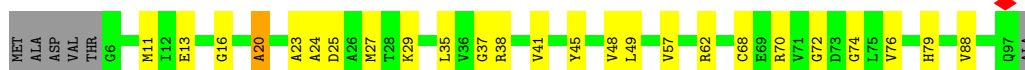
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ai:  69% 20% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bi:  68% 24% 6%



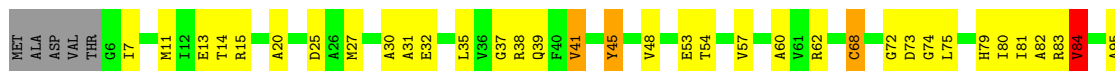
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ci:  61% 28% 5% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Di:  58% 32% 6%

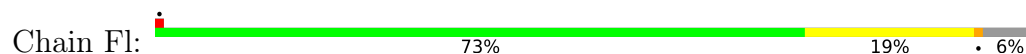


- Molecule 1: Major carboxysome shell protein CsoS1A

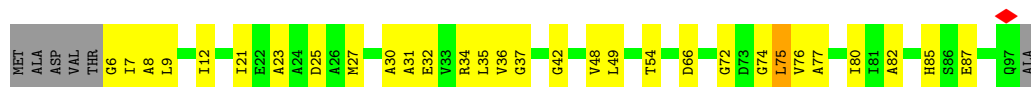
Chain Ei:  73% 19% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



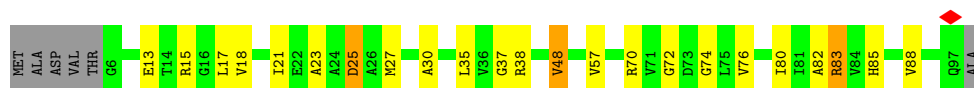
- Molecule 1: Major carboxysome shell protein CsoS1A



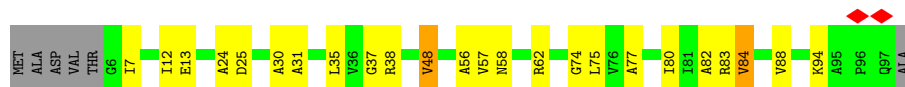
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



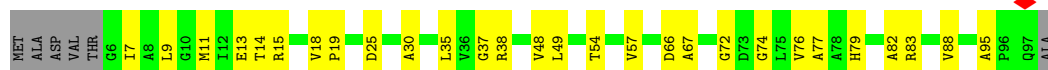
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dk:  73% 19% • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ek:  65% 29% 6%



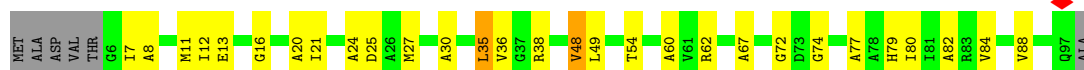
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fk:  70% 22% • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gk:  64% 28% • 6%



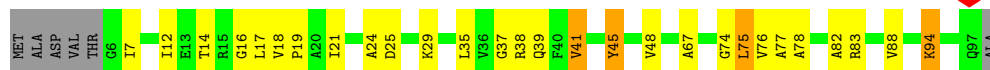
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ao:  64% 27% • • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bo:  65% 24% • 6%

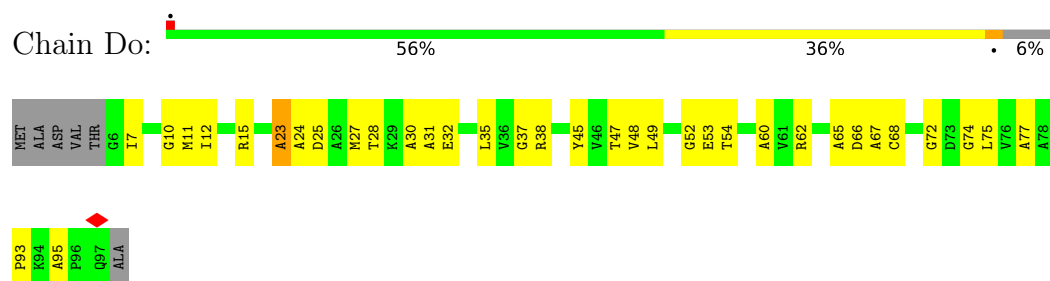


- Molecule 1: Major carboxysome shell protein CsoS1A

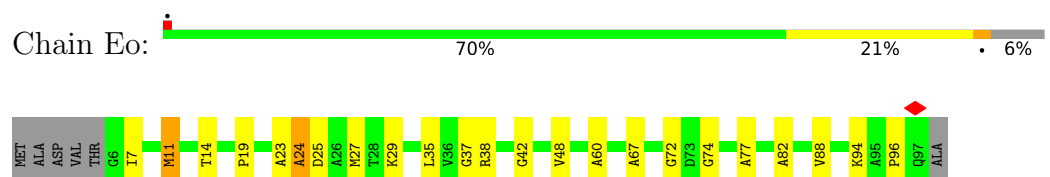
Chain Co:  73% 17% • 6%



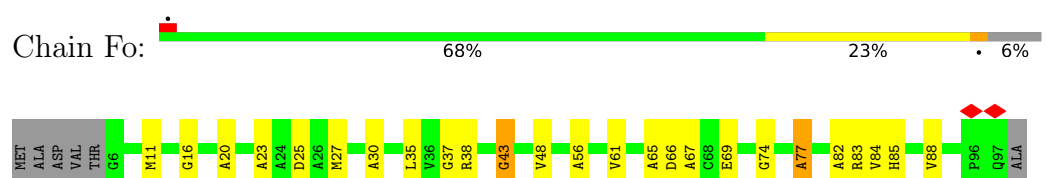
- Molecule 1: Major carboxysome shell protein CsoS1A



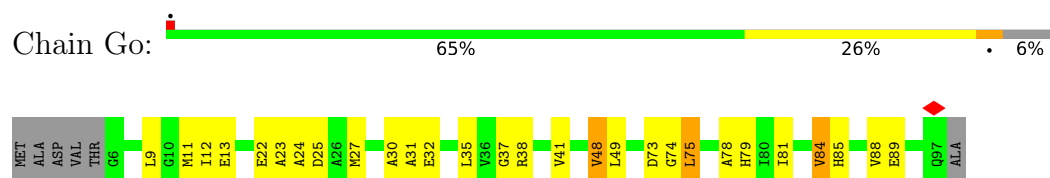
- Molecule 1: Major carboxysome shell protein CsoS1A



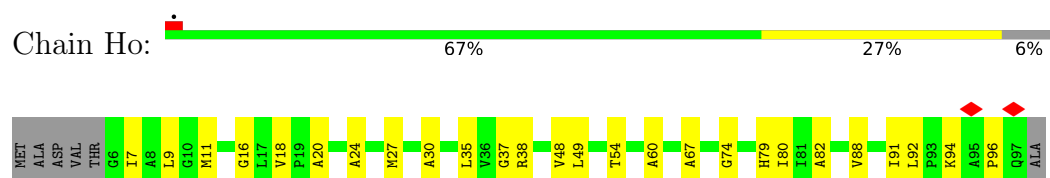
- Molecule 1: Major carboxysome shell protein CsoS1A



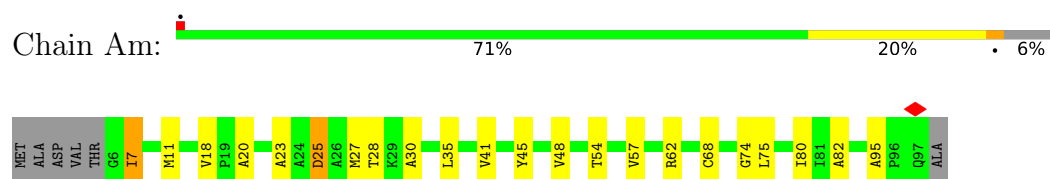
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

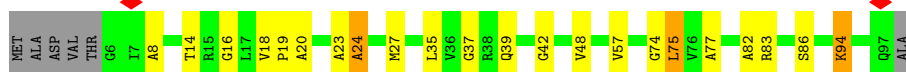


- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bm:  71% 19% 6%



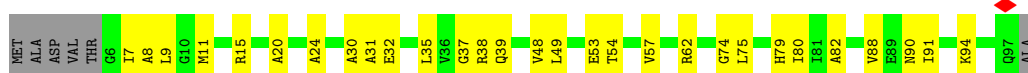
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Cm:  64% 28% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dm:  64% 30% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Em:  72% 21% 6%



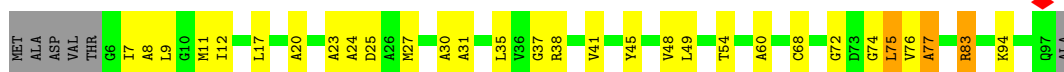
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fm:  65% 27% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gm:  63% 28% 6%



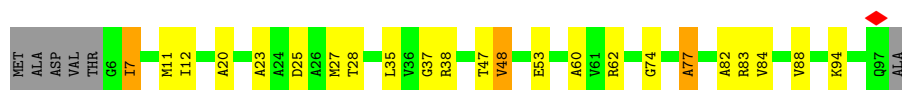
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Hm:  71% 20% 6%



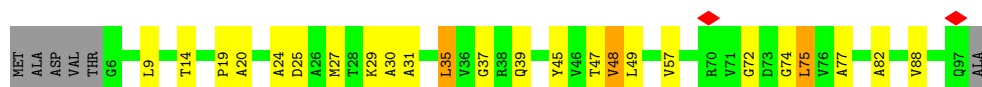
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain An:  70% 20% 6%



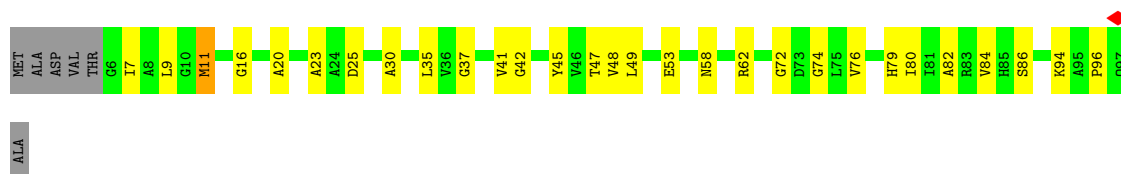
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bn:  69% 21% 6%



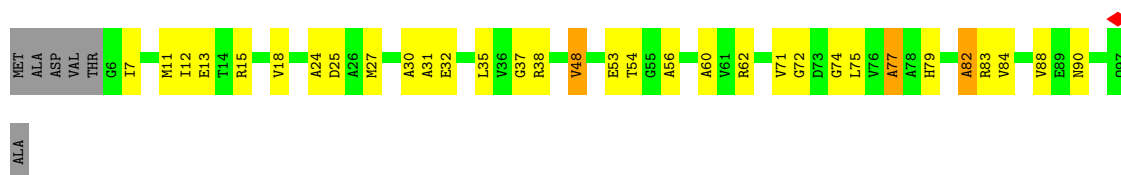
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Cn:  64% 29% 6%



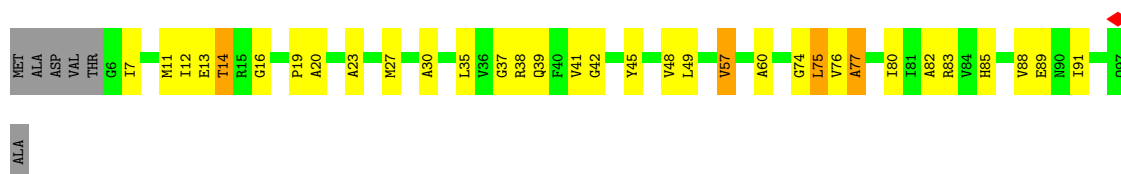
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dn:  61% 30% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain En:  60% 30% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fn:  64% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A



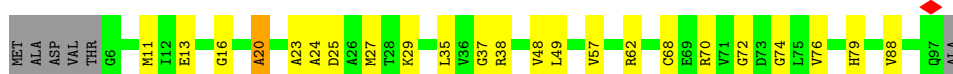
- Molecule 1: Major carboxysome shell protein CsoS1A



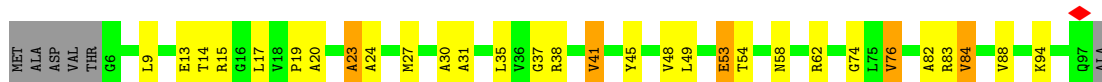
- Molecule 1: Major carboxysome shell protein CsoS1A



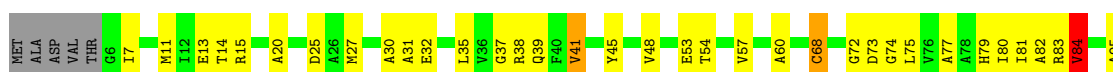
- Molecule 1: Major carboxysome shell protein CsoS1A



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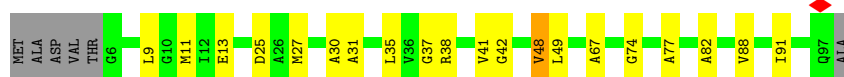
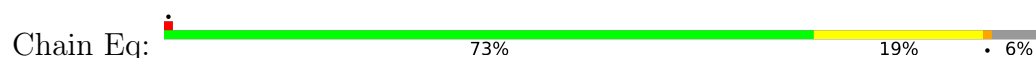


- Molecule 1: Major carboxysome shell protein CsoS1A

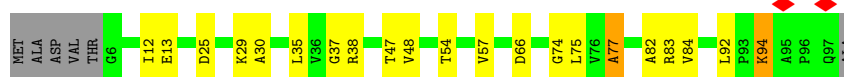
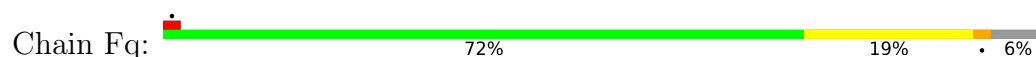




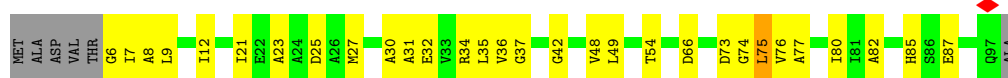
- Molecule 1: Major carboxysome shell protein CsoS1A



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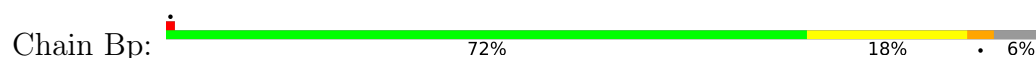
- Molecule 1: Major carboxysome shell protein CsoS1A



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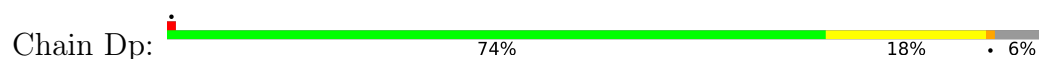
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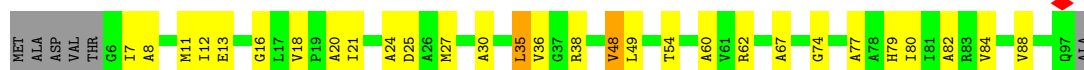
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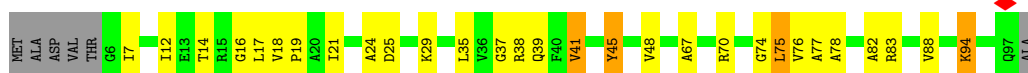


- Molecule 1: Major carboxysome shell protein CsoS1A

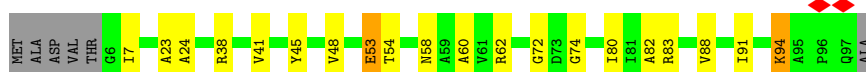




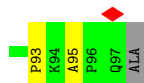
- Molecule 1: Major carboxysome shell protein CsoS1A



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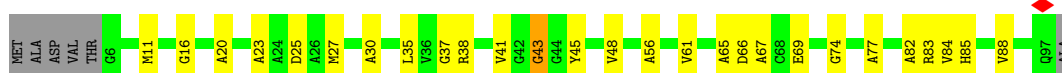
- Molecule 1: Major carboxysome shell protein CsoS1A



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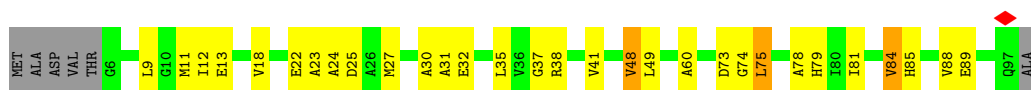


- Molecule 1: Major carboxysome shell protein CsoS1A



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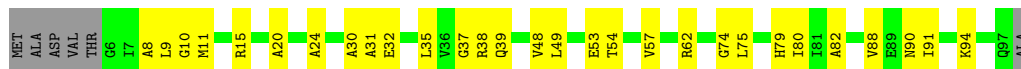
- Molecule 1: Major carboxysome shell protein CsoS1A



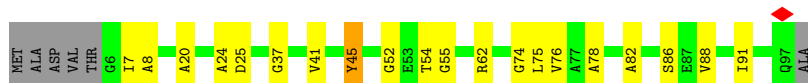
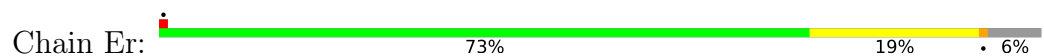
- Molecule 1: Major carboxysome shell protein CsoS1A



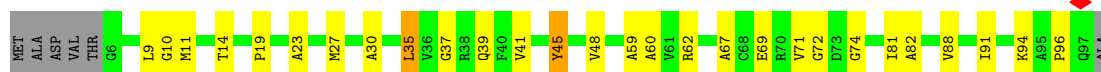
- Molecule 1: Major carboxysome shell protein CsoS1A



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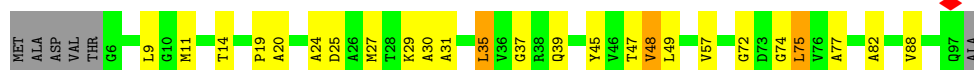
- Molecule 1: Major carboxysome shell protein CsoS1A



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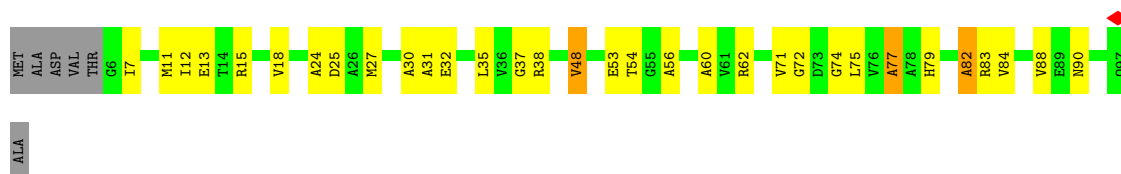
- Molecule 1: Major carboxysome shell protein CsoS1A



ALA

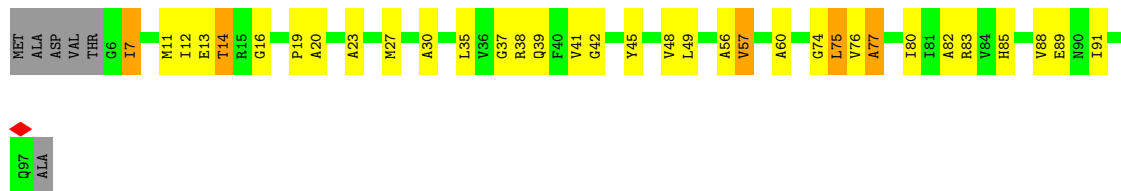
- Molecule 1: Major carboxysome shell protein CsoS1A





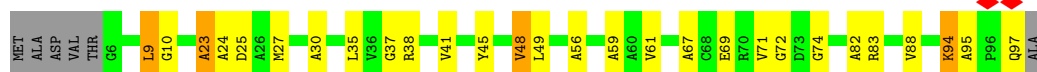
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Es: 59% 30% 5% 6%



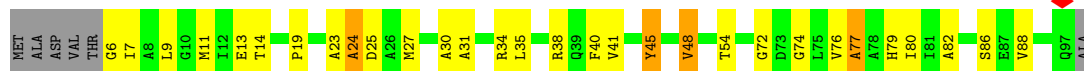
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fs: 65% 24% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gs: 63% 27% 6%



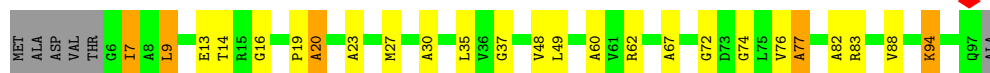
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Hs: 64% 28% 6%



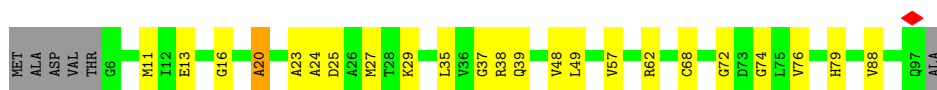
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Av: 68% 20% 5% 6%

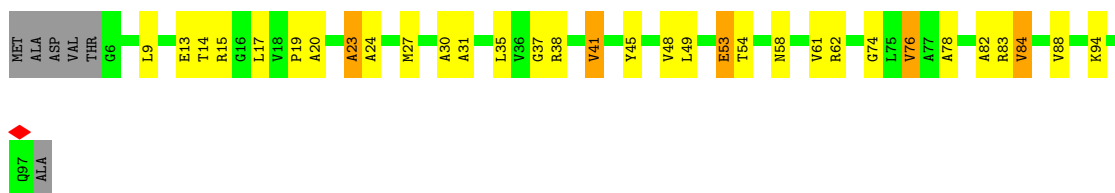


- Molecule 1: Major carboxysome shell protein CsoS1A

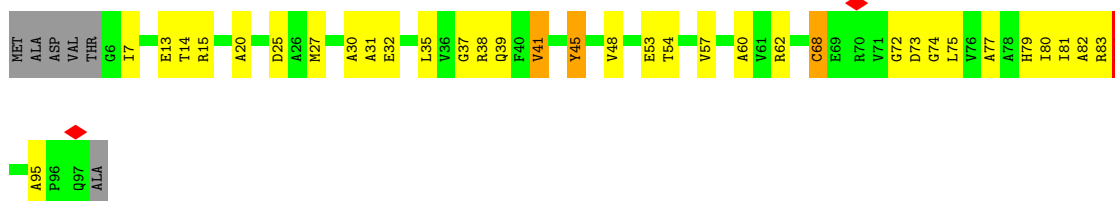
Chain Bv: 70% 22% 6%



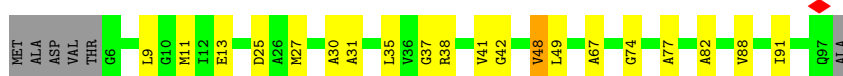
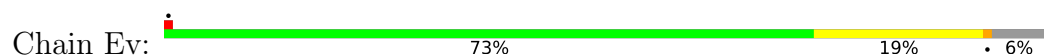
- Molecule 1: Major carboxysome shell protein CsoS1A



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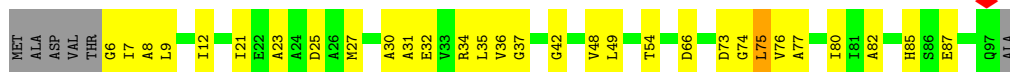
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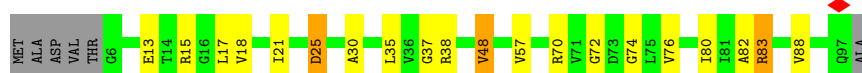
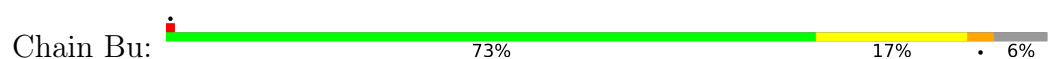
- Molecule 1: Major carboxysome shell protein CsoS1A



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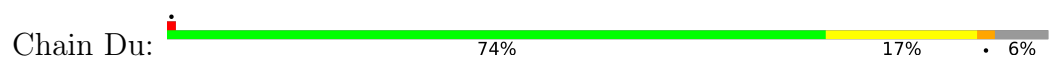
- Molecule 1: Major carboxysome shell protein CsoS1A



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- Molecule 1: Major carboxysome shell protein CsoS1A

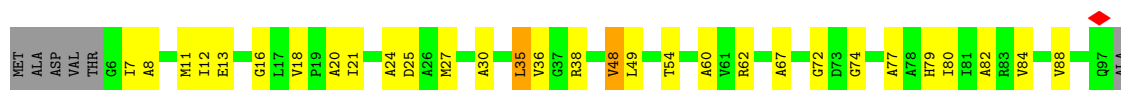


- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gu:  63% 29% 6%



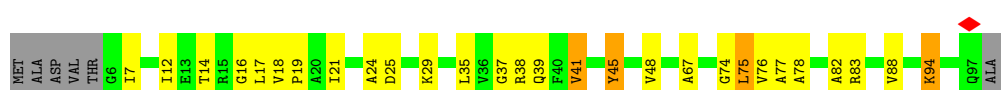
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ay:  63% 29% 6%



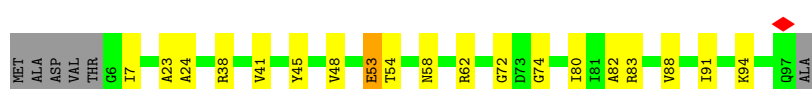
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain By:  65% 24% 6%



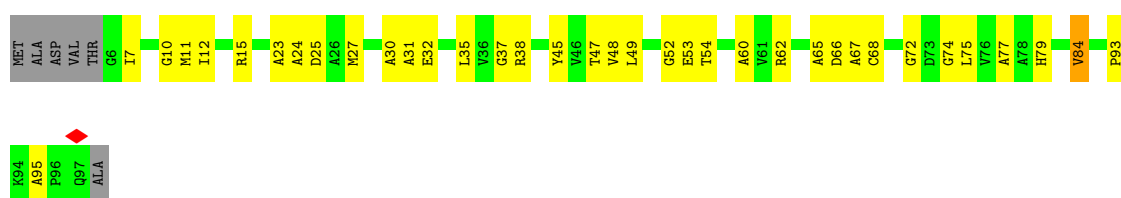
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Cy:  74% 18% 6%



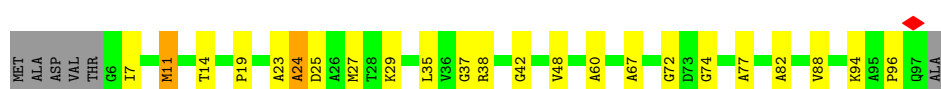
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dy:  57% 36% 6%

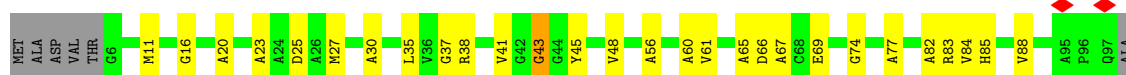


- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Ey:  70% 21% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A



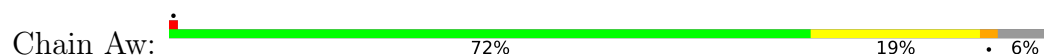
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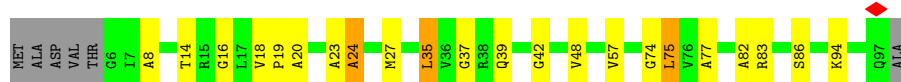
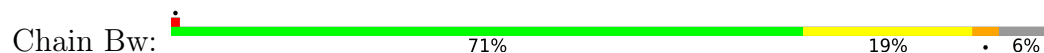
- Molecule 1: Major carboxysome shell protein CsoS1A



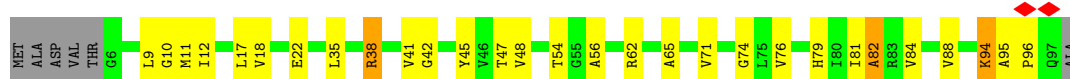
- Molecule 1: Major carboxysome shell protein CsoS1A



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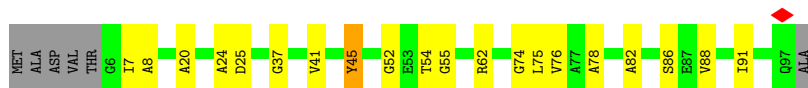
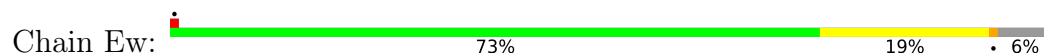


- Molecule 1: Major carboxysome shell protein CsoS1A

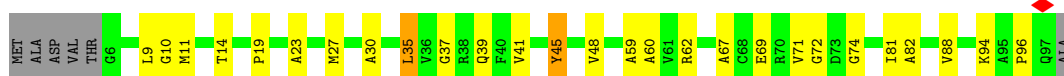




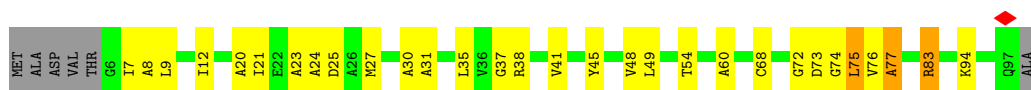
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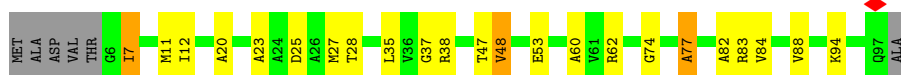
- Molecule 1: Major carboxysome shell protein CsoS1A



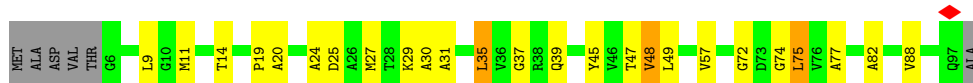
- Molecule 1: Major carboxysome shell protein CsoS1A



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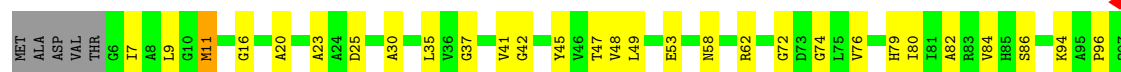


- Molecule 1: Major carboxysome shell protein CsoS1A



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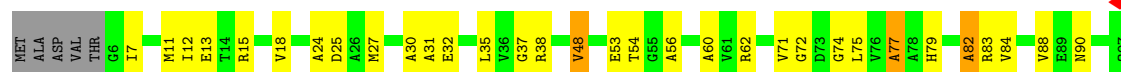
Chain Cx:  64% 29% 6%



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dx:  61% 30% 6%



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

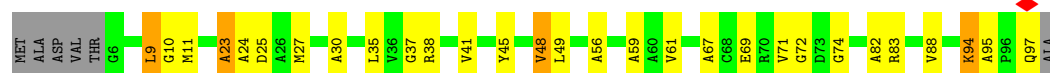
Chain Ex:  60% 29% 5% 6%



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Fx:  64% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Gx:  64% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Hx:  63% 30% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AA:  66% 22% 5% 6%



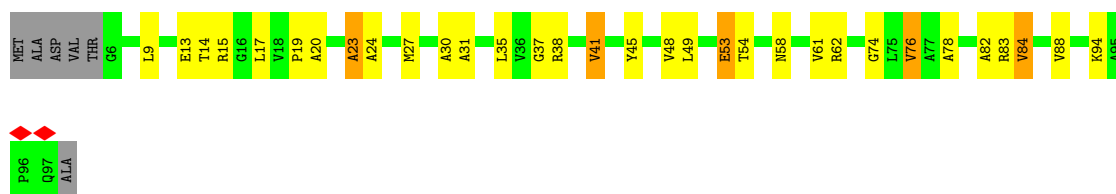
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BA:  67% 26% 6%



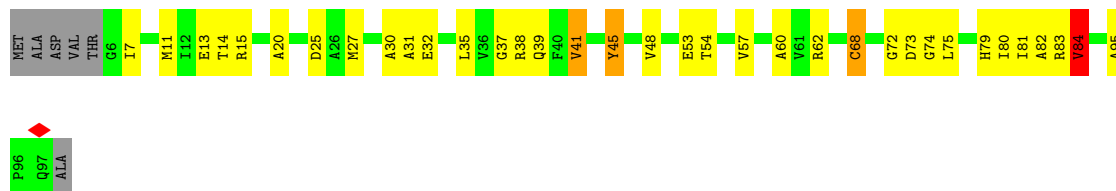
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CA:  61% 28% 5% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DA:  58% 32% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain EA:  73% 19% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FA:  71% 20% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GA: 



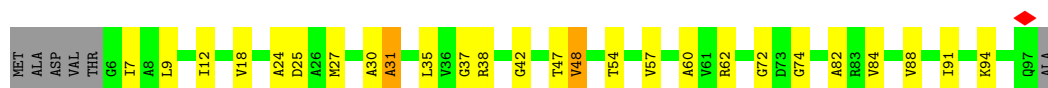
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HA: 



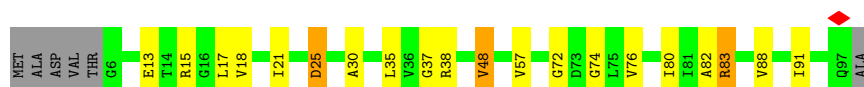
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Az: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Bz: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Cz: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Dz: 



- Molecule 1: Major carboxysome shell protein CsoS1A

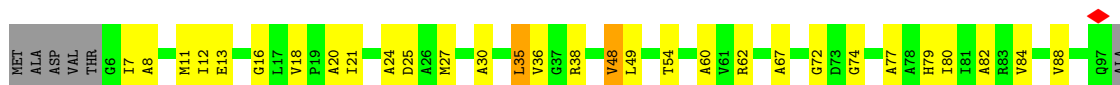
Chain Ez: 



- Molecule 1: Major carboxysome shell protein CsoS1A



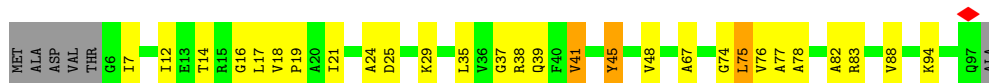
- Molecule 1: Major carboxysome shell protein CsoS1A



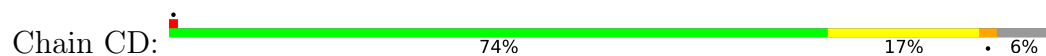
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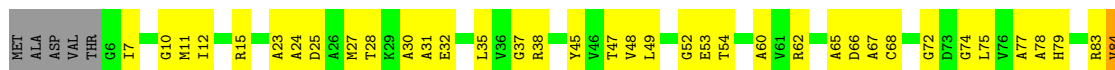
- Molecule 1: Major carboxysome shell protein CsoS1A

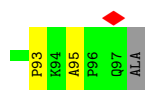


- Molecule 1: Major carboxysome shell protein CsoS1A

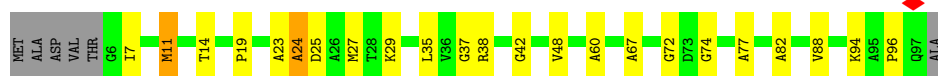


- Molecule 1: Major carboxysome shell protein CsoS1A

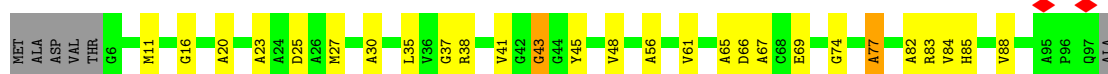




- Molecule 1: Major carboxysome shell protein CsoS1A



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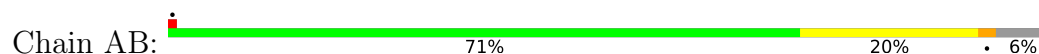
- Molecule 1: Major carboxysome shell protein CsoS1A



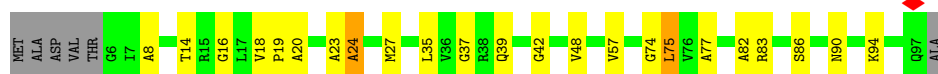
- Molecule 1: Major carboxysome shell protein CsoS1A



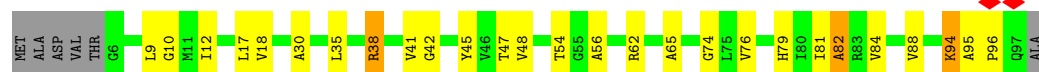
- Molecule 1: Major carboxysome shell protein CsoS1A



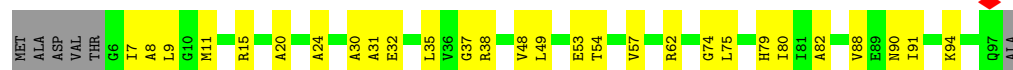
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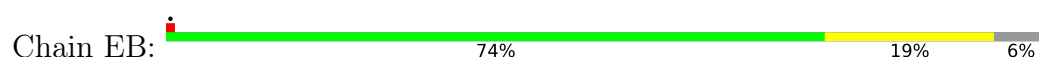
- Molecule 1: Major carboxysome shell protein CsoS1A



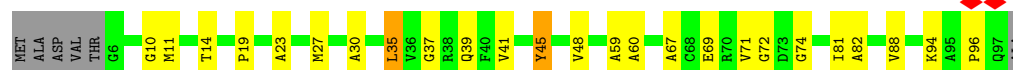
- Molecule 1: Major carboxysome shell protein CsoS1A



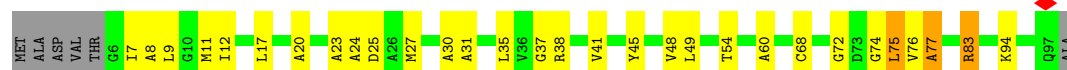
- Molecule 1: Major carboxysome shell protein CsoS1A



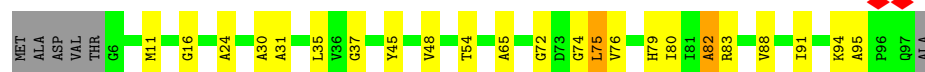
- Molecule 1: Major carboxysome shell protein CsoS1A



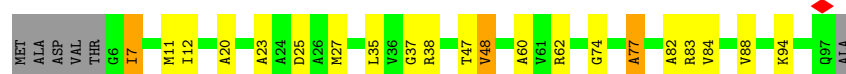
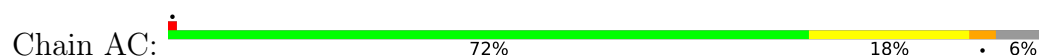
- Molecule 1: Major carboxysome shell protein CsoS1A



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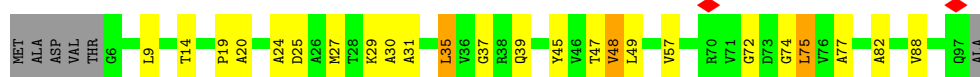


- Molecule 1: Major carboxysome shell protein CsoS1A



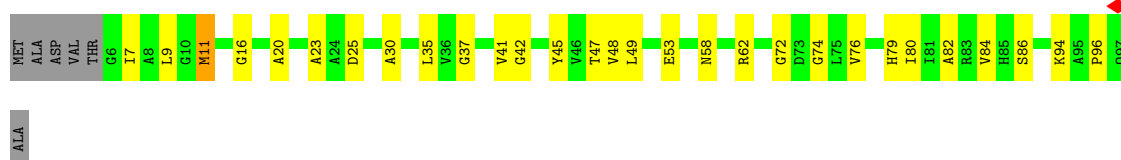
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BC: 



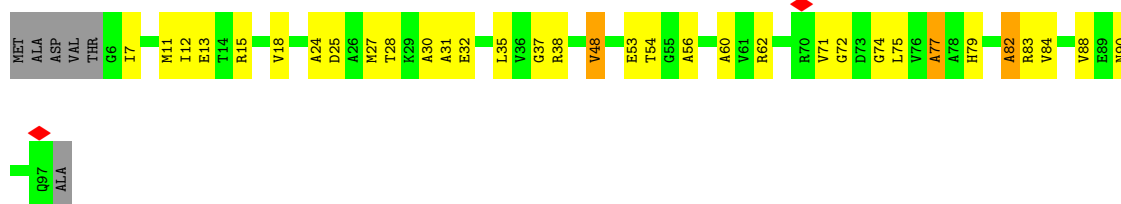
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CC: 



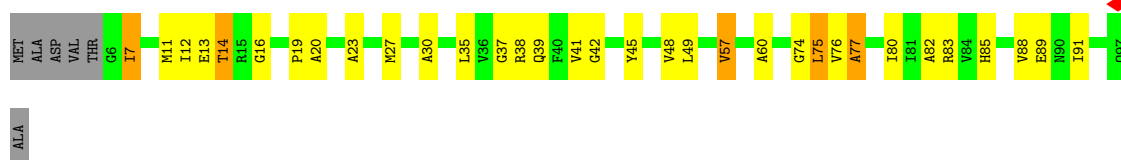
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DC: 



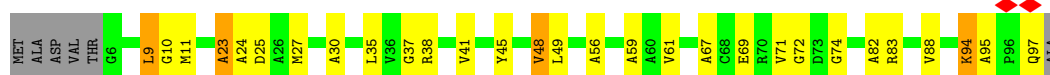
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain EC: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FC: 



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GC: 



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



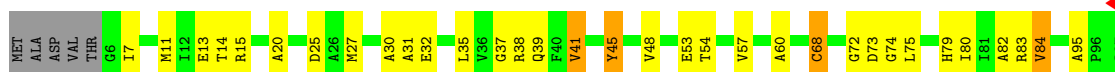
- Molecule 1: Major carboxysome shell protein CsoS1A



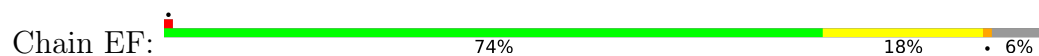
- Molecule 1: Major carboxysome shell protein CsoS1A

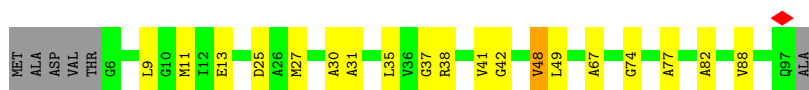


- Molecule 1: Major carboxysome shell protein CsoS1A



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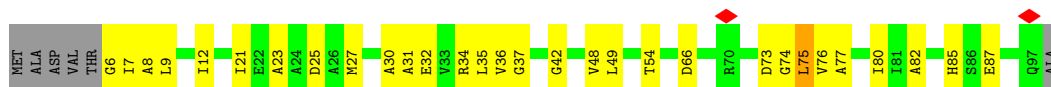




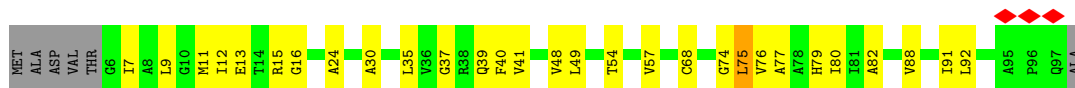
- Molecule 1: Major carboxysome shell protein CsoS1A



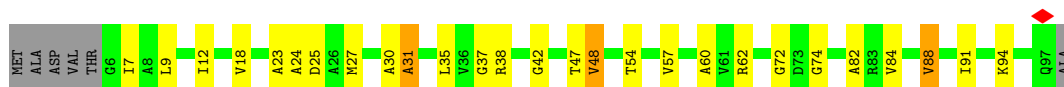
- Molecule 1: Major carboxysome shell protein CsoS1A



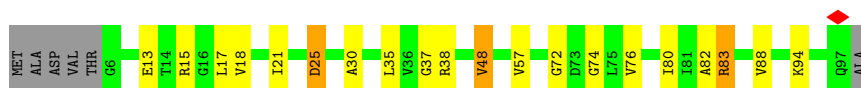
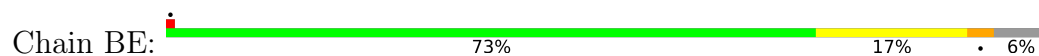
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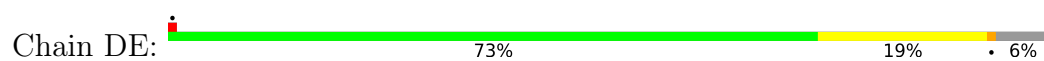
- Molecule 1: Major carboxysome shell protein CsoS1A



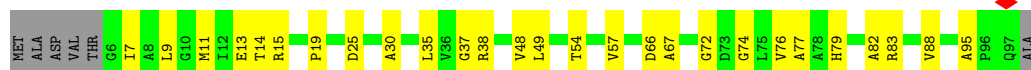
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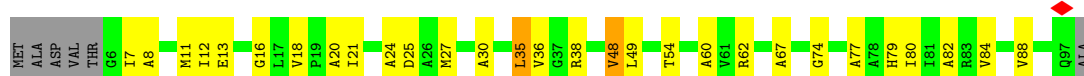
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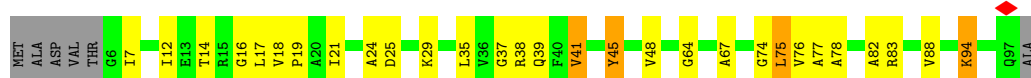
- Molecule 1: Major carboxysome shell protein CsoS1A



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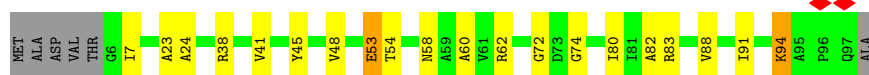


- Molecule 1: Major carboxysome shell protein CsoS1A



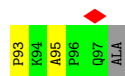
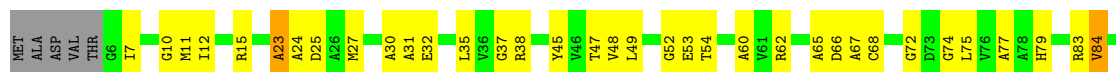
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CI:  73% 18% 6%



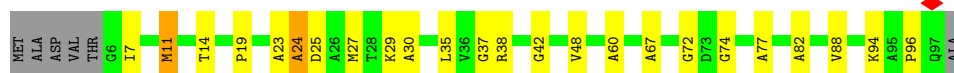
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DI:  56% 36% 6%



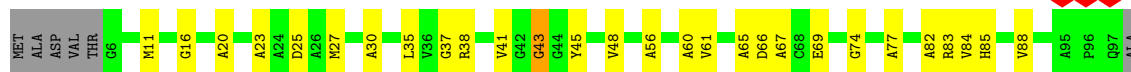
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain EI:  69% 22% 6%



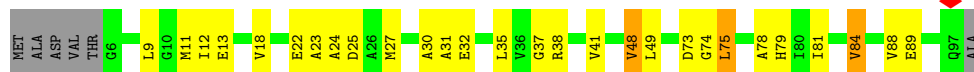
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FI:  65% 28% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GI:  65% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HI:  67% 27% 6%



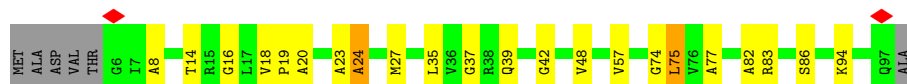
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AG:  71% 20% 6%



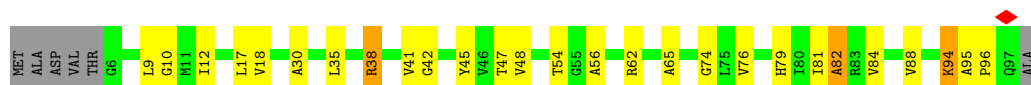
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BG:  71% 20% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CG:  66% 24% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DG:  64% 30% 6%



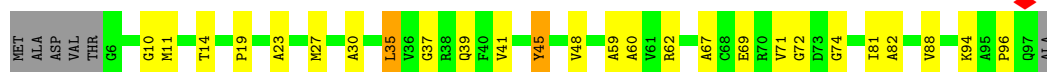
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain EG:  76% 18% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FG:  67% 24% 6%



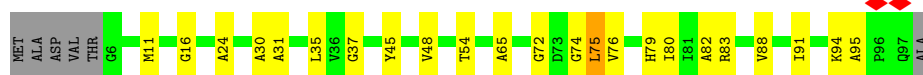
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GG:  64% 27% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HG:  70% 22% 6%



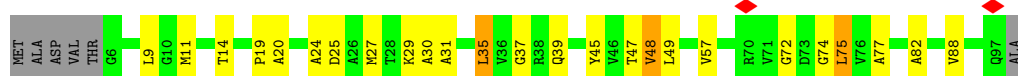
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AH:  71% 19% 6%



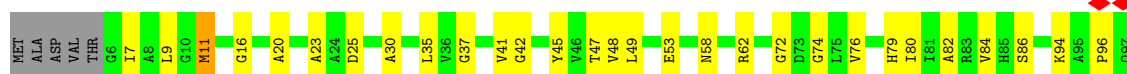
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BH:  68% 22% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CH:  64% 29% 6%



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DH:  61% 30% 6%



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

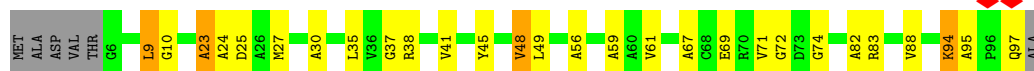
Chain EH:  59% 30% 5% 6%





- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FH: 65% 24% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GH: 64% 26% 6%



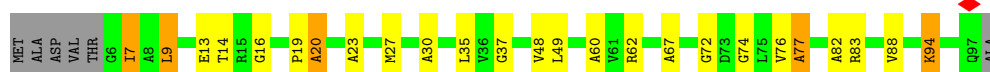
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HH: 64% 27% 6%



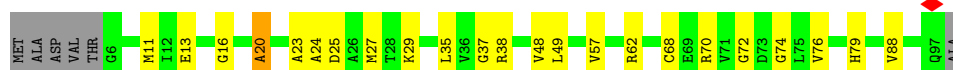
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AK: 68% 20% 5% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BK: 70% 22% 6%

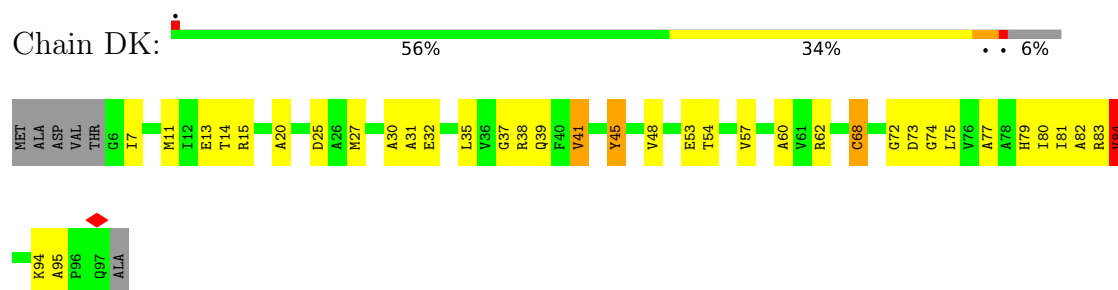


- Molecule 1: Major carboxysome shell protein CsoS1A

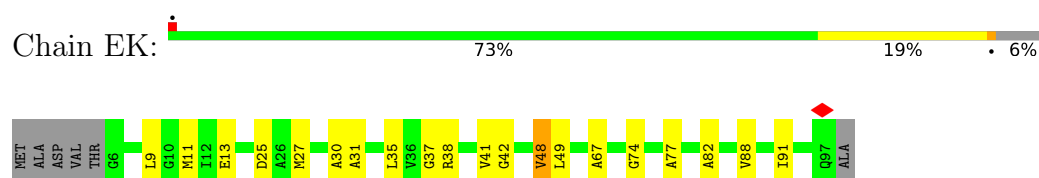
Chain CK: 61% 28% 5% 6%



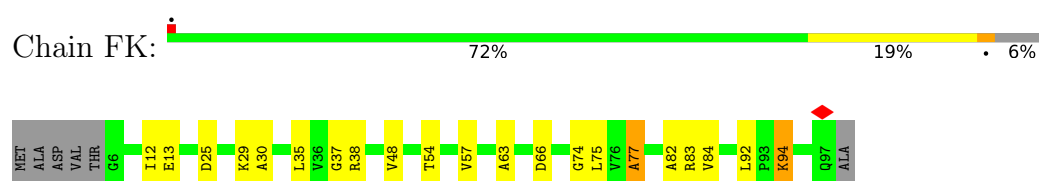
- Molecule 1: Major carboxysome shell protein CsoS1A



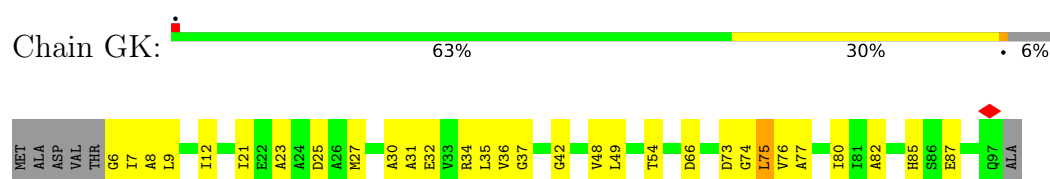
- Molecule 1: Major carboxysome shell protein CsoS1A



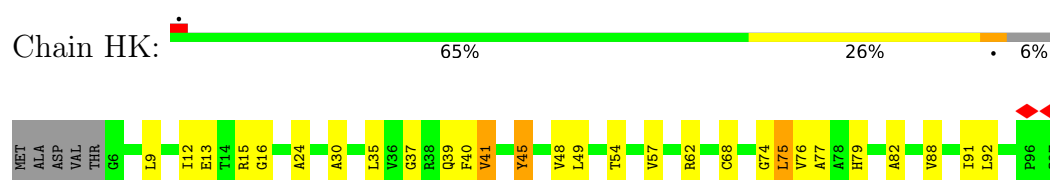
- Molecule 1: Major carboxysome shell protein CsoS1A



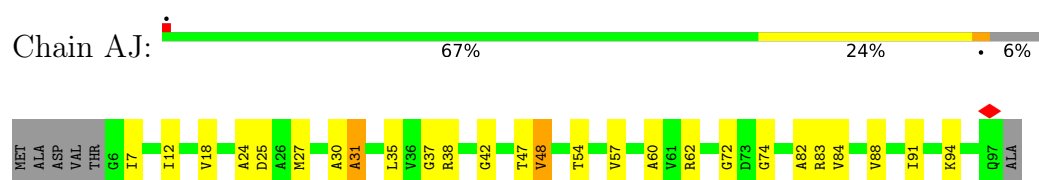
- Molecule 1: Major carboxysome shell protein CsoS1A



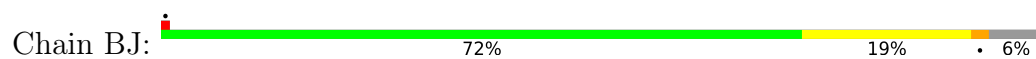
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



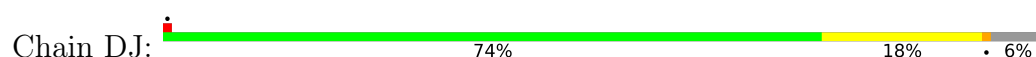
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



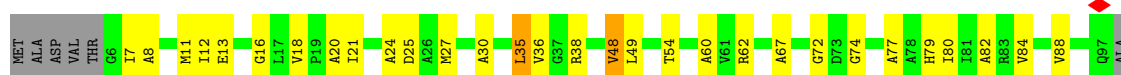
- Molecule 1: Major carboxysome shell protein CsoS1A



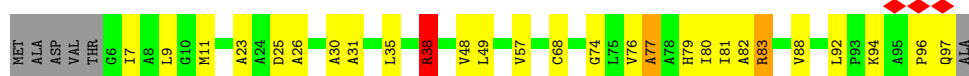
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AN:  63% 29% •• 6%



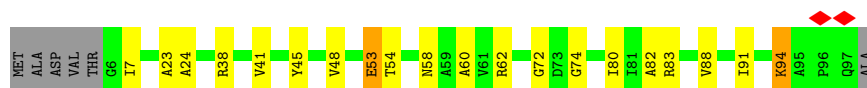
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BN:  64% 24% 5% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CN:  73% 18% • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DN:  59% 34% • 6%



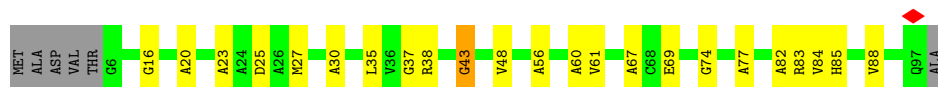
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain EN:  69% 22% • 6%



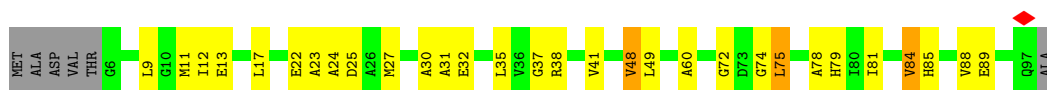
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FN:  70% 22% • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GN:  63% 28% • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



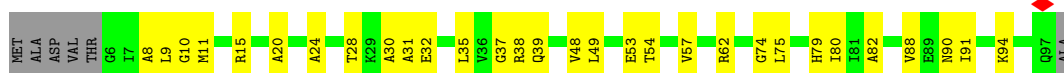
- Molecule 1: Major carboxysome shell protein CsoS1A



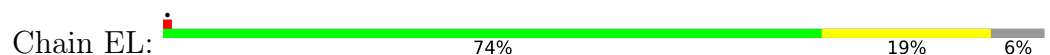
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

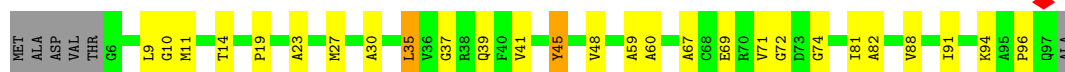


- Molecule 1: Major carboxysome shell protein CsoS1A



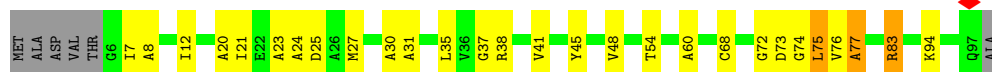
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FL:  66% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GL:  65% 26% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HL:  68% 24% 6%



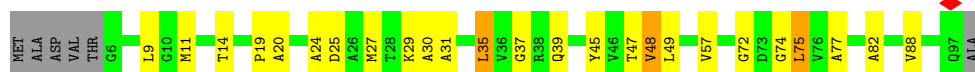
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AM:  68% 22% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BM:  68% 22% 6%



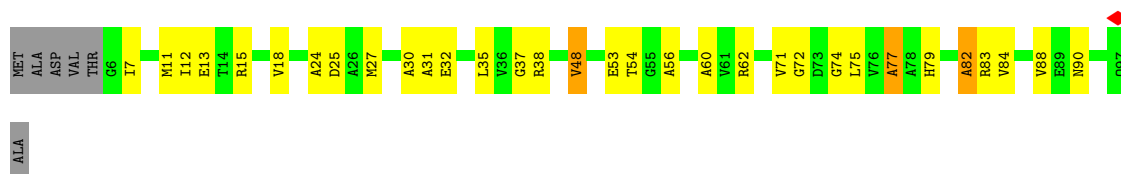
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CM:  64% 29% 6%

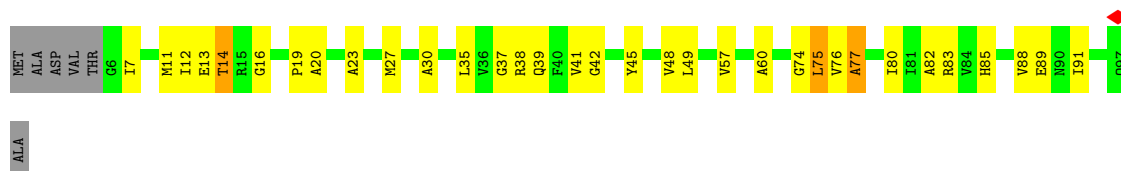


- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DM:  61% 30% 6%



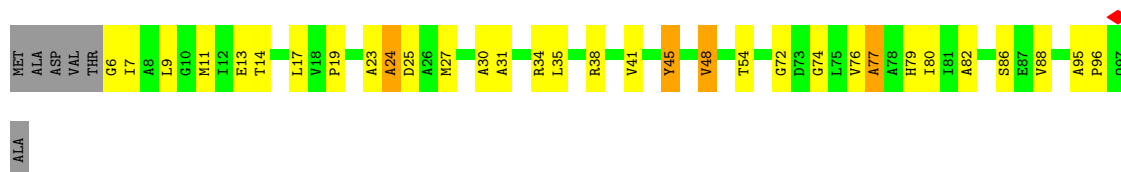
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



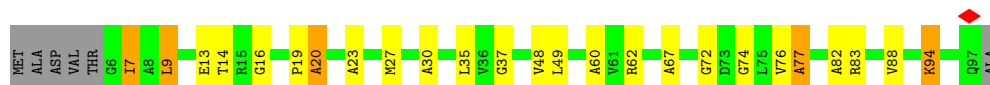
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



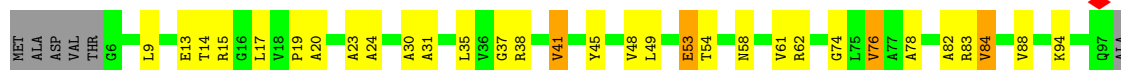
- Molecule 1: Major carboxysome shell protein CsoS1A



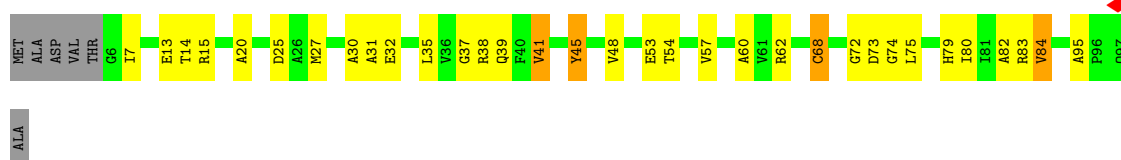
- Molecule 1: Major carboxysome shell protein CsoS1A



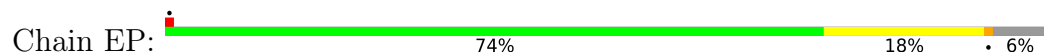
- Molecule 1: Major carboxysome shell protein CsoS1A



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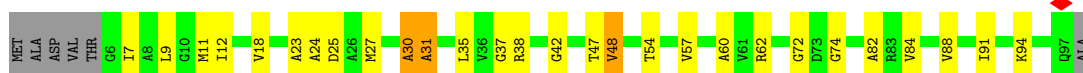


- Molecule 1: Major carboxysome shell protein CsoS1A

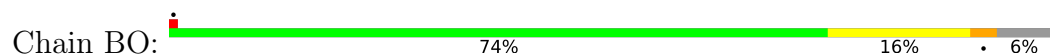




- Molecule 1: Major carboxysome shell protein CsoS1A



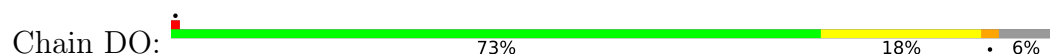
- Molecule 1: Major carboxysome shell protein CsoS1A



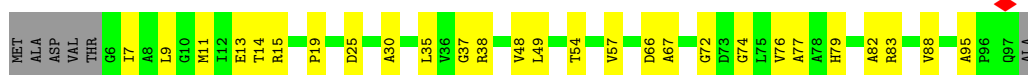
- Molecule 1: Major carboxysome shell protein CsoS1A



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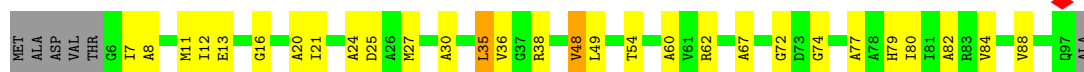
- Molecule 1: Major carboxysome shell protein CsoS1A



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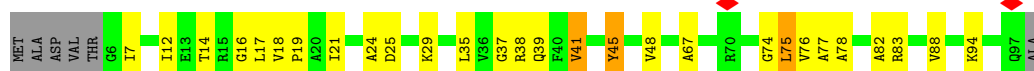
- Molecule 1: Major carboxysome shell protein CsoS1A



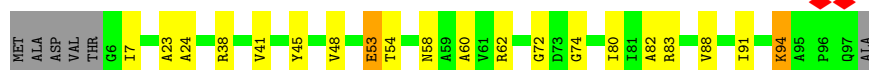
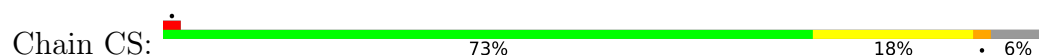
- Molecule 1: Major carboxysome shell protein CsoS1A



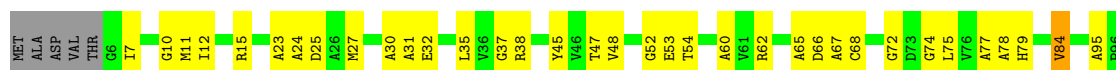
- Molecule 1: Major carboxysome shell protein CsoS1A



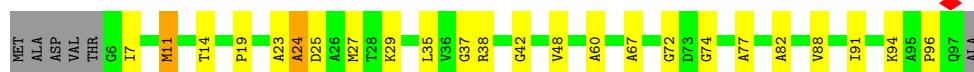
- Molecule 1: Major carboxysome shell protein CsoS1A



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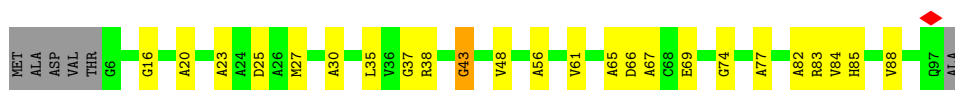


- Molecule 1: Major carboxysome shell protein CsoS1A



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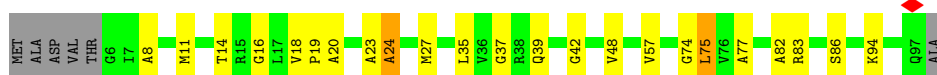
- Molecule 1: Major carboxysome shell protein CsoS1A



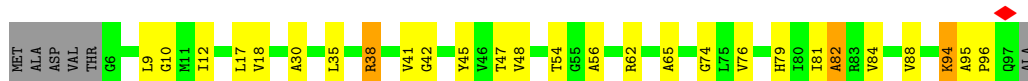
- Molecule 1: Major carboxysome shell protein CsoS1A



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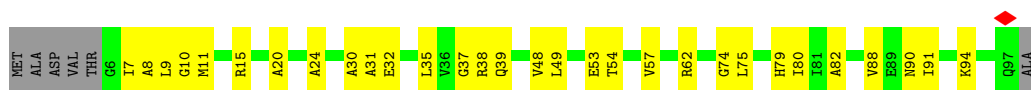


- Molecule 1: Major carboxysome shell protein CsoS1A

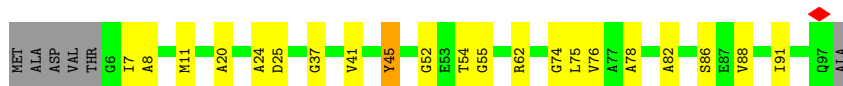
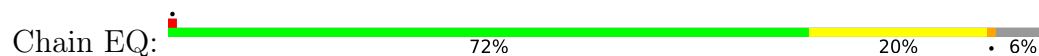


- Molecule 1: Major carboxysome shell protein CsoS1A





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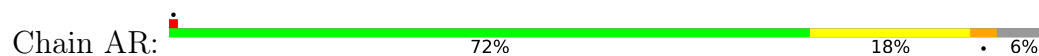
- Molecule 1: Major carboxysome shell protein CsoS1A



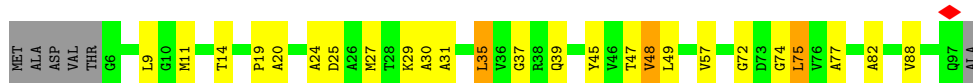
- Molecule 1: Major carboxysome shell protein CsoS1A



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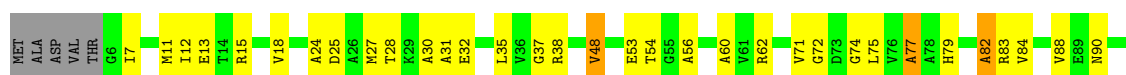
Chain CR: 



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DR: 



Q97
ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

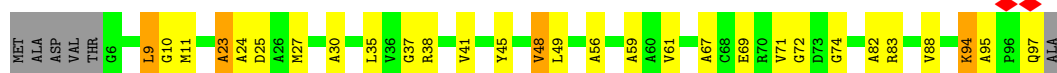
Chain ER: 



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FR: 



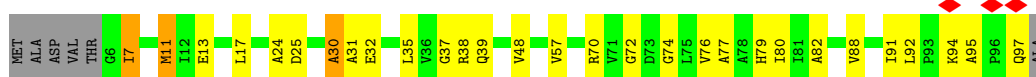
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GR: 

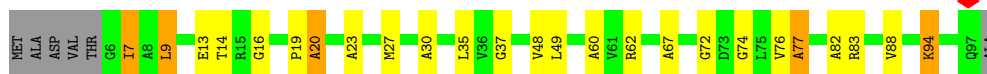


- Molecule 1: Major carboxysome shell protein CsoS1A

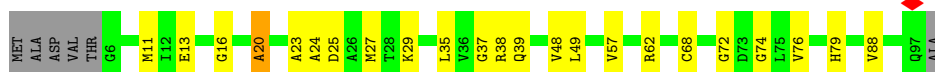
Chain HR: 



- Molecule 1: Major carboxysome shell protein CsoS1A



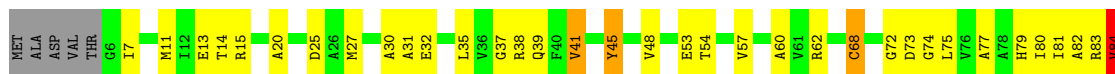
- Molecule 1: Major carboxysome shell protein CsoS1A



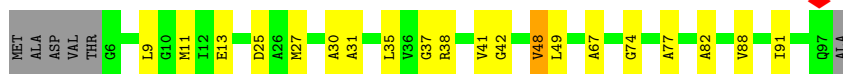
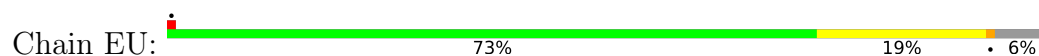
- Molecule 1: Major carboxysome shell protein CsoS1A



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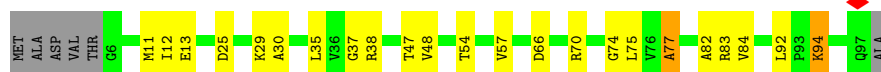


- Molecule 1: Major carboxysome shell protein CsoS1A



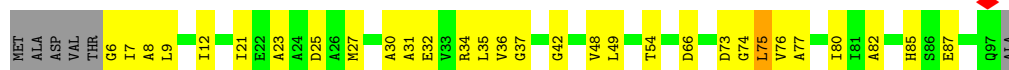
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FU:  70% 21% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GU:  63% 30% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HU:  64% 29% 6%



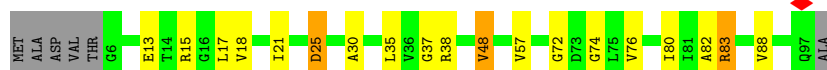
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AT:  65% 24% 6%



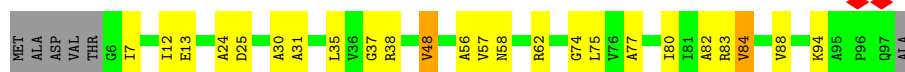
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BT:  74% 16% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CT:  69% 22% 6%



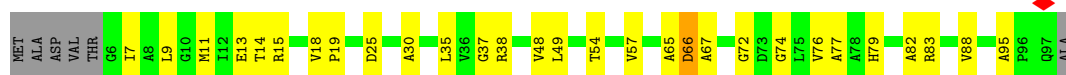
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DT:  74% 18% 6%



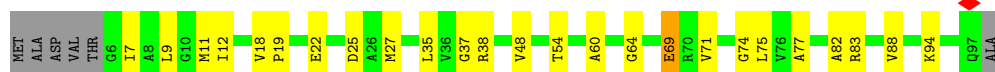
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain ET:  64% 29% • 6%



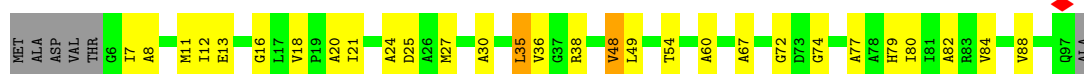
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FT:  68% 24% • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GT:  64% 28% • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HT:  66% 24% • • 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AX:  64% 27% • • 6%



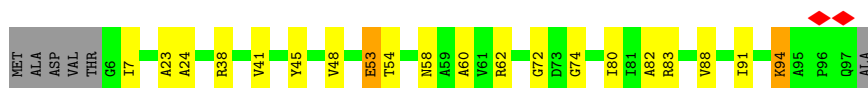
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BX:  63% 28% • 6%

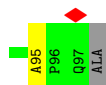


- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CX:  73% 18% • 6%



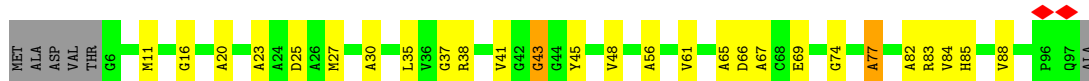
- Molecule 1: Major carboxysome shell protein CsoS1A



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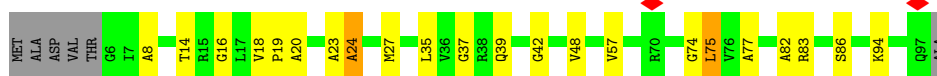
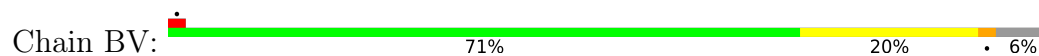


- Molecule 1: Major carboxysome shell protein CsoS1A





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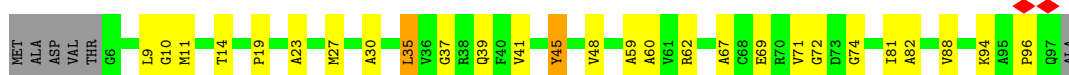
- Molecule 1: Major carboxysome shell protein CsoS1A



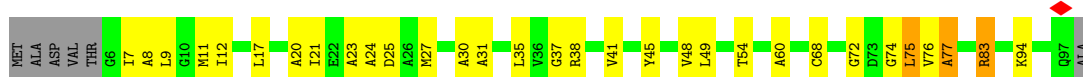
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A



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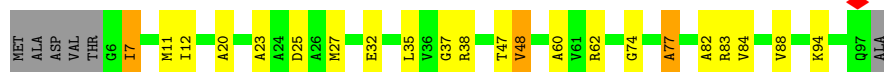
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HV:  71% 20% 6%



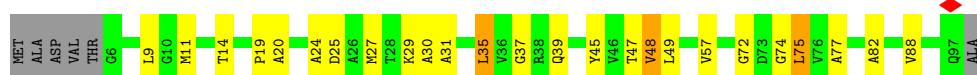
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain AW:  71% 19% 6%



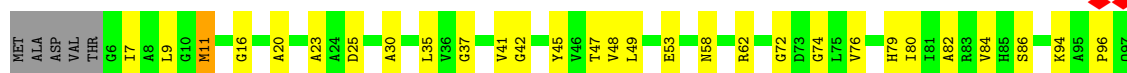
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain BW:  68% 22% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain CW:  64% 29% 6%



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

Chain DW:  61% 30% 6%



ALA

- Molecule 1: Major carboxysome shell protein CsoS1A

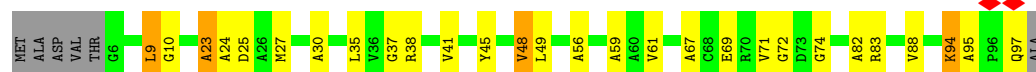
Chain EW:  59% 30% 5% 6%





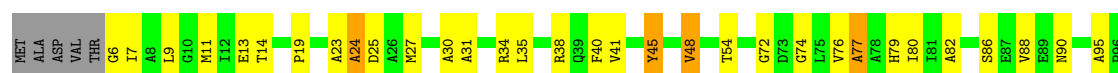
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain FW: 65% 24% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain GW: 61% 29% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain HW: 63% 28% 6%



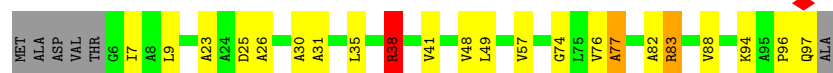
- Molecule 1: Major carboxysome shell protein CsoS1A

Chain H1: 71% 19% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain H6: 71% 19% 6%



- Molecule 1: Major carboxysome shell protein CsoS1A

Chain Hf: 68% 22% 6%



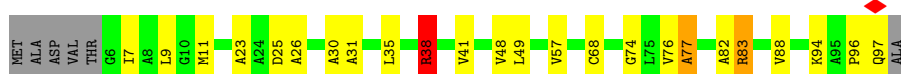
- Molecule 1: Major carboxysome shell protein CsoS1A



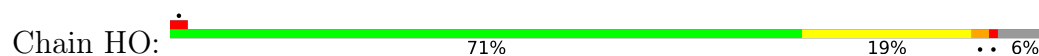
- Molecule 1: Major carboxysome shell protein CsoS1A



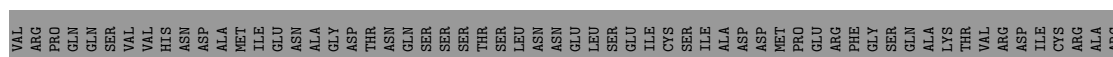
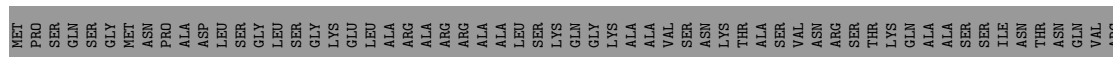
- Molecule 1: Major carboxysome shell protein CsoS1A



- Molecule 1: Major carboxysome shell protein CsoS1A

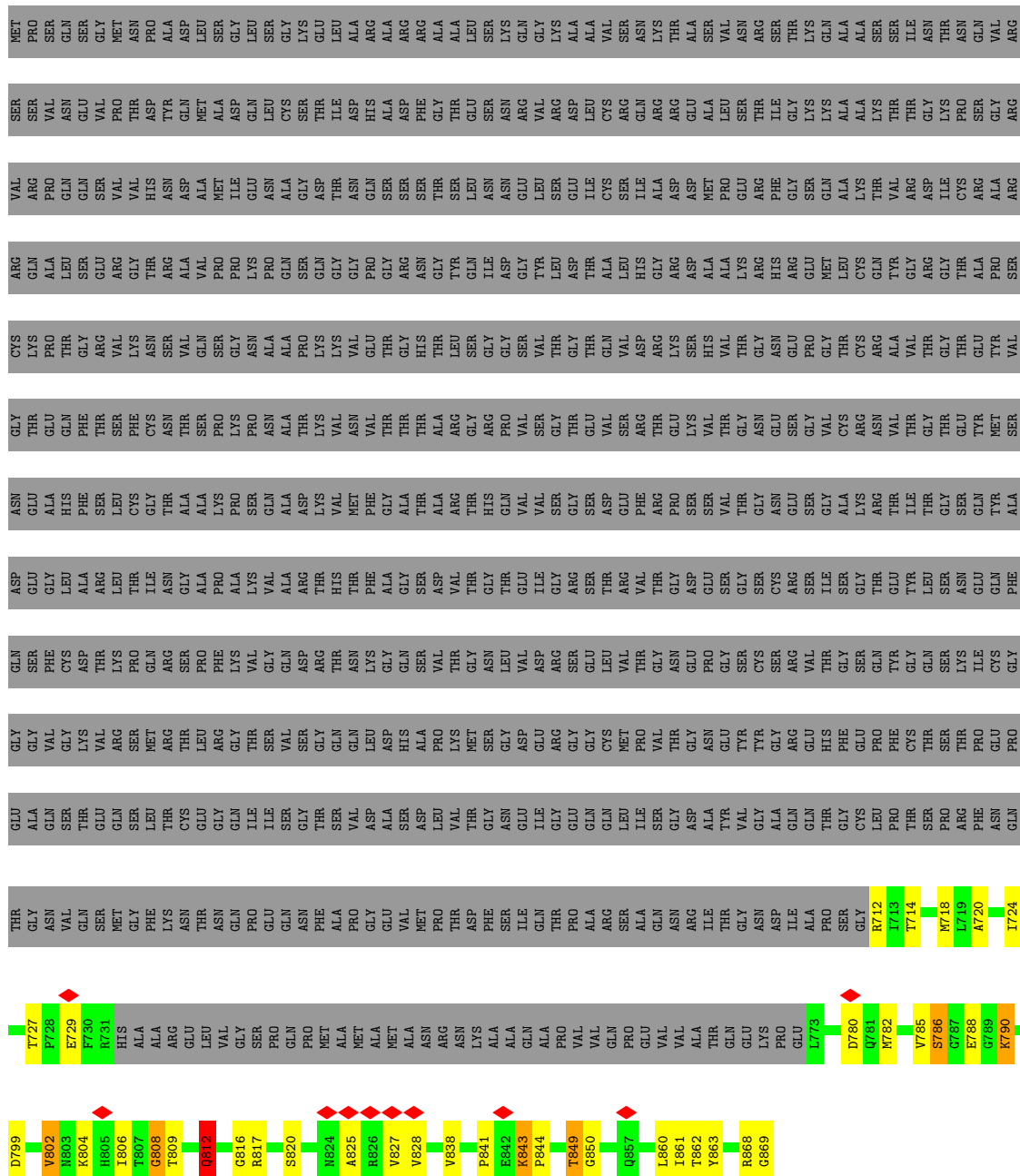


- Molecule 2: Carboxysome assembly protein CsoS2B

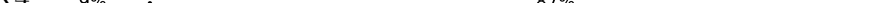




- Molecule 2: Carboxysome assembly protein CsoS2B



- Molecule 2: Carboxysome assembly protein CsoS2B

Chain X4:  9% 87%

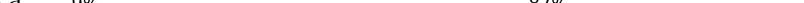
[illegible]

- Molecule 2: Carboxysome assembly protein CsoS2B

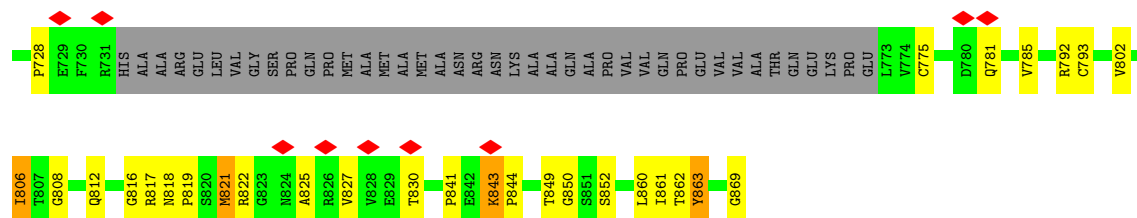
Chain X7: 10% 87%

[illegible]



Chain Xa:  9% 87%

THR	GLY	GLN	ASP	ASN	GLY	ASN	GLY	GLU	GLY	THR	MET
ASN	GLY	SER	GLY	GLY	GLU	GLU	ALA	THR	THR	GLN	PRO
VAL	VAL	PHE	GLY	ALA	ALA	ALA	HIS	GLN	GLU	PRO	SER
GLN	GLY	CYS	ASP	ALA	ALA	ALA	PHE	THR	SER	GLN	ASN
SER	VAL	THR	ARG	ARG	ARG	ARG	SER	THR	THR	SER	GLY
MET	GLN	LYS	THR	LEU	LEU	LEU	LEU	SER	VAL	PRO	MET
GLY	ARG	PRO	ILE	THR	GLY	GLY	CYS	PHE	THR	ASN	GLY
THR	THR	GLN	THR	THR	THR	THR	ASN	ASN	GLY	HIS	THR
ASN	THR	ARG	ASN	GLY	ALA	ALA	THR	VAL	VAL	ALA	ASP
THR	GLY	PRO	ALA	ALA	ALA	ALA	SER	GLN	GLN	ALA	LEU
ASN	GLY	PHE	PRO	GLY	PRO	LYS	LYS	LYS	ASP	MET	SER
GLN	GLY	GLY	VAL	GLY	GLY	VAL	VAL	GLN	GLY	ILE	LEU
ASN	SER	ASP	GLY	ALA	ALA	ALA	PHE	GLY	PRO	GLN	GLY
PHE	GLY	ARG	THR	ALA	GLY	GLY	ALA	THR	THR	GLY	LYS
ALA	ASP	GLN	ALA	GLY	ALA	ALA	ALA	THR	GLY	GLY	ARG
VAL	SER	HIS	GLY	THR	THR	THR	THR	THR	GLY	ILE	SER
MET	ASP	ALA	SER	GLY	THR	THR	THR	THR	HIS	ASN	ARG
PRO	LEU	PRO	ASP	VAL	VAL	VAL	ALA	ALA	LEU	TYR	GLY
THR	VAL	THR	THR	THR	ARG	ARG	ALA	ARG	THR	SER	ALA
ASP	THR	GLY	THR	GLY	THR	THR	GLY	GLY	ASP	LEU	LEU
PHE	GLY	ASN	GLY	ASN	GLY	HIS	GLN	PRO	GLY	ILE	SER
SER	ASN	LEU	THR	THR	THR	THR	GLY	GLY	ASP	ASN	LYS
ILE	GLY	VAL	ASP	ILE	GLY	ILE	VAL	VAL	SER	GLY	GLN
GLY	ILE	ASP	GLY	GLY	GLY	GLY	VAL	THR	TYR	VAL	ARG
THR	GLY	ARG	GLY	GLY	GLY	GLY	THR	THR	GLY	THR	LYS
ALA	GLN	GLY	GLY	GLY	GLY	SER	SER	THR	GLY	THR	THR
ARG	GLN	LEU	SER	CYS	THR	THR	ASP	VAL	VAL	CYS	VAL
SER	LEU	MET	THR	MET	GLU	GLU	GLY	ARG	LEU	SER	SER
ALA	ILE	PRO	THR	PRO	THR	VAL	THR	PHE	ALA	GLN	ASN
ASN	VAL	GLY	THR	VAL	GLY	GLY	GLY	THR	GLY	ARG	THR
THR	GLY	ASN	GLY	GLY	GLY	GLY	PRO	GLY	ASP	ASP	GLY
ILE	ALA	ASN	GLY	ASN	PRO	VAL	SER	SER	ALA	MET	SER
THR	GLY	GLY	SER	THR	THR	THR	VAL	THR	PRO	GLY	VAL
GLY	VAL	THR	GLY	TYR	VAL	GLY	GLY	LYS	GLY	THR	ASN
ASN	GLY	ALA	SER	TYR	GLY	CYS	GLY	ARG	GLY	THR	THR
ILE	GLN	ARG	GLY	ARG	GLY	ARG	ASN	GLY	LYS	PHE	SER
ALA	GLN	GLY	THR	THR	SER	THR	THR	GLY	ASN	GLY	LYS
PRO	GLY	SER	GLY	THR	GLY	LYS	CYS	ARG	CYS	ALA	ALA
R712	LEU	PRO	THR	THR	THR	THR	GLN	ARG	ARG	THR	SER
I713	PRO	PHE	TYR	GLY	GLY	ILE	ILE	THR	GLY	VAL	THR
P716	THR	THR	THR	THR	GLY	THR	GLN	THR	GLY	ARG	ILE
L719	PRO	SER	SER	THR	THR	THR	GLN	THR	GLY	ASP	ASN
A720	PHE	THR	THR	THR	GLY	GLY	ILE	THR	GLY	THR	GLN
THR	ASN	GLY	GLN	THR	THR	THR	CYS	TYR	MET	PRO	VAL



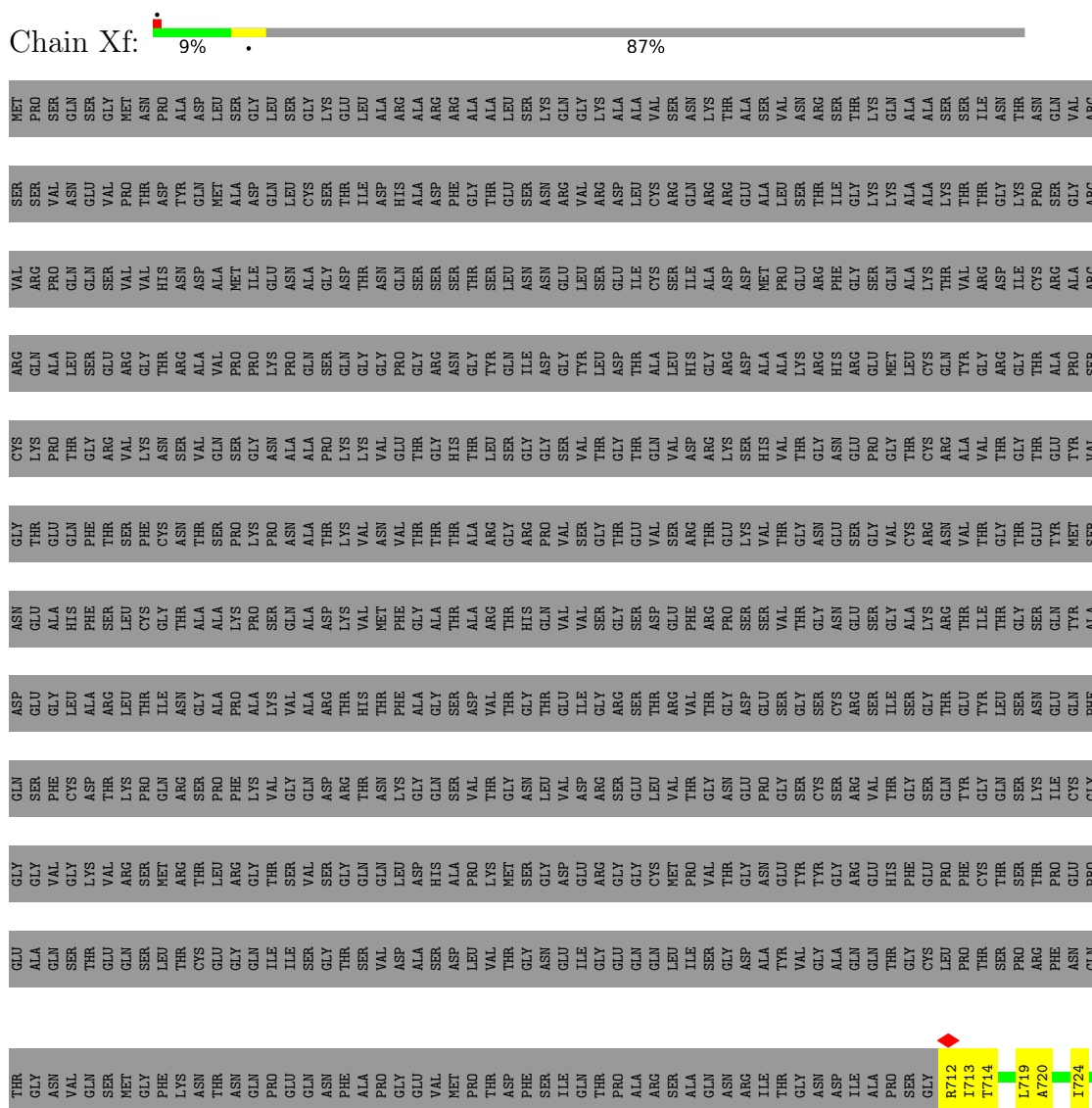
- Molecule 2: Carboxysome assembly protein CsoS2B

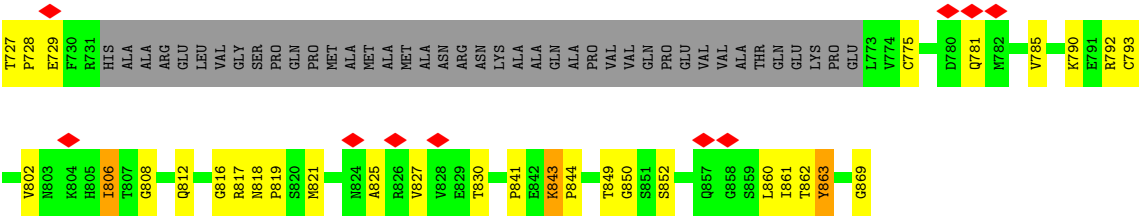
Chain Xe: 10% 87%

VAL	SER	MET
ARG	SER	PRO
PRO	VAL	SER
GLN	ASN	GLN
GLN	GLU	SER
SER	VAL	GLY
VAL	PRO	MET
VAL	THR	ASN
HIS	ASP	PRO
ASN	TYR	ALA
ASP	GLN	ASP
ALA	MET	LEU
MET	ALA	SER
ILE	ASP	GLY
GLU	GLN	LEU
ASN	LEU	SER
ALA	CYS	GLY
GLY	SER	LYS
ASP	THR	GLU
THR	ILE	LEU
ASN	HIS	ARG
GLN	ASP	ALA
SER	ASP	ARG
SER	PHE	ARG
THR	GLY	ALA
THR	THR	ALA
LEU	GLU	LEU
ASN	SER	SER
ASN	ASN	LYS
LEU	ARG	GLN
GLU	VAL	GLY
SER	ARG	LYS
GLU	ASP	ALA
ILE	LEU	ALA
CYS	CTS	VAL
SER	ARG	SER
ILE	GLN	ASN
ALA	ARG	LYS
ASP	ARG	THR
ASP	GLU	ALA
MET	ALA	SER
PRO	LEU	VAL
GLU	SER	ASN
PHE	THR	ARG
GLY	ILE	SER
SER	GLY	THR
GLN	LYS	LYS
ALA	ALA	GLN
ALA	ALA	ALA
LYS	LYS	ALA
THR	THR	SER
VAL	THR	SER
ARG	THR	ILE
ASP	GLY	ASN
ILE	LYS	THR
ILE	LYS	THR
CYS	PRO	ASN
ARG	SER	GLN
ALA	GLY	VAL

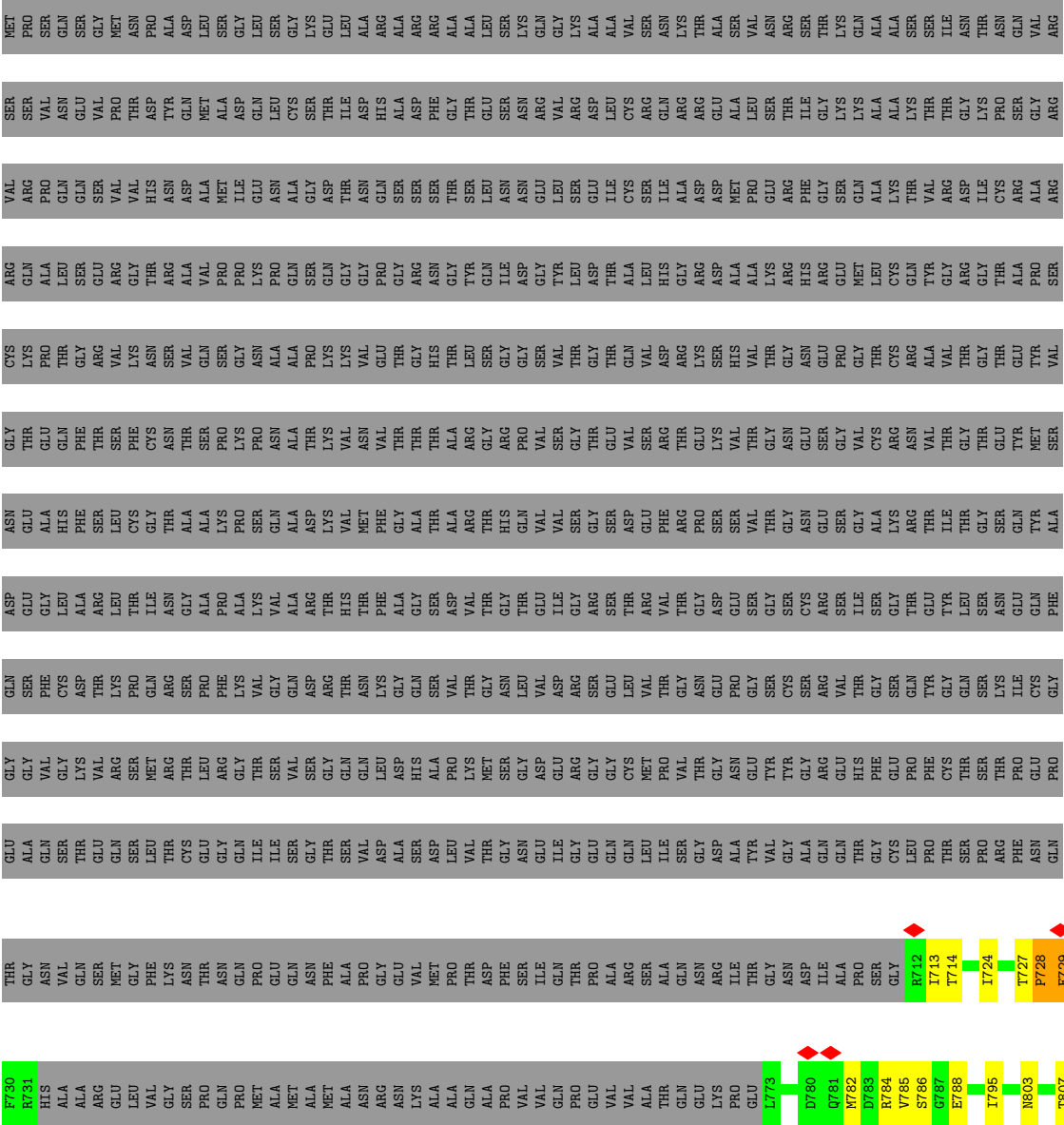
[illegible]

- Molecule 2: Carboxysome assembly protein CsoS2B



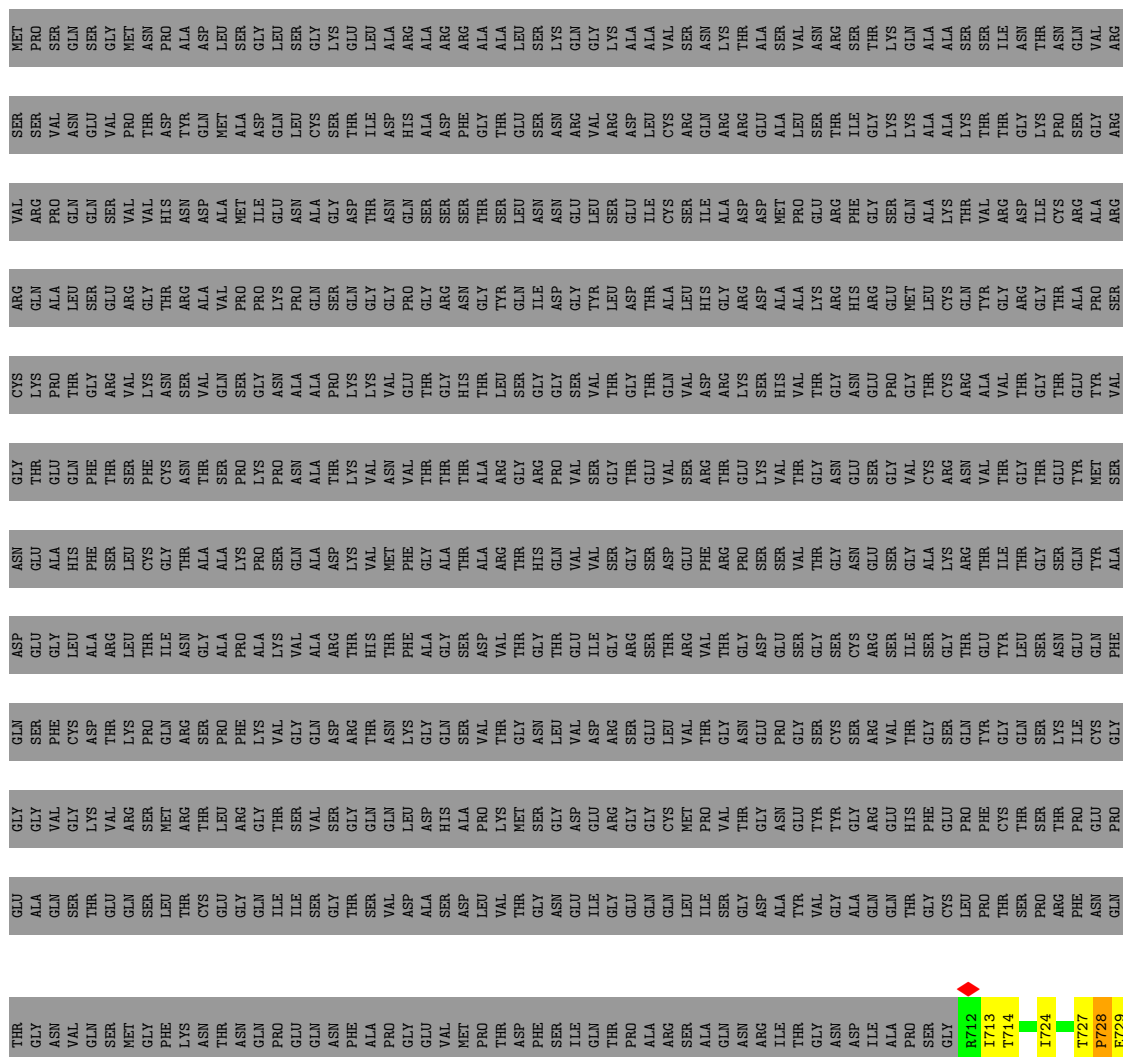


• Molecule 2: Carboxysome assembly protein CsoS2B

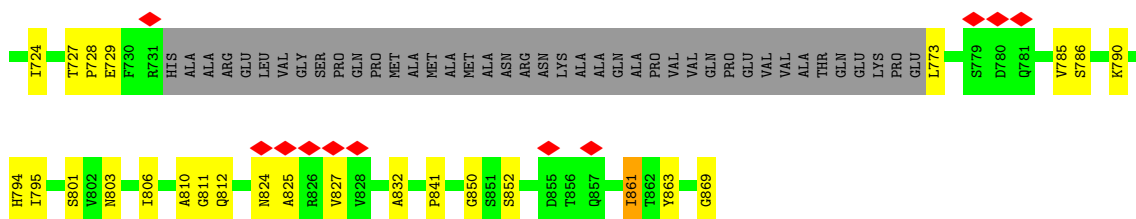


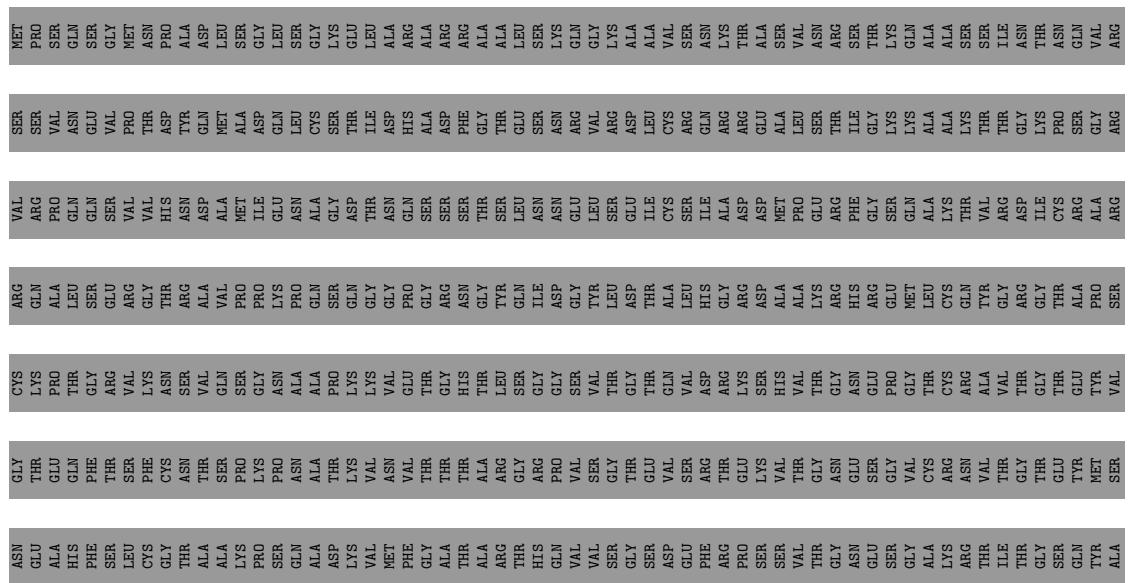
• Molecule 2: Carboxysome assembly protein CsoS2B



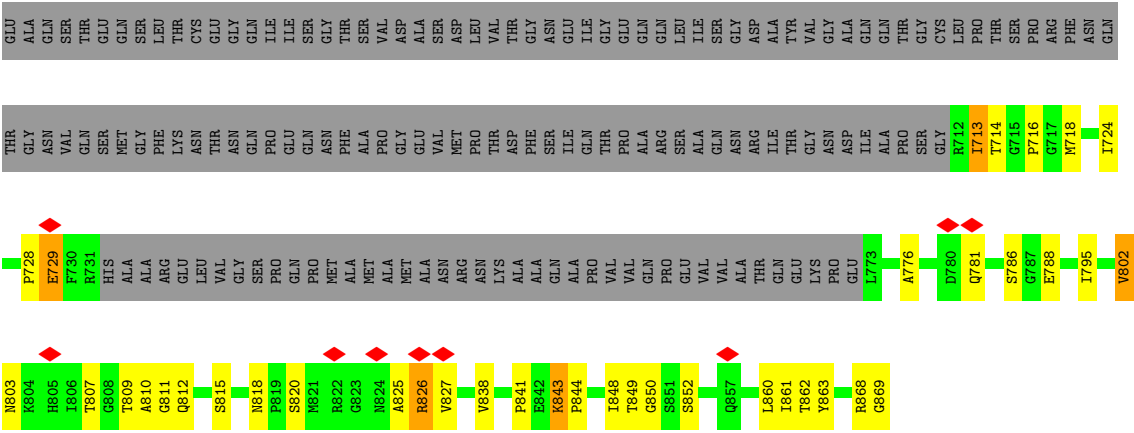




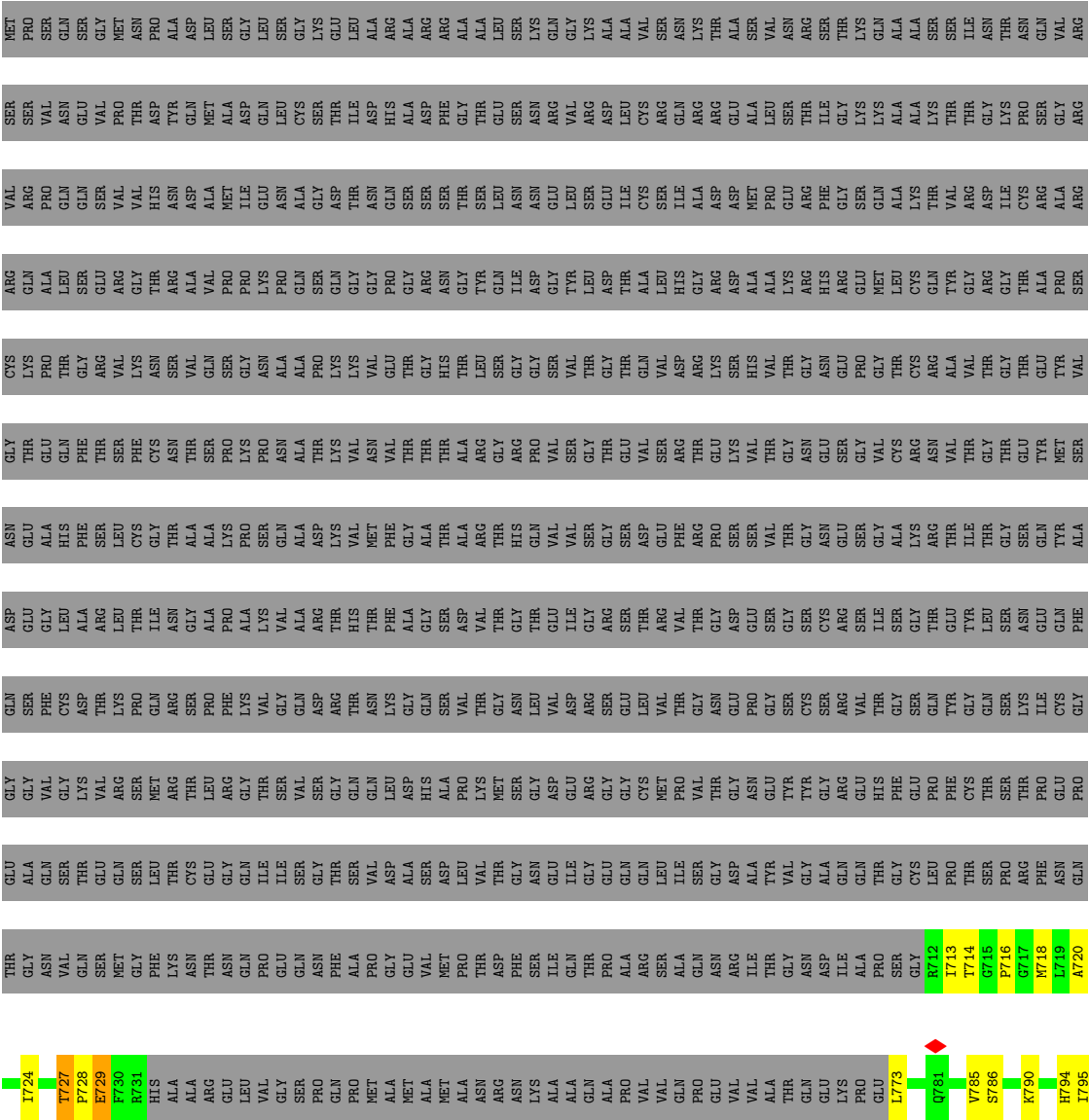
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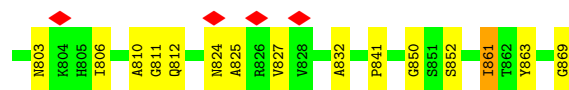






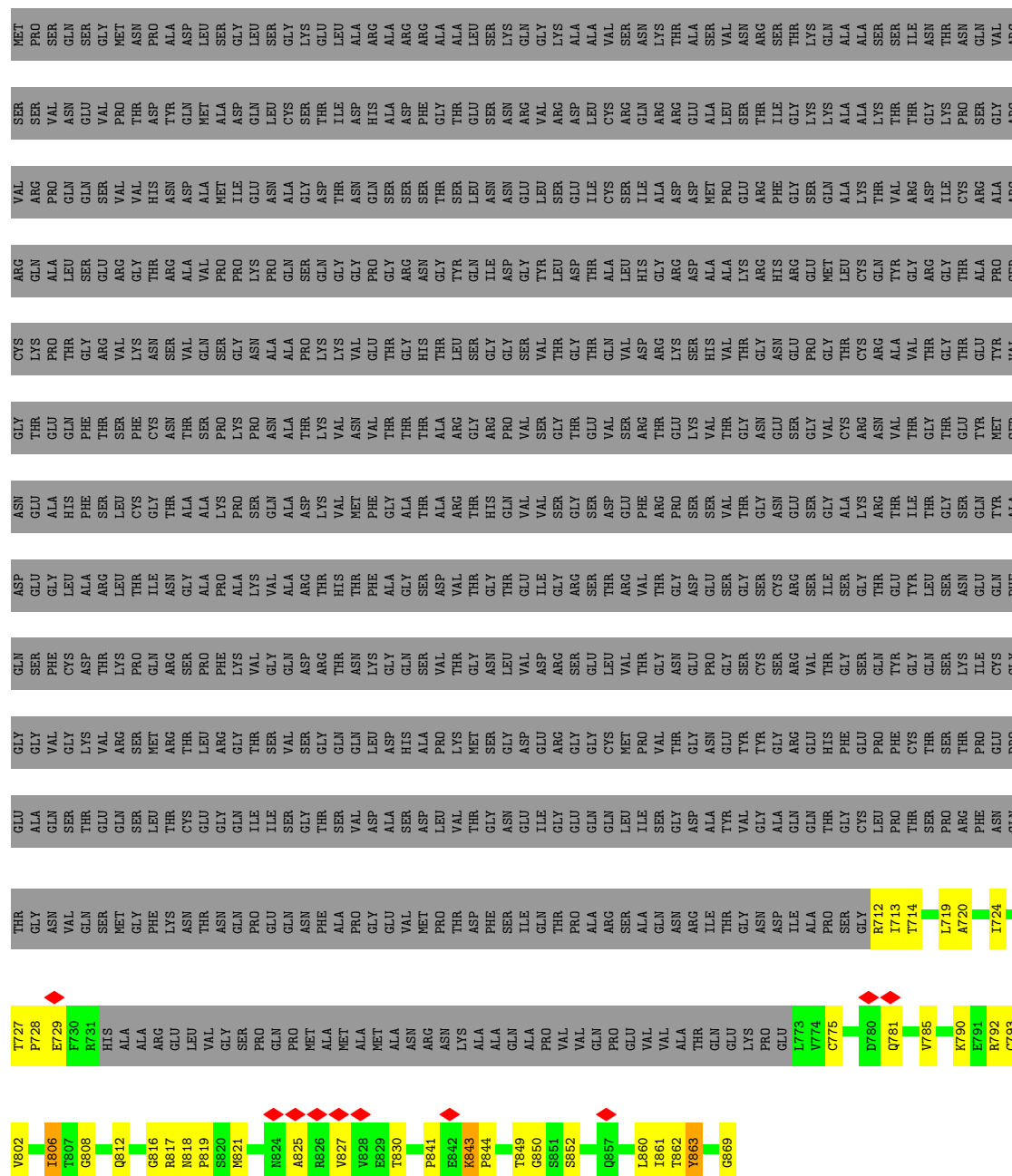
● Molecule 2: Carboxysome assembly protein CsoS2B





• Molecule 2: Carboxysome assembly protein CsoS2B

Chain Xu: 9% 87%



• Molecule 2: Carboxysome assembly protein CsoS2B

Chain Xy: 10% 87%

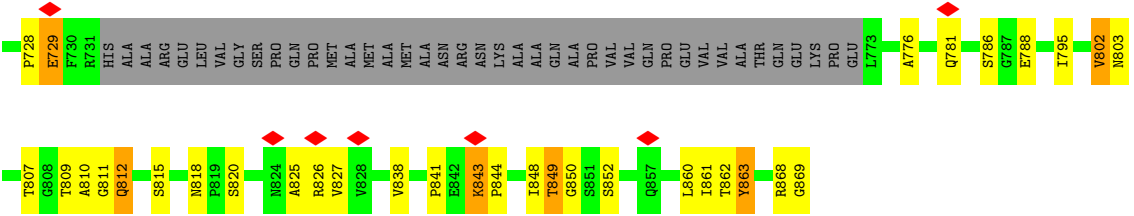
G808	T809
S815	G816
G817	R817
N818	P819
S820	S820
N824	A825
R826	V827
V828	S830
N835	P841
S846	T849
Q857	L860
L860	T861
T862	Y863
G866	A867
R868	G869

Chain Xw: 9% 87%

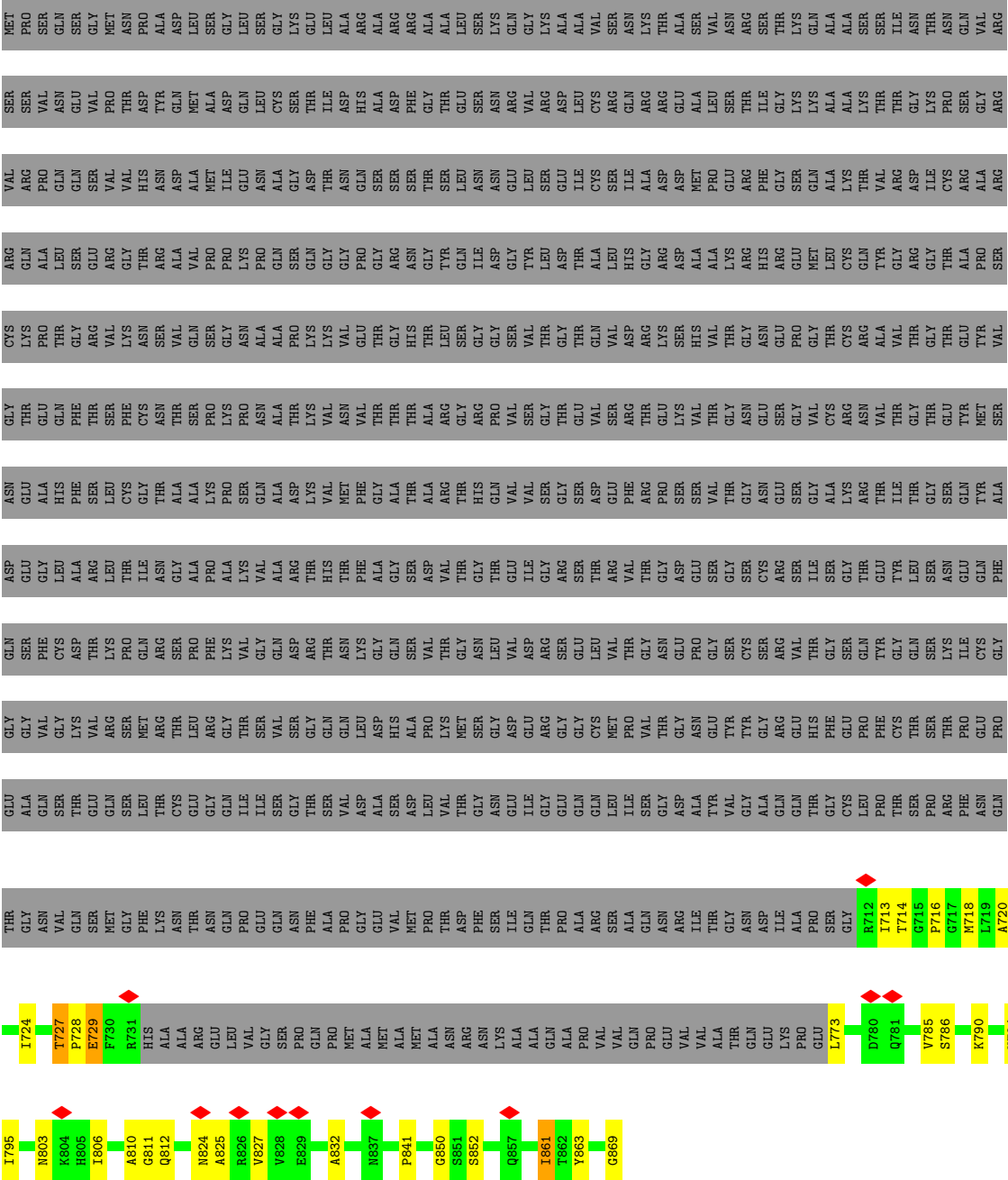








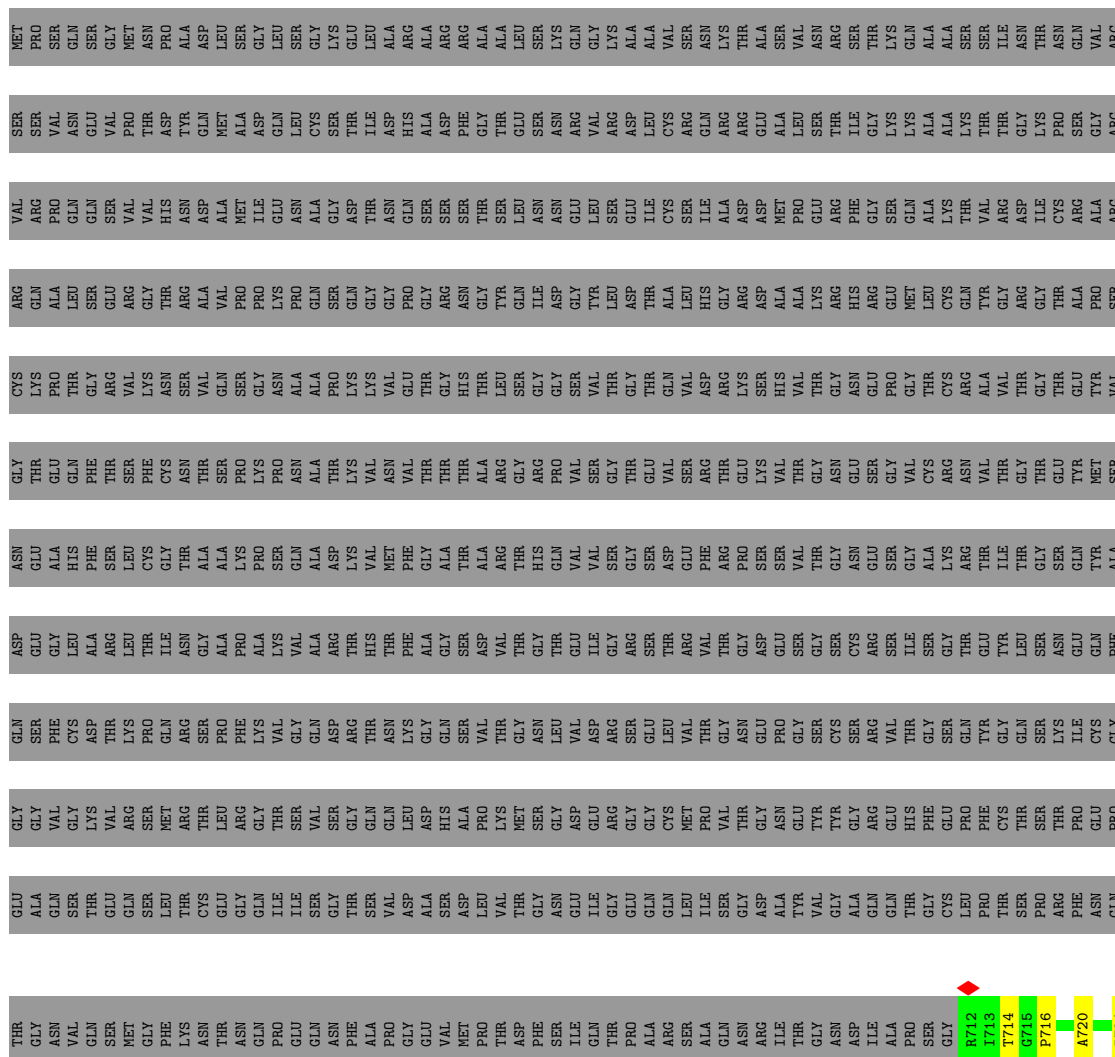
• Molecule 2: Carboxysome assembly protein CsoS2B



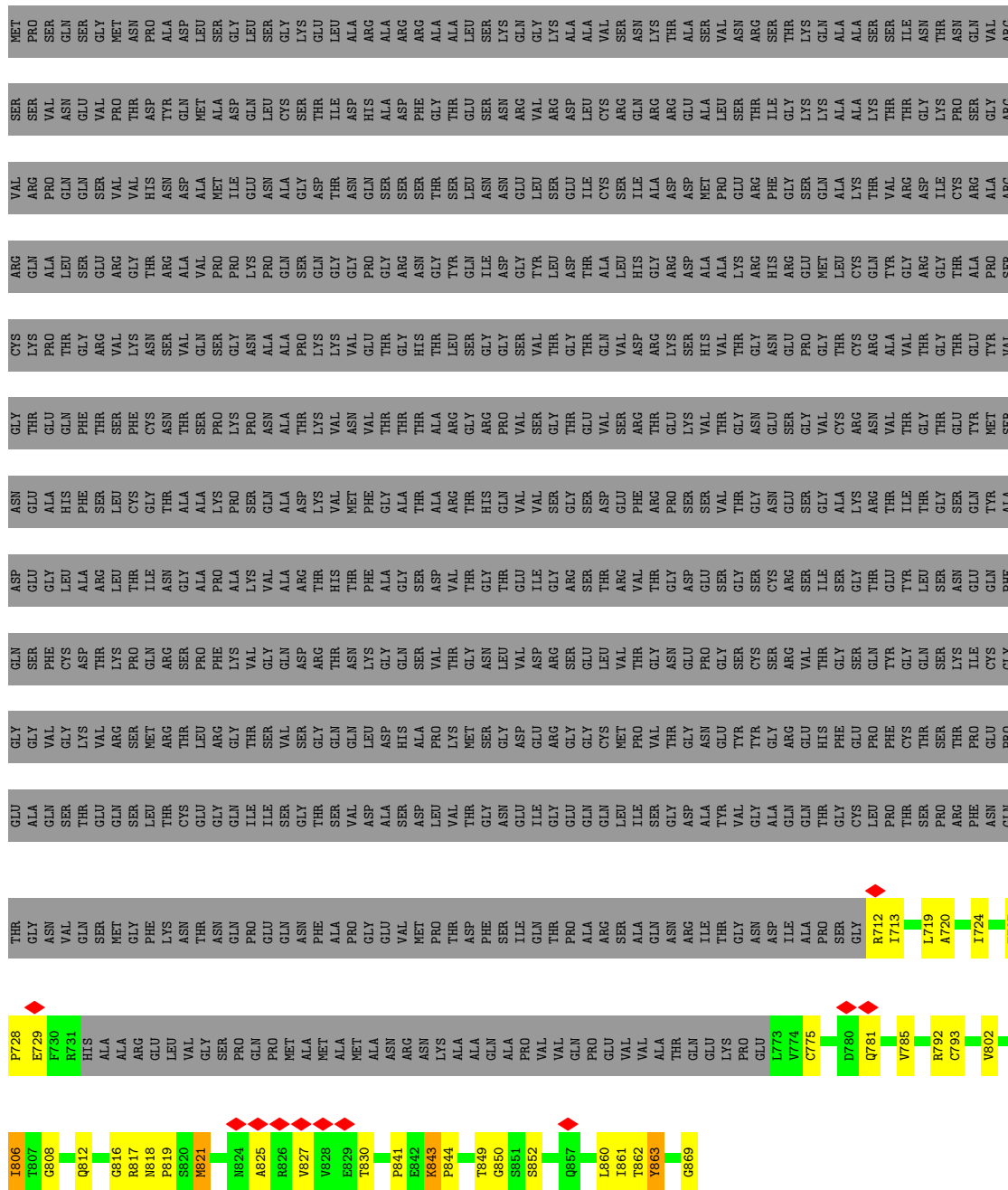
• Molecule 2: Carboxysome assembly protein CsoS2B



- Molecule 2: Carboxysome assembly protein CsoS2B



- Molecule 2: Carboxysome assembly protein CsoS2B



- Molecule 2: Carboxysome assembly protein CsoS2B

Chain XS: 10% 87%

[illegible]

- Molecule 2: Carboxysome assembly protein CsoS2B

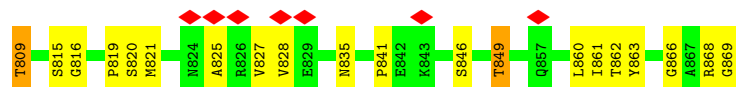
Chain XQ: 9% 87%

MET	PRO	ASP	GLN	SER	GLY	MET	ASN	PRO	ALA	ASP	SER	LEU	SER	GLY	LYS	GLU	LEU	ALA	ARG	ARG	ALA	LEU	SER	SER	LYS	GLN	GLY	LYS	VAL	SER	ASN	ARG	SER	THR	ALA	SER	VAL	ASN	THR	GLN	ALA	ALA	SER	SER	THR	ILE	ASN	THR	ASN	GLN	VAL	PRO
SER	SER	VAL	ASN	GLU	VAL	PRO	THR	ASP	TYR	ALA	GLN	MET	ALA	GLN	SER	THR	ILE	ASP	ALA	ASP	THR	GLU	SER	ASN	ASN	ARG	VAL	LYS	GLY	ALA	LEU	SER	THR	THR	ALA	ALA	LEU	LYS	LYS	THR	THR	GLY	GLN	PRO	SER	GLY	VAL	PRO				

- Molecule 2: Carboxysome assembly protein CsoS2B

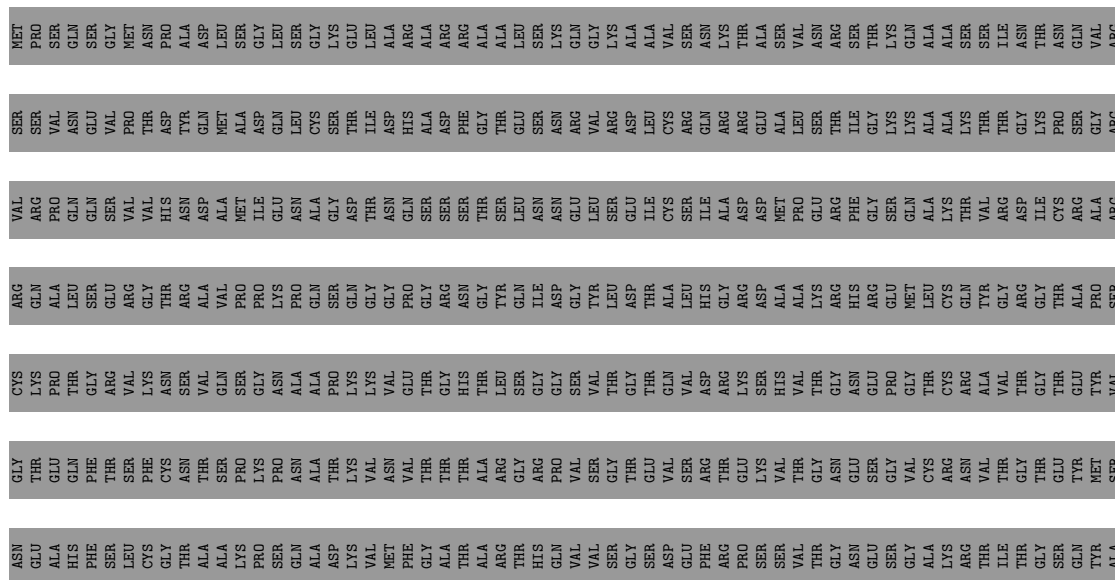


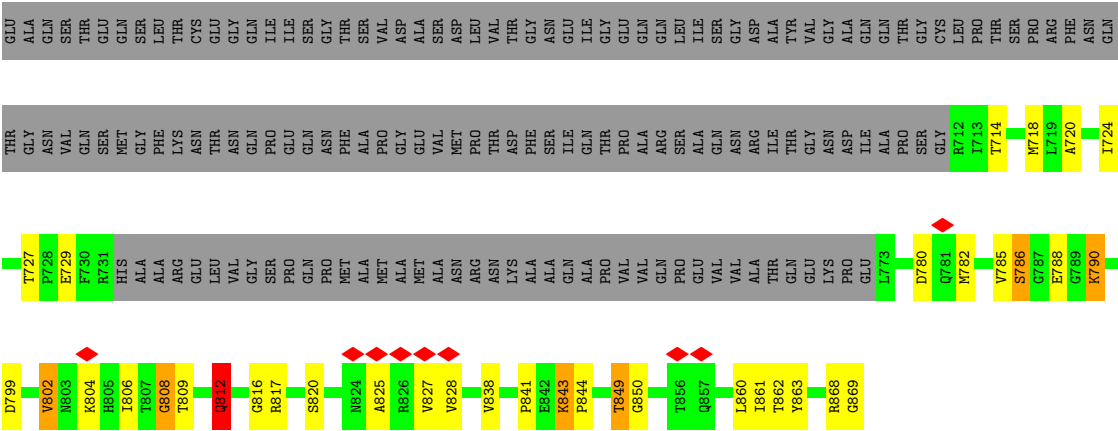




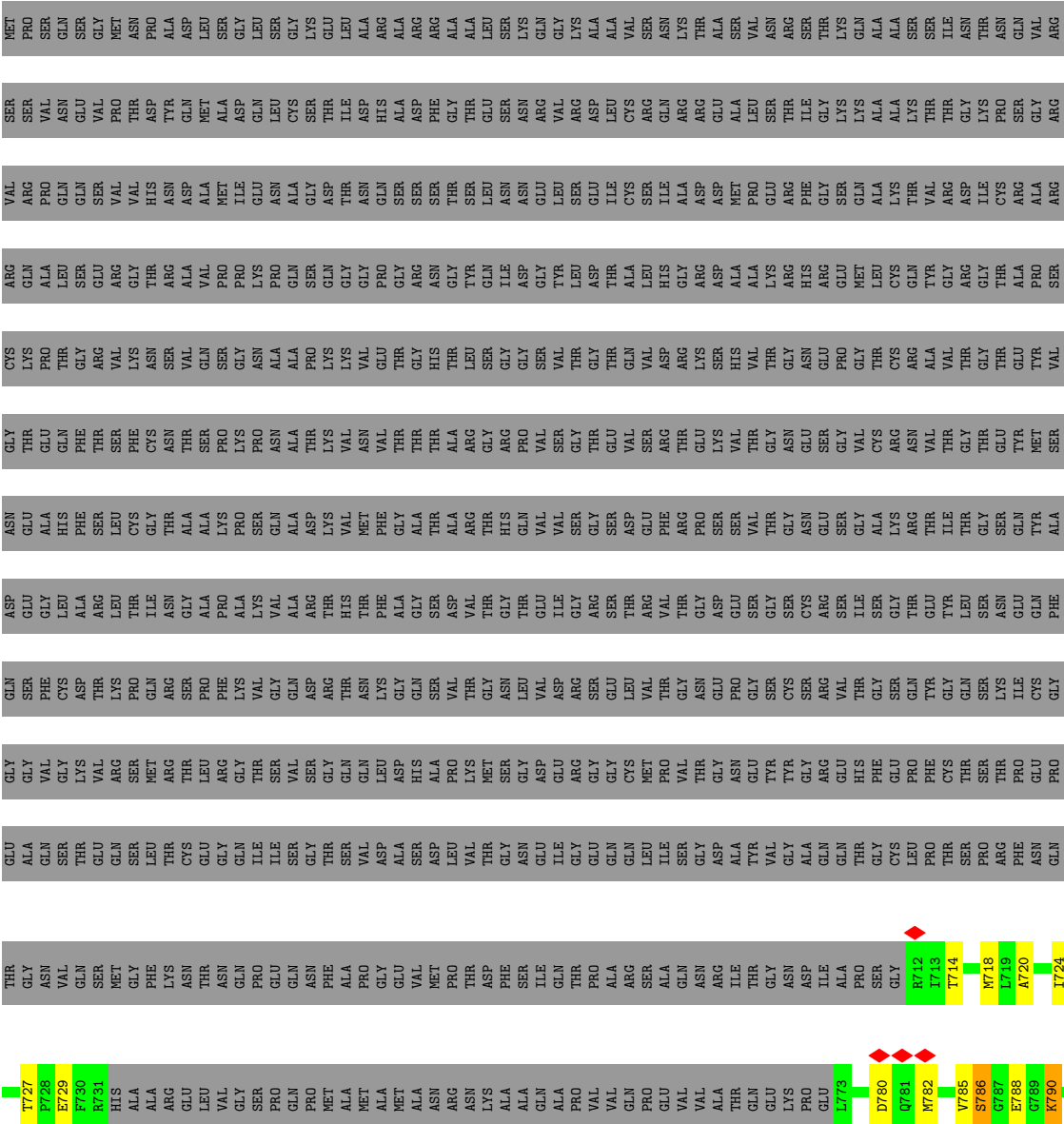
- Molecule 2: Carboxysome assembly protein CsoS2B





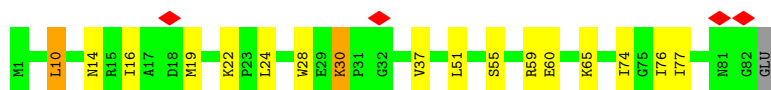
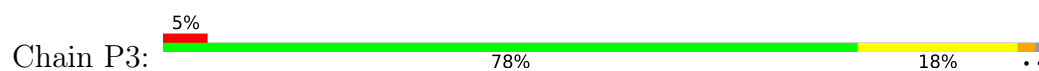


● Molecule 2: Carboxysome assembly protein CsoS2B

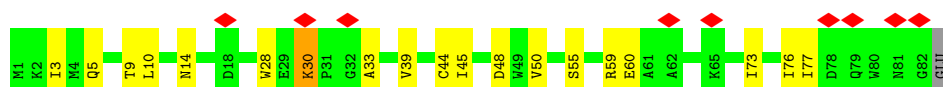
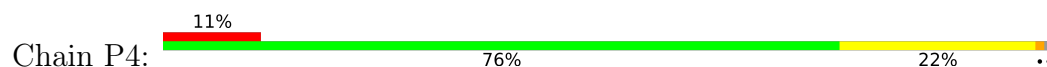




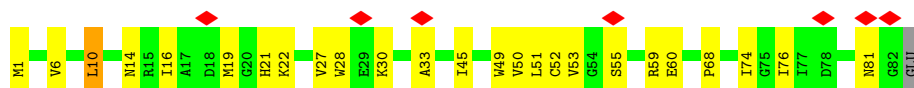
- Molecule 3: Carboxysome shell vertex protein CsoS4A



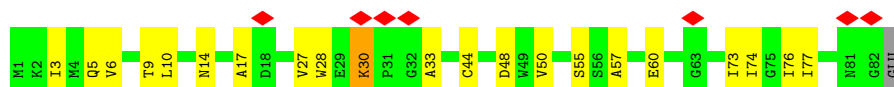
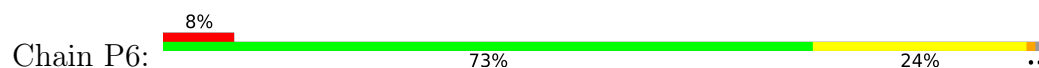
- Molecule 3: Carboxysome shell vertex protein CsoS4A



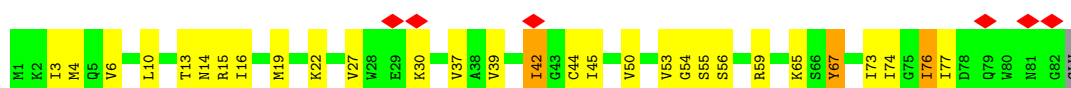
- Molecule 3: Carboxysome shell vertex protein CsoS4A



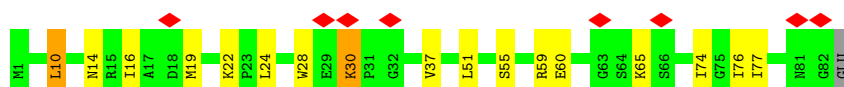
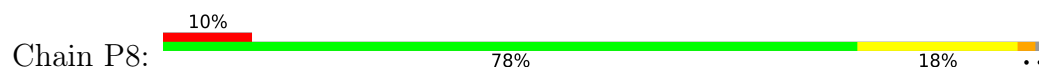
- Molecule 3: Carboxysome shell vertex protein CsoS4A



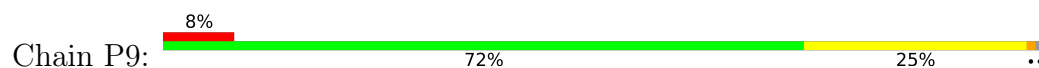
- Molecule 3: Carboxysome shell vertex protein CsoS4A

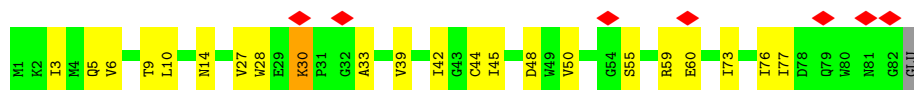


- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A

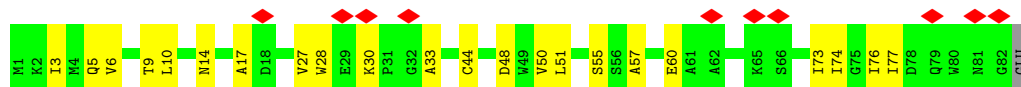
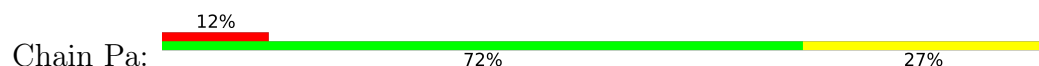




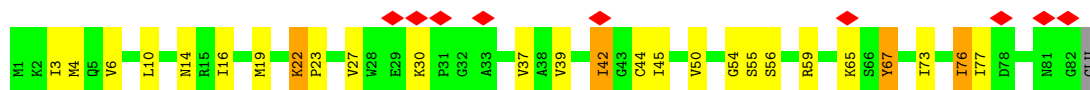
- Molecule 3: Carboxysome shell vertex protein CsoS4A



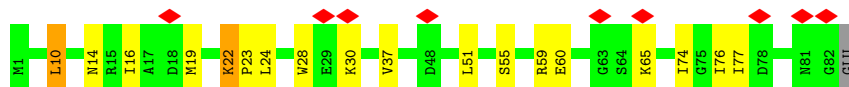
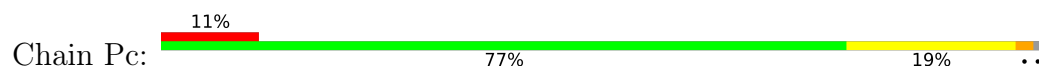
- Molecule 3: Carboxysome shell vertex protein CsoS4A



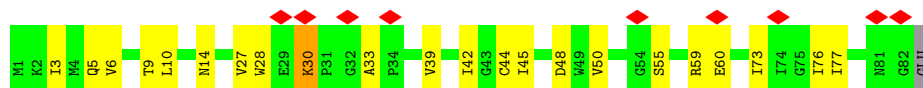
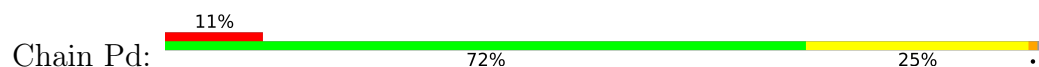
- Molecule 3: Carboxysome shell vertex protein CsoS4A



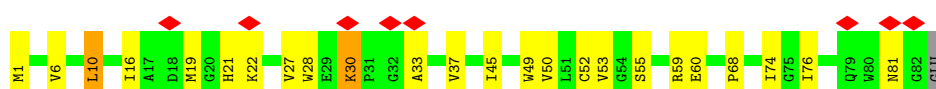
- Molecule 3: Carboxysome shell vertex protein CsoS4A



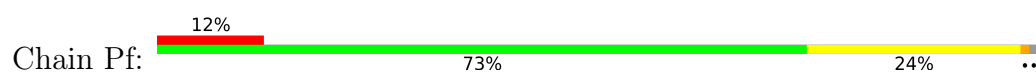
- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A



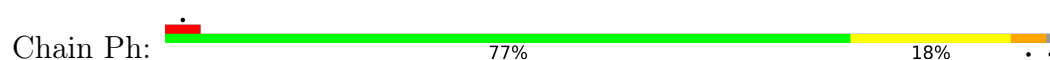
- Molecule 3: Carboxysome shell vertex protein CsoS4A



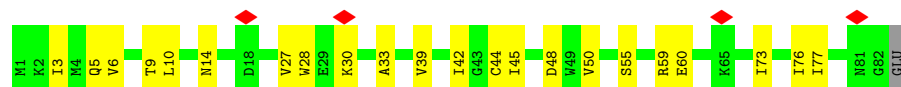
- Molecule 3: Carboxysome shell vertex protein CsoS4A



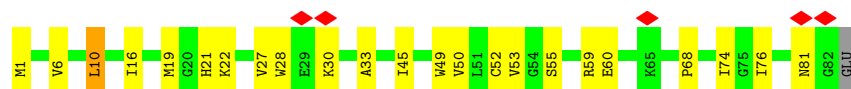
- Molecule 3: Carboxysome shell vertex protein CsoS4A



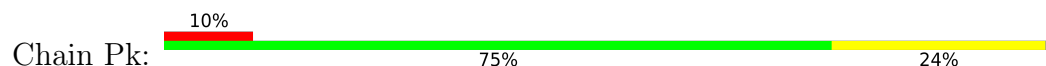
- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A



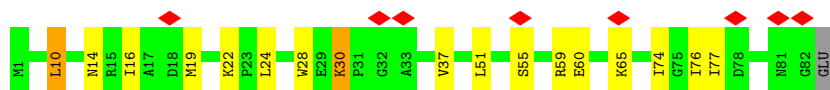
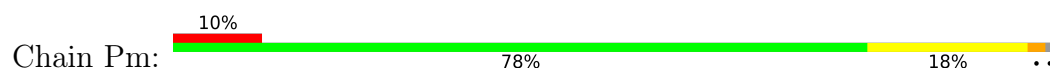
- Molecule 3: Carboxysome shell vertex protein CsoS4A



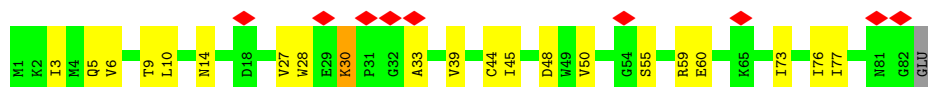
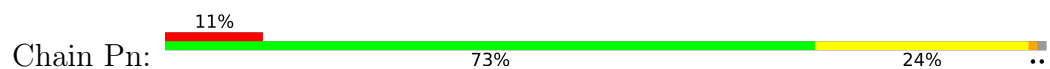
- Molecule 3: Carboxysome shell vertex protein CsoS4A



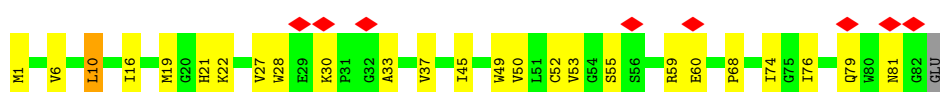
- Molecule 3: Carboxysome shell vertex protein CsoS4A



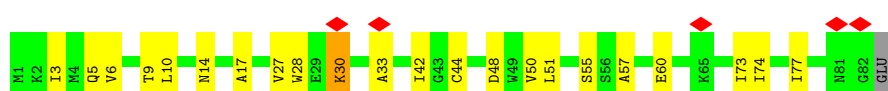
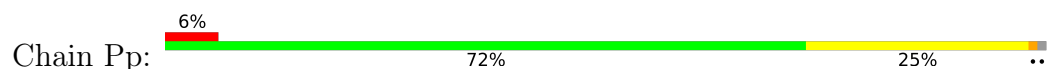
- Molecule 3: Carboxysome shell vertex protein CsoS4A



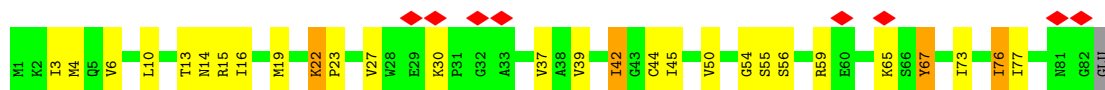
- Molecule 3: Carboxysome shell vertex protein CsoS4A



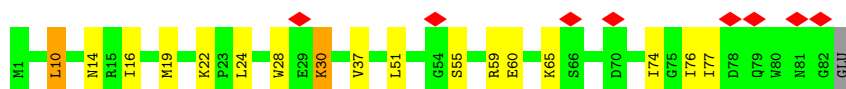
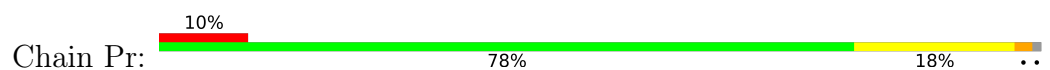
- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A

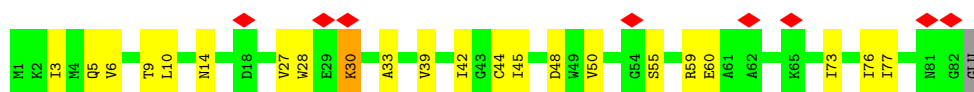


- Molecule 3: Carboxysome shell vertex protein CsoS4A

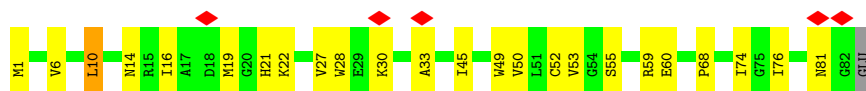


- Molecule 3: Carboxysome shell vertex protein CsoS4A





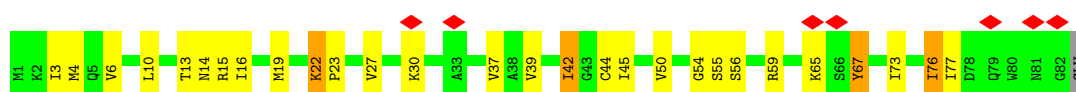
- Molecule 3: Carboxysome shell vertex protein CsoS4A



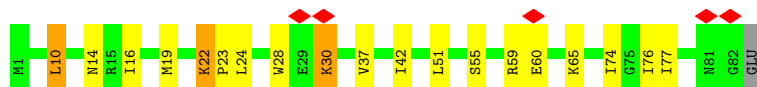
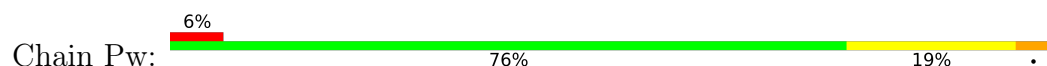
- Molecule 3: Carboxysome shell vertex protein CsoS4A



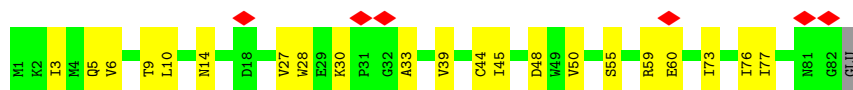
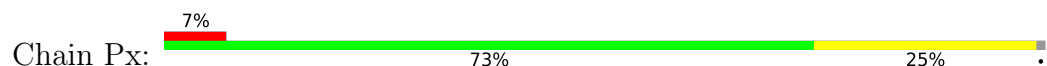
- Molecule 3: Carboxysome shell vertex protein CsoS4A



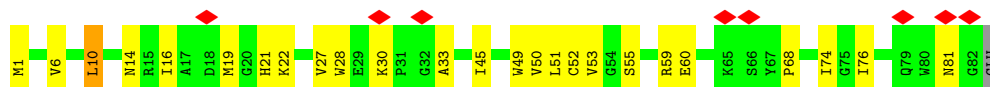
- Molecule 3: Carboxysome shell vertex protein CsoS4A



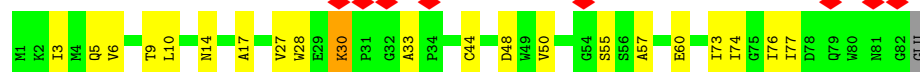
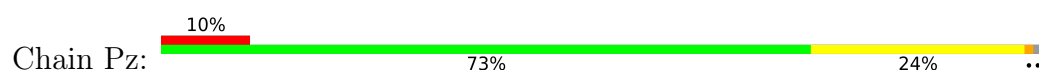
- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A



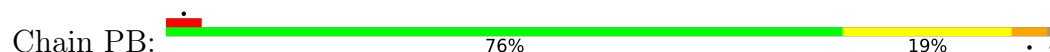
- Molecule 3: Carboxysome shell vertex protein CsoS4A



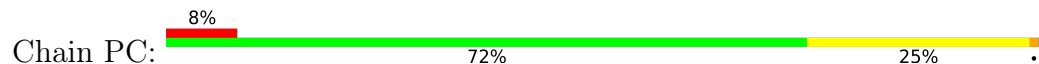
- Molecule 3: Carboxysome shell vertex protein CsoS4A



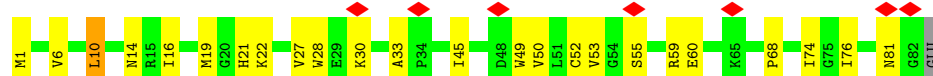
- Molecule 3: Carboxysome shell vertex protein CsoS4A



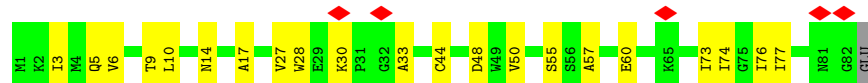
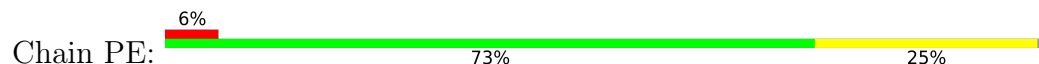
- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A



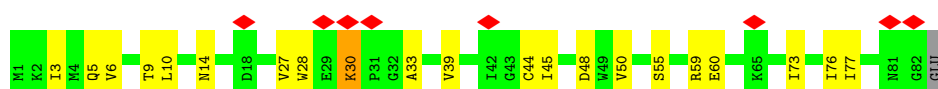
● Molecule 3: Carboxysome shell vertex protein CsoS4A

Chain PG:  6% 76% 20% ..



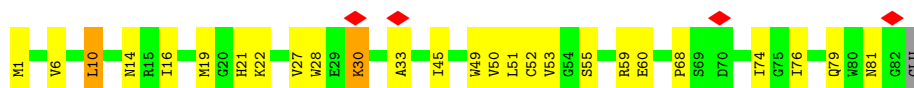
● Molecule 3: Carboxysome shell vertex protein CsoS4A

Chain PH:  10% 73% 24% ..



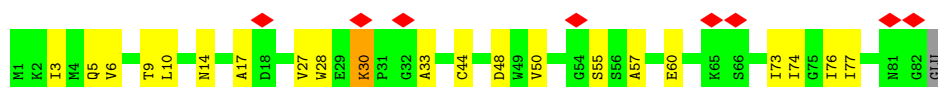
● Molecule 3: Carboxysome shell vertex protein CsoS4A

Chain PK:  5% 67% 29% ..



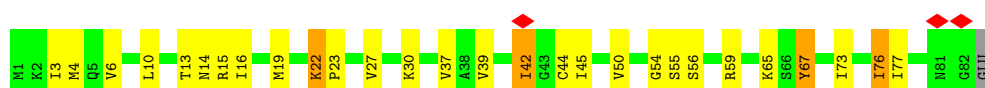
● Molecule 3: Carboxysome shell vertex protein CsoS4A

Chain PJ:  10% 73% 24% ..



● Molecule 3: Carboxysome shell vertex protein CsoS4A

Chain PN:  1% 65% 29% 5% .



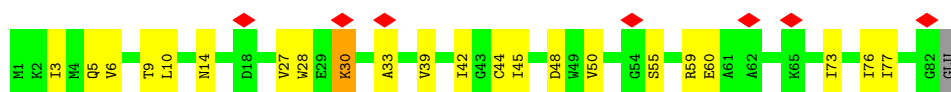
● Molecule 3: Carboxysome shell vertex protein CsoS4A

Chain PL:  13% 77% 20% ..

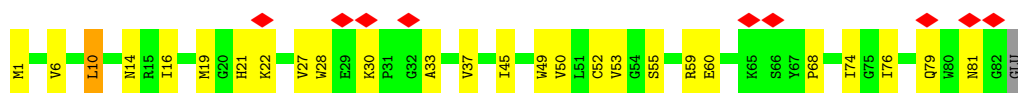


● Molecule 3: Carboxysome shell vertex protein CsoS4A

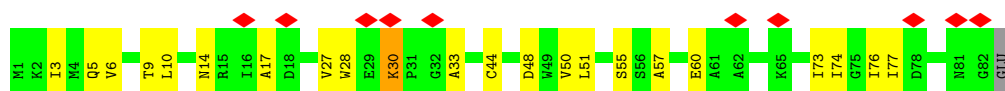
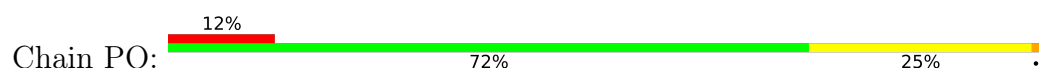
Chain PM:  8% 72% 25% ..



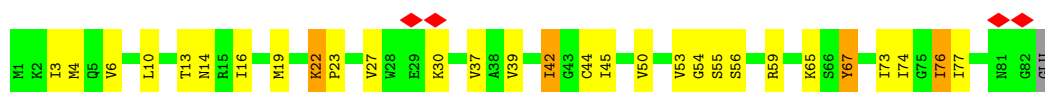
- Molecule 3: Carboxysome shell vertex protein CsoS4A



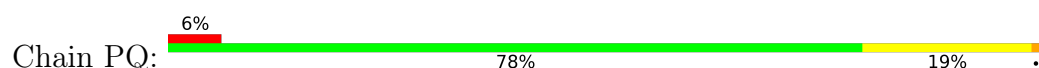
- Molecule 3: Carboxysome shell vertex protein CsoS4A



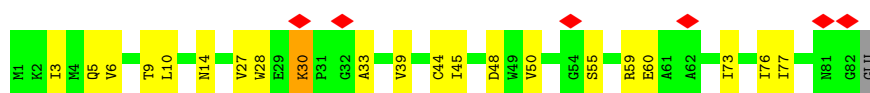
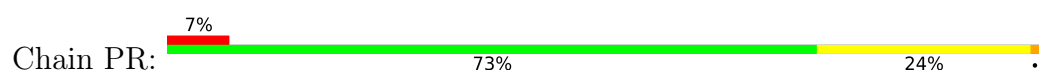
- Molecule 3: Carboxysome shell vertex protein CsoS4A



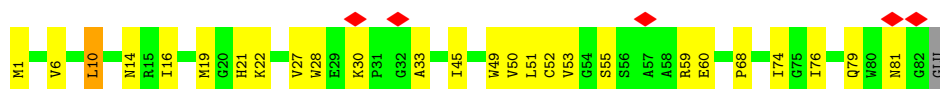
- Molecule 3: Carboxysome shell vertex protein CsoS4A



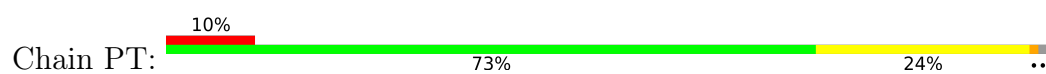
- Molecule 3: Carboxysome shell vertex protein CsoS4A



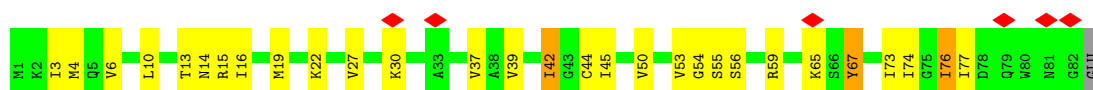
- Molecule 3: Carboxysome shell vertex protein CsoS4A



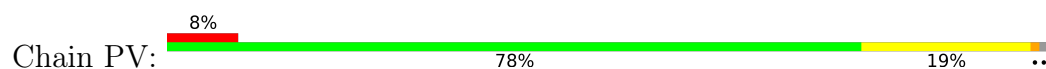
- Molecule 3: Carboxysome shell vertex protein CsoS4A



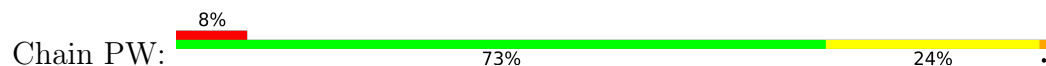
- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A



- Molecule 3: Carboxysome shell vertex protein CsoS4A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40177	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.813	Depositor
Minimum map value	-0.956	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.3	Depositor
Map size ($\text{\AA}$)	530.0, 530.0, 530.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A0	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	A1	1.84	3/662 (0.5%)	1.38	9/897 (1.0%)
1	A2	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	A3	1.70	3/662 (0.5%)	1.37	5/897 (0.6%)
1	A4	1.80	5/662 (0.8%)	1.39	8/897 (0.9%)
1	A5	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	A6	1.84	3/662 (0.5%)	1.38	9/897 (1.0%)
1	A7	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	A8	1.70	3/662 (0.5%)	1.37	5/897 (0.6%)
1	A9	1.80	5/662 (0.8%)	1.39	8/897 (0.9%)
1	AA	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	AB	1.69	2/662 (0.3%)	1.37	7/897 (0.8%)
1	AC	1.80	5/662 (0.8%)	1.40	8/897 (0.9%)
1	AD	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	AE	1.84	4/662 (0.6%)	1.38	9/897 (1.0%)
1	AF	1.82	3/662 (0.5%)	1.30	8/897 (0.9%)
1	AG	1.70	3/662 (0.5%)	1.37	5/897 (0.6%)
1	AH	1.80	5/662 (0.8%)	1.39	8/897 (0.9%)
1	AI	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	AJ	1.84	2/662 (0.3%)	1.38	9/897 (1.0%)
1	AK	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	AL	1.70	3/662 (0.5%)	1.37	5/897 (0.6%)
1	AM	1.80	5/662 (0.8%)	1.39	8/897 (0.9%)
1	AN	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	AO	1.84	3/662 (0.5%)	1.38	9/897 (1.0%)
1	AP	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	AQ	1.69	3/662 (0.5%)	1.37	7/897 (0.8%)
1	AR	1.80	5/662 (0.8%)	1.39	8/897 (0.9%)
1	AS	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	AT	1.84	4/662 (0.6%)	1.38	9/897 (1.0%)
1	AU	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	AV	1.70	2/662 (0.3%)	1.37	5/897 (0.6%)
1	AW	1.80	5/662 (0.8%)	1.40	8/897 (0.9%)
1	AX	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Aa	1.84	4/662 (0.6%)	1.38	9/897 (1.0%)
1	Ab	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	Ac	1.70	2/662 (0.3%)	1.37	5/897 (0.6%)
1	Ad	1.80	5/662 (0.8%)	1.39	8/897 (0.9%)
1	Ae	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	Af	1.84	3/662 (0.5%)	1.38	9/897 (1.0%)
1	Ag	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	Ah	1.69	3/662 (0.5%)	1.37	7/897 (0.8%)
1	Ai	1.80	5/662 (0.8%)	1.40	8/897 (0.9%)
1	Aj	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	Ak	1.84	4/662 (0.6%)	1.38	9/897 (1.0%)
1	Al	1.82	2/662 (0.3%)	1.30	9/897 (1.0%)
1	Am	1.70	3/662 (0.5%)	1.37	5/897 (0.6%)
1	An	1.80	5/662 (0.8%)	1.40	8/897 (0.9%)
1	Ao	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	Ap	1.84	4/662 (0.6%)	1.38	9/897 (1.0%)
1	Aq	1.82	2/662 (0.3%)	1.30	9/897 (1.0%)
1	Ar	1.70	3/662 (0.5%)	1.37	5/897 (0.6%)
1	As	1.80	5/662 (0.8%)	1.39	8/897 (0.9%)
1	At	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	Au	1.84	4/662 (0.6%)	1.38	9/897 (1.0%)
1	Av	1.82	3/662 (0.5%)	1.30	9/897 (1.0%)
1	Aw	1.69	3/662 (0.5%)	1.37	5/897 (0.6%)
1	Ax	1.80	5/662 (0.8%)	1.39	8/897 (0.9%)
1	Ay	1.85	6/662 (0.9%)	1.41	13/897 (1.4%)
1	Az	1.84	3/662 (0.5%)	1.38	9/897 (1.0%)
1	B0	1.74	2/662 (0.3%)	1.37	11/897 (1.2%)
1	B1	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	B2	1.81	3/662 (0.5%)	1.32	6/897 (0.7%)
1	B3	1.82	3/662 (0.5%)	1.42	12/897 (1.3%)
1	B4	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	B5	1.74	2/662 (0.3%)	1.37	11/897 (1.2%)
1	B6	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	B7	1.81	4/662 (0.6%)	1.33	6/897 (0.7%)
1	B8	1.82	3/662 (0.5%)	1.42	12/897 (1.3%)
1	B9	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	BA	1.81	4/662 (0.6%)	1.32	6/897 (0.7%)
1	BB	1.82	3/662 (0.5%)	1.43	12/897 (1.3%)
1	BC	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	BD	1.74	2/662 (0.3%)	1.36	11/897 (1.2%)
1	BE	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	BF	1.81	4/662 (0.6%)	1.33	6/897 (0.7%)
1	BG	1.82	3/662 (0.5%)	1.42	12/897 (1.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BH	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	BI	1.74	3/662 (0.5%)	1.37	11/897 (1.2%)
1	BJ	1.73	1/662 (0.2%)	1.32	8/897 (0.9%)
1	BK	1.81	3/662 (0.5%)	1.32	6/897 (0.7%)
1	BL	1.82	3/662 (0.5%)	1.43	12/897 (1.3%)
1	BM	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	BN	1.74	3/662 (0.5%)	1.37	11/897 (1.2%)
1	BO	1.74	1/662 (0.2%)	1.32	9/897 (1.0%)
1	BP	1.81	4/662 (0.6%)	1.33	5/897 (0.6%)
1	BQ	1.82	3/662 (0.5%)	1.42	12/897 (1.3%)
1	BR	1.79	7/662 (1.1%)	1.35	5/897 (0.6%)
1	BS	1.74	2/662 (0.3%)	1.36	11/897 (1.2%)
1	BT	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	BU	1.81	4/662 (0.6%)	1.33	6/897 (0.7%)
1	BV	1.82	3/662 (0.5%)	1.42	12/897 (1.3%)
1	BW	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	BX	1.74	2/662 (0.3%)	1.37	11/897 (1.2%)
1	Ba	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	Bb	1.81	4/662 (0.6%)	1.33	6/897 (0.7%)
1	Bc	1.82	3/662 (0.5%)	1.42	12/897 (1.3%)
1	Bd	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	Be	1.74	2/662 (0.3%)	1.37	11/897 (1.2%)
1	Bf	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	Bg	1.81	3/662 (0.5%)	1.33	6/897 (0.7%)
1	Bh	1.82	3/662 (0.5%)	1.42	12/897 (1.3%)
1	Bi	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	Bj	1.74	3/662 (0.5%)	1.37	11/897 (1.2%)
1	Bk	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	Bl	1.81	3/662 (0.5%)	1.33	6/897 (0.7%)
1	Bm	1.83	3/662 (0.5%)	1.43	12/897 (1.3%)
1	Bn	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	Bo	1.74	2/662 (0.3%)	1.37	11/897 (1.2%)
1	Bp	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	Bq	1.81	3/662 (0.5%)	1.32	6/897 (0.7%)
1	Br	1.82	3/662 (0.5%)	1.42	12/897 (1.3%)
1	Bs	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	Bt	1.74	2/662 (0.3%)	1.37	11/897 (1.2%)
1	Bu	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)
1	Bv	1.81	4/662 (0.6%)	1.33	6/897 (0.7%)
1	Bw	1.82	4/662 (0.6%)	1.42	12/897 (1.3%)
1	Bx	1.80	7/662 (1.1%)	1.35	5/897 (0.6%)
1	By	1.74	2/662 (0.3%)	1.37	11/897 (1.2%)
1	Bz	1.73	1/662 (0.2%)	1.32	9/897 (1.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	C0	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	C1	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	C2	1.80	5/662 (0.8%)	1.40	10/897 (1.1%)
1	C3	1.83	5/662 (0.8%)	1.43	10/897 (1.1%)
1	C4	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	C5	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	C6	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	C7	1.80	5/662 (0.8%)	1.40	10/897 (1.1%)
1	C8	1.83	6/662 (0.9%)	1.43	10/897 (1.1%)
1	C9	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	CA	1.80	5/662 (0.8%)	1.39	10/897 (1.1%)
1	CB	1.83	6/662 (0.9%)	1.43	10/897 (1.1%)
1	CC	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	CD	1.80	1/662 (0.2%)	1.31	4/897 (0.4%)
1	CE	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	CF	1.80	5/662 (0.8%)	1.40	10/897 (1.1%)
1	CG	1.83	6/662 (0.9%)	1.43	10/897 (1.1%)
1	CH	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	CI	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	CJ	1.83	3/662 (0.5%)	1.35	7/897 (0.8%)
1	CK	1.80	5/662 (0.8%)	1.40	10/897 (1.1%)
1	CL	1.83	5/662 (0.8%)	1.43	10/897 (1.1%)
1	CM	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	CN	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	CO	1.83	3/662 (0.5%)	1.35	7/897 (0.8%)
1	CP	1.80	5/662 (0.8%)	1.39	10/897 (1.1%)
1	CQ	1.83	6/662 (0.9%)	1.43	10/897 (1.1%)
1	CR	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	CS	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	CT	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	CU	1.80	5/662 (0.8%)	1.40	10/897 (1.1%)
1	CV	1.83	5/662 (0.8%)	1.43	10/897 (1.1%)
1	CW	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	CX	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	Ca	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	Cb	1.80	5/662 (0.8%)	1.40	10/897 (1.1%)
1	Cc	1.83	5/662 (0.8%)	1.43	10/897 (1.1%)
1	Cd	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	Ce	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	Cf	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	Cg	1.80	5/662 (0.8%)	1.40	10/897 (1.1%)
1	Ch	1.83	6/662 (0.9%)	1.43	10/897 (1.1%)
1	Ci	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Cj	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	Ck	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	Cl	1.80	5/662 (0.8%)	1.39	10/897 (1.1%)
1	Cm	1.83	6/662 (0.9%)	1.43	10/897 (1.1%)
1	Cn	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	Co	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	Cp	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	Cq	1.80	5/662 (0.8%)	1.40	10/897 (1.1%)
1	Cr	1.83	6/662 (0.9%)	1.43	10/897 (1.1%)
1	Cs	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	Ct	1.80	2/662 (0.3%)	1.31	4/897 (0.4%)
1	Cu	1.83	3/662 (0.5%)	1.35	7/897 (0.8%)
1	Cv	1.80	5/662 (0.8%)	1.39	10/897 (1.1%)
1	Cw	1.83	6/662 (0.9%)	1.43	10/897 (1.1%)
1	Cx	1.80	4/662 (0.6%)	1.32	10/897 (1.1%)
1	Cy	1.80	1/662 (0.2%)	1.31	4/897 (0.4%)
1	Cz	1.83	3/662 (0.5%)	1.34	7/897 (0.8%)
1	D0	1.81	6/662 (0.9%)	1.40	10/897 (1.1%)
1	D1	1.74	2/662 (0.3%)	1.29	8/897 (0.9%)
1	D2	1.87	8/662 (1.2%)	1.43	15/897 (1.7%)
1	D3	1.81	5/662 (0.8%)	1.39	10/897 (1.1%)
1	D4	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	D5	1.81	7/662 (1.1%)	1.40	10/897 (1.1%)
1	D6	1.75	2/662 (0.3%)	1.29	8/897 (0.9%)
1	D7	1.87	8/662 (1.2%)	1.44	14/897 (1.6%)
1	D8	1.81	5/662 (0.8%)	1.39	11/897 (1.2%)
1	D9	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	DA	1.87	8/662 (1.2%)	1.44	14/897 (1.6%)
1	DB	1.81	3/662 (0.5%)	1.39	11/897 (1.2%)
1	DC	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	DD	1.82	7/662 (1.1%)	1.39	10/897 (1.1%)
1	DE	1.75	2/662 (0.3%)	1.29	8/897 (0.9%)
1	DF	1.87	8/662 (1.2%)	1.44	14/897 (1.6%)
1	DG	1.81	5/662 (0.8%)	1.39	10/897 (1.1%)
1	DH	1.80	5/662 (0.8%)	1.35	8/897 (0.9%)
1	DI	1.81	7/662 (1.1%)	1.40	10/897 (1.1%)
1	DJ	1.75	1/662 (0.2%)	1.29	8/897 (0.9%)
1	DK	1.87	8/662 (1.2%)	1.44	15/897 (1.7%)
1	DL	1.81	5/662 (0.8%)	1.39	10/897 (1.1%)
1	DM	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	DN	1.81	6/662 (0.9%)	1.40	10/897 (1.1%)
1	DO	1.75	2/662 (0.3%)	1.29	9/897 (1.0%)
1	DP	1.87	8/662 (1.2%)	1.44	14/897 (1.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	DQ	1.81	5/662 (0.8%)	1.39	11/897 (1.2%)
1	DR	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	DS	1.81	6/662 (0.9%)	1.39	10/897 (1.1%)
1	DT	1.75	1/662 (0.2%)	1.29	8/897 (0.9%)
1	DU	1.87	8/662 (1.2%)	1.44	15/897 (1.7%)
1	DV	1.81	5/662 (0.8%)	1.39	10/897 (1.1%)
1	DW	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	DX	1.81	7/662 (1.1%)	1.39	11/897 (1.2%)
1	Da	1.75	1/662 (0.2%)	1.29	8/897 (0.9%)
1	Db	1.87	8/662 (1.2%)	1.44	15/897 (1.7%)
1	Dc	1.81	5/662 (0.8%)	1.39	10/897 (1.1%)
1	Dd	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	De	1.81	7/662 (1.1%)	1.39	11/897 (1.2%)
1	Df	1.74	1/662 (0.2%)	1.29	8/897 (0.9%)
1	Dg	1.87	8/662 (1.2%)	1.43	15/897 (1.7%)
1	Dh	1.81	5/662 (0.8%)	1.39	10/897 (1.1%)
1	Di	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	Dj	1.81	7/662 (1.1%)	1.39	10/897 (1.1%)
1	Dk	1.75	2/662 (0.3%)	1.29	8/897 (0.9%)
1	Dl	1.87	8/662 (1.2%)	1.44	14/897 (1.6%)
1	Dm	1.81	4/662 (0.6%)	1.39	11/897 (1.2%)
1	Dn	1.80	5/662 (0.8%)	1.35	8/897 (0.9%)
1	Do	1.82	6/662 (0.9%)	1.40	10/897 (1.1%)
1	Dp	1.75	2/662 (0.3%)	1.29	8/897 (0.9%)
1	Dq	1.86	7/662 (1.1%)	1.44	15/897 (1.7%)
1	Dr	1.81	4/662 (0.6%)	1.39	10/897 (1.1%)
1	Ds	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	Dt	1.81	7/662 (1.1%)	1.40	11/897 (1.2%)
1	Du	1.75	1/662 (0.2%)	1.29	9/897 (1.0%)
1	Dv	1.87	8/662 (1.2%)	1.43	15/897 (1.7%)
1	Dw	1.81	4/662 (0.6%)	1.38	10/897 (1.1%)
1	Dx	1.79	5/662 (0.8%)	1.35	8/897 (0.9%)
1	Dy	1.81	6/662 (0.9%)	1.39	10/897 (1.1%)
1	Dz	1.75	2/662 (0.3%)	1.29	9/897 (1.0%)
1	E0	1.80	3/662 (0.5%)	1.35	10/897 (1.1%)
1	E1	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	E2	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	E3	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	E4	1.82	7/662 (1.1%)	1.29	8/897 (0.9%)
1	E5	1.80	3/662 (0.5%)	1.35	10/897 (1.1%)
1	E6	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	E7	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	E8	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	E9	1.82	8/662 (1.2%)	1.29	8/897 (0.9%)
1	EA	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	EB	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	EC	1.82	7/662 (1.1%)	1.29	9/897 (1.0%)
1	ED	1.80	3/662 (0.5%)	1.35	10/897 (1.1%)
1	EE	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	EF	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	EG	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	EH	1.82	8/662 (1.2%)	1.29	9/897 (1.0%)
1	EI	1.80	4/662 (0.6%)	1.35	10/897 (1.1%)
1	EJ	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	EK	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	EL	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	EM	1.82	6/662 (0.9%)	1.29	8/897 (0.9%)
1	EN	1.80	3/662 (0.5%)	1.35	10/897 (1.1%)
1	EO	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	EP	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	EQ	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	ER	1.82	7/662 (1.1%)	1.29	9/897 (1.0%)
1	ES	1.80	3/662 (0.5%)	1.35	10/897 (1.1%)
1	ET	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	EU	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	EV	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	EW	1.82	8/662 (1.2%)	1.29	9/897 (1.0%)
1	EX	1.80	4/662 (0.6%)	1.35	10/897 (1.1%)
1	Ea	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	Eb	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	Ec	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	Ed	1.82	8/662 (1.2%)	1.29	9/897 (1.0%)
1	Ee	1.80	4/662 (0.6%)	1.35	10/897 (1.1%)
1	Ef	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	Eg	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	Eh	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	Ei	1.82	7/662 (1.1%)	1.29	8/897 (0.9%)
1	Ej	1.80	3/662 (0.5%)	1.35	10/897 (1.1%)
1	Ek	1.77	3/662 (0.5%)	1.36	9/897 (1.0%)
1	El	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	Em	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	En	1.82	7/662 (1.1%)	1.29	8/897 (0.9%)
1	Eo	1.80	3/662 (0.5%)	1.35	10/897 (1.1%)
1	Ep	1.78	3/662 (0.5%)	1.36	9/897 (1.0%)
1	Eq	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	Er	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Es	1.82	8/662 (1.2%)	1.29	9/897 (1.0%)
1	Et	1.80	4/662 (0.6%)	1.35	10/897 (1.1%)
1	Eu	1.78	3/662 (0.5%)	1.36	9/897 (1.0%)
1	Ev	1.77	2/662 (0.3%)	1.29	8/897 (0.9%)
1	Ew	1.74	3/662 (0.5%)	1.32	7/897 (0.8%)
1	Ex	1.82	7/662 (1.1%)	1.29	9/897 (1.0%)
1	Ey	1.80	3/662 (0.5%)	1.35	10/897 (1.1%)
1	Ez	1.78	3/662 (0.5%)	1.35	9/897 (1.0%)
1	F0	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	F1	1.77	2/662 (0.3%)	1.32	8/897 (0.9%)
1	F2	1.77	3/662 (0.5%)	1.41	10/897 (1.1%)
1	F3	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	F4	1.82	3/662 (0.5%)	1.42	11/897 (1.2%)
1	F5	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	F6	1.77	2/662 (0.3%)	1.32	8/897 (0.9%)
1	F7	1.77	3/662 (0.5%)	1.41	10/897 (1.1%)
1	F8	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	F9	1.81	3/662 (0.5%)	1.42	11/897 (1.2%)
1	FA	1.77	2/662 (0.3%)	1.41	10/897 (1.1%)
1	FB	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	FC	1.82	3/662 (0.5%)	1.42	11/897 (1.2%)
1	FD	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	FE	1.77	2/662 (0.3%)	1.32	8/897 (0.9%)
1	FF	1.78	3/662 (0.5%)	1.41	10/897 (1.1%)
1	FG	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	FH	1.81	2/662 (0.3%)	1.43	11/897 (1.2%)
1	FI	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	FJ	1.77	1/662 (0.2%)	1.32	8/897 (0.9%)
1	FK	1.77	3/662 (0.5%)	1.41	10/897 (1.1%)
1	FL	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	FM	1.82	3/662 (0.5%)	1.42	11/897 (1.2%)
1	FN	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	FO	1.77	1/662 (0.2%)	1.32	8/897 (0.9%)
1	FP	1.77	3/662 (0.5%)	1.41	10/897 (1.1%)
1	FQ	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	FR	1.81	3/662 (0.5%)	1.42	11/897 (1.2%)
1	FS	1.78	2/662 (0.3%)	1.34	9/897 (1.0%)
1	FT	1.77	2/662 (0.3%)	1.32	8/897 (0.9%)
1	FU	1.78	3/662 (0.5%)	1.41	10/897 (1.1%)
1	FV	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	FW	1.81	2/662 (0.3%)	1.43	11/897 (1.2%)
1	FX	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	Fa	1.77	2/662 (0.3%)	1.32	8/897 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Fb	1.78	4/662 (0.6%)	1.41	10/897 (1.1%)
1	Fc	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	Fd	1.81	2/662 (0.3%)	1.43	11/897 (1.2%)
1	Fe	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	Ff	1.77	1/662 (0.2%)	1.32	8/897 (0.9%)
1	Fg	1.77	3/662 (0.5%)	1.41	10/897 (1.1%)
1	Fh	1.89	7/662 (1.1%)	1.43	7/897 (0.8%)
1	Fi	1.82	2/662 (0.3%)	1.42	11/897 (1.2%)
1	Fj	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	Fk	1.77	2/662 (0.3%)	1.32	8/897 (0.9%)
1	Fl	1.77	2/662 (0.3%)	1.41	10/897 (1.1%)
1	Fm	1.88	7/662 (1.1%)	1.43	7/897 (0.8%)
1	Fn	1.82	2/662 (0.3%)	1.42	11/897 (1.2%)
1	Fo	1.78	3/662 (0.5%)	1.34	9/897 (1.0%)
1	Fp	1.77	1/662 (0.2%)	1.32	8/897 (0.9%)
1	Fq	1.78	3/662 (0.5%)	1.41	10/897 (1.1%)
1	Fr	1.89	7/662 (1.1%)	1.43	7/897 (0.8%)
1	Fs	1.81	2/662 (0.3%)	1.42	11/897 (1.2%)
1	Ft	1.78	2/662 (0.3%)	1.34	9/897 (1.0%)
1	Fu	1.77	2/662 (0.3%)	1.32	8/897 (0.9%)
1	Fv	1.78	3/662 (0.5%)	1.41	10/897 (1.1%)
1	Fw	1.89	7/662 (1.1%)	1.43	7/897 (0.8%)
1	Fx	1.81	2/662 (0.3%)	1.43	11/897 (1.2%)
1	Fy	1.78	3/662 (0.5%)	1.33	9/897 (1.0%)
1	Fz	1.77	3/662 (0.5%)	1.32	8/897 (0.9%)
1	G0	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	G1	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	G2	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	G3	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	G4	1.86	5/662 (0.8%)	1.40	8/897 (0.9%)
1	G5	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	G6	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	G7	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	G8	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	G9	1.86	5/662 (0.8%)	1.40	10/897 (1.1%)
1	GA	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	GB	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	GC	1.86	5/662 (0.8%)	1.40	10/897 (1.1%)
1	GD	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	GE	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	GF	1.80	3/662 (0.5%)	1.37	10/897 (1.1%)
1	GG	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	GH	1.85	5/662 (0.8%)	1.40	10/897 (1.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GI	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	GJ	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	GK	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	GL	1.81	2/662 (0.3%)	1.34	10/897 (1.1%)
1	GM	1.85	5/662 (0.8%)	1.40	10/897 (1.1%)
1	GN	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	GO	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	GP	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	GQ	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	GR	1.86	5/662 (0.8%)	1.40	8/897 (0.9%)
1	GS	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	GT	1.75	4/662 (0.6%)	1.32	11/897 (1.2%)
1	GU	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	GV	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	GW	1.86	5/662 (0.8%)	1.40	10/897 (1.1%)
1	GX	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	Ga	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	Gb	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	Gc	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	Gd	1.86	5/662 (0.8%)	1.40	8/897 (0.9%)
1	Ge	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	Gf	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	Gg	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	Gh	1.81	2/662 (0.3%)	1.34	10/897 (1.1%)
1	Gi	1.85	5/662 (0.8%)	1.40	10/897 (1.1%)
1	Gj	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	Gk	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	Gl	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	Gm	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	Gn	1.86	5/662 (0.8%)	1.40	10/897 (1.1%)
1	Go	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	Gp	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	Gq	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	Gr	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	Gs	1.86	5/662 (0.8%)	1.40	8/897 (0.9%)
1	Gt	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	Gu	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	Gv	1.79	3/662 (0.5%)	1.37	10/897 (1.1%)
1	Gw	1.82	2/662 (0.3%)	1.34	10/897 (1.1%)
1	Gx	1.86	5/662 (0.8%)	1.39	8/897 (0.9%)
1	Gy	1.83	2/662 (0.3%)	1.33	7/897 (0.8%)
1	Gz	1.75	4/662 (0.6%)	1.33	11/897 (1.2%)
1	H0	1.73	0/662	1.36	11/897 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	H1	1.82	4/662 (0.6%)	1.23	8/897 (0.9%)
1	H2	1.75	3/662 (0.5%)	1.32	8/897 (0.9%)
1	H3	1.76	2/662 (0.3%)	1.39	11/897 (1.2%)
1	H4	1.76	4/662 (0.6%)	1.32	8/897 (0.9%)
1	H5	1.73	0/662	1.36	11/897 (1.2%)
1	H6	1.83	4/662 (0.6%)	1.21	7/897 (0.8%)
1	H7	1.75	3/662 (0.5%)	1.32	8/897 (0.9%)
1	H8	1.76	3/662 (0.5%)	1.39	11/897 (1.2%)
1	H9	1.76	5/662 (0.8%)	1.32	8/897 (0.9%)
1	HA	1.75	3/662 (0.5%)	1.32	8/897 (0.9%)
1	HB	1.76	3/662 (0.5%)	1.39	11/897 (1.2%)
1	HC	1.76	4/662 (0.6%)	1.32	8/897 (0.9%)
1	HD	1.74	0/662	1.36	11/897 (1.2%)
1	HE	1.83	5/662 (0.8%)	1.24	8/897 (0.9%)
1	HF	1.75	2/662 (0.3%)	1.32	8/897 (0.9%)
1	HG	1.76	3/662 (0.5%)	1.39	11/897 (1.2%)
1	HH	1.75	3/662 (0.5%)	1.32	8/897 (0.9%)
1	HI	1.73	0/662	1.36	11/897 (1.2%)
1	HJ	1.83	4/662 (0.6%)	1.23	8/897 (0.9%)
1	HK	1.75	3/662 (0.5%)	1.32	8/897 (0.9%)
1	HL	1.76	3/662 (0.5%)	1.39	11/897 (1.2%)
1	HM	1.76	4/662 (0.6%)	1.32	8/897 (0.9%)
1	HN	1.74	0/662	1.36	11/897 (1.2%)
1	HO	1.83	4/662 (0.6%)	1.22	7/897 (0.8%)
1	HP	1.75	3/662 (0.5%)	1.32	8/897 (0.9%)
1	HQ	1.76	3/662 (0.5%)	1.39	11/897 (1.2%)
1	HR	1.76	5/662 (0.8%)	1.32	8/897 (0.9%)
1	HS	1.74	0/662	1.36	11/897 (1.2%)
1	HT	1.83	4/662 (0.6%)	1.23	8/897 (0.9%)
1	HU	1.75	2/662 (0.3%)	1.32	8/897 (0.9%)
1	HV	1.76	2/662 (0.3%)	1.39	11/897 (1.2%)
1	HW	1.76	3/662 (0.5%)	1.32	8/897 (0.9%)
1	HX	1.73	0/662	1.35	11/897 (1.2%)
1	Ha	1.83	4/662 (0.6%)	1.23	8/897 (0.9%)
1	Hb	1.75	2/662 (0.3%)	1.32	8/897 (0.9%)
1	Hc	1.76	2/662 (0.3%)	1.39	11/897 (1.2%)
1	Hd	1.76	3/662 (0.5%)	1.32	8/897 (0.9%)
1	He	1.73	0/662	1.36	11/897 (1.2%)
1	Hf	1.83	4/662 (0.6%)	1.23	8/897 (0.9%)
1	Hg	1.75	3/662 (0.5%)	1.32	8/897 (0.9%)
1	Hh	1.76	2/662 (0.3%)	1.39	11/897 (1.2%)
1	Hi	1.76	4/662 (0.6%)	1.32	8/897 (0.9%)
1	Hj	1.74	0/662	1.36	11/897 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Hk	1.83	4/662 (0.6%)	1.23	8/897 (0.9%)
1	Hl	1.75	3/662 (0.5%)	1.32	8/897 (0.9%)
1	Hm	1.76	2/662 (0.3%)	1.39	11/897 (1.2%)
1	Hn	1.75	4/662 (0.6%)	1.32	8/897 (0.9%)
1	Ho	1.73	0/662	1.36	11/897 (1.2%)
1	Hp	1.83	4/662 (0.6%)	1.23	8/897 (0.9%)
1	Hq	1.75	2/662 (0.3%)	1.32	8/897 (0.9%)
1	Hr	1.76	3/662 (0.5%)	1.39	11/897 (1.2%)
1	Hs	1.76	3/662 (0.5%)	1.32	8/897 (0.9%)
1	Ht	1.73	0/662	1.35	11/897 (1.2%)
1	Hu	1.83	4/662 (0.6%)	1.22	7/897 (0.8%)
1	Hv	1.75	2/662 (0.3%)	1.32	8/897 (0.9%)
1	Hw	1.76	3/662 (0.5%)	1.39	11/897 (1.2%)
1	Hx	1.76	4/662 (0.6%)	1.32	8/897 (0.9%)
1	Hy	1.73	0/662	1.36	11/897 (1.2%)
1	Hz	1.83	4/662 (0.6%)	1.23	8/897 (0.9%)
2	X0	1.38	0/873	1.38	15/1176 (1.3%)
2	X1	1.38	2/873 (0.2%)	1.33	9/1176 (0.8%)
2	X2	1.41	1/873 (0.1%)	1.39	11/1176 (0.9%)
2	X3	1.37	2/873 (0.2%)	1.61	13/1176 (1.1%)
2	X4	1.42	2/873 (0.2%)	1.41	15/1176 (1.3%)
2	X5	1.38	0/873	1.38	15/1176 (1.3%)
2	X6	1.38	2/873 (0.2%)	1.33	9/1176 (0.8%)
2	X7	1.41	1/873 (0.1%)	1.39	9/1176 (0.8%)
2	X8	1.37	2/873 (0.2%)	1.61	13/1176 (1.1%)
2	X9	1.42	2/873 (0.2%)	1.41	16/1176 (1.4%)
2	XA	1.41	1/873 (0.1%)	1.39	11/1176 (0.9%)
2	XB	1.38	2/873 (0.2%)	1.61	13/1176 (1.1%)
2	XC	1.42	2/873 (0.2%)	1.41	15/1176 (1.3%)
2	XD	1.38	0/873	1.38	15/1176 (1.3%)
2	XE	1.38	2/873 (0.2%)	1.32	9/1176 (0.8%)
2	XF	1.41	1/873 (0.1%)	1.39	11/1176 (0.9%)
2	XG	1.36	2/873 (0.2%)	1.61	13/1176 (1.1%)
2	XH	1.42	2/873 (0.2%)	1.41	17/1176 (1.4%)
2	XI	1.38	0/873	1.38	14/1176 (1.2%)
2	XJ	1.38	2/873 (0.2%)	1.32	9/1176 (0.8%)
2	XK	1.41	1/873 (0.1%)	1.39	11/1176 (0.9%)
2	XL	1.37	2/873 (0.2%)	1.61	13/1176 (1.1%)
2	XM	1.42	2/873 (0.2%)	1.41	15/1176 (1.3%)
2	XN	1.38	0/873	1.38	15/1176 (1.3%)
2	XO	1.38	2/873 (0.2%)	1.32	9/1176 (0.8%)
2	XP	1.41	1/873 (0.1%)	1.39	9/1176 (0.8%)
2	XQ	1.37	2/873 (0.2%)	1.61	13/1176 (1.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	XR	1.42	2/873 (0.2%)	1.41	17/1176 (1.4%)
2	XS	1.38	0/873	1.38	15/1176 (1.3%)
2	XT	1.38	2/873 (0.2%)	1.33	9/1176 (0.8%)
2	XU	1.41	1/873 (0.1%)	1.39	9/1176 (0.8%)
2	XV	1.37	2/873 (0.2%)	1.62	13/1176 (1.1%)
2	XW	1.42	2/873 (0.2%)	1.41	17/1176 (1.4%)
2	XX	1.38	0/873	1.38	14/1176 (1.2%)
2	Xa	1.38	2/873 (0.2%)	1.32	9/1176 (0.8%)
2	Xb	1.41	1/873 (0.1%)	1.39	9/1176 (0.8%)
2	Xc	1.37	2/873 (0.2%)	1.61	13/1176 (1.1%)
2	Xd	1.42	2/873 (0.2%)	1.41	16/1176 (1.4%)
2	Xe	1.38	0/873	1.38	14/1176 (1.2%)
2	Xf	1.38	2/873 (0.2%)	1.33	9/1176 (0.8%)
2	Xg	1.41	1/873 (0.1%)	1.39	11/1176 (0.9%)
2	Xh	1.37	2/873 (0.2%)	1.61	13/1176 (1.1%)
2	Xi	1.42	2/873 (0.2%)	1.41	15/1176 (1.3%)
2	Xj	1.38	0/873	1.38	14/1176 (1.2%)
2	Xk	1.38	2/873 (0.2%)	1.32	9/1176 (0.8%)
2	Xl	1.41	1/873 (0.1%)	1.39	9/1176 (0.8%)
2	Xm	1.37	2/873 (0.2%)	1.61	13/1176 (1.1%)
2	Xn	1.42	2/873 (0.2%)	1.41	17/1176 (1.4%)
2	Xo	1.38	0/873	1.38	14/1176 (1.2%)
2	Xp	1.38	2/873 (0.2%)	1.33	9/1176 (0.8%)
2	Xq	1.41	1/873 (0.1%)	1.39	9/1176 (0.8%)
2	Xr	1.38	2/873 (0.2%)	1.62	13/1176 (1.1%)
2	Xs	1.42	2/873 (0.2%)	1.41	16/1176 (1.4%)
2	Xt	1.38	0/873	1.38	14/1176 (1.2%)
2	Xu	1.38	2/873 (0.2%)	1.32	9/1176 (0.8%)
2	Xv	1.41	1/873 (0.1%)	1.39	11/1176 (0.9%)
2	Xw	1.38	2/873 (0.2%)	1.62	13/1176 (1.1%)
2	Xx	1.42	2/873 (0.2%)	1.41	16/1176 (1.4%)
2	Xy	1.38	0/873	1.38	14/1176 (1.2%)
2	Xz	1.38	2/873 (0.2%)	1.33	9/1176 (0.8%)
3	P0	1.29	0/624	1.43	11/848 (1.3%)
3	P1	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	P2	1.28	1/624 (0.2%)	1.32	9/848 (1.1%)
3	P3	1.26	0/624	1.35	5/848 (0.6%)
3	P4	1.20	0/624	1.35	5/848 (0.6%)
3	P5	1.29	0/624	1.43	11/848 (1.3%)
3	P6	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	P7	1.28	0/624	1.32	9/848 (1.1%)
3	P8	1.26	0/624	1.35	5/848 (0.6%)
3	P9	1.20	0/624	1.35	5/848 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	PA	1.28	0/624	1.32	9/848 (1.1%)
3	PB	1.26	0/624	1.35	5/848 (0.6%)
3	PC	1.20	0/624	1.35	5/848 (0.6%)
3	PD	1.30	0/624	1.43	11/848 (1.3%)
3	PE	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	PF	1.28	0/624	1.32	9/848 (1.1%)
3	PG	1.26	0/624	1.35	5/848 (0.6%)
3	PH	1.20	0/624	1.35	5/848 (0.6%)
3	PI	1.30	0/624	1.43	11/848 (1.3%)
3	PJ	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	PK	1.28	1/624 (0.2%)	1.32	9/848 (1.1%)
3	PL	1.26	0/624	1.35	5/848 (0.6%)
3	PM	1.20	0/624	1.35	5/848 (0.6%)
3	PN	1.29	0/624	1.42	11/848 (1.3%)
3	PO	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	PP	1.28	1/624 (0.2%)	1.32	9/848 (1.1%)
3	PQ	1.26	0/624	1.35	5/848 (0.6%)
3	PR	1.20	0/624	1.35	5/848 (0.6%)
3	PS	1.29	0/624	1.42	11/848 (1.3%)
3	PT	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	PU	1.28	1/624 (0.2%)	1.32	9/848 (1.1%)
3	PV	1.26	0/624	1.35	5/848 (0.6%)
3	PW	1.20	0/624	1.35	5/848 (0.6%)
3	PX	1.30	0/624	1.42	11/848 (1.3%)
3	Pa	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	Pb	1.28	0/624	1.32	9/848 (1.1%)
3	Pc	1.26	0/624	1.35	5/848 (0.6%)
3	Pd	1.20	0/624	1.35	5/848 (0.6%)
3	Pe	1.30	0/624	1.43	11/848 (1.3%)
3	Pf	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	Pg	1.28	0/624	1.32	9/848 (1.1%)
3	Ph	1.26	0/624	1.35	5/848 (0.6%)
3	Pi	1.20	0/624	1.35	5/848 (0.6%)
3	Pj	1.29	0/624	1.42	11/848 (1.3%)
3	Pk	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	Pl	1.28	0/624	1.31	9/848 (1.1%)
3	Pm	1.26	0/624	1.35	5/848 (0.6%)
3	Pn	1.20	0/624	1.35	5/848 (0.6%)
3	Po	1.29	0/624	1.43	11/848 (1.3%)
3	Pp	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	Pq	1.28	1/624 (0.2%)	1.32	9/848 (1.1%)
3	Pr	1.26	0/624	1.35	5/848 (0.6%)
3	Ps	1.20	0/624	1.35	5/848 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	Pt	1.30	0/624	1.42	11/848 (1.3%)
3	Pu	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
3	Pv	1.28	0/624	1.32	9/848 (1.1%)
3	Pw	1.26	0/624	1.35	5/848 (0.6%)
3	Px	1.20	0/624	1.35	5/848 (0.6%)
3	Py	1.29	0/624	1.43	11/848 (1.3%)
3	Pz	1.20	1/624 (0.2%)	1.33	5/848 (0.6%)
All	All	1.70	1862/407580 (0.5%)	1.37	5491/552000 (1.0%)

All (1862) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Bl	13	GLU	CA-C	-7.26	1.44	1.52
1	Bv	13	GLU	CA-C	-7.26	1.44	1.52
1	B7	13	GLU	CA-C	-7.26	1.44	1.52
1	BP	13	GLU	CA-C	-7.26	1.44	1.52
1	GW	24	ALA	CA-C	-7.25	1.43	1.52
1	B2	13	GLU	CA-C	-7.23	1.44	1.52
1	BK	13	GLU	CA-C	-7.23	1.44	1.52
1	BU	13	GLU	CA-C	-7.23	1.44	1.52
1	Bq	13	GLU	CA-C	-7.22	1.44	1.52
1	Bb	13	GLU	CA-C	-7.21	1.44	1.52
1	BF	13	GLU	CA-C	-7.21	1.44	1.52
1	DA	13	GLU	CA-C	-7.20	1.44	1.52
1	GH	24	ALA	CA-C	-7.20	1.43	1.52
1	D7	13	GLU	CA-C	-7.19	1.44	1.52
1	Gd	24	ALA	CA-C	-7.19	1.43	1.52
1	DP	13	GLU	CA-C	-7.19	1.44	1.52
1	BA	13	GLU	CA-C	-7.19	1.44	1.52
1	Bg	13	GLU	CA-C	-7.18	1.44	1.52
1	Dv	13	GLU	CA-C	-7.17	1.44	1.52
1	Gs	24	ALA	CA-C	-7.17	1.43	1.52
1	Dg	13	GLU	CA-C	-7.17	1.44	1.52
1	Dl	13	GLU	CA-C	-7.17	1.44	1.52
1	DF	13	GLU	CA-C	-7.17	1.44	1.52
1	Dq	13	GLU	CA-C	-7.16	1.44	1.52
1	HB	31	ALA	CA-C	-7.16	1.44	1.52
1	BC	31	ALA	CA-C	-7.14	1.43	1.52
1	D2	13	GLU	CA-C	-7.14	1.44	1.52
1	DK	13	GLU	CA-C	-7.14	1.44	1.52
1	Db	13	GLU	CA-C	-7.13	1.44	1.52
1	Gi	24	ALA	CA-C	-7.13	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	GS	31	ALA	CA-C	-7.13	1.43	1.52
1	DU	13	GLU	CA-C	-7.13	1.44	1.52
1	Gx	24	ALA	CA-C	-7.13	1.43	1.52
1	H3	31	ALA	CA-C	-7.13	1.44	1.52
1	HQ	31	ALA	CA-C	-7.13	1.44	1.52
1	GM	24	ALA	CA-C	-7.13	1.43	1.52
1	H8	31	ALA	CA-C	-7.13	1.44	1.52
1	GD	31	ALA	CA-C	-7.13	1.43	1.52
1	Hh	31	ALA	CA-C	-7.12	1.44	1.52
1	G4	24	ALA	CA-C	-7.12	1.43	1.52
1	HL	31	ALA	CA-C	-7.11	1.44	1.52
1	Go	31	ALA	CA-C	-7.10	1.43	1.52
1	B9	31	ALA	CA-C	-7.10	1.43	1.52
1	Hw	31	ALA	CA-C	-7.09	1.44	1.52
1	Hm	31	ALA	CA-C	-7.09	1.44	1.52
1	BM	31	ALA	CA-C	-7.09	1.43	1.52
1	Bn	31	ALA	CA-C	-7.08	1.43	1.52
1	G0	31	ALA	CA-C	-7.08	1.43	1.52
1	Gn	24	ALA	CA-C	-7.07	1.43	1.52
1	Hc	31	ALA	CA-C	-7.07	1.44	1.52
1	HG	31	ALA	CA-C	-7.07	1.44	1.52
1	G9	24	ALA	CA-C	-7.06	1.43	1.52
1	GR	24	ALA	CA-C	-7.06	1.43	1.52
1	Bs	31	ALA	CA-C	-7.05	1.43	1.52
1	Bx	31	ALA	CA-C	-7.05	1.43	1.52
1	Gy	31	ALA	CA-C	-7.05	1.43	1.52
1	Bd	31	ALA	CA-C	-7.05	1.43	1.52
1	BW	31	ALA	CA-C	-7.05	1.43	1.52
1	GI	31	ALA	CA-C	-7.04	1.43	1.52
1	Gj	31	ALA	CA-C	-7.04	1.43	1.52
1	BR	31	ALA	CA-C	-7.04	1.43	1.52
1	G5	31	ALA	CA-C	-7.03	1.44	1.52
1	GN	31	ALA	CA-C	-7.03	1.44	1.52
1	B4	31	ALA	CA-C	-7.03	1.43	1.52
1	Ge	31	ALA	CA-C	-7.03	1.44	1.52
1	Bi	31	ALA	CA-C	-7.03	1.43	1.52
1	Hr	31	ALA	CA-C	-7.03	1.44	1.52
1	Gt	31	ALA	CA-C	-7.02	1.44	1.52
1	BH	31	ALA	CA-C	-7.00	1.43	1.52
1	HV	31	ALA	CA-C	-7.00	1.44	1.52
1	GC	24	ALA	CA-C	-7.00	1.43	1.52
1	GX	31	ALA	CA-C	-6.99	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Cg	20	ALA	CA-C	-6.80	1.44	1.52
1	DB	31	ALA	CA-C	-6.79	1.44	1.52
1	C2	20	ALA	CA-C	-6.79	1.44	1.52
1	CA	20	ALA	CA-C	-6.79	1.44	1.52
1	CF	20	ALA	CA-C	-6.78	1.44	1.52
1	Cb	20	ALA	CA-C	-6.78	1.44	1.52
1	CU	20	ALA	CA-C	-6.78	1.44	1.52
1	Cq	20	ALA	CA-C	-6.78	1.44	1.52
1	D8	31	ALA	CA-C	-6.76	1.44	1.52
1	DQ	31	ALA	CA-C	-6.76	1.44	1.52
1	CK	20	ALA	CA-C	-6.75	1.44	1.52
1	Dw	31	ALA	CA-C	-6.75	1.44	1.52
1	Cv	20	ALA	CA-C	-6.74	1.44	1.52
1	C7	20	ALA	CA-C	-6.73	1.44	1.52
1	DV	31	ALA	CA-C	-6.73	1.44	1.52
1	Dm	31	ALA	CA-C	-6.71	1.44	1.52
1	Cl	20	ALA	CA-C	-6.69	1.44	1.52
1	D3	31	ALA	CA-C	-6.69	1.44	1.52
1	DL	31	ALA	CA-C	-6.69	1.44	1.52
1	CP	20	ALA	CA-C	-6.69	1.44	1.52
1	Dc	31	ALA	CA-C	-6.67	1.44	1.52
1	Dh	31	ALA	CA-C	-6.67	1.44	1.52
1	Dr	31	ALA	CA-C	-6.67	1.44	1.52
1	DG	31	ALA	CA-C	-6.62	1.44	1.52
1	DD	45	TYR	CA-C	-6.61	1.44	1.52
1	CD	23	ALA	C-O	-6.59	1.16	1.24
1	CS	23	ALA	C-O	-6.56	1.16	1.24
1	DI	45	TYR	CA-C	-6.54	1.44	1.52
1	Cj	23	ALA	C-O	-6.53	1.16	1.24
1	Co	23	ALA	C-O	-6.53	1.16	1.24
1	D0	45	TYR	CA-C	-6.53	1.44	1.52
1	Do	45	TYR	CA-C	-6.52	1.44	1.52
1	C0	23	ALA	C-O	-6.51	1.16	1.24
1	FL	10	GLY	CA-C	-6.51	1.47	1.52
1	De	45	TYR	CA-C	-6.51	1.44	1.52
1	Dj	45	TYR	CA-C	-6.51	1.44	1.52
1	Dt	45	TYR	CA-C	-6.50	1.44	1.52
1	Cl	24	ALA	CA-C	-6.50	1.44	1.52
1	Ct	23	ALA	C-O	-6.49	1.16	1.24
1	Cy	23	ALA	C-O	-6.49	1.16	1.24
1	CX	23	ALA	C-O	-6.49	1.16	1.24
1	D5	45	TYR	CA-C	-6.49	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	DN	45	TYR	CA-C	-6.49	1.44	1.52
1	F3	10	GLY	CA-C	-6.48	1.47	1.52
1	FB	10	GLY	CA-C	-6.48	1.47	1.52
1	FG	10	GLY	CA-C	-6.48	1.47	1.52
1	C5	23	ALA	C-O	-6.48	1.16	1.24
1	Fc	10	GLY	CA-C	-6.47	1.47	1.52
1	Fh	10	GLY	CA-C	-6.47	1.47	1.52
1	Cb	24	ALA	CA-C	-6.47	1.44	1.52
1	Cl	31	ALA	CA-C	-6.47	1.44	1.52
1	Fr	10	GLY	CA-C	-6.47	1.47	1.52
1	Fw	10	GLY	CA-C	-6.47	1.47	1.52
1	CA	24	ALA	CA-C	-6.46	1.44	1.52
1	F8	10	GLY	CA-C	-6.46	1.47	1.52
1	C2	31	ALA	CA-C	-6.46	1.44	1.52
1	Ce	23	ALA	C-O	-6.46	1.16	1.24
1	Cg	31	ALA	CA-C	-6.46	1.44	1.52
1	GF	31	ALA	CA-C	-6.45	1.44	1.52
1	DS	45	TYR	CA-C	-6.45	1.44	1.52
1	CP	24	ALA	CA-C	-6.45	1.44	1.52
1	Cq	31	ALA	CA-C	-6.45	1.44	1.52
1	Cq	24	ALA	CA-C	-6.44	1.44	1.52
1	C7	31	ALA	CA-C	-6.44	1.44	1.52
1	CP	31	ALA	CA-C	-6.44	1.44	1.52
1	DX	45	TYR	CA-C	-6.44	1.44	1.52
1	FV	10	GLY	CA-C	-6.44	1.47	1.52
1	C2	24	ALA	CA-C	-6.44	1.44	1.52
1	CF	31	ALA	CA-C	-6.44	1.44	1.52
1	C7	24	ALA	CA-C	-6.44	1.44	1.52
1	Dy	45	TYR	CA-C	-6.44	1.44	1.52
1	CK	24	ALA	CA-C	-6.44	1.44	1.52
1	Cb	31	ALA	CA-C	-6.44	1.44	1.52
1	CU	31	ALA	CA-C	-6.44	1.44	1.52
1	Cg	24	ALA	CA-C	-6.43	1.44	1.52
1	CF	24	ALA	CA-C	-6.43	1.44	1.52
1	CI	23	ALA	C-O	-6.43	1.16	1.24
1	CN	23	ALA	C-O	-6.43	1.16	1.24
1	Cv	24	ALA	CA-C	-6.43	1.44	1.52
1	CA	31	ALA	CA-C	-6.42	1.44	1.52
1	CU	24	ALA	CA-C	-6.40	1.44	1.52
1	GK	31	ALA	CA-C	-6.40	1.44	1.52
1	CK	31	ALA	CA-C	-6.40	1.44	1.52
1	FQ	10	GLY	CA-C	-6.40	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Cv	31	ALA	CA-C	-6.39	1.44	1.52
1	Gb	31	ALA	CA-C	-6.39	1.44	1.52
1	GU	31	ALA	CA-C	-6.39	1.44	1.52
1	Bt	39	GLN	CA-C	-6.39	1.44	1.52
1	Gq	31	ALA	CA-C	-6.38	1.44	1.52
1	Bo	39	GLN	CA-C	-6.38	1.44	1.52
1	Be	39	GLN	CA-C	-6.38	1.44	1.52
1	BX	39	GLN	CA-C	-6.38	1.44	1.52
1	CA	13	GLU	CA-C	-6.37	1.45	1.52
1	B5	39	GLN	CA-C	-6.37	1.44	1.52
1	BN	39	GLN	CA-C	-6.37	1.44	1.52
1	Gv	31	ALA	CA-C	-6.36	1.44	1.52
1	CK	13	GLU	CA-C	-6.36	1.45	1.52
1	Gg	31	ALA	CA-C	-6.36	1.44	1.52
1	Fm	10	GLY	CA-C	-6.36	1.47	1.52
1	BS	39	GLN	CA-C	-6.35	1.44	1.52
1	GA	31	ALA	CA-C	-6.35	1.44	1.52
1	G2	31	ALA	CA-C	-6.34	1.44	1.52
1	B0	39	GLN	CA-C	-6.34	1.44	1.52
1	Bj	39	GLN	CA-C	-6.33	1.45	1.52
1	BI	39	GLN	CA-C	-6.33	1.45	1.52
1	Eg	13	GLU	CA-C	-6.32	1.45	1.52
1	C7	13	GLU	CA-C	-6.31	1.45	1.52
1	CP	13	GLU	CA-C	-6.31	1.45	1.52
1	Eq	13	GLU	CA-C	-6.31	1.45	1.52
1	Cg	13	GLU	CA-C	-6.31	1.45	1.52
1	Eb	13	GLU	CA-C	-6.30	1.45	1.52
1	E2	13	GLU	CA-C	-6.30	1.45	1.52
1	By	39	GLN	CA-C	-6.29	1.45	1.52
1	Cl	13	GLU	CA-C	-6.29	1.45	1.52
1	G7	31	ALA	CA-C	-6.29	1.44	1.52
1	BD	39	GLN	CA-C	-6.29	1.45	1.52
1	GP	31	ALA	CA-C	-6.29	1.44	1.52
1	Gl	31	ALA	CA-C	-6.29	1.44	1.52
1	GS	13	GLU	CA-C	-6.29	1.45	1.52
1	C2	13	GLU	CA-C	-6.28	1.45	1.52
1	EU	13	GLU	CA-C	-6.28	1.45	1.52
1	Ev	13	GLU	CA-C	-6.28	1.45	1.52
1	CF	13	GLU	CA-C	-6.27	1.45	1.52
1	EK	13	GLU	CA-C	-6.27	1.45	1.52
1	EO	35	LEU	CA-C	-6.27	1.44	1.52
1	Gj	13	GLU	CA-C	-6.26	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	GD	13	GLU	CA-C	-6.26	1.45	1.52
1	Cq	13	GLU	CA-C	-6.26	1.45	1.52
1	Cv	13	GLU	CA-C	-6.26	1.45	1.52
1	E7	13	GLU	CA-C	-6.25	1.45	1.52
1	EP	13	GLU	CA-C	-6.25	1.45	1.52
1	Cb	13	GLU	CA-C	-6.24	1.45	1.52
1	CU	13	GLU	CA-C	-6.24	1.45	1.52
1	G0	13	GLU	CA-C	-6.23	1.45	1.52
1	EF	13	GLU	CA-C	-6.23	1.45	1.52
1	El	13	GLU	CA-C	-6.23	1.45	1.52
1	Ep	35	LEU	CA-C	-6.22	1.44	1.52
1	DF	31	ALA	CA-C	-6.22	1.44	1.52
1	Go	13	GLU	CA-C	-6.21	1.45	1.52
1	EA	13	GLU	CA-C	-6.21	1.45	1.52
1	E6	35	LEU	CA-C	-6.21	1.44	1.52
1	GX	13	GLU	CA-C	-6.21	1.45	1.52
1	Av	13	GLU	CA-C	-6.21	1.45	1.52
1	Ez	35	LEU	CA-C	-6.20	1.44	1.52
1	EJ	35	LEU	CA-C	-6.20	1.44	1.52
1	Gy	13	GLU	CA-C	-6.20	1.45	1.52
1	Eu	35	LEU	CA-C	-6.20	1.44	1.52
1	Db	31	ALA	CA-C	-6.19	1.44	1.52
1	Dg	31	ALA	CA-C	-6.19	1.44	1.52
1	Gt	13	GLU	CA-C	-6.19	1.45	1.52
1	DU	31	ALA	CA-C	-6.19	1.44	1.52
1	EE	35	LEU	CA-C	-6.19	1.44	1.52
1	DA	31	ALA	CA-C	-6.18	1.44	1.52
1	E1	35	LEU	CA-C	-6.18	1.44	1.52
1	D7	31	ALA	CA-C	-6.17	1.44	1.52
1	DP	31	ALA	CA-C	-6.17	1.44	1.52
1	Ea	35	LEU	CA-C	-6.17	1.44	1.52
1	Ef	35	LEU	CA-C	-6.17	1.44	1.52
1	ET	35	LEU	CA-C	-6.17	1.44	1.52
1	Ek	35	LEU	CA-C	-6.17	1.44	1.52
1	GI	13	GLU	CA-C	-6.17	1.45	1.52
1	D2	31	ALA	CA-C	-6.17	1.44	1.52
1	Ge	13	GLU	CA-C	-6.17	1.45	1.52
1	DK	31	ALA	CA-C	-6.17	1.44	1.52
1	Dq	31	ALA	CA-C	-6.17	1.44	1.52
1	Bx	57	VAL	C-O	-6.16	1.17	1.24
1	G5	13	GLU	CA-C	-6.16	1.45	1.52
1	GN	13	GLU	CA-C	-6.16	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Dv	31	ALA	CA-C	-6.15	1.44	1.52
1	Bl	57	VAL	C-O	-6.15	1.16	1.24
1	Eu	13	GLU	CA-C	-6.15	1.45	1.52
1	AF	13	GLU	CA-C	-6.15	1.45	1.52
1	A2	13	GLU	CA-C	-6.14	1.45	1.52
1	BF	57	VAL	C-O	-6.14	1.16	1.24
1	AK	13	GLU	CA-C	-6.14	1.45	1.52
1	B7	57	VAL	C-O	-6.13	1.16	1.24
1	BP	57	VAL	C-O	-6.13	1.16	1.24
1	Bb	57	VAL	C-O	-6.13	1.16	1.24
1	BC	35	LEU	CA-C	-6.13	1.45	1.52
1	BU	57	VAL	C-O	-6.13	1.16	1.24
1	Aq	13	GLU	CA-C	-6.13	1.45	1.52
1	Bi	57	VAL	C-O	-6.12	1.17	1.24
1	Dl	31	ALA	CA-C	-6.12	1.44	1.52
1	Ez	13	GLU	CA-C	-6.12	1.45	1.52
1	A7	13	GLU	CA-C	-6.12	1.45	1.52
1	AP	13	GLU	CA-C	-6.12	1.45	1.52
1	EO	13	GLU	CA-C	-6.12	1.45	1.52
1	E6	13	GLU	CA-C	-6.11	1.45	1.52
1	Ab	13	GLU	CA-C	-6.11	1.45	1.52
1	Ef	13	GLU	CA-C	-6.11	1.45	1.52
1	AU	13	GLU	CA-C	-6.11	1.45	1.52
1	Bq	57	VAL	C-O	-6.11	1.16	1.24
1	BV	39	GLN	CA-C	-6.11	1.45	1.52
1	Ek	13	GLU	CA-C	-6.11	1.45	1.52
1	AA	13	GLU	CA-C	-6.09	1.45	1.52
1	BA	57	VAL	C-O	-6.09	1.16	1.24
1	BQ	39	GLN	CA-C	-6.09	1.45	1.52
1	E1	13	GLU	CA-C	-6.09	1.45	1.52
1	EJ	13	GLU	CA-C	-6.09	1.45	1.52
1	Ag	13	GLU	CA-C	-6.09	1.45	1.52
1	BG	39	GLN	CA-C	-6.09	1.45	1.52
1	BM	57	VAL	C-O	-6.08	1.17	1.24
1	B8	39	GLN	CA-C	-6.08	1.45	1.52
1	B4	57	VAL	C-O	-6.08	1.17	1.24
1	B2	57	VAL	C-O	-6.08	1.17	1.24
1	BH	35	LEU	CA-C	-6.08	1.45	1.52
1	BK	57	VAL	C-O	-6.08	1.17	1.24
1	BW	35	LEU	CA-C	-6.08	1.45	1.52
1	B3	39	GLN	CA-C	-6.07	1.45	1.52
1	Bm	39	GLN	CA-C	-6.07	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Br	39	GLN	CA-C	-6.07	1.45	1.52
1	Bw	39	GLN	CA-C	-6.07	1.45	1.52
1	BB	39	GLN	CA-C	-6.07	1.45	1.52
1	Bc	39	GLN	CA-C	-6.07	1.45	1.52
1	Bd	35	LEU	CA-C	-6.07	1.45	1.52
1	Bh	39	GLN	CA-C	-6.07	1.45	1.52
1	Bi	35	LEU	CA-C	-6.07	1.45	1.52
1	Cp	56	ALA	CA-C	-6.06	1.44	1.52
1	Bs	35	LEU	CA-C	-6.06	1.45	1.52
1	Bx	35	LEU	CA-C	-6.06	1.45	1.52
1	Ea	13	GLU	CA-C	-6.06	1.45	1.52
1	ET	13	GLU	CA-C	-6.06	1.45	1.52
1	Al	13	GLU	CA-C	-6.05	1.45	1.52
1	EE	13	GLU	CA-C	-6.05	1.45	1.52
1	B4	35	LEU	CA-C	-6.05	1.45	1.52
1	BM	35	LEU	CA-C	-6.05	1.45	1.52
1	Ep	13	GLU	CA-C	-6.05	1.45	1.52
1	B9	35	LEU	CA-C	-6.05	1.45	1.52
1	Bn	35	LEU	CA-C	-6.04	1.45	1.52
1	Ca	56	ALA	CA-C	-6.04	1.45	1.52
1	Bg	57	VAL	C-O	-6.04	1.17	1.24
1	CT	56	ALA	CA-C	-6.04	1.45	1.52
1	Bd	57	VAL	C-O	-6.04	1.17	1.24
1	BH	57	VAL	C-O	-6.04	1.17	1.24
1	BW	57	VAL	C-O	-6.04	1.17	1.24
1	Bn	57	VAL	C-O	-6.03	1.17	1.24
1	BL	24	ALA	CA-C	-6.03	1.45	1.52
1	BL	39	GLN	CA-C	-6.03	1.45	1.52
1	BR	35	LEU	CA-C	-6.03	1.45	1.52
1	Bv	57	VAL	C-O	-6.03	1.17	1.24
1	Cf	56	ALA	CA-C	-6.02	1.45	1.52
1	CJ	56	ALA	CA-C	-6.02	1.45	1.52
1	Bs	57	VAL	C-O	-6.02	1.17	1.24
1	AE	31	ALA	CA-C	-6.02	1.45	1.52
1	AD	45	TYR	CA-C	-6.01	1.45	1.52
1	B9	57	VAL	C-O	-6.00	1.17	1.24
1	BR	57	VAL	C-O	-6.00	1.17	1.24
1	BC	57	VAL	C-O	-6.00	1.17	1.24
1	CE	56	ALA	CA-C	-6.00	1.45	1.52
1	Ao	45	TYR	CA-C	-6.00	1.45	1.52
1	Aj	45	TYR	CA-C	-6.00	1.45	1.52
1	Br	24	ALA	CA-C	-5.98	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Cu	56	ALA	CA-C	-5.98	1.45	1.52
1	C1	56	ALA	CA-C	-5.97	1.45	1.52
1	As	47	THR	CA-C	-5.97	1.45	1.52
1	Ax	47	THR	CA-C	-5.97	1.45	1.52
1	Ak	31	ALA	CA-C	-5.97	1.45	1.52
1	AS	45	TYR	CA-C	-5.97	1.45	1.52
1	A0	45	TYR	CA-C	-5.96	1.45	1.52
1	Bh	24	ALA	CA-C	-5.96	1.45	1.52
1	Ap	31	ALA	CA-C	-5.96	1.45	1.52
1	Bw	24	ALA	CA-C	-5.96	1.45	1.52
1	B3	24	ALA	CA-C	-5.96	1.45	1.52
1	Ad	47	THR	CA-C	-5.96	1.45	1.52
1	AW	47	THR	CA-C	-5.96	1.45	1.52
1	GC	31	ALA	CA-C	-5.95	1.45	1.52
1	Ck	56	ALA	CA-C	-5.95	1.45	1.52
1	AI	31	ALA	CA-C	-5.95	1.45	1.52
1	AI	45	TYR	CA-C	-5.95	1.45	1.52
1	BV	24	ALA	CA-C	-5.95	1.45	1.52
2	Xp	720	ALA	CA-C	-5.94	1.45	1.53
1	AH	47	THR	CA-C	-5.94	1.45	1.52
1	A5	45	TYR	CA-C	-5.94	1.45	1.52
1	AN	45	TYR	CA-C	-5.94	1.45	1.52
1	A6	31	ALA	CA-C	-5.94	1.45	1.52
1	C6	56	ALA	CA-C	-5.94	1.45	1.52
1	Aa	31	ALA	CA-C	-5.94	1.45	1.52
1	Bc	24	ALA	CA-C	-5.94	1.45	1.52
1	AO	31	ALA	CA-C	-5.94	1.45	1.52
1	CO	56	ALA	CA-C	-5.94	1.45	1.52
1	AT	31	ALA	CA-C	-5.94	1.45	1.52
1	AC	47	THR	CA-C	-5.93	1.45	1.52
1	BB	24	ALA	CA-C	-5.93	1.45	1.52
1	GB	31	ALA	CA-C	-5.93	1.45	1.52
1	A5	31	ALA	CA-C	-5.92	1.45	1.52
1	Au	31	ALA	CA-C	-5.92	1.45	1.52
1	Ay	45	TYR	CA-C	-5.92	1.45	1.52
1	AN	31	ALA	CA-C	-5.92	1.45	1.52
1	Ai	47	THR	CA-C	-5.92	1.45	1.52
1	Ae	31	ALA	CA-C	-5.92	1.45	1.52
1	Aj	31	ALA	CA-C	-5.92	1.45	1.52
1	AX	31	ALA	CA-C	-5.92	1.45	1.52
1	Gm	31	ALA	CA-C	-5.92	1.45	1.52
1	Fw	23	ALA	C-O	-5.92	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Cz	56	ALA	CA-C	-5.91	1.45	1.52
1	BG	24	ALA	CA-C	-5.91	1.45	1.52
1	A4	47	THR	CA-C	-5.91	1.45	1.52
1	Af	31	ALA	CA-C	-5.91	1.45	1.52
1	AM	47	THR	CA-C	-5.91	1.45	1.52
1	A1	31	ALA	CA-C	-5.91	1.45	1.52
1	Az	31	ALA	CA-C	-5.91	1.45	1.52
1	AJ	31	ALA	CA-C	-5.91	1.45	1.52
1	B8	24	ALA	CA-C	-5.91	1.45	1.52
1	BQ	24	ALA	CA-C	-5.91	1.45	1.52
1	AS	31	ALA	CA-C	-5.90	1.45	1.52
1	G8	31	ALA	CA-C	-5.90	1.45	1.52
1	An	47	THR	CA-C	-5.90	1.45	1.52
2	XE	720	ALA	CA-C	-5.90	1.45	1.53
1	Ae	45	TYR	CA-C	-5.90	1.45	1.52
1	At	31	ALA	CA-C	-5.90	1.45	1.52
1	Gr	31	ALA	CA-C	-5.90	1.45	1.52
1	Ay	31	ALA	CA-C	-5.90	1.45	1.52
1	Gw	31	ALA	CA-C	-5.90	1.45	1.52
1	AX	45	TYR	CA-C	-5.90	1.45	1.52
1	Bm	24	ALA	CA-C	-5.90	1.45	1.52
2	Xa	720	ALA	CA-C	-5.89	1.45	1.53
1	Gc	31	ALA	CA-C	-5.89	1.45	1.52
1	Gh	31	ALA	CA-C	-5.89	1.45	1.52
2	XT	720	ALA	CA-C	-5.89	1.45	1.53
1	GV	31	ALA	CA-C	-5.89	1.45	1.52
1	G3	31	ALA	CA-C	-5.89	1.45	1.52
1	A9	47	THR	CA-C	-5.89	1.45	1.52
1	GQ	31	ALA	CA-C	-5.89	1.45	1.52
1	AR	47	THR	CA-C	-5.89	1.45	1.52
1	Fm	23	ALA	C-O	-5.89	1.17	1.24
1	Fh	23	ALA	C-O	-5.89	1.17	1.24
1	GG	31	ALA	CA-C	-5.89	1.45	1.52
1	FG	23	ALA	C-O	-5.88	1.17	1.24
2	Xu	720	ALA	CA-C	-5.88	1.45	1.53
1	Gn	31	ALA	CA-C	-5.88	1.45	1.52
1	At	45	TYR	CA-C	-5.88	1.45	1.52
1	FQ	60	ALA	CA-C	-5.88	1.45	1.52
1	AD	31	ALA	CA-C	-5.88	1.45	1.52
2	XO	720	ALA	CA-C	-5.88	1.45	1.53
1	G4	31	ALA	CA-C	-5.87	1.45	1.52
1	G9	31	ALA	CA-C	-5.87	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	GM	31	ALA	CA-C	-5.87	1.45	1.52
1	A0	31	ALA	CA-C	-5.87	1.45	1.52
1	Ao	31	ALA	CA-C	-5.87	1.45	1.52
1	Gx	31	ALA	CA-C	-5.87	1.45	1.52
1	F8	23	ALA	C-O	-5.86	1.17	1.24
1	FQ	23	ALA	C-O	-5.86	1.17	1.24
1	FB	23	ALA	C-O	-5.86	1.17	1.24
1	FL	23	ALA	C-O	-5.86	1.17	1.24
1	F3	23	ALA	C-O	-5.85	1.17	1.24
1	Gd	31	ALA	CA-C	-5.85	1.45	1.52
1	Gi	31	ALA	CA-C	-5.85	1.45	1.52
1	GW	31	ALA	CA-C	-5.85	1.45	1.52
1	FO	64	GLY	CA-C	-5.85	1.45	1.52
1	Gs	31	ALA	CA-C	-5.85	1.45	1.52
2	XJ	720	ALA	CA-C	-5.85	1.45	1.53
1	FB	60	ALA	CA-C	-5.84	1.45	1.52
1	GH	31	ALA	CA-C	-5.84	1.45	1.52
1	Fc	23	ALA	C-O	-5.84	1.17	1.24
1	GR	31	ALA	CA-C	-5.84	1.45	1.52
1	FV	23	ALA	C-O	-5.84	1.17	1.24
2	Xf	720	ALA	CA-C	-5.84	1.45	1.53
2	X1	720	ALA	CA-C	-5.83	1.45	1.53
2	Xz	720	ALA	CA-C	-5.83	1.45	1.53
1	Fu	64	GLY	CA-C	-5.83	1.45	1.52
1	F8	60	ALA	CA-C	-5.82	1.45	1.52
1	GL	31	ALA	CA-C	-5.82	1.45	1.52
1	Hx	13	GLU	CA-C	-5.82	1.45	1.52
2	XL	817	ARG	CA-C	-5.82	1.45	1.52
1	Ff	64	GLY	CA-C	-5.82	1.45	1.52
2	XQ	817	ARG	CA-C	-5.81	1.45	1.52
2	X8	817	ARG	CA-C	-5.81	1.45	1.52
1	Fk	64	GLY	CA-C	-5.81	1.45	1.52
1	F1	64	GLY	CA-C	-5.81	1.45	1.52
1	Fz	64	GLY	CA-C	-5.81	1.45	1.52
1	F6	64	GLY	CA-C	-5.81	1.45	1.52
2	Xr	817	ARG	CA-C	-5.81	1.45	1.52
2	X6	720	ALA	CA-C	-5.80	1.45	1.53
1	Fh	60	ALA	CA-C	-5.80	1.45	1.52
2	Xk	720	ALA	CA-C	-5.80	1.45	1.53
2	Xm	817	ARG	CA-C	-5.80	1.45	1.52
2	Xc	817	ARG	CA-C	-5.79	1.45	1.52
2	XV	817	ARG	CA-C	-5.79	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	XB	817	ARG	CA-C	-5.79	1.45	1.52
1	Hd	13	GLU	CA-C	-5.79	1.45	1.52
1	HW	13	GLU	CA-C	-5.79	1.45	1.52
1	F3	60	ALA	CA-C	-5.78	1.45	1.52
2	Xh	817	ARG	CA-C	-5.78	1.45	1.52
1	Fr	23	ALA	C-O	-5.78	1.17	1.24
1	Fm	60	ALA	CA-C	-5.78	1.45	1.52
1	Hn	13	GLU	CA-C	-5.78	1.45	1.52
2	X3	817	ARG	CA-C	-5.76	1.45	1.52
1	FL	60	ALA	CA-C	-5.76	1.45	1.52
1	FJ	64	GLY	CA-C	-5.76	1.45	1.52
2	XG	817	ARG	CA-C	-5.75	1.45	1.52
1	HM	13	GLU	CA-C	-5.75	1.45	1.52
1	H4	13	GLU	CA-C	-5.75	1.45	1.52
1	Dv	37	GLY	CA-C	-5.74	1.46	1.51
1	Fp	64	GLY	CA-C	-5.74	1.45	1.52
1	Fa	64	GLY	CA-C	-5.74	1.45	1.52
1	Gp	13	GLU	CA-C	-5.74	1.45	1.52
1	FT	64	GLY	CA-C	-5.74	1.45	1.52
1	Dq	37	GLY	CA-C	-5.74	1.46	1.51
1	Hi	13	GLU	CA-C	-5.73	1.45	1.52
1	FE	64	GLY	CA-C	-5.73	1.45	1.52
1	H9	13	GLU	CA-C	-5.72	1.45	1.52
1	DB	30	ALA	CA-C	-5.72	1.45	1.52
2	Xw	817	ARG	CA-C	-5.72	1.45	1.52
1	HC	13	GLU	CA-C	-5.72	1.45	1.52
1	Fw	60	ALA	CA-C	-5.71	1.45	1.52
1	Dh	30	ALA	CA-C	-5.71	1.45	1.52
1	Gu	13	GLU	CA-C	-5.71	1.45	1.52
1	HH	13	GLU	CA-C	-5.71	1.45	1.52
1	Hs	13	GLU	CA-C	-5.71	1.45	1.52
1	HR	13	GLU	CA-C	-5.71	1.45	1.52
1	Db	37	GLY	CA-C	-5.71	1.46	1.51
1	DU	37	GLY	CA-C	-5.71	1.46	1.51
1	DV	30	ALA	CA-C	-5.71	1.45	1.52
1	D3	30	ALA	CA-C	-5.71	1.45	1.52
1	Dr	30	ALA	CA-C	-5.70	1.45	1.52
1	Fc	60	ALA	CA-C	-5.70	1.45	1.52
1	Fr	60	ALA	CA-C	-5.70	1.45	1.52
1	FV	60	ALA	CA-C	-5.70	1.45	1.52
1	DF	37	GLY	CA-C	-5.70	1.46	1.51
1	Dc	30	ALA	CA-C	-5.69	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	DG	30	ALA	CA-C	-5.69	1.45	1.52
1	Ga	13	GLU	CA-C	-5.68	1.45	1.52
1	Cx	11	MET	CA-C	-5.68	1.45	1.52
1	EQ	45	TYR	CA-C	-5.68	1.45	1.52
1	GT	13	GLU	CA-C	-5.68	1.45	1.52
1	Gf	13	GLU	CA-C	-5.68	1.45	1.52
1	Dw	30	ALA	CA-C	-5.68	1.45	1.52
1	DL	30	ALA	CA-C	-5.68	1.45	1.52
1	H6	31	ALA	CA-C	-5.68	1.45	1.52
1	HO	31	ALA	CA-C	-5.68	1.45	1.52
1	D8	30	ALA	CA-C	-5.68	1.45	1.52
1	Ai	60	ALA	CA-C	-5.68	1.45	1.52
1	DQ	30	ALA	CA-C	-5.68	1.45	1.52
1	D2	37	GLY	CA-C	-5.68	1.46	1.51
1	F3	35	LEU	CA-C	-5.68	1.45	1.52
1	Ci	11	MET	CA-C	-5.68	1.45	1.52
1	Em	45	TYR	CA-C	-5.68	1.45	1.52
1	DK	37	GLY	CA-C	-5.68	1.46	1.51
1	FL	35	LEU	CA-C	-5.68	1.45	1.52
1	Ew	45	TYR	CA-C	-5.67	1.45	1.52
1	FG	60	ALA	CA-C	-5.67	1.45	1.52
1	G1	13	GLU	CA-C	-5.67	1.45	1.52
1	E8	45	TYR	CA-C	-5.67	1.45	1.52
1	GJ	13	GLU	CA-C	-5.67	1.45	1.52
1	G6	13	GLU	CA-C	-5.67	1.45	1.52
1	Cn	23	ALA	C-O	-5.67	1.17	1.24
1	GO	13	GLU	CA-C	-5.67	1.45	1.52
1	E3	45	TYR	CA-C	-5.66	1.45	1.52
1	F8	35	LEU	CA-C	-5.66	1.45	1.52
1	EB	45	TYR	CA-C	-5.66	1.45	1.52
1	EL	45	TYR	CA-C	-5.66	1.45	1.52
1	Er	45	TYR	CA-C	-5.66	1.45	1.52
1	GE	13	GLU	CA-C	-5.66	1.45	1.52
1	CC	23	ALA	C-O	-5.66	1.17	1.24
1	Fm	35	LEU	CA-C	-5.66	1.45	1.52
1	HM	11	MET	CA-C	-5.65	1.45	1.52
1	FQ	35	LEU	CA-C	-5.65	1.45	1.52
1	Ec	45	TYR	CA-C	-5.64	1.45	1.52
1	Eh	45	TYR	CA-C	-5.64	1.45	1.52
1	C9	11	MET	CA-C	-5.64	1.45	1.52
1	Dg	37	GLY	CA-C	-5.64	1.46	1.51
1	As	20	ALA	CA-C	-5.64	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Fw	35	LEU	CA-C	-5.64	1.45	1.52
1	Ax	20	ALA	CA-C	-5.64	1.45	1.52
1	CR	11	MET	CA-C	-5.64	1.45	1.52
1	Dl	37	GLY	CA-C	-5.63	1.46	1.51
1	FG	35	LEU	CA-C	-5.63	1.45	1.52
1	C9	23	ALA	C-O	-5.63	1.17	1.24
1	Ad	20	ALA	CA-C	-5.63	1.45	1.52
1	CR	23	ALA	C-O	-5.63	1.17	1.24
1	AW	20	ALA	CA-C	-5.63	1.45	1.52
1	Fc	35	LEU	CA-C	-5.63	1.45	1.52
1	Ci	23	ALA	C-O	-5.63	1.17	1.24
1	FV	35	LEU	CA-C	-5.63	1.45	1.52
1	A4	60	ALA	CA-C	-5.63	1.45	1.52
1	C4	11	MET	CA-C	-5.63	1.45	1.52
1	Fl	13	GLU	CA-C	-5.63	1.46	1.52
1	Dm	30	ALA	CA-C	-5.63	1.45	1.52
1	CC	11	MET	CA-C	-5.63	1.45	1.52
1	DC	56	ALA	CA-C	-5.63	1.45	1.52
1	HJ	31	ALA	CA-C	-5.63	1.45	1.52
1	CM	11	MET	CA-C	-5.63	1.45	1.52
1	DM	56	ALA	CA-C	-5.63	1.45	1.52
1	H1	31	ALA	CA-C	-5.63	1.45	1.52
1	Dn	56	ALA	CA-C	-5.62	1.45	1.52
1	Fh	35	LEU	CA-C	-5.62	1.45	1.52
1	EH	60	ALA	CA-C	-5.62	1.45	1.52
1	D9	56	ALA	CA-C	-5.62	1.45	1.52
1	DR	56	ALA	CA-C	-5.62	1.45	1.52
1	Cx	23	ALA	C-O	-5.62	1.17	1.24
1	E9	60	ALA	CA-C	-5.62	1.45	1.52
1	Hi	11	MET	CA-C	-5.62	1.45	1.52
1	EC	60	ALA	CA-C	-5.62	1.45	1.52
1	AM	20	ALA	CA-C	-5.62	1.45	1.52
1	ER	60	ALA	CA-C	-5.62	1.45	1.52
1	Hk	31	ALA	CA-C	-5.62	1.45	1.52
1	Hz	31	ALA	CA-C	-5.62	1.45	1.52
1	C4	23	ALA	C-O	-5.62	1.17	1.24
1	Ex	60	ALA	CA-C	-5.62	1.45	1.52
1	Gz	13	GLU	CA-C	-5.62	1.45	1.52
1	CM	23	ALA	C-O	-5.62	1.17	1.24
1	Cs	11	MET	CA-C	-5.61	1.45	1.52
1	AH	60	ALA	CA-C	-5.61	1.45	1.52
1	EW	60	ALA	CA-C	-5.61	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D7	37	GLY	CA-C	-5.61	1.46	1.51
1	An	20	ALA	CA-C	-5.61	1.45	1.52
1	AH	20	ALA	CA-C	-5.61	1.45	1.52
1	A4	20	ALA	CA-C	-5.61	1.45	1.52
1	A9	20	ALA	CA-C	-5.61	1.45	1.52
1	AR	20	ALA	CA-C	-5.61	1.45	1.52
1	H9	11	MET	CA-C	-5.61	1.45	1.52
1	Ha	31	ALA	CA-C	-5.61	1.45	1.52
1	HR	11	MET	CA-C	-5.61	1.45	1.52
1	HT	31	ALA	CA-C	-5.61	1.45	1.52
1	Hf	31	ALA	CA-C	-5.61	1.45	1.52
1	H4	11	MET	CA-C	-5.61	1.45	1.52
1	Cd	11	MET	CA-C	-5.61	1.45	1.52
1	Hs	11	MET	CA-C	-5.61	1.45	1.52
1	FB	35	LEU	CA-C	-5.61	1.45	1.52
1	CW	11	MET	CA-C	-5.61	1.45	1.52
1	Gk	13	GLU	CA-C	-5.60	1.46	1.52
1	AR	60	ALA	CA-C	-5.60	1.45	1.52
1	En	60	ALA	CA-C	-5.60	1.45	1.52
1	As	60	ALA	CA-C	-5.60	1.45	1.52
1	AC	20	ALA	CA-C	-5.60	1.45	1.52
1	DP	37	GLY	CA-C	-5.60	1.46	1.51
1	DU	20	ALA	CA-C	-5.60	1.45	1.52
1	EV	45	TYR	CA-C	-5.60	1.45	1.52
1	Hn	11	MET	CA-C	-5.60	1.45	1.52
1	EM	60	ALA	CA-C	-5.60	1.45	1.52
1	Bm	57	VAL	C-O	-5.60	1.17	1.24
1	Dv	20	ALA	CA-C	-5.60	1.45	1.52
1	HH	11	MET	CA-C	-5.60	1.45	1.52
1	Hp	31	ALA	CA-C	-5.60	1.45	1.52
1	BB	57	VAL	C-O	-5.60	1.17	1.24
1	EG	45	TYR	CA-C	-5.60	1.45	1.52
1	Hu	31	ALA	CA-C	-5.60	1.45	1.52
1	E4	60	ALA	CA-C	-5.60	1.45	1.52
1	Cd	23	ALA	C-O	-5.59	1.17	1.24
1	AM	60	ALA	CA-C	-5.59	1.45	1.52
1	CW	23	ALA	C-O	-5.59	1.17	1.24
1	HO	26	ALA	CA-C	-5.59	1.45	1.52
1	Bw	57	VAL	C-O	-5.59	1.17	1.24
1	DW	56	ALA	CA-C	-5.59	1.45	1.52
1	DA	37	GLY	CA-C	-5.59	1.46	1.51
1	Cn	11	MET	CA-C	-5.59	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CH	11	MET	CA-C	-5.59	1.45	1.52
1	EI	23	ALA	C-O	-5.59	1.17	1.24
1	Hd	11	MET	CA-C	-5.58	1.45	1.52
1	D4	56	ALA	CA-C	-5.58	1.45	1.52
1	B8	57	VAL	C-O	-5.58	1.17	1.24
1	Ds	56	ALA	CA-C	-5.58	1.45	1.52
1	Ax	60	ALA	CA-C	-5.58	1.45	1.52
1	Ad	60	ALA	CA-C	-5.58	1.45	1.52
1	Hp	57	VAL	C-O	-5.58	1.17	1.24
1	Hx	11	MET	CA-C	-5.58	1.45	1.52
1	AW	60	ALA	CA-C	-5.58	1.45	1.52
1	HW	11	MET	CA-C	-5.58	1.45	1.52
1	Dg	20	ALA	CA-C	-5.58	1.45	1.52
1	FA	13	GLU	CA-C	-5.58	1.46	1.52
1	HE	57	VAL	C-O	-5.58	1.17	1.24
1	Ha	57	VAL	C-O	-5.58	1.17	1.24
1	Ai	20	ALA	CA-C	-5.58	1.45	1.52
1	HE	23	ALA	C-O	-5.58	1.17	1.24
1	DH	56	ALA	CA-C	-5.58	1.45	1.52
1	HT	57	VAL	C-O	-5.58	1.17	1.24
1	Hf	57	VAL	C-O	-5.58	1.17	1.24
1	Ed	60	ALA	CA-C	-5.57	1.45	1.52
1	Cs	23	ALA	C-O	-5.57	1.17	1.24
1	Et	23	ALA	C-O	-5.57	1.17	1.24
1	CH	23	ALA	C-O	-5.57	1.17	1.24
1	FK	13	GLU	CA-C	-5.57	1.46	1.52
1	F7	13	GLU	CA-C	-5.57	1.46	1.52
1	An	60	ALA	CA-C	-5.57	1.45	1.52
1	Fv	13	GLU	CA-C	-5.57	1.46	1.52
1	BQ	57	VAL	C-O	-5.57	1.17	1.24
1	Ei	60	ALA	CA-C	-5.56	1.45	1.52
1	D2	20	ALA	CA-C	-5.56	1.45	1.52
1	A9	60	ALA	CA-C	-5.56	1.45	1.52
1	Fg	13	GLU	CA-C	-5.56	1.46	1.52
1	Dq	20	ALA	CA-C	-5.56	1.45	1.52
1	DK	20	ALA	CA-C	-5.56	1.45	1.52
1	Dd	56	ALA	CA-C	-5.56	1.45	1.52
1	Di	56	ALA	CA-C	-5.56	1.45	1.52
1	Fr	35	LEU	CA-C	-5.56	1.45	1.52
1	HJ	57	VAL	C-O	-5.56	1.17	1.24
1	HT	23	ALA	C-O	-5.56	1.17	1.24
1	H6	23	ALA	C-O	-5.56	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	HO	23	ALA	C-O	-5.56	1.17	1.24
1	Dx	56	ALA	CA-C	-5.55	1.45	1.52
1	F2	13	GLU	CA-C	-5.55	1.46	1.52
1	AC	60	ALA	CA-C	-5.55	1.45	1.52
1	HC	11	MET	CA-C	-5.55	1.45	1.52
1	HE	31	ALA	CA-C	-5.55	1.46	1.52
1	Es	60	ALA	CA-C	-5.55	1.45	1.52
1	Bh	57	VAL	C-O	-5.55	1.17	1.24
1	D7	20	ALA	CA-C	-5.54	1.45	1.52
1	DP	20	ALA	CA-C	-5.54	1.45	1.52
1	Ee	23	ALA	C-O	-5.54	1.17	1.24
1	EX	23	ALA	C-O	-5.54	1.17	1.24
1	Hk	23	ALA	C-O	-5.54	1.17	1.24
1	Db	20	ALA	CA-C	-5.54	1.45	1.52
1	CO	13	GLU	CA-C	-5.54	1.46	1.52
1	Ey	23	ALA	C-O	-5.54	1.17	1.24
1	Ck	13	GLU	CA-C	-5.54	1.46	1.52
1	FP	13	GLU	CA-C	-5.53	1.46	1.52
1	B3	57	VAL	C-O	-5.53	1.17	1.24
1	Ha	23	ALA	C-O	-5.53	1.17	1.24
1	Hp	26	ALA	CA-C	-5.53	1.45	1.52
1	Hp	23	ALA	C-O	-5.53	1.17	1.24
1	Hu	23	ALA	C-O	-5.53	1.17	1.24
1	Bc	57	VAL	C-O	-5.52	1.17	1.24
1	BV	57	VAL	C-O	-5.52	1.17	1.24
1	Cp	13	GLU	CA-C	-5.52	1.46	1.52
1	DF	20	ALA	CA-C	-5.52	1.45	1.52
1	C6	13	GLU	CA-C	-5.52	1.46	1.52
1	Hu	57	VAL	C-O	-5.52	1.17	1.24
1	E0	23	ALA	C-O	-5.52	1.17	1.24
1	Eo	23	ALA	C-O	-5.52	1.17	1.24
1	DA	20	ALA	CA-C	-5.52	1.45	1.52
1	HJ	23	ALA	C-O	-5.52	1.17	1.24
1	ES	23	ALA	C-O	-5.52	1.17	1.24
1	H1	23	ALA	C-O	-5.52	1.17	1.24
1	Hx	23	ALA	C-O	-5.52	1.17	1.24
1	H6	26	ALA	CA-C	-5.52	1.45	1.52
1	Dl	20	ALA	CA-C	-5.51	1.45	1.52
1	E5	23	ALA	C-O	-5.51	1.17	1.24
1	Cf	13	GLU	CA-C	-5.51	1.46	1.52
1	Ej	23	ALA	C-O	-5.51	1.17	1.24
1	ED	23	ALA	C-O	-5.51	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	EN	23	ALA	C-O	-5.51	1.17	1.24
1	Hz	26	ALA	CA-C	-5.51	1.45	1.52
1	En	20	ALA	CA-C	-5.51	1.45	1.52
1	HE	26	ALA	CA-C	-5.51	1.45	1.52
1	Hf	23	ALA	C-O	-5.51	1.17	1.24
1	Hk	26	ALA	CA-C	-5.51	1.45	1.52
1	Fb	13	GLU	CA-C	-5.50	1.46	1.52
1	Br	57	VAL	C-O	-5.50	1.17	1.24
1	Fq	13	GLU	CA-C	-5.49	1.46	1.52
1	BL	57	VAL	C-O	-5.49	1.17	1.24
1	Eh	20	ALA	CA-C	-5.49	1.45	1.52
1	Ha	26	ALA	CA-C	-5.49	1.45	1.52
1	HT	26	ALA	CA-C	-5.49	1.45	1.52
1	Dl	38	ARG	CA-C	-5.48	1.45	1.52
1	Ft	20	ALA	CA-C	-5.48	1.45	1.52
1	AD	25	ASP	CA-C	-5.48	1.45	1.52
1	FF	13	GLU	CA-C	-5.48	1.46	1.52
1	DN	47	THR	CA-C	-5.48	1.46	1.52
1	Hu	26	ALA	CA-C	-5.48	1.45	1.52
1	Fe	20	ALA	CA-C	-5.48	1.45	1.52
1	FX	20	ALA	CA-C	-5.48	1.45	1.52
1	Cu	13	GLU	CA-C	-5.48	1.46	1.52
1	HJ	26	ALA	CA-C	-5.48	1.45	1.52
1	Hl	26	ALA	CA-C	-5.48	1.45	1.52
1	ER	20	ALA	CA-C	-5.47	1.45	1.52
1	DA	38	ARG	CA-C	-5.47	1.45	1.52
1	HO	57	VAL	C-O	-5.47	1.17	1.24
1	BG	57	VAL	C-O	-5.46	1.17	1.24
1	EM	20	ALA	CA-C	-5.46	1.45	1.52
1	Ca	13	GLU	CA-C	-5.46	1.46	1.52
1	CT	13	GLU	CA-C	-5.46	1.46	1.52
1	C1	13	GLU	CA-C	-5.46	1.46	1.52
1	Cz	13	GLU	CA-C	-5.46	1.46	1.52
1	CJ	13	GLU	CA-C	-5.46	1.46	1.52
1	FU	13	GLU	CA-C	-5.46	1.46	1.52
3	PO	17	ALA	CA-C	-5.45	1.45	1.52
1	Em	20	ALA	CA-C	-5.45	1.45	1.52
1	Hf	26	ALA	CA-C	-5.45	1.45	1.52
1	Ao	25	ASP	CA-C	-5.45	1.46	1.52
1	Ex	20	ALA	CA-C	-5.44	1.45	1.52
1	F5	20	ALA	CA-C	-5.44	1.45	1.52
1	E9	20	ALA	CA-C	-5.44	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Cm	47	THR	CA-C	-5.44	1.46	1.52
1	FN	20	ALA	CA-C	-5.44	1.45	1.52
1	Fj	20	ALA	CA-C	-5.44	1.45	1.52
1	AN	39	GLN	CA-C	-5.44	1.46	1.52
1	CE	13	GLU	CA-C	-5.44	1.46	1.52
1	FI	20	ALA	CA-C	-5.44	1.45	1.52
1	BO	13	GLU	CA-C	-5.44	1.46	1.52
1	Ei	20	ALA	CA-C	-5.43	1.45	1.52
1	BJ	13	GLU	CA-C	-5.43	1.46	1.52
1	E4	20	ALA	CA-C	-5.43	1.45	1.52
1	EC	20	ALA	CA-C	-5.43	1.45	1.52
1	D7	38	ARG	CA-C	-5.43	1.46	1.52
1	DP	38	ARG	CA-C	-5.43	1.46	1.52
1	E3	20	ALA	CA-C	-5.42	1.45	1.52
1	A0	25	ASP	CA-C	-5.42	1.46	1.52
1	Aj	25	ASP	CA-C	-5.42	1.46	1.52
3	Pz	17	ALA	CA-C	-5.42	1.45	1.52
1	EL	20	ALA	CA-C	-5.42	1.45	1.52
1	AS	25	ASP	CA-C	-5.42	1.46	1.52
1	Fo	20	ALA	CA-C	-5.42	1.45	1.52
1	Dt	47	THR	CA-C	-5.42	1.46	1.52
1	Fy	20	ALA	CA-C	-5.42	1.45	1.52
1	Dt	23	ALA	C-O	-5.42	1.17	1.24
1	Dy	23	ALA	C-O	-5.42	1.17	1.24
3	Pk	17	ALA	CA-C	-5.42	1.45	1.52
1	Fr	39	GLN	CA-C	-5.42	1.45	1.52
1	Fw	39	GLN	CA-C	-5.42	1.45	1.52
1	AG	25	ASP	CA-C	-5.42	1.46	1.52
1	E8	20	ALA	CA-C	-5.41	1.45	1.52
1	GF	42	GLY	C-O	-5.41	1.19	1.23
1	EX	11	MET	CA-C	-5.41	1.45	1.52
1	B1	13	GLU	CA-C	-5.41	1.46	1.52
1	Gn	9	LEU	CA-C	-5.41	1.46	1.52
1	AI	39	GLN	CA-C	-5.41	1.46	1.52
1	AX	39	GLN	CA-C	-5.41	1.46	1.52
1	D5	47	THR	CA-C	-5.41	1.46	1.52
1	At	39	GLN	CA-C	-5.41	1.46	1.52
1	Er	20	ALA	CA-C	-5.41	1.45	1.52
1	Ew	20	ALA	CA-C	-5.41	1.45	1.52
1	DD	23	ALA	C-O	-5.41	1.17	1.24
1	BE	13	GLU	CA-C	-5.41	1.46	1.52
1	DI	47	THR	CA-C	-5.41	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H1	57	VAL	C-O	-5.41	1.17	1.24
1	H2	57	VAL	C-O	-5.41	1.17	1.24
1	Ar	25	ASP	CA-C	-5.41	1.46	1.52
1	Ay	39	GLN	CA-C	-5.41	1.46	1.52
1	D5	23	ALA	C-O	-5.40	1.17	1.24
1	D0	47	THR	CA-C	-5.40	1.46	1.52
1	Ch	9	LEU	CA-C	-5.40	1.45	1.52
3	Pp	17	ALA	CA-C	-5.40	1.45	1.52
1	DN	23	ALA	C-O	-5.40	1.17	1.24
1	Dj	47	THR	CA-C	-5.40	1.46	1.52
1	FG	39	GLN	CA-C	-5.40	1.45	1.52
1	De	47	THR	CA-C	-5.40	1.46	1.52
1	DX	47	THR	CA-C	-5.40	1.46	1.52
1	Ed	20	ALA	CA-C	-5.40	1.45	1.52
1	Bk	13	GLU	CA-C	-5.40	1.46	1.52
1	EW	20	ALA	CA-C	-5.40	1.45	1.52
1	Ba	13	GLU	CA-C	-5.39	1.46	1.52
1	Bf	13	GLU	CA-C	-5.39	1.46	1.52
1	Es	20	ALA	CA-C	-5.39	1.45	1.52
1	Cw	9	LEU	CA-C	-5.39	1.45	1.52
1	DD	47	THR	CA-C	-5.39	1.46	1.52
1	A5	25	ASP	CA-C	-5.39	1.46	1.52
1	D0	23	ALA	C-O	-5.39	1.17	1.24
1	Fc	39	GLN	CA-C	-5.39	1.45	1.52
1	GC	9	LEU	CA-C	-5.39	1.46	1.52
1	EH	20	ALA	CA-C	-5.39	1.45	1.52
1	AN	25	ASP	CA-C	-5.39	1.46	1.52
1	DS	23	ALA	C-O	-5.39	1.17	1.24
1	FV	39	GLN	CA-C	-5.39	1.45	1.52
3	P6	17	ALA	CA-C	-5.39	1.45	1.52
3	PT	17	ALA	CA-C	-5.39	1.45	1.52
1	B6	13	GLU	CA-C	-5.39	1.46	1.52
1	F0	20	ALA	CA-C	-5.39	1.45	1.52
1	Dq	38	ARG	CA-C	-5.39	1.46	1.52
1	Dv	38	ARG	CA-C	-5.39	1.46	1.52
1	A8	25	ASP	CA-C	-5.39	1.46	1.52
1	Ae	39	GLN	CA-C	-5.39	1.46	1.52
1	Ch	47	THR	CA-C	-5.39	1.46	1.52
1	DF	38	ARG	CA-C	-5.39	1.46	1.52
1	AQ	25	ASP	CA-C	-5.39	1.46	1.52
1	Aj	39	GLN	CA-C	-5.38	1.46	1.52
1	H6	57	VAL	C-O	-5.38	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A3	25	ASP	CA-C	-5.38	1.46	1.52
1	Ec	20	ALA	CA-C	-5.38	1.45	1.52
1	Aw	25	ASP	CA-C	-5.38	1.46	1.52
1	FD	20	ALA	CA-C	-5.38	1.45	1.52
1	EG	20	ALA	CA-C	-5.38	1.45	1.52
1	AL	25	ASP	CA-C	-5.38	1.46	1.52
1	EV	20	ALA	CA-C	-5.38	1.45	1.52
1	Db	38	ARG	CA-C	-5.38	1.46	1.52
1	Dg	38	ARG	CA-C	-5.38	1.46	1.52
1	DU	38	ARG	CA-C	-5.38	1.46	1.52
1	Hk	57	VAL	C-O	-5.38	1.17	1.24
1	Am	25	ASP	CA-C	-5.38	1.46	1.52
1	Bu	13	GLU	CA-C	-5.37	1.46	1.52
1	D2	38	ARG	CA-C	-5.37	1.46	1.52
3	Pa	17	ALA	CA-C	-5.37	1.45	1.52
1	Ah	25	ASP	CA-C	-5.37	1.46	1.52
1	DK	38	ARG	CA-C	-5.37	1.46	1.52
1	A5	39	GLN	CA-C	-5.37	1.46	1.52
1	C3	47	THR	CA-C	-5.37	1.46	1.52
1	Ac	25	ASP	CA-C	-5.37	1.46	1.52
1	Cr	9	LEU	CA-C	-5.37	1.45	1.52
1	AV	25	ASP	CA-C	-5.37	1.46	1.52
1	CQ	47	THR	CA-C	-5.37	1.46	1.52
1	C8	47	THR	CA-C	-5.37	1.46	1.52
1	Bn	47	THR	CA-C	-5.37	1.46	1.52
1	EB	20	ALA	CA-C	-5.37	1.45	1.52
1	Do	47	THR	CA-C	-5.36	1.46	1.52
3	PE	17	ALA	CA-C	-5.36	1.45	1.52
1	Dy	52	GLY	C-O	-5.36	1.18	1.23
1	DI	23	ALA	C-O	-5.36	1.17	1.24
1	AS	39	GLN	CA-C	-5.36	1.46	1.52
1	DX	23	ALA	C-O	-5.36	1.17	1.24
1	G9	9	LEU	CA-C	-5.36	1.46	1.52
1	GR	9	LEU	CA-C	-5.36	1.46	1.52
3	P1	17	ALA	CA-C	-5.36	1.45	1.52
1	AB	25	ASP	CA-C	-5.36	1.46	1.52
1	Ee	11	MET	CA-C	-5.36	1.46	1.52
1	Ej	11	MET	CA-C	-5.36	1.46	1.52
1	Hh	11	MET	CA-C	-5.36	1.46	1.52
1	De	23	ALA	C-O	-5.35	1.17	1.24
1	E5	11	MET	CA-C	-5.35	1.46	1.52
1	EN	11	MET	CA-C	-5.35	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Dy	47	THR	CA-C	-5.35	1.46	1.52
1	ED	11	MET	CA-C	-5.35	1.46	1.52
1	EI	11	MET	CA-C	-5.35	1.46	1.52
1	Ay	25	ASP	CA-C	-5.35	1.46	1.52
1	AD	39	GLN	CA-C	-5.35	1.46	1.52
1	AF	9	LEU	CA-C	-5.35	1.46	1.52
1	Gg	42	GLY	C-O	-5.35	1.19	1.23
1	Dj	23	ALA	C-O	-5.35	1.17	1.24
1	Gd	9	LEU	CA-C	-5.35	1.46	1.52
1	F3	39	GLN	CA-C	-5.34	1.46	1.52
1	Bp	13	GLU	CA-C	-5.34	1.46	1.52
1	FB	39	GLN	CA-C	-5.34	1.46	1.52
1	FL	39	GLN	CA-C	-5.34	1.46	1.52
1	Gq	42	GLY	C-O	-5.34	1.19	1.23
1	El	31	ALA	CA-C	-5.34	1.46	1.52
3	PJ	17	ALA	CA-C	-5.34	1.45	1.52
1	G4	9	LEU	CA-C	-5.34	1.46	1.52
1	Ae	25	ASP	CA-C	-5.34	1.46	1.52
1	Cc	9	LEU	CA-C	-5.34	1.46	1.52
1	At	25	ASP	CA-C	-5.34	1.46	1.52
1	Bx	47	THR	CA-C	-5.34	1.46	1.52
1	GM	9	LEU	CA-C	-5.34	1.46	1.52
1	AX	25	ASP	CA-C	-5.34	1.46	1.52
1	CV	9	LEU	CA-C	-5.34	1.46	1.52
1	Bt	45	TYR	CA-C	-5.34	1.46	1.52
1	BT	13	GLU	CA-C	-5.34	1.46	1.52
1	Hr	11	MET	CA-C	-5.33	1.46	1.52
1	Hw	11	MET	CA-C	-5.33	1.46	1.52
1	CB	47	THR	CA-C	-5.33	1.46	1.52
1	DI	52	GLY	C-O	-5.33	1.18	1.23
1	CL	47	THR	CA-C	-5.33	1.46	1.52
1	EQ	20	ALA	CA-C	-5.33	1.46	1.52
1	Ax	12	ILE	C-O	-5.33	1.18	1.24
1	C3	9	LEU	CA-C	-5.33	1.46	1.52
1	H8	11	MET	CA-C	-5.33	1.46	1.52
1	CL	9	LEU	CA-C	-5.33	1.46	1.52
1	DS	47	THR	CA-C	-5.33	1.46	1.52
1	HQ	11	MET	CA-C	-5.33	1.46	1.52
1	Ei	14	THR	CA-C	-5.33	1.46	1.52
1	Cn	53	GLU	CA-C	-5.33	1.46	1.53
1	CV	47	THR	CA-C	-5.33	1.46	1.52
1	A0	39	GLN	CA-C	-5.33	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E0	11	MET	CA-C	-5.33	1.46	1.52
1	Et	11	MET	CA-C	-5.33	1.46	1.52
1	Fs	23	ALA	C-O	-5.33	1.17	1.24
1	Ey	11	MET	CA-C	-5.33	1.46	1.52
1	ES	11	MET	CA-C	-5.33	1.46	1.52
1	D0	52	GLY	C-O	-5.33	1.18	1.23
1	Ch	10	GLY	CA-C	-5.33	1.47	1.51
1	Cw	47	THR	CA-C	-5.33	1.46	1.52
1	CG	9	LEU	CA-C	-5.33	1.46	1.52
1	BH	47	THR	CA-C	-5.33	1.46	1.52
1	DS	52	GLY	C-O	-5.33	1.18	1.23
1	Ai	12	ILE	C-O	-5.32	1.18	1.24
1	GH	9	LEU	CA-C	-5.32	1.46	1.52
1	FQ	39	GLN	CA-C	-5.32	1.46	1.52
1	BR	47	THR	CA-C	-5.32	1.46	1.52
1	EU	31	ALA	CA-C	-5.32	1.46	1.52
1	AW	12	ILE	C-O	-5.32	1.18	1.24
1	DW	13	GLU	CA-C	-5.32	1.46	1.52
1	Gb	42	GLY	C-O	-5.32	1.19	1.23
1	Gu	35	LEU	CA-C	-5.32	1.46	1.52
1	GU	42	GLY	C-O	-5.32	1.19	1.23
1	Ab	9	LEU	CA-C	-5.32	1.46	1.52
1	Bz	13	GLU	CA-C	-5.32	1.46	1.52
1	AU	9	LEU	CA-C	-5.32	1.46	1.52
1	C8	9	LEU	CA-C	-5.32	1.46	1.52
1	B9	47	THR	CA-C	-5.32	1.46	1.52
1	HA	57	VAL	C-O	-5.32	1.18	1.24
1	CQ	9	LEU	CA-C	-5.32	1.46	1.52
1	H3	11	MET	CA-C	-5.32	1.46	1.52
1	HB	11	MET	CA-C	-5.32	1.46	1.52
1	HL	11	MET	CA-C	-5.32	1.46	1.52
1	HV	11	MET	CA-C	-5.32	1.46	1.52
1	Fh	39	GLN	CA-C	-5.31	1.46	1.52
1	A2	9	LEU	CA-C	-5.31	1.46	1.52
1	Cc	47	THR	CA-C	-5.31	1.46	1.52
1	GW	9	LEU	CA-C	-5.31	1.46	1.52
1	D5	52	GLY	C-O	-5.31	1.18	1.23
1	C8	10	GLY	CA-C	-5.31	1.47	1.51
1	DN	52	GLY	C-O	-5.31	1.18	1.23
1	A7	9	LEU	CA-C	-5.31	1.46	1.52
1	E7	31	ALA	CA-C	-5.31	1.46	1.52
3	Pf	17	ALA	CA-C	-5.31	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Gi	9	LEU	CA-C	-5.31	1.46	1.52
1	Gs	9	LEU	CA-C	-5.31	1.46	1.52
1	EP	31	ALA	CA-C	-5.31	1.46	1.52
1	Hc	11	MET	CA-C	-5.31	1.46	1.52
1	Do	23	ALA	C-O	-5.31	1.18	1.24
1	Aq	9	LEU	CA-C	-5.31	1.46	1.52
1	BC	47	THR	CA-C	-5.31	1.46	1.52
1	AK	9	LEU	CA-C	-5.31	1.46	1.52
1	Bi	47	THR	CA-C	-5.31	1.46	1.52
1	Ao	39	GLN	CA-C	-5.31	1.46	1.52
1	CG	47	THR	CA-C	-5.31	1.46	1.52
1	Be	45	TYR	CA-C	-5.30	1.46	1.52
1	Gc	20	ALA	C-O	-5.30	1.18	1.24
1	Dd	13	GLU	CA-C	-5.30	1.46	1.52
1	Bj	45	TYR	CA-C	-5.30	1.46	1.52
1	GL	20	ALA	C-O	-5.30	1.18	1.24
1	GV	20	ALA	C-O	-5.30	1.18	1.24
1	En	14	THR	CA-C	-5.30	1.46	1.52
1	EH	14	THR	CA-C	-5.30	1.46	1.52
1	Cm	10	GLY	CA-C	-5.30	1.47	1.51
1	EW	14	THR	CA-C	-5.30	1.46	1.52
1	F8	39	GLN	CA-C	-5.30	1.46	1.52
1	Hm	11	MET	CA-C	-5.30	1.46	1.52
1	GG	20	ALA	C-O	-5.30	1.18	1.24
1	BX	45	TYR	CA-C	-5.30	1.46	1.52
1	C9	53	GLU	CA-C	-5.30	1.46	1.53
1	Dt	52	GLY	C-O	-5.30	1.18	1.23
1	DM	13	GLU	CA-C	-5.30	1.46	1.52
1	B4	47	THR	CA-C	-5.29	1.46	1.52
3	Pu	17	ALA	CA-C	-5.29	1.45	1.52
1	FC	23	ALA	C-O	-5.29	1.18	1.24
1	AI	25	ASP	CA-C	-5.29	1.46	1.52
1	DH	13	GLU	CA-C	-5.29	1.46	1.52
1	BM	47	THR	CA-C	-5.29	1.46	1.52
1	FS	20	ALA	CA-C	-5.29	1.45	1.52
1	B5	45	TYR	CA-C	-5.29	1.46	1.52
1	Gf	35	LEU	CA-C	-5.29	1.46	1.52
1	BD	45	TYR	CA-C	-5.29	1.46	1.52
1	HG	11	MET	CA-C	-5.29	1.46	1.52
1	BN	45	TYR	CA-C	-5.29	1.46	1.52
1	Gx	9	LEU	CA-C	-5.29	1.46	1.52
1	Gz	35	LEU	CA-C	-5.29	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Bd	47	THR	CA-C	-5.29	1.46	1.52
1	Ao	13	GLU	CA-C	-5.29	1.46	1.52
1	BW	47	THR	CA-C	-5.29	1.46	1.52
1	A4	12	ILE	C-O	-5.29	1.18	1.24
1	Cr	47	THR	CA-C	-5.29	1.46	1.52
1	Ex	14	THR	CA-C	-5.29	1.46	1.52
1	DD	52	GLY	C-O	-5.29	1.18	1.23
1	EK	31	ALA	CA-C	-5.29	1.46	1.52
1	AM	12	ILE	C-O	-5.29	1.18	1.24
1	G2	42	GLY	C-O	-5.29	1.19	1.23
1	AP	9	LEU	CA-C	-5.29	1.46	1.52
1	C4	53	GLU	CA-C	-5.29	1.46	1.53
1	Cm	9	LEU	CA-C	-5.29	1.46	1.52
1	Bs	45	TYR	CA-C	-5.29	1.46	1.52
1	CC	53	GLU	CA-C	-5.29	1.46	1.53
1	CM	53	GLU	CA-C	-5.29	1.46	1.53
1	F4	23	ALA	C-O	-5.28	1.18	1.24
1	Ds	13	GLU	CA-C	-5.28	1.46	1.52
1	Dx	13	GLU	CA-C	-5.28	1.46	1.52
1	CB	9	LEU	CA-C	-5.28	1.46	1.52
1	EM	60	ALA	C-O	-5.28	1.18	1.24
1	Hl	57	VAL	C-O	-5.28	1.18	1.24
1	G1	35	LEU	CA-C	-5.28	1.46	1.52
1	E4	14	THR	CA-C	-5.28	1.46	1.52
1	Cd	53	GLU	CA-C	-5.28	1.46	1.53
1	Fx	23	ALA	C-O	-5.28	1.18	1.24
1	GJ	35	LEU	CA-C	-5.28	1.46	1.52
1	CW	53	GLU	CA-C	-5.28	1.46	1.53
1	Eo	11	MET	CA-C	-5.28	1.46	1.52
1	EM	14	THR	CA-C	-5.28	1.46	1.52
1	CR	53	GLU	CA-C	-5.28	1.46	1.53
1	Eb	31	ALA	CA-C	-5.28	1.46	1.52
1	Al	9	LEU	CA-C	-5.28	1.46	1.52
1	Eq	31	ALA	CA-C	-5.28	1.46	1.52
1	Ds	71	VAL	CA-C	-5.28	1.46	1.52
1	Gv	42	GLY	C-O	-5.28	1.19	1.23
1	Dx	71	VAL	CA-C	-5.28	1.46	1.52
1	H7	57	VAL	C-O	-5.28	1.18	1.24
1	G6	35	LEU	CA-C	-5.28	1.46	1.52
1	De	52	GLY	C-O	-5.28	1.18	1.23
1	Dj	52	GLY	C-O	-5.28	1.18	1.23
2	Xn	776	ALA	CA-C	-5.28	1.47	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	GK	42	GLY	C-O	-5.28	1.19	1.23
1	HP	57	VAL	C-O	-5.28	1.18	1.24
1	CQ	10	GLY	CA-C	-5.28	1.47	1.51
1	C3	10	GLY	CA-C	-5.27	1.47	1.51
1	Fm	39	GLN	CA-C	-5.27	1.46	1.52
1	D4	13	GLU	CA-C	-5.27	1.46	1.52
1	Cc	10	GLY	CA-C	-5.27	1.47	1.51
1	Cr	10	GLY	CA-C	-5.27	1.47	1.51
1	Fw	60	ALA	C-O	-5.27	1.18	1.24
1	DC	13	GLU	CA-C	-5.27	1.46	1.52
1	CH	53	GLU	CA-C	-5.27	1.46	1.53
1	FM	23	ALA	C-O	-5.27	1.18	1.24
1	CV	10	GLY	CA-C	-5.27	1.47	1.51
1	B0	45	TYR	CA-C	-5.27	1.46	1.52
1	Ci	53	GLU	CA-C	-5.27	1.46	1.53
1	Di	71	VAL	CA-C	-5.27	1.46	1.52
1	BS	45	TYR	CA-C	-5.27	1.46	1.52
1	F3	45	TYR	CA-C	-5.27	1.46	1.52
1	D9	13	GLU	CA-C	-5.27	1.46	1.52
1	GE	36	VAL	C-O	-5.27	1.19	1.24
1	DR	13	GLU	CA-C	-5.27	1.46	1.52
1	Do	52	GLY	C-O	-5.27	1.18	1.23
1	AH	12	ILE	C-O	-5.27	1.18	1.24
1	E2	31	ALA	CA-C	-5.27	1.46	1.52
1	F3	60	ALA	C-O	-5.27	1.18	1.24
1	D4	71	VAL	CA-C	-5.27	1.46	1.52
1	EA	31	ALA	CA-C	-5.27	1.46	1.52
1	FL	60	ALA	C-O	-5.27	1.18	1.24
1	DM	71	VAL	CA-C	-5.27	1.46	1.52
1	Di	13	GLU	CA-C	-5.26	1.46	1.52
1	Fd	23	ALA	C-O	-5.26	1.18	1.24
1	Fq	57	VAL	C-O	-5.26	1.18	1.24
1	Cw	10	GLY	CA-C	-5.26	1.47	1.51
1	FW	23	ALA	C-O	-5.26	1.18	1.24
1	Ed	14	THR	CA-C	-5.26	1.46	1.52
2	Xp	806	ILE	CA-C	-5.26	1.46	1.52
1	By	45	TYR	CA-C	-5.26	1.46	1.52
1	Gh	20	ALA	C-O	-5.26	1.18	1.24
1	Fv	57	VAL	C-O	-5.26	1.18	1.24
1	G3	20	ALA	C-O	-5.26	1.18	1.24
1	F9	23	ALA	C-O	-5.26	1.18	1.24
1	Fc	60	ALA	C-O	-5.26	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	DH	71	VAL	CA-C	-5.26	1.46	1.52
1	FV	60	ALA	C-O	-5.26	1.18	1.24
1	Dd	71	VAL	CA-C	-5.25	1.46	1.52
1	Ag	9	LEU	CA-C	-5.25	1.46	1.52
1	Bs	47	THR	CA-C	-5.25	1.46	1.52
1	CG	54	THR	C-O	-5.25	1.18	1.24
1	DW	71	VAL	CA-C	-5.25	1.46	1.52
1	Gp	35	LEU	CA-C	-5.25	1.46	1.52
1	Cs	53	GLU	CA-C	-5.25	1.46	1.53
1	Fw	45	TYR	CA-C	-5.25	1.46	1.52
1	Cx	53	GLU	CA-C	-5.25	1.46	1.53
1	AA	9	LEU	CA-C	-5.25	1.46	1.52
1	Ev	31	ALA	CA-C	-5.25	1.46	1.52
1	DX	52	GLY	C-O	-5.25	1.18	1.23
1	GO	35	LEU	CA-C	-5.25	1.46	1.52
1	Dn	71	VAL	CA-C	-5.25	1.46	1.52
1	FL	45	TYR	CA-C	-5.25	1.46	1.52
1	E9	14	THR	CA-C	-5.25	1.46	1.52
1	Dn	13	GLU	CA-C	-5.25	1.46	1.52
1	As	12	ILE	C-O	-5.25	1.18	1.24
1	DE	24	ALA	CA-C	-5.25	1.46	1.52
1	FG	45	TYR	CA-C	-5.25	1.46	1.52
1	AH	37	GLY	CA-C	-5.25	1.46	1.51
1	Es	14	THR	CA-C	-5.25	1.46	1.52
1	Av	9	LEU	CA-C	-5.25	1.46	1.52
1	AD	13	GLU	CA-C	-5.25	1.46	1.52
1	A0	13	GLU	CA-C	-5.24	1.46	1.52
1	G8	20	ALA	C-O	-5.24	1.18	1.24
1	Ad	12	ILE	C-O	-5.24	1.18	1.24
1	Bn	45	TYR	CA-C	-5.24	1.46	1.52
1	GQ	20	ALA	C-O	-5.24	1.18	1.24
1	Gk	35	LEU	CA-C	-5.24	1.46	1.52
1	Fn	23	ALA	C-O	-5.24	1.18	1.24
1	FH	23	ALA	C-O	-5.24	1.18	1.24
1	H2	57	VAL	C-O	-5.24	1.18	1.24
1	Dp	24	ALA	CA-C	-5.24	1.46	1.52
1	Bx	45	TYR	CA-C	-5.24	1.46	1.52
2	XT	806	ILE	CA-C	-5.24	1.46	1.52
1	Dl	39	GLN	CA-C	-5.24	1.46	1.52
1	Fm	45	TYR	CA-C	-5.24	1.46	1.52
1	DC	71	VAL	CA-C	-5.24	1.46	1.52
1	BI	45	TYR	CA-C	-5.24	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	FV	45	TYR	CA-C	-5.24	1.46	1.52
1	Fi	23	ALA	C-O	-5.24	1.18	1.24
1	HK	57	VAL	C-O	-5.24	1.18	1.24
1	Gr	20	ALA	C-O	-5.23	1.18	1.24
1	Gw	20	ALA	C-O	-5.23	1.18	1.24
1	FR	23	ALA	C-O	-5.23	1.18	1.24
1	Bd	45	TYR	CA-C	-5.23	1.46	1.52
1	At	13	GLU	CA-C	-5.23	1.46	1.52
1	BW	45	TYR	CA-C	-5.23	1.46	1.52
1	B9	45	TYR	CA-C	-5.23	1.46	1.52
1	Fb	57	VAL	C-O	-5.23	1.18	1.24
1	Ga	35	LEU	CA-C	-5.23	1.46	1.52
1	Fg	57	VAL	C-O	-5.23	1.18	1.24
1	Bi	45	TYR	CA-C	-5.23	1.46	1.52
1	EF	31	ALA	CA-C	-5.23	1.46	1.52
1	BR	45	TYR	CA-C	-5.23	1.46	1.52
1	FU	57	VAL	C-O	-5.23	1.18	1.24
1	GT	35	LEU	CA-C	-5.23	1.46	1.52
1	B4	45	TYR	CA-C	-5.23	1.46	1.52
1	Eg	31	ALA	CA-C	-5.23	1.46	1.52
1	BC	45	TYR	CA-C	-5.23	1.46	1.52
1	BM	45	TYR	CA-C	-5.23	1.46	1.52
1	Fh	60	ALA	C-O	-5.23	1.18	1.24
1	FG	60	ALA	C-O	-5.23	1.18	1.24
1	AN	13	GLU	CA-C	-5.23	1.46	1.52
2	Xn	810	ALA	CA-C	-5.23	1.46	1.52
1	Fr	45	TYR	CA-C	-5.23	1.46	1.52
2	XH	810	ALA	CA-C	-5.23	1.46	1.52
1	G7	42	GLY	C-O	-5.22	1.19	1.23
1	Hb	57	VAL	C-O	-5.22	1.18	1.24
1	Fc	45	TYR	CA-C	-5.22	1.46	1.52
2	Xd	810	ALA	CA-C	-5.22	1.46	1.52
1	Hg	57	VAL	C-O	-5.22	1.18	1.24
1	Fh	45	TYR	CA-C	-5.22	1.46	1.52
1	Bo	45	TYR	CA-C	-5.22	1.46	1.52
1	GP	42	GLY	C-O	-5.22	1.19	1.23
1	HR	31	ALA	CA-C	-5.22	1.46	1.52
1	HU	57	VAL	C-O	-5.22	1.18	1.24
2	XW	810	ALA	CA-C	-5.22	1.46	1.52
1	F2	57	VAL	C-O	-5.22	1.18	1.24
1	D9	71	VAL	CA-C	-5.22	1.46	1.52
1	Hx	31	ALA	CA-C	-5.22	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	FK	57	VAL	C-O	-5.22	1.18	1.24
1	En	60	ALA	C-O	-5.22	1.18	1.24
1	EH	60	ALA	C-O	-5.22	1.18	1.24
1	Ea	57	VAL	C-O	-5.22	1.18	1.24
1	Ef	57	VAL	C-O	-5.22	1.18	1.24
1	Ei	60	ALA	C-O	-5.22	1.18	1.24
1	DO	24	ALA	CA-C	-5.22	1.46	1.52
1	DR	71	VAL	CA-C	-5.22	1.46	1.52
1	ER	14	THR	CA-C	-5.22	1.46	1.52
1	ET	57	VAL	C-O	-5.22	1.18	1.24
2	Xs	810	ALA	CA-C	-5.22	1.46	1.52
2	Xx	810	ALA	CA-C	-5.22	1.46	1.52
1	AO	47	THR	CA-C	-5.22	1.46	1.52
1	A9	12	ILE	C-O	-5.21	1.18	1.24
2	XC	810	ALA	CA-C	-5.21	1.46	1.52
1	AR	12	ILE	C-O	-5.21	1.18	1.24
1	Cc	54	THR	C-O	-5.21	1.18	1.24
1	Hq	57	VAL	C-O	-5.21	1.18	1.24
1	CV	54	THR	C-O	-5.21	1.18	1.24
1	Ed	60	ALA	C-O	-5.21	1.18	1.24
1	AC	12	ILE	C-O	-5.21	1.18	1.24
1	EC	60	ALA	C-O	-5.21	1.18	1.24
1	GE	35	LEU	CA-C	-5.21	1.46	1.52
2	X4	776	ALA	CA-C	-5.21	1.47	1.53
1	EC	14	THR	CA-C	-5.21	1.46	1.52
2	XC	776	ALA	CA-C	-5.21	1.47	1.53
1	FQ	45	TYR	CA-C	-5.21	1.46	1.52
1	D6	24	ALA	CA-C	-5.21	1.46	1.52
1	F8	45	TYR	CA-C	-5.21	1.46	1.52
1	Da	24	ALA	CA-C	-5.21	1.46	1.52
1	Ep	57	VAL	C-O	-5.21	1.18	1.24
1	BH	45	TYR	CA-C	-5.21	1.46	1.52
1	DT	24	ALA	CA-C	-5.21	1.46	1.52
2	X9	776	ALA	CA-C	-5.21	1.47	1.53
1	Gl	42	GLY	C-O	-5.21	1.19	1.23
1	Eo	24	ALA	CA-C	-5.21	1.46	1.52
2	Xs	776	ALA	CA-C	-5.21	1.47	1.53
2	Xx	776	ALA	CA-C	-5.21	1.47	1.53
1	EW	60	ALA	C-O	-5.21	1.18	1.24
1	A5	13	GLU	CA-C	-5.21	1.46	1.52
1	Aj	13	GLU	CA-C	-5.21	1.46	1.52
1	Ay	13	GLU	CA-C	-5.21	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	EH	30	ALA	CA-C	-5.21	1.46	1.52
2	X9	810	ALA	CA-C	-5.20	1.46	1.52
1	Ga	36	VAL	C-O	-5.20	1.19	1.24
2	Xd	776	ALA	CA-C	-5.20	1.47	1.53
1	Dg	39	GLN	CA-C	-5.20	1.46	1.52
1	Af	47	THR	CA-C	-5.20	1.46	1.52
1	Gf	36	VAL	C-O	-5.20	1.19	1.24
2	Xi	776	ALA	CA-C	-5.20	1.47	1.53
1	Cm	56	ALA	C-O	-5.20	1.18	1.24
1	Ey	24	ALA	CA-C	-5.20	1.46	1.52
2	XR	810	ALA	CA-C	-5.20	1.46	1.52
1	AT	47	THR	CA-C	-5.20	1.46	1.52
2	XW	776	ALA	CA-C	-5.20	1.47	1.53
2	X4	810	ALA	CA-C	-5.20	1.46	1.52
1	Hv	57	VAL	C-O	-5.20	1.18	1.24
1	AB	20	ALA	CA-C	-5.20	1.46	1.52
1	CG	10	GLY	CA-C	-5.20	1.47	1.51
2	XM	810	ALA	CA-C	-5.20	1.46	1.52
1	G1	36	VAL	C-O	-5.20	1.19	1.24
1	Fr	60	ALA	C-O	-5.20	1.18	1.24
1	Cw	54	THR	C-O	-5.20	1.18	1.24
1	GB	20	ALA	C-O	-5.20	1.18	1.24
1	HF	57	VAL	C-O	-5.20	1.18	1.24
1	Gm	20	ALA	C-O	-5.20	1.18	1.24
1	AI	24	ALA	CA-C	-5.20	1.46	1.52
1	CT	57	VAL	C-O	-5.20	1.18	1.24
1	Fm	60	ALA	C-O	-5.20	1.18	1.24
1	Az	47	THR	CA-C	-5.20	1.46	1.52
1	AS	13	GLU	CA-C	-5.20	1.46	1.52
1	AQ	20	ALA	CA-C	-5.20	1.46	1.52
1	D1	24	ALA	CA-C	-5.19	1.46	1.52
1	Dz	24	ALA	CA-C	-5.19	1.46	1.52
1	CB	10	GLY	CA-C	-5.19	1.47	1.51
1	CL	10	GLY	CA-C	-5.19	1.47	1.51
1	F7	57	VAL	C-O	-5.19	1.18	1.24
1	E0	24	ALA	CA-C	-5.19	1.46	1.52
1	An	12	ILE	C-O	-5.19	1.18	1.24
1	Ds	37	GLY	CA-C	-5.19	1.46	1.51
1	Ay	24	ALA	CA-C	-5.19	1.46	1.52
1	EE	57	VAL	C-O	-5.19	1.18	1.24
2	XH	776	ALA	CA-C	-5.19	1.47	1.53
1	FP	57	VAL	C-O	-5.19	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	ES	24	ALA	CA-C	-5.19	1.46	1.52
1	FF	57	VAL	C-O	-5.19	1.18	1.24
1	AE	47	THR	CA-C	-5.19	1.46	1.52
1	FQ	60	ALA	C-O	-5.19	1.18	1.24
1	Cx	47	THR	CA-C	-5.19	1.46	1.52
1	DD	31	ALA	CA-C	-5.19	1.46	1.52
1	DR	37	GLY	CA-C	-5.19	1.46	1.51
1	A8	20	ALA	CA-C	-5.18	1.46	1.52
1	C8	56	ALA	C-O	-5.18	1.18	1.24
1	Hi	31	ALA	CA-C	-5.18	1.46	1.52
1	Cr	54	THR	C-O	-5.18	1.18	1.24
1	Es	60	ALA	C-O	-5.18	1.18	1.24
1	Du	24	ALA	CA-C	-5.18	1.46	1.52
1	CB	54	THR	C-O	-5.18	1.18	1.24
1	D7	39	GLN	CA-C	-5.18	1.46	1.52
1	F8	60	ALA	C-O	-5.18	1.18	1.24
1	E9	60	ALA	C-O	-5.18	1.18	1.24
1	Df	24	ALA	CA-C	-5.18	1.46	1.52
2	Xi	810	ALA	CA-C	-5.18	1.46	1.52
1	ER	60	ALA	C-O	-5.18	1.18	1.24
1	Gu	36	VAL	C-O	-5.18	1.19	1.24
2	X6	806	ILE	CA-C	-5.18	1.46	1.52
1	H9	31	ALA	CA-C	-5.18	1.46	1.52
2	Xa	806	ILE	CA-C	-5.18	1.46	1.52
1	Ae	13	GLU	CA-C	-5.18	1.46	1.52
1	Ad	37	GLY	CA-C	-5.18	1.46	1.51
2	Xf	806	ILE	CA-C	-5.18	1.46	1.52
1	Ej	24	ALA	CA-C	-5.18	1.46	1.52
1	Gz	20	ALA	C-O	-5.18	1.18	1.24
1	FB	60	ALA	C-O	-5.18	1.18	1.24
2	XO	806	ILE	CA-C	-5.18	1.46	1.52
1	AW	37	GLY	CA-C	-5.18	1.46	1.51
1	At	24	ALA	CA-C	-5.18	1.46	1.52
1	Gx	45	TYR	CA-C	-5.18	1.46	1.52
1	B2	20	ALA	C-O	-5.18	1.18	1.24
1	G6	36	VAL	C-O	-5.18	1.19	1.24
1	Es	30	ALA	CA-C	-5.18	1.46	1.52
1	AD	24	ALA	CA-C	-5.18	1.46	1.52
1	BK	20	ALA	C-O	-5.18	1.18	1.24
1	E4	60	ALA	C-O	-5.17	1.18	1.24
1	Ek	57	VAL	C-O	-5.17	1.18	1.24
1	Hn	31	ALA	CA-C	-5.17	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	FB	45	TYR	CA-C	-5.17	1.46	1.52
1	B7	20	ALA	C-O	-5.17	1.18	1.24
1	GJ	36	VAL	C-O	-5.17	1.19	1.24
1	BP	20	ALA	C-O	-5.17	1.18	1.24
1	A1	47	THR	CA-C	-5.17	1.46	1.52
1	Ai	37	GLY	CA-C	-5.17	1.46	1.51
1	Dk	24	ALA	CA-C	-5.17	1.46	1.52
1	CM	47	THR	CA-C	-5.17	1.46	1.52
1	H4	31	ALA	CA-C	-5.17	1.46	1.52
1	Di	31	ALA	CA-C	-5.17	1.46	1.52
1	Ak	47	THR	CA-C	-5.17	1.46	1.52
1	HM	31	ALA	CA-C	-5.17	1.46	1.52
1	GT	20	ALA	C-O	-5.17	1.18	1.24
1	Dg	14	THR	CA-C	-5.17	1.46	1.52
1	Gk	20	ALA	C-O	-5.17	1.18	1.24
1	BF	20	ALA	C-O	-5.17	1.18	1.24
1	E5	24	ALA	CA-C	-5.17	1.46	1.52
1	E6	57	VAL	C-O	-5.17	1.18	1.24
1	Ao	24	ALA	CA-C	-5.17	1.46	1.52
1	Eu	57	VAL	C-O	-5.17	1.18	1.24
1	GA	42	GLY	C-O	-5.17	1.19	1.23
1	ED	24	ALA	CA-C	-5.17	1.46	1.52
1	EI	24	ALA	CA-C	-5.17	1.46	1.52
1	DH	37	GLY	CA-C	-5.17	1.46	1.51
1	C3	54	THR	C-O	-5.17	1.18	1.24
1	CL	54	THR	C-O	-5.17	1.18	1.24
2	XR	776	ALA	CA-C	-5.17	1.47	1.53
1	D2	14	THR	CA-C	-5.16	1.46	1.52
1	Gz	36	VAL	C-O	-5.16	1.19	1.24
2	Xk	806	ILE	CA-C	-5.16	1.46	1.52
2	XE	806	ILE	CA-C	-5.16	1.46	1.52
1	AN	24	ALA	CA-C	-5.16	1.46	1.52
1	A0	24	ALA	CA-C	-5.16	1.46	1.52
1	Dt	10	GLY	CA-C	-5.16	1.47	1.52
1	AS	24	ALA	CA-C	-5.16	1.46	1.52
1	E1	57	VAL	C-O	-5.16	1.18	1.24
1	A6	47	THR	CA-C	-5.16	1.46	1.52
1	As	37	GLY	CA-C	-5.16	1.46	1.51
1	Ez	57	VAL	C-O	-5.16	1.18	1.24
1	EJ	57	VAL	C-O	-5.16	1.18	1.24
1	BC	20	ALA	C-O	-5.16	1.18	1.24
1	GH	13	GLU	CA-C	-5.16	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D7	14	THR	CA-C	-5.16	1.46	1.52
1	Ed	30	ALA	CA-C	-5.16	1.46	1.52
1	Aj	24	ALA	CA-C	-5.16	1.46	1.52
1	Dh	20	ALA	C-O	-5.16	1.18	1.24
1	Ei	30	ALA	CA-C	-5.16	1.46	1.52
1	Am	20	ALA	CA-C	-5.16	1.46	1.52
1	EB	24	ALA	CA-C	-5.16	1.46	1.52
1	DP	14	THR	CA-C	-5.16	1.46	1.52
2	XP	794	HIS	CA-C	-5.16	1.46	1.52
1	EW	30	ALA	CA-C	-5.16	1.46	1.52
1	Bn	39	GLN	CA-C	-5.15	1.46	1.52
1	Ah	20	ALA	CA-C	-5.15	1.46	1.52
1	Dq	14	THR	CA-C	-5.15	1.46	1.52
1	Gp	36	VAL	C-O	-5.15	1.19	1.24
1	Ft	56	ALA	C-O	-5.15	1.18	1.24
1	Bv	20	ALA	C-O	-5.15	1.18	1.24
1	Fy	56	ALA	C-O	-5.15	1.18	1.24
1	Dd	37	GLY	CA-C	-5.15	1.46	1.51
1	Di	37	GLY	CA-C	-5.15	1.46	1.51
1	Dv	39	GLN	CA-C	-5.15	1.46	1.52
1	Au	47	THR	CA-C	-5.15	1.46	1.52
1	EN	24	ALA	CA-C	-5.15	1.46	1.52
1	DW	37	GLY	CA-C	-5.15	1.46	1.51
1	Dn	31	ALA	CA-C	-5.15	1.46	1.52
2	X1	806	ILE	CA-C	-5.15	1.46	1.52
1	Ae	24	ALA	CA-C	-5.15	1.46	1.52
2	Xz	806	ILE	CA-C	-5.15	1.46	1.52
1	AX	24	ALA	CA-C	-5.15	1.46	1.52
1	Aa	47	THR	CA-C	-5.14	1.46	1.52
1	Cc	56	ALA	C-O	-5.14	1.18	1.24
1	Bg	20	ALA	C-O	-5.14	1.18	1.24
1	Gk	36	VAL	C-O	-5.14	1.19	1.24
1	Do	31	ALA	CA-C	-5.14	1.46	1.52
1	Dv	14	THR	CA-C	-5.14	1.46	1.52
1	CQ	56	ALA	C-O	-5.14	1.18	1.24
1	BU	20	ALA	C-O	-5.14	1.18	1.24
1	CV	56	ALA	C-O	-5.14	1.18	1.24
1	D5	31	ALA	CA-C	-5.14	1.46	1.52
1	CG	56	ALA	C-O	-5.14	1.18	1.24
1	DN	31	ALA	CA-C	-5.14	1.46	1.52
1	DP	39	GLN	CA-C	-5.14	1.46	1.52
1	Bn	20	ALA	C-O	-5.14	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CB	56	ALA	C-O	-5.14	1.18	1.24
1	A5	24	ALA	CA-C	-5.14	1.46	1.52
1	Bb	20	ALA	C-O	-5.14	1.18	1.24
1	Ch	54	THR	C-O	-5.14	1.18	1.24
1	Fl	57	VAL	C-O	-5.14	1.18	1.24
1	En	30	ALA	CA-C	-5.14	1.46	1.52
1	Cp	57	VAL	C-O	-5.14	1.18	1.24
1	Aw	20	ALA	CA-C	-5.14	1.46	1.52
1	Dx	31	ALA	CA-C	-5.14	1.46	1.52
1	DA	14	THR	CA-C	-5.14	1.46	1.52
1	GC	13	GLU	CA-C	-5.14	1.46	1.52
1	AL	20	ALA	CA-C	-5.14	1.46	1.52
1	D2	39	GLN	CA-C	-5.14	1.46	1.52
1	A4	37	GLY	CA-C	-5.14	1.46	1.51
1	C8	54	THR	C-O	-5.14	1.18	1.24
1	Bi	39	GLN	CA-C	-5.14	1.46	1.52
1	Gi	13	GLU	CA-C	-5.14	1.46	1.52
1	Bl	20	ALA	C-O	-5.14	1.18	1.24
1	Ap	47	THR	CA-C	-5.14	1.46	1.52
1	DA	39	GLN	CA-C	-5.14	1.46	1.52
1	DK	39	GLN	CA-C	-5.14	1.46	1.52
1	AM	37	GLY	CA-C	-5.14	1.46	1.51
1	CQ	54	THR	C-O	-5.14	1.18	1.24
2	XB	843	LYS	CA-C	-5.14	1.48	1.53
1	A3	20	ALA	CA-C	-5.13	1.46	1.52
1	Db	14	THR	CA-C	-5.13	1.46	1.52
1	Cn	47	THR	CA-C	-5.13	1.46	1.52
1	Ct	60	ALA	C-O	-5.13	1.18	1.24
1	DF	14	THR	CA-C	-5.13	1.46	1.52
1	DS	31	ALA	CA-C	-5.13	1.46	1.52
1	DU	14	THR	CA-C	-5.13	1.46	1.52
1	GT	36	VAL	C-O	-5.13	1.19	1.24
2	Xu	806	ILE	CA-C	-5.13	1.46	1.52
1	Dy	31	ALA	CA-C	-5.13	1.46	1.52
1	HC	31	ALA	CA-C	-5.13	1.46	1.52
1	C4	47	THR	CA-C	-5.13	1.46	1.52
1	Dl	14	THR	CA-C	-5.13	1.46	1.52
1	Bq	20	ALA	C-O	-5.13	1.18	1.24
1	BA	20	ALA	C-O	-5.13	1.18	1.24
1	GE	20	ALA	C-O	-5.13	1.18	1.24
1	BH	39	GLN	CA-C	-5.13	1.46	1.52
1	DJ	24	ALA	CA-C	-5.13	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	GM	13	GLU	CA-C	-5.13	1.46	1.52
2	XM	776	ALA	CA-C	-5.13	1.47	1.53
1	Gd	45	TYR	CA-C	-5.13	1.46	1.52
1	Gi	45	TYR	CA-C	-5.13	1.46	1.52
1	Hl	13	GLU	CA-C	-5.13	1.46	1.52
1	GW	45	TYR	CA-C	-5.13	1.46	1.52
1	G9	45	TYR	CA-C	-5.13	1.46	1.52
1	Ee	24	ALA	CA-C	-5.13	1.46	1.52
1	Gp	20	ALA	C-O	-5.13	1.18	1.24
2	XJ	806	ILE	CA-C	-5.13	1.46	1.52
1	GR	45	TYR	CA-C	-5.13	1.46	1.52
2	XV	843	LYS	CA-C	-5.13	1.48	1.53
1	Ca	57	VAL	C-O	-5.13	1.18	1.24
1	Ga	20	ALA	C-O	-5.13	1.18	1.24
1	Cm	54	THR	C-O	-5.13	1.18	1.24
1	Gs	45	TYR	CA-C	-5.13	1.46	1.52
1	G6	20	ALA	C-O	-5.12	1.18	1.24
1	AI	13	GLU	CA-C	-5.12	1.46	1.52
1	EH	13	GLU	CA-C	-5.12	1.46	1.52
1	CU	23	ALA	C-O	-5.12	1.18	1.24
1	D0	31	ALA	CA-C	-5.12	1.46	1.52
2	XA	794	HIS	CA-C	-5.12	1.46	1.52
1	EO	57	VAL	C-O	-5.12	1.18	1.24
1	E8	24	ALA	CA-C	-5.12	1.46	1.52
1	C9	47	THR	CA-C	-5.12	1.46	1.52
1	Bd	39	GLN	CA-C	-5.12	1.46	1.52
1	Ds	31	ALA	CA-C	-5.12	1.46	1.52
1	Gs	13	GLU	CA-C	-5.12	1.46	1.52
1	CE	57	VAL	C-O	-5.12	1.18	1.24
1	DK	14	THR	CA-C	-5.12	1.46	1.52
1	GK	66	ASP	CA-C	-5.12	1.46	1.52
1	CO	57	VAL	C-O	-5.12	1.18	1.24
1	AX	13	GLU	CA-C	-5.12	1.46	1.52
1	BW	39	GLN	CA-C	-5.12	1.46	1.52
1	G9	13	GLU	CA-C	-5.12	1.46	1.52
1	GR	13	GLU	CA-C	-5.12	1.46	1.52
1	B4	39	GLN	CA-C	-5.12	1.46	1.52
1	Fe	56	ALA	C-O	-5.12	1.18	1.24
1	Fj	56	ALA	C-O	-5.12	1.18	1.24
1	Et	24	ALA	CA-C	-5.12	1.46	1.52
1	Gv	66	ASP	CA-C	-5.12	1.46	1.52
1	BM	39	GLN	CA-C	-5.12	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Ah	11	MET	CA-C	-5.12	1.46	1.52
1	Bx	39	GLN	CA-C	-5.12	1.46	1.52
1	D9	37	GLY	CA-C	-5.12	1.46	1.51
1	Ex	60	ALA	C-O	-5.12	1.18	1.24
1	CH	47	THR	CA-C	-5.12	1.46	1.52
1	DH	31	ALA	CA-C	-5.12	1.46	1.52
1	G1	20	ALA	C-O	-5.11	1.18	1.24
1	D9	31	ALA	CA-C	-5.11	1.46	1.52
1	GJ	20	ALA	C-O	-5.11	1.18	1.24
1	DL	10	GLY	CA-C	-5.11	1.47	1.52
2	XQ	843	LYS	CA-C	-5.11	1.48	1.53
1	DR	31	ALA	CA-C	-5.11	1.46	1.52
1	BW	20	ALA	C-O	-5.11	1.18	1.24
1	EC	30	ALA	CA-C	-5.11	1.46	1.52
1	GO	20	ALA	C-O	-5.11	1.18	1.24
1	Dd	31	ALA	CA-C	-5.11	1.46	1.52
1	Gf	20	ALA	C-O	-5.11	1.18	1.24
1	DW	31	ALA	CA-C	-5.11	1.46	1.52
1	EW	13	GLU	CA-C	-5.11	1.46	1.52
1	H7	13	GLU	CA-C	-5.11	1.46	1.52
2	Xv	794	HIS	CA-C	-5.11	1.46	1.52
1	AG	20	ALA	CA-C	-5.11	1.46	1.52
1	EX	24	ALA	CA-C	-5.11	1.46	1.52
1	D4	31	ALA	CA-C	-5.11	1.46	1.52
1	DM	31	ALA	CA-C	-5.11	1.46	1.52
1	E9	30	ALA	CA-C	-5.11	1.46	1.52
1	Cr	56	ALA	C-O	-5.11	1.18	1.24
1	DC	37	GLY	CA-C	-5.11	1.46	1.51
1	HH	31	ALA	CA-C	-5.11	1.46	1.52
1	HP	13	GLU	CA-C	-5.11	1.46	1.52
1	CW	47	THR	CA-C	-5.11	1.46	1.52
1	FW	56	ALA	C-O	-5.11	1.18	1.24
1	Cd	47	THR	CA-C	-5.10	1.46	1.52
1	Ci	47	THR	CA-C	-5.10	1.46	1.52
1	DI	10	GLY	CA-C	-5.10	1.47	1.52
1	G4	45	TYR	CA-C	-5.10	1.46	1.52
1	A9	37	GLY	CA-C	-5.10	1.46	1.51
1	De	31	ALA	CA-C	-5.10	1.46	1.52
1	Dj	31	ALA	CA-C	-5.10	1.46	1.52
1	GM	45	TYR	CA-C	-5.10	1.46	1.52
1	AR	37	GLY	CA-C	-5.10	1.46	1.51
1	F5	56	ALA	C-O	-5.10	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B9	20	ALA	C-O	-5.10	1.18	1.24
1	Hd	31	ALA	CA-C	-5.10	1.46	1.52
2	Xl	794	HIS	CA-C	-5.10	1.46	1.52
1	FN	56	ALA	C-O	-5.10	1.18	1.24
1	DL	39	GLN	CA-C	-5.10	1.46	1.52
1	BR	20	ALA	C-O	-5.10	1.18	1.24
1	HW	31	ALA	CA-C	-5.10	1.46	1.52
1	Fg	63	ALA	CA-C	-5.10	1.46	1.52
1	Dt	31	ALA	CA-C	-5.10	1.46	1.52
1	Gx	13	GLU	CA-C	-5.10	1.46	1.52
1	FI	56	ALA	C-O	-5.10	1.18	1.24
1	AJ	47	THR	CA-C	-5.10	1.46	1.52
1	D4	37	GLY	CA-C	-5.10	1.46	1.51
1	De	10	GLY	CA-C	-5.10	1.47	1.52
1	DI	31	ALA	CA-C	-5.10	1.46	1.52
1	DM	37	GLY	CA-C	-5.10	1.46	1.51
1	CQ	30	ALA	CA-C	-5.10	1.46	1.52
1	DX	10	GLY	CA-C	-5.10	1.47	1.52
1	FX	56	ALA	C-O	-5.10	1.18	1.24
1	An	37	GLY	CA-C	-5.10	1.46	1.51
1	GC	45	TYR	CA-C	-5.10	1.46	1.52
1	EL	24	ALA	CA-C	-5.10	1.46	1.52
1	GO	36	VAL	C-O	-5.10	1.19	1.24
1	Db	39	GLN	CA-C	-5.09	1.46	1.52
1	Eh	24	ALA	CA-C	-5.09	1.46	1.52
1	DI	83	ARG	CA-C	-5.09	1.46	1.52
1	Cm	30	ALA	CA-C	-5.09	1.46	1.52
1	Dt	83	ARG	CA-C	-5.09	1.46	1.52
1	Fs	56	ALA	C-O	-5.09	1.18	1.24
1	Fx	56	ALA	C-O	-5.09	1.18	1.24
1	Bd	20	ALA	C-O	-5.09	1.18	1.24
1	D3	20	ALA	C-O	-5.09	1.18	1.24
1	E4	30	ALA	CA-C	-5.09	1.46	1.52
1	Ax	37	GLY	CA-C	-5.09	1.46	1.51
1	FA	57	VAL	C-O	-5.09	1.18	1.24
1	FD	77	ALA	CA-C	-5.09	1.46	1.52
1	EM	30	ALA	CA-C	-5.09	1.46	1.52
1	HP	45	TYR	C-O	-5.09	1.17	1.24
1	Ed	13	GLU	CA-C	-5.09	1.46	1.52
1	Dj	10	GLY	CA-C	-5.09	1.47	1.52
2	Xc	843	LYS	CA-C	-5.09	1.48	1.53
1	G4	13	GLU	CA-C	-5.09	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Gb	66	ASP	CA-C	-5.09	1.46	1.52
2	Xq	794	HIS	CA-C	-5.09	1.46	1.52
1	Hs	31	ALA	CA-C	-5.09	1.46	1.52
1	DK	45	TYR	CA-C	-5.09	1.46	1.52
1	GU	66	ASP	CA-C	-5.09	1.46	1.52
1	Dx	37	GLY	CA-C	-5.08	1.46	1.51
2	X2	794	HIS	CA-C	-5.08	1.46	1.52
1	B9	39	GLN	CA-C	-5.08	1.46	1.52
1	Hg	45	TYR	C-O	-5.08	1.17	1.24
1	Fo	77	ALA	CA-C	-5.08	1.46	1.52
1	Gn	13	GLU	CA-C	-5.08	1.46	1.52
1	Aw	11	MET	CA-C	-5.08	1.46	1.52
1	AL	11	MET	CA-C	-5.08	1.46	1.52
1	BR	39	GLN	CA-C	-5.08	1.46	1.52
1	G2	66	ASP	CA-C	-5.08	1.46	1.52
1	C3	56	ALA	C-O	-5.08	1.18	1.24
1	E3	24	ALA	CA-C	-5.08	1.46	1.52
1	Ac	20	ALA	CA-C	-5.08	1.46	1.52
1	Gd	13	GLU	CA-C	-5.08	1.46	1.52
1	Gn	45	TYR	CA-C	-5.08	1.46	1.52
1	CA	23	ALA	C-O	-5.08	1.18	1.24
1	GH	45	TYR	CA-C	-5.08	1.46	1.52
1	HK	13	GLU	CA-C	-5.08	1.46	1.52
1	CL	56	ALA	C-O	-5.08	1.18	1.24
1	CR	47	THR	CA-C	-5.08	1.46	1.52
1	DU	39	GLN	CA-C	-5.08	1.46	1.52
1	AV	20	ALA	CA-C	-5.08	1.46	1.52
1	GW	13	GLU	CA-C	-5.08	1.46	1.52
2	X8	843	LYS	CA-C	-5.08	1.48	1.53
1	C6	57	VAL	C-O	-5.08	1.18	1.24
1	Dn	37	GLY	CA-C	-5.08	1.46	1.51
1	Gu	20	ALA	C-O	-5.08	1.18	1.24
1	FH	56	ALA	C-O	-5.08	1.18	1.24
1	Em	24	ALA	CA-C	-5.08	1.46	1.52
1	Cq	23	ALA	C-O	-5.08	1.18	1.24
1	Ex	30	ALA	CA-C	-5.08	1.46	1.52
1	EG	24	ALA	CA-C	-5.08	1.46	1.52
1	FK	63	ALA	CA-C	-5.08	1.46	1.52
2	X7	794	HIS	CA-C	-5.08	1.46	1.52
1	Gl	66	ASP	CA-C	-5.08	1.46	1.52
1	HC	32	GLU	CA-C	-5.08	1.47	1.53
1	EQ	24	ALA	CA-C	-5.08	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	XU	794	HIS	CA-C	-5.08	1.46	1.52
1	C1	57	VAL	C-O	-5.07	1.18	1.24
1	F4	56	ALA	C-O	-5.07	1.18	1.24
2	Xb	794	HIS	CA-C	-5.07	1.46	1.52
1	Dc	20	ALA	C-O	-5.07	1.18	1.24
1	Cz	57	VAL	C-O	-5.07	1.18	1.24
1	CJ	57	VAL	C-O	-5.07	1.18	1.24
1	FM	56	ALA	C-O	-5.07	1.18	1.24
1	DV	20	ALA	C-O	-5.07	1.18	1.24
1	D5	10	GLY	CA-C	-5.07	1.47	1.52
1	Fd	56	ALA	C-O	-5.07	1.18	1.24
1	Fi	56	ALA	C-O	-5.07	1.18	1.24
1	Dr	39	GLN	CA-C	-5.07	1.46	1.52
1	Er	24	ALA	CA-C	-5.07	1.46	1.52
1	DD	10	GLY	CA-C	-5.07	1.47	1.52
1	C8	30	ALA	CA-C	-5.07	1.46	1.52
1	Dq	39	GLN	CA-C	-5.07	1.46	1.52
1	DA	45	TYR	CA-C	-5.07	1.46	1.52
1	Bi	20	ALA	C-O	-5.07	1.18	1.24
1	Dr	10	GLY	CA-C	-5.07	1.48	1.52
1	Bs	39	GLN	CA-C	-5.07	1.46	1.52
1	HA	13	GLU	CA-C	-5.07	1.46	1.52
1	DF	45	TYR	CA-C	-5.07	1.46	1.52
1	ER	30	ALA	CA-C	-5.07	1.46	1.52
1	A7	20	ALA	CA-C	-5.07	1.46	1.52
1	D7	45	TYR	CA-C	-5.07	1.46	1.52
1	Ec	24	ALA	CA-C	-5.07	1.46	1.52
1	Cs	47	THR	CA-C	-5.07	1.46	1.52
1	Cw	56	ALA	C-O	-5.07	1.18	1.24
1	GF	66	ASP	CA-C	-5.07	1.46	1.52
1	DG	10	GLY	CA-C	-5.07	1.48	1.52
1	AP	20	ALA	CA-C	-5.07	1.46	1.52
1	DP	45	TYR	CA-C	-5.07	1.46	1.52
1	EV	24	ALA	CA-C	-5.07	1.46	1.52
1	A3	11	MET	CA-C	-5.06	1.46	1.52
1	B4	20	ALA	C-O	-5.06	1.18	1.24
1	Ch	56	ALA	C-O	-5.06	1.18	1.24
1	Dk	47	THR	CA-C	-5.06	1.46	1.52
1	Es	13	GLU	CA-C	-5.06	1.46	1.52
2	Xh	843	LYS	CA-C	-5.06	1.48	1.53
1	Hq	13	GLU	CA-C	-5.06	1.46	1.52
1	Dc	39	GLN	CA-C	-5.06	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Dh	39	GLN	CA-C	-5.06	1.46	1.52
1	Cv	23	ALA	C-O	-5.06	1.18	1.24
1	AC	37	GLY	CA-C	-5.06	1.46	1.51
1	EM	13	GLU	CA-C	-5.06	1.46	1.52
1	DX	31	ALA	CA-C	-5.06	1.46	1.52
1	DV	39	GLN	CA-C	-5.06	1.46	1.52
1	D3	39	GLN	CA-C	-5.06	1.46	1.52
1	E4	13	GLU	CA-C	-5.06	1.46	1.52
1	Hb	13	GLU	CA-C	-5.06	1.46	1.52
1	De	83	ARG	CA-C	-5.06	1.46	1.52
1	Hg	13	GLU	CA-C	-5.06	1.46	1.52
1	Cf	57	VAL	C-O	-5.06	1.18	1.24
1	Dl	45	TYR	CA-C	-5.06	1.46	1.52
1	Co	60	ALA	C-O	-5.06	1.18	1.24
1	Bx	20	ALA	C-O	-5.06	1.18	1.24
1	EC	13	GLU	CA-C	-5.06	1.46	1.52
1	FN	60	ALA	C-O	-5.06	1.18	1.24
1	FR	56	ALA	C-O	-5.06	1.18	1.24
1	Dm	20	ALA	C-O	-5.06	1.18	1.24
1	Dw	20	ALA	C-O	-5.06	1.18	1.24
1	DG	20	ALA	C-O	-5.06	1.18	1.24
2	Xr	843	LYS	CA-C	-5.06	1.48	1.53
1	C5	60	ALA	C-O	-5.05	1.18	1.24
2	X3	843	LYS	CA-C	-5.05	1.48	1.53
1	Dc	10	GLY	CA-C	-5.05	1.48	1.52
1	Dh	10	GLY	CA-C	-5.05	1.48	1.52
1	Fk	9	LEU	CA-C	-5.05	1.46	1.52
1	Ap	88	VAL	C-O	-5.05	1.18	1.24
1	EH	57	VAL	C-O	-5.05	1.18	1.24
1	CN	60	ALA	C-O	-5.05	1.18	1.24
1	DV	10	GLY	CA-C	-5.05	1.48	1.52
1	H2	13	GLU	CA-C	-5.05	1.46	1.52
1	Cu	57	VAL	C-O	-5.05	1.18	1.24
2	XF	794	HIS	CA-C	-5.05	1.46	1.52
1	HR	57	VAL	C-O	-5.05	1.18	1.24
1	Cb	23	ALA	C-O	-5.05	1.18	1.24
1	Cg	23	ALA	C-O	-5.05	1.18	1.24
1	Ei	13	GLU	CA-C	-5.05	1.46	1.52
1	HA	45	TYR	C-O	-5.05	1.17	1.24
1	HK	45	TYR	C-O	-5.05	1.17	1.24
1	Hv	13	GLU	CA-C	-5.05	1.46	1.52
1	FC	10	GLY	CA-C	-5.05	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	DF	39	GLN	CA-C	-5.05	1.46	1.52
1	HF	13	GLU	CA-C	-5.05	1.46	1.52
1	DG	39	GLN	CA-C	-5.05	1.46	1.52
1	DS	10	GLY	CA-C	-5.05	1.47	1.52
1	F2	63	ALA	CA-C	-5.05	1.46	1.52
1	G7	66	ASP	CA-C	-5.05	1.46	1.52
1	F9	56	ALA	C-O	-5.05	1.18	1.24
1	Fb	47	THR	CA-C	-5.05	1.46	1.52
1	Ce	60	ALA	C-O	-5.05	1.18	1.24
1	Cj	60	ALA	C-O	-5.05	1.18	1.24
1	Gq	66	ASP	CA-C	-5.05	1.46	1.52
1	GP	66	ASP	CA-C	-5.05	1.46	1.52
1	CX	60	ALA	C-O	-5.05	1.18	1.24
1	F0	56	ALA	C-O	-5.04	1.18	1.24
1	BM	20	ALA	C-O	-5.04	1.18	1.24
1	CP	23	ALA	C-O	-5.04	1.18	1.24
1	FS	56	ALA	C-O	-5.04	1.18	1.24
1	FU	47	THR	CA-C	-5.04	1.46	1.52
1	AT	88	VAL	C-O	-5.04	1.18	1.24
1	DX	83	ARG	CA-C	-5.04	1.46	1.52
2	Xm	843	LYS	CA-C	-5.04	1.48	1.53
1	D2	45	TYR	CA-C	-5.04	1.46	1.52
1	Cr	30	ALA	CA-C	-5.04	1.46	1.52
1	Fu	9	LEU	CA-C	-5.04	1.46	1.52
1	BF	39	GLN	CA-C	-5.04	1.46	1.52
1	Fn	56	ALA	C-O	-5.04	1.18	1.24
1	CF	23	ALA	C-O	-5.04	1.18	1.24
2	XL	843	LYS	CA-C	-5.04	1.48	1.53
1	Ag	20	ALA	CA-C	-5.04	1.46	1.52
1	Do	10	GLY	CA-C	-5.04	1.47	1.52
1	Es	56	ALA	N-CA	-5.04	1.40	1.46
1	BC	39	GLN	CA-C	-5.04	1.46	1.52
1	FC	56	ALA	C-O	-5.04	1.18	1.24
3	PP	79	GLN	CA-C	-5.04	1.46	1.52
1	D3	10	GLY	CA-C	-5.04	1.48	1.52
1	Ex	13	GLU	CA-C	-5.04	1.46	1.52
1	DC	31	ALA	CA-C	-5.04	1.46	1.52
1	B7	39	GLN	CA-C	-5.04	1.46	1.52
1	C7	23	ALA	C-O	-5.04	1.18	1.24
1	Ed	57	VAL	C-O	-5.04	1.18	1.24
1	Ei	57	VAL	C-O	-5.04	1.18	1.24
1	Ck	57	VAL	C-O	-5.04	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BA	39	GLN	CA-C	-5.04	1.46	1.52
1	DL	20	ALA	C-O	-5.04	1.18	1.24
1	BP	39	GLN	CA-C	-5.04	1.46	1.52
1	FT	9	LEU	CA-C	-5.04	1.46	1.52
1	EW	57	VAL	C-O	-5.04	1.18	1.24
1	C2	23	ALA	C-O	-5.03	1.18	1.24
1	D6	47	THR	CA-C	-5.03	1.46	1.52
1	F6	9	LEU	CA-C	-5.03	1.46	1.52
1	D0	10	GLY	CA-C	-5.03	1.47	1.52
1	Gg	66	ASP	CA-C	-5.03	1.46	1.52
1	Hi	32	GLU	CA-C	-5.03	1.47	1.53
1	Hr	83	ARG	CA-C	-5.03	1.46	1.52
1	CC	47	THR	CA-C	-5.03	1.46	1.52
1	CK	23	ALA	C-O	-5.03	1.18	1.24
1	DO	47	THR	CA-C	-5.03	1.46	1.52
1	H2	45	TYR	C-O	-5.03	1.18	1.24
1	D8	20	ALA	C-O	-5.03	1.18	1.24
1	Bj	24	ALA	CA-C	-5.03	1.46	1.52
1	DQ	20	ALA	C-O	-5.03	1.18	1.24
1	A2	20	ALA	CA-C	-5.03	1.46	1.52
1	F0	77	ALA	CA-C	-5.03	1.46	1.52
1	Ap	9	LEU	CA-C	-5.03	1.46	1.52
1	Ar	20	ALA	CA-C	-5.03	1.46	1.52
1	Fv	63	ALA	CA-C	-5.03	1.46	1.52
1	Au	9	LEU	CA-C	-5.03	1.46	1.52
1	AA	20	ALA	CA-C	-5.03	1.46	1.52
1	AE	88	VAL	C-O	-5.03	1.18	1.24
1	BI	64	GLY	CA-C	-5.03	1.46	1.52
1	BH	20	ALA	C-O	-5.03	1.18	1.24
1	AK	20	ALA	CA-C	-5.03	1.46	1.52
3	PU	79	GLN	CA-C	-5.03	1.46	1.52
1	Fe	77	ALA	CA-C	-5.03	1.46	1.52
1	FX	77	ALA	CA-C	-5.03	1.46	1.52
1	H7	45	TYR	C-O	-5.03	1.18	1.24
1	H9	32	GLU	CA-C	-5.03	1.47	1.53
1	Hl	45	TYR	C-O	-5.03	1.18	1.24
1	Ak	9	LEU	CA-C	-5.03	1.46	1.52
1	Et	30	ALA	CA-C	-5.03	1.46	1.52
1	Hx	32	GLU	CA-C	-5.03	1.47	1.53
1	AE	9	LEU	CA-C	-5.03	1.46	1.52
1	DE	47	THR	CA-C	-5.03	1.46	1.52
1	HM	57	VAL	C-O	-5.03	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	HR	32	GLU	CA-C	-5.03	1.47	1.53
1	F1	9	LEU	CA-C	-5.03	1.46	1.52
1	Dj	83	ARG	CA-C	-5.03	1.46	1.52
1	Am	11	MET	CA-C	-5.03	1.46	1.52
1	Es	57	VAL	C-O	-5.03	1.18	1.24
2	Xw	843	LYS	CA-C	-5.03	1.48	1.53
1	Ex	57	VAL	C-O	-5.03	1.18	1.24
1	Fz	9	LEU	CA-C	-5.03	1.46	1.52
1	CB	30	ALA	CA-C	-5.03	1.46	1.52
1	FE	9	LEU	CA-C	-5.03	1.46	1.52
1	CI	60	ALA	C-O	-5.03	1.18	1.24
1	AG	11	MET	CA-C	-5.03	1.46	1.52
1	Aa	88	VAL	C-O	-5.02	1.18	1.24
1	Dm	39	GLN	CA-C	-5.02	1.46	1.52
1	HB	83	ARG	CA-C	-5.02	1.46	1.52
1	HL	83	ARG	CA-C	-5.02	1.46	1.52
1	H4	32	GLU	CA-C	-5.02	1.47	1.53
1	F9	10	GLY	CA-C	-5.02	1.47	1.52
1	Fo	56	ALA	C-O	-5.02	1.18	1.24
1	HU	13	GLU	CA-C	-5.02	1.46	1.52
1	C0	60	ALA	C-O	-5.02	1.18	1.24
1	Aa	9	LEU	CA-C	-5.02	1.46	1.52
2	Xg	794	HIS	CA-C	-5.02	1.46	1.52
1	Af	9	LEU	CA-C	-5.02	1.46	1.52
1	Dz	47	THR	CA-C	-5.02	1.46	1.52
1	Fz	30	ALA	CA-C	-5.02	1.46	1.52
1	FI	60	ALA	C-O	-5.02	1.18	1.24
1	CG	30	ALA	CA-C	-5.02	1.46	1.52
2	XK	794	HIS	CA-C	-5.02	1.46	1.52
1	BN	24	ALA	CA-C	-5.02	1.46	1.52
1	CS	60	ALA	C-O	-5.02	1.18	1.24
1	AT	9	LEU	CA-C	-5.02	1.46	1.52
1	H8	83	ARG	CA-C	-5.02	1.46	1.52
1	Db	45	TYR	CA-C	-5.02	1.46	1.52
1	Hw	83	ARG	CA-C	-5.02	1.46	1.52
1	HG	83	ARG	CA-C	-5.02	1.46	1.52
1	HQ	83	ARG	CA-C	-5.02	1.46	1.52
1	DU	45	TYR	CA-C	-5.02	1.46	1.52
1	E9	57	VAL	C-O	-5.02	1.18	1.24
1	Dg	45	TYR	CA-C	-5.02	1.46	1.52
1	Fj	60	ALA	C-O	-5.02	1.18	1.24
1	En	57	VAL	C-O	-5.02	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Fy	60	ALA	C-O	-5.02	1.18	1.24
1	Cw	11	MET	CA-C	-5.02	1.46	1.52
1	Ew	24	ALA	CA-C	-5.02	1.46	1.52
1	HE	26	ALA	C-O	-5.02	1.18	1.24
1	ER	57	VAL	C-O	-5.02	1.18	1.24
1	GA	66	ASP	CA-C	-5.02	1.46	1.52
1	D1	47	THR	CA-C	-5.01	1.46	1.52
1	F5	60	ALA	C-O	-5.01	1.18	1.24
1	E4	57	VAL	C-O	-5.01	1.18	1.24
3	Pq	79	GLN	CA-C	-5.01	1.46	1.52
1	Bs	20	ALA	C-O	-5.01	1.18	1.24
1	Bv	39	GLN	CA-C	-5.01	1.46	1.52
1	FD	56	ALA	C-O	-5.01	1.18	1.24
1	EC	57	VAL	C-O	-5.01	1.18	1.24
1	FF	47	THR	CA-C	-5.01	1.46	1.52
1	Fq	47	THR	CA-C	-5.01	1.46	1.52
1	Ar	11	MET	CA-C	-5.01	1.46	1.52
1	A1	9	LEU	CA-C	-5.01	1.46	1.52
1	F7	63	ALA	CA-C	-5.01	1.46	1.52
1	A6	9	LEU	CA-C	-5.01	1.46	1.52
1	A8	11	MET	CA-C	-5.01	1.46	1.52
1	D8	10	GLY	CA-C	-5.01	1.48	1.52
1	E9	13	GLU	CA-C	-5.01	1.46	1.52
1	E9	56	ALA	N-CA	-5.01	1.40	1.46
1	H9	57	VAL	C-O	-5.01	1.18	1.24
1	Ch	30	ALA	CA-C	-5.01	1.46	1.52
1	Cl	23	ALA	C-O	-5.01	1.18	1.24
1	Hn	57	VAL	C-O	-5.01	1.18	1.24
1	Az	9	LEU	CA-C	-5.01	1.46	1.52
1	FP	63	ALA	CA-C	-5.01	1.46	1.52
1	AO	9	LEU	CA-C	-5.01	1.46	1.52
1	AQ	11	MET	CA-C	-5.01	1.46	1.52
1	DQ	10	GLY	CA-C	-5.01	1.48	1.52
1	ER	13	GLU	CA-C	-5.01	1.46	1.52
2	XG	843	LYS	CA-C	-5.01	1.48	1.53
1	Fa	9	LEU	CA-C	-5.01	1.46	1.52
1	Ed	56	ALA	N-CA	-5.01	1.40	1.46
1	Dp	47	THR	CA-C	-5.01	1.46	1.52
1	Dy	10	GLY	CA-C	-5.01	1.47	1.52
1	AF	20	ALA	CA-C	-5.01	1.46	1.52
1	EW	56	ALA	N-CA	-5.01	1.40	1.46
1	Ee	30	ALA	CA-C	-5.01	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	En	13	GLU	CA-C	-5.01	1.46	1.52
1	EX	30	ALA	CA-C	-5.01	1.46	1.52
1	F4	10	GLY	CA-C	-5.00	1.47	1.52
1	Av	20	ALA	CA-C	-5.00	1.46	1.52
1	Dv	45	TYR	CA-C	-5.00	1.46	1.52
1	EI	30	ALA	CA-C	-5.00	1.46	1.52
1	FM	10	GLY	CA-C	-5.00	1.47	1.52
3	P2	79	GLN	CA-C	-5.00	1.46	1.52
1	Fb	63	ALA	CA-C	-5.00	1.46	1.52
1	Ak	88	VAL	C-O	-5.00	1.18	1.24
1	DB	20	ALA	C-O	-5.00	1.18	1.24
1	EH	56	ALA	N-CA	-5.00	1.40	1.46
3	PK	79	GLN	CA-C	-5.00	1.46	1.52
1	FR	10	GLY	CA-C	-5.00	1.47	1.52
1	D5	83	ARG	CA-C	-5.00	1.46	1.52
1	D8	39	GLN	CA-C	-5.00	1.46	1.52
1	Ab	20	ALA	CA-C	-5.00	1.46	1.52
1	Bb	39	GLN	CA-C	-5.00	1.46	1.52
1	Au	88	VAL	C-O	-5.00	1.18	1.24
1	Bw	35	LEU	CA-C	-5.00	1.46	1.52
1	Dw	39	GLN	CA-C	-5.00	1.46	1.52
1	DD	83	ARG	CA-C	-5.00	1.46	1.52
1	DN	83	ARG	CA-C	-5.00	1.46	1.52
1	DQ	39	GLN	CA-C	-5.00	1.46	1.52
1	AU	20	ALA	CA-C	-5.00	1.46	1.52
1	BU	39	GLN	CA-C	-5.00	1.46	1.52

All (5491) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Xw	808	GLY	N-CA-C	29.61	148.31	112.49
2	Xr	808	GLY	N-CA-C	29.61	148.31	112.49
2	Xc	808	GLY	N-CA-C	29.60	148.31	112.49
2	XL	808	GLY	N-CA-C	29.60	148.31	112.49
2	X3	808	GLY	N-CA-C	29.60	148.30	112.49
2	Xh	808	GLY	N-CA-C	29.60	148.30	112.49
2	XQ	808	GLY	N-CA-C	29.59	148.30	112.49
2	X8	808	GLY	N-CA-C	29.59	148.30	112.49
2	XB	808	GLY	N-CA-C	29.59	148.29	112.49
2	XG	808	GLY	N-CA-C	29.58	148.28	112.49
2	XV	808	GLY	N-CA-C	29.57	148.27	112.49
2	Xm	808	GLY	N-CA-C	29.57	148.26	112.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	PH	55	SER	N-CA-C	20.14	132.62	111.07
3	PR	55	SER	N-CA-C	20.12	132.60	111.07
3	PT	55	SER	N-CA-C	20.12	132.60	111.07
3	Pd	55	SER	N-CA-C	20.11	132.59	111.07
3	Ps	55	SER	N-CA-C	20.09	132.57	111.07
3	PE	55	SER	N-CA-C	20.09	132.57	111.07
3	Pu	55	SER	N-CA-C	20.09	132.56	111.07
3	P9	55	SER	N-CA-C	20.08	132.56	111.07
3	Pp	55	SER	N-CA-C	20.08	132.56	111.07
3	PW	55	SER	N-CA-C	20.08	132.56	111.07
3	Pa	55	SER	N-CA-C	20.08	132.55	111.07
3	PC	55	SER	N-CA-C	20.07	132.55	111.07
3	P1	55	SER	N-CA-C	20.07	132.55	111.07
3	PJ	55	SER	N-CA-C	20.07	132.55	111.07
3	P4	55	SER	N-CA-C	20.07	132.54	111.07
3	Pn	55	SER	N-CA-C	20.07	132.54	111.07
3	Px	55	SER	N-CA-C	20.06	132.54	111.07
3	Pz	55	SER	N-CA-C	20.06	132.53	111.07
3	PM	55	SER	N-CA-C	20.06	132.54	111.07
3	Pi	55	SER	N-CA-C	20.05	132.53	111.07
3	PO	55	SER	N-CA-C	20.05	132.52	111.07
3	P6	55	SER	N-CA-C	20.04	132.51	111.07
3	Pf	55	SER	N-CA-C	20.04	132.51	111.07
3	Pk	55	SER	N-CA-C	20.01	132.48	111.07
3	Pr	55	SER	N-CA-C	17.85	130.17	111.07
3	Pc	55	SER	N-CA-C	17.84	130.15	111.07
3	Ph	55	SER	N-CA-C	17.82	130.14	111.07
3	PQ	55	SER	N-CA-C	17.81	130.13	111.07
3	PV	55	SER	N-CA-C	17.81	130.13	111.07
3	PG	55	SER	N-CA-C	17.80	130.12	111.07
3	P8	55	SER	N-CA-C	17.80	130.11	111.07
3	P3	55	SER	N-CA-C	17.79	130.11	111.07
3	PL	55	SER	N-CA-C	17.79	130.11	111.07
3	Pm	55	SER	N-CA-C	17.79	130.11	111.07
3	Pw	55	SER	N-CA-C	17.78	130.09	111.07
3	PB	55	SER	N-CA-C	17.78	130.09	111.07
3	Py	55	SER	N-CA-C	16.88	129.13	111.07
3	PI	55	SER	N-CA-C	16.87	129.12	111.07
3	P5	55	SER	N-CA-C	16.86	129.11	111.07
3	P0	55	SER	N-CA-C	16.86	129.11	111.07
3	PS	55	SER	N-CA-C	16.86	129.11	111.07
3	Pe	55	SER	N-CA-C	16.86	129.10	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	PD	55	SER	N-CA-C	16.85	129.10	111.07
3	Pt	55	SER	N-CA-C	16.84	129.09	111.07
3	PN	55	SER	N-CA-C	16.84	129.09	111.07
3	PX	55	SER	N-CA-C	16.84	129.09	111.07
3	Po	55	SER	N-CA-C	16.83	129.08	111.07
3	Pj	55	SER	N-CA-C	16.82	129.07	111.07
1	CX	74	GLY	N-CA-C	13.96	129.28	110.43
1	Ct	74	GLY	N-CA-C	13.94	129.25	110.43
1	CN	74	GLY	N-CA-C	13.94	129.25	110.43
1	C5	74	GLY	N-CA-C	13.94	129.25	110.43
1	CI	74	GLY	N-CA-C	13.94	129.25	110.43
1	Ce	74	GLY	N-CA-C	13.94	129.25	110.43
1	Cy	74	GLY	N-CA-C	13.93	129.24	110.43
1	Cj	74	GLY	N-CA-C	13.93	129.23	110.43
1	C0	74	GLY	N-CA-C	13.91	129.21	110.43
1	CS	74	GLY	N-CA-C	13.91	129.21	110.43
1	CD	74	GLY	N-CA-C	13.90	129.19	110.43
1	Co	74	GLY	N-CA-C	13.89	129.18	110.43
1	BB	74	GLY	N-CA-C	13.54	131.12	111.76
1	B8	74	GLY	N-CA-C	13.54	131.12	111.76
1	Bm	74	GLY	N-CA-C	13.54	131.12	111.76
1	BL	74	GLY	N-CA-C	13.54	131.12	111.76
1	Br	74	GLY	N-CA-C	13.53	131.10	111.76
1	Bw	74	GLY	N-CA-C	13.53	131.10	111.76
2	XA	811	GLY	N-CA-C	13.53	128.19	112.50
1	B3	74	GLY	N-CA-C	13.52	131.10	111.76
1	BQ	74	GLY	N-CA-C	13.52	131.09	111.76
1	Bh	74	GLY	N-CA-C	13.52	131.09	111.76
1	Bc	74	GLY	N-CA-C	13.49	131.06	111.76
2	Xl	811	GLY	N-CA-C	13.49	128.15	112.50
1	CF	74	GLY	N-CA-C	13.49	131.05	111.76
1	BV	74	GLY	N-CA-C	13.49	131.06	111.76
1	BG	74	GLY	N-CA-C	13.49	131.05	111.76
1	CA	74	GLY	N-CA-C	13.49	131.04	111.76
1	Cq	74	GLY	N-CA-C	13.48	131.04	111.76
2	X7	811	GLY	N-CA-C	13.47	128.13	112.50
1	Cl	74	GLY	N-CA-C	13.47	131.02	111.76
1	C7	74	GLY	N-CA-C	13.47	131.02	111.76
2	Xg	811	GLY	N-CA-C	13.46	128.12	112.50
2	XP	811	GLY	N-CA-C	13.46	128.12	112.50
2	X2	811	GLY	N-CA-C	13.46	128.12	112.50
1	Cb	74	GLY	N-CA-C	13.46	131.00	111.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CU	74	GLY	N-CA-C	13.46	131.00	111.76
2	XU	811	GLY	N-CA-C	13.46	128.11	112.50
1	C2	74	GLY	N-CA-C	13.46	131.00	111.76
1	CP	74	GLY	N-CA-C	13.45	131.00	111.76
1	Cg	74	GLY	N-CA-C	13.45	131.00	111.76
1	CK	74	GLY	N-CA-C	13.45	131.00	111.76
2	Xb	811	GLY	N-CA-C	13.44	128.09	112.50
2	Xv	811	GLY	N-CA-C	13.44	128.09	112.50
2	XF	811	GLY	N-CA-C	13.44	128.09	112.50
1	Cv	74	GLY	N-CA-C	13.44	130.97	111.76
2	Xq	811	GLY	N-CA-C	13.43	128.08	112.50
2	XK	811	GLY	N-CA-C	13.42	128.06	112.50
1	FW	74	GLY	N-CA-C	12.12	126.79	110.43
1	FH	74	GLY	N-CA-C	12.11	126.77	110.43
1	Fs	74	GLY	N-CA-C	12.09	126.75	110.43
1	Fd	74	GLY	N-CA-C	12.08	126.74	110.43
1	FM	74	GLY	N-CA-C	12.07	126.72	110.43
1	F4	74	GLY	N-CA-C	12.06	126.72	110.43
1	Fi	74	GLY	N-CA-C	12.05	126.70	110.43
1	F9	74	GLY	N-CA-C	12.05	126.70	110.43
1	Fx	74	GLY	N-CA-C	12.05	126.70	110.43
1	FR	74	GLY	N-CA-C	12.05	126.70	110.43
1	AW	74	GLY	N-CA-C	12.04	131.87	112.84
1	Fn	74	GLY	N-CA-C	12.04	126.68	110.43
1	Ai	74	GLY	N-CA-C	12.01	131.82	112.84
1	FC	74	GLY	N-CA-C	12.01	126.65	110.43
1	An	74	GLY	N-CA-C	12.01	131.81	112.84
1	AC	74	GLY	N-CA-C	12.00	131.80	112.84
1	At	74	GLY	N-CA-C	12.00	126.25	111.85
1	AI	74	GLY	N-CA-C	12.00	126.25	111.85
1	Ae	74	GLY	N-CA-C	11.98	126.23	111.85
1	AN	74	GLY	N-CA-C	11.98	126.23	111.85
1	AX	74	GLY	N-CA-C	11.96	126.20	111.85
1	Aj	74	GLY	N-CA-C	11.95	126.19	111.85
1	A5	74	GLY	N-CA-C	11.94	126.18	111.85
1	Ay	74	GLY	N-CA-C	11.94	126.18	111.85
1	A0	74	GLY	N-CA-C	11.89	126.12	111.85
1	Ao	74	GLY	N-CA-C	11.89	126.11	111.85
1	AS	74	GLY	N-CA-C	11.88	126.10	111.85
1	AD	74	GLY	N-CA-C	11.86	126.09	111.85
1	FB	74	GLY	N-CA-C	11.85	128.70	111.76
1	FQ	74	GLY	N-CA-C	11.84	128.69	111.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Fh	74	GLY	N-CA-C	11.83	128.68	111.76
1	FL	74	GLY	N-CA-C	11.83	128.67	111.76
1	F3	74	GLY	N-CA-C	11.82	128.67	111.76
1	Fw	74	GLY	N-CA-C	11.82	128.66	111.76
1	F8	74	GLY	N-CA-C	11.81	128.65	111.76
1	Fc	74	GLY	N-CA-C	11.81	128.64	111.76
1	FV	74	GLY	N-CA-C	11.79	128.61	111.76
1	Fr	74	GLY	N-CA-C	11.78	128.61	111.76
1	Fm	74	GLY	N-CA-C	11.78	128.60	111.76
1	FG	74	GLY	N-CA-C	11.77	128.59	111.76
2	XS	861	ILE	N-CA-C	-11.59	91.00	108.85
2	Xo	861	ILE	N-CA-C	-11.58	91.02	108.85
2	X0	861	ILE	N-CA-C	-11.57	91.03	108.85
2	Xt	861	ILE	N-CA-C	-11.57	91.03	108.85
2	Xy	861	ILE	N-CA-C	-11.57	91.04	108.85
2	XN	861	ILE	N-CA-C	-11.57	91.04	108.85
2	Xj	861	ILE	N-CA-C	-11.56	91.04	108.85
2	XX	861	ILE	N-CA-C	-11.56	91.04	108.85
2	X5	861	ILE	N-CA-C	-11.56	91.05	108.85
2	Xe	861	ILE	N-CA-C	-11.56	91.05	108.85
2	XD	861	ILE	N-CA-C	-11.56	91.05	108.85
2	XI	861	ILE	N-CA-C	-11.54	91.07	108.85
1	HK	74	GLY	N-CA-C	11.47	130.22	112.45
1	HU	74	GLY	N-CA-C	11.45	130.20	112.45
1	Hq	74	GLY	N-CA-C	11.45	130.20	112.45
1	HF	74	GLY	N-CA-C	11.45	130.20	112.45
1	HA	74	GLY	N-CA-C	11.45	130.19	112.45
1	Hv	74	GLY	N-CA-C	11.44	130.18	112.45
1	Hl	74	GLY	N-CA-C	11.44	130.17	112.45
1	H2	74	GLY	N-CA-C	11.43	130.17	112.45
1	Hg	74	GLY	N-CA-C	11.43	130.17	112.45
1	Hb	74	GLY	N-CA-C	11.43	130.17	112.45
1	H7	74	GLY	N-CA-C	11.42	130.15	112.45
1	HP	74	GLY	N-CA-C	11.42	130.15	112.45
1	GH	74	GLY	N-CA-C	11.34	125.74	110.43
1	GW	74	GLY	N-CA-C	11.34	125.74	110.43
1	Gn	74	GLY	N-CA-C	11.33	125.73	110.43
1	Db	74	GLY	N-CA-C	11.32	127.95	111.76
1	DU	74	GLY	N-CA-C	11.32	127.95	111.76
1	Gd	74	GLY	N-CA-C	11.32	125.71	110.43
1	Dq	74	GLY	N-CA-C	11.32	127.94	111.76
1	Gx	74	GLY	N-CA-C	11.32	125.71	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Gi	74	GLY	N-CA-C	11.32	125.71	110.43
1	DF	74	GLY	N-CA-C	11.31	127.94	111.76
1	Gs	74	GLY	N-CA-C	11.31	125.70	110.43
1	GM	74	GLY	N-CA-C	11.31	125.70	110.43
1	G9	74	GLY	N-CA-C	11.31	125.70	110.43
1	GC	74	GLY	N-CA-C	11.30	125.69	110.43
1	G4	74	GLY	N-CA-C	11.30	125.68	110.43
1	Dv	74	GLY	N-CA-C	11.30	127.92	111.76
1	DA	74	GLY	N-CA-C	11.30	127.92	111.76
1	Dg	74	GLY	N-CA-C	11.29	127.91	111.76
1	DK	74	GLY	N-CA-C	11.29	127.91	111.76
1	DP	74	GLY	N-CA-C	11.29	127.90	111.76
1	GR	74	GLY	N-CA-C	11.29	125.67	110.43
1	D2	74	GLY	N-CA-C	11.28	127.90	111.76
1	D7	74	GLY	N-CA-C	11.27	127.88	111.76
1	Dl	74	GLY	N-CA-C	11.27	127.87	111.76
1	Ek	74	GLY	N-CA-C	11.03	130.26	112.84
1	Ef	74	GLY	N-CA-C	11.02	130.26	112.84
1	E6	74	GLY	N-CA-C	11.02	130.25	112.84
1	Ep	74	GLY	N-CA-C	11.02	130.25	112.84
1	Ez	74	GLY	N-CA-C	11.02	130.25	112.84
1	Ea	74	GLY	N-CA-C	11.02	130.25	112.84
1	Eu	74	GLY	N-CA-C	11.01	130.23	112.84
1	E1	74	GLY	N-CA-C	11.00	130.23	112.84
1	EJ	74	GLY	N-CA-C	11.00	130.23	112.84
1	EO	74	GLY	N-CA-C	11.00	130.23	112.84
1	EE	74	GLY	N-CA-C	10.99	130.21	112.84
1	ET	74	GLY	N-CA-C	10.99	130.21	112.84
1	AH	74	GLY	N-CA-C	10.99	131.87	112.53
1	Ad	74	GLY	N-CA-C	10.98	131.85	112.53
1	AR	74	GLY	N-CA-C	10.98	131.85	112.53
1	BH	74	GLY	N-CA-C	10.98	127.56	112.52
1	As	74	GLY	N-CA-C	10.97	131.84	112.53
1	Hi	74	GLY	N-CA-C	10.97	131.48	112.83
1	Hn	74	GLY	N-CA-C	10.97	131.48	112.83
1	HC	74	GLY	N-CA-C	10.96	131.47	112.83
1	H4	74	GLY	N-CA-C	10.96	131.47	112.83
1	HM	74	GLY	N-CA-C	10.96	131.47	112.83
1	A9	74	GLY	N-CA-C	10.96	131.82	112.53
1	H9	74	GLY	N-CA-C	10.96	131.46	112.83
1	Hd	74	GLY	N-CA-C	10.96	131.46	112.83
1	A4	74	GLY	N-CA-C	10.96	131.81	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Hs	74	GLY	N-CA-C	10.95	131.45	112.83
1	Ax	74	GLY	N-CA-C	10.96	131.81	112.53
1	HH	74	GLY	N-CA-C	10.95	131.45	112.83
1	AM	74	GLY	N-CA-C	10.95	131.80	112.53
1	BM	74	GLY	N-CA-C	10.94	127.51	112.52
1	BW	74	GLY	N-CA-C	10.94	127.51	112.52
1	Hx	74	GLY	N-CA-C	10.94	131.43	112.83
1	HW	74	GLY	N-CA-C	10.94	131.43	112.83
1	B4	74	GLY	N-CA-C	10.94	127.50	112.52
1	Bd	74	GLY	N-CA-C	10.94	127.50	112.52
1	BC	74	GLY	N-CA-C	10.94	127.50	112.52
1	HR	74	GLY	N-CA-C	10.92	131.40	112.83
1	Bi	74	GLY	N-CA-C	10.92	127.48	112.52
1	B9	74	GLY	N-CA-C	10.91	127.47	112.52
1	Bx	74	GLY	N-CA-C	10.91	127.47	112.52
1	Dt	74	GLY	N-CA-C	10.91	127.47	112.52
1	Bs	74	GLY	N-CA-C	10.90	127.46	112.52
1	BR	74	GLY	N-CA-C	10.90	127.45	112.52
1	Bn	74	GLY	N-CA-C	10.88	127.42	112.52
1	Dj	74	GLY	N-CA-C	10.87	127.41	112.52
1	De	74	GLY	N-CA-C	10.86	127.40	112.52
1	DX	74	GLY	N-CA-C	10.86	127.40	112.52
1	Do	74	GLY	N-CA-C	10.86	127.39	112.52
1	DI	74	GLY	N-CA-C	10.85	127.38	112.52
1	D0	74	GLY	N-CA-C	10.84	127.37	112.52
1	D5	74	GLY	N-CA-C	10.84	127.36	112.52
1	Dy	74	GLY	N-CA-C	10.84	127.36	112.52
1	DD	74	GLY	N-CA-C	10.84	127.36	112.52
1	CC	74	GLY	N-CA-C	10.84	132.38	112.77
1	CW	74	GLY	N-CA-C	10.84	132.38	112.77
1	DN	74	GLY	N-CA-C	10.84	127.36	112.52
1	Ci	74	GLY	N-CA-C	10.83	132.37	112.77
1	DS	74	GLY	N-CA-C	10.82	127.35	112.52
1	C4	74	GLY	N-CA-C	10.82	132.35	112.77
1	Cx	74	GLY	N-CA-C	10.82	132.35	112.77
1	CM	74	GLY	N-CA-C	10.82	132.35	112.77
1	C9	74	GLY	N-CA-C	10.81	132.34	112.77
1	Cd	74	GLY	N-CA-C	10.81	132.33	112.77
1	Cs	74	GLY	N-CA-C	10.81	132.33	112.77
1	CR	74	GLY	N-CA-C	10.79	132.29	112.77
1	Cn	74	GLY	N-CA-C	10.79	132.29	112.77
1	CH	74	GLY	N-CA-C	10.79	132.29	112.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bg	74	GLY	N-CA-C	10.57	130.80	112.83
1	Bb	74	GLY	N-CA-C	10.56	130.78	112.83
1	BF	74	GLY	N-CA-C	10.56	130.78	112.83
1	Fq	74	GLY	N-CA-C	10.56	131.88	112.77
1	FU	74	GLY	N-CA-C	10.56	131.88	112.77
1	B2	74	GLY	N-CA-C	10.55	130.77	112.83
1	FF	74	GLY	N-CA-C	10.55	131.87	112.77
1	BU	74	GLY	N-CA-C	10.55	130.77	112.83
1	Bv	74	GLY	N-CA-C	10.55	130.76	112.83
1	Fb	74	GLY	N-CA-C	10.55	131.86	112.77
1	FK	74	GLY	N-CA-C	10.54	131.84	112.77
1	Bq	74	GLY	N-CA-C	10.53	130.73	112.83
1	BK	74	GLY	N-CA-C	10.53	130.74	112.83
1	Fl	74	GLY	N-CA-C	10.53	131.83	112.77
1	Fg	74	GLY	N-CA-C	10.53	131.82	112.77
1	F7	74	GLY	N-CA-C	10.52	131.82	112.77
1	FP	74	GLY	N-CA-C	10.52	131.82	112.77
1	F2	74	GLY	N-CA-C	10.52	131.81	112.77
1	BA	74	GLY	N-CA-C	10.52	130.71	112.83
1	FA	74	GLY	N-CA-C	10.52	131.81	112.77
1	Fv	74	GLY	N-CA-C	10.52	131.80	112.77
1	B7	74	GLY	N-CA-C	10.51	130.69	112.83
1	Bl	74	GLY	N-CA-C	10.50	130.68	112.83
1	BP	74	GLY	N-CA-C	10.48	130.65	112.83
1	CV	94	LYS	N-CA-C	10.36	122.65	111.36
1	Cm	94	LYS	N-CA-C	10.35	122.64	111.36
1	CB	94	LYS	N-CA-C	10.35	122.64	111.36
1	Bv	76	VAL	N-CA-C	-10.34	101.85	111.67
1	BK	76	VAL	N-CA-C	-10.33	101.86	111.67
1	C8	94	LYS	N-CA-C	10.32	122.61	111.36
1	Cc	94	LYS	N-CA-C	10.32	122.61	111.36
1	Ch	94	LYS	N-CA-C	10.32	122.61	111.36
1	BU	76	VAL	N-CA-C	-10.32	101.86	111.67
1	B2	76	VAL	N-CA-C	-10.32	101.87	111.67
1	B7	76	VAL	N-CA-C	-10.32	101.87	111.67
1	Cr	94	LYS	N-CA-C	10.32	122.61	111.36
1	Cw	94	LYS	N-CA-C	10.32	122.61	111.36
1	CQ	94	LYS	N-CA-C	10.31	122.60	111.36
1	Bl	76	VAL	N-CA-C	-10.31	101.87	111.67
1	CL	94	LYS	N-CA-C	10.31	122.60	111.36
2	XO	808	GLY	N-CA-C	10.31	137.61	113.18
1	Bq	76	VAL	N-CA-C	-10.31	101.88	111.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Xz	808	GLY	N-CA-C	10.30	137.60	113.18
1	BA	76	VAL	N-CA-C	-10.30	101.89	111.67
1	Bb	76	VAL	N-CA-C	-10.30	101.89	111.67
1	Bg	76	VAL	N-CA-C	-10.30	101.89	111.67
2	X6	808	GLY	N-CA-C	10.30	137.58	113.18
1	C3	94	LYS	N-CA-C	10.29	122.58	111.36
1	BP	76	VAL	N-CA-C	-10.29	101.89	111.67
2	Xk	808	GLY	N-CA-C	10.28	137.55	113.18
2	Xf	808	GLY	N-CA-C	10.28	137.53	113.18
2	Xp	808	GLY	N-CA-C	10.28	137.53	113.18
2	XE	808	GLY	N-CA-C	10.27	137.53	113.18
2	XT	808	GLY	N-CA-C	10.27	137.53	113.18
2	Xa	808	GLY	N-CA-C	10.27	137.52	113.18
1	CG	94	LYS	N-CA-C	10.27	122.55	111.36
2	X1	808	GLY	N-CA-C	10.27	137.51	113.18
2	XJ	808	GLY	N-CA-C	10.27	137.51	113.18
2	Xu	808	GLY	N-CA-C	10.26	137.49	113.18
1	BF	76	VAL	N-CA-C	-10.25	101.93	111.67
2	Xu	861	ILE	N-CA-C	-10.19	93.75	108.53
1	DH	74	GLY	N-CA-C	10.19	126.33	111.76
2	XJ	861	ILE	N-CA-C	-10.18	93.77	108.53
2	Xp	861	ILE	N-CA-C	-10.18	93.77	108.53
2	XE	861	ILE	N-CA-C	-10.18	93.77	108.53
2	X1	861	ILE	N-CA-C	-10.17	93.78	108.53
2	Xa	861	ILE	N-CA-C	-10.17	93.79	108.53
2	Xf	861	ILE	N-CA-C	-10.16	93.79	108.53
1	Dd	74	GLY	N-CA-C	10.16	126.29	111.76
1	DW	74	GLY	N-CA-C	10.16	126.29	111.76
2	X6	861	ILE	N-CA-C	-10.16	93.80	108.53
2	Xk	861	ILE	N-CA-C	-10.16	93.80	108.53
1	GQ	74	GLY	N-CA-C	10.14	126.27	111.76
2	XT	861	ILE	N-CA-C	-10.14	93.82	108.53
2	XO	861	ILE	N-CA-C	-10.14	93.83	108.53
1	Ds	74	GLY	N-CA-C	10.14	126.26	111.76
1	GB	74	GLY	N-CA-C	10.14	126.26	111.76
2	Xz	861	ILE	N-CA-C	-10.13	93.84	108.53
1	HS	82	ALA	N-CA-C	10.13	122.40	111.36
1	Dn	74	GLY	N-CA-C	10.12	126.24	111.76
1	Dx	74	GLY	N-CA-C	10.12	126.24	111.76
1	D4	74	GLY	N-CA-C	10.12	126.23	111.76
1	DM	74	GLY	N-CA-C	10.12	126.23	111.76
1	Fk	74	GLY	N-CA-C	10.12	131.54	112.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	FE	74	GLY	N-CA-C	10.12	131.54	112.62
1	G8	74	GLY	N-CA-C	10.12	126.23	111.76
1	F6	74	GLY	N-CA-C	10.12	131.53	112.62
1	Gh	74	GLY	N-CA-C	10.12	126.23	111.76
1	Gw	74	GLY	N-CA-C	10.12	126.22	111.76
1	Fz	74	GLY	N-CA-C	10.12	131.53	112.62
1	FJ	74	GLY	N-CA-C	10.12	131.53	112.62
1	GL	74	GLY	N-CA-C	10.12	126.22	111.76
1	FO	74	GLY	N-CA-C	10.12	131.53	112.62
1	Di	74	GLY	N-CA-C	10.11	126.22	111.76
1	H0	82	ALA	N-CA-C	10.11	122.38	111.36
1	Fp	74	GLY	N-CA-C	10.10	131.51	112.62
1	Fu	74	GLY	N-CA-C	10.10	131.51	112.62
1	D9	74	GLY	N-CA-C	10.10	126.20	111.76
1	Fa	74	GLY	N-CA-C	10.10	131.51	112.62
1	DR	74	GLY	N-CA-C	10.10	126.20	111.76
1	FT	74	GLY	N-CA-C	10.10	131.51	112.62
1	G3	74	GLY	N-CA-C	10.10	126.20	111.76
1	F1	74	GLY	N-CA-C	10.10	131.50	112.62
1	Gr	74	GLY	N-CA-C	10.10	126.20	111.76
1	GV	74	GLY	N-CA-C	10.10	126.20	111.76
1	HD	82	ALA	N-CA-C	10.09	122.36	111.36
1	Gc	74	GLY	N-CA-C	10.09	126.19	111.76
1	Gm	74	GLY	N-CA-C	10.09	126.18	111.76
1	H5	82	ALA	N-CA-C	10.08	122.35	111.36
1	HN	82	ALA	N-CA-C	10.08	122.35	111.36
1	Ff	74	GLY	N-CA-C	10.08	131.47	112.62
1	Hy	82	ALA	N-CA-C	10.08	122.35	111.36
1	GG	74	GLY	N-CA-C	10.08	126.17	111.76
1	Hj	82	ALA	N-CA-C	10.08	122.34	111.36
1	DC	74	GLY	N-CA-C	10.08	126.17	111.76
1	HX	82	ALA	N-CA-C	10.06	122.33	111.36
1	He	82	ALA	N-CA-C	10.06	122.33	111.36
1	Ho	82	ALA	N-CA-C	10.06	122.32	111.36
1	El	74	GLY	N-CA-C	10.04	130.84	112.37
1	Ht	82	ALA	N-CA-C	10.03	122.29	111.36
1	HI	82	ALA	N-CA-C	10.03	122.29	111.36
1	EP	74	GLY	N-CA-C	10.03	130.82	112.37
1	CQ	42	GLY	N-CA-C	-10.03	101.95	112.08
1	E7	74	GLY	N-CA-C	10.03	130.82	112.37
1	Ev	74	GLY	N-CA-C	10.03	130.82	112.37
1	E2	74	GLY	N-CA-C	10.02	130.80	112.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EA	74	GLY	N-CA-C	10.02	130.80	112.37
1	EK	74	GLY	N-CA-C	10.02	130.80	112.37
1	Eq	74	GLY	N-CA-C	10.01	130.80	112.37
1	Eb	74	GLY	N-CA-C	10.01	130.78	112.37
1	EF	74	GLY	N-CA-C	10.01	130.78	112.37
1	Eg	74	GLY	N-CA-C	10.01	130.78	112.37
1	EU	74	GLY	N-CA-C	10.00	130.77	112.37
1	DA	38	ARG	N-CA-C	-9.99	91.87	108.76
1	D7	38	ARG	N-CA-C	-9.99	91.87	108.76
1	DP	38	ARG	N-CA-C	-9.99	91.87	108.76
1	Dl	38	ARG	N-CA-C	-9.99	91.88	108.76
1	CB	42	GLY	N-CA-C	-9.99	101.99	112.08
1	C8	42	GLY	N-CA-C	-9.99	101.99	112.08
1	Cm	42	GLY	N-CA-C	-9.98	102.00	112.08
1	Dq	38	ARG	N-CA-C	-9.98	91.89	108.76
1	D2	38	ARG	N-CA-C	-9.97	91.90	108.76
1	DF	38	ARG	N-CA-C	-9.97	91.90	108.76
1	Ch	42	GLY	N-CA-C	-9.97	102.01	112.08
1	DK	38	ARG	N-CA-C	-9.97	91.92	108.76
1	Db	38	ARG	N-CA-C	-9.96	91.92	108.76
1	DU	38	ARG	N-CA-C	-9.96	91.92	108.76
1	Dv	38	ARG	N-CA-C	-9.96	91.93	108.76
1	Cw	42	GLY	N-CA-C	-9.96	102.02	112.08
1	Dg	38	ARG	N-CA-C	-9.95	91.94	108.76
1	C3	42	GLY	N-CA-C	-9.95	102.03	112.08
1	CL	42	GLY	N-CA-C	-9.95	102.03	112.08
1	Cc	42	GLY	N-CA-C	-9.92	102.06	112.08
1	CV	42	GLY	N-CA-C	-9.91	102.07	112.08
1	CG	42	GLY	N-CA-C	-9.89	102.09	112.08
1	Cr	42	GLY	N-CA-C	-9.89	102.09	112.08
2	Xg	810	ALA	N-CA-C	9.85	125.62	112.13
2	XP	810	ALA	N-CA-C	9.84	125.61	112.13
2	Xl	810	ALA	N-CA-C	9.83	125.59	112.13
2	XU	810	ALA	N-CA-C	9.83	125.59	112.13
2	X7	810	ALA	N-CA-C	9.82	125.58	112.13
2	XK	810	ALA	N-CA-C	9.82	125.58	112.13
2	Xv	810	ALA	N-CA-C	9.81	125.58	112.13
2	XF	810	ALA	N-CA-C	9.81	125.58	112.13
1	Cr	74	GLY	N-CA-C	9.81	130.53	112.77
2	X2	810	ALA	N-CA-C	9.80	125.56	112.13
1	CG	74	GLY	N-CA-C	9.80	130.51	112.77
1	Ch	74	GLY	N-CA-C	9.80	130.51	112.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CL	74	GLY	N-CA-C	9.80	130.51	112.77
2	XA	810	ALA	N-CA-C	9.80	125.55	112.13
1	C8	74	GLY	N-CA-C	9.80	130.50	112.77
1	CQ	74	GLY	N-CA-C	9.80	130.50	112.77
2	Xb	810	ALA	N-CA-C	9.79	125.55	112.13
1	Cc	74	GLY	N-CA-C	9.79	130.50	112.77
1	CB	74	GLY	N-CA-C	9.79	130.50	112.77
1	CV	74	GLY	N-CA-C	9.79	130.50	112.77
1	Bj	82	ALA	N-CA-C	9.79	122.03	111.36
1	Cm	74	GLY	N-CA-C	9.79	130.49	112.77
1	Cw	74	GLY	N-CA-C	9.79	130.48	112.77
1	C3	74	GLY	N-CA-C	9.78	130.48	112.77
1	BI	82	ALA	N-CA-C	9.78	122.02	111.36
1	B5	82	ALA	N-CA-C	9.77	122.00	111.36
1	Be	82	ALA	N-CA-C	9.76	122.00	111.36
1	BN	82	ALA	N-CA-C	9.76	122.00	111.36
2	Xq	810	ALA	N-CA-C	9.75	125.49	112.13
1	Bt	82	ALA	N-CA-C	9.75	121.99	111.36
1	BX	82	ALA	N-CA-C	9.75	121.99	111.36
1	BD	82	ALA	N-CA-C	9.75	121.98	111.36
1	By	82	ALA	N-CA-C	9.74	121.98	111.36
1	Bo	82	ALA	N-CA-C	9.74	121.98	111.36
1	B0	82	ALA	N-CA-C	9.74	121.98	111.36
1	EC	74	GLY	N-CA-C	9.71	127.50	112.45
1	BS	82	ALA	N-CA-C	9.71	121.94	111.36
1	Ei	74	GLY	N-CA-C	9.70	127.48	112.45
1	E9	74	GLY	N-CA-C	9.69	127.47	112.45
1	En	74	GLY	N-CA-C	9.69	127.47	112.45
1	EM	74	GLY	N-CA-C	9.69	127.46	112.45
1	ER	74	GLY	N-CA-C	9.69	127.46	112.45
1	Ex	74	GLY	N-CA-C	9.68	127.46	112.45
1	E4	74	GLY	N-CA-C	9.68	127.45	112.45
1	EW	74	GLY	N-CA-C	9.68	127.45	112.45
1	EH	74	GLY	N-CA-C	9.66	127.43	112.45
1	Ed	74	GLY	N-CA-C	9.65	127.41	112.45
1	Es	74	GLY	N-CA-C	9.63	127.38	112.45
1	GO	74	GLY	N-CA-C	9.49	130.37	112.62
1	Gf	74	GLY	N-CA-C	9.48	130.35	112.62
1	GT	74	GLY	N-CA-C	9.48	130.35	112.62
1	G6	74	GLY	N-CA-C	9.48	130.34	112.62
1	Ga	74	GLY	N-CA-C	9.47	130.34	112.62
1	Gz	74	GLY	N-CA-C	9.47	130.34	112.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	GE	74	GLY	N-CA-C	9.46	130.32	112.62
1	Gk	74	GLY	N-CA-C	9.46	130.31	112.62
1	G1	74	GLY	N-CA-C	9.46	130.31	112.62
1	Gu	74	GLY	N-CA-C	9.46	130.30	112.62
1	Gp	74	GLY	N-CA-C	9.45	130.29	112.62
1	GJ	74	GLY	N-CA-C	9.44	130.28	112.62
1	ED	74	GLY	N-CA-C	9.40	125.20	111.76
1	ES	74	GLY	N-CA-C	9.40	125.20	111.76
1	EN	74	GLY	N-CA-C	9.39	125.19	111.76
1	Ey	74	GLY	N-CA-C	9.38	125.18	111.76
1	DM	54	THR	N-CA-C	9.39	121.11	111.07
1	Ej	74	GLY	N-CA-C	9.38	125.18	111.76
1	E5	74	GLY	N-CA-C	9.38	125.17	111.76
1	E0	74	GLY	N-CA-C	9.38	125.17	111.76
1	Ee	74	GLY	N-CA-C	9.38	125.17	111.76
1	Eo	74	GLY	N-CA-C	9.37	125.16	111.76
1	Dn	54	THR	N-CA-C	9.37	121.10	111.07
1	Et	74	GLY	N-CA-C	9.37	125.16	111.76
1	D4	54	THR	N-CA-C	9.35	121.08	111.07
1	Dx	54	THR	N-CA-C	9.35	121.08	111.07
1	EX	74	GLY	N-CA-C	9.35	125.14	111.76
1	DC	54	THR	N-CA-C	9.35	121.08	111.07
1	EI	74	GLY	N-CA-C	9.35	125.13	111.76
1	DH	54	THR	N-CA-C	9.34	121.07	111.07
1	Dd	54	THR	N-CA-C	9.34	121.06	111.07
1	DR	54	THR	N-CA-C	9.34	121.06	111.07
1	DW	54	THR	N-CA-C	9.34	121.06	111.07
1	D9	54	THR	N-CA-C	9.33	121.05	111.07
1	Di	54	THR	N-CA-C	9.33	121.05	111.07
1	CE	94	LYS	N-CA-C	9.32	121.52	111.36
1	CO	94	LYS	N-CA-C	9.31	121.50	111.36
1	Ds	54	THR	N-CA-C	9.30	121.03	111.07
1	Cu	94	LYS	N-CA-C	9.29	121.49	111.36
2	Xx	815	SER	N-CA-C	9.29	121.41	111.28
1	CJ	94	LYS	N-CA-C	9.28	121.48	111.36
1	HB	76	VAL	N-CA-C	-9.28	102.86	111.67
1	C6	94	LYS	N-CA-C	9.27	121.47	111.36
1	Ca	94	LYS	N-CA-C	9.27	121.47	111.36
1	Cf	94	LYS	N-CA-C	9.27	121.47	111.36
2	Xn	815	SER	N-CA-C	9.27	121.39	111.28
1	CT	94	LYS	N-CA-C	9.27	121.46	111.36
1	C1	94	LYS	N-CA-C	9.27	121.46	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	XC	815	SER	N-CA-C	9.26	121.38	111.28
1	Ck	94	LYS	N-CA-C	9.26	121.45	111.36
2	Xi	815	SER	N-CA-C	9.26	121.37	111.28
1	Cp	94	LYS	N-CA-C	9.26	121.45	111.36
2	XR	815	SER	N-CA-C	9.25	121.37	111.28
2	X4	815	SER	N-CA-C	9.25	121.36	111.28
1	Cz	94	LYS	N-CA-C	9.25	121.44	111.36
2	XM	815	SER	N-CA-C	9.25	121.36	111.28
1	HQ	76	VAL	N-CA-C	-9.25	102.89	111.67
1	H8	76	VAL	N-CA-C	-9.24	102.89	111.67
1	HL	76	VAL	N-CA-C	-9.24	102.89	111.67
2	Xs	815	SER	N-CA-C	9.24	121.35	111.28
2	X9	815	SER	N-CA-C	9.24	121.35	111.28
1	Hm	76	VAL	N-CA-C	-9.23	102.90	111.67
1	HG	76	VAL	N-CA-C	-9.23	102.90	111.67
1	H3	76	VAL	N-CA-C	-9.23	102.90	111.67
1	Hc	76	VAL	N-CA-C	-9.23	102.90	111.67
2	Xd	815	SER	N-CA-C	9.23	121.34	111.28
2	XW	815	SER	N-CA-C	9.23	121.34	111.28
1	HG	30	ALA	N-CA-C	9.21	121.32	111.28
1	HV	76	VAL	N-CA-C	-9.21	102.92	111.67
2	XH	815	SER	N-CA-C	9.21	121.32	111.28
1	Hw	76	VAL	N-CA-C	-9.20	102.93	111.67
1	Hr	76	VAL	N-CA-C	-9.20	102.94	111.67
1	Hh	76	VAL	N-CA-C	-9.19	102.94	111.67
1	Hr	30	ALA	N-CA-C	9.19	121.29	111.28
1	HQ	30	ALA	N-CA-C	9.19	121.29	111.28
1	Hc	30	ALA	N-CA-C	9.18	121.29	111.28
1	HB	30	ALA	N-CA-C	9.18	121.28	111.28
1	HV	30	ALA	N-CA-C	9.17	121.28	111.28
1	H8	30	ALA	N-CA-C	9.15	121.26	111.28
1	Hm	30	ALA	N-CA-C	9.15	121.25	111.28
1	H3	30	ALA	N-CA-C	9.14	121.25	111.28
1	HL	30	ALA	N-CA-C	9.14	121.25	111.28
1	Hh	30	ALA	N-CA-C	9.14	121.24	111.28
1	Es	37	GLY	N-CA-C	9.12	124.51	110.91
1	EH	37	GLY	N-CA-C	9.12	124.50	110.91
1	Hw	30	ALA	N-CA-C	9.11	121.21	111.28
1	Ed	37	GLY	N-CA-C	9.10	124.47	110.91
1	EW	37	GLY	N-CA-C	9.10	124.47	110.91
1	EC	37	GLY	N-CA-C	9.08	124.44	110.91
1	E4	37	GLY	N-CA-C	9.08	124.43	110.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EM	37	GLY	N-CA-C	9.08	124.43	110.91
1	Ex	37	GLY	N-CA-C	9.07	124.43	110.91
1	ER	37	GLY	N-CA-C	9.07	124.43	110.91
1	E9	37	GLY	N-CA-C	9.06	124.42	110.91
2	XC	850	GLY	N-CA-C	-9.06	103.34	111.95
1	En	37	GLY	N-CA-C	9.06	124.41	110.91
2	XR	850	GLY	N-CA-C	-9.05	103.36	111.95
1	Ei	37	GLY	N-CA-C	9.04	124.38	110.91
2	Xx	861	ILE	N-CA-C	-9.04	94.92	108.85
2	XH	850	GLY	N-CA-C	-9.04	103.36	111.95
2	Xn	850	GLY	N-CA-C	-9.04	103.37	111.95
2	Xx	850	GLY	N-CA-C	-9.03	103.38	111.95
2	X9	850	GLY	N-CA-C	-9.03	103.38	111.95
2	Xs	850	GLY	N-CA-C	-9.02	103.38	111.95
2	XM	850	GLY	N-CA-C	-9.01	103.39	111.95
2	X4	850	GLY	N-CA-C	-9.00	103.40	111.95
2	Xd	850	GLY	N-CA-C	-8.99	103.41	111.95
2	XW	850	GLY	N-CA-C	-8.99	103.41	111.95
2	Xi	850	GLY	N-CA-C	-8.97	103.43	111.95
1	Bw	37	GLY	N-CA-C	8.92	124.21	110.91
1	Fl	82	ALA	N-CA-C	8.91	120.99	111.28
1	FF	82	ALA	N-CA-C	8.90	120.98	111.28
1	BL	37	GLY	N-CA-C	8.90	124.17	110.91
1	Fv	82	ALA	N-CA-C	8.89	120.97	111.28
1	Fg	82	ALA	N-CA-C	8.89	120.97	111.28
1	B3	37	GLY	N-CA-C	8.88	124.15	110.91
1	F7	82	ALA	N-CA-C	8.88	120.96	111.28
1	Br	37	GLY	N-CA-C	8.88	124.15	110.91
1	FP	82	ALA	N-CA-C	8.88	120.96	111.28
2	Xw	861	ILE	N-CA-C	-8.88	95.40	108.89
1	F2	82	ALA	N-CA-C	8.88	120.95	111.28
1	Bc	37	GLY	N-CA-C	8.87	124.13	110.91
1	Bh	37	GLY	N-CA-C	8.87	124.13	110.91
1	BG	37	GLY	N-CA-C	8.87	124.13	110.91
1	Fb	82	ALA	N-CA-C	8.87	120.95	111.28
2	Xr	861	ILE	N-CA-C	-8.87	95.41	108.89
1	Fq	82	ALA	N-CA-C	8.86	120.94	111.28
3	Pv	81	ASN	N-CA-C	-8.86	95.50	109.50
1	DG	74	GLY	N-CA-C	8.86	128.81	112.77
1	Dc	74	GLY	N-CA-C	8.86	128.80	112.77
1	Bm	37	GLY	N-CA-C	8.86	124.11	110.91
2	XG	861	ILE	N-CA-C	-8.86	95.42	108.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B8	37	GLY	N-CA-C	8.86	124.11	110.91
1	FA	82	ALA	N-CA-C	8.85	120.93	111.28
1	DL	74	GLY	N-CA-C	8.85	128.79	112.77
3	PF	81	ASN	N-CA-C	-8.85	95.52	109.50
2	Xc	861	ILE	N-CA-C	-8.85	95.44	108.89
1	Dw	74	GLY	N-CA-C	8.85	128.78	112.77
1	BV	37	GLY	N-CA-C	8.85	124.09	110.91
1	D3	74	GLY	N-CA-C	8.84	128.78	112.77
2	X3	861	ILE	N-CA-C	-8.84	95.45	108.89
1	Dh	74	GLY	N-CA-C	8.84	128.78	112.77
1	BB	37	GLY	N-CA-C	8.84	124.09	110.91
2	Xh	861	ILE	N-CA-C	-8.84	95.45	108.89
2	XL	861	ILE	N-CA-C	-8.84	95.45	108.89
1	BQ	37	GLY	N-CA-C	8.84	124.08	110.91
1	DV	74	GLY	N-CA-C	8.84	128.77	112.77
3	P2	81	ASN	N-CA-C	-8.84	95.54	109.50
3	PK	81	ASN	N-CA-C	-8.84	95.54	109.50
1	Dm	74	GLY	N-CA-C	8.84	128.76	112.77
2	XV	861	ILE	N-CA-C	-8.84	95.46	108.89
3	Pq	81	ASN	N-CA-C	-8.83	95.55	109.50
1	FU	82	ALA	N-CA-C	8.83	120.91	111.28
2	Xm	861	ILE	N-CA-C	-8.83	95.46	108.89
1	D8	74	GLY	N-CA-C	8.83	128.75	112.77
3	PP	81	ASN	N-CA-C	-8.83	95.55	109.50
3	Pb	81	ASN	N-CA-C	-8.83	95.55	109.50
3	Pg	81	ASN	N-CA-C	-8.83	95.55	109.50
3	Pl	81	ASN	N-CA-C	-8.83	95.55	109.50
1	FK	82	ALA	N-CA-C	8.83	120.90	111.28
1	DQ	74	GLY	N-CA-C	8.83	128.75	112.77
2	XB	861	ILE	N-CA-C	-8.82	95.48	108.89
3	P7	81	ASN	N-CA-C	-8.82	95.56	109.50
1	Dr	74	GLY	N-CA-C	8.82	128.74	112.77
3	PA	81	ASN	N-CA-C	-8.82	95.57	109.50
1	DB	74	GLY	N-CA-C	8.82	128.73	112.77
2	X8	861	ILE	N-CA-C	-8.81	95.49	108.89
3	PU	81	ASN	N-CA-C	-8.80	95.59	109.50
2	XQ	861	ILE	N-CA-C	-8.80	95.52	108.89
3	PF	55	SER	N-CA-C	8.78	123.18	110.10
3	Pq	55	SER	N-CA-C	8.77	123.17	110.10
3	Pb	55	SER	N-CA-C	8.77	123.17	110.10
1	AQ	74	GLY	N-CA-C	8.77	126.04	112.45
3	PU	55	SER	N-CA-C	8.77	123.17	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ar	74	GLY	N-CA-C	8.77	126.04	112.45
1	A8	74	GLY	N-CA-C	8.76	126.03	112.45
3	P7	55	SER	N-CA-C	8.76	123.15	110.10
1	Aw	74	GLY	N-CA-C	8.76	126.02	112.45
3	PP	55	SER	N-CA-C	8.76	123.15	110.10
1	A3	74	GLY	N-CA-C	8.75	126.02	112.45
3	P2	55	SER	N-CA-C	8.75	123.14	110.10
3	Pg	55	SER	N-CA-C	8.75	123.14	110.10
1	AV	74	GLY	N-CA-C	8.75	126.01	112.45
1	AB	74	GLY	N-CA-C	8.75	126.01	112.45
1	Ac	74	GLY	N-CA-C	8.74	126.00	112.45
1	AG	74	GLY	N-CA-C	8.74	126.00	112.45
3	PK	55	SER	N-CA-C	8.74	123.12	110.10
1	AL	74	GLY	N-CA-C	8.74	125.99	112.45
3	Pl	55	SER	N-CA-C	8.73	123.11	110.10
1	Am	74	GLY	N-CA-C	8.73	125.98	112.45
1	AS	82	ALA	N-CA-C	8.73	120.80	111.28
3	Pv	55	SER	N-CA-C	8.73	123.11	110.10
1	Aj	82	ALA	N-CA-C	8.73	120.79	111.28
1	Ah	74	GLY	N-CA-C	8.72	125.97	112.45
3	PA	55	SER	N-CA-C	8.72	123.10	110.10
1	A0	82	ALA	N-CA-C	8.72	120.78	111.28
2	XK	812	GLN	N-CA-C	-8.72	103.06	114.31
1	Ay	82	ALA	N-CA-C	8.72	120.78	111.28
2	Xg	812	GLN	N-CA-C	-8.71	103.07	114.31
2	XF	812	GLN	N-CA-C	-8.71	103.07	114.31
2	Xv	812	GLN	N-CA-C	-8.71	103.08	114.31
1	AX	82	ALA	N-CA-C	8.71	120.77	111.28
1	BT	74	GLY	N-CA-C	8.70	128.52	112.77
1	A5	82	ALA	N-CA-C	8.70	120.76	111.28
1	AN	82	ALA	N-CA-C	8.70	120.76	111.28
1	Bp	74	GLY	N-CA-C	8.69	128.51	112.77
1	Bu	74	GLY	N-CA-C	8.69	128.50	112.77
2	XA	812	GLN	N-CA-C	-8.69	103.10	114.31
2	X2	812	GLN	N-CA-C	-8.69	103.10	114.31
2	Xq	812	GLN	N-CA-C	-8.69	103.10	114.31
1	Ao	82	ALA	N-CA-C	8.69	120.75	111.28
1	BE	74	GLY	N-CA-C	8.69	128.50	112.77
1	AI	82	ALA	N-CA-C	8.69	120.75	111.28
2	XU	812	GLN	N-CA-C	-8.69	103.10	114.31
2	Xb	812	GLN	N-CA-C	-8.69	103.10	114.31
1	Bk	74	GLY	N-CA-C	8.69	128.49	112.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B1	74	GLY	N-CA-C	8.68	128.48	112.77
2	X7	812	GLN	N-CA-C	-8.68	103.11	114.31
2	XP	812	GLN	N-CA-C	-8.68	103.12	114.31
1	Bf	74	GLY	N-CA-C	8.68	128.47	112.77
1	Ba	74	GLY	N-CA-C	8.68	128.47	112.77
2	Xl	812	GLN	N-CA-C	-8.68	103.12	114.31
1	B6	74	GLY	N-CA-C	8.67	128.47	112.77
1	AD	82	ALA	N-CA-C	8.66	120.72	111.28
1	Ae	82	ALA	N-CA-C	8.66	120.72	111.28
1	Bz	74	GLY	N-CA-C	8.66	128.45	112.77
1	EV	76	VAL	N-CA-C	-8.66	104.88	111.90
1	BJ	74	GLY	N-CA-C	8.66	128.44	112.77
1	EG	76	VAL	N-CA-C	-8.65	104.89	111.90
1	BO	74	GLY	N-CA-C	8.65	128.43	112.77
1	At	82	ALA	N-CA-C	8.65	120.71	111.28
1	Eh	76	VAL	N-CA-C	-8.61	104.93	111.90
1	Ec	76	VAL	N-CA-C	-8.60	104.93	111.90
1	Er	76	VAL	N-CA-C	-8.60	104.94	111.90
1	EB	76	VAL	N-CA-C	-8.59	104.94	111.90
1	E3	76	VAL	N-CA-C	-8.59	104.94	111.90
1	Em	76	VAL	N-CA-C	-8.59	104.94	111.90
1	EL	76	VAL	N-CA-C	-8.59	104.95	111.90
1	E8	76	VAL	N-CA-C	-8.57	104.95	111.90
1	Ew	76	VAL	N-CA-C	-8.57	104.95	111.90
1	EQ	76	VAL	N-CA-C	-8.57	104.95	111.90
2	Xn	861	ILE	N-CA-C	-8.56	94.90	108.86
2	XC	861	ILE	N-CA-C	-8.56	94.91	108.86
2	X4	861	ILE	N-CA-C	-8.56	94.91	108.86
2	XM	861	ILE	N-CA-C	-8.56	94.91	108.86
2	Xd	861	ILE	N-CA-C	-8.55	94.92	108.86
2	Xi	861	ILE	N-CA-C	-8.55	94.92	108.86
2	Xs	861	ILE	N-CA-C	-8.55	94.92	108.86
2	XW	861	ILE	N-CA-C	-8.55	94.92	108.86
2	X9	861	ILE	N-CA-C	-8.54	94.93	108.86
2	XH	861	ILE	N-CA-C	-8.54	94.93	108.86
2	XR	861	ILE	N-CA-C	-8.54	94.94	108.86
1	Aw	95	ALA	N-CA-C	-8.54	98.35	108.25
1	Ah	95	ALA	N-CA-C	-8.53	98.35	108.25
1	FN	82	ALA	N-CA-C	8.53	120.66	111.36
1	A3	95	ALA	N-CA-C	-8.53	98.36	108.25
1	AL	95	ALA	N-CA-C	-8.53	98.36	108.25
1	A8	95	ALA	N-CA-C	-8.53	98.36	108.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AQ	95	ALA	N-CA-C	-8.53	98.36	108.25
1	AB	95	ALA	N-CA-C	-8.52	98.36	108.25
1	FV	37	GLY	N-CA-C	8.52	123.61	110.91
1	FQ	37	GLY	N-CA-C	8.52	123.60	110.91
1	Ac	95	ALA	N-CA-C	-8.51	98.37	108.25
1	Fc	37	GLY	N-CA-C	8.51	123.60	110.91
1	AG	95	ALA	N-CA-C	-8.51	98.37	108.25
1	AV	95	ALA	N-CA-C	-8.51	98.37	108.25
1	Fo	82	ALA	N-CA-C	8.51	120.64	111.36
1	F5	82	ALA	N-CA-C	8.51	120.64	111.36
1	Ft	82	ALA	N-CA-C	8.51	120.64	111.36
1	Ar	95	ALA	N-CA-C	-8.51	98.38	108.25
1	F3	37	GLY	N-CA-C	8.50	123.58	110.91
1	Fy	82	ALA	N-CA-C	8.50	120.62	111.36
1	AF	82	ALA	N-CA-C	8.50	120.17	111.07
1	FX	82	ALA	N-CA-C	8.50	120.62	111.36
1	F8	37	GLY	N-CA-C	8.49	123.57	110.91
1	FD	82	ALA	N-CA-C	8.49	120.62	111.36
1	Fj	82	ALA	N-CA-C	8.49	120.62	111.36
1	Fw	37	GLY	N-CA-C	8.49	123.56	110.91
1	Ag	82	ALA	N-CA-C	8.49	120.16	111.07
1	Av	82	ALA	N-CA-C	8.49	120.15	111.07
1	FL	37	GLY	N-CA-C	8.49	123.56	110.91
1	Fe	82	ALA	N-CA-C	8.49	120.61	111.36
1	F0	82	ALA	N-CA-C	8.48	120.61	111.36
1	Dj	54	THR	N-CA-C	8.48	120.15	111.07
1	Fh	37	GLY	N-CA-C	8.48	123.55	110.91
1	FB	37	GLY	N-CA-C	8.48	123.55	110.91
1	Ab	82	ALA	N-CA-C	8.48	120.14	111.07
1	Fm	37	GLY	N-CA-C	8.48	123.54	110.91
1	Fr	37	GLY	N-CA-C	8.48	123.54	110.91
1	Az	54	THR	N-CA-C	8.48	120.14	111.07
1	Am	95	ALA	N-CA-C	-8.48	98.42	108.25
1	EI	7	ILE	N-CA-C	-8.48	104.19	113.43
1	FG	37	GLY	N-CA-C	8.48	123.54	110.91
1	AT	54	THR	N-CA-C	8.48	120.14	111.07
1	A2	82	ALA	N-CA-C	8.47	120.14	111.07
1	Dp	82	ALA	N-CA-C	8.47	120.51	111.28
1	D0	54	THR	N-CA-C	8.47	120.13	111.07
1	Aq	82	ALA	N-CA-C	8.47	120.13	111.07
1	AU	82	ALA	N-CA-C	8.46	120.13	111.07
1	Do	54	THR	N-CA-C	8.46	120.12	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DD	54	THR	N-CA-C	8.46	120.12	111.07
1	Df	82	ALA	N-CA-C	8.46	120.50	111.28
1	DS	54	THR	N-CA-C	8.46	120.12	111.07
1	Ak	54	THR	N-CA-C	8.46	120.12	111.07
1	A1	54	THR	N-CA-C	8.46	120.12	111.07
1	DX	54	THR	N-CA-C	8.46	120.12	111.07
1	A6	54	THR	N-CA-C	8.45	120.11	111.07
1	Ey	7	ILE	N-CA-C	-8.45	104.22	113.43
1	Dy	54	THR	N-CA-C	8.45	120.11	111.07
1	D5	54	THR	N-CA-C	8.45	120.11	111.07
1	Da	82	ALA	N-CA-C	8.45	120.49	111.28
1	AA	82	ALA	N-CA-C	8.45	120.11	111.07
1	AK	82	ALA	N-CA-C	8.45	120.11	111.07
1	Af	54	THR	N-CA-C	8.44	120.11	111.07
1	Gl	74	GLY	N-CA-C	8.45	122.93	110.60
1	FI	82	ALA	N-CA-C	8.45	120.57	111.36
1	DT	82	ALA	N-CA-C	8.45	120.49	111.28
1	Dt	54	THR	N-CA-C	8.44	120.11	111.07
1	E0	7	ILE	N-CA-C	-8.44	104.23	113.43
1	Eo	7	ILE	N-CA-C	-8.44	104.23	113.43
1	DI	54	THR	N-CA-C	8.44	120.10	111.07
1	Ee	7	ILE	N-CA-C	-8.44	104.23	113.43
1	Dk	82	ALA	N-CA-C	8.44	120.48	111.28
1	Gv	74	GLY	N-CA-C	8.44	122.92	110.60
1	Ap	54	THR	N-CA-C	8.44	120.10	111.07
1	Hr	37	GLY	N-CA-C	8.44	122.31	111.09
1	Au	54	THR	N-CA-C	8.44	120.10	111.07
1	Aa	54	THR	N-CA-C	8.44	120.10	111.07
1	AJ	54	THR	N-CA-C	8.44	120.10	111.07
1	E5	7	ILE	N-CA-C	-8.43	104.24	113.43
1	GA	74	GLY	N-CA-C	8.43	122.91	110.60
1	AE	54	THR	N-CA-C	8.43	120.09	111.07
1	FS	82	ALA	N-CA-C	8.43	120.55	111.36
1	A7	82	ALA	N-CA-C	8.43	120.09	111.07
1	Ej	7	ILE	N-CA-C	-8.43	104.24	113.43
1	Gq	74	GLY	N-CA-C	8.43	122.91	110.60
1	AP	82	ALA	N-CA-C	8.43	120.09	111.07
1	D1	82	ALA	N-CA-C	8.43	120.47	111.28
1	ED	7	ILE	N-CA-C	-8.43	104.24	113.43
1	EN	7	ILE	N-CA-C	-8.43	104.24	113.43
1	HV	37	GLY	N-CA-C	8.43	122.30	111.09
1	G2	74	GLY	N-CA-C	8.43	122.90	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	De	54	THR	N-CA-C	8.43	120.08	111.07
1	Al	82	ALA	N-CA-C	8.43	120.08	111.07
1	DE	82	ALA	N-CA-C	8.43	120.47	111.28
1	AO	54	THR	N-CA-C	8.42	120.08	111.07
1	Hh	37	GLY	N-CA-C	8.42	122.29	111.09
1	Du	82	ALA	N-CA-C	8.42	120.46	111.28
1	Fj	74	GLY	N-CA-C	8.42	127.35	112.53
1	ES	7	ILE	N-CA-C	-8.42	104.26	113.43
1	D6	82	ALA	N-CA-C	8.41	120.45	111.28
1	DN	54	THR	N-CA-C	8.41	120.07	111.07
1	DO	82	ALA	N-CA-C	8.41	120.45	111.28
1	Et	7	ILE	N-CA-C	-8.41	104.26	113.43
1	DJ	82	ALA	N-CA-C	8.41	120.45	111.28
1	G7	74	GLY	N-CA-C	8.41	122.88	110.60
1	GP	74	GLY	N-CA-C	8.41	122.88	110.60
1	EX	7	ILE	N-CA-C	-8.41	104.26	113.43
1	Gg	74	GLY	N-CA-C	8.41	122.88	110.60
1	F0	74	GLY	N-CA-C	8.41	127.32	112.53
1	Hc	37	GLY	N-CA-C	8.40	122.27	111.09
1	H3	37	GLY	N-CA-C	8.40	122.27	111.09
1	Dz	82	ALA	N-CA-C	8.40	120.44	111.28
1	Fo	74	GLY	N-CA-C	8.40	127.32	112.53
1	GK	74	GLY	N-CA-C	8.40	122.87	110.60
1	F5	74	GLY	N-CA-C	8.40	127.31	112.53
1	Gb	74	GLY	N-CA-C	8.40	122.86	110.60
1	FN	74	GLY	N-CA-C	8.39	127.30	112.53
1	HL	37	GLY	N-CA-C	8.39	122.25	111.09
1	FD	74	GLY	N-CA-C	8.39	127.29	112.53
1	FS	74	GLY	N-CA-C	8.39	127.29	112.53
1	HG	37	GLY	N-CA-C	8.39	122.25	111.09
1	Fe	74	GLY	N-CA-C	8.38	127.27	112.53
1	FX	74	GLY	N-CA-C	8.38	127.27	112.53
1	Fy	74	GLY	N-CA-C	8.38	127.27	112.53
1	Hw	37	GLY	N-CA-C	8.38	122.23	111.09
1	H8	37	GLY	N-CA-C	8.37	122.22	111.09
1	HB	37	GLY	N-CA-C	8.37	122.22	111.09
1	BS	74	GLY	N-CA-C	8.37	127.92	112.77
1	HQ	37	GLY	N-CA-C	8.37	122.22	111.09
1	FI	74	GLY	N-CA-C	8.37	127.26	112.53
1	Cp	74	GLY	N-CA-C	8.37	127.76	112.37
1	Bo	74	GLY	N-CA-C	8.36	127.90	112.77
1	Bj	74	GLY	N-CA-C	8.36	127.90	112.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	GU	74	GLY	N-CA-C	8.36	122.80	110.60
1	Ft	74	GLY	N-CA-C	8.36	127.24	112.53
1	By	74	GLY	N-CA-C	8.36	127.90	112.77
1	CE	74	GLY	N-CA-C	8.36	127.74	112.37
1	Bt	74	GLY	N-CA-C	8.35	127.89	112.77
1	GF	74	GLY	N-CA-C	8.35	122.79	110.60
1	CT	74	GLY	N-CA-C	8.35	127.74	112.37
1	Ca	74	GLY	N-CA-C	8.35	127.73	112.37
1	Hm	37	GLY	N-CA-C	8.35	122.19	111.09
1	B5	74	GLY	N-CA-C	8.35	127.87	112.77
1	B0	74	GLY	N-CA-C	8.35	127.88	112.77
1	FP	94	LYS	N-CA-C	8.35	120.46	111.36
1	BD	74	GLY	N-CA-C	8.34	127.87	112.77
1	C6	74	GLY	N-CA-C	8.34	127.72	112.37
1	Ck	74	GLY	N-CA-C	8.34	127.72	112.37
1	CJ	74	GLY	N-CA-C	8.34	127.72	112.37
1	C1	74	GLY	N-CA-C	8.34	127.71	112.37
1	Be	74	GLY	N-CA-C	8.34	127.86	112.77
1	FA	94	LYS	N-CA-C	8.34	120.44	111.36
1	CB	82	ALA	N-CA-C	8.34	120.37	111.28
1	BX	74	GLY	N-CA-C	8.34	127.86	112.77
1	Ch	82	ALA	N-CA-C	8.33	120.36	111.28
1	Cu	74	GLY	N-CA-C	8.33	127.70	112.37
1	Cm	82	ALA	N-CA-C	8.33	120.36	111.28
1	BN	74	GLY	N-CA-C	8.33	127.85	112.77
1	C8	82	ALA	N-CA-C	8.33	120.36	111.28
1	Fg	94	LYS	N-CA-C	8.33	120.44	111.36
1	Cz	74	GLY	N-CA-C	8.33	127.69	112.37
1	CQ	82	ALA	N-CA-C	8.33	120.36	111.28
1	CO	74	GLY	N-CA-C	8.32	127.69	112.37
1	Fl	94	LYS	N-CA-C	8.32	120.43	111.36
1	Cf	74	GLY	N-CA-C	8.32	127.67	112.37
1	BI	74	GLY	N-CA-C	8.32	127.82	112.77
1	Cc	82	ALA	N-CA-C	8.31	120.34	111.28
1	Cr	82	ALA	N-CA-C	8.31	120.34	111.28
1	C3	82	ALA	N-CA-C	8.31	120.34	111.28
1	CL	82	ALA	N-CA-C	8.31	120.34	111.28
1	FU	94	LYS	N-CA-C	8.30	120.41	111.36
1	F7	94	LYS	N-CA-C	8.30	120.41	111.36
1	Fb	94	LYS	N-CA-C	8.30	120.41	111.36
1	FF	94	LYS	N-CA-C	8.30	120.41	111.36
1	Cw	82	ALA	N-CA-C	8.30	120.33	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Fq	94	LYS	N-CA-C	8.30	120.41	111.36
1	CG	82	ALA	N-CA-C	8.30	120.33	111.28
1	CV	82	ALA	N-CA-C	8.30	120.32	111.28
1	F2	94	LYS	N-CA-C	8.29	120.40	111.36
1	FK	94	LYS	N-CA-C	8.29	120.40	111.36
1	Fv	94	LYS	N-CA-C	8.25	120.35	111.36
1	HE	74	GLY	N-CA-C	8.22	127.49	112.37
1	HT	74	GLY	N-CA-C	8.22	127.49	112.37
1	Hp	74	GLY	N-CA-C	8.20	127.46	112.37
1	Hk	74	GLY	N-CA-C	8.20	127.46	112.37
1	Ha	74	GLY	N-CA-C	8.20	127.45	112.37
1	HJ	74	GLY	N-CA-C	8.20	127.45	112.37
1	Hz	74	GLY	N-CA-C	8.19	127.44	112.37
1	H6	74	GLY	N-CA-C	8.19	127.43	112.37
1	HO	74	GLY	N-CA-C	8.19	127.43	112.37
1	H1	74	GLY	N-CA-C	8.18	127.43	112.37
1	AR	82	ALA	N-CA-C	8.18	120.19	111.28
1	Aq	30	ALA	N-CA-C	8.17	120.27	111.36
1	Hf	74	GLY	N-CA-C	8.17	127.41	112.37
1	Hu	74	GLY	N-CA-C	8.17	127.41	112.37
1	AC	82	ALA	N-CA-C	8.16	120.18	111.28
1	An	82	ALA	N-CA-C	8.15	120.16	111.28
1	A9	82	ALA	N-CA-C	8.14	120.16	111.28
1	Ai	82	ALA	N-CA-C	8.14	120.15	111.28
1	Ax	82	ALA	N-CA-C	8.14	120.15	111.28
1	Ab	30	ALA	N-CA-C	8.14	120.23	111.36
1	A2	30	ALA	N-CA-C	8.12	120.21	111.36
1	AK	30	ALA	N-CA-C	8.12	120.21	111.36
1	Ag	30	ALA	N-CA-C	8.12	120.21	111.36
1	AF	30	ALA	N-CA-C	8.12	120.21	111.36
1	AJ	42	GLY	N-CA-C	-8.12	103.88	112.08
1	A4	82	ALA	N-CA-C	8.11	120.12	111.28
1	Dj	38	ARG	N-CA-C	-8.11	95.27	109.06
1	AU	30	ALA	N-CA-C	8.11	120.20	111.36
1	AT	42	GLY	N-CA-C	-8.11	103.89	112.08
1	Ap	42	GLY	N-CA-C	-8.11	103.89	112.08
1	Dy	38	ARG	N-CA-C	-8.11	95.28	109.06
1	AM	82	ALA	N-CA-C	8.11	120.12	111.28
1	A7	30	ALA	N-CA-C	8.10	120.19	111.36
1	Al	30	ALA	N-CA-C	8.10	120.19	111.36
1	Aa	42	GLY	N-CA-C	-8.10	103.90	112.08
1	Do	38	ARG	N-CA-C	-8.10	95.29	109.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AP	30	ALA	N-CA-C	8.10	120.19	111.36
1	Az	42	GLY	N-CA-C	-8.10	103.90	112.08
1	D5	38	ARG	N-CA-C	-8.10	95.30	109.06
1	Dt	38	ARG	N-CA-C	-8.10	95.30	109.06
1	AA	30	ALA	N-CA-C	8.09	120.18	111.36
1	AH	82	ALA	N-CA-C	8.09	120.10	111.28
1	A6	42	GLY	N-CA-C	-8.09	103.91	112.08
1	Av	30	ALA	N-CA-C	8.09	120.17	111.36
1	DN	38	ARG	N-CA-C	-8.09	95.31	109.06
1	A1	42	GLY	N-CA-C	-8.09	103.91	112.08
1	De	38	ARG	N-CA-C	-8.08	95.32	109.06
1	Ak	42	GLY	N-CA-C	-8.08	103.92	112.08
1	As	82	ALA	N-CA-C	8.08	120.09	111.28
1	AO	42	GLY	N-CA-C	-8.08	103.92	112.08
1	Ad	82	ALA	N-CA-C	8.08	120.09	111.28
1	Af	42	GLY	N-CA-C	-8.08	103.92	112.08
1	DD	38	ARG	N-CA-C	-8.08	95.33	109.06
1	D0	38	ARG	N-CA-C	-8.08	95.33	109.06
1	DI	38	ARG	N-CA-C	-8.07	95.33	109.06
1	DS	38	ARG	N-CA-C	-8.07	95.34	109.06
1	Au	42	GLY	N-CA-C	-8.07	103.93	112.08
1	AW	82	ALA	N-CA-C	8.06	120.07	111.28
1	AE	42	GLY	N-CA-C	-8.06	103.94	112.08
1	DX	38	ARG	N-CA-C	-8.05	95.37	109.06
1	Ap	74	GLY	N-CA-C	8.04	127.33	112.77
1	AV	30	ALA	N-CA-C	8.04	120.05	111.28
1	AG	30	ALA	N-CA-C	8.04	120.04	111.28
1	Ac	30	ALA	N-CA-C	8.03	120.04	111.28
1	Gs	76	VAL	N-CA-C	-8.03	104.04	111.67
1	AL	30	ALA	N-CA-C	8.03	120.04	111.28
1	A3	30	ALA	N-CA-C	8.03	120.03	111.28
1	GB	54	THR	N-CA-C	8.03	119.66	111.07
1	AB	30	ALA	N-CA-C	8.02	120.03	111.28
1	GH	76	VAL	N-CA-C	-8.02	104.05	111.67
1	Aa	74	GLY	N-CA-C	8.01	127.27	112.77
1	AT	74	GLY	N-CA-C	8.01	127.27	112.77
1	A8	30	ALA	N-CA-C	8.01	120.01	111.28
1	Gd	76	VAL	N-CA-C	-8.01	104.06	111.67
1	Ah	30	ALA	N-CA-C	8.01	120.01	111.28
1	Aw	30	ALA	N-CA-C	8.01	120.01	111.28
1	Am	30	ALA	N-CA-C	8.01	120.00	111.28
1	Au	74	GLY	N-CA-C	8.01	127.26	112.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	GW	76	VAL	N-CA-C	-8.00	104.07	111.67
1	AQ	30	ALA	N-CA-C	8.00	120.00	111.28
1	G4	76	VAL	N-CA-C	-8.00	104.07	111.67
1	G8	54	THR	N-CA-C	8.00	119.63	111.07
1	GQ	54	THR	N-CA-C	8.00	119.63	111.07
1	A1	74	GLY	N-CA-C	7.99	127.24	112.77
1	Ar	30	ALA	N-CA-C	7.99	119.99	111.28
1	AE	74	GLY	N-CA-C	7.99	127.24	112.77
1	Gi	76	VAL	N-CA-C	-7.99	104.08	111.67
1	G9	76	VAL	N-CA-C	-7.99	104.08	111.67
1	AJ	74	GLY	N-CA-C	7.99	127.23	112.77
1	GR	76	VAL	N-CA-C	-7.99	104.08	111.67
1	GC	76	VAL	N-CA-C	-7.99	104.08	111.67
1	Af	74	GLY	N-CA-C	7.99	127.22	112.77
1	Gx	76	VAL	N-CA-C	-7.98	104.08	111.67
1	Az	74	GLY	N-CA-C	7.98	127.22	112.77
1	Gm	54	THR	N-CA-C	7.98	119.61	111.07
1	A6	74	GLY	N-CA-C	7.98	127.22	112.77
3	Po	42	ILE	CB-CA-C	-7.98	99.99	110.84
1	AO	74	GLY	N-CA-C	7.98	127.22	112.77
1	GL	54	THR	N-CA-C	7.98	119.61	111.07
3	Py	42	ILE	CB-CA-C	-7.98	99.99	110.84
3	PD	42	ILE	CB-CA-C	-7.98	99.99	110.84
3	Pt	42	ILE	CB-CA-C	-7.97	100.00	110.84
3	Pe	42	ILE	CB-CA-C	-7.97	100.00	110.84
3	P5	42	ILE	CB-CA-C	-7.97	100.00	110.84
1	Gn	76	VAL	N-CA-C	-7.97	104.10	111.67
1	GG	54	THR	N-CA-C	7.97	119.59	111.07
3	PN	42	ILE	CB-CA-C	-7.97	100.00	110.84
1	GM	76	VAL	N-CA-C	-7.97	104.10	111.67
1	Ak	74	GLY	N-CA-C	7.96	127.19	112.77
1	Gr	54	THR	N-CA-C	7.96	119.59	111.07
3	PI	42	ILE	CB-CA-C	-7.96	100.01	110.84
1	G3	54	THR	N-CA-C	7.96	119.58	111.07
1	Gw	54	THR	N-CA-C	7.96	119.58	111.07
3	P0	42	ILE	CB-CA-C	-7.95	100.03	110.84
3	PS	42	ILE	CB-CA-C	-7.95	100.03	110.84
1	Gc	54	THR	N-CA-C	7.95	119.58	111.07
1	GV	54	THR	N-CA-C	7.95	119.58	111.07
3	Pj	42	ILE	CB-CA-C	-7.95	100.03	110.84
1	Gh	54	THR	N-CA-C	7.95	119.57	111.07
3	PX	42	ILE	CB-CA-C	-7.95	100.03	110.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BL	82	ALA	N-CA-C	7.90	119.97	111.36
1	Gl	36	VAL	N-CA-C	-7.89	104.19	113.42
1	GA	36	VAL	N-CA-C	-7.88	104.20	113.42
1	Bc	82	ALA	N-CA-C	7.87	119.94	111.36
1	BV	82	ALA	N-CA-C	7.87	119.94	111.36
1	Br	82	ALA	N-CA-C	7.87	119.93	111.36
1	Bw	82	ALA	N-CA-C	7.87	119.93	111.36
1	B3	82	ALA	N-CA-C	7.86	119.93	111.36
1	G7	36	VAL	N-CA-C	-7.86	104.22	113.42
1	Bh	82	ALA	N-CA-C	7.86	119.93	111.36
1	BG	82	ALA	N-CA-C	7.86	119.92	111.36
1	GP	36	VAL	N-CA-C	-7.86	104.23	113.42
1	G2	36	VAL	N-CA-C	-7.84	104.25	113.42
1	Bm	82	ALA	N-CA-C	7.83	119.89	111.36
1	GF	36	VAL	N-CA-C	-7.83	104.27	113.42
1	Gv	36	VAL	N-CA-C	-7.82	104.27	113.42
1	Gb	36	VAL	N-CA-C	-7.82	104.27	113.42
1	B8	82	ALA	N-CA-C	7.81	119.87	111.36
1	BQ	82	ALA	N-CA-C	7.81	119.87	111.36
1	DG	82	ALA	N-CA-C	7.81	119.79	111.28
1	Gq	36	VAL	N-CA-C	-7.80	104.29	113.42
1	GK	36	VAL	N-CA-C	-7.80	104.29	113.42
1	DQ	82	ALA	N-CA-C	7.80	119.78	111.28
1	Gg	36	VAL	N-CA-C	-7.79	104.30	113.42
1	DV	82	ALA	N-CA-C	7.79	119.77	111.28
1	GU	36	VAL	N-CA-C	-7.79	104.31	113.42
2	Xj	807	THR	N-CA-C	-7.79	97.26	109.72
1	BB	82	ALA	N-CA-C	7.78	119.84	111.36
1	Dr	82	ALA	N-CA-C	7.78	119.76	111.28
1	D8	82	ALA	N-CA-C	7.78	119.76	111.28
2	Xt	807	THR	N-CA-C	-7.78	97.27	109.72
2	Xe	807	THR	N-CA-C	-7.78	97.28	109.72
1	Dh	82	ALA	N-CA-C	7.78	119.76	111.28
2	XX	807	THR	N-CA-C	-7.78	97.28	109.72
2	XD	807	THR	N-CA-C	-7.77	97.29	109.72
1	D3	82	ALA	N-CA-C	7.77	119.75	111.28
1	DL	82	ALA	N-CA-C	7.77	119.75	111.28
1	Dc	82	ALA	N-CA-C	7.77	119.75	111.28
2	Xs	807	THR	N-CA-C	-7.77	98.10	110.14
1	DB	82	ALA	N-CA-C	7.77	119.75	111.28
2	Xy	807	THR	N-CA-C	-7.76	97.30	109.72
2	XH	807	THR	N-CA-C	-7.76	98.11	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	XI	807	THR	N-CA-C	-7.76	97.31	109.72
2	X5	807	THR	N-CA-C	-7.76	97.31	109.72
1	Dw	82	ALA	N-CA-C	7.76	119.73	111.28
1	Dm	82	ALA	N-CA-C	7.75	119.73	111.28
2	Xd	807	THR	N-CA-C	-7.75	98.12	110.14
2	XC	807	THR	N-CA-C	-7.75	98.13	110.14
2	X0	807	THR	N-CA-C	-7.75	97.32	109.72
2	XN	807	THR	N-CA-C	-7.75	97.32	109.72
2	XS	807	THR	N-CA-C	-7.74	97.33	109.72
2	Xo	807	THR	N-CA-C	-7.74	97.33	109.72
2	XW	807	THR	N-CA-C	-7.74	98.15	110.14
2	XM	807	THR	N-CA-C	-7.73	98.15	110.14
2	X4	807	THR	N-CA-C	-7.73	98.16	110.14
2	Xx	807	THR	N-CA-C	-7.72	98.17	110.14
1	GU	37	GLY	N-CA-C	7.71	122.40	110.91
2	Xn	807	THR	N-CA-C	-7.71	98.19	110.14
2	X9	807	THR	N-CA-C	-7.71	98.19	110.14
2	XR	807	THR	N-CA-C	-7.71	98.19	110.14
1	Gl	37	GLY	N-CA-C	7.71	122.39	110.91
1	G7	37	GLY	N-CA-C	7.70	122.38	110.91
2	Xi	807	THR	N-CA-C	-7.70	98.20	110.14
1	Fs	82	ALA	N-CA-C	7.70	119.67	111.28
1	GA	37	GLY	N-CA-C	7.69	122.37	110.91
1	GP	37	GLY	N-CA-C	7.69	122.37	110.91
1	Gv	37	GLY	N-CA-C	7.69	122.37	110.91
1	Gb	37	GLY	N-CA-C	7.69	122.36	110.91
3	Pr	22	LYS	N-CA-C	7.69	119.40	109.64
1	G2	37	GLY	N-CA-C	7.68	122.36	110.91
1	Fn	82	ALA	N-CA-C	7.68	119.65	111.28
1	FH	82	ALA	N-CA-C	7.68	119.65	111.28
1	Gg	37	GLY	N-CA-C	7.68	122.35	110.91
1	Gq	37	GLY	N-CA-C	7.68	122.35	110.91
1	Fx	82	ALA	N-CA-C	7.68	119.65	111.28
1	GF	37	GLY	N-CA-C	7.67	122.35	110.91
1	FR	82	ALA	N-CA-C	7.67	119.64	111.28
1	Fd	82	ALA	N-CA-C	7.67	119.64	111.28
1	FM	82	ALA	N-CA-C	7.67	119.64	111.28
2	XR	809	THR	N-CA-C	7.67	119.64	111.28
1	FC	82	ALA	N-CA-C	7.67	119.64	111.28
2	X9	809	THR	N-CA-C	7.66	119.63	111.28
1	DX	7	ILE	N-CA-C	7.66	118.46	110.72
3	PB	22	LYS	N-CA-C	7.66	119.37	109.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CI	82	ALA	N-CA-C	7.66	119.71	111.36
1	Fs	67	ALA	N-CA-C	7.66	119.41	111.14
1	F9	82	ALA	N-CA-C	7.66	119.62	111.28
2	XC	809	THR	N-CA-C	7.66	119.62	111.28
3	Pc	22	LYS	N-CA-C	7.65	119.36	109.64
1	F4	82	ALA	N-CA-C	7.65	119.62	111.28
1	GK	37	GLY	N-CA-C	7.65	122.31	110.91
2	X4	809	THR	N-CA-C	7.65	119.61	111.28
1	Cj	82	ALA	N-CA-C	7.65	119.70	111.36
1	Cy	82	ALA	N-CA-C	7.65	119.69	111.36
2	XM	809	THR	N-CA-C	7.65	119.62	111.28
2	Xx	809	THR	N-CA-C	7.65	119.61	111.28
3	Pm	22	LYS	N-CA-C	7.64	119.35	109.64
1	Dt	7	ILE	N-CA-C	7.64	118.44	110.72
2	Xs	809	THR	N-CA-C	7.64	119.61	111.28
3	PV	22	LYS	N-CA-C	7.64	119.35	109.64
1	CX	82	ALA	N-CA-C	7.64	119.69	111.36
1	C5	82	ALA	N-CA-C	7.64	119.69	111.36
1	Fi	82	ALA	N-CA-C	7.64	119.61	111.28
2	Xd	809	THR	N-CA-C	7.64	119.61	111.28
3	P8	22	LYS	N-CA-C	7.64	119.34	109.64
3	PQ	22	LYS	N-CA-C	7.64	119.34	109.64
1	Dj	7	ILE	N-CA-C	7.63	118.43	110.72
3	P3	22	LYS	N-CA-C	7.63	119.33	109.64
3	Pw	22	LYS	N-CA-C	7.63	119.33	109.64
1	DD	7	ILE	N-CA-C	7.63	118.43	110.72
1	Ce	82	ALA	N-CA-C	7.63	119.67	111.36
1	Fd	67	ALA	N-CA-C	7.63	119.38	111.14
2	Xi	809	THR	N-CA-C	7.63	119.59	111.28
1	FW	82	ALA	N-CA-C	7.63	119.60	111.28
1	CN	82	ALA	N-CA-C	7.63	119.67	111.36
2	Xn	809	THR	N-CA-C	7.62	119.59	111.28
1	De	7	ILE	N-CA-C	7.62	118.42	110.72
2	Xn	781	GLN	N-CA-C	7.62	121.83	109.40
1	Co	82	ALA	N-CA-C	7.62	119.67	111.36
1	C0	82	ALA	N-CA-C	7.62	119.66	111.36
2	XH	809	THR	N-CA-C	7.62	119.58	111.28
3	PL	22	LYS	N-CA-C	7.62	119.31	109.64
1	CD	82	ALA	N-CA-C	7.61	119.66	111.36
2	XC	781	GLN	N-CA-C	7.61	121.81	109.40
3	PG	22	LYS	N-CA-C	7.61	119.30	109.64
2	XW	781	GLN	N-CA-C	7.61	121.80	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BD	76	VAL	N-CA-C	-7.61	104.44	111.67
2	Xi	781	GLN	N-CA-C	7.61	121.80	109.40
1	FH	67	ALA	N-CA-C	7.61	119.36	111.14
1	DS	7	ILE	N-CA-C	7.61	118.40	110.72
2	Xd	781	GLN	N-CA-C	7.61	121.80	109.40
1	Fx	67	ALA	N-CA-C	7.61	119.35	111.14
1	BS	76	VAL	N-CA-C	-7.60	104.45	111.67
2	X9	781	GLN	N-CA-C	7.60	121.79	109.40
2	Xx	781	GLN	N-CA-C	7.60	121.79	109.40
2	XR	781	GLN	N-CA-C	7.60	121.79	109.40
2	XW	809	THR	N-CA-C	7.60	119.57	111.28
1	B0	76	VAL	N-CA-C	-7.60	104.45	111.67
3	Ph	22	LYS	N-CA-C	7.60	119.29	109.64
2	XH	781	GLN	N-CA-C	7.60	121.78	109.40
1	FW	67	ALA	N-CA-C	7.60	119.34	111.14
1	D5	7	ILE	N-CA-C	7.60	118.39	110.72
2	X4	781	GLN	N-CA-C	7.60	121.78	109.40
1	D0	7	ILE	N-CA-C	7.59	118.39	110.72
1	Ct	82	ALA	N-CA-C	7.59	119.64	111.36
1	DI	7	ILE	N-CA-C	7.59	118.39	110.72
1	AC	94	LYS	N-CA-C	7.59	119.64	111.36
2	XM	781	GLN	N-CA-C	7.59	121.77	109.40
1	Fi	67	ALA	N-CA-C	7.59	119.33	111.14
1	BN	76	VAL	N-CA-C	-7.59	104.46	111.67
2	Xs	781	GLN	N-CA-C	7.58	121.76	109.40
1	F9	67	ALA	N-CA-C	7.58	119.33	111.14
1	CS	82	ALA	N-CA-C	7.58	119.62	111.36
1	B5	76	VAL	N-CA-C	-7.58	104.47	111.67
1	Do	7	ILE	N-CA-C	7.58	118.37	110.72
1	F4	67	ALA	N-CA-C	7.58	119.32	111.14
1	FC	67	ALA	N-CA-C	7.58	119.32	111.14
1	Be	76	VAL	N-CA-C	-7.57	104.48	111.67
1	Fn	67	ALA	N-CA-C	7.57	119.32	111.14
1	Bt	76	VAL	N-CA-C	-7.57	104.48	111.67
1	DN	7	ILE	N-CA-C	7.57	118.36	110.72
1	DR	7	ILE	N-CA-C	7.56	118.36	110.72
1	Bo	76	VAL	N-CA-C	-7.56	104.48	111.67
1	Bj	76	VAL	N-CA-C	-7.56	104.49	111.67
1	As	94	LYS	N-CA-C	7.56	119.60	111.36
1	BX	76	VAL	N-CA-C	-7.56	104.49	111.67
1	AM	94	LYS	N-CA-C	7.56	119.60	111.36
1	An	94	LYS	N-CA-C	7.55	119.59	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	FM	67	ALA	N-CA-C	7.55	119.30	111.14
1	Ai	94	LYS	N-CA-C	7.55	119.59	111.36
1	DC	7	ILE	N-CA-C	7.55	118.35	110.72
1	FR	67	ALA	N-CA-C	7.55	119.30	111.14
1	Ad	94	LYS	N-CA-C	7.55	119.59	111.36
1	By	76	VAL	N-CA-C	-7.55	104.50	111.67
1	Ds	7	ILE	N-CA-C	7.55	118.34	110.72
1	Dx	7	ILE	N-CA-C	7.55	118.34	110.72
1	AH	94	LYS	N-CA-C	7.55	119.58	111.36
1	Dn	7	ILE	N-CA-C	7.54	118.34	110.72
1	A4	94	LYS	N-CA-C	7.54	119.58	111.36
1	A9	94	LYS	N-CA-C	7.54	119.58	111.36
1	Az	94	LYS	N-CA-C	7.54	119.58	111.36
1	DH	7	ILE	N-CA-C	7.54	118.34	110.72
1	AR	94	LYS	N-CA-C	7.54	119.58	111.36
1	AW	94	LYS	N-CA-C	7.54	119.58	111.36
1	C1	37	GLY	N-CA-C	7.54	122.14	110.91
1	Ax	94	LYS	N-CA-C	7.54	119.58	111.36
1	D9	7	ILE	N-CA-C	7.54	118.33	110.72
1	Ca	37	GLY	N-CA-C	7.54	122.14	110.91
1	Dd	7	ILE	N-CA-C	7.54	118.33	110.72
1	Dy	7	ILE	N-CA-C	7.54	118.33	110.72
1	GE	82	ALA	N-CA-C	7.54	119.50	111.28
1	AJ	94	LYS	N-CA-C	7.54	119.58	111.36
1	Cf	37	GLY	N-CA-C	7.54	122.14	110.91
1	Gp	82	ALA	N-CA-C	7.54	119.50	111.28
1	BI	76	VAL	N-CA-C	-7.54	104.51	111.67
1	Cp	37	GLY	N-CA-C	7.53	122.13	110.91
1	GJ	82	ALA	N-CA-C	7.53	119.49	111.28
1	DW	7	ILE	N-CA-C	7.53	118.33	110.72
1	D4	7	ILE	N-CA-C	7.53	118.32	110.72
1	A6	94	LYS	N-CA-C	7.53	119.56	111.36
1	C6	37	GLY	N-CA-C	7.53	122.13	110.91
1	Fh	94	LYS	N-CA-C	7.53	119.56	111.36
1	Au	94	LYS	N-CA-C	7.53	119.56	111.36
1	CE	37	GLY	N-CA-C	7.53	122.12	110.91
1	CO	37	GLY	N-CA-C	7.53	122.13	110.91
1	CJ	37	GLY	N-CA-C	7.53	122.12	110.91
1	GT	82	ALA	N-CA-C	7.53	119.48	111.28
1	Ga	82	ALA	N-CA-C	7.52	119.48	111.28
1	G1	82	ALA	N-CA-C	7.52	119.48	111.28
1	Ck	37	GLY	N-CA-C	7.52	122.12	110.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	FL	94	LYS	N-CA-C	7.52	119.56	111.36
1	Cu	37	GLY	N-CA-C	7.52	122.11	110.91
1	Cz	37	GLY	N-CA-C	7.52	122.11	110.91
1	F3	94	LYS	N-CA-C	7.52	119.55	111.36
1	Fm	94	LYS	N-CA-C	7.52	119.55	111.36
1	HS	74	GLY	N-CA-C	7.52	126.37	112.77
1	CT	37	GLY	N-CA-C	7.51	122.11	110.91
1	A1	94	LYS	N-CA-C	7.51	119.55	111.36
1	Ht	74	GLY	N-CA-C	7.51	126.36	112.77
1	Gf	82	ALA	N-CA-C	7.51	119.46	111.28
1	F8	94	LYS	N-CA-C	7.50	119.54	111.36
1	Af	94	LYS	N-CA-C	7.50	119.54	111.36
1	Ho	74	GLY	N-CA-C	7.50	126.35	112.77
1	FB	94	LYS	N-CA-C	7.50	119.54	111.36
1	FQ	94	LYS	N-CA-C	7.50	119.53	111.36
1	FV	94	LYS	N-CA-C	7.50	119.53	111.36
1	AE	94	LYS	N-CA-C	7.50	119.53	111.36
1	Fw	94	LYS	N-CA-C	7.49	119.53	111.36
1	HD	74	GLY	N-CA-C	7.49	126.33	112.77
1	AO	94	LYS	N-CA-C	7.49	119.53	111.36
1	He	74	GLY	N-CA-C	7.49	126.33	112.77
1	H0	74	GLY	N-CA-C	7.49	126.33	112.77
1	Ap	94	LYS	N-CA-C	7.49	119.52	111.36
1	AT	94	LYS	N-CA-C	7.49	119.53	111.36
1	Di	7	ILE	N-CA-C	7.49	118.28	110.72
1	G6	82	ALA	N-CA-C	7.48	119.44	111.28
1	Aa	94	LYS	N-CA-C	7.48	119.52	111.36
1	HN	74	GLY	N-CA-C	7.48	126.32	112.77
1	Fc	94	LYS	N-CA-C	7.48	119.52	111.36
1	HX	74	GLY	N-CA-C	7.48	126.31	112.77
1	DM	7	ILE	N-CA-C	7.48	118.27	110.72
1	H5	74	GLY	N-CA-C	7.47	126.30	112.77
1	Gu	82	ALA	N-CA-C	7.47	119.42	111.28
1	GO	82	ALA	N-CA-C	7.47	119.42	111.28
1	Hj	74	GLY	N-CA-C	7.47	126.29	112.77
1	Hy	74	GLY	N-CA-C	7.47	126.29	112.77
1	Gk	82	ALA	N-CA-C	7.47	119.42	111.28
1	Ak	94	LYS	N-CA-C	7.46	119.50	111.36
1	Gz	82	ALA	N-CA-C	7.46	119.42	111.28
1	DV	38	ARG	N-CA-C	-7.46	95.48	108.69
1	HI	74	GLY	N-CA-C	7.46	126.28	112.77
1	DG	38	ARG	N-CA-C	-7.45	95.50	108.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Dx	38	ARG	N-CA-C	-7.45	95.50	108.69
1	FG	94	LYS	N-CA-C	7.45	119.48	111.36
1	DR	38	ARG	N-CA-C	-7.45	95.51	108.69
1	Dp	74	GLY	N-CA-C	7.44	126.24	112.77
1	Du	74	GLY	N-CA-C	7.44	126.24	112.77
1	Gj	38	ARG	N-CA-C	-7.44	96.19	108.76
1	Fr	94	LYS	N-CA-C	7.44	119.47	111.36
1	DC	38	ARG	N-CA-C	-7.44	95.52	108.69
1	D3	38	ARG	N-CA-C	-7.44	95.53	108.69
1	Dc	38	ARG	N-CA-C	-7.44	95.53	108.69
1	D4	38	ARG	N-CA-C	-7.43	95.53	108.69
1	Df	74	GLY	N-CA-C	7.43	126.23	112.77
1	Dr	38	ARG	N-CA-C	-7.43	95.53	108.69
1	DW	38	ARG	N-CA-C	-7.43	95.53	108.69
1	DB	38	ARG	N-CA-C	-7.43	95.54	108.69
1	DL	38	ARG	N-CA-C	-7.43	95.54	108.69
1	D9	38	ARG	N-CA-C	-7.43	95.54	108.69
1	Di	38	ARG	N-CA-C	-7.43	95.54	108.69
1	D8	38	ARG	N-CA-C	-7.43	95.54	108.69
1	Dn	38	ARG	N-CA-C	-7.43	95.54	108.69
1	DQ	38	ARG	N-CA-C	-7.43	95.54	108.69
1	Dh	38	ARG	N-CA-C	-7.43	95.54	108.69
1	GD	38	ARG	N-CA-C	-7.43	96.21	108.76
1	DM	38	ARG	N-CA-C	-7.43	95.54	108.69
1	G0	38	ARG	N-CA-C	-7.42	96.22	108.76
1	Dm	38	ARG	N-CA-C	-7.42	95.55	108.69
1	AD	54	THR	N-CA-C	7.42	119.01	111.07
1	Ao	54	THR	N-CA-C	7.42	119.01	111.07
1	Go	38	ARG	N-CA-C	-7.42	96.22	108.76
1	Dw	38	ARG	N-CA-C	-7.42	95.56	108.69
1	D1	74	GLY	N-CA-C	7.42	126.20	112.77
1	G5	38	ARG	N-CA-C	-7.42	96.22	108.76
1	Gt	38	ARG	N-CA-C	-7.42	96.22	108.76
1	GS	38	ARG	N-CA-C	-7.42	96.22	108.76
1	DJ	74	GLY	N-CA-C	7.42	126.19	112.77
3	P2	22	LYS	N-CA-C	7.42	120.40	109.50
1	DO	74	GLY	N-CA-C	7.41	126.19	112.77
1	Dd	38	ARG	N-CA-C	-7.41	95.57	108.69
1	Ay	54	THR	N-CA-C	7.41	119.00	111.07
1	Da	74	GLY	N-CA-C	7.41	126.18	112.77
1	GN	38	ARG	N-CA-C	-7.41	96.24	108.76
3	PP	22	LYS	N-CA-C	7.41	120.39	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DT	74	GLY	N-CA-C	7.41	126.18	112.77
1	D6	74	GLY	N-CA-C	7.41	126.18	112.77
3	Pl	22	LYS	N-CA-C	7.41	120.39	109.50
1	Dk	74	GLY	N-CA-C	7.41	126.18	112.77
1	GI	38	ARG	N-CA-C	-7.41	96.24	108.76
1	Ge	38	ARG	N-CA-C	-7.40	96.25	108.76
1	Ds	38	ARG	N-CA-C	-7.40	95.59	108.69
1	Dz	74	GLY	N-CA-C	7.40	126.17	112.77
1	DH	38	ARG	N-CA-C	-7.40	95.59	108.69
1	GX	38	ARG	N-CA-C	-7.40	96.25	108.76
3	Pb	22	LYS	N-CA-C	7.40	120.38	109.50
3	Pv	22	LYS	N-CA-C	7.40	120.38	109.50
3	Pg	22	LYS	N-CA-C	7.40	120.38	109.50
1	Gy	38	ARG	N-CA-C	-7.40	96.26	108.76
3	PU	22	LYS	N-CA-C	7.40	120.38	109.50
3	PF	22	LYS	N-CA-C	7.40	120.37	109.50
1	DE	74	GLY	N-CA-C	7.39	126.16	112.77
1	Aj	54	THR	N-CA-C	7.39	118.98	111.07
3	P7	22	LYS	N-CA-C	7.39	120.36	109.50
3	PK	22	LYS	N-CA-C	7.39	120.36	109.50
3	Pq	22	LYS	N-CA-C	7.39	120.36	109.50
1	A0	54	THR	N-CA-C	7.38	118.97	111.07
1	Hk	30	ALA	N-CA-C	7.38	119.33	111.28
1	A5	54	THR	N-CA-C	7.38	118.97	111.07
1	AN	54	THR	N-CA-C	7.38	118.97	111.07
1	CA	37	GLY	N-CA-C	7.38	121.91	110.91
3	PA	22	LYS	N-CA-C	7.38	120.35	109.50
1	HT	30	ALA	N-CA-C	7.38	119.32	111.28
3	PA	33	ALA	CA-C-N	-7.37	111.87	119.83
3	PA	33	ALA	C-N-CA	-7.37	111.87	119.83
2	XG	827	VAL	N-CA-C	7.37	117.32	106.85
1	Ha	30	ALA	N-CA-C	7.37	119.31	111.28
1	HJ	30	ALA	N-CA-C	7.36	119.31	111.28
3	PP	33	ALA	CA-C-N	-7.36	111.88	119.83
3	PP	33	ALA	C-N-CA	-7.36	111.88	119.83
1	Hx	30	ALA	N-CA-C	7.36	119.31	111.28
2	XV	827	VAL	N-CA-C	7.36	117.30	106.85
1	CP	37	GLY	N-CA-C	7.36	121.88	110.91
1	AS	54	THR	N-CA-C	7.36	118.94	111.07
1	HE	30	ALA	N-CA-C	7.36	119.30	111.28
1	H6	30	ALA	N-CA-C	7.36	119.30	111.28
1	Hp	30	ALA	N-CA-C	7.36	119.30	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Xr	827	VAL	N-CA-C	7.36	117.29	106.85
1	Hu	30	ALA	N-CA-C	7.35	119.30	111.28
1	Ae	54	THR	N-CA-C	7.35	118.94	111.07
1	Bp	82	ALA	N-CA-C	7.35	119.38	111.36
1	BT	82	ALA	N-CA-C	7.35	119.37	111.36
1	C7	37	GLY	N-CA-C	7.35	121.86	110.91
1	Ba	82	ALA	N-CA-C	7.35	119.37	111.36
2	Xc	827	VAL	N-CA-C	7.35	117.29	106.85
1	AI	54	THR	N-CA-C	7.35	118.93	111.07
1	Cv	37	GLY	N-CA-C	7.34	121.85	110.91
3	Pv	33	ALA	CA-C-N	-7.34	111.90	119.83
3	Pv	33	ALA	C-N-CA	-7.34	111.90	119.83
3	P7	33	ALA	CA-C-N	-7.34	111.90	119.83
3	P7	33	ALA	C-N-CA	-7.34	111.90	119.83
1	Bz	82	ALA	N-CA-C	7.34	119.36	111.36
1	GC	38	ARG	N-CA-C	-7.34	96.30	108.34
1	CU	37	GLY	N-CA-C	7.34	121.85	110.91
1	G9	38	ARG	N-CA-C	-7.34	96.30	108.34
1	GR	38	ARG	N-CA-C	-7.34	96.30	108.34
1	BO	82	ALA	N-CA-C	7.34	119.36	111.36
3	PF	33	ALA	CA-C-N	-7.33	111.91	119.83
3	PF	33	ALA	C-N-CA	-7.33	111.91	119.83
1	H1	30	ALA	N-CA-C	7.33	119.27	111.28
1	HO	30	ALA	N-CA-C	7.33	119.27	111.28
1	BE	82	ALA	N-CA-C	7.33	119.35	111.36
3	Pb	33	ALA	CA-C-N	-7.33	111.92	119.83
3	Pb	33	ALA	C-N-CA	-7.33	111.92	119.83
1	Cq	37	GLY	N-CA-C	7.33	121.83	110.91
3	PU	33	ALA	CA-C-N	-7.33	111.92	119.83
3	PU	33	ALA	C-N-CA	-7.33	111.92	119.83
2	XB	827	VAL	N-CA-C	7.33	117.26	106.85
1	C2	37	GLY	N-CA-C	7.33	121.83	110.91
1	CK	37	GLY	N-CA-C	7.33	121.83	110.91
3	P2	33	ALA	CA-C-N	-7.33	111.92	119.83
3	P2	33	ALA	C-N-CA	-7.33	111.92	119.83
3	PK	33	ALA	CA-C-N	-7.33	111.92	119.83
3	PK	33	ALA	C-N-CA	-7.33	111.92	119.83
2	XQ	827	VAL	N-CA-C	7.33	117.25	106.85
1	Hf	30	ALA	N-CA-C	7.33	119.27	111.28
1	B1	82	ALA	N-CA-C	7.32	119.34	111.36
1	Gn	38	ARG	N-CA-C	-7.32	96.33	108.34
1	Gx	38	ARG	N-CA-C	-7.32	96.33	108.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X3	827	VAL	N-CA-C	7.32	117.25	106.85
1	AX	54	THR	N-CA-C	7.32	118.90	111.07
1	Cg	37	GLY	N-CA-C	7.32	121.81	110.91
2	Xh	827	VAL	N-CA-C	7.32	117.24	106.85
3	Pq	33	ALA	CA-C-N	-7.32	111.93	119.83
3	Pq	33	ALA	C-N-CA	-7.32	111.93	119.83
1	Cb	37	GLY	N-CA-C	7.32	121.81	110.91
1	GH	38	ARG	N-CA-C	-7.32	96.34	108.34
2	XL	827	VAL	N-CA-C	7.32	117.24	106.85
1	B6	82	ALA	N-CA-C	7.32	119.33	111.36
1	Bf	82	ALA	N-CA-C	7.32	119.33	111.36
1	CF	37	GLY	N-CA-C	7.32	121.81	110.91
1	Gd	38	ARG	N-CA-C	-7.31	96.34	108.34
1	GW	38	ARG	N-CA-C	-7.31	96.34	108.34
1	G4	38	ARG	N-CA-C	-7.31	96.35	108.34
1	Gi	38	ARG	N-CA-C	-7.31	96.35	108.34
1	Cl	37	GLY	N-CA-C	7.31	121.80	110.91
3	Pl	33	ALA	CA-C-N	-7.31	111.93	119.83
3	Pl	33	ALA	C-N-CA	-7.31	111.93	119.83
1	BJ	82	ALA	N-CA-C	7.31	119.33	111.36
1	Bu	82	ALA	N-CA-C	7.31	119.33	111.36
2	Xm	827	VAL	N-CA-C	7.31	117.23	106.85
1	Bk	82	ALA	N-CA-C	7.31	119.32	111.36
3	Pg	33	ALA	CA-C-N	-7.30	111.94	119.83
3	Pg	33	ALA	C-N-CA	-7.30	111.94	119.83
2	Xw	827	VAL	N-CA-C	7.30	117.22	106.85
2	X8	827	VAL	N-CA-C	7.30	117.22	106.85
1	At	54	THR	N-CA-C	7.29	118.88	111.07
1	GM	38	ARG	N-CA-C	-7.29	96.38	108.34
1	Gs	38	ARG	N-CA-C	-7.29	96.38	108.34
1	EO	82	ALA	N-CA-C	7.29	119.23	111.28
2	XB	782	MET	N-CA-C	-7.27	96.67	108.52
2	Xm	782	MET	N-CA-C	-7.27	96.67	108.52
1	Ek	82	ALA	N-CA-C	7.27	119.20	111.28
1	EJ	82	ALA	N-CA-C	7.27	119.20	111.28
1	E6	82	ALA	N-CA-C	7.27	119.20	111.28
1	E1	82	ALA	N-CA-C	7.26	119.19	111.28
2	XQ	816	GLY	N-CA-C	7.26	123.66	114.66
2	XV	816	GLY	N-CA-C	7.26	123.66	114.66
2	Xw	816	GLY	N-CA-C	7.25	123.65	114.66
2	XQ	782	MET	N-CA-C	-7.25	96.69	108.52
2	Xr	816	GLY	N-CA-C	7.25	123.66	114.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	XV	782	MET	N-CA-C	-7.25	96.70	108.52
2	Xh	782	MET	N-CA-C	-7.25	96.70	108.52
1	Eu	82	ALA	N-CA-C	7.25	119.18	111.28
1	Ez	82	ALA	N-CA-C	7.25	119.18	111.28
2	X8	782	MET	N-CA-C	-7.25	96.71	108.52
2	XB	816	GLY	N-CA-C	7.25	123.65	114.66
2	Xc	816	GLY	N-CA-C	7.25	123.64	114.66
2	X3	782	MET	N-CA-C	-7.24	96.71	108.52
2	Xw	782	MET	N-CA-C	-7.24	96.72	108.52
1	Au	30	ALA	N-CA-C	7.24	119.25	111.36
2	X8	816	GLY	N-CA-C	7.24	123.64	114.66
1	Ef	82	ALA	N-CA-C	7.24	119.17	111.28
1	Fk	82	ALA	N-CA-C	7.24	119.17	111.28
2	XG	816	GLY	N-CA-C	7.23	123.63	114.66
1	DP	82	ALA	N-CA-C	7.23	119.16	111.28
2	Xc	782	MET	N-CA-C	-7.23	96.73	108.52
2	Xm	816	GLY	N-CA-C	7.23	123.62	114.66
2	Xr	782	MET	N-CA-C	-7.23	96.73	108.52
2	XG	782	MET	N-CA-C	-7.23	96.73	108.52
1	Aa	30	ALA	N-CA-C	7.23	119.24	111.36
1	AT	30	ALA	N-CA-C	7.23	119.24	111.36
1	AE	30	ALA	N-CA-C	7.23	119.24	111.36
2	XL	782	MET	N-CA-C	-7.23	96.74	108.52
1	A1	30	ALA	N-CA-C	7.22	119.23	111.36
1	Ap	30	ALA	N-CA-C	7.22	119.22	111.36
2	X3	816	GLY	N-CA-C	7.21	123.61	114.66
1	AO	30	ALA	N-CA-C	7.21	119.22	111.36
1	Ep	82	ALA	N-CA-C	7.21	119.14	111.28
1	Ea	82	ALA	N-CA-C	7.21	119.14	111.28
1	EE	82	ALA	N-CA-C	7.21	119.14	111.28
2	Xh	816	GLY	N-CA-C	7.21	123.60	114.66
1	DF	82	ALA	N-CA-C	7.20	119.13	111.28
1	Fu	82	ALA	N-CA-C	7.20	119.12	111.28
1	D7	82	ALA	N-CA-C	7.20	119.12	111.28
1	F6	82	ALA	N-CA-C	7.20	119.12	111.28
2	XL	816	GLY	N-CA-C	7.20	123.58	114.66
1	F1	82	ALA	N-CA-C	7.19	119.12	111.28
1	Af	30	ALA	N-CA-C	7.19	119.20	111.36
1	FJ	82	ALA	N-CA-C	7.19	119.12	111.28
1	D2	82	ALA	N-CA-C	7.19	119.12	111.28
1	Az	30	ALA	N-CA-C	7.19	119.20	111.36
1	Db	82	ALA	N-CA-C	7.19	119.12	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ff	82	ALA	N-CA-C	7.19	119.12	111.28
1	Dv	82	ALA	N-CA-C	7.19	119.12	111.28
1	A6	30	ALA	N-CA-C	7.19	119.19	111.36
1	CC	30	ALA	N-CA-C	7.19	119.11	111.28
1	AJ	30	ALA	N-CA-C	7.18	119.19	111.36
1	ET	82	ALA	N-CA-C	7.18	119.11	111.28
1	Dq	68	CYS	N-CA-C	7.18	121.63	113.01
1	Fp	82	ALA	N-CA-C	7.18	119.11	111.28
1	FO	82	ALA	N-CA-C	7.18	119.11	111.28
1	CR	30	ALA	N-CA-C	7.18	119.11	111.28
1	Fa	82	ALA	N-CA-C	7.18	119.10	111.28
1	DI	82	ALA	N-CA-C	7.18	119.10	111.28
1	DU	82	ALA	N-CA-C	7.18	119.10	111.28
1	Db	68	CYS	N-CA-C	7.17	121.61	113.01
1	Cn	30	ALA	N-CA-C	7.17	119.09	111.28
1	Dg	68	CYS	N-CA-C	7.17	121.61	113.01
1	C9	30	ALA	N-CA-C	7.16	119.09	111.28
1	DK	68	CYS	N-CA-C	7.16	121.61	113.01
1	Dg	82	ALA	N-CA-C	7.16	119.09	111.28
1	Cs	30	ALA	N-CA-C	7.16	119.09	111.28
1	DU	68	CYS	N-CA-C	7.16	121.60	113.01
1	CW	30	ALA	N-CA-C	7.16	119.08	111.28
1	Dq	82	ALA	N-CA-C	7.16	119.08	111.28
1	FE	82	ALA	N-CA-C	7.16	119.08	111.28
1	DK	82	ALA	N-CA-C	7.16	119.08	111.28
1	D2	68	CYS	N-CA-C	7.15	121.59	113.01
1	DA	82	ALA	N-CA-C	7.15	119.08	111.28
1	DF	68	CYS	N-CA-C	7.15	121.59	113.01
1	FT	82	ALA	N-CA-C	7.15	119.08	111.28
1	Fz	82	ALA	N-CA-C	7.15	119.07	111.28
1	Ak	30	ALA	N-CA-C	7.15	119.15	111.36
1	DP	68	CYS	N-CA-C	7.15	121.59	113.01
1	CR	76	VAL	N-CA-C	-7.14	105.42	111.56
1	D7	68	CYS	N-CA-C	7.14	121.58	113.01
1	Cd	30	ALA	N-CA-C	7.14	119.06	111.28
1	Dv	68	CYS	N-CA-C	7.14	121.58	113.01
1	Gu	54	THR	N-CA-C	7.14	118.71	111.07
2	XN	820	SER	N-CA-C	7.14	120.30	109.23
1	CW	76	VAL	N-CA-C	-7.14	105.42	111.56
2	Xj	820	SER	N-CA-C	7.13	120.29	109.23
2	XD	820	SER	N-CA-C	7.13	120.29	109.23
2	XI	820	SER	N-CA-C	7.13	120.29	109.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CM	30	ALA	N-CA-C	7.13	119.06	111.28
1	GE	54	THR	N-CA-C	7.13	118.70	111.07
1	DI	68	CYS	N-CA-C	7.13	121.56	113.01
1	HI	38	ARG	N-CA-C	-7.13	96.94	109.06
2	Xe	820	SER	N-CA-C	7.12	120.27	109.23
1	Ci	30	ALA	N-CA-C	7.12	119.05	111.28
2	X5	820	SER	N-CA-C	7.12	120.27	109.23
1	Cs	76	VAL	N-CA-C	-7.12	105.44	111.56
1	GJ	54	THR	N-CA-C	7.12	118.69	111.07
2	XX	820	SER	N-CA-C	7.12	120.27	109.23
1	Hj	38	ARG	N-CA-C	-7.12	96.96	109.06
1	C4	30	ALA	N-CA-C	7.12	119.04	111.28
1	H0	38	ARG	N-CA-C	-7.12	96.96	109.06
1	Gf	54	THR	N-CA-C	7.12	118.69	111.07
1	Ht	38	ARG	N-CA-C	-7.12	96.96	109.06
1	He	38	ARG	N-CA-C	-7.11	96.97	109.06
1	Gk	54	THR	N-CA-C	7.11	118.68	111.07
1	Cn	76	VAL	N-CA-C	-7.11	105.44	111.56
1	Cx	76	VAL	N-CA-C	-7.11	105.44	111.56
1	CH	30	ALA	N-CA-C	7.11	119.03	111.28
1	CM	76	VAL	N-CA-C	-7.11	105.44	111.56
1	Ci	76	VAL	N-CA-C	-7.11	105.44	111.56
1	C4	76	VAL	N-CA-C	-7.11	105.44	111.56
1	Ga	54	THR	N-CA-C	7.11	118.68	111.07
1	DA	68	CYS	N-CA-C	7.11	121.54	113.01
1	HD	38	ARG	N-CA-C	-7.11	96.97	109.06
1	G1	54	THR	N-CA-C	7.11	118.67	111.07
1	Cd	76	VAL	N-CA-C	-7.11	105.45	111.56
2	Xt	820	SER	N-CA-C	7.11	120.25	109.23
2	Xy	820	SER	N-CA-C	7.11	120.24	109.23
1	Ho	38	ARG	N-CA-C	-7.10	96.98	109.06
1	H5	38	ARG	N-CA-C	-7.10	96.99	109.06
1	C9	76	VAL	N-CA-C	-7.10	105.45	111.56
1	Hy	38	ARG	N-CA-C	-7.10	96.98	109.06
1	Gz	54	THR	N-CA-C	7.10	118.67	111.07
2	X0	820	SER	N-CA-C	7.10	120.24	109.23
1	G6	54	THR	N-CA-C	7.10	118.67	111.07
2	Xo	820	SER	N-CA-C	7.10	120.23	109.23
1	GO	54	THR	N-CA-C	7.10	118.67	111.07
1	HS	38	ARG	N-CA-C	-7.09	97.00	109.06
2	XS	820	SER	N-CA-C	7.09	120.23	109.23
1	HX	38	ARG	N-CA-C	-7.09	97.00	109.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AI	30	ALA	N-CA-C	7.09	119.09	111.36
1	HN	38	ARG	N-CA-C	-7.09	97.00	109.06
1	Cx	30	ALA	N-CA-C	7.09	119.01	111.28
1	GT	54	THR	N-CA-C	7.09	118.66	111.07
1	CH	76	VAL	N-CA-C	-7.09	105.46	111.56
1	Ae	30	ALA	N-CA-C	7.07	119.06	111.36
1	CC	76	VAL	N-CA-C	-7.07	105.48	111.56
1	AX	30	ALA	N-CA-C	7.07	119.06	111.36
1	Gp	54	THR	N-CA-C	7.06	118.62	111.07
1	A0	30	ALA	N-CA-C	7.05	119.05	111.36
1	At	30	ALA	N-CA-C	7.05	119.05	111.36
1	Hz	68	CYS	N-CA-C	7.05	121.14	112.54
1	Ao	30	ALA	N-CA-C	7.04	119.04	111.36
1	AD	30	ALA	N-CA-C	7.04	119.03	111.36
1	AS	30	ALA	N-CA-C	7.04	119.03	111.36
1	Hk	68	CYS	N-CA-C	7.04	121.13	112.54
1	Aa	37	GLY	N-CA-C	7.03	122.24	110.56
2	Xj	849	THR	N-CA-C	-7.03	98.72	109.41
1	AE	37	GLY	N-CA-C	7.03	122.24	110.56
1	AT	37	GLY	N-CA-C	7.03	122.24	110.56
1	Ap	37	GLY	N-CA-C	7.03	122.23	110.56
1	A1	37	GLY	N-CA-C	7.03	122.23	110.56
1	AJ	37	GLY	N-CA-C	7.03	122.23	110.56
1	A5	30	ALA	N-CA-C	7.02	119.01	111.36
1	Au	37	GLY	N-CA-C	7.02	122.21	110.56
2	Xy	849	THR	N-CA-C	-7.01	98.75	109.41
1	H1	68	CYS	N-CA-C	7.01	121.09	112.54
2	Xt	849	THR	N-CA-C	-7.01	98.75	109.41
2	X5	849	THR	N-CA-C	-7.01	98.76	109.41
2	XN	849	THR	N-CA-C	-7.01	98.76	109.41
2	X0	849	THR	N-CA-C	-7.01	98.76	109.41
2	XS	849	THR	N-CA-C	-7.01	98.76	109.41
1	Ha	68	CYS	N-CA-C	7.01	121.09	112.54
1	Ay	30	ALA	N-CA-C	7.01	119.00	111.36
1	Hf	68	CYS	N-CA-C	7.01	121.09	112.54
1	Dl	41	VAL	N-CA-C	7.00	117.80	110.72
2	Xo	849	THR	N-CA-C	-7.00	98.76	109.41
1	Ak	37	GLY	N-CA-C	7.00	122.19	110.56
1	Hp	68	CYS	N-CA-C	7.00	121.08	112.54
1	HE	68	CYS	N-CA-C	7.00	121.08	112.54
1	Cf	82	ALA	N-CA-C	7.00	118.91	111.28
1	Aj	30	ALA	N-CA-C	7.00	118.99	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A6	37	GLY	N-CA-C	7.00	122.18	110.56
2	Xe	849	THR	N-CA-C	-7.00	98.78	109.41
1	Bg	38	ARG	N-CA-C	-7.00	96.94	108.76
1	El	82	ALA	N-CA-C	7.00	118.91	111.28
1	Bq	38	ARG	N-CA-C	-7.00	96.94	108.76
1	Cp	82	ALA	N-CA-C	7.00	118.91	111.28
1	AO	37	GLY	N-CA-C	7.00	122.17	110.56
1	Af	37	GLY	N-CA-C	7.00	122.17	110.56
1	Bv	38	ARG	N-CA-C	-7.00	96.94	108.76
2	XI	849	THR	N-CA-C	-6.99	98.78	109.41
2	XX	849	THR	N-CA-C	-6.99	98.78	109.41
1	Az	37	GLY	N-CA-C	6.99	122.17	110.56
2	XD	849	THR	N-CA-C	-6.99	98.78	109.41
1	Ca	82	ALA	N-CA-C	6.99	118.90	111.28
1	CT	82	ALA	N-CA-C	6.99	118.90	111.28
1	BF	38	ARG	N-CA-C	-6.99	96.96	108.76
1	B2	38	ARG	N-CA-C	-6.98	96.96	108.76
1	Bj	83	ARG	N-CA-C	-6.98	97.52	108.90
1	BK	38	ARG	N-CA-C	-6.98	96.96	108.76
1	Bb	38	ARG	N-CA-C	-6.98	96.96	108.76
1	HJ	68	CYS	N-CA-C	6.98	121.06	112.54
1	AN	30	ALA	N-CA-C	6.98	118.97	111.36
1	Dg	83	ARG	N-CA-C	-6.98	97.19	109.06
1	BA	38	ARG	N-CA-C	-6.98	96.96	108.76
1	CJ	82	ALA	N-CA-C	6.98	118.89	111.28
1	HT	68	CYS	N-CA-C	6.98	121.05	112.54
1	DA	41	VAL	N-CA-C	6.97	117.76	110.72
1	DF	83	ARG	N-CA-C	-6.97	97.20	109.06
1	C1	82	ALA	N-CA-C	6.97	118.88	111.28
1	B7	38	ARG	N-CA-C	-6.97	96.98	108.76
1	Dv	83	ARG	N-CA-C	-6.97	97.21	109.06
1	BP	38	ARG	N-CA-C	-6.97	96.98	108.76
1	D2	83	ARG	N-CA-C	-6.97	97.21	109.06
1	D7	41	VAL	N-CA-C	6.97	117.76	110.72
1	CB	17	LEU	N-CA-C	6.97	118.95	111.36
1	DK	83	ARG	N-CA-C	-6.97	97.21	109.06
1	DP	41	VAL	N-CA-C	6.97	117.76	110.72
1	By	83	ARG	N-CA-C	-6.97	97.55	108.90
1	E7	82	ALA	N-CA-C	6.96	118.87	111.28
1	BU	38	ARG	N-CA-C	-6.96	96.99	108.76
1	D7	83	ARG	N-CA-C	-6.96	97.22	109.06
1	C6	82	ALA	N-CA-C	6.96	118.87	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Db	83	ARG	N-CA-C	-6.96	97.23	109.06
1	Dq	83	ARG	N-CA-C	-6.96	97.23	109.06
2	Xz	843	LYS	N-CA-C	6.96	118.48	109.64
1	CE	82	ALA	N-CA-C	6.96	118.86	111.28
1	EK	82	ALA	N-CA-C	6.96	118.86	111.28
1	Aq	37	GLY	N-CA-C	6.96	121.28	110.91
1	Cz	82	ALA	N-CA-C	6.96	118.86	111.28
1	EF	82	ALA	N-CA-C	6.96	118.86	111.28
1	DP	83	ARG	N-CA-C	-6.95	97.24	109.06
1	Ab	37	GLY	N-CA-C	6.95	121.27	110.91
1	AU	37	GLY	N-CA-C	6.95	121.27	110.91
1	DU	83	ARG	N-CA-C	-6.95	97.24	109.06
1	Dl	83	ARG	N-CA-C	-6.95	97.25	109.06
2	XJ	843	LYS	N-CA-C	6.95	118.47	109.64
2	XT	843	LYS	N-CA-C	6.94	118.46	109.64
1	Df	38	ARG	N-CA-C	-6.94	97.03	108.76
1	Bl	38	ARG	N-CA-C	-6.94	97.03	108.76
1	Av	37	GLY	N-CA-C	6.94	121.25	110.91
1	DA	83	ARG	N-CA-C	-6.94	97.26	109.06
1	Ck	82	ALA	N-CA-C	6.94	118.84	111.28
1	EA	82	ALA	N-CA-C	6.94	118.85	111.28
1	EP	82	ALA	N-CA-C	6.94	118.84	111.28
1	E2	82	ALA	N-CA-C	6.94	118.84	111.28
1	DK	41	VAL	N-CA-C	6.94	117.73	110.72
1	Eg	82	ALA	N-CA-C	6.94	118.84	111.28
1	DT	38	ARG	N-CA-C	-6.94	97.04	108.76
1	Cm	17	LEU	N-CA-C	6.94	118.92	111.36
1	CC	7	ILE	N-CA-C	6.94	118.76	112.17
1	DJ	38	ARG	N-CA-C	-6.94	97.04	108.76
2	X6	843	LYS	N-CA-C	6.93	118.45	109.64
1	Dp	38	ARG	N-CA-C	-6.93	97.05	108.76
1	HC	37	GLY	N-CA-C	6.93	122.07	110.56
2	XE	843	LYS	N-CA-C	6.93	118.44	109.64
1	HM	37	GLY	N-CA-C	6.93	122.07	110.56
1	Eb	82	ALA	N-CA-C	6.93	118.83	111.28
1	Dq	41	VAL	N-CA-C	6.93	117.72	110.72
1	EU	82	ALA	N-CA-C	6.93	118.83	111.28
2	Xa	843	LYS	N-CA-C	6.93	118.44	109.64
1	Hi	37	GLY	N-CA-C	6.93	122.06	110.56
1	AF	37	GLY	N-CA-C	6.93	121.23	110.91
1	A2	37	GLY	N-CA-C	6.93	121.23	110.91
1	D1	38	ARG	N-CA-C	-6.93	97.05	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ev	82	ALA	N-CA-C	6.93	118.83	111.28
1	CO	82	ALA	N-CA-C	6.93	118.83	111.28
1	Da	38	ARG	N-CA-C	-6.92	97.06	108.76
1	Hx	37	GLY	N-CA-C	6.92	122.05	110.56
2	XO	843	LYS	N-CA-C	6.92	118.43	109.64
1	DF	41	VAL	N-CA-C	6.92	117.71	110.72
2	X1	843	LYS	N-CA-C	6.92	118.43	109.64
1	H9	37	GLY	N-CA-C	6.92	122.05	110.56
1	D2	41	VAL	N-CA-C	6.92	117.71	110.72
1	DE	38	ARG	N-CA-C	-6.92	97.07	108.76
1	C8	17	LEU	N-CA-C	6.92	118.90	111.36
1	Hn	37	GLY	N-CA-C	6.92	122.04	110.56
1	Ag	37	GLY	N-CA-C	6.92	121.22	110.91
1	Hs	37	GLY	N-CA-C	6.92	122.04	110.56
1	Du	38	ARG	N-CA-C	-6.92	97.07	108.76
1	AK	37	GLY	N-CA-C	6.92	121.22	110.91
2	Xk	843	LYS	N-CA-C	6.92	118.42	109.64
1	H4	37	GLY	N-CA-C	6.91	122.04	110.56
1	A7	37	GLY	N-CA-C	6.91	121.21	110.91
1	Hd	37	GLY	N-CA-C	6.91	122.04	110.56
2	Xp	843	LYS	N-CA-C	6.91	118.42	109.64
1	AP	37	GLY	N-CA-C	6.91	121.21	110.91
1	CQ	17	LEU	N-CA-C	6.91	118.89	111.36
1	HW	37	GLY	N-CA-C	6.91	122.04	110.56
1	FS	43	GLY	N-CA-C	-6.91	105.78	115.32
2	Xu	843	LYS	N-CA-C	6.91	118.42	109.64
1	Fj	43	GLY	N-CA-C	-6.91	105.78	115.32
2	Xt	816	GLY	N-CA-C	6.91	121.02	112.73
1	CL	17	LEU	N-CA-C	6.91	118.89	111.36
1	D6	38	ARG	N-CA-C	-6.91	97.09	108.76
1	Db	41	VAL	N-CA-C	6.91	117.70	110.72
1	Fo	43	GLY	N-CA-C	-6.91	105.79	115.32
1	Eq	82	ALA	N-CA-C	6.91	118.81	111.28
1	DU	41	VAL	N-CA-C	6.91	117.70	110.72
1	Cu	82	ALA	N-CA-C	6.91	118.81	111.28
1	AA	37	GLY	N-CA-C	6.91	121.20	110.91
1	DO	38	ARG	N-CA-C	-6.91	97.09	108.76
1	Dz	38	ARG	N-CA-C	-6.90	97.09	108.76
3	PD	56	SER	N-CA-C	-6.90	105.40	114.31
3	Po	56	SER	N-CA-C	-6.90	105.41	114.31
1	Dk	38	ARG	N-CA-C	-6.90	97.10	108.76
1	FN	43	GLY	N-CA-C	-6.90	105.80	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Gf	7	ILE	N-CA-C	6.90	117.69	110.72
1	Ch	17	LEU	N-CA-C	6.90	118.88	111.36
1	Dg	41	VAL	N-CA-C	6.90	117.69	110.72
3	PI	56	SER	N-CA-C	-6.90	105.41	114.31
2	Xe	816	GLY	N-CA-C	6.90	121.00	112.73
1	Al	37	GLY	N-CA-C	6.90	121.19	110.91
1	Fy	43	GLY	N-CA-C	-6.90	105.80	115.32
1	F5	43	GLY	N-CA-C	-6.89	105.81	115.32
2	Xf	843	LYS	N-CA-C	6.89	118.40	109.64
2	Xw	849	THR	N-CA-C	-6.89	98.93	109.41
1	HH	37	GLY	N-CA-C	6.89	122.00	110.56
1	FD	43	GLY	N-CA-C	-6.89	105.81	115.32
1	FI	43	GLY	N-CA-C	-6.89	105.81	115.32
1	HR	37	GLY	N-CA-C	6.89	122.00	110.56
1	Cs	82	ALA	N-CA-C	6.89	118.87	111.36
2	X5	816	GLY	N-CA-C	6.89	121.00	112.73
1	C3	17	LEU	N-CA-C	6.89	118.87	111.36
2	Xj	816	GLY	N-CA-C	6.89	121.00	112.73
1	Dv	41	VAL	N-CA-C	6.89	117.68	110.72
3	Py	56	SER	N-CA-C	-6.89	105.42	114.31
2	XI	816	GLY	N-CA-C	6.89	121.00	112.73
2	XX	816	GLY	N-CA-C	6.89	121.00	112.73
1	F0	43	GLY	N-CA-C	-6.89	105.81	115.32
1	He	20	ALA	N-CA-C	6.89	118.78	111.28
3	Pe	56	SER	N-CA-C	-6.89	105.42	114.31
1	Ci	82	ALA	N-CA-C	6.89	118.87	111.36
2	Xo	816	GLY	N-CA-C	6.89	120.99	112.73
2	XS	816	GLY	N-CA-C	6.89	121.00	112.73
1	HX	20	ALA	N-CA-C	6.89	118.78	111.28
3	PX	56	SER	N-CA-C	-6.89	105.42	114.31
3	P0	56	SER	N-CA-C	-6.88	105.43	114.31
2	X0	816	GLY	N-CA-C	6.88	120.99	112.73
1	Ht	20	ALA	N-CA-C	6.88	118.78	111.28
1	Fe	43	GLY	N-CA-C	-6.88	105.83	115.32
1	Cc	17	LEU	N-CA-C	6.88	118.86	111.36
3	Pt	56	SER	N-CA-C	-6.88	105.44	114.31
1	GC	48	VAL	CB-CA-C	6.88	121.08	110.83
1	HI	20	ALA	N-CA-C	6.88	118.78	111.28
1	CV	17	LEU	N-CA-C	6.88	118.86	111.36
3	P5	56	SER	N-CA-C	-6.88	105.44	114.31
3	PN	56	SER	N-CA-C	-6.88	105.44	114.31
2	Xh	849	THR	N-CA-C	-6.87	98.96	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G8	37	GLY	N-CA-C	6.87	121.15	110.91
3	Pj	56	SER	N-CA-C	-6.87	105.45	114.31
2	Xy	816	GLY	N-CA-C	6.87	120.97	112.73
1	Gw	37	GLY	N-CA-C	6.87	121.15	110.91
1	CH	7	ILE	N-CA-C	6.87	118.70	112.17
1	C9	7	ILE	N-CA-C	6.87	118.70	112.17
1	G9	48	VAL	CB-CA-C	6.87	121.07	110.83
1	CM	94	LYS	N-CA-C	6.87	118.85	111.36
1	GR	48	VAL	CB-CA-C	6.87	121.07	110.83
1	FX	43	GLY	N-CA-C	-6.87	105.84	115.32
2	Xc	849	THR	N-CA-C	-6.87	98.97	109.41
1	Cw	17	LEU	N-CA-C	6.87	118.84	111.36
2	XB	849	THR	N-CA-C	-6.87	98.97	109.41
2	XG	849	THR	N-CA-C	-6.87	98.97	109.41
1	G3	37	GLY	N-CA-C	6.86	121.14	110.91
1	C9	82	ALA	N-CA-C	6.86	118.84	111.36
1	Ft	43	GLY	N-CA-C	-6.86	105.85	115.32
1	Cs	94	LYS	N-CA-C	6.86	118.84	111.36
1	Cx	82	ALA	N-CA-C	6.86	118.84	111.36
1	CG	17	LEU	N-CA-C	6.86	118.84	111.36
1	GQ	37	GLY	N-CA-C	6.86	121.14	110.91
2	X3	849	THR	N-CA-C	-6.86	98.98	109.41
1	Gm	37	GLY	N-CA-C	6.86	121.13	110.91
1	Gu	7	ILE	N-CA-C	6.86	117.65	110.72
2	XL	849	THR	N-CA-C	-6.86	98.98	109.41
1	CR	7	ILE	N-CA-C	6.86	118.69	112.17
1	Gi	48	VAL	CB-CA-C	6.86	121.05	110.83
1	Gz	7	ILE	N-CA-C	6.86	117.65	110.72
2	XN	816	GLY	N-CA-C	6.86	120.96	112.73
1	GL	37	GLY	N-CA-C	6.86	121.13	110.91
1	H5	20	ALA	N-CA-C	6.86	118.76	111.28
1	Gh	37	GLY	N-CA-C	6.86	121.13	110.91
1	Gk	7	ILE	N-CA-C	6.86	117.65	110.72
1	HN	20	ALA	N-CA-C	6.86	118.76	111.28
1	Cn	82	ALA	N-CA-C	6.86	118.83	111.36
1	Hy	20	ALA	N-CA-C	6.86	118.75	111.28
1	CM	7	ILE	N-CA-C	6.86	118.69	112.17
1	G1	7	ILE	N-CA-C	6.86	117.64	110.72
1	C4	82	ALA	N-CA-C	6.86	118.83	111.36
1	Ho	20	ALA	N-CA-C	6.86	118.75	111.28
1	Gn	48	VAL	CB-CA-C	6.86	121.05	110.83
1	Cr	17	LEU	N-CA-C	6.86	118.83	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	XD	816	GLY	N-CA-C	6.86	120.96	112.73
1	CM	82	ALA	N-CA-C	6.86	118.83	111.36
1	CR	82	ALA	N-CA-C	6.86	118.83	111.36
1	CU	38	ARG	N-CA-C	-6.86	97.17	108.76
1	Fz	38	ARG	N-CA-C	-6.85	97.79	109.24
1	GB	37	GLY	N-CA-C	6.85	121.12	110.91
1	CC	82	ALA	N-CA-C	6.85	118.83	111.36
1	CF	38	ARG	N-CA-C	-6.85	97.18	108.76
1	Ci	7	ILE	N-CA-C	6.85	118.68	112.17
1	Cq	38	ARG	N-CA-C	-6.85	97.18	108.76
1	GG	37	GLY	N-CA-C	6.85	121.12	110.91
1	GO	7	ILE	N-CA-C	6.85	117.64	110.72
1	Cd	82	ALA	N-CA-C	6.85	118.83	111.36
2	XV	849	THR	N-CA-C	-6.85	99.00	109.41
3	PS	56	SER	N-CA-C	-6.85	105.48	114.31
1	Ff	38	ARG	N-CA-C	-6.85	97.81	109.24
1	Hj	20	ALA	N-CA-C	6.85	118.74	111.28
2	X8	849	THR	N-CA-C	-6.85	99.00	109.41
1	Fk	38	ARG	N-CA-C	-6.84	97.81	109.24
1	Cs	7	ILE	N-CA-C	6.84	118.67	112.17
2	Xr	849	THR	N-CA-C	-6.84	99.01	109.41
1	Cb	38	ARG	N-CA-C	-6.84	97.20	108.76
1	GH	48	VAL	CB-CA-C	6.84	121.03	110.83
1	C4	94	LYS	N-CA-C	6.84	118.82	111.36
1	Cd	94	LYS	N-CA-C	6.84	118.82	111.36
1	Cn	7	ILE	N-CA-C	6.84	118.67	112.17
2	Xt	803	ASN	N-CA-C	6.84	119.02	109.31
1	Cx	7	ILE	N-CA-C	6.84	118.67	112.17
1	CH	94	LYS	N-CA-C	6.84	118.82	111.36
1	CW	94	LYS	N-CA-C	6.84	118.82	111.36
1	G4	48	VAL	CB-CA-C	6.84	121.02	110.83
1	G6	7	ILE	N-CA-C	6.84	117.63	110.72
1	Cv	38	ARG	N-CA-C	-6.84	97.20	108.76
1	Gd	48	VAL	CB-CA-C	6.84	121.02	110.83
1	Gs	48	VAL	CB-CA-C	6.84	121.02	110.83
1	Gx	48	VAL	CB-CA-C	6.84	121.02	110.83
1	Cd	7	ILE	N-CA-C	6.84	118.66	112.17
1	CW	7	ILE	N-CA-C	6.84	118.66	112.17
2	Xm	849	THR	N-CA-C	-6.83	99.02	109.41
1	Gr	37	GLY	N-CA-C	6.83	121.09	110.91
1	CH	82	ALA	N-CA-C	6.83	118.81	111.36
2	XQ	849	THR	N-CA-C	-6.83	99.02	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Gc	37	GLY	N-CA-C	6.83	121.09	110.91
1	GV	37	GLY	N-CA-C	6.83	121.09	110.91
1	Hd	82	ALA	N-CA-C	6.83	118.72	111.28
2	Xo	803	ASN	N-CA-C	6.83	119.01	109.31
1	HW	82	ALA	N-CA-C	6.83	118.72	111.28
1	F6	38	ARG	N-CA-C	-6.83	97.84	109.24
1	Cx	94	LYS	N-CA-C	6.83	118.80	111.36
1	C4	7	ILE	N-CA-C	6.83	118.66	112.17
2	X0	803	ASN	N-CA-C	6.83	119.00	109.31
1	Cg	38	ARG	N-CA-C	-6.83	97.23	108.76
2	Xy	803	ASN	N-CA-C	6.83	119.00	109.31
2	XI	803	ASN	N-CA-C	6.83	119.00	109.31
2	XS	803	ASN	N-CA-C	6.83	119.00	109.31
1	F1	38	ARG	N-CA-C	-6.82	97.84	109.24
1	H0	20	ALA	N-CA-C	6.82	118.72	111.28
1	Ga	7	ILE	N-CA-C	6.82	117.61	110.72
1	FJ	38	ARG	N-CA-C	-6.82	97.84	109.24
1	GJ	7	ILE	N-CA-C	6.82	117.61	110.72
1	C2	38	ARG	N-CA-C	-6.82	97.23	108.76
1	HC	82	ALA	N-CA-C	6.82	118.72	111.28
1	CK	38	ARG	N-CA-C	-6.82	97.23	108.76
1	Ci	94	LYS	N-CA-C	6.82	118.79	111.36
1	Cn	94	LYS	N-CA-C	6.82	118.79	111.36
1	Hn	82	ALA	N-CA-C	6.82	118.71	111.28
1	C7	38	ARG	N-CA-C	-6.82	97.24	108.76
1	H9	82	ALA	N-CA-C	6.82	118.71	111.28
1	C9	94	LYS	N-CA-C	6.82	118.79	111.36
1	Hi	82	ALA	N-CA-C	6.82	118.71	111.28
1	HD	20	ALA	N-CA-C	6.82	118.71	111.28
1	GE	7	ILE	N-CA-C	6.82	117.61	110.72
1	HH	82	ALA	N-CA-C	6.82	118.71	111.28
1	CW	82	ALA	N-CA-C	6.82	118.79	111.36
1	GW	48	VAL	CB-CA-C	6.82	120.98	110.83
2	X5	803	ASN	N-CA-C	6.81	118.98	109.31
1	H4	82	ALA	N-CA-C	6.81	118.71	111.28
2	Xe	803	ASN	N-CA-C	6.81	118.98	109.31
2	Xj	803	ASN	N-CA-C	6.81	118.98	109.31
2	XD	803	ASN	N-CA-C	6.81	118.98	109.31
2	XN	803	ASN	N-CA-C	6.81	118.98	109.31
2	XX	803	ASN	N-CA-C	6.81	118.98	109.31
1	GM	48	VAL	CB-CA-C	6.81	120.98	110.83
1	Cl	38	ARG	N-CA-C	-6.81	97.25	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bm	42	GLY	N-CA-C	-6.81	102.80	111.72
1	Hs	82	ALA	N-CA-C	6.81	118.70	111.28
1	CC	94	LYS	N-CA-C	6.81	118.78	111.36
1	Gm	30	ALA	N-CA-C	6.80	118.70	111.28
1	CA	38	ARG	N-CA-C	-6.80	97.26	108.76
1	CP	38	ARG	N-CA-C	-6.80	97.26	108.76
1	EG	7	ILE	N-CA-C	-6.80	106.37	112.90
1	Hx	82	ALA	N-CA-C	6.80	118.69	111.28
1	EB	7	ILE	N-CA-C	-6.80	106.37	112.90
1	Fp	38	ARG	N-CA-C	-6.80	97.89	109.24
1	Fa	38	ARG	N-CA-C	-6.79	97.89	109.24
1	HR	82	ALA	N-CA-C	6.79	118.69	111.28
1	GB	30	ALA	N-CA-C	6.79	118.68	111.28
1	HM	82	ALA	N-CA-C	6.79	118.68	111.28
1	G8	30	ALA	N-CA-C	6.79	118.68	111.28
1	Er	7	ILE	N-CA-C	-6.79	106.38	112.90
1	BL	42	GLY	N-CA-C	-6.79	102.83	111.72
1	Fi	30	ALA	N-CA-C	6.79	118.68	111.28
1	GL	30	ALA	N-CA-C	6.79	118.68	111.28
1	CR	94	LYS	N-CA-C	6.79	118.76	111.36
1	Bh	42	GLY	N-CA-C	-6.78	102.83	111.72
1	HS	20	ALA	N-CA-C	6.78	118.67	111.28
1	FG	30	ALA	N-CA-C	6.78	118.67	111.28
1	B3	42	GLY	N-CA-C	-6.78	102.84	111.72
1	BB	42	GLY	N-CA-C	-6.78	102.84	111.72
1	EQ	7	ILE	N-CA-C	-6.78	106.39	112.90
1	BM	82	ALA	N-CA-C	6.78	118.75	111.36
1	Gp	7	ILE	N-CA-C	6.78	117.57	110.72
1	Ec	7	ILE	N-CA-C	-6.77	106.40	112.90
1	Bd	82	ALA	N-CA-C	6.77	118.74	111.36
1	Bs	82	ALA	N-CA-C	6.77	118.74	111.36
1	BW	82	ALA	N-CA-C	6.77	118.74	111.36
1	Bw	42	GLY	N-CA-C	-6.77	102.85	111.72
1	E8	7	ILE	N-CA-C	-6.77	106.40	112.90
1	B8	42	GLY	N-CA-C	-6.77	102.86	111.72
1	Em	7	ILE	N-CA-C	-6.76	106.41	112.90
1	Br	42	GLY	N-CA-C	-6.76	102.86	111.72
1	GQ	30	ALA	N-CA-C	6.76	118.65	111.28
1	Fr	30	ALA	N-CA-C	6.76	118.65	111.28
1	Ew	7	ILE	N-CA-C	-6.76	106.41	112.90
1	BG	42	GLY	N-CA-C	-6.76	102.86	111.72
1	B9	82	ALA	N-CA-C	6.76	118.73	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BC	82	ALA	N-CA-C	6.76	118.73	111.36
1	BR	82	ALA	N-CA-C	6.76	118.73	111.36
1	G3	30	ALA	N-CA-C	6.76	118.64	111.28
1	Bc	42	GLY	N-CA-C	-6.76	102.87	111.72
1	Hq	82	ALA	N-CA-C	6.76	118.64	111.28
1	Fc	30	ALA	N-CA-C	6.75	118.64	111.28
1	Bi	82	ALA	N-CA-C	6.75	118.72	111.36
1	Gw	30	ALA	N-CA-C	6.75	118.64	111.28
1	FF	37	GLY	N-CA-C	6.75	120.97	110.91
1	FV	30	ALA	N-CA-C	6.75	118.64	111.28
1	Bn	82	ALA	N-CA-C	6.75	118.72	111.36
1	CV	76	VAL	N-CA-C	-6.75	105.75	111.56
1	Fd	30	ALA	N-CA-C	6.75	118.64	111.28
1	FM	30	ALA	N-CA-C	6.75	118.63	111.28
1	Ek	37	GLY	N-CA-C	6.75	120.70	110.18
1	CF	41	VAL	N-CA-C	6.75	117.53	110.72
1	EV	7	ILE	N-CA-C	-6.75	106.42	112.90
1	F9	30	ALA	N-CA-C	6.74	118.63	111.28
1	Ay	37	GLY	N-CA-C	6.74	120.95	110.91
1	FR	30	ALA	N-CA-C	6.74	118.63	111.28
1	AX	37	GLY	N-CA-C	6.74	120.96	110.91
1	F4	30	ALA	N-CA-C	6.74	118.63	111.28
1	Hb	82	ALA	N-CA-C	6.74	118.63	111.28
1	Gh	30	ALA	N-CA-C	6.74	118.63	111.28
1	AD	37	GLY	N-CA-C	6.74	120.95	110.91
1	HU	82	ALA	N-CA-C	6.74	118.63	111.28
1	Fs	30	ALA	N-CA-C	6.74	118.63	111.28
1	BH	82	ALA	N-CA-C	6.74	118.70	111.36
1	FA	37	GLY	N-CA-C	6.74	120.95	110.91
1	E3	7	ILE	N-CA-C	-6.74	106.43	112.90
1	Ao	37	GLY	N-CA-C	6.74	120.94	110.91
1	EL	7	ILE	N-CA-C	-6.74	106.43	112.90
1	B4	82	ALA	N-CA-C	6.73	118.70	111.36
1	A0	37	GLY	N-CA-C	6.73	120.94	110.91
1	At	37	GLY	N-CA-C	6.73	120.94	110.91
1	BV	42	GLY	N-CA-C	-6.73	102.90	111.72
1	A5	37	GLY	N-CA-C	6.73	120.94	110.91
1	Aj	37	GLY	N-CA-C	6.73	120.94	110.91
1	Eu	37	GLY	N-CA-C	6.73	120.68	110.18
1	FH	30	ALA	N-CA-C	6.73	118.62	111.28
1	AN	37	GLY	N-CA-C	6.73	120.94	110.91
1	Cb	41	VAL	N-CA-C	6.73	117.51	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Eh	7	ILE	N-CA-C	-6.73	106.44	112.90
1	Gr	30	ALA	N-CA-C	6.73	118.61	111.28
1	HF	82	ALA	N-CA-C	6.73	118.61	111.28
1	E6	37	GLY	N-CA-C	6.73	120.67	110.18
1	BQ	42	GLY	N-CA-C	-6.73	102.91	111.72
1	Fb	37	GLY	N-CA-C	6.72	120.93	110.91
1	Fh	30	ALA	N-CA-C	6.72	118.61	111.28
1	Fn	30	ALA	N-CA-C	6.72	118.61	111.28
1	AI	37	GLY	N-CA-C	6.72	120.93	110.91
1	FU	37	GLY	N-CA-C	6.72	120.93	110.91
1	Gc	30	ALA	N-CA-C	6.72	118.61	111.28
1	CK	41	VAL	N-CA-C	6.72	117.51	110.72
1	CU	41	VAL	N-CA-C	6.72	117.51	110.72
1	GV	30	ALA	N-CA-C	6.72	118.61	111.28
1	F3	30	ALA	N-CA-C	6.72	118.61	111.28
1	FC	30	ALA	N-CA-C	6.72	118.61	111.28
1	H7	82	ALA	N-CA-C	6.72	118.61	111.28
1	AS	37	GLY	N-CA-C	6.72	120.92	110.91
1	E1	37	GLY	N-CA-C	6.72	120.66	110.18
1	Fq	37	GLY	N-CA-C	6.72	120.92	110.91
1	Fv	37	GLY	N-CA-C	6.72	120.92	110.91
1	Ez	37	GLY	N-CA-C	6.72	120.66	110.18
1	BE	76	VAL	N-CA-C	-6.72	105.29	111.67
1	EJ	37	GLY	N-CA-C	6.72	120.66	110.18
1	FP	37	GLY	N-CA-C	6.72	120.92	110.91
1	Fw	30	ALA	N-CA-C	6.71	118.60	111.28
1	EE	37	GLY	N-CA-C	6.71	120.66	110.18
1	FK	37	GLY	N-CA-C	6.71	120.91	110.91
1	FL	30	ALA	N-CA-C	6.71	118.60	111.28
1	Ea	37	GLY	N-CA-C	6.71	120.65	110.18
1	Ae	37	GLY	N-CA-C	6.71	120.91	110.91
1	Cl	41	VAL	N-CA-C	6.71	117.50	110.72
1	FW	30	ALA	N-CA-C	6.71	118.60	111.28
1	F2	37	GLY	N-CA-C	6.71	120.91	110.91
1	Fg	37	GLY	N-CA-C	6.71	120.91	110.91
1	CG	76	VAL	N-CA-C	-6.71	105.79	111.56
1	HK	82	ALA	N-CA-C	6.71	118.59	111.28
1	Cc	76	VAL	N-CA-C	-6.71	105.79	111.56
1	Ch	76	VAL	N-CA-C	-6.71	105.79	111.56
1	Bk	76	VAL	N-CA-C	-6.71	105.30	111.67
1	Bx	82	ALA	N-CA-C	6.71	118.67	111.36
1	F7	37	GLY	N-CA-C	6.71	120.90	110.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Hl	82	ALA	N-CA-C	6.71	118.59	111.28
1	Cv	41	VAL	N-CA-C	6.71	117.49	110.72
1	Bu	76	VAL	N-CA-C	-6.71	105.30	111.67
1	Fx	30	ALA	N-CA-C	6.71	118.59	111.28
1	HP	82	ALA	N-CA-C	6.71	118.59	111.28
1	Ba	76	VAL	N-CA-C	-6.70	105.31	111.67
1	Cq	41	VAL	N-CA-C	6.70	117.49	110.72
1	EO	37	GLY	N-CA-C	6.70	120.63	110.18
1	C2	41	VAL	N-CA-C	6.70	117.49	110.72
1	Hg	82	ALA	N-CA-C	6.70	118.58	111.28
1	Ef	37	GLY	N-CA-C	6.70	120.63	110.18
1	Ep	37	GLY	N-CA-C	6.70	120.62	110.18
1	Bz	76	VAL	N-CA-C	-6.70	105.31	111.67
1	F8	30	ALA	N-CA-C	6.69	118.57	111.28
1	Cg	41	VAL	N-CA-C	6.69	117.48	110.72
1	B6	76	VAL	N-CA-C	-6.69	105.31	111.67
1	FB	30	ALA	N-CA-C	6.69	118.57	111.28
1	Fm	30	ALA	N-CA-C	6.69	118.57	111.28
1	Cr	76	VAL	N-CA-C	-6.69	105.81	111.56
2	XS	809	THR	N-CA-C	6.69	118.57	111.28
1	BT	76	VAL	N-CA-C	-6.69	105.32	111.67
1	ET	37	GLY	N-CA-C	6.69	120.61	110.18
1	H2	82	ALA	N-CA-C	6.68	118.57	111.28
1	HA	82	ALA	N-CA-C	6.68	118.56	111.28
1	C7	41	VAL	N-CA-C	6.68	117.47	110.72
1	F1	37	GLY	N-CA-C	6.68	120.86	110.91
1	Bp	76	VAL	N-CA-C	-6.68	105.32	111.67
1	Dg	84	VAL	N-CA-C	-6.68	98.57	108.85
2	XD	809	THR	N-CA-C	6.68	118.56	111.28
1	Cm	76	VAL	N-CA-C	-6.67	105.82	111.56
1	DQ	54	THR	N-CA-C	6.67	118.21	111.07
1	Ew	82	ALA	N-CA-C	6.67	118.55	111.28
1	GG	30	ALA	N-CA-C	6.67	118.55	111.28
1	C3	76	VAL	N-CA-C	-6.67	105.82	111.56
1	Dv	84	VAL	N-CA-C	-6.67	98.58	108.85
1	AT	82	ALA	N-CA-C	6.67	118.55	111.28
1	FQ	30	ALA	N-CA-C	6.66	118.54	111.28
1	CA	41	VAL	N-CA-C	6.66	117.45	110.72
1	B1	76	VAL	N-CA-C	-6.66	105.34	111.67
1	BI	41	VAL	N-CA-C	6.66	117.45	110.72
1	Bf	76	VAL	N-CA-C	-6.66	105.34	111.67
1	Aa	82	ALA	N-CA-C	6.66	118.53	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EG	82	ALA	N-CA-C	6.66	118.53	111.28
1	Dw	54	THR	N-CA-C	6.65	118.19	111.07
2	X0	809	THR	N-CA-C	6.65	118.53	111.28
1	Cm	95	ALA	N-CA-C	-6.65	100.53	108.25
1	DA	84	VAL	N-CA-C	-6.65	98.60	108.85
1	BD	83	ARG	N-CA-C	-6.65	97.52	108.76
1	DB	54	THR	N-CA-C	6.65	118.19	111.07
1	BN	83	ARG	N-CA-C	-6.65	97.52	108.76
1	D2	84	VAL	N-CA-C	-6.65	98.61	108.85
1	Dh	54	THR	N-CA-C	6.65	118.19	111.07
1	DK	84	VAL	N-CA-C	-6.65	98.61	108.85
1	EL	82	ALA	N-CA-C	6.65	118.53	111.28
1	BO	76	VAL	N-CA-C	-6.65	105.35	111.67
1	B0	83	ARG	N-CA-C	-6.65	97.52	108.76
1	Az	82	ALA	N-CA-C	6.65	118.53	111.28
1	CB	76	VAL	N-CA-C	-6.65	105.84	111.56
1	Db	84	VAL	N-CA-C	-6.65	98.61	108.85
1	Dm	54	THR	N-CA-C	6.65	118.18	111.07
1	DU	84	VAL	N-CA-C	-6.65	98.61	108.85
1	Bo	83	ARG	N-CA-C	-6.65	97.53	108.76
1	C8	76	VAL	N-CA-C	-6.64	105.85	111.56
1	Cw	76	VAL	N-CA-C	-6.64	105.85	111.56
1	DP	84	VAL	N-CA-C	-6.64	98.62	108.85
1	A6	82	ALA	N-CA-C	6.64	118.52	111.28
1	D8	54	THR	N-CA-C	6.64	118.18	111.07
1	Hv	82	ALA	N-CA-C	6.64	118.52	111.28
1	BJ	76	VAL	N-CA-C	-6.64	105.36	111.67
1	AO	82	ALA	N-CA-C	6.64	118.52	111.28
1	Dq	84	VAL	N-CA-C	-6.64	98.62	108.85
1	AJ	82	ALA	N-CA-C	6.64	118.52	111.28
1	B5	83	ARG	N-CA-C	-6.64	97.54	108.76
1	D7	84	VAL	N-CA-C	-6.64	98.62	108.85
2	Xj	809	THR	N-CA-C	6.64	118.52	111.28
1	Bt	83	ARG	N-CA-C	-6.64	97.54	108.76
1	Dl	84	VAL	N-CA-C	-6.64	98.63	108.85
1	Bo	41	VAL	N-CA-C	6.64	117.42	110.72
1	DF	84	VAL	N-CA-C	-6.64	98.63	108.85
2	Xo	809	THR	N-CA-C	6.64	118.51	111.28
2	XN	809	THR	N-CA-C	6.64	118.51	111.28
1	Be	83	ARG	N-CA-C	-6.63	97.55	108.76
1	By	41	VAL	N-CA-C	6.63	117.42	110.72
2	X5	809	THR	N-CA-C	6.63	118.51	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D3	54	THR	N-CA-C	6.63	118.17	111.07
1	DL	54	THR	N-CA-C	6.63	118.17	111.07
1	B5	41	VAL	N-CA-C	6.63	117.42	110.72
1	E8	82	ALA	N-CA-C	6.63	118.51	111.28
1	Ak	82	ALA	N-CA-C	6.63	118.51	111.28
1	BI	83	ARG	N-CA-C	-6.63	97.55	108.76
1	CP	41	VAL	N-CA-C	6.63	117.42	110.72
1	EQ	82	ALA	N-CA-C	6.63	118.51	111.28
1	BX	83	ARG	N-CA-C	-6.63	97.56	108.76
1	E3	82	ALA	N-CA-C	6.63	118.50	111.28
1	AE	82	ALA	N-CA-C	6.63	118.50	111.28
1	B0	41	VAL	N-CA-C	6.63	117.41	110.72
1	Ap	82	ALA	N-CA-C	6.63	118.50	111.28
1	BS	83	ARG	N-CA-C	-6.63	97.56	108.76
1	Dc	54	THR	N-CA-C	6.62	118.16	111.07
1	DV	54	THR	N-CA-C	6.62	118.16	111.07
1	Be	41	VAL	N-CA-C	6.62	117.41	110.72
1	Ec	82	ALA	N-CA-C	6.62	118.50	111.28
1	Er	82	ALA	N-CA-C	6.62	118.50	111.28
2	Xy	809	THR	N-CA-C	6.62	118.50	111.28
1	CL	95	ALA	N-CA-C	-6.62	100.57	108.25
1	BX	41	VAL	N-CA-C	6.62	117.41	110.72
1	EV	82	ALA	N-CA-C	6.62	118.50	111.28
1	Eh	82	ALA	N-CA-C	6.62	118.50	111.28
1	Em	82	ALA	N-CA-C	6.62	118.49	111.28
1	FH	38	ARG	N-CA-C	-6.62	98.19	109.24
1	Fs	38	ARG	N-CA-C	-6.62	98.19	109.24
1	Fj	30	ALA	N-CA-C	6.61	118.49	111.28
1	Dr	54	THR	N-CA-C	6.61	118.15	111.07
1	CL	76	VAL	N-CA-C	-6.61	105.87	111.56
1	GX	48	VAL	CB-CA-C	6.61	120.68	110.83
1	Af	82	ALA	N-CA-C	6.61	118.49	111.28
2	Xl	850	GLY	N-CA-C	-6.61	104.33	112.33
1	Go	48	VAL	CB-CA-C	6.61	120.68	110.83
1	Bj	41	VAL	N-CA-C	6.61	117.39	110.72
1	EB	82	ALA	N-CA-C	6.61	118.48	111.28
1	AS	38	ARG	N-CA-C	-6.61	97.59	108.76
1	CQ	95	ALA	N-CA-C	-6.61	100.58	108.25
1	A1	82	ALA	N-CA-C	6.61	118.48	111.28
2	Xv	850	GLY	N-CA-C	-6.61	104.34	112.33
1	C8	95	ALA	N-CA-C	-6.60	100.59	108.25
2	Xg	850	GLY	N-CA-C	-6.60	104.34	112.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BD	41	VAL	N-CA-C	6.60	117.39	110.72
1	CQ	76	VAL	N-CA-C	-6.60	105.88	111.56
1	Fn	38	ARG	N-CA-C	-6.60	98.21	109.24
1	BN	41	VAL	N-CA-C	6.60	117.39	110.72
1	FW	38	ARG	N-CA-C	-6.60	98.21	109.24
1	G0	48	VAL	CB-CA-C	6.60	120.66	110.83
1	Fd	38	ARG	N-CA-C	-6.60	98.22	109.24
2	Xf	817	ARG	N-CA-C	6.60	119.03	111.11
1	Gt	48	VAL	CB-CA-C	6.60	120.66	110.83
2	XK	850	GLY	N-CA-C	-6.60	104.34	112.33
1	AX	38	ARG	N-CA-C	-6.60	97.61	108.76
1	Gy	48	VAL	CB-CA-C	6.59	120.66	110.83
1	GD	48	VAL	CB-CA-C	6.59	120.66	110.83
1	Cc	95	ALA	N-CA-C	-6.59	100.60	108.25
1	Ch	95	ALA	N-CA-C	-6.59	100.60	108.25
1	DG	54	THR	N-CA-C	6.59	118.12	111.07
1	CV	95	ALA	N-CA-C	-6.59	100.60	108.25
1	C3	95	ALA	N-CA-C	-6.59	100.60	108.25
1	F9	38	ARG	N-CA-C	-6.59	98.23	109.24
2	Xe	809	THR	N-CA-C	6.59	118.47	111.28
1	Ao	38	ARG	N-CA-C	-6.59	97.62	108.76
1	Cq	94	LYS	N-CA-C	6.59	118.55	111.36
2	XX	809	THR	N-CA-C	6.59	118.47	111.28
2	X2	850	GLY	N-CA-C	-6.59	104.36	112.33
1	Ct	94	LYS	N-CA-C	6.59	118.54	111.36
1	AN	38	ARG	N-CA-C	-6.59	97.62	108.76
1	CP	94	LYS	N-CA-C	6.59	118.54	111.36
1	FR	38	ARG	N-CA-C	-6.59	98.24	109.24
1	Ge	48	VAL	CB-CA-C	6.59	120.65	110.83
1	Cy	94	LYS	N-CA-C	6.59	118.54	111.36
1	FN	30	ALA	N-CA-C	6.59	118.46	111.28
1	Cb	94	LYS	N-CA-C	6.58	118.54	111.36
1	F4	38	ARG	N-CA-C	-6.58	98.25	109.24
1	Cr	95	ALA	N-CA-C	-6.58	100.61	108.25
2	Xu	817	ARG	N-CA-C	6.58	119.01	111.11
1	FC	38	ARG	N-CA-C	-6.58	98.25	109.24
1	FM	38	ARG	N-CA-C	-6.58	98.25	109.24
1	Ay	38	ARG	N-CA-C	-6.58	97.64	108.76
2	XE	817	ARG	N-CA-C	6.58	119.01	111.11
1	A0	38	ARG	N-CA-C	-6.58	97.64	108.76
1	Ae	38	ARG	N-CA-C	-6.58	97.64	108.76
1	Cl	94	LYS	N-CA-C	6.58	118.53	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BS	41	VAL	N-CA-C	6.58	117.36	110.72
1	Cg	94	LYS	N-CA-C	6.58	118.53	111.36
2	Xq	850	GLY	N-CA-C	-6.58	104.37	112.33
1	CD	94	LYS	N-CA-C	6.58	118.53	111.36
1	G5	48	VAL	CB-CA-C	6.58	120.63	110.83
1	Fi	38	ARG	N-CA-C	-6.58	98.26	109.24
1	GI	48	VAL	CB-CA-C	6.58	120.63	110.83
1	GN	48	VAL	CB-CA-C	6.58	120.63	110.83
2	XO	817	ARG	N-CA-C	6.58	119.00	111.11
1	A5	38	ARG	N-CA-C	-6.57	97.65	108.76
1	CI	94	LYS	N-CA-C	6.57	118.53	111.36
3	PV	30	LYS	N-CA-C	-6.57	100.62	108.25
1	Bt	41	VAL	N-CA-C	6.57	117.36	110.72
1	Fy	30	ALA	N-CA-C	6.57	118.44	111.28
1	AI	38	ARG	N-CA-C	-6.57	97.65	108.76
1	GS	48	VAL	CB-CA-C	6.57	120.62	110.83
3	Ph	30	LYS	N-CA-C	-6.57	100.63	108.25
1	Au	82	ALA	N-CA-C	6.57	118.44	111.28
1	Fx	38	ARG	N-CA-C	-6.57	98.27	109.24
1	AD	38	ARG	N-CA-C	-6.57	97.66	108.76
1	CF	94	LYS	N-CA-C	6.57	118.52	111.36
1	F5	30	ALA	N-CA-C	6.57	118.44	111.28
2	Xa	817	ARG	N-CA-C	6.57	118.99	111.11
1	Aj	38	ARG	N-CA-C	-6.57	97.66	108.76
2	Xk	817	ARG	N-CA-C	6.57	118.99	111.11
1	At	38	ARG	N-CA-C	-6.57	97.66	108.76
2	Xt	809	THR	N-CA-C	6.57	118.44	111.28
2	XI	809	THR	N-CA-C	6.57	118.44	111.28
1	CU	94	LYS	N-CA-C	6.57	118.52	111.36
1	C5	94	LYS	N-CA-C	6.56	118.51	111.36
1	C0	94	LYS	N-CA-C	6.56	118.51	111.36
1	Fo	30	ALA	N-CA-C	6.56	118.43	111.28
1	Gq	76	VAL	N-CA-C	-6.56	105.35	111.45
1	Du	69	GLU	N-CA-C	6.56	118.43	111.28
1	Cw	95	ALA	N-CA-C	-6.56	100.64	108.25
1	CS	94	LYS	N-CA-C	6.56	118.51	111.36
1	FR	94	LYS	N-CA-C	6.56	118.23	111.14
1	C2	94	LYS	N-CA-C	6.56	118.51	111.36
2	X7	850	GLY	N-CA-C	-6.56	104.39	112.33
2	Xp	817	ARG	N-CA-C	6.56	118.98	111.11
1	CB	95	ALA	N-CA-C	-6.56	100.64	108.25
2	XP	850	GLY	N-CA-C	-6.56	104.39	112.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G2	54	THR	N-CA-C	6.56	118.98	111.11
1	Gj	48	VAL	CB-CA-C	6.56	120.60	110.83
1	Cv	94	LYS	N-CA-C	6.56	118.51	111.36
1	GA	76	VAL	N-CA-C	-6.56	105.35	111.45
2	XA	850	GLY	N-CA-C	-6.56	104.39	112.33
1	FC	94	LYS	N-CA-C	6.56	118.22	111.14
1	CG	95	ALA	N-CA-C	-6.56	100.64	108.25
1	Co	94	LYS	N-CA-C	6.56	118.51	111.36
1	CK	94	LYS	N-CA-C	6.56	118.51	111.36
1	FU	77	ALA	N-CA-C	6.56	119.29	108.99
1	Ce	94	LYS	N-CA-C	6.56	118.51	111.36
1	FX	30	ALA	N-CA-C	6.56	118.43	111.28
2	X1	817	ARG	N-CA-C	6.55	118.97	111.11
1	C7	94	LYS	N-CA-C	6.55	118.50	111.36
1	Gv	54	THR	N-CA-C	6.55	118.97	111.11
2	XF	850	GLY	N-CA-C	-6.55	104.40	112.33
1	CN	94	LYS	N-CA-C	6.55	118.50	111.36
2	X6	817	ARG	N-CA-C	6.55	118.97	111.11
1	Gl	76	VAL	N-CA-C	-6.55	105.36	111.45
1	Dz	69	GLU	N-CA-C	6.55	118.42	111.28
3	PL	30	LYS	N-CA-C	-6.55	100.65	108.25
3	Pc	30	LYS	N-CA-C	-6.55	100.65	108.25
1	Df	69	GLU	N-CA-C	6.55	118.42	111.28
1	Fn	94	LYS	N-CA-C	6.55	118.21	111.14
1	CA	94	LYS	N-CA-C	6.55	118.50	111.36
2	Xb	850	GLY	N-CA-C	-6.55	104.41	112.33
1	Gg	54	THR	N-CA-C	6.55	118.97	111.11
2	Xz	817	ARG	N-CA-C	6.55	118.97	111.11
2	XU	850	GLY	N-CA-C	-6.55	104.41	112.33
3	P3	30	LYS	N-CA-C	-6.55	100.66	108.25
1	F0	30	ALA	N-CA-C	6.55	118.42	111.28
1	Da	69	GLU	N-CA-C	6.55	118.42	111.28
3	Pn	30	LYS	CA-C-N	-6.55	113.24	119.85
3	Pn	30	LYS	C-N-CA	-6.55	113.24	119.85
1	DE	69	GLU	N-CA-C	6.55	118.42	111.28
1	AC	38	ARG	N-CA-C	-6.54	97.74	108.41
1	Fg	83	ARG	N-CA-C	-6.54	98.23	108.90
1	Fx	94	LYS	N-CA-C	6.54	118.21	111.14
1	FK	83	ARG	N-CA-C	-6.54	98.23	108.90
2	XJ	817	ARG	N-CA-C	6.54	118.96	111.11
1	Cj	94	LYS	N-CA-C	6.54	118.49	111.36
1	Fv	77	ALA	N-CA-C	6.54	119.26	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	PB	30	LYS	N-CA-C	-6.54	100.66	108.25
2	XT	817	ARG	N-CA-C	6.54	118.96	111.11
1	F2	77	ALA	N-CA-C	6.54	119.25	108.99
1	B0	38	ARG	N-CA-C	-6.54	97.12	108.69
1	Gb	54	THR	N-CA-C	6.54	118.96	111.11
3	Pw	30	LYS	N-CA-C	-6.54	100.67	108.25
1	CX	94	LYS	N-CA-C	6.54	118.49	111.36
1	Fi	94	LYS	N-CA-C	6.54	118.20	111.14
1	Bo	38	ARG	N-CA-C	-6.54	97.12	108.69
1	Fq	77	ALA	N-CA-C	6.54	119.25	108.99
1	DT	69	GLU	N-CA-C	6.54	118.41	111.28
1	F9	94	LYS	N-CA-C	6.54	118.20	111.14
3	PQ	30	LYS	N-CA-C	-6.54	100.67	108.25
1	D1	69	GLU	N-CA-C	6.53	118.40	111.28
3	P8	30	LYS	N-CA-C	-6.53	100.67	108.25
1	Fg	77	ALA	N-CA-C	6.53	119.25	108.99
1	Fv	83	ARG	N-CA-C	-6.53	98.25	108.90
1	FK	77	ALA	N-CA-C	6.53	119.25	108.99
1	G7	54	THR	N-CA-C	6.53	118.95	111.11
1	Hg	37	GLY	N-CA-C	6.53	120.10	110.63
1	Dp	69	GLU	N-CA-C	6.53	118.40	111.28
1	GK	54	THR	N-CA-C	6.53	118.95	111.11
1	Fb	83	ARG	N-CA-C	-6.53	98.26	108.90
1	BD	38	ARG	N-CA-C	-6.53	97.13	108.69
1	FH	94	LYS	N-CA-C	6.53	118.19	111.14
1	GK	76	VAL	N-CA-C	-6.53	105.38	111.45
1	FS	30	ALA	N-CA-C	6.53	118.40	111.28
1	FU	83	ARG	N-CA-C	-6.53	98.26	108.90
1	Fq	83	ARG	N-CA-C	-6.53	98.26	108.90
1	GA	54	THR	N-CA-C	6.53	118.94	111.11
1	F4	94	LYS	N-CA-C	6.53	118.19	111.14
1	Gl	54	THR	N-CA-C	6.53	118.94	111.11
3	Pr	30	LYS	N-CA-C	-6.53	100.68	108.25
1	GU	54	THR	N-CA-C	6.53	118.94	111.11
1	G7	76	VAL	N-CA-C	-6.53	105.38	111.45
1	Gb	76	VAL	N-CA-C	-6.53	105.38	111.45
1	HK	37	GLY	N-CA-C	6.53	120.09	110.63
1	GU	76	VAL	N-CA-C	-6.53	105.38	111.45
1	DX	67	ALA	N-CA-C	6.53	118.98	111.02
1	F2	83	ARG	N-CA-C	-6.52	98.27	108.90
1	Fb	77	ALA	N-CA-C	6.52	119.23	108.99
1	FA	83	ARG	N-CA-C	-6.52	98.27	108.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	PG	30	LYS	N-CA-C	-6.52	100.68	108.25
1	Fl	83	ARG	N-CA-C	-6.52	98.27	108.90
3	Pm	30	LYS	N-CA-C	-6.52	100.69	108.25
1	GF	54	THR	N-CA-C	6.52	118.94	111.11
1	H2	37	GLY	N-CA-C	6.52	120.08	110.63
1	Gj	74	GLY	N-CA-C	6.52	120.23	110.97
1	Ax	38	ARG	N-CA-C	-6.52	97.74	108.76
1	FD	30	ALA	N-CA-C	6.52	118.39	111.28
1	DI	67	ALA	N-CA-C	6.52	118.97	111.02
1	D6	69	GLU	N-CA-C	6.52	118.38	111.28
1	Fd	94	LYS	N-CA-C	6.52	118.18	111.14
1	Bj	38	ARG	N-CA-C	-6.52	97.16	108.69
1	Hl	37	GLY	N-CA-C	6.52	120.08	110.63
1	DO	69	GLU	N-CA-C	6.52	118.38	111.28
1	B5	38	ARG	N-CA-C	-6.51	97.16	108.69
1	F7	77	ALA	N-CA-C	6.51	119.22	108.99
1	F7	83	ARG	N-CA-C	-6.51	98.28	108.90
1	Fe	30	ALA	N-CA-C	6.51	118.38	111.28
1	Dk	69	GLU	N-CA-C	6.51	118.38	111.28
1	DC	30	ALA	N-CA-C	6.51	118.38	111.28
1	FF	77	ALA	N-CA-C	6.51	119.22	108.99
1	HH	94	LYS	N-CA-C	6.51	118.46	111.36
1	BN	38	ARG	N-CA-C	-6.51	97.16	108.69
1	HW	94	LYS	N-CA-C	6.51	118.46	111.36
1	G2	76	VAL	N-CA-C	-6.51	105.39	111.45
1	Be	38	ARG	N-CA-C	-6.51	97.17	108.69
1	By	38	ARG	N-CA-C	-6.51	97.17	108.69
1	BX	38	ARG	N-CA-C	-6.51	97.17	108.69
1	G5	74	GLY	N-CA-C	6.51	120.21	110.97
2	Xz	849	THR	N-CA-C	-6.51	99.43	109.52
1	GD	74	GLY	N-CA-C	6.51	120.21	110.97
1	GN	74	GLY	N-CA-C	6.51	120.21	110.97
1	G0	74	GLY	N-CA-C	6.51	120.21	110.97
2	Xa	849	THR	N-CA-C	-6.51	99.43	109.52
1	Fl	77	ALA	N-CA-C	6.51	119.21	108.99
2	XT	849	THR	N-CA-C	-6.51	99.43	109.52
1	Di	82	ALA	N-CA-C	6.50	118.37	111.28
1	FP	83	ARG	N-CA-C	-6.50	98.30	108.90
2	X1	849	THR	N-CA-C	-6.50	99.44	109.52
1	Dx	82	ALA	N-CA-C	6.50	118.37	111.28
1	Ez	30	ALA	N-CA-C	6.50	118.37	111.28
2	XE	849	THR	N-CA-C	-6.50	99.44	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DM	30	ALA	N-CA-C	6.50	118.37	111.28
1	FM	94	LYS	N-CA-C	6.50	118.16	111.14
1	GX	74	GLY	N-CA-C	6.50	120.20	110.97
1	GS	74	GLY	N-CA-C	6.50	120.20	110.97
1	Gy	74	GLY	N-CA-C	6.50	120.20	110.97
1	DJ	69	GLU	N-CA-C	6.50	118.36	111.28
1	BS	38	ARG	N-CA-C	-6.50	97.19	108.69
1	D4	82	ALA	N-CA-C	6.50	118.36	111.28
1	Gg	76	VAL	N-CA-C	-6.50	105.41	111.45
2	Xf	849	THR	N-CA-C	-6.50	99.45	109.52
1	GF	76	VAL	N-CA-C	-6.50	105.41	111.45
1	HF	37	GLY	N-CA-C	6.50	120.05	110.63
1	GI	74	GLY	N-CA-C	6.50	120.20	110.97
1	DW	82	ALA	N-CA-C	6.50	118.36	111.28
1	Hb	37	GLY	N-CA-C	6.50	120.05	110.63
1	Ek	30	ALA	N-CA-C	6.50	118.36	111.28
1	Bt	38	ARG	N-CA-C	-6.50	97.19	108.69
1	Hv	37	GLY	N-CA-C	6.50	120.05	110.63
1	BI	38	ARG	N-CA-C	-6.50	97.19	108.69
1	GP	54	THR	N-CA-C	6.50	118.91	111.11
1	GP	76	VAL	N-CA-C	-6.50	105.41	111.45
2	XO	849	THR	N-CA-C	-6.50	99.45	109.52
1	De	67	ALA	N-CA-C	6.49	118.94	111.02
1	Dt	67	ALA	N-CA-C	6.49	118.94	111.02
2	Xu	849	THR	N-CA-C	-6.49	99.45	109.52
1	FA	77	ALA	N-CA-C	6.49	119.19	108.99
1	FP	77	ALA	N-CA-C	6.49	119.19	108.99
1	Go	74	GLY	N-CA-C	6.49	120.19	110.97
1	Hq	37	GLY	N-CA-C	6.49	120.04	110.63
1	DH	82	ALA	N-CA-C	6.49	118.36	111.28
1	Ge	74	GLY	N-CA-C	6.49	120.19	110.97
2	XJ	849	THR	N-CA-C	-6.49	99.46	109.52
2	X6	849	THR	N-CA-C	-6.49	99.46	109.52
1	Gq	54	THR	N-CA-C	6.49	118.90	111.11
1	H7	37	GLY	N-CA-C	6.49	120.04	110.63
1	D9	82	ALA	N-CA-C	6.49	118.35	111.28
1	FF	83	ARG	N-CA-C	-6.49	98.33	108.90
1	HP	37	GLY	N-CA-C	6.49	120.04	110.63
2	Xp	849	THR	N-CA-C	-6.49	99.47	109.52
1	Gv	76	VAL	N-CA-C	-6.49	105.42	111.45
1	DH	30	ALA	N-CA-C	6.49	118.35	111.28
1	DS	67	ALA	N-CA-C	6.49	118.93	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ft	30	ALA	N-CA-C	6.48	118.35	111.28
1	FW	94	LYS	N-CA-C	6.48	118.14	111.14
1	HA	37	GLY	N-CA-C	6.48	120.03	110.63
1	HC	94	LYS	N-CA-C	6.48	118.43	111.36
1	D0	67	ALA	N-CA-C	6.48	118.92	111.02
2	Xk	849	THR	N-CA-C	-6.48	99.48	109.52
1	E6	30	ALA	N-CA-C	6.48	118.34	111.28
1	Ds	30	ALA	N-CA-C	6.48	118.34	111.28
1	Dx	30	ALA	N-CA-C	6.48	118.34	111.28
3	P9	30	LYS	CA-C-N	-6.48	113.31	119.85
3	P9	30	LYS	C-N-CA	-6.48	113.31	119.85
1	Gt	74	GLY	N-CA-C	6.48	120.17	110.97
3	PR	30	LYS	CA-C-N	-6.48	113.31	119.85
3	PR	30	LYS	C-N-CA	-6.48	113.31	119.85
1	D4	30	ALA	N-CA-C	6.48	118.34	111.28
1	Ai	38	ARG	N-CA-C	-6.48	97.72	108.34
1	FI	30	ALA	N-CA-C	6.48	118.34	111.28
1	HU	37	GLY	N-CA-C	6.48	120.02	110.63
1	Dd	82	ALA	N-CA-C	6.47	118.34	111.28
1	Do	67	ALA	N-CA-C	6.47	118.92	111.02
3	PH	30	LYS	CA-C-N	-6.47	113.31	119.85
3	PH	30	LYS	C-N-CA	-6.47	113.31	119.85
1	Dd	30	ALA	N-CA-C	6.47	118.34	111.28
1	Di	30	ALA	N-CA-C	6.47	118.34	111.28
1	Ds	82	ALA	N-CA-C	6.47	118.33	111.28
1	DW	30	ALA	N-CA-C	6.47	118.34	111.28
1	D5	67	ALA	N-CA-C	6.47	118.91	111.02
1	A4	38	ARG	N-CA-C	-6.47	97.73	108.34
1	D9	30	ALA	N-CA-C	6.47	118.33	111.28
1	Hd	94	LYS	N-CA-C	6.47	118.41	111.36
3	Pd	30	LYS	CA-C-N	-6.47	113.31	119.85
3	Pd	30	LYS	C-N-CA	-6.47	113.31	119.85
3	Pi	30	LYS	CA-C-N	-6.47	113.31	119.85
3	Pi	30	LYS	C-N-CA	-6.47	113.31	119.85
1	Hn	94	LYS	N-CA-C	6.47	118.41	111.36
1	Fs	94	LYS	N-CA-C	6.47	118.13	111.14
3	PC	30	LYS	CA-C-N	-6.47	113.32	119.85
3	PC	30	LYS	C-N-CA	-6.47	113.32	119.85
1	EJ	30	ALA	N-CA-C	6.47	118.33	111.28
1	AM	38	ARG	N-CA-C	-6.47	97.73	108.34
1	DM	82	ALA	N-CA-C	6.47	118.33	111.28
1	DR	30	ALA	N-CA-C	6.47	118.33	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	PW	30	LYS	CA-C-N	-6.47	113.32	119.85
3	PW	30	LYS	C-N-CA	-6.47	113.32	119.85
1	Ad	38	ARG	N-CA-C	-6.47	97.73	108.34
1	Hs	94	LYS	N-CA-C	6.47	118.41	111.36
1	DC	82	ALA	N-CA-C	6.47	118.33	111.28
1	Ef	30	ALA	N-CA-C	6.46	118.33	111.28
1	An	38	ARG	N-CA-C	-6.46	97.74	108.34
1	A9	38	ARG	N-CA-C	-6.46	97.74	108.34
3	Ps	30	LYS	CA-C-N	-6.46	113.32	119.85
3	Ps	30	LYS	C-N-CA	-6.46	113.32	119.85
1	DD	67	ALA	N-CA-C	6.46	118.91	111.02
1	E1	30	ALA	N-CA-C	6.46	118.32	111.28
1	EO	30	ALA	N-CA-C	6.46	118.32	111.28
1	AR	38	ARG	N-CA-C	-6.46	97.75	108.34
1	DR	82	ALA	N-CA-C	6.46	118.32	111.28
1	H9	94	LYS	N-CA-C	6.46	118.40	111.36
1	Fu	38	ARG	N-CA-C	-6.46	97.85	108.76
1	HR	94	LYS	N-CA-C	6.46	118.40	111.36
3	Px	30	LYS	CA-C-N	-6.46	113.33	119.85
3	Px	30	LYS	C-N-CA	-6.46	113.33	119.85
3	Pf	30	LYS	CA-C-N	-6.45	113.33	119.85
3	Pf	30	LYS	C-N-CA	-6.45	113.33	119.85
1	Dy	67	ALA	N-CA-C	6.45	118.89	111.02
3	P4	30	LYS	CA-C-N	-6.45	113.33	119.85
3	P4	30	LYS	C-N-CA	-6.45	113.33	119.85
1	Hi	94	LYS	N-CA-C	6.45	118.39	111.36
3	PM	30	LYS	CA-C-N	-6.45	113.33	119.85
3	PM	30	LYS	C-N-CA	-6.45	113.33	119.85
1	HD	30	ALA	N-CA-C	6.45	118.31	111.28
1	DN	67	ALA	N-CA-C	6.45	118.89	111.02
1	H4	94	LYS	N-CA-C	6.45	118.39	111.36
1	Dj	67	ALA	N-CA-C	6.45	118.89	111.02
1	Dn	82	ALA	N-CA-C	6.45	118.31	111.28
1	As	38	ARG	N-CA-C	-6.45	97.77	108.34
1	Hj	30	ALA	N-CA-C	6.45	118.31	111.28
1	Ep	30	ALA	N-CA-C	6.45	118.31	111.28
1	Ea	30	ALA	N-CA-C	6.45	118.31	111.28
1	FO	38	ARG	N-CA-C	-6.45	97.87	108.76
1	ET	30	ALA	N-CA-C	6.45	118.31	111.28
1	CV	54	THR	N-CA-C	6.45	118.31	111.28
1	H0	30	ALA	N-CA-C	6.44	118.30	111.28
1	HS	30	ALA	N-CA-C	6.44	118.30	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EE	30	ALA	N-CA-C	6.44	118.30	111.28
1	AH	38	ARG	N-CA-C	-6.44	97.78	108.34
1	AW	38	ARG	N-CA-C	-6.44	97.78	108.34
1	Eu	30	ALA	N-CA-C	6.44	118.30	111.28
1	HI	30	ALA	N-CA-C	6.44	118.30	111.28
1	Hx	94	LYS	N-CA-C	6.43	118.37	111.36
3	Pp	30	LYS	CA-C-N	-6.43	113.36	119.85
3	Pp	30	LYS	C-N-CA	-6.43	113.36	119.85
1	Hy	30	ALA	N-CA-C	6.43	118.29	111.28
1	CG	54	THR	N-CA-C	6.43	118.29	111.28
1	He	30	ALA	N-CA-C	6.42	118.28	111.28
3	PE	30	LYS	CA-C-N	-6.42	113.36	119.85
3	PE	30	LYS	C-N-CA	-6.42	113.36	119.85
1	FT	38	ARG	N-CA-C	-6.42	97.91	108.76
1	Gp	38	ARG	N-CA-C	-6.42	97.91	108.76
3	Pu	30	LYS	CA-C-N	-6.42	113.36	119.85
3	Pu	30	LYS	C-N-CA	-6.42	113.36	119.85
3	Pk	30	LYS	CA-C-N	-6.42	113.37	119.85
3	Pk	30	LYS	C-N-CA	-6.42	113.37	119.85
1	Cr	54	THR	N-CA-C	6.42	118.28	111.28
1	BJ	37	GLY	N-CA-C	6.42	120.47	110.91
1	HM	94	LYS	N-CA-C	6.42	118.36	111.36
3	P1	30	LYS	CA-C-N	-6.42	113.37	119.85
3	P1	30	LYS	C-N-CA	-6.42	113.37	119.85
1	Di	83	ARG	N-CA-C	-6.42	98.15	109.06
1	GE	38	ARG	N-CA-C	-6.42	97.92	108.76
3	PJ	30	LYS	CA-C-N	-6.42	113.37	119.85
3	PJ	30	LYS	C-N-CA	-6.42	113.37	119.85
1	Cc	54	THR	N-CA-C	6.42	118.27	111.28
1	Ho	30	ALA	N-CA-C	6.42	118.27	111.28
3	Pa	30	LYS	CA-C-N	-6.41	113.37	119.85
3	Pa	30	LYS	C-N-CA	-6.41	113.37	119.85
1	H5	30	ALA	N-CA-C	6.41	118.27	111.28
1	D9	83	ARG	N-CA-C	-6.41	98.16	109.06
1	DR	83	ARG	N-CA-C	-6.41	98.16	109.06
1	Dn	83	ARG	N-CA-C	-6.41	98.16	109.06
1	Ds	83	ARG	N-CA-C	-6.41	98.16	109.06
1	FE	38	ARG	N-CA-C	-6.41	97.93	108.76
1	HN	30	ALA	N-CA-C	6.41	118.27	111.28
1	Hh	74	GLY	N-CA-C	6.41	124.37	112.77
1	Dn	30	ALA	N-CA-C	6.41	118.26	111.28
3	P6	30	LYS	CA-C-N	-6.41	113.38	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P6	30	LYS	C-N-CA	-6.41	113.38	119.85
1	Ht	30	ALA	N-CA-C	6.41	118.26	111.28
1	Gk	38	ARG	N-CA-C	-6.40	97.94	108.76
1	Bu	37	GLY	N-CA-C	6.40	120.45	110.91
1	AB	82	ALA	N-CA-C	6.40	118.26	111.28
3	PT	30	LYS	CA-C-N	-6.40	113.38	119.85
3	PT	30	LYS	C-N-CA	-6.40	113.38	119.85
1	HX	30	ALA	N-CA-C	6.40	118.26	111.28
1	Dd	83	ARG	N-CA-C	-6.40	98.17	109.06
1	Aj	7	ILE	N-CA-C	6.40	118.25	112.17
1	Bq	37	GLY	N-CA-C	6.40	120.45	110.91
1	Ao	45	TYR	N-CA-C	-6.40	98.77	109.07
1	DC	83	ARG	N-CA-C	-6.40	98.18	109.06
1	D4	83	ARG	N-CA-C	-6.40	98.18	109.06
1	Gz	38	ARG	N-CA-C	-6.40	97.94	108.76
1	Am	82	ALA	N-CA-C	6.40	118.25	111.28
3	Pz	30	LYS	CA-C-N	-6.40	113.39	119.85
3	Pz	30	LYS	C-N-CA	-6.40	113.39	119.85
1	C3	54	THR	N-CA-C	6.40	118.25	111.28
1	BP	37	GLY	N-CA-C	6.40	120.44	110.91
1	Hm	74	GLY	N-CA-C	6.39	124.34	112.77
1	AX	45	TYR	N-CA-C	-6.39	98.78	109.07
1	AN	7	ILE	N-CA-C	6.39	118.24	112.17
1	DM	83	ARG	N-CA-C	-6.39	98.19	109.06
1	DW	83	ARG	N-CA-C	-6.39	98.19	109.06
1	G6	38	ARG	N-CA-C	-6.39	97.96	108.76
1	Bb	37	GLY	N-CA-C	6.39	120.43	110.91
1	GO	38	ARG	N-CA-C	-6.39	97.96	108.76
1	AS	7	ILE	N-CA-C	6.39	118.24	112.17
1	Ga	38	ARG	N-CA-C	-6.39	97.96	108.76
1	Gf	38	ARG	N-CA-C	-6.39	97.96	108.76
1	HG	74	GLY	N-CA-C	6.39	124.34	112.77
1	GT	38	ARG	N-CA-C	-6.39	97.96	108.76
1	B1	37	GLY	N-CA-C	6.39	120.43	110.91
1	Bf	37	GLY	N-CA-C	6.39	120.43	110.91
1	Hw	74	GLY	N-CA-C	6.39	124.33	112.77
1	Bp	37	GLY	N-CA-C	6.39	120.42	110.91
1	Cw	54	THR	N-CA-C	6.39	118.24	111.28
1	BF	37	GLY	N-CA-C	6.39	120.43	110.91
1	H3	74	GLY	N-CA-C	6.38	124.33	112.77
1	Ao	7	ILE	N-CA-C	6.38	118.24	112.17
1	DH	83	ARG	N-CA-C	-6.38	98.21	109.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HL	74	GLY	N-CA-C	6.38	124.33	112.77
1	BO	37	GLY	N-CA-C	6.38	120.42	110.91
1	Aj	45	TYR	N-CA-C	-6.38	98.79	109.07
1	BE	37	GLY	N-CA-C	6.38	120.42	110.91
1	At	45	TYR	N-CA-C	-6.38	98.80	109.07
1	EG	74	GLY	N-CA-C	6.38	124.32	112.77
1	H8	74	GLY	N-CA-C	6.38	124.32	112.77
1	Ch	54	THR	N-CA-C	6.38	118.23	111.28
1	A5	45	TYR	N-CA-C	-6.38	98.80	109.07
1	Ae	45	TYR	N-CA-C	-6.38	98.80	109.07
1	AD	45	TYR	N-CA-C	-6.38	98.80	109.07
1	AN	45	TYR	N-CA-C	-6.38	98.80	109.07
1	G1	38	ARG	N-CA-C	-6.38	97.98	108.76
1	A0	45	TYR	N-CA-C	-6.38	98.81	109.07
1	Cm	54	THR	N-CA-C	6.38	118.23	111.28
1	CL	54	THR	N-CA-C	6.38	118.23	111.28
1	HQ	74	GLY	N-CA-C	6.38	124.31	112.77
1	Ba	37	GLY	N-CA-C	6.38	120.41	110.91
1	BT	37	GLY	N-CA-C	6.38	120.41	110.91
1	Hc	74	GLY	N-CA-C	6.37	124.31	112.77
1	Em	74	GLY	N-CA-C	6.37	124.31	112.77
1	Dx	83	ARG	N-CA-C	-6.37	98.22	109.06
3	PO	30	LYS	CA-C-N	-6.37	113.41	119.85
3	PO	30	LYS	C-N-CA	-6.37	113.41	119.85
1	CQ	54	THR	N-CA-C	6.37	118.23	111.28
1	B2	37	GLY	N-CA-C	6.37	120.41	110.91
1	B7	37	GLY	N-CA-C	6.37	120.40	110.91
1	E8	74	GLY	N-CA-C	6.37	124.30	112.77
3	Pj	22	LYS	N-CA-C	6.37	117.73	109.64
1	Dv	95	ALA	N-CA-C	-6.37	102.48	108.22
1	Ew	74	GLY	N-CA-C	6.37	124.30	112.77
2	X5	729	GLU	N-CA-C	6.37	118.22	111.28
1	E3	74	GLY	N-CA-C	6.37	124.30	112.77
1	C8	54	THR	N-CA-C	6.37	118.22	111.28
1	Bl	37	GLY	N-CA-C	6.37	120.40	110.91
1	AI	45	TYR	N-CA-C	-6.37	98.81	109.07
1	HB	74	GLY	N-CA-C	6.37	124.30	112.77
3	PI	30	LYS	CA-C-N	-6.37	113.20	119.76
3	PI	30	LYS	C-N-CA	-6.37	113.20	119.76
1	A8	82	ALA	N-CA-C	6.37	118.22	111.28
1	Er	74	GLY	N-CA-C	6.37	124.29	112.77
1	Hr	74	GLY	N-CA-C	6.37	124.29	112.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A0	7	ILE	N-CA-C	6.37	118.22	112.17
1	CB	54	THR	N-CA-C	6.37	118.22	111.28
2	XS	729	GLU	N-CA-C	6.37	118.22	111.28
1	At	7	ILE	N-CA-C	6.36	118.22	112.17
1	Gu	38	ARG	N-CA-C	-6.36	98.00	108.76
1	BK	37	GLY	N-CA-C	6.36	120.39	110.91
3	PS	22	LYS	N-CA-C	6.36	117.72	109.64
1	Ay	7	ILE	N-CA-C	6.36	118.21	112.17
1	B6	37	GLY	N-CA-C	6.36	120.39	110.91
1	Ec	74	GLY	N-CA-C	6.36	124.28	112.77
1	Eh	74	GLY	N-CA-C	6.36	124.28	112.77
3	Pq	30	LYS	CA-C-N	-6.36	112.96	119.83
3	Pq	30	LYS	C-N-CA	-6.36	112.96	119.83
1	GJ	38	ARG	N-CA-C	-6.36	98.01	108.76
1	A3	82	ALA	N-CA-C	6.36	118.21	111.28
1	AL	82	ALA	N-CA-C	6.36	118.21	111.28
1	AS	45	TYR	N-CA-C	-6.36	98.83	109.07
3	PX	30	LYS	CA-C-N	-6.36	113.21	119.76
3	PX	30	LYS	C-N-CA	-6.36	113.21	119.76
1	AD	7	ILE	N-CA-C	6.36	118.21	112.17
2	XN	729	GLU	N-CA-C	6.36	118.21	111.28
1	EV	74	GLY	N-CA-C	6.36	124.27	112.77
2	XI	729	GLU	N-CA-C	6.35	118.21	111.28
1	Bg	37	GLY	N-CA-C	6.35	120.38	110.91
3	Pj	30	LYS	CA-C-N	-6.35	113.22	119.76
3	Pj	30	LYS	C-N-CA	-6.35	113.22	119.76
3	PD	22	LYS	N-CA-C	6.35	117.71	109.64
1	EB	74	GLY	N-CA-C	6.35	124.27	112.77
1	EL	74	GLY	N-CA-C	6.35	124.27	112.77
1	BU	37	GLY	N-CA-C	6.35	120.38	110.91
1	HV	74	GLY	N-CA-C	6.35	124.27	112.77
1	A5	7	ILE	N-CA-C	6.35	118.20	112.17
2	Xj	729	GLU	N-CA-C	6.35	118.20	111.28
1	Ar	82	ALA	N-CA-C	6.35	118.20	111.28
2	X0	729	GLU	N-CA-C	6.35	118.20	111.28
1	AQ	82	ALA	N-CA-C	6.35	118.20	111.28
1	EQ	74	GLY	N-CA-C	6.35	124.26	112.77
1	Ac	82	ALA	N-CA-C	6.35	118.20	111.28
1	Dl	95	ALA	N-CA-C	-6.35	102.51	108.22
1	Bk	37	GLY	N-CA-C	6.35	120.37	110.91
1	Ay	45	TYR	N-CA-C	-6.35	98.85	109.07
3	PN	22	LYS	N-CA-C	6.35	117.70	109.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P0	22	LYS	N-CA-C	6.35	117.70	109.64
3	Pb	30	LYS	CA-C-N	-6.35	112.98	119.83
3	Pb	30	LYS	C-N-CA	-6.35	112.98	119.83
1	BA	37	GLY	N-CA-C	6.35	120.36	110.91
3	P5	22	LYS	N-CA-C	6.34	117.70	109.64
2	Xt	729	GLU	N-CA-C	6.34	118.20	111.28
1	Hr	54	THR	N-CA-C	6.34	117.86	111.07
2	Xw	850	GLY	N-CA-C	-6.34	105.67	112.08
2	Xe	729	GLU	N-CA-C	6.34	118.19	111.28
1	Ah	82	ALA	N-CA-C	6.34	118.19	111.28
1	Bv	37	GLY	N-CA-C	6.34	120.36	110.91
3	Py	30	LYS	CA-C-N	-6.34	113.23	119.76
3	Py	30	LYS	C-N-CA	-6.34	113.23	119.76
1	Aw	82	ALA	N-CA-C	6.34	118.19	111.28
1	Hw	54	THR	N-CA-C	6.34	117.85	111.07
3	PF	30	LYS	CA-C-N	-6.34	112.98	119.83
3	PF	30	LYS	C-N-CA	-6.34	112.98	119.83
1	Db	95	ALA	N-CA-C	-6.34	102.52	108.22
3	Po	22	LYS	N-CA-C	6.34	117.69	109.64
1	AI	7	ILE	N-CA-C	6.34	118.19	112.17
3	P5	30	LYS	CA-C-N	-6.33	113.23	119.76
3	P5	30	LYS	C-N-CA	-6.33	113.23	119.76
2	Xo	729	GLU	N-CA-C	6.33	118.19	111.28
1	D2	95	ALA	N-CA-C	-6.33	102.52	108.22
3	Py	22	LYS	N-CA-C	6.33	117.69	109.64
1	DK	95	ALA	N-CA-C	-6.33	102.52	108.22
1	Ae	7	ILE	N-CA-C	6.33	118.19	112.17
1	Bz	37	GLY	N-CA-C	6.33	120.34	110.91
1	DP	95	ALA	N-CA-C	-6.33	102.52	108.22
2	XB	850	GLY	N-CA-C	-6.33	105.69	112.08
3	Pe	30	LYS	CA-C-N	-6.33	113.24	119.76
3	Pe	30	LYS	C-N-CA	-6.33	113.24	119.76
1	Dq	95	ALA	N-CA-C	-6.33	102.52	108.22
2	XD	729	GLU	N-CA-C	6.33	118.18	111.28
1	AG	82	ALA	N-CA-C	6.33	118.18	111.28
1	H3	54	THR	N-CA-C	6.33	117.84	111.07
2	Xy	729	GLU	N-CA-C	6.33	118.17	111.28
1	HL	54	THR	N-CA-C	6.33	117.84	111.07
1	HV	54	THR	N-CA-C	6.32	117.84	111.07
3	PP	30	LYS	CA-C-N	-6.32	113.00	119.83
3	PP	30	LYS	C-N-CA	-6.32	113.00	119.83
1	F9	83	ARG	N-CA-C	-6.32	98.08	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DQ	30	ALA	N-CA-C	6.32	118.17	111.28
1	FR	83	ARG	N-CA-C	-6.32	98.08	108.76
1	F4	83	ARG	N-CA-C	-6.32	98.09	108.76
1	FW	83	ARG	N-CA-C	-6.32	98.09	108.76
1	Hh	54	THR	N-CA-C	6.31	117.82	111.07
1	Fi	83	ARG	N-CA-C	-6.31	98.09	108.76
1	DF	95	ALA	N-CA-C	-6.31	102.54	108.22
1	HQ	54	THR	N-CA-C	6.31	117.83	111.07
3	PU	30	LYS	CA-C-N	-6.31	113.01	119.83
3	PU	30	LYS	C-N-CA	-6.31	113.01	119.83
1	Hm	54	THR	N-CA-C	6.31	117.82	111.07
1	H8	54	THR	N-CA-C	6.31	117.82	111.07
1	Hh	82	ALA	N-CA-C	6.31	118.16	111.28
1	HG	54	THR	N-CA-C	6.31	117.82	111.07
2	XX	729	GLU	N-CA-C	6.31	118.16	111.28
1	Fh	83	ARG	N-CA-C	-6.31	98.10	108.76
3	PA	30	LYS	CA-C-N	-6.31	113.02	119.83
3	PA	30	LYS	C-N-CA	-6.31	113.02	119.83
1	FH	83	ARG	N-CA-C	-6.31	98.10	108.76
1	Hw	82	ALA	N-CA-C	6.31	118.15	111.28
1	DB	30	ALA	N-CA-C	6.31	118.15	111.28
1	D7	95	ALA	N-CA-C	-6.30	102.55	108.22
3	P7	30	LYS	CA-C-N	-6.30	113.02	119.83
3	P7	30	LYS	C-N-CA	-6.30	113.02	119.83
1	Hc	54	THR	N-CA-C	6.30	117.81	111.07
3	Pv	30	LYS	CA-C-N	-6.30	113.02	119.83
3	Pv	30	LYS	C-N-CA	-6.30	113.02	119.83
1	HB	54	THR	N-CA-C	6.30	117.82	111.07
1	FC	83	ARG	N-CA-C	-6.30	98.11	108.76
3	PI	22	LYS	N-CA-C	6.30	117.64	109.64
3	Pe	22	LYS	N-CA-C	6.30	117.64	109.64
3	Pg	30	LYS	CA-C-N	-6.30	113.03	119.83
3	Pg	30	LYS	C-N-CA	-6.30	113.03	119.83
1	Fx	83	ARG	N-CA-C	-6.30	98.11	108.76
3	P2	30	LYS	CA-C-N	-6.30	113.03	119.83
3	P2	30	LYS	C-N-CA	-6.30	113.03	119.83
3	Pt	30	LYS	CA-C-N	-6.30	113.27	119.76
3	Pt	30	LYS	C-N-CA	-6.30	113.27	119.76
1	Hc	82	ALA	N-CA-C	6.30	118.14	111.28
1	Fd	83	ARG	N-CA-C	-6.30	98.12	108.76
1	AX	7	ILE	N-CA-C	6.30	118.15	112.17
1	AV	82	ALA	N-CA-C	6.30	118.14	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HV	82	ALA	N-CA-C	6.30	118.14	111.28
1	Fs	83	ARG	N-CA-C	-6.29	98.12	108.76
3	PN	30	LYS	CA-C-N	-6.29	113.28	119.76
3	PN	30	LYS	C-N-CA	-6.29	113.28	119.76
1	Dg	95	ALA	N-CA-C	-6.29	102.56	108.22
1	DA	95	ALA	N-CA-C	-6.29	102.56	108.22
1	DU	95	ALA	N-CA-C	-6.29	102.56	108.22
1	Dh	30	ALA	N-CA-C	6.29	118.14	111.28
3	P0	30	LYS	CA-C-N	-6.29	113.28	119.76
3	P0	30	LYS	C-N-CA	-6.29	113.28	119.76
3	Pl	30	LYS	CA-C-N	-6.29	113.04	119.83
3	Pl	30	LYS	C-N-CA	-6.29	113.04	119.83
1	D8	30	ALA	N-CA-C	6.29	118.13	111.28
1	Dm	30	ALA	N-CA-C	6.29	118.13	111.28
1	DG	30	ALA	N-CA-C	6.29	118.13	111.28
3	PX	22	LYS	N-CA-C	6.29	117.62	109.64
3	Pt	22	LYS	N-CA-C	6.28	117.62	109.64
1	HG	82	ALA	N-CA-C	6.28	118.13	111.28
1	H8	82	ALA	N-CA-C	6.28	118.13	111.28
1	AF	74	GLY	N-CA-C	6.28	124.14	112.77
3	Po	30	LYS	CA-C-N	-6.28	113.30	119.76
3	Po	30	LYS	C-N-CA	-6.28	113.30	119.76
3	PD	30	LYS	CA-C-N	-6.28	113.30	119.76
3	PD	30	LYS	C-N-CA	-6.28	113.30	119.76
1	DL	30	ALA	N-CA-C	6.28	118.12	111.28
1	Hr	82	ALA	N-CA-C	6.27	118.12	111.28
3	PK	30	LYS	CA-C-N	-6.27	113.06	119.83
3	PK	30	LYS	C-N-CA	-6.27	113.06	119.83
1	Dr	30	ALA	N-CA-C	6.26	118.11	111.28
1	HB	82	ALA	N-CA-C	6.26	118.11	111.28
1	HQ	82	ALA	N-CA-C	6.26	118.11	111.28
1	A2	74	GLY	N-CA-C	6.26	124.11	112.77
1	AK	74	GLY	N-CA-C	6.26	124.11	112.77
1	D3	30	ALA	N-CA-C	6.26	118.11	111.28
1	H3	82	ALA	N-CA-C	6.26	118.11	111.28
1	Ab	74	GLY	N-CA-C	6.26	124.11	112.77
1	Hm	82	ALA	N-CA-C	6.26	118.10	111.28
1	AU	74	GLY	N-CA-C	6.26	124.11	112.77
1	FW	37	GLY	N-CA-C	6.26	120.24	110.91
1	Gb	7	ILE	N-CA-C	6.26	117.04	110.72
1	GK	7	ILE	N-CA-C	6.26	117.04	110.72
1	GU	7	ILE	N-CA-C	6.26	117.04	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Fs	37	GLY	N-CA-C	6.26	120.23	110.91
1	Dw	30	ALA	N-CA-C	6.26	118.10	111.28
1	GA	7	ILE	N-CA-C	6.26	117.04	110.72
1	AP	74	GLY	N-CA-C	6.26	124.09	112.77
1	Aq	74	GLY	N-CA-C	6.25	124.09	112.77
1	GF	7	ILE	N-CA-C	6.25	117.04	110.72
1	AA	74	GLY	N-CA-C	6.25	124.09	112.77
3	PS	30	LYS	CA-C-N	-6.25	113.32	119.76
3	PS	30	LYS	C-N-CA	-6.25	113.32	119.76
1	Dc	30	ALA	N-CA-C	6.25	118.09	111.28
1	Ag	74	GLY	N-CA-C	6.25	124.09	112.77
1	AH	37	GLY	N-CA-C	6.25	120.50	110.87
1	CG	38	ARG	N-CA-C	-6.25	98.20	108.76
1	A7	74	GLY	N-CA-C	6.25	124.08	112.77
1	Ch	38	ARG	N-CA-C	-6.25	98.20	108.76
1	FC	37	GLY	N-CA-C	6.25	120.22	110.91
1	F9	37	GLY	N-CA-C	6.25	120.22	110.91
1	CL	38	ARG	N-CA-C	-6.25	98.20	108.76
1	DV	30	ALA	N-CA-C	6.25	118.09	111.28
1	ES	42	GLY	N-CA-C	-6.24	98.38	113.18
1	A9	37	GLY	N-CA-C	6.24	120.48	110.87
1	Gg	7	ILE	N-CA-C	6.24	117.02	110.72
1	Cc	38	ARG	N-CA-C	-6.24	98.22	108.76
1	Eo	42	GLY	N-CA-C	-6.24	98.39	113.18
1	Fx	37	GLY	N-CA-C	6.24	120.21	110.91
2	Xr	850	GLY	N-CA-C	-6.24	105.67	112.04
1	C3	38	ARG	N-CA-C	-6.24	98.22	108.76
1	ER	76	VAL	N-CA-C	-6.24	105.65	111.45
1	G7	7	ILE	N-CA-C	6.24	117.02	110.72
1	Cm	38	ARG	N-CA-C	-6.24	98.22	108.76
1	Fd	37	GLY	N-CA-C	6.24	120.20	110.91
1	Fi	37	GLY	N-CA-C	6.24	120.20	110.91
1	Al	74	GLY	N-CA-C	6.24	124.06	112.77
1	Gq	7	ILE	N-CA-C	6.24	117.02	110.72
1	Av	74	GLY	N-CA-C	6.24	124.06	112.77
1	AC	37	GLY	N-CA-C	6.24	120.47	110.87
1	DK	54	THR	N-CA-C	6.24	118.08	111.28
2	XQ	850	GLY	N-CA-C	-6.24	105.68	112.04
1	Ad	37	GLY	N-CA-C	6.23	120.47	110.87
1	AW	37	GLY	N-CA-C	6.23	120.47	110.87
1	G2	7	ILE	N-CA-C	6.23	117.02	110.72
1	A4	37	GLY	N-CA-C	6.23	120.47	110.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F4	37	GLY	N-CA-C	6.23	120.20	110.91
1	Hh	75	LEU	CA-CB-CG	6.23	138.12	116.30
1	Gl	7	ILE	N-CA-C	6.23	117.02	110.72
1	Hr	75	LEU	CA-CB-CG	6.23	138.12	116.30
1	AM	37	GLY	N-CA-C	6.23	120.47	110.87
1	FM	37	GLY	N-CA-C	6.23	120.20	110.91
1	EP	41	VAL	N-CA-C	6.23	117.01	110.72
2	X8	850	GLY	N-CA-C	-6.23	105.68	112.04
2	Xm	850	GLY	N-CA-C	-6.23	105.68	112.04
2	X3	850	GLY	N-CA-C	-6.23	105.69	112.04
1	EN	42	GLY	N-CA-C	-6.23	98.41	113.18
2	XL	850	GLY	N-CA-C	-6.23	105.69	112.04
1	Cw	38	ARG	N-CA-C	-6.23	98.23	108.76
1	E0	42	GLY	N-CA-C	-6.23	98.42	113.18
1	H8	75	LEU	CA-CB-CG	6.23	138.10	116.30
1	Fn	37	GLY	N-CA-C	6.23	120.19	110.91
1	Cr	38	ARG	N-CA-C	-6.23	98.23	108.76
1	AR	37	GLY	N-CA-C	6.23	120.46	110.87
1	C8	38	ARG	N-CA-C	-6.22	98.24	108.76
1	Hc	75	LEU	CA-CB-CG	6.22	138.08	116.30
1	FM	83	ARG	N-CA-C	-6.22	98.13	108.34
1	FR	37	GLY	N-CA-C	6.22	120.19	110.91
1	H3	75	LEU	CA-CB-CG	6.22	138.08	116.30
1	ED	42	GLY	N-CA-C	-6.22	98.43	113.18
1	Hm	75	LEU	CA-CB-CG	6.22	138.07	116.30
1	FH	37	GLY	N-CA-C	6.22	120.18	110.91
1	HQ	75	LEU	CA-CB-CG	6.22	138.07	116.30
1	Ai	37	GLY	N-CA-C	6.22	120.45	110.87
1	An	37	GLY	N-CA-C	6.22	120.45	110.87
1	Ax	37	GLY	N-CA-C	6.22	120.45	110.87
1	HG	75	LEU	CA-CB-CG	6.22	138.07	116.30
1	CV	38	ARG	N-CA-C	-6.22	98.25	108.76
2	Xc	850	GLY	N-CA-C	-6.22	105.70	112.04
1	HL	75	LEU	CA-CB-CG	6.22	138.06	116.30
1	DP	54	THR	N-CA-C	6.22	118.06	111.28
1	E5	42	GLY	N-CA-C	-6.22	98.45	113.18
1	Ey	42	GLY	N-CA-C	-6.22	98.44	113.18
1	HL	82	ALA	N-CA-C	6.22	118.06	111.28
1	As	37	GLY	N-CA-C	6.21	120.44	110.87
1	Hw	75	LEU	CA-CB-CG	6.21	138.05	116.30
1	CB	38	ARG	N-CA-C	-6.21	98.26	108.76
1	GP	7	ILE	N-CA-C	6.21	117.00	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HV	75	LEU	CA-CB-CG	6.21	138.05	116.30
1	EW	76	VAL	N-CA-C	-6.21	105.67	111.45
1	Ej	42	GLY	N-CA-C	-6.21	98.46	113.18
2	XG	850	GLY	N-CA-C	-6.21	105.70	112.04
1	HB	75	LEU	CA-CB-CG	6.21	138.03	116.30
1	CK	76	VAL	N-CA-C	-6.21	106.47	111.81
1	CQ	38	ARG	N-CA-C	-6.21	98.27	108.76
1	Ex	76	VAL	N-CA-C	-6.21	105.68	111.45
1	D2	54	THR	N-CA-C	6.20	118.04	111.28
1	Dl	54	THR	N-CA-C	6.20	118.04	111.28
1	En	76	VAL	N-CA-C	-6.20	105.68	111.45
1	EA	41	VAL	N-CA-C	6.20	116.98	110.72
1	E9	76	VAL	N-CA-C	-6.20	105.68	111.45
1	Cg	76	VAL	N-CA-C	-6.20	106.48	111.81
1	Ev	41	VAL	N-CA-C	6.20	116.98	110.72
1	Ee	42	GLY	N-CA-C	-6.20	98.48	113.18
2	Xh	850	GLY	N-CA-C	-6.20	105.72	112.04
1	EI	42	GLY	N-CA-C	-6.20	98.48	113.18
1	EX	42	GLY	N-CA-C	-6.20	98.48	113.18
1	D7	54	THR	N-CA-C	6.20	118.04	111.28
1	Eb	41	VAL	N-CA-C	6.20	116.98	110.72
1	El	41	VAL	N-CA-C	6.20	116.98	110.72
1	Dq	54	THR	N-CA-C	6.20	118.04	111.28
1	Et	42	GLY	N-CA-C	-6.20	98.49	113.18
1	Dv	54	THR	N-CA-C	6.20	118.04	111.28
1	EU	41	VAL	N-CA-C	6.20	116.98	110.72
1	E2	41	VAL	N-CA-C	6.20	116.98	110.72
1	Dg	54	THR	N-CA-C	6.20	118.03	111.28
1	EK	41	VAL	N-CA-C	6.20	116.98	110.72
1	EC	76	VAL	N-CA-C	-6.19	105.69	111.45
1	CA	76	VAL	N-CA-C	-6.19	106.48	111.81
1	Gv	7	ILE	N-CA-C	6.19	116.97	110.72
1	Eg	41	VAL	N-CA-C	6.19	116.97	110.72
1	DA	54	THR	N-CA-C	6.19	118.03	111.28
2	XV	850	GLY	N-CA-C	-6.19	105.73	112.04
1	E4	76	VAL	N-CA-C	-6.19	105.70	111.45
1	DP	95	ALA	CA-C-N	-6.19	113.58	120.14
1	DP	95	ALA	C-N-CA	-6.19	113.58	120.14
1	Ed	76	VAL	N-CA-C	-6.18	105.70	111.45
1	Dq	95	ALA	CA-C-N	-6.18	113.58	120.14
1	Dq	95	ALA	C-N-CA	-6.18	113.58	120.14
1	D7	95	ALA	CA-C-N	-6.18	113.59	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D7	95	ALA	C-N-CA	-6.18	113.59	120.14
1	DU	95	ALA	CA-C-N	-6.18	113.59	120.14
1	DU	95	ALA	C-N-CA	-6.18	113.59	120.14
1	E7	41	VAL	N-CA-C	6.18	116.96	110.72
1	EF	41	VAL	N-CA-C	6.18	116.96	110.72
2	XS	808	GLY	N-CA-C	6.18	127.83	113.18
1	Es	76	VAL	N-CA-C	-6.18	105.70	111.45
1	CP	76	VAL	N-CA-C	-6.18	106.50	111.81
1	DU	54	THR	N-CA-C	6.17	118.01	111.28
1	Db	54	THR	N-CA-C	6.17	118.00	111.28
1	DF	95	ALA	CA-C-N	-6.17	113.60	120.14
1	DF	95	ALA	C-N-CA	-6.17	113.60	120.14
1	Dv	95	ALA	CA-C-N	-6.17	113.60	120.14
1	Dv	95	ALA	C-N-CA	-6.17	113.60	120.14
1	Cb	76	VAL	N-CA-C	-6.16	106.51	111.81
1	Eq	41	VAL	N-CA-C	6.16	116.94	110.72
2	X0	808	GLY	N-CA-C	6.16	127.77	113.18
1	Hp	38	ARG	N-CA-C	-6.16	98.59	109.06
1	C2	76	VAL	N-CA-C	-6.16	106.52	111.81
1	Ei	76	VAL	N-CA-C	-6.16	105.73	111.45
1	DA	95	ALA	CA-C-N	-6.16	113.61	120.14
1	DA	95	ALA	C-N-CA	-6.16	113.61	120.14
1	Cq	76	VAL	N-CA-C	-6.15	106.52	111.81
1	Cv	76	VAL	N-CA-C	-6.15	106.52	111.81
1	EH	76	VAL	N-CA-C	-6.15	105.73	111.45
1	EM	76	VAL	N-CA-C	-6.15	105.73	111.45
2	XD	808	GLY	N-CA-C	6.15	127.76	113.18
1	CU	76	VAL	N-CA-C	-6.15	106.52	111.81
2	Xt	808	GLY	N-CA-C	6.15	127.75	113.18
2	Xy	808	GLY	N-CA-C	6.15	127.75	113.18
1	Db	95	ALA	CA-C-N	-6.15	113.62	120.14
1	Db	95	ALA	C-N-CA	-6.15	113.62	120.14
1	Dg	95	ALA	CA-C-N	-6.15	113.62	120.14
1	Dg	95	ALA	C-N-CA	-6.15	113.62	120.14
1	Cl	76	VAL	N-CA-C	-6.15	106.52	111.81
1	Hk	38	ARG	N-CA-C	-6.15	98.61	109.06
2	Xj	808	GLY	N-CA-C	6.15	127.75	113.18
1	C7	76	VAL	N-CA-C	-6.14	106.53	111.81
1	Gw	38	ARG	N-CA-C	-6.14	98.61	109.06
1	DF	54	THR	N-CA-C	6.14	117.98	111.28
1	HO	38	ARG	N-CA-C	-6.14	98.61	109.06
1	Dl	95	ALA	CA-C-N	-6.14	113.63	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Dl	95	ALA	C-N-CA	-6.14	113.63	120.14
2	Xo	808	GLY	N-CA-C	6.14	127.73	113.18
2	X5	808	GLY	N-CA-C	6.14	127.73	113.18
1	Eo	82	ALA	N-CA-C	6.14	118.05	111.36
1	Es	82	ALA	N-CA-C	6.14	117.97	111.28
2	XN	808	GLY	N-CA-C	6.14	127.73	113.18
1	D2	95	ALA	CA-C-N	-6.14	113.64	120.14
1	D2	95	ALA	C-N-CA	-6.14	113.64	120.14
1	Hz	38	ARG	N-CA-C	-6.14	98.63	109.06
1	CF	76	VAL	N-CA-C	-6.13	106.53	111.81
1	ER	82	ALA	N-CA-C	6.13	117.97	111.28
2	Xe	808	GLY	N-CA-C	6.13	127.71	113.18
2	XX	808	GLY	N-CA-C	6.13	127.71	113.18
1	Gr	38	ARG	N-CA-C	-6.13	98.64	109.06
1	Hf	38	ARG	N-CA-C	-6.13	98.64	109.06
1	Ha	38	ARG	N-CA-C	-6.13	98.64	109.06
1	Gh	38	ARG	N-CA-C	-6.13	98.64	109.06
2	XI	808	GLY	N-CA-C	6.13	127.70	113.18
1	GL	38	ARG	N-CA-C	-6.13	98.65	109.06
1	HT	38	ARG	N-CA-C	-6.13	98.65	109.06
1	H6	38	ARG	N-CA-C	-6.13	98.64	109.06
1	Et	82	ALA	N-CA-C	6.12	118.03	111.36
1	EI	82	ALA	N-CA-C	6.12	118.03	111.36
1	DK	95	ALA	CA-C-N	-6.12	113.65	120.14
1	DK	95	ALA	C-N-CA	-6.12	113.65	120.14
1	G3	38	ARG	N-CA-C	-6.12	98.66	109.06
1	HJ	38	ARG	N-CA-C	-6.12	98.66	109.06
1	H1	38	ARG	N-CA-C	-6.12	98.66	109.06
1	Gc	38	ARG	N-CA-C	-6.12	98.66	109.06
1	Ex	82	ALA	N-CA-C	6.12	117.95	111.28
1	HE	38	ARG	N-CA-C	-6.12	98.66	109.06
2	Xi	729	GLU	N-CA-C	6.12	118.03	111.36
1	ES	82	ALA	N-CA-C	6.12	118.03	111.36
1	E0	82	ALA	N-CA-C	6.11	118.03	111.36
1	Ee	82	ALA	N-CA-C	6.11	118.02	111.36
1	E9	82	ALA	N-CA-C	6.11	117.94	111.28
1	E5	82	ALA	N-CA-C	6.11	118.02	111.36
1	EN	82	ALA	N-CA-C	6.11	118.02	111.36
1	Hu	38	ARG	N-CA-C	-6.11	98.67	109.06
1	E4	82	ALA	N-CA-C	6.11	117.94	111.28
1	Ei	82	ALA	N-CA-C	6.11	117.94	111.28
2	Xx	729	GLU	N-CA-C	6.11	118.02	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EM	82	ALA	N-CA-C	6.11	117.94	111.28
1	GV	38	ARG	N-CA-C	-6.11	98.68	109.06
1	GG	38	ARG	N-CA-C	-6.10	98.69	109.06
1	Ej	82	ALA	N-CA-C	6.10	118.01	111.36
2	XM	729	GLU	N-CA-C	6.09	118.00	111.36
1	En	82	ALA	N-CA-C	6.09	117.92	111.28
1	GB	38	ARG	N-CA-C	-6.09	98.70	109.06
1	Ey	82	ALA	N-CA-C	6.09	118.00	111.36
1	Gm	38	ARG	N-CA-C	-6.09	98.71	109.06
1	Gv	30	ALA	N-CA-C	6.09	117.92	111.28
2	X4	729	GLU	N-CA-C	6.09	117.99	111.36
1	GQ	38	ARG	N-CA-C	-6.08	98.72	109.06
1	Ed	82	ALA	N-CA-C	6.08	117.91	111.28
1	EC	82	ALA	N-CA-C	6.08	117.91	111.28
1	EW	82	ALA	N-CA-C	6.08	117.91	111.28
1	G8	38	ARG	N-CA-C	-6.08	98.72	109.06
1	ED	82	ALA	N-CA-C	6.08	117.99	111.36
2	X9	729	GLU	N-CA-C	6.08	117.98	111.36
1	GK	30	ALA	N-CA-C	6.08	117.90	111.28
2	XR	729	GLU	N-CA-C	6.08	117.98	111.36
1	EX	82	ALA	N-CA-C	6.08	117.98	111.36
1	EH	82	ALA	N-CA-C	6.07	117.89	111.28
2	Xn	729	GLU	N-CA-C	6.07	117.97	111.36
1	G7	30	ALA	N-CA-C	6.06	117.89	111.28
2	XH	729	GLU	N-CA-C	6.06	117.97	111.36
1	GP	30	ALA	N-CA-C	6.06	117.89	111.28
1	GU	30	ALA	N-CA-C	6.06	117.89	111.28
1	Gb	30	ALA	N-CA-C	6.06	117.89	111.28
1	Gl	30	ALA	N-CA-C	6.06	117.88	111.28
1	AE	48	VAL	CB-CA-C	6.05	119.59	110.63
2	Xd	729	GLU	N-CA-C	6.05	117.96	111.36
1	GA	30	ALA	N-CA-C	6.05	117.87	111.28
1	G2	30	ALA	N-CA-C	6.04	117.87	111.28
1	Dm	37	GLY	N-CA-C	6.04	119.92	110.91
1	Gq	30	ALA	N-CA-C	6.04	117.87	111.28
1	D3	37	GLY	N-CA-C	6.04	119.91	110.91
1	GF	30	ALA	N-CA-C	6.04	117.86	111.28
1	DV	37	GLY	N-CA-C	6.04	119.91	110.91
1	Dh	37	GLY	N-CA-C	6.04	119.91	110.91
1	Au	48	VAL	CB-CA-C	6.04	119.56	110.63
2	XC	729	GLU	N-CA-C	6.04	117.94	111.36
1	Aa	48	VAL	CB-CA-C	6.04	119.56	110.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Af	48	VAL	CB-CA-C	6.04	119.56	110.63
1	ER	38	ARG	N-CA-C	-6.04	98.56	108.76
1	En	38	ARG	N-CA-C	-6.03	98.56	108.76
1	Ap	48	VAL	CB-CA-C	6.03	119.56	110.63
1	A6	48	VAL	CB-CA-C	6.03	119.55	110.63
1	Ed	38	ARG	N-CA-C	-6.03	98.57	108.76
2	Xs	729	GLU	N-CA-C	6.03	117.93	111.36
1	EC	38	ARG	N-CA-C	-6.03	98.57	108.76
1	DL	37	GLY	N-CA-C	6.03	119.89	110.91
1	AO	48	VAL	CB-CA-C	6.03	119.55	110.63
1	Gg	30	ALA	N-CA-C	6.03	117.85	111.28
1	Es	38	ARG	N-CA-C	-6.03	98.57	108.76
1	DB	37	GLY	N-CA-C	6.03	119.89	110.91
1	EH	38	ARG	N-CA-C	-6.03	98.58	108.76
2	XI	782	MET	N-CA-C	-6.03	99.08	108.90
1	A1	48	VAL	CB-CA-C	6.02	119.55	110.63
1	Cq	83	ARG	N-CA-C	-6.02	98.82	109.06
2	XX	782	MET	N-CA-C	-6.02	99.08	108.90
2	XN	782	MET	N-CA-C	-6.02	99.08	108.90
1	E9	38	ARG	N-CA-C	-6.02	98.59	108.76
2	XD	782	MET	N-CA-C	-6.02	99.09	108.90
1	H5	54	THR	N-CA-C	6.02	117.84	111.28
1	D8	37	GLY	N-CA-C	6.02	119.88	110.91
2	Xe	782	MET	N-CA-C	-6.02	99.09	108.90
1	Dc	37	GLY	N-CA-C	6.02	119.88	110.91
1	Dw	37	GLY	N-CA-C	6.02	119.88	110.91
1	HN	54	THR	N-CA-C	6.02	117.84	111.28
2	XW	843	LYS	N-CA-C	6.02	117.47	109.83
2	Xt	782	MET	N-CA-C	-6.02	99.09	108.90
2	XS	782	MET	N-CA-C	-6.02	99.09	108.90
2	X0	782	MET	N-CA-C	-6.01	99.10	108.90
2	Xo	782	MET	N-CA-C	-6.01	99.09	108.90
2	Xs	843	LYS	N-CA-C	6.01	117.47	109.83
2	Xx	843	LYS	N-CA-C	6.01	117.47	109.83
1	Hy	54	THR	N-CA-C	6.01	117.83	111.28
1	H0	54	THR	N-CA-C	6.01	117.83	111.28
1	HA	30	ALA	N-CA-C	6.01	117.83	111.28
1	Az	48	VAL	CB-CA-C	6.01	119.53	110.63
1	HS	54	THR	N-CA-C	6.01	117.83	111.28
2	XW	729	GLU	N-CA-C	6.01	117.91	111.36
1	AT	48	VAL	CB-CA-C	6.01	119.53	110.63
1	EW	38	ARG	N-CA-C	-6.01	98.61	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X5	782	MET	N-CA-C	-6.01	99.11	108.90
1	Hj	54	THR	N-CA-C	6.01	117.83	111.28
1	Ez	38	ARG	N-CA-C	-6.01	98.85	109.06
1	Dr	37	GLY	N-CA-C	6.00	119.86	110.91
1	Ex	38	ARG	N-CA-C	-6.00	98.61	108.76
2	XH	843	LYS	N-CA-C	6.00	117.46	109.83
1	AJ	48	VAL	CB-CA-C	6.00	119.52	110.63
1	CU	83	ARG	N-CA-C	-6.00	98.85	109.06
1	E4	38	ARG	N-CA-C	-6.00	98.61	108.76
2	Xd	843	LYS	N-CA-C	6.00	117.45	109.83
1	Ho	54	THR	N-CA-C	6.00	117.83	111.28
1	HD	54	THR	N-CA-C	6.00	117.82	111.28
2	XE	850	GLY	N-CA-C	-6.00	106.25	111.95
1	EM	38	ARG	N-CA-C	-6.00	98.61	108.76
2	XR	843	LYS	N-CA-C	6.00	117.45	109.83
2	X4	843	LYS	N-CA-C	6.00	117.45	109.83
1	Cb	83	ARG	N-CA-C	-6.00	98.86	109.06
2	Xp	850	GLY	N-CA-C	-6.00	106.25	111.95
2	XM	843	LYS	N-CA-C	6.00	117.45	109.83
2	Xz	850	GLY	N-CA-C	-6.00	106.25	111.95
2	Xj	782	MET	N-CA-C	-6.00	99.12	108.90
2	Xn	843	LYS	N-CA-C	6.00	117.45	109.83
1	DQ	37	GLY	N-CA-C	6.00	119.85	110.91
2	Xi	843	LYS	N-CA-C	6.00	117.44	109.83
1	Ek	38	ARG	N-CA-C	-6.00	98.87	109.06
1	Ei	38	ARG	N-CA-C	-5.99	98.63	108.76
1	Ak	48	VAL	CB-CA-C	5.99	119.50	110.63
1	Ew	78	ALA	N-CA-C	-5.99	98.08	108.69
1	C7	83	ARG	N-CA-C	-5.99	98.87	109.06
1	CF	83	ARG	N-CA-C	-5.99	98.87	109.06
2	X9	843	LYS	N-CA-C	5.99	117.44	109.83
1	Cl	83	ARG	N-CA-C	-5.99	98.87	109.06
2	XC	843	LYS	N-CA-C	5.99	117.44	109.83
1	Cg	83	ARG	N-CA-C	-5.99	98.88	109.06
1	Er	78	ALA	N-CA-C	-5.99	98.09	108.69
1	DP	30	ALA	N-CA-C	5.99	117.48	111.07
1	EV	78	ALA	N-CA-C	-5.99	98.09	108.69
1	E6	38	ARG	N-CA-C	-5.99	98.89	109.06
2	Xj	728	PRO	N-CA-C	-5.99	105.21	113.53
1	DG	37	GLY	N-CA-C	5.99	119.83	110.91
2	XO	850	GLY	N-CA-C	-5.99	106.26	111.95
1	He	54	THR	N-CA-C	5.98	117.80	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	83	ARG	N-CA-C	-5.98	98.89	109.06
1	Ai	48	VAL	CB-CA-C	5.98	119.74	110.83
1	EE	38	ARG	N-CA-C	-5.98	98.89	109.06
1	CK	83	ARG	N-CA-C	-5.98	98.89	109.06
1	EL	78	ALA	N-CA-C	-5.98	98.10	108.69
2	Xy	782	MET	N-CA-C	-5.98	99.15	108.90
1	Hl	30	ALA	N-CA-C	5.98	117.80	111.28
1	Cv	83	ARG	N-CA-C	-5.98	98.90	109.06
1	CA	83	ARG	N-CA-C	-5.98	98.90	109.06
1	Ec	78	ALA	N-CA-C	-5.98	98.11	108.69
1	H7	30	ALA	N-CA-C	5.97	117.79	111.28
1	Em	78	ALA	N-CA-C	-5.97	98.11	108.69
1	Eu	38	ARG	N-CA-C	-5.97	98.90	109.06
1	Ef	38	ARG	N-CA-C	-5.97	98.91	109.06
1	Ep	38	ARG	N-CA-C	-5.97	98.91	109.06
1	EB	78	ALA	N-CA-C	-5.97	98.12	108.69
1	AH	48	VAL	CB-CA-C	5.97	119.73	110.83
1	EO	38	ARG	N-CA-C	-5.97	98.91	109.06
1	E3	78	ALA	N-CA-C	-5.97	98.12	108.69
1	E8	78	ALA	N-CA-C	-5.97	98.12	108.69
1	Eh	78	ALA	N-CA-C	-5.97	98.12	108.69
1	HI	54	THR	N-CA-C	5.97	117.79	111.28
2	XJ	850	GLY	N-CA-C	-5.97	106.28	111.95
2	XD	728	PRO	N-CA-C	-5.97	105.23	113.53
2	XT	850	GLY	N-CA-C	-5.97	106.28	111.95
3	PB	30	LYS	CA-C-N	-5.97	113.61	119.76
3	PB	30	LYS	C-N-CA	-5.97	113.61	119.76
1	EG	78	ALA	N-CA-C	-5.97	98.13	108.69
1	Ad	48	VAL	CB-CA-C	5.96	119.72	110.83
1	AR	48	VAL	CB-CA-C	5.96	119.72	110.83
1	Ea	38	ARG	N-CA-C	-5.96	98.92	109.06
1	ET	38	ARG	N-CA-C	-5.96	98.92	109.06
2	Xa	850	GLY	N-CA-C	-5.96	106.29	111.95
1	CP	83	ARG	N-CA-C	-5.96	98.92	109.06
1	E1	38	ARG	N-CA-C	-5.96	98.93	109.06
1	A4	48	VAL	CB-CA-C	5.96	119.71	110.83
1	BH	37	GLY	N-CA-C	5.96	119.79	110.91
1	HP	30	ALA	N-CA-C	5.96	117.78	111.28
2	X5	728	PRO	N-CA-C	-5.96	105.25	113.53
2	XN	728	PRO	N-CA-C	-5.96	105.25	113.53
1	Ag	67	ALA	N-CA-C	5.95	117.57	111.14
2	Xk	850	GLY	N-CA-C	-5.95	106.29	111.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	PF	49	TRP	N-CA-C	-5.95	99.53	109.24
1	EQ	78	ALA	N-CA-C	-5.95	98.15	108.69
1	HX	54	THR	N-CA-C	5.95	117.77	111.28
2	X0	728	PRO	N-CA-C	-5.95	105.26	113.53
1	Bd	37	GLY	N-CA-C	5.95	119.78	110.91
2	XS	728	PRO	N-CA-C	-5.95	105.26	113.53
1	Av	67	ALA	N-CA-C	5.95	117.57	111.14
1	Hv	30	ALA	N-CA-C	5.95	117.77	111.28
1	EJ	38	ARG	N-CA-C	-5.95	98.94	109.06
1	Ht	54	THR	N-CA-C	5.95	117.76	111.28
1	Bs	37	GLY	N-CA-C	5.95	119.77	110.91
1	AM	48	VAL	CB-CA-C	5.95	119.69	110.83
3	PQ	30	LYS	CA-C-N	-5.95	113.63	119.76
3	PQ	30	LYS	C-N-CA	-5.95	113.63	119.76
2	X6	850	GLY	N-CA-C	-5.95	106.30	111.95
3	Pl	49	TRP	N-CA-C	-5.95	99.55	109.24
1	Eu	95	ALA	CA-C-N	-5.95	113.81	119.76
1	Eu	95	ALA	C-N-CA	-5.95	113.81	119.76
2	Xy	728	PRO	N-CA-C	-5.95	105.27	113.53
1	Ax	48	VAL	CB-CA-C	5.95	119.69	110.83
1	AW	48	VAL	CB-CA-C	5.95	119.69	110.83
2	XG	828	VAL	N-CA-C	-5.95	99.18	107.80
1	AA	67	ALA	N-CA-C	5.94	117.56	111.14
1	A7	67	ALA	N-CA-C	5.94	117.56	111.14
1	D7	30	ALA	N-CA-C	5.94	117.43	111.07
1	Hg	30	ALA	N-CA-C	5.94	117.76	111.28
1	HF	30	ALA	N-CA-C	5.94	117.76	111.28
1	AK	67	ALA	N-CA-C	5.94	117.56	111.14
1	DK	30	ALA	N-CA-C	5.94	117.43	111.07
1	A9	48	VAL	CB-CA-C	5.94	119.68	110.83
3	Pm	30	LYS	CA-C-N	-5.94	113.64	119.76
3	Pm	30	LYS	C-N-CA	-5.94	113.64	119.76
3	P7	49	TRP	N-CA-C	-5.94	99.56	109.24
3	Pv	49	TRP	N-CA-C	-5.94	99.56	109.24
3	Pb	49	TRP	N-CA-C	-5.93	99.57	109.24
3	Pq	49	TRP	N-CA-C	-5.93	99.57	109.24
1	As	48	VAL	CB-CA-C	5.93	119.67	110.83
2	XL	828	VAL	N-CA-C	-5.93	99.19	107.80
1	H2	30	ALA	N-CA-C	5.93	117.75	111.28
3	P2	49	TRP	N-CA-C	-5.93	99.57	109.24
2	Xu	850	GLY	N-CA-C	-5.93	106.31	111.95
2	Xw	828	VAL	N-CA-C	-5.93	99.20	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	PA	49	TRP	N-CA-C	-5.93	99.57	109.24
3	PP	49	TRP	N-CA-C	-5.93	99.57	109.24
1	AU	67	ALA	N-CA-C	5.93	117.55	111.14
3	PU	49	TRP	N-CA-C	-5.93	99.57	109.24
1	BW	37	GLY	N-CA-C	5.93	119.75	110.91
2	XI	728	PRO	N-CA-C	-5.93	105.29	113.53
2	X1	850	GLY	N-CA-C	-5.93	106.32	111.95
2	Xc	828	VAL	N-CA-C	-5.93	99.20	107.80
3	PK	49	TRP	N-CA-C	-5.93	99.58	109.24
2	X3	828	VAL	N-CA-C	-5.93	99.21	107.80
3	Pg	49	TRP	N-CA-C	-5.93	99.58	109.24
1	A2	67	ALA	N-CA-C	5.92	117.54	111.14
2	Xe	728	PRO	N-CA-C	-5.92	105.29	113.53
1	Fm	67	ALA	N-CA-C	5.92	117.54	111.14
1	DA	30	ALA	N-CA-C	5.92	117.41	111.07
1	HK	30	ALA	N-CA-C	5.92	117.74	111.28
1	FN	67	ALA	N-CA-C	5.92	117.82	111.36
2	XV	828	VAL	N-CA-C	-5.92	99.21	107.80
1	FX	67	ALA	N-CA-C	5.92	117.82	111.36
2	Xo	728	PRO	N-CA-C	-5.92	105.30	113.53
1	ET	95	ALA	CA-C-N	-5.92	113.84	119.76
1	ET	95	ALA	C-N-CA	-5.92	113.84	119.76
1	HT	82	ALA	N-CA-C	5.92	119.76	112.54
1	Fe	67	ALA	N-CA-C	5.92	117.81	111.36
1	Ep	95	ALA	CA-C-N	-5.92	113.84	119.76
1	Ep	95	ALA	C-N-CA	-5.92	113.84	119.76
2	XB	828	VAL	N-CA-C	-5.92	99.22	107.80
1	D2	30	ALA	N-CA-C	5.92	117.40	111.07
1	CP	82	ALA	N-CA-C	5.92	118.68	111.82
1	AF	67	ALA	N-CA-C	5.92	117.53	111.14
1	B4	37	GLY	N-CA-C	5.91	119.72	110.91
1	Dl	30	ALA	N-CA-C	5.91	117.40	111.07
1	FQ	67	ALA	N-CA-C	5.91	117.53	111.14
1	Ab	67	ALA	N-CA-C	5.91	117.52	111.14
1	Al	67	ALA	N-CA-C	5.91	117.53	111.14
3	P8	30	LYS	CA-C-N	-5.91	113.67	119.76
3	P8	30	LYS	C-N-CA	-5.91	113.67	119.76
1	An	48	VAL	CB-CA-C	5.91	119.64	110.83
1	Bx	37	GLY	N-CA-C	5.91	119.72	110.91
1	AC	48	VAL	CB-CA-C	5.91	119.64	110.83
2	X8	828	VAL	N-CA-C	-5.91	99.23	107.80
2	Xr	828	VAL	N-CA-C	-5.91	99.23	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F8	67	ALA	N-CA-C	5.91	117.52	111.14
1	Bn	37	GLY	N-CA-C	5.91	119.71	110.91
1	C7	82	ALA	N-CA-C	5.91	118.67	111.82
1	Db	30	ALA	N-CA-C	5.91	117.39	111.07
1	Ea	95	ALA	CA-C-N	-5.91	113.86	119.76
1	Ea	95	ALA	C-N-CA	-5.91	113.86	119.76
1	Dg	30	ALA	N-CA-C	5.91	117.39	111.07
2	Xh	828	VAL	N-CA-C	-5.91	99.24	107.80
1	Bi	37	GLY	N-CA-C	5.91	119.71	110.91
1	Dq	30	ALA	N-CA-C	5.91	117.39	111.07
1	Dv	30	ALA	N-CA-C	5.91	117.39	111.07
1	AP	67	ALA	N-CA-C	5.91	117.52	111.14
2	XX	728	PRO	N-CA-C	-5.91	105.32	113.53
1	CA	82	ALA	N-CA-C	5.90	118.67	111.82
1	FI	67	ALA	N-CA-C	5.90	117.80	111.36
1	EX	67	ALA	N-CA-C	5.90	117.39	111.07
1	E1	95	ALA	CA-C-N	-5.90	113.86	119.76
1	E1	95	ALA	C-N-CA	-5.90	113.86	119.76
1	F5	67	ALA	N-CA-C	5.90	117.79	111.36
1	Ft	67	ALA	N-CA-C	5.90	117.79	111.36
2	Xt	728	PRO	N-CA-C	-5.90	105.33	113.53
1	Ez	95	ALA	CA-C-N	-5.90	113.86	119.76
1	Ez	95	ALA	C-N-CA	-5.90	113.86	119.76
1	EE	95	ALA	CA-C-N	-5.90	113.86	119.76
1	EE	95	ALA	C-N-CA	-5.90	113.86	119.76
1	EJ	95	ALA	CA-C-N	-5.90	113.86	119.76
1	EJ	95	ALA	C-N-CA	-5.90	113.86	119.76
1	HU	30	ALA	N-CA-C	5.90	117.72	111.28
1	Cg	82	ALA	N-CA-C	5.90	118.67	111.82
1	Fj	67	ALA	N-CA-C	5.90	117.79	111.36
1	Cq	82	ALA	N-CA-C	5.90	118.66	111.82
1	Hf	82	ALA	N-CA-C	5.90	119.74	112.54
1	Cl	82	ALA	N-CA-C	5.90	118.66	111.82
1	E6	95	ALA	CA-C-N	-5.90	113.86	119.76
1	E6	95	ALA	C-N-CA	-5.90	113.86	119.76
2	Xf	850	GLY	N-CA-C	-5.90	106.35	111.95
1	CF	82	ALA	N-CA-C	5.90	118.66	111.82
1	HJ	82	ALA	N-CA-C	5.90	119.73	112.54
1	HN	37	GLY	N-CA-C	5.90	120.35	110.56
1	Hu	82	ALA	N-CA-C	5.90	119.73	112.54
1	Hb	30	ALA	N-CA-C	5.90	117.71	111.28
1	H5	37	GLY	N-CA-C	5.89	120.34	110.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B9	37	GLY	N-CA-C	5.89	119.69	110.91
1	HD	37	GLY	N-CA-C	5.89	120.34	110.56
1	Ek	95	ALA	CA-C-N	-5.89	113.87	119.76
1	Ek	95	ALA	C-N-CA	-5.89	113.87	119.76
1	Hy	37	GLY	N-CA-C	5.89	120.34	110.56
2	XQ	828	VAL	N-CA-C	-5.89	99.25	107.80
1	Hz	82	ALA	N-CA-C	5.89	119.73	112.54
1	BM	37	GLY	N-CA-C	5.89	119.69	110.91
1	BC	37	GLY	N-CA-C	5.89	119.69	110.91
1	HI	37	GLY	N-CA-C	5.89	120.34	110.56
1	Aq	67	ALA	N-CA-C	5.89	117.50	111.14
1	BA	68	CYS	N-CA-C	5.89	120.08	113.01
1	Fy	67	ALA	N-CA-C	5.89	117.78	111.36
1	C2	82	ALA	N-CA-C	5.88	118.64	111.82
1	B7	68	CYS	N-CA-C	5.88	120.07	113.01
1	Bg	68	CYS	N-CA-C	5.88	120.07	113.01
1	Ef	95	ALA	CA-C-N	-5.88	113.88	119.76
1	Ef	95	ALA	C-N-CA	-5.88	113.88	119.76
1	Hj	37	GLY	N-CA-C	5.88	120.33	110.56
1	CK	82	ALA	N-CA-C	5.88	118.64	111.82
1	Ho	37	GLY	N-CA-C	5.88	120.33	110.56
2	Xm	828	VAL	N-CA-C	-5.88	99.27	107.80
1	H0	37	GLY	N-CA-C	5.88	120.32	110.56
1	Ha	82	ALA	N-CA-C	5.88	119.72	112.54
1	FB	67	ALA	N-CA-C	5.88	117.49	111.14
1	HF	40	PHE	N-CA-C	5.88	118.64	111.82
1	HE	82	ALA	N-CA-C	5.88	119.72	112.54
1	GL	94	LYS	N-CA-C	5.88	117.77	111.36
1	BR	37	GLY	N-CA-C	5.88	119.67	110.91
1	BU	68	CYS	N-CA-C	5.88	120.06	113.01
1	H1	82	ALA	N-CA-C	5.88	119.71	112.54
1	F3	67	ALA	N-CA-C	5.88	117.49	111.14
1	Cb	82	ALA	N-CA-C	5.88	118.64	111.82
1	DF	30	ALA	N-CA-C	5.88	117.36	111.07
1	CU	82	ALA	N-CA-C	5.88	118.64	111.82
1	H6	82	ALA	N-CA-C	5.88	119.71	112.54
1	F0	67	ALA	N-CA-C	5.88	117.77	111.36
1	Fo	67	ALA	N-CA-C	5.88	117.77	111.36
1	FS	67	ALA	N-CA-C	5.88	117.77	111.36
1	Hk	82	ALA	N-CA-C	5.88	119.71	112.54
1	He	37	GLY	N-CA-C	5.88	120.31	110.56
1	Ht	37	GLY	N-CA-C	5.88	120.31	110.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Cv	82	ALA	N-CA-C	5.88	118.64	111.82
1	HX	37	GLY	N-CA-C	5.88	120.31	110.56
1	Ee	67	ALA	N-CA-C	5.87	117.36	111.07
1	Fc	67	ALA	N-CA-C	5.87	117.48	111.14
1	Ej	67	ALA	N-CA-C	5.87	117.36	111.07
1	Fh	67	ALA	N-CA-C	5.87	117.48	111.14
1	Bl	68	CYS	N-CA-C	5.87	120.06	113.01
1	BP	68	CYS	N-CA-C	5.87	120.06	113.01
1	EO	95	ALA	CA-C-N	-5.87	113.89	119.76
1	EO	95	ALA	C-N-CA	-5.87	113.89	119.76
1	Hq	30	ALA	N-CA-C	5.87	117.68	111.28
1	Et	67	ALA	N-CA-C	5.87	117.35	111.07
1	DU	30	ALA	N-CA-C	5.87	117.35	111.07
1	B2	68	CYS	N-CA-C	5.87	120.05	113.01
1	BK	68	CYS	N-CA-C	5.87	120.05	113.01
1	Fr	67	ALA	N-CA-C	5.87	117.47	111.14
1	Fw	67	ALA	N-CA-C	5.86	117.47	111.14
1	Hp	82	ALA	N-CA-C	5.86	119.69	112.54
1	ED	67	ALA	N-CA-C	5.86	117.34	111.07
1	HS	37	GLY	N-CA-C	5.86	120.29	110.56
1	HO	82	ALA	N-CA-C	5.86	119.69	112.54
3	P3	30	LYS	CA-C-N	-5.86	113.73	119.76
3	P3	30	LYS	C-N-CA	-5.86	113.73	119.76
1	Hb	40	PHE	N-CA-C	5.86	118.61	111.82
1	Eo	67	ALA	N-CA-C	5.86	117.34	111.07
3	PL	30	LYS	CA-C-N	-5.86	113.73	119.76
3	PL	30	LYS	C-N-CA	-5.86	113.73	119.76
1	FV	67	ALA	N-CA-C	5.86	117.47	111.14
1	E5	67	ALA	N-CA-C	5.86	117.33	111.07
1	Gh	94	LYS	N-CA-C	5.86	117.74	111.36
1	Ey	67	ALA	N-CA-C	5.86	117.34	111.07
2	Xv	803	ASN	N-CA-C	5.85	118.93	109.86
3	Pw	30	LYS	CA-C-N	-5.85	113.73	119.76
3	Pw	30	LYS	C-N-CA	-5.85	113.73	119.76
1	Bq	68	CYS	N-CA-C	5.85	120.03	113.01
1	Bv	68	CYS	N-CA-C	5.85	120.03	113.01
1	FD	67	ALA	N-CA-C	5.85	117.74	111.36
1	Hq	40	PHE	N-CA-C	5.85	118.61	111.82
1	Bb	68	CYS	N-CA-C	5.85	120.03	113.01
1	H7	40	PHE	N-CA-C	5.85	118.60	111.82
1	FL	67	ALA	N-CA-C	5.85	117.45	111.14
2	X2	803	ASN	N-CA-C	5.84	118.92	109.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Hl	40	PHE	N-CA-C	5.84	118.60	111.82
1	Bt	94	LYS	N-CA-C	5.84	117.73	111.36
1	HL	94	LYS	N-CA-C	5.84	117.73	111.36
1	BF	68	CYS	N-CA-C	5.84	120.02	113.01
1	FG	67	ALA	N-CA-C	5.84	117.45	111.14
2	X7	803	ASN	N-CA-C	5.84	118.91	109.86
1	HU	40	PHE	N-CA-C	5.83	118.59	111.82
3	PG	30	LYS	CA-C-N	-5.83	113.75	119.76
3	PG	30	LYS	C-N-CA	-5.83	113.75	119.76
1	G3	94	LYS	N-CA-C	5.83	117.72	111.36
1	G8	94	LYS	N-CA-C	5.83	117.72	111.36
2	XK	803	ASN	N-CA-C	5.83	118.90	109.86
1	EJ	67	ALA	N-CA-C	5.83	118.39	111.33
1	HP	40	PHE	N-CA-C	5.83	118.58	111.82
1	GQ	94	LYS	N-CA-C	5.83	117.72	111.36
1	H8	94	LYS	N-CA-C	5.83	117.72	111.36
1	HQ	94	LYS	N-CA-C	5.83	117.72	111.36
1	Hm	94	LYS	N-CA-C	5.83	117.71	111.36
2	Xp	827	VAL	N-CA-C	5.83	116.25	107.80
2	XF	803	ASN	N-CA-C	5.83	118.89	109.86
1	EI	67	ALA	N-CA-C	5.83	117.31	111.07
1	E7	37	GLY	N-CA-C	5.83	121.63	111.14
1	E6	67	ALA	N-CA-C	5.83	118.38	111.33
2	XA	803	ASN	N-CA-C	5.83	118.89	109.86
1	GB	94	LYS	N-CA-C	5.83	117.71	111.36
1	HK	40	PHE	N-CA-C	5.83	118.58	111.82
1	EP	37	GLY	N-CA-C	5.83	121.63	111.14
1	HW	76	VAL	N-CA-C	-5.83	106.14	111.67
1	E0	67	ALA	N-CA-C	5.82	117.30	111.07
1	Ez	67	ALA	N-CA-C	5.82	118.38	111.33
1	HH	76	VAL	N-CA-C	-5.82	106.14	111.67
1	ES	67	ALA	N-CA-C	5.82	117.30	111.07
3	Pc	30	LYS	CA-C-N	-5.82	113.76	119.76
3	Pc	30	LYS	C-N-CA	-5.82	113.76	119.76
3	Ph	30	LYS	CA-C-N	-5.82	113.76	119.76
3	Ph	30	LYS	C-N-CA	-5.82	113.76	119.76
1	El	37	GLY	N-CA-C	5.82	121.62	111.14
1	ET	67	ALA	N-CA-C	5.82	118.37	111.33
3	PV	30	LYS	CA-C-N	-5.82	113.76	119.76
3	PV	30	LYS	C-N-CA	-5.82	113.76	119.76
1	H2	40	PHE	N-CA-C	5.82	118.57	111.82
1	Hh	94	LYS	N-CA-C	5.82	117.70	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EO	67	ALA	N-CA-C	5.82	118.37	111.33
1	Hg	40	PHE	N-CA-C	5.82	118.57	111.82
1	HA	40	PHE	N-CA-C	5.82	118.56	111.82
1	HE	76	VAL	N-CA-C	-5.82	106.14	111.67
1	E1	67	ALA	N-CA-C	5.81	118.37	111.33
1	HB	94	LYS	N-CA-C	5.81	117.70	111.36
2	Xb	803	ASN	N-CA-C	5.81	118.87	109.86
1	Gm	94	LYS	N-CA-C	5.81	117.70	111.36
1	EA	37	GLY	N-CA-C	5.81	121.60	111.14
2	XP	803	ASN	N-CA-C	5.81	118.87	109.86
1	H3	94	LYS	N-CA-C	5.81	117.69	111.36
1	Fp	54	THR	N-CA-C	5.81	118.08	111.11
1	FE	54	THR	N-CA-C	5.81	118.08	111.11
1	GG	94	LYS	N-CA-C	5.81	117.69	111.36
1	Eg	37	GLY	N-CA-C	5.81	121.59	111.14
2	Xg	803	ASN	N-CA-C	5.81	118.86	109.86
1	Gw	94	LYS	N-CA-C	5.81	117.69	111.36
1	EN	67	ALA	N-CA-C	5.81	117.28	111.07
2	Xl	803	ASN	N-CA-C	5.80	118.86	109.86
2	Xq	803	ASN	N-CA-C	5.80	118.86	109.86
1	Ev	37	GLY	N-CA-C	5.80	121.59	111.14
1	Eu	67	ALA	N-CA-C	5.80	118.35	111.33
1	EU	37	GLY	N-CA-C	5.80	121.59	111.14
2	XW	713	ILE	N-CA-C	-5.80	102.09	109.58
1	Gc	94	LYS	N-CA-C	5.80	117.69	111.36
1	BC	75	LEU	CA-CB-CG	5.80	136.61	116.30
2	XU	803	ASN	N-CA-C	5.80	118.85	109.86
1	Bn	75	LEU	CA-CB-CG	5.80	136.61	116.30
1	Hp	76	VAL	N-CA-C	-5.80	106.16	111.67
3	Pr	30	LYS	CA-C-N	-5.80	113.78	119.76
3	Pr	30	LYS	C-N-CA	-5.80	113.78	119.76
1	Bk	48	VAL	CB-CA-C	5.80	119.21	110.63
1	Hv	40	PHE	N-CA-C	5.80	118.55	111.82
1	CP	17	LEU	CA-C-N	-5.80	116.59	120.24
1	CP	17	LEU	C-N-CA	-5.80	116.59	120.24
1	BW	75	LEU	CA-CB-CG	5.80	136.60	116.30
1	Eq	37	GLY	N-CA-C	5.80	121.58	111.14
2	XO	827	VAL	N-CA-C	5.80	116.21	107.80
1	Hf	76	VAL	N-CA-C	-5.80	106.16	111.67
1	Ek	67	ALA	N-CA-C	5.80	118.34	111.33
1	BN	94	LYS	N-CA-C	5.80	117.68	111.36
1	E2	37	GLY	N-CA-C	5.79	121.57	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bj	94	LYS	N-CA-C	5.79	117.68	111.36
1	EK	37	GLY	N-CA-C	5.79	121.57	111.14
1	Be	94	LYS	N-CA-C	5.79	117.68	111.36
1	B9	75	LEU	CA-CB-CG	5.79	136.57	116.30
1	Eb	37	GLY	N-CA-C	5.79	121.56	111.14
1	Ea	67	ALA	N-CA-C	5.79	118.34	111.33
1	Cg	17	LEU	CA-C-N	-5.79	116.59	120.24
1	Cg	17	LEU	C-N-CA	-5.79	116.59	120.24
1	Bo	94	LYS	N-CA-C	5.79	117.67	111.36
1	Hr	94	LYS	N-CA-C	5.79	117.67	111.36
1	BH	75	LEU	CA-CB-CG	5.79	136.57	116.30
1	BR	75	LEU	CA-CB-CG	5.79	136.57	116.30
1	B6	48	VAL	CB-CA-C	5.79	119.20	110.63
1	Bd	75	LEU	CA-CB-CG	5.79	136.56	116.30
1	Bi	75	LEU	CA-CB-CG	5.79	136.56	116.30
1	Hk	76	VAL	N-CA-C	-5.79	106.17	111.67
2	Xa	827	VAL	N-CA-C	5.79	116.19	107.80
1	Hc	94	LYS	N-CA-C	5.79	117.67	111.36
2	Xf	827	VAL	N-CA-C	5.79	116.19	107.80
1	Fi	95	ALA	CA-C-N	-5.79	113.97	119.76
1	Fi	95	ALA	C-N-CA	-5.79	113.97	119.76
1	BM	75	LEU	CA-CB-CG	5.79	136.56	116.30
2	XT	827	VAL	N-CA-C	5.79	116.19	107.80
1	Fa	54	THR	N-CA-C	5.79	118.05	111.11
1	EF	37	GLY	N-CA-C	5.79	121.56	111.14
1	HG	94	LYS	N-CA-C	5.79	117.67	111.36
2	XH	713	ILE	N-CA-C	-5.79	102.11	109.58
1	B4	75	LEU	CA-CB-CG	5.79	136.55	116.30
2	Xd	713	ILE	N-CA-C	-5.79	102.12	109.58
1	Ef	67	ALA	N-CA-C	5.79	118.33	111.33
1	Bw	18	VAL	CA-C-N	-5.79	112.63	119.05
1	Bw	18	VAL	C-N-CA	-5.79	112.63	119.05
1	DQ	75	LEU	CA-CB-CG	5.79	136.55	116.30
1	Hx	76	VAL	N-CA-C	-5.79	106.17	111.67
1	Hd	76	VAL	N-CA-C	-5.78	106.17	111.67
1	BI	94	LYS	N-CA-C	5.78	117.66	111.36
1	Bx	75	LEU	CA-CB-CG	5.78	136.54	116.30
1	BO	48	VAL	CB-CA-C	5.78	119.19	110.63
1	HV	94	LYS	N-CA-C	5.78	117.66	111.36
1	Bz	48	VAL	CB-CA-C	5.78	119.19	110.63
1	DB	75	LEU	CA-CB-CG	5.78	136.53	116.30
2	XE	827	VAL	N-CA-C	5.78	116.18	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D3	75	LEU	CA-CB-CG	5.78	136.52	116.30
1	D8	75	LEU	CA-CB-CG	5.78	136.52	116.30
1	Dh	75	LEU	CA-CB-CG	5.78	136.52	116.30
1	Bs	75	LEU	CA-CB-CG	5.78	136.52	116.30
1	DL	75	LEU	CA-CB-CG	5.78	136.52	116.30
2	X1	827	VAL	N-CA-C	5.78	116.17	107.80
1	Dr	75	LEU	CA-CB-CG	5.78	136.52	116.30
1	Dw	75	LEU	CA-CB-CG	5.78	136.52	116.30
1	BX	94	LYS	N-CA-C	5.78	117.66	111.36
1	Dm	75	LEU	CA-CB-CG	5.77	136.50	116.30
1	DV	75	LEU	CA-CB-CG	5.77	136.50	116.30
1	Ba	48	VAL	CB-CA-C	5.77	119.17	110.63
1	BT	48	VAL	CB-CA-C	5.77	119.17	110.63
1	Br	18	VAL	CA-C-N	-5.77	112.65	119.05
1	Br	18	VAL	C-N-CA	-5.77	112.65	119.05
1	B5	94	LYS	N-CA-C	5.77	117.65	111.36
2	X6	827	VAL	N-CA-C	5.77	116.16	107.80
1	B8	18	VAL	CA-C-N	-5.77	112.65	119.05
1	B8	18	VAL	C-N-CA	-5.77	112.65	119.05
1	Dc	75	LEU	CA-CB-CG	5.77	136.49	116.30
1	Ff	54	THR	N-CA-C	5.77	118.03	111.11
1	Bm	18	VAL	CA-C-N	-5.77	112.65	119.05
1	Bm	18	VAL	C-N-CA	-5.77	112.65	119.05
1	Bp	48	VAL	CB-CA-C	5.77	119.17	110.63
2	Xs	713	ILE	N-CA-C	-5.77	102.14	109.58
1	BD	94	LYS	N-CA-C	5.77	117.65	111.36
1	DG	75	LEU	CA-CB-CG	5.77	136.49	116.30
1	BQ	18	VAL	CA-C-N	-5.77	112.65	119.05
1	BQ	18	VAL	C-N-CA	-5.77	112.65	119.05
1	GV	94	LYS	N-CA-C	5.77	117.65	111.36
2	Xi	713	ILE	N-CA-C	-5.77	102.14	109.58
2	Xk	827	VAL	N-CA-C	5.77	116.16	107.80
2	XJ	827	VAL	N-CA-C	5.77	116.16	107.80
1	CU	17	LEU	CA-C-N	-5.77	116.61	120.24
1	CU	17	LEU	C-N-CA	-5.77	116.61	120.24
1	Ha	76	VAL	N-CA-C	-5.76	106.19	111.67
1	Ep	67	ALA	N-CA-C	5.76	118.31	111.33
1	FR	95	ALA	CA-C-N	-5.76	114.00	119.76
1	FR	95	ALA	C-N-CA	-5.76	114.00	119.76
1	HT	76	VAL	N-CA-C	-5.76	106.19	111.67
1	B0	94	LYS	N-CA-C	5.76	117.64	111.36
1	BS	94	LYS	N-CA-C	5.76	117.64	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Gr	94	LYS	N-CA-C	5.76	117.64	111.36
1	BB	18	VAL	CA-C-N	-5.76	112.66	119.05
1	BB	18	VAL	C-N-CA	-5.76	112.66	119.05
1	Hu	76	VAL	N-CA-C	-5.76	106.20	111.67
1	HO	76	VAL	N-CA-C	-5.76	106.20	111.67
2	X4	713	ILE	N-CA-C	-5.76	102.15	109.58
1	Hw	94	LYS	N-CA-C	5.76	117.64	111.36
1	FC	95	ALA	CA-C-N	-5.76	114.00	119.76
1	FC	95	ALA	C-N-CA	-5.76	114.00	119.76
1	HC	76	VAL	N-CA-C	-5.76	106.20	111.67
1	FJ	54	THR	N-CA-C	5.76	118.02	111.11
1	GL	77	ALA	N-CA-C	5.76	118.03	108.99
2	XM	713	ILE	N-CA-C	-5.76	102.15	109.58
1	Fd	95	ALA	CA-C-N	-5.76	114.00	119.76
1	Fd	95	ALA	C-N-CA	-5.76	114.00	119.76
1	EE	67	ALA	N-CA-C	5.75	118.29	111.33
1	BL	18	VAL	CA-C-N	-5.75	112.66	119.05
1	BL	18	VAL	C-N-CA	-5.75	112.66	119.05
1	GV	77	ALA	N-CA-C	5.75	118.03	108.99
1	B1	48	VAL	CB-CA-C	5.75	119.15	110.63
2	Xu	827	VAL	N-CA-C	5.75	116.14	107.80
1	BJ	48	VAL	CB-CA-C	5.75	119.15	110.63
1	F1	54	THR	N-CA-C	5.75	118.01	111.11
1	Bf	48	VAL	CB-CA-C	5.75	119.14	110.63
1	By	94	LYS	N-CA-C	5.75	117.63	111.36
1	FH	95	ALA	CA-C-N	-5.75	114.01	119.76
1	FH	95	ALA	C-N-CA	-5.75	114.01	119.76
1	Hs	76	VAL	N-CA-C	-5.75	106.21	111.67
1	C2	17	LEU	CA-C-N	-5.75	116.62	120.24
1	C2	17	LEU	C-N-CA	-5.75	116.62	120.24
1	F4	95	ALA	CA-C-N	-5.75	114.01	119.76
1	F4	95	ALA	C-N-CA	-5.75	114.01	119.76
1	CK	17	LEU	CA-C-N	-5.75	116.62	120.24
1	CK	17	LEU	C-N-CA	-5.75	116.62	120.24
1	FT	54	THR	N-CA-C	5.75	118.01	111.11
1	H6	76	VAL	N-CA-C	-5.75	106.21	111.67
1	H9	76	VAL	N-CA-C	-5.75	106.21	111.67
1	Hi	76	VAL	N-CA-C	-5.75	106.21	111.67
1	Gm	77	ALA	N-CA-C	5.75	118.01	108.99
1	B3	18	VAL	CA-C-N	-5.75	112.67	119.05
1	B3	18	VAL	C-N-CA	-5.75	112.67	119.05
1	Bc	18	VAL	CA-C-N	-5.74	112.67	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bc	18	VAL	C-N-CA	-5.74	112.67	119.05
1	Fk	7	ILE	CB-CA-C	-5.74	104.64	111.65
2	XC	713	ILE	N-CA-C	-5.74	102.17	109.58
1	BV	18	VAL	CA-C-N	-5.74	112.67	119.05
1	BV	18	VAL	C-N-CA	-5.74	112.67	119.05
1	H1	76	VAL	N-CA-C	-5.74	106.21	111.67
1	Bu	48	VAL	CB-CA-C	5.74	119.13	110.63
1	Hx	76	VAL	N-CA-C	-5.74	106.22	111.67
1	GG	77	ALA	N-CA-C	5.74	118.00	108.99
1	FV	82	ALA	N-CA-C	5.74	118.48	111.82
1	H4	76	VAL	N-CA-C	-5.74	106.22	111.67
1	C7	17	LEU	CA-C-N	-5.74	116.62	120.24
1	C7	17	LEU	C-N-CA	-5.74	116.62	120.24
2	X9	713	ILE	N-CA-C	-5.74	102.18	109.58
1	Eg	67	ALA	N-CA-C	5.74	117.53	111.28
1	Cq	17	LEU	CA-C-N	-5.74	116.62	120.24
1	Cq	17	LEU	C-N-CA	-5.74	116.62	120.24
1	Gr	77	ALA	N-CA-C	5.74	118.00	108.99
1	Fu	54	THR	N-CA-C	5.74	118.00	111.11
1	HR	76	VAL	N-CA-C	-5.74	106.22	111.67
2	XR	713	ILE	N-CA-C	-5.74	102.18	109.58
1	Fs	95	ALA	CA-C-N	-5.74	114.02	119.76
1	Fs	95	ALA	C-N-CA	-5.74	114.02	119.76
1	Cb	17	LEU	CA-C-N	-5.74	116.63	120.24
1	Cb	17	LEU	C-N-CA	-5.74	116.63	120.24
1	Gh	77	ALA	N-CA-C	5.74	117.99	108.99
1	Fw	82	ALA	N-CA-C	5.73	118.47	111.82
2	Xz	719	LEU	N-CA-C	5.73	118.10	110.53
1	FO	54	THR	N-CA-C	5.73	117.99	111.11
1	Fn	95	ALA	CA-C-N	-5.73	114.03	119.76
1	Fn	95	ALA	C-N-CA	-5.73	114.03	119.76
1	BE	48	VAL	CB-CA-C	5.73	119.11	110.63
1	FW	95	ALA	CA-C-N	-5.73	114.03	119.76
1	FW	95	ALA	C-N-CA	-5.73	114.03	119.76
1	Gc	77	ALA	N-CA-C	5.73	117.99	108.99
1	Gw	77	ALA	N-CA-C	5.73	117.99	108.99
1	G3	77	ALA	N-CA-C	5.73	117.98	108.99
1	G8	77	ALA	N-CA-C	5.73	117.98	108.99
1	F9	95	ALA	CA-C-N	-5.73	114.03	119.76
1	F9	95	ALA	C-N-CA	-5.73	114.03	119.76
2	Xx	713	ILE	N-CA-C	-5.73	102.19	109.58
1	Hn	76	VAL	N-CA-C	-5.72	106.23	111.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Fh	82	ALA	N-CA-C	5.72	118.46	111.82
1	Cv	17	LEU	CA-C-N	-5.72	116.63	120.24
1	Cv	17	LEU	C-N-CA	-5.72	116.63	120.24
1	FE	7	ILE	CB-CA-C	-5.72	104.67	111.65
1	BG	18	VAL	CA-C-N	-5.72	112.70	119.05
1	BG	18	VAL	C-N-CA	-5.72	112.70	119.05
1	EU	67	ALA	N-CA-C	5.72	117.52	111.28
2	Xz	827	VAL	N-CA-C	5.72	116.09	107.80
1	El	67	ALA	N-CA-C	5.72	117.51	111.28
2	Xn	713	ILE	N-CA-C	-5.72	102.20	109.58
1	Fp	7	ILE	CB-CA-C	-5.72	104.67	111.65
1	FM	95	ALA	CA-C-N	-5.72	114.04	119.76
1	FM	95	ALA	C-N-CA	-5.72	114.04	119.76
1	Cl	17	LEU	CA-C-N	-5.72	116.64	120.24
1	Cl	17	LEU	C-N-CA	-5.72	116.64	120.24
1	EH	16	GLY	N-CA-C	5.72	118.69	112.29
1	AN	94	LYS	N-CA-C	5.72	117.59	111.36
1	GQ	77	ALA	N-CA-C	5.72	117.96	108.99
1	Fc	82	ALA	N-CA-C	5.71	118.45	111.82
1	En	16	GLY	N-CA-C	5.71	118.69	112.29
1	Fx	95	ALA	CA-C-N	-5.71	114.05	119.76
1	Fx	95	ALA	C-N-CA	-5.71	114.05	119.76
1	AX	94	LYS	N-CA-C	5.71	117.59	111.36
2	XV	780	ASP	N-CA-C	5.71	117.51	111.28
1	FO	7	ILE	CB-CA-C	-5.71	104.68	111.65
1	Fz	54	THR	N-CA-C	5.71	117.96	111.11
2	XG	780	ASP	N-CA-C	5.71	117.50	111.28
1	F6	7	ILE	CB-CA-C	-5.71	104.69	111.65
1	Eb	67	ALA	N-CA-C	5.71	117.50	111.28
1	Fr	82	ALA	N-CA-C	5.71	118.44	111.82
1	Ex	16	GLY	N-CA-C	5.71	118.68	112.29
1	Fz	7	ILE	CB-CA-C	-5.71	104.69	111.65
1	AI	94	LYS	N-CA-C	5.71	117.58	111.36
1	F6	54	THR	N-CA-C	5.70	117.95	111.11
1	Bh	18	VAL	CA-C-N	-5.70	112.72	119.05
1	Bh	18	VAL	C-N-CA	-5.70	112.72	119.05
1	CA	17	LEU	CA-C-N	-5.70	116.65	120.24
1	CA	17	LEU	C-N-CA	-5.70	116.65	120.24
1	EF	67	ALA	N-CA-C	5.70	117.50	111.28
1	HJ	76	VAL	N-CA-C	-5.70	106.25	111.67
1	E2	67	ALA	N-CA-C	5.70	117.50	111.28
1	F3	82	ALA	N-CA-C	5.70	118.43	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AF	77	ALA	N-CA-C	5.70	118.49	108.75
1	Fa	7	ILE	CB-CA-C	-5.70	104.70	111.65
1	Ff	7	ILE	CB-CA-C	-5.70	104.70	111.65
1	GB	77	ALA	N-CA-C	5.70	117.94	108.99
1	FJ	7	ILE	CB-CA-C	-5.70	104.70	111.65
1	BQ	20	ALA	N-CA-C	5.70	117.49	111.28
1	E7	67	ALA	N-CA-C	5.70	117.49	111.28
2	XQ	817	ARG	N-CA-C	5.70	117.49	111.28
1	H6	83	ARG	N-CA-C	-5.70	98.61	108.69
2	X8	817	ARG	N-CA-C	5.70	117.49	111.28
2	Xc	780	ASP	N-CA-C	5.70	117.49	111.28
2	Xr	780	ASP	N-CA-C	5.70	117.49	111.28
1	HO	83	ARG	N-CA-C	-5.70	98.61	108.69
1	EA	67	ALA	N-CA-C	5.69	117.49	111.28
1	Fu	7	ILE	CB-CA-C	-5.69	104.70	111.65
1	FT	7	ILE	CB-CA-C	-5.69	104.70	111.65
1	Fk	54	THR	N-CA-C	5.69	117.94	111.11
1	GD	30	ALA	N-CA-C	5.69	117.48	111.28
1	EC	16	GLY	N-CA-C	5.69	118.66	112.29
2	XO	719	LEU	N-CA-C	5.69	118.04	110.53
1	H1	83	ARG	N-CA-C	-5.69	98.62	108.69
1	Hk	83	ARG	N-CA-C	-5.69	98.62	108.69
1	E9	16	GLY	N-CA-C	5.69	118.66	112.29
1	ER	16	GLY	N-CA-C	5.69	118.66	112.29
1	A5	94	LYS	N-CA-C	5.69	117.56	111.36
1	Es	16	GLY	N-CA-C	5.69	118.66	112.29
1	F1	7	ILE	CB-CA-C	-5.68	104.72	111.65
2	X6	719	LEU	N-CA-C	5.68	118.03	110.53
1	Ev	67	ALA	N-CA-C	5.68	117.48	111.28
1	HJ	83	ARG	N-CA-C	-5.68	98.63	108.69
1	Hf	83	ARG	N-CA-C	-5.68	98.63	108.69
2	XB	817	ARG	N-CA-C	5.68	117.48	111.28
1	Bm	20	ALA	N-CA-C	5.68	117.47	111.28
1	HM	76	VAL	N-CA-C	-5.68	106.27	111.67
1	EP	67	ALA	N-CA-C	5.68	117.47	111.28
1	AU	77	ALA	N-CA-C	5.68	118.47	108.75
1	Ed	16	GLY	N-CA-C	5.68	118.65	112.29
1	EW	16	GLY	N-CA-C	5.68	118.65	112.29
2	Xk	719	LEU	N-CA-C	5.68	118.03	110.53
1	Ay	94	LYS	N-CA-C	5.68	117.55	111.36
1	BV	94	LYS	N-CA-C	5.68	117.55	111.36
1	Hz	83	ARG	N-CA-C	-5.68	98.64	108.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X3	780	ASP	N-CA-C	5.68	117.47	111.28
1	A0	94	LYS	N-CA-C	5.68	117.55	111.36
1	Fm	82	ALA	N-CA-C	5.68	118.41	111.82
2	XL	780	ASP	N-CA-C	5.68	117.47	111.28
2	Xf	719	LEU	N-CA-C	5.68	118.02	110.53
1	Eq	67	ALA	N-CA-C	5.68	117.47	111.28
2	Xm	817	ARG	N-CA-C	5.68	117.47	111.28
1	E4	16	GLY	N-CA-C	5.67	118.64	112.29
1	Ae	94	LYS	N-CA-C	5.67	117.55	111.36
1	Hp	83	ARG	N-CA-C	-5.67	98.64	108.69
1	AD	94	LYS	N-CA-C	5.67	117.55	111.36
1	EM	16	GLY	N-CA-C	5.67	118.64	112.29
1	B3	94	LYS	N-CA-C	5.67	117.54	111.36
1	HT	83	ARG	N-CA-C	-5.67	98.65	108.69
1	FG	82	ALA	N-CA-C	5.67	118.40	111.82
1	AM	83	ARG	N-CA-C	-5.67	99.77	109.24
2	XB	780	ASP	N-CA-C	5.67	117.46	111.28
1	F7	38	ARG	N-CA-C	-5.67	99.18	108.76
1	F8	82	ALA	N-CA-C	5.67	118.39	111.82
1	An	83	ARG	N-CA-C	-5.67	99.77	109.24
1	AH	83	ARG	N-CA-C	-5.67	99.77	109.24
1	Hu	83	ARG	N-CA-C	-5.67	98.66	108.69
1	Bw	94	LYS	N-CA-C	5.67	117.54	111.36
1	CF	17	LEU	CA-C-N	-5.67	116.67	120.24
1	CF	17	LEU	C-N-CA	-5.67	116.67	120.24
1	EK	67	ALA	N-CA-C	5.67	117.46	111.28
1	CO	30	ALA	N-CA-C	5.67	117.46	111.28
1	B8	20	ALA	N-CA-C	5.67	117.45	111.28
1	BG	20	ALA	N-CA-C	5.67	117.45	111.28
1	G5	30	ALA	N-CA-C	5.66	117.45	111.28
1	Ab	77	ALA	N-CA-C	5.66	118.43	108.75
1	Ha	83	ARG	N-CA-C	-5.66	98.67	108.69
1	Cf	31	ALA	N-CA-C	5.66	116.56	108.74
2	Xw	817	ARG	N-CA-C	5.66	117.45	111.28
1	BB	94	LYS	N-CA-C	5.66	117.53	111.36
1	FK	38	ARG	N-CA-C	-5.66	99.19	108.76
1	AW	83	ARG	N-CA-C	-5.66	99.78	109.24
2	XV	817	ARG	N-CA-C	5.66	117.45	111.28
2	XL	817	ARG	N-CA-C	5.66	117.45	111.28
1	BQ	94	LYS	N-CA-C	5.66	117.53	111.36
1	A4	83	ARG	N-CA-C	-5.66	99.79	109.24
1	B8	94	LYS	N-CA-C	5.66	117.53	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bc	94	LYS	N-CA-C	5.66	117.53	111.36
1	Bh	20	ALA	N-CA-C	5.66	117.45	111.28
1	Bh	94	LYS	N-CA-C	5.66	117.53	111.36
2	Xh	780	ASP	N-CA-C	5.66	117.45	111.28
1	Fl	38	ARG	N-CA-C	-5.66	99.19	108.76
2	Xu	719	LEU	N-CA-C	5.66	118.00	110.53
1	FA	38	ARG	N-CA-C	-5.66	99.19	108.76
1	FB	82	ALA	N-CA-C	5.66	118.39	111.82
1	FP	38	ARG	N-CA-C	-5.66	99.19	108.76
1	AR	83	ARG	N-CA-C	-5.66	99.79	109.24
2	XT	719	LEU	N-CA-C	5.66	118.00	110.53
2	X1	719	LEU	N-CA-C	5.66	118.00	110.53
2	X3	817	ARG	N-CA-C	5.66	117.45	111.28
1	As	83	ARG	N-CA-C	-5.66	99.79	109.24
1	Bw	20	ALA	N-CA-C	5.66	117.45	111.28
1	Ax	83	ARG	N-CA-C	-5.66	99.79	109.24
2	XJ	719	LEU	N-CA-C	5.66	118.00	110.53
1	FL	82	ALA	N-CA-C	5.66	118.38	111.82
1	GS	30	ALA	N-CA-C	5.66	117.45	111.28
1	Ad	83	ARG	N-CA-C	-5.66	99.79	109.24
2	Xc	817	ARG	N-CA-C	5.66	117.45	111.28
1	G0	30	ALA	N-CA-C	5.66	117.44	111.28
1	Aj	94	LYS	N-CA-C	5.66	117.52	111.36
1	Br	20	ALA	N-CA-C	5.66	117.44	111.28
1	GE	77	ALA	N-CA-C	5.66	118.42	108.75
1	FU	38	ARG	N-CA-C	-5.66	99.20	108.76
1	CJ	30	ALA	N-CA-C	5.65	117.44	111.28
1	A9	83	ARG	N-CA-C	-5.65	99.80	109.24
1	Aq	77	ALA	N-CA-C	5.65	118.42	108.75
2	Xp	719	LEU	N-CA-C	5.65	117.99	110.53
1	Br	94	LYS	N-CA-C	5.65	117.52	111.36
2	XD	815	SER	N-CA-C	5.65	117.24	111.14
1	HE	77	ALA	N-CA-C	5.65	117.86	108.99
1	BG	94	LYS	N-CA-C	5.65	117.52	111.36
1	EG	37	GLY	N-CA-C	5.65	121.31	111.14
1	HJ	77	ALA	N-CA-C	5.65	117.86	108.99
1	BL	94	LYS	N-CA-C	5.65	117.52	111.36
1	H1	77	ALA	N-CA-C	5.65	117.86	108.99
2	X8	780	ASP	N-CA-C	5.65	117.44	111.28
1	Hf	77	ALA	N-CA-C	5.65	117.86	108.99
1	At	94	LYS	N-CA-C	5.65	117.52	111.36
1	BB	20	ALA	N-CA-C	5.65	117.44	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AS	94	LYS	N-CA-C	5.65	117.52	111.36
1	Ck	30	ALA	N-CA-C	5.65	117.44	111.28
2	Xw	780	ASP	N-CA-C	5.65	117.44	111.28
1	FF	38	ARG	N-CA-C	-5.65	99.21	108.76
1	AK	77	ALA	N-CA-C	5.65	118.41	108.75
2	Xr	817	ARG	N-CA-C	5.65	117.44	111.28
1	C6	30	ALA	N-CA-C	5.65	117.44	111.28
1	Bm	94	LYS	N-CA-C	5.65	117.52	111.36
1	AC	83	ARG	N-CA-C	-5.65	99.81	109.24
1	HE	83	ARG	N-CA-C	-5.65	98.70	108.69
1	Gy	30	ALA	N-CA-C	5.65	117.43	111.28
1	Bc	20	ALA	N-CA-C	5.64	117.43	111.28
1	GN	30	ALA	N-CA-C	5.64	117.43	111.28
1	BV	20	ALA	N-CA-C	5.64	117.43	111.28
1	G1	77	ALA	N-CA-C	5.64	118.40	108.75
1	F2	38	ARG	N-CA-C	-5.64	99.23	108.76
1	B3	20	ALA	N-CA-C	5.64	117.43	111.28
1	Fb	38	ARG	N-CA-C	-5.64	99.23	108.76
1	Ga	77	ALA	N-CA-C	5.64	118.40	108.75
1	Bk	38	ARG	N-CA-C	-5.64	98.70	108.69
1	Gu	77	ALA	N-CA-C	5.64	118.40	108.75
1	HT	77	ALA	N-CA-C	5.64	117.85	108.99
1	A2	77	ALA	N-CA-C	5.64	118.39	108.75
2	X0	815	SER	N-CA-C	5.64	117.23	111.14
1	Ca	31	ALA	N-CA-C	5.64	116.52	108.74
1	Ag	77	ALA	N-CA-C	5.64	118.39	108.75
1	Fg	38	ARG	N-CA-C	-5.64	99.23	108.76
1	Ai	83	ARG	N-CA-C	-5.64	99.82	109.24
1	Go	30	ALA	N-CA-C	5.64	117.43	111.28
1	Gz	77	ALA	N-CA-C	5.64	118.39	108.75
1	Hu	77	ALA	N-CA-C	5.64	117.84	108.99
1	Ck	31	ALA	N-CA-C	5.64	116.52	108.74
1	Cu	30	ALA	N-CA-C	5.64	117.43	111.28
1	AP	77	ALA	N-CA-C	5.64	118.39	108.75
1	A7	77	ALA	N-CA-C	5.64	118.39	108.75
1	GJ	77	ALA	N-CA-C	5.64	118.39	108.75
1	BL	20	ALA	N-CA-C	5.64	117.42	111.28
1	BO	38	ARG	N-CA-C	-5.64	98.72	108.69
1	FQ	82	ALA	N-CA-C	5.64	118.36	111.82
1	Ha	77	ALA	N-CA-C	5.63	117.84	108.99
2	Xa	719	LEU	N-CA-C	5.63	117.97	110.53
1	Ge	30	ALA	N-CA-C	5.63	117.42	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ec	37	GLY	N-CA-C	5.63	121.28	111.14
1	Gj	30	ALA	N-CA-C	5.63	117.42	111.28
1	Ei	16	GLY	N-CA-C	5.63	118.60	112.29
1	Ao	94	LYS	N-CA-C	5.63	117.50	111.36
1	Bp	38	ARG	N-CA-C	-5.63	98.72	108.69
1	Cz	30	ALA	N-CA-C	5.63	117.42	111.28
1	GX	30	ALA	N-CA-C	5.63	117.42	111.28
1	EB	37	GLY	N-CA-C	5.63	121.28	111.14
1	Hp	77	ALA	N-CA-C	5.63	117.83	108.99
1	EV	37	GLY	N-CA-C	5.63	121.28	111.14
2	XG	817	ARG	N-CA-C	5.63	117.42	111.28
1	Em	37	GLY	N-CA-C	5.63	121.27	111.14
1	Fq	38	ARG	N-CA-C	-5.63	99.25	108.76
1	Cp	31	ALA	N-CA-C	5.63	116.51	108.74
1	C1	30	ALA	N-CA-C	5.63	117.42	111.28
1	C1	31	ALA	N-CA-C	5.63	116.51	108.74
1	G6	77	ALA	N-CA-C	5.63	118.37	108.75
1	GO	67	ALA	N-CA-C	5.63	117.86	111.11
1	B6	38	ARG	N-CA-C	-5.63	98.73	108.69
1	Gp	77	ALA	N-CA-C	5.63	118.37	108.75
1	CE	31	ALA	N-CA-C	5.63	116.50	108.74
2	XS	815	SER	N-CA-C	5.63	117.22	111.14
2	XQ	780	ASP	N-CA-C	5.63	117.41	111.28
1	GT	77	ALA	N-CA-C	5.63	118.37	108.75
1	H6	77	ALA	N-CA-C	5.63	117.83	108.99
1	Hx	77	ALA	N-CA-C	5.63	117.82	108.99
1	E8	37	GLY	N-CA-C	5.62	121.27	111.14
1	Al	77	ALA	N-CA-C	5.62	118.37	108.75
1	Er	37	GLY	N-CA-C	5.62	121.27	111.14
1	AA	77	ALA	N-CA-C	5.62	118.37	108.75
1	CH	20	ALA	N-CA-C	5.62	117.41	111.28
1	EQ	37	GLY	N-CA-C	5.62	121.27	111.14
2	Xm	780	ASP	N-CA-C	5.62	117.41	111.28
1	C6	31	ALA	N-CA-C	5.62	116.50	108.74
1	Cs	20	ALA	N-CA-C	5.62	117.41	111.28
1	Cu	31	ALA	N-CA-C	5.62	116.50	108.74
1	Bz	38	ARG	N-CA-C	-5.62	98.74	108.69
1	GI	30	ALA	N-CA-C	5.62	117.41	111.28
1	CO	31	ALA	N-CA-C	5.62	116.50	108.74
1	E3	37	GLY	N-CA-C	5.62	121.26	111.14
1	Gf	67	ALA	N-CA-C	5.62	117.86	111.11
2	Xh	817	ARG	N-CA-C	5.62	117.41	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Av	77	ALA	N-CA-C	5.62	118.36	108.75
1	Bu	38	ARG	N-CA-C	-5.62	98.74	108.69
1	CE	30	ALA	N-CA-C	5.62	117.41	111.28
1	Gf	77	ALA	N-CA-C	5.62	118.36	108.75
2	Xo	815	SER	N-CA-C	5.62	117.21	111.14
1	Cx	20	ALA	N-CA-C	5.62	117.41	111.28
1	D6	16	GLY	CA-C-O	-5.62	118.57	122.22
1	Bf	38	ARG	N-CA-C	-5.62	98.75	108.69
1	Fv	38	ARG	N-CA-C	-5.62	99.27	108.76
1	BE	38	ARG	N-CA-C	-5.62	98.74	108.69
1	Gt	30	ALA	N-CA-C	5.62	117.40	111.28
1	B1	38	ARG	N-CA-C	-5.62	98.75	108.69
1	D1	16	GLY	CA-C-O	-5.62	118.57	122.22
1	Ci	20	ALA	N-CA-C	5.62	117.40	111.28
1	Gp	67	ALA	N-CA-C	5.62	117.85	111.11
1	DJ	16	GLY	CA-C-O	-5.62	118.57	122.22
1	GO	77	ALA	N-CA-C	5.62	118.35	108.75
1	CT	31	ALA	N-CA-C	5.62	116.49	108.74
1	Hk	77	ALA	N-CA-C	5.62	117.81	108.99
2	Xt	815	SER	N-CA-C	5.61	117.20	111.14
1	Ba	38	ARG	N-CA-C	-5.61	98.76	108.69
1	Fk	94	LYS	N-CA-C	5.61	117.48	111.36
1	DO	16	GLY	CA-C-O	-5.61	118.57	122.22
2	Xj	815	SER	N-CA-C	5.61	117.20	111.14
1	EL	37	GLY	N-CA-C	5.61	121.24	111.14
1	FO	94	LYS	N-CA-C	5.61	117.48	111.36
1	Gk	77	ALA	N-CA-C	5.61	118.34	108.75
1	C9	20	ALA	N-CA-C	5.61	117.39	111.28
1	Cf	30	ALA	N-CA-C	5.61	117.39	111.28
1	As	77	ALA	N-CA-C	5.61	117.80	108.99
1	BJ	38	ARG	N-CA-C	-5.61	98.76	108.69
1	BT	38	ARG	N-CA-C	-5.61	98.77	108.69
1	G6	67	ALA	N-CA-C	5.61	117.84	111.11
1	Df	16	GLY	CA-C-O	-5.61	118.58	122.22
1	Gl	77	ALA	N-CA-C	5.61	117.59	109.07
1	Gu	67	ALA	N-CA-C	5.61	117.84	111.11
1	GJ	67	ALA	N-CA-C	5.61	117.84	111.11
2	XN	815	SER	N-CA-C	5.61	117.19	111.14
1	CR	20	ALA	N-CA-C	5.61	117.39	111.28
1	DT	16	GLY	CA-C-O	-5.61	118.58	122.22
1	G1	67	ALA	N-CA-C	5.60	117.83	111.11
1	Gz	67	ALA	N-CA-C	5.60	117.83	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Cd	20	ALA	N-CA-C	5.60	117.39	111.28
1	Dk	16	GLY	CA-C-O	-5.60	118.58	122.22
2	Xy	815	SER	N-CA-C	5.60	117.19	111.14
1	GA	77	ALA	N-CA-C	5.60	117.59	109.07
1	CM	20	ALA	N-CA-C	5.60	117.39	111.28
1	GP	77	ALA	N-CA-C	5.60	117.58	109.07
1	CW	20	ALA	N-CA-C	5.60	117.39	111.28
1	Cn	20	ALA	N-CA-C	5.60	117.39	111.28
1	CJ	31	ALA	N-CA-C	5.60	116.47	108.74
2	X5	815	SER	N-CA-C	5.60	117.19	111.14
1	Ew	37	GLY	N-CA-C	5.60	121.22	111.14
2	XE	719	LEU	N-CA-C	5.60	117.92	110.53
1	Ca	30	ALA	N-CA-C	5.60	117.38	111.28
1	Fp	94	LYS	N-CA-C	5.60	117.46	111.36
1	C4	20	ALA	N-CA-C	5.59	117.38	111.28
2	Xe	815	SER	N-CA-C	5.59	117.18	111.14
1	Ej	94	LYS	N-CA-C	5.59	117.46	111.36
1	HO	77	ALA	N-CA-C	5.59	117.77	108.99
1	Ff	94	LYS	N-CA-C	5.59	117.45	111.36
1	CC	20	ALA	N-CA-C	5.59	117.37	111.28
1	AQ	54	THR	N-CA-C	5.59	117.82	111.11
1	Ga	67	ALA	N-CA-C	5.59	117.81	111.11
1	GT	67	ALA	N-CA-C	5.59	117.81	111.11
1	F1	94	LYS	N-CA-C	5.59	117.45	111.36
1	Eh	37	GLY	N-CA-C	5.59	121.20	111.14
1	Do	84	VAL	N-CA-C	-5.59	103.96	110.05
1	Fz	94	LYS	N-CA-C	5.59	117.45	111.36
1	FE	94	LYS	N-CA-C	5.59	117.45	111.36
1	G7	77	ALA	N-CA-C	5.58	117.56	109.07
1	Cp	30	ALA	N-CA-C	5.58	117.37	111.28
1	A3	54	THR	N-CA-C	5.58	117.81	111.11
1	Am	54	THR	N-CA-C	5.58	117.81	111.11
1	Cz	31	ALA	N-CA-C	5.58	116.45	108.74
1	AH	77	ALA	N-CA-C	5.58	117.76	108.99
1	D5	84	VAL	N-CA-C	-5.58	103.97	110.05
1	Gk	67	ALA	N-CA-C	5.58	117.81	111.11
1	DN	84	VAL	N-CA-C	-5.58	103.97	110.05
1	DD	84	VAL	N-CA-C	-5.58	103.97	110.05
1	GE	67	ALA	N-CA-C	5.58	117.81	111.11
1	GF	77	ALA	N-CA-C	5.58	117.55	109.07
1	ED	94	LYS	N-CA-C	5.58	117.44	111.36
1	EI	94	LYS	N-CA-C	5.58	117.44	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	XI	815	SER	N-CA-C	5.58	117.16	111.14
1	Ah	54	THR	N-CA-C	5.57	117.80	111.11
1	BD	37	GLY	N-CA-C	5.57	119.21	110.91
1	EN	94	LYS	N-CA-C	5.57	117.44	111.36
1	Aw	54	THR	N-CA-C	5.57	117.80	111.11
1	FP	92	LEU	N-CA-C	5.57	116.91	109.83
1	Dj	84	VAL	N-CA-C	-5.57	103.98	110.05
1	An	77	ALA	N-CA-C	5.57	117.73	108.99
1	Bt	37	GLY	N-CA-C	5.57	119.21	110.91
1	FJ	94	LYS	N-CA-C	5.57	117.43	111.36
1	F6	94	LYS	N-CA-C	5.57	117.43	111.36
1	D0	84	VAL	N-CA-C	-5.57	103.98	110.05
1	DS	84	VAL	N-CA-C	-5.57	103.98	110.05
1	Ad	77	ALA	N-CA-C	5.57	117.73	108.99
1	GA	80	ILE	N-CA-C	5.57	116.14	108.12
1	BI	37	GLY	N-CA-C	5.57	119.20	110.91
1	BG	75	LEU	CA-CB-CG	5.57	135.78	116.30
1	BL	83	ARG	N-CA-C	-5.57	99.35	108.76
1	AM	77	ALA	N-CA-C	5.57	117.73	108.99
1	CT	30	ALA	N-CA-C	5.57	117.35	111.28
2	XX	815	SER	N-CA-C	5.57	117.15	111.14
1	AW	77	ALA	N-CA-C	5.57	117.73	108.99
1	A8	54	THR	N-CA-C	5.57	117.79	111.11
1	Ee	94	LYS	N-CA-C	5.57	117.43	111.36
1	Dt	84	VAL	N-CA-C	-5.57	103.98	110.05
1	AC	77	ALA	N-CA-C	5.56	117.73	108.99
1	BQ	75	LEU	CA-CB-CG	5.56	135.77	116.30
1	A9	77	ALA	N-CA-C	5.56	117.72	108.99
1	Be	37	GLY	N-CA-C	5.56	119.20	110.91
1	BX	37	GLY	N-CA-C	5.56	119.20	110.91
1	Bc	75	LEU	CA-CB-CG	5.56	135.76	116.30
1	Bm	75	LEU	CA-CB-CG	5.56	135.76	116.30
1	B8	75	LEU	CA-CB-CG	5.56	135.76	116.30
1	Fl	92	LEU	N-CA-C	5.56	116.89	109.83
1	Dy	84	VAL	N-CA-C	-5.56	103.99	110.05
1	B5	37	GLY	N-CA-C	5.56	119.19	110.91
1	Da	16	GLY	CA-C-O	-5.56	118.61	122.22
1	De	84	VAL	N-CA-C	-5.56	103.99	110.05
1	Bc	83	ARG	N-CA-C	-5.56	99.37	108.76
1	Du	16	GLY	CA-C-O	-5.56	118.61	122.22
1	BG	83	ARG	N-CA-C	-5.56	99.37	108.76
1	FT	94	LYS	N-CA-C	5.56	117.42	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BV	83	ARG	N-CA-C	-5.56	99.37	108.76
1	Br	83	ARG	N-CA-C	-5.55	99.37	108.76
1	Gv	77	ALA	N-CA-C	5.55	117.51	109.07
1	Dz	16	GLY	CA-C-O	-5.55	118.61	122.22
1	BB	83	ARG	N-CA-C	-5.55	99.37	108.76
1	GF	80	ILE	N-CA-C	5.55	116.12	108.12
1	ES	94	LYS	N-CA-C	5.55	117.41	111.36
1	G2	77	ALA	N-CA-C	5.55	117.51	109.07
1	B3	75	LEU	CA-CB-CG	5.55	135.73	116.30
1	E5	94	LYS	N-CA-C	5.55	117.41	111.36
1	E0	94	LYS	N-CA-C	5.55	117.41	111.36
1	Bj	37	GLY	N-CA-C	5.55	119.18	110.91
1	Eo	94	LYS	N-CA-C	5.55	117.41	111.36
1	AB	54	THR	N-CA-C	5.55	117.77	111.11
1	BN	37	GLY	N-CA-C	5.55	119.18	110.91
1	AL	54	THR	N-CA-C	5.55	117.77	111.11
1	HS	67	ALA	N-CA-C	5.55	117.14	111.14
1	B0	37	GLY	N-CA-C	5.55	119.18	110.91
1	B8	83	ARG	N-CA-C	-5.55	99.38	108.76
1	Fa	94	LYS	N-CA-C	5.55	117.41	111.36
1	Et	94	LYS	N-CA-C	5.55	117.41	111.36
1	By	37	GLY	N-CA-C	5.55	119.18	110.91
1	BB	75	LEU	CA-CB-CG	5.55	135.72	116.30
1	AG	54	THR	N-CA-C	5.55	117.77	111.11
1	EX	94	LYS	N-CA-C	5.55	117.41	111.36
1	BV	75	LEU	CA-CB-CG	5.55	135.72	116.30
1	B3	83	ARG	N-CA-C	-5.55	99.38	108.76
1	Br	75	LEU	CA-CB-CG	5.55	135.71	116.30
1	Bw	75	LEU	CA-CB-CG	5.55	135.71	116.30
1	GU	77	ALA	N-CA-C	5.55	117.50	109.07
1	A4	77	ALA	N-CA-C	5.54	117.70	108.99
1	Dp	16	GLY	CA-C-O	-5.54	118.62	122.22
1	Ac	54	THR	N-CA-C	5.54	117.76	111.11
1	Bh	75	LEU	CA-CB-CG	5.54	135.71	116.30
1	BL	75	LEU	CA-CB-CG	5.54	135.71	116.30
1	HS	96	PRO	CA-C-O	-5.54	115.25	122.12
1	AV	54	THR	N-CA-C	5.54	117.76	111.11
1	Gb	77	ALA	N-CA-C	5.54	117.49	109.07
1	Bo	37	GLY	N-CA-C	5.54	119.17	110.91
1	Gv	80	ILE	N-CA-C	5.54	116.10	108.12
1	Bw	83	ARG	N-CA-C	-5.54	99.40	108.76
1	AR	77	ALA	N-CA-C	5.54	117.69	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bm	83	ARG	N-CA-C	-5.54	99.40	108.76
1	Fu	94	LYS	N-CA-C	5.54	117.40	111.36
1	Ho	96	PRO	CA-C-O	-5.54	115.25	122.12
1	BS	37	GLY	N-CA-C	5.54	119.16	110.91
1	Gg	77	ALA	N-CA-C	5.54	117.48	109.07
1	Ey	94	LYS	N-CA-C	5.54	117.39	111.36
1	G2	80	ILE	N-CA-C	5.53	116.09	108.12
1	F7	92	LEU	N-CA-C	5.53	116.86	109.83
1	He	67	ALA	N-CA-C	5.53	117.12	111.14
1	Gq	77	ALA	N-CA-C	5.53	117.48	109.07
1	Ax	77	ALA	N-CA-C	5.53	117.68	108.99
1	HX	67	ALA	N-CA-C	5.53	117.12	111.14
1	BQ	83	ARG	N-CA-C	-5.53	99.41	108.76
1	G7	80	ILE	N-CA-C	5.53	116.08	108.12
1	Gg	80	ILE	N-CA-C	5.53	116.08	108.12
1	GH	77	ALA	N-CA-C	5.53	117.67	108.99
1	H0	67	ALA	N-CA-C	5.53	117.11	111.14
1	HI	67	ALA	N-CA-C	5.53	117.11	111.14
1	GK	77	ALA	N-CA-C	5.53	117.47	109.07
1	Gb	80	ILE	N-CA-C	5.53	116.08	108.12
1	Gq	80	ILE	N-CA-C	5.53	116.08	108.12
1	GU	80	ILE	N-CA-C	5.53	116.08	108.12
1	DX	84	VAL	N-CA-C	-5.53	104.03	110.05
1	F2	92	LEU	N-CA-C	5.52	116.84	109.83
1	Ho	67	ALA	N-CA-C	5.52	117.11	111.14
1	DA	7	ILE	N-CA-C	5.52	116.30	110.72
1	FK	92	LEU	N-CA-C	5.52	116.84	109.83
1	GK	80	ILE	N-CA-C	5.52	116.07	108.12
2	Xi	850	GLY	CA-C-O	-5.52	118.63	122.22
3	Po	67	TYR	N-CA-C	5.52	116.65	109.64
3	PS	67	TYR	N-CA-C	5.52	116.65	109.64
1	D7	7	ILE	N-CA-C	5.52	116.29	110.72
1	Fb	92	LEU	N-CA-C	5.52	116.84	109.83
1	Ar	54	THR	N-CA-C	5.52	117.73	111.11
1	Hy	67	ALA	N-CA-C	5.52	117.10	111.14
2	Xx	850	GLY	CA-C-O	-5.52	118.63	122.22
1	FA	92	LEU	N-CA-C	5.52	116.84	109.83
1	H0	96	PRO	CA-C-O	-5.52	115.28	122.12
1	Fq	92	LEU	N-CA-C	5.52	116.84	109.83
1	FU	92	LEU	N-CA-C	5.52	116.84	109.83
1	Ht	67	ALA	N-CA-C	5.52	117.10	111.14
2	XL	720	ALA	N-CA-C	5.52	119.00	111.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bh	83	ARG	N-CA-C	-5.51	99.44	108.76
1	Ai	77	ALA	N-CA-C	5.51	117.65	108.99
1	Fv	92	LEU	N-CA-C	5.51	116.83	109.83
1	DI	84	VAL	N-CA-C	-5.51	104.04	110.05
1	Hj	67	ALA	N-CA-C	5.51	117.09	111.14
2	XH	803	ASN	N-CA-C	5.51	117.14	109.31
1	FN	37	GLY	N-CA-C	5.51	119.12	110.91
1	Gl	80	ILE	N-CA-C	5.51	116.05	108.12
1	HD	96	PRO	CA-C-O	-5.51	115.29	122.12
1	FF	92	LEU	N-CA-C	5.51	116.83	109.83
1	DE	16	GLY	CA-C-O	-5.51	118.64	122.22
1	GP	80	ILE	N-CA-C	5.51	116.05	108.12
1	H5	96	PRO	CA-C-O	-5.51	115.29	122.12
1	FX	37	GLY	N-CA-C	5.50	119.11	110.91
2	Xm	720	ALA	N-CA-C	5.50	118.98	111.39
3	P0	67	TYR	N-CA-C	5.50	116.63	109.64
1	H5	67	ALA	N-CA-C	5.50	117.08	111.14
1	Gd	77	ALA	N-CA-C	5.50	117.62	108.99
2	Xd	803	ASN	N-CA-C	5.50	117.11	109.31
1	Hj	96	PRO	CA-C-O	-5.50	115.31	122.12
1	Fo	37	GLY	N-CA-C	5.50	119.10	110.91
1	Dv	7	ILE	N-CA-C	5.50	116.27	110.72
1	Hy	16	GLY	CA-C-O	-5.50	118.65	122.22
3	Py	67	TYR	N-CA-C	5.50	116.62	109.64
1	Gx	77	ALA	N-CA-C	5.50	117.62	108.99
3	PD	67	TYR	N-CA-C	5.50	116.62	109.64
2	XW	803	ASN	N-CA-C	5.50	117.11	109.31
1	F0	37	GLY	N-CA-C	5.50	119.10	110.91
1	FI	37	GLY	N-CA-C	5.50	119.10	110.91
1	Fg	92	LEU	N-CA-C	5.49	116.81	109.83
1	DP	7	ILE	N-CA-C	5.49	116.27	110.72
2	X3	720	ALA	N-CA-C	5.49	118.97	111.39
1	Fj	37	GLY	N-CA-C	5.49	119.09	110.91
2	XC	803	ASN	N-CA-C	5.49	117.11	109.31
1	HI	96	PRO	CA-C-O	-5.49	115.31	122.12
1	AP	94	LYS	N-CA-C	5.49	117.34	111.36
2	Xi	803	ASN	N-CA-C	5.49	117.11	109.31
1	AA	94	LYS	N-CA-C	5.49	117.34	111.36
1	Eb	38	ARG	N-CA-C	-5.49	99.49	108.76
1	Fe	37	GLY	N-CA-C	5.49	119.08	110.91
1	El	38	ARG	N-CA-C	-5.49	99.49	108.76
1	Gs	77	ALA	N-CA-C	5.49	117.60	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EP	38	ARG	N-CA-C	-5.49	99.49	108.76
1	EU	38	ARG	N-CA-C	-5.49	99.49	108.76
2	Xr	720	ALA	N-CA-C	5.49	118.96	111.39
1	G9	77	ALA	N-CA-C	5.49	117.60	108.99
3	Pe	67	TYR	N-CA-C	5.49	116.61	109.64
1	Dl	7	ILE	N-CA-C	5.49	116.26	110.72
1	HC	95	ALA	N-CA-C	-5.49	101.89	108.25
3	PI	67	TYR	N-CA-C	5.49	116.61	109.64
1	GM	77	ALA	N-CA-C	5.49	117.60	108.99
3	PX	67	TYR	N-CA-C	5.49	116.61	109.64
2	Xs	803	ASN	N-CA-C	5.48	117.10	109.31
1	DK	7	ILE	N-CA-C	5.48	116.26	110.72
1	HN	67	ALA	N-CA-C	5.48	117.06	111.14
2	Xc	720	ALA	N-CA-C	5.48	118.96	111.39
2	XV	720	ALA	N-CA-C	5.48	118.96	111.39
1	Gn	77	ALA	N-CA-C	5.48	117.60	108.99
2	Xn	803	ASN	N-CA-C	5.48	117.09	109.31
2	Xw	720	ALA	N-CA-C	5.48	118.95	111.39
1	HD	67	ALA	N-CA-C	5.48	117.06	111.14
1	CR	42	GLY	N-CA-C	-5.48	104.54	111.72
2	X4	803	ASN	N-CA-C	5.48	117.09	109.31
1	Ft	37	GLY	N-CA-C	5.48	119.08	110.91
1	Fy	37	GLY	N-CA-C	5.48	119.08	110.91
1	GR	77	ALA	N-CA-C	5.48	117.59	108.99
2	XG	720	ALA	N-CA-C	5.48	118.95	111.39
1	F5	37	GLY	N-CA-C	5.48	119.07	110.91
2	X9	803	ASN	N-CA-C	5.48	117.09	109.31
1	EA	38	ARG	N-CA-C	-5.48	99.50	108.76
2	XR	803	ASN	N-CA-C	5.48	117.09	109.31
1	Gs	82	ALA	N-CA-C	5.48	117.25	111.28
1	Hy	96	PRO	CA-C-O	-5.48	115.33	122.12
1	GC	82	ALA	N-CA-C	5.48	117.25	111.28
1	EF	38	ARG	N-CA-C	-5.48	99.50	108.76
2	XQ	720	ALA	N-CA-C	5.48	118.95	111.39
1	GW	77	ALA	N-CA-C	5.48	117.59	108.99
2	X8	720	ALA	N-CA-C	5.48	118.95	111.39
1	Gp	30	ALA	N-CA-C	5.48	117.25	111.28
1	GC	77	ALA	N-CA-C	5.48	117.59	108.99
1	E7	38	ARG	N-CA-C	-5.47	99.51	108.76
1	Fp	37	GLY	N-CA-C	5.47	119.07	110.91
1	HN	96	PRO	CA-C-O	-5.47	115.33	122.12
2	Xh	720	ALA	N-CA-C	5.47	118.94	111.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Gn	82	ALA	N-CA-C	5.47	117.24	111.28
1	Eq	38	ARG	N-CA-C	-5.47	99.51	108.76
1	Ev	38	ARG	N-CA-C	-5.47	99.51	108.76
3	P5	67	TYR	N-CA-C	5.47	116.59	109.64
1	G4	77	ALA	N-CA-C	5.47	117.58	108.99
1	Fa	37	GLY	N-CA-C	5.47	119.06	110.91
1	He	96	PRO	CA-C-O	-5.47	115.34	122.12
3	Pj	67	TYR	N-CA-C	5.47	116.59	109.64
1	FT	37	GLY	N-CA-C	5.47	119.06	110.91
1	E2	38	ARG	N-CA-C	-5.47	99.52	108.76
1	C9	42	GLY	N-CA-C	-5.47	104.56	111.72
1	Dg	7	ILE	N-CA-C	5.47	116.24	110.72
2	Xx	803	ASN	N-CA-C	5.47	117.08	109.31
1	Gz	30	ALA	N-CA-C	5.47	117.24	111.28
1	FE	37	GLY	N-CA-C	5.47	119.06	110.91
1	HH	95	ALA	N-CA-C	-5.47	101.91	108.25
1	D2	7	ILE	N-CA-C	5.47	116.24	110.72
3	Pt	67	TYR	N-CA-C	5.47	116.58	109.64
2	XH	850	GLY	CA-C-O	-5.47	118.67	122.22
1	Gk	30	ALA	N-CA-C	5.46	117.24	111.28
1	FD	37	GLY	N-CA-C	5.46	119.05	110.91
1	FJ	37	GLY	N-CA-C	5.46	119.05	110.91
1	GR	82	ALA	N-CA-C	5.46	117.24	111.28
2	XB	720	ALA	N-CA-C	5.46	118.93	111.39
1	Ga	30	ALA	N-CA-C	5.46	117.23	111.28
1	Eg	38	ARG	N-CA-C	-5.46	99.53	108.76
1	Gx	82	ALA	N-CA-C	5.46	117.23	111.28
1	H9	95	ALA	N-CA-C	-5.46	101.91	108.25
1	GJ	30	ALA	N-CA-C	5.46	117.23	111.28
3	PN	67	TYR	N-CA-C	5.46	116.58	109.64
2	XM	803	ASN	N-CA-C	5.46	117.07	109.31
1	Ff	37	GLY	N-CA-C	5.46	119.04	110.91
1	FS	37	GLY	N-CA-C	5.46	119.04	110.91
1	HR	95	ALA	N-CA-C	-5.46	101.92	108.25
1	EK	38	ARG	N-CA-C	-5.46	99.54	108.76
1	Gi	82	ALA	N-CA-C	5.46	117.23	111.28
1	G1	30	ALA	N-CA-C	5.45	117.22	111.28
1	Bj	67	ALA	N-CA-C	5.45	117.22	111.28
1	HX	96	PRO	CA-C-O	-5.45	115.36	122.12
1	GT	30	ALA	N-CA-C	5.45	117.22	111.28
2	X4	850	GLY	CA-C-O	-5.45	118.68	122.22
1	Hj	16	GLY	CA-C-O	-5.45	118.68	122.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bu	83	ARG	N-CA-C	-5.45	100.02	108.90
1	CH	42	GLY	N-CA-C	-5.45	104.58	111.72
2	XM	850	GLY	CA-C-O	-5.45	118.68	122.22
1	Gd	82	ALA	N-CA-C	5.45	117.22	111.28
1	Gi	77	ALA	N-CA-C	5.45	117.54	108.99
1	Dq	7	ILE	N-CA-C	5.45	116.22	110.72
1	Ht	96	PRO	CA-C-O	-5.45	115.36	122.12
1	GW	82	ALA	N-CA-C	5.45	117.22	111.28
1	G6	30	ALA	N-CA-C	5.45	117.22	111.28
1	G4	82	ALA	N-CA-C	5.44	117.21	111.28
1	A7	94	LYS	N-CA-C	5.44	117.29	111.36
1	Ci	42	GLY	N-CA-C	-5.44	104.59	111.72
1	F1	37	GLY	N-CA-C	5.44	119.02	110.91
1	Gf	30	ALA	N-CA-C	5.44	117.21	111.28
1	Ho	16	GLY	CA-C-O	-5.44	118.68	122.22
1	GE	30	ALA	N-CA-C	5.44	117.21	111.28
1	FS	83	ARG	N-CA-C	-5.44	99.56	108.76
1	FX	83	ARG	N-CA-C	-5.44	99.56	108.76
1	Bf	83	ARG	N-CA-C	-5.44	100.03	108.90
1	Fj	83	ARG	N-CA-C	-5.44	99.56	108.76
1	Al	94	LYS	N-CA-C	5.44	117.29	111.36
1	C4	42	GLY	N-CA-C	-5.44	104.59	111.72
1	CC	42	GLY	N-CA-C	-5.44	104.59	111.72
1	CM	42	GLY	N-CA-C	-5.44	104.59	111.72
1	CW	42	GLY	N-CA-C	-5.44	104.59	111.72
1	H0	16	GLY	CA-C-O	-5.44	118.69	122.22
1	Hd	95	ALA	N-CA-C	-5.44	101.94	108.25
1	Hi	95	ALA	N-CA-C	-5.44	101.94	108.25
1	Bo	67	ALA	N-CA-C	5.44	117.21	111.28
1	Fu	37	GLY	N-CA-C	5.44	119.01	110.91
1	HD	16	GLY	CA-C-O	-5.44	118.69	122.22
1	HW	95	ALA	N-CA-C	-5.44	101.94	108.25
2	Xd	850	GLY	CA-C-O	-5.43	118.69	122.22
1	Fy	83	ARG	N-CA-C	-5.43	99.58	108.76
2	XW	850	GLY	CA-C-O	-5.43	118.69	122.22
1	G9	82	ALA	N-CA-C	5.43	117.20	111.28
1	BJ	83	ARG	N-CA-C	-5.43	100.05	108.90
1	Gu	30	ALA	N-CA-C	5.43	117.20	111.28
1	H4	95	ALA	N-CA-C	-5.43	101.95	108.25
1	Fe	83	ARG	N-CA-C	-5.43	99.58	108.76
1	Cx	42	GLY	N-CA-C	-5.43	104.61	111.72
1	GH	82	ALA	N-CA-C	5.43	117.20	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HM	95	ALA	N-CA-C	-5.43	101.95	108.25
1	F5	83	ARG	N-CA-C	-5.43	99.59	108.76
1	Ft	83	ARG	N-CA-C	-5.43	99.59	108.76
1	Hs	95	ALA	N-CA-C	-5.43	101.95	108.25
1	EU	30	ALA	N-CA-C	5.43	117.28	111.36
1	B1	83	ARG	N-CA-C	-5.43	100.05	108.90
1	Hn	95	ALA	N-CA-C	-5.43	101.95	108.25
1	Bz	83	ARG	N-CA-C	-5.43	100.05	108.90
1	FN	83	ARG	N-CA-C	-5.43	99.59	108.76
1	BS	67	ALA	N-CA-C	5.42	117.19	111.28
1	DS	37	GLY	N-CA-C	5.42	118.99	110.91
1	FD	83	ARG	N-CA-C	-5.42	99.59	108.76
1	B5	67	ALA	N-CA-C	5.42	117.19	111.28
1	F6	37	GLY	N-CA-C	5.42	118.99	110.91
1	F0	83	ARG	N-CA-C	-5.42	99.60	108.76
1	Bp	83	ARG	N-CA-C	-5.42	100.06	108.90
2	Xt	835	ASN	N-CA-C	-5.42	106.86	112.93
1	FO	37	GLY	N-CA-C	5.42	118.99	110.91
1	Hx	95	ALA	N-CA-C	-5.42	101.96	108.25
2	XA	861	ILE	N-CA-C	-5.42	100.67	108.53
1	B6	83	ARG	N-CA-C	-5.42	100.07	108.90
1	Cd	42	GLY	N-CA-C	-5.42	104.62	111.72
1	Bk	83	ARG	N-CA-C	-5.42	100.07	108.90
1	Cn	42	GLY	N-CA-C	-5.42	104.62	111.72
1	EA	30	ALA	N-CA-C	5.42	117.27	111.36
1	BI	67	ALA	N-CA-C	5.42	117.19	111.28
1	BO	83	ARG	N-CA-C	-5.42	100.07	108.90
1	GO	30	ALA	N-CA-C	5.42	117.19	111.28
1	B0	67	ALA	N-CA-C	5.42	117.19	111.28
1	D0	37	GLY	N-CA-C	5.42	118.98	110.91
1	Fo	83	ARG	N-CA-C	-5.42	99.61	108.76
1	DD	37	GLY	N-CA-C	5.42	118.98	110.91
2	XP	861	ILE	N-CA-C	-5.42	100.68	108.53
1	Cs	42	GLY	N-CA-C	-5.42	104.63	111.72
1	Fk	37	GLY	N-CA-C	5.41	118.97	110.91
1	Dt	37	GLY	N-CA-C	5.41	118.97	110.91
1	Ab	94	LYS	N-CA-C	5.41	117.26	111.36
2	Xe	835	ASN	N-CA-C	-5.41	106.87	112.93
1	Ag	94	LYS	N-CA-C	5.41	117.26	111.36
1	Av	94	LYS	N-CA-C	5.41	117.26	111.36
1	DF	7	ILE	N-CA-C	5.41	116.19	110.72
1	BN	67	ALA	N-CA-C	5.41	117.18	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	GM	82	ALA	N-CA-C	5.41	117.18	111.28
1	BE	83	ARG	N-CA-C	-5.41	100.08	108.90
2	X7	861	ILE	N-CA-C	-5.41	100.69	108.53
1	Db	7	ILE	N-CA-C	5.41	116.18	110.72
1	Fz	37	GLY	N-CA-C	5.41	118.97	110.91
1	FI	83	ARG	N-CA-C	-5.41	99.63	108.76
1	Do	37	GLY	N-CA-C	5.40	118.96	110.91
1	Eq	30	ALA	N-CA-C	5.40	117.25	111.36
2	XX	828	VAL	N-CA-C	-5.40	99.77	107.77
1	Dy	37	GLY	N-CA-C	5.40	118.96	110.91
1	BD	67	ALA	N-CA-C	5.40	117.17	111.28
1	CG	81	ILE	CB-CA-C	-5.40	104.78	111.32
1	AK	94	LYS	N-CA-C	5.40	117.25	111.36
3	PE	33	ALA	CA-C-N	-5.40	114.20	119.76
3	PE	33	ALA	C-N-CA	-5.40	114.20	119.76
1	Be	67	ALA	N-CA-C	5.40	117.16	111.28
1	A2	94	LYS	N-CA-C	5.40	117.24	111.36
2	X0	835	ASN	N-CA-C	-5.40	106.89	112.93
1	El	30	ALA	N-CA-C	5.40	117.24	111.36
2	XS	835	ASN	N-CA-C	-5.40	106.89	112.93
1	H5	16	GLY	CA-C-O	-5.40	118.71	122.22
1	E7	30	ALA	N-CA-C	5.40	117.24	111.36
2	Xg	795	ILE	N-CA-C	-5.40	100.11	107.99
2	Xv	861	ILE	N-CA-C	-5.40	100.71	108.53
2	Xb	795	ILE	N-CA-C	-5.39	100.11	107.99
1	Cc	81	ILE	CB-CA-C	-5.39	104.79	111.32
1	Fg	30	ALA	N-CA-C	5.39	117.16	111.28
1	Ev	30	ALA	N-CA-C	5.39	117.24	111.36
2	XI	835	ASN	N-CA-C	-5.39	106.89	112.93
1	Bt	67	ALA	N-CA-C	5.39	117.16	111.28
1	EF	30	ALA	N-CA-C	5.39	117.24	111.36
1	DU	7	ILE	N-CA-C	5.39	116.17	110.72
1	D5	37	GLY	N-CA-C	5.39	118.94	110.91
1	Ba	83	ARG	N-CA-C	-5.39	100.11	108.90
1	De	37	GLY	N-CA-C	5.39	118.94	110.91
3	Pp	33	ALA	CA-C-N	-5.39	114.21	119.76
3	Pp	33	ALA	C-N-CA	-5.39	114.21	119.76
1	Cr	81	ILE	CB-CA-C	-5.39	104.80	111.32
1	Es	42	GLY	N-CA-C	-5.39	100.41	113.18
1	HD	94	LYS	N-CA-C	5.39	117.23	111.36
2	XF	795	ILE	N-CA-C	-5.39	100.12	107.99
1	BT	83	ARG	N-CA-C	-5.39	100.11	108.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DX	37	GLY	N-CA-C	5.39	118.94	110.91
1	DI	37	GLY	N-CA-C	5.39	118.94	110.91
2	Xo	835	ASN	N-CA-C	-5.39	106.90	112.93
1	AF	94	LYS	N-CA-C	5.39	117.23	111.36
2	X2	861	ILE	N-CA-C	-5.38	100.72	108.53
1	Aq	94	LYS	N-CA-C	5.38	117.23	111.36
1	By	67	ALA	N-CA-C	5.38	117.15	111.28
1	FF	30	ALA	N-CA-C	5.38	117.15	111.28
2	XK	861	ILE	N-CA-C	-5.38	100.72	108.53
1	HS	16	GLY	CA-C-O	-5.38	118.72	122.22
2	X5	835	ASN	N-CA-C	-5.38	106.90	112.93
1	D6	54	THR	N-CA-C	5.38	117.15	111.28
2	X9	850	GLY	CA-C-O	-5.38	118.72	122.22
2	Xe	828	VAL	N-CA-C	-5.38	99.80	107.77
1	Ex	42	GLY	N-CA-C	-5.38	100.43	113.18
2	XI	828	VAL	N-CA-C	-5.38	99.81	107.77
1	Eb	30	ALA	N-CA-C	5.38	117.22	111.36
2	Xv	795	ILE	N-CA-C	-5.38	100.14	107.99
1	E5	72	GLY	N-CA-C	5.38	120.86	111.50
1	E0	72	GLY	N-CA-C	5.38	120.86	111.50
1	C8	81	ILE	CB-CA-C	-5.38	104.81	111.32
2	Xl	861	ILE	N-CA-C	-5.38	100.73	108.53
1	ED	72	GLY	N-CA-C	5.38	120.86	111.50
1	CV	81	ILE	CB-CA-C	-5.38	104.81	111.32
2	X7	795	ILE	N-CA-C	-5.38	100.14	107.99
1	Df	54	THR	N-CA-C	5.38	117.14	111.28
1	Et	72	GLY	N-CA-C	5.38	120.86	111.50
1	EC	42	GLY	N-CA-C	-5.38	100.44	113.18
1	CL	81	ILE	CB-CA-C	-5.38	104.81	111.32
1	DQ	20	ALA	N-CA-C	5.38	117.22	111.36
1	Cz	38	ARG	N-CA-C	-5.38	99.18	108.69
1	ER	42	GLY	N-CA-C	-5.38	100.44	113.18
2	XU	795	ILE	N-CA-C	-5.38	100.14	107.99
1	AX	68	CYS	N-CA-C	5.38	119.84	113.28
2	X2	795	ILE	N-CA-C	-5.37	100.14	107.99
1	He	16	GLY	CA-C-O	-5.37	118.73	122.22
1	Dj	37	GLY	N-CA-C	5.37	118.92	110.91
2	XD	835	ASN	N-CA-C	-5.37	106.91	112.93
1	DO	54	THR	N-CA-C	5.37	117.14	111.28
1	HX	16	GLY	CA-C-O	-5.37	118.73	122.22
1	C3	81	ILE	CB-CA-C	-5.37	104.82	111.32
1	Fl	30	ALA	N-CA-C	5.37	117.14	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Xq	795	ILE	N-CA-C	-5.37	100.15	107.99
1	CB	81	ILE	CB-CA-C	-5.37	104.82	111.32
2	XC	850	GLY	CA-C-O	-5.37	118.73	122.22
2	XN	835	ASN	N-CA-C	-5.37	106.91	112.93
2	XP	795	ILE	N-CA-C	-5.37	100.15	107.99
1	E9	42	GLY	N-CA-C	-5.37	100.45	113.18
1	En	42	GLY	N-CA-C	-5.37	100.45	113.18
1	Cw	81	ILE	CB-CA-C	-5.37	104.82	111.32
1	EH	42	GLY	N-CA-C	-5.37	100.45	113.18
1	E4	42	GLY	N-CA-C	-5.37	100.46	113.18
1	Ed	42	GLY	N-CA-C	-5.37	100.46	113.18
1	Dz	54	THR	N-CA-C	5.37	117.13	111.28
1	HI	16	GLY	CA-C-O	-5.37	118.73	122.22
1	CJ	38	ARG	N-CA-C	-5.37	99.19	108.69
1	DN	37	GLY	N-CA-C	5.37	118.91	110.91
1	EM	42	GLY	N-CA-C	-5.37	100.46	113.18
1	AU	94	LYS	N-CA-C	5.37	117.21	111.36
1	AI	68	CYS	N-CA-C	5.37	119.83	113.28
2	Xl	795	ILE	N-CA-C	-5.37	100.16	107.99
1	Cm	81	ILE	CB-CA-C	-5.36	104.83	111.32
1	Cu	38	ARG	N-CA-C	-5.36	99.20	108.69
1	EP	30	ALA	N-CA-C	5.36	117.20	111.36
1	CQ	81	ILE	CB-CA-C	-5.36	104.83	111.32
2	XX	835	ASN	N-CA-C	-5.36	106.92	112.93
3	Pa	33	ALA	CA-C-N	-5.36	114.24	119.76
3	Pa	33	ALA	C-N-CA	-5.36	114.24	119.76
2	Xt	828	VAL	N-CA-C	-5.36	99.83	107.77
1	EI	72	GLY	N-CA-C	5.36	120.83	111.50
1	C1	38	ARG	N-CA-C	-5.36	99.20	108.69
1	Dh	20	ALA	N-CA-C	5.36	117.20	111.36
1	GN	37	GLY	N-CA-C	5.36	119.12	110.87
1	ES	72	GLY	N-CA-C	5.36	120.83	111.50
2	Xg	861	ILE	N-CA-C	-5.36	100.76	108.53
1	EN	72	GLY	N-CA-C	5.36	120.82	111.50
1	E2	30	ALA	N-CA-C	5.36	117.20	111.36
1	C6	38	ARG	N-CA-C	-5.36	99.21	108.69
1	Ej	72	GLY	N-CA-C	5.36	120.82	111.50
1	Ei	42	GLY	N-CA-C	-5.36	100.48	113.18
1	Ht	16	GLY	CA-C-O	-5.36	118.74	122.22
1	Ey	72	GLY	N-CA-C	5.36	120.82	111.50
1	FA	54	THR	N-CA-C	5.36	117.54	111.11
1	CO	38	ARG	N-CA-C	-5.36	99.21	108.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BX	67	ALA	N-CA-C	5.36	117.12	111.28
1	F2	30	ALA	N-CA-C	5.36	117.12	111.28
1	Ee	72	GLY	N-CA-C	5.36	120.82	111.50
1	Fc	81	ILE	N-CA-C	-5.36	98.76	107.28
2	Xy	828	VAL	N-CA-C	-5.36	99.84	107.77
1	FA	30	ALA	N-CA-C	5.36	117.12	111.28
1	EK	30	ALA	N-CA-C	5.36	117.20	111.36
1	F7	30	ALA	N-CA-C	5.35	117.12	111.28
1	Eg	30	ALA	N-CA-C	5.35	117.20	111.36
2	Xj	828	VAL	N-CA-C	-5.35	99.85	107.77
1	Eo	72	GLY	N-CA-C	5.35	120.81	111.50
1	EW	42	GLY	N-CA-C	-5.35	100.49	113.18
2	X5	828	VAL	N-CA-C	-5.35	99.85	107.77
1	Fb	30	ALA	N-CA-C	5.35	117.11	111.28
1	Ca	38	ARG	N-CA-C	-5.35	99.22	108.69
1	Ch	81	ILE	CB-CA-C	-5.35	104.84	111.32
1	Fh	81	ILE	N-CA-C	-5.35	98.77	107.28
2	Xy	835	ASN	N-CA-C	-5.35	106.93	112.93
1	AS	68	CYS	N-CA-C	5.35	119.81	113.28
1	FU	30	ALA	N-CA-C	5.35	117.11	111.28
1	CT	38	ARG	N-CA-C	-5.35	99.22	108.69
1	Ck	38	ARG	N-CA-C	-5.35	99.22	108.69
1	Ao	68	CYS	N-CA-C	5.35	119.81	113.28
1	Ho	94	LYS	N-CA-C	5.35	117.19	111.36
1	Cp	38	ARG	N-CA-C	-5.35	99.22	108.69
2	XK	795	ILE	N-CA-C	-5.35	100.18	107.99
1	D1	54	THR	N-CA-C	5.35	117.11	111.28
1	A0	68	CYS	N-CA-C	5.35	119.81	113.28
2	Xb	861	ILE	N-CA-C	-5.35	100.77	108.53
1	Ae	68	CYS	N-CA-C	5.35	119.81	113.28
1	HI	94	LYS	N-CA-C	5.35	117.19	111.36
1	FP	30	ALA	N-CA-C	5.35	117.11	111.28
1	Ge	37	GLY	N-CA-C	5.35	119.11	110.87
1	Dm	20	ALA	N-CA-C	5.35	117.19	111.36
3	PT	33	ALA	CA-C-N	-5.35	114.25	119.76
3	PT	33	ALA	C-N-CA	-5.35	114.25	119.76
2	Xn	850	GLY	CA-C-O	-5.35	118.75	122.22
1	Fv	30	ALA	N-CA-C	5.35	117.11	111.28
2	XF	861	ILE	N-CA-C	-5.35	100.78	108.53
1	Aj	95	ALA	N-CA-C	-5.34	101.99	108.14
1	DB	20	ALA	N-CA-C	5.34	117.19	111.36
1	AN	68	CYS	N-CA-C	5.34	119.80	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	XN	828	VAL	N-CA-C	-5.34	99.86	107.77
1	FL	81	ILE	N-CA-C	-5.34	98.78	107.28
1	At	68	CYS	N-CA-C	5.34	119.80	113.28
1	F3	81	ILE	N-CA-C	-5.34	98.79	107.28
2	Xq	861	ILE	N-CA-C	-5.34	100.79	108.53
2	XD	828	VAL	N-CA-C	-5.34	99.86	107.77
2	XU	861	ILE	N-CA-C	-5.34	100.78	108.53
1	D8	20	ALA	N-CA-C	5.34	117.18	111.36
1	Ci	16	GLY	CA-C-O	-5.34	118.75	122.22
2	Xo	828	VAL	N-CA-C	-5.34	99.87	107.77
1	Fr	81	ILE	N-CA-C	-5.34	98.79	107.28
1	CE	38	ARG	N-CA-C	-5.34	99.24	108.69
1	HN	16	GLY	CA-C-O	-5.34	118.75	122.22
1	BL	16	GLY	CA-C-O	-5.34	118.55	122.23
1	FV	81	ILE	N-CA-C	-5.34	98.79	107.28
2	X0	828	VAL	N-CA-C	-5.34	99.87	107.77
2	Xj	835	ASN	N-CA-C	-5.34	106.95	112.93
2	XA	795	ILE	N-CA-C	-5.34	100.20	107.99
1	GS	37	GLY	N-CA-C	5.34	119.09	110.87
2	XS	828	VAL	N-CA-C	-5.34	99.87	107.77
1	F7	54	THR	N-CA-C	5.34	117.51	111.11
1	Fb	54	THR	N-CA-C	5.34	117.51	111.11
1	Cf	38	ARG	N-CA-C	-5.34	99.24	108.69
1	Ay	95	ALA	N-CA-C	-5.34	102.00	108.14
1	GI	37	GLY	N-CA-C	5.34	119.09	110.87
1	FU	54	THR	N-CA-C	5.34	117.51	111.11
1	D3	20	ALA	N-CA-C	5.33	117.17	111.36
3	Pf	33	ALA	CA-C-N	-5.33	114.27	119.76
3	Pf	33	ALA	C-N-CA	-5.33	114.27	119.76
1	Dk	54	THR	N-CA-C	5.33	117.09	111.28
1	Du	54	THR	N-CA-C	5.33	117.09	111.28
1	Fw	81	ILE	N-CA-C	-5.33	98.80	107.28
2	XR	850	GLY	CA-C-O	-5.33	118.75	122.22
1	EX	72	GLY	N-CA-C	5.33	120.78	111.50
3	P1	33	ALA	CA-C-N	-5.33	114.27	119.76
3	P1	33	ALA	C-N-CA	-5.33	114.27	119.76
1	He	94	LYS	N-CA-C	5.33	117.17	111.36
1	Dj	30	ALA	N-CA-C	5.33	117.09	111.28
1	Gj	37	GLY	N-CA-C	5.33	119.08	110.87
1	Go	37	GLY	N-CA-C	5.33	119.08	110.87
1	Hy	94	LYS	N-CA-C	5.33	117.17	111.36
1	BI	16	GLY	N-CA-C	5.33	118.26	112.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	FK	54	THR	N-CA-C	5.33	117.51	111.11
3	PJ	33	ALA	CA-C-N	-5.33	114.27	119.76
3	PJ	33	ALA	C-N-CA	-5.33	114.27	119.76
1	DM	77	ALA	N-CA-C	5.33	117.19	108.55
1	HX	94	LYS	N-CA-C	5.33	117.17	111.36
1	F8	81	ILE	N-CA-C	-5.33	98.81	107.28
1	Gt	37	GLY	N-CA-C	5.33	119.08	110.87
1	Fg	54	THR	N-CA-C	5.33	117.50	111.11
1	Ao	95	ALA	N-CA-C	-5.33	102.01	108.14
1	Go	41	VAL	N-CA-C	5.33	116.10	110.72
1	DC	77	ALA	N-CA-C	5.33	117.18	108.55
1	DE	54	THR	N-CA-C	5.33	117.09	111.28
1	FQ	81	ILE	N-CA-C	-5.33	98.81	107.28
1	GX	37	GLY	N-CA-C	5.33	119.08	110.87
1	A0	95	ALA	N-CA-C	-5.33	102.01	108.14
1	H0	94	LYS	N-CA-C	5.33	117.17	111.36
1	Bt	16	GLY	N-CA-C	5.33	118.25	112.29
1	Dr	20	ALA	N-CA-C	5.33	117.17	111.36
2	Xs	850	GLY	CA-C-O	-5.33	118.76	122.22
1	F2	54	THR	N-CA-C	5.32	117.50	111.11
1	A5	68	CYS	N-CA-C	5.32	119.78	113.28
1	Fm	81	ILE	N-CA-C	-5.32	98.82	107.28
1	DT	54	THR	N-CA-C	5.32	117.08	111.28
1	Be	16	GLY	N-CA-C	5.32	118.25	112.29
1	FG	81	ILE	N-CA-C	-5.32	98.82	107.28
1	A5	95	ALA	N-CA-C	-5.32	102.02	108.14
1	Da	54	THR	N-CA-C	5.32	117.08	111.28
1	Gj	41	VAL	N-CA-C	5.32	116.09	110.72
1	Fq	30	ALA	N-CA-C	5.32	117.08	111.28
1	Ht	94	LYS	N-CA-C	5.32	117.16	111.36
1	GD	37	GLY	N-CA-C	5.32	119.06	110.87
1	DJ	54	THR	N-CA-C	5.32	117.08	111.28
1	AN	95	ALA	N-CA-C	-5.32	102.02	108.14
1	BX	16	GLY	N-CA-C	5.32	118.25	112.29
1	G0	37	GLY	N-CA-C	5.32	119.06	110.87
3	Pd	33	ALA	CA-C-N	-5.32	114.28	119.76
3	Pd	33	ALA	C-N-CA	-5.32	114.28	119.76
1	Dt	30	ALA	N-CA-C	5.32	117.08	111.28
1	FK	30	ALA	N-CA-C	5.32	117.08	111.28
3	PW	33	ALA	CA-C-N	-5.32	114.28	119.76
3	PW	33	ALA	C-N-CA	-5.32	114.28	119.76
1	G5	37	GLY	N-CA-C	5.32	119.06	110.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Dp	54	THR	N-CA-C	5.32	117.08	111.28
1	DI	30	ALA	N-CA-C	5.32	117.08	111.28
1	FP	54	THR	N-CA-C	5.32	117.49	111.11
1	Bm	16	GLY	CA-C-O	-5.32	118.56	122.23
1	Dw	20	ALA	N-CA-C	5.32	117.15	111.36
1	AD	68	CYS	N-CA-C	5.32	119.77	113.28
1	GD	41	VAL	N-CA-C	5.32	116.09	110.72
1	FF	54	THR	N-CA-C	5.32	117.49	111.11
1	H5	94	LYS	N-CA-C	5.31	117.15	111.36
1	Gy	37	GLY	N-CA-C	5.31	119.05	110.87
1	BD	16	GLY	N-CA-C	5.31	118.24	112.29
1	GX	41	VAL	N-CA-C	5.31	116.09	110.72
1	De	30	ALA	N-CA-C	5.31	117.07	111.28
1	Dd	77	ALA	N-CA-C	5.31	117.16	108.55
1	Ej	38	ARG	N-CA-C	-5.31	99.78	108.76
1	Gt	41	VAL	N-CA-C	5.31	116.09	110.72
1	DX	30	ALA	N-CA-C	5.31	117.07	111.28
1	D4	77	ALA	N-CA-C	5.31	117.15	108.55
1	Ge	41	VAL	N-CA-C	5.31	116.08	110.72
1	Dc	20	ALA	N-CA-C	5.31	117.15	111.36
1	Bh	16	GLY	CA-C-O	-5.31	118.57	122.23
1	B3	16	GLY	CA-C-O	-5.31	118.57	122.23
1	D9	77	ALA	N-CA-C	5.31	117.15	108.55
1	Aj	68	CYS	N-CA-C	5.31	119.76	113.28
1	AD	95	ALA	N-CA-C	-5.31	102.03	108.14
1	ED	37	GLY	N-CA-C	5.31	118.82	110.91
1	AI	95	ALA	CA-C-N	-5.31	113.20	119.84
1	AI	95	ALA	C-N-CA	-5.31	113.20	119.84
1	DN	30	ALA	N-CA-C	5.31	117.07	111.28
1	E2	42	GLY	N-CA-C	-5.31	101.14	111.01
1	B0	16	GLY	N-CA-C	5.31	118.23	112.29
1	Fq	54	THR	N-CA-C	5.31	117.48	111.11
1	Bw	16	GLY	CA-C-O	-5.31	118.57	122.23
1	DL	20	ALA	N-CA-C	5.31	117.15	111.36
1	BS	16	GLY	N-CA-C	5.31	118.23	112.29
3	Ps	33	ALA	CA-C-N	-5.31	114.30	119.76
3	Ps	33	ALA	C-N-CA	-5.31	114.30	119.76
2	Xm	812	GLN	N-CA-C	-5.31	105.61	111.71
1	E7	42	GLY	N-CA-C	-5.30	101.14	111.01
2	Xh	812	GLN	N-CA-C	-5.30	105.61	111.71
1	Dy	30	ALA	N-CA-C	5.30	117.06	111.28
1	D5	30	ALA	N-CA-C	5.30	117.06	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	By	77	ALA	N-CA-C	5.30	117.82	108.75
1	Eb	42	GLY	N-CA-C	-5.30	101.15	111.01
1	Bj	16	GLY	N-CA-C	5.30	118.23	112.29
1	Eq	42	GLY	N-CA-C	-5.30	101.15	111.01
3	Pz	33	ALA	CA-C-N	-5.30	114.30	119.76
3	Pz	33	ALA	C-N-CA	-5.30	114.30	119.76
1	FB	81	ILE	N-CA-C	-5.30	98.85	107.28
1	DH	77	ALA	N-CA-C	5.30	117.14	108.55
2	XQ	812	GLN	N-CA-C	-5.30	105.61	111.71
1	D0	30	ALA	N-CA-C	5.30	117.06	111.28
3	P9	33	ALA	CA-C-N	-5.30	114.30	119.76
3	P9	33	ALA	C-N-CA	-5.30	114.30	119.76
3	Pu	33	ALA	CA-C-N	-5.30	114.30	119.76
3	Pu	33	ALA	C-N-CA	-5.30	114.30	119.76
1	EA	42	GLY	N-CA-C	-5.30	101.15	111.01
1	GI	41	VAL	N-CA-C	5.30	116.07	110.72
1	Dn	77	ALA	N-CA-C	5.30	117.13	108.55
1	Fv	54	THR	N-CA-C	5.30	117.47	111.11
1	B5	16	GLY	N-CA-C	5.30	118.22	112.29
3	P4	33	ALA	CA-C-N	-5.30	114.31	119.76
3	P4	33	ALA	C-N-CA	-5.30	114.31	119.76
3	P6	33	ALA	CA-C-N	-5.30	114.31	119.76
3	P6	33	ALA	C-N-CA	-5.30	114.31	119.76
1	Ae	95	ALA	N-CA-C	-5.30	102.05	108.14
1	Ey	37	GLY	N-CA-C	5.30	118.80	110.91
3	Px	33	ALA	CA-C-N	-5.30	114.31	119.76
3	Px	33	ALA	C-N-CA	-5.30	114.31	119.76
1	BI	77	ALA	N-CA-C	5.30	117.81	108.75
3	PO	33	ALA	CA-C-N	-5.30	114.31	119.76
3	PO	33	ALA	C-N-CA	-5.30	114.31	119.76
1	AS	95	ALA	N-CA-C	-5.30	102.05	108.14
1	AX	95	ALA	N-CA-C	-5.30	102.05	108.14
1	G0	41	VAL	N-CA-C	5.29	116.07	110.72
1	Be	77	ALA	N-CA-C	5.29	117.80	108.75
1	Di	77	ALA	N-CA-C	5.29	117.13	108.55
1	Ay	68	CYS	N-CA-C	5.29	119.74	113.28
1	Dx	77	ALA	N-CA-C	5.29	117.13	108.55
1	EU	42	GLY	N-CA-C	-5.29	101.17	111.01
1	BX	77	ALA	N-CA-C	5.29	117.80	108.75
2	X3	812	GLN	N-CA-C	-5.29	105.62	111.71
1	Eg	42	GLY	N-CA-C	-5.29	101.17	111.01
1	Ev	42	GLY	N-CA-C	-5.29	101.17	111.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DG	20	ALA	N-CA-C	5.29	117.13	111.36
3	PH	33	ALA	CA-C-N	-5.29	114.31	119.76
3	PH	33	ALA	C-N-CA	-5.29	114.31	119.76
1	EP	42	GLY	N-CA-C	-5.29	101.17	111.01
1	HS	94	LYS	N-CA-C	5.29	117.13	111.36
1	DR	77	ALA	N-CA-C	5.29	117.12	108.55
2	XB	812	GLN	N-CA-C	-5.29	105.62	111.71
1	Fl	54	THR	N-CA-C	5.29	117.46	111.11
3	Pn	33	ALA	CA-C-N	-5.29	114.31	119.76
3	Pn	33	ALA	C-N-CA	-5.29	114.31	119.76
1	DV	20	ALA	N-CA-C	5.29	117.13	111.36
1	Hj	94	LYS	N-CA-C	5.29	117.12	111.36
3	Pi	33	ALA	CA-C-N	-5.29	114.31	119.76
3	Pi	33	ALA	C-N-CA	-5.29	114.31	119.76
1	Bo	16	GLY	N-CA-C	5.29	118.21	112.29
1	Ds	77	ALA	N-CA-C	5.29	117.12	108.55
1	Hc	16	GLY	CA-C-O	-5.29	118.78	122.22
1	Hh	16	GLY	CA-C-O	-5.29	118.78	122.22
1	Et	38	ARG	N-CA-C	-5.29	99.83	108.76
1	EF	42	GLY	N-CA-C	-5.29	101.17	111.01
1	EK	42	GLY	N-CA-C	-5.29	101.18	111.01
2	XL	812	GLN	N-CA-C	-5.29	105.63	111.71
1	HV	16	GLY	CA-C-O	-5.29	118.78	122.22
1	E0	38	ARG	N-CA-C	-5.29	99.83	108.76
1	Aj	95	ALA	CA-C-N	-5.29	113.23	119.84
1	Aj	95	ALA	C-N-CA	-5.29	113.23	119.84
1	Bj	77	ALA	N-CA-C	5.29	117.79	108.75
1	By	16	GLY	N-CA-C	5.29	118.21	112.29
1	Ey	38	ARG	N-CA-C	-5.29	99.83	108.76
1	ES	38	ARG	N-CA-C	-5.29	99.83	108.76
1	E5	38	ARG	N-CA-C	-5.28	99.83	108.76
1	Ee	38	ARG	N-CA-C	-5.28	99.83	108.76
1	Bc	16	GLY	CA-C-O	-5.28	118.58	122.23
1	Eo	37	GLY	N-CA-C	5.28	118.78	110.91
1	At	95	ALA	N-CA-C	-5.28	102.06	108.14
1	BN	16	GLY	N-CA-C	5.28	118.21	112.29
1	EN	38	ARG	N-CA-C	-5.28	99.83	108.76
1	HN	94	LYS	N-CA-C	5.28	117.12	111.36
1	DW	77	ALA	N-CA-C	5.28	117.11	108.55
2	X8	812	GLN	N-CA-C	-5.28	105.64	111.71
1	El	42	GLY	N-CA-C	-5.28	101.19	111.01
1	Do	30	ALA	N-CA-C	5.28	117.04	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HA	16	GLY	N-CA-C	5.28	118.20	112.29
1	EI	38	ARG	N-CA-C	-5.28	99.83	108.76
1	G5	41	VAL	N-CA-C	5.28	116.05	110.72
1	Ae	95	ALA	CA-C-N	-5.28	113.24	119.84
1	Ae	95	ALA	C-N-CA	-5.28	113.24	119.84
1	Ej	37	GLY	N-CA-C	5.28	118.78	110.91
1	Bt	77	ALA	N-CA-C	5.28	117.78	108.75
2	Xw	812	GLN	N-CA-C	-5.28	105.64	111.71
1	E5	37	GLY	N-CA-C	5.28	118.77	110.91
1	E0	37	GLY	N-CA-C	5.28	118.77	110.91
1	Hv	16	GLY	N-CA-C	5.28	118.20	112.29
1	Gy	41	VAL	N-CA-C	5.28	116.05	110.72
1	HB	16	GLY	CA-C-O	-5.28	118.79	122.22
1	HC	30	ALA	N-CA-C	5.28	117.03	111.28
1	BV	16	GLY	CA-C-O	-5.28	118.59	122.23
1	A5	95	ALA	CA-C-N	-5.28	113.25	119.84
1	A5	95	ALA	C-N-CA	-5.28	113.25	119.84
1	B5	77	ALA	N-CA-C	5.28	117.77	108.75
1	AI	95	ALA	N-CA-C	-5.28	102.07	108.14
1	BG	16	GLY	CA-C-O	-5.28	118.59	122.23
1	CM	16	GLY	CA-C-O	-5.28	118.79	122.22
1	GS	41	VAL	N-CA-C	5.28	116.05	110.72
1	H8	16	GLY	CA-C-O	-5.27	118.79	122.22
3	Pk	33	ALA	CA-C-N	-5.27	114.33	119.76
3	Pk	33	ALA	C-N-CA	-5.27	114.33	119.76
1	Eo	38	ARG	N-CA-C	-5.27	99.85	108.76
1	Et	37	GLY	N-CA-C	5.27	118.77	110.91
1	DD	30	ALA	N-CA-C	5.27	117.03	111.28
1	BE	30	ALA	N-CA-C	5.27	117.03	111.28
1	GE	16	GLY	N-CA-C	5.27	116.96	111.95
1	DS	30	ALA	N-CA-C	5.27	117.03	111.28
1	Ay	95	ALA	CA-C-N	-5.27	113.25	119.84
1	Ay	95	ALA	C-N-CA	-5.27	113.25	119.84
1	BQ	16	GLY	CA-C-O	-5.27	118.59	122.23
1	B0	77	ALA	N-CA-C	5.27	117.76	108.75
1	Ee	37	GLY	N-CA-C	5.27	118.76	110.91
1	At	95	ALA	CA-C-N	-5.27	113.25	119.84
1	At	95	ALA	C-N-CA	-5.27	113.25	119.84
3	PR	33	ALA	CA-C-N	-5.27	114.33	119.76
3	PR	33	ALA	C-N-CA	-5.27	114.33	119.76
1	Bz	30	ALA	N-CA-C	5.27	117.02	111.28
1	GO	49	LEU	N-CA-C	5.27	117.66	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	GQ	8	ALA	N-CA-C	5.27	117.51	110.35
1	Dv	37	GLY	N-CA-C	5.27	118.98	110.87
1	HQ	16	GLY	CA-C-O	-5.27	118.80	122.22
1	EX	38	ARG	N-CA-C	-5.27	99.86	108.76
1	Hn	30	ALA	N-CA-C	5.26	117.02	111.28
1	DA	37	GLY	N-CA-C	5.26	118.98	110.87
1	EN	37	GLY	N-CA-C	5.26	118.75	110.91
1	AX	95	ALA	CA-C-N	-5.26	113.26	119.84
1	AX	95	ALA	C-N-CA	-5.26	113.26	119.84
2	Xc	812	GLN	N-CA-C	-5.26	105.66	111.71
1	ED	38	ARG	N-CA-C	-5.26	99.86	108.76
1	GE	49	LEU	N-CA-C	5.26	117.66	108.76
1	EG	54	THR	N-CA-C	5.26	116.70	111.07
1	H7	16	GLY	N-CA-C	5.26	118.18	112.29
1	Gf	49	LEU	N-CA-C	5.26	117.65	108.76
1	Fj	16	GLY	CA-C-O	-5.26	118.80	122.22
1	HP	16	GLY	N-CA-C	5.26	118.18	112.29
1	BS	77	ALA	N-CA-C	5.26	117.75	108.75
1	GT	49	LEU	N-CA-C	5.26	117.65	108.76
1	A0	95	ALA	CA-C-N	-5.26	113.27	119.84
1	A0	95	ALA	C-N-CA	-5.26	113.27	119.84
1	B8	16	GLY	CA-C-O	-5.26	118.60	122.23
3	PM	33	ALA	CA-C-N	-5.26	114.34	119.76
3	PM	33	ALA	C-N-CA	-5.26	114.34	119.76
3	PC	33	ALA	CA-C-N	-5.26	114.34	119.76
3	PC	33	ALA	C-N-CA	-5.26	114.34	119.76
1	DK	37	GLY	N-CA-C	5.26	118.97	110.87
1	BN	77	ALA	N-CA-C	5.26	117.74	108.75
1	Gp	16	GLY	N-CA-C	5.26	116.94	111.95
2	XK	729	GLU	N-CA-C	5.26	117.01	111.28
1	BJ	30	ALA	N-CA-C	5.26	117.01	111.28
1	GN	41	VAL	N-CA-C	5.26	116.03	110.72
1	G6	49	LEU	N-CA-C	5.25	117.64	108.76
1	Hg	16	GLY	N-CA-C	5.25	118.18	112.29
2	XG	812	GLN	N-CA-C	-5.25	105.67	111.71
1	Hl	16	GLY	N-CA-C	5.25	118.17	112.29
1	Gk	49	LEU	N-CA-C	5.25	117.64	108.76
1	AD	95	ALA	CA-C-N	-5.25	113.27	119.84
1	AD	95	ALA	C-N-CA	-5.25	113.27	119.84
1	BD	77	ALA	N-CA-C	5.25	117.73	108.75
1	AN	95	ALA	CA-C-N	-5.25	113.27	119.84
1	AN	95	ALA	C-N-CA	-5.25	113.27	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DP	37	GLY	N-CA-C	5.25	118.96	110.87
1	EV	54	THR	N-CA-C	5.25	116.69	111.07
1	B1	30	ALA	N-CA-C	5.25	117.00	111.28
1	G1	49	LEU	N-CA-C	5.25	117.64	108.76
1	Bk	30	ALA	N-CA-C	5.25	117.00	111.28
1	Bp	30	ALA	N-CA-C	5.25	117.00	111.28
1	Gz	49	LEU	N-CA-C	5.25	117.64	108.76
1	EI	37	GLY	N-CA-C	5.25	118.73	110.91
1	GJ	49	LEU	N-CA-C	5.25	117.64	108.76
1	D2	37	GLY	N-CA-C	5.25	118.95	110.87
1	D7	37	GLY	N-CA-C	5.25	118.95	110.87
1	Ga	49	LEU	N-CA-C	5.25	117.63	108.76
1	Bo	77	ALA	N-CA-C	5.25	117.73	108.75
1	Ao	95	ALA	CA-C-N	-5.25	113.28	119.84
1	Ao	95	ALA	C-N-CA	-5.25	113.28	119.84
1	Gu	49	LEU	N-CA-C	5.25	117.63	108.76
1	ES	37	GLY	N-CA-C	5.25	118.73	110.91
1	G8	8	ALA	N-CA-C	5.25	117.49	110.35
2	Xb	729	GLU	N-CA-C	5.25	117.00	111.28
1	EQ	54	THR	N-CA-C	5.25	116.68	111.07
1	B6	30	ALA	N-CA-C	5.25	117.00	111.28
1	EX	37	GLY	N-CA-C	5.25	118.72	110.91
2	XV	812	GLN	N-CA-C	-5.25	105.68	111.71
1	H2	16	GLY	N-CA-C	5.24	118.16	112.29
1	E3	54	THR	N-CA-C	5.24	116.68	111.07
1	H3	16	GLY	CA-C-O	-5.24	118.81	122.22
1	Ec	54	THR	N-CA-C	5.24	116.68	111.07
1	Dl	37	GLY	N-CA-C	5.24	118.94	110.87
2	XA	729	GLU	N-CA-C	5.24	116.99	111.28
1	EB	54	THR	N-CA-C	5.24	116.68	111.07
1	HG	16	GLY	CA-C-O	-5.24	118.81	122.22
1	GL	8	ALA	N-CA-C	5.24	117.48	110.35
1	HL	16	GLY	CA-C-O	-5.24	118.81	122.22
1	HR	30	ALA	N-CA-C	5.24	116.99	111.28
1	HW	30	ALA	N-CA-C	5.24	116.99	111.28
1	Gh	8	ALA	N-CA-C	5.24	117.47	110.35
1	Gr	8	ALA	N-CA-C	5.24	117.47	110.35
1	GG	8	ALA	N-CA-C	5.24	117.47	110.35
1	BO	30	ALA	N-CA-C	5.24	116.99	111.28
1	H9	30	ALA	N-CA-C	5.24	116.99	111.28
1	Ba	30	ALA	N-CA-C	5.24	116.99	111.28
1	Dq	37	GLY	N-CA-C	5.24	118.93	110.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Hq	16	GLY	N-CA-C	5.24	118.16	112.29
1	Db	37	GLY	N-CA-C	5.24	118.93	110.87
1	Ez	54	THR	N-CA-C	5.24	116.67	111.07
1	HK	16	GLY	N-CA-C	5.24	118.15	112.29
2	XU	729	GLU	N-CA-C	5.24	116.99	111.28
2	Xr	812	GLN	N-CA-C	-5.24	105.69	111.71
2	Xq	729	GLU	N-CA-C	5.23	116.98	111.28
1	E8	54	THR	N-CA-C	5.23	116.67	111.07
1	Dz	30	ALA	N-CA-C	5.23	116.98	111.28
1	DF	37	GLY	N-CA-C	5.23	118.93	110.87
1	DL	8	ALA	N-CA-C	5.23	117.61	110.55
1	En	77	ALA	N-CA-C	5.23	117.69	108.75
2	Xq	720	ALA	N-CA-C	5.23	118.61	111.39
1	HM	30	ALA	N-CA-C	5.23	116.98	111.28
1	AS	95	ALA	CA-C-N	-5.23	113.30	119.84
1	AS	95	ALA	C-N-CA	-5.23	113.30	119.84
1	G3	8	ALA	N-CA-C	5.23	117.46	110.35
1	Gc	8	ALA	N-CA-C	5.23	117.46	110.35
2	Xg	720	ALA	N-CA-C	5.23	118.60	111.39
1	Dh	8	ALA	N-CA-C	5.23	117.61	110.55
1	Gp	49	LEU	N-CA-C	5.23	117.60	108.76
1	Hr	16	GLY	CA-C-O	-5.23	118.82	122.22
2	XA	720	ALA	N-CA-C	5.23	118.60	111.39
1	HU	16	GLY	N-CA-C	5.23	118.15	112.29
1	E4	77	ALA	N-CA-C	5.23	117.69	108.75
1	Ed	77	ALA	N-CA-C	5.23	117.69	108.75
1	Dg	37	GLY	N-CA-C	5.23	118.92	110.87
2	Xl	729	GLU	N-CA-C	5.23	116.98	111.28
1	EC	77	ALA	N-CA-C	5.23	117.69	108.75
1	EM	77	ALA	N-CA-C	5.23	117.69	108.75
1	Gt	78	ALA	N-CA-C	-5.22	99.44	108.69
1	Ew	54	THR	N-CA-C	5.22	116.66	111.07
1	C4	16	GLY	CA-C-O	-5.22	118.83	122.22
1	Fy	16	GLY	CA-C-O	-5.22	118.83	122.22
1	GB	8	ALA	N-CA-C	5.22	117.45	110.35
2	XU	720	ALA	N-CA-C	5.22	118.60	111.39
1	EW	77	ALA	N-CA-C	5.22	117.68	108.75
1	Es	77	ALA	N-CA-C	5.22	117.68	108.75
1	CH	16	GLY	CA-C-O	-5.22	118.83	122.22
1	EH	77	ALA	N-CA-C	5.22	117.68	108.75
1	DQ	8	ALA	N-CA-C	5.22	117.60	110.55
1	H4	30	ALA	N-CA-C	5.22	116.97	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ga	16	GLY	N-CA-C	5.22	116.91	111.95
1	Ei	77	ALA	N-CA-C	5.22	117.68	108.75
1	Dm	8	ALA	N-CA-C	5.22	117.59	110.55
1	Er	54	THR	N-CA-C	5.22	116.66	111.07
2	XF	729	GLU	N-CA-C	5.22	116.97	111.28
1	DO	41	VAL	N-CA-C	5.22	115.99	110.72
1	GT	16	GLY	N-CA-C	5.22	116.91	111.95
1	Ex	77	ALA	N-CA-C	5.22	117.67	108.75
1	GT	7	ILE	N-CA-C	5.22	117.61	111.09
1	GV	8	ALA	N-CA-C	5.22	117.44	110.35
2	X2	729	GLU	N-CA-C	5.21	116.97	111.28
1	E9	77	ALA	N-CA-C	5.21	117.67	108.75
1	Hb	16	GLY	N-CA-C	5.21	118.13	112.29
1	Hg	41	VAL	N-CA-C	5.21	120.19	109.34
2	Xg	729	GLU	N-CA-C	5.21	116.96	111.28
1	Eh	54	THR	N-CA-C	5.21	116.65	111.07
1	Gm	8	ALA	N-CA-C	5.21	117.44	110.35
1	EL	54	THR	N-CA-C	5.21	116.65	111.07
1	ER	77	ALA	N-CA-C	5.21	117.67	108.75
1	DU	37	GLY	N-CA-C	5.21	118.90	110.87
2	X7	729	GLU	N-CA-C	5.21	116.96	111.28
2	XP	729	GLU	N-CA-C	5.21	116.96	111.28
1	Gw	8	ALA	N-CA-C	5.21	117.44	110.35
1	BB	16	GLY	CA-C-O	-5.21	118.63	122.23
2	XF	720	ALA	N-CA-C	5.21	118.58	111.39
1	Ge	78	ALA	N-CA-C	-5.21	99.47	108.69
1	Hx	30	ALA	N-CA-C	5.21	116.96	111.28
1	GX	78	ALA	N-CA-C	-5.21	99.47	108.69
2	X7	720	ALA	N-CA-C	5.21	118.58	111.39
1	D8	8	ALA	N-CA-C	5.21	117.58	110.55
2	Xb	720	ALA	N-CA-C	5.21	118.58	111.39
1	AF	16	GLY	CA-C-O	-5.21	118.64	122.23
1	CR	16	GLY	CA-C-O	-5.21	118.83	122.22
1	Fo	16	GLY	CA-C-O	-5.21	118.83	122.22
1	Go	78	ALA	N-CA-C	-5.21	99.47	108.69
3	PD	65	LYS	N-CA-C	-5.21	105.61	111.28
1	EE	54	THR	N-CA-C	5.21	116.64	111.07
1	GI	78	ALA	N-CA-C	-5.21	99.47	108.69
1	BT	30	ALA	N-CA-C	5.21	116.95	111.28
1	Bf	30	ALA	N-CA-C	5.21	116.95	111.28
1	Bu	30	ALA	N-CA-C	5.21	116.95	111.28
3	PN	65	LYS	N-CA-C	-5.21	105.61	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F0	16	GLY	CA-C-O	-5.20	118.84	122.22
1	G0	78	ALA	N-CA-C	-5.20	99.48	108.69
1	Hd	30	ALA	N-CA-C	5.20	116.95	111.28
1	Hi	30	ALA	N-CA-C	5.20	116.95	111.28
1	Em	54	THR	N-CA-C	5.20	116.64	111.07
1	Ft	16	GLY	CA-C-O	-5.20	118.84	122.22
1	CN	38	ARG	N-CA-C	-5.20	100.55	109.24
1	FS	16	GLY	CA-C-O	-5.20	118.84	122.22
1	GS	78	ALA	N-CA-C	-5.20	99.48	108.69
1	Br	16	GLY	CA-C-O	-5.20	118.64	122.23
1	Gy	78	ALA	N-CA-C	-5.20	99.48	108.69
1	FI	16	GLY	CA-C-O	-5.20	118.84	122.22
2	Xn	818	ASN	CA-C-N	-5.20	114.44	119.90
2	Xn	818	ASN	C-N-CA	-5.20	114.44	119.90
1	D3	8	ALA	N-CA-C	5.20	117.57	110.55
1	Cd	16	GLY	CA-C-O	-5.20	118.84	122.22
1	Bi	30	ALA	N-CA-C	5.20	117.03	111.36
1	GH	30	ALA	N-CA-C	5.20	116.95	111.28
1	CW	16	GLY	CA-C-O	-5.20	118.84	122.22
1	HF	41	VAL	N-CA-C	5.20	120.15	109.34
1	Cj	38	ARG	N-CA-C	-5.20	100.56	109.24
1	Hs	30	ALA	N-CA-C	5.20	116.94	111.28
1	Hv	41	VAL	N-CA-C	5.20	120.15	109.34
1	Cy	38	ARG	N-CA-C	-5.20	100.56	109.24
1	CD	38	ARG	N-CA-C	-5.20	100.56	109.24
1	H2	41	VAL	N-CA-C	5.19	120.14	109.34
2	X2	720	ALA	N-CA-C	5.19	118.56	111.39
1	G5	78	ALA	N-CA-C	-5.19	99.50	108.69
3	P0	65	LYS	N-CA-C	-5.19	105.62	111.28
1	Cs	16	GLY	CA-C-O	-5.19	118.84	122.22
2	Xs	818	ASN	CA-C-N	-5.19	114.45	119.90
2	Xs	818	ASN	C-N-CA	-5.19	114.45	119.90
2	Xv	720	ALA	N-CA-C	5.19	118.56	111.39
1	HK	41	VAL	N-CA-C	5.19	120.14	109.34
1	GR	54	THR	N-CA-C	5.19	117.34	111.11
1	Hb	41	VAL	N-CA-C	5.19	120.14	109.34
3	Pj	65	LYS	N-CA-C	-5.19	105.62	111.28
3	Py	65	LYS	N-CA-C	-5.19	105.62	111.28
1	Hw	16	GLY	CA-C-O	-5.19	118.85	122.22
1	HA	41	VAL	N-CA-C	5.19	120.14	109.34
1	Gz	16	GLY	N-CA-C	5.19	116.88	111.95
1	GO	16	GLY	N-CA-C	5.19	116.88	111.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HU	41	VAL	N-CA-C	5.19	120.14	109.34
1	ET	54	THR	N-CA-C	5.19	116.62	111.07
1	DV	8	ALA	N-CA-C	5.19	117.56	110.55
1	E1	54	THR	N-CA-C	5.19	116.62	111.07
1	H7	41	VAL	N-CA-C	5.19	120.13	109.34
1	GD	78	ALA	N-CA-C	-5.19	99.51	108.69
1	DB	8	ALA	N-CA-C	5.19	117.55	110.55
1	EJ	54	THR	N-CA-C	5.19	116.62	111.07
1	HP	41	VAL	N-CA-C	5.19	120.13	109.34
1	CS	38	ARG	N-CA-C	-5.19	100.58	109.24
1	C5	38	ARG	N-CA-C	-5.19	100.58	109.24
1	Ee	77	ALA	N-CA-C	5.19	117.62	108.75
1	Gd	30	ALA	N-CA-C	5.19	116.93	111.28
1	Af	38	ARG	N-CA-C	-5.19	99.51	108.69
1	Ej	77	ALA	N-CA-C	5.19	117.62	108.75
1	Ap	38	ARG	N-CA-C	-5.19	99.51	108.69
1	CI	38	ARG	N-CA-C	-5.19	100.58	109.24
2	XK	720	ALA	N-CA-C	5.19	118.55	111.39
2	XP	720	ALA	N-CA-C	5.19	118.55	111.39
1	EX	77	ALA	N-CA-C	5.19	117.62	108.75
2	Xl	720	ALA	N-CA-C	5.18	118.55	111.39
1	Bn	30	ALA	N-CA-C	5.18	117.01	111.36
2	Xv	729	GLU	N-CA-C	5.18	116.93	111.28
1	GN	78	ALA	N-CA-C	-5.18	99.52	108.69
1	GT	8	ALA	N-CA-C	5.18	117.81	110.50
3	P5	65	LYS	N-CA-C	-5.18	105.63	111.28
1	C9	16	GLY	CA-C-O	-5.18	118.85	122.22
1	Ea	54	THR	N-CA-C	5.18	116.62	111.07
1	Ga	8	ALA	N-CA-C	5.18	117.81	110.50
1	Ef	54	THR	N-CA-C	5.18	116.62	111.07
1	Gj	78	ALA	N-CA-C	-5.18	99.52	108.69
1	Co	38	ARG	N-CA-C	-5.18	100.59	109.24
1	Eo	77	ALA	N-CA-C	5.18	117.61	108.75
1	Gs	30	ALA	N-CA-C	5.18	116.93	111.28
1	Dw	8	ALA	N-CA-C	5.18	117.55	110.55
1	Gx	30	ALA	N-CA-C	5.18	116.93	111.28
1	Az	38	ARG	N-CA-C	-5.18	99.52	108.69
1	HF	16	GLY	N-CA-C	5.18	118.09	112.29
1	Aa	38	ARG	N-CA-C	-5.18	99.52	108.69
1	Dc	8	ALA	N-CA-C	5.18	117.54	110.55
1	Hm	16	GLY	CA-C-O	-5.18	118.85	122.22
1	Aq	16	GLY	CA-C-O	-5.18	118.66	122.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Fx	10	GLY	N-CA-C	-5.18	102.12	111.19
1	CC	16	GLY	CA-C-O	-5.18	118.85	122.22
1	HH	30	ALA	N-CA-C	5.18	116.93	111.28
1	B4	30	ALA	N-CA-C	5.18	117.00	111.36
1	Fe	16	GLY	CA-C-O	-5.18	118.85	122.22
1	Ek	54	THR	N-CA-C	5.18	116.61	111.07
1	Et	77	ALA	N-CA-C	5.18	117.61	108.75
1	Ey	77	ALA	N-CA-C	5.18	117.61	108.75
1	GE	8	ALA	N-CA-C	5.18	117.80	110.50
1	AJ	38	ARG	N-CA-C	-5.18	99.52	108.69
1	BM	30	ALA	N-CA-C	5.18	117.00	111.36
1	F5	16	GLY	CA-C-O	-5.18	118.85	122.22
1	C0	38	ARG	N-CA-C	-5.18	100.59	109.24
1	FN	16	GLY	CA-C-O	-5.18	118.86	122.22
1	GW	30	ALA	N-CA-C	5.18	116.92	111.28
1	G1	16	GLY	N-CA-C	5.18	116.87	111.95
1	E5	77	ALA	N-CA-C	5.18	117.60	108.75
1	E6	54	THR	N-CA-C	5.18	116.61	111.07
2	X9	818	ASN	CA-C-N	-5.18	114.47	119.90
2	X9	818	ASN	C-N-CA	-5.18	114.47	119.90
1	Hl	41	VAL	N-CA-C	5.18	120.11	109.34
1	Gp	8	ALA	N-CA-C	5.18	117.80	110.50
1	HB	95	ALA	CA-C-N	-5.18	114.65	120.14
1	HB	95	ALA	C-N-CA	-5.18	114.65	120.14
1	FC	10	GLY	N-CA-C	-5.18	102.13	111.19
1	GJ	16	GLY	N-CA-C	5.18	116.87	111.95
1	EO	54	THR	N-CA-C	5.18	116.61	111.07
2	XR	818	ASN	CA-C-N	-5.18	114.47	119.90
2	XR	818	ASN	C-N-CA	-5.18	114.47	119.90
1	BW	30	ALA	N-CA-C	5.18	117.00	111.36
1	Ag	16	GLY	CA-C-O	-5.17	118.66	122.23
2	Xn	811	GLY	N-CA-C	-5.17	100.92	113.18
1	Fs	10	GLY	N-CA-C	-5.17	102.14	111.19
2	XC	818	ASN	CA-C-N	-5.17	114.47	119.90
2	XC	818	ASN	C-N-CA	-5.17	114.47	119.90
1	Bd	30	ALA	N-CA-C	5.17	117.00	111.36
1	Bs	30	ALA	N-CA-C	5.17	117.00	111.36
1	EI	77	ALA	N-CA-C	5.17	117.60	108.75
1	Au	38	ARG	N-CA-C	-5.17	99.54	108.69
1	AO	38	ARG	N-CA-C	-5.17	99.54	108.69
1	DO	30	ALA	N-CA-C	5.17	116.92	111.28
2	Xx	811	GLY	N-CA-C	-5.17	100.93	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D6	41	VAL	N-CA-C	5.17	115.94	110.72
1	Gi	54	THR	N-CA-C	5.17	117.31	111.11
1	G4	54	THR	N-CA-C	5.17	117.31	111.11
1	Al	16	GLY	CA-C-O	-5.17	118.67	122.23
1	FD	16	GLY	CA-C-O	-5.17	118.86	122.22
1	GH	54	THR	N-CA-C	5.17	117.31	111.11
3	PS	65	LYS	N-CA-C	-5.17	105.65	111.28
1	FR	10	GLY	N-CA-C	-5.17	102.15	111.19
1	Gd	54	THR	N-CA-C	5.17	117.31	111.11
3	Po	65	LYS	N-CA-C	-5.17	105.65	111.28
1	DG	8	ALA	N-CA-C	5.17	117.52	110.55
1	GM	54	THR	N-CA-C	5.17	117.31	111.11
1	GW	54	THR	N-CA-C	5.17	117.31	111.11
1	G1	8	ALA	N-CA-C	5.16	117.78	110.50
1	B9	30	ALA	N-CA-C	5.16	116.99	111.36
1	Hq	41	VAL	N-CA-C	5.16	120.08	109.34
1	Bx	30	ALA	N-CA-C	5.16	116.99	111.36
1	FH	10	GLY	N-CA-C	-5.16	102.15	111.19
2	XH	811	GLY	N-CA-C	-5.16	100.94	113.18
1	GJ	8	ALA	N-CA-C	5.16	117.78	110.50
2	Xd	818	ASN	CA-C-N	-5.16	114.48	119.90
2	Xd	818	ASN	C-N-CA	-5.16	114.48	119.90
1	Ak	38	ARG	N-CA-C	-5.16	99.55	108.69
1	Ct	38	ARG	N-CA-C	-5.16	100.62	109.24
1	BH	30	ALA	N-CA-C	5.16	116.99	111.36
1	ES	77	ALA	N-CA-C	5.16	117.58	108.75
1	BR	30	ALA	N-CA-C	5.16	116.99	111.36
2	XW	818	ASN	CA-C-N	-5.16	114.48	119.90
2	XW	818	ASN	C-N-CA	-5.16	114.48	119.90
1	A1	38	ARG	N-CA-C	-5.16	99.56	108.69
1	G6	8	ALA	N-CA-C	5.16	117.78	110.50
1	Da	41	VAL	N-CA-C	5.16	115.93	110.72
1	Df	41	VAL	N-CA-C	5.16	115.93	110.72
1	GO	8	ALA	N-CA-C	5.16	117.78	110.50
1	AT	38	ARG	N-CA-C	-5.16	99.56	108.69
1	DT	41	VAL	N-CA-C	5.16	115.93	110.72
1	Fd	10	GLY	N-CA-C	-5.16	102.16	111.19
1	Hh	95	ALA	CA-C-N	-5.16	114.67	120.14
1	Hh	95	ALA	C-N-CA	-5.16	114.67	120.14
1	Dr	8	ALA	N-CA-C	5.16	117.51	110.55
1	Gs	54	THR	N-CA-C	5.16	117.30	111.11
2	XR	811	GLY	N-CA-C	-5.16	100.95	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D6	30	ALA	N-CA-C	5.16	116.90	111.28
1	F4	10	GLY	N-CA-C	-5.16	102.17	111.19
1	G4	30	ALA	N-CA-C	5.16	116.90	111.28
2	X4	811	GLY	N-CA-C	-5.16	100.96	113.18
1	G6	16	GLY	N-CA-C	5.16	116.85	111.95
1	E0	77	ALA	N-CA-C	5.16	117.56	108.75
3	Pe	65	LYS	N-CA-C	-5.16	105.66	111.28
2	Xs	811	GLY	N-CA-C	-5.16	100.96	113.18
1	EN	77	ALA	N-CA-C	5.16	117.57	108.75
3	PX	65	LYS	N-CA-C	-5.16	105.66	111.28
1	A6	38	ARG	N-CA-C	-5.15	99.57	108.69
2	X9	811	GLY	N-CA-C	-5.15	100.97	113.18
2	XH	818	ASN	CA-C-N	-5.15	114.49	119.90
2	XH	818	ASN	C-N-CA	-5.15	114.49	119.90
1	Dk	41	VAL	N-CA-C	5.15	115.92	110.72
2	Xx	818	ASN	CA-C-N	-5.15	114.49	119.90
2	Xx	818	ASN	C-N-CA	-5.15	114.49	119.90
1	F9	10	GLY	N-CA-C	-5.15	102.18	111.19
1	G9	54	THR	N-CA-C	5.15	117.29	111.11
1	Ce	38	ARG	N-CA-C	-5.15	100.64	109.24
2	Xd	811	GLY	N-CA-C	-5.15	100.97	113.18
1	Dk	30	ALA	N-CA-C	5.15	116.89	111.28
2	XW	811	GLY	N-CA-C	-5.15	100.97	113.18
1	Cn	16	GLY	CA-C-O	-5.15	118.87	122.22
1	Fn	10	GLY	N-CA-C	-5.15	102.18	111.19
1	Gn	30	ALA	N-CA-C	5.15	116.89	111.28
3	Pt	65	LYS	N-CA-C	-5.15	105.67	111.28
1	CX	38	ARG	N-CA-C	-5.15	100.64	109.24
1	D1	41	VAL	N-CA-C	5.15	115.92	110.72
1	Hn	17	LEU	N-CA-C	5.15	118.72	112.23
1	Dp	41	VAL	N-CA-C	5.15	115.92	110.72
1	Ep	54	THR	N-CA-C	5.15	116.58	111.07
1	Ft	38	ARG	N-CA-C	-5.15	100.06	108.76
1	Du	41	VAL	N-CA-C	5.15	115.92	110.72
1	Eu	54	THR	N-CA-C	5.15	116.58	111.07
1	GC	54	THR	N-CA-C	5.15	117.29	111.11
1	Ab	16	GLY	CA-C-O	-5.15	118.68	122.23
1	Gf	8	ALA	N-CA-C	5.15	117.76	110.50
1	Gx	54	THR	N-CA-C	5.15	117.28	111.11
1	AU	16	GLY	CA-C-O	-5.15	118.68	122.23
1	Fe	38	ARG	N-CA-C	-5.14	100.06	108.76
1	Gk	8	ALA	N-CA-C	5.14	117.75	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Gu	8	ALA	N-CA-C	5.14	117.75	110.50
1	Gz	8	ALA	N-CA-C	5.14	117.75	110.50
1	DE	41	VAL	N-CA-C	5.14	115.92	110.72
2	XM	811	GLY	N-CA-C	-5.14	100.99	113.18
1	FX	38	ARG	N-CA-C	-5.14	100.06	108.76
1	Fi	10	GLY	N-CA-C	-5.14	102.19	111.19
2	Xi	811	GLY	N-CA-C	-5.14	100.99	113.18
1	Hx	17	LEU	N-CA-C	5.14	118.71	112.23
1	ED	77	ALA	N-CA-C	5.14	117.55	108.75
1	FD	38	ARG	N-CA-C	-5.14	100.07	108.76
1	BC	30	ALA	N-CA-C	5.14	116.97	111.36
3	PI	54	GLY	N-CA-C	5.14	125.37	113.18
1	FM	10	GLY	N-CA-C	-5.14	102.19	111.19
1	G9	30	ALA	N-CA-C	5.14	116.88	111.28
1	AE	38	ARG	N-CA-C	-5.14	99.59	108.69
1	FN	38	ARG	N-CA-C	-5.14	100.07	108.76
1	Fo	38	ARG	N-CA-C	-5.14	100.07	108.76
2	XC	811	GLY	N-CA-C	-5.14	101.00	113.18
1	AK	16	GLY	CA-C-O	-5.14	118.68	122.23
1	FW	10	GLY	N-CA-C	-5.14	102.20	111.19
1	F0	38	ARG	N-CA-C	-5.14	100.08	108.76
1	Gf	16	GLY	N-CA-C	5.14	116.83	111.95
1	Fy	38	ARG	N-CA-C	-5.14	100.08	108.76
1	GM	30	ALA	N-CA-C	5.14	116.88	111.28
1	FS	38	ARG	N-CA-C	-5.14	100.08	108.76
1	F5	38	ARG	N-CA-C	-5.14	100.08	108.76
2	XM	818	ASN	CA-C-N	-5.14	114.51	119.90
2	XM	818	ASN	C-N-CA	-5.14	114.51	119.90
1	GU	8	ALA	N-CA-C	5.14	117.31	110.53
2	X4	818	ASN	CA-C-N	-5.13	114.51	119.90
2	X4	818	ASN	C-N-CA	-5.13	114.51	119.90
3	P0	76	ILE	N-CA-C	-5.13	100.92	108.11
1	Gc	83	ARG	N-CA-C	-5.13	100.33	109.06
1	Fj	38	ARG	N-CA-C	-5.13	100.08	108.76
1	Gi	30	ALA	N-CA-C	5.13	116.88	111.28
1	Hi	17	LEU	N-CA-C	5.13	118.70	112.23
1	FI	38	ARG	N-CA-C	-5.13	100.08	108.76
1	FO	83	ARG	N-CA-C	-5.13	100.53	108.90
3	PS	76	ILE	N-CA-C	-5.13	100.92	108.11
1	GR	30	ALA	N-CA-C	5.13	116.88	111.28
1	GV	83	ARG	N-CA-C	-5.13	100.33	109.06
1	Gr	83	ARG	N-CA-C	-5.13	100.33	109.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P0	54	GLY	N-CA-C	5.13	125.34	113.18
1	Gb	8	ALA	N-CA-C	5.13	117.30	110.53
1	Al	76	VAL	N-CA-C	-5.13	106.68	111.45
3	PI	65	LYS	N-CA-C	-5.13	105.69	111.28
3	PS	54	GLY	N-CA-C	5.13	125.34	113.18
1	Av	16	GLY	CA-C-O	-5.13	118.69	122.23
1	GB	83	ARG	N-CA-C	-5.13	100.34	109.06
1	GC	30	ALA	N-CA-C	5.13	116.87	111.28
1	GL	83	ARG	N-CA-C	-5.13	100.34	109.06
1	G3	83	ARG	N-CA-C	-5.13	100.34	109.06
1	H4	17	LEU	N-CA-C	5.13	118.69	112.23
3	Py	54	GLY	N-CA-C	5.13	125.33	113.18
1	GG	83	ARG	N-CA-C	-5.13	100.34	109.06
1	HH	17	LEU	N-CA-C	5.13	118.69	112.23
3	PN	54	GLY	N-CA-C	5.13	125.34	113.18
1	GL	76	VAL	N-CA-C	-5.13	106.68	111.45
1	HM	17	LEU	N-CA-C	5.13	118.69	112.23
1	Fu	83	ARG	N-CA-C	-5.13	100.55	108.90
3	PD	76	ILE	N-CA-C	-5.13	100.93	108.11
3	Pj	54	GLY	N-CA-C	5.12	125.33	113.18
1	Gh	83	ARG	N-CA-C	-5.12	100.35	109.06
3	Pt	76	ILE	N-CA-C	-5.12	100.94	108.11
1	Gr	76	VAL	N-CA-C	-5.12	106.68	111.45
1	Hw	95	ALA	CA-C-N	-5.12	114.71	120.14
1	Hw	95	ALA	C-N-CA	-5.12	114.71	120.14
1	Gm	83	ARG	N-CA-C	-5.12	100.35	109.06
1	Gn	54	THR	N-CA-C	5.12	117.26	111.11
1	BF	16	GLY	CA-C-O	-5.12	118.69	122.23
1	Gw	83	ARG	N-CA-C	-5.12	100.35	109.06
1	Cx	16	GLY	CA-C-O	-5.12	118.89	122.22
1	Fz	83	ARG	N-CA-C	-5.12	100.55	108.90
1	HC	17	LEU	N-CA-C	5.12	118.68	112.23
1	GG	76	VAL	N-CA-C	-5.12	106.69	111.45
1	HV	95	ALA	CA-C-N	-5.12	114.71	120.14
1	HV	95	ALA	C-N-CA	-5.12	114.71	120.14
1	H3	95	ALA	CA-C-N	-5.12	114.71	120.14
1	H3	95	ALA	C-N-CA	-5.12	114.71	120.14
1	Hd	17	LEU	N-CA-C	5.12	118.68	112.23
1	Dz	41	VAL	N-CA-C	5.12	115.89	110.72
1	GB	76	VAL	N-CA-C	-5.12	106.69	111.45
1	HK	54	THR	N-CA-C	5.12	116.55	111.07
1	DJ	41	VAL	N-CA-C	5.12	115.89	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	16	GLY	CA-C-O	-5.12	118.70	122.23
3	P5	54	GLY	N-CA-C	5.12	125.31	113.18
3	Pe	54	GLY	N-CA-C	5.12	125.31	113.18
1	Fk	83	ARG	N-CA-C	-5.12	100.56	108.90
1	Gk	16	GLY	N-CA-C	5.12	116.81	111.95
3	PI	42	ILE	N-CA-C	-5.12	101.04	108.36
3	PX	54	GLY	N-CA-C	5.12	125.31	113.18
1	HW	17	LEU	N-CA-C	5.12	118.68	112.23
1	H9	17	LEU	N-CA-C	5.12	118.68	112.23
1	HR	17	LEU	N-CA-C	5.12	118.68	112.23
1	G2	8	ALA	N-CA-C	5.12	117.28	110.53
3	Po	76	ILE	N-CA-C	-5.12	100.95	108.11
3	PD	54	GLY	N-CA-C	5.12	125.30	113.18
1	GK	8	ALA	N-CA-C	5.12	117.28	110.53
1	FJ	83	ARG	N-CA-C	-5.12	100.56	108.90
1	Gm	76	VAL	N-CA-C	-5.11	106.69	111.45
1	Gq	8	ALA	N-CA-C	5.11	117.28	110.53
1	D1	30	ALA	N-CA-C	5.11	116.85	111.28
3	Po	54	GLY	N-CA-C	5.11	125.30	113.18
1	H8	95	ALA	CA-C-N	-5.11	114.72	120.14
1	H8	95	ALA	C-N-CA	-5.11	114.72	120.14
1	Gc	76	VAL	N-CA-C	-5.11	106.70	111.45
1	Cn	37	GLY	N-CA-C	5.11	118.53	110.91
1	Bq	16	GLY	CA-C-O	-5.11	118.70	122.23
3	Pt	54	GLY	N-CA-C	5.11	125.29	113.18
1	G8	83	ARG	N-CA-C	-5.11	100.38	109.06
3	Pe	42	ILE	N-CA-C	-5.11	101.06	108.36
1	Ff	83	ARG	N-CA-C	-5.11	100.57	108.90
1	Gu	16	GLY	N-CA-C	5.11	116.80	111.95
1	CH	37	GLY	N-CA-C	5.11	118.52	110.91
1	DN	95	ALA	CA-C-N	-5.11	114.54	119.90
1	DN	95	ALA	C-N-CA	-5.11	114.54	119.90
3	PN	42	ILE	N-CA-C	-5.11	101.06	108.36
1	GQ	83	ARG	N-CA-C	-5.11	100.38	109.06
1	F6	83	ARG	N-CA-C	-5.11	100.58	108.90
3	Pj	76	ILE	N-CA-C	-5.11	100.96	108.11
1	Gv	8	ALA	N-CA-C	5.11	117.27	110.53
1	Gh	76	VAL	N-CA-C	-5.10	106.70	111.45
3	PX	42	ILE	N-CA-C	-5.10	101.06	108.36
1	Hm	95	ALA	CA-C-N	-5.10	114.73	120.14
1	Hm	95	ALA	C-N-CA	-5.10	114.73	120.14
1	Hs	17	LEU	N-CA-C	5.10	118.66	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DQ	94	LYS	N-CA-C	5.10	116.92	111.36
1	G3	76	VAL	N-CA-C	-5.10	106.71	111.45
1	F1	83	ARG	N-CA-C	-5.10	100.59	108.90
1	C4	37	GLY	N-CA-C	5.10	118.51	110.91
1	A7	16	GLY	CA-C-O	-5.10	118.71	122.23
3	Pj	42	ILE	N-CA-C	-5.10	101.07	108.36
1	Du	30	ALA	N-CA-C	5.10	116.84	111.28
3	Py	76	ILE	N-CA-C	-5.10	100.97	108.11
1	DB	94	LYS	N-CA-C	5.10	116.92	111.36
1	AP	16	GLY	CA-C-O	-5.10	118.71	122.23
3	P5	42	ILE	N-CA-C	-5.10	101.07	108.36
1	G8	76	VAL	N-CA-C	-5.10	106.71	111.45
1	C9	37	GLY	N-CA-C	5.10	118.50	110.91
1	Bb	16	GLY	CA-C-O	-5.10	118.71	122.23
3	Py	42	ILE	N-CA-C	-5.10	101.07	108.36
1	GA	8	ALA	N-CA-C	5.10	117.26	110.53
2	XC	802	VAL	N-CA-C	5.10	116.06	108.46
3	P5	76	ILE	N-CA-C	-5.10	100.97	108.11
1	G7	8	ALA	N-CA-C	5.10	117.26	110.53
1	Cd	37	GLY	N-CA-C	5.10	118.50	110.91
1	Gg	8	ALA	N-CA-C	5.10	117.26	110.53
3	Pt	42	ILE	N-CA-C	-5.10	101.07	108.36
3	PN	76	ILE	N-CA-C	-5.10	100.97	108.11
1	Hg	54	THR	N-CA-C	5.09	116.52	111.07
1	Ci	37	GLY	N-CA-C	5.09	118.50	110.91
2	Xi	818	ASN	CA-C-N	-5.09	114.55	119.90
2	Xi	818	ASN	C-N-CA	-5.09	114.55	119.90
1	Cx	37	GLY	N-CA-C	5.09	118.50	110.91
1	DJ	30	ALA	N-CA-C	5.09	116.83	111.28
1	A7	76	VAL	N-CA-C	-5.09	106.72	111.45
1	HI	54	THR	N-CA-C	5.09	116.52	111.07
1	GP	8	ALA	N-CA-C	5.09	117.25	110.53
1	H7	54	THR	N-CA-C	5.09	116.52	111.07
3	P0	42	ILE	N-CA-C	-5.09	101.08	108.36
1	D8	94	LYS	N-CA-C	5.09	116.91	111.36
3	PD	42	ILE	N-CA-C	-5.09	101.08	108.36
1	GF	8	ALA	N-CA-C	5.09	117.25	110.53
1	HL	95	ALA	CA-C-N	-5.09	114.75	120.14
1	HL	95	ALA	C-N-CA	-5.09	114.75	120.14
3	PS	42	ILE	N-CA-C	-5.09	101.08	108.36
1	GQ	76	VAL	N-CA-C	-5.09	106.72	111.45
1	DT	30	ALA	N-CA-C	5.09	116.83	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Pe	76	ILE	N-CA-C	-5.09	100.99	108.11
1	Hc	95	ALA	CA-C-N	-5.09	114.75	120.14
1	Hc	95	ALA	C-N-CA	-5.09	114.75	120.14
1	Gl	8	ALA	N-CA-C	5.09	117.25	110.53
1	HA	54	THR	N-CA-C	5.09	116.51	111.07
1	DE	30	ALA	N-CA-C	5.09	116.82	111.28
2	X9	802	VAL	N-CA-C	5.08	116.04	108.46
2	Xs	802	VAL	N-CA-C	5.08	116.03	108.46
1	Do	95	ALA	CA-C-N	-5.08	114.56	119.90
1	Do	95	ALA	C-N-CA	-5.08	114.56	119.90
3	Po	42	ILE	N-CA-C	-5.08	101.09	108.36
1	Dt	95	ALA	CA-C-N	-5.08	114.56	119.90
1	Dt	95	ALA	C-N-CA	-5.08	114.56	119.90
1	GV	76	VAL	N-CA-C	-5.08	106.73	111.45
1	Fa	83	ARG	N-CA-C	-5.08	100.62	108.90
1	Df	30	ALA	N-CA-C	5.08	116.82	111.28
3	PI	76	ILE	N-CA-C	-5.08	101.00	108.11
1	Aq	76	VAL	N-CA-C	-5.08	106.73	111.45
1	HQ	95	ALA	CA-C-N	-5.08	114.76	120.14
1	HQ	95	ALA	C-N-CA	-5.08	114.76	120.14
2	Xr	804	LYS	N-CA-C	5.08	116.81	111.28
1	H2	54	THR	N-CA-C	5.08	116.50	111.07
1	Fp	83	ARG	N-CA-C	-5.08	100.63	108.90
1	CC	37	GLY	N-CA-C	5.08	118.47	110.91
1	CR	37	GLY	N-CA-C	5.08	118.47	110.91
1	FX	16	GLY	CA-C-O	-5.08	118.92	122.22
3	PX	76	ILE	N-CA-C	-5.08	101.00	108.11
1	CW	37	GLY	N-CA-C	5.08	118.47	110.91
1	Hb	54	THR	N-CA-C	5.07	116.50	111.07
1	Da	30	ALA	N-CA-C	5.07	116.81	111.28
2	XR	802	VAL	N-CA-C	5.07	116.02	108.46
1	AA	16	GLY	CA-C-O	-5.07	118.73	122.23
1	Cs	37	GLY	N-CA-C	5.07	118.47	110.91
1	HG	95	ALA	CA-C-N	-5.07	114.77	120.14
1	HG	95	ALA	C-N-CA	-5.07	114.77	120.14
1	HP	54	THR	N-CA-C	5.07	116.50	111.07
1	Dj	95	ALA	CA-C-N	-5.07	114.58	119.90
1	Dj	95	ALA	C-N-CA	-5.07	114.58	119.90
1	HF	54	THR	N-CA-C	5.07	116.49	111.07
1	FE	83	ARG	N-CA-C	-5.07	100.64	108.90
1	DI	95	ALA	CA-C-N	-5.07	114.58	119.90
1	DI	95	ALA	C-N-CA	-5.07	114.58	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	EH	7	ILE	N-CA-C	5.07	116.98	112.17
1	BU	16	GLY	CA-C-O	-5.07	118.73	122.23
1	Gw	76	VAL	N-CA-C	-5.07	106.74	111.45
2	Xp	816	GLY	N-CA-C	5.06	119.87	113.24
1	Gn	95	ALA	CA-C-N	-5.06	114.74	119.85
1	Gn	95	ALA	C-N-CA	-5.06	114.74	119.85
1	CM	37	GLY	N-CA-C	5.06	118.45	110.91
1	D5	95	ALA	CA-C-N	-5.06	114.59	119.90
1	D5	95	ALA	C-N-CA	-5.06	114.59	119.90
1	A2	76	VAL	N-CA-C	-5.06	106.75	111.45
1	AA	76	VAL	N-CA-C	-5.06	106.75	111.45
1	FT	83	ARG	N-CA-C	-5.06	100.66	108.90
1	DV	94	LYS	N-CA-C	5.06	116.87	111.36
1	B2	16	GLY	CA-C-O	-5.06	118.74	122.23
2	Xd	802	VAL	N-CA-C	5.06	115.99	108.46
1	Dy	95	ALA	CA-C-N	-5.06	114.59	119.90
1	Dy	95	ALA	C-N-CA	-5.06	114.59	119.90
2	Xx	802	VAL	N-CA-C	5.06	115.99	108.46
2	Xz	816	GLY	N-CA-C	5.06	119.86	113.24
1	BK	16	GLY	CA-C-O	-5.06	118.74	122.23
2	XW	802	VAL	N-CA-C	5.06	115.99	108.46
1	AQ	17	LEU	CA-C-N	-5.05	117.06	120.24
1	AQ	17	LEU	C-N-CA	-5.05	117.06	120.24
2	X1	816	GLY	N-CA-C	5.05	119.86	113.24
1	Dp	30	ALA	N-CA-C	5.05	116.79	111.28
1	DS	95	ALA	CA-C-N	-5.05	114.60	119.90
1	DS	95	ALA	C-N-CA	-5.05	114.60	119.90
2	X4	802	VAL	N-CA-C	5.05	115.98	108.46
2	Xn	802	VAL	N-CA-C	5.05	115.98	108.46
1	Hv	54	THR	N-CA-C	5.05	116.47	111.07
1	DL	94	LYS	N-CA-C	5.05	116.86	111.36
1	Bg	16	GLY	CA-C-O	-5.05	118.75	122.23
2	Xk	816	GLY	N-CA-C	5.05	119.85	113.24
1	Dm	94	LYS	N-CA-C	5.05	116.86	111.36
1	DG	94	LYS	N-CA-C	5.05	116.86	111.36
1	Bu	25	ASP	N-CA-C	-5.04	105.67	111.07
1	Bz	25	ASP	N-CA-C	-5.04	105.67	111.07
2	XH	802	VAL	N-CA-C	5.04	115.98	108.46
1	Ab	76	VAL	N-CA-C	-5.04	106.76	111.45
1	BV	8	ALA	N-CA-C	5.04	117.61	110.50
2	XG	804	LYS	N-CA-C	5.04	116.78	111.28
2	Xa	816	GLY	N-CA-C	5.04	119.84	113.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	De	95	ALA	CA-C-N	-5.04	114.61	119.90
1	De	95	ALA	C-N-CA	-5.04	114.61	119.90
2	Xf	816	GLY	N-CA-C	5.04	119.84	113.24
1	Bw	8	ALA	N-CA-C	5.04	117.61	110.50
1	AP	76	VAL	N-CA-C	-5.04	106.76	111.45
1	Hq	54	THR	N-CA-C	5.04	116.46	111.07
2	X6	816	GLY	N-CA-C	5.04	119.84	113.24
1	Ba	25	ASP	N-CA-C	-5.04	105.68	111.07
1	Ed	7	ILE	N-CA-C	5.04	116.96	112.17
2	Xh	804	LYS	N-CA-C	5.04	116.77	111.28
1	BL	8	ALA	N-CA-C	5.04	117.60	110.50
1	HU	54	THR	N-CA-C	5.04	116.46	111.07
1	BT	25	ASP	N-CA-C	-5.04	105.68	111.07
1	EW	7	ILE	N-CA-C	5.04	116.96	112.17
1	D0	95	ALA	CA-C-N	-5.04	114.61	119.90
1	D0	95	ALA	C-N-CA	-5.04	114.61	119.90
1	Hr	95	ALA	CA-C-N	-5.04	114.80	120.14
1	Hr	95	ALA	C-N-CA	-5.04	114.80	120.14
1	GC	95	ALA	CA-C-N	-5.04	114.76	119.85
1	GC	95	ALA	C-N-CA	-5.04	114.76	119.85
1	D3	94	LYS	N-CA-C	5.04	116.85	111.36
3	Pq	52	CYS	N-CA-C	5.04	116.83	108.02
3	Pv	52	CYS	N-CA-C	5.04	116.83	108.02
2	Xu	816	GLY	N-CA-C	5.04	119.84	113.24
1	BA	16	GLY	CA-C-O	-5.04	118.76	122.23
2	XE	816	GLY	N-CA-C	5.04	119.84	113.24
2	Xc	804	LYS	N-CA-C	5.04	116.77	111.28
1	B3	8	ALA	N-CA-C	5.03	117.60	110.50
3	Pg	52	CYS	N-CA-C	5.03	116.83	108.02
2	Xi	802	VAL	N-CA-C	5.03	115.96	108.46
2	Xn	849	THR	N-CA-C	-5.03	101.72	109.52
1	Es	7	ILE	N-CA-C	5.03	116.95	112.17
1	Av	76	VAL	N-CA-C	-5.03	106.77	111.45
1	Ex	7	ILE	N-CA-C	5.03	116.95	112.17
1	BE	25	ASP	N-CA-C	-5.03	105.68	111.07
1	AK	76	VAL	N-CA-C	-5.03	106.77	111.45
3	PK	52	CYS	N-CA-C	5.03	116.83	108.02
2	XO	816	GLY	N-CA-C	5.03	119.83	113.24
3	PU	52	CYS	N-CA-C	5.03	116.83	108.02
2	XT	816	GLY	N-CA-C	5.03	119.83	113.24
1	Dc	94	LYS	N-CA-C	5.03	116.84	111.36
1	Bv	16	GLY	CA-C-O	-5.03	118.76	122.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Pl	52	CYS	N-CA-C	5.03	116.82	108.02
1	Bp	25	ASP	N-CA-C	-5.03	105.69	111.07
1	DD	95	ALA	CA-C-N	-5.03	114.62	119.90
1	DD	95	ALA	C-N-CA	-5.03	114.62	119.90
2	XF	727	THR	CA-C-N	-5.03	113.47	119.05
2	XF	727	THR	C-N-CA	-5.03	113.47	119.05
3	P2	52	CYS	N-CA-C	5.03	116.82	108.02
1	Dh	94	LYS	N-CA-C	5.03	116.84	111.36
1	Dm	7	ILE	N-CA-C	5.03	115.80	110.72
1	Dt	85	HIS	N-CA-C	-5.03	103.89	110.53
1	Dv	77	ALA	N-CA-C	5.03	116.70	108.76
2	XW	849	THR	N-CA-C	-5.03	101.73	109.52
3	Pb	52	CYS	N-CA-C	5.03	116.81	108.02
1	Bc	8	ALA	N-CA-C	5.03	117.59	110.50
1	Bh	8	ALA	N-CA-C	5.03	117.59	110.50
1	Dw	94	LYS	N-CA-C	5.03	116.84	111.36
2	Xw	804	LYS	N-CA-C	5.03	116.76	111.28
1	EC	7	ILE	N-CA-C	5.03	116.94	112.17
1	BG	8	ALA	N-CA-C	5.03	117.59	110.50
2	XJ	816	GLY	N-CA-C	5.03	119.82	113.24
1	B1	25	ASP	N-CA-C	-5.02	105.69	111.07
3	PF	52	CYS	N-CA-C	5.02	116.81	108.02
2	XM	802	VAL	N-CA-C	5.02	115.95	108.46
2	X3	804	LYS	N-CA-C	5.02	116.75	111.28
1	B6	25	ASP	N-CA-C	-5.02	105.70	111.07
2	XH	849	THR	N-CA-C	-5.02	101.73	109.52
2	XL	804	LYS	N-CA-C	5.02	116.75	111.28
1	BO	25	ASP	N-CA-C	-5.02	105.70	111.07
2	XR	826	ARG	N-CA-C	5.02	116.38	109.15
1	G9	95	ALA	CA-C-N	-5.02	114.78	119.85
1	G9	95	ALA	C-N-CA	-5.02	114.78	119.85
2	Xn	826	ARG	N-CA-C	5.02	116.38	109.15
1	Br	8	ALA	N-CA-C	5.02	117.58	110.50
3	PA	52	CYS	N-CA-C	5.02	116.81	108.02
1	DK	77	ALA	N-CA-C	5.02	116.69	108.76
3	P7	52	CYS	N-CA-C	5.02	116.80	108.02
1	Ag	76	VAL	N-CA-C	-5.02	106.78	111.45
2	Xg	727	THR	CA-C-N	-5.02	113.48	119.05
2	Xg	727	THR	C-N-CA	-5.02	113.48	119.05
2	XQ	804	LYS	N-CA-C	5.02	116.75	111.28
2	X8	804	LYS	N-CA-C	5.02	116.75	111.28
3	PP	52	CYS	N-CA-C	5.02	116.80	108.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DO	84	VAL	N-CA-C	-5.02	101.20	108.97
1	BQ	8	ALA	N-CA-C	5.02	117.57	110.50
2	XB	804	LYS	N-CA-C	5.02	116.75	111.28
1	D2	77	ALA	N-CA-C	5.01	116.68	108.76
1	GM	95	ALA	CA-C-N	-5.01	114.79	119.85
1	GM	95	ALA	C-N-CA	-5.01	114.79	119.85
1	DX	95	ALA	CA-C-N	-5.01	114.64	119.90
1	DX	95	ALA	C-N-CA	-5.01	114.64	119.90
1	Du	84	VAL	N-CA-C	-5.01	101.20	108.97
2	XV	804	LYS	N-CA-C	5.01	116.74	111.28
1	Bf	25	ASP	N-CA-C	-5.01	105.71	111.07
1	BB	8	ALA	N-CA-C	5.01	117.56	110.50
1	GW	95	ALA	CA-C-N	-5.01	114.79	119.85
1	GW	95	ALA	C-N-CA	-5.01	114.79	119.85
2	X2	727	THR	CA-C-N	-5.01	113.49	119.05
2	X2	727	THR	C-N-CA	-5.01	113.49	119.05
1	B8	8	ALA	N-CA-C	5.01	117.56	110.50
1	Ah	17	LEU	CA-C-N	-5.01	117.08	120.24
1	Ah	17	LEU	C-N-CA	-5.01	117.08	120.24
1	Gi	95	ALA	CA-C-N	-5.01	114.79	119.85
1	Gi	95	ALA	C-N-CA	-5.01	114.79	119.85
1	Bl	16	GLY	CA-C-O	-5.01	118.77	122.23
2	XA	727	THR	CA-C-N	-5.01	113.49	119.05
2	XA	727	THR	C-N-CA	-5.01	113.49	119.05
2	XK	727	THR	CA-C-N	-5.01	113.49	119.05
2	XK	727	THR	C-N-CA	-5.01	113.49	119.05
1	AU	76	VAL	N-CA-C	-5.01	106.79	111.45
2	X0	811	GLY	N-CA-C	5.01	120.08	110.86
1	De	85	HIS	N-CA-C	-5.01	103.92	110.53
1	AB	17	LEU	CA-C-N	-5.01	117.08	120.24
1	AB	17	LEU	C-N-CA	-5.01	117.08	120.24
2	XS	811	GLY	N-CA-C	5.01	120.08	110.86
1	Dg	77	ALA	N-CA-C	5.01	116.67	108.76
1	Dr	94	LYS	N-CA-C	5.01	116.82	111.36
2	Xv	727	THR	CA-C-N	-5.01	113.49	119.05
2	Xv	727	THR	C-N-CA	-5.01	113.49	119.05
2	Xx	826	ARG	N-CA-C	5.01	116.36	109.15
2	XH	863	TYR	N-CA-C	-5.01	102.48	109.69
1	Db	77	ALA	N-CA-C	5.00	116.67	108.76
1	B7	16	GLY	CA-C-O	-5.00	118.78	122.23
1	D8	7	ILE	N-CA-C	5.00	115.77	110.72
2	Xd	849	THR	N-CA-C	-5.00	101.76	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Bm	8	ALA	N-CA-C	5.00	117.56	110.50
1	Dz	84	VAL	N-CA-C	-5.00	101.22	108.97
1	DB	7	ILE	N-CA-C	5.00	115.77	110.72
1	DQ	7	ILE	N-CA-C	5.00	115.77	110.72
1	DX	85	HIS	N-CA-C	-5.00	103.93	110.53
2	Xm	804	LYS	N-CA-C	5.00	116.73	111.28
2	X5	811	GLY	N-CA-C	5.00	120.06	110.86
2	X9	849	THR	N-CA-C	-5.00	101.77	109.52
1	Bk	25	ASP	N-CA-C	-5.00	105.72	111.07
1	Dq	77	ALA	N-CA-C	5.00	116.66	108.76
2	Xs	826	ARG	N-CA-C	5.00	116.35	109.15
2	XD	811	GLY	N-CA-C	5.00	120.06	110.86
1	GH	95	ALA	CA-C-N	-5.00	114.80	119.85
1	GH	95	ALA	C-N-CA	-5.00	114.80	119.85
2	XN	811	GLY	N-CA-C	5.00	120.06	110.86
1	ER	7	ILE	N-CA-C	5.00	116.92	112.17
2	XR	849	THR	N-CA-C	-5.00	101.77	109.52
1	DU	77	ALA	N-CA-C	5.00	116.66	108.76
2	XW	863	TYR	N-CA-C	-5.00	102.49	109.69

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A0	656	0	677	15	0
1	A1	656	0	677	22	0
1	A2	656	0	677	17	0
1	A3	656	0	677	13	0
1	A4	656	0	677	13	0
1	A5	656	0	677	13	0
1	A6	656	0	677	20	0
1	A7	656	0	677	18	0
1	A8	656	0	677	15	0
1	A9	656	0	677	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	656	0	677	19	0
1	AB	656	0	677	14	0
1	AC	656	0	677	11	0
1	AD	656	0	677	14	0
1	AE	656	0	677	18	0
1	AF	656	0	677	16	0
1	AG	656	0	677	14	0
1	AH	656	0	677	12	0
1	AI	656	0	677	13	0
1	AJ	656	0	677	20	0
1	AK	656	0	677	14	0
1	AL	656	0	677	15	0
1	AM	656	0	677	13	0
1	AN	656	0	677	13	0
1	AO	656	0	677	22	0
1	AP	656	0	677	16	0
1	AQ	656	0	677	14	0
1	AR	656	0	677	11	0
1	AS	656	0	677	14	0
1	AT	656	0	677	22	0
1	AU	656	0	677	14	0
1	AV	656	0	677	15	0
1	AW	656	0	677	13	0
1	AX	656	0	677	14	0
1	Aa	656	0	677	18	0
1	Ab	656	0	677	17	0
1	Ac	656	0	677	15	0
1	Ad	656	0	677	13	0
1	Ae	656	0	677	15	0
1	Af	656	0	677	21	0
1	Ag	656	0	677	15	0
1	Ah	656	0	677	13	0
1	Ai	656	0	677	12	0
1	Aj	656	0	677	14	0
1	Ak	656	0	677	21	0
1	Al	656	0	677	17	0
1	Am	656	0	677	15	0
1	An	656	0	677	12	0
1	Ao	656	0	677	14	0
1	Ap	656	0	677	17	0
1	Aq	656	0	677	15	0
1	Ar	656	0	677	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	As	656	0	677	13	0
1	At	656	0	677	15	0
1	Au	656	0	677	21	0
1	Av	656	0	677	14	0
1	Aw	656	0	677	13	0
1	Ax	656	0	677	11	0
1	Ay	656	0	677	13	0
1	Az	656	0	677	19	0
1	B0	656	0	677	14	0
1	B1	656	0	677	13	0
1	B2	656	0	677	12	0
1	B3	656	0	677	10	0
1	B4	656	0	677	13	0
1	B5	656	0	677	14	0
1	B6	656	0	677	15	0
1	B7	656	0	677	12	0
1	B8	656	0	677	9	0
1	B9	656	0	677	13	0
1	BA	656	0	677	13	0
1	BB	656	0	677	10	0
1	BC	656	0	677	12	0
1	BD	656	0	677	12	0
1	BE	656	0	677	13	0
1	BF	656	0	677	12	0
1	BG	656	0	677	9	0
1	BH	656	0	677	13	0
1	BI	656	0	677	13	0
1	BJ	656	0	677	14	0
1	BK	656	0	677	12	0
1	BL	656	0	677	10	0
1	BM	656	0	677	13	0
1	BN	656	0	677	15	0
1	BO	656	0	677	12	0
1	BP	656	0	677	11	0
1	BQ	656	0	677	10	0
1	BR	656	0	677	13	0
1	BS	656	0	677	13	0
1	BT	656	0	677	12	0
1	BU	656	0	677	11	0
1	BV	656	0	677	9	0
1	BW	656	0	677	13	0
1	BX	656	0	677	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Ba	656	0	677	14	0
1	Bb	656	0	677	11	0
1	Bc	656	0	677	10	0
1	Bd	656	0	677	13	0
1	Be	656	0	677	14	0
1	Bf	656	0	677	14	0
1	Bg	656	0	677	12	0
1	Bh	656	0	677	11	0
1	Bi	656	0	677	13	0
1	Bj	656	0	677	14	0
1	Bk	656	0	677	15	0
1	Bl	656	0	677	13	0
1	Bm	656	0	677	10	0
1	Bn	656	0	677	12	0
1	Bo	656	0	677	13	0
1	Bp	656	0	677	14	0
1	Bq	656	0	677	12	0
1	Br	656	0	677	10	0
1	Bs	656	0	677	13	0
1	Bt	656	0	677	14	0
1	Bu	656	0	677	13	0
1	Bv	656	0	677	12	0
1	Bw	656	0	677	9	0
1	Bx	656	0	677	13	0
1	By	656	0	677	13	0
1	Bz	656	0	677	13	0
1	C0	656	0	677	11	0
1	C1	656	0	677	11	0
1	C2	656	0	677	10	0
1	C3	656	0	677	11	0
1	C4	656	0	677	12	0
1	C5	656	0	677	11	0
1	C6	656	0	677	11	0
1	C7	656	0	677	12	0
1	C8	656	0	677	11	0
1	C9	656	0	677	11	0
1	CA	656	0	677	12	0
1	CB	656	0	677	11	0
1	CC	656	0	677	12	0
1	CD	656	0	677	11	0
1	CE	656	0	677	11	0
1	CF	656	0	677	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CG	656	0	677	11	0
1	CH	656	0	677	11	0
1	CI	656	0	677	11	0
1	CJ	656	0	677	11	0
1	CK	656	0	677	12	0
1	CL	656	0	677	12	0
1	CM	656	0	677	11	0
1	CN	656	0	677	11	0
1	CO	656	0	677	11	0
1	CP	656	0	677	11	0
1	CQ	656	0	677	11	0
1	CR	656	0	677	11	0
1	CS	656	0	677	11	0
1	CT	656	0	677	11	0
1	CU	656	0	677	12	0
1	CV	656	0	677	11	0
1	CW	656	0	677	11	0
1	CX	656	0	677	11	0
1	Ca	656	0	677	11	0
1	Cb	656	0	677	12	0
1	Cc	656	0	677	11	0
1	Cd	656	0	677	11	0
1	Ce	656	0	677	11	0
1	Cf	656	0	677	11	0
1	Cg	656	0	677	12	0
1	Ch	656	0	677	11	0
1	Ci	656	0	677	11	0
1	Cj	656	0	677	11	0
1	Ck	656	0	677	11	0
1	Cl	656	0	677	12	0
1	Cm	656	0	677	11	0
1	Cn	656	0	677	12	0
1	Co	656	0	677	12	0
1	Cp	656	0	677	11	0
1	Cq	656	0	677	11	0
1	Cr	656	0	677	12	0
1	Cs	656	0	677	12	0
1	Ct	656	0	677	11	0
1	Cu	656	0	677	11	0
1	Cv	656	0	677	12	0
1	Cw	656	0	677	12	0
1	Cx	656	0	677	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Cy	656	0	677	10	0
1	Cz	656	0	677	11	0
1	D0	656	0	677	18	0
1	D1	656	0	677	13	0
1	D2	656	0	677	16	0
1	D3	656	0	677	19	0
1	D4	656	0	677	18	0
1	D5	656	0	677	20	0
1	D6	656	0	677	14	0
1	D7	656	0	677	20	0
1	D8	656	0	677	22	0
1	D9	656	0	677	24	0
1	DA	656	0	677	22	0
1	DB	656	0	677	22	0
1	DC	656	0	677	21	0
1	DD	656	0	677	20	0
1	DE	656	0	677	11	0
1	DF	656	0	677	16	0
1	DG	656	0	677	23	0
1	DH	656	0	677	18	0
1	DI	656	0	677	22	0
1	DJ	656	0	677	11	0
1	DK	656	0	677	21	0
1	DL	656	0	677	18	0
1	DM	656	0	677	20	0
1	DN	656	0	677	18	0
1	DO	656	0	677	14	0
1	DP	656	0	677	20	0
1	DQ	656	0	677	17	0
1	DR	656	0	677	21	0
1	DS	656	0	677	18	0
1	DT	656	0	677	11	0
1	DU	656	0	677	21	0
1	DV	656	0	677	23	0
1	DW	656	0	677	18	0
1	DX	656	0	677	18	0
1	Da	656	0	677	10	0
1	Db	656	0	677	15	0
1	Dc	656	0	677	21	0
1	Dd	656	0	677	18	0
1	De	656	0	677	23	0
1	Df	656	0	677	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Dg	656	0	677	26	0
1	Dh	656	0	677	19	0
1	Di	656	0	677	21	0
1	Dj	656	0	677	19	0
1	Dk	656	0	677	13	0
1	Dl	656	0	677	22	0
1	Dm	656	0	677	23	0
1	Dn	656	0	677	28	0
1	Do	656	0	677	20	0
1	Dp	656	0	677	9	0
1	Dq	656	0	677	17	0
1	Dr	656	0	677	22	0
1	Ds	656	0	677	18	0
1	Dt	656	0	677	23	0
1	Du	656	0	677	15	0
1	Dv	656	0	677	19	0
1	Dw	656	0	677	19	0
1	Dx	656	0	677	20	0
1	Dy	656	0	677	18	0
1	Dz	656	0	677	14	0
1	E0	656	0	677	13	0
1	E1	656	0	677	14	0
1	E2	656	0	677	10	0
1	E3	656	0	677	6	0
1	E4	656	0	677	12	0
1	E5	656	0	677	13	0
1	E6	656	0	677	14	0
1	E7	656	0	677	9	0
1	E8	656	0	677	5	0
1	E9	656	0	677	12	0
1	EA	656	0	677	10	0
1	EB	656	0	677	5	0
1	EC	656	0	677	12	0
1	ED	656	0	677	12	0
1	EE	656	0	677	12	0
1	EF	656	0	677	9	0
1	EG	656	0	677	4	0
1	EH	656	0	677	12	0
1	EI	656	0	677	12	0
1	EJ	656	0	677	13	0
1	EK	656	0	677	10	0
1	EL	656	0	677	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	EM	656	0	677	12	0
1	EN	656	0	677	13	0
1	EO	656	0	677	11	0
1	EP	656	0	677	9	0
1	EQ	656	0	677	7	0
1	ER	656	0	677	12	0
1	ES	656	0	677	13	0
1	ET	656	0	677	13	0
1	EU	656	0	677	9	0
1	EV	656	0	677	8	0
1	EW	656	0	677	12	0
1	EX	656	0	677	12	0
1	Ea	656	0	677	13	0
1	Eb	656	0	677	9	0
1	Ec	656	0	677	6	0
1	Ed	656	0	677	12	0
1	Ee	656	0	677	13	0
1	Ef	656	0	677	14	0
1	Eg	656	0	677	10	0
1	EH	656	0	677	7	0
1	Ei	656	0	677	11	0
1	Ej	656	0	677	13	0
1	Ek	656	0	677	14	0
1	El	656	0	677	10	0
1	Em	656	0	677	6	0
1	En	656	0	677	12	0
1	Eo	656	0	677	12	0
1	Ep	656	0	677	13	0
1	Eq	656	0	677	9	0
1	Er	656	0	677	6	0
1	Es	656	0	677	12	0
1	Et	656	0	677	12	0
1	Eu	656	0	677	12	0
1	Ev	656	0	677	10	0
1	Ew	656	0	677	6	0
1	Ex	656	0	677	12	0
1	Ey	656	0	677	12	0
1	Ez	656	0	677	14	0
1	F0	656	0	677	11	0
1	F1	656	0	677	13	0
1	F2	656	0	677	7	0
1	F3	656	0	677	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F4	656	0	677	13	0
1	F5	656	0	677	13	0
1	F6	656	0	677	12	0
1	F7	656	0	677	5	0
1	F8	656	0	677	14	0
1	F9	656	0	677	13	0
1	FA	656	0	677	8	0
1	FB	656	0	677	13	0
1	FC	656	0	677	14	0
1	FD	656	0	677	13	0
1	FE	656	0	677	11	0
1	FF	656	0	677	7	0
1	FG	656	0	677	13	0
1	FH	656	0	677	13	0
1	FI	656	0	677	13	0
1	FJ	656	0	677	11	0
1	FK	656	0	677	6	0
1	FL	656	0	677	14	0
1	FM	656	0	677	13	0
1	FN	656	0	677	10	0
1	FO	656	0	677	11	0
1	FP	656	0	677	5	0
1	FQ	656	0	677	14	0
1	FR	656	0	677	14	0
1	FS	656	0	677	11	0
1	FT	656	0	677	11	0
1	FU	656	0	677	8	0
1	FV	656	0	677	13	0
1	FW	656	0	677	13	0
1	FX	656	0	677	13	0
1	Fa	656	0	677	11	0
1	Fb	656	0	677	6	0
1	Fc	656	0	677	14	0
1	Fd	656	0	677	13	0
1	Fe	656	0	677	11	0
1	Ff	656	0	677	11	0
1	Fg	656	0	677	7	0
1	Fh	656	0	677	14	0
1	Fi	656	0	677	13	0
1	Fj	656	0	677	11	0
1	Fk	656	0	677	10	0
1	Fl	656	0	677	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Fm	656	0	677	15	0
1	Fn	656	0	677	14	0
1	Fo	656	0	677	12	0
1	Fp	656	0	677	11	0
1	Fq	656	0	677	6	0
1	Fr	656	0	677	16	0
1	Fs	656	0	677	13	0
1	Ft	656	0	677	13	0
1	Fu	656	0	677	10	0
1	Fv	656	0	677	6	0
1	Fw	656	0	677	14	0
1	Fx	656	0	677	14	0
1	Fy	656	0	677	13	0
1	Fz	656	0	677	12	0
1	G0	656	0	677	19	0
1	G1	656	0	677	15	0
1	G2	656	0	677	18	0
1	G3	656	0	677	19	0
1	G4	656	0	677	20	0
1	G5	656	0	677	20	0
1	G6	656	0	677	21	0
1	G7	656	0	677	19	0
1	G8	656	0	677	21	0
1	G9	656	0	677	17	0
1	GA	656	0	677	25	0
1	GB	656	0	677	22	0
1	GC	656	0	677	19	0
1	GD	656	0	677	21	0
1	GE	656	0	677	15	0
1	GF	656	0	677	21	0
1	GG	656	0	677	18	0
1	GH	656	0	677	18	0
1	GI	656	0	677	21	0
1	GJ	656	0	677	19	0
1	GK	656	0	677	17	0
1	GL	656	0	677	18	0
1	GM	656	0	677	21	0
1	GN	656	0	677	27	0
1	GO	656	0	677	19	0
1	GP	656	0	677	23	0
1	GQ	656	0	677	19	0
1	GR	656	0	677	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GS	656	0	677	21	0
1	GT	656	0	677	19	0
1	GU	656	0	677	17	0
1	GV	656	0	677	22	0
1	GW	656	0	677	20	0
1	GX	656	0	677	23	0
1	Ga	656	0	677	17	0
1	Gb	656	0	677	19	0
1	Gc	656	0	677	19	0
1	Gd	656	0	677	19	0
1	Ge	656	0	677	23	0
1	Gf	656	0	677	15	0
1	Gg	656	0	677	23	0
1	Gh	656	0	677	19	0
1	Gi	656	0	677	21	0
1	Gj	656	0	677	19	0
1	Gk	656	0	677	19	0
1	Gl	656	0	677	17	0
1	Gm	656	0	677	20	0
1	Gn	656	0	677	18	0
1	Go	656	0	677	19	0
1	Gp	656	0	677	18	0
1	Gq	656	0	677	20	0
1	Gr	656	0	677	18	0
1	Gs	656	0	677	19	0
1	Gt	656	0	677	24	0
1	Gu	656	0	677	19	0
1	Gv	656	0	677	19	0
1	Gw	656	0	677	19	0
1	Gx	656	0	677	19	0
1	Gy	656	0	677	20	0
1	Gz	656	0	677	20	0
1	H0	656	0	677	17	0
1	H1	656	0	677	13	0
1	H2	656	0	677	22	0
1	H3	656	0	677	17	0
1	H4	656	0	677	23	0
1	H5	656	0	677	25	0
1	H6	656	0	677	15	0
1	H7	656	0	677	20	0
1	H8	656	0	677	18	0
1	H9	656	0	677	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	HA	656	0	677	20	0
1	HB	656	0	677	18	0
1	HC	656	0	677	21	0
1	HD	656	0	677	18	0
1	HE	656	0	677	17	0
1	HF	656	0	677	22	0
1	HG	656	0	677	17	0
1	HH	656	0	677	25	0
1	HI	656	0	677	25	0
1	HJ	656	0	677	18	0
1	HK	656	0	677	28	0
1	HL	656	0	677	16	0
1	HM	656	0	677	29	0
1	HN	656	0	677	25	0
1	HO	656	0	677	15	0
1	HP	656	0	677	19	0
1	HQ	656	0	677	22	0
1	HR	656	0	677	22	0
1	HS	656	0	677	25	0
1	HT	656	0	677	20	0
1	HU	656	0	677	25	0
1	HV	656	0	677	17	0
1	HW	656	0	677	26	0
1	HX	656	0	677	19	0
1	Ha	656	0	677	17	0
1	Hb	656	0	677	19	0
1	Hc	656	0	677	18	0
1	Hd	656	0	677	22	0
1	He	656	0	677	25	0
1	Hf	656	0	677	17	0
1	Hg	656	0	677	26	0
1	Hh	656	0	677	15	0
1	Hi	656	0	677	22	0
1	Hj	656	0	677	25	0
1	Hk	656	0	677	16	0
1	Hl	656	0	677	20	0
1	Hm	656	0	677	18	0
1	Kn	656	0	677	26	0
1	Ho	656	0	677	19	0
1	Hp	656	0	677	15	0
1	Hq	656	0	677	21	0
1	Hr	656	0	677	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Hs	656	0	677	23	0
1	Ht	656	0	677	23	0
1	Hu	656	0	677	17	0
1	Hv	656	0	677	27	0
1	Hw	656	0	677	18	0
1	Hx	656	0	677	25	0
1	Hy	656	0	677	26	0
1	Hz	656	0	677	16	0
2	X0	859	0	838	25	0
2	X1	859	0	837	27	0
2	X2	859	0	838	27	0
2	X3	859	0	836	27	0
2	X4	859	0	838	24	0
2	X5	859	0	838	29	0
2	X6	859	0	837	26	0
2	X7	859	0	838	23	0
2	X8	859	0	838	25	0
2	X9	859	0	838	26	0
2	XA	859	0	838	23	0
2	XB	859	0	838	24	0
2	XC	859	0	838	22	0
2	XD	859	0	838	24	0
2	XE	859	0	837	29	0
2	XF	859	0	838	25	0
2	XG	859	0	838	23	0
2	XH	859	0	838	25	0
2	XI	859	0	838	22	0
2	XJ	859	0	838	26	0
2	XK	859	0	838	25	0
2	XL	859	0	836	26	0
2	XM	859	0	838	29	0
2	XN	859	0	838	27	0
2	XO	859	0	837	26	0
2	XP	859	0	838	22	0
2	XQ	859	0	836	30	0
2	XR	859	0	838	22	0
2	XS	859	0	838	27	0
2	XT	859	0	837	28	0
2	XU	859	0	838	23	0
2	XV	859	0	838	22	0
2	XW	859	0	838	26	0
2	XX	859	0	838	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Xa	859	0	837	28	0
2	Xb	859	0	838	29	0
2	Xc	859	0	838	22	0
2	Xd	859	0	838	25	0
2	Xe	859	0	838	21	0
2	Xf	859	0	837	27	0
2	Xg	859	0	838	25	0
2	Xh	859	0	836	27	0
2	Xi	859	0	838	23	0
2	Xj	859	0	838	28	0
2	Xk	859	0	837	24	0
2	Xl	859	0	838	23	0
2	Xm	859	0	838	24	0
2	Xn	859	0	838	22	0
2	Xo	859	0	838	23	0
2	Xp	859	0	837	28	0
2	Xq	859	0	838	25	0
2	Xr	859	0	838	23	0
2	Xs	859	0	838	24	0
2	Xt	859	0	838	21	0
2	Xu	859	0	837	27	0
2	Xv	859	0	838	24	0
2	Xw	859	0	836	27	0
2	Xx	859	0	838	28	0
2	Xy	859	0	838	28	0
2	Xz	859	0	837	27	0
3	P0	612	0	628	19	0
3	P1	612	0	628	12	0
3	P2	612	0	628	15	0
3	P3	612	0	628	15	0
3	P4	612	0	628	14	0
3	P5	612	0	628	20	0
3	P6	612	0	628	13	0
3	P7	612	0	628	16	0
3	P8	612	0	628	16	0
3	P9	612	0	628	16	0
3	PA	612	0	628	16	0
3	PB	612	0	628	18	0
3	PC	612	0	628	16	0
3	PD	612	0	628	19	0
3	PE	612	0	628	12	0
3	PF	612	0	628	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	PG	612	0	628	16	0
3	PH	612	0	628	15	0
3	PI	612	0	628	18	0
3	PJ	612	0	628	13	0
3	PK	612	0	628	17	0
3	PL	612	0	628	16	0
3	PM	612	0	628	16	0
3	PN	612	0	628	19	0
3	PO	612	0	628	14	0
3	PP	612	0	628	17	0
3	PQ	612	0	628	14	0
3	PR	612	0	628	15	0
3	PS	612	0	628	19	0
3	PT	612	0	628	13	0
3	PU	612	0	628	16	0
3	PV	612	0	628	14	0
3	PW	612	0	628	15	0
3	PX	612	0	628	19	0
3	Pa	612	0	628	13	0
3	Pb	612	0	628	18	0
3	Pc	612	0	628	16	0
3	Pd	612	0	628	16	0
3	Pe	612	0	628	17	0
3	Pf	612	0	628	13	0
3	Pg	612	0	628	16	0
3	Ph	612	0	628	17	0
3	Pi	612	0	628	15	0
3	Pj	612	0	628	20	0
3	Pk	612	0	628	11	0
3	Pl	612	0	628	14	0
3	Pm	612	0	628	15	0
3	Pn	612	0	628	15	0
3	Po	612	0	628	20	0
3	Pp	612	0	628	14	0
3	Pq	612	0	628	15	0
3	Pr	612	0	628	16	0
3	Ps	612	0	628	16	0
3	Pt	612	0	628	19	0
3	Pu	612	0	628	12	0
3	Pv	612	0	628	15	0
3	Pw	612	0	628	17	0
3	Px	612	0	628	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Py	612	0	628	19	0
3	Pz	612	0	628	13	0
All	All	403140	0	412899	6677	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (6677) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xp:714:THR:OG1	1:HI:79:HIS:ND1	1.56	1.38
2:X9:714:THR:HG23	1:HQ:79:HIS:ND1	1.38	1.38
1:Hn:79:HIS:ND1	2:XT:714:THR:OG1	1.58	1.35
1:He:79:HIS:ND1	2:XE:714:THR:OG1	1.59	1.34
2:Xf:714:THR:OG1	1:HB:79:HIS:ND1	1.58	1.33
1:H8:79:HIS:ND1	2:Xu:714:THR:OG1	1.61	1.32
1:D9:32:GLU:OE1	1:AQ:7:ILE:CD1	1.75	1.32
1:HN:79:HIS:ND1	2:XW:714:THR:HG23	1.42	1.31
1:Hj:79:HIS:ND1	2:Xs:714:THR:HG23	1.42	1.30
1:Hg:79:HIS:ND1	2:XJ:714:THR:OG1	1.65	1.30
1:Hy:79:HIS:ND1	2:XH:714:THR:HG23	1.42	1.29
2:Xx:714:THR:HG23	1:HM:79:HIS:ND1	1.47	1.29
1:H5:79:HIS:ND1	2:Xd:714:THR:HG23	1.42	1.29
2:X4:714:THR:HG23	1:HS:79:HIS:ND1	1.45	1.29
2:XC:714:THR:HG23	1:HK:79:HIS:ND1	1.49	1.25
1:Hx:79:HIS:ND1	2:XM:714:THR:HG23	1.49	1.23
1:Hv:79:HIS:ND1	2:XR:714:THR:HG23	1.51	1.23
1:Hg:79:HIS:NE2	1:GN:22:GLU:OE2	1.70	1.21
2:Xn:714:THR:HG23	1:HT:79:HIS:ND1	1.55	1.20
1:Gj:22:GLU:OE2	1:HB:79:HIS:NE2	1.74	1.19
2:Xi:714:THR:HG23	1:HU:79:HIS:ND1	1.56	1.19
1:Hn:79:HIS:NE2	1:GX:22:GLU:OE2	1.75	1.18
1:G5:22:GLU:OE2	1:Hm:79:HIS:NE2	1.77	1.17
1:H8:79:HIS:NE2	1:Gy:22:GLU:OE2	1.76	1.17
1:DN:32:GLU:HB2	1:AW:7:ILE:HD11	1.26	1.16
1:Go:22:GLU:OE2	1:Hr:79:HIS:NE2	1.79	1.16
1:D9:32:GLU:OE1	1:AQ:7:ILE:HD12	1.34	1.15
1:De:32:GLU:HB2	1:AE:7:ILE:HD11	1.19	1.15
1:Ap:7:ILE:HD11	1:DI:32:GLU:HB2	1.22	1.14
1:GS:22:GLU:OE2	1:Hv:79:HIS:NE2	1.79	1.14
1:G0:22:GLU:OE2	1:Hc:79:HIS:NE2	1.79	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Df:32:GLU:OE2	1:AB:7:ILE:CD1	1.96	1.14
1:GD:22:GLU:OE2	1:HG:79:HIS:NE2	1.79	1.13
1:Dy:32:GLU:HB2	1:AH:7:ILE:HD11	1.26	1.13
1:A1:7:ILE:HD11	1:Dm:32:GLU:HB2	1.31	1.13
1:Dj:32:GLU:HB2	1:As:7:ILE:HD11	1.26	1.12
1:Af:7:ILE:HD11	1:DB:32:GLU:HB2	1.29	1.11
1:A4:7:ILE:HD11	1:DS:32:GLU:HB2	1.26	1.11
1:Gj:35:LEU:HD21	1:HB:91:ILE:HG21	1.27	1.11
1:D1:32:GLU:OE2	1:Am:7:ILE:CD1	1.99	1.11
1:Dg:32:GLU:HB2	1:AJ:7:ILE:HD11	1.15	1.10
1:GS:35:LEU:HD21	1:HV:91:ILE:HG21	1.32	1.10
1:Dn:32:GLU:HB2	1:AT:7:ILE:HD11	1.25	1.10
1:GD:35:LEU:HD21	1:HG:91:ILE:HG21	1.32	1.10
1:A8:7:ILE:CD1	1:Du:32:GLU:OE2	2.00	1.10
1:D8:32:GLU:HB2	1:Au:7:ILE:HD11	1.31	1.10
1:AC:7:ILE:HD11	1:DK:32:GLU:HB2	1.32	1.10
1:H8:91:ILE:HG21	1:Gy:35:LEU:HD21	1.32	1.09
1:Go:35:LEU:HD21	1:Hr:91:ILE:HG21	1.32	1.09
1:Aa:7:ILE:HD11	1:Dt:32:GLU:HB2	1.24	1.09
1:A6:7:ILE:HD11	1:Dc:32:GLU:HB2	1.34	1.08
1:G0:35:LEU:HD21	1:Hc:91:ILE:HG21	1.32	1.08
1:Ai:7:ILE:HD11	1:DU:32:GLU:HB2	1.32	1.08
1:D5:32:GLU:HB2	1:Ad:7:ILE:HD11	1.26	1.08
1:G5:35:LEU:HD21	1:Hm:91:ILE:HG21	1.28	1.08
1:Dv:32:GLU:HB2	1:AR:7:ILE:HD11	1.29	1.07
1:Dk:32:GLU:OE2	1:Ar:7:ILE:CD1	2.02	1.07
1:Dz:32:GLU:OE2	1:AG:7:ILE:CD1	2.02	1.07
1:DO:32:GLU:OE2	1:AV:7:ILE:CD1	2.02	1.07
1:D6:32:GLU:OE2	1:Ac:7:ILE:CD1	2.02	1.07
1:AO:7:ILE:HD11	1:DV:32:GLU:HB2	1.34	1.07
2:X4:728:PRO:O	1:DS:62:ARG:NH1	1.87	1.06
1:D9:32:GLU:OE1	1:AQ:7:ILE:HD11	1.53	1.06
1:DN:62:ARG:NH1	2:XW:728:PRO:O	1.89	1.06
1:Ak:7:ILE:HD11	1:Dr:32:GLU:HB2	1.34	1.06
1:D5:62:ARG:NH1	2:Xd:728:PRO:O	1.89	1.06
1:Gt:22:GLU:OE2	1:HI:79:HIS:NE2	1.88	1.06
1:He:79:HIS:NE2	1:GI:22:GLU:OE2	1.88	1.05
1:Az:7:ILE:HD11	1:DG:32:GLU:HB2	1.34	1.05
1:A9:7:ILE:HD11	1:DQ:32:GLU:HB2	1.38	1.05
1:Dy:62:ARG:NH1	2:XH:728:PRO:O	1.89	1.05
1:Dj:62:ARG:NH1	2:Xs:728:PRO:O	1.89	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:De:32:GLU:CB	1:AE:7:ILE:HD11	1.86	1.04
1:Ge:22:GLU:OE2	1:Ht:79:HIS:NE2	1.91	1.03
1:Dg:32:GLU:CB	1:Aj:7:ILE:HD11	1.87	1.03
1:Ap:7:ILE:HD11	1:Di:32:GLU:CB	1.87	1.03
1:Aa:7:ILE:HD11	1:Dt:32:GLU:CB	1.90	1.02
2:Xv:729:GLU:HA	1:DR:62:ARG:HH12	1.24	1.02
1:De:62:ARG:NH1	2:XE:728:PRO:O	1.93	1.01
2:Xp:728:PRO:O	1:DI:62:ARG:NH1	1.93	1.01
1:An:7:ILE:HD11	1:DT:32:GLU:HB2	1.43	1.00
1:Dx:32:GLU:HB2	1:AM:7:ILE:HD11	1.43	1.00
1:Gj:35:LEU:CD2	1:HB:91:ILE:HG21	1.91	1.00
1:G5:73:ASP:OD2	1:Hm:45:TYR:OH	1.78	1.00
1:A8:7:ILE:HD12	1:Du:32:GLU:OE2	1.62	0.99
1:Di:62:ARG:HH12	2:XU:729:GLU:HA	1.26	0.99
1:Gj:73:ASP:OD2	1:HB:45:TYR:OH	1.80	0.99
1:D1:32:GLU:OE2	1:Am:7:ILE:HD12	1.61	0.99
1:G5:35:LEU:CD2	1:Hm:91:ILE:HG21	1.93	0.99
2:Xa:728:PRO:O	1:Dt:62:ARG:NH1	1.96	0.98
2:Xx:729:GLU:HA	1:DM:62:ARG:HH12	1.28	0.98
1:GD:73:ASP:OD2	1:HG:45:TYR:OH	1.81	0.98
1:Go:73:ASP:OD2	1:Hr:45:TYR:OH	1.81	0.98
1:Dq:32:GLU:HB2	1:AD:7:ILE:HD11	1.44	0.98
1:G0:73:ASP:OD2	1:Hc:45:TYR:OH	1.81	0.98
1:Df:32:GLU:OE2	1:AB:7:ILE:HD11	1.63	0.97
1:Dk:32:GLU:OE2	1:Ar:7:ILE:HD12	1.64	0.97
1:Db:32:GLU:HB2	1:Ao:7:ILE:HD11	1.46	0.97
1:Ax:7:ILE:HD11	1:DM:32:GLU:HB2	1.43	0.97
1:DC:62:ARG:HH12	2:XK:729:GLU:HA	1.26	0.97
1:D0:62:ARG:NH1	2:XF:728:PRO:O	1.97	0.97
1:D9:32:GLU:CD	1:AQ:7:ILE:HD12	1.88	0.97
1:GA:17:LEU:CD2	1:HK:39:GLN:OE1	2.13	0.97
1:A0:7:ILE:HD11	1:DF:32:GLU:HB2	1.46	0.96
1:Dz:32:GLU:OE2	1:AG:7:ILE:HD12	1.64	0.96
1:GS:73:ASP:OD2	1:HV:45:TYR:OH	1.81	0.96
1:Df:32:GLU:OE2	1:AB:7:ILE:HD12	1.59	0.96
1:Hv:39:GLN:OE1	1:GP:17:LEU:CD2	2.14	0.96
1:Dx:62:ARG:HH12	2:XM:729:GLU:HA	1.30	0.96
1:GO:35:LEU:HD11	1:GO:48:VAL:HG23	1.48	0.96
1:Gk:35:LEU:HD11	1:Gk:48:VAL:HG23	1.48	0.95
1:Gz:35:LEU:HD11	1:Gz:48:VAL:HG23	1.48	0.95
1:D0:32:GLU:HB2	1:AF:7:ILE:HD11	1.48	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Hn:91:ILE:HG21	1:GX:35:LEU:HD21	1.48	0.95
2:X2:728:PRO:O	1:DX:62:ARG:NH1	1.99	0.95
1:H8:91:ILE:HG21	1:Gy:35:LEU:CD2	1.96	0.95
1:G1:35:LEU:HD11	1:G1:48:VAL:HG23	1.48	0.95
1:Hn:45:TYR:OH	1:GX:73:ASP:OD2	1.82	0.95
1:G6:35:LEU:HD11	1:G6:48:VAL:HG23	1.48	0.95
1:GE:35:LEU:HD11	1:GE:48:VAL:HG23	1.48	0.95
1:DO:32:GLU:OE2	1:AV:7:ILE:HD11	1.67	0.95
1:GS:35:LEU:CD2	1:HV:91:ILE:HG21	1.97	0.95
1:Ga:35:LEU:HD11	1:Ga:48:VAL:HG23	1.48	0.95
1:H8:45:TYR:OH	1:Gy:73:ASP:OD2	1.84	0.94
1:GJ:35:LEU:HD11	1:GJ:48:VAL:HG23	1.48	0.94
1:GT:35:LEU:HD11	1:GT:48:VAL:HG23	1.48	0.94
1:G0:35:LEU:CD2	1:Hc:91:ILE:HG21	1.97	0.94
1:D6:32:GLU:OE2	1:Ac:7:ILE:HD11	1.67	0.94
2:Xq:728:PRO:O	1:DD:62:ARG:NH1	2.01	0.94
1:Dz:32:GLU:OE2	1:AG:7:ILE:HD11	1.67	0.94
1:Gu:35:LEU:HD11	1:Gu:48:VAL:HG23	1.48	0.94
1:D2:32:GLU:HB2	1:AX:7:ILE:HD11	1.47	0.94
1:D9:62:ARG:HH12	2:XQ:729:GLU:HA	1.32	0.94
1:GD:35:LEU:CD2	1:HG:91:ILE:HG21	1.97	0.94
1:D6:32:GLU:OE2	1:Ac:7:ILE:HD12	1.64	0.94
1:Go:35:LEU:CD2	1:Hr:91:ILE:HG21	1.97	0.93
1:DO:32:GLU:OE2	1:AV:7:ILE:HD12	1.64	0.93
1:A8:7:ILE:HD11	1:Du:32:GLU:OE2	1.67	0.93
1:Aq:7:ILE:HD11	1:DD:32:GLU:HB2	1.51	0.93
1:A2:7:ILE:HD11	1:DX:32:GLU:HB2	1.49	0.93
2:X9:714:THR:CG2	1:HQ:79:HIS:ND1	2.31	0.93
1:Dk:32:GLU:OE2	1:Ar:7:ILE:HD11	1.67	0.93
1:Gp:35:LEU:HD11	1:Gp:48:VAL:HG23	1.48	0.93
1:Gt:35:LEU:HD21	1:HI:91:ILE:HG21	1.49	0.93
1:Hv:39:GLN:OE1	1:GP:17:LEU:HD21	1.69	0.93
1:Gf:35:LEU:HD11	1:Gf:48:VAL:HG23	1.48	0.92
1:D1:32:GLU:OE2	1:Am:7:ILE:HD11	1.65	0.92
2:Xb:728:PRO:O	1:Do:62:ARG:NH1	2.03	0.92
1:GA:17:LEU:HD21	1:HK:39:GLN:OE1	1.69	0.92
1:He:91:ILE:HG21	1:GI:35:LEU:HD21	1.50	0.92
1:Af:7:ILE:HD11	1:DB:32:GLU:CB	1.99	0.91
1:Ge:35:LEU:HD21	1:Ht:91:ILE:HG21	1.51	0.91
1:Ab:7:ILE:HD11	1:Do:32:GLU:HB2	1.52	0.91
1:G7:73:ASP:OD2	1:HQ:45:TYR:OH	1.88	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HN:79:HIS:ND1	2:XW:714:THR:CG2	2.33	0.91
1:H5:79:HIS:ND1	2:Xd:714:THR:CG2	2.33	0.90
1:A1:7:ILE:HD11	1:Dm:32:GLU:CB	2.02	0.90
1:Hq:91:ILE:HD13	1:GB:35:LEU:HD21	1.53	0.90
1:Hj:79:HIS:ND1	2:Xs:714:THR:CG2	2.33	0.90
1:G8:35:LEU:HD21	1:HF:91:ILE:HD13	1.54	0.90
1:G2:35:LEU:HD11	1:G2:48:VAL:HG13	1.54	0.90
1:Hy:79:HIS:ND1	2:XH:714:THR:CG2	2.33	0.90
1:Gg:17:LEU:CD2	1:HU:39:GLN:OE1	2.21	0.89
2:Xg:729:GLU:HA	1:DJ:62:ARG:HH12	1.37	0.89
1:D8:32:GLU:CB	1:Au:7:ILE:HD11	2.03	0.89
1:Hb:91:ILE:HD13	1:Gm:35:LEU:HD21	1.55	0.88
1:Dw:62:ARG:HH12	2:XA:729:GLU:HA	1.38	0.88
1:GU:35:LEU:HD11	1:GU:48:VAL:HG13	1.55	0.88
1:GF:35:LEU:HD11	1:GF:48:VAL:HG13	1.55	0.88
1:Gg:35:LEU:HD11	1:Gg:48:VAL:HG13	1.54	0.88
1:GK:35:LEU:HD11	1:GK:48:VAL:HG13	1.54	0.88
1:GA:35:LEU:HD11	1:GA:48:VAL:HG13	1.55	0.88
1:GP:35:LEU:HD11	1:GP:48:VAL:HG13	1.54	0.87
1:G7:35:LEU:CD2	1:HQ:91:ILE:HG21	2.04	0.87
1:Gg:17:LEU:HD21	1:HU:39:GLN:OE1	1.75	0.87
1:Gq:35:LEU:HD11	1:Gq:48:VAL:HG13	1.54	0.87
1:AN:7:ILE:HD11	1:DW:32:GLU:HB2	1.57	0.87
1:DL:62:ARG:HH12	2:XP:729:GLU:HA	1.38	0.87
1:D3:62:ARG:HH12	2:X7:729:GLU:HA	1.38	0.87
1:G7:35:LEU:HD11	1:G7:48:VAL:HG13	1.54	0.87
1:Gl:35:LEU:HD11	1:Gl:48:VAL:HG13	1.54	0.87
2:Xa:713:ILE:CG2	1:Ht:80:ILE:HD12	2.04	0.87
1:Hg:91:ILE:HG21	1:GN:35:LEU:HD21	1.54	0.87
1:Gv:35:LEU:HD11	1:Gv:48:VAL:HG13	1.55	0.87
1:A6:7:ILE:HD11	1:Dc:32:GLU:CB	2.05	0.86
1:AO:7:ILE:HD11	1:DV:32:GLU:CB	2.05	0.86
1:Dn:32:GLU:CB	1:AT:7:ILE:HD11	2.05	0.86
1:Ak:7:ILE:HD11	1:Dr:32:GLU:CB	2.05	0.86
1:Gt:73:ASP:OD2	1:HI:45:TYR:OH	1.94	0.86
1:Av:7:ILE:HD11	1:DR:32:GLU:HB2	1.56	0.86
2:X9:729:GLU:HA	1:DQ:62:ARG:HH12	1.41	0.86
1:Dh:62:ARG:HH12	2:Xl:729:GLU:HA	1.38	0.86
1:Aj:7:ILE:HD11	1:Ds:32:GLU:HB2	1.57	0.86
1:Hx:45:TYR:OH	1:GK:73:ASP:OD2	1.94	0.86
1:Az:7:ILE:HD11	1:DG:32:GLU:CB	2.05	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Gv:73:ASP:OD2	1:HM:45:TYR:OH	1.93	0.85
2:Xp:713:ILE:CG2	1:HI:80:ILE:HD12	2.06	0.85
1:DC:32:GLU:HB2	1:AK:7:ILE:HD11	1.59	0.85
1:H2:91:ILE:HD13	1:GV:35:LEU:HD21	1.55	0.85
1:Gb:35:LEU:HD11	1:Gb:48:VAL:HG13	1.55	0.85
2:X4:714:THR:CG2	1:HS:79:HIS:ND1	2.36	0.85
1:D3:32:GLU:HB2	1:A7:7:ILE:HD11	1.58	0.85
2:Xw:712:ARG:HH12	1:HA:65:ALA:HB1	1.42	0.85
1:A5:7:ILE:HD11	1:Dd:32:GLU:HB2	1.57	0.85
1:Ba:35:LEU:HD11	1:Ba:48:VAL:HG22	1.59	0.85
1:Ag:7:ILE:HD11	1:DJ:32:GLU:HB2	1.58	0.85
1:Bk:35:LEU:HD11	1:Bk:48:VAL:HG22	1.59	0.85
1:BE:35:LEU:HD11	1:BE:48:VAL:HG22	1.59	0.85
1:B1:35:LEU:HD11	1:B1:48:VAL:HG22	1.59	0.84
1:D5:32:GLU:CB	1:Ad:7:ILE:HD11	2.07	0.84
1:Ge:73:ASP:OD2	1:Ht:45:TYR:OH	1.94	0.84
1:Dh:32:GLU:HB2	1:Al:7:ILE:HD11	1.58	0.84
1:BO:35:LEU:HD11	1:BO:48:VAL:HG22	1.59	0.84
1:Ay:7:ILE:HD11	1:DH:32:GLU:HB2	1.57	0.84
1:He:45:TYR:OH	1:GI:73:ASP:OD2	1.93	0.84
1:Bf:35:LEU:HD11	1:Bf:48:VAL:HG22	1.59	0.84
1:Ap:7:ILE:HD11	1:DI:32:GLU:CG	2.07	0.84
2:Xh:712:ARG:HH12	1:HI:65:ALA:HB1	1.41	0.84
1:D4:32:GLU:HB2	1:AS:7:ILE:HD11	1.58	0.84
1:Dy:32:GLU:CB	1:AH:7:ILE:HD11	2.07	0.84
2:Xw:712:ARG:NH1	1:HA:65:ALA:HB1	1.93	0.84
2:Xn:729:GLU:HA	1:DT:62:ARG:HH12	1.42	0.84
1:Dw:32:GLU:HB2	1:AA:7:ILE:HD11	1.58	0.84
2:X3:712:ARG:HH12	1:H7:65:ALA:HB1	1.42	0.84
1:Gc:72:GLY:HA2	1:HE:77:ALA:HB2	1.58	0.84
1:Dj:32:GLU:CB	1:As:7:ILE:HD11	2.07	0.83
2:Xq:714:THR:HG1	1:HD:79:HIS:HD1	1.23	0.83
1:BT:35:LEU:HD11	1:BT:48:VAL:HG22	1.59	0.83
2:X3:712:ARG:NH1	1:H7:65:ALA:HB1	1.93	0.83
1:Bz:35:LEU:HD11	1:Bz:48:VAL:HG22	1.59	0.83
1:DL:32:GLU:HB2	1:AP:7:ILE:HD11	1.58	0.83
2:XL:712:ARG:HH12	1:HP:65:ALA:HB1	1.42	0.83
1:Gj:35:LEU:CD2	1:HB:91:ILE:CG2	2.56	0.83
1:B6:35:LEU:HD11	1:B6:48:VAL:HG22	1.59	0.83
1:A4:7:ILE:HD11	1:DS:32:GLU:CB	2.08	0.83
1:G8:72:GLY:HA2	1:HF:77:ALA:HB2	1.61	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G5:35:LEU:CD2	1:Hm:91:ILE:CG2	2.57	0.83
2:Xq:716:PRO:HD3	1:HD:80:ILE:O	1.77	0.83
1:Bp:35:LEU:HD11	1:Bp:48:VAL:HG22	1.59	0.83
1:GH:35:LEU:HD11	1:GH:48:VAL:HG22	1.61	0.83
1:GW:35:LEU:HD11	1:GW:48:VAL:HG22	1.61	0.83
1:Gf:72:GLY:HA2	1:HJ:77:ALA:HB2	1.59	0.83
1:He:80:ILE:HD12	2:XE:713:ILE:CG2	2.10	0.82
1:Gs:35:LEU:HD11	1:Gs:48:VAL:HG22	1.61	0.82
2:XL:712:ARG:NH1	1:HP:65:ALA:HB1	1.93	0.82
1:Gn:35:LEU:HD11	1:Gn:48:VAL:HG22	1.61	0.82
1:Gv:25:ASP:HA	1:HM:88:VAL:HG21	1.61	0.82
1:Gx:35:LEU:HD11	1:Gx:48:VAL:HG22	1.61	0.82
1:Hp:77:ALA:HB2	1:GG:72:GLY:HA2	1.61	0.82
2:Xz:712:ARG:HA	2:Xz:712:ARG:HE	1.45	0.82
2:X6:712:ARG:HA	2:X6:712:ARG:HE	1.45	0.82
2:XO:712:ARG:HA	2:XO:712:ARG:HE	1.45	0.82
1:GR:35:LEU:HD11	1:GR:48:VAL:HG22	1.61	0.82
1:H2:77:ALA:HB2	1:GV:72:GLY:HA2	1.62	0.82
1:Bu:35:LEU:HD11	1:Bu:48:VAL:HG22	1.59	0.82
2:XE:712:ARG:HA	2:XE:712:ARG:HE	1.45	0.82
2:XJ:712:ARG:HA	2:XJ:712:ARG:HE	1.45	0.82
1:Df:62:ARG:HH12	2:XB:729:GLU:HA	1.45	0.82
1:Dn:32:GLU:CD	1:AT:7:ILE:HD13	2.04	0.82
1:GC:35:LEU:HD11	1:GC:48:VAL:HG22	1.61	0.82
1:Gi:35:LEU:HD11	1:Gi:48:VAL:HG22	1.61	0.81
1:BJ:35:LEU:HD11	1:BJ:48:VAL:HG22	1.59	0.81
1:G4:35:LEU:HD11	1:G4:48:VAL:HG22	1.61	0.81
2:Xh:712:ARG:NH1	1:Hl:65:ALA:HB1	1.93	0.81
2:Xk:712:ARG:HA	2:Xk:712:ARG:HE	1.45	0.81
1:H0:80:ILE:O	2:XF:716:PRO:HD3	1.80	0.81
1:De:32:GLU:CG	1:AE:7:ILE:HD11	2.10	0.81
1:Gd:35:LEU:HD11	1:Gd:48:VAL:HG22	1.61	0.81
1:G9:35:LEU:HD11	1:G9:48:VAL:HG22	1.61	0.81
1:DN:32:GLU:CB	1:AW:7:ILE:HD11	2.07	0.81
2:Xf:712:ARG:HA	2:Xf:712:ARG:HE	1.45	0.81
2:X2:716:PRO:HD3	1:HX:80:ILE:O	1.81	0.81
2:Xb:716:PRO:HD3	1:Ho:80:ILE:O	1.80	0.81
1:Aa:7:ILE:HD11	1:Dt:32:GLU:CG	2.10	0.81
1:Ha:77:ALA:HB2	1:Gr:72:GLY:HA2	1.63	0.81
1:Hg:39:GLN:OE1	1:GN:17:LEU:HD21	1.80	0.81
2:Xu:712:ARG:HA	2:Xu:712:ARG:HE	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Di:32:GLU:HB2	1:Au:7:ILE:HD11	1.62	0.80
2:xa:712:ARG:HA	2:xa:712:ARG:HE	1.45	0.80
1:GM:35:LEU:HD11	1:GM:48:VAL:HG22	1.61	0.80
2:X1:712:ARG:HA	2:X1:712:ARG:HE	1.45	0.80
1:Dn:62:ARG:HH12	2:XT:729:GLU:HA	1.46	0.80
1:Hx:88:VAL:HG21	1:GK:25:ASP:HA	1.63	0.80
2:Xp:712:ARG:HA	2:Xp:712:ARG:HE	1.45	0.80
1:Dy:35:LEU:HD11	1:Dy:48:VAL:HG13	1.64	0.80
1:Bd:35:LEU:HD11	1:Bd:48:VAL:HG23	1.64	0.80
1:Df:32:GLU:CD	1:AB:7:ILE:HD12	2.06	0.80
2:XT:712:ARG:HA	2:XT:712:ARG:HE	1.45	0.80
1:De:35:LEU:HD11	1:De:48:VAL:HG13	1.64	0.80
1:Dp:32:GLU:HB2	1:AI:7:ILE:HD11	1.64	0.80
1:Bx:35:LEU:HD11	1:Bx:48:VAL:HG23	1.64	0.80
1:DI:35:LEU:HD11	1:DI:48:VAL:HG13	1.64	0.80
1:B5:35:LEU:HD11	1:B5:48:VAL:HG13	1.64	0.80
1:H5:45:TYR:OH	1:Gb:73:ASP:OD2	2.00	0.80
1:Hy:45:TYR:OH	1:GF:73:ASP:OD2	2.00	0.80
1:B0:35:LEU:HD11	1:B0:48:VAL:HG13	1.64	0.79
2:Xb:714:THR:HG1	1:Ho:79:HIS:HD1	1.30	0.79
1:Dj:35:LEU:HD11	1:Dj:48:VAL:HG13	1.64	0.79
1:BS:35:LEU:HD11	1:BS:48:VAL:HG13	1.64	0.79
1:Be:35:LEU:HD11	1:Be:48:VAL:HG13	1.64	0.79
1:DN:35:LEU:HD11	1:DN:48:VAL:HG13	1.64	0.79
1:Dt:35:LEU:HD11	1:Dt:48:VAL:HG13	1.64	0.79
1:Bs:35:LEU:HD11	1:Bs:48:VAL:HG23	1.64	0.79
1:BR:35:LEU:HD11	1:BR:48:VAL:HG23	1.64	0.79
1:DD:35:LEU:HD11	1:DD:48:VAL:HG13	1.64	0.79
1:B9:35:LEU:HD11	1:B9:48:VAL:HG23	1.64	0.79
1:Bi:35:LEU:HD11	1:Bi:48:VAL:HG23	1.64	0.79
1:BD:35:LEU:HD11	1:BD:48:VAL:HG13	1.64	0.79
1:BC:35:LEU:HD11	1:BC:48:VAL:HG23	1.64	0.79
1:D1:32:GLU:CD	1:Am:7:ILE:HD12	2.07	0.79
1:By:35:LEU:HD11	1:By:48:VAL:HG13	1.64	0.79
1:G0:35:LEU:CD2	1:Hc:91:ILE:CG2	2.61	0.79
2:XC:714:THR:CG2	1:HK:79:HIS:ND1	2.40	0.79
1:H8:91:ILE:CG2	1:Gy:35:LEU:CD2	2.61	0.79
1:Hn:80:ILE:HD12	2:XT:713:ILE:CG2	2.12	0.79
1:BX:35:LEU:HD11	1:BX:48:VAL:HG13	1.64	0.79
1:BW:35:LEU:HD11	1:BW:48:VAL:HG23	1.64	0.79
1:DS:35:LEU:HD11	1:DS:48:VAL:HG13	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D1:62:ARG:HH12	2:Xm:729:GLU:HA	1.48	0.78
1:D0:35:LEU:HD11	1:D0:48:VAL:HG13	1.64	0.78
1:GS:35:LEU:CD2	1:HV:91:ILE:CG2	2.61	0.78
1:D5:35:LEU:HD11	1:D5:48:VAL:HG13	1.64	0.78
1:HN:45:TYR:OH	1:GU:73:ASP:OD2	2.00	0.78
1:D6:62:ARG:HH12	2:Xc:729:GLU:HA	1.49	0.78
1:Gl:25:ASP:HA	1:HT:88:VAL:HG21	1.66	0.78
1:Go:35:LEU:CD2	1:Hr:91:ILE:CG2	2.61	0.78
1:GD:35:LEU:CD2	1:HG:91:ILE:CG2	2.61	0.78
1:BI:35:LEU:HD11	1:BI:48:VAL:HG13	1.64	0.78
1:BN:35:LEU:HD11	1:BN:48:VAL:HG13	1.64	0.78
2:X9:713:ILE:HD11	1:HQ:62:ARG:HA	1.66	0.78
1:Hj:45:TYR:OH	1:Gq:73:ASP:OD2	2.00	0.78
1:Hh:91:ILE:HG21	1:Gk:35:LEU:CD2	2.14	0.78
1:BM:35:LEU:HD11	1:BM:48:VAL:HG23	1.64	0.78
1:DO:62:ARG:HH12	2:XV:729:GLU:HA	1.49	0.78
2:Xy:863:TYR:HD2	2:Xy:869:GLY:HA3	1.49	0.78
1:Hw:91:ILE:HG21	1:Gz:35:LEU:CD2	2.14	0.78
2:XN:863:TYR:HD2	2:XN:869:GLY:HA3	1.49	0.78
1:DX:35:LEU:HD11	1:DX:48:VAL:HG13	1.64	0.78
1:Bo:35:LEU:HD11	1:Bo:48:VAL:HG13	1.64	0.78
1:Do:35:LEU:HD11	1:Do:48:VAL:HG13	1.64	0.78
1:Hq:77:ALA:HB2	1:GB:72:GLY:HA2	1.64	0.78
1:Bj:35:LEU:HD11	1:Bj:48:VAL:HG13	1.64	0.78
2:Xo:863:TYR:HD2	2:Xo:869:GLY:HA3	1.49	0.78
1:B4:35:LEU:HD11	1:B4:48:VAL:HG23	1.64	0.77
1:H3:91:ILE:HG21	1:G6:35:LEU:CD2	2.14	0.77
2:Xj:863:TYR:HD2	2:Xj:869:GLY:HA3	1.49	0.77
1:Bt:35:LEU:HD11	1:Bt:48:VAL:HG13	1.64	0.77
2:XS:863:TYR:HD2	2:XS:869:GLY:HA3	1.49	0.77
1:D9:32:GLU:CD	1:AQ:7:ILE:CD1	2.49	0.77
1:Da:32:GLU:HB2	1:At:7:ILE:HD11	1.67	0.77
1:Ae:7:ILE:HD11	1:DE:32:GLU:HB2	1.67	0.77
1:Bn:35:LEU:HD11	1:Bn:48:VAL:HG23	1.64	0.77
1:Hv:88:VAL:HG21	1:GP:25:ASP:HA	1.67	0.77
1:GA:25:ASP:HA	1:HK:88:VAL:HG21	1.65	0.77
2:Xx:714:THR:CG2	1:HM:79:HIS:ND1	2.41	0.77
1:HL:91:ILE:HG21	1:GO:35:LEU:CD2	2.14	0.77
2:Xg:716:PRO:HD3	1:HJ:80:ILE:O	1.84	0.77
2:XD:863:TYR:HD2	2:XD:869:GLY:HA3	1.49	0.77
1:BH:35:LEU:HD11	1:BH:48:VAL:HG23	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Hj:88:VAL:HG21	1:Gq:25:ASP:HA	1.67	0.77
1:Hn:91:ILE:HG21	1:GX:35:LEU:CD2	2.15	0.77
1:HN:88:VAL:HG21	1:GU:25:ASP:HA	1.67	0.77
1:D6:32:GLU:CD	1:Ac:7:ILE:HD12	2.10	0.77
1:Hb:77:ALA:HB2	1:Gm:72:GLY:HA2	1.67	0.77
2:Xl:863:TYR:HD2	2:Xl:869:GLY:HA3	1.49	0.77
2:XX:863:TYR:HD2	2:XX:869:GLY:HA3	1.49	0.77
2:Xn:713:ILE:HD11	1:HT:62:ARG:HA	1.65	0.76
1:Du:62:ARG:HH12	2:X8:729:GLU:HA	1.48	0.76
2:Xe:863:TYR:HD2	2:Xe:869:GLY:HA3	1.49	0.76
1:DO:32:GLU:CD	1:AV:7:ILE:HD12	2.10	0.76
2:X5:863:TYR:HD2	2:X5:869:GLY:HA3	1.49	0.76
2:X0:863:TYR:HD2	2:X0:869:GLY:HA3	1.49	0.76
1:Dk:62:ARG:HH12	2:Xr:729:GLU:HA	1.49	0.76
2:Xw:812:GLN:HE22	1:Hx:70:ARG:HD2	1.51	0.76
1:HH:70:ARG:HD2	2:XG:812:GLN:HE22	1.51	0.76
2:XC:713:ILE:HD11	1:HK:62:ARG:HA	1.67	0.76
2:Xt:863:TYR:HD2	2:Xt:869:GLY:HA3	1.49	0.76
1:Hy:88:VAL:HG21	1:GF:25:ASP:HA	1.67	0.76
1:H5:88:VAL:HG21	1:Gb:25:ASP:HA	1.67	0.75
1:Dk:32:GLU:CD	1:Ar:7:ILE:HD12	2.10	0.75
1:Hn:70:ARG:HD2	2:Xm:812:GLN:HE22	1.51	0.75
1:HL:79:HIS:ND1	2:XP:714:THR:OG1	2.17	0.75
1:H9:70:ARG:HD2	2:X8:812:GLN:HE22	1.51	0.75
2:Xv:729:GLU:HA	1:DR:62:ARG:NH1	2.02	0.75
1:HW:70:ARG:HD2	2:XV:812:GLN:HE22	1.51	0.75
1:H9:88:VAL:HG21	1:GR:25:ASP:HA	1.69	0.75
2:Xh:812:GLN:HE22	1:Hi:70:ARG:HD2	1.51	0.75
1:Hd:70:ARG:HD2	2:Xc:812:GLN:HE22	1.51	0.75
1:AC:7:ILE:HD11	1:DK:32:GLU:CB	2.16	0.75
1:A4:35:LEU:HD11	1:A4:48:VAL:HG22	1.69	0.75
1:Ai:35:LEU:HD11	1:Ai:48:VAL:HG22	1.69	0.75
1:Dz:62:ARG:HH12	2:XG:729:GLU:HA	1.49	0.75
1:Hx:79:HIS:ND1	2:XM:714:THR:CG2	2.42	0.75
1:Dz:32:GLU:CD	1:AG:7:ILE:HD12	2.10	0.75
1:AR:35:LEU:HD11	1:AR:48:VAL:HG22	1.69	0.75
1:A8:7:ILE:HD12	1:Du:32:GLU:CD	2.11	0.75
1:A9:35:LEU:HD11	1:A9:48:VAL:HG22	1.69	0.75
1:Fm:35:LEU:HD11	1:Fm:48:VAL:HG13	1.69	0.75
1:HC:70:ARG:HD2	2:XB:812:GLN:HE22	1.51	0.75
1:Ax:35:LEU:HD11	1:Ax:48:VAL:HG22	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Hg:91:ILE:HG21	1:GN:35:LEU:CD2	2.16	0.74
1:Hw:79:HIS:ND1	2:XA:714:THR:OG1	2.17	0.74
1:FG:35:LEU:HD11	1:FG:48:VAL:HG13	1.69	0.74
1:AH:35:LEU:HD11	1:AH:48:VAL:HG22	1.69	0.74
2:XL:812:GLN:HE22	1:HM:70:ARG:HD2	1.51	0.74
1:AM:35:LEU:HD11	1:AM:48:VAL:HG22	1.69	0.74
2:Xy:729:GLU:HA	1:DH:62:ARG:HH12	1.52	0.74
2:XD:860:LEU:HD12	2:XD:868:ARG:HD3	1.69	0.74
2:XN:729:GLU:HA	1:DW:62:ARG:HH12	1.52	0.74
1:FV:35:LEU:HD11	1:FV:48:VAL:HG13	1.69	0.74
1:Hg:39:GLN:OE1	1:GN:17:LEU:CD2	2.36	0.74
1:Gj:35:LEU:HD23	1:HB:91:ILE:CG2	2.17	0.74
1:As:35:LEU:HD11	1:As:48:VAL:HG22	1.69	0.74
2:XQ:812:GLN:HE22	1:HR:70:ARG:HD2	1.51	0.74
2:XX:860:LEU:HD12	2:XX:868:ARG:HD3	1.69	0.74
1:F1:35:LEU:HD11	1:F1:48:VAL:HG13	1.70	0.74
1:C6:35:LEU:HD11	1:C6:48:VAL:HG23	1.70	0.74
1:Ad:35:LEU:HD11	1:Ad:48:VAL:HG22	1.69	0.74
2:XS:860:LEU:HD12	2:XS:868:ARG:HD3	1.69	0.74
2:X5:860:LEU:HD12	2:X5:868:ARG:HD3	1.69	0.74
2:XN:860:LEU:HD12	2:XN:868:ARG:HD3	1.69	0.74
1:C1:35:LEU:HD11	1:C1:48:VAL:HG23	1.69	0.74
1:G7:35:LEU:HD23	1:HQ:91:ILE:CG2	2.18	0.74
1:Hs:70:ARG:HD2	2:Xr:812:GLN:HE22	1.51	0.74
2:XI:860:LEU:HD12	2:XI:868:ARG:HD3	1.69	0.74
1:An:35:LEU:HD11	1:An:48:VAL:HG22	1.69	0.74
1:FB:35:LEU:HD11	1:FB:48:VAL:HG13	1.69	0.74
1:GC:25:ASP:HA	1:Hf:88:VAL:HG21	1.68	0.74
1:CE:35:LEU:HD11	1:CE:48:VAL:HG23	1.70	0.74
1:Fr:35:LEU:HD11	1:Fr:48:VAL:HG13	1.69	0.74
2:Xy:860:LEU:HD12	2:Xy:868:ARG:HD3	1.70	0.74
1:FE:35:LEU:HD11	1:FE:48:VAL:HG13	1.70	0.74
1:FQ:35:LEU:HD11	1:FQ:48:VAL:HG13	1.69	0.74
1:Hv:62:ARG:HA	2:XR:713:ILE:HD11	1.68	0.74
1:Fu:35:LEU:HD11	1:Fu:48:VAL:HG13	1.70	0.74
1:Cz:35:LEU:HD11	1:Cz:48:VAL:HG23	1.69	0.74
1:FL:35:LEU:HD11	1:FL:48:VAL:HG13	1.69	0.74
1:Ca:35:LEU:HD11	1:Ca:48:VAL:HG23	1.70	0.74
1:Fa:35:LEU:HD11	1:Fa:48:VAL:HG13	1.70	0.74
2:Xe:860:LEU:HD12	2:Xe:868:ARG:HD3	1.69	0.74
1:G2:25:ASP:HA	1:HS:88:VAL:HG21	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D4:62:ARG:HH12	2:XS:729:GLU:HA	1.53	0.73
1:Gj:35:LEU:HD11	1:Gj:48:VAL:HG22	1.70	0.73
1:Gt:35:LEU:HD11	1:Gt:48:VAL:HG22	1.70	0.73
1:Gy:35:LEU:HD11	1:Gy:48:VAL:HG22	1.70	0.73
1:CJ:35:LEU:HD11	1:CJ:48:VAL:HG23	1.70	0.73
1:FJ:35:LEU:HD11	1:FJ:48:VAL:HG13	1.70	0.73
2:Xj:862:THR:HG21	1:Fh:71:VAL:HG22	1.70	0.73
1:AC:35:LEU:HD11	1:AC:48:VAL:HG22	1.69	0.73
1:FO:35:LEU:HD11	1:FO:48:VAL:HG13	1.70	0.73
1:G7:35:LEU:HD21	1:HQ:91:ILE:HG21	1.68	0.73
1:Hj:92:LEU:CD2	1:Gq:21:ILE:HD13	2.19	0.73
2:Xx:713:ILE:HD11	1:HM:62:ARG:HA	1.71	0.73
1:HC:80:ILE:O	2:XK:716:PRO:HD3	1.88	0.73
2:XS:862:THR:HG21	1:FQ:71:VAL:HG22	1.70	0.73
1:G5:35:LEU:HD11	1:G5:48:VAL:HG22	1.70	0.73
2:X3:812:GLN:HE22	1:H4:70:ARG:HD2	1.51	0.73
1:G4:35:LEU:HD21	1:H7:91:ILE:HD13	1.70	0.73
2:X0:860:LEU:HD12	2:X0:868:ARG:HD3	1.69	0.73
1:Ff:35:LEU:HD11	1:Ff:48:VAL:HG13	1.70	0.73
2:Xj:729:GLU:HA	1:Ds:62:ARG:HH12	1.52	0.73
1:DC:35:LEU:HD11	1:DC:48:VAL:HG23	1.71	0.73
1:G5:35:LEU:HD23	1:Hm:91:ILE:CG2	2.19	0.73
1:H5:92:LEU:CD2	1:Gb:21:ILE:HD13	2.19	0.73
1:G9:25:ASP:HA	1:Hu:88:VAL:HG21	1.70	0.73
1:Ge:35:LEU:HD11	1:Ge:48:VAL:HG22	1.70	0.73
1:DH:35:LEU:HD11	1:DH:48:VAL:HG23	1.71	0.73
1:GM:35:LEU:HD21	1:HP:91:ILE:HD13	1.70	0.73
1:EX:35:LEU:HD11	1:EX:48:VAL:HG13	1.71	0.73
1:F8:35:LEU:HD11	1:F8:48:VAL:HG13	1.69	0.73
2:Xj:860:LEU:HD12	2:Xj:868:ARG:HD3	1.69	0.73
1:Fp:35:LEU:HD11	1:Fp:48:VAL:HG13	1.70	0.73
1:Du:35:LEU:HD11	1:Du:48:VAL:HG13	1.71	0.73
1:AO:25:ASP:HA	1:FO:88:VAL:HG21	1.71	0.73
2:X5:729:GLU:HA	1:Dd:62:ARG:HH12	1.52	0.73
2:X5:862:THR:HG21	1:F3:71:VAL:HG22	1.71	0.73
1:G7:25:ASP:HA	1:HQ:88:VAL:HG21	1.70	0.73
1:Da:35:LEU:HD11	1:Da:48:VAL:HG13	1.71	0.73
1:Cf:35:LEU:HD11	1:Cf:48:VAL:HG23	1.69	0.73
2:Xt:862:THR:HG21	1:Fr:71:VAL:HG22	1.70	0.73
1:Fz:35:LEU:HD11	1:Fz:48:VAL:HG13	1.70	0.73
1:AJ:25:ASP:HA	1:FJ:88:VAL:HG21	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HN:92:LEU:CD2	1:GU:21:ILE:HD13	2.19	0.73
1:A3:7:ILE:HD12	1:D7:32:GLU:CD	2.14	0.73
2:X0:862:THR:HG21	1:F8:71:VAL:HG22	1.70	0.73
1:Fk:35:LEU:HD11	1:Fk:48:VAL:HG13	1.70	0.73
1:Cp:35:LEU:HD11	1:Cp:48:VAL:HG23	1.70	0.73
1:Et:35:LEU:HD11	1:Et:48:VAL:HG13	1.71	0.73
1:Dx:35:LEU:HD11	1:Dx:48:VAL:HG23	1.71	0.73
1:AT:25:ASP:HA	1:FT:88:VAL:HG21	1.71	0.73
1:DW:35:LEU:HD11	1:DW:48:VAL:HG23	1.71	0.73
1:A1:25:ASP:HA	1:F1:88:VAL:HG21	1.71	0.73
1:F3:35:LEU:HD11	1:F3:48:VAL:HG13	1.69	0.73
1:E0:35:LEU:HD11	1:E0:48:VAL:HG13	1.71	0.73
1:D9:35:LEU:HD11	1:D9:48:VAL:HG23	1.71	0.73
1:Fc:35:LEU:HD11	1:Fc:48:VAL:HG13	1.69	0.73
2:Xo:860:LEU:HD12	2:Xo:868:ARG:HD3	1.70	0.73
1:Dn:35:LEU:HD11	1:Dn:48:VAL:HG23	1.71	0.73
1:DR:35:LEU:HD11	1:DR:48:VAL:HG23	1.71	0.73
1:DT:35:LEU:HD11	1:DT:48:VAL:HG13	1.71	0.73
1:G2:73:ASP:OD2	1:HS:45:TYR:OH	2.03	0.73
1:H4:79:HIS:HD1	2:XS:714:THR:CB	2.02	0.73
1:Fw:35:LEU:HD11	1:Fw:48:VAL:HG13	1.69	0.73
1:AE:25:ASP:HA	1:FE:88:VAL:HG21	1.71	0.73
1:GS:35:LEU:HD11	1:GS:48:VAL:HG22	1.70	0.73
1:FT:35:LEU:HD11	1:FT:48:VAL:HG13	1.70	0.73
1:F6:35:LEU:HD11	1:F6:48:VAL:HG13	1.70	0.72
1:G0:35:LEU:HD11	1:G0:48:VAL:HG22	1.70	0.72
1:Af:7:ILE:HD11	1:DB:32:GLU:CG	2.19	0.72
1:Ej:35:LEU:HD11	1:Ej:48:VAL:HG13	1.71	0.72
1:Ck:35:LEU:HD11	1:Ck:48:VAL:HG23	1.70	0.72
2:Xy:862:THR:HG21	1:Fw:71:VAL:HG22	1.70	0.72
1:Aw:7:ILE:HD12	1:DA:32:GLU:CD	2.14	0.72
1:Az:25:ASP:HA	1:Fz:88:VAL:HG21	1.71	0.72
2:XN:714:THR:CB	1:HW:79:HIS:HD1	2.02	0.72
1:CO:35:LEU:HD11	1:CO:48:VAL:HG23	1.70	0.72
1:CT:35:LEU:HD11	1:CT:48:VAL:HG23	1.70	0.72
1:Dd:35:LEU:HD11	1:Dd:48:VAL:HG23	1.71	0.72
1:Ah:7:ILE:HD12	1:Dl:32:GLU:CD	2.14	0.72
1:Cu:35:LEU:HD11	1:Cu:48:VAL:HG23	1.70	0.72
2:Xl:862:THR:HG21	1:FG:71:VAL:HG22	1.70	0.72
1:Ae:28:THR:O	1:HE:83:ARG:NH1	2.22	0.72
1:Gi:35:LEU:HD21	1:Hi:91:ILE:HD13	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Eo:35:LEU:HD11	1:Eo:48:VAL:HG13	1.71	0.72
1:Ds:35:LEU:HD11	1:Ds:48:VAL:HG23	1.71	0.72
1:Gx:17:LEU:HD21	1:HA:39:GLN:OE1	1.89	0.72
1:Dz:35:LEU:HD11	1:Dz:48:VAL:HG13	1.71	0.72
1:GD:35:LEU:HD11	1:GD:48:VAL:HG22	1.70	0.72
2:XD:862:THR:HG21	1:FB:71:VAL:HG22	1.70	0.72
1:AL:7:ILE:HD12	1:DP:32:GLU:CD	2.14	0.72
1:ES:35:LEU:HD11	1:ES:48:VAL:HG13	1.71	0.72
2:X5:714:THR:CB	1:Hd:79:HIS:HD1	2.02	0.72
1:G4:17:LEU:HD21	1:H7:39:GLN:OE1	1.89	0.72
2:Xe:862:THR:HG21	1:Fc:71:VAL:HG22	1.70	0.72
1:Hq:7:ILE:HD11	1:AD:32:GLU:HG3	1.70	0.72
1:GI:35:LEU:HD11	1:GI:48:VAL:HG22	1.70	0.72
1:AS:35:LEU:HD11	1:AS:48:VAL:HG13	1.72	0.72
1:Df:35:LEU:HD11	1:Df:48:VAL:HG13	1.71	0.72
1:Gi:17:LEU:HD21	1:HI:39:GLN:OE1	1.89	0.72
2:Xt:860:LEU:HD12	2:Xt:868:ARG:HD3	1.70	0.72
1:Gx:35:LEU:HD21	1:HA:91:ILE:HD13	1.70	0.72
1:D1:35:LEU:HD11	1:D1:48:VAL:HG13	1.71	0.72
1:H4:80:ILE:HD12	2:XS:713:ILE:CG2	2.20	0.72
2:Xj:714:THR:CB	1:Hs:79:HIS:HD1	2.02	0.72
1:Ak:25:ASP:HA	1:Fk:88:VAL:HG21	1.71	0.72
2:Xy:714:THR:CB	1:HH:79:HIS:HD1	2.02	0.72
1:GN:35:LEU:HD11	1:GN:48:VAL:HG22	1.70	0.72
2:XN:862:THR:HG21	1:FL:71:VAL:HG22	1.71	0.72
1:AW:35:LEU:HD11	1:AW:48:VAL:HG22	1.69	0.72
1:Ee:35:LEU:HD11	1:Ee:48:VAL:HG13	1.71	0.72
1:Gg:25:ASP:HA	1:HU:88:VAL:HG21	1.71	0.72
1:Dk:35:LEU:HD11	1:Dk:48:VAL:HG13	1.71	0.72
1:Go:35:LEU:HD11	1:Go:48:VAL:HG22	1.70	0.72
1:Dp:35:LEU:HD11	1:Dp:48:VAL:HG13	1.71	0.72
2:Xv:716:PRO:HD3	1:HR:80:ILE:O	1.89	0.72
1:Hy:92:LEU:CD2	1:GF:21:ILE:HD13	2.19	0.72
1:A5:35:LEU:HD11	1:A5:48:VAL:HG13	1.72	0.72
1:D6:35:LEU:HD11	1:D6:48:VAL:HG13	1.71	0.72
1:At:35:LEU:HD11	1:At:48:VAL:HG13	1.72	0.72
1:EI:35:LEU:HD11	1:EI:48:VAL:HG13	1.71	0.72
1:GX:35:LEU:HD11	1:GX:48:VAL:HG22	1.70	0.72
1:DE:35:LEU:HD11	1:DE:48:VAL:HG13	1.71	0.72
1:GL:25:ASP:HA	1:HW:88:VAL:HG21	1.72	0.72
1:DO:35:LEU:HD11	1:DO:48:VAL:HG13	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Fh:35:LEU:HD11	1:Fh:48:VAL:HG13	1.69	0.72
1:Hi:77:ALA:HB2	1:GT:72:GLY:HA2	1.72	0.72
2:Xo:862:THR:HG21	1:Fm:71:VAL:HG22	1.70	0.72
1:EN:35:LEU:HD11	1:EN:48:VAL:HG13	1.71	0.72
1:GM:17:LEU:HD21	1:HP:39:GLN:OE1	1.89	0.72
1:A0:35:LEU:HD11	1:A0:48:VAL:HG13	1.72	0.71
1:Di:62:ARG:NH1	2:XU:729:GLU:HA	2.03	0.71
1:Hi:80:ILE:O	2:XU:716:PRO:HD3	1.90	0.71
1:D4:35:LEU:HD11	1:D4:48:VAL:HG23	1.71	0.71
2:Xb:714:THR:OG1	1:Ho:79:HIS:ND1	2.17	0.71
1:Aq:7:ILE:HD11	1:DD:32:GLU:CB	2.20	0.71
1:Ap:7:ILE:CD1	1:DI:32:GLU:HG3	2.20	0.71
1:Hv:79:HIS:ND1	2:XR:714:THR:CG2	2.42	0.71
1:E5:35:LEU:HD11	1:E5:48:VAL:HG13	1.71	0.71
1:A6:25:ASP:HA	1:F6:88:VAL:HG21	1.71	0.71
1:Di:35:LEU:HD11	1:Di:48:VAL:HG23	1.71	0.71
1:Ap:25:ASP:HA	1:Fp:88:VAL:HG21	1.71	0.71
1:Gt:35:LEU:CD2	1:HI:91:ILE:HG21	2.21	0.71
1:DJ:35:LEU:HD11	1:DJ:48:VAL:HG13	1.71	0.71
1:A1:7:ILE:HD11	1:Dm:32:GLU:CG	2.20	0.71
2:X5:713:ILE:CG2	1:Hd:80:ILE:HD12	2.21	0.71
1:Hx:62:ARG:HA	2:XM:713:ILE:HD11	1.72	0.71
1:Ae:35:LEU:HD11	1:Ae:48:VAL:HG13	1.72	0.71
1:Gs:25:ASP:HA	1:Hk:88:VAL:HG21	1.73	0.71
2:XX:862:THR:HG21	1:FV:71:VAL:HG22	1.70	0.71
1:Au:25:ASP:HA	1:Fu:88:VAL:HG21	1.71	0.71
1:GH:25:ASP:HA	1:Hz:88:VAL:HG21	1.73	0.71
1:H3:91:ILE:HG21	1:G6:35:LEU:HD21	1.73	0.71
1:Gd:25:ASP:HA	1:H6:88:VAL:HG21	1.73	0.71
1:Af:25:ASP:HA	1:Ff:88:VAL:HG21	1.71	0.71
1:Gn:25:ASP:HA	1:H1:88:VAL:HG21	1.70	0.71
1:Ey:35:LEU:HD11	1:Ey:48:VAL:HG13	1.71	0.71
2:Xy:713:ILE:CG2	1:HH:80:ILE:HD12	2.21	0.71
1:Hw:91:ILE:HG21	1:Gz:35:LEU:HD21	1.73	0.71
1:AI:35:LEU:HD11	1:AI:48:VAL:HG13	1.72	0.71
2:XN:713:ILE:CG2	1:HW:80:ILE:HD12	2.21	0.71
1:Bs:25:ASP:HA	1:Es:88:VAL:HG21	1.73	0.71
1:ED:35:LEU:HD11	1:ED:48:VAL:HG13	1.71	0.71
1:D0:32:GLU:CB	1:AF:7:ILE:HD11	2.19	0.71
1:Hg:91:ILE:HD13	1:GN:35:LEU:HD21	1.71	0.71
2:Xj:713:ILE:CG2	1:Hs:80:ILE:HD12	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AX:35:LEU:HD11	1:AX:48:VAL:HG13	1.72	0.71
1:A8:28:THR:O	1:Hu:83:ARG:NH1	2.24	0.71
1:Bi:25:ASP:HA	1:Et:88:VAL:HG21	1.73	0.71
2:Xp:712:ARG:HA	2:Xp:712:ARG:NE	2.06	0.71
1:Aj:35:LEU:HD11	1:Aj:48:VAL:HG13	1.72	0.70
2:XA:712:ARG:HA	2:XA:712:ARG:NE	2.06	0.70
2:XE:712:ARG:HA	2:XE:712:ARG:NE	2.06	0.70
1:BM:25:ASP:HA	1:EM:88:VAL:HG21	1.73	0.70
1:DM:35:LEU:HD11	1:DM:48:VAL:HG23	1.71	0.70
1:A2:7:ILE:HD11	1:DX:32:GLU:CB	2.21	0.70
1:Aa:25:ASP:HA	1:Fa:88:VAL:HG21	1.71	0.70
2:Xf:729:GLU:HA	1:DB:62:ARG:HH12	1.56	0.70
1:Dn:32:GLU:CD	1:AT:7:ILE:CD1	2.63	0.70
3:P1:14:ASN:HD22	3:P5:42:ILE:HG21	1.56	0.70
1:B4:25:ASP:HA	1:E4:88:VAL:HG21	1.73	0.70
1:Dg:32:GLU:CG	1:AJ:7:ILE:HD11	2.22	0.70
2:Xf:712:ARG:HA	2:Xf:712:ARG:NE	2.07	0.70
1:Ao:35:LEU:HD11	1:Ao:48:VAL:HG13	1.72	0.70
1:Ap:7:ILE:CD1	1:DI:32:GLU:CG	2.68	0.70
1:BH:25:ASP:HA	1:EH:88:VAL:HG21	1.73	0.70
1:AN:35:LEU:HD11	1:AN:48:VAL:HG13	1.72	0.70
1:Af:7:ILE:CD1	1:DB:32:GLU:CD	2.64	0.70
3:Pz:14:ASN:HD22	3:PD:42:ILE:HG21	1.56	0.70
1:DU:35:LEU:HD11	1:DU:48:VAL:HG13	1.74	0.70
1:D7:35:LEU:HD11	1:D7:48:VAL:HG13	1.74	0.70
1:H9:65:ALA:HB1	2:XQ:712:ARG:HH12	1.56	0.70
1:He:91:ILE:HG21	1:GI:35:LEU:CD2	2.21	0.70
1:Gh:25:ASP:HA	1:Hs:88:VAL:HG21	1.72	0.70
1:Ay:35:LEU:HD11	1:Ay:48:VAL:HG13	1.72	0.70
2:XJ:712:ARG:HA	2:XJ:712:ARG:NE	2.06	0.70
2:XO:712:ARG:HA	2:XO:712:ARG:NE	2.06	0.70
3:PO:14:ASN:HD22	3:PS:42:ILE:HG21	1.56	0.70
1:A1:7:ILE:CD1	1:Dm:32:GLU:CD	2.64	0.70
1:G3:25:ASP:HA	1:Hd:88:VAL:HG21	1.72	0.70
1:A4:7:ILE:CD1	1:DS:32:GLU:HB2	2.16	0.70
1:Gc:25:ASP:HA	1:HE:88:VAL:HG21	1.73	0.70
3:Pf:14:ASN:HD22	3:Pj:42:ILE:HG21	1.56	0.70
1:Dv:35:LEU:HD11	1:Dv:48:VAL:HG13	1.74	0.70
1:Fv:35:LEU:HD11	1:Fv:48:VAL:HG13	1.74	0.70
2:XX:729:GLU:CA	1:DM:62:ARG:HH12	2.03	0.70
3:PT:14:ASN:HD22	3:PX:42:ILE:HG21	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X6:712:ARG:HA	2:X6:712:ARG:NE	2.06	0.70
1:Db:35:LEU:HD11	1:Db:48:VAL:HG13	1.74	0.70
1:De:32:GLU:CG	1:AE:7:ILE:CD1	2.70	0.70
2:Xf:714:THR:OG1	1:HB:79:HIS:CE1	2.44	0.70
1:Dl:35:LEU:HD11	1:Dl:48:VAL:HG13	1.74	0.70
2:Xk:712:ARG:HA	2:Xk:712:ARG:NE	2.06	0.70
3:Pk:14:ASN:HD22	3:Po:42:ILE:HG21	1.56	0.70
1:FP:35:LEU:HD11	1:FP:48:VAL:HG13	1.74	0.70
3:Pa:14:ASN:HD22	3:Pe:42:ILE:HG21	1.56	0.70
1:Bn:25:ASP:HA	1:En:88:VAL:HG21	1.73	0.70
1:FF:35:LEU:HD11	1:FF:48:VAL:HG13	1.74	0.70
1:AH:77:ALA:HB2	1:DH:72:GLY:HA2	1.74	0.70
1:FU:35:LEU:HD11	1:FU:48:VAL:HG13	1.74	0.70
2:Xm:863:TYR:HD2	2:Xm:869:GLY:HA3	1.57	0.70
1:F2:35:LEU:HD11	1:F2:48:VAL:HG13	1.74	0.70
1:A4:77:ALA:HB2	1:D4:72:GLY:HA2	1.74	0.70
1:B9:25:ASP:HA	1:E9:88:VAL:HG21	1.73	0.70
1:Hj:62:ARG:HA	2:Xs:713:ILE:HD11	1.74	0.70
2:Xu:712:ARG:HA	2:Xu:712:ARG:NE	2.06	0.70
1:AD:35:LEU:HD11	1:AD:48:VAL:HG13	1.72	0.70
3:PE:14:ASN:HD22	3:PI:42:ILE:HG21	1.56	0.70
1:BR:25:ASP:HA	1:ER:88:VAL:HG21	1.73	0.70
2:XB:863:TYR:HD2	2:XB:869:GLY:HA3	1.57	0.70
2:XV:863:TYR:HD2	2:XV:869:GLY:HA3	1.57	0.70
2:X3:863:TYR:HD2	2:X3:869:GLY:HA3	1.57	0.69
1:H4:88:VAL:HG21	1:GQ:25:ASP:HA	1.73	0.69
1:H8:91:ILE:CG2	1:Gy:35:LEU:HD23	2.21	0.69
1:Fg:35:LEU:HD11	1:Fg:48:VAL:HG13	1.74	0.69
1:Hh:91:ILE:HG21	1:Gk:35:LEU:HD21	1.73	0.69
1:AR:77:ALA:HB2	1:DR:72:GLY:HA2	1.74	0.69
1:GW:25:ASP:HA	1:HO:88:VAL:HG21	1.73	0.69
3:P6:14:ASN:HD22	3:P0:42:ILE:HG21	1.56	0.69
1:A9:77:ALA:HB2	1:D9:72:GLY:HA2	1.74	0.69
1:Hb:7:ILE:HD11	1:Ao:32:GLU:HG3	1.71	0.69
1:Bd:25:ASP:HA	1:Ed:88:VAL:HG21	1.73	0.69
1:Dg:35:LEU:HD11	1:Dg:48:VAL:HG13	1.74	0.69
1:An:77:ALA:HB2	1:Dn:72:GLY:HA2	1.74	0.69
1:Dq:35:LEU:HD11	1:Dq:48:VAL:HG13	1.74	0.69
1:Gw:25:ASP:HA	1:HH:88:VAL:HG21	1.72	0.69
2:XO:713:ILE:CG2	1:HV:80:ILE:HD12	2.22	0.69
1:Fq:35:LEU:HD11	1:Fq:48:VAL:HG13	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xz:712:ARG:HA	2:Xz:712:ARG:NE	2.06	0.69
1:AC:77:ALA:HB2	1:DC:72:GLY:HA2	1.74	0.69
2:X6:713:ILE:CG2	1:Hc:80:ILE:HD12	2.22	0.69
1:A0:32:GLU:HG3	1:HF:7:ILE:HD11	1.74	0.69
1:Fb:35:LEU:HD11	1:Fb:48:VAL:HG13	1.74	0.69
1:Aa:7:ILE:CD1	1:Dt:32:GLU:HG3	2.23	0.69
2:Xi:713:ILE:HD11	1:HU:62:ARG:HA	1.73	0.69
1:HL:91:ILE:HG21	1:GO:35:LEU:HD21	1.73	0.69
2:XQ:863:TYR:HD2	2:XQ:869:GLY:HA3	1.57	0.69
2:XT:712:ARG:HA	2:XT:712:ARG:NE	2.06	0.69
2:Xi:714:THR:CG2	1:HU:79:HIS:ND1	2.47	0.69
3:Pp:14:ASN:HD22	3:Pt:42:ILE:HG21	1.56	0.69
1:DA:35:LEU:HD11	1:DA:48:VAL:HG13	1.74	0.69
1:DF:35:LEU:HD11	1:DF:48:VAL:HG13	1.74	0.69
1:FK:35:LEU:HD11	1:FK:48:VAL:HG13	1.74	0.69
1:F7:35:LEU:HD11	1:F7:48:VAL:HG13	1.74	0.69
1:Ab:7:ILE:HD11	1:Do:32:GLU:CB	2.22	0.69
1:Bx:25:ASP:HA	1:Ex:88:VAL:HG21	1.73	0.69
2:XX:863:TYR:CD2	2:XX:869:GLY:HA3	2.28	0.69
2:Xa:713:ILE:HG21	1:Ht:80:ILE:HD12	1.75	0.69
2:Xh:863:TYR:HD2	2:Xh:869:GLY:HA3	1.57	0.69
1:Dv:32:GLU:CB	1:AR:7:ILE:HD11	2.14	0.69
1:Gv:35:LEU:CD2	1:HM:91:ILE:HG21	2.22	0.69
1:Gu:72:GLY:HA2	1:HR:77:ALA:HB2	1.74	0.69
1:FA:35:LEU:HD11	1:FA:48:VAL:HG13	1.74	0.69
1:G0:35:LEU:HD23	1:Hc:91:ILE:CG2	2.23	0.69
1:De:32:GLU:HG3	1:AE:7:ILE:CD1	2.22	0.69
1:Ad:77:ALA:HB2	1:Dd:72:GLY:HA2	1.74	0.69
1:Gi:17:LEU:CD2	1:Hi:39:GLN:OE1	2.41	0.69
1:Bm:35:LEU:HD11	1:Bm:48:VAL:HG13	1.75	0.69
1:Cp:24:ALA:HB2	1:Cp:48:VAL:HG21	1.75	0.69
3:Pu:14:ASN:HD22	3:Py:42:ILE:HG21	1.56	0.69
1:Ax:77:ALA:HB2	1:Dx:72:GLY:HA2	1.74	0.69
2:XD:863:TYR:CD2	2:XD:869:GLY:HA3	2.28	0.69
1:BC:25:ASP:HA	1:EC:88:VAL:HG21	1.73	0.69
1:DC:62:ARG:NH1	2:XK:729:GLU:HA	2.04	0.69
1:BL:35:LEU:HD11	1:BL:48:VAL:HG13	1.75	0.69
1:GM:17:LEU:CD2	1:HP:39:GLN:OE1	2.41	0.69
1:CO:24:ALA:HB2	1:CO:48:VAL:HG21	1.75	0.69
2:Xc:863:TYR:HD2	2:Xc:869:GLY:HA3	1.57	0.69
1:G4:17:LEU:CD2	1:H7:39:GLN:OE1	2.41	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X0:863:TYR:CD2	2:X0:869:GLY:HA3	2.28	0.69
1:H8:79:HIS:CE1	2:Xu:714:THR:OG1	2.43	0.69
1:Aa:7:ILE:CD1	1:Dt:32:GLU:CG	2.71	0.69
1:Ai:77:ALA:HB2	1:Di:72:GLY:HA2	1.74	0.69
1:AB:28:THR:O	1:Hf:83:ARG:NH1	2.24	0.69
1:CE:24:ALA:HB2	1:CE:48:VAL:HG21	1.75	0.69
3:PJ:14:ASN:HD22	3:PN:42:ILE:HG21	1.56	0.69
1:CT:24:ALA:HB2	1:CT:48:VAL:HG21	1.75	0.69
1:D2:35:LEU:HD11	1:D2:48:VAL:HG13	1.74	0.69
2:X1:712:ARG:HA	2:X1:712:ARG:NE	2.06	0.69
2:Xa:713:ILE:HG21	1:Ht:80:ILE:CD1	2.23	0.69
1:Hn:88:VAL:HG21	1:GX:25:ASP:HA	1.72	0.69
2:Xz:713:ILE:CG2	1:HG:80:ILE:HD12	2.22	0.69
1:HN:62:ARG:HA	2:XW:713:ILE:HD11	1.74	0.69
1:GS:35:LEU:HD23	1:HV:91:ILE:CG2	2.23	0.69
1:C1:24:ALA:HB2	1:C1:48:VAL:HG21	1.75	0.68
1:Gh:72:GLY:HA2	1:Hs:77:ALA:HB2	1.75	0.68
1:Go:35:LEU:HD23	1:Hr:91:ILE:CG2	2.22	0.68
1:Bw:35:LEU:HD11	1:Bw:48:VAL:HG13	1.75	0.68
1:Gx:17:LEU:CD2	1:HA:39:GLN:OE1	2.41	0.68
1:BG:35:LEU:HD11	1:BG:48:VAL:HG13	1.75	0.68
1:AW:77:ALA:HB2	1:DW:72:GLY:HA2	1.74	0.68
1:Fl:35:LEU:HD11	1:Fl:48:VAL:HG13	1.74	0.68
1:Ck:24:ALA:HB2	1:Ck:48:VAL:HG21	1.75	0.68
1:Gw:72:GLY:HA2	1:HH:77:ALA:HB2	1.75	0.68
1:GL:72:GLY:HA2	1:HW:77:ALA:HB2	1.75	0.68
1:D3:35:LEU:HD11	1:D3:48:VAL:HG13	1.76	0.68
1:B8:35:LEU:HD11	1:B8:48:VAL:HG13	1.75	0.68
1:Dc:35:LEU:HD11	1:Dc:48:VAL:HG13	1.76	0.68
1:Ak:7:ILE:HD11	1:Dr:32:GLU:CG	2.23	0.68
2:Xv:729:GLU:CA	1:DR:62:ARG:HH12	2.03	0.68
1:BB:35:LEU:HD11	1:BB:48:VAL:HG13	1.75	0.68
1:DK:35:LEU:HD11	1:DK:48:VAL:HG13	1.74	0.68
1:DP:35:LEU:HD11	1:DP:48:VAL:HG13	1.74	0.68
1:DV:35:LEU:HD11	1:DV:48:VAL:HG13	1.76	0.68
1:Dx:62:ARG:HH12	2:XM:729:GLU:CA	2.04	0.68
1:Ge:35:LEU:CD2	1:Ht:91:ILE:HG21	2.23	0.68
1:Gr:7:ILE:HG21	1:Gr:83:ARG:HG3	1.76	0.68
1:Hy:62:ARG:HA	2:XH:713:ILE:HD11	1.74	0.68
1:G2:21:ILE:HD13	1:HS:92:LEU:CD2	2.23	0.68
1:D5:32:GLU:HB2	1:Ad:7:ILE:CD1	2.16	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X5:863:TYR:CD2	2:X5:869:GLY:HA3	2.28	0.68
1:H4:77:ALA:HB2	1:GQ:72:GLY:HA2	1.75	0.68
1:C6:24:ALA:HB2	1:C6:48:VAL:HG21	1.75	0.68
2:Xe:863:TYR:CD2	2:Xe:869:GLY:HA3	2.28	0.68
2:Xk:713:ILE:CG2	1:Hr:80:ILE:HD12	2.22	0.68
1:Dm:35:LEU:HD11	1:Dm:48:VAL:HG13	1.76	0.68
1:Gm:7:ILE:HG21	1:Gm:83:ARG:HG3	1.76	0.68
1:Cu:24:ALA:HB2	1:Cu:48:VAL:HG21	1.75	0.68
2:Xl:863:TYR:CD2	2:Xl:869:GLY:HA3	2.28	0.68
1:GM:25:ASP:HA	1:HP:88:VAL:HG21	1.76	0.68
2:Xr:863:TYR:HD2	2:Xr:869:GLY:HA3	1.57	0.68
1:A6:7:ILE:HD11	1:Dc:32:GLU:CG	2.23	0.68
1:Dg:32:GLU:CD	1:Aj:7:ILE:HD13	2.19	0.68
1:Gh:7:ILE:HG21	1:Gh:83:ARG:HG3	1.76	0.68
2:Xo:863:TYR:CD2	2:Xo:869:GLY:HA3	2.28	0.68
1:Br:35:LEU:HD11	1:Br:48:VAL:HG13	1.75	0.68
1:As:77:ALA:HB2	1:Ds:72:GLY:HA2	1.74	0.68
1:GD:35:LEU:HD23	1:HG:91:ILE:CG2	2.23	0.68
1:Bc:35:LEU:HD11	1:Bc:48:VAL:HG13	1.75	0.68
2:Xx:729:GLU:HA	1:DM:62:ARG:NH1	2.07	0.68
1:AO:7:ILE:HD11	1:DV:32:GLU:CG	2.23	0.68
1:H5:62:ARG:HA	2:Xd:713:ILE:HD11	1.74	0.68
1:B3:35:LEU:HD11	1:B3:48:VAL:HG13	1.75	0.68
1:G3:7:ILE:HG21	1:G3:83:ARG:HG3	1.76	0.68
1:G8:7:ILE:HG21	1:G8:83:ARG:HG3	1.76	0.68
1:Gc:7:ILE:HG21	1:Gc:83:ARG:HG3	1.76	0.68
1:Gf:25:ASP:HA	1:HJ:88:VAL:HG21	1.76	0.68
2:Xw:863:TYR:HD2	2:Xw:869:GLY:HA3	1.57	0.68
1:GB:7:ILE:HG21	1:GB:83:ARG:HG3	1.76	0.68
1:DC:62:ARG:HH12	2:XK:729:GLU:CA	2.05	0.68
2:XL:863:TYR:HD2	2:XL:869:GLY:HA3	1.57	0.68
2:XS:863:TYR:CD2	2:XS:869:GLY:HA3	2.28	0.68
1:Bh:35:LEU:HD11	1:Bh:48:VAL:HG13	1.75	0.68
2:XG:863:TYR:HD2	2:XG:869:GLY:HA3	1.57	0.68
2:X1:729:GLU:HA	1:Dm:62:ARG:HH12	1.59	0.67
1:H9:65:ALA:HB1	2:XQ:712:ARG:NH1	2.09	0.67
1:Ah:35:LEU:HD11	1:Ah:48:VAL:HG13	1.76	0.67
2:Xl:806:ILE:HG21	1:Gk:80:ILE:HD12	1.76	0.67
1:Am:35:LEU:HD11	1:Am:48:VAL:HG13	1.77	0.67
2:Xq:714:THR:OG1	1:HD:79:HIS:ND1	2.19	0.67
2:XA:806:ILE:HG21	1:Gz:80:ILE:HD12	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:24:ALA:HB2	1:CJ:48:VAL:HG21	1.75	0.67
1:GL:7:ILE:HG21	1:GL:83:ARG:HG3	1.76	0.67
1:D8:35:LEU:HD11	1:D8:48:VAL:HG13	1.76	0.67
1:Ak:7:ILE:CD1	1:Dr:32:GLU:CD	2.68	0.67
2:Xy:863:TYR:CD2	2:Xy:869:GLY:HA3	2.28	0.67
1:Az:7:ILE:CD1	1:DG:32:GLU:CD	2.68	0.67
1:AM:77:ALA:HB2	1:DM:72:GLY:HA2	1.74	0.67
1:BW:25:ASP:HA	1:EW:88:VAL:HG21	1.73	0.67
2:X8:863:TYR:HD2	2:X8:869:GLY:HA3	1.57	0.67
1:Hy:91:ILE:HG21	1:GF:35:LEU:CD2	2.24	0.67
1:DG:35:LEU:HD11	1:DG:48:VAL:HG13	1.76	0.67
1:DL:35:LEU:HD11	1:DL:48:VAL:HG13	1.76	0.67
1:H2:7:ILE:HD11	1:AX:32:GLU:HG3	1.75	0.67
1:Ac:35:LEU:HD11	1:Ac:48:VAL:HG13	1.76	0.67
1:Dh:35:LEU:HD11	1:Dh:48:VAL:HG13	1.76	0.67
1:Hw:80:ILE:O	2:XA:716:PRO:HD3	1.94	0.67
1:DB:35:LEU:HD11	1:DB:48:VAL:HG13	1.76	0.67
1:GG:7:ILE:HG21	1:GG:83:ARG:HG3	1.76	0.67
1:H5:91:ILE:HG21	1:Gb:35:LEU:CD2	2.24	0.67
1:A8:35:LEU:HD11	1:A8:48:VAL:HG13	1.76	0.67
1:Ca:24:ALA:HB2	1:Ca:48:VAL:HG21	1.75	0.67
1:Ha:83:ARG:NH1	1:At:28:THR:O	2.28	0.67
1:Bi:88:VAL:HG21	1:Fi:25:ASP:HA	1.77	0.67
1:Hx:91:ILE:HG21	1:GK:35:LEU:CD2	2.24	0.67
2:XF:806:ILE:HG21	1:GE:80:ILE:HD12	1.77	0.67
1:BH:88:VAL:HG21	1:FH:25:ASP:HA	1.77	0.67
1:G3:72:GLY:HA2	1:Hd:77:ALA:HB2	1.75	0.67
1:G4:25:ASP:HA	1:H7:88:VAL:HG21	1.76	0.67
2:Xe:714:THR:CB	1:HE:79:HIS:HD1	2.05	0.67
1:Cf:24:ALA:HB2	1:Cf:48:VAL:HG21	1.75	0.67
1:Hp:88:VAL:HG21	1:GG:25:ASP:HA	1.76	0.67
1:Aw:35:LEU:HD11	1:Aw:48:VAL:HG13	1.76	0.67
1:Az:7:ILE:HD11	1:DG:32:GLU:CG	2.23	0.67
2:XN:863:TYR:CD2	2:XN:869:GLY:HA3	2.28	0.67
1:B4:88:VAL:HG21	1:F4:25:ASP:HA	1.77	0.67
2:Xj:863:TYR:CD2	2:Xj:869:GLY:HA3	2.28	0.67
1:Hh:80:ILE:O	2:Xl:716:PRO:HD3	1.95	0.67
1:Gi:25:ASP:HA	1:Hi:88:VAL:HG21	1.76	0.67
1:AG:35:LEU:HD11	1:AG:48:VAL:HG13	1.76	0.67
1:AO:7:ILE:CD1	1:DV:32:GLU:CD	2.68	0.67
1:Hj:91:ILE:HG21	1:Gq:35:LEU:CD2	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xk:729:GLU:HA	1:Dr:62:ARG:HH12	1.60	0.67
2:Xp:713:ILE:HG21	1:HI:80:ILE:CD1	2.24	0.67
1:AL:35:LEU:HD11	1:AL:48:VAL:HG13	1.76	0.67
1:HL:80:ILE:O	2:XP:716:PRO:HD3	1.95	0.67
1:DQ:35:LEU:HD11	1:DQ:48:VAL:HG13	1.76	0.67
2:Xt:863:TYR:CD2	2:Xt:869:GLY:HA3	2.28	0.67
1:Ar:35:LEU:HD11	1:Ar:48:VAL:HG13	1.76	0.67
1:Bs:88:VAL:HG21	1:Fs:25:ASP:HA	1.77	0.67
1:GV:7:ILE:HG21	1:GV:83:ARG:HG3	1.76	0.67
1:G2:35:LEU:CD2	1:HS:91:ILE:HG21	2.25	0.67
1:A3:35:LEU:HD11	1:A3:48:VAL:HG13	1.76	0.67
1:Hg:88:VAL:HG21	1:GN:25:ASP:HA	1.77	0.67
1:Gw:7:ILE:HG21	1:Gw:83:ARG:HG3	1.76	0.67
1:BM:88:VAL:HG21	1:FM:25:ASP:HA	1.77	0.67
2:XO:729:GLU:HA	1:DV:62:ARG:HH12	1.60	0.67
1:BV:35:LEU:HD11	1:BV:48:VAL:HG13	1.75	0.67
2:X1:713:ILE:CG2	1:Hm:80:ILE:HD12	2.24	0.66
1:B9:88:VAL:HG21	1:F9:25:ASP:HA	1.77	0.66
1:Bn:88:VAL:HG21	1:Fn:25:ASP:HA	1.77	0.66
1:Bq:25:ASP:HA	1:Eq:88:VAL:HG21	1.77	0.66
1:Bx:88:VAL:HG21	1:Fx:25:ASP:HA	1.77	0.66
1:Cz:24:ALA:HB2	1:Cz:48:VAL:HG21	1.75	0.66
1:BC:88:VAL:HG21	1:FC:25:ASP:HA	1.77	0.66
1:BF:25:ASP:HA	1:EF:88:VAL:HG21	1.77	0.66
1:HN:91:ILE:HG21	1:GU:35:LEU:CD2	2.24	0.66
1:AQ:35:LEU:HD11	1:AQ:48:VAL:HG13	1.76	0.66
1:BQ:35:LEU:HD11	1:BQ:48:VAL:HG13	1.75	0.66
1:H3:80:ILE:O	2:X7:716:PRO:HD3	1.95	0.66
1:D8:32:GLU:CG	1:Au:7:ILE:HD11	2.24	0.66
1:Hp:83:ARG:NH1	1:AI:28:THR:O	2.26	0.66
2:Xz:729:GLU:HA	1:DG:62:ARG:HH12	1.60	0.66
2:XP:806:ILE:HG21	1:GO:80:ILE:HD12	1.76	0.66
1:BU:25:ASP:HA	1:EU:88:VAL:HG21	1.77	0.66
1:B2:25:ASP:HA	1:E2:88:VAL:HG21	1.77	0.66
1:Dr:35:LEU:HD11	1:Dr:48:VAL:HG13	1.76	0.66
1:Gx:25:ASP:HA	1:HA:88:VAL:HG21	1.76	0.66
1:BP:25:ASP:HA	1:EP:88:VAL:HG21	1.77	0.66
1:B7:25:ASP:HA	1:E7:88:VAL:HG21	1.77	0.66
1:D8:62:ARG:HH12	2:Xu:729:GLU:HA	1.60	0.66
1:Dw:35:LEU:HD11	1:Dw:48:VAL:HG13	1.76	0.66
2:X4:713:ILE:HD11	1:HS:62:ARG:HA	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A6:7:ILE:CD1	1:Dc:32:GLU:CD	2.68	0.66
1:Bg:25:ASP:HA	1:Eg:88:VAL:HG21	1.77	0.66
1:GQ:7:ILE:HG21	1:GQ:83:ARG:HG3	1.76	0.66
1:AV:35:LEU:HD11	1:AV:48:VAL:HG13	1.76	0.66
1:Df:32:GLU:CD	1:AB:7:ILE:CD1	2.68	0.66
2:X7:806:ILE:HG21	1:G6:80:ILE:HD12	1.76	0.66
2:Xw:860:LEU:HD12	2:Xw:868:ARG:HD3	1.78	0.66
2:X2:806:ILE:HG21	1:G1:80:ILE:HD12	1.76	0.66
2:Xg:806:ILE:HG21	1:Gf:80:ILE:HD12	1.76	0.66
2:Xp:713:ILE:HG21	1:HI:80:ILE:HD12	1.77	0.66
1:Ex:35:LEU:HD11	1:Ex:48:VAL:HG13	1.78	0.66
2:X3:860:LEU:HD12	2:X3:868:ARG:HD3	1.78	0.66
2:X6:729:GLU:HA	1:Dc:62:ARG:HH12	1.60	0.66
2:Xg:729:GLU:HA	1:DJ:62:ARG:NH1	2.11	0.66
2:Xh:860:LEU:HD12	2:Xh:868:ARG:HD3	1.78	0.66
1:Ei:35:LEU:HD11	1:Ei:48:VAL:HG13	1.78	0.66
2:XL:860:LEU:HD12	2:XL:868:ARG:HD3	1.78	0.66
2:Xq:806:ILE:HG21	1:Gp:80:ILE:HD12	1.76	0.66
2:Xv:806:ILE:HG21	1:Gu:80:ILE:HD12	1.76	0.66
2:XK:806:ILE:HG21	1:GJ:80:ILE:HD12	1.77	0.66
2:XU:806:ILE:HG21	1:GT:80:ILE:HD12	1.76	0.66
1:E4:35:LEU:HD11	1:E4:48:VAL:HG13	1.78	0.65
1:Gu:25:ASP:HA	1:HR:88:VAL:HG21	1.78	0.65
1:DN:32:GLU:HB2	1:AW:7:ILE:CD1	2.16	0.65
1:D0:28:THR:O	1:AF:83:ARG:NH1	2.29	0.65
1:G8:25:ASP:HA	1:HF:88:VAL:HG21	1.79	0.65
1:GA:35:LEU:CD2	1:HK:91:ILE:HG21	2.26	0.65
1:BW:88:VAL:HG21	1:FW:25:ASP:HA	1.77	0.65
1:Bl:25:ASP:HA	1:El:88:VAL:HG21	1.77	0.65
1:Am:28:THR:O	1:H1:83:ARG:NH1	2.27	0.65
1:DC:28:THR:O	1:AK:83:ARG:NH1	2.30	0.65
1:AO:62:ARG:HG2	2:XO:724:ILE:HG13	1.79	0.65
2:XQ:860:LEU:HD12	2:XQ:868:ARG:HD3	1.78	0.65
1:AT:35:LEU:HD11	1:AT:48:VAL:HG22	1.78	0.65
1:EW:35:LEU:HD11	1:EW:48:VAL:HG13	1.78	0.65
1:D8:32:GLU:CD	1:Au:7:ILE:CD1	2.70	0.65
1:Aa:62:ARG:HG2	2:Xa:724:ILE:HG13	1.79	0.65
2:Xf:713:ILE:CG2	1:HB:80:ILE:HD12	2.26	0.65
1:Hn:80:ILE:CD1	2:XT:713:ILE:HG21	2.26	0.65
1:HC:77:ALA:HB2	1:GJ:72:GLY:HA2	1.77	0.65
2:XH:844:PRO:HG2	2:XH:860:LEU:HD11	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G7:35:LEU:HD23	1:HQ:91:ILE:HG21	1.73	0.65
1:Af:62:ARG:HG2	2:Xf:724:ILE:HG13	1.79	0.65
1:BA:25:ASP:HA	1:EA:88:VAL:HG21	1.77	0.65
1:Az:35:LEU:HD11	1:Az:48:VAL:HG22	1.78	0.65
2:X4:844:PRO:HG2	2:X4:860:LEU:HD11	1.79	0.65
1:A6:35:LEU:HD11	1:A6:48:VAL:HG22	1.78	0.65
1:E9:35:LEU:HD11	1:E9:48:VAL:HG13	1.78	0.65
1:Ak:62:ARG:HG2	2:Xk:724:ILE:HG13	1.79	0.65
1:AB:35:LEU:HD11	1:AB:48:VAL:HG13	1.76	0.65
1:BK:25:ASP:HA	1:EK:88:VAL:HG21	1.77	0.65
2:Xc:860:LEU:HD12	2:Xc:868:ARG:HD3	1.78	0.65
1:H8:35:LEU:HD11	1:H8:48:VAL:HG22	1.79	0.65
2:XM:844:PRO:HG2	2:XM:860:LEU:HD11	1.79	0.65
1:BR:88:VAL:HG21	1:FR:25:ASP:HA	1.77	0.65
2:XR:844:PRO:HG2	2:XR:860:LEU:HD11	1.79	0.65
2:Xm:860:LEU:HD12	2:Xm:868:ARG:HD3	1.78	0.65
1:A2:83:ARG:NH1	1:DX:28:THR:O	2.30	0.65
1:H8:80:ILE:HD12	2:Xu:713:ILE:CG2	2.27	0.65
2:Xs:844:PRO:HG2	2:Xs:860:LEU:HD11	1.79	0.65
1:EM:35:LEU:HD11	1:EM:48:VAL:HG13	1.78	0.65
1:HV:35:LEU:HD11	1:HV:48:VAL:HG22	1.79	0.65
1:Bb:25:ASP:HA	1:Eb:88:VAL:HG21	1.77	0.65
1:Ed:35:LEU:HD11	1:Ed:48:VAL:HG13	1.78	0.65
1:Af:35:LEU:HD11	1:Af:48:VAL:HG22	1.78	0.65
1:Bv:25:ASP:HA	1:Ev:88:VAL:HG21	1.77	0.65
1:A1:7:ILE:HD13	1:Dm:32:GLU:CD	2.21	0.65
1:G3:73:ASP:OD2	1:Hd:45:TYR:OH	2.08	0.65
2:Xb:806:ILE:HG21	1:Ga:80:ILE:HD12	1.76	0.65
2:Xi:844:PRO:HG2	2:Xi:860:LEU:HD11	1.79	0.65
1:Dn:32:GLU:OE1	1:AT:7:ILE:HD13	1.97	0.65
1:Az:62:ARG:HG2	2:Xz:724:ILE:HG13	1.79	0.65
1:AE:35:LEU:HD11	1:AE:48:VAL:HG22	1.78	0.65
1:AJ:62:ARG:HG2	2:XJ:724:ILE:HG13	1.79	0.65
2:Xr:860:LEU:HD12	2:Xr:868:ARG:HD3	1.78	0.65
2:XB:860:LEU:HD12	2:XB:868:ARG:HD3	1.78	0.65
2:XV:860:LEU:HD12	2:XV:868:ARG:HD3	1.78	0.65
1:H4:80:ILE:CD1	2:XS:713:ILE:CG2	2.75	0.64
1:F9:35:LEU:HD11	1:F9:48:VAL:HG23	1.79	0.64
1:Bd:88:VAL:HG21	1:Fd:25:ASP:HA	1.77	0.64
1:Fi:35:LEU:HD11	1:Fi:48:VAL:HG23	1.79	0.64
1:HB:35:LEU:HD11	1:HB:48:VAL:HG22	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HC:88:VAL:HG21	1:GJ:25:ASP:HA	1.79	0.64
1:G8:35:LEU:HD11	1:G8:48:VAL:HG13	1.80	0.64
1:Af:7:ILE:HD13	1:DB:32:GLU:CD	2.21	0.64
1:Ak:35:LEU:HD11	1:Ak:48:VAL:HG22	1.78	0.64
1:En:35:LEU:HD11	1:En:48:VAL:HG13	1.78	0.64
2:Xw:729:GLU:HA	1:DA:62:ARG:HH12	1.62	0.64
1:FW:35:LEU:HD11	1:FW:48:VAL:HG23	1.79	0.64
1:B2:24:ALA:HB2	1:B2:48:VAL:HG11	1.80	0.64
2:X0:841:PRO:HG3	1:F8:69:GLU:HG2	1.80	0.64
1:Gf:72:GLY:CA	1:HJ:77:ALA:HB2	2.26	0.64
1:Ap:35:LEU:HD11	1:Ap:48:VAL:HG22	1.78	0.64
1:Es:35:LEU:HD11	1:Es:48:VAL:HG13	1.78	0.64
1:Hv:91:ILE:HG21	1:GP:35:LEU:CD2	2.27	0.64
2:XG:860:LEU:HD12	2:XG:868:ARG:HD3	1.78	0.64
1:H2:88:VAL:HG21	1:GV:25:ASP:HA	1.80	0.64
1:Gc:35:LEU:HD11	1:Gc:48:VAL:HG13	1.80	0.64
2:Xx:844:PRO:HG2	2:Xx:860:LEU:HD11	1.79	0.64
1:A1:35:LEU:HD11	1:A1:48:VAL:HG22	1.78	0.64
1:Aa:35:LEU:HD11	1:Aa:48:VAL:HG22	1.78	0.64
1:Ha:88:VAL:HG21	1:Gr:25:ASP:HA	1.79	0.64
2:Xh:729:GLU:HA	1:DI:62:ARG:HH12	1.62	0.64
1:Fs:35:LEU:HD11	1:Fs:48:VAL:HG23	1.79	0.64
1:EC:35:LEU:HD11	1:EC:48:VAL:HG13	1.78	0.64
1:AG:28:THR:O	1:Hz:83:ARG:NH1	2.29	0.64
2:Xd:844:PRO:HG2	2:Xd:860:LEU:HD11	1.79	0.64
1:Hr:35:LEU:HD11	1:Hr:48:VAL:HG22	1.79	0.64
1:Bv:24:ALA:HB2	1:Bv:48:VAL:HG11	1.80	0.64
1:Hw:24:ALA:HB2	1:Hw:48:VAL:HG21	1.80	0.64
1:AJ:35:LEU:HD11	1:AJ:48:VAL:HG22	1.78	0.64
1:ER:35:LEU:HD11	1:ER:48:VAL:HG13	1.78	0.64
1:GV:35:LEU:HD11	1:GV:48:VAL:HG13	1.80	0.64
1:A1:62:ARG:HG2	2:X1:724:ILE:HG13	1.79	0.64
2:Xj:841:PRO:HG3	1:Fh:69:GLU:HG2	1.80	0.64
1:Hm:35:LEU:HD11	1:Hm:48:VAL:HG22	1.79	0.64
1:Au:35:LEU:HD11	1:Au:48:VAL:HG22	1.78	0.64
1:Au:62:ARG:HG2	2:Xu:724:ILE:HG13	1.79	0.64
2:Xx:860:LEU:HD12	2:Xx:868:ARG:HD3	1.80	0.64
1:HL:24:ALA:HB2	1:HL:48:VAL:HG21	1.80	0.64
2:X8:860:LEU:HD12	2:X8:868:ARG:HD3	1.78	0.64
1:H3:35:LEU:HD11	1:H3:48:VAL:HG22	1.79	0.64
2:X3:729:GLU:HA	1:D7:62:ARG:HH12	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X9:860:LEU:HD12	2:X9:868:ARG:HD3	1.80	0.64
1:Hh:35:LEU:HD11	1:Hh:48:VAL:HG22	1.79	0.64
1:Hq:88:VAL:HG21	1:GB:25:ASP:HA	1.80	0.64
1:Ap:62:ARG:HG2	2:Xp:724:ILE:HG13	1.79	0.64
2:Xy:841:PRO:HG3	1:Fw:69:GLU:HG2	1.80	0.64
2:XC:844:PRO:HG2	2:XC:860:LEU:HD11	1.79	0.64
1:EH:35:LEU:HD11	1:EH:48:VAL:HG13	1.78	0.64
2:XL:844:PRO:HG2	2:XL:860:LEU:HD11	1.80	0.64
1:HQ:35:LEU:HD11	1:HQ:48:VAL:HG22	1.79	0.64
1:H8:24:ALA:HB2	1:H8:48:VAL:HG21	1.80	0.64
1:He:80:ILE:CD1	2:XE:713:ILE:HG21	2.28	0.64
3:Pc:59:ARG:HH22	3:Pd:60:GLU:HG3	1.63	0.64
1:Hh:24:ALA:HB2	1:Hh:48:VAL:HG21	1.80	0.64
1:Hi:88:VAL:HG21	1:GT:25:ASP:HA	1.78	0.64
1:Hr:24:ALA:HB2	1:Hr:48:VAL:HG21	1.80	0.64
1:Dv:32:GLU:HB2	1:AR:7:ILE:CD1	2.19	0.64
1:Gv:21:ILE:HD13	1:HM:92:LEU:CD2	2.27	0.64
2:XD:841:PRO:HG3	1:FB:69:GLU:HG2	1.80	0.64
1:Ac:28:THR:O	1:H6:83:ARG:NH1	2.29	0.64
1:Fh:35:LEU:HD11	1:Fh:48:VAL:HG23	1.79	0.64
2:XC:860:LEU:HD12	2:XC:868:ARG:HD3	1.80	0.64
2:XL:729:GLU:HA	1:DP:62:ARG:HH12	1.62	0.64
1:AO:35:LEU:HD11	1:AO:48:VAL:HG22	1.78	0.64
2:X5:713:ILE:CG2	1:Hd:80:ILE:CD1	2.76	0.63
1:G3:35:LEU:HD11	1:G3:48:VAL:HG13	1.80	0.63
3:P8:59:ARG:HH22	3:P9:60:GLU:HG3	1.63	0.63
1:Ai:7:ILE:HD11	1:DU:32:GLU:CB	2.17	0.63
2:Xi:860:LEU:HD12	2:Xi:868:ARG:HD3	1.80	0.63
1:Av:83:ARG:NH1	1:DR:28:THR:O	2.30	0.63
3:PG:59:ARG:HH22	3:PH:60:GLU:HG3	1.63	0.63
2:XH:860:LEU:HD12	2:XH:868:ARG:HD3	1.80	0.63
2:X8:844:PRO:HG2	2:X8:860:LEU:HD11	1.80	0.63
1:B7:24:ALA:HB2	1:B7:48:VAL:HG11	1.80	0.63
1:Bb:24:ALA:HB2	1:Bb:48:VAL:HG11	1.80	0.63
2:Xd:860:LEU:HD12	2:Xd:868:ARG:HD3	1.80	0.63
2:Xh:844:PRO:HG2	2:Xh:860:LEU:HD11	1.80	0.63
2:Xo:841:PRO:HG3	1:Fm:69:GLU:HG2	1.80	0.63
1:Dx:62:ARG:NH1	2:XM:729:GLU:HA	2.08	0.63
3:PB:59:ARG:HH22	3:PC:60:GLU:HG3	1.63	0.63
1:HG:35:LEU:HD11	1:HG:48:VAL:HG22	1.79	0.63
3:PL:59:ARG:HH22	3:PM:60:GLU:HG3	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XM:860:LEU:HD12	2:XM:868:ARG:HD3	1.80	0.63
2:XS:841:PRO:HG3	1:FQ:69:GLU:HG2	1.80	0.63
1:HQ:24:ALA:HB2	1:HQ:48:VAL:HG21	1.80	0.63
2:X5:841:PRO:HG3	1:F3:69:GLU:HG2	1.80	0.63
1:Ha:79:HIS:HD1	2:Xt:714:THR:CB	2.10	0.63
1:Gm:35:LEU:HD11	1:Gm:48:VAL:HG13	1.80	0.63
1:Fx:35:LEU:HD11	1:Fx:48:VAL:HG23	1.79	0.63
1:FC:35:LEU:HD11	1:FC:48:VAL:HG23	1.79	0.63
1:AE:62:ARG:HG2	2:XE:724:ILE:HG13	1.79	0.63
2:XW:844:PRO:HG2	2:XW:860:LEU:HD11	1.79	0.63
2:Xr:844:PRO:HG2	2:Xr:860:LEU:HD11	1.80	0.63
2:X1:802:VAL:HG13	2:X1:806:ILE:HB	1.81	0.63
2:Xe:841:PRO:HG3	1:Fc:69:GLU:HG2	1.79	0.63
1:Dj:32:GLU:HB2	1:As:7:ILE:CD1	2.16	0.63
2:Xn:844:PRO:HG2	2:Xn:860:LEU:HD11	1.79	0.63
2:XO:802:VAL:HG13	2:XO:806:ILE:HB	1.81	0.63
1:AV:28:THR:O	1:HO:83:ARG:NH1	2.29	0.63
1:H2:39:GLN:OE1	1:GV:17:LEU:HD21	1.99	0.63
1:A6:62:ARG:HG2	2:X6:724:ILE:HG13	1.79	0.63
1:Dg:32:GLU:CD	1:AJ:7:ILE:CD1	2.72	0.63
1:Gh:35:LEU:HD11	1:Gh:48:VAL:HG13	1.80	0.63
1:Ai:88:VAL:HG21	1:Di:25:ASP:HA	1.81	0.63
1:Hn:91:ILE:CG2	1:GX:35:LEU:CD2	2.76	0.63
2:Xp:802:VAL:HG13	2:Xp:806:ILE:HB	1.81	0.63
2:Xt:825:ALA:CB	1:Dr:15:ARG:HE	2.12	0.63
2:XJ:802:VAL:HG13	2:XJ:806:ILE:HB	1.81	0.63
1:FR:35:LEU:HD11	1:FR:48:VAL:HG23	1.79	0.63
3:PV:59:ARG:HH22	3:PW:60:GLU:HG3	1.63	0.63
2:Xc:844:PRO:HG2	2:Xc:860:LEU:HD11	1.80	0.63
2:XG:844:PRO:HG2	2:XG:860:LEU:HD11	1.80	0.63
1:F4:35:LEU:HD11	1:F4:48:VAL:HG23	1.79	0.63
2:X9:844:PRO:HG2	2:X9:860:LEU:HD11	1.79	0.63
2:Xf:802:VAL:HG13	2:Xf:806:ILE:HB	1.81	0.63
2:Xt:841:PRO:HG3	1:Fr:69:GLU:HG2	1.80	0.63
1:Gr:35:LEU:HD11	1:Gr:48:VAL:HG13	1.80	0.63
2:Xs:860:LEU:HD12	2:Xs:868:ARG:HD3	1.80	0.63
1:Dy:32:GLU:HB2	1:AH:7:ILE:CD1	2.16	0.63
2:XN:713:ILE:CG2	1:HW:80:ILE:CD1	2.76	0.63
1:GQ:35:LEU:HD11	1:GQ:48:VAL:HG13	1.80	0.63
2:XB:844:PRO:HG2	2:XB:860:LEU:HD11	1.80	0.63
2:X5:825:ALA:CB	1:D3:15:ARG:HE	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G8:17:LEU:HD21	1:HF:39:GLN:OE1	1.98	0.63
1:Fd:35:LEU:HD11	1:Fd:48:VAL:HG23	1.79	0.63
1:Bg:24:ALA:HB2	1:Bg:48:VAL:HG11	1.80	0.63
1:As:88:VAL:HG21	1:Ds:25:ASP:HA	1.81	0.63
1:GL:73:ASP:OD2	1:HW:45:TYR:OH	2.08	0.63
1:Ax:88:VAL:HG21	1:Dx:25:ASP:HA	1.81	0.63
2:XE:802:VAL:HG13	2:XE:806:ILE:HB	1.81	0.63
1:GL:35:LEU:HD11	1:GL:48:VAL:HG13	1.80	0.63
2:X3:844:PRO:HG2	2:X3:860:LEU:HD11	1.80	0.63
1:Gh:73:ASP:OD2	1:Hs:45:TYR:OH	2.08	0.63
1:BA:24:ALA:HB2	1:BA:48:VAL:HG11	1.80	0.63
1:BU:24:ALA:HB2	1:BU:48:VAL:HG11	1.80	0.63
1:HV:24:ALA:HB2	1:HV:48:VAL:HG21	1.80	0.63
1:He:80:ILE:HD12	2:XE:713:ILE:HG21	1.80	0.62
2:Xw:844:PRO:HG2	2:Xw:860:LEU:HD11	1.80	0.62
3:Pw:59:ARG:HH22	3:Px:60:GLU:HG3	1.63	0.62
1:BP:24:ALA:HB2	1:BP:48:VAL:HG11	1.80	0.62
2:XQ:844:PRO:HG2	2:XQ:860:LEU:HD11	1.80	0.62
3:PQ:59:ARG:HH22	3:PR:60:GLU:HG3	1.63	0.62
1:Hc:24:ALA:HB2	1:Hc:48:VAL:HG21	1.80	0.62
1:Hc:35:LEU:HD11	1:Hc:48:VAL:HG22	1.79	0.62
2:Xj:713:ILE:CG2	1:Hs:80:ILE:CD1	2.76	0.62
1:Bl:24:ALA:HB2	1:Bl:48:VAL:HG11	1.80	0.62
2:Xn:860:LEU:HD12	2:Xn:868:ARG:HD3	1.80	0.62
3:Pr:59:ARG:HH22	3:Ps:60:GLU:HG3	1.63	0.62
1:AT:62:ARG:HG2	2:XT:724:ILE:HG13	1.79	0.62
2:XW:860:LEU:HD12	2:XW:868:ARG:HD3	1.80	0.62
1:A9:7:ILE:HD11	1:DQ:32:GLU:CB	2.24	0.62
1:G9:72:GLY:HA2	1:Hu:77:ALA:HB2	1.82	0.62
1:Di:62:ARG:HH12	2:XU:729:GLU:CA	2.06	0.62
1:Bq:24:ALA:HB2	1:Bq:48:VAL:HG11	1.80	0.62
1:HL:35:LEU:HD11	1:HL:48:VAL:HG22	1.79	0.62
1:FM:35:LEU:HD11	1:FM:48:VAL:HG23	1.79	0.62
1:H3:91:ILE:CG2	1:G6:35:LEU:HD23	2.29	0.62
3:P3:59:ARG:HH22	3:P4:60:GLU:HG3	1.63	0.62
1:A4:88:VAL:HG21	1:D4:25:ASP:HA	1.81	0.62
1:A9:88:VAL:HG21	1:D9:25:ASP:HA	1.81	0.62
1:Gc:72:GLY:CA	1:HE:77:ALA:HB2	2.29	0.62
2:Xy:713:ILE:CG2	1:HH:80:ILE:CD1	2.76	0.62
1:GB:35:LEU:HD11	1:GB:48:VAL:HG13	1.80	0.62
1:GG:35:LEU:HD11	1:GG:48:VAL:HG13	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FH:35:LEU:HD11	1:FH:48:VAL:HG23	1.79	0.62
1:BK:24:ALA:HB2	1:BK:48:VAL:HG11	1.80	0.62
2:XN:841:PRO:HG3	1:FL:69:GLU:HG2	1.80	0.62
2:XT:802:VAL:HG13	2:XT:806:ILE:HB	1.81	0.62
1:H3:77:ALA:HB2	1:G6:72:GLY:HA2	1.82	0.62
2:Xe:825:ALA:CB	1:Dc:15:ARG:HE	2.12	0.62
2:Xj:825:ALA:CB	1:Dh:15:ARG:HE	2.12	0.62
2:Xk:802:VAL:HG13	2:Xk:806:ILE:HB	1.81	0.62
1:Hm:24:ALA:HB2	1:Hm:48:VAL:HG21	1.80	0.62
3:Pm:59:ARG:HH22	3:Pn:60:GLU:HG3	1.63	0.62
1:HL:91:ILE:CG2	1:GO:35:LEU:HD23	2.29	0.62
2:XV:844:PRO:HG2	2:XV:860:LEU:HD11	1.80	0.62
1:H5:80:ILE:O	2:Xd:716:PRO:HD3	2.00	0.62
2:X4:860:LEU:HD12	2:X4:868:ARG:HD3	1.80	0.62
1:Ga:21:ILE:HD13	1:Ho:92:LEU:CD2	2.30	0.62
3:Ph:59:ARG:HH22	3:Pi:60:GLU:HG3	1.63	0.62
1:Gt:35:LEU:CD2	1:HI:91:ILE:CG2	2.77	0.62
1:Ar:28:THR:O	1:Hk:83:ARG:NH1	2.29	0.62
2:Xu:802:VAL:HG13	2:Xu:806:ILE:HB	1.81	0.62
1:HB:24:ALA:HB2	1:HB:48:VAL:HG21	1.80	0.62
1:HG:24:ALA:HB2	1:HG:48:VAL:HG21	1.80	0.62
1:HN:91:ILE:HG21	1:GU:35:LEU:HD21	1.82	0.62
2:XN:825:ALA:CB	1:DL:15:ARG:HE	2.12	0.62
2:Xm:844:PRO:HG2	2:Xm:860:LEU:HD11	1.80	0.62
1:G7:21:ILE:HD13	1:HQ:92:LEU:CD2	2.28	0.62
2:X6:802:VAL:HG13	2:X6:806:ILE:HB	1.81	0.62
1:Gg:35:LEU:CD2	1:HU:91:ILE:HG21	2.30	0.62
1:Gf:88:VAL:HG21	1:Hf:25:ASP:HA	1.82	0.62
2:Xo:825:ALA:CB	1:Dm:15:ARG:HE	2.12	0.62
1:Hy:91:ILE:HG21	1:GF:35:LEU:HD21	1.82	0.62
1:Hw:35:LEU:HD11	1:Hw:48:VAL:HG22	1.79	0.62
1:BF:24:ALA:HB2	1:BF:48:VAL:HG11	1.80	0.62
2:XX:841:PRO:HG3	1:FV:69:GLU:HG2	1.80	0.62
1:Gk:88:VAL:HG21	1:Hk:25:ASP:HA	1.82	0.62
1:An:88:VAL:HG21	1:Dn:25:ASP:HA	1.81	0.62
1:Gv:35:LEU:HD23	1:HM:91:ILE:CG2	2.30	0.62
1:Gw:35:LEU:HD11	1:Gw:48:VAL:HG13	1.80	0.62
2:Xz:802:VAL:HG13	2:Xz:806:ILE:HB	1.81	0.62
1:H3:24:ALA:HB2	1:H3:48:VAL:HG21	1.80	0.62
2:Xy:825:ALA:CB	1:Dw:15:ARG:HE	2.12	0.62
2:XD:825:ALA:CB	1:DB:15:ARG:HE	2.12	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XI:841:PRO:HG3	1:FG:69:GLU:HG2	1.80	0.62
1:GJ:88:VAL:HG21	1:HJ:25:ASP:HA	1.82	0.62
1:AM:88:VAL:HG21	1:DM:25:ASP:HA	1.81	0.62
2:XS:825:ALA:CB	1:DQ:15:ARG:HE	2.12	0.62
2:XR:860:LEU:HD12	2:XR:868:ARG:HD3	1.80	0.62
1:G7:35:LEU:CD2	1:HQ:91:ILE:CG2	2.76	0.62
1:Hh:77:ALA:HB2	1:Gk:72:GLY:HA2	1.82	0.62
1:Hn:80:ILE:CD1	2:XT:713:ILE:CG2	2.78	0.62
1:Hv:91:ILE:HD13	1:GP:35:LEU:HD21	1.81	0.62
3:PU:1:MET:HG2	3:PU:74:ILE:HD11	1.82	0.62
2:X0:825:ALA:CB	1:D8:15:ARG:HE	2.12	0.61
1:Hg:80:ILE:HD12	2:XJ:713:ILE:CG2	2.30	0.61
1:Ef:7:ILE:HD11	1:Ef:83:ARG:HD2	1.82	0.61
1:Hh:91:ILE:CG2	1:Gk:35:LEU:HD23	2.29	0.61
1:Cl:88:VAL:HG21	1:El:25:ASP:HA	1.82	0.61
1:Ek:7:ILE:HD11	1:Ek:83:ARG:HD2	1.82	0.61
1:Gp:88:VAL:HG21	1:Hp:25:ASP:HA	1.82	0.61
1:Hy:80:ILE:O	2:XH:716:PRO:HD3	2.00	0.61
1:Hw:91:ILE:CG2	1:Gz:35:LEU:HD23	2.29	0.61
2:XI:825:ALA:CB	1:DG:15:ARG:HE	2.12	0.61
1:AR:88:VAL:HG21	1:DR:25:ASP:HA	1.81	0.61
1:G6:88:VAL:HG21	1:H6:25:ASP:HA	1.82	0.61
1:Ad:88:VAL:HG21	1:Dd:25:ASP:HA	1.81	0.61
1:Gw:73:ASP:OD2	1:HH:45:TYR:OH	2.09	0.61
1:Hw:91:ILE:HG21	1:Gz:35:LEU:HD23	1.83	0.61
1:GC:72:GLY:HA2	1:Hf:77:ALA:HB2	1.81	0.61
1:HN:80:ILE:O	2:XW:716:PRO:HD3	2.00	0.61
1:Hj:80:ILE:O	2:Xs:716:PRO:HD3	2.00	0.61
1:Hw:77:ALA:HB2	1:Gz:72:GLY:HA2	1.82	0.61
2:XC:729:GLU:HA	1:DK:62:ARG:HH12	1.66	0.61
1:HP:35:LEU:HD11	1:HP:48:VAL:HG13	1.83	0.61
1:H2:35:LEU:HD11	1:H2:48:VAL:HG13	1.83	0.61
1:Cg:88:VAL:HG21	1:Eg:25:ASP:HA	1.82	0.61
1:Dt:35:LEU:CD1	1:Dt:48:VAL:HG13	2.31	0.61
1:Gs:40:PHE:CE1	1:Hk:41:VAL:HG13	2.36	0.61
3:Pv:1:MET:HG2	3:Pv:74:ILE:HD11	1.82	0.61
1:GA:25:ASP:CA	1:HK:88:VAL:HG21	2.31	0.61
1:AC:88:VAL:HG21	1:DC:25:ASP:HA	1.81	0.61
1:CP:88:VAL:HG21	1:EP:25:ASP:HA	1.82	0.61
3:Pb:59:ARG:HH22	3:Pa:60:GLU:HG3	1.66	0.61
2:Xa:802:VAL:HG13	2:Xa:806:ILE:HB	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dj:35:LEU:CD1	1:Dj:48:VAL:HG13	2.31	0.61
1:Hi:35:LEU:HD11	1:Hi:48:VAL:HG13	1.83	0.61
3:Pv:59:ARG:HH22	3:Pu:60:GLU:HG3	1.66	0.61
2:XN:714:THR:HG1	1:HW:79:HIS:CG	2.09	0.61
1:DX:35:LEU:CD1	1:DX:48:VAL:HG13	2.31	0.61
2:XX:825:ALA:CB	1:DV:15:ARG:HE	2.12	0.61
1:A6:7:ILE:HD13	1:Dc:32:GLU:CD	2.25	0.61
1:HA:35:LEU:HD11	1:HA:48:VAL:HG13	1.83	0.61
1:DD:35:LEU:CD1	1:DD:48:VAL:HG13	2.31	0.61
1:CK:88:VAL:HG21	1:EK:25:ASP:HA	1.82	0.61
3:PP:1:MET:HG2	3:PP:74:ILE:HD11	1.82	0.61
1:GT:88:VAL:HG21	1:HT:25:ASP:HA	1.82	0.61
1:AW:88:VAL:HG21	1:DW:25:ASP:HA	1.81	0.61
3:P7:59:ARG:HH22	3:P6:60:GLU:HG3	1.66	0.61
1:Gd:40:PHE:CE1	1:H6:41:VAL:HG13	2.36	0.61
1:Hj:91:ILE:HG21	1:Gq:35:LEU:HD21	1.82	0.61
2:Xn:714:THR:CG2	1:HT:79:HIS:ND1	2.49	0.61
1:Gp:21:ILE:HD13	1:HD:92:LEU:CD2	2.31	0.61
1:Cv:88:VAL:HG21	1:Ev:25:ASP:HA	1.82	0.61
1:Aw:7:ILE:CD1	1:DA:32:GLU:CD	2.74	0.61
3:PK:59:ARG:HH22	3:PJ:60:GLU:HG3	1.66	0.61
3:PU:59:ARG:HH22	3:PT:60:GLU:HG3	1.66	0.61
1:H5:91:ILE:HG21	1:Gb:35:LEU:HD21	1.82	0.61
1:D9:62:ARG:HH12	2:XQ:729:GLU:CA	2.10	0.61
1:Bn:35:LEU:CD1	1:Bn:48:VAL:HG23	2.31	0.61
1:Ez:7:ILE:HD11	1:Ez:83:ARG:HD2	1.82	0.61
1:BC:35:LEU:CD1	1:BC:48:VAL:HG23	2.31	0.61
1:AH:88:VAL:HG21	1:DH:25:ASP:HA	1.81	0.61
1:HL:77:ALA:HB2	1:GO:72:GLY:HA2	1.82	0.61
1:BM:35:LEU:CD1	1:BM:48:VAL:HG23	2.31	0.61
1:BW:35:LEU:CD1	1:BW:48:VAL:HG23	2.31	0.61
1:H7:35:LEU:HD11	1:H7:48:VAL:HG13	1.83	0.61
1:D0:32:GLU:HB2	1:AF:7:ILE:CD1	2.29	0.61
3:Py:10:LEU:HD11	3:Pw:77:ILE:HG12	1.83	0.61
1:Gz:88:VAL:HG21	1:Hz:25:ASP:HA	1.82	0.61
1:HF:35:LEU:HD11	1:HF:48:VAL:HG13	1.83	0.61
3:PF:59:ARG:HH22	3:PE:60:GLU:HG3	1.66	0.61
3:PK:1:MET:HG2	3:PK:74:ILE:HD11	1.82	0.61
1:EJ:7:ILE:HD11	1:EJ:83:ARG:HD2	1.83	0.61
1:AL:7:ILE:CD1	1:DP:32:GLU:CD	2.74	0.61
1:D8:32:GLU:CD	1:Au:7:ILE:HD13	2.26	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ea:7:ILE:HD11	1:Ea:83:ARG:HD2	1.82	0.61
3:Pq:1:MET:HG2	3:Pq:74:ILE:HD11	1.82	0.61
1:Dv:62:ARG:HH12	2:XR:729:GLU:HA	1.66	0.61
1:Gu:88:VAL:HG21	1:Hu:25:ASP:HA	1.82	0.61
1:GA:35:LEU:HD21	1:HK:91:ILE:HD13	1.83	0.61
1:DI:35:LEU:CD1	1:DI:48:VAL:HG13	2.31	0.61
1:GH:40:PHE:CE1	1:Hx:41:VAL:HG13	2.36	0.61
1:HL:91:ILE:HG21	1:GO:35:LEU:HD23	1.83	0.61
1:Hq:79:HIS:HD1	2:XD:714:THR:CB	2.12	0.60
1:Ep:7:ILE:HD11	1:Ep:83:ARG:HD2	1.82	0.60
1:Gt:25:ASP:HA	1:HI:88:VAL:HG21	1.83	0.60
3:Pt:10:LEU:HD11	3:Pr:77:ILE:HG12	1.83	0.60
1:Hx:92:LEU:CD2	1:GK:21:ILE:HD13	2.30	0.60
3:PN:10:LEU:HD11	3:PL:77:ILE:HG12	1.83	0.60
1:GO:88:VAL:HG21	1:HO:25:ASP:HA	1.82	0.60
1:CU:88:VAL:HG21	1:EU:25:ASP:HA	1.82	0.60
1:ET:7:ILE:HD11	1:ET:83:ARG:HD2	1.82	0.60
1:G1:88:VAL:HG21	1:H1:25:ASP:HA	1.82	0.60
1:G5:25:ASP:HA	1:Hm:88:VAL:HG21	1.83	0.60
1:D0:35:LEU:CD1	1:D0:48:VAL:HG13	2.31	0.60
1:Hb:35:LEU:HD11	1:Hb:48:VAL:HG13	1.83	0.60
3:Pb:1:MET:HG2	3:Pb:74:ILE:HD11	1.82	0.60
1:Ga:88:VAL:HG21	1:Ha:25:ASP:HA	1.82	0.60
1:Ak:7:ILE:HD13	1:Dr:32:GLU:CD	2.25	0.60
1:Hp:77:ALA:HB2	1:GG:72:GLY:CA	2.31	0.60
1:Ds:15:ARG:HE	2:Xr:825:ALA:CB	2.15	0.60
1:Hv:35:LEU:HD11	1:Hv:48:VAL:HG13	1.83	0.60
1:Gu:35:LEU:CD2	1:HR:91:ILE:HG21	2.32	0.60
1:CE:25:ASP:HA	1:DE:88:VAL:HG21	1.83	0.60
1:HK:35:LEU:HD11	1:HK:48:VAL:HG13	1.83	0.60
3:PP:59:ARG:HH22	3:PO:60:GLU:HG3	1.66	0.60
1:BR:35:LEU:CD1	1:BR:48:VAL:HG23	2.31	0.60
1:HU:35:LEU:HD11	1:HU:48:VAL:HG13	1.83	0.60
1:E1:7:ILE:HD11	1:E1:83:ARG:HD2	1.82	0.60
1:C7:88:VAL:HG21	1:E7:25:ASP:HA	1.82	0.60
1:E6:7:ILE:HD11	1:E6:83:ARG:HD2	1.82	0.60
1:B9:35:LEU:CD1	1:B9:48:VAL:HG23	2.31	0.60
1:Bs:35:LEU:CD1	1:Bs:48:VAL:HG23	2.31	0.60
3:PF:1:MET:HG2	3:PF:74:ILE:HD11	1.82	0.60
1:AO:7:ILE:HD13	1:DV:32:GLU:CD	2.25	0.60
1:C2:88:VAL:HG21	1:E2:25:ASP:HA	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P2:1:MET:HG2	3:P2:74:ILE:HD11	1.82	0.60
1:D6:32:GLU:CD	1:Ac:7:ILE:CD1	2.72	0.60
2:X6:713:ILE:HG21	1:Hc:80:ILE:CD1	2.32	0.60
1:Cb:88:VAL:HG21	1:Eb:25:ASP:HA	1.82	0.60
1:Dn:15:ARG:HE	2:Xm:825:ALA:CB	2.15	0.60
1:Cq:88:VAL:HG21	1:Eq:25:ASP:HA	1.82	0.60
1:Hq:35:LEU:HD11	1:Hq:48:VAL:HG13	1.83	0.60
1:Cp:25:ASP:HA	1:Dp:88:VAL:HG21	1.83	0.60
1:GE:88:VAL:HG21	1:HE:25:ASP:HA	1.82	0.60
1:D5:11:MET:HE3	1:D5:79:HIS:HB3	1.84	0.60
2:X3:825:ALA:CB	1:D4:15:ARG:HE	2.15	0.60
3:Pg:1:MET:HG2	3:Pg:74:ILE:HD11	1.82	0.60
3:Pj:10:LEU:HD11	3:Ph:77:ILE:HG12	1.83	0.60
1:Gn:40:PHE:CE1	1:H1:41:VAL:HG13	2.37	0.60
2:Xp:714:THR:OG1	1:HI:79:HIS:CE1	2.49	0.60
1:Cu:25:ASP:HA	1:Du:88:VAL:HG21	1.84	0.60
1:CA:88:VAL:HG21	1:EA:25:ASP:HA	1.82	0.60
1:GA:35:LEU:HD23	1:HK:91:ILE:HG21	1.84	0.60
3:PA:59:ARG:HH22	3:Pz:60:GLU:HG3	1.66	0.60
3:PI:10:LEU:HD11	3:PG:77:ILE:HG12	1.83	0.60
1:CJ:25:ASP:HA	1:DJ:88:VAL:HG21	1.84	0.60
1:DN:35:LEU:CD1	1:DN:48:VAL:HG13	2.31	0.60
1:Ah:7:ILE:CD1	1:Dl:32:GLU:CD	2.74	0.60
2:Xh:825:ALA:CB	1:Di:15:ARG:HE	2.15	0.60
2:Xk:713:ILE:HG21	1:Hr:80:ILE:CD1	2.32	0.60
3:Pq:59:ARG:HH22	3:Pp:60:GLU:HG3	1.66	0.60
1:Dy:11:MET:HE3	1:Dy:79:HIS:HB3	1.84	0.60
1:Hx:91:ILE:CG2	1:GK:35:LEU:HD23	2.32	0.60
1:DC:15:ARG:HE	2:XB:825:ALA:CB	2.15	0.60
1:CO:25:ASP:HA	1:DO:88:VAL:HG21	1.84	0.60
2:XO:713:ILE:HG21	1:Hv:80:ILE:CD1	2.32	0.60
1:Hb:88:VAL:HG21	1:Gm:25:ASP:HA	1.83	0.60
1:Ak:24:ALA:HB2	1:Ak:48:VAL:HG21	1.84	0.60
1:Hq:39:GLN:OE1	1:GB:17:LEU:HD21	2.01	0.60
1:Az:24:ALA:HB2	1:Az:48:VAL:HG21	1.84	0.60
1:HN:35:LEU:HD11	1:HN:48:VAL:HG13	1.84	0.60
1:DS:35:LEU:CD1	1:DS:48:VAL:HG13	2.31	0.60
2:XQ:825:ALA:CB	1:DR:15:ARG:HE	2.15	0.60
1:AT:24:ALA:HB2	1:AT:48:VAL:HG21	1.84	0.60
1:GW:40:PHE:CE1	1:HO:41:VAL:HG13	2.36	0.60
1:A1:24:ALA:HB2	1:A1:48:VAL:HG21	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A3:7:ILE:CD1	1:D7:32:GLU:CD	2.74	0.60
1:H0:35:LEU:HD11	1:H0:48:VAL:HG13	1.84	0.60
3:P1:59:ARG:HH22	3:Pk:60:GLU:HG3	1.66	0.60
1:Ap:24:ALA:HB2	1:Ap:48:VAL:HG21	1.84	0.60
1:Az:7:ILE:HD13	1:DG:32:GLU:CD	2.26	0.60
1:DX:11:MET:HE3	1:DX:79:HIS:HB3	1.84	0.60
2:X2:714:THR:OG1	1:HX:79:HIS:ND1	2.21	0.60
1:C1:25:ASP:HA	1:D1:88:VAL:HG21	1.84	0.60
1:C6:25:ASP:HA	1:D6:88:VAL:HG21	1.84	0.60
1:De:35:LEU:CD1	1:De:48:VAL:HG13	2.31	0.60
1:Hg:35:LEU:HD11	1:Hg:48:VAL:HG13	1.83	0.60
1:Af:24:ALA:HB2	1:Af:48:VAL:HG21	1.84	0.60
1:Ho:35:LEU:HD11	1:Ho:48:VAL:HG13	1.84	0.60
1:Gn:72:GLY:HA2	1:H1:77:ALA:HB2	1.84	0.60
1:Dy:35:LEU:CD1	1:Dy:48:VAL:HG13	2.31	0.60
1:CF:88:VAL:HG21	1:EF:25:ASP:HA	1.82	0.60
1:HS:35:LEU:HD11	1:HS:48:VAL:HG13	1.84	0.60
1:Hu:35:LEU:HD11	1:Hu:48:VAL:HG13	1.84	0.60
2:X1:713:ILE:HG21	1:Hm:80:ILE:CD1	2.32	0.60
3:P5:10:LEU:HD11	3:P3:77:ILE:HG12	1.83	0.60
1:D0:11:MET:HE3	1:D0:79:HIS:HB3	1.84	0.60
1:Ca:25:ASP:HA	1:Da:88:VAL:HG21	1.84	0.60
1:Aq:83:ARG:NH1	1:DD:28:THR:O	2.34	0.60
1:Eu:7:ILE:HD11	1:Eu:83:ARG:HD2	1.82	0.60
2:Xw:825:ALA:CB	1:Dx:15:ARG:HE	2.15	0.60
1:HI:35:LEU:HD11	1:HI:48:VAL:HG13	1.84	0.60
1:BL:24:ALA:HB2	1:BL:48:VAL:HG11	1.84	0.60
1:DS:11:MET:HE3	1:DS:79:HIS:HB3	1.84	0.60
3:PT:10:LEU:HD11	3:PX:77:ILE:HG12	1.84	0.60
1:HX:35:LEU:HD11	1:HX:48:VAL:HG13	1.84	0.60
3:P2:59:ARG:HH22	3:P1:60:GLU:HG3	1.66	0.59
2:X4:716:PRO:HD3	1:HS:80:ILE:O	2.02	0.59
1:A8:7:ILE:CD1	1:Du:32:GLU:CD	2.73	0.59
1:Ge:25:ASP:HA	1:Ht:88:VAL:HG21	1.84	0.59
1:Hg:91:ILE:CG2	1:GN:35:LEU:CD2	2.80	0.59
3:Pg:59:ARG:HH22	3:Pf:60:GLU:HG3	1.66	0.59
1:Au:24:ALA:HB2	1:Au:48:VAL:HG21	1.84	0.59
1:Hf:35:LEU:HD11	1:Hf:48:VAL:HG13	1.84	0.59
3:P1:10:LEU:HD11	3:P5:77:ILE:HG12	1.85	0.59
1:A6:24:ALA:HB2	1:A6:48:VAL:HG21	1.84	0.59
1:G8:17:LEU:CD2	1:HF:39:GLN:OE1	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ge:35:LEU:CD2	1:Ht:91:ILE:CG2	2.80	0.59
1:Dd:15:ARG:HE	2:Xc:825:ALA:CB	2.15	0.59
1:Gj:35:LEU:HD23	1:HB:91:ILE:HG23	1.84	0.59
1:An:28:THR:O	1:HT:83:ARG:NH1	2.32	0.59
2:Xz:713:ILE:HG21	1:HG:80:ILE:CD1	2.32	0.59
1:DN:11:MET:HE3	1:DN:79:HIS:HB3	1.84	0.59
1:CT:25:ASP:HA	1:DT:88:VAL:HG21	1.84	0.59
2:XV:863:TYR:CD2	2:XV:869:GLY:HA3	2.38	0.59
1:G2:35:LEU:HD21	1:HS:91:ILE:HG21	1.85	0.59
1:H5:35:LEU:HD11	1:H5:48:VAL:HG13	1.84	0.59
1:Do:35:LEU:CD1	1:Do:48:VAL:HG13	2.31	0.59
1:Hp:35:LEU:HD11	1:Hp:48:VAL:HG13	1.84	0.59
1:GC:40:PHE:CE1	1:Hf:41:VAL:HG13	2.37	0.59
1:EE:7:ILE:HD11	1:EE:83:ARG:HD2	1.82	0.59
1:DI:11:MET:HE3	1:DI:79:HIS:HB3	1.84	0.59
1:DH:15:ARG:HE	2:XG:825:ALA:CB	2.15	0.59
3:PO:10:LEU:HD11	3:PS:77:ILE:HG12	1.85	0.59
3:P7:1:MET:HG2	3:P7:74:ILE:HD11	1.82	0.59
1:B8:24:ALA:HB2	1:B8:48:VAL:HG11	1.84	0.59
1:A9:53:GLU:OE1	1:HQ:53:GLU:HG3	2.03	0.59
1:Aa:24:ALA:HB2	1:Aa:48:VAL:HG21	1.84	0.59
3:Pe:10:LEU:HD11	3:Pc:77:ILE:HG12	1.83	0.59
1:Dg:32:GLU:HB2	1:AJ:7:ILE:CD1	2.10	0.59
3:Pl:1:MET:HG2	3:Pl:74:ILE:HD11	1.82	0.59
3:PD:10:LEU:HD11	3:PB:77:ILE:HG12	1.83	0.59
1:H1:35:LEU:HD11	1:H1:48:VAL:HG13	1.84	0.59
1:D5:35:LEU:CD1	1:D5:48:VAL:HG13	2.31	0.59
1:Ea:14:THR:HB	1:Ea:19:PRO:HB2	1.85	0.59
1:He:91:ILE:CG2	1:GI:35:LEU:CD2	2.79	0.59
1:Bh:24:ALA:HB2	1:Bh:48:VAL:HG11	1.84	0.59
1:Do:11:MET:HE3	1:Do:79:HIS:HB3	1.84	0.59
1:Br:24:ALA:HB2	1:Br:48:VAL:HG11	1.84	0.59
1:Hy:35:LEU:HD11	1:Hy:48:VAL:HG13	1.84	0.59
2:Xy:784:ARG:HH22	1:Cw:65:ALA:HB3	1.68	0.59
1:AE:24:ALA:HB2	1:AE:48:VAL:HG21	1.84	0.59
1:EE:14:THR:HB	1:EE:19:PRO:HB2	1.85	0.59
2:XL:825:ALA:CB	1:DM:15:ARG:HE	2.15	0.59
1:H2:39:GLN:OE1	1:GV:17:LEU:CD2	2.50	0.59
1:He:35:LEU:HD11	1:He:48:VAL:HG13	1.84	0.59
1:Bd:35:LEU:CD1	1:Bd:48:VAL:HG23	2.31	0.59
1:Dj:11:MET:HE3	1:Dj:79:HIS:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ao:25:ASP:HA	1:Fo:88:VAL:HG21	1.85	0.59
3:Po:10:LEU:HD11	3:Pm:77:ILE:HG12	1.83	0.59
1:Hv:91:ILE:HG21	1:GP:35:LEU:HD23	1.84	0.59
1:Hx:91:ILE:HG21	1:GK:35:LEU:HD23	1.84	0.59
3:PE:10:LEU:HD11	3:PI:77:ILE:HG12	1.85	0.59
1:BH:35:LEU:CD1	1:BH:48:VAL:HG23	2.31	0.59
1:EO:7:ILE:HD11	1:EO:83:ARG:HD2	1.82	0.59
1:B6:83:ARG:NH1	1:E0:29:LYS:O	2.36	0.59
3:P6:10:LEU:HD11	3:P0:77:ILE:HG12	1.85	0.59
1:Ab:83:ARG:NH1	1:Do:28:THR:O	2.35	0.59
1:Gg:35:LEU:HD21	1:HU:91:ILE:HD13	1.83	0.59
1:Cf:25:ASP:HA	1:Df:88:VAL:HG21	1.84	0.59
1:Aj:25:ASP:HA	1:Fj:88:VAL:HG21	1.85	0.59
1:Hh:91:ILE:HG21	1:Gk:35:LEU:HD23	1.82	0.59
2:Xh:863:TYR:CD2	2:Xh:869:GLY:HA3	2.38	0.59
1:Ep:14:THR:HB	1:Ep:19:PRO:HB2	1.85	0.59
1:Bz:83:ARG:NH1	1:ED:29:LYS:O	2.36	0.59
1:AI:25:ASP:HA	1:FI:88:VAL:HG21	1.85	0.59
3:PS:10:LEU:HD11	3:PQ:77:ILE:HG12	1.83	0.59
1:HT:35:LEU:HD11	1:HT:48:VAL:HG13	1.84	0.59
1:H3:91:ILE:HG21	1:G6:35:LEU:HD23	1.83	0.59
1:Gj:25:ASP:HA	1:HB:88:VAL:HG21	1.84	0.59
1:Hj:91:ILE:CG2	1:Gq:35:LEU:HD23	2.33	0.59
1:Bi:35:LEU:CD1	1:Bi:48:VAL:HG23	2.31	0.59
1:At:25:ASP:HA	1:Ft:88:VAL:HG21	1.85	0.59
3:PA:1:MET:HG2	3:PA:74:ILE:HD11	1.82	0.59
1:AN:25:ASP:HA	1:FN:88:VAL:HG21	1.85	0.59
1:AX:25:ASP:HA	1:FX:88:VAL:HG21	1.85	0.59
1:DW:15:ARG:HE	2:XV:825:ALA:CB	2.15	0.59
2:Xe:784:ARG:HH22	1:Cc:65:ALA:HB3	1.68	0.59
1:Di:28:THR:O	1:AU:83:ARG:NH1	2.35	0.59
1:HD:35:LEU:HD11	1:HD:48:VAL:HG13	1.84	0.59
1:BJ:83:ARG:NH1	1:EN:29:LYS:O	2.36	0.59
2:XL:863:TYR:CD2	2:XL:869:GLY:HA3	2.38	0.59
1:ET:14:THR:HB	1:ET:19:PRO:HB2	1.85	0.59
1:BV:24:ALA:HB2	1:BV:48:VAL:HG11	1.85	0.59
2:XB:863:TYR:CD2	2:XB:869:GLY:HA3	2.38	0.59
1:B1:83:ARG:NH1	1:E5:29:LYS:O	2.36	0.59
1:G5:35:LEU:HD23	1:Hm:91:ILE:HG23	1.85	0.59
2:X0:714:THR:CB	1:HF:79:HIS:HD1	2.10	0.59
3:P0:10:LEU:HD11	3:P8:77:ILE:HG12	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D9:15:ARG:HE	2:X8:825:ALA:CB	2.15	0.59
1:He:88:VAL:HG21	1:GI:25:ASP:HA	1.85	0.59
1:Bk:83:ARG:NH1	1:Eo:29:LYS:O	2.36	0.59
2:Xt:784:ARG:HH22	1:Cr:65:ALA:HB3	1.68	0.59
1:AD:25:ASP:HA	1:FD:88:VAL:HG21	1.85	0.59
1:DD:11:MET:HE3	1:DD:79:HIS:HB3	1.84	0.59
1:HJ:35:LEU:HD11	1:HJ:48:VAL:HG13	1.84	0.59
1:Ba:83:ARG:NH1	1:Ee:29:LYS:O	2.36	0.58
1:Hy:91:ILE:CG2	1:GF:35:LEU:HD23	2.33	0.58
1:Dz:32:GLU:CD	1:AG:7:ILE:CD1	2.72	0.58
2:XI:784:ARG:HH22	1:CG:65:ALA:HB3	1.68	0.58
2:XN:784:ARG:HH22	1:CL:65:ALA:HB3	1.68	0.58
1:Bk:72:GLY:HA2	1:Ek:77:ALA:HB2	1.85	0.58
1:Bm:24:ALA:HB2	1:Bm:48:VAL:HG11	1.85	0.58
1:Bp:72:GLY:HA2	1:Ep:77:ALA:HB2	1.86	0.58
1:Dt:11:MET:HE3	1:Dt:79:HIS:HB3	1.84	0.58
1:Eu:14:THR:HB	1:Eu:19:PRO:HB2	1.85	0.58
1:BG:24:ALA:HB2	1:BG:48:VAL:HG11	1.84	0.58
1:HN:91:ILE:CG2	1:GU:35:LEU:HD23	2.33	0.58
1:Hk:35:LEU:HD11	1:Hk:48:VAL:HG13	1.84	0.58
1:Hz:35:LEU:HD11	1:Hz:48:VAL:HG13	1.84	0.58
1:G2:35:LEU:HD23	1:HS:91:ILE:CG2	2.34	0.58
1:B4:35:LEU:CD1	1:B4:48:VAL:HG23	2.31	0.58
1:A0:25:ASP:HA	1:F0:88:VAL:HG21	1.85	0.58
1:Gg:35:LEU:HD23	1:HU:91:ILE:HG21	1.84	0.58
1:Ck:25:ASP:HA	1:Dk:88:VAL:HG21	1.84	0.58
3:Pp:10:LEU:HD11	3:Pt:77:ILE:HG12	1.85	0.58
3:Pz:10:LEU:HD11	3:PD:77:ILE:HG12	1.85	0.58
1:AO:24:ALA:HB2	1:AO:48:VAL:HG21	1.84	0.58
1:BT:83:ARG:NH1	1:EX:29:LYS:O	2.36	0.58
2:X3:863:TYR:CD2	2:X3:869:GLY:HA3	2.38	0.58
3:Pa:10:LEU:HD11	3:Pe:77:ILE:HG12	1.85	0.58
1:Hi:92:LEU:CD2	1:GT:21:ILE:HD13	2.33	0.58
1:Bx:35:LEU:CD1	1:Bx:48:VAL:HG23	2.31	0.58
1:GA:35:LEU:HD23	1:HK:91:ILE:CG2	2.34	0.58
1:Cz:25:ASP:HA	1:Dz:88:VAL:HG21	1.84	0.58
1:BB:24:ALA:HB2	1:BB:48:VAL:HG11	1.85	0.58
1:FF:66:ASP:HB2	2:XF:790:LYS:HE3	1.86	0.58
2:XX:784:ARG:HH22	1:CV:65:ALA:HB3	1.68	0.58
2:Xc:863:TYR:CD2	2:Xc:869:GLY:HA3	2.38	0.58
1:Bc:24:ALA:HB2	1:Bc:48:VAL:HG11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Af:7:ILE:CD1	1:DB:32:GLU:CG	2.82	0.58
1:Bf:83:ARG:NH1	1:Ej:29:LYS:O	2.36	0.58
1:Hi:92:LEU:HD21	1:GT:21:ILE:HD13	1.86	0.58
2:Xo:784:ARG:HH22	1:Cm:65:ALA:HB3	1.68	0.58
1:Bp:83:ARG:NH1	1:Et:29:LYS:O	2.36	0.58
1:Bu:72:GLY:HA2	1:Eu:77:ALA:HB2	1.85	0.58
1:Hy:80:ILE:HD12	2:XH:713:ILE:HG22	1.85	0.58
2:Xw:863:TYR:CD2	2:Xw:869:GLY:HA3	2.38	0.58
3:PX:10:LEU:HD11	3:PV:77:ILE:HG12	1.83	0.58
1:B3:24:ALA:HB2	1:B3:48:VAL:HG11	1.84	0.58
1:De:11:MET:HE3	1:De:79:HIS:HB3	1.84	0.58
3:Pf:10:LEU:HD11	3:Pj:77:ILE:HG12	1.84	0.58
1:Fq:66:ASP:HB2	2:Xq:790:LYS:HE3	1.86	0.58
1:Gp:35:LEU:HD21	1:HD:91:ILE:HG21	1.86	0.58
1:Bw:24:ALA:HB2	1:Bw:48:VAL:HG11	1.84	0.58
1:H5:91:ILE:CG2	1:Gb:35:LEU:HD23	2.33	0.58
1:Bz:72:GLY:HA2	1:Ez:77:ALA:HB2	1.85	0.58
1:Ez:14:THR:HB	1:Ez:19:PRO:HB2	1.85	0.58
3:PJ:10:LEU:HD11	3:PN:77:ILE:HG12	1.85	0.58
1:FP:66:ASP:HB2	2:XP:790:LYS:HE3	1.86	0.58
1:BO:83:ARG:NH1	1:ES:29:LYS:O	2.36	0.58
1:BQ:24:ALA:HB2	1:BQ:48:VAL:HG11	1.85	0.58
2:X5:784:ARG:HH22	1:C3:65:ALA:HB3	1.68	0.58
1:Ba:72:GLY:HA2	1:Ea:77:ALA:HB2	1.85	0.58
1:Gd:72:GLY:HA2	1:H6:77:ALA:HB2	1.86	0.58
1:Fl:66:ASP:HB2	2:Xl:790:LYS:HE3	1.86	0.58
2:Xq:716:PRO:CD	1:HD:80:ILE:O	2.48	0.58
1:Gp:35:LEU:CD2	1:HD:91:ILE:HG21	2.34	0.58
1:HC:91:ILE:HG21	1:GJ:35:LEU:CD2	2.33	0.58
1:BE:72:GLY:HA2	1:EE:77:ALA:HB2	1.85	0.58
1:HE:35:LEU:HD11	1:HE:48:VAL:HG13	1.84	0.58
3:PG:60:GLU:HG2	3:PG:65:LYS:HA	1.86	0.58
1:FK:66:ASP:HB2	2:XK:790:LYS:HE3	1.86	0.58
1:FU:66:ASP:HB2	2:XU:790:LYS:HE3	1.86	0.58
1:B6:72:GLY:HA2	1:E6:77:ALA:HB2	1.85	0.58
1:Ed:7:ILE:HD11	1:Ed:83:ARG:HD3	1.86	0.58
1:Ef:14:THR:HB	1:Ef:19:PRO:HB2	1.85	0.58
1:Hj:35:LEU:HD11	1:Hj:48:VAL:HG13	1.84	0.58
2:Xp:712:ARG:HE	2:Xp:712:ARG:CA	2.17	0.58
1:Ay:25:ASP:HA	1:Fy:88:VAL:HG21	1.85	0.58
1:B1:72:GLY:HA2	1:E1:77:ALA:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F5:35:LEU:HD11	1:F5:48:VAL:HG13	1.86	0.58
1:H3:88:VAL:HG21	1:G6:25:ASP:HA	1.86	0.58
1:E4:7:ILE:HD11	1:E4:83:ARG:HD3	1.86	0.58
2:X0:784:ARG:HH22	1:C8:65:ALA:HB3	1.68	0.58
1:Dk:32:GLU:CD	1:Ar:7:ILE:CD1	2.72	0.58
1:Ht:35:LEU:HD11	1:Ht:48:VAL:HG13	1.84	0.58
1:CA:35:LEU:HD11	1:CA:48:VAL:HG13	1.86	0.58
1:AJ:24:ALA:HB2	1:AJ:48:VAL:HG21	1.84	0.58
3:PV:60:GLU:HG2	3:PV:65:LYS:HA	1.86	0.58
1:H6:35:LEU:HD11	1:H6:48:VAL:HG13	1.84	0.58
2:Xr:863:TYR:CD2	2:Xr:869:GLY:HA3	2.38	0.58
1:D1:32:GLU:CD	1:Am:7:ILE:CD1	2.69	0.57
1:A0:7:ILE:HD11	1:DF:32:GLU:CB	2.29	0.57
1:Cb:35:LEU:HD11	1:Cb:48:VAL:HG13	1.86	0.57
1:Hb:39:GLN:OE1	1:Gm:17:LEU:HD21	2.04	0.57
1:Gv:35:LEU:HD23	1:HM:91:ILE:HG21	1.83	0.57
1:Hv:88:VAL:HG21	1:GP:25:ASP:CA	2.33	0.57
1:Bu:83:ARG:NH1	1:Ey:29:LYS:O	2.36	0.57
1:Hw:88:VAL:HG21	1:Gz:25:ASP:HA	1.86	0.57
1:Ex:7:ILE:HD11	1:Ex:83:ARG:HD3	1.86	0.57
2:XD:784:ARG:HH22	1:CB:65:ALA:HB3	1.68	0.57
1:EH:7:ILE:HD11	1:EH:83:ARG:HD3	1.86	0.57
3:PQ:60:GLU:HG2	3:PQ:65:LYS:HA	1.86	0.57
1:E1:14:THR:HB	1:E1:19:PRO:HB2	1.85	0.57
1:H5:80:ILE:HD12	2:Xd:713:ILE:HG22	1.85	0.57
1:E6:14:THR:HB	1:E6:19:PRO:HB2	1.85	0.57
1:Fb:66:ASP:HB2	2:Xb:790:LYS:HE3	1.86	0.57
1:Fg:66:ASP:HB2	2:Xg:790:LYS:HE3	1.86	0.57
1:Cl:35:LEU:HD11	1:Cl:48:VAL:HG13	1.86	0.57
1:En:7:ILE:HD11	1:En:83:ARG:HD3	1.86	0.57
2:Xq:863:TYR:HD2	2:Xq:869:GLY:HA3	1.69	0.57
3:Pw:60:GLU:HG2	3:Pw:65:LYS:HA	1.86	0.57
1:CK:35:LEU:HD11	1:CK:48:VAL:HG13	1.86	0.57
1:BJ:72:GLY:HA2	1:EJ:77:ALA:HB2	1.85	0.57
1:EO:14:THR:HB	1:EO:19:PRO:HB2	1.85	0.57
1:AS:25:ASP:HA	1:FS:88:VAL:HG21	1.85	0.57
1:E9:7:ILE:HD11	1:E9:83:ARG:HD3	1.86	0.57
1:Ha:35:LEU:HD11	1:Ha:48:VAL:HG13	1.84	0.57
1:Ae:25:ASP:HA	1:Fe:88:VAL:HG21	1.85	0.57
1:Ag:83:ARG:NH1	1:DJ:28:THR:O	2.37	0.57
2:Xi:729:GLU:HA	1:DU:62:ARG:HH12	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xz:712:ARG:HE	2:Xz:712:ARG:CA	2.17	0.57
1:GD:25:ASP:HA	1:HG:88:VAL:HG21	1.87	0.57
1:BE:83:ARG:NH1	1:EI:29:LYS:O	2.36	0.57
1:EM:7:ILE:HD11	1:EM:83:ARG:HD3	1.86	0.57
1:HO:35:LEU:HD11	1:HO:48:VAL:HG13	1.84	0.57
2:X2:863:TYR:HD2	2:X2:869:GLY:HA3	1.69	0.57
1:G1:21:ILE:HD13	1:HX:92:LEU:CD2	2.33	0.57
1:A5:25:ASP:HA	1:F5:88:VAL:HG21	1.85	0.57
2:Xb:863:TYR:HD2	2:Xb:869:GLY:HA3	1.69	0.57
1:Fe:35:LEU:HD11	1:Fe:48:VAL:HG13	1.86	0.57
1:Bf:72:GLY:HA2	1:Ef:77:ALA:HB2	1.85	0.57
2:Xj:784:ARG:HH22	1:Ch:65:ALA:HB3	1.68	0.57
1:Ek:14:THR:HB	1:Ek:19:PRO:HB2	1.85	0.57
3:Pk:10:LEU:HD11	3:Po:77:ILE:HG12	1.84	0.57
1:Hv:91:ILE:CG2	1:GP:35:LEU:HD23	2.34	0.57
2:Xv:863:TYR:HD2	2:Xv:869:GLY:HA3	1.69	0.57
1:EJ:14:THR:HB	1:EJ:19:PRO:HB2	1.85	0.57
1:HN:80:ILE:HD12	2:XW:713:ILE:HG22	1.85	0.57
3:PL:60:GLU:HG2	3:PL:65:LYS:HA	1.86	0.57
2:XS:784:ARG:HH22	1:CQ:65:ALA:HB3	1.68	0.57
1:GQ:24:ALA:HB2	1:GQ:48:VAL:HG11	1.87	0.57
2:XQ:863:TYR:CD2	2:XQ:869:GLY:HA3	2.38	0.57
2:X5:786:SER:HB2	1:C3:79:HIS:ND1	2.20	0.57
1:C7:35:LEU:HD11	1:C7:48:VAL:HG13	1.86	0.57
1:Hp:79:HIS:HD1	2:XI:714:THR:CB	2.11	0.57
1:Gw:24:ALA:HB2	1:Gw:48:VAL:HG11	1.87	0.57
2:XA:863:TYR:HD2	2:XA:869:GLY:HA3	1.69	0.57
1:HL:88:VAL:HG21	1:GO:25:ASP:HA	1.86	0.57
2:XP:863:TYR:HD2	2:XP:869:GLY:HA3	1.69	0.57
2:XU:863:TYR:HD2	2:XU:869:GLY:HA3	1.69	0.57
2:XG:863:TYR:CD2	2:XG:869:GLY:HA3	2.38	0.57
1:H4:45:TYR:OH	1:GQ:73:ASP:OD2	2.10	0.57
1:H0:80:ILE:O	2:XF:716:PRO:CD	2.52	0.57
3:P8:60:GLU:HG2	3:P8:65:LYS:HA	1.86	0.57
2:Xg:863:TYR:HD2	2:Xg:869:GLY:HA3	1.69	0.57
1:CF:35:LEU:HD11	1:CF:48:VAL:HG13	1.86	0.57
2:XE:712:ARG:HE	2:XE:712:ARG:CA	2.17	0.57
2:XI:786:SER:HB2	1:CG:79:HIS:ND1	2.20	0.57
1:CG:18:VAL:HG22	1:DG:11:MET:HB3	1.87	0.57
2:XN:786:SER:HB2	1:CL:79:HIS:ND1	2.20	0.57
1:CU:35:LEU:HD11	1:CU:48:VAL:HG13	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:72:GLY:HA2	1:ET:77:ALA:HB2	1.85	0.57
1:F7:66:ASP:HB2	2:X7:790:LYS:HE3	1.86	0.57
1:F0:35:LEU:HD11	1:F0:48:VAL:HG13	1.86	0.57
1:H0:79:HIS:ND1	2:XF:714:THR:OG1	2.24	0.57
1:Dg:32:GLU:CG	1:AJ:7:ILE:CD1	2.82	0.57
1:Et:7:ILE:HD11	1:Et:83:ARG:HD3	1.86	0.57
1:Gm:24:ALA:HB2	1:Gm:48:VAL:HG11	1.87	0.57
1:Fy:35:LEU:HD11	1:Fy:48:VAL:HG13	1.86	0.57
2:XF:863:TYR:HD2	2:XF:869:GLY:HA3	1.69	0.57
1:H2:80:ILE:HD12	2:XX:713:ILE:CG2	2.35	0.57
1:Ag:7:ILE:HD11	1:DJ:32:GLU:CB	2.34	0.57
1:Fj:35:LEU:HD11	1:Fj:48:VAL:HG13	1.86	0.57
3:Pu:10:LEU:HD11	3:Py:77:ILE:HG12	1.85	0.57
2:Xy:786:SER:HB2	1:Cw:79:HIS:ND1	2.20	0.57
1:FA:66:ASP:HB2	2:XA:790:LYS:HE3	1.86	0.57
1:GV:24:ALA:HB2	1:GV:48:VAL:HG11	1.87	0.57
2:Xm:863:TYR:CD2	2:Xm:869:GLY:HA3	2.38	0.57
1:F2:66:ASP:HB2	2:X2:790:LYS:HE3	1.86	0.57
3:P3:60:GLU:HG2	3:P3:65:LYS:HA	1.86	0.57
1:Cc:88:VAL:HG21	1:Ec:25:ASP:HA	1.87	0.57
1:Dw:32:GLU:OE2	1:AA:7:ILE:HD11	2.05	0.57
1:Dw:62:ARG:NH1	2:XA:729:GLU:HA	2.17	0.57
3:PB:60:GLU:HG2	3:PB:65:LYS:HA	1.86	0.57
1:HN:88:VAL:HG21	1:GU:25:ASP:CA	2.35	0.57
1:GS:25:ASP:HA	1:HV:88:VAL:HG21	1.87	0.57
2:X8:863:TYR:CD2	2:X8:869:GLY:HA3	2.38	0.57
1:G0:25:ASP:HA	1:Hc:88:VAL:HG21	1.87	0.57
1:He:79:HIS:CE1	2:XE:714:THR:OG1	2.51	0.57
2:Xo:786:SER:HB2	1:Cm:79:HIS:ND1	2.20	0.57
1:Cq:35:LEU:HD11	1:Cq:48:VAL:HG13	1.86	0.57
1:Ft:35:LEU:HD11	1:Ft:48:VAL:HG13	1.86	0.57
1:AM:62:ARG:HG2	2:XM:724:ILE:HG13	1.87	0.57
1:FS:35:LEU:HD11	1:FS:48:VAL:HG13	1.86	0.57
1:AW:62:ARG:HG2	2:XW:724:ILE:HG13	1.87	0.57
1:EW:7:ILE:HD11	1:EW:83:ARG:HD3	1.86	0.57
1:C2:35:LEU:HD11	1:C2:48:VAL:HG13	1.86	0.56
2:X7:863:TYR:HD2	2:X7:869:GLY:HA3	1.69	0.56
1:Ab:7:ILE:CD1	1:Do:32:GLU:HB2	2.33	0.56
3:Pm:60:GLU:HG2	3:Pm:65:LYS:HA	1.86	0.56
1:Es:7:ILE:HD11	1:Es:83:ARG:HD3	1.86	0.56
1:Fv:66:ASP:HB2	2:Xv:790:LYS:HE3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:18:VAL:HG22	1:DL:11:MET:HB3	1.87	0.56
1:D3:32:GLU:OE2	1:A7:7:ILE:HD11	2.05	0.56
1:G3:24:ALA:HB2	1:G3:48:VAL:HG11	1.87	0.56
1:Dh:28:THR:O	1:Al:83:ARG:NH1	2.39	0.56
1:Dh:32:GLU:OE2	1:Al:7:ILE:HD11	2.05	0.56
1:Hh:88:VAL:HG21	1:Gk:25:ASP:HA	1.86	0.56
2:Xt:786:SER:HB2	1:Cr:79:HIS:ND1	2.20	0.56
1:As:62:ARG:HG2	2:Xs:724:ILE:HG13	1.87	0.56
1:Hy:88:VAL:HG21	1:GF:25:ASP:CA	2.35	0.56
2:X2:841:PRO:HG3	1:F1:69:GLU:O	2.06	0.56
1:H5:88:VAL:HG21	1:Gb:25:ASP:CA	2.35	0.56
1:A3:25:ASP:HA	1:F3:88:VAL:HG21	1.88	0.56
1:C8:88:VAL:HG21	1:E8:25:ASP:HA	1.87	0.56
2:Xb:716:PRO:CD	1:Ho:80:ILE:O	2.51	0.56
1:Ga:35:LEU:HD21	1:Ho:91:ILE:HG21	1.88	0.56
1:Ac:25:ASP:HA	1:Fc:88:VAL:HG21	1.88	0.56
1:Ad:62:ARG:HG2	2:Xd:724:ILE:HG13	1.87	0.56
1:Cg:35:LEU:HD11	1:Cg:48:VAL:HG13	1.86	0.56
1:Hj:80:ILE:HD12	2:Xs:713:ILE:HG22	1.85	0.56
2:Xl:841:PRO:HG3	1:Fk:69:GLU:O	2.06	0.56
1:Gp:25:ASP:HA	1:HD:88:VAL:HG21	1.86	0.56
1:Gs:72:GLY:HA2	1:Hk:77:ALA:HB2	1.86	0.56
1:Cv:35:LEU:HD11	1:Cv:48:VAL:HG13	1.86	0.56
1:Aw:25:ASP:HA	1:Fw:88:VAL:HG21	1.88	0.56
1:Cw:88:VAL:HG21	1:Ew:25:ASP:HA	1.87	0.56
2:Xw:802:VAL:HG13	2:Xw:806:ILE:HB	1.88	0.56
1:BC:24:ALA:HB2	1:BC:48:VAL:HG21	1.88	0.56
1:FI:35:LEU:HD11	1:FI:48:VAL:HG13	1.86	0.56
1:GH:72:GLY:HA2	1:Hz:77:ALA:HB2	1.86	0.56
1:GL:24:ALA:HB2	1:GL:48:VAL:HG11	1.87	0.56
2:XS:786:SER:HB2	1:CQ:79:HIS:ND1	2.20	0.56
1:CQ:18:VAL:HG22	1:DQ:11:MET:HB3	1.87	0.56
1:CQ:88:VAL:HG21	1:EQ:25:ASP:HA	1.87	0.56
1:ER:7:ILE:HD11	1:ER:83:ARG:HD3	1.86	0.56
2:XX:786:SER:HB2	1:CV:79:HIS:ND1	2.20	0.56
2:X3:802:VAL:HG13	2:X3:806:ILE:HB	1.88	0.56
1:G9:40:PHE:CE1	1:Hu:41:VAL:HG13	2.41	0.56
2:Xb:841:PRO:HG3	1:Fa:69:GLU:O	2.06	0.56
1:Cc:18:VAL:HG22	1:Dc:11:MET:HB3	1.87	0.56
3:Pc:60:GLU:HG2	3:Pc:65:LYS:HA	1.86	0.56
1:Gf:25:ASP:OD2	1:HJ:81:ILE:HG21	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xh:802:VAL:HG13	2:Xh:806:ILE:HB	1.88	0.56
3:Ph:60:GLU:HG2	3:Ph:65:LYS:HA	1.86	0.56
2:Xl:863:TYR:HD2	2:Xl:869:GLY:HA3	1.69	0.56
1:Fo:35:LEU:HD11	1:Fo:48:VAL:HG13	1.86	0.56
3:Pr:60:GLU:HG2	3:Pr:65:LYS:HA	1.86	0.56
2:Xv:841:PRO:HG3	1:Fu:69:GLU:O	2.06	0.56
1:GG:24:ALA:HB2	1:GG:48:VAL:HG11	1.87	0.56
2:XG:802:VAL:HG13	2:XG:806:ILE:HB	1.88	0.56
1:H2:79:HIS:HD1	2:XX:714:THR:CB	2.10	0.56
1:H0:92:LEU:CD2	1:GE:21:ILE:HD13	2.36	0.56
2:X0:713:ILE:CG2	1:HF:80:ILE:HD12	2.36	0.56
1:Aa:7:ILE:HD11	1:Dt:32:GLU:HG3	1.87	0.56
1:Ga:25:ASP:HA	1:Ho:88:VAL:HG21	1.88	0.56
1:An:62:ARG:HG2	2:Xn:724:ILE:HG13	1.87	0.56
1:Gr:24:ALA:HB2	1:Gr:48:VAL:HG11	1.87	0.56
2:XA:841:PRO:HG3	1:Fz:69:GLU:O	2.06	0.56
2:XD:786:SER:HB2	1:CB:79:HIS:ND1	2.20	0.56
1:GB:24:ALA:HB2	1:GB:48:VAL:HG11	1.87	0.56
2:XL:802:VAL:HG13	2:XL:806:ILE:HB	1.88	0.56
1:CP:35:LEU:HD11	1:CP:48:VAL:HG13	1.86	0.56
1:BO:72:GLY:HA2	1:EO:77:ALA:HB2	1.86	0.56
1:AQ:25:ASP:HA	1:FQ:88:VAL:HG21	1.88	0.56
2:XU:841:PRO:HG3	1:FT:69:GLU:O	2.06	0.56
1:CV:88:VAL:HG21	1:EV:25:ASP:HA	1.87	0.56
1:D3:28:THR:O	1:A7:83:ARG:NH1	2.38	0.56
2:X0:786:SER:HB2	1:C8:79:HIS:ND1	2.20	0.56
1:A8:25:ASP:HA	1:F8:88:VAL:HG21	1.88	0.56
2:Xe:786:SER:HB2	1:Cc:79:HIS:ND1	2.20	0.56
1:Hj:88:VAL:HG21	1:Gq:25:ASP:CA	2.35	0.56
2:Xj:786:SER:HB2	1:Ch:79:HIS:ND1	2.20	0.56
1:Ai:7:ILE:CD1	1:DU:32:GLU:HB2	2.21	0.56
1:Bn:24:ALA:HB2	1:Bn:48:VAL:HG21	1.88	0.56
1:Hy:80:ILE:HD12	2:XH:713:ILE:CG2	2.36	0.56
1:Gx:72:GLY:HA2	1:HA:77:ALA:HB2	1.88	0.56
1:FD:35:LEU:HD11	1:FD:48:VAL:HG13	1.86	0.56
1:FN:35:LEU:HD11	1:FN:48:VAL:HG13	1.86	0.56
2:XB:802:VAL:HG13	2:XB:806:ILE:HB	1.88	0.56
1:G4:72:GLY:HA2	1:H7:77:ALA:HB2	1.88	0.56
1:G7:25:ASP:HA	1:HQ:88:VAL:CG2	2.36	0.56
1:Ab:35:LEU:HD11	1:Ab:48:VAL:HG13	1.88	0.56
1:Ha:77:ALA:HB2	1:Gr:72:GLY:CA	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ai:62:ARG:HG2	2:Xi:724:ILE:HG13	1.87	0.56
1:Aq:35:LEU:HD11	1:Aq:48:VAL:HG13	1.88	0.56
1:Av:35:LEU:HD11	1:Av:48:VAL:HG13	1.88	0.56
1:AC:7:ILE:CD1	1:DK:32:GLU:HB2	2.21	0.56
1:DL:28:THR:O	1:AP:83:ARG:NH1	2.38	0.56
2:XT:712:ARG:HE	2:XT:712:ARG:CA	2.17	0.56
1:A1:7:ILE:CD1	1:Dm:32:GLU:CG	2.84	0.56
1:G8:24:ALA:HB2	1:G8:48:VAL:HG11	1.87	0.56
1:Hi:91:ILE:HG21	1:GT:35:LEU:CD2	2.35	0.56
1:Dw:28:THR:O	1:AA:83:ARG:NH1	2.39	0.56
1:CB:18:VAL:HG22	1:DB:11:MET:HB3	1.87	0.56
1:CG:88:VAL:HG21	1:EG:25:ASP:HA	1.87	0.56
1:D2:32:GLU:CB	1:AX:7:ILE:HD11	2.30	0.56
1:C3:18:VAL:HG22	1:D3:11:MET:HB3	1.87	0.56
1:A9:62:ARG:HG2	2:X9:724:ILE:HG13	1.87	0.56
2:Xb:713:ILE:CG2	1:Ho:80:ILE:HD12	2.35	0.56
1:Cr:18:VAL:HG22	1:Dr:11:MET:HB3	1.87	0.56
1:Gu:72:GLY:CA	1:HR:77:ALA:HB2	2.35	0.56
1:CB:88:VAL:HG21	1:EB:25:ASP:HA	1.87	0.56
1:AC:62:ARG:HG2	2:XC:724:ILE:HG13	1.87	0.56
1:DH:15:ARG:HE	2:XG:825:ALA:HB3	1.71	0.56
2:XK:841:PRO:HG3	1:FJ:69:GLU:O	2.06	0.56
1:DL:32:GLU:OE2	1:AP:7:ILE:HD11	2.05	0.56
2:XO:712:ARG:HE	2:XO:712:ARG:CA	2.17	0.56
2:XQ:825:ALA:HB3	1:DR:15:ARG:HE	1.71	0.56
1:BR:24:ALA:HB2	1:BR:48:VAL:HG21	1.88	0.56
1:AV:25:ASP:HA	1:FV:88:VAL:HG21	1.88	0.56
1:CV:18:VAL:HG22	1:DV:11:MET:HB3	1.87	0.56
1:GW:72:GLY:HA2	1:HO:77:ALA:HB2	1.86	0.56
2:X1:712:ARG:HE	2:X1:712:ARG:CA	2.17	0.56
1:C3:88:VAL:HG21	1:E3:25:ASP:HA	1.87	0.56
2:X4:713:ILE:HG22	1:HS:80:ILE:HD12	1.88	0.56
1:H0:91:ILE:HG21	1:GE:35:LEU:CD2	2.35	0.56
3:Pq:10:LEU:HD21	3:Pp:77:ILE:HG12	1.88	0.56
1:Gv:35:LEU:HD21	1:HM:91:ILE:HG21	1.87	0.56
1:AF:35:LEU:HD11	1:AF:48:VAL:HG13	1.88	0.56
2:XF:841:PRO:HG3	1:FE:69:GLU:O	2.06	0.56
2:XP:841:PRO:HG3	1:FO:69:GLU:O	2.06	0.56
1:FX:35:LEU:HD11	1:FX:48:VAL:HG13	1.86	0.56
1:C8:18:VAL:HG22	1:D8:11:MET:HB3	1.87	0.55
1:D9:15:ARG:HE	2:X8:825:ALA:HB3	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bd:24:ALA:HB2	1:Bd:48:VAL:HG21	1.88	0.55
3:Pg:10:LEU:HD21	3:Pf:77:ILE:HG12	1.88	0.55
1:Gh:24:ALA:HB2	1:Gh:48:VAL:HG11	1.87	0.55
1:Hi:77:ALA:HB2	1:GT:72:GLY:CA	2.36	0.55
1:Go:25:ASP:HA	1:Hr:88:VAL:HG21	1.87	0.55
2:Xq:841:PRO:HG3	1:Fp:69:GLU:O	2.06	0.55
1:Cr:88:VAL:HG21	1:Er:25:ASP:HA	1.87	0.55
1:GA:21:ILE:HD13	1:HK:92:LEU:CD2	2.36	0.55
1:EC:7:ILE:HD11	1:EC:83:ARG:HD3	1.86	0.55
1:AL:25:ASP:HA	1:FL:88:VAL:HG21	1.88	0.55
1:CM:35:LEU:HD11	1:CM:48:VAL:HG13	1.89	0.55
2:XQ:802:VAL:HG13	2:XQ:806:ILE:HB	1.88	0.55
1:C4:35:LEU:HD11	1:C4:48:VAL:HG13	1.89	0.55
1:Hj:80:ILE:HD12	2:Xs:713:ILE:CG2	2.36	0.55
1:Ch:18:VAL:HG22	1:Dh:11:MET:HB3	1.87	0.55
1:Bi:24:ALA:HB2	1:Bi:48:VAL:HG21	1.88	0.55
1:Ci:35:LEU:HD11	1:Ci:48:VAL:HG13	1.89	0.55
2:Xn:729:GLU:HA	1:DT:62:ARG:NH1	2.17	0.55
1:Dq:32:GLU:CB	1:AD:7:ILE:HD11	2.28	0.55
1:Ar:25:ASP:HA	1:Fr:88:VAL:HG21	1.88	0.55
1:Bs:24:ALA:HB2	1:Bs:48:VAL:HG21	1.88	0.55
1:Ax:62:ARG:HG2	2:Xx:724:ILE:HG13	1.87	0.55
1:AB:25:ASP:HA	1:FB:88:VAL:HG21	1.88	0.55
2:XK:863:TYR:HD2	2:XK:869:GLY:HA3	1.69	0.55
1:A2:35:LEU:HD11	1:A2:48:VAL:HG13	1.88	0.55
3:P2:10:LEU:HD21	3:P1:77:ILE:HG12	1.88	0.55
2:X3:825:ALA:HB3	1:D4:15:ARG:HE	1.71	0.55
2:X7:841:PRO:HG3	1:F6:69:GLU:O	2.06	0.55
1:Ch:88:VAL:HG21	1:Eh:25:ASP:HA	1.87	0.55
1:Cm:88:VAL:HG21	1:Em:25:ASP:HA	1.87	0.55
1:AH:62:ARG:HG2	2:XH:724:ILE:HG13	1.87	0.55
2:XL:825:ALA:HB3	1:DM:15:ARG:HE	1.71	0.55
2:Xm:802:VAL:HG13	2:Xm:806:ILE:HB	1.88	0.55
1:Dd:15:ARG:HE	2:Xc:825:ALA:HB3	1.71	0.55
1:Go:35:LEU:HD23	1:Hr:91:ILE:HG23	1.89	0.55
1:Ds:15:ARG:HE	2:Xr:825:ALA:HB3	1.71	0.55
1:Hv:92:LEU:CD2	1:GP:21:ILE:HD13	2.37	0.55
1:Cx:35:LEU:HD11	1:Cx:48:VAL:HG13	1.89	0.55
2:XI:825:ALA:HB3	1:DG:15:ARG:HE	1.72	0.55
3:PK:10:LEU:HD21	3:PJ:77:ILE:HG12	1.88	0.55
1:HN:80:ILE:HD12	2:XW:713:ILE:CG2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EU:35:LEU:HD11	1:EU:48:VAL:HG13	1.88	0.55
3:PU:10:LEU:HD21	3:PT:77:ILE:HG12	1.88	0.55
2:XV:802:VAL:HG13	2:XV:806:ILE:HB	1.88	0.55
1:Cm:18:VAL:HG22	1:Dm:11:MET:HB3	1.87	0.55
1:Hq:39:GLN:OE1	1:GB:17:LEU:CD2	2.54	0.55
1:Cw:18:VAL:HG22	1:Dw:11:MET:HB3	1.87	0.55
1:Bx:24:ALA:HB2	1:Bx:48:VAL:HG21	1.88	0.55
3:PA:10:LEU:HD21	3:Pz:77:ILE:HG12	1.88	0.55
3:PB:10:LEU:HD21	3:PC:77:ILE:HG12	1.89	0.55
1:AK:35:LEU:HD11	1:AK:48:VAL:HG13	1.88	0.55
2:X8:802:VAL:HG13	2:X8:806:ILE:HB	1.88	0.55
1:E7:35:LEU:CD1	1:E7:48:VAL:HG13	2.37	0.55
1:Ga:35:LEU:CD2	1:Ho:91:ILE:HG21	2.36	0.55
1:Gc:24:ALA:HB2	1:Gc:48:VAL:HG11	1.87	0.55
2:Xj:825:ALA:HB3	1:Dh:15:ARG:HE	1.72	0.55
1:Bh:35:LEU:CD1	1:Bh:48:VAL:HG13	2.37	0.55
3:PG:10:LEU:HD21	3:PH:77:ILE:HG12	1.89	0.55
1:AP:35:LEU:HD11	1:AP:48:VAL:HG13	1.88	0.55
1:AU:35:LEU:HD11	1:AU:48:VAL:HG13	1.88	0.55
1:E2:35:LEU:CD1	1:E2:48:VAL:HG13	2.37	0.55
1:B4:24:ALA:HB2	1:B4:48:VAL:HG21	1.88	0.55
2:Xa:712:ARG:HE	2:Xa:712:ARG:CA	2.17	0.55
2:Xg:841:PRO:HG3	1:Ff:69:GLU:O	2.06	0.55
1:Ah:25:ASP:HA	1:Fh:88:VAL:HG21	1.88	0.55
1:Cs:35:LEU:HD11	1:Cs:48:VAL:HG13	1.89	0.55
3:Pw:10:LEU:HD21	3:Px:77:ILE:HG12	1.89	0.55
1:GA:25:ASP:HA	1:HK:88:VAL:CG2	2.36	0.55
2:Xz:713:ILE:HG21	1:HG:80:ILE:HD12	1.88	0.55
1:BB:35:LEU:CD1	1:BB:48:VAL:HG13	2.37	0.55
1:BH:24:ALA:HB2	1:BH:48:VAL:HG21	1.88	0.55
1:EK:35:LEU:CD1	1:EK:48:VAL:HG13	2.37	0.55
1:CL:88:VAL:HG21	1:EL:25:ASP:HA	1.87	0.55
1:DO:32:GLU:CD	1:AV:7:ILE:CD1	2.72	0.55
1:AR:62:ARG:HG2	2:XR:724:ILE:HG13	1.87	0.55
1:DW:15:ARG:HE	2:XV:825:ALA:HB3	1.71	0.55
1:B8:35:LEU:CD1	1:B8:48:VAL:HG13	2.37	0.55
1:B9:24:ALA:HB2	1:B9:48:VAL:HG21	1.88	0.55
1:Gg:35:LEU:HD23	1:HU:91:ILE:CG2	2.37	0.55
1:Gp:24:ALA:HB2	1:Gp:48:VAL:HG21	1.89	0.55
2:Xw:712:ARG:HH12	1:HA:65:ALA:CB	2.18	0.55
2:X2:716:PRO:CD	1:HX:80:ILE:O	2.53	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G4:35:LEU:CD2	1:H7:91:ILE:HD13	2.37	0.55
1:A7:35:LEU:HD11	1:A7:48:VAL:HG13	1.88	0.55
1:H0:91:ILE:HG21	1:GE:35:LEU:HD21	1.89	0.55
2:Xb:863:TYR:CD2	2:Xb:869:GLY:HA3	2.42	0.55
3:Pc:10:LEU:HD21	3:Pd:77:ILE:HG12	1.89	0.55
2:Xj:713:ILE:HG21	1:Hs:80:ILE:CD1	2.37	0.55
1:El:35:LEU:HD11	1:El:48:VAL:HG13	1.88	0.55
1:EA:35:LEU:CD1	1:EA:48:VAL:HG13	2.37	0.55
1:EK:35:LEU:HD11	1:EK:48:VAL:HG13	1.89	0.55
2:XL:712:ARG:HH12	1:HP:65:ALA:CB	2.18	0.55
1:GM:72:GLY:HA2	1:HP:77:ALA:HB2	1.88	0.55
2:XP:863:TYR:CD2	2:XP:869:GLY:HA3	2.42	0.55
2:XX:825:ALA:HB3	1:DV:15:ARG:HE	1.72	0.55
1:G7:21:ILE:HD13	1:HQ:92:LEU:HD21	1.88	0.55
2:Xf:713:ILE:HG21	1:HB:80:ILE:CD1	2.35	0.55
1:Gl:21:ILE:HD13	1:HT:92:LEU:CD2	2.37	0.55
2:Xq:713:ILE:CG2	1:HD:80:ILE:HD12	2.37	0.55
2:Xv:863:TYR:CD2	2:Xv:869:GLY:HA3	2.42	0.55
1:Fw:59:ALA:HB1	2:Xw:788:GLU:HG2	1.89	0.55
1:AA:35:LEU:HD11	1:AA:48:VAL:HG13	1.88	0.55
1:DC:15:ARG:HE	2:XB:825:ALA:HB3	1.71	0.55
2:XF:863:TYR:CD2	2:XF:869:GLY:HA3	2.42	0.55
1:AG:25:ASP:HA	1:FG:88:VAL:HG21	1.88	0.55
1:CH:35:LEU:HD11	1:CH:48:VAL:HG13	1.89	0.55
3:PP:10:LEU:HD21	3:PO:77:ILE:HG12	1.88	0.55
2:Xr:802:VAL:HG13	2:Xr:806:ILE:HB	1.88	0.55
1:H5:80:ILE:HD12	2:Xd:713:ILE:CG2	2.36	0.54
1:H3:92:LEU:HD21	1:G6:21:ILE:HD13	1.88	0.54
1:A4:62:ARG:HG2	2:X4:724:ILE:HG13	1.87	0.54
3:Pb:10:LEU:HD21	3:Pa:77:ILE:HG12	1.88	0.54
1:Cd:35:LEU:HD11	1:Cd:48:VAL:HG13	1.89	0.54
1:Eg:35:LEU:HD11	1:Eg:48:VAL:HG13	1.88	0.54
1:Hg:91:ILE:CG2	1:GN:35:LEU:HD23	2.37	0.54
1:Al:35:LEU:HD11	1:Al:48:VAL:HG13	1.88	0.54
1:Gu:21:ILE:HD13	1:HR:92:LEU:CD2	2.37	0.54
1:Gx:35:LEU:CD2	1:HA:91:ILE:HD13	2.37	0.54
1:EA:35:LEU:HD11	1:EA:48:VAL:HG13	1.88	0.54
2:XD:825:ALA:HB3	1:DB:15:ARG:HE	1.72	0.54
1:BG:35:LEU:CD1	1:BG:48:VAL:HG13	2.37	0.54
1:HL:92:LEU:HD21	1:GO:21:ILE:HD13	1.88	0.54
3:PL:10:LEU:HD21	3:PM:77:ILE:HG12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:9:LEU:HD11	1:BM:49:LEU:HD23	1.89	0.54
1:BM:24:ALA:HB2	1:BM:48:VAL:HG21	1.88	0.54
1:BQ:35:LEU:CD1	1:BQ:48:VAL:HG13	2.37	0.54
1:FQ:59:ALA:HB1	2:XQ:788:GLU:HG2	1.90	0.54
3:PQ:10:LEU:HD21	3:PR:77:ILE:HG12	1.89	0.54
1:CR:35:LEU:HD11	1:CR:48:VAL:HG13	1.89	0.54
2:X5:713:ILE:HG21	1:Hd:80:ILE:CD1	2.37	0.54
1:H4:80:ILE:CD1	2:XS:713:ILE:HG21	2.37	0.54
3:P7:10:LEU:HD21	3:P6:77:ILE:HG12	1.88	0.54
1:Eb:35:LEU:CD1	1:Eb:48:VAL:HG13	2.37	0.54
1:Eg:35:LEU:CD1	1:Eg:48:VAL:HG13	2.37	0.54
1:El:35:LEU:CD1	1:El:48:VAL:HG13	2.37	0.54
3:Pl:10:LEU:HD21	3:Pk:77:ILE:HG12	1.88	0.54
2:Xk:712:ARG:HE	2:Xk:712:ARG:CA	2.17	0.54
1:Cn:35:LEU:HD11	1:Cn:48:VAL:HG13	1.89	0.54
1:Eq:35:LEU:CD1	1:Eq:48:VAL:HG13	2.37	0.54
1:Hw:92:LEU:HD21	1:Gz:21:ILE:HD13	1.88	0.54
2:XS:825:ALA:HB3	1:DQ:15:ARG:HE	1.72	0.54
1:GR:41:VAL:HB	1:GR:45:TYR:HB2	1.90	0.54
2:Xc:802:VAL:HG13	2:Xc:806:ILE:HB	1.88	0.54
1:A2:7:ILE:CD1	1:DX:32:GLU:HB2	2.31	0.54
1:B3:35:LEU:CD1	1:B3:48:VAL:HG13	2.37	0.54
1:E7:35:LEU:HD11	1:E7:48:VAL:HG13	1.88	0.54
1:Gd:41:VAL:HB	1:Gd:45:TYR:HB2	1.90	0.54
1:Ag:35:LEU:HD11	1:Ag:48:VAL:HG13	1.88	0.54
1:Gi:72:GLY:HA2	1:Hi:77:ALA:HB2	1.88	0.54
1:Gn:41:VAL:HB	1:Gn:45:TYR:HB2	1.90	0.54
1:BH:9:LEU:HD11	1:BH:49:LEU:HD23	1.89	0.54
1:GH:41:VAL:HB	1:GH:45:TYR:HB2	1.90	0.54
1:EP:35:LEU:CD1	1:EP:48:VAL:HG13	2.37	0.54
1:H8:80:ILE:CD1	2:Xu:713:ILE:HG21	2.37	0.54
1:H8:91:ILE:HG23	1:Gy:35:LEU:HD23	1.88	0.54
1:Gf:24:ALA:HB2	1:Gf:48:VAL:HG21	1.89	0.54
1:Hh:92:LEU:HD21	1:Gk:21:ILE:HD13	1.88	0.54
1:Dn:15:ARG:HE	2:Xm:825:ALA:HB3	1.71	0.54
1:Hn:91:ILE:CG2	1:GX:35:LEU:HD23	2.37	0.54
2:Xq:863:TYR:CD2	2:Xq:869:GLY:HA3	2.42	0.54
3:Pr:10:LEU:HD21	3:Ps:77:ILE:HG12	1.89	0.54
1:BR:9:LEU:HD11	1:BR:49:LEU:HD23	1.89	0.54
1:EU:35:LEU:CD1	1:EU:48:VAL:HG13	2.37	0.54
2:XU:863:TYR:CD2	2:XU:869:GLY:HA3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BV:35:LEU:CD1	1:BV:48:VAL:HG13	2.37	0.54
1:BW:24:ALA:HB2	1:BW:48:VAL:HG21	1.88	0.54
2:Xr:714:THR:HA	2:Xr:718:MET:HG3	1.90	0.54
1:F7:29:LYS:HA	1:C6:83:ARG:HH21	1.73	0.54
1:Hb:79:HIS:HD1	2:Xo:714:THR:CB	2.15	0.54
1:Be:12:ILE:HG23	1:Be:75:LEU:HD12	1.90	0.54
2:Xh:825:ALA:HB3	1:Di:15:ARG:HE	1.71	0.54
1:Gi:35:LEU:CD2	1:Hi:91:ILE:HD13	2.37	0.54
1:Am:25:ASP:HA	1:Fm:88:VAL:HG21	1.88	0.54
1:Hx:91:ILE:HG21	1:GK:35:LEU:HD21	1.89	0.54
1:EF:35:LEU:CD1	1:EF:48:VAL:HG13	2.37	0.54
1:EF:35:LEU:HD11	1:EF:48:VAL:HG13	1.88	0.54
3:PF:10:LEU:HD21	3:PE:77:ILE:HG12	1.88	0.54
2:XN:713:ILE:HG21	1:HW:80:ILE:CD1	2.37	0.54
1:G1:35:LEU:CD2	1:HX:91:ILE:HG21	2.37	0.54
3:P3:10:LEU:HD21	3:P4:77:ILE:HG12	1.89	0.54
1:G4:41:VAL:HB	1:G4:45:TYR:HB2	1.90	0.54
2:Xe:825:ALA:HB3	1:Dc:15:ARG:HE	1.72	0.54
2:Xg:863:TYR:CD2	2:Xg:869:GLY:HA3	2.42	0.54
2:Xf:712:ARG:HE	2:Xf:712:ARG:CA	2.17	0.54
1:Fq:29:LYS:HA	1:Cp:83:ARG:HH21	1.73	0.54
2:Xt:825:ALA:HB3	1:Dr:15:ARG:HE	1.72	0.54
1:Bx:9:LEU:HD11	1:Bx:49:LEU:HD23	1.89	0.54
2:XA:863:TYR:CD2	2:XA:869:GLY:HA3	2.42	0.54
1:GC:25:ASP:CA	1:Hf:88:VAL:HG21	2.37	0.54
1:CI:72:GLY:HA2	1:DI:77:ALA:HB2	1.90	0.54
1:FU:29:LYS:HA	1:CT:83:ARG:HH21	1.73	0.54
1:B0:12:ILE:HG23	1:B0:75:LEU:HD12	1.90	0.54
1:H8:88:VAL:HG21	1:Gy:25:ASP:HA	1.89	0.54
3:P8:10:LEU:HD21	3:P9:77:ILE:HG12	1.89	0.54
1:G9:41:VAL:HB	1:G9:45:TYR:HB2	1.90	0.54
1:Fb:29:LYS:HA	1:Ca:83:ARG:HH21	1.73	0.54
3:Ph:10:LEU:HD21	3:Pi:77:ILE:HG12	1.89	0.54
1:Bn:9:LEU:HD11	1:Bn:49:LEU:HD23	1.89	0.54
1:Fr:59:ALA:HB1	2:Xr:788:GLU:HG2	1.89	0.54
1:Fs:69:GLU:HG2	2:Xr:841:PRO:HG3	1.90	0.54
1:CC:35:LEU:HD11	1:CC:48:VAL:HG13	1.89	0.54
1:FF:29:LYS:HA	1:CE:83:ARG:HH21	1.73	0.54
2:X2:863:TYR:CD2	2:X2:869:GLY:HA3	2.42	0.54
1:D3:32:GLU:CB	1:A7:7:ILE:HD11	2.35	0.54
1:B9:9:LEU:HD11	1:B9:49:LEU:HD23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Eb:35:LEU:HD11	1:Eb:48:VAL:HG13	1.89	0.54
1:Bc:35:LEU:CD1	1:Bc:48:VAL:HG13	2.37	0.54
1:Bd:9:LEU:HD11	1:Bd:49:LEU:HD23	1.89	0.54
2:Xh:841:PRO:HG3	1:Fi:69:GLU:HG2	1.90	0.54
1:Fm:59:ALA:HB1	2:Xm:788:GLU:HG2	1.90	0.54
3:Pm:10:LEU:HD21	3:Pn:77:ILE:HG12	1.89	0.54
1:Fv:29:LYS:HA	1:Cu:83:ARG:HH21	1.73	0.54
1:Bw:35:LEU:CD1	1:Bw:48:VAL:HG13	2.37	0.54
1:BC:9:LEU:HD11	1:BC:49:LEU:HD23	1.89	0.54
1:FP:29:LYS:HA	1:CO:83:ARG:HH21	1.73	0.54
1:E2:35:LEU:HD11	1:E2:48:VAL:HG13	1.88	0.54
2:X2:806:ILE:HG21	1:G1:80:ILE:CD1	2.38	0.54
1:G6:24:ALA:HB2	1:G6:48:VAL:HG21	1.89	0.54
1:G9:25:ASP:HA	1:Hu:88:VAL:CG2	2.38	0.54
2:X9:863:TYR:HD2	2:X9:869:GLY:HA3	1.73	0.54
1:Fc:59:ALA:HB1	2:Xc:788:GLU:HG2	1.90	0.54
1:Eq:35:LEU:HD11	1:Eq:48:VAL:HG13	1.88	0.54
1:Ev:35:LEU:HD11	1:Ev:48:VAL:HG13	1.89	0.54
2:Xu:712:ARG:HE	2:Xu:712:ARG:CA	2.17	0.54
2:Xw:841:PRO:HG3	1:Fx:69:GLU:HG2	1.90	0.54
1:CD:72:GLY:HA2	1:DD:77:ALA:HB2	1.90	0.54
1:FB:59:ALA:HB1	2:XB:788:GLU:HG2	1.90	0.54
1:GJ:24:ALA:HB2	1:GJ:48:VAL:HG21	1.89	0.54
1:G1:25:ASP:HA	1:HX:88:VAL:HG21	1.90	0.54
1:C9:35:LEU:HD11	1:C9:48:VAL:HG13	1.89	0.54
1:Gh:23:ALA:O	1:Gh:27:MET:HG3	2.08	0.54
1:Gi:41:VAL:HB	1:Gi:45:TYR:HB2	1.90	0.54
2:Xl:863:TYR:CD2	2:Xl:869:GLY:HA3	2.42	0.54
1:Gk:24:ALA:HB2	1:Gk:48:VAL:HG21	1.89	0.54
1:Bo:12:ILE:HG23	1:Bo:75:LEU:HD12	1.90	0.54
1:FA:29:LYS:HA	1:Cz:83:ARG:HH21	1.73	0.54
1:CN:72:GLY:HA2	1:DN:77:ALA:HB2	1.90	0.54
1:BX:12:ILE:HG23	1:BX:75:LEU:HD12	1.90	0.54
1:CW:35:LEU:HD11	1:CW:48:VAL:HG13	1.89	0.54
1:GW:41:VAL:HB	1:GW:45:TYR:HB2	1.90	0.54
2:X6:713:ILE:HG21	1:Hc:80:ILE:HD12	1.88	0.53
1:A0:72:GLY:HA2	1:F0:77:ALA:HB2	1.90	0.53
1:Hb:39:GLN:OE1	1:Gm:17:LEU:CD2	2.57	0.53
1:Ga:21:ILE:HD13	1:Ho:92:LEU:HD21	1.89	0.53
2:Xa:785:VAL:HG21	1:Ce:62:ARG:HG2	1.90	0.53
1:Ce:72:GLY:HA2	1:De:77:ALA:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bi:9:LEU:HD11	1:Bi:49:LEU:HD23	1.89	0.53
1:Fn:69:GLU:HG2	2:Xm:841:PRO:HG3	1.90	0.53
1:Bt:12:ILE:HG23	1:Bt:75:LEU:HD12	1.90	0.53
1:Ev:35:LEU:CD1	1:Ev:48:VAL:HG13	2.37	0.53
3:Pv:10:LEU:HD21	3:Pu:77:ILE:HG12	1.88	0.53
2:Xy:713:ILE:HG21	1:HH:80:ILE:CD1	2.37	0.53
1:Ax:53:GLU:OE1	1:HM:53:GLU:HG3	2.09	0.53
2:XK:825:ALA:HB3	1:DJ:15:ARG:HE	1.74	0.53
2:XL:841:PRO:HG3	1:FM:69:GLU:HG2	1.90	0.53
2:XP:806:ILE:HG21	1:GO:80:ILE:CD1	2.38	0.53
2:XR:863:TYR:HD2	2:XR:869:GLY:HA3	1.73	0.53
3:PV:10:LEU:HD21	3:PW:77:ILE:HG12	1.89	0.53
2:XV:714:THR:HA	2:XV:718:MET:HG3	1.91	0.53
1:G0:35:LEU:HD23	1:Hc:91:ILE:HG23	1.89	0.53
2:Xo:825:ALA:HB3	1:Dm:15:ARG:HE	1.72	0.53
1:Hn:91:ILE:HG23	1:GX:35:LEU:HD23	1.89	0.53
1:Ct:72:GLY:HA2	1:Dt:77:ALA:HB2	1.90	0.53
2:Xv:825:ALA:HB3	1:Du:15:ARG:HE	1.74	0.53
1:Cy:72:GLY:HA2	1:Dy:77:ALA:HB2	1.90	0.53
1:BA:35:LEU:HD11	1:BA:48:VAL:HG13	1.91	0.53
1:GA:73:ASP:OD2	1:HK:45:TYR:OH	2.16	0.53
1:HC:77:ALA:HB2	1:GJ:72:GLY:CA	2.39	0.53
2:XJ:712:ARG:HE	2:XJ:712:ARG:CA	2.17	0.53
2:XJ:844:PRO:HG2	2:XJ:860:LEU:HD11	1.91	0.53
1:CL:96:PRO:HG2	1:DL:90:ASN:HD22	1.74	0.53
1:EP:35:LEU:HD11	1:EP:48:VAL:HG13	1.88	0.53
1:GQ:23:ALA:O	1:GQ:27:MET:HG3	2.09	0.53
1:GV:23:ALA:O	1:GV:27:MET:HG3	2.09	0.53
2:X2:825:ALA:HB3	1:D1:15:ARG:HE	1.74	0.53
2:X1:713:ILE:HG21	1:Hm:80:ILE:HD12	1.89	0.53
2:X5:825:ALA:HB3	1:D3:15:ARG:HE	1.72	0.53
2:X4:713:ILE:CG2	1:HS:80:ILE:HD12	2.39	0.53
2:X4:863:TYR:HD2	2:X4:869:GLY:HA3	1.73	0.53
2:X6:712:ARG:HE	2:X6:712:ARG:CA	2.17	0.53
2:X6:785:VAL:HG21	1:C0:62:ARG:HG2	1.90	0.53
1:H0:88:VAL:HG21	1:GE:25:ASP:HA	1.90	0.53
3:P0:16:ILE:HG13	3:P0:19:MET:HG3	1.91	0.53
1:F8:59:ALA:HB1	2:X8:788:GLU:HG2	1.90	0.53
1:Bb:35:LEU:HD11	1:Bb:48:VAL:HG13	1.91	0.53
2:Xd:863:TYR:HD2	2:Xd:869:GLY:HA3	1.73	0.53
3:Po:16:ILE:HG13	3:Po:19:MET:HG3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bm:35:LEU:CD1	1:Bm:48:VAL:HG13	2.37	0.53
2:Xq:806:ILE:HG21	1:Gp:80:ILE:CD1	2.38	0.53
2:Xy:825:ALA:HB3	1:Dw:15:ARG:HE	1.72	0.53
1:Gx:41:VAL:HB	1:Gx:45:TYR:HB2	1.90	0.53
2:Xz:781:GLN:HG2	2:Xz:792:ARG:HB3	1.90	0.53
1:GB:23:ALA:O	1:GB:27:MET:HG3	2.09	0.53
2:XC:863:TYR:HD2	2:XC:869:GLY:HA3	1.73	0.53
1:GS:35:LEU:HD23	1:HV:91:ILE:HG23	1.89	0.53
1:AX:72:GLY:HA2	1:FX:77:ALA:HB2	1.90	0.53
1:C5:72:GLY:HA2	1:D5:77:ALA:HB2	1.90	0.53
2:X3:841:PRO:HG3	1:F4:69:GLU:HG2	1.90	0.53
1:G8:23:ALA:O	1:G8:27:MET:HG3	2.08	0.53
1:Fd:69:GLU:HG2	2:Xc:841:PRO:HG3	1.90	0.53
1:Gg:73:ASP:OD2	1:HU:45:TYR:OH	2.20	0.53
2:Xk:781:GLN:HG2	2:Xk:792:ARG:HB3	1.91	0.53
1:Gn:25:ASP:HA	1:H1:88:VAL:CG2	2.38	0.53
1:Hs:35:LEU:HD11	1:Hs:48:VAL:HG13	1.91	0.53
1:Hx:53:GLU:HG3	1:AM:53:GLU:OE1	2.08	0.53
2:XA:825:ALA:HB3	1:Dz:15:ARG:HE	1.74	0.53
1:AD:72:GLY:HA2	1:FD:77:ALA:HB2	1.90	0.53
2:XH:863:TYR:HD2	2:XH:869:GLY:HA3	1.73	0.53
1:HN:92:LEU:HD21	1:GU:21:ILE:HD13	1.91	0.53
3:PN:16:ILE:HG13	3:PN:19:MET:HG3	1.91	0.53
1:GM:25:ASP:CA	1:HP:88:VAL:HG21	2.37	0.53
1:GT:24:ALA:HB2	1:GT:48:VAL:HG21	1.89	0.53
1:HW:35:LEU:HD11	1:HW:48:VAL:HG13	1.91	0.53
2:X1:785:VAL:HG21	1:C5:62:ARG:HG2	1.90	0.53
1:H5:92:LEU:HD21	1:Gb:21:ILE:HD13	1.91	0.53
1:C9:72:GLY:HA2	1:D9:77:ALA:HB2	1.91	0.53
2:Xg:806:ILE:HG21	1:Gf:80:ILE:CD1	2.38	0.53
2:Xf:843:LYS:HE3	2:Xf:860:LEU:HD13	1.91	0.53
1:Bl:35:LEU:HD11	1:Bl:48:VAL:HG13	1.91	0.53
2:Xl:825:ALA:HB3	1:Dk:15:ARG:HE	1.74	0.53
3:Pt:16:ILE:HG13	3:Pt:19:MET:HG3	1.91	0.53
1:F5:71:VAL:HG22	2:Xr:862:THR:HG21	1.91	0.53
1:Az:7:ILE:CD1	1:DG:32:GLU:CG	2.87	0.53
1:GD:35:LEU:HD23	1:HG:91:ILE:HG23	1.89	0.53
1:GC:25:ASP:HA	1:Hf:88:VAL:CG2	2.37	0.53
1:BF:35:LEU:HD11	1:BF:48:VAL:HG13	1.91	0.53
2:XF:806:ILE:HG21	1:GE:80:ILE:CD1	2.38	0.53
1:GE:24:ALA:HB2	1:GE:48:VAL:HG21	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:96:PRO:HG2	1:DG:90:ASN:HD22	1.74	0.53
2:XO:713:ILE:HG21	1:HV:80:ILE:HD12	1.88	0.53
1:AX:57:VAL:HG12	1:AX:80:ILE:HG12	1.91	0.53
1:A5:57:VAL:HG12	1:A5:80:ILE:HG12	1.91	0.53
1:B4:9:LEU:HD11	1:B4:49:LEU:HD23	1.89	0.53
1:B7:35:LEU:HD11	1:B7:48:VAL:HG13	1.91	0.53
2:X7:863:TYR:CD2	2:X7:869:GLY:HA3	2.42	0.53
2:X6:781:GLN:HG2	2:X6:792:ARG:HB3	1.91	0.53
2:X6:844:PRO:HG2	2:X6:860:LEU:HD11	1.91	0.53
2:X0:825:ALA:HB3	1:D8:15:ARG:HE	1.72	0.53
1:F9:71:VAL:HG22	2:X8:862:THR:HG21	1.91	0.53
1:Ab:62:ARG:HG2	2:Xb:724:ILE:HG13	1.91	0.53
1:Ga:24:ALA:HB2	1:Ga:48:VAL:HG21	1.89	0.53
1:Bj:12:ILE:HG23	1:Bj:75:LEU:HD12	1.90	0.53
1:Ch:96:PRO:HG2	1:Dh:90:ASN:HD22	1.74	0.53
1:Fh:59:ALA:HB1	2:Xh:788:GLU:HG2	1.90	0.53
1:Gm:23:ALA:O	1:Gm:27:MET:HG3	2.09	0.53
1:Br:35:LEU:CD1	1:Br:48:VAL:HG13	2.37	0.53
1:Bs:9:LEU:HD11	1:Bs:49:LEU:HD23	1.89	0.53
1:Gs:41:VAL:HB	1:Gs:45:TYR:HB2	1.90	0.53
2:Xs:863:TYR:HD2	2:Xs:869:GLY:HA3	1.73	0.53
2:Xu:843:LYS:HE3	2:Xu:860:LEU:HD13	1.91	0.53
2:Xw:862:THR:HG21	1:Fx:71:VAL:HG22	1.91	0.53
2:Xz:785:VAL:HG21	1:CD:62:ARG:HG2	1.90	0.53
1:AI:57:VAL:HG12	1:AI:80:ILE:HG12	1.91	0.53
2:XK:863:TYR:CD2	2:XK:869:GLY:HA3	2.42	0.53
1:GO:24:ALA:HB2	1:GO:48:VAL:HG21	1.89	0.53
1:CS:72:GLY:HA2	1:DS:77:ALA:HB2	1.90	0.53
1:HQ:65:ALA:HB1	1:HQ:75:LEU:HD11	1.91	0.53
2:XQ:862:THR:HG21	1:FR:71:VAL:HG22	1.91	0.53
1:AU:62:ARG:HG2	2:XU:724:ILE:HG13	1.91	0.53
1:BW:9:LEU:HD11	1:BW:49:LEU:HD23	1.89	0.53
1:FW:71:VAL:HG22	2:XV:862:THR:HG21	1.91	0.53
1:C0:72:GLY:HA2	1:D0:77:ALA:HB2	1.90	0.53
2:Xi:863:TYR:HD2	2:Xi:869:GLY:HA3	1.73	0.53
2:Xk:843:LYS:HE3	2:Xk:860:LEU:HD13	1.91	0.53
1:Aq:62:ARG:HG2	2:Xq:724:ILE:HG13	1.91	0.53
2:Xq:825:ALA:HB3	1:Dp:15:ARG:HE	1.74	0.53
1:Av:62:ARG:HG2	2:Xv:724:ILE:HG13	1.91	0.53
2:Xv:806:ILE:HG21	1:Gu:80:ILE:CD1	2.38	0.53
1:Gu:24:ALA:HB2	1:Gu:48:VAL:HG21	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dw:32:GLU:CB	1:AA:7:ILE:HD11	2.35	0.53
2:XE:844:PRO:HG2	2:XE:860:LEU:HD11	1.91	0.53
1:HH:35:LEU:HD11	1:HH:48:VAL:HG13	1.91	0.53
1:FK:29:LYS:HA	1:CJ:83:ARG:HH21	1.73	0.53
2:XJ:785:VAL:HG21	1:CN:62:ARG:HG2	1.90	0.53
1:BN:12:ILE:HG23	1:BN:75:LEU:HD12	1.90	0.53
1:GM:41:VAL:HB	1:GM:45:TYR:HB2	1.90	0.53
1:AS:57:VAL:HG12	1:AS:80:ILE:HG12	1.91	0.53
2:XQ:841:PRO:HG3	1:FR:69:GLU:HG2	1.90	0.53
2:XT:785:VAL:HG21	1:CX:62:ARG:HG2	1.90	0.53
2:XW:863:TYR:HD2	2:XW:869:GLY:HA3	1.73	0.53
1:F3:59:ALA:HB1	2:X3:788:GLU:HG2	1.90	0.53
1:G3:72:GLY:CA	1:Hd:77:ALA:HB2	2.39	0.53
1:Cc:96:PRO:HG2	1:Dc:90:ASN:HD22	1.74	0.53
1:Fg:29:LYS:HA	1:Cf:83:ARG:HH21	1.73	0.53
1:Gg:25:ASP:CA	1:HU:88:VAL:HG21	2.39	0.53
2:Xf:785:VAL:HG21	1:Cj:62:ARG:HG2	1.90	0.53
2:Xn:863:TYR:HD2	2:Xn:869:GLY:HA3	1.73	0.53
2:Xp:785:VAL:HG21	1:Ct:62:ARG:HG2	1.90	0.53
1:Gu:21:ILE:HD13	1:HR:92:LEU:HD21	1.90	0.53
2:Xu:844:PRO:HG2	2:Xu:860:LEU:HD11	1.91	0.53
2:Xz:843:LYS:HE3	2:Xz:860:LEU:HD13	1.91	0.53
1:FC:69:GLU:HG2	2:XB:841:PRO:HG3	1.90	0.53
1:HC:35:LEU:HD11	1:HC:48:VAL:HG13	1.91	0.53
2:XN:825:ALA:HB3	1:DL:15:ARG:HE	1.72	0.53
2:XO:843:LYS:HE3	2:XO:860:LEU:HD13	1.91	0.53
2:XT:844:PRO:HG2	2:XT:860:LEU:HD11	1.91	0.53
1:CX:72:GLY:HA2	1:DX:77:ALA:HB2	1.90	0.53
3:P7:76:ILE:HB	3:P9:14:ASN:HD21	1.74	0.53
1:H8:65:ALA:HB1	1:H8:75:LEU:HD11	1.91	0.53
2:Xe:825:ALA:HB3	1:Dc:15:ARG:HH21	1.74	0.53
1:Gc:23:ALA:O	1:Gc:27:MET:HG3	2.09	0.53
1:Cj:72:GLY:HA2	1:Dj:77:ALA:HB2	1.90	0.53
2:Xj:714:THR:HG1	1:Hs:79:HIS:CG	2.10	0.53
1:Gi:25:ASP:CA	1:Hi:88:VAL:HG21	2.37	0.53
1:Dn:62:ARG:HH12	2:XT:729:GLU:CA	2.20	0.53
2:Xp:844:PRO:HG2	2:Xp:860:LEU:HD11	1.91	0.53
2:Xt:825:ALA:HB3	1:Dr:15:ARG:HH21	1.74	0.53
2:Xx:863:TYR:HD2	2:Xx:869:GLY:HA3	1.73	0.53
2:XK:806:ILE:HG21	1:GJ:80:ILE:CD1	2.38	0.53
2:XM:863:TYR:HD2	2:XM:869:GLY:HA3	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XO:785:VAL:HG21	1:CS:62:ARG:HG2	1.90	0.53
1:AS:72:GLY:HA2	1:FS:77:ALA:HB2	1.91	0.53
1:BS:12:ILE:HG23	1:BS:75:LEU:HD12	1.90	0.53
2:XT:781:GLN:HG2	2:XT:792:ARG:HB3	1.91	0.53
1:FV:59:ALA:HB1	2:XV:788:GLU:HG2	1.90	0.53
1:B2:35:LEU:HD11	1:B2:48:VAL:HG13	1.91	0.53
1:G1:35:LEU:HD21	1:HX:91:ILE:HG21	1.90	0.53
2:X1:844:PRO:HG2	2:X1:860:LEU:HD11	1.91	0.53
2:X5:825:ALA:HB3	1:D3:15:ARG:HH21	1.74	0.53
1:G4:25:ASP:CA	1:H7:88:VAL:HG21	2.37	0.53
1:A6:7:ILE:CD1	1:Dc:32:GLU:CG	2.87	0.53
2:X6:843:LYS:HE3	2:X6:860:LEU:HD13	1.91	0.53
1:H9:88:VAL:HG21	1:GR:25:ASP:CA	2.37	0.53
2:Xb:806:ILE:HG21	1:Ga:80:ILE:CD1	2.38	0.53
2:Xb:825:ALA:HB3	1:Da:15:ARG:HE	1.74	0.53
2:Xa:844:PRO:HG2	2:Xa:860:LEU:HD11	1.91	0.53
1:Dh:62:ARG:NH1	2:Xl:729:GLU:HA	2.17	0.53
1:Fl:29:LYS:HA	1:Ck:83:ARG:HH21	1.73	0.53
1:Ao:72:GLY:HA2	1:Fo:77:ALA:HB2	1.91	0.53
3:Pq:76:ILE:HB	3:Ps:14:ASN:HD21	1.74	0.53
1:By:12:ILE:HG23	1:By:75:LEU:HD12	1.90	0.53
2:XD:825:ALA:HB3	1:DB:15:ARG:HH21	1.74	0.53
2:XF:825:ALA:HB3	1:DE:15:ARG:HE	1.74	0.53
1:BI:12:ILE:HG23	1:BI:75:LEU:HD12	1.90	0.53
1:BL:35:LEU:CD1	1:BL:48:VAL:HG13	2.37	0.53
2:XL:862:THR:HG21	1:FM:71:VAL:HG22	1.91	0.53
1:BU:35:LEU:HD11	1:BU:48:VAL:HG13	1.91	0.53
3:PX:16:ILE:HG13	3:PX:19:MET:HG3	1.91	0.53
1:A1:7:ILE:HD11	1:Dm:32:GLU:CD	2.33	0.52
1:Dg:32:GLU:OE2	1:AJ:7:ILE:CD1	2.57	0.52
1:Ao:57:VAL:HG12	1:Ao:80:ILE:HG12	1.91	0.52
1:Cm:96:PRO:HG2	1:Dm:90:ASN:HD22	1.74	0.52
2:Xp:781:GLN:HG2	2:Xp:792:ARG:HB3	1.91	0.52
1:Hr:65:ALA:HB1	1:Hr:75:LEU:HD11	1.91	0.52
1:Bv:35:LEU:HD11	1:Bv:48:VAL:HG13	1.91	0.52
3:Pv:76:ILE:HB	3:Px:14:ASN:HD21	1.74	0.52
2:Xw:825:ALA:HB3	1:Dx:15:ARG:HE	1.71	0.52
1:GC:41:VAL:HB	1:GC:45:TYR:HB2	1.90	0.52
3:PF:76:ILE:HB	3:PH:14:ASN:HD21	1.74	0.52
3:PK:76:ILE:HB	3:PM:14:ASN:HD21	1.74	0.52
1:GL:23:ALA:O	1:GL:27:MET:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FW:69:GLU:HG2	2:XV:841:PRO:HG3	1.90	0.52
1:G1:24:ALA:HB2	1:G1:48:VAL:HG21	1.89	0.52
1:G3:23:ALA:O	1:G3:27:MET:HG3	2.09	0.52
1:G8:25:ASP:CA	1:HF:88:VAL:HG21	2.39	0.52
1:G9:25:ASP:CA	1:Hu:88:VAL:HG21	2.37	0.52
3:Pb:76:ILE:HB	3:Pd:14:ASN:HD21	1.74	0.52
2:Xf:781:GLN:HG2	2:Xf:792:ARG:HB3	1.91	0.52
1:Hj:92:LEU:HD21	1:Gq:21:ILE:HD13	1.91	0.52
1:Al:62:ARG:HG2	2:Xl:724:ILE:HG13	1.91	0.52
3:Pl:76:ILE:HB	3:Pn:14:ASN:HD21	1.74	0.52
1:Co:72:GLY:HA2	1:Do:77:ALA:HB2	1.90	0.52
1:Fm:71:VAL:HG22	2:Xm:862:THR:HG21	1.91	0.52
1:Hn:35:LEU:HD11	1:Hn:48:VAL:HG13	1.91	0.52
1:At:72:GLY:HA2	1:Ft:77:ALA:HB2	1.90	0.52
1:AA:62:ARG:HG2	2:XA:724:ILE:HG13	1.91	0.52
1:FC:71:VAL:HG22	2:XB:862:THR:HG21	1.91	0.52
1:BK:35:LEU:HD11	1:BK:48:VAL:HG13	1.91	0.52
2:XJ:713:ILE:HD12	2:XJ:713:ILE:N	2.25	0.52
1:DL:32:GLU:CB	1:AP:7:ILE:HD11	2.35	0.52
1:FL:59:ALA:HB1	2:XL:788:GLU:HG2	1.90	0.52
1:GM:35:LEU:CD2	1:HP:91:ILE:HD13	2.37	0.52
2:XP:825:ALA:HB3	1:DO:15:ARG:HE	1.74	0.52
2:XU:825:ALA:HB3	1:DT:15:ARG:HE	1.74	0.52
2:XX:825:ALA:HB3	1:DV:15:ARG:HH21	1.74	0.52
2:X1:781:GLN:HG2	2:X1:792:ARG:HB3	1.91	0.52
1:A5:72:GLY:HA2	1:F5:77:ALA:HB2	1.91	0.52
1:B5:12:ILE:HG23	1:B5:75:LEU:HD12	1.90	0.52
1:H4:35:LEU:HD11	1:H4:48:VAL:HG13	1.91	0.52
1:A7:62:ARG:HG2	2:X7:724:ILE:HG13	1.91	0.52
2:Xk:844:PRO:HG2	2:Xk:860:LEU:HD11	1.91	0.52
1:Hm:65:ALA:HB1	1:Hm:75:LEU:HD11	1.91	0.52
1:HB:65:ALA:HB1	1:HB:75:LEU:HD11	1.91	0.52
2:XE:713:ILE:N	2:XE:713:ILE:HD12	2.25	0.52
1:FG:59:ALA:HB1	2:XG:788:GLU:HG2	1.89	0.52
1:GG:23:ALA:O	1:GG:27:MET:HG3	2.09	0.52
1:AK:62:ARG:HG2	2:XK:724:ILE:HG13	1.91	0.52
2:XJ:781:GLN:HG2	2:XJ:792:ARG:HB3	1.91	0.52
1:CQ:96:PRO:HG2	1:DQ:90:ASN:HD22	1.74	0.52
1:DR:24:ALA:HB2	1:DR:48:VAL:HG21	1.92	0.52
2:XU:806:ILE:HG21	1:GT:80:ILE:CD1	2.38	0.52
1:AV:62:ARG:HG2	2:XV:724:ILE:HG13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:96:PRO:HG2	1:DV:90:ASN:HD22	1.74	0.52
1:F2:29:LYS:HA	1:C1:83:ARG:HH21	1.73	0.52
2:X2:713:ILE:CG2	1:HX:80:ILE:HD12	2.39	0.52
1:C9:79:HIS:ND1	2:X8:786:SER:HB2	2.25	0.52
2:XA:781:GLN:HG2	2:XA:792:ARG:HB3	1.91	0.52
1:Ae:57:VAL:HG12	1:Ae:80:ILE:HG12	1.91	0.52
1:Aj:72:GLY:HA2	1:Fj:77:ALA:HB2	1.90	0.52
3:Pj:3:ILE:HG23	3:Pj:77:ILE:HD13	1.91	0.52
1:Hi:91:ILE:HG21	1:GT:35:LEU:HD21	1.91	0.52
1:Ak:7:ILE:CD1	1:Dr:32:GLU:CG	2.87	0.52
2:Xp:843:LYS:HE3	2:Xp:860:LEU:HD13	1.91	0.52
1:Ar:62:ARG:HG2	2:Xr:724:ILE:HG13	1.92	0.52
1:Cr:96:PRO:HG2	1:Dr:90:ASN:HD22	1.74	0.52
1:Ay:57:VAL:HG12	1:Ay:80:ILE:HG12	1.91	0.52
2:Xz:713:ILE:N	2:Xz:713:ILE:HD12	2.25	0.52
2:Xz:844:PRO:HG2	2:Xz:860:LEU:HD11	1.91	0.52
3:PD:16:ILE:HG13	3:PD:19:MET:HG3	1.91	0.52
1:CB:96:PRO:HG2	1:DB:90:ASN:HD22	1.74	0.52
2:XE:843:LYS:HE3	2:XE:860:LEU:HD13	1.91	0.52
2:XJ:843:LYS:HE3	2:XJ:860:LEU:HD13	1.91	0.52
1:AL:62:ARG:HG2	2:XL:724:ILE:HG13	1.92	0.52
1:AP:62:ARG:HG2	2:XP:724:ILE:HG13	1.91	0.52
3:PP:76:ILE:HB	3:PR:14:ASN:HD21	1.74	0.52
2:XO:844:PRO:HG2	2:XO:860:LEU:HD11	1.91	0.52
1:CR:72:GLY:HA2	1:DR:77:ALA:HB2	1.91	0.52
1:H2:88:VAL:HG21	1:GV:25:ASP:CA	2.40	0.52
1:A3:62:ARG:HG2	2:X3:724:ILE:HG13	1.92	0.52
1:C4:72:GLY:HA2	1:D4:77:ALA:HB2	1.91	0.52
1:H4:79:HIS:ND1	2:XS:714:THR:OG1	1.86	0.52
1:Cd:72:GLY:HA2	1:Dd:77:ALA:HB2	1.91	0.52
1:Ag:62:ARG:HG2	2:Xg:724:ILE:HG13	1.91	0.52
2:Xk:713:ILE:HD12	2:Xk:713:ILE:N	2.25	0.52
1:Gr:23:ALA:O	1:Gr:27:MET:HG3	2.09	0.52
1:Cs:72:GLY:HA2	1:Ds:77:ALA:HB2	1.91	0.52
1:Gv:25:ASP:CA	1:HM:88:VAL:HG21	2.34	0.52
2:Xu:781:GLN:HG2	2:Xu:792:ARG:HB3	1.91	0.52
1:Aw:62:ARG:HG2	2:Xw:724:ILE:HG13	1.92	0.52
2:Xw:786:SER:HB2	1:Cx:79:HIS:ND1	2.25	0.52
1:CC:72:GLY:HA2	1:DC:77:ALA:HB2	1.91	0.52
1:AI:72:GLY:HA2	1:FI:77:ALA:HB2	1.90	0.52
1:DM:24:ALA:HB2	1:DM:48:VAL:HG21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:PS:3:ILE:HG23	3:PS:77:ILE:HD13	1.91	0.52
2:X1:713:ILE:HD12	2:X1:713:ILE:N	2.25	0.52
1:Gl:25:ASP:HA	1:HT:88:VAL:CG2	2.39	0.52
2:Xp:713:ILE:HD12	2:Xp:713:ILE:N	2.25	0.52
1:Cw:96:PRO:HG2	1:Dw:90:ASN:HD22	1.74	0.52
1:Gw:72:GLY:CA	1:HH:77:ALA:HB2	2.39	0.52
1:FH:69:GLU:HG2	2:XG:841:PRO:HG3	1.90	0.52
1:AN:57:VAL:HG12	1:AN:80:ILE:HG12	1.91	0.52
1:HL:77:ALA:HB2	1:GO:72:GLY:CA	2.39	0.52
1:CM:72:GLY:HA2	1:DM:77:ALA:HB2	1.91	0.52
1:AO:7:ILE:CD1	1:DV:32:GLU:CG	2.87	0.52
1:DW:24:ALA:HB2	1:DW:48:VAL:HG21	1.92	0.52
1:B5:88:VAL:HG21	1:F5:25:ASP:HA	1.92	0.52
3:P0:3:ILE:HG23	3:P0:77:ILE:HD13	1.91	0.52
1:D8:32:GLU:CG	1:Au:7:ILE:CD1	2.87	0.52
1:G8:72:GLY:CA	1:HF:77:ALA:HB2	2.35	0.52
1:F9:69:GLU:HG2	2:X8:841:PRO:HG3	1.90	0.52
3:Pe:16:ILE:HG13	3:Pe:19:MET:HG3	1.91	0.52
1:Bg:35:LEU:HD11	1:Bg:48:VAL:HG13	1.91	0.52
2:Xl:806:ILE:HG21	1:Gk:80:ILE:CD1	2.38	0.52
1:Gu:35:LEU:HD21	1:HR:91:ILE:HG21	1.90	0.52
1:Hy:92:LEU:HD21	1:GF:21:ILE:HD13	1.91	0.52
1:Gw:23:ALA:O	1:Gw:27:MET:HG3	2.08	0.52
1:Gx:25:ASP:CA	1:HA:88:VAL:HG21	2.38	0.52
3:PA:76:ILE:HB	3:PC:14:ASN:HD21	1.74	0.52
1:Gz:24:ALA:HB2	1:Gz:48:VAL:HG21	1.89	0.52
1:BD:12:ILE:HG23	1:BD:75:LEU:HD12	1.90	0.52
1:DC:24:ALA:HB2	1:DC:48:VAL:HG21	1.92	0.52
1:BI:88:VAL:HG21	1:FI:25:ASP:HA	1.92	0.52
3:PI:16:ILE:HG13	3:PI:19:MET:HG3	1.91	0.52
1:HM:35:LEU:HD11	1:HM:48:VAL:HG13	1.91	0.52
3:PU:76:ILE:HB	3:PW:14:ASN:HD21	1.74	0.52
1:CW:72:GLY:HA2	1:DW:77:ALA:HB2	1.91	0.52
1:CW:79:HIS:ND1	2:XV:786:SER:HB2	2.25	0.52
1:A2:62:ARG:HG2	2:X2:724:ILE:HG13	1.91	0.52
1:A0:57:VAL:HG12	1:A0:80:ILE:HG12	1.91	0.52
1:B0:88:VAL:HG21	1:F0:25:ASP:HA	1.92	0.52
1:A8:62:ARG:HG2	2:X8:724:ILE:HG13	1.92	0.52
1:C8:96:PRO:HG2	1:D8:90:ASN:HD22	1.74	0.52
1:H9:35:LEU:HD11	1:H9:48:VAL:HG13	1.91	0.52
1:Dd:24:ALA:HB2	1:Dd:48:VAL:HG21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Fd:71:VAL:HG22	2:Xc:862:THR:HG21	1.91	0.52
2:Xj:825:ALA:HB3	1:Dh:15:ARG:HH21	1.74	0.52
3:Pj:16:ILE:HG13	3:Pj:19:MET:HG3	1.91	0.52
3:Po:3:ILE:HG23	3:Po:77:ILE:HD13	1.91	0.52
1:Dm:24:ALA:HB2	1:Dm:48:VAL:HG11	1.92	0.52
2:Xn:713:ILE:CD1	1:HT:62:ARG:HA	2.38	0.52
1:Hp:91:ILE:HD13	1:GG:35:LEU:HD21	1.92	0.52
1:BP:35:LEU:HD11	1:BP:48:VAL:HG13	1.91	0.52
1:BS:88:VAL:HG21	1:FS:25:ASP:HA	1.92	0.52
1:C3:96:PRO:HG2	1:D3:90:ASN:HD22	1.74	0.52
2:X6:713:ILE:HD12	2:X6:713:ILE:N	2.25	0.52
1:B9:77:ALA:HB2	1:F9:72:GLY:HA2	1.92	0.52
1:Gb:9:LEU:HD11	1:Gb:49:LEU:HD23	1.92	0.52
3:Pe:3:ILE:HG23	3:Pe:77:ILE:HD13	1.92	0.52
1:Cd:79:HIS:ND1	2:Xc:786:SER:HB2	2.25	0.52
3:Pg:76:ILE:HB	3:Pi:14:ASN:HD21	1.74	0.52
1:Aj:57:VAL:HG12	1:Aj:80:ILE:HG12	1.91	0.52
1:Bn:77:ALA:HB2	1:Fn:72:GLY:HA2	1.92	0.52
1:Cn:72:GLY:HA2	1:Dn:77:ALA:HB2	1.91	0.52
1:Bq:35:LEU:HD11	1:Bq:48:VAL:HG13	1.91	0.52
1:GF:9:LEU:HD11	1:GF:49:LEU:HD23	1.92	0.52
2:XE:785:VAL:HG21	1:CI:62:ARG:HG2	1.90	0.52
1:DH:24:ALA:HB2	1:DH:48:VAL:HG21	1.92	0.52
3:PS:16:ILE:HG13	3:PS:19:MET:HG3	1.91	0.52
1:DQ:24:ALA:HB2	1:DQ:48:VAL:HG11	1.92	0.52
1:DV:24:ALA:HB2	1:DV:48:VAL:HG11	1.92	0.52
3:P2:76:ILE:HB	3:P4:14:ASN:HD21	1.74	0.52
2:X7:825:ALA:HB3	1:D6:15:ARG:HE	1.74	0.52
2:Xg:825:ALA:HB3	1:Df:15:ARG:HE	1.74	0.52
2:Xf:713:ILE:HG21	1:HB:80:ILE:HD12	1.92	0.52
2:Xf:713:ILE:HD12	2:Xf:713:ILE:N	2.25	0.52
1:Ah:62:ARG:HG2	2:Xh:724:ILE:HG13	1.92	0.52
1:Hw:65:ALA:HB1	1:Hw:75:LEU:HD11	1.91	0.52
1:GA:9:LEU:HD11	1:GA:49:LEU:HD23	1.92	0.52
1:AD:57:VAL:HG12	1:AD:80:ILE:HG12	1.91	0.52
1:AB:62:ARG:HG2	2:XB:724:ILE:HG13	1.92	0.52
1:HL:65:ALA:HB1	1:HL:75:LEU:HD11	1.91	0.52
2:Xa:713:ILE:N	2:Xa:713:ILE:HD12	2.25	0.51
1:Do:27:MET:HE1	1:Do:48:VAL:HG12	1.92	0.51
1:At:57:VAL:HG12	1:At:80:ILE:HG12	1.91	0.51
1:Cs:79:HIS:ND1	2:Xr:786:SER:HB2	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Gs:40:PHE:HE1	1:Hk:41:VAL:HG13	1.75	0.51
2:Xu:785:VAL:HG21	1:Cy:62:ARG:HG2	1.91	0.51
3:Py:16:ILE:HG13	3:Py:19:MET:HG3	1.91	0.51
1:Hx:88:VAL:HG21	1:GK:25:ASP:CA	2.37	0.51
1:DD:27:MET:HE1	1:DD:48:VAL:HG12	1.92	0.51
3:PD:3:ILE:HG23	3:PD:77:ILE:HD13	1.91	0.51
2:XE:781:GLN:HG2	2:XE:792:ARG:HB3	1.90	0.51
1:DI:27:MET:HE1	1:DI:48:VAL:HG12	1.93	0.51
2:Xl:825:ALA:HB3	1:DG:15:ARG:HH21	1.74	0.51
1:CH:72:GLY:HA2	1:DH:77:ALA:HB2	1.91	0.51
1:BM:77:ALA:HB2	1:FM:72:GLY:HA2	1.92	0.51
1:GP:9:LEU:HD11	1:GP:49:LEU:HD23	1.92	0.51
2:XO:713:ILE:HD12	2:XO:713:ILE:N	2.25	0.51
1:BR:77:ALA:HB2	1:FR:72:GLY:HA2	1.92	0.51
1:BX:88:VAL:HG21	1:FX:25:ASP:HA	1.92	0.51
1:H2:77:ALA:HB2	1:GV:72:GLY:CA	2.36	0.51
1:G1:11:MET:HE3	1:G1:79:HIS:HB3	1.93	0.51
1:Hc:65:ALA:HB1	1:Hc:75:LEU:HD11	1.91	0.51
1:Af:7:ILE:HG12	1:DB:32:GLU:OE2	2.10	0.51
1:Ah:7:ILE:HG13	1:DI:32:GLU:OE2	2.11	0.51
1:Hh:65:ALA:HB1	1:Hh:75:LEU:HD11	1.91	0.51
2:Xh:862:THR:HG21	1:Fi:71:VAL:HG22	1.91	0.51
1:Ci:72:GLY:HA2	1:Di:77:ALA:HB2	1.91	0.51
1:Gq:9:LEU:HD11	1:Gq:49:LEU:HD23	1.92	0.51
1:Hq:80:ILE:HD12	2:XD:713:ILE:CG2	2.40	0.51
1:By:88:VAL:HG21	1:Fy:25:ASP:HA	1.92	0.51
1:Dx:24:ALA:HB2	1:Dx:48:VAL:HG21	1.92	0.51
1:HC:92:LEU:CD2	1:GJ:21:ILE:HD13	2.40	0.51
1:HG:65:ALA:HB1	1:HG:75:LEU:HD11	1.91	0.51
1:CJ:88:VAL:HG21	1:EJ:25:ASP:HA	1.93	0.51
2:XL:786:SER:HB2	1:CM:79:HIS:ND1	2.25	0.51
2:XS:825:ALA:HB3	1:DQ:15:ARG:HH21	1.74	0.51
1:HR:35:LEU:HD11	1:HR:48:VAL:HG13	1.91	0.51
2:X3:786:SER:HB2	1:C4:79:HIS:ND1	2.25	0.51
2:X0:825:ALA:HB3	1:D8:15:ARG:HH21	1.74	0.51
1:D9:24:ALA:HB2	1:D9:48:VAL:HG21	1.92	0.51
1:Ck:88:VAL:HG21	1:Ek:25:ASP:HA	1.93	0.51
2:Xu:713:ILE:N	2:Xu:713:ILE:HD12	2.25	0.51
1:Gz:11:MET:HE3	1:Gz:79:HIS:HB3	1.93	0.51
1:DG:24:ALA:HB2	1:DG:48:VAL:HG11	1.92	0.51
1:BH:77:ALA:HB2	1:FH:72:GLY:HA2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:72:GLY:HA2	1:FN:77:ALA:HB2	1.90	0.51
2:XN:825:ALA:HB3	1:DL:15:ARG:HH21	1.74	0.51
1:BT:18:VAL:HG22	1:ET:11:MET:HB3	1.93	0.51
2:XT:843:LYS:HE3	2:XT:860:LEU:HD13	1.91	0.51
1:BW:77:ALA:HB2	1:FW:72:GLY:HA2	1.93	0.51
1:C1:88:VAL:HG21	1:E1:25:ASP:HA	1.93	0.51
3:P5:16:ILE:HG13	3:P5:19:MET:HG3	1.91	0.51
1:H3:92:LEU:CD2	1:G6:21:ILE:HD13	2.41	0.51
1:Ca:77:ALA:HB2	1:Ea:72:GLY:HA2	1.93	0.51
1:Ca:88:VAL:HG21	1:Ea:25:ASP:HA	1.93	0.51
2:Xa:843:LYS:HE3	2:Xa:860:LEU:HD13	1.91	0.51
1:Ae:72:GLY:HA2	1:Fe:77:ALA:HB2	1.90	0.51
1:Be:88:VAL:HG21	1:Fe:25:ASP:HA	1.92	0.51
2:Xf:844:PRO:HG2	2:Xf:860:LEU:HD11	1.91	0.51
1:Hh:92:LEU:CD2	1:Gk:21:ILE:HD13	2.41	0.51
1:Ck:77:ALA:HB2	1:Ek:72:GLY:HA2	1.93	0.51
2:Xk:785:VAL:HG21	1:Co:62:ARG:HG2	1.90	0.51
1:Gn:40:PHE:HE1	1:H1:41:VAL:HG13	1.76	0.51
1:Dr:24:ALA:HB2	1:Dr:48:VAL:HG11	1.92	0.51
1:Hw:92:LEU:CD2	1:Gz:21:ILE:HD13	2.41	0.51
2:XA:806:ILE:HG21	1:Gz:80:ILE:CD1	2.38	0.51
1:FH:71:VAL:HG22	2:XG:862:THR:HG21	1.91	0.51
1:AL:7:ILE:HG13	1:DP:32:GLU:OE2	2.11	0.51
1:DL:24:ALA:HB2	1:DL:48:VAL:HG11	1.92	0.51
2:XQ:786:SER:HB2	1:CR:79:HIS:ND1	2.25	0.51
1:A5:88:VAL:HG21	1:D5:25:ASP:HA	1.93	0.51
1:D5:27:MET:HE1	1:D5:48:VAL:HG12	1.92	0.51
1:B4:77:ALA:HB2	1:F4:72:GLY:HA2	1.92	0.51
1:D8:24:ALA:HB2	1:D8:48:VAL:HG11	1.92	0.51
1:Hd:35:LEU:HD11	1:Hd:48:VAL:HG13	1.91	0.51
1:Cf:88:VAL:HG21	1:Ef:25:ASP:HA	1.93	0.51
1:Hi:35:LEU:HD11	1:Hi:48:VAL:HG13	1.91	0.51
2:Xo:825:ALA:HB3	1:Dm:15:ARG:HH21	1.74	0.51
1:Dn:32:GLU:CG	1:AT:7:ILE:HD11	2.40	0.51
1:Hv:88:VAL:CG2	1:GP:25:ASP:HA	2.39	0.51
1:DB:24:ALA:HB2	1:DB:48:VAL:HG11	1.92	0.51
1:AG:62:ARG:HG2	2:XG:724:ILE:HG13	1.92	0.51
1:HP:9:LEU:HD11	1:HP:49:LEU:HD23	1.93	0.51
2:XO:781:GLN:HG2	2:XO:792:ARG:HB3	1.91	0.51
1:CT:88:VAL:HG21	1:ET:25:ASP:HA	1.93	0.51
2:XT:713:ILE:HD12	2:XT:713:ILE:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HV:65:ALA:HB1	1:HV:75:LEU:HD11	1.91	0.51
2:X1:843:LYS:HE3	2:X1:860:LEU:HD13	1.91	0.51
1:H3:65:ALA:HB1	1:H3:75:LEU:HD11	1.91	0.51
1:H7:68:CYS:SG	1:H7:75:LEU:HB2	2.51	0.51
1:A0:88:VAL:HG21	1:D0:25:ASP:HA	1.93	0.51
1:H9:45:TYR:OH	1:GR:73:ASP:OD2	2.21	0.51
1:Hb:9:LEU:HD11	1:Hb:49:LEU:HD23	1.93	0.51
1:Ba:88:VAL:HG21	1:Fa:25:ASP:HA	1.93	0.51
1:Ao:88:VAL:HG21	1:Do:25:ASP:HA	1.93	0.51
1:Am:62:ARG:HG2	2:Xm:724:ILE:HG13	1.92	0.51
1:Cn:79:HIS:ND1	2:Xm:786:SER:HB2	2.25	0.51
1:Cn:80:ILE:HD12	2:Xm:785:VAL:HG11	1.93	0.51
1:Cn:96:PRO:HG2	1:Dn:90:ASN:HD22	1.76	0.51
1:Dn:24:ALA:HB2	1:Dn:48:VAL:HG21	1.92	0.51
1:Hq:9:LEU:HD11	1:Hq:49:LEU:HD23	1.93	0.51
1:Hq:77:ALA:HB2	1:GB:72:GLY:CA	2.37	0.51
3:Pt:3:ILE:HG23	3:Pt:77:ILE:HD13	1.91	0.51
2:Xy:825:ALA:HB3	1:Dw:15:ARG:HH21	1.74	0.51
1:Bx:77:ALA:HB2	1:Fx:72:GLY:HA2	1.92	0.51
1:Cz:77:ALA:HB2	1:Ez:72:GLY:HA2	1.93	0.51
1:AF:62:ARG:HG2	2:XF:724:ILE:HG13	1.91	0.51
1:HF:68:CYS:SG	1:HF:75:LEU:HB2	2.51	0.51
1:GE:11:MET:HE3	1:GE:79:HIS:HB3	1.93	0.51
1:HL:92:LEU:CD2	1:GO:21:ILE:HD13	2.41	0.51
1:AQ:62:ARG:HG2	2:XQ:724:ILE:HG13	1.92	0.51
1:HU:68:CYS:SG	1:HU:75:LEU:HB2	2.51	0.51
1:H2:68:CYS:SG	1:H2:75:LEU:HB2	2.51	0.51
1:H3:77:ALA:HB2	1:G6:72:GLY:CA	2.39	0.51
1:G7:9:LEU:HD11	1:G7:49:LEU:HD23	1.92	0.51
2:X7:806:ILE:HG21	1:G6:80:ILE:CD1	2.38	0.51
1:C9:80:ILE:HD12	2:X8:785:VAL:HG11	1.93	0.51
1:Dc:24:ALA:HB2	1:Dc:48:VAL:HG11	1.92	0.51
1:Dg:62:ARG:HH12	2:XJ:729:GLU:HA	1.76	0.51
1:Bf:18:VAL:HG22	1:Ef:11:MET:HB3	1.93	0.51
2:Xh:712:ARG:HH12	1:Hl:65:ALA:CB	2.18	0.51
1:Di:24:ALA:HB2	1:Di:48:VAL:HG21	1.92	0.51
1:Hl:9:LEU:HD11	1:Hl:49:LEU:HD23	1.93	0.51
1:Ay:72:GLY:HA2	1:Fy:77:ALA:HB2	1.91	0.51
1:Dy:27:MET:HE1	1:Dy:48:VAL:HG12	1.92	0.51
3:Py:3:ILE:HG23	3:Py:77:ILE:HD13	1.92	0.51
1:Dw:24:ALA:HB2	1:Dw:48:VAL:HG11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Hw:77:ALA:HB2	1:Gz:72:GLY:CA	2.40	0.51
2:Xx:713:ILE:HG22	1:HM:80:ILE:HD12	1.92	0.51
1:BD:88:VAL:HG21	1:FD:25:ASP:HA	1.92	0.51
1:AI:88:VAL:HG21	1:DI:25:ASP:HA	1.93	0.51
1:BN:88:VAL:HG21	1:FN:25:ASP:HA	1.92	0.51
2:XL:785:VAL:HG11	1:CM:80:ILE:HD12	1.93	0.51
1:GO:11:MET:HE3	1:GO:79:HIS:HB3	1.93	0.51
1:C1:77:ALA:HB2	1:E1:72:GLY:HA2	1.93	0.51
1:G4:24:ALA:HB2	1:G4:48:VAL:HG21	1.93	0.51
1:G9:24:ALA:HB2	1:G9:48:VAL:HG21	1.93	0.51
1:Dj:27:MET:HE1	1:Dj:48:VAL:HG12	1.93	0.51
1:Hh:77:ALA:HB2	1:Gk:72:GLY:CA	2.40	0.51
2:Xh:786:SER:HB2	1:Ci:79:HIS:ND1	2.25	0.51
1:Dn:32:GLU:HG3	1:AT:83:ARG:NH1	2.26	0.51
1:Dt:27:MET:HE1	1:Dt:48:VAL:HG12	1.92	0.51
1:Gv:9:LEU:HD11	1:Gv:49:LEU:HD23	1.92	0.51
1:Cu:88:VAL:HG21	1:Eu:25:ASP:HA	1.93	0.51
1:Hx:35:LEU:HD11	1:Hx:48:VAL:HG13	1.91	0.51
1:Az:7:ILE:HD11	1:DG:32:GLU:CD	2.36	0.51
3:PI:3:ILE:HG23	3:PI:77:ILE:HD13	1.91	0.51
1:HK:68:CYS:SG	1:HK:75:LEU:HB2	2.51	0.51
1:GL:72:GLY:CA	1:HW:77:ALA:HB2	2.39	0.51
1:CW:96:PRO:HG2	1:DW:90:ASN:HD22	1.76	0.51
1:G2:25:ASP:CA	1:HS:88:VAL:HG21	2.39	0.51
3:P5:3:ILE:HG23	3:P5:77:ILE:HD13	1.91	0.51
2:X3:862:THR:HG21	1:F4:71:VAL:HG22	1.91	0.51
1:H7:9:LEU:HD11	1:H7:49:LEU:HD23	1.93	0.51
1:Ag:28:THR:O	1:HJ:83:ARG:NH1	2.41	0.51
1:HI:68:CYS:SG	1:HI:75:LEU:HB2	2.51	0.51
1:Gn:25:ASP:CA	1:H1:88:VAL:HG21	2.39	0.51
1:Gp:21:ILE:HD13	1:HD:92:LEU:HD21	1.92	0.51
1:Gs:24:ALA:HB2	1:Gs:48:VAL:HG21	1.93	0.51
1:Gs:25:ASP:HA	1:Hk:88:VAL:CG2	2.41	0.51
1:HA:68:CYS:SG	1:HA:75:LEU:HB2	2.51	0.51
1:CC:96:PRO:HG2	1:DC:90:ASN:HD22	1.76	0.51
1:GK:9:LEU:HD11	1:GK:49:LEU:HD23	1.92	0.51
1:CO:77:ALA:HB2	1:EO:72:GLY:HA2	1.93	0.51
1:F3:35:LEU:O	1:F3:96:PRO:HG3	2.12	0.51
1:D4:24:ALA:HB2	1:D4:48:VAL:HG21	1.92	0.51
1:Bd:77:ALA:HB2	1:Fd:72:GLY:HA2	1.92	0.51
1:Cd:80:ILE:HD12	2:Xc:785:VAL:HG11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cf:77:ALA:HB2	1:Ef:72:GLY:HA2	1.93	0.51
1:Bt:88:VAL:HG21	1:Ft:25:ASP:HA	1.92	0.51
1:Hv:9:LEU:HD11	1:Hv:49:LEU:HD23	1.93	0.51
1:Gx:24:ALA:HB2	1:Gx:48:VAL:HG21	1.93	0.51
1:AA:88:VAL:HG21	1:DA:25:ASP:HA	1.93	0.51
1:CC:80:ILE:HD12	2:XB:785:VAL:HG11	1.93	0.51
1:CH:79:HIS:ND1	2:XG:786:SER:HB2	2.25	0.51
1:BJ:18:VAL:HG22	1:EJ:11:MET:HB3	1.93	0.51
1:GJ:11:MET:HE3	1:GJ:79:HIS:HB3	1.93	0.51
1:HP:68:CYS:SG	1:HP:75:LEU:HB2	2.51	0.51
1:GU:9:LEU:HD11	1:GU:49:LEU:HD23	1.92	0.51
1:GT:11:MET:HE3	1:GT:79:HIS:HB3	1.93	0.51
2:Xm:714:THR:HA	2:Xm:718:MET:HG3	1.93	0.51
1:B6:88:VAL:HG21	1:F6:25:ASP:HA	1.93	0.50
1:C6:88:VAL:HG21	1:E6:25:ASP:HA	1.93	0.50
1:H8:80:ILE:HD12	2:Xu:713:ILE:HG21	1.92	0.50
1:C9:96:PRO:HG2	1:D9:90:ASN:HD22	1.76	0.50
1:Hb:80:ILE:HD12	2:Xo:713:ILE:CG2	2.40	0.50
1:Fh:35:LEU:O	1:Fh:96:PRO:HG3	2.12	0.50
1:Gt:11:MET:HB3	1:Ht:18:VAL:HG22	1.94	0.50
1:Ds:24:ALA:HB2	1:Ds:48:VAL:HG21	1.92	0.50
1:Fw:35:LEU:O	1:Fw:96:PRO:HG3	2.11	0.50
1:Bz:18:VAL:HG22	1:Ez:11:MET:HB3	1.93	0.50
1:BC:77:ALA:HB2	1:FC:72:GLY:HA2	1.92	0.50
1:FG:35:LEU:O	1:FG:96:PRO:HG3	2.12	0.50
1:FL:35:LEU:O	1:FL:96:PRO:HG3	2.11	0.50
3:PX:3:ILE:HG23	3:PX:77:ILE:HD13	1.92	0.50
1:H4:92:LEU:CD2	1:GQ:21:ILE:HD13	2.41	0.50
1:Hb:68:CYS:SG	1:Hb:75:LEU:HB2	2.51	0.50
1:De:27:MET:HE1	1:De:48:VAL:HG12	1.93	0.50
1:Ge:11:MET:HB3	1:He:18:VAL:HG22	1.94	0.50
1:Ac:62:ARG:HG2	2:Xc:724:ILE:HG13	1.92	0.50
1:Ci:96:PRO:HG2	1:Di:90:ASN:HD22	1.76	0.50
1:Bk:88:VAL:HG21	1:Fk:25:ASP:HA	1.93	0.50
1:Aq:7:ILE:CD1	1:DD:32:GLU:HB2	2.30	0.50
1:Cs:96:PRO:HG2	1:Ds:90:ASN:HD22	1.76	0.50
1:Gv:21:ILE:HD13	1:HM:92:LEU:HD21	1.93	0.50
1:Hv:68:CYS:SG	1:Hv:75:LEU:HB2	2.51	0.50
1:Gy:11:MET:HB3	1:Hy:18:VAL:HG22	1.94	0.50
1:Hy:91:ILE:HG21	1:GF:35:LEU:HD23	1.94	0.50
1:Cx:72:GLY:HA2	1:Dx:77:ALA:HB2	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HA:9:LEU:HD11	1:HA:49:LEU:HD23	1.93	0.50
1:FB:35:LEU:O	1:FB:96:PRO:HG3	2.11	0.50
1:CC:79:HIS:ND1	2:XB:786:SER:HB2	2.25	0.50
1:HC:91:ILE:HG21	1:GJ:35:LEU:HD21	1.92	0.50
1:GI:11:MET:HB3	1:HI:18:VAL:HG22	1.94	0.50
1:EN:14:THR:HB	1:EN:19:PRO:HB2	1.94	0.50
1:CO:88:VAL:HG21	1:EO:25:ASP:HA	1.93	0.50
1:AS:88:VAL:HG21	1:DS:25:ASP:HA	1.93	0.50
1:FQ:35:LEU:O	1:FQ:96:PRO:HG3	2.11	0.50
1:AU:88:VAL:HG21	1:DU:25:ASP:HA	1.94	0.50
1:HU:9:LEU:HD11	1:HU:49:LEU:HD23	1.93	0.50
1:CT:77:ALA:HB2	1:ET:72:GLY:HA2	1.93	0.50
1:G1:21:ILE:HD13	1:HX:92:LEU:HD21	1.92	0.50
1:D3:24:ALA:HB2	1:D3:48:VAL:HG11	1.92	0.50
1:B4:14:THR:HB	1:B4:19:PRO:HB2	1.94	0.50
1:B9:72:GLY:HA2	1:E9:77:ALA:HB2	1.94	0.50
1:Bb:72:GLY:HA2	1:Eb:77:ALA:HB2	1.94	0.50
1:Hg:91:ILE:HG23	1:GN:35:LEU:HD23	1.94	0.50
1:Bo:88:VAL:HG21	1:Fo:25:ASP:HA	1.92	0.50
1:Go:11:MET:HB3	1:Ho:18:VAL:HG22	1.94	0.50
1:Gn:79:HIS:CE1	2:Xm:808:GLY:HA2	2.47	0.50
1:Hn:79:HIS:CE1	2:XT:714:THR:OG1	2.54	0.50
1:Hq:68:CYS:SG	1:Hq:75:LEU:HB2	2.51	0.50
1:Fr:35:LEU:O	1:Fr:96:PRO:HG3	2.12	0.50
1:Gs:79:HIS:CE1	2:Xr:808:GLY:HA2	2.47	0.50
1:BC:14:THR:HB	1:BC:19:PRO:HB2	1.93	0.50
1:BF:72:GLY:HA2	1:EF:77:ALA:HB2	1.94	0.50
1:CE:88:VAL:HG21	1:EE:25:ASP:HA	1.93	0.50
1:DN:27:MET:HE1	1:DN:48:VAL:HG12	1.92	0.50
3:PN:3:ILE:HG23	3:PN:77:ILE:HD13	1.91	0.50
1:GS:11:MET:HB3	1:HS:18:VAL:HG22	1.94	0.50
2:XQ:808:GLY:HA2	1:GR:79:HIS:CE1	2.47	0.50
2:X8:713:ILE:HD11	1:Hu:62:ARG:HA	1.94	0.50
1:G2:9:LEU:HD11	1:G2:49:LEU:HD23	1.92	0.50
1:A1:7:ILE:HG12	1:Dm:32:GLU:OE2	2.11	0.50
1:B5:29:LYS:HE2	3:P5:45:ILE:HG22	1.94	0.50
1:G5:11:MET:HB3	1:H5:18:VAL:HG22	1.94	0.50
1:G6:11:MET:HE3	1:G6:79:HIS:HB3	1.93	0.50
1:B9:14:THR:HB	1:B9:19:PRO:HB2	1.94	0.50
1:Eb:9:LEU:HD11	1:Eb:49:LEU:HD23	1.94	0.50
1:Hg:68:CYS:SG	1:Hg:75:LEU:HB2	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bn:72:GLY:HA2	1:En:77:ALA:HB2	1.93	0.50
1:Bq:72:GLY:HA2	1:Eq:77:ALA:HB2	1.94	0.50
1:Gt:35:LEU:HD23	1:Hi:91:ILE:HG23	1.93	0.50
1:Av:88:VAL:HG21	1:Dv:25:ASP:HA	1.93	0.50
1:GC:24:ALA:HB2	1:GC:48:VAL:HG21	1.93	0.50
1:BE:88:VAL:HG21	1:FE:25:ASP:HA	1.93	0.50
1:BH:14:THR:HB	1:BH:19:PRO:HB2	1.93	0.50
1:BM:14:THR:HB	1:BM:19:PRO:HB2	1.94	0.50
1:AP:77:ALA:HB2	1:DP:72:GLY:HA2	1.94	0.50
1:DS:27:MET:HE1	1:DS:48:VAL:HG12	1.93	0.50
1:AX:88:VAL:HG21	1:DX:25:ASP:HA	1.93	0.50
1:DX:27:MET:HE1	1:DX:48:VAL:HG12	1.93	0.50
1:EX:14:THR:HB	1:EX:19:PRO:HB2	1.94	0.50
1:GW:24:ALA:HB2	1:GW:48:VAL:HG21	1.93	0.50
1:A2:88:VAL:HG21	1:D2:25:ASP:HA	1.93	0.50
1:E2:9:LEU:HD11	1:E2:49:LEU:HD23	1.94	0.50
1:H2:9:LEU:HD11	1:H2:49:LEU:HD23	1.93	0.50
1:B1:18:VAL:HG22	1:E1:11:MET:HB3	1.93	0.50
1:A3:7:ILE:HG13	1:D7:32:GLU:OE2	2.11	0.50
1:Be:29:LYS:HE2	3:Pe:45:ILE:HG22	1.94	0.50
1:De:32:GLU:HG3	1:AE:7:ILE:HD13	1.94	0.50
1:Gg:9:LEU:HD11	1:Gg:49:LEU:HD23	1.92	0.50
1:Bj:29:LYS:HE2	3:Pj:45:ILE:HG22	1.94	0.50
1:Bi:29:LYS:HE2	3:Pi:45:ILE:HG22	1.94	0.50
1:Bl:72:GLY:HA2	1:El:77:ALA:HB2	1.94	0.50
1:Gp:11:MET:HE3	1:Gp:79:HIS:HB3	1.93	0.50
1:Et:14:THR:HB	1:Et:19:PRO:HB2	1.94	0.50
1:Bs:29:LYS:HE2	3:Ps:45:ILE:HG22	1.94	0.50
2:Xw:785:VAL:HG11	1:Cx:80:ILE:HD12	1.93	0.50
1:BA:72:GLY:HA2	1:EA:77:ALA:HB2	1.94	0.50
3:PA:16:ILE:HD11	3:PA:68:PRO:HG3	1.94	0.50
1:GD:11:MET:HB3	1:HD:18:VAL:HG22	1.94	0.50
1:BC:72:GLY:HA2	1:EC:77:ALA:HB2	1.94	0.50
1:BH:72:GLY:HA2	1:EH:77:ALA:HB2	1.94	0.50
1:HN:24:ALA:HB2	1:HN:48:VAL:HG11	1.94	0.50
1:BO:18:VAL:HG22	1:EO:11:MET:HB3	1.93	0.50
1:BO:88:VAL:HG21	1:FO:25:ASP:HA	1.93	0.50
1:EU:9:LEU:HD11	1:EU:49:LEU:HD23	1.94	0.50
1:BT:88:VAL:HG21	1:FT:25:ASP:HA	1.93	0.50
1:BW:14:THR:HB	1:BW:19:PRO:HB2	1.93	0.50
1:B1:25:ASP:HA	1:E1:88:VAL:HG21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B1:88:VAL:HG21	1:F1:25:ASP:HA	1.93	0.50
1:A6:7:ILE:HD11	1:Dc:32:GLU:CD	2.36	0.50
1:C6:77:ALA:HB2	1:E6:72:GLY:HA2	1.93	0.50
1:G0:11:MET:HB3	1:H0:18:VAL:HG22	1.94	0.50
1:Gh:25:ASP:CA	1:Hs:88:VAL:HG21	2.41	0.50
2:Xh:785:VAL:HG11	1:Ci:80:ILE:HD12	1.93	0.50
1:A1:88:VAL:HG21	1:Dl:25:ASP:HA	1.93	0.50
1:Gk:11:MET:HE3	1:Gk:79:HIS:HB3	1.93	0.50
1:By:29:LYS:HE2	3:Py:45:ILE:HG22	1.94	0.50
1:Aw:7:ILE:HG13	1:DA:32:GLU:OE2	2.11	0.50
1:Bz:25:ASP:HA	1:Ez:88:VAL:HG21	1.94	0.50
1:Cz:88:VAL:HG21	1:Ez:25:ASP:HA	1.93	0.50
1:ED:24:ALA:HB2	1:ED:48:VAL:HG11	1.94	0.50
3:PD:59:ARG:HH22	3:PB:60:GLU:HG3	1.77	0.50
1:HC:79:HIS:ND1	2:XK:714:THR:OG1	2.28	0.50
1:CI:91:ILE:HG22	1:EI:96:PRO:HB3	1.94	0.50
1:EI:24:ALA:HB2	1:EI:48:VAL:HG11	1.94	0.50
1:HI:24:ALA:HB2	1:HI:48:VAL:HG11	1.94	0.50
1:GH:25:ASP:HA	1:Hz:88:VAL:CG2	2.41	0.50
1:AO:7:ILE:HD11	1:DV:32:GLU:CD	2.36	0.50
1:BO:25:ASP:HA	1:EO:88:VAL:HG21	1.94	0.50
2:X3:785:VAL:HG11	1:C4:80:ILE:HD12	1.93	0.50
1:F8:35:LEU:O	1:F8:96:PRO:HG3	2.12	0.50
1:Ba:25:ASP:HA	1:Ea:88:VAL:HG21	1.94	0.50
1:He:24:ALA:HB2	1:He:48:VAL:HG11	1.94	0.50
1:Hg:91:ILE:HD13	1:GN:35:LEU:CD2	2.40	0.50
1:Gf:11:MET:HE3	1:Gf:79:HIS:HB3	1.93	0.50
1:El:9:LEU:HD11	1:El:49:LEU:HD23	1.94	0.50
3:Po:59:ARG:HH22	3:Pm:60:GLU:HG3	1.77	0.50
1:Hn:80:ILE:HD12	2:XT:713:ILE:HG23	1.93	0.50
1:Ct:91:ILE:HG22	1:Et:96:PRO:HB3	1.94	0.50
1:Ey:24:ALA:HB2	1:Ey:48:VAL:HG11	1.94	0.50
1:Cx:96:PRO:HG2	1:Dx:90:ASN:HD22	1.76	0.50
1:Hx:80:ILE:HD12	2:XM:713:ILE:HG22	1.94	0.50
1:GC:79:HIS:CE1	2:XB:808:GLY:HA2	2.47	0.50
1:HF:9:LEU:HD11	1:HF:49:LEU:HD23	1.93	0.50
1:CE:77:ALA:HB2	1:EE:72:GLY:HA2	1.93	0.50
1:BI:29:LYS:HE2	3:PI:45:ILE:HG22	1.94	0.50
1:GH:40:PHE:HE1	1:Hz:41:VAL:HG13	1.75	0.50
1:AN:88:VAL:HG21	1:DN:25:ASP:HA	1.93	0.50
1:GN:11:MET:HB3	1:HN:18:VAL:HG22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BU:72:GLY:HA2	1:EU:77:ALA:HB2	1.94	0.50
1:BT:25:ASP:HA	1:ET:88:VAL:HG21	1.94	0.50
3:PX:59:ARG:HH22	3:PV:60:GLU:HG3	1.77	0.50
1:BW:29:LYS:HE2	3:PW:45:ILE:HG22	1.94	0.50
1:G2:35:LEU:HD23	1:HS:91:ILE:HG21	1.92	0.50
1:H5:24:ALA:HB2	1:H5:48:VAL:HG11	1.94	0.50
2:X3:714:THR:HA	2:X3:718:MET:HG3	1.94	0.50
2:X3:808:GLY:HA2	1:G4:79:HIS:CE1	2.47	0.50
1:B4:72:GLY:HA2	1:E4:77:ALA:HB2	1.93	0.50
1:Ba:18:VAL:HG22	1:Ea:11:MET:HB3	1.93	0.50
1:Ag:88:VAL:HG21	1:Dg:25:ASP:HA	1.93	0.50
1:Hg:9:LEU:HD11	1:Hg:49:LEU:HD23	1.93	0.50
1:Hg:79:HIS:CE1	1:GN:22:GLU:OE2	2.58	0.50
1:Aj:88:VAL:HG21	1:Dj:25:ASP:HA	1.93	0.50
1:Ej:14:THR:HB	1:Ej:19:PRO:HB2	1.93	0.50
1:Gj:12:ILE:HG23	1:Gj:75:LEU:HD12	1.94	0.50
1:Bi:77:ALA:HB2	1:Fi:72:GLY:HA2	1.92	0.50
1:Bp:18:VAL:HG22	1:Ep:11:MET:HB3	1.93	0.50
1:Ht:24:ALA:HB2	1:Ht:48:VAL:HG11	1.94	0.50
1:Gs:25:ASP:CA	1:Hk:88:VAL:HG21	2.41	0.50
1:Dv:62:ARG:NH1	2:XR:729:GLU:HA	2.27	0.50
1:Hy:24:ALA:HB2	1:Hy:48:VAL:HG11	1.94	0.50
2:Xw:808:GLY:HA2	1:Gx:79:HIS:CE1	2.47	0.50
1:Bz:88:VAL:HG21	1:Fz:25:ASP:HA	1.93	0.50
1:GD:12:ILE:HG23	1:GD:75:LEU:HD12	1.94	0.50
1:AK:77:ALA:HB2	1:DK:72:GLY:HA2	1.94	0.50
1:Ae:88:VAL:HG21	1:De:25:ASP:HA	1.93	0.50
1:Ce:91:ILE:HG22	1:Ee:96:PRO:HB3	1.94	0.50
1:Ee:14:THR:HB	1:Ee:19:PRO:HB2	1.94	0.50
1:Bd:29:LYS:HE2	3:Pd:45:ILE:HG22	1.94	0.50
1:Bf:88:VAL:HG21	1:Ff:25:ASP:HA	1.93	0.50
1:Gh:72:GLY:CA	1:Hs:77:ALA:HB2	2.39	0.50
2:Xh:808:GLY:HA2	1:Gi:79:HIS:CE1	2.47	0.50
2:Xk:713:ILE:HG21	1:Hr:80:ILE:HD12	1.88	0.50
1:Bp:25:ASP:HA	1:Ep:88:VAL:HG21	1.94	0.50
1:At:88:VAL:HG21	1:Dt:25:ASP:HA	1.93	0.50
1:Bt:29:LYS:HE2	3:Pt:45:ILE:HG22	1.94	0.50
1:Bs:14:THR:HB	1:Bs:19:PRO:HB2	1.93	0.50
1:Bu:88:VAL:HG21	1:Fu:25:ASP:HA	1.93	0.50
1:Gu:35:LEU:HD23	1:HR:91:ILE:CG2	2.42	0.50
1:Ey:14:THR:HB	1:Ey:19:PRO:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GI:12:ILE:HG23	1:GI:75:LEU:HD12	1.94	0.50
1:CH:80:ILE:HD12	2:XG:785:VAL:HG11	1.93	0.50
1:GH:24:ALA:HB2	1:GH:48:VAL:HG21	1.93	0.50
1:CJ:77:ALA:HB2	1:EJ:72:GLY:HA2	1.93	0.50
3:PS:59:ARG:HH22	3:PQ:60:GLU:HG3	1.77	0.50
3:PU:16:ILE:HD11	3:PU:68:PRO:HG3	1.94	0.50
1:GX:11:MET:HB3	1:HX:18:VAL:HG22	1.94	0.50
1:BW:72:GLY:HA2	1:EW:77:ALA:HB2	1.93	0.50
1:E5:24:ALA:HB2	1:E5:48:VAL:HG11	1.94	0.49
1:G3:21:ILE:HD13	1:Hd:92:LEU:CD2	2.42	0.49
2:X3:712:ARG:HH12	1:H7:65:ALA:CB	2.18	0.49
3:P0:59:ARG:HH22	3:P8:60:GLU:HG3	1.77	0.49
1:Ga:11:MET:HE3	1:Ga:79:HIS:HB3	1.93	0.49
1:Gc:35:LEU:HD21	1:HE:91:ILE:HD13	1.94	0.49
1:Gd:40:PHE:HE1	1:H6:41:VAL:HG13	1.75	0.49
1:Gh:21:ILE:HD13	1:Hs:92:LEU:CD2	2.42	0.49
1:Bi:72:GLY:HA2	1:Ei:77:ALA:HB2	1.93	0.49
1:Fi:24:ALA:HB2	1:Fi:48:VAL:HG21	1.94	0.49
1:Gi:24:ALA:HB2	1:Gi:48:VAL:HG21	1.93	0.49
1:Bk:18:VAL:HG22	1:Ek:11:MET:HB3	1.93	0.49
1:Bk:25:ASP:HA	1:Ek:88:VAL:HG21	1.94	0.49
1:Aq:77:ALA:HB2	1:Dq:72:GLY:HA2	1.94	0.49
3:Pq:60:GLU:HG3	3:Ps:59:ARG:HH22	1.77	0.49
1:Gt:12:ILE:HG23	1:Gt:75:LEU:HD12	1.94	0.49
1:Gu:11:MET:HE3	1:Gu:79:HIS:HB3	1.93	0.49
1:Gy:12:ILE:HG23	1:Gy:75:LEU:HD12	1.94	0.49
2:Xy:714:THR:OG1	1:HH:79:HIS:ND1	1.87	0.49
1:Bx:14:THR:HB	1:Bx:19:PRO:HB2	1.94	0.49
1:GC:40:PHE:HE1	1:Hf:41:VAL:HG13	1.77	0.49
1:HC:92:LEU:HD21	1:GJ:21:ILE:HD13	1.93	0.49
1:AF:77:ALA:HB2	1:DF:72:GLY:HA2	1.94	0.49
1:HK:9:LEU:HD11	1:HK:49:LEU:HD23	1.93	0.49
1:BN:29:LYS:HE2	3:PN:45:ILE:HG22	1.94	0.49
1:BM:29:LYS:HE2	3:PM:45:ILE:HG22	1.94	0.49
2:XQ:785:VAL:HG11	1:CR:80:ILE:HD12	1.93	0.49
1:CR:96:PRO:HG2	1:DR:90:ASN:HD22	1.76	0.49
1:AU:77:ALA:HB2	1:DU:72:GLY:HA2	1.94	0.49
2:X2:825:ALA:CB	1:D1:15:ARG:HE	2.26	0.49
1:G5:12:ILE:HG23	1:G5:75:LEU:HD12	1.94	0.49
1:Ab:77:ALA:HB2	1:Db:72:GLY:HA2	1.94	0.49
1:Bd:72:GLY:HA2	1:Ed:77:ALA:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Gd:24:ALA:HB2	1:Gd:48:VAL:HG21	1.93	0.49
1:Bf:25:ASP:HA	1:Ef:88:VAL:HG21	1.94	0.49
1:Bj:88:VAL:HG21	1:Fj:25:ASP:HA	1.92	0.49
1:Hh:91:ILE:CG2	1:Gk:35:LEU:CD2	2.87	0.49
2:Xh:714:THR:HA	2:Xh:718:MET:HG3	1.94	0.49
1:Gl:9:LEU:HD11	1:Gl:49:LEU:HD23	1.92	0.49
3:Pl:16:ILE:HD11	3:Pl:68:PRO:HG3	1.94	0.49
1:Co:91:ILE:HG22	1:Eo:96:PRO:HB3	1.94	0.49
1:Go:12:ILE:HG23	1:Go:75:LEU:HD12	1.94	0.49
1:Bn:14:THR:HB	1:Bn:19:PRO:HB2	1.94	0.49
1:Aq:88:VAL:HG21	1:Dq:25:ASP:HA	1.94	0.49
1:Bs:77:ALA:HB2	1:Fs:72:GLY:HA2	1.92	0.49
1:Ay:28:THR:O	1:HH:83:ARG:NH1	2.45	0.49
1:Ay:88:VAL:HG21	1:Dy:25:ASP:HA	1.93	0.49
1:AD:88:VAL:HG21	1:DD:25:ASP:HA	1.93	0.49
1:GG:27:MET:HE1	1:GG:48:VAL:HG12	1.94	0.49
1:AK:88:VAL:HG21	1:DK:25:ASP:HA	1.93	0.49
1:BJ:25:ASP:HA	1:EJ:88:VAL:HG21	1.94	0.49
1:AN:28:THR:O	1:HW:83:ARG:NH1	2.45	0.49
1:CM:25:ASP:HA	1:DM:88:VAL:HG21	1.94	0.49
1:GM:24:ALA:HB2	1:GM:48:VAL:HG21	1.93	0.49
1:AP:88:VAL:HG21	1:DP:25:ASP:HA	1.94	0.49
2:XQ:714:THR:HA	2:XQ:718:MET:HG3	1.94	0.49
1:BR:72:GLY:HA2	1:ER:77:ALA:HB2	1.94	0.49
3:PU:60:GLU:HG3	3:PW:59:ARG:HH22	1.77	0.49
1:H4:77:ALA:HB2	1:GQ:72:GLY:CA	2.40	0.49
1:A7:88:VAL:HG21	1:D7:25:ASP:HA	1.94	0.49
1:E7:9:LEU:HD11	1:E7:49:LEU:HD23	1.94	0.49
3:P7:60:GLU:HG3	3:P9:59:ARG:HH22	1.78	0.49
1:C0:91:ILE:HG22	1:E0:96:PRO:HB3	1.94	0.49
1:H0:80:ILE:HD12	2:XF:713:ILE:CG2	2.42	0.49
1:G9:79:HIS:CE1	2:X8:808:GLY:HA2	2.47	0.49
1:Fc:35:LEU:O	1:Fc:96:PRO:HG3	2.12	0.49
1:Bd:14:THR:HB	1:Bd:19:PRO:HB2	1.93	0.49
1:Cd:96:PRO:HG2	1:Dd:90:ASN:HD22	1.76	0.49
1:Eg:9:LEU:HD11	1:Eg:49:LEU:HD23	1.94	0.49
1:Ej:24:ALA:HB2	1:Ej:48:VAL:HG11	1.94	0.49
1:Dh:24:ALA:HB2	1:Dh:48:VAL:HG11	1.92	0.49
1:Di:25:ASP:HA	1:Di:88:VAL:HG21	1.95	0.49
1:Bo:29:LYS:HE2	3:Po:45:ILE:HG22	1.94	0.49
2:Xn:716:PRO:HD3	1:HT:80:ILE:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dp:32:GLU:CB	1:Al:7:ILE:HD11	2.40	0.49
1:Bs:72:GLY:HA2	1:Es:77:ALA:HB2	1.93	0.49
1:Fs:24:ALA:HB2	1:Fs:48:VAL:HG21	1.94	0.49
1:Hv:45:TYR:OH	1:GP:73:ASP:OD2	2.19	0.49
1:Bu:18:VAL:HG22	1:Eu:11:MET:HB3	1.93	0.49
1:Cy:91:ILE:HG22	1:Ey:96:PRO:HB3	1.94	0.49
2:Xx:713:ILE:CD1	1:HM:62:ARG:HA	2.41	0.49
1:ED:14:THR:HB	1:ED:19:PRO:HB2	1.94	0.49
1:EF:9:LEU:HD11	1:EF:49:LEU:HD23	1.94	0.49
1:Al:77:ALA:HB2	1:DI:72:GLY:HA2	1.95	0.49
1:CH:96:PRO:HG2	1:DH:90:ASN:HD22	1.76	0.49
1:GH:79:HIS:CE1	2:XG:808:GLY:HA2	2.47	0.49
1:GL:21:ILE:HD13	1:HW:92:LEU:CD2	2.42	0.49
2:XL:808:GLY:HA2	1:GM:79:HIS:CE1	2.47	0.49
3:PP:16:ILE:HD11	3:PP:68:PRO:HG3	1.94	0.49
1:GR:77:ALA:HB2	1:HR:72:GLY:HA2	1.95	0.49
1:C4:96:PRO:HG2	1:D4:90:ASN:HD22	1.76	0.49
1:B6:18:VAL:HG22	1:E6:11:MET:HB3	1.93	0.49
1:Fa:12:ILE:HG23	1:Fa:75:LEU:CD1	2.43	0.49
1:Ge:12:ILE:HG23	1:Ge:75:LEU:HD12	1.94	0.49
3:Pe:59:ARG:HH22	3:Pc:60:GLU:HG3	1.77	0.49
1:Gc:25:ASP:CA	1:HE:88:VAL:HG21	2.42	0.49
1:Gd:25:ASP:CA	1:H6:88:VAL:HG21	2.42	0.49
1:Dg:73:ASP:HA	2:Xi:826:ARG:HE	1.78	0.49
3:Pj:59:ARG:HH22	3:Ph:60:GLU:HG3	1.77	0.49
1:An:7:ILE:HD11	1:DT:32:GLU:CB	2.27	0.49
2:Xq:825:ALA:CB	1:Dp:15:ARG:HE	2.26	0.49
1:Cp:77:ALA:HB2	1:Ep:72:GLY:HA2	1.93	0.49
1:At:77:ALA:HB2	1:Dt:72:GLY:HA2	1.95	0.49
1:Cu:77:ALA:HB2	1:Eu:72:GLY:HA2	1.93	0.49
1:Fy:85:HIS:HB3	1:Fy:88:VAL:HG23	1.95	0.49
1:Gw:21:ILE:HD13	1:HH:92:LEU:CD2	2.42	0.49
1:Hx:92:LEU:HD21	1:GK:21:ILE:HD13	1.94	0.49
1:GA:35:LEU:HD21	1:HK:91:ILE:HG21	1.93	0.49
1:BC:29:LYS:HE2	3:PC:45:ILE:HG22	1.94	0.49
1:FC:24:ALA:HB2	1:FC:48:VAL:HG21	1.94	0.49
1:BE:18:VAL:HG22	1:EE:11:MET:HB3	1.93	0.49
1:BH:29:LYS:HE2	3:PH:45:ILE:HG22	1.94	0.49
1:BJ:88:VAL:HG21	1:FJ:25:ASP:HA	1.93	0.49
3:PN:59:ARG:HH22	3:PL:60:GLU:HG3	1.77	0.49
1:BM:72:GLY:HA2	1:EM:77:ALA:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GR:24:ALA:HB2	1:GR:48:VAL:HG21	1.93	0.49
1:HX:24:ALA:HB2	1:HX:48:VAL:HG11	1.94	0.49
1:E5:14:THR:HB	1:E5:19:PRO:HB2	1.94	0.49
2:X5:825:ALA:HB1	1:D3:15:ARG:HE	1.78	0.49
1:B4:29:LYS:HE2	3:P4:45:ILE:HG22	1.94	0.49
1:H4:83:ARG:NH1	1:AS:28:THR:O	2.45	0.49
1:G0:12:ILE:HG23	1:G0:75:LEU:HD12	1.94	0.49
1:H0:24:ALA:HB2	1:H0:48:VAL:HG11	1.94	0.49
1:G9:77:ALA:HB2	1:H9:72:GLY:HA2	1.95	0.49
3:Pb:16:ILE:HD11	3:Pb:68:PRO:HG3	1.94	0.49
1:Bg:72:GLY:HA2	1:Eg:77:ALA:HB2	1.94	0.49
2:Xg:825:ALA:CB	1:Df:15:ARG:HE	2.26	0.49
1:Bj:24:ALA:HB2	1:Bj:48:VAL:HG11	1.94	0.49
1:Hj:24:ALA:HB2	1:Hj:48:VAL:HG11	1.94	0.49
1:Hq:88:VAL:HG21	1:GB:25:ASP:CA	2.42	0.49
3:Pq:16:ILE:HD11	3:Pq:68:PRO:HG3	1.94	0.49
1:Cp:88:VAL:HG21	1:Ep:25:ASP:HA	1.93	0.49
1:Ft:85:HIS:HB3	1:Ft:88:VAL:HG23	1.95	0.49
1:Cs:80:ILE:HD12	2:Xr:785:VAL:HG11	1.93	0.49
1:Hy:91:ILE:CG2	1:GF:35:LEU:CD2	2.90	0.49
2:XA:825:ALA:CB	1:Dz:15:ARG:HE	2.26	0.49
1:AF:88:VAL:HG21	1:DF:25:ASP:HA	1.93	0.49
1:BI:24:ALA:HB2	1:BI:48:VAL:HG11	1.95	0.49
1:DL:62:ARG:NH1	2:XP:729:GLU:HA	2.17	0.49
1:FW:24:ALA:HB2	1:FW:48:VAL:HG21	1.94	0.49
1:A2:77:ALA:HB2	1:D2:72:GLY:HA2	1.94	0.49
1:A5:77:ALA:HB2	1:D5:72:GLY:HA2	1.95	0.49
1:C5:91:ILE:HG22	1:E5:96:PRO:HB3	1.94	0.49
1:G4:77:ALA:HB2	1:H4:72:GLY:HA2	1.95	0.49
1:D0:27:MET:HE1	1:D0:48:VAL:HG12	1.92	0.49
1:Ee:24:ALA:HB2	1:Ee:48:VAL:HG11	1.94	0.49
1:Fe:85:HIS:HB3	1:Fe:88:VAL:HG23	1.95	0.49
1:Gg:35:LEU:HD11	1:Gg:48:VAL:CG1	2.37	0.49
1:Ff:12:ILE:HG23	1:Ff:75:LEU:CD1	2.43	0.49
1:Aj:28:THR:O	1:Hs:83:ARG:NH1	2.46	0.49
1:Ho:24:ALA:HB2	1:Ho:48:VAL:HG11	1.94	0.49
1:Bn:29:LYS:HE2	3:Pn:45:ILE:HG22	1.94	0.49
1:Cn:9:LEU:HD11	1:Cn:49:LEU:HD23	1.95	0.49
1:Dp:62:ARG:HH12	2:XI:729:GLU:HA	1.78	0.49
1:Av:77:ALA:HB2	1:Dv:72:GLY:HA2	1.94	0.49
2:Xv:825:ALA:CB	1:Du:15:ARG:HE	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Pv:16:ILE:HD11	3:Pv:68:PRO:HG3	1.94	0.49
3:Pv:60:GLU:HG3	3:Px:59:ARG:HH22	1.78	0.49
1:Gw:25:ASP:CA	1:HH:88:VAL:HG21	2.41	0.49
1:Bx:72:GLY:HA2	1:Ex:77:ALA:HB2	1.94	0.49
1:Gx:77:ALA:HB2	1:Hx:72:GLY:HA2	1.95	0.49
1:EA:9:LEU:HD11	1:EA:49:LEU:HD23	1.94	0.49
1:HD:24:ALA:HB2	1:HD:48:VAL:HG11	1.94	0.49
2:XK:825:ALA:CB	1:DJ:15:ARG:HE	2.26	0.49
3:PK:16:ILE:HD11	3:PK:68:PRO:HG3	1.94	0.49
1:BS:24:ALA:HB2	1:BS:48:VAL:HG11	1.94	0.49
2:XU:825:ALA:CB	1:DT:15:ARG:HE	2.26	0.49
1:GV:27:MET:HE1	1:GV:48:VAL:HG12	1.95	0.49
1:CW:25:ASP:HA	1:DW:88:VAL:HG21	1.95	0.49
3:P2:16:ILE:HD11	3:P2:68:PRO:HG3	1.94	0.49
1:H5:91:ILE:CG2	1:Gb:35:LEU:CD2	2.90	0.49
1:G3:25:ASP:CA	1:Hd:88:VAL:HG21	2.41	0.49
2:X7:825:ALA:CB	1:D6:15:ARG:HE	2.26	0.49
1:F9:24:ALA:HB2	1:F9:48:VAL:HG21	1.94	0.49
1:Af:7:ILE:HD11	1:DB:32:GLU:CD	2.35	0.49
1:Cj:91:ILE:HG22	1:Ej:96:PRO:HB3	1.94	0.49
1:Eo:24:ALA:HB2	1:Eo:48:VAL:HG11	1.94	0.49
1:Gn:77:ALA:HB2	1:Hn:72:GLY:HA2	1.95	0.49
1:Bp:88:VAL:HG21	1:Fp:25:ASP:HA	1.93	0.49
1:Ep:9:LEU:HD11	1:Ep:49:LEU:HD23	1.95	0.49
1:Bv:72:GLY:HA2	1:Ev:77:ALA:HB2	1.94	0.49
1:Bx:27:MET:HE1	1:Bx:48:VAL:HG22	1.95	0.49
1:Bx:29:LYS:HE2	3:Px:45:ILE:HG22	1.94	0.49
1:BD:29:LYS:HE2	3:PD:45:ILE:HG22	1.94	0.49
1:FD:85:HIS:HB3	1:FD:88:VAL:HG23	1.95	0.49
3:PF:60:GLU:HG3	3:PH:59:ARG:HH22	1.78	0.49
3:PK:60:GLU:HG3	3:PM:59:ARG:HH22	1.77	0.49
3:PS:44:CYS:SG	3:PS:73:ILE:HG21	2.53	0.49
1:BR:14:THR:HB	1:BR:19:PRO:HB2	1.94	0.49
1:AT:31:ALA:HB3	1:AT:60:ALA:HB2	1.95	0.49
1:EX:24:ALA:HB2	1:EX:48:VAL:HG11	1.94	0.49
1:B2:72:GLY:HA2	1:E2:77:ALA:HB2	1.94	0.49
1:A7:77:ALA:HB2	1:D7:72:GLY:HA2	1.94	0.49
1:D7:73:ASP:HA	2:X9:826:ARG:HE	1.78	0.49
1:F0:85:HIS:HB3	1:F0:88:VAL:HG23	1.95	0.49
3:P0:44:CYS:SG	3:P0:73:ILE:HG21	2.53	0.49
1:He:91:ILE:CG2	1:GI:35:LEU:HD23	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Gd:25:ASP:HA	1:H6:88:VAL:CG2	2.41	0.49
3:Pj:44:CYS:SG	3:Pj:73:ILE:HG21	2.53	0.49
3:Pl:60:GLU:HG3	3:Pn:59:ARG:HH22	1.78	0.49
1:Ak:31:ALA:HB3	1:Ak:60:ALA:HB2	1.95	0.49
1:Fm:35:LEU:O	1:Fm:96:PRO:HG3	2.11	0.49
1:Cn:25:ASP:HA	1:Dn:88:VAL:HG21	1.94	0.49
1:Gn:24:ALA:HB2	1:Gn:48:VAL:HG21	1.93	0.49
1:Gr:27:MET:HE1	1:Gr:48:VAL:HG12	1.95	0.49
1:Gw:27:MET:HE1	1:Gw:48:VAL:HG12	1.95	0.49
1:Fz:12:ILE:HG23	1:Fz:75:LEU:CD1	2.43	0.49
1:CC:25:ASP:HA	1:DC:88:VAL:HG21	1.94	0.49
2:XC:729:GLU:HA	1:DK:62:ARG:NH1	2.26	0.49
1:FH:24:ALA:HB2	1:FH:48:VAL:HG21	1.95	0.49
1:BN:24:ALA:HB2	1:BN:48:VAL:HG11	1.94	0.49
1:FN:85:HIS:HB3	1:FN:88:VAL:HG23	1.95	0.49
1:HS:24:ALA:HB2	1:HS:48:VAL:HG11	1.94	0.49
1:BR:29:LYS:HE2	3:PR:45:ILE:HG22	1.94	0.49
1:FR:24:ALA:HB2	1:FR:48:VAL:HG21	1.94	0.49
1:CX:91:ILE:HG22	1:EX:96:PRO:HB3	1.94	0.49
2:XG:714:THR:HA	2:XG:718:MET:HG3	1.94	0.49
1:G3:27:MET:HE1	1:G3:48:VAL:HG12	1.94	0.49
1:E0:24:ALA:HB2	1:E0:48:VAL:HG11	1.94	0.49
2:X9:713:ILE:CD1	1:HQ:62:ARG:HA	2.41	0.49
2:Xe:825:ALA:HB1	1:Dc:15:ARG:HE	1.78	0.49
1:Et:24:ALA:HB2	1:Et:48:VAL:HG11	1.94	0.49
2:XD:825:ALA:HB1	1:DB:15:ARG:HE	1.78	0.49
1:GC:77:ALA:HB2	1:HC:72:GLY:HA2	1.95	0.49
2:XF:825:ALA:CB	1:DE:15:ARG:HE	2.26	0.49
1:EI:14:THR:HB	1:EI:19:PRO:HB2	1.94	0.49
1:CH:9:LEU:HD11	1:CH:49:LEU:HD23	1.95	0.49
1:EK:9:LEU:HD11	1:EK:49:LEU:HD23	1.94	0.49
1:AJ:31:ALA:HB3	1:AJ:60:ALA:HB2	1.95	0.49
1:BP:72:GLY:HA2	1:EP:77:ALA:HB2	1.94	0.49
1:FO:12:ILE:HG23	1:FO:75:LEU:CD1	2.43	0.49
1:ES:14:THR:HB	1:ES:19:PRO:HB2	1.94	0.49
1:CR:9:LEU:HD11	1:CR:49:LEU:HD23	1.95	0.49
1:FV:35:LEU:O	1:FV:96:PRO:HG3	2.12	0.49
1:C4:9:LEU:HD11	1:C4:49:LEU:HD23	1.95	0.49
1:B7:72:GLY:HA2	1:E7:77:ALA:HB2	1.94	0.49
3:Pa:3:ILE:HG23	3:Pa:77:ILE:HD13	1.95	0.49
1:Gc:27:MET:HE1	1:Gc:48:VAL:HG12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Fd:23:ALA:O	1:Fd:27:MET:HG3	2.13	0.49
1:Ef:9:LEU:HD11	1:Ef:49:LEU:HD23	1.95	0.49
1:Dh:32:GLU:CB	1:Al:7:ILE:HD11	2.35	0.49
1:Bi:14:THR:HB	1:Bi:19:PRO:HB2	1.94	0.49
2:Xo:825:ALA:HB1	1:Dm:15:ARG:HE	1.78	0.49
1:Dq:73:ASP:HA	2:Xs:826:ARG:HE	1.78	0.49
1:Eq:9:LEU:HD11	1:Eq:49:LEU:HD23	1.94	0.49
1:Gt:35:LEU:HD23	1:HI:91:ILE:CG2	2.42	0.49
1:Ev:9:LEU:HD11	1:Ev:49:LEU:HD23	1.94	0.49
1:Bu:25:ASP:HA	1:Eu:88:VAL:HG21	1.94	0.49
1:Fu:12:ILE:HG23	1:Fu:75:LEU:CD1	2.43	0.49
1:Cx:9:LEU:HD11	1:Cx:49:LEU:HD23	1.95	0.49
1:FC:23:ALA:O	1:FC:27:MET:HG3	2.13	0.49
1:CF:15:ARG:NH1	1:CF:76:VAL:HG22	2.28	0.49
1:BK:72:GLY:HA2	1:EK:77:ALA:HB2	1.94	0.49
1:DK:73:ASP:HA	2:XM:826:ARG:HE	1.78	0.49
1:EN:24:ALA:HB2	1:EN:48:VAL:HG11	1.94	0.49
2:XN:714:THR:OG1	1:HW:79:HIS:ND1	1.87	0.49
2:XL:714:THR:HA	2:XL:718:MET:HG3	1.94	0.49
1:BM:27:MET:HE1	1:BM:48:VAL:HG22	1.95	0.49
3:PP:60:GLU:HG3	3:PR:59:ARG:HH22	1.78	0.49
1:ES:24:ALA:HB2	1:ES:48:VAL:HG11	1.94	0.49
1:FS:85:HIS:HB3	1:FS:88:VAL:HG23	1.95	0.49
1:CU:15:ARG:NH1	1:CU:76:VAL:HG22	2.28	0.49
1:AX:77:ALA:HB2	1:DX:72:GLY:HA2	1.95	0.49
1:GX:12:ILE:HG23	1:GX:75:LEU:HD12	1.94	0.49
1:BW:27:MET:HE1	1:BW:48:VAL:HG22	1.95	0.49
1:DW:79:HIS:ND1	2:XV:820:SER:HB2	2.28	0.49
1:GW:77:ALA:HB2	1:HW:72:GLY:HA2	1.95	0.49
3:P2:60:GLU:HG3	3:P4:59:ARG:HH22	1.77	0.48
3:P5:59:ARG:HH22	3:P3:60:GLU:HG3	1.77	0.48
3:P6:3:ILE:HG23	3:P6:77:ILE:HD13	1.95	0.48
1:E0:14:THR:HB	1:E0:19:PRO:HB2	1.94	0.48
1:C9:9:LEU:HD11	1:C9:49:LEU:HD23	1.95	0.48
1:Gd:79:HIS:CE1	2:Xc:808:GLY:HA2	2.47	0.48
3:Pg:60:GLU:HG3	3:Pi:59:ARG:HH22	1.78	0.48
3:Pf:3:ILE:HG23	3:Pf:77:ILE:HD13	1.95	0.48
1:Gj:11:MET:HB3	1:Hj:18:VAL:HG22	1.94	0.48
2:Xj:825:ALA:HB1	1:Dh:15:ARG:HE	1.78	0.48
2:XI:825:ALA:CB	1:Dk:15:ARG:HE	2.26	0.48
1:Bo:24:ALA:HB2	1:Bo:48:VAL:HG11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dn:79:HIS:ND1	2:Xm:820:SER:HB2	2.28	0.48
3:Pu:3:ILE:HG23	3:Pu:77:ILE:HD13	1.95	0.48
1:Cw:35:LEU:HD11	1:Cw:48:VAL:HG13	1.95	0.48
2:Xw:714:THR:HA	2:Xw:718:MET:HG3	1.94	0.48
1:BD:24:ALA:HB2	1:BD:48:VAL:HG11	1.94	0.48
1:CC:9:LEU:HD11	1:CC:49:LEU:HD23	1.95	0.48
1:BE:25:ASP:HA	1:EE:88:VAL:HG21	1.94	0.48
3:PI:44:CYS:SG	3:PI:73:ILE:HG21	2.53	0.48
3:PX:44:CYS:SG	3:PX:73:ILE:HG21	2.53	0.48
1:F5:85:HIS:HB3	1:F5:88:VAL:HG23	1.95	0.48
1:C7:15:ARG:NH1	1:C7:76:VAL:HG22	2.28	0.48
1:A6:31:ALA:HB3	1:A6:60:ALA:HB2	1.95	0.48
1:B0:29:LYS:HE2	3:P0:45:ILE:HG22	1.94	0.48
3:Pb:60:GLU:HG3	3:Pd:59:ARG:HH22	1.77	0.48
1:Ga:18:VAL:HG22	1:Ho:11:MET:HB3	1.94	0.48
1:Fc:27:MET:HE1	1:Fc:48:VAL:HG12	1.95	0.48
1:Bd:27:MET:HE1	1:Bd:48:VAL:HG22	1.95	0.48
1:Fj:85:HIS:HB3	1:Fj:88:VAL:HG23	1.95	0.48
1:Ci:9:LEU:HD11	1:Ci:49:LEU:HD23	1.95	0.48
1:Dl:73:ASP:HA	2:Xn:826:ARG:HE	1.78	0.48
1:Ek:9:LEU:HD11	1:Ek:49:LEU:HD23	1.95	0.48
1:Fp:12:ILE:HG23	1:Fp:75:LEU:CD1	2.43	0.48
1:Gt:22:GLU:OE2	1:HI:79:HIS:CE1	2.63	0.48
3:Pt:44:CYS:SG	3:Pt:73:ILE:HG21	2.53	0.48
1:Ds:79:HIS:ND1	2:Xr:820:SER:HB2	2.28	0.48
1:Fs:23:ALA:O	1:Fs:27:MET:HG3	2.13	0.48
1:Dv:73:ASP:HA	2:Xx:826:ARG:HE	1.78	0.48
1:Hv:91:ILE:HG21	1:GP:35:LEU:HD21	1.95	0.48
2:Xw:820:SER:HB2	1:Dx:79:HIS:ND1	2.28	0.48
1:CD:41:VAL:HB	1:CD:45:TYR:HB2	1.96	0.48
1:CD:91:ILE:HG22	1:ED:96:PRO:HB3	1.94	0.48
3:PC:3:ILE:HG23	3:PC:77:ILE:HD13	1.95	0.48
1:FE:12:ILE:HG23	1:FE:75:LEU:CD1	2.43	0.48
1:CG:35:LEU:HD11	1:CG:48:VAL:HG13	1.95	0.48
1:FJ:12:ILE:HG23	1:FJ:75:LEU:CD1	2.43	0.48
1:GN:12:ILE:HG23	1:GN:75:LEU:HD12	1.94	0.48
1:CM:96:PRO:HG2	1:DM:90:ASN:HD22	1.76	0.48
2:XP:825:ALA:CB	1:DO:15:ARG:HE	2.26	0.48
1:EO:9:LEU:HD11	1:EO:49:LEU:HD23	1.95	0.48
1:CV:35:LEU:HD11	1:CV:48:VAL:HG13	1.95	0.48
1:F3:27:MET:HE1	1:F3:48:VAL:HG12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X3:820:SER:HB2	1:D4:79:HIS:ND1	2.28	0.48
1:B7:62:ARG:HB3	3:P7:21:HIS:CG	2.49	0.48
1:G0:11:MET:HE3	1:G0:79:HIS:HB3	1.96	0.48
1:B9:29:LYS:HE2	3:P9:45:ILE:HG22	1.94	0.48
1:F9:23:ALA:O	1:F9:27:MET:HG3	2.13	0.48
1:Ea:9:LEU:HD11	1:Ea:49:LEU:HD23	1.95	0.48
2:Xa:713:ILE:HG23	1:Ht:80:ILE:HD12	1.93	0.48
1:Ae:77:ALA:HB2	1:De:72:GLY:HA2	1.95	0.48
1:Cc:35:LEU:HD11	1:Cc:48:VAL:HG13	1.95	0.48
1:Hi:80:ILE:HD12	2:XU:713:ILE:CG2	2.43	0.48
1:Go:11:MET:HE3	1:Go:79:HIS:HB3	1.95	0.48
3:Pt:59:ARG:HH22	3:Pr:60:GLU:HG3	1.77	0.48
3:Py:44:CYS:SG	3:Py:73:ILE:HG21	2.53	0.48
1:CA:15:ARG:NH1	1:CA:76:VAL:HG22	2.29	0.48
1:Az:31:ALA:HB3	1:Az:60:ALA:HB2	1.95	0.48
3:Pz:3:ILE:HG23	3:Pz:77:ILE:HD13	1.95	0.48
1:BF:62:ARG:HB3	3:PF:21:HIS:CG	2.49	0.48
1:EE:9:LEU:HD11	1:EE:49:LEU:HD23	1.95	0.48
1:AN:77:ALA:HB2	1:DN:72:GLY:HA2	1.95	0.48
1:CN:91:ILE:HG22	1:EN:96:PRO:HB3	1.94	0.48
3:PM:3:ILE:HG23	3:PM:77:ILE:HD13	1.95	0.48
1:EP:9:LEU:HD11	1:EP:49:LEU:HD23	1.94	0.48
1:AO:31:ALA:HB3	1:AO:60:ALA:HB2	1.95	0.48
1:CS:41:VAL:HB	1:CS:45:TYR:HB2	1.95	0.48
1:GW:79:HIS:CE1	2:XV:808:GLY:HA2	2.47	0.48
1:B5:24:ALA:HB2	1:B5:48:VAL:HG11	1.94	0.48
3:P7:16:ILE:HD11	3:P7:68:PRO:HG3	1.94	0.48
1:B0:24:ALA:HB2	1:B0:48:VAL:HG11	1.94	0.48
1:Ab:88:VAL:HG21	1:Db:25:ASP:HA	1.94	0.48
1:Cb:15:ARG:NH1	1:Cb:76:VAL:HG22	2.28	0.48
1:Cg:15:ARG:NH1	1:Cg:76:VAL:HG22	2.28	0.48
1:Fh:27:MET:HE1	1:Fh:48:VAL:HG12	1.95	0.48
1:Cl:15:ARG:NH1	1:Cl:76:VAL:HG22	2.28	0.48
1:Co:41:VAL:HB	1:Co:45:TYR:HB2	1.95	0.48
3:Po:44:CYS:SG	3:Po:73:ILE:HG21	2.53	0.48
1:Ap:31:ALA:HB3	1:Ap:60:ALA:HB2	1.95	0.48
1:Hp:9:LEU:HD11	1:Hp:49:LEU:HD23	1.96	0.48
1:Cs:9:LEU:HD11	1:Cs:49:LEU:HD23	1.95	0.48
1:Cv:15:ARG:NH1	1:Cv:76:VAL:HG22	2.28	0.48
1:Hv:91:ILE:HD13	1:GP:35:LEU:CD2	2.44	0.48
1:Au:31:ALA:HB3	1:Au:60:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Gy:11:MET:HE3	1:Gy:79:HIS:HB3	1.96	0.48
1:CI:41:VAL:HB	1:CI:45:TYR:HB2	1.95	0.48
1:GH:77:ALA:HB2	1:HH:72:GLY:HA2	1.95	0.48
1:GN:11:MET:HE3	1:GN:79:HIS:HB3	1.96	0.48
2:XL:820:SER:HB2	1:DM:79:HIS:ND1	2.28	0.48
1:FM:24:ALA:HB2	1:FM:48:VAL:HG21	1.94	0.48
1:AS:77:ALA:HB2	1:DS:72:GLY:HA2	1.95	0.48
1:GQ:27:MET:HE1	1:GQ:48:VAL:HG12	1.94	0.48
1:BX:24:ALA:HB2	1:BX:48:VAL:HG11	1.95	0.48
1:BX:29:LYS:HE2	3:PX:45:ILE:HG22	1.94	0.48
1:FV:27:MET:HE1	1:FV:48:VAL:HG12	1.95	0.48
3:PW:3:ILE:HG23	3:PW:77:ILE:HD13	1.95	0.48
1:A5:28:THR:O	1:Hd:83:ARG:NH1	2.45	0.48
3:P5:44:CYS:SG	3:P5:73:ILE:HG21	2.53	0.48
1:C3:35:LEU:HD11	1:C3:48:VAL:HG13	1.95	0.48
1:D3:9:LEU:HD11	1:D3:49:LEU:HD23	1.96	0.48
3:P4:3:ILE:HG23	3:P4:77:ILE:HD13	1.95	0.48
1:C0:41:VAL:HB	1:C0:45:TYR:HB2	1.95	0.48
1:Dd:79:HIS:ND1	2:Xc:820:SER:HB2	2.28	0.48
1:Gd:77:ALA:HB2	1:Hd:72:GLY:HA2	1.95	0.48
1:Ag:77:ALA:HB2	1:Dg:72:GLY:HA2	1.94	0.48
1:Bg:62:ARG:HB3	3:Pg:21:HIS:CG	2.49	0.48
1:Hj:80:ILE:CD1	2:Xs:713:ILE:CG2	2.92	0.48
1:Al:77:ALA:HB2	1:Dl:72:GLY:HA2	1.94	0.48
1:Eo:14:THR:HB	1:Eo:19:PRO:HB2	1.94	0.48
1:Hn:88:VAL:HG21	1:GX:25:ASP:CA	2.43	0.48
1:Bt:24:ALA:HB2	1:Bt:48:VAL:HG11	1.94	0.48
1:Gt:18:VAL:HG22	1:HI:11:MET:HB3	1.95	0.48
2:Xt:825:ALA:HB1	1:Dr:15:ARG:HE	1.78	0.48
3:Py:59:ARG:HH22	3:Pw:60:GLU:HG3	1.77	0.48
1:Fx:24:ALA:HB2	1:Fx:48:VAL:HG21	1.94	0.48
2:Xz:825:ALA:HB3	1:DD:15:ARG:HE	1.79	0.48
1:DH:79:HIS:ND1	2:XG:820:SER:HB2	2.28	0.48
1:EJ:9:LEU:HD11	1:EJ:49:LEU:HD23	1.95	0.48
1:DP:73:ASP:HA	2:XR:826:ARG:HE	1.78	0.48
1:BS:29:LYS:HE2	3:PS:45:ILE:HG22	1.94	0.48
1:DQ:9:LEU:HD11	1:DQ:49:LEU:HD23	1.96	0.48
2:XT:825:ALA:HB3	1:DX:15:ARG:HE	1.79	0.48
1:GW:40:PHE:HE1	1:HO:41:VAL:HG13	1.75	0.48
1:A1:31:ALA:HB3	1:A1:60:ALA:HB2	1.95	0.48
1:E1:9:LEU:HD11	1:E1:49:LEU:HD23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C5:41:VAL:HB	1:C5:45:TYR:HB2	1.95	0.48
1:G5:11:MET:HE3	1:G5:79:HIS:HB3	1.96	0.48
1:F4:41:VAL:HB	1:F4:45:TYR:HB2	1.96	0.48
2:Xb:825:ALA:CB	1:Da:15:ARG:HE	2.26	0.48
2:Xa:825:ALA:HB3	1:De:15:ARG:HE	1.79	0.48
1:Be:24:ALA:HB2	1:Be:48:VAL:HG11	1.94	0.48
1:Cd:9:LEU:HD11	1:Cd:49:LEU:HD23	1.95	0.48
1:Fd:24:ALA:HB2	1:Fd:48:VAL:HG21	1.94	0.48
1:Dg:41:VAL:HB	1:Dg:45:TYR:HB2	1.96	0.48
1:Gh:27:MET:HE1	1:Gh:48:VAL:HG12	1.94	0.48
1:Fk:12:ILE:HG23	1:Fk:75:LEU:CD1	2.43	0.48
1:Ao:77:ALA:HB2	1:Do:72:GLY:HA2	1.95	0.48
1:Eu:9:LEU:HD11	1:Eu:49:LEU:HD23	1.95	0.48
2:Xu:825:ALA:HB3	1:Dy:15:ARG:HE	1.79	0.48
1:Ay:77:ALA:HB2	1:Dy:72:GLY:HA2	1.95	0.48
1:AD:77:ALA:HB2	1:DD:72:GLY:HA2	1.95	0.48
3:PD:44:CYS:SG	3:PD:73:ILE:HG21	2.53	0.48
1:DF:73:ASP:HA	2:XH:826:ARG:HE	1.78	0.48
3:PI:59:ARG:HH22	3:PG:60:GLU:HG3	1.77	0.48
3:PN:44:CYS:SG	3:PN:73:ILE:HG21	2.53	0.48
1:GL:27:MET:HE1	1:GL:48:VAL:HG12	1.94	0.48
1:CM:9:LEU:HD11	1:CM:49:LEU:HD23	1.95	0.48
1:GM:77:ALA:HB2	1:HM:72:GLY:HA2	1.95	0.48
3:PO:3:ILE:HG23	3:PO:77:ILE:HD13	1.95	0.48
1:CS:91:ILE:HG22	1:ES:96:PRO:HB3	1.94	0.48
1:CR:25:ASP:HA	1:DR:88:VAL:HG21	1.95	0.48
1:GX:11:MET:HE3	1:GX:79:HIS:HB3	1.96	0.48
1:CW:80:ILE:HD12	2:XV:785:VAL:HG11	1.93	0.48
1:B2:62:ARG:HB3	3:P2:21:HIS:CG	2.49	0.48
1:G4:96:PRO:HB2	1:H7:91:ILE:HG22	1.96	0.48
1:E6:9:LEU:HD11	1:E6:49:LEU:HD23	1.95	0.48
1:G8:27:MET:HE1	1:G8:48:VAL:HG12	1.94	0.48
1:C9:25:ASP:HA	1:D9:88:VAL:HG21	1.94	0.48
1:Aj:77:ALA:HB2	1:Dj:72:GLY:HA2	1.95	0.48
1:Fh:24:ALA:HB2	1:Fh:48:VAL:HG21	1.94	0.48
1:Cs:25:ASP:HA	1:Ds:88:VAL:HG21	1.95	0.48
1:Bv:62:ARG:HB3	3:Pv:21:HIS:CG	2.49	0.48
1:Ez:9:LEU:HD11	1:Ez:49:LEU:HD23	1.95	0.48
1:HD:27:MET:HG2	1:HD:60:ALA:O	2.14	0.48
1:DC:79:HIS:ND1	2:XB:820:SER:HB2	2.28	0.48
1:AE:31:ALA:HB3	1:AE:60:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XE:825:ALA:HB3	1:DI:15:ARG:HE	1.79	0.48
1:HN:80:ILE:CD1	2:XW:713:ILE:CG2	2.92	0.48
1:FL:27:MET:HE1	1:FL:48:VAL:HG12	1.96	0.48
1:GL:25:ASP:CA	1:HW:88:VAL:HG21	2.41	0.48
2:XO:825:ALA:HB3	1:DS:15:ARG:HE	1.79	0.48
1:GS:12:ILE:HG23	1:GS:75:LEU:HD12	1.94	0.48
1:FQ:27:MET:HE1	1:FQ:48:VAL:HG12	1.95	0.48
1:FR:41:VAL:HB	1:FR:45:TYR:HB2	1.96	0.48
1:FT:12:ILE:HG23	1:FT:75:LEU:CD1	2.43	0.48
1:HT:9:LEU:HD11	1:HT:49:LEU:HD23	1.96	0.48
1:FX:85:HIS:HB3	1:FX:88:VAL:HG23	1.95	0.48
1:DV:9:LEU:HD11	1:DV:49:LEU:HD23	1.96	0.48
1:FW:41:VAL:HB	1:FW:45:TYR:HB2	1.96	0.48
1:H5:27:MET:HG2	1:H5:60:ALA:O	2.14	0.48
1:F6:12:ILE:HG23	1:F6:75:LEU:CD1	2.43	0.48
1:A0:77:ALA:HB2	1:D0:72:GLY:HA2	1.95	0.48
3:P9:3:ILE:HG23	3:P9:77:ILE:HD13	1.95	0.48
1:Aa:31:ALA:HB3	1:Aa:60:ALA:HB2	1.95	0.48
1:Ae:7:ILE:HD11	1:DE:32:GLU:CB	2.41	0.48
1:He:27:MET:HG2	1:He:60:ALA:O	2.14	0.48
1:Cg:41:VAL:HB	1:Cg:45:TYR:HB2	1.96	0.48
2:Xk:825:ALA:HB3	1:Do:15:ARG:HE	1.79	0.48
3:Pk:3:ILE:HG23	3:Pk:77:ILE:HD13	1.95	0.48
1:Fh:23:ALA:O	1:Fh:27:MET:HG3	2.13	0.48
2:Xt:788:GLU:HG3	1:Cr:82:ALA:H	1.79	0.48
1:Fr:27:MET:HE1	1:Fr:48:VAL:HG12	1.95	0.48
1:By:24:ALA:HB2	1:By:48:VAL:HG11	1.95	0.48
1:AA:77:ALA:HB2	1:DA:72:GLY:HA2	1.94	0.48
2:XA:825:ALA:HB3	1:Dz:15:ARG:HH21	1.79	0.48
1:GD:11:MET:HE3	1:GD:79:HIS:HB3	1.96	0.48
1:GB:27:MET:HE1	1:GB:48:VAL:HG12	1.94	0.48
1:FI:85:HIS:HB3	1:FI:88:VAL:HG23	1.95	0.48
3:PH:3:ILE:HG23	3:PH:77:ILE:HD13	1.95	0.48
1:CN:41:VAL:HB	1:CN:45:TYR:HB2	1.95	0.48
3:PR:3:ILE:HG23	3:PR:77:ILE:HD13	1.95	0.48
2:XX:788:GLU:HG3	1:CV:82:ALA:H	1.79	0.48
1:GW:25:ASP:CA	1:HO:88:VAL:HG21	2.42	0.48
1:H6:9:LEU:HD11	1:H6:49:LEU:HD23	1.96	0.48
1:C2:15:ARG:NH1	1:C2:76:VAL:HG22	2.28	0.48
1:D2:41:VAL:HB	1:D2:45:TYR:HB2	1.96	0.48
1:D2:73:ASP:HA	2:X4:826:ARG:HE	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F4:23:ALA:O	1:F4:27:MET:HG3	2.14	0.48
2:X7:825:ALA:HB3	1:D6:15:ARG:HH21	1.79	0.48
1:B6:25:ASP:HA	1:E6:88:VAL:HG21	1.94	0.48
1:D8:9:LEU:HD11	1:D8:49:LEU:HD23	1.96	0.48
1:Ce:41:VAL:HB	1:Ce:45:TYR:HB2	1.95	0.48
1:Bg:11:MET:HE3	1:Bg:79:HIS:HB3	1.96	0.48
1:Af:31:ALA:HB3	1:Af:60:ALA:HB2	1.95	0.48
2:Xf:818:ASN:HA	2:Xf:819:PRO:HD3	1.80	0.48
1:Bl:62:ARG:HB3	3:Pl:21:HIS:CG	2.49	0.48
2:Xl:825:ALA:HB3	1:Dk:15:ARG:HH21	1.79	0.48
2:Xl:841:PRO:HG3	1:Fk:69:GLU:HG2	1.96	0.48
1:Fo:85:HIS:HB3	1:Fo:88:VAL:HG23	1.95	0.48
1:Fm:27:MET:HE1	1:Fm:48:VAL:HG12	1.95	0.48
3:Pp:3:ILE:HG23	3:Pp:77:ILE:HD13	1.95	0.48
1:Ht:27:MET:HG2	1:Ht:60:ALA:O	2.14	0.48
1:Fx:23:ALA:O	1:Fx:27:MET:HG3	2.13	0.48
1:BA:62:ARG:HB3	3:PA:21:HIS:CG	2.49	0.48
3:PI:10:LEU:HG	3:PI:37:VAL:HG21	1.96	0.48
1:DK:41:VAL:HB	1:DK:45:TYR:HB2	1.96	0.48
1:FM:23:ALA:O	1:FM:27:MET:HG3	2.13	0.48
1:CP:15:ARG:NH1	1:CP:76:VAL:HG22	2.28	0.48
2:XP:825:ALA:HB3	1:DO:15:ARG:HH21	1.79	0.48
1:Hf:9:LEU:HD11	1:Hf:49:LEU:HD23	1.96	0.48
1:Hk:9:LEU:HD11	1:Hk:49:LEU:HD23	1.96	0.48
2:X6:825:ALA:HB3	1:D0:15:ARG:HE	1.79	0.48
1:Db:32:GLU:CB	1:Ao:7:ILE:HD11	2.30	0.48
1:Bc:27:MET:HE1	1:Bc:48:VAL:HG12	1.96	0.48
1:Cd:25:ASP:HA	1:Dd:88:VAL:HG21	1.95	0.48
1:Gg:21:ILE:HD13	1:HU:92:LEU:CD2	2.44	0.48
1:Cj:41:VAL:HB	1:Cj:45:TYR:HB2	1.96	0.48
1:Cl:41:VAL:HB	1:Cl:45:TYR:HB2	1.96	0.48
1:Gp:18:VAL:HG22	1:HD:11:MET:HB3	1.95	0.48
1:Gt:11:MET:HE3	1:Gt:79:HIS:HB3	1.96	0.48
1:Au:62:ARG:HA	2:Xu:724:ILE:HD11	1.96	0.48
1:Hy:27:MET:HG2	1:Hy:60:ALA:O	2.14	0.48
1:BF:11:MET:HE3	1:BF:79:HIS:HB3	1.96	0.48
3:PF:16:ILE:HD11	3:PF:68:PRO:HG3	1.94	0.48
1:DG:9:LEU:HD11	1:DG:49:LEU:HD23	1.96	0.48
1:BL:27:MET:HE1	1:BL:48:VAL:HG12	1.96	0.48
3:PS:10:LEU:HG	3:PS:37:VAL:HG21	1.96	0.48
1:CQ:35:LEU:HD11	1:CQ:48:VAL:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ER:11:MET:HG2	1:ER:49:LEU:HD23	1.96	0.48
1:CX:41:VAL:HB	1:CX:45:TYR:HB2	1.95	0.48
1:CW:9:LEU:HD11	1:CW:49:LEU:HD23	1.95	0.48
1:F1:12:ILE:HG23	1:F1:75:LEU:CD1	2.43	0.47
2:X1:825:ALA:HB3	1:D5:15:ARG:HE	1.79	0.47
2:X5:788:GLU:HG3	1:C3:82:ALA:H	1.79	0.47
1:C4:25:ASP:HA	1:D4:88:VAL:HG21	1.95	0.47
1:C7:41:VAL:HB	1:C7:45:TYR:HB2	1.96	0.47
1:Gb:35:LEU:HD11	1:Gb:48:VAL:CG1	2.37	0.47
1:Ha:91:ILE:HD13	1:Gr:35:LEU:HD21	1.95	0.47
1:Hg:88:VAL:HG21	1:GN:25:ASP:CA	2.42	0.47
1:Hj:27:MET:HG2	1:Hj:60:ALA:O	2.14	0.47
3:Pj:10:LEU:HG	3:Pj:37:VAL:HG21	1.96	0.47
1:Bl:88:VAL:HG21	1:Fl:25:ASP:HA	1.96	0.47
1:Dl:41:VAL:HB	1:Dl:45:TYR:HB2	1.96	0.47
2:Xo:788:GLU:HG3	1:Cm:82:ALA:H	1.79	0.47
1:Bq:11:MET:HE3	1:Bq:79:HIS:HB3	1.96	0.47
1:Cq:15:ARG:NH1	1:Cq:76:VAL:HG22	2.28	0.47
1:Hv:15:ARG:HG3	1:Hv:76:VAL:HG23	1.96	0.47
1:Hy:80:ILE:CD1	2:XH:713:ILE:CG2	2.92	0.47
2:Xx:716:PRO:HD3	1:HM:80:ILE:O	2.13	0.47
1:BA:11:MET:HE3	1:BA:79:HIS:HB3	1.96	0.47
1:HA:15:ARG:HG3	1:HA:76:VAL:HG23	1.96	0.47
3:PA:60:GLU:HG3	3:PC:59:ARG:HH22	1.78	0.47
1:DB:9:LEU:HD11	1:DB:49:LEU:HD23	1.96	0.47
1:AE:62:ARG:HA	2:XE:724:ILE:HD11	1.96	0.47
1:CH:25:ASP:HA	1:DH:88:VAL:HG21	1.95	0.47
1:CK:41:VAL:HB	1:CK:45:TYR:HB2	1.96	0.47
2:XK:841:PRO:HG3	1:FJ:69:GLU:HG2	1.96	0.47
1:HJ:9:LEU:HD11	1:HJ:49:LEU:HD23	1.96	0.47
2:XJ:825:ALA:HB3	1:DN:15:ARG:HE	1.79	0.47
1:CL:35:LEU:HD11	1:CL:48:VAL:HG13	1.95	0.47
2:XS:825:ALA:HB1	1:DQ:15:ARG:HE	1.78	0.47
1:B2:11:MET:HE3	1:B2:79:HIS:HB3	1.96	0.47
1:E5:27:MET:HE1	1:E5:48:VAL:HG12	1.96	0.47
1:B7:88:VAL:HG21	1:F7:25:ASP:HA	1.97	0.47
1:E0:27:MET:HE1	1:E0:48:VAL:HG12	1.97	0.47
1:Bb:88:VAL:HG21	1:Fb:25:ASP:HA	1.97	0.47
2:Xb:841:PRO:HG3	1:Fa:69:GLU:HG2	1.96	0.47
1:He:91:ILE:HG23	1:GI:35:LEU:HD23	1.96	0.47
3:Pc:19:MET:CE	3:Pc:24:LEU:HD21	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Pg:16:ILE:HD11	3:Pg:68:PRO:HG3	1.94	0.47
1:Gj:11:MET:HE3	1:Gj:79:HIS:HB3	1.96	0.47
1:Fi:23:ALA:O	1:Fi:27:MET:HG3	2.13	0.47
1:Gi:77:ALA:HB2	1:Hi:72:GLY:HA2	1.95	0.47
1:Gm:27:MET:HE1	1:Gm:48:VAL:HG12	1.95	0.47
3:Pn:3:ILE:HG23	3:Pn:77:ILE:HD13	1.95	0.47
1:Cq:41:VAL:HB	1:Cq:45:TYR:HB2	1.96	0.47
1:Br:27:MET:HE1	1:Br:48:VAL:HG12	1.96	0.47
1:Bs:27:MET:HE1	1:Bs:48:VAL:HG22	1.95	0.47
1:Cy:41:VAL:HB	1:Cy:45:TYR:HB2	1.95	0.47
1:Cx:25:ASP:HA	1:Dx:88:VAL:HG21	1.95	0.47
2:XD:788:GLU:HG3	1:CB:82:ALA:H	1.79	0.47
1:EC:11:MET:HG2	1:EC:49:LEU:HD23	1.96	0.47
1:HF:15:ARG:HG3	1:HF:76:VAL:HG23	1.96	0.47
2:XF:825:ALA:HB3	1:DE:15:ARG:HH21	1.79	0.47
1:FG:27:MET:HE1	1:FG:48:VAL:HG12	1.95	0.47
1:BH:27:MET:HE1	1:BH:48:VAL:HG22	1.95	0.47
1:FH:23:ALA:O	1:FH:27:MET:HG3	2.13	0.47
1:AM:77:ALA:HB2	1:DM:72:GLY:CA	2.44	0.47
1:FM:41:VAL:HB	1:FM:45:TYR:HB2	1.96	0.47
1:HS:27:MET:HG2	1:HS:60:ALA:O	2.14	0.47
1:BQ:27:MET:HE1	1:BQ:48:VAL:HG12	1.96	0.47
2:XQ:820:SER:HB2	1:DR:79:HIS:ND1	2.28	0.47
1:BU:11:MET:HE3	1:BU:79:HIS:HB3	1.96	0.47
1:DU:73:ASP:HA	2:XW:826:ARG:HE	1.78	0.47
1:G2:21:ILE:HD13	1:HS:92:LEU:HD21	1.94	0.47
1:H5:91:ILE:HG21	1:Gb:35:LEU:HD23	1.94	0.47
2:Xe:729:GLU:HA	1:DE:62:ARG:HH12	1.80	0.47
3:Pe:44:CYS:SG	3:Pe:73:ILE:HG21	2.53	0.47
1:Hj:91:ILE:HG21	1:Gq:35:LEU:HD23	1.93	0.47
2:Xh:820:SER:HB2	1:Di:79:HIS:ND1	2.28	0.47
2:Xk:713:ILE:CG2	1:Hr:80:ILE:CD1	2.91	0.47
3:Pm:19:MET:CE	3:Pm:24:LEU:HD21	2.45	0.47
1:En:11:MET:HG2	1:En:49:LEU:HD23	1.96	0.47
1:Ap:7:ILE:HD13	1:DI:32:GLU:HG3	1.93	0.47
1:Et:27:MET:HE1	1:Et:48:VAL:HG12	1.96	0.47
2:Xy:788:GLU:HG3	1:Cw:82:ALA:H	1.79	0.47
3:Py:10:LEU:HG	3:Py:37:VAL:HG21	1.96	0.47
2:XA:841:PRO:HG3	1:Fz:69:GLU:HG2	1.96	0.47
1:BC:27:MET:HE1	1:BC:48:VAL:HG22	1.95	0.47
1:BF:88:VAL:HG21	1:FF:25:ASP:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:41:VAL:HB	1:CF:45:TYR:HB2	1.96	0.47
1:HI:27:MET:HG2	1:HI:60:ALA:O	2.14	0.47
1:BK:62:ARG:HB3	3:PK:21:HIS:CG	2.49	0.47
1:GK:35:LEU:HD11	1:GK:48:VAL:CG1	2.37	0.47
1:BP:88:VAL:HG21	1:FP:25:ASP:HA	1.97	0.47
2:XP:841:PRO:HG3	1:FO:69:GLU:HG2	1.96	0.47
1:BR:27:MET:HE1	1:BR:48:VAL:HG22	1.95	0.47
1:BU:88:VAL:HG21	1:FU:25:ASP:HA	1.97	0.47
3:PT:3:ILE:HG23	3:PT:77:ILE:HD13	1.95	0.47
3:PV:19:MET:CE	3:PV:24:LEU:HD21	2.45	0.47
1:H5:80:ILE:CD1	2:Xd:713:ILE:CG2	2.92	0.47
3:P3:19:MET:CE	3:P3:24:LEU:HD21	2.45	0.47
1:F4:24:ALA:HB2	1:F4:48:VAL:HG21	1.94	0.47
2:X6:818:ASN:HA	2:X6:819:PRO:HD3	1.80	0.47
1:Ge:23:ALA:O	1:Ge:27:MET:HG3	2.15	0.47
2:Xe:714:THR:OG1	1:HE:79:HIS:ND1	1.87	0.47
1:Fd:41:VAL:HB	1:Fd:45:TYR:HB2	1.96	0.47
1:Gg:35:LEU:CD2	1:HU:91:ILE:HD13	2.44	0.47
1:Hg:80:ILE:CD1	2:XJ:713:ILE:HG21	2.44	0.47
1:Gf:21:ILE:HD13	1:HJ:92:LEU:CD2	2.44	0.47
1:Ej:27:MET:HE1	1:Ej:48:VAL:HG12	1.96	0.47
1:Ch:35:LEU:HD11	1:Ch:48:VAL:HG13	1.95	0.47
1:Bs:35:LEU:HD21	1:Es:91:ILE:HD13	1.97	0.47
2:Xv:841:PRO:HG3	1:Fu:69:GLU:HG2	1.96	0.47
2:Xx:713:ILE:CG2	1:HM:80:ILE:HD12	2.45	0.47
1:FA:94:LYS:HE3	1:FA:94:LYS:HB2	1.78	0.47
1:FC:41:VAL:HB	1:FC:45:TYR:HB2	1.96	0.47
1:GI:23:ALA:O	1:GI:27:MET:HG3	2.15	0.47
1:BG:27:MET:HE1	1:BG:48:VAL:HG12	1.96	0.47
1:BK:11:MET:HE3	1:BK:79:HIS:HB3	1.96	0.47
1:HK:15:ARG:HG3	1:HK:76:VAL:HG23	1.96	0.47
2:XN:788:GLU:HG3	1:CL:82:ALA:H	1.79	0.47
1:BP:11:MET:HE3	1:BP:79:HIS:HB3	1.96	0.47
2:XS:788:GLU:HG3	1:CQ:82:ALA:H	1.79	0.47
1:ET:9:LEU:HD11	1:ET:49:LEU:HD23	1.95	0.47
1:GW:25:ASP:HA	1:HO:88:VAL:CG2	2.41	0.47
1:B4:35:LEU:HD21	1:E4:91:ILE:HD13	1.97	0.47
1:B9:35:LEU:HD21	1:E9:91:ILE:HD13	1.97	0.47
1:D9:79:HIS:ND1	2:X8:820:SER:HB2	2.28	0.47
1:Bb:20:ALA:HB1	1:Bb:48:VAL:CG2	2.45	0.47
1:Db:73:ASP:HA	2:Xd:826:ARG:HE	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ee:27:MET:HE1	1:Ee:48:VAL:HG12	1.96	0.47
3:Pd:3:ILE:HG23	3:Pd:77:ILE:HD13	1.95	0.47
1:Bg:88:VAL:HG21	1:Fg:25:ASP:HA	1.97	0.47
1:Bi:11:MET:HE3	1:Bi:11:MET:HB2	1.76	0.47
1:Bl:20:ALA:HB1	1:Bl:48:VAL:CG2	2.45	0.47
1:Ak:62:ARG:HA	2:Xk:724:ILE:HD11	1.96	0.47
3:Po:10:LEU:HG	3:Po:37:VAL:HG21	1.96	0.47
1:Bm:27:MET:HE1	1:Bm:48:VAL:HG12	1.96	0.47
1:Bn:27:MET:HE1	1:Bn:48:VAL:HG22	1.95	0.47
1:Fh:41:VAL:HB	1:Fh:45:TYR:HB2	1.96	0.47
1:Dq:57:VAL:HG12	1:Dq:80:ILE:HG23	1.97	0.47
3:Pr:19:MET:CE	3:Pr:24:LEU:HD21	2.45	0.47
1:Es:11:MET:HG2	1:Es:49:LEU:HD23	1.96	0.47
1:Bv:88:VAL:HG21	1:Fv:25:ASP:HA	1.97	0.47
1:Fw:27:MET:HE1	1:Fw:48:VAL:HG12	1.95	0.47
1:BB:27:MET:HE1	1:BB:48:VAL:HG12	1.96	0.47
1:GH:25:ASP:CA	1:Hh:88:VAL:HG21	2.41	0.47
1:BK:20:ALA:HB1	1:BK:48:VAL:CG2	2.45	0.47
3:PJ:3:ILE:HG23	3:PJ:77:ILE:HD13	1.95	0.47
1:HN:27:MET:HG2	1:HN:60:ALA:O	2.14	0.47
1:GS:11:MET:HE3	1:GS:79:HIS:HB3	1.96	0.47
1:BU:20:ALA:HB1	1:BU:48:VAL:CG2	2.45	0.47
1:BU:62:ARG:HB3	3:PU:21:HIS:CG	2.49	0.47
1:CU:41:VAL:HB	1:CU:45:TYR:HB2	1.96	0.47
1:DU:57:VAL:HG12	1:DU:80:ILE:HG23	1.97	0.47
1:BV:27:MET:HE1	1:BV:48:VAL:HG12	1.96	0.47
1:B2:20:ALA:HB1	1:B2:48:VAL:CG2	2.45	0.47
1:D3:62:ARG:NH1	2:X7:729:GLU:HA	2.17	0.47
1:B4:27:MET:HE1	1:B4:48:VAL:HG22	1.95	0.47
1:A7:94:LYS:HB3	1:A7:94:LYS:HE2	1.64	0.47
1:D7:57:VAL:HG12	1:D7:80:ILE:HG23	1.97	0.47
1:A6:7:ILE:HG12	1:Dc:32:GLU:OE2	2.15	0.47
1:H0:27:MET:HG2	1:H0:60:ALA:O	2.14	0.47
1:Db:41:VAL:HB	1:Db:45:TYR:HB2	1.96	0.47
1:Ad:11:MET:HB3	1:Dd:18:VAL:HG22	1.97	0.47
1:Bd:35:LEU:HD21	1:Ed:91:ILE:HD13	1.97	0.47
1:Dg:57:VAL:HG12	1:Dg:80:ILE:HG23	1.97	0.47
2:Xg:825:ALA:HB3	1:Df:15:ARG:HH21	1.79	0.47
1:El:27:MET:HE1	1:El:48:VAL:HG12	1.97	0.47
1:Dq:41:VAL:HB	1:Dq:45:TYR:HB2	1.96	0.47
1:Ct:41:VAL:HB	1:Ct:45:TYR:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cr:35:LEU:HD11	1:Cr:48:VAL:HG13	1.95	0.47
1:Dr:9:LEU:HD11	1:Dr:49:LEU:HD23	1.96	0.47
3:Ps:3:ILE:HG23	3:Ps:77:ILE:HD13	1.95	0.47
1:Hx:80:ILE:O	2:XM:716:PRO:HD3	2.14	0.47
3:Px:3:ILE:HG23	3:Px:77:ILE:HD13	1.95	0.47
1:BA:88:VAL:HG21	1:FA:25:ASP:HA	1.97	0.47
1:CA:41:VAL:HB	1:CA:45:TYR:HB2	1.96	0.47
1:DA:73:ASP:HA	2:XC:826:ARG:HE	1.78	0.47
1:FB:27:MET:HE1	1:FB:48:VAL:HG12	1.96	0.47
1:DF:41:VAL:HB	1:DF:45:TYR:HB2	1.96	0.47
1:HE:9:LEU:HD11	1:HE:49:LEU:HD23	1.96	0.47
1:GM:25:ASP:HA	1:HP:88:VAL:CG2	2.44	0.47
2:XU:841:PRO:HG3	1:FT:69:GLU:HG2	1.96	0.47
1:AT:62:ARG:HA	2:XT:724:ILE:HD11	1.96	0.47
3:PX:3:ILE:HG23	3:PX:77:ILE:CD1	2.45	0.47
2:Xc:790:LYS:HE2	2:Xc:790:LYS:HB2	1.45	0.47
1:H2:15:ARG:HG3	1:H2:76:VAL:HG23	1.96	0.47
2:X2:718:MET:HE3	2:X2:718:MET:HB3	1.65	0.47
1:A1:7:ILE:CD1	1:Dm:32:GLU:OE2	2.63	0.47
3:P1:3:ILE:HG23	3:P1:77:ILE:HD13	1.95	0.47
1:G3:24:ALA:HA	1:G3:27:MET:HE2	1.97	0.47
1:A4:11:MET:HB3	1:D4:18:VAL:HG22	1.97	0.47
1:B7:20:ALA:HB1	1:B7:48:VAL:CG2	2.45	0.47
2:X7:841:PRO:HG3	1:F6:69:GLU:HG2	1.96	0.47
1:B0:94:LYS:HA	1:B0:94:LYS:HD3	1.75	0.47
1:G0:23:ALA:O	1:G0:27:MET:HG3	2.15	0.47
1:B8:27:MET:HE1	1:B8:48:VAL:HG12	1.96	0.47
1:C8:35:LEU:HD11	1:C8:48:VAL:HG13	1.95	0.47
1:F8:27:MET:HE1	1:F8:48:VAL:HG12	1.96	0.47
1:E9:11:MET:HG2	1:E9:49:LEU:HD23	1.96	0.47
1:H9:80:ILE:HD12	2:XQ:713:ILE:CG2	2.44	0.47
1:Db:57:VAL:HG12	1:Db:80:ILE:HG23	1.97	0.47
1:Hb:15:ARG:HG3	1:Hb:76:VAL:HG23	1.96	0.47
1:Ce:58:ASN:HA	1:Ce:80:ILE:HD11	1.96	0.47
1:Ge:11:MET:HE3	1:Ge:79:HIS:HB3	1.96	0.47
1:Bg:20:ALA:HB1	1:Bg:48:VAL:CG2	2.45	0.47
2:Xf:825:ALA:HB3	1:Dj:15:ARG:HE	1.79	0.47
1:Fj:61:VAL:HG12	2:Xj:795:ILE:HD12	1.97	0.47
1:Gh:24:ALA:HA	1:Gh:27:MET:HE2	1.97	0.47
3:Ph:19:MET:CE	3:Ph:24:LEU:HD21	2.45	0.47
1:Bi:27:MET:HE1	1:Bi:48:VAL:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Gi:96:PRO:HB2	1:Hi:91:ILE:HG22	1.96	0.47
3:Pi:3:ILE:HG23	3:Pi:77:ILE:HD13	1.95	0.47
1:Bl:11:MET:HE3	1:Bl:79:HIS:HB3	1.96	0.47
1:Gl:25:ASP:CA	1:HT:88:VAL:HG21	2.40	0.47
1:Cm:35:LEU:HD11	1:Cm:48:VAL:HG13	1.96	0.47
1:An:53:GLU:OE1	1:HT:53:GLU:HG3	2.14	0.47
1:Bq:20:ALA:HB1	1:Bq:48:VAL:CG2	2.45	0.47
1:Bq:62:ARG:HB3	3:Pq:21:HIS:CG	2.49	0.47
1:Bq:88:VAL:HG21	1:Fq:25:ASP:HA	1.97	0.47
2:Xq:825:ALA:HB3	1:Dp:15:ARG:HH21	1.79	0.47
1:Ap:62:ARG:HA	2:Xp:724:ILE:HD11	1.96	0.47
2:Xp:825:ALA:HB3	1:Dt:15:ARG:HE	1.79	0.47
1:Gt:35:LEU:HD21	1:Hi:91:ILE:CG2	2.29	0.47
3:Pt:10:LEU:HG	3:Pt:37:VAL:HG21	1.96	0.47
1:Ff:41:VAL:HB	1:Ff:45:TYR:HB2	1.96	0.47
1:Gs:77:ALA:HB2	1:Hs:72:GLY:HA2	1.95	0.47
1:Bv:20:ALA:HB1	1:Bv:48:VAL:CG2	2.45	0.47
1:Cv:41:VAL:HB	1:Cv:45:TYR:HB2	1.96	0.47
2:Xv:825:ALA:HB3	1:Du:15:ARG:HH21	1.79	0.47
1:Bw:27:MET:HE1	1:Bw:48:VAL:HG12	1.96	0.47
1:Ex:11:MET:HG2	1:Ex:49:LEU:HD23	1.96	0.47
2:Xx:713:ILE:CG2	1:HM:80:ILE:CD1	2.93	0.47
1:Az:7:ILE:HG12	1:DG:32:GLU:OE2	2.15	0.47
1:ED:27:MET:HE1	1:ED:48:VAL:HG12	1.97	0.47
1:CB:35:LEU:HD11	1:CB:48:VAL:HG13	1.95	0.47
1:BC:35:LEU:HD21	1:EC:91:ILE:HD13	1.97	0.47
1:HC:91:ILE:CG2	1:GJ:35:LEU:HD23	2.44	0.47
2:XF:841:PRO:HG3	1:FE:69:GLU:HG2	1.96	0.47
3:PE:3:ILE:HG23	3:PE:77:ILE:HD13	1.95	0.47
1:CK:15:ARG:NH1	1:CK:76:VAL:HG22	2.28	0.47
2:XN:825:ALA:HB1	1:DL:15:ARG:HE	1.78	0.47
3:PN:10:LEU:HG	3:PN:37:VAL:HG21	1.96	0.47
1:FL:14:THR:HB	1:FL:19:PRO:HB2	1.97	0.47
1:AP:20:ALA:HB1	1:AP:48:VAL:CG2	2.45	0.47
1:BP:62:ARG:HB3	3:PP:21:HIS:CG	2.49	0.47
1:DP:57:VAL:HG12	1:DP:80:ILE:HG23	1.97	0.47
3:PS:3:ILE:HG23	3:PS:77:ILE:CD1	2.45	0.47
3:PQ:19:MET:CE	3:PQ:24:LEU:HD21	2.45	0.47
1:FU:94:LYS:HB2	1:FU:94:LYS:HE3	1.78	0.47
1:HX:27:MET:HG2	1:HX:60:ALA:O	2.14	0.47
1:Hu:9:LEU:HD11	1:Hu:49:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E2:27:MET:HE1	1:E2:48:VAL:HG12	1.97	0.47
1:C5:58:ASN:HA	1:C5:80:ILE:CD1	2.45	0.47
3:P5:3:ILE:HG23	3:P5:77:ILE:CD1	2.45	0.47
1:B7:11:MET:HE3	1:B7:79:HIS:HB3	1.96	0.47
1:F0:61:VAL:HG12	2:X0:795:ILE:HD12	1.97	0.47
3:P0:10:LEU:HG	3:P0:37:VAL:HG21	1.96	0.47
1:B9:27:MET:HE1	1:B9:48:VAL:HG22	1.95	0.47
1:Bb:11:MET:HE3	1:Bb:79:HIS:HB3	1.96	0.47
1:Bb:62:ARG:HB3	3:Pb:21:HIS:CG	2.49	0.47
1:Cb:41:VAL:HB	1:Cb:45:TYR:HB2	1.96	0.47
1:Ge:35:LEU:HD23	1:Ht:91:ILE:HG23	1.96	0.47
1:He:79:HIS:CE1	1:GI:22:GLU:OE2	2.62	0.47
2:Xe:788:GLU:HG3	1:Cc:82:ALA:H	1.79	0.47
1:Ag:20:ALA:HB1	1:Ag:48:VAL:CG2	2.45	0.47
1:Fh:14:THR:HB	1:Fh:19:PRO:HB2	1.97	0.47
1:Dl:57:VAL:HG12	1:Dl:80:ILE:HG23	1.97	0.47
3:Po:3:ILE:HG23	3:Po:77:ILE:CD1	2.45	0.47
3:Ps:30:LYS:HB2	3:Ps:30:LYS:HE3	1.74	0.47
1:Ev:27:MET:HE1	1:Ev:48:VAL:HG12	1.97	0.47
1:Hv:62:ARG:HA	2:XR:713:ILE:CD1	2.41	0.47
1:Ax:11:MET:HB3	1:Dx:18:VAL:HG22	1.97	0.47
1:Fx:41:VAL:HB	1:Fx:45:TYR:HB2	1.96	0.47
1:DA:57:VAL:HG12	1:DA:80:ILE:HG23	1.97	0.47
1:GD:23:ALA:O	1:GD:27:MET:HG3	2.15	0.47
1:GC:72:GLY:CA	1:Hf:77:ALA:HB2	2.43	0.47
1:EI:27:MET:HE1	1:EI:48:VAL:HG12	1.97	0.47
1:FH:41:VAL:HB	1:FH:45:TYR:HB2	1.96	0.47
1:EM:11:MET:HG2	1:EM:49:LEU:HD23	1.96	0.47
1:GM:96:PRO:HB2	1:HP:91:ILE:HG22	1.96	0.47
1:AO:7:ILE:HG12	1:DV:32:GLU:OE2	2.15	0.47
1:CS:58:ASN:HA	1:CS:80:ILE:HD11	1.96	0.47
1:AR:77:ALA:HB2	1:DR:72:GLY:CA	2.44	0.47
1:CX:58:ASN:HA	1:CX:80:ILE:CD1	2.45	0.47
3:PX:10:LEU:HG	3:PX:37:VAL:HG21	1.96	0.47
1:BW:35:LEU:HD21	1:EW:91:ILE:HD13	1.97	0.47
1:Hx:9:LEU:HD11	1:Hx:49:LEU:HD23	1.96	0.47
1:HO:9:LEU:HD11	1:HO:49:LEU:HD23	1.96	0.47
1:D2:57:VAL:HG12	1:D2:80:ILE:HG23	1.97	0.47
3:P5:37:VAL:HB	3:P3:51:LEU:HD11	1.97	0.47
1:D7:15:ARG:HE	2:X9:825:ALA:CB	2.28	0.47
1:A6:62:ARG:HA	2:X6:724:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X0:714:THR:OG1	1:HF:79:HIS:ND1	1.86	0.47
2:X0:788:GLU:HG3	1:C8:82:ALA:H	1.79	0.47
1:E9:57:VAL:HG12	1:E9:80:ILE:HG23	1.97	0.47
1:Hb:11:MET:HE3	1:Hb:11:MET:HB2	1.89	0.47
2:Xb:825:ALA:HB3	1:Da:15:ARG:HH21	1.79	0.47
1:Ce:58:ASN:HA	1:Ce:80:ILE:CD1	2.45	0.47
1:Dc:9:LEU:HD11	1:Dc:49:LEU:HD23	1.96	0.47
1:Gc:21:ILE:HD13	1:HE:92:LEU:CD2	2.44	0.47
1:Dg:15:ARG:HE	2:Xi:825:ALA:CB	2.28	0.47
1:Hg:15:ARG:HG3	1:Hg:76:VAL:HG23	1.96	0.47
1:Bh:27:MET:HE1	1:Bh:48:VAL:HG12	1.96	0.47
1:Hi:15:ARG:HG3	1:Hi:76:VAL:HG23	1.96	0.47
1:Co:58:ASN:HA	1:Co:80:ILE:CD1	2.45	0.47
1:Co:58:ASN:HA	1:Co:80:ILE:HD11	1.96	0.47
1:Ho:27:MET:HG2	1:Ho:60:ALA:O	2.14	0.47
1:Dq:15:ARG:HE	2:Xs:825:ALA:CB	2.28	0.47
1:Gp:35:LEU:HD23	1:HD:91:ILE:CG2	2.45	0.47
1:Gt:23:ALA:O	1:Gt:27:MET:HG3	2.15	0.47
2:Xv:714:THR:OG1	1:HR:79:HIS:ND1	2.28	0.47
1:Gy:23:ALA:O	1:Gy:27:MET:HG3	2.15	0.47
2:XC:713:ILE:CD1	1:HK:62:ARG:HA	2.41	0.47
1:BF:20:ALA:HB1	1:BF:48:VAL:CG2	2.45	0.47
2:XI:825:ALA:HB1	1:DG:15:ARG:HE	1.78	0.47
3:PI:3:ILE:HG23	3:PI:77:ILE:CD1	2.45	0.47
1:EH:11:MET:HG2	1:EH:49:LEU:HD23	1.96	0.47
1:DK:15:ARG:HE	2:XM:825:ALA:CB	2.28	0.47
1:CN:94:LYS:HE3	1:CN:94:LYS:HB3	1.73	0.47
3:PN:3:ILE:HG23	3:PN:77:ILE:CD1	2.45	0.47
3:PL:19:MET:CE	3:PL:24:LEU:HD21	2.45	0.47
2:XO:818:ASN:HA	2:XO:819:PRO:HD3	1.81	0.47
2:XX:825:ALA:HB1	1:DV:15:ARG:HE	1.78	0.47
1:FV:14:THR:HB	1:FV:19:PRO:HB2	1.97	0.47
1:FW:23:ALA:O	1:FW:27:MET:HG3	2.13	0.47
1:E4:57:VAL:HG12	1:E4:80:ILE:HG23	1.97	0.47
1:H0:92:LEU:HD21	1:GE:21:ILE:HD13	1.95	0.47
1:F8:14:THR:HB	1:F8:19:PRO:HB2	1.97	0.47
1:Aa:7:ILE:HD13	1:Dt:32:GLU:HG3	1.96	0.47
1:Ed:11:MET:HG2	1:Ed:49:LEU:HD23	1.96	0.47
1:Hg:79:HIS:CE1	2:XJ:714:THR:OG1	2.54	0.47
1:Hj:91:ILE:CG2	1:Gq:35:LEU:CD2	2.90	0.47
3:Pj:16:ILE:HG12	3:Ph:74:ILE:HB	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EI:57:VAL:HG12	1:EI:80:ILE:HG23	1.97	0.47
1:CT:58:ASN:HA	1:CT:80:ILE:CD1	2.45	0.47
3:PT:16:ILE:HG12	3:PR:74:ILE:HB	1.97	0.47
1:DV:41:VAL:HB	1:DV:45:TYR:HB2	1.96	0.47
2:XY:825:ALA:HB1	1:DW:15:ARG:HE	1.78	0.47
1:BX:35:LEU:HD21	1:EX:91:ILE:HD13	1.97	0.47
1:EX:57:VAL:HG12	1:EX:80:ILE:HG23	1.97	0.47
1:CD:58:ASN:HA	1:CD:80:ILE:HD11	1.96	0.47
1:HC:91:ILE:HG21	1:GJ:35:LEU:HD23	1.96	0.47
1:EE:11:MET:HB2	1:EE:11:MET:HE3	1.68	0.47
1:CI:58:ASN:HA	1:CI:80:ILE:CD1	2.45	0.47
1:GI:11:MET:HE3	1:GI:79:HIS:HB3	1.96	0.47
1:EH:57:VAL:HG12	1:EH:80:ILE:HG23	1.97	0.47
1:GL:24:ALA:HA	1:GL:27:MET:HE2	1.97	0.47
1:BP:20:ALA:HB1	1:BP:48:VAL:CG2	2.45	0.47
1:DP:41:VAL:HB	1:DP:45:TYR:HB2	1.96	0.47
1:GS:23:ALA:O	1:GS:27:MET:HG3	2.15	0.47
1:FR:23:ALA:O	1:FR:27:MET:HG3	2.14	0.47
2:XU:825:ALA:HB3	1:DT:15:ARG:HH21	1.79	0.47
1:H1:9:LEU:HD11	1:H1:49:LEU:HD23	1.96	0.47
2:X8:714:THR:HA	2:X8:718:MET:HG3	1.96	0.47
1:A7:20:ALA:HB1	1:A7:48:VAL:CG2	2.45	0.46
1:G7:25:ASP:CA	1:HQ:88:VAL:HG21	2.42	0.46
1:H0:11:MET:HB3	1:GE:18:VAL:HG22	1.96	0.46
1:D8:32:GLU:OE2	1:Au:7:ILE:HG12	2.15	0.46
1:G8:24:ALA:HA	1:G8:27:MET:HE2	1.97	0.46
1:Ha:9:LEU:HD11	1:Ha:49:LEU:HD23	1.96	0.46
2:Xj:788:GLU:HG3	1:Ch:82:ALA:H	1.79	0.46
3:Pj:37:VAL:HB	3:Ph:51:LEU:HD11	1.97	0.46
1:Ak:7:ILE:HG12	1:Dr:32:GLU:OE2	2.15	0.46
1:DV:57:VAL:HG12	1:DV:80:ILE:HG23	1.97	0.46
1:Cy:58:ASN:HA	1:Cy:80:ILE:CD1	2.45	0.46
3:Py:16:ILE:HG12	3:Pw:74:ILE:HB	1.97	0.46
1:Gw:24:ALA:HA	1:Gw:27:MET:HE2	1.97	0.46
1:Gx:96:PRO:HB2	1:HA:91:ILE:HG22	1.96	0.46
1:FD:61:VAL:HG12	2:XD:795:ILE:HD12	1.97	0.46
1:AF:20:ALA:HB1	1:AF:48:VAL:CG2	2.45	0.46
1:DF:15:ARG:HE	2:XH:825:ALA:CB	2.28	0.46
1:FE:27:MET:HG2	1:FE:60:ALA:O	2.16	0.46
1:CI:53:GLU:HG2	1:CI:54:THR:N	2.31	0.46
2:XI:788:GLU:HG3	1:CG:82:ALA:H	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:62:ARG:HA	2:XO:724:ILE:HD11	1.96	0.46
1:HR:7:ILE:H	1:HR:7:ILE:HG13	1.57	0.46
1:A2:20:ALA:HB1	1:A2:48:VAL:CG2	2.45	0.46
1:B2:88:VAL:HG21	1:F2:25:ASP:HA	1.97	0.46
2:X2:825:ALA:HB3	1:D1:15:ARG:HH21	1.79	0.46
1:B3:27:MET:HE1	1:B3:48:VAL:HG12	1.96	0.46
1:F6:27:MET:HG2	1:F6:60:ALA:O	2.16	0.46
1:E0:27:MET:HG2	1:E0:60:ALA:O	2.16	0.46
3:P8:19:MET:CE	3:P8:24:LEU:HD21	2.45	0.46
1:Ca:58:ASN:O	1:Ca:62:ARG:HG3	2.16	0.46
1:Fe:61:VAL:HG12	2:Xe:795:ILE:HD12	1.97	0.46
3:Pe:16:ILE:HG12	3:Pc:74:ILE:HB	1.98	0.46
1:Fc:11:MET:HE3	1:Fc:11:MET:HB2	1.82	0.46
1:Fc:41:VAL:HB	1:Fc:45:TYR:HB2	1.98	0.46
3:Pj:3:ILE:HG23	3:Pj:77:ILE:CD1	2.45	0.46
1:Al:20:ALA:HB1	1:Al:48:VAL:CG2	2.45	0.46
1:Et:27:MET:HG2	1:Et:60:ALA:O	2.16	0.46
2:Xt:821:MET:HB2	2:Xt:821:MET:HE3	1.68	0.46
3:Py:37:VAL:HB	3:Pw:51:LEU:HD11	1.97	0.46
2:Xw:790:LYS:HE2	2:Xw:790:LYS:HB2	1.45	0.46
3:Pw:19:MET:CE	3:Pw:24:LEU:HD21	2.45	0.46
2:XA:825:ALA:HB1	1:Dz:73:ASP:O	2.16	0.46
1:Az:62:ARG:HA	2:Xz:724:ILE:HD11	1.96	0.46
1:EC:57:VAL:HG12	1:EC:80:ILE:HG23	1.97	0.46
1:GF:35:LEU:HD11	1:GF:48:VAL:CG1	2.37	0.46
1:BI:14:THR:HB	1:BI:19:PRO:HB2	1.98	0.46
3:PI:16:ILE:HG12	3:PG:74:ILE:HB	1.97	0.46
1:BH:35:LEU:HD21	1:EH:91:ILE:HD13	1.97	0.46
2:XK:773:LEU:HD21	2:XM:841:PRO:HD3	1.97	0.46
2:XK:825:ALA:HB3	1:DJ:15:ARG:HH21	1.79	0.46
1:CJ:58:ASN:O	1:CJ:62:ARG:HG3	2.16	0.46
1:BM:35:LEU:HD21	1:EM:91:ILE:HD13	1.97	0.46
1:CP:41:VAL:HB	1:CP:45:TYR:HB2	1.96	0.46
3:PS:37:VAL:HB	3:PQ:51:LEU:HD11	1.97	0.46
1:FQ:41:VAL:HB	1:FQ:45:TYR:HB2	1.98	0.46
1:GQ:24:ALA:HA	1:GQ:27:MET:HE2	1.97	0.46
1:FT:27:MET:HG2	1:FT:60:ALA:O	2.16	0.46
1:CX:58:ASN:HA	1:CX:80:ILE:HD11	1.96	0.46
1:FX:61:VAL:HG12	2:XX:795:ILE:HD12	1.97	0.46
1:GX:23:ALA:O	1:GX:27:MET:HG3	2.15	0.46
2:X2:841:PRO:HG3	1:F1:69:GLU:HG2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A1:62:ARG:HA	2:X1:724:ILE:HD11	1.96	0.46
1:G1:18:VAL:HG22	1:HX:11:MET:HB3	1.96	0.46
1:G5:23:ALA:O	1:G5:27:MET:HG3	2.15	0.46
3:P5:10:LEU:HG	3:P5:37:VAL:HG21	1.96	0.46
2:X7:818:ASN:HA	2:X7:819:PRO:HD3	1.82	0.46
2:Xb:825:ALA:HB1	1:Da:73:ASP:O	2.16	0.46
3:Pe:3:ILE:HG23	3:Pe:77:ILE:CD1	2.45	0.46
1:Gc:25:ASP:HA	1:HE:88:VAL:CG2	2.42	0.46
1:Eg:27:MET:HE1	1:Eg:48:VAL:HG12	1.97	0.46
1:Cj:53:GLU:HG2	1:Cj:54:THR:N	2.30	0.46
1:Ej:27:MET:HG2	1:Ej:60:ALA:O	2.16	0.46
1:Dh:9:LEU:HD11	1:Dh:49:LEU:HD23	1.96	0.46
1:Fi:41:VAL:HB	1:Fi:45:TYR:HB2	1.96	0.46
1:Fm:14:THR:HB	1:Fm:19:PRO:HB2	1.97	0.46
1:An:11:MET:HB3	1:Dn:18:VAL:HG22	1.97	0.46
1:Av:20:ALA:HB1	1:Av:48:VAL:CG2	2.45	0.46
1:Fu:27:MET:HG2	1:Fu:60:ALA:O	2.16	0.46
1:Dw:9:LEU:HD11	1:Dw:49:LEU:HD23	1.96	0.46
1:Fw:41:VAL:HB	1:Fw:45:TYR:HB2	1.98	0.46
1:DA:15:ARG:HE	2:XC:825:ALA:CB	2.28	0.46
1:DA:41:VAL:HB	1:DA:45:TYR:HB2	1.96	0.46
2:XA:818:ASN:HA	2:XA:819:PRO:HD3	1.82	0.46
2:XF:773:LEU:HD21	2:XH:841:PRO:HD3	1.98	0.46
1:CN:58:ASN:HA	1:CN:80:ILE:CD1	2.45	0.46
1:EN:27:MET:HE1	1:EN:48:VAL:HG12	1.96	0.46
1:GN:23:ALA:O	1:GN:27:MET:HG3	2.15	0.46
2:XP:825:ALA:HB1	1:DO:73:ASP:O	2.16	0.46
1:BR:35:LEU:HD21	1:ER:91:ILE:HD13	1.97	0.46
1:DU:41:VAL:HB	1:DU:45:TYR:HB2	1.96	0.46
1:BX:14:THR:HB	1:BX:19:PRO:HB2	1.98	0.46
1:CX:94:LYS:HE3	1:CX:94:LYS:HB3	1.73	0.46
2:X2:773:LEU:HD21	2:X4:841:PRO:HD3	1.97	0.46
1:C5:58:ASN:HA	1:C5:80:ILE:HD11	1.96	0.46
1:G5:24:ALA:HB2	1:G5:48:VAL:HG21	1.97	0.46
1:H4:80:ILE:HD11	2:XS:713:ILE:HG21	1.97	0.46
1:D7:41:VAL:HB	1:D7:45:TYR:HB2	1.96	0.46
1:C0:58:ASN:HA	1:C0:80:ILE:CD1	2.45	0.46
3:P0:37:VAL:HB	3:P8:51:LEU:HD11	1.97	0.46
1:A9:11:MET:HB3	1:D9:18:VAL:HG22	1.97	0.46
1:F9:41:VAL:HB	1:F9:45:TYR:HB2	1.96	0.46
1:G9:72:GLY:CA	1:Hu:77:ALA:HB2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Eb:27:MET:HE1	1:Eb:48:VAL:HG12	1.97	0.46
2:Xg:841:PRO:HG3	1:Ff:69:GLU:HG2	1.96	0.46
1:Ai:11:MET:HB3	1:Di:18:VAL:HG22	1.97	0.46
1:Ei:11:MET:HG2	1:Ei:49:LEU:HD23	1.96	0.46
1:An:77:ALA:HB2	1:Dn:72:GLY:CA	2.44	0.46
1:Aq:20:ALA:HB1	1:Aq:48:VAL:CG2	2.45	0.46
2:Xq:773:LEU:HD21	2:Xs:841:PRO:HD3	1.98	0.46
1:Ct:58:ASN:HA	1:Ct:80:ILE:HD11	1.97	0.46
1:Cu:58:ASN:O	1:Cu:62:ARG:HG3	2.16	0.46
1:BA:20:ALA:HB1	1:BA:48:VAL:CG2	2.45	0.46
1:Cz:58:ASN:O	1:Cz:62:ARG:HG3	2.16	0.46
3:PD:3:ILE:HG23	3:PD:77:ILE:CD1	2.45	0.46
3:PD:37:VAL:HB	3:PB:51:LEU:HD11	1.97	0.46
1:FB:41:VAL:HB	1:FB:45:TYR:HB2	1.98	0.46
1:BI:94:LYS:HA	1:BI:94:LYS:HD3	1.75	0.46
3:PG:19:MET:CE	3:PG:24:LEU:HD21	2.45	0.46
1:FJ:27:MET:HG2	1:FJ:60:ALA:O	2.16	0.46
2:XJ:790:LYS:HB2	2:XJ:790:LYS:HE2	1.76	0.46
1:DL:9:LEU:HD11	1:DL:49:LEU:HD23	1.96	0.46
1:CS:58:ASN:HA	1:CS:80:ILE:CD1	2.45	0.46
1:GS:24:ALA:HB2	1:GS:48:VAL:HG21	1.97	0.46
1:FQ:14:THR:HB	1:FQ:19:PRO:HB2	1.97	0.46
3:PQ:37:VAL:HG23	3:PR:3:ILE:HD11	1.98	0.46
1:ER:12:ILE:HG23	1:ER:75:LEU:HD12	1.98	0.46
1:AW:11:MET:HB3	1:DW:18:VAL:HG22	1.97	0.46
1:EW:11:MET:HG2	1:EW:49:LEU:HD23	1.96	0.46
1:EW:57:VAL:HG12	1:EW:80:ILE:HG23	1.97	0.46
1:C2:41:VAL:HB	1:C2:45:TYR:HB2	1.96	0.46
3:P5:16:ILE:HG12	3:P3:74:ILE:HB	1.98	0.46
1:C0:53:GLU:HG2	1:C0:54:THR:N	2.31	0.46
1:Ee:27:MET:HG2	1:Ee:60:ALA:O	2.16	0.46
1:Gj:23:ALA:O	1:Gj:27:MET:HG3	2.15	0.46
3:Ph:37:VAL:HG23	3:Pi:3:ILE:HD11	1.98	0.46
2:Xl:773:LEU:HD21	2:Xn:841:PRO:HD3	1.98	0.46
1:Ak:7:ILE:HD11	1:Dr:32:GLU:CD	2.36	0.46
1:Fo:61:VAL:HG12	2:Xo:795:ILE:HD12	1.97	0.46
3:Po:16:ILE:HG12	3:Pm:74:ILE:HB	1.97	0.46
1:Dm:9:LEU:HD11	1:Dm:49:LEU:HD23	1.96	0.46
1:En:12:ILE:HG23	1:En:75:LEU:HD12	1.98	0.46
1:Eq:27:MET:HE1	1:Eq:48:VAL:HG12	1.97	0.46
1:Hq:15:ARG:HG3	1:Hq:76:VAL:HG23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xq:841:PRO:HG3	1:Fp:69:GLU:HG2	1.96	0.46
1:As:11:MET:HB3	1:Ds:18:VAL:HG22	1.97	0.46
1:Bv:11:MET:HE3	1:Bv:79:HIS:HB3	1.96	0.46
1:Gy:24:ALA:HB2	1:Gy:48:VAL:HG21	1.97	0.46
2:Xy:713:ILE:HG21	1:HH:80:ILE:HD11	1.98	0.46
1:AA:20:ALA:HB1	1:AA:48:VAL:CG2	2.45	0.46
3:PB:19:MET:CE	3:PB:24:LEU:HD21	2.45	0.46
1:AC:77:ALA:HB2	1:DC:72:GLY:CA	2.44	0.46
1:AH:11:MET:HB3	1:DH:18:VAL:HG22	1.97	0.46
1:AK:20:ALA:HB1	1:AK:48:VAL:CG2	2.45	0.46
1:EN:27:MET:HG2	1:EN:60:ALA:O	2.16	0.46
2:XN:713:ILE:HG21	1:HW:80:ILE:HD11	1.97	0.46
1:EM:12:ILE:HG23	1:EM:75:LEU:HD12	1.98	0.46
1:HP:15:ARG:HG3	1:HP:76:VAL:HG23	1.96	0.46
1:CS:53:GLU:HG2	1:CS:54:THR:N	2.31	0.46
1:AR:11:MET:HB3	1:DR:18:VAL:HG22	1.97	0.46
1:F5:61:VAL:HG12	2:X5:795:ILE:HD12	1.97	0.46
2:X7:773:LEU:HD21	2:X9:841:PRO:HD3	1.98	0.46
3:P0:3:ILE:HG23	3:P0:77:ILE:CD1	2.45	0.46
1:F8:41:VAL:HB	1:F8:45:TYR:HB2	1.98	0.46
1:Fa:27:MET:HG2	1:Fa:60:ALA:O	2.16	0.46
3:Pe:10:LEU:HG	3:Pe:37:VAL:HG21	1.96	0.46
2:Xg:773:LEU:HD21	2:Xi:841:PRO:HD3	1.98	0.46
1:Ef:11:MET:HE3	1:Ef:11:MET:HB2	1.68	0.46
1:Ff:27:MET:HG2	1:Ff:60:ALA:O	2.16	0.46
1:Ei:12:ILE:HG23	1:Ei:75:LEU:HD12	1.98	0.46
1:Eo:27:MET:HG2	1:Eo:60:ALA:O	2.16	0.46
1:Bm:35:LEU:HD21	1:Em:91:ILE:HD13	1.97	0.46
3:Pn:30:LYS:HB2	3:Pn:30:LYS:HE3	1.74	0.46
1:Fp:27:MET:HG2	1:Fp:60:ALA:O	2.16	0.46
3:Pt:3:ILE:HG23	3:Pt:77:ILE:CD1	2.45	0.46
1:Es:57:VAL:HG12	1:Es:80:ILE:HG23	1.97	0.46
1:Dv:15:ARG:HE	2:Xx:825:ALA:CB	2.28	0.46
2:Xv:773:LEU:HD21	2:Xx:841:PRO:HD3	1.97	0.46
2:Xu:841:PRO:HG3	1:Fy:69:GLU:HG2	1.98	0.46
1:Ey:27:MET:HE1	1:Ey:48:VAL:HG12	1.97	0.46
1:Fw:14:THR:HB	1:Fw:19:PRO:HB2	1.97	0.46
1:GB:24:ALA:HA	1:GB:27:MET:HE2	1.97	0.46
1:EC:12:ILE:HG23	1:EC:75:LEU:HD12	1.98	0.46
1:EH:12:ILE:HG23	1:EH:75:LEU:HD12	1.98	0.46
1:CN:53:GLU:HG2	1:CN:54:THR:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EM:57:VAL:HG12	1:EM:80:ILE:HG23	1.97	0.46
1:CO:58:ASN:O	1:CO:62:ARG:HG3	2.16	0.46
1:FO:22:GLU:HG2	1:FO:71:VAL:HG21	1.98	0.46
3:PT:30:LYS:HB2	3:PT:30:LYS:HE3	1.74	0.46
1:EX:27:MET:HE1	1:EX:48:VAL:HG12	1.97	0.46
1:GX:24:ALA:HB2	1:GX:48:VAL:HG21	1.97	0.46
2:XB:714:THR:HA	2:XB:718:MET:HG3	1.97	0.46
1:B1:83:ARG:NH1	1:E5:29:LYS:HA	2.31	0.46
1:H7:15:ARG:HG3	1:H7:76:VAL:HG23	1.96	0.46
1:C6:58:ASN:O	1:C6:62:ARG:HG3	2.16	0.46
1:C9:41:VAL:HB	1:C9:45:TYR:HB2	1.98	0.46
1:Hb:77:ALA:HB2	1:Gm:72:GLY:CA	2.40	0.46
1:Aa:62:ARG:HA	2:Xa:724:ILE:HD11	1.96	0.46
1:Ce:53:GLU:HG2	1:Ce:54:THR:N	2.30	0.46
3:Pe:37:VAL:HB	3:Pc:51:LEU:HD11	1.98	0.46
1:Gc:24:ALA:HA	1:Gc:27:MET:HE2	1.97	0.46
1:Af:7:ILE:CD1	1:DB:32:GLU:OE2	2.64	0.46
1:Cf:58:ASN:O	1:Cf:62:ARG:HG3	2.16	0.46
2:Xf:841:PRO:HG3	1:Fj:69:GLU:HG2	1.98	0.46
1:Gi:25:ASP:HA	1:Hi:88:VAL:CG2	2.44	0.46
3:Po:37:VAL:HB	3:Pm:51:LEU:HD11	1.98	0.46
2:Xp:716:PRO:HD2	1:Hi:80:ILE:O	2.16	0.46
1:Gv:35:LEU:HD11	1:Gv:48:VAL:CG1	2.37	0.46
3:PB:37:VAL:HG23	3:PC:3:ILE:HD11	1.98	0.46
1:AC:11:MET:HB3	1:DC:18:VAL:HG22	1.97	0.46
1:BE:83:ARG:NH1	1:EI:29:LYS:HA	2.31	0.46
1:CE:58:ASN:O	1:CE:62:ARG:HG3	2.16	0.46
1:CI:58:ASN:HA	1:CI:80:ILE:HD11	1.96	0.46
1:DK:57:VAL:HG12	1:DK:80:ILE:HG23	1.97	0.46
2:XK:825:ALA:HB1	1:DJ:73:ASP:O	2.16	0.46
1:BJ:83:ARG:HH12	1:EN:29:LYS:HA	1.81	0.46
1:CN:58:ASN:HA	1:CN:80:ILE:HD11	1.96	0.46
3:PL:37:VAL:HG23	3:PM:3:ILE:HD11	1.98	0.46
1:CR:41:VAL:HB	1:CR:45:TYR:HB2	1.98	0.46
2:XU:825:ALA:HB1	1:DT:73:ASP:O	2.16	0.46
1:CX:53:GLU:HG2	1:CX:54:THR:N	2.31	0.46
2:X1:818:ASN:HA	2:X1:819:PRO:HD3	1.80	0.46
1:E5:27:MET:HG2	1:E5:60:ALA:O	2.16	0.46
1:E6:11:MET:HE3	1:E6:11:MET:HB2	1.68	0.46
1:C0:58:ASN:HA	1:C0:80:ILE:HD11	1.96	0.46
1:G8:41:VAL:HB	1:G8:45:TYR:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X9:716:PRO:HD3	1:HQ:80:ILE:O	2.14	0.46
1:Ab:20:ALA:HB1	1:Ab:48:VAL:CG2	2.45	0.46
1:Ef:11:MET:HE3	1:Ef:79:HIS:HB3	1.98	0.46
1:Cj:58:ASN:HA	1:Cj:80:ILE:HD11	1.96	0.46
1:Fh:41:VAL:HB	1:Fh:45:TYR:HB2	1.98	0.46
1:Go:24:ALA:HB2	1:Go:48:VAL:HG21	1.97	0.46
1:Fm:41:VAL:HB	1:Fm:45:TYR:HB2	1.98	0.46
1:Gm:41:VAL:HB	1:Gm:45:TYR:HB2	1.98	0.46
1:Ft:61:VAL:HG12	2:Xt:795:ILE:HD12	1.97	0.46
1:By:14:THR:HB	1:By:19:PRO:HB2	1.98	0.46
3:Py:3:ILE:HG23	3:Py:77:ILE:CD1	2.45	0.46
1:GA:35:LEU:CD2	1:HK:91:ILE:HD13	2.46	0.46
1:Bz:83:ARG:NH1	1:ED:29:LYS:HA	2.31	0.46
1:GD:24:ALA:HB2	1:GD:48:VAL:HG21	1.97	0.46
1:CF:30:ALA:O	1:GF:82:ALA:HB3	2.16	0.46
2:XF:825:ALA:HB1	1:DE:73:ASP:O	2.16	0.46
1:FG:14:THR:HB	1:FG:19:PRO:HB2	1.97	0.46
1:GG:24:ALA:HA	1:GG:27:MET:HE2	1.97	0.46
1:BK:88:VAL:HG21	1:FK:25:ASP:HA	1.97	0.46
1:CT:58:ASN:O	1:CT:62:ARG:HG3	2.16	0.46
1:CW:41:VAL:HB	1:CW:45:TYR:HB2	1.98	0.46
1:D2:15:ARG:HE	2:X4:825:ALA:CB	2.28	0.46
2:X2:825:ALA:HB1	1:D1:73:ASP:O	2.16	0.46
2:X0:713:ILE:CG2	1:HF:80:ILE:CD1	2.94	0.46
2:X0:825:ALA:HB1	1:D8:15:ARG:HE	1.78	0.46
1:Ge:35:LEU:HD23	1:Ht:91:ILE:CG2	2.45	0.46
1:Aj:62:ARG:HG2	2:Xj:724:ILE:HG13	1.98	0.46
1:Di:11:MET:HE3	1:Di:79:HIS:HB3	1.98	0.46
1:Ek:11:MET:HE3	1:Ek:79:HIS:HB3	1.98	0.46
1:Eo:27:MET:HE1	1:Eo:48:VAL:HG12	1.96	0.46
1:Fr:41:VAL:HB	1:Fr:45:TYR:HB2	1.98	0.46
1:Cu:12:ILE:HB	1:Cu:48:VAL:HG13	1.98	0.46
1:Fy:61:VAL:HG12	2:Xy:795:ILE:HD12	1.97	0.46
1:Ex:12:ILE:HG23	1:Ex:75:LEU:HD12	1.98	0.46
1:Fx:94:LYS:HE3	1:Fx:94:LYS:HB3	1.70	0.46
1:CD:53:GLU:HG2	1:CD:54:THR:N	2.30	0.46
2:XD:821:MET:HB2	2:XD:821:MET:HE3	1.68	0.46
3:PD:16:ILE:HG12	3:PB:74:ILE:HB	1.97	0.46
1:DF:57:VAL:HG12	1:DF:80:ILE:HG23	1.97	0.46
1:EF:27:MET:HE1	1:EF:48:VAL:HG12	1.97	0.46
1:FE:22:GLU:HG2	1:FE:71:VAL:HG21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HN:91:ILE:CG2	1:GU:35:LEU:CD2	2.90	0.46
1:DM:11:MET:HE3	1:DM:79:HIS:HB3	1.98	0.46
1:DP:15:ARG:HE	2:XR:825:ALA:CB	2.28	0.46
1:EP:27:MET:HE1	1:EP:48:VAL:HG12	1.97	0.46
1:BO:83:ARG:NH1	1:ES:29:LYS:HA	2.31	0.46
1:BO:83:ARG:HH12	1:ES:29:LYS:HA	1.81	0.46
1:ES:27:MET:HE1	1:ES:48:VAL:HG12	1.97	0.46
1:AU:20:ALA:HB1	1:AU:48:VAL:CG2	2.45	0.46
1:BV:27:MET:CE	1:BV:48:VAL:HG12	2.46	0.46
1:GV:41:VAL:HB	1:GV:45:TYR:HB2	1.98	0.46
1:Hu:11:MET:HE3	1:Hu:11:MET:HB2	1.88	0.46
1:A2:27:MET:HG2	1:A2:60:ALA:O	2.16	0.46
1:A5:62:ARG:HG2	2:X5:724:ILE:HG13	1.98	0.46
1:B5:94:LYS:HA	1:B5:94:LYS:HD3	1.75	0.46
1:C5:24:ALA:HB2	1:C5:48:VAL:HG11	1.98	0.46
1:G3:41:VAL:HB	1:G3:45:TYR:HB2	1.98	0.46
1:D4:11:MET:HE3	1:D4:79:HIS:HB3	1.98	0.46
1:E7:27:MET:HE1	1:E7:48:VAL:HG12	1.97	0.46
1:G7:35:LEU:HD11	1:G7:48:VAL:CG1	2.37	0.46
1:F9:94:LYS:HE3	1:F9:94:LYS:HB3	1.70	0.46
3:Pc:37:VAL:HG23	3:Pd:3:ILE:HD11	1.98	0.46
2:Xg:718:MET:HB3	2:Xg:718:MET:HE3	1.65	0.46
1:Af:30:ALA:O	1:HB:82:ALA:HB3	2.15	0.46
1:Af:62:ARG:HA	2:Xf:724:ILE:HD11	1.96	0.46
1:Gh:41:VAL:HB	1:Gh:45:TYR:HB2	1.98	0.46
1:Bk:83:ARG:NH1	1:Eo:29:LYS:HA	2.31	0.46
1:Bn:35:LEU:HD21	1:En:91:ILE:HD13	1.97	0.46
1:Bp:83:ARG:NH1	1:Et:29:LYS:HA	2.31	0.46
1:Hp:79:HIS:ND1	2:XI:714:THR:OG1	1.92	0.46
1:Br:35:LEU:HD21	1:Er:91:ILE:HD13	1.97	0.46
1:Gr:24:ALA:HA	1:Gr:27:MET:HE2	1.97	0.46
1:Gs:11:MET:HE3	1:Gs:79:HIS:HB3	1.98	0.46
1:Gv:23:ALA:O	1:Gv:27:MET:HG3	2.16	0.46
1:Cy:58:ASN:HA	1:Cy:80:ILE:HD11	1.96	0.46
1:Ey:27:MET:HG2	1:Ey:60:ALA:O	2.16	0.46
1:GA:23:ALA:O	1:GA:27:MET:HG3	2.16	0.46
2:Xz:790:LYS:HB2	2:Xz:790:LYS:HE2	1.76	0.46
1:CD:24:ALA:HB2	1:CD:48:VAL:HG11	1.98	0.46
1:ED:27:MET:HG2	1:ED:60:ALA:O	2.16	0.46
1:GB:41:VAL:HB	1:GB:45:TYR:HB2	1.98	0.46
1:CC:41:VAL:HB	1:CC:45:TYR:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XE:841:PRO:HG3	1:FI:69:GLU:HG2	1.98	0.46
1:AI:62:ARG:HG2	2:XI:724:ILE:HG13	1.98	0.46
1:BG:27:MET:CE	1:BG:48:VAL:HG12	2.46	0.46
1:FH:94:LYS:HE3	1:FH:94:LYS:HB3	1.70	0.46
1:BJ:83:ARG:NH1	1:EN:29:LYS:HA	2.31	0.46
1:FJ:22:GLU:HG2	1:FJ:71:VAL:HG21	1.98	0.46
1:FO:27:MET:HG2	1:FO:60:ALA:O	2.16	0.46
1:ER:14:THR:HB	1:ER:19:PRO:HB2	1.98	0.46
1:HU:15:ARG:HG3	1:HU:76:VAL:HG23	1.96	0.46
1:AW:77:ALA:HB2	1:DW:72:GLY:CA	2.44	0.46
1:A2:9:LEU:HD11	1:A2:49:LEU:HD23	1.98	0.45
1:C3:94:LYS:HE3	1:C3:94:LYS:HB3	1.79	0.45
1:A4:77:ALA:HB2	1:D4:72:GLY:CA	2.44	0.45
1:G6:27:MET:HG2	1:G6:60:ALA:O	2.17	0.45
1:C0:24:ALA:HB2	1:C0:48:VAL:HG11	1.98	0.45
2:X9:863:TYR:CD2	2:X9:869:GLY:HA3	2.51	0.45
1:Ab:27:MET:HG2	1:Ab:60:ALA:O	2.16	0.45
1:Db:15:ARG:HE	2:Xd:825:ALA:CB	2.28	0.45
2:Xb:773:LEU:HD21	2:Xd:841:PRO:HD3	1.98	0.45
1:Ce:24:ALA:HB2	1:Ce:48:VAL:HG11	1.98	0.45
1:Ge:18:VAL:HG22	1:Ht:11:MET:HB3	1.97	0.45
1:Cd:41:VAL:HB	1:Cd:45:TYR:HB2	1.98	0.45
1:Bi:35:LEU:HD21	1:Ei:91:ILE:HD13	1.97	0.45
1:Ci:41:VAL:HB	1:Ci:45:TYR:HB2	1.98	0.45
2:Xi:729:GLU:HA	1:DU:62:ARG:NH1	2.31	0.45
1:Di:15:ARG:HE	2:Xn:825:ALA:CB	2.28	0.45
3:Pm:37:VAL:HG23	3:Pn:3:ILE:HD11	1.98	0.45
1:Bp:83:ARG:HH12	1:Et:29:LYS:HA	1.81	0.45
1:Cp:12:ILE:HB	1:Cp:48:VAL:HG13	1.98	0.45
1:Ep:11:MET:HE3	1:Ep:79:HIS:HB3	1.98	0.45
1:Av:27:MET:HG2	1:Av:60:ALA:O	2.16	0.45
2:Xv:825:ALA:HB1	1:Du:73:ASP:O	2.16	0.45
1:Bx:11:MET:HE3	1:Bx:11:MET:HB2	1.76	0.45
1:EA:27:MET:HE1	1:EA:48:VAL:HG12	1.97	0.45
1:Ez:11:MET:HE3	1:Ez:79:HIS:HB3	1.98	0.45
1:AD:62:ARG:HG2	2:XD:724:ILE:HG13	1.98	0.45
1:FB:14:THR:HB	1:FB:19:PRO:HB2	1.97	0.45
1:EC:14:THR:HB	1:EC:19:PRO:HB2	1.98	0.45
1:AF:9:LEU:HD11	1:AF:49:LEU:HD23	1.98	0.45
1:GF:23:ALA:O	1:GF:27:MET:HG3	2.17	0.45
1:BE:83:ARG:HH12	1:EI:29:LYS:HA	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XE:818:ASN:HA	2:XE:819:PRO:HD3	1.80	0.45
1:FG:41:VAL:HB	1:FG:45:TYR:HB2	1.97	0.45
1:AJ:62:ARG:HA	2:XJ:724:ILE:HD11	1.96	0.45
1:BL:27:MET:CE	1:BL:48:VAL:HG12	2.46	0.45
1:CP:30:ALA:O	1:GP:82:ALA:HB3	2.16	0.45
1:CO:12:ILE:HB	1:CO:48:VAL:HG13	1.98	0.45
1:BQ:27:MET:CE	1:BQ:48:VAL:HG12	2.46	0.45
1:EU:27:MET:HE1	1:EU:48:VAL:HG12	1.97	0.45
1:GV:24:ALA:HA	1:GV:27:MET:HE2	1.97	0.45
1:EW:14:THR:HB	1:EW:19:PRO:HB2	1.99	0.45
2:XG:790:LYS:HB2	2:XG:790:LYS:HE2	1.45	0.45
1:C2:30:ALA:O	1:G2:82:ALA:HB3	2.16	0.45
1:C1:58:ASN:O	1:C1:62:ARG:HG3	2.16	0.45
1:C1:84:VAL:HG12	1:C1:88:VAL:HB	1.98	0.45
1:C5:53:GLU:HG2	1:C5:54:THR:N	2.30	0.45
1:C4:41:VAL:HB	1:C4:45:TYR:HB2	1.98	0.45
1:H4:11:MET:HE3	1:H4:11:MET:HB2	1.88	0.45
1:C7:30:ALA:O	1:G7:82:ALA:HB3	2.16	0.45
1:H7:12:ILE:HG23	1:H7:75:LEU:HD12	1.98	0.45
1:A0:62:ARG:HG2	2:X0:724:ILE:HG13	1.98	0.45
1:G8:25:ASP:HA	1:HF:88:VAL:CG2	2.46	0.45
3:P8:37:VAL:HG23	3:P9:3:ILE:HD11	1.98	0.45
1:E9:14:THR:HB	1:E9:19:PRO:HB2	1.98	0.45
1:Ba:83:ARG:NH1	1:Ee:29:LYS:HA	2.31	0.45
1:Bc:27:MET:CE	1:Bc:48:VAL:HG12	2.46	0.45
2:Xd:863:TYR:CD2	2:Xd:869:GLY:HA3	2.51	0.45
1:Cg:30:ALA:O	1:Gg:82:ALA:HB3	2.16	0.45
1:Bf:83:ARG:NH1	1:Ej:29:LYS:HA	2.31	0.45
1:Cf:12:ILE:HB	1:Cf:48:VAL:HG13	1.98	0.45
1:Ff:22:GLU:HG2	1:Ff:71:VAL:HG21	1.98	0.45
1:Cj:58:ASN:HA	1:Cj:80:ILE:CD1	2.45	0.45
1:Hi:91:ILE:CG2	1:GT:35:LEU:HD23	2.46	0.45
2:Xl:825:ALA:HB1	1:Dk:73:ASP:O	2.16	0.45
1:Ck:84:VAL:HG12	1:Ck:88:VAL:HB	1.98	0.45
1:Gk:27:MET:HG2	1:Gk:60:ALA:O	2.17	0.45
2:Xk:841:PRO:HG3	1:Fo:69:GLU:HG2	1.98	0.45
1:Fh:94:LYS:HE3	1:Fh:94:LYS:HB3	1.70	0.45
1:Cq:30:ALA:O	1:Gq:82:ALA:HB3	2.16	0.45
1:Cp:58:ASN:O	1:Cp:62:ARG:HG3	2.16	0.45
3:Pp:30:LYS:HB2	3:Pp:30:LYS:HE3	1.74	0.45
1:Br:27:MET:CE	1:Br:48:VAL:HG12	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cs:11:MET:HE3	1:Cs:11:MET:HB2	1.89	0.45
1:Cs:41:VAL:HB	1:Cs:45:TYR:HB2	1.98	0.45
1:Cu:84:VAL:HG12	1:Cu:88:VAL:HB	1.98	0.45
1:Hx:80:ILE:HD12	2:XM:713:ILE:CG2	2.46	0.45
1:Cz:84:VAL:HG12	1:Cz:88:VAL:HB	1.98	0.45
1:Fz:27:MET:HG2	1:Fz:60:ALA:O	2.16	0.45
1:CC:11:MET:HE3	1:CC:11:MET:HB2	1.89	0.45
2:XC:863:TYR:CD2	2:XC:869:GLY:HA3	2.51	0.45
1:FI:61:VAL:HG12	2:XI:795:ILE:HD12	1.97	0.45
1:GI:24:ALA:HB2	1:GI:48:VAL:HG21	1.97	0.45
1:AK:27:MET:HG2	1:AK:60:ALA:O	2.16	0.45
1:AN:62:ARG:HG2	2:XN:724:ILE:HG13	1.98	0.45
2:XO:841:PRO:HG3	1:FS:69:GLU:HG2	1.98	0.45
1:CS:24:ALA:HB2	1:CS:48:VAL:HG11	1.98	0.45
1:DR:11:MET:HE3	1:DR:79:HIS:HB3	1.98	0.45
2:XT:841:PRO:HG3	1:FX:69:GLU:HG2	1.98	0.45
1:C1:12:ILE:HB	1:C1:48:VAL:HG13	1.98	0.45
1:E1:11:MET:HE3	1:E1:79:HIS:HB3	1.98	0.45
2:X5:713:ILE:HG21	1:Hd:80:ILE:HD11	1.98	0.45
1:B3:27:MET:CE	1:B3:48:VAL:HG12	2.46	0.45
3:P3:37:VAL:HG23	3:P4:3:ILE:HD11	1.98	0.45
1:A7:27:MET:HG2	1:A7:60:ALA:O	2.16	0.45
1:C6:84:VAL:HG12	1:C6:88:VAL:HB	1.98	0.45
3:P0:16:ILE:HG12	3:P8:74:ILE:HB	1.97	0.45
1:Cb:14:THR:HB	1:Cb:19:PRO:HB2	1.99	0.45
1:Cb:30:ALA:O	1:Gb:82:ALA:HB3	2.16	0.45
1:Fc:14:THR:HB	1:Fc:19:PRO:HB2	1.97	0.45
1:Ed:14:THR:HB	1:Ed:19:PRO:HB2	1.99	0.45
1:Ag:27:MET:HG2	1:Ag:60:ALA:O	2.17	0.45
1:Hj:92:LEU:HD23	1:Gq:21:ILE:HD13	1.98	0.45
1:Bh:35:LEU:HD21	1:Eh:91:ILE:HD13	1.97	0.45
1:Gl:23:ALA:O	1:Gl:27:MET:HG3	2.16	0.45
1:Ck:58:ASN:O	1:Ck:62:ARG:HG3	2.16	0.45
1:Fk:27:MET:HG2	1:Fk:60:ALA:O	2.16	0.45
1:Go:23:ALA:O	1:Go:27:MET:HG3	2.15	0.45
1:En:57:VAL:HG12	1:En:80:ILE:HG23	1.97	0.45
1:Gn:11:MET:HE3	1:Gn:79:HIS:HB3	1.98	0.45
2:Xq:825:ALA:HB1	1:Dp:73:ASP:O	2.16	0.45
1:Fp:22:GLU:HG2	1:Fp:71:VAL:HG21	1.98	0.45
1:Bt:94:LYS:HD3	1:Bt:94:LYS:HA	1.75	0.45
1:Gt:24:ALA:HB2	1:Gt:48:VAL:HG21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Fr:11:MET:HE3	1:Fr:11:MET:HB2	1.82	0.45
1:Es:14:THR:HB	1:Es:19:PRO:HB2	1.99	0.45
1:Fu:22:GLU:HG2	1:Fu:71:VAL:HG21	1.98	0.45
1:Gu:18:VAL:HG22	1:HR:11:MET:HB3	1.99	0.45
1:Gu:35:LEU:HD23	1:HR:91:ILE:HG21	1.95	0.45
1:Gw:41:VAL:HB	1:Gw:45:TYR:HB2	1.98	0.45
2:Xx:863:TYR:CD2	2:Xx:869:GLY:HA3	2.51	0.45
1:AA:94:LYS:HE2	1:AA:94:LYS:HB3	1.64	0.45
1:CD:58:ASN:HA	1:CD:80:ILE:CD1	2.45	0.45
3:PD:10:LEU:HG	3:PD:37:VAL:HG21	1.96	0.45
1:CI:24:ALA:HB2	1:CI:48:VAL:HG11	1.98	0.45
3:PI:37:VAL:HB	3:PG:51:LEU:HD11	1.97	0.45
3:PG:37:VAL:HG23	3:PH:3:ILE:HD11	1.98	0.45
1:GJ:27:MET:HG2	1:GJ:60:ALA:O	2.17	0.45
2:XJ:841:PRO:HG3	1:FN:69:GLU:HG2	1.98	0.45
1:BN:14:THR:HB	1:BN:19:PRO:HB2	1.98	0.45
1:FN:61:VAL:HG12	2:XN:795:ILE:HD12	1.97	0.45
1:AM:11:MET:HB3	1:DM:18:VAL:HG22	1.97	0.45
1:GM:11:MET:HE3	1:GM:79:HIS:HB3	1.98	0.45
1:CO:84:VAL:HG12	1:CO:88:VAL:HB	1.98	0.45
1:FS:61:VAL:HG12	2:XS:795:ILE:HD12	1.97	0.45
1:AR:25:ASP:HA	1:FR:88:VAL:HG21	1.99	0.45
1:CU:58:ASN:O	1:CU:62:ARG:HG3	2.17	0.45
1:BT:83:ARG:NH1	1:EX:29:LYS:HA	2.31	0.45
1:CT:84:VAL:HG12	1:CT:88:VAL:HB	1.98	0.45
1:FT:22:GLU:HG2	1:FT:71:VAL:HG21	1.98	0.45
3:PV:37:VAL:HG23	3:PW:3:ILE:HD11	1.98	0.45
1:HW:11:MET:HE3	1:HW:11:MET:HB2	1.88	0.45
1:G2:23:ALA:O	1:G2:27:MET:HG3	2.16	0.45
1:H2:80:ILE:CD1	2:XX:713:ILE:CG2	2.94	0.45
2:X1:841:PRO:HG3	1:F5:69:GLU:HG2	1.98	0.45
2:X5:714:THR:OG1	1:Hd:79:HIS:ND1	1.87	0.45
1:E4:11:MET:HG2	1:E4:49:LEU:HD23	1.96	0.45
1:A7:9:LEU:HD11	1:A7:49:LEU:HD23	1.99	0.45
1:B6:83:ARG:NH1	1:E0:29:LYS:HA	2.31	0.45
1:G0:24:ALA:HB2	1:G0:48:VAL:HG21	1.97	0.45
1:A9:25:ASP:HA	1:F9:88:VAL:HG21	1.99	0.45
1:Aa:11:MET:HE3	1:Aa:11:MET:HB2	1.91	0.45
1:Ca:12:ILE:HB	1:Ca:48:VAL:HG13	1.98	0.45
1:Fa:22:GLU:HG2	1:Fa:71:VAL:HG21	1.98	0.45
1:Ed:12:ILE:HG23	1:Ed:75:LEU:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Af:88:VAL:O	1:Af:91:ILE:HG12	2.17	0.45
1:Cj:94:LYS:HE3	1:Cj:94:LYS:HB3	1.73	0.45
1:Ao:62:ARG:HG2	2:Xo:724:ILE:HG13	1.98	0.45
1:Bm:14:THR:HB	1:Bm:19:PRO:HB2	1.99	0.45
1:Gm:24:ALA:HA	1:Gm:27:MET:HE2	1.97	0.45
1:Cq:14:THR:HB	1:Cq:19:PRO:HB2	1.99	0.45
1:Gq:23:ALA:O	1:Gq:27:MET:HG3	2.16	0.45
1:Gu:27:MET:HG2	1:Gu:60:ALA:O	2.17	0.45
1:By:94:LYS:HD3	1:By:94:LYS:HA	1.75	0.45
1:Gx:11:MET:HE3	1:Gx:79:HIS:HB3	1.99	0.45
1:Bz:83:ARG:HH12	1:ED:29:LYS:HA	1.81	0.45
1:Fz:22:GLU:HG2	1:Fz:71:VAL:HG21	1.98	0.45
1:Gz:27:MET:HG2	1:Gz:60:ALA:O	2.17	0.45
1:BD:14:THR:HB	1:BD:19:PRO:HB2	1.98	0.45
1:GH:11:MET:HE3	1:GH:79:HIS:HB3	1.98	0.45
1:CK:30:ALA:O	1:GK:82:ALA:HB3	2.16	0.45
1:CK:58:ASN:O	1:CK:62:ARG:HG3	2.17	0.45
1:CP:14:THR:HB	1:CP:19:PRO:HB2	1.99	0.45
1:GO:27:MET:HG2	1:GO:60:ALA:O	2.17	0.45
3:PS:16:ILE:HG12	3:PQ:74:ILE:HB	1.97	0.45
1:ER:57:VAL:HG12	1:ER:80:ILE:HG23	1.97	0.45
1:DU:15:ARG:HE	2:XW:825:ALA:CB	2.28	0.45
1:HU:12:ILE:HG23	1:HU:75:LEU:HD12	1.98	0.45
1:EX:27:MET:HG2	1:EX:60:ALA:O	2.16	0.45
1:BV:35:LEU:HD21	1:EV:91:ILE:HD13	1.97	0.45
1:DW:11:MET:HE3	1:DW:79:HIS:HB3	1.98	0.45
1:GW:11:MET:HE3	1:GW:79:HIS:HB3	1.99	0.45
1:F1:27:MET:HG2	1:F1:60:ALA:O	2.16	0.45
1:B3:35:LEU:HD21	1:E3:91:ILE:HD13	1.97	0.45
1:F3:14:THR:HB	1:F3:19:PRO:HB2	1.97	0.45
1:F3:41:VAL:HB	1:F3:45:TYR:HB2	1.98	0.45
1:H4:80:ILE:HD12	2:XS:713:ILE:HG22	1.98	0.45
1:C7:14:THR:HB	1:C7:19:PRO:HB2	1.99	0.45
1:H0:91:ILE:CG2	1:GE:35:LEU:HD23	2.47	0.45
1:D8:32:GLU:CD	1:Au:7:ILE:HD11	2.40	0.45
1:G9:21:ILE:HD13	1:Hu:92:LEU:CD2	2.47	0.45
1:Fb:94:LYS:HE3	1:Fb:94:LYS:HB2	1.78	0.45
1:Hb:88:VAL:HG21	1:Gm:25:ASP:CA	2.45	0.45
1:Ce:94:LYS:HB3	1:Ce:94:LYS:HE3	1.73	0.45
1:Cf:84:VAL:HG12	1:Cf:88:VAL:HB	1.98	0.45
1:Df:62:ARG:NH1	2:XB:729:GLU:HA	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ak:72:GLY:HA2	1:Fk:77:ALA:HB2	1.99	0.45
1:Co:24:ALA:HB2	1:Co:48:VAL:HG11	1.98	0.45
1:Aq:27:MET:HG2	1:Aq:60:ALA:O	2.16	0.45
1:Es:12:ILE:HG23	1:Es:75:LEU:HD12	1.98	0.45
3:Pw:37:VAL:HG23	3:Px:3:ILE:HD11	1.98	0.45
1:Dx:11:MET:HE3	1:Dx:79:HIS:HB3	1.98	0.45
1:Cz:12:ILE:HB	1:Cz:48:VAL:HG13	1.98	0.45
1:DD:68:CYS:SG	1:DD:75:LEU:HB2	2.57	0.45
1:EI:27:MET:HG2	1:EI:60:ALA:O	2.16	0.45
1:GG:12:ILE:HG23	1:GG:75:LEU:HD12	1.99	0.45
1:GG:41:VAL:HB	1:GG:45:TYR:HB2	1.98	0.45
1:BL:35:LEU:HD21	1:EL:91:ILE:HD13	1.97	0.45
1:FL:41:VAL:HB	1:FL:45:TYR:HB2	1.98	0.45
1:BS:14:THR:HB	1:BS:19:PRO:HB2	1.98	0.45
1:EQ:11:MET:HE3	1:EQ:11:MET:HB2	1.89	0.45
1:GQ:12:ILE:HG23	1:GQ:75:LEU:HD12	1.99	0.45
1:BT:83:ARG:HH12	1:EX:29:LYS:HA	1.81	0.45
1:GT:27:MET:HG2	1:GT:60:ALA:O	2.17	0.45
1:F1:22:GLU:HG2	1:F1:71:VAL:HG21	1.98	0.45
1:G1:27:MET:HG2	1:G1:60:ALA:O	2.17	0.45
1:C7:58:ASN:O	1:C7:62:ARG:HG3	2.17	0.45
1:G7:23:ALA:O	1:G7:27:MET:HG3	2.16	0.45
2:X7:825:ALA:HB1	1:D6:73:ASP:O	2.16	0.45
1:B8:35:LEU:HD21	1:E8:91:ILE:HD13	1.97	0.45
1:Ge:24:ALA:HB2	1:Ge:48:VAL:HG21	1.97	0.45
1:Hg:12:ILE:HG23	1:Hg:75:LEU:HD12	1.98	0.45
1:Cj:24:ALA:HB2	1:Cj:48:VAL:HG11	1.98	0.45
1:Gh:12:ILE:HG23	1:Gh:75:LEU:HD12	1.99	0.45
1:Ei:14:THR:HB	1:Ei:19:PRO:HB2	1.99	0.45
1:Hi:11:MET:HB3	1:GT:18:VAL:HG22	1.98	0.45
1:Co:53:GLU:HG2	1:Co:54:THR:N	2.31	0.45
1:Gp:27:MET:HG2	1:Gp:60:ALA:O	2.17	0.45
1:Ct:53:GLU:HG2	1:Ct:54:THR:N	2.30	0.45
1:Hv:92:LEU:HD21	1:GP:21:ILE:HD13	1.99	0.45
1:Bu:83:ARG:NH1	1:Ey:29:LYS:HA	2.31	0.45
1:Eu:11:MET:HE3	1:Eu:79:HIS:HB3	1.98	0.45
1:Dy:68:CYS:SG	1:Dy:75:LEU:HB2	2.57	0.45
1:Cw:94:LYS:HE3	1:Cw:94:LYS:HB3	1.79	0.45
1:Hx:62:ARG:HA	2:XM:713:ILE:CD1	2.42	0.45
2:XA:773:LEU:HD21	2:XC:841:PRO:HD3	1.98	0.45
1:Az:88:VAL:O	1:Az:91:ILE:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DF:27:MET:HE1	1:DF:48:VAL:HG12	1.99	0.45
2:XF:718:MET:HB3	2:XF:718:MET:HE3	1.66	0.45
1:AE:88:VAL:O	1:AE:91:ILE:HG12	2.17	0.45
1:CI:88:VAL:HG21	1:EI:25:ASP:HA	1.99	0.45
1:BG:35:LEU:HD21	1:EG:91:ILE:HD13	1.97	0.45
1:GH:80:ILE:HD12	2:XG:806:ILE:HG21	1.99	0.45
1:EK:27:MET:HE1	1:EK:48:VAL:HG12	1.97	0.45
1:AJ:72:GLY:HA2	1:FJ:77:ALA:HB2	1.99	0.45
1:GN:24:ALA:HB2	1:GN:48:VAL:HG21	1.97	0.45
2:XN:713:ILE:HG22	1:HW:80:ILE:HD12	1.98	0.45
3:PN:16:ILE:HG12	3:PL:74:ILE:HB	1.97	0.45
3:PX:16:ILE:HG12	3:PV:74:ILE:HB	1.98	0.45
1:EV:11:MET:HE3	1:EV:11:MET:HB2	1.89	0.45
1:H2:11:MET:HE3	1:H2:11:MET:HB2	1.89	0.45
1:C5:94:LYS:HE3	1:C5:94:LYS:HB3	1.73	0.45
2:X3:790:LYS:HE2	2:X3:790:LYS:HB2	1.45	0.45
1:A4:25:ASP:HA	1:F4:88:VAL:HG21	1.99	0.45
3:P4:44:CYS:SG	3:P4:73:ILE:HG21	2.57	0.45
2:Xb:818:ASN:HA	2:Xb:819:PRO:HD3	1.82	0.45
1:Ek:11:MET:HE3	1:Ek:11:MET:HB2	1.68	0.45
1:Co:58:ASN:O	1:Co:62:ARG:HG3	2.17	0.45
1:Fm:11:MET:HE3	1:Fm:11:MET:HB2	1.81	0.45
1:Dq:27:MET:HE1	1:Dq:48:VAL:HG12	1.99	0.45
1:Hq:24:ALA:HB2	1:Hq:48:VAL:HG11	1.99	0.45
2:Xq:718:MET:HE3	2:Xq:718:MET:HB3	1.65	0.45
1:At:62:ARG:HG2	2:Xt:724:ILE:HG13	1.99	0.45
1:Ct:24:ALA:HB2	1:Ct:48:VAL:HG11	1.98	0.45
1:Dt:68:CYS:SG	1:Dt:75:LEU:HB2	2.57	0.45
3:Pt:37:VAL:HB	3:Pr:51:LEU:HD11	1.97	0.45
1:Fr:14:THR:HB	1:Fr:19:PRO:HB2	1.97	0.45
1:Gr:41:VAL:HB	1:Gr:45:TYR:HB2	1.98	0.45
2:Xs:863:TYR:CD2	2:Xs:869:GLY:HA3	2.51	0.45
1:Cv:58:ASN:O	1:Cv:62:ARG:HG3	2.17	0.45
1:Dv:27:MET:HE1	1:Dv:48:VAL:HG12	1.99	0.45
1:Cy:88:VAL:HG21	1:Ey:25:ASP:HA	1.99	0.45
1:Bw:35:LEU:HD21	1:Ew:91:ILE:HD13	1.97	0.45
1:HA:12:ILE:HG23	1:HA:75:LEU:HD12	1.98	0.45
1:AD:9:LEU:HD11	1:AD:49:LEU:HD23	1.99	0.45
1:EF:11:MET:HE3	1:EF:11:MET:HB2	1.87	0.45
1:AK:35:LEU:HD11	1:AK:48:VAL:CG1	2.47	0.45
1:DK:27:MET:HE1	1:DK:48:VAL:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HK:24:ALA:HB2	1:HK:48:VAL:HG11	1.99	0.45
1:GP:23:ALA:O	1:GP:27:MET:HG3	2.16	0.45
1:HP:24:ALA:HB2	1:HP:48:VAL:HG11	1.99	0.45
1:CS:88:VAL:HG21	1:ES:25:ASP:HA	1.99	0.45
3:PR:30:LYS:HB2	3:PR:30:LYS:HE3	1.74	0.45
1:DU:27:MET:HE1	1:DU:48:VAL:HG12	1.99	0.45
1:HU:24:ALA:HB2	1:HU:48:VAL:HG11	1.99	0.45
1:AX:62:ARG:HG2	2:XX:724:ILE:HG13	1.98	0.45
1:AW:25:ASP:HA	1:FW:88:VAL:HG21	1.99	0.45
1:BW:11:MET:HE3	1:BW:11:MET:HB2	1.76	0.45
1:B5:14:THR:HB	1:B5:19:PRO:HB2	1.98	0.45
1:A6:72:GLY:HA2	1:F6:77:ALA:HB2	1.99	0.45
2:X6:841:PRO:HG3	1:F0:69:GLU:O	2.17	0.45
1:B0:14:THR:HB	1:B0:19:PRO:HB2	1.98	0.45
1:C9:58:ASN:O	1:C9:62:ARG:HG3	2.17	0.45
1:G9:80:ILE:HD12	2:X8:806:ILE:HG21	1.99	0.45
1:H9:91:ILE:HG21	1:GR:35:LEU:CD2	2.47	0.45
1:Ab:35:LEU:HD11	1:Ab:48:VAL:CG1	2.47	0.45
2:Xa:716:PRO:HD2	1:Ht:80:ILE:O	2.17	0.45
2:Xa:841:PRO:HG3	1:Fe:69:GLU:HG2	1.98	0.45
1:Bc:35:LEU:HD21	1:Ec:91:ILE:HD13	1.97	0.45
1:Bf:83:ARG:HH12	1:Ej:29:LYS:HA	1.81	0.45
1:Gj:24:ALA:HB2	1:Gj:48:VAL:HG21	1.97	0.45
1:Bh:27:MET:CE	1:Bh:48:VAL:HG12	2.46	0.45
2:Xi:714:THR:HA	2:Xi:718:MET:HG3	1.99	0.45
1:Al:94:LYS:HB3	1:Al:94:LYS:HE2	1.64	0.45
1:Cl:30:ALA:O	1:Gl:82:ALA:HB3	2.16	0.45
1:Bo:14:THR:HB	1:Bo:19:PRO:HB2	1.98	0.45
1:Dn:11:MET:HE3	1:Dn:79:HIS:HB3	1.98	0.45
2:Xn:714:THR:HA	2:Xn:718:MET:HG3	1.99	0.45
1:Aq:9:LEU:HD11	1:Aq:49:LEU:HD23	1.98	0.45
2:Xq:785:VAL:HG11	1:Cp:80:ILE:CD1	2.47	0.45
1:Cy:53:GLU:HG2	1:Cy:54:THR:N	2.30	0.45
1:Ax:25:ASP:HA	1:Fx:88:VAL:HG21	1.99	0.45
2:Xz:841:PRO:HG3	1:FD:69:GLU:HG2	1.98	0.45
1:BB:35:LEU:HD21	1:EB:91:ILE:HD13	1.97	0.45
1:CF:14:THR:HB	1:CF:19:PRO:HB2	1.99	0.45
1:AI:9:LEU:HD11	1:AI:49:LEU:HD23	1.99	0.45
1:DI:68:CYS:SG	1:DI:75:LEU:HB2	2.57	0.45
1:BG:14:THR:HB	1:BG:19:PRO:HB2	1.99	0.45
1:CN:24:ALA:HB2	1:CN:48:VAL:HG11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:27:MET:HG2	1:AP:60:ALA:O	2.16	0.45
1:CS:58:ASN:O	1:CS:62:ARG:HG3	2.17	0.45
2:XS:821:MET:HB2	2:XS:821:MET:HE3	1.68	0.45
1:BQ:35:LEU:HD21	1:EQ:91:ILE:HD13	1.97	0.45
2:XR:863:TYR:CD2	2:XR:869:GLY:HA3	2.51	0.45
2:XT:841:PRO:HG3	1:FX:69:GLU:O	2.17	0.45
1:DX:68:CYS:SG	1:DX:75:LEU:HB2	2.57	0.45
1:FX:11:MET:HE3	1:FX:11:MET:HB2	1.87	0.45
1:EW:12:ILE:HG23	1:EW:75:LEU:HD12	1.98	0.45
3:PW:44:CYS:SG	3:PW:73:ILE:HG21	2.57	0.45
1:C2:14:THR:HB	1:C2:19:PRO:HB2	1.99	0.45
1:E4:12:ILE:HG23	1:E4:75:LEU:HD12	1.98	0.45
1:H4:88:VAL:HG21	1:GQ:25:ASP:CA	2.42	0.45
1:D7:27:MET:HE1	1:D7:48:VAL:HG12	1.99	0.45
1:E7:9:LEU:HG	1:E7:11:MET:HG3	1.99	0.45
1:B6:83:ARG:HH12	1:E0:29:LYS:HA	1.81	0.45
2:X6:713:ILE:CG2	1:Hc:80:ILE:CD1	2.91	0.45
2:X6:841:PRO:HG3	1:F0:69:GLU:HG2	1.98	0.45
1:A0:9:LEU:HD11	1:A0:49:LEU:HD23	1.99	0.45
3:P9:30:LYS:HB2	3:P9:30:LYS:HE3	1.74	0.45
3:P9:44:CYS:SG	3:P9:73:ILE:HG21	2.57	0.45
1:Hb:24:ALA:HB2	1:Hb:48:VAL:HG11	1.99	0.45
3:Pb:1:MET:HE1	3:Pd:39:VAL:HG23	1.99	0.45
1:Aa:72:GLY:HA2	1:Fa:77:ALA:HB2	1.99	0.45
1:Be:94:LYS:HD3	1:Be:94:LYS:HA	1.75	0.45
1:He:80:ILE:O	2:XE:716:PRO:HD2	2.16	0.45
3:Pd:44:CYS:SG	3:Pd:73:ILE:HG21	2.57	0.45
2:Xg:727:THR:O	2:Xg:728:PRO:C	2.58	0.45
2:Xg:785:VAL:HG11	1:Cf:80:ILE:CD1	2.47	0.45
1:Dj:68:CYS:SG	1:Dj:75:LEU:HB2	2.57	0.45
1:Al:27:MET:HG2	1:Al:60:ALA:O	2.16	0.45
1:El:9:LEU:HG	1:El:11:MET:HG3	1.99	0.45
1:Gl:72:GLY:CA	1:HT:77:ALA:HB2	2.47	0.45
2:Xk:841:PRO:HG3	1:Fo:69:GLU:O	2.17	0.45
3:Pk:44:CYS:SG	3:Pk:73:ILE:HG21	2.57	0.45
1:Bm:77:ALA:HB2	1:Fm:72:GLY:HA2	1.99	0.45
1:En:14:THR:HB	1:En:19:PRO:HB2	1.98	0.45
3:Pq:1:MET:HE1	3:Ps:39:VAL:HG23	1.99	0.45
1:Ct:88:VAL:HG21	1:Et:25:ASP:HA	1.99	0.45
3:Ps:44:CYS:SG	3:Ps:73:ILE:HG21	2.57	0.45
1:Ev:9:LEU:HG	1:Ev:11:MET:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bu:83:ARG:HH12	1:Ey:29:LYS:HA	1.81	0.45
1:CA:14:THR:HB	1:CA:19:PRO:HB2	1.99	0.45
1:CE:84:VAL:HG12	1:CE:88:VAL:HB	1.98	0.45
1:EJ:11:MET:HE3	1:EJ:79:HIS:HB3	1.98	0.45
2:XL:806:ILE:HG21	1:GM:80:ILE:HD12	1.99	0.45
1:CP:58:ASN:O	1:CP:62:ARG:HG3	2.17	0.45
1:EP:9:LEU:HG	1:EP:11:MET:HG3	1.99	0.45
3:PP:1:MET:HE1	3:PR:39:VAL:HG23	1.99	0.45
1:EU:9:LEU:HG	1:EU:11:MET:HG3	1.99	0.45
1:CX:24:ALA:HB2	1:CX:48:VAL:HG11	1.98	0.45
3:PX:37:VAL:HB	3:PV:51:LEU:HD11	1.97	0.45
2:XW:714:THR:HA	2:XW:718:MET:HG3	1.99	0.45
1:A1:72:GLY:HA2	1:F1:77:ALA:HB2	1.99	0.45
1:A5:9:LEU:HD11	1:A5:49:LEU:HD23	1.99	0.45
1:G4:25:ASP:HA	1:H7:88:VAL:CG2	2.44	0.45
2:X7:718:MET:HE3	2:X7:718:MET:HB3	1.65	0.45
1:A9:77:ALA:HB2	1:D9:72:GLY:CA	2.44	0.45
1:Ba:83:ARG:HH12	1:Ee:29:LYS:HA	1.81	0.45
1:Be:14:THR:HB	1:Be:19:PRO:HB2	1.98	0.45
1:Ge:9:LEU:HD11	1:Ge:49:LEU:HD23	1.99	0.45
1:Ge:22:GLU:OE2	1:Ht:79:HIS:CE1	2.66	0.45
1:Gc:41:VAL:HB	1:Gc:45:TYR:HB2	1.98	0.45
1:Bf:94:LYS:HA	1:Bf:94:LYS:HD3	1.70	0.45
1:Cj:88:VAL:HG21	1:Ej:25:ASP:HA	1.99	0.45
2:Xj:713:ILE:HG21	1:Hs:80:ILE:HD11	1.98	0.45
1:Ai:77:ALA:HB2	1:Di:72:GLY:CA	2.44	0.45
1:Al:9:LEU:HD11	1:Al:49:LEU:HD23	1.99	0.45
1:Gn:80:ILE:HD12	2:Xm:806:ILE:HG21	1.99	0.45
1:Hq:12:ILE:HG23	1:Hq:75:LEU:HD12	1.98	0.45
1:Cp:84:VAL:HG12	1:Cp:88:VAL:HB	1.98	0.45
2:Xp:841:PRO:HG3	1:Ft:69:GLU:HG2	1.98	0.45
1:At:9:LEU:HD11	1:At:49:LEU:HD23	1.99	0.45
1:Bw:14:THR:HB	1:Bw:19:PRO:HB2	1.99	0.45
1:Gw:12:ILE:HG23	1:Gw:75:LEU:HD12	1.99	0.45
2:Xz:841:PRO:HG3	1:FD:69:GLU:O	2.17	0.45
1:GB:12:ILE:HG23	1:GB:75:LEU:HD12	1.99	0.45
1:FC:94:LYS:HB3	1:FC:94:LYS:HE3	1.70	0.45
1:HF:24:ALA:HB2	1:HF:48:VAL:HG11	1.99	0.45
2:XF:785:VAL:HG11	1:CE:80:ILE:CD1	2.47	0.45
1:AE:72:GLY:HA2	1:FE:77:ALA:HB2	1.99	0.45
1:GG:68:CYS:SG	1:GG:75:LEU:HB2	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HH:7:ILE:H	1:HH:7:ILE:HG13	1.57	0.45
1:CK:14:THR:HB	1:CK:19:PRO:HB2	1.99	0.45
1:CN:88:VAL:HG21	1:EN:25:ASP:HA	1.99	0.45
3:PN:37:VAL:HB	3:PL:51:LEU:HD11	1.97	0.45
1:DM:27:MET:HG2	1:DM:60:ALA:O	2.17	0.45
2:XP:773:LEU:HD21	2:XR:841:PRO:HD3	1.98	0.45
1:CS:94:LYS:HB3	1:CS:94:LYS:HE3	1.73	0.45
1:ES:27:MET:HG2	1:ES:60:ALA:O	2.16	0.45
1:AU:9:LEU:HD11	1:AU:49:LEU:HD23	1.98	0.45
1:GU:23:ALA:O	1:GU:27:MET:HG3	2.16	0.45
1:CW:58:ASN:O	1:CW:62:ARG:HG3	2.17	0.45
1:H2:12:ILE:HG23	1:H2:75:LEU:HD12	1.98	0.44
1:H2:24:ALA:HB2	1:H2:48:VAL:HG11	1.99	0.44
1:C5:88:VAL:HG21	1:E5:25:ASP:HA	1.99	0.44
1:G3:12:ILE:HG23	1:G3:75:LEU:HD12	1.99	0.44
2:X3:806:ILE:HG21	1:G4:80:ILE:HD12	1.99	0.44
1:E4:14:THR:HB	1:E4:19:PRO:HB2	1.99	0.44
1:A6:88:VAL:O	1:A6:91:ILE:HG12	2.17	0.44
1:B6:70:ARG:HD3	1:B6:70:ARG:HA	1.79	0.44
1:C6:12:ILE:HB	1:C6:48:VAL:HG13	1.98	0.44
1:D0:68:CYS:SG	1:D0:75:LEU:HB2	2.57	0.44
1:B8:27:MET:CE	1:B8:48:VAL:HG12	2.46	0.44
1:Gb:23:ALA:O	1:Gb:27:MET:HG3	2.16	0.44
1:Da:32:GLU:CB	1:At:7:ILE:HD11	2.43	0.44
1:Ea:11:MET:HE3	1:Ea:79:HIS:HB3	1.98	0.44
1:Ga:35:LEU:HD23	1:Ho:91:ILE:CG2	2.48	0.44
1:Ha:79:HIS:ND1	2:Xt:714:THR:OG1	1.91	0.44
1:Gd:11:MET:HE3	1:Gd:79:HIS:HB3	1.98	0.44
1:Gf:27:MET:HG2	1:Gf:60:ALA:O	2.17	0.44
2:Xf:841:PRO:HG3	1:Fj:69:GLU:O	2.17	0.44
3:Pf:30:LYS:HE3	3:Pf:30:LYS:HB2	1.74	0.44
1:Bh:77:ALA:HB2	1:Fh:72:GLY:HA2	1.99	0.44
1:HI:12:ILE:HG23	1:HI:75:LEU:HD12	1.99	0.44
1:HI:24:ALA:HB2	1:HI:48:VAL:HG11	1.99	0.44
3:Pl:1:MET:HE1	3:Pn:39:VAL:HG23	1.99	0.44
1:Bm:27:MET:CE	1:Bm:48:VAL:HG12	2.46	0.44
1:Cn:58:ASN:O	1:Cn:62:ARG:HG3	2.17	0.44
1:Hq:79:HIS:ND1	2:XD:714:THR:OG1	1.89	0.44
1:Bt:14:THR:HB	1:Bt:19:PRO:HB2	1.98	0.44
3:Pr:37:VAL:HG23	3:Ps:3:ILE:HD11	1.98	0.44
1:Gs:80:ILE:HD12	2:Xr:806:ILE:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xs:714:THR:HA	2:Xs:718:MET:HG3	1.99	0.44
1:Au:88:VAL:O	1:Au:91:ILE:HG12	2.17	0.44
2:Xu:818:ASN:HA	2:Xu:819:PRO:HD3	1.80	0.44
2:Xu:841:PRO:HG3	1:Fy:69:GLU:O	2.17	0.44
1:Bw:27:MET:CE	1:Bw:48:VAL:HG12	2.46	0.44
2:Xw:729:GLU:HA	1:DA:62:ARG:NH1	2.31	0.44
1:Ax:28:THR:O	1:HM:83:ARG:NH1	2.49	0.44
1:Cx:41:VAL:HB	1:Cx:45:TYR:HB2	1.98	0.44
1:CA:30:ALA:O	1:GA:82:ALA:HB3	2.16	0.44
1:CA:58:ASN:O	1:CA:62:ARG:HG3	2.17	0.44
1:EA:9:LEU:HG	1:EA:11:MET:HG3	1.99	0.44
3:Pz:44:CYS:SG	3:Pz:73:ILE:HG21	2.57	0.44
1:CD:58:ASN:O	1:CD:62:ARG:HG3	2.17	0.44
1:BB:27:MET:CE	1:BB:48:VAL:HG12	2.46	0.44
1:CC:58:ASN:O	1:CC:62:ARG:HG3	2.17	0.44
1:AF:27:MET:HG2	1:AF:60:ALA:O	2.16	0.44
3:PJ:44:CYS:SG	3:PJ:73:ILE:HG21	2.57	0.44
1:DN:68:CYS:SG	1:DN:75:LEU:HB2	2.57	0.44
3:PM:44:CYS:SG	3:PM:73:ILE:HG21	2.57	0.44
1:DP:27:MET:HE1	1:DP:48:VAL:HG12	1.99	0.44
2:XP:785:VAL:HG11	1:CO:80:ILE:CD1	2.47	0.44
1:AU:27:MET:HG2	1:AU:60:ALA:O	2.17	0.44
1:CU:30:ALA:O	1:GU:82:ALA:HB3	2.16	0.44
2:XU:773:LEU:HD21	2:XW:841:PRO:HD3	1.98	0.44
1:CX:88:VAL:HG21	1:EX:25:ASP:HA	1.99	0.44
2:XX:821:MET:HB2	2:XX:821:MET:HE3	1.68	0.44
1:C2:58:ASN:O	1:C2:62:ARG:HG3	2.17	0.44
2:X2:785:VAL:HG11	1:C1:80:ILE:CD1	2.47	0.44
1:E1:11:MET:HE3	1:E1:11:MET:HB2	1.68	0.44
1:G4:11:MET:HE3	1:G4:79:HIS:HB3	1.98	0.44
2:X7:785:VAL:HG11	1:C6:80:ILE:CD1	2.47	0.44
1:E9:12:ILE:HG23	1:E9:75:LEU:HD12	1.98	0.44
1:G9:11:MET:HE3	1:G9:79:HIS:HB3	1.98	0.44
1:G9:40:PHE:HE1	1:Hu:41:VAL:HG13	1.81	0.44
1:Bb:23:ALA:O	1:Bb:27:MET:HG3	2.18	0.44
1:Ha:11:MET:HE3	1:Ha:11:MET:HB2	1.88	0.44
3:Pa:44:CYS:SG	3:Pa:73:ILE:HG21	2.57	0.44
1:Ce:58:ASN:O	1:Ce:62:ARG:HG3	2.17	0.44
1:Dd:11:MET:HE3	1:Dd:79:HIS:HB3	1.98	0.44
1:Bg:23:ALA:O	1:Bg:27:MET:HG3	2.18	0.44
1:Cg:58:ASN:O	1:Cg:62:ARG:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Pf:44:CYS:SG	3:Pf:73:ILE:HG21	2.57	0.44
1:Ci:58:ASN:O	1:Ci:62:ARG:HG3	2.17	0.44
1:Gi:11:MET:HE3	1:Gi:79:HIS:HB3	1.98	0.44
1:Al:35:LEU:HD11	1:Al:48:VAL:CG1	2.47	0.44
1:Bl:23:ALA:O	1:Bl:27:MET:HG3	2.18	0.44
1:El:11:MET:HE3	1:El:11:MET:HB2	1.87	0.44
1:Bk:70:ARG:HD3	1:Bk:70:ARG:HA	1.79	0.44
1:Bk:83:ARG:HH12	1:Eo:29:LYS:HA	1.81	0.44
1:Ck:12:ILE:HB	1:Ck:48:VAL:HG13	1.98	0.44
1:Ap:88:VAL:O	1:Ap:91:ILE:HG12	2.17	0.44
1:Br:14:THR:HB	1:Br:19:PRO:HB2	1.99	0.44
1:Cs:58:ASN:O	1:Cs:62:ARG:HG3	2.17	0.44
1:Au:72:GLY:HA2	1:Fu:77:ALA:HB2	1.99	0.44
3:Px:44:CYS:SG	3:Px:73:ILE:HG21	2.57	0.44
2:Xz:818:ASN:HA	2:Xz:819:PRO:HD3	1.81	0.44
1:CF:58:ASN:O	1:CF:62:ARG:HG3	2.17	0.44
1:CI:58:ASN:O	1:CI:62:ARG:HG3	2.17	0.44
1:AK:9:LEU:HD11	1:AK:49:LEU:HD23	1.98	0.44
1:GK:23:ALA:O	1:GK:27:MET:HG3	2.16	0.44
1:CJ:12:ILE:HB	1:CJ:48:VAL:HG13	1.98	0.44
1:CM:41:VAL:HB	1:CM:45:TYR:HB2	1.98	0.44
1:HP:12:ILE:HG23	1:HP:75:LEU:HD12	1.98	0.44
2:XO:841:PRO:HG3	1:FS:69:GLU:O	2.17	0.44
1:GS:9:LEU:HD11	1:GS:49:LEU:HD23	2.00	0.44
1:GR:11:MET:HE3	1:GR:79:HIS:HB3	1.98	0.44
3:PR:44:CYS:SG	3:PR:73:ILE:HG21	2.57	0.44
1:AU:35:LEU:HD11	1:AU:48:VAL:CG1	2.47	0.44
2:XU:785:VAL:HG11	1:CT:80:ILE:CD1	2.47	0.44
1:BV:14:THR:HB	1:BV:19:PRO:HB2	1.99	0.44
1:E2:9:LEU:HG	1:E2:11:MET:HG3	1.99	0.44
1:E2:11:MET:HE3	1:E2:11:MET:HB2	1.87	0.44
1:D5:68:CYS:SG	1:D5:75:LEU:HB2	2.57	0.44
1:G5:9:LEU:HD11	1:G5:49:LEU:HD23	1.99	0.44
1:E6:11:MET:HE3	1:E6:79:HIS:HB3	1.98	0.44
1:F6:22:GLU:HG2	1:F6:71:VAL:HG21	1.98	0.44
1:C8:41:VAL:HB	1:C8:45:TYR:HB2	2.00	0.44
1:D9:11:MET:HE3	1:D9:79:HIS:HB3	1.98	0.44
1:H9:11:MET:HE3	1:H9:11:MET:HB2	1.88	0.44
1:Cb:58:ASN:O	1:Cb:62:ARG:HG3	2.17	0.44
1:Eb:11:MET:HE3	1:Eb:11:MET:HB2	1.87	0.44
2:Xb:785:VAL:HG11	1:Ca:80:ILE:CD1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:He:11:MET:HB3	1:Gi:18:VAL:HG22	1.99	0.44
1:Bc:77:ALA:HB2	1:Fc:72:GLY:HA2	1.99	0.44
1:Gc:68:CYS:SG	1:Gc:75:LEU:HB2	2.57	0.44
1:Cd:80:ILE:CD1	2:Xc:785:VAL:HG11	2.48	0.44
1:Gg:23:ALA:O	1:Gg:27:MET:HG3	2.16	0.44
2:Xi:863:TYR:CD2	2:Xi:869:GLY:HA3	2.51	0.44
1:Dl:27:MET:HE1	1:Dl:48:VAL:HG12	1.99	0.44
1:Cv:30:ALA:O	1:Gv:82:ALA:HB3	2.16	0.44
1:Hx:80:ILE:CD1	2:XM:713:ILE:CG2	2.95	0.44
1:GA:72:GLY:HA2	1:HK:77:ALA:HB2	1.99	0.44
3:PA:1:MET:HE1	3:PC:39:VAL:HG23	1.99	0.44
1:Az:72:GLY:HA2	1:Fz:77:ALA:HB2	1.99	0.44
2:Xz:775:CYS:HA	2:Xz:793:CYS:HA	2.00	0.44
1:BB:14:THR:HB	1:BB:19:PRO:HB2	1.99	0.44
1:CB:41:VAL:HB	1:CB:45:TYR:HB2	2.00	0.44
1:GE:27:MET:HG2	1:GE:60:ALA:O	2.16	0.44
2:XE:841:PRO:HG3	1:FI:69:GLU:O	2.17	0.44
3:PE:44:CYS:SG	3:PE:73:ILE:HG21	2.57	0.44
1:DH:11:MET:HE3	1:DH:79:HIS:HB3	1.98	0.44
1:DH:27:MET:HG2	1:DH:60:ALA:O	2.18	0.44
1:FH:61:VAL:HG12	2:XH:795:ILE:HD12	2.00	0.44
1:GH:72:GLY:CA	1:Hx:77:ALA:HB2	2.48	0.44
3:PK:1:MET:HE1	3:PM:39:VAL:HG23	1.99	0.44
1:AJ:88:VAL:O	1:AJ:91:ILE:HG12	2.17	0.44
2:XJ:841:PRO:HG3	1:FN:69:GLU:O	2.17	0.44
2:XL:729:GLU:HA	1:DP:62:ARG:NH1	2.31	0.44
1:EM:14:THR:HB	1:EM:19:PRO:HB2	1.99	0.44
1:HM:38:ARG:HH22	1:HM:97:GLN:HE21	1.66	0.44
1:AS:62:ARG:HG2	2:XS:724:ILE:HG13	1.98	0.44
1:AS:94:LYS:HE2	1:AS:94:LYS:HB3	1.85	0.44
1:BQ:14:THR:HB	1:BQ:19:PRO:HB2	1.99	0.44
2:XQ:785:VAL:HG11	1:CR:80:ILE:CD1	2.48	0.44
1:BU:23:ALA:O	1:BU:27:MET:HG3	2.17	0.44
1:ET:11:MET:HE3	1:ET:79:HIS:HB3	1.98	0.44
2:XT:775:CYS:HA	2:XT:793:CYS:HA	2.00	0.44
1:AX:9:LEU:HD11	1:AX:49:LEU:HD23	1.99	0.44
1:FV:41:VAL:HB	1:FV:45:TYR:HB2	1.98	0.44
1:HW:38:ARG:HH22	1:HW:97:GLN:HE21	1.66	0.44
1:G3:68:CYS:SG	1:G3:75:LEU:HB2	2.57	0.44
1:F4:61:VAL:HG12	2:X4:795:ILE:HD12	2.00	0.44
2:X4:713:ILE:CG2	1:HS:80:ILE:CD1	2.95	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A7:35:LEU:HD11	1:A7:48:VAL:CG1	2.47	0.44
3:P6:44:CYS:SG	3:P6:73:ILE:HG21	2.57	0.44
1:F8:11:MET:HE3	1:F8:11:MET:HB2	1.81	0.44
1:Ab:9:LEU:HD11	1:Ab:49:LEU:HD23	1.98	0.44
1:Ce:88:VAL:HG21	1:Ee:25:ASP:HA	1.99	0.44
1:Ad:25:ASP:HA	1:Fd:88:VAL:HG21	1.99	0.44
2:Xd:714:THR:HA	2:Xd:718:MET:HG3	1.99	0.44
1:Ag:9:LEU:HD11	1:Ag:49:LEU:HD23	1.98	0.44
1:Dg:27:MET:HE1	1:Dg:48:VAL:HG12	1.99	0.44
2:Xg:825:ALA:HB1	1:Df:73:ASP:O	2.16	0.44
1:Gf:21:ILE:HD13	1:HJ:92:LEU:HD21	1.98	0.44
2:Xh:806:ILE:HG21	1:Gi:80:ILE:HD12	1.99	0.44
1:Ai:25:ASP:HA	1:Fi:88:VAL:HG21	1.99	0.44
1:Fn:61:VAL:HG12	2:Xn:795:ILE:HD12	2.00	0.44
1:Hn:38:ARG:HH22	1:Hn:97:GLN:HE21	1.66	0.44
1:Hn:79:HIS:CE1	1:GX:22:GLU:OE2	2.62	0.44
1:Aq:35:LEU:HD11	1:Aq:48:VAL:CG1	2.47	0.44
1:Cq:58:ASN:O	1:Cq:62:ARG:HG3	2.17	0.44
2:Xp:775:CYS:HA	2:Xp:793:CYS:HA	2.00	0.44
2:Xv:785:VAL:HG11	1:Cu:80:ILE:CD1	2.47	0.44
1:AC:25:ASP:HA	1:FC:88:VAL:HG21	1.99	0.44
1:CC:80:ILE:CD1	2:XB:785:VAL:HG11	2.48	0.44
1:GC:80:ILE:HD12	2:XB:806:ILE:HG21	1.99	0.44
3:PC:44:CYS:SG	3:PC:73:ILE:HG21	2.57	0.44
1:HF:12:ILE:HG23	1:HF:75:LEU:HD12	1.98	0.44
1:CG:94:LYS:HE3	1:CG:94:LYS:HB3	1.79	0.44
2:XH:714:THR:HA	2:XH:718:MET:HG3	1.99	0.44
2:XJ:775:CYS:HA	2:XJ:793:CYS:HA	2.00	0.44
1:AN:9:LEU:HD11	1:AN:49:LEU:HD23	1.99	0.44
3:PO:44:CYS:SG	3:PO:73:ILE:HG21	2.57	0.44
1:AS:9:LEU:HD11	1:AS:49:LEU:HD23	1.99	0.44
1:GQ:68:CYS:SG	1:GQ:75:LEU:HB2	2.57	0.44
1:AT:88:VAL:O	1:AT:91:ILE:HG12	2.17	0.44
1:CT:12:ILE:HB	1:CT:48:VAL:HG13	1.98	0.44
1:CV:41:VAL:HB	1:CV:45:TYR:HB2	2.00	0.44
1:Hz:11:MET:HE3	1:Hz:11:MET:HB2	1.88	0.44
1:B1:83:ARG:HH12	1:E5:29:LYS:HA	1.81	0.44
1:C3:41:VAL:HB	1:C3:45:TYR:HB2	2.00	0.44
2:X9:714:THR:HA	2:X9:718:MET:HG3	1.99	0.44
1:Ca:84:VAL:HG12	1:Ca:88:VAL:HB	1.98	0.44
1:Ga:27:MET:HG2	1:Ga:60:ALA:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:De:68:CYS:SG	1:De:75:LEU:HB2	2.57	0.44
1:Ad:77:ALA:HB2	1:Dd:72:GLY:CA	2.44	0.44
1:Ed:57:VAL:HG12	1:Ed:80:ILE:HG23	1.97	0.44
1:Gd:72:GLY:CA	1:H6:77:ALA:HB2	2.48	0.44
1:Hg:11:MET:HE3	1:Hg:11:MET:HB2	1.88	0.44
1:Gh:68:CYS:SG	1:Gh:75:LEU:HB2	2.58	0.44
1:Di:27:MET:HG2	1:Di:60:ALA:O	2.18	0.44
1:Cl:58:ASN:O	1:Cl:62:ARG:HG3	2.17	0.44
1:Co:88:VAL:HG21	1:Eo:25:ASP:HA	1.99	0.44
1:Do:68:CYS:SG	1:Do:75:LEU:HB2	2.57	0.44
1:Dn:27:MET:HG2	1:Dn:60:ALA:O	2.17	0.44
1:Bp:94:LYS:HD3	1:Bp:94:LYS:HA	1.70	0.44
1:Cr:94:LYS:HE3	1:Cr:94:LYS:HB3	1.79	0.44
1:Gv:25:ASP:HA	1:HM:88:VAL:CG2	2.41	0.44
1:Hv:12:ILE:HG23	1:Hv:75:LEU:HD12	1.99	0.44
3:Pv:1:MET:HE1	3:Px:39:VAL:HG23	1.99	0.44
1:Ay:62:ARG:HG2	2:Xy:724:ILE:HG13	1.98	0.44
2:Xw:785:VAL:HG11	1:Cx:80:ILE:CD1	2.48	0.44
2:Xw:806:ILE:HG21	1:Gx:80:ILE:HD12	1.99	0.44
1:Cx:58:ASN:O	1:Cx:62:ARG:HG3	2.17	0.44
2:Xx:714:THR:HA	2:Xx:718:MET:HG3	1.99	0.44
1:AD:94:LYS:HE2	1:AD:94:LYS:HB3	1.85	0.44
1:GD:9:LEU:HD11	1:GD:49:LEU:HD23	1.99	0.44
1:BB:77:ALA:HB2	1:FB:72:GLY:HA2	1.99	0.44
1:DC:11:MET:HE3	1:DC:79:HIS:HB3	1.98	0.44
1:BF:23:ALA:O	1:BF:27:MET:HG3	2.18	0.44
2:XE:775:CYS:HA	2:XE:793:CYS:HA	2.00	0.44
1:HH:38:ARG:HH22	1:HH:97:GLN:HE21	1.66	0.44
1:GL:41:VAL:HB	1:GL:45:TYR:HB2	1.98	0.44
1:GL:68:CYS:SG	1:GL:75:LEU:HB2	2.57	0.44
2:XL:785:VAL:HG11	1:CM:80:ILE:CD1	2.48	0.44
1:AP:35:LEU:HD11	1:AP:48:VAL:CG1	2.47	0.44
1:CR:58:ASN:O	1:CR:62:ARG:HG3	2.17	0.44
1:FR:61:VAL:HG12	2:XR:795:ILE:HD12	2.00	0.44
1:AU:94:LYS:HB3	1:AU:94:LYS:HE2	1.64	0.44
1:GX:9:LEU:HD11	1:GX:49:LEU:HD23	1.99	0.44
1:GW:80:ILE:HD12	2:XV:806:ILE:HG21	1.99	0.44
3:PW:30:LYS:HB2	3:PW:30:LYS:HE3	1.74	0.44
2:XB:790:LYS:HE2	2:XB:790:LYS:HB2	1.45	0.44
2:X1:841:PRO:HG3	1:F5:69:GLU:O	2.17	0.44
1:C5:58:ASN:O	1:C5:62:ARG:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H7:24:ALA:HB2	1:H7:48:VAL:HG11	1.99	0.44
1:B8:14:THR:HB	1:B8:19:PRO:HB2	1.99	0.44
1:G8:12:ILE:HG23	1:G8:75:LEU:HD12	1.99	0.44
1:Aa:88:VAL:O	1:Aa:91:ILE:HG12	2.17	0.44
1:Ae:62:ARG:HG2	2:Xe:724:ILE:HG13	1.98	0.44
1:Gd:80:ILE:HD12	2:Xc:806:ILE:HG21	1.99	0.44
1:Cg:14:THR:HB	1:Cg:19:PRO:HB2	1.99	0.44
2:Xg:714:THR:OG1	1:HJ:79:HIS:ND1	2.34	0.44
1:Af:11:MET:HE3	1:Af:11:MET:HB2	1.91	0.44
1:Ch:41:VAL:HB	1:Ch:45:TYR:HB2	2.00	0.44
2:Xl:785:VAL:HG11	1:Ck:80:ILE:CD1	2.47	0.44
1:Ak:88:VAL:O	1:Ak:91:ILE:HG12	2.17	0.44
1:Co:94:LYS:HE3	1:Co:94:LYS:HB3	1.73	0.44
1:Gm:12:ILE:HG23	1:Gm:75:LEU:HD12	1.99	0.44
2:Xn:863:TYR:CD2	2:Xn:869:GLY:HA3	2.51	0.44
1:Bp:70:ARG:HA	1:Bp:70:ARG:HD3	1.78	0.44
1:Cp:12:ILE:HG23	1:Cp:75:LEU:CD1	2.48	0.44
3:Pp:44:CYS:SG	3:Pp:73:ILE:HG21	2.57	0.44
1:Gt:9:LEU:HD11	1:Gt:49:LEU:HD23	1.99	0.44
1:Gt:25:ASP:CA	1:HI:88:VAL:HG21	2.48	0.44
1:Cr:41:VAL:HB	1:Cr:45:TYR:HB2	2.00	0.44
1:Cs:80:ILE:CD1	2:Xr:785:VAL:HG11	2.48	0.44
1:Av:9:LEU:HD11	1:Av:49:LEU:HD23	1.98	0.44
1:Hv:24:ALA:HB2	1:Hv:48:VAL:HG11	1.99	0.44
1:Gw:68:CYS:SG	1:Gw:75:LEU:HB2	2.58	0.44
1:AA:9:LEU:HD11	1:AA:49:LEU:HD23	1.99	0.44
1:CE:12:ILE:HB	1:CE:48:VAL:HG13	1.98	0.44
1:GI:9:LEU:HD11	1:GI:49:LEU:HD23	1.99	0.44
1:AK:94:LYS:HE2	1:AK:94:LYS:HB3	1.64	0.44
1:BN:94:LYS:HA	1:BN:94:LYS:HD3	1.75	0.44
1:CN:58:ASN:O	1:CN:62:ARG:HG3	2.17	0.44
1:GL:12:ILE:HG23	1:GL:75:LEU:HD12	1.99	0.44
1:GV:12:ILE:HG23	1:GV:75:LEU:HD12	1.99	0.44
1:GV:68:CYS:SG	1:GV:75:LEU:HB2	2.57	0.44
2:XW:863:TYR:CD2	2:XW:869:GLY:HA3	2.51	0.44
2:X3:729:GLU:HA	1:D7:62:ARG:NH1	2.31	0.44
1:D4:27:MET:HG2	1:D4:60:ALA:O	2.18	0.44
2:X4:714:THR:HA	2:X4:718:MET:HG3	1.99	0.44
1:F9:61:VAL:HG12	2:X9:795:ILE:HD12	2.00	0.44
1:Dd:27:MET:HG2	1:Dd:60:ALA:O	2.18	0.44
1:Fd:61:VAL:HG12	2:Xd:795:ILE:HD12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bj:94:LYS:HD3	1:Bj:94:LYS:HA	1.75	0.44
1:Ah:18:VAL:HG22	1:Fh:11:MET:HB3	2.00	0.44
1:Gq:35:LEU:HD11	1:Gq:48:VAL:CG1	2.37	0.44
1:Ap:72:GLY:HA2	1:Fp:77:ALA:HB2	1.99	0.44
1:Bt:25:ASP:HA	1:Et:88:VAL:HG21	2.00	0.44
1:Gr:12:ILE:HG23	1:Gr:75:LEU:HD12	1.99	0.44
1:Hs:7:ILE:H	1:Hs:7:ILE:HG13	1.57	0.44
1:Av:35:LEU:HD11	1:Av:48:VAL:CG1	2.47	0.44
2:Xu:790:LYS:HB2	2:Xu:790:LYS:HE2	1.76	0.44
3:Pu:44:CYS:SG	3:Pu:73:ILE:HG21	2.57	0.44
1:Hw:91:ILE:CG2	1:Gz:35:LEU:CD2	2.87	0.44
1:Ex:14:THR:HB	1:Ex:19:PRO:HB2	1.99	0.44
1:BA:23:ALA:O	1:BA:27:MET:HG3	2.18	0.44
1:HA:24:ALA:HB2	1:HA:48:VAL:HG11	1.99	0.44
1:FD:11:MET:HE3	1:FD:11:MET:HB2	1.87	0.44
1:GB:68:CYS:SG	1:GB:75:LEU:HB2	2.58	0.44
1:EF:9:LEU:HG	1:EF:11:MET:HG3	1.99	0.44
1:BE:72:GLY:CA	1:EE:77:ALA:HB2	2.48	0.44
1:EE:11:MET:HE3	1:EE:79:HIS:HB3	1.98	0.44
1:BI:25:ASP:HA	1:EI:88:VAL:HG21	2.00	0.44
1:EK:9:LEU:HG	1:EK:11:MET:HG3	1.99	0.44
1:HK:12:ILE:HG23	1:HK:75:LEU:HD12	1.98	0.44
1:BL:14:THR:HB	1:BL:19:PRO:HB2	1.99	0.44
1:CL:94:LYS:HE3	1:CL:94:LYS:HB3	1.79	0.44
1:CQ:94:LYS:HE3	1:CQ:94:LYS:HB3	1.79	0.44
1:FU:11:MET:HE3	1:FU:11:MET:HB2	1.94	0.44
1:A1:88:VAL:O	1:A1:91:ILE:HG12	2.17	0.44
3:P7:1:MET:HE1	3:P9:39:VAL:HG23	1.99	0.44
1:B0:25:ASP:HA	1:E0:88:VAL:HG21	2.00	0.44
1:C0:58:ASN:O	1:C0:62:ARG:HG3	2.17	0.44
1:C0:88:VAL:HG21	1:E0:25:ASP:HA	1.99	0.44
1:G8:68:CYS:SG	1:G8:75:LEU:HB2	2.57	0.44
1:Eb:9:LEU:HG	1:Eb:11:MET:HG3	1.99	0.44
2:Xb:718:MET:HE3	2:Xb:718:MET:HB3	1.66	0.44
1:Ag:35:LEU:HD11	1:Ag:48:VAL:CG1	2.47	0.44
1:Gg:35:LEU:HD21	1:HU:91:ILE:HG21	2.00	0.44
3:Pg:1:MET:HE1	3:Pi:39:VAL:HG23	1.99	0.44
1:Bj:14:THR:HB	1:Bj:19:PRO:HB2	1.98	0.44
1:Cl:14:THR:HB	1:Cl:19:PRO:HB2	1.99	0.44
1:Cn:41:VAL:HB	1:Cn:45:TYR:HB2	1.98	0.44
3:Pn:44:CYS:SG	3:Pn:73:ILE:HG21	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Bq:23:ALA:O	1:Bq:27:MET:HG3	2.18	0.44
2:Xp:841:PRO:HG3	1:Ft:69:GLU:O	2.17	0.44
1:Hs:38:ARG:HH22	1:Hs:97:GLN:HE21	1.66	0.44
2:Xv:718:MET:HB3	2:Xv:718:MET:HE3	1.65	0.44
1:Eu:11:MET:HE3	1:Eu:11:MET:HB2	1.68	0.44
1:Ax:77:ALA:HB2	1:Dx:72:GLY:CA	2.44	0.44
1:AA:35:LEU:HD11	1:AA:48:VAL:CG1	2.47	0.44
2:XA:785:VAL:HG11	1:Cz:80:ILE:CD1	2.47	0.44
1:CD:94:LYS:HB3	1:CD:94:LYS:HE3	1.73	0.44
3:PB:30:LYS:HB2	3:PB:30:LYS:HE3	1.79	0.44
1:BG:77:ALA:HB2	1:FG:72:GLY:HA2	2.00	0.44
1:CH:41:VAL:HB	1:CH:45:TYR:HB2	1.98	0.44
1:BL:77:ALA:HB2	1:FL:72:GLY:HA2	1.99	0.44
1:CM:58:ASN:O	1:CM:62:ARG:HG3	2.17	0.44
1:FM:61:VAL:HG12	2:XM:795:ILE:HD12	2.00	0.44
1:AP:94:LYS:HB3	1:AP:94:LYS:HE2	1.64	0.44
1:DS:68:CYS:SG	1:DS:75:LEU:HB2	2.57	0.44
1:CU:14:THR:HB	1:CU:19:PRO:HB2	1.99	0.44
3:PT:44:CYS:SG	3:PT:73:ILE:HG21	2.57	0.44
1:D5:27:MET:CE	1:D5:48:VAL:HG12	2.48	0.44
2:X5:713:ILE:HG22	1:Hd:80:ILE:HD12	1.98	0.44
1:A8:18:VAL:HG22	1:F8:11:MET:HB3	2.00	0.44
1:Hb:12:ILE:HG23	1:Hb:75:LEU:HD12	1.98	0.44
1:Ba:72:GLY:CA	1:Ea:77:ALA:HB2	2.48	0.44
1:Da:62:ARG:HH12	2:Xt:729:GLU:HA	1.81	0.44
1:Cd:58:ASN:O	1:Cd:62:ARG:HG3	2.17	0.44
2:Xf:790:LYS:HB2	2:Xf:790:LYS:HE2	1.76	0.44
1:Cj:58:ASN:O	1:Cj:62:ARG:HG3	2.17	0.44
3:Pj:14:ASN:HD21	3:Ph:76:ILE:HB	1.83	0.44
1:Bh:14:THR:HB	1:Bh:19:PRO:HB2	1.99	0.44
3:Pi:44:CYS:SG	3:Pi:73:ILE:HG21	2.57	0.44
1:Gm:68:CYS:SG	1:Gm:75:LEU:HB2	2.58	0.44
1:An:25:ASP:HA	1:Fm:88:VAL:HG21	1.99	0.44
1:Dn:32:GLU:CD	1:AT:7:ILE:HD11	2.43	0.44
1:Gn:72:GLY:CA	1:H1:77:ALA:HB2	2.47	0.44
1:Ct:58:ASN:O	1:Ct:62:ARG:HG3	2.17	0.44
1:Br:77:ALA:HB2	1:Fr:72:GLY:HA2	1.99	0.44
1:Cy:24:ALA:HB2	1:Cy:48:VAL:HG11	1.98	0.44
1:Aw:18:VAL:HG22	1:Fw:11:MET:HB3	2.00	0.44
1:Az:7:ILE:CD1	1:DG:32:GLU:OE2	2.66	0.44
1:AH:77:ALA:HB2	1:DH:72:GLY:CA	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DN:27:MET:CE	1:DN:48:VAL:HG12	2.48	0.44
1:BM:11:MET:HB2	1:BM:11:MET:HE3	1.77	0.44
1:BP:23:ALA:O	1:BP:27:MET:HG3	2.18	0.44
2:XP:727:THR:O	2:XP:728:PRO:C	2.58	0.44
1:EO:11:MET:HE3	1:EO:79:HIS:HB3	1.98	0.44
1:BS:25:ASP:HA	1:ES:88:VAL:HG21	2.00	0.44
1:DS:27:MET:CE	1:DS:48:VAL:HG12	2.48	0.44
1:CT:12:ILE:HG23	1:CT:75:LEU:CD1	2.48	0.44
1:CW:80:ILE:CD1	2:XV:785:VAL:HG11	2.48	0.44
1:FW:61:VAL:HG12	2:XW:795:ILE:HD12	2.00	0.44
3:P2:1:MET:HE1	3:P4:39:VAL:HG23	1.99	0.43
1:A3:18:VAL:HG22	1:F3:11:MET:HB3	2.00	0.43
1:H4:38:ARG:HH22	1:H4:97:GLN:HE21	1.66	0.43
1:A6:18:VAL:HG22	1:F6:11:MET:HB3	2.00	0.43
1:C6:12:ILE:HG23	1:C6:75:LEU:CD1	2.48	0.43
2:X6:775:CYS:HA	2:X6:793:CYS:HA	2.00	0.43
2:Xa:841:PRO:HG3	1:Fe:69:GLU:O	2.17	0.43
1:He:80:ILE:CD1	2:XE:713:ILE:CG2	2.85	0.43
1:Dc:11:MET:HE3	1:Dc:79:HIS:HB3	2.00	0.43
1:Aj:9:LEU:HD11	1:Aj:49:LEU:HD23	1.99	0.43
3:Ph:19:MET:HE1	3:Ph:24:LEU:HD21	2.00	0.43
1:Fk:22:GLU:HG2	1:Fk:71:VAL:HG21	1.98	0.43
1:Ao:9:LEU:HD11	1:Ao:49:LEU:HD23	1.99	0.43
1:Go:9:LEU:HD11	1:Go:49:LEU:HD23	2.00	0.43
1:Ap:18:VAL:HG22	1:Fp:11:MET:HB3	2.00	0.43
1:Ar:18:VAL:HG22	1:Fr:11:MET:HB3	2.00	0.43
1:Dr:11:MET:HE3	1:Dr:79:HIS:HB3	2.00	0.43
1:Gv:6:GLY:N	1:Gv:34:ARG:HH12	2.16	0.43
1:Ay:9:LEU:HD11	1:Ay:49:LEU:HD23	1.99	0.43
1:By:25:ASP:HA	1:Ey:88:VAL:HG21	2.00	0.43
3:Pw:19:MET:HE1	3:Pw:24:LEU:HD21	2.00	0.43
1:DA:27:MET:HE1	1:DA:48:VAL:HG12	1.99	0.43
1:DB:11:MET:HE3	1:DB:79:HIS:HB3	2.00	0.43
1:CH:58:ASN:O	1:CH:62:ARG:HG3	2.17	0.43
2:XH:812:GLN:HE21	2:XH:812:GLN:HB2	1.71	0.43
1:CJ:84:VAL:HG12	1:CJ:88:VAL:HB	1.98	0.43
1:EJ:11:MET:HE3	1:EJ:11:MET:HB2	1.68	0.43
1:HJ:94:LYS:HE2	1:HJ:94:LYS:HB2	1.87	0.43
1:AL:18:VAL:HG22	1:FL:11:MET:HB3	2.00	0.43
1:AM:25:ASP:HA	1:FM:88:VAL:HG21	1.99	0.43
2:XM:714:THR:HA	2:XM:718:MET:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XM:863:TYR:CD2	2:XM:869:GLY:HA3	2.51	0.43
1:AQ:18:VAL:HG22	1:FQ:11:MET:HB3	2.00	0.43
1:AT:72:GLY:HA2	1:FT:77:ALA:HB2	1.99	0.43
1:BX:25:ASP:HA	1:EX:88:VAL:HG21	2.00	0.43
3:P1:44:CYS:SG	3:P1:73:ILE:HG21	2.57	0.43
1:B5:25:ASP:HA	1:E5:88:VAL:HG21	2.00	0.43
1:B3:14:THR:HB	1:B3:19:PRO:HB2	1.99	0.43
1:C4:58:ASN:O	1:C4:62:ARG:HG3	2.17	0.43
3:P8:19:MET:HE1	3:P8:24:LEU:HD21	2.00	0.43
3:P9:50:VAL:HB	3:P9:73:ILE:HG23	2.00	0.43
1:Ca:12:ILE:HG23	1:Ca:75:LEU:CD1	2.48	0.43
1:De:27:MET:CE	1:De:48:VAL:HG12	2.48	0.43
1:Bc:14:THR:HB	1:Bc:19:PRO:HB2	1.99	0.43
1:Gc:12:ILE:HG23	1:Gc:75:LEU:HD12	1.99	0.43
1:Ck:12:ILE:HG23	1:Ck:75:LEU:CD1	2.48	0.43
1:Cn:80:ILE:CD1	2:Xm:785:VAL:HG11	2.48	0.43
1:Ds:11:MET:HE3	1:Ds:79:HIS:HB3	1.98	0.43
1:Ev:11:MET:HE3	1:Ev:11:MET:HB2	1.88	0.43
1:Dx:12:ILE:HG23	1:Dx:75:LEU:CD1	2.49	0.43
1:Fx:61:VAL:HG12	2:Xx:795:ILE:HD12	2.00	0.43
1:Gx:25:ASP:HA	1:HA:88:VAL:CG2	2.44	0.43
1:Hx:38:ARG:HH22	1:Hx:97:GLN:HE21	1.66	0.43
1:AA:27:MET:HG2	1:AA:60:ALA:O	2.16	0.43
1:Bz:72:GLY:CA	1:Ez:77:ALA:HB2	2.48	0.43
3:Pz:5:GLN:HA	3:Pz:48:ASP:O	2.19	0.43
1:GC:11:MET:HE3	1:GC:79:HIS:HB3	1.99	0.43
1:HC:38:ARG:HH22	1:HC:97:GLN:HE21	1.66	0.43
3:PF:1:MET:HE1	3:PH:39:VAL:HG23	1.99	0.43
3:PH:44:CYS:SG	3:PH:73:ILE:HG21	2.57	0.43
1:CO:12:ILE:HG23	1:CO:75:LEU:CD1	2.48	0.43
1:BQ:77:ALA:HB2	1:FQ:72:GLY:HA2	1.99	0.43
2:XQ:806:ILE:HG21	1:GR:80:ILE:HD12	1.99	0.43
3:PQ:16:ILE:HG13	3:PQ:19:MET:HG2	2.01	0.43
1:AV:23:ALA:O	1:AV:27:MET:HG3	2.18	0.43
1:BV:23:ALA:O	1:BV:27:MET:HG3	2.19	0.43
3:PW:5:GLN:HA	3:PW:48:ASP:O	2.19	0.43
1:B2:23:ALA:O	1:B2:27:MET:HG3	2.18	0.43
1:D2:27:MET:HE1	1:D2:48:VAL:HG12	1.99	0.43
1:H2:80:ILE:HD12	2:XX:713:ILE:HG22	2.00	0.43
1:A1:30:ALA:O	1:Hm:82:ALA:HB3	2.18	0.43
3:P5:14:ASN:HD21	3:P3:76:ILE:HB	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P3:16:ILE:HG13	3:P3:19:MET:HG2	2.00	0.43
1:D4:12:ILE:HG23	1:D4:75:LEU:CD1	2.49	0.43
3:P4:50:VAL:HB	3:P4:73:ILE:HG23	2.00	0.43
1:D0:27:MET:CE	1:D0:48:VAL:HG12	2.48	0.43
1:H8:82:ALA:HB3	1:Au:30:ALA:O	2.18	0.43
1:C9:11:MET:HE3	1:C9:11:MET:HB2	1.89	0.43
1:D9:12:ILE:HG23	1:D9:75:LEU:CD1	2.49	0.43
3:P9:5:GLN:HA	3:P9:48:ASP:O	2.19	0.43
1:Be:25:ASP:HA	1:Ee:88:VAL:HG21	2.00	0.43
1:Ac:23:ALA:O	1:Ac:27:MET:HG3	2.19	0.43
2:Xf:775:CYS:HA	2:Xf:793:CYS:HA	2.00	0.43
1:Hi:38:ARG:HH22	1:Hi:97:GLN:HE21	1.66	0.43
1:Hi:80:ILE:CD1	2:XU:713:ILE:CG2	2.96	0.43
1:Bl:70:ARG:HA	1:Bl:70:ARG:HD3	1.86	0.43
1:Gl:35:LEU:HD11	1:Gl:48:VAL:CG1	2.37	0.43
1:Ak:7:ILE:CD1	1:Dr:32:GLU:OE2	2.66	0.43
1:Fo:65:ALA:O	1:Fo:66:ASP:C	2.61	0.43
1:Am:23:ALA:O	1:Am:27:MET:HG3	2.19	0.43
1:As:25:ASP:HA	1:Fs:88:VAL:HG21	1.99	0.43
1:As:77:ALA:HB2	1:Ds:72:GLY:CA	2.44	0.43
1:Hv:11:MET:HE3	1:Hv:11:MET:HB2	1.88	0.43
2:Xv:727:THR:O	2:Xv:728:PRO:C	2.58	0.43
1:Du:35:LEU:CD1	1:Du:48:VAL:HG13	2.46	0.43
1:Gy:9:LEU:HD11	1:Gy:49:LEU:HD23	1.99	0.43
1:Aw:23:ALA:O	1:Aw:27:MET:HG3	2.19	0.43
1:GA:21:ILE:HD13	1:HK:92:LEU:HD21	1.99	0.43
3:PB:19:MET:HE1	3:PB:24:LEU:HD21	2.00	0.43
2:XK:727:THR:O	2:XK:728:PRO:C	2.58	0.43
1:BN:25:ASP:HA	1:EN:88:VAL:HG21	2.00	0.43
1:AP:9:LEU:HD11	1:AP:49:LEU:HD23	1.98	0.43
1:AO:88:VAL:O	1:AO:91:ILE:HG12	2.17	0.43
1:BQ:23:ALA:O	1:BQ:27:MET:HG3	2.19	0.43
1:GQ:41:VAL:HB	1:GQ:45:TYR:HB2	1.98	0.43
2:XR:714:THR:HA	2:XR:718:MET:HG3	1.99	0.43
3:PV:16:ILE:HG13	3:PV:19:MET:HG2	2.00	0.43
3:PV:19:MET:HE1	3:PV:24:LEU:HD21	2.00	0.43
1:DW:27:MET:HG2	1:DW:60:ALA:O	2.18	0.43
1:HW:7:ILE:H	1:HW:7:ILE:HG13	1.57	0.43
2:Xm:843:LYS:HE3	2:Xm:860:LEU:HD13	2.01	0.43
1:B5:18:VAL:HB	1:B5:19:PRO:HD3	2.01	0.43
3:P3:19:MET:HE1	3:P3:24:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P8:16:ILE:HG13	3:P8:19:MET:HG2	2.00	0.43
1:C9:80:ILE:CD1	2:X8:785:VAL:HG11	2.48	0.43
1:Ae:9:LEU:HD11	1:Ae:49:LEU:HD23	1.99	0.43
1:Be:75:LEU:HD11	1:Be:78:ALA:HB2	2.01	0.43
1:Dd:12:ILE:HG23	1:Dd:75:LEU:CD1	2.49	0.43
1:Dd:82:ALA:HB3	1:Hd:30:ALA:O	2.19	0.43
1:Eg:9:LEU:HG	1:Eg:11:MET:HG3	1.99	0.43
2:Xg:716:PRO:CD	1:HJ:80:ILE:O	2.63	0.43
1:Af:72:GLY:HA2	1:Ff:77:ALA:HB2	1.99	0.43
3:Pf:5:GLN:HA	3:Pf:48:ASP:O	2.19	0.43
2:Xh:790:LYS:HE2	2:Xh:790:LYS:HB2	1.45	0.43
1:Bm:23:ALA:O	1:Bm:27:MET:HG3	2.18	0.43
3:Pm:19:MET:HE1	3:Pm:24:LEU:HD21	2.00	0.43
1:Hn:82:ALA:HB3	1:AT:30:ALA:O	2.18	0.43
3:Pn:50:VAL:HB	3:Pn:73:ILE:HG23	2.00	0.43
1:Bp:57:VAL:HG12	1:Bp:80:ILE:HG23	2.01	0.43
1:Cv:14:THR:HB	1:Cv:19:PRO:HB2	1.99	0.43
1:Fv:94:LYS:HB2	1:Fv:94:LYS:HE3	1.78	0.43
1:Dx:82:ALA:HB3	1:Hx:30:ALA:O	2.19	0.43
1:CD:88:VAL:HG21	1:ED:25:ASP:HA	1.99	0.43
1:DD:27:MET:CE	1:DD:48:VAL:HG12	2.48	0.43
1:AF:35:LEU:HD11	1:AF:48:VAL:CG1	2.47	0.43
1:BI:75:LEU:HD11	1:BI:78:ALA:HB2	2.01	0.43
3:PI:14:ASN:HD21	3:PG:76:ILE:HB	1.83	0.43
1:AH:25:ASP:HA	1:FH:88:VAL:HG21	1.99	0.43
1:CH:80:ILE:CD1	2:XG:785:VAL:HG11	2.48	0.43
1:EH:14:THR:HB	1:EH:19:PRO:HB2	1.99	0.43
2:XK:785:VAL:HG11	1:CJ:80:ILE:CD1	2.47	0.43
1:BJ:70:ARG:HA	1:BJ:70:ARG:HD3	1.79	0.43
1:BN:75:LEU:HD11	1:BN:78:ALA:HB2	2.01	0.43
1:GM:23:ALA:O	1:GM:27:MET:HG3	2.19	0.43
1:AO:7:ILE:CD1	1:DV:32:GLU:OE2	2.66	0.43
1:AO:72:GLY:HA2	1:FO:77:ALA:HB2	1.99	0.43
1:DR:12:ILE:HG23	1:DR:75:LEU:CD1	2.49	0.43
1:DR:27:MET:HG2	1:DR:60:ALA:O	2.17	0.43
2:XU:818:ASN:HA	2:XU:819:PRO:HD3	1.82	0.43
1:BT:72:GLY:CA	1:ET:77:ALA:HB2	2.48	0.43
3:PT:50:VAL:HB	3:PT:73:ILE:HG23	2.00	0.43
1:CX:58:ASN:O	1:CX:62:ARG:HG3	2.17	0.43
1:GW:72:GLY:CA	1:HO:77:ALA:HB2	2.48	0.43
3:PW:50:VAL:HB	3:PW:73:ILE:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X3:785:VAL:HG11	1:C4:80:ILE:CD1	2.48	0.43
1:B7:23:ALA:O	1:B7:27:MET:HG3	2.18	0.43
3:P6:50:VAL:HB	3:P6:73:ILE:HG23	2.00	0.43
2:X0:713:ILE:HG22	1:HF:80:ILE:HD12	2.00	0.43
1:H9:83:ARG:NH1	1:AQ:28:THR:O	2.51	0.43
1:Ab:94:LYS:HE2	1:Ab:94:LYS:HB3	1.64	0.43
1:Db:68:CYS:SG	1:Db:75:LEU:HD13	2.59	0.43
1:Aa:18:VAL:HG22	1:Fa:11:MET:HB3	2.01	0.43
2:Xa:775:CYS:HA	2:Xa:793:CYS:HA	2.00	0.43
2:Xa:818:ASN:HA	2:Xa:819:PRO:HD3	1.80	0.43
2:Xe:785:VAL:HG21	1:Cc:62:ARG:HG2	2.01	0.43
1:Bf:70:ARG:HD3	1:Bf:70:ARG:HA	1.79	0.43
1:Bj:18:VAL:HB	1:Bj:19:PRO:HD3	2.01	0.43
2:Xj:714:THR:OG1	1:Hs:79:HIS:ND1	1.87	0.43
3:Pl:6:VAL:HA	3:Pl:27:VAL:HG12	2.01	0.43
3:Pk:5:GLN:HA	3:Pk:48:ASP:O	2.19	0.43
3:Pn:5:GLN:HA	3:Pn:48:ASP:O	2.19	0.43
3:Pq:6:VAL:HA	3:Pq:27:VAL:HG12	2.01	0.43
3:Pt:14:ASN:HD21	3:Pr:76:ILE:HB	1.84	0.43
1:Au:18:VAL:HG22	1:Fu:11:MET:HB3	2.00	0.43
3:Pu:5:GLN:HA	3:Pu:48:ASP:O	2.19	0.43
1:Cy:58:ASN:O	1:Cy:62:ARG:HG3	2.17	0.43
3:PC:50:VAL:HB	3:PC:73:ILE:HG23	2.00	0.43
1:HF:11:MET:HE3	1:HF:11:MET:HB2	1.88	0.43
1:BI:41:VAL:HB	1:BI:45:TYR:HB2	2.01	0.43
1:DG:11:MET:HE3	1:DG:79:HIS:HB3	2.00	0.43
2:XH:863:TYR:CD2	2:XH:869:GLY:HA3	2.51	0.43
1:BK:23:ALA:O	1:BK:27:MET:HG3	2.18	0.43
1:DM:12:ILE:HG23	1:DM:75:LEU:CD1	2.49	0.43
2:XS:785:VAL:HG21	1:CQ:62:ARG:HG2	2.01	0.43
1:BR:11:MET:HE3	1:BR:11:MET:HB2	1.76	0.43
1:CU:84:VAL:HG12	1:CU:88:VAL:HB	2.01	0.43
3:PU:1:MET:HE1	3:PW:39:VAL:HG23	1.99	0.43
3:PT:5:GLN:HA	3:PT:48:ASP:O	2.19	0.43
1:BV:77:ALA:HB2	1:FV:72:GLY:HA2	1.99	0.43
1:G2:6:GLY:N	1:G2:34:ARG:HH12	2.16	0.43
1:H2:88:VAL:CG2	1:GV:25:ASP:HA	2.47	0.43
1:D5:27:MET:HG2	1:D5:60:ALA:O	2.19	0.43
2:X5:785:VAL:HG21	1:C3:62:ARG:HG2	2.01	0.43
1:A7:23:ALA:O	1:A7:27:MET:HG3	2.19	0.43
1:G7:6:GLY:N	1:G7:34:ARG:HH12	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P0:14:ASN:HD21	3:P8:76:ILE:HB	1.83	0.43
1:Ba:57:VAL:HG12	1:Ba:80:ILE:HG23	2.01	0.43
1:Ba:70:ARG:HA	1:Ba:70:ARG:HD3	1.78	0.43
1:Ha:92:LEU:CD2	1:Gr:21:ILE:HD13	2.49	0.43
3:Pe:14:ASN:HD21	3:Pc:76:ILE:HB	1.83	0.43
1:Af:18:VAL:HG22	1:Ff:11:MET:HB3	2.00	0.43
1:Bj:75:LEU:HD11	1:Bj:78:ALA:HB2	2.01	0.43
3:Pj:39:VAL:HG21	3:Pj:67:TYR:HE2	1.84	0.43
1:Fi:61:VAL:HG12	2:Xi:795:ILE:HD12	2.00	0.43
1:Gi:23:ALA:O	1:Gi:27:MET:HG3	2.19	0.43
1:Bl:29:LYS:HE2	3:Pl:45:ILE:HG22	2.01	0.43
1:Ak:18:VAL:HG22	1:Fk:11:MET:HB3	2.00	0.43
2:Xk:775:CYS:HA	2:Xk:793:CYS:HA	2.00	0.43
3:Po:39:VAL:HG21	3:Po:67:TYR:HE2	1.84	0.43
1:Dm:11:MET:HE3	1:Dm:79:HIS:HB3	2.00	0.43
1:Bt:75:LEU:HD11	1:Bt:78:ALA:HB2	2.01	0.43
1:Cu:12:ILE:HG23	1:Cu:75:LEU:CD1	2.48	0.43
3:Py:39:VAL:HG21	3:Py:67:TYR:HE2	1.84	0.43
1:Cw:41:VAL:HB	1:Cw:45:TYR:HB2	2.00	0.43
1:DA:68:CYS:SG	1:DA:75:LEU:HD13	2.59	0.43
1:BD:18:VAL:HB	1:BD:19:PRO:HD3	2.01	0.43
1:BD:75:LEU:HD11	1:BD:78:ALA:HB2	2.01	0.43
1:AB:18:VAL:HG22	1:FB:11:MET:HB3	2.00	0.43
1:DI:27:MET:CE	1:DI:48:VAL:HG12	2.48	0.43
3:PG:16:ILE:HG13	3:PG:19:MET:HG2	2.01	0.43
1:EK:11:MET:HE3	1:EK:11:MET:HB2	1.87	0.43
1:BJ:72:GLY:CA	1:EJ:77:ALA:HB2	2.48	0.43
1:BN:18:VAL:HB	1:BN:19:PRO:HD3	2.01	0.43
3:PN:14:ASN:HD21	3:PL:76:ILE:HB	1.83	0.43
1:DM:82:ALA:HB3	1:HM:30:ALA:O	2.19	0.43
1:BO:72:GLY:CA	1:EO:77:ALA:HB2	2.48	0.43
2:XO:775:CYS:HA	2:XO:793:CYS:HA	2.00	0.43
3:PO:5:GLN:HA	3:PO:48:ASP:O	2.19	0.43
1:CQ:41:VAL:HB	1:CQ:45:TYR:HB2	2.00	0.43
3:PR:50:VAL:HB	3:PR:73:ILE:HG23	2.00	0.43
1:DX:27:MET:CE	1:DX:48:VAL:HG12	2.48	0.43
3:PX:14:ASN:HD21	3:PV:76:ILE:HB	1.83	0.43
2:Xr:843:LYS:HE3	2:Xr:860:LEU:HD13	2.01	0.43
1:B1:72:GLY:CA	1:E1:77:ALA:HB2	2.48	0.43
3:P1:50:VAL:HB	3:P1:73:ILE:HG23	2.01	0.43
1:B3:23:ALA:O	1:B3:27:MET:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D3:11:MET:HE3	1:D3:79:HIS:HB3	2.00	0.43
1:D7:68:CYS:SG	1:D7:75:LEU:HD13	2.59	0.43
1:B6:72:GLY:CA	1:E6:77:ALA:HB2	2.48	0.43
1:G0:9:LEU:HD11	1:G0:49:LEU:HD23	1.99	0.43
1:Ab:23:ALA:O	1:Ab:27:MET:HG3	2.19	0.43
1:Db:27:MET:HE1	1:Db:48:VAL:HG12	1.99	0.43
3:Pa:50:VAL:HB	3:Pa:73:ILE:HG23	2.01	0.43
3:Pd:50:VAL:HB	3:Pd:73:ILE:HG23	2.01	0.43
1:Dg:32:GLU:HG3	1:AJ:83:ARG:NH1	2.33	0.43
1:Gg:6:GLY:N	1:Gg:34:ARG:HH12	2.16	0.43
1:Hg:77:ALA:HB2	1:GN:72:GLY:HA2	2.00	0.43
1:Gj:9:LEU:HD11	1:Gj:49:LEU:HD23	1.99	0.43
1:Gj:84:VAL:HG13	1:Gj:88:VAL:HB	2.01	0.43
1:Bh:23:ALA:O	1:Bh:27:MET:HG3	2.19	0.43
3:Pi:50:VAL:HB	3:Pi:73:ILE:HG23	2.01	0.43
1:Dl:68:CYS:SG	1:Dl:75:LEU:HD13	2.59	0.43
2:Xl:718:MET:HE3	2:Xl:718:MET:HB3	1.65	0.43
1:Do:27:MET:CE	1:Do:48:VAL:HG12	2.48	0.43
1:Hn:11:MET:HB3	1:GX:18:VAL:HG22	2.00	0.43
1:Cq:84:VAL:HG12	1:Cq:88:VAL:HB	2.01	0.43
1:Gq:6:GLY:N	1:Gq:34:ARG:HH12	2.16	0.43
1:Ft:65:ALA:O	1:Ft:66:ASP:C	2.61	0.43
1:Ar:23:ALA:O	1:Ar:27:MET:HG3	2.19	0.43
1:Br:23:ALA:O	1:Br:27:MET:HG3	2.19	0.43
1:Ds:12:ILE:HG23	1:Ds:75:LEU:CD1	2.48	0.43
1:Ds:27:MET:HG2	1:Ds:60:ALA:O	2.18	0.43
1:Gs:72:GLY:CA	1:Hk:77:ALA:HB2	2.48	0.43
3:Pv:6:VAL:HA	3:Pv:27:VAL:HG12	2.01	0.43
1:Dw:11:MET:HE3	1:Dw:79:HIS:HB3	2.00	0.43
3:Px:50:VAL:HB	3:Px:73:ILE:HG23	2.00	0.43
1:BA:29:LYS:HE2	3:PA:45:ILE:HG22	2.01	0.43
3:PD:6:VAL:HA	3:PD:27:VAL:HG12	2.01	0.43
1:BB:23:ALA:O	1:BB:27:MET:HG3	2.19	0.43
1:DC:27:MET:HG2	1:DC:60:ALA:O	2.18	0.43
1:DC:82:ALA:HB3	1:HC:30:ALA:O	2.19	0.43
1:CF:84:VAL:HG12	1:CF:88:VAL:HB	2.01	0.43
1:AE:12:ILE:HD12	1:AE:27:MET:SD	2.59	0.43
1:BE:57:VAL:HG12	1:BE:80:ILE:HG23	2.01	0.43
1:AG:18:VAL:HG22	1:FG:11:MET:HB3	2.00	0.43
1:FG:11:MET:HE3	1:FG:11:MET:HB2	1.81	0.43
1:DH:82:ALA:HB3	1:HH:30:ALA:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GH:23:ALA:O	1:GH:27:MET:HG3	2.19	0.43
1:BK:70:ARG:HA	1:BK:70:ARG:HD3	1.86	0.43
1:CJ:12:ILE:HG23	1:CJ:75:LEU:CD1	2.48	0.43
1:DS:27:MET:HG2	1:DS:60:ALA:O	2.19	0.43
3:PR:5:GLN:HA	3:PR:48:ASP:O	2.18	0.43
1:BT:57:VAL:HG12	1:BT:80:ILE:HG23	2.01	0.43
1:DW:82:ALA:HB3	1:HW:30:ALA:O	2.19	0.43
1:C1:12:ILE:HG23	1:C1:75:LEU:CD1	2.48	0.43
1:B5:41:VAL:HB	1:B5:45:TYR:HB2	2.01	0.43
1:A3:23:ALA:O	1:A3:27:MET:HG3	2.19	0.43
3:P6:5:GLN:HA	3:P6:48:ASP:O	2.19	0.43
1:D0:27:MET:HG2	1:D0:60:ALA:O	2.19	0.43
1:B8:77:ALA:HB2	1:F8:72:GLY:HA2	1.99	0.43
1:D9:27:MET:HG2	1:D9:60:ALA:O	2.17	0.43
1:Gb:6:GLY:N	1:Gb:34:ARG:HH12	2.16	0.43
1:Hb:79:HIS:ND1	2:Xo:714:THR:OG1	1.90	0.43
3:Pb:6:VAL:HA	3:Pb:27:VAL:HG12	2.01	0.43
1:Bc:23:ALA:O	1:Bc:27:MET:HG3	2.19	0.43
1:Ag:72:GLY:HA2	1:Fg:77:ALA:HB2	2.01	0.43
1:Cf:12:ILE:HG23	1:Cf:75:LEU:CD1	2.48	0.43
1:Bj:41:VAL:HB	1:Bj:45:TYR:HB2	2.01	0.43
1:Dj:27:MET:CE	1:Dj:48:VAL:HG12	2.48	0.43
1:Ei:23:ALA:O	1:Ei:27:MET:HG3	2.19	0.43
1:Gl:6:GLY:N	1:Gl:34:ARG:HH12	2.16	0.43
1:Bo:75:LEU:HD11	1:Bo:78:ALA:HB2	2.01	0.43
2:Xo:785:VAL:HG21	1:Cm:62:ARG:HG2	2.01	0.43
1:Am:18:VAL:HG22	1:Fm:11:MET:HB3	2.00	0.43
3:Pp:5:GLN:HA	3:Pp:48:ASP:O	2.19	0.43
1:Dt:27:MET:HG2	1:Dt:60:ALA:O	2.19	0.43
1:Dt:27:MET:CE	1:Dt:48:VAL:HG12	2.48	0.43
1:Gr:68:CYS:SG	1:Gr:75:LEU:HB2	2.57	0.43
1:Av:72:GLY:HA2	1:Fv:77:ALA:HB2	2.01	0.43
1:Bv:23:ALA:O	1:Bv:27:MET:HG3	2.18	0.43
1:Au:12:ILE:HD12	1:Au:27:MET:SD	2.59	0.43
3:Pu:50:VAL:HB	3:Pu:73:ILE:HG23	2.01	0.43
3:Py:6:VAL:HA	3:Py:27:VAL:HG12	2.01	0.43
1:Bw:77:ALA:HB2	1:Fw:72:GLY:HA2	1.99	0.43
1:Dx:27:MET:HG2	1:Dx:60:ALA:O	2.17	0.43
1:Az:12:ILE:HD12	1:Az:27:MET:SD	2.59	0.43
1:FC:61:VAL:HG12	2:XC:795:ILE:HD12	2.00	0.43
3:PC:5:GLN:HA	3:PC:48:ASP:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:70:ARG:HA	1:BF:70:ARG:HD3	1.86	0.43
1:GF:6:GLY:N	1:GF:34:ARG:HH12	2.16	0.43
3:PE:50:VAL:HB	3:PE:73:ILE:HG23	2.01	0.43
2:XI:785:VAL:HG21	1:CG:62:ARG:HG2	2.01	0.43
3:PH:30:LYS:HB2	3:PH:30:LYS:HE3	1.74	0.43
1:GK:6:GLY:N	1:GK:34:ARG:HH12	2.16	0.43
1:GN:84:VAL:HG13	1:GN:88:VAL:HB	2.01	0.43
1:EP:11:MET:HE3	1:EP:11:MET:HB2	1.87	0.43
3:PQ:19:MET:HE1	3:PQ:24:LEU:HD21	2.00	0.43
1:GU:6:GLY:N	1:GU:34:ARG:HH12	2.16	0.43
1:BX:17:LEU:O	1:BX:21:ILE:HG12	2.19	0.43
3:PX:6:VAL:HA	3:PX:27:VAL:HG12	2.01	0.43
2:X8:843:LYS:HE3	2:X8:860:LEU:HD13	2.01	0.43
1:A2:35:LEU:HD11	1:A2:48:VAL:CG1	2.47	0.43
1:A1:12:ILE:HD12	1:A1:27:MET:SD	2.59	0.43
1:E4:23:ALA:O	1:E4:27:MET:HG3	2.19	0.43
1:C7:84:VAL:HG12	1:C7:88:VAL:HB	2.01	0.43
3:P7:6:VAL:HA	3:P7:27:VAL:HG12	2.01	0.43
1:B0:17:LEU:O	1:B0:21:ILE:HG12	2.19	0.43
1:B8:23:ALA:O	1:B8:27:MET:HG3	2.19	0.43
1:H9:92:LEU:CD2	1:GR:21:ILE:HD13	2.49	0.43
1:Bb:70:ARG:HA	1:Bb:70:ARG:HD3	1.86	0.43
1:Cb:84:VAL:HG12	1:Cb:88:VAL:HB	2.01	0.43
1:Ed:23:ALA:O	1:Ed:27:MET:HG3	2.19	0.43
1:Ed:41:VAL:HB	1:Ed:45:TYR:HB2	2.01	0.43
3:Pg:6:VAL:HA	3:Pg:27:VAL:HG12	2.01	0.43
3:Pg:53:VAL:HB	3:Pg:74:ILE:HD13	2.01	0.43
3:Pf:50:VAL:HB	3:Pf:73:ILE:HG23	2.01	0.43
1:Bj:17:LEU:O	1:Bj:21:ILE:HG12	2.19	0.43
1:Ah:23:ALA:O	1:Ah:27:MET:HG3	2.18	0.43
1:Di:12:ILE:HG23	1:Di:75:LEU:CD1	2.49	0.43
1:Aq:23:ALA:O	1:Aq:27:MET:HG3	2.19	0.43
1:Ap:12:ILE:HD12	1:Ap:27:MET:SD	2.59	0.43
1:H _p :92:LEU:CD2	1:GG:21:ILE:HD13	2.48	0.43
3:Pp:50:VAL:HB	3:Pp:73:ILE:HG23	2.01	0.43
1:F _s :61:VAL:HG12	2:X _s :795:ILE:HD12	2.00	0.43
1:AA:23:ALA:O	1:AA:27:MET:HG3	2.19	0.43
1:GA:17:LEU:HD23	1:HK:39:GLN:OE1	2.11	0.43
1:GA:72:GLY:CA	1:HK:77:ALA:HB2	2.49	0.43
2:XA:727:THR:O	2:XA:728:PRO:C	2.58	0.43
1:Dz:35:LEU:CD1	1:Dz:48:VAL:HG13	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XC:714:THR:HA	2:XC:718:MET:HG3	1.99	0.43
1:DH:12:ILE:HG23	1:DH:75:LEU:CD1	2.49	0.43
3:PK:6:VAL:HA	3:PK:27:VAL:HG12	2.01	0.43
3:PJ:50:VAL:HB	3:PJ:73:ILE:HG23	2.01	0.43
3:PL:16:ILE:HG13	3:PL:19:MET:HG2	2.01	0.43
1:AO:12:ILE:HD12	1:AO:27:MET:SD	2.59	0.43
1:AO:18:VAL:HG22	1:FO:11:MET:HB3	2.00	0.43
3:PO:50:VAL:HB	3:PO:73:ILE:HG23	2.00	0.43
1:AS:61:VAL:HG12	2:XS:724:ILE:HD12	2.01	0.43
2:XQ:790:LYS:HE2	2:XQ:790:LYS:HB2	1.45	0.43
2:XQ:843:LYS:HE3	2:XQ:860:LEU:HD13	2.01	0.43
1:GR:23:ALA:O	1:GR:27:MET:HG3	2.19	0.43
1:HU:11:MET:HE3	1:HU:11:MET:HB2	1.89	0.43
3:PU:6:VAL:HA	3:PU:27:VAL:HG12	2.01	0.43
1:D2:68:CYS:SG	1:D2:75:LEU:HD13	2.59	0.43
1:B1:57:VAL:HG12	1:B1:80:ILE:HG23	2.01	0.43
1:A5:61:VAL:HG12	2:X5:724:ILE:HD12	2.01	0.43
1:B3:77:ALA:HB2	1:F3:72:GLY:HA2	1.99	0.43
3:P3:14:ASN:HD21	3:P4:76:ILE:CG1	2.32	0.43
3:P4:5:GLN:HA	3:P4:48:ASP:O	2.19	0.43
1:A6:7:ILE:CD1	1:Dc:32:GLU:OE2	2.66	0.43
1:D9:62:ARG:NH1	2:XQ:729:GLU:HA	2.16	0.43
2:X9:713:ILE:HG22	1:HQ:80:ILE:HD12	2.01	0.43
1:Ac:18:VAL:HG22	1:Fc:11:MET:HB3	2.00	0.43
1:Gd:23:ALA:O	1:Gd:27:MET:HG3	2.19	0.43
3:Pd:5:GLN:HA	3:Pd:48:ASP:O	2.19	0.43
1:Hg:24:ALA:HB2	1:Hg:48:VAL:HG11	1.99	0.43
2:Xh:785:VAL:HG11	1:Ci:80:ILE:CD1	2.48	0.43
1:Gl:35:LEU:CD2	1:HT:91:ILE:HG21	2.49	0.43
2:Xl:727:THR:O	2:Xl:728:PRO:C	2.58	0.43
1:Bo:94:LYS:HD3	1:Bo:94:LYS:HA	1.75	0.43
1:Do:27:MET:HG2	1:Do:60:ALA:O	2.19	0.43
1:Eq:9:LEU:HG	1:Eq:11:MET:HG3	1.99	0.43
3:Pr:16:ILE:HG13	3:Pr:19:MET:HG2	2.00	0.43
3:Ps:5:GLN:HA	3:Ps:48:ASP:O	2.19	0.43
2:Xu:775:CYS:HA	2:Xu:793:CYS:HA	2.00	0.43
1:By:41:VAL:HB	1:By:45:TYR:HB2	2.01	0.43
1:Dy:27:MET:HG2	1:Dy:60:ALA:O	2.19	0.43
1:Dy:27:MET:CE	1:Dy:48:VAL:HG12	2.48	0.43
1:Hy:92:LEU:HD23	1:GF:21:ILE:HD13	1.98	0.43
2:Xw:843:LYS:HE3	2:Xw:860:LEU:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Pw:16:ILE:HG13	3:Pw:19:MET:HG2	2.01	0.43
1:GA:6:GLY:N	1:GA:34:ARG:HH12	2.16	0.43
1:AD:61:VAL:HG12	2:XD:724:ILE:HD12	2.01	0.43
1:GD:81:ILE:HG21	1:GD:84:VAL:HG23	2.01	0.43
1:AB:23:ALA:O	1:AB:27:MET:HG3	2.19	0.43
1:EC:23:ALA:O	1:EC:27:MET:HG3	2.19	0.43
1:CE:12:ILE:HG23	1:CE:75:LEU:CD1	2.48	0.43
1:BI:17:LEU:O	1:BI:21:ILE:HG12	2.19	0.43
3:PI:6:VAL:HA	3:PI:27:VAL:HG12	2.01	0.43
3:PG:14:ASN:HD21	3:PH:76:ILE:CG1	2.32	0.43
1:AN:61:VAL:HG12	2:XN:724:ILE:HD12	2.01	0.43
3:PN:39:VAL:HG21	3:PN:67:TYR:HE2	1.84	0.43
3:PM:5:GLN:HA	3:PM:48:ASP:O	2.19	0.43
1:DP:15:ARG:HE	2:XR:825:ALA:HB3	1.84	0.43
1:GP:6:GLY:N	1:GP:34:ARG:HH12	2.16	0.43
1:DQ:11:MET:HE3	1:DQ:79:HIS:HB3	2.00	0.43
1:H6:94:LYS:HE2	1:H6:94:LYS:HB2	1.87	0.43
1:A2:72:GLY:HA2	1:F2:77:ALA:HB2	2.01	0.42
2:X1:775:CYS:HA	2:X1:793:CYS:HA	2.00	0.42
1:D5:24:ALA:HB2	1:D5:48:VAL:HG11	2.01	0.42
1:F4:94:LYS:HE3	1:F4:94:LYS:HB3	1.70	0.42
3:P7:19:MET:SD	3:P6:74:ILE:HD12	2.59	0.42
1:B6:57:VAL:HG12	1:B6:80:ILE:HG23	2.01	0.42
1:Ab:72:GLY:HA2	1:Fb:77:ALA:HB2	2.01	0.42
1:Gc:77:ALA:HB2	1:Hc:72:GLY:HA2	2.01	0.42
3:Pc:19:MET:HE1	3:Pc:24:LEU:HD21	2.00	0.42
1:Dg:68:CYS:SG	1:Dg:75:LEU:HD13	2.59	0.42
1:Dj:24:ALA:HB2	1:Dj:48:VAL:HG11	2.01	0.42
1:Ah:7:ILE:CD1	1:DI:32:GLU:OE1	2.67	0.42
1:Hi:91:ILE:HG21	1:GT:35:LEU:HD23	2.01	0.42
2:Xk:869:GLY:HA2	1:Em:62:ARG:HD3	2.01	0.42
1:Bo:18:VAL:HB	1:Bo:19:PRO:HD3	2.01	0.42
1:Dn:12:ILE:HG23	1:Dn:75:LEU:CD1	2.49	0.42
1:Bp:72:GLY:CA	1:Ep:77:ALA:HB2	2.48	0.42
1:Av:23:ALA:O	1:Av:27:MET:HG3	2.19	0.42
1:Av:94:LYS:HE2	1:Av:94:LYS:HB3	1.64	0.42
1:Bu:72:GLY:CA	1:Eu:77:ALA:HB2	2.48	0.42
2:Xy:785:VAL:HG21	1:Cw:62:ARG:HG2	2.01	0.42
1:Dw:88:VAL:O	1:Dw:91:ILE:HG12	2.19	0.42
1:Cz:12:ILE:HG23	1:Cz:75:LEU:CD1	2.48	0.42
1:BD:17:LEU:O	1:BD:21:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:PB:14:ASN:HD21	3:PC:76:ILE:CG1	2.32	0.42
1:AF:72:GLY:HA2	1:FF:77:ALA:HB2	2.01	0.42
3:PF:53:VAL:HB	3:PF:74:ILE:HD13	2.01	0.42
1:AI:61:VAL:HG12	2:XI:724:ILE:HD12	2.01	0.42
1:CG:41:VAL:HB	1:CG:45:TYR:HB2	2.00	0.42
2:YN:821:MET:HE3	2:YN:821:MET:HB2	1.68	0.42
3:PO:30:LYS:HB2	3:PO:30:LYS:HE3	1.74	0.42
2:XT:790:LYS:HB2	2:XT:790:LYS:HE2	1.76	0.42
1:GX:84:VAL:HG13	1:GX:88:VAL:HB	2.01	0.42
1:AV:18:VAL:HG22	1:FV:11:MET:HB3	2.00	0.42
1:EW:41:VAL:HB	1:EW:45:TYR:HB2	2.01	0.42
1:C2:84:VAL:HG12	1:C2:88:VAL:HB	2.01	0.42
1:F2:11:MET:HE3	1:F2:11:MET:HB2	1.94	0.42
3:P2:19:MET:SD	3:P1:74:ILE:HD12	2.60	0.42
1:B5:75:LEU:HD11	1:B5:78:ALA:HB2	2.01	0.42
1:F5:65:ALA:O	1:F5:66:ASP:C	2.61	0.42
2:X5:727:THR:O	2:X5:728:PRO:C	2.61	0.42
2:X3:843:LYS:HE3	2:X3:860:LEU:HD13	2.01	0.42
1:G4:23:ALA:O	1:G4:27:MET:HG3	2.19	0.42
1:H4:79:HIS:CG	2:XS:714:THR:HG1	2.09	0.42
1:E9:41:VAL:HB	1:E9:45:TYR:HB2	2.01	0.42
1:Cc:41:VAL:HB	1:Cc:45:TYR:HB2	2.00	0.42
1:Gc:27:MET:HG2	1:Gc:60:ALA:O	2.20	0.42
1:Hd:38:ARG:HH22	1:Hd:97:GLN:HE21	1.66	0.42
1:Ai:23:ALA:O	1:Ai:27:MET:HG3	2.20	0.42
1:Al:23:ALA:O	1:Al:27:MET:HG3	2.19	0.42
3:Pl:50:VAL:HG12	3:Pl:76:ILE:HG12	2.01	0.42
1:Bo:25:ASP:HA	1:Eo:88:VAL:HG21	2.00	0.42
1:Go:84:VAL:HG13	1:Go:88:VAL:HB	2.01	0.42
1:An:23:ALA:O	1:An:27:MET:HG3	2.20	0.42
1:Hn:91:ILE:CG2	1:GX:35:LEU:HD21	2.31	0.42
1:Dq:68:CYS:SG	1:Dq:75:LEU:HD13	2.59	0.42
3:Pq:19:MET:SD	3:Pp:74:ILE:HD12	2.59	0.42
2:Xp:869:GLY:HA2	1:Er:62:ARG:HD3	2.01	0.42
1:Hv:77:ALA:HB2	1:GP:72:GLY:HA2	2.00	0.42
2:Xy:714:THR:HG1	1:HH:79:HIS:CG	2.09	0.42
1:Gw:27:MET:HG2	1:Gw:60:ALA:O	2.19	0.42
1:Ax:23:ALA:O	1:Ax:27:MET:HG3	2.20	0.42
1:Bz:57:VAL:HG12	1:Bz:80:ILE:HG23	2.01	0.42
1:BD:41:VAL:HB	1:BD:45:TYR:HB2	2.01	0.42
1:GB:27:MET:HG2	1:GB:60:ALA:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DC:12:ILE:HG23	1:DC:75:LEU:CD1	2.49	0.42
1:BF:29:LYS:HE2	3:PF:45:ILE:HG22	2.01	0.42
1:DF:68:CYS:SG	1:DF:75:LEU:HD13	2.59	0.42
3:PF:6:VAL:HA	3:PF:27:VAL:HG12	2.01	0.42
3:PF:19:MET:SD	3:PE:74:ILE:HD12	2.60	0.42
2:XE:869:GLY:HA2	1:EG:62:ARG:HD3	2.01	0.42
1:AG:23:ALA:O	1:AG:27:MET:HG3	2.19	0.42
1:DG:88:VAL:O	1:DG:91:ILE:HG12	2.20	0.42
1:BH:11:MET:HE3	1:BH:11:MET:HB2	1.77	0.42
3:PH:50:VAL:HB	3:PH:73:ILE:HG23	2.01	0.42
3:PK:19:MET:SD	3:PJ:74:ILE:HD12	2.60	0.42
1:BJ:94:LYS:HA	1:BJ:94:LYS:HD3	1.70	0.42
1:HJ:11:MET:HE3	1:HJ:11:MET:HB2	1.88	0.42
1:CL:41:VAL:HB	1:CL:45:TYR:HB2	2.00	0.42
1:EM:41:VAL:HB	1:EM:45:TYR:HB2	2.01	0.42
2:XP:818:ASN:HA	2:XP:819:PRO:HD3	1.82	0.42
3:PP:6:VAL:HA	3:PP:27:VAL:HG12	2.01	0.42
3:PP:50:VAL:HG12	3:PP:76:ILE:HG12	2.01	0.42
1:AO:11:MET:HE3	1:AO:11:MET:HB2	1.91	0.42
1:AT:12:ILE:HD12	1:AT:27:MET:SD	2.59	0.42
1:DX:24:ALA:HB2	1:DX:48:VAL:HG11	2.01	0.42
1:DW:12:ILE:HG23	1:DW:75:LEU:CD1	2.48	0.42
1:H6:96:PRO:O	1:H6:97:GLN:C	2.62	0.42
2:Xc:843:LYS:HE3	2:Xc:860:LEU:HD13	2.01	0.42
1:Hk:96:PRO:O	1:Hk:97:GLN:C	2.62	0.42
1:Hz:94:LYS:HE2	1:Hz:94:LYS:HB2	1.87	0.42
1:D2:15:ARG:HE	2:X4:825:ALA:HB3	1.84	0.42
1:A1:11:MET:HE3	1:A1:11:MET:HB2	1.91	0.42
1:F1:18:VAL:O	1:F1:19:PRO:C	2.62	0.42
2:X1:727:THR:O	2:X1:728:PRO:C	2.61	0.42
1:G5:81:ILE:HG21	1:G5:84:VAL:HG23	2.01	0.42
1:D3:88:VAL:O	1:D3:91:ILE:HG12	2.19	0.42
1:H3:91:ILE:CG2	1:G6:35:LEU:CD2	2.87	0.42
1:D4:82:ALA:HB3	1:H4:30:ALA:O	2.19	0.42
2:X4:863:TYR:CD2	2:X4:869:GLY:HA3	2.51	0.42
1:B6:94:LYS:HD3	1:B6:94:LYS:HA	1.70	0.42
1:E6:15:ARG:HG3	1:E6:76:VAL:CG2	2.49	0.42
1:B0:41:VAL:HB	1:B0:45:TYR:HB2	2.01	0.42
1:G0:81:ILE:HG21	1:G0:84:VAL:HG23	2.01	0.42
1:C8:84:VAL:HG12	1:C8:88:VAL:HB	2.02	0.42
1:Bb:29:LYS:HE2	3:Pb:45:ILE:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Pe:39:VAL:HG21	3:Pe:67:TYR:HE2	1.84	0.42
1:Bd:11:MET:HB2	1:Bd:11:MET:HE3	1.76	0.42
1:Cd:11:MET:HE3	1:Cd:79:HIS:HB3	2.02	0.42
1:Ag:23:ALA:O	1:Ag:27:MET:HG3	2.19	0.42
1:Bg:29:LYS:HE2	3:Pg:45:ILE:HG22	2.01	0.42
1:Eg:11:MET:HE3	1:Eg:11:MET:HB2	1.87	0.42
1:Bj:25:ASP:HA	1:Ej:88:VAL:HG21	2.00	0.42
1:Dh:11:MET:HE3	1:Dh:79:HIS:HB3	2.00	0.42
1:Di:82:ALA:HB3	1:Hi:30:ALA:O	2.19	0.42
1:Gl:21:ILE:HD13	1:HT:92:LEU:HD21	2.01	0.42
1:Ek:15:ARG:HG3	1:Ek:76:VAL:CG2	2.50	0.42
1:Bo:17:LEU:O	1:Bo:21:ILE:HG12	2.19	0.42
3:Po:14:ASN:HD21	3:Pm:76:ILE:HB	1.83	0.42
1:Cm:41:VAL:HB	1:Cm:45:TYR:HB2	2.00	0.42
1:Gm:77:ALA:HB2	1:Hm:72:GLY:HA2	2.01	0.42
1:Dn:82:ALA:HB3	1:Hn:30:ALA:O	2.19	0.42
1:At:94:LYS:HE2	1:At:94:LYS:HB3	1.85	0.42
1:Dr:88:VAL:O	1:Dr:91:ILE:HG12	2.19	0.42
1:Dv:15:ARG:HE	2:Xx:825:ALA:HB3	1.84	0.42
1:Dv:68:CYS:SG	1:Dv:75:LEU:HD13	2.59	0.42
3:Pv:50:VAL:HG12	3:Pv:76:ILE:HG12	2.02	0.42
1:Aw:7:ILE:CD1	1:DA:32:GLU:OE1	2.67	0.42
1:Az:18:VAL:HG22	1:Fz:11:MET:HB3	2.01	0.42
2:XD:785:VAL:HG21	1:CB:62:ARG:HG2	2.01	0.42
2:XD:818:ASN:HA	2:XD:819:PRO:HD3	1.93	0.42
3:PD:14:ASN:HD21	3:PB:76:ILE:HB	1.83	0.42
3:PD:39:VAL:HG21	3:PD:67:TYR:HE2	1.84	0.42
3:PB:16:ILE:HG13	3:PB:19:MET:HG2	2.00	0.42
1:FC:59:ALA:HB1	2:XC:788:GLU:HG2	2.02	0.42
1:AK:23:ALA:O	1:AK:27:MET:HG3	2.19	0.42
1:BK:29:LYS:HE2	3:PK:45:ILE:HG22	2.01	0.42
2:XK:718:MET:HE3	2:XK:718:MET:HB3	1.65	0.42
1:BJ:57:VAL:HG12	1:BJ:80:ILE:HG23	2.01	0.42
3:PJ:5:GLN:HA	3:PJ:48:ASP:O	2.19	0.42
1:DN:27:MET:HG2	1:DN:60:ALA:O	2.19	0.42
1:GN:9:LEU:HD11	1:GN:49:LEU:HD23	1.99	0.42
1:HN:83:ARG:NH2	1:AW:32:GLU:HG3	2.34	0.42
1:EM:23:ALA:O	1:EM:27:MET:HG3	2.19	0.42
1:DP:68:CYS:SG	1:DP:75:LEU:HD13	2.59	0.42
1:BO:57:VAL:HG12	1:BO:80:ILE:HG23	2.01	0.42
1:EO:15:ARG:HG3	1:EO:76:VAL:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XO:869:GLY:HA2	1:EQ:62:ARG:HD3	2.01	0.42
1:ER:41:VAL:HB	1:ER:45:TYR:HB2	2.01	0.42
1:HR:38:ARG:HH22	1:HR:97:GLN:HE21	1.66	0.42
2:XX:785:VAL:HG21	1:CV:62:ARG:HG2	2.01	0.42
2:XB:843:LYS:HE3	2:XB:860:LEU:HD13	2.01	0.42
2:XG:843:LYS:HE3	2:XG:860:LEU:HD13	2.01	0.42
1:B2:29:LYS:HE2	3:P2:45:ILE:HG22	2.01	0.42
1:G1:35:LEU:HD23	1:HX:91:ILE:CG2	2.49	0.42
1:D7:15:ARG:HE	2:X9:825:ALA:HB3	1.84	0.42
1:H7:11:MET:HE3	1:H7:11:MET:HB2	1.89	0.42
1:D0:24:ALA:HB2	1:D0:48:VAL:HG11	2.01	0.42
3:P0:39:VAL:HG21	3:P0:67:TYR:HE2	1.84	0.42
1:D8:11:MET:HE3	1:D8:79:HIS:HB3	2.00	0.42
1:Ea:15:ARG:HG3	1:Ea:76:VAL:CG2	2.50	0.42
3:Pd:30:LYS:HB2	3:Pd:30:LYS:HE3	1.74	0.42
1:Dg:15:ARG:HE	2:Xi:825:ALA:HB3	1.84	0.42
1:Gg:25:ASP:HA	1:HU:88:VAL:CG2	2.43	0.42
1:Dj:27:MET:HG2	1:Dj:60:ALA:O	2.19	0.42
3:Pj:6:VAL:HA	3:Pj:27:VAL:HG12	2.01	0.42
1:Gh:77:ALA:HB2	1:Hh:72:GLY:HA2	2.01	0.42
1:Hi:7:ILE:H	1:Hi:7:ILE:HG13	1.57	0.42
1:Ak:11:MET:HE3	1:Ak:11:MET:HB2	1.91	0.42
1:Bk:57:VAL:HG12	1:Bk:80:ILE:HG23	2.01	0.42
1:Bo:41:VAL:HB	1:Bo:45:TYR:HB2	2.01	0.42
2:Xo:821:MET:HE3	2:Xo:821:MET:HB2	1.68	0.42
1:Cn:11:MET:HE3	1:Cn:79:HIS:HB3	2.02	0.42
1:Hp:96:PRO:O	1:Hp:97:GLN:C	2.62	0.42
2:Xp:713:ILE:CG2	1:HI:80:ILE:CD1	2.81	0.42
1:Bt:17:LEU:O	1:Bt:21:ILE:HG12	2.19	0.42
1:Bt:18:VAL:HB	1:Bt:19:PRO:HD3	2.01	0.42
1:Gr:27:MET:HG2	1:Gr:60:ALA:O	2.20	0.42
1:F8:94:LYS:HE3	1:F8:94:LYS:HB3	1.70	0.42
1:Gs:23:ALA:O	1:Gs:27:MET:HG3	2.19	0.42
1:Bv:29:LYS:HE2	3:Pv:45:ILE:HG22	2.01	0.42
1:Hv:77:ALA:HB2	1:GP:72:GLY:CA	2.49	0.42
2:Xy:818:ASN:HA	2:Xy:819:PRO:HD3	1.93	0.42
3:Py:14:ASN:HD21	3:Pw:76:ILE:HB	1.83	0.42
1:Ex:41:VAL:HB	1:Ex:45:TYR:HB2	2.01	0.42
1:Gx:23:ALA:O	1:Gx:27:MET:HG3	2.19	0.42
1:DA:15:ARG:HE	2:XC:825:ALA:HB3	1.84	0.42
1:EA:11:MET:HE3	1:EA:11:MET:HB2	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GC:23:ALA:O	1:GC:27:MET:HG3	2.19	0.42
1:AF:23:ALA:O	1:AF:27:MET:HG3	2.19	0.42
1:DI:27:MET:HG2	1:DI:60:ALA:O	2.19	0.42
1:FI:65:ALA:O	1:FI:66:ASP:C	2.61	0.42
1:CK:84:VAL:HG12	1:CK:88:VAL:HB	2.01	0.42
1:GN:81:ILE:HG21	1:GN:84:VAL:HG23	2.01	0.42
1:CL:84:VAL:HG12	1:CL:88:VAL:HB	2.02	0.42
3:PL:19:MET:HE1	3:PL:24:LEU:HD21	2.00	0.42
1:CM:11:MET:HE3	1:CM:79:HIS:HB3	2.02	0.42
1:FM:94:LYS:HB3	1:FM:94:LYS:HE3	1.70	0.42
3:PM:30:LYS:HB2	3:PM:30:LYS:HE3	1.74	0.42
1:CP:9:LEU:HD11	1:CP:49:LEU:HD23	2.02	0.42
1:HP:11:MET:HE3	1:HP:11:MET:HB2	1.89	0.42
3:PP:19:MET:SD	3:PO:74:ILE:HD12	2.59	0.42
1:BS:41:VAL:HB	1:BS:45:TYR:HB2	2.01	0.42
3:PS:14:ASN:HD21	3:PQ:76:ILE:HB	1.83	0.42
1:DQ:88:VAL:O	1:DQ:91:ILE:HG12	2.20	0.42
1:ER:23:ALA:O	1:ER:27:MET:HG3	2.19	0.42
1:DU:68:CYS:SG	1:DU:75:LEU:HD13	2.59	0.42
1:GX:81:ILE:HG21	1:GX:84:VAL:HG23	2.01	0.42
3:PX:50:VAL:HG12	3:PX:76:ILE:HG12	2.01	0.42
1:GV:27:MET:HG2	1:GV:60:ALA:O	2.20	0.42
1:AW:23:ALA:O	1:AW:27:MET:HG3	2.20	0.42
1:H2:92:LEU:CD2	1:GV:21:ILE:HD13	2.49	0.42
1:D5:65:ALA:O	1:D5:66:ASP:C	2.62	0.42
1:A3:7:ILE:CD1	1:D7:32:GLU:OE1	2.67	0.42
1:F4:59:ALA:HB1	2:X4:788:GLU:HG2	2.02	0.42
2:X0:821:MET:HB2	2:X0:821:MET:HE3	1.68	0.42
3:P0:6:VAL:HA	3:P0:27:VAL:HG12	2.01	0.42
1:G8:27:MET:HG2	1:G8:60:ALA:O	2.20	0.42
1:H9:88:VAL:CG2	1:GR:25:ASP:HA	2.44	0.42
1:Db:15:ARG:HH21	2:Xd:825:ALA:HB3	1.85	0.42
1:Ha:38:ARG:NH2	1:Ha:97:GLN:HE21	2.18	0.42
1:Be:18:VAL:HB	1:Be:19:PRO:HD3	2.01	0.42
2:Xe:821:MET:HE3	2:Xe:821:MET:HB2	1.68	0.42
3:Pc:16:ILE:HG13	3:Pc:19:MET:HG2	2.00	0.42
1:Af:12:ILE:HD12	1:Af:27:MET:SD	2.59	0.42
1:Ef:15:ARG:HG3	1:Ef:76:VAL:CG2	2.49	0.42
3:Ph:14:ASN:HD21	3:Pi:76:ILE:CG1	2.32	0.42
1:Al:72:GLY:HA2	1:Fl:77:ALA:HB2	2.01	0.42
1:Di:15:ARG:HE	2:Xn:825:ALA:HB3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Do:24:ALA:HB2	1:Do:48:VAL:HG11	2.01	0.42
1:Cm:84:VAL:HG12	1:Cm:88:VAL:HB	2.02	0.42
1:Dn:32:GLU:CG	1:AT:7:ILE:CD1	2.97	0.42
1:Bq:29:LYS:HE2	3:Pq:45:ILE:HG22	2.01	0.42
1:Dq:15:ARG:HH21	2:Xs:825:ALA:HB3	1.85	0.42
1:As:11:MET:HE3	1:As:11:MET:HB2	1.92	0.42
1:Bw:23:ALA:O	1:Bw:27:MET:HG3	2.19	0.42
1:CA:84:VAL:HG12	1:CA:88:VAL:HB	2.01	0.42
1:GA:35:LEU:HD11	1:GA:48:VAL:CG1	2.37	0.42
2:Xz:869:GLY:HA2	1:EB:62:ARG:HD3	2.01	0.42
1:DD:24:ALA:HB2	1:DD:48:VAL:HG11	2.01	0.42
1:GD:84:VAL:HG13	1:GD:88:VAL:HB	2.01	0.42
3:PD:50:VAL:HG12	3:PD:76:ILE:HG12	2.01	0.42
1:CB:84:VAL:HG12	1:CB:88:VAL:HB	2.02	0.42
1:AE:18:VAL:HG22	1:FE:11:MET:HB3	2.00	0.42
2:XE:790:LYS:HB2	2:XE:790:LYS:HE2	1.76	0.42
1:GG:27:MET:HG2	1:GG:60:ALA:O	2.19	0.42
1:AH:23:ALA:O	1:AH:27:MET:HG3	2.20	0.42
1:CK:9:LEU:HD11	1:CK:49:LEU:HD23	2.02	0.42
1:DK:68:CYS:SG	1:DK:75:LEU:HD13	2.59	0.42
3:PK:53:VAL:HB	3:PK:74:ILE:HD13	2.01	0.42
1:DN:24:ALA:HB2	1:DN:48:VAL:HG11	2.01	0.42
1:BL:23:ALA:O	1:BL:27:MET:HG3	2.19	0.42
1:DL:11:MET:HE3	1:DL:79:HIS:HB3	2.00	0.42
1:FM:9:LEU:HD11	1:FM:49:LEU:HD23	2.02	0.42
1:BP:29:LYS:HE2	3:PP:45:ILE:HG22	2.01	0.42
1:AR:23:ALA:O	1:AR:27:MET:HG3	2.20	0.42
1:DR:82:ALA:HB3	1:HR:30:ALA:O	2.19	0.42
1:FR:11:MET:HE3	1:FR:11:MET:HB2	1.90	0.42
1:FR:59:ALA:HB1	2:XR:788:GLU:HG2	2.02	0.42
1:HT:38:ARG:NH2	1:HT:97:GLN:HE21	2.18	0.42
1:FW:94:LYS:HE3	1:FW:94:LYS:HB3	1.70	0.42
1:A2:14:THR:HB	1:A2:19:PRO:HB2	2.02	0.42
1:A2:23:ALA:O	1:A2:27:MET:HG3	2.19	0.42
3:P2:6:VAL:HA	3:P2:27:VAL:HG12	2.01	0.42
3:P5:50:VAL:HG12	3:P5:76:ILE:HG12	2.01	0.42
1:B0:18:VAL:HB	1:B0:19:PRO:HD3	2.01	0.42
2:X0:785:VAL:HG21	1:C8:62:ARG:HG2	2.01	0.42
1:B9:11:MET:HE3	1:B9:11:MET:HB2	1.76	0.42
1:G9:23:ALA:O	1:G9:27:MET:HG3	2.19	0.42
1:H9:38:ARG:HH22	1:H9:97:GLN:HE21	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X9:843:LYS:HD2	2:X9:860:LEU:HD13	2.02	0.42
1:Cb:9:LEU:HD11	1:Cb:49:LEU:HD23	2.02	0.42
1:Aa:12:ILE:HD12	1:Aa:27:MET:SD	2.59	0.42
1:Ba:94:LYS:HD3	1:Ba:94:LYS:HA	1.70	0.42
2:Xa:869:GLY:HA2	1:Ec:62:ARG:HD3	2.01	0.42
1:Ae:61:VAL:HG12	2:Xe:724:ILE:HD12	2.01	0.42
3:Pe:6:VAL:HA	3:Pe:27:VAL:HG12	2.01	0.42
1:Cc:84:VAL:HG12	1:Cc:88:VAL:HB	2.02	0.42
1:Ag:14:THR:HB	1:Ag:19:PRO:HB2	2.02	0.42
1:Aj:94:LYS:HE2	1:Aj:94:LYS:HB3	1.85	0.42
1:Fi:59:ALA:HB1	2:Xi:788:GLU:HG2	2.02	0.42
1:Ak:12:ILE:HD12	1:Ak:27:MET:SD	2.59	0.42
3:Po:50:VAL:HG12	3:Po:76:ILE:HG12	2.01	0.42
1:Dq:27:MET:HG2	1:Dq:60:ALA:O	2.20	0.42
3:Pq:50:VAL:HG12	3:Pq:76:ILE:HG12	2.02	0.42
3:Pt:39:VAL:HG21	3:Pt:67:TYR:HE2	1.84	0.42
1:Ds:82:ALA:HB3	1:Hs:30:ALA:O	2.19	0.42
1:Ay:61:VAL:HG12	2:Xy:724:ILE:HD12	2.01	0.42
1:By:17:LEU:O	1:By:21:ILE:HG12	2.19	0.42
1:By:18:VAL:HB	1:By:19:PRO:HD3	2.01	0.42
1:Fy:23:ALA:O	1:Fy:27:MET:HG3	2.20	0.42
3:Pw:14:ASN:HD21	3:Px:76:ILE:CG1	2.32	0.42
3:PA:6:VAL:HA	3:PA:27:VAL:HG12	2.01	0.42
1:Ez:15:ARG:HG3	1:Ez:76:VAL:CG2	2.50	0.42
3:Pz:30:LYS:HE3	3:Pz:30:LYS:HB2	1.74	0.42
1:FB:11:MET:HE3	1:FB:11:MET:HB2	1.81	0.42
1:AC:23:ALA:O	1:AC:27:MET:HG3	2.20	0.42
1:CF:9:LEU:HD11	1:CF:49:LEU:HD23	2.02	0.42
3:PF:50:VAL:HG12	3:PF:76:ILE:HG12	2.01	0.42
1:BG:23:ALA:O	1:BG:27:MET:HG3	2.19	0.42
1:GG:77:ALA:HB2	1:HG:72:GLY:HA2	2.01	0.42
1:CH:11:MET:HE3	1:CH:79:HIS:HB3	2.02	0.42
3:PK:50:VAL:HG12	3:PK:76:ILE:HG12	2.02	0.42
1:BN:17:LEU:O	1:BN:21:ILE:HG12	2.19	0.42
1:GL:77:ALA:HB2	1:HL:72:GLY:HA2	2.01	0.42
2:XL:843:LYS:HE3	2:XL:860:LEU:HD13	2.01	0.42
2:XM:838:VAL:HA	2:XM:839:PRO:HD3	1.96	0.42
1:AP:14:THR:HB	1:AP:19:PRO:HB2	2.02	0.42
1:DP:15:ARG:HH21	2:XR:825:ALA:HB3	1.85	0.42
3:PS:6:VAL:HA	3:PS:27:VAL:HG12	2.01	0.42
3:PS:50:VAL:HG12	3:PS:76:ILE:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FQ:11:MET:HE3	1:FQ:11:MET:HB2	1.82	0.42
1:DU:27:MET:HG2	1:DU:60:ALA:O	2.20	0.42
3:PU:19:MET:SD	3:PT:74:ILE:HD12	2.60	0.42
1:AX:61:VAL:HG12	2:XX:724:ILE:HD12	2.01	0.42
1:BX:75:LEU:HD11	1:BX:78:ALA:HB2	2.01	0.42
1:AV:41:VAL:HB	1:AV:45:TYR:HB2	2.02	0.42
1:DV:11:MET:HE3	1:DV:79:HIS:HB3	2.00	0.42
1:EW:23:ALA:O	1:EW:27:MET:HG3	2.19	0.42
1:D2:15:ARG:HH21	2:X4:825:ALA:HB3	1.85	0.42
1:B1:94:LYS:HA	1:B1:94:LYS:HD3	1.70	0.42
1:H5:11:MET:HE3	1:H5:11:MET:HB2	1.89	0.42
1:G3:35:LEU:HD21	1:Hd:91:ILE:HG21	2.01	0.42
3:P3:30:LYS:HB2	3:P3:30:LYS:HE3	1.79	0.42
1:C7:53:GLU:HG2	1:C7:54:THR:N	2.35	0.42
1:Fe:65:ALA:O	1:Fe:66:ASP:C	2.61	0.42
1:Dc:88:VAL:O	1:Dc:91:ILE:HG12	2.20	0.42
1:Ad:11:MET:HE3	1:Ad:11:MET:HB2	1.92	0.42
2:Xh:729:GLU:HA	1:Dl:62:ARG:NH1	2.31	0.42
1:Ci:11:MET:HE3	1:Ci:79:HIS:HB3	2.02	0.42
1:Go:81:ILE:HG21	1:Go:84:VAL:HG23	2.01	0.42
3:Pm:16:ILE:HG13	3:Pm:19:MET:HG2	2.00	0.42
1:Aq:14:THR:HB	1:Aq:19:PRO:HB2	2.02	0.42
1:Dq:15:ARG:HE	2:Xs:825:ALA:HB3	1.84	0.42
3:Pq:53:VAL:HB	3:Pq:74:ILE:HD13	2.01	0.42
1:Ep:15:ARG:HG3	1:Ep:76:VAL:CG2	2.49	0.42
1:Hp:88:VAL:HG21	1:GG:25:ASP:CA	2.46	0.42
1:Cr:84:VAL:HG12	1:Cr:88:VAL:HB	2.02	0.42
1:Es:23:ALA:O	1:Es:27:MET:HG3	2.19	0.42
2:Xu:863:TYR:HD2	2:Xu:869:GLY:CA	2.33	0.42
2:Xy:713:ILE:HG22	1:HH:80:ILE:HD12	1.98	0.42
1:Ex:23:ALA:O	1:Ex:27:MET:HG3	2.19	0.42
2:XA:832:ALA:HB1	1:Bz:15:ARG:HG2	2.02	0.42
1:DF:79:HIS:ND1	2:XH:820:SER:HB2	2.35	0.42
2:XF:727:THR:O	2:XF:728:PRO:C	2.58	0.42
3:PH:5:GLN:HA	3:PH:48:ASP:O	2.19	0.42
1:AJ:12:ILE:HD12	1:AJ:27:MET:SD	2.59	0.42
1:GL:27:MET:HG2	1:GL:60:ALA:O	2.20	0.42
3:PM:50:VAL:HB	3:PM:73:ILE:HG23	2.01	0.42
3:PP:53:VAL:HB	3:PP:74:ILE:HD13	2.01	0.42
3:PS:39:VAL:HG21	3:PS:67:TYR:HE2	1.84	0.42
2:XR:812:GLN:HE21	2:XR:812:GLN:HB2	1.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FX:23:ALA:O	1:FX:27:MET:HG3	2.20	0.42
3:PV:14:ASN:HD21	3:PW:76:ILE:CG1	2.32	0.42
1:GW:23:ALA:O	1:GW:27:MET:HG3	2.19	0.42
1:H1:38:ARG:NH2	1:H1:97:GLN:HE21	2.18	0.42
1:Hf:96:PRO:O	1:Hf:97:GLN:C	2.62	0.42
1:C2:9:LEU:HD11	1:C2:49:LEU:HD23	2.02	0.42
1:D2:79:HIS:ND1	2:X4:820:SER:HB2	2.35	0.42
1:A1:18:VAL:HG22	1:F1:11:MET:HB3	2.01	0.42
1:A3:41:VAL:HB	1:A3:45:TYR:HB2	2.02	0.42
1:A4:32:GLU:HG3	1:HS:83:ARG:NH2	2.34	0.42
1:A7:72:GLY:HA2	1:F7:77:ALA:HB2	2.01	0.42
1:D7:27:MET:HG2	1:D7:60:ALA:O	2.20	0.42
2:X6:713:ILE:HG21	1:Hc:80:ILE:HD11	2.02	0.42
2:X6:863:TYR:HD2	2:X6:869:GLY:CA	2.33	0.42
1:H0:11:MET:HE3	1:H0:11:MET:HB2	1.89	0.42
1:D9:82:ALA:HB3	1:H9:30:ALA:O	2.19	0.42
1:Db:79:HIS:ND1	2:Xd:820:SER:HB2	2.35	0.42
3:Pb:53:VAL:HB	3:Pb:74:ILE:HD13	2.01	0.42
2:Xa:822:ARG:HE	2:Xa:822:ARG:HB3	1.73	0.42
1:Ge:85:HIS:HB3	1:Ge:88:VAL:HG23	2.02	0.42
3:Pc:14:ASN:HD21	3:Pd:76:ILE:CG1	2.32	0.42
1:Cg:53:GLU:HG2	1:Cg:54:THR:N	2.35	0.42
1:Gh:35:LEU:HD21	1:Hs:91:ILE:HG21	2.01	0.42
2:Xl:818:ASN:HA	2:Xl:819:PRO:HD3	1.82	0.42
1:Fo:23:ALA:O	1:Fo:27:MET:HG3	2.20	0.42
1:Fh:9:LEU:HD11	1:Fh:49:LEU:HD23	2.02	0.42
1:Gn:23:ALA:O	1:Gn:27:MET:HG3	2.19	0.42
1:Cq:9:LEU:HD11	1:Cq:49:LEU:HD23	2.02	0.42
1:Gt:84:VAL:HG13	1:Gt:88:VAL:HB	2.01	0.42
1:As:23:ALA:O	1:As:27:MET:HG3	2.20	0.42
1:Bs:11:MET:HB2	1:Bs:11:MET:HE3	1.76	0.42
3:Ps:50:VAL:HB	3:Ps:73:ILE:HG23	2.01	0.42
1:Bu:57:VAL:HG12	1:Bu:80:ILE:HG23	2.01	0.42
1:By:75:LEU:HD11	1:By:78:ALA:HB2	2.01	0.42
1:Fx:11:MET:HE3	1:Fx:11:MET:HB2	1.90	0.42
1:FA:11:MET:HE3	1:FA:11:MET:HB2	1.94	0.42
2:XA:806:ILE:HD11	1:Gz:62:ARG:HA	2.02	0.42
3:Pz:50:VAL:HB	3:Pz:73:ILE:HG23	2.01	0.42
3:PI:39:VAL:HG21	3:PI:67:TYR:HE2	1.84	0.42
1:AG:41:VAL:HB	1:AG:45:TYR:HB2	2.02	0.42
1:GH:88:VAL:HG21	1:HH:25:ASP:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XK:832:ALA:HB1	1:BJ:15:ARG:HG2	2.02	0.42
3:PJ:30:LYS:HB2	3:PJ:30:LYS:HE3	1.74	0.42
3:PN:6:VAL:HA	3:PN:27:VAL:HG12	2.01	0.42
2:XM:821:MET:HB3	2:XM:821:MET:HE3	1.82	0.42
1:AP:23:ALA:O	1:AP:27:MET:HG3	2.19	0.42
1:DP:79:HIS:ND1	2:XR:820:SER:HB2	2.35	0.42
1:BS:17:LEU:O	1:BS:21:ILE:HG12	2.19	0.42
1:GS:84:VAL:HG13	1:GS:88:VAL:HB	2.01	0.42
1:AQ:41:VAL:HB	1:AQ:45:TYR:HB2	2.02	0.42
1:GU:12:ILE:HG23	1:GU:75:LEU:HD12	2.02	0.42
3:PU:53:VAL:HB	3:PU:74:ILE:HD13	2.01	0.42
1:ET:15:ARG:HG3	1:ET:76:VAL:CG2	2.50	0.42
3:PX:39:VAL:HG21	3:PX:67:TYR:HE2	1.84	0.42
1:FW:9:LEU:HD11	1:FW:49:LEU:HD23	2.02	0.42
1:Hf:11:MET:HE3	1:Hf:11:MET:HB2	1.88	0.42
1:Hz:96:PRO:O	1:Hz:97:GLN:C	2.62	0.42
2:X1:713:ILE:HG21	1:Hm:80:ILE:HD11	2.01	0.42
1:A6:12:ILE:HD12	1:A6:27:MET:SD	2.59	0.42
1:Db:27:MET:HG2	1:Db:60:ALA:O	2.20	0.42
3:Pa:5:GLN:HA	3:Pa:48:ASP:O	2.19	0.42
1:Fd:59:ALA:HB1	2:Xd:788:GLU:HG2	2.02	0.42
1:Cg:9:LEU:HD11	1:Cg:49:LEU:HD23	2.02	0.42
1:Fg:11:MET:HE3	1:Fg:11:MET:HB2	1.94	0.42
3:Pg:30:LYS:HE3	3:Pg:30:LYS:HB2	1.94	0.42
3:Ph:16:ILE:HG13	3:Ph:19:MET:HG2	2.00	0.42
1:Gi:88:VAL:HG21	1:Hi:25:ASP:HA	2.02	0.42
1:Cl:84:VAL:HG12	1:Cl:88:VAL:HB	2.01	0.42
2:Xl:806:ILE:HD11	1:Gk:62:ARG:HA	2.02	0.42
1:Bk:72:GLY:CA	1:Ek:77:ALA:HB2	2.48	0.42
1:Ao:62:ARG:HA	2:Xo:724:ILE:HD11	2.02	0.42
1:Am:41:VAL:HB	1:Am:45:TYR:HB2	2.02	0.42
1:Dm:88:VAL:O	1:Dm:91:ILE:HG12	2.20	0.42
3:Pm:14:ASN:HD21	3:Pn:76:ILE:HD12	1.85	0.42
1:At:61:VAL:HG12	2:Xt:724:ILE:HD12	2.01	0.42
1:Gt:81:ILE:HG21	1:Gt:84:VAL:HG23	2.01	0.42
2:Xv:806:ILE:HD11	1:Gu:62:ARG:HA	2.02	0.42
3:Pw:14:ASN:HD21	3:Px:76:ILE:HD12	1.85	0.42
2:Xx:838:VAL:HA	2:Xx:839:PRO:HD3	1.96	0.42
1:DA:79:HIS:ND1	2:XC:820:SER:HB2	2.35	0.42
3:PA:19:MET:SD	3:Pz:74:ILE:HD12	2.59	0.42
3:PA:50:VAL:HG12	3:PA:76:ILE:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dz:61:VAL:O	1:Dz:62:ARG:C	2.62	0.42
1:CC:11:MET:HE3	1:CC:79:HIS:HB3	2.02	0.42
1:EE:15:ARG:HG3	1:EE:76:VAL:CG2	2.49	0.42
1:CG:84:VAL:HG12	1:CG:88:VAL:HB	2.02	0.42
3:PG:19:MET:HE1	3:PG:24:LEU:HD21	2.00	0.42
1:EH:41:VAL:HB	1:EH:45:TYR:HB2	2.01	0.42
1:HH:11:MET:HE3	1:HH:11:MET:HB2	1.88	0.42
1:HJ:35:LEU:CD1	1:HJ:48:VAL:HG13	2.50	0.42
3:PN:50:VAL:HG12	3:PN:76:ILE:HG12	2.01	0.42
3:PL:14:ASN:HD21	3:PM:76:ILE:CG1	2.32	0.42
1:AM:23:ALA:O	1:AM:27:MET:HG3	2.20	0.42
1:HM:7:ILE:H	1:HM:7:ILE:HG13	1.57	0.42
1:DP:27:MET:HG2	1:DP:60:ALA:O	2.20	0.42
1:AS:62:ARG:HA	2:XS:724:ILE:HD11	2.02	0.42
1:BS:75:LEU:HD11	1:BS:78:ALA:HB2	2.01	0.42
1:DS:24:ALA:HB2	1:DS:48:VAL:HG11	2.01	0.42
1:GS:85:HIS:HB3	1:GS:88:VAL:HG23	2.02	0.42
1:AQ:23:ALA:O	1:AQ:27:MET:HG3	2.19	0.42
1:AU:72:GLY:HA2	1:FU:77:ALA:HB2	2.01	0.42
1:DU:79:HIS:ND1	2:XW:820:SER:HB2	2.35	0.42
2:XU:727:THR:O	2:XU:728:PRO:C	2.58	0.42
1:AT:18:VAL:HG22	1:FT:11:MET:HB3	2.01	0.42
1:A2:94:LYS:HB3	1:A2:94:LYS:HE2	1.64	0.42
2:X1:790:LYS:HB2	2:X1:790:LYS:HE2	1.76	0.42
1:A5:94:LYS:HE2	1:A5:94:LYS:HB3	1.85	0.42
1:H5:83:ARG:NH2	1:Ad:32:GLU:HG3	2.34	0.42
1:G3:27:MET:HG2	1:G3:60:ALA:O	2.20	0.42
1:B4:11:MET:HB2	1:B4:11:MET:HE3	1.76	0.42
2:X4:843:LYS:HD2	2:X4:860:LEU:HD13	2.02	0.42
3:P4:30:LYS:HB2	3:P4:30:LYS:HE3	1.74	0.42
1:B7:29:LYS:HE2	3:P7:45:ILE:HG22	2.01	0.42
1:D7:79:HIS:ND1	2:X9:820:SER:HB2	2.35	0.42
1:G7:12:ILE:HG23	1:G7:75:LEU:HD12	2.02	0.42
1:B0:75:LEU:HD11	1:B0:78:ALA:HB2	2.01	0.42
1:G0:84:VAL:HG13	1:G0:88:VAL:HB	2.01	0.42
1:G8:21:ILE:HD13	1:HF:92:LEU:CD2	2.49	0.42
1:A9:7:ILE:HG13	1:DQ:32:GLU:OE2	2.20	0.42
1:Ab:14:THR:HB	1:Ab:19:PRO:HB2	2.02	0.42
3:Pb:19:MET:SD	3:Pa:74:ILE:HD12	2.59	0.42
3:Pb:50:VAL:HG12	3:Pb:76:ILE:HG12	2.02	0.42
1:Be:17:LEU:O	1:Be:21:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:De:27:MET:HG2	1:De:60:ALA:O	2.19	0.42
1:Dg:15:ARG:HH21	2:Xi:825:ALA:HB3	1.85	0.42
2:Xg:832:ALA:HB1	1:Bf:15:ARG:HG2	2.02	0.42
3:Pg:19:MET:SD	3:Pf:74:ILE:HD12	2.60	0.42
1:Bf:57:VAL:HG12	1:Bf:80:ILE:HG23	2.01	0.42
1:Aj:61:VAL:HG12	2:Xj:724:ILE:HD12	2.01	0.42
1:Dj:65:ALA:O	1:Dj:66:ASP:C	2.62	0.42
3:Pj:50:VAL:HG12	3:Pj:76:ILE:HG12	2.01	0.42
2:Xi:713:ILE:CD1	1:HU:62:ARG:HA	2.45	0.42
1:Ho:11:MET:HE3	1:Ho:11:MET:HB2	1.89	0.42
3:Po:6:VAL:HA	3:Po:27:VAL:HG12	2.01	0.42
1:En:23:ALA:O	1:En:27:MET:HG3	2.19	0.42
1:Aq:72:GLY:HA2	1:Fq:77:ALA:HB2	2.01	0.42
1:Bt:41:VAL:HB	1:Bt:45:TYR:HB2	2.01	0.42
1:Dt:24:ALA:HB2	1:Dt:48:VAL:HG11	2.01	0.42
2:Xu:869:GLY:HA2	1:Ew:62:ARG:HD3	2.01	0.42
1:Gy:85:HIS:HB3	1:Gy:88:VAL:HG23	2.02	0.42
1:Hx:83:ARG:NH1	1:AM:28:THR:O	2.51	0.42
2:Xx:843:LYS:HD2	2:Xx:860:LEU:HD13	2.02	0.42
1:HA:11:MET:HE3	1:HA:11:MET:HB2	1.89	0.42
3:PA:53:VAL:HB	3:PA:74:ILE:HD13	2.01	0.42
2:Xz:713:ILE:CG2	1:HG:80:ILE:CD1	2.91	0.42
1:EC:41:VAL:HB	1:EC:45:TYR:HB2	2.01	0.42
1:GF:12:ILE:HG23	1:GF:75:LEU:HD12	2.02	0.42
1:HE:38:ARG:NH2	1:HE:97:GLN:HE21	2.18	0.42
1:HE:96:PRO:O	1:HE:97:GLN:C	2.62	0.42
1:AK:14:THR:HB	1:AK:19:PRO:HB2	2.02	0.42
1:DK:15:ARG:HE	2:XM:825:ALA:HB3	1.84	0.42
1:AJ:18:VAL:HG22	1:FJ:11:MET:HB3	2.00	0.42
1:HJ:38:ARG:NH2	1:HJ:97:GLN:HE21	2.18	0.42
1:HJ:96:PRO:O	1:HJ:97:GLN:C	2.62	0.42
2:XJ:863:TYR:HD2	2:XJ:869:GLY:CA	2.33	0.42
1:GL:35:LEU:HD21	1:HW:91:ILE:HG21	2.01	0.42
3:PL:14:ASN:HD21	3:PM:76:ILE:HD12	1.85	0.42
1:AP:72:GLY:HA2	1:FP:77:ALA:HB2	2.01	0.42
1:CP:84:VAL:HG12	1:CP:88:VAL:HB	2.01	0.42
1:BS:18:VAL:HB	1:BS:19:PRO:HD3	2.01	0.42
1:CQ:84:VAL:HG12	1:CQ:88:VAL:HB	2.02	0.42
1:GQ:77:ALA:HB2	1:HQ:72:GLY:HA2	2.01	0.42
1:CU:9:LEU:HD11	1:CU:49:LEU:HD23	2.02	0.42
1:HT:96:PRO:O	1:HT:97:GLN:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:41:VAL:HB	1:BX:45:TYR:HB2	2.01	0.42
1:E1:15:ARG:HG3	1:E1:76:VAL:CG2	2.50	0.41
2:X1:830:THR:HG22	1:F5:43:GLY:O	2.20	0.41
3:P1:6:VAL:HA	3:P1:27:VAL:HG12	2.03	0.41
1:B5:17:LEU:O	1:B5:21:ILE:HG12	2.19	0.41
1:F5:23:ALA:O	1:F5:27:MET:HG3	2.20	0.41
2:X6:727:THR:O	2:X6:728:PRO:C	2.62	0.41
2:X6:869:GLY:HA2	1:E8:62:ARG:HD3	2.01	0.41
3:P8:14:ASN:HD21	3:P9:76:ILE:CG1	2.32	0.41
1:H9:77:ALA:HB2	1:GR:72:GLY:HA2	2.01	0.41
1:H9:79:HIS:HA	2:XQ:714:THR:O	2.20	0.41
1:Db:15:ARG:HE	2:Xd:825:ALA:HB3	1.84	0.41
1:Gb:12:ILE:HG23	1:Gb:75:LEU:HD12	2.02	0.41
1:Ge:25:ASP:CA	1:Ht:88:VAL:HG21	2.48	0.41
1:Cg:84:VAL:HG12	1:Cg:88:VAL:HB	2.01	0.41
1:Dg:32:GLU:HG3	1:AJ:83:ARG:HH11	1.85	0.41
3:Pg:50:VAL:HG12	3:Pg:76:ILE:HG12	2.02	0.41
2:Xj:785:VAL:HG21	1:Ch:62:ARG:HG2	2.01	0.41
1:Em:8:ALA:HB3	1:Em:52:GLY:O	2.20	0.41
1:Ct:94:LYS:HB3	1:Ct:94:LYS:HE3	1.73	0.41
1:Fr:62:ARG:HH22	2:Xr:799:ASP:HB2	1.85	0.41
1:Gr:77:ALA:HB2	1:Hr:72:GLY:HA2	2.01	0.41
3:Pr:14:ASN:HD21	3:Ps:76:ILE:HD12	1.85	0.41
1:Es:41:VAL:HB	1:Es:45:TYR:HB2	2.01	0.41
1:F5:9:LEU:HD11	1:F5:49:LEU:HD23	2.02	0.41
1:Eu:15:ARG:HG3	1:Eu:76:VAL:CG2	2.50	0.41
1:Ay:62:ARG:HA	2:Xy:724:ILE:HD11	2.02	0.41
3:Py:50:VAL:HG12	3:Py:76:ILE:HG12	2.01	0.41
3:Px:6:VAL:HA	3:Px:27:VAL:HG12	2.02	0.41
1:CA:53:GLU:HG2	1:CA:54:THR:N	2.35	0.41
2:Xz:863:TYR:HD2	2:Xz:869:GLY:CA	2.33	0.41
1:AD:62:ARG:HA	2:XD:724:ILE:HD11	2.02	0.41
1:BD:25:ASP:HA	1:ED:88:VAL:HG21	2.00	0.41
1:GB:77:ALA:HB2	1:HB:72:GLY:HA2	2.01	0.41
1:DF:27:MET:HG2	1:DF:60:ALA:O	2.20	0.41
1:BI:18:VAL:HB	1:BI:19:PRO:HD3	2.01	0.41
1:FI:11:MET:HE3	1:FI:11:MET:HB2	1.87	0.41
1:EH:23:ALA:O	1:EH:27:MET:HG3	2.19	0.41
2:XK:806:ILE:HD11	1:GJ:62:ARG:HA	2.02	0.41
2:XJ:869:GLY:HA2	1:EL:62:ARG:HD3	2.01	0.41
2:XN:785:VAL:HG21	1:CL:62:ARG:HG2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:90:ASN:HD22	1:AL:90:ASN:HA	1.72	0.41
1:GM:88:VAL:HG21	1:HM:25:ASP:HA	2.02	0.41
1:DS:65:ALA:O	1:DS:66:ASP:C	2.62	0.41
1:EQ:8:ALA:HB3	1:EQ:52:GLY:O	2.20	0.41
3:PQ:14:ASN:HD21	3:PR:76:ILE:CG1	2.32	0.41
1:AU:23:ALA:O	1:AU:27:MET:HG3	2.19	0.41
2:XT:863:TYR:HD2	2:XT:869:GLY:CA	2.33	0.41
1:GV:11:MET:HE3	1:GV:11:MET:HB2	1.99	0.41
1:Hf:38:ARG:NH2	1:Hf:97:GLN:HE21	2.18	0.41
2:X2:818:ASN:HA	2:X2:819:PRO:HD3	1.82	0.41
2:X2:832:ALA:HB1	1:B1:15:ARG:HG2	2.02	0.41
3:P2:53:VAL:HB	3:P2:74:ILE:HD13	2.01	0.41
1:B5:35:LEU:HD21	1:E5:91:ILE:HD13	2.03	0.41
3:P5:39:VAL:HG21	3:P5:67:TYR:HE2	1.84	0.41
1:C4:11:MET:HE3	1:C4:79:HIS:HB3	2.02	0.41
1:F4:9:LEU:HD11	1:F4:49:LEU:HD23	2.02	0.41
2:X6:822:ARG:HE	2:X6:822:ARG:HB3	1.73	0.41
3:P0:50:VAL:HG12	3:P0:76:ILE:HG12	2.01	0.41
1:A8:23:ALA:O	1:A8:27:MET:HG3	2.19	0.41
1:E9:23:ALA:O	1:E9:27:MET:HG3	2.19	0.41
3:P9:6:VAL:HA	3:P9:27:VAL:HG12	2.03	0.41
2:Xb:727:THR:O	2:Xb:728:PRO:C	2.58	0.41
1:Fe:23:ALA:O	1:Fe:27:MET:HG3	2.20	0.41
2:Xg:818:ASN:HA	2:Xg:819:PRO:HD3	1.82	0.41
1:Fj:23:ALA:O	1:Fj:27:MET:HG3	2.20	0.41
1:Hj:83:ARG:NH2	1:As:32:GLU:HG3	2.34	0.41
1:Bh:94:LYS:HA	1:Bh:94:LYS:HD3	1.90	0.41
1:Dh:57:VAL:HG12	1:Dh:80:ILE:HG23	2.03	0.41
3:Pi:5:GLN:HA	3:Pi:48:ASP:O	2.19	0.41
3:Pi:6:VAL:HA	3:Pi:27:VAL:HG12	2.03	0.41
1:Dl:15:ARG:HH21	2:Xn:825:ALA:HB3	1.85	0.41
1:Dl:27:MET:HG2	1:Dl:60:ALA:O	2.20	0.41
1:Gl:12:ILE:HG23	1:Gl:75:LEU:HD12	2.02	0.41
1:Gl:85:HIS:ND1	1:Gl:87:GLU:HG3	2.35	0.41
3:Pk:50:VAL:HB	3:Pk:73:ILE:HG23	2.01	0.41
1:Fm:9:LEU:HG	1:Fm:11:MET:HG3	2.02	0.41
1:Fm:62:ARG:HH22	2:Xm:799:ASP:HB2	1.86	0.41
1:Cn:11:MET:HE3	1:Cn:11:MET:HB2	1.89	0.41
1:Fm:59:ALA:HB1	2:Xn:788:GLU:HG2	2.02	0.41
1:Fq:94:LYS:HE3	1:Fq:94:LYS:HB2	1.78	0.41
3:Pt:50:VAL:HG12	3:Pt:76:ILE:HG12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cv:84:VAL:HG12	1:Cv:88:VAL:HB	2.01	0.41
2:Xv:713:ILE:CG2	1:HR:80:ILE:HD12	2.50	0.41
1:Gu:11:MET:HE3	1:Gu:11:MET:HB2	1.99	0.41
1:Dy:24:ALA:HB2	1:Dy:48:VAL:HG11	2.01	0.41
3:Py:22:LYS:HD3	3:Py:23:PRO:HD2	2.03	0.41
1:Gw:77:ALA:HB2	1:Hw:72:GLY:HA2	2.01	0.41
1:Gx:88:VAL:HG21	1:Hx:25:ASP:HA	2.02	0.41
1:DA:27:MET:HG2	1:DA:60:ALA:O	2.20	0.41
1:GA:85:HIS:ND1	1:GA:87:GLU:HG3	2.35	0.41
1:Fz:11:MET:HE3	1:Fz:11:MET:HB2	1.99	0.41
1:DD:27:MET:HG2	1:DD:60:ALA:O	2.19	0.41
1:GD:85:HIS:HB3	1:GD:88:VAL:HG23	2.02	0.41
1:GC:21:ILE:HD13	1:Hf:92:LEU:CD2	2.50	0.41
1:DE:35:LEU:CD1	1:DE:48:VAL:HG13	2.47	0.41
3:PE:5:GLN:HA	3:PE:48:ASP:O	2.19	0.41
3:PE:6:VAL:HA	3:PE:27:VAL:HG12	2.03	0.41
1:FI:23:ALA:O	1:FI:27:MET:HG3	2.20	0.41
1:GI:81:ILE:HG21	1:GI:84:VAL:HG23	2.01	0.41
1:GI:84:VAL:HG13	1:GI:88:VAL:HB	2.01	0.41
1:HI:9:LEU:HD11	1:HI:49:LEU:HD23	2.03	0.41
1:BN:18:VAL:HG22	1:EN:11:MET:HB3	2.02	0.41
1:BN:41:VAL:HB	1:BN:45:TYR:HB2	2.01	0.41
1:AM:11:MET:HE3	1:AM:11:MET:HB2	1.92	0.41
2:XO:727:THR:O	2:XO:728:PRO:C	2.62	0.41
1:BU:29:LYS:HE2	3:PU:45:ILE:HG22	2.01	0.41
1:DU:15:ARG:HE	2:XW:825:ALA:HB3	1.84	0.41
2:XT:869:GLY:HA2	1:EV:62:ARG:HD3	2.01	0.41
1:DX:27:MET:HG2	1:DX:60:ALA:O	2.19	0.41
1:HX:9:LEU:HD11	1:HX:49:LEU:HD23	2.03	0.41
3:PV:14:ASN:HD21	3:PW:76:ILE:HD12	1.85	0.41
1:AW:11:MET:HE3	1:AW:11:MET:HB2	1.92	0.41
1:Hu:96:PRO:O	1:Hu:97:GLN:C	2.62	0.41
1:Hx:38:ARG:NH2	1:Hx:97:GLN:HE21	2.18	0.41
1:HO:96:PRO:O	1:HO:97:GLN:C	2.62	0.41
3:P1:5:GLN:HA	3:P1:48:ASP:O	2.19	0.41
1:B5:18:VAL:HG22	1:E5:11:MET:HB3	2.02	0.41
1:G5:84:VAL:HG13	1:G5:88:VAL:HB	2.01	0.41
1:E3:8:ALA:HB3	1:E3:52:GLY:O	2.20	0.41
1:F3:9:LEU:HG	1:F3:11:MET:HG3	2.02	0.41
1:A4:23:ALA:O	1:A4:27:MET:HG3	2.20	0.41
1:G4:88:VAL:HG21	1:H4:25:ASP:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F9:59:ALA:HB1	2:X9:788:GLU:HG2	2.02	0.41
1:Ea:11:MET:HE3	1:Ea:11:MET:HB2	1.68	0.41
1:Ha:96:PRO:O	1:Ha:97:GLN:C	2.62	0.41
1:Be:41:VAL:HB	1:Be:45:TYR:HB2	2.01	0.41
1:Ge:81:ILE:HG21	1:Ge:84:VAL:HG23	2.01	0.41
1:Ge:84:VAL:HG13	1:Ge:88:VAL:HB	2.01	0.41
3:Pe:22:LYS:HD3	3:Pe:23:PRO:HD2	2.02	0.41
1:Ad:23:ALA:O	1:Ad:27:MET:HG3	2.20	0.41
1:Fd:9:LEU:HD11	1:Fd:49:LEU:HD23	2.02	0.41
1:Gg:85:HIS:ND1	1:Gg:87:GLU:HG3	2.36	0.41
1:Gj:85:HIS:HB3	1:Gj:88:VAL:HG23	2.02	0.41
1:Ch:84:VAL:HG12	1:Ch:88:VAL:HB	2.02	0.41
2:Xh:843:LYS:HE3	2:Xh:860:LEU:HD13	2.01	0.41
1:Fi:94:LYS:HB3	1:Fi:94:LYS:HE3	1.70	0.41
1:En:41:VAL:HB	1:En:45:TYR:HB2	2.01	0.41
1:Cq:53:GLU:HG2	1:Cq:54:THR:N	2.35	0.41
2:Xq:832:ALA:HB1	1:Bp:15:ARG:HG2	2.02	0.41
1:Gp:27:MET:HE1	1:Gp:48:VAL:HG22	2.03	0.41
2:Xp:830:THR:HG22	1:Ft:43:GLY:O	2.20	0.41
2:Xp:863:TYR:HD2	2:Xp:869:GLY:CA	2.33	0.41
3:Pp:42:ILE:HD13	3:Pp:42:ILE:HA	1.91	0.41
3:Pr:14:ASN:HD21	3:Ps:76:ILE:CG1	2.32	0.41
1:F5:59:ALA:HB1	2:Xs:788:GLU:HG2	2.02	0.41
1:Dv:79:HIS:ND1	2:Xx:820:SER:HB2	2.35	0.41
1:Dv:81:ILE:HG21	1:Dv:84:VAL:HG23	2.03	0.41
1:Gv:85:HIS:ND1	1:Gv:87:GLU:HG3	2.36	0.41
3:Pv:19:MET:SD	3:Pu:74:ILE:HD12	2.60	0.41
3:Pv:53:VAL:HB	3:Pv:74:ILE:HD13	2.01	0.41
3:Px:5:GLN:HA	3:Px:48:ASP:O	2.19	0.41
3:PA:68:PRO:HA	3:Pz:57:ALA:HB1	2.02	0.41
3:PB:14:ASN:HD21	3:PC:76:ILE:HD12	1.85	0.41
1:FF:11:MET:HE3	1:FF:11:MET:HB2	1.94	0.41
2:XE:830:THR:HG22	1:FI:43:GLY:O	2.21	0.41
1:DI:24:ALA:HB2	1:DI:48:VAL:HG11	2.01	0.41
2:XI:818:ASN:HA	2:XI:819:PRO:HD3	1.93	0.41
1:AK:72:GLY:HA2	1:FK:77:ALA:HB2	2.01	0.41
1:HN:92:LEU:HD23	1:GU:21:ILE:HD13	1.98	0.41
1:DL:88:VAL:O	1:DL:91:ILE:HG12	2.19	0.41
1:BP:70:ARG:HA	1:BP:70:ARG:HD3	1.86	0.41
3:PO:6:VAL:HA	3:PO:27:VAL:HG12	2.02	0.41
3:PS:22:LYS:HD3	3:PS:23:PRO:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GT:27:MET:HE1	1:GT:48:VAL:HG22	2.03	0.41
1:FW:59:ALA:HB1	2:XW:788:GLU:HG2	2.01	0.41
1:H1:96:PRO:O	1:H1:97:GLN:C	2.62	0.41
1:D2:81:ILE:HG21	1:D2:84:VAL:HG23	2.03	0.41
2:X1:869:GLY:HA2	1:E3:62:ARG:HD3	2.01	0.41
1:G3:77:ALA:HB2	1:H3:72:GLY:HA2	2.01	0.41
1:G7:85:HIS:ND1	1:G7:87:GLU:HG3	2.35	0.41
2:X7:806:ILE:HD11	1:G6:62:ARG:HA	2.02	0.41
3:P7:53:VAL:HB	3:P7:74:ILE:HD13	2.01	0.41
3:P7:68:PRO:HA	3:P6:57:ALA:HB1	2.03	0.41
1:C0:94:LYS:HB3	1:C0:94:LYS:HE3	1.73	0.41
1:A8:41:VAL:HB	1:A8:45:TYR:HB2	2.02	0.41
1:A8:90:ASN:HD22	1:A8:90:ASN:HA	1.72	0.41
1:C8:22:GLU:HG2	1:C8:71:VAL:HG21	2.03	0.41
3:P8:30:LYS:HE3	3:P8:30:LYS:HB2	1.79	0.41
2:X9:729:GLU:HA	1:DQ:62:ARG:NH1	2.21	0.41
1:Gb:85:HIS:ND1	1:Gb:87:GLU:HG3	2.36	0.41
1:Ha:88:VAL:CG2	1:Gr:25:ASP:HA	2.48	0.41
1:Ac:57:VAL:HG12	1:Ac:80:ILE:HG12	2.03	0.41
2:Xd:812:GLN:HE21	2:Xd:812:GLN:HB2	1.71	0.41
2:Xf:863:TYR:HD2	2:Xf:869:GLY:CA	2.33	0.41
1:Bj:18:VAL:HG22	1:Ej:11:MET:HB3	2.02	0.41
1:Ch:22:GLU:HG2	1:Ch:71:VAL:HG21	2.03	0.41
1:Dh:88:VAL:O	1:Dh:91:ILE:HG12	2.19	0.41
3:Ph:30:LYS:HE3	3:Ph:30:LYS:HB2	1.79	0.41
1:Ai:32:GLU:HG3	1:HU:83:ARG:NH2	2.36	0.41
1:Gl:72:GLY:HA2	1:HT:77:ALA:HB2	2.02	0.41
2:Xl:832:ALA:HB1	1:Bk:15:ARG:HG2	2.02	0.41
3:Pl:19:MET:SD	3:Pk:74:ILE:HD12	2.59	0.41
1:Gk:27:MET:HE1	1:Gk:48:VAL:HG22	2.03	0.41
1:Ao:61:VAL:HG12	2:Xo:724:ILE:HD12	2.01	0.41
1:Gm:27:MET:HG2	1:Gm:60:ALA:O	2.19	0.41
3:Pn:6:VAL:HA	3:Pn:27:VAL:HG12	2.02	0.41
2:Xp:818:ASN:HA	2:Xp:819:PRO:HD3	1.81	0.41
1:Ht:9:LEU:HD11	1:Ht:49:LEU:HD23	2.02	0.41
2:Xt:785:VAL:HG21	1:Cr:62:ARG:HG2	2.01	0.41
1:Dr:57:VAL:HG12	1:Dr:80:ILE:HG23	2.02	0.41
3:Pr:19:MET:HE1	3:Pr:24:LEU:HD21	2.00	0.41
3:Pr:30:LYS:HB2	3:Pr:30:LYS:HE3	1.79	0.41
1:Bu:70:ARG:HA	1:Bu:70:ARG:HD3	1.79	0.41
1:AA:14:THR:HB	1:AA:19:PRO:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GA:12:ILE:HG23	1:GA:75:LEU:HD12	2.02	0.41
1:Ez:11:MET:HE3	1:Ez:11:MET:HB2	1.68	0.41
1:BD:18:VAL:HG22	1:ED:11:MET:HB3	2.02	0.41
1:DD:65:ALA:O	1:DD:66:ASP:C	2.62	0.41
1:FD:23:ALA:O	1:FD:27:MET:HG3	2.20	0.41
1:CB:94:LYS:HE3	1:CB:94:LYS:HB3	1.79	0.41
1:GB:9:LEU:HD11	1:GB:49:LEU:HD23	2.03	0.41
3:PB:16:ILE:HG23	3:PC:42:ILE:HD11	2.03	0.41
3:PB:42:ILE:HD13	3:PB:42:ILE:HA	1.81	0.41
3:PF:68:PRO:HA	3:PE:57:ALA:HB1	2.02	0.41
1:HE:11:MET:HE3	1:HE:11:MET:HB2	1.88	0.41
1:DI:65:ALA:O	1:DI:66:ASP:C	2.62	0.41
1:AG:57:VAL:HG12	1:AG:80:ILE:HG12	2.03	0.41
3:PG:42:ILE:HD13	3:PG:42:ILE:HA	1.81	0.41
1:FH:59:ALA:HB1	2:XH:788:GLU:HG2	2.02	0.41
1:DK:27:MET:HG2	1:DK:60:ALA:O	2.20	0.41
3:PK:68:PRO:HA	3:PJ:57:ALA:HB1	2.03	0.41
1:BN:35:LEU:HD21	1:EN:91:ILE:HD13	2.03	0.41
1:EL:8:ALA:HB3	1:EL:52:GLY:O	2.20	0.41
2:XP:806:ILE:HD11	1:GO:62:ARG:HA	2.02	0.41
1:HS:9:LEU:HD11	1:HS:49:LEU:HD23	2.03	0.41
1:GQ:9:LEU:HD11	1:GQ:49:LEU:HD23	2.03	0.41
1:FR:94:LYS:HE3	1:FR:94:LYS:HB3	1.70	0.41
1:GR:88:VAL:HG21	1:HR:25:ASP:HA	2.02	0.41
1:BX:18:VAL:HB	1:BX:19:PRO:HD3	2.01	0.41
1:CV:22:GLU:HG2	1:CV:71:VAL:HG21	2.03	0.41
1:GV:77:ALA:HB2	1:HV:72:GLY:HA2	2.01	0.41
3:Pb:51:LEU:HD12	3:Pb:51:LEU:HA	1.88	0.41
1:Ga:27:MET:HE1	1:Ga:48:VAL:HG22	2.03	0.41
1:De:24:ALA:HB2	1:De:48:VAL:HG11	2.01	0.41
1:De:49:LEU:HD13	1:De:93:PRO:HG3	2.03	0.41
3:Pe:50:VAL:HG12	3:Pe:76:ILE:HG12	2.01	0.41
1:Bc:11:MET:HE3	1:Bc:11:MET:HB2	1.99	0.41
1:Dg:81:ILE:HG21	1:Dg:84:VAL:HG23	2.03	0.41
1:Gj:81:ILE:HG21	1:Gj:84:VAL:HG23	2.01	0.41
1:Gj:84:VAL:CG1	1:Gj:89:GLU:HG2	2.51	0.41
1:Gh:27:MET:HG2	1:Gh:60:ALA:O	2.20	0.41
3:Ph:16:ILE:HG23	3:Pi:42:ILE:HD11	2.03	0.41
2:Xi:843:LYS:HD2	2:Xi:860:LEU:HD13	2.02	0.41
2:Xk:830:THR:HG22	1:Fo:43:GLY:O	2.20	0.41
1:Bo:18:VAL:HG22	1:Eo:11:MET:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cm:22:GLU:HG2	1:Cm:71:VAL:HG21	2.03	0.41
1:Hp:38:ARG:NH2	1:Hp:97:GLN:HE21	2.18	0.41
1:Gt:84:VAL:CG1	1:Gt:89:GLU:HG2	2.51	0.41
1:Ar:57:VAL:HG12	1:Ar:80:ILE:HG12	2.03	0.41
1:Cs:11:MET:HE3	1:Cs:79:HIS:HB3	2.02	0.41
1:Cv:9:LEU:HD11	1:Cv:49:LEU:HD23	2.02	0.41
2:Xv:832:ALA:HB1	1:Bu:15:ARG:HG2	2.02	0.41
3:Pv:68:PRO:HA	3:Pu:57:ALA:HB1	2.02	0.41
1:Du:62:ARG:NH1	2:X8:729:GLU:HA	2.26	0.41
1:Hy:83:ARG:NH2	1:AH:32:GLU:HG3	2.34	0.41
1:Aw:7:ILE:HD11	1:DA:32:GLU:OE1	2.21	0.41
1:Aw:41:VAL:HB	1:Aw:45:TYR:HB2	2.02	0.41
1:Ew:8:ALA:HB3	1:Ew:52:GLY:O	2.20	0.41
1:Fx:59:ALA:HB1	2:Xx:788:GLU:HG2	2.02	0.41
1:AA:72:GLY:HA2	1:FA:77:ALA:HB2	2.01	0.41
3:Pz:6:VAL:HA	3:Pz:27:VAL:HG12	2.02	0.41
3:PD:22:LYS:HD3	3:PD:23:PRO:HD2	2.03	0.41
1:AB:68:CYS:SG	1:AB:75:LEU:HB2	2.61	0.41
1:DB:88:VAL:O	1:DB:91:ILE:HG12	2.20	0.41
1:EB:8:ALA:HB3	1:EB:52:GLY:O	2.20	0.41
1:FC:11:MET:HE3	1:FC:11:MET:HB2	1.90	0.41
1:HC:80:ILE:HD12	2:XK:713:ILE:CG2	2.50	0.41
2:XE:863:TYR:HD2	2:XE:869:GLY:CA	2.33	0.41
1:AG:68:CYS:SG	1:AG:75:LEU:HB2	2.61	0.41
1:EG:8:ALA:HB3	1:EG:52:GLY:O	2.21	0.41
1:GG:9:LEU:HD11	1:GG:49:LEU:HD23	2.03	0.41
1:DK:15:ARG:HH21	2:XM:825:ALA:HB3	1.85	0.41
1:EJ:15:ARG:HG3	1:EJ:76:VAL:CG2	2.50	0.41
1:FJ:18:VAL:O	1:FJ:19:PRO:C	2.62	0.41
1:GN:84:VAL:CG1	1:GN:89:GLU:HG2	2.51	0.41
1:AL:7:ILE:CD1	1:DP:32:GLU:OE1	2.67	0.41
1:AL:23:ALA:O	1:AL:27:MET:HG3	2.19	0.41
1:AL:57:VAL:HG12	1:AL:80:ILE:HG12	2.03	0.41
1:FM:59:ALA:HB1	2:XM:788:GLU:HG2	2.02	0.41
3:PM:6:VAL:HA	3:PM:27:VAL:HG12	2.02	0.41
1:CP:53:GLU:HG2	1:CP:54:THR:N	2.35	0.41
1:GO:27:MET:HE1	1:GO:48:VAL:HG22	2.03	0.41
1:FS:65:ALA:O	1:FS:66:ASP:C	2.61	0.41
1:AQ:90:ASN:HD22	1:AQ:90:ASN:HA	1.72	0.41
1:GQ:27:MET:HG2	1:GQ:60:ALA:O	2.19	0.41
3:PQ:14:ASN:HD21	3:PR:76:ILE:HD12	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FR:9:LEU:HD11	1:FR:49:LEU:HD23	2.02	0.41
1:CU:61:VAL:CG1	1:CU:78:ALA:HB1	2.51	0.41
1:DU:81:ILE:HG21	1:DU:84:VAL:HG23	2.03	0.41
3:PT:6:VAL:HA	3:PT:27:VAL:HG12	2.03	0.41
1:AX:94:LYS:HE2	1:AX:94:LYS:HB3	1.85	0.41
1:BX:18:VAL:HG22	1:EX:11:MET:HB3	2.02	0.41
1:DV:88:VAL:O	1:DV:91:ILE:HG12	2.19	0.41
1:CW:11:MET:HE3	1:CW:79:HIS:HB3	2.02	0.41
1:GW:88:VAL:HG21	1:HW:25:ASP:HA	2.02	0.41
1:Hk:35:LEU:CD1	1:Hk:48:VAL:HG13	2.50	0.41
1:Hu:38:ARG:NH2	1:Hu:97:GLN:HE21	2.18	0.41
1:D2:27:MET:HG2	1:D2:60:ALA:O	2.20	0.41
1:G2:35:LEU:HD11	1:G2:48:VAL:CG1	2.37	0.41
1:G2:85:HIS:ND1	1:G2:87:GLU:HG3	2.36	0.41
3:P5:6:VAL:HA	3:P5:27:VAL:HG12	2.01	0.41
3:P5:13:THR:HG21	1:E3:55:GLY:HA2	2.03	0.41
1:A3:57:VAL:HG12	1:A3:80:ILE:HG12	2.03	0.41
1:G3:9:LEU:HD11	1:G3:49:LEU:HD23	2.03	0.41
1:H4:91:ILE:HG21	1:GQ:35:LEU:HD21	2.03	0.41
1:B7:35:LEU:HD21	1:E7:91:ILE:HD13	2.03	0.41
3:P6:6:VAL:HA	3:P6:27:VAL:HG12	2.02	0.41
1:A0:61:VAL:HG12	2:X0:724:ILE:HD12	2.01	0.41
1:A0:62:ARG:HA	2:X0:724:ILE:HD11	2.02	0.41
1:D8:57:VAL:HG12	1:D8:80:ILE:HG23	2.03	0.41
1:D8:88:VAL:O	1:D8:91:ILE:HG12	2.20	0.41
1:F8:62:ARG:HH22	2:X8:799:ASP:HB2	1.86	0.41
2:X9:838:VAL:HA	2:X9:839:PRO:HD3	1.96	0.41
2:Xb:713:ILE:CG2	1:Ho:80:ILE:CD1	2.98	0.41
1:Ge:84:VAL:CG1	1:Ge:89:GLU:HG2	2.51	0.41
1:He:80:ILE:HD12	2:XE:713:ILE:HG23	1.99	0.41
1:Gc:9:LEU:HD11	1:Gc:49:LEU:HD23	2.03	0.41
3:Pc:16:ILE:HG23	3:Pd:42:ILE:HD11	2.03	0.41
1:Cg:23:ALA:O	1:Cg:27:MET:HG3	2.21	0.41
1:Dg:79:HIS:ND1	2:Xi:820:SER:HB2	2.35	0.41
2:Xf:869:GLY:HA2	1:Eh:62:ARG:HD3	2.01	0.41
1:Ah:41:VAL:HB	1:Ah:45:TYR:HB2	2.02	0.41
1:Eh:8:ALA:HB3	1:Eh:52:GLY:O	2.20	0.41
3:Ph:14:ASN:HD21	3:Pi:76:ILE:HD12	1.85	0.41
1:Ei:41:VAL:HB	1:Ei:45:TYR:HB2	2.01	0.41
1:Dm:11:MET:HE3	1:Dm:11:MET:HB2	1.99	0.41
1:Gm:11:MET:HE3	1:Gm:11:MET:HB2	1.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dq:81:ILE:HG21	1:Dq:84:VAL:HG23	2.03	0.41
1:Gp:11:MET:HE3	1:Gp:11:MET:HB2	1.99	0.41
1:Ft:11:MET:HE3	1:Ft:11:MET:HB2	1.87	0.41
1:Ar:41:VAL:HB	1:Ar:45:TYR:HB2	2.02	0.41
1:Er:8:ALA:HB3	1:Er:52:GLY:O	2.20	0.41
1:Bv:11:MET:HE3	1:Bv:11:MET:HB2	2.00	0.41
1:Cv:53:GLU:HG2	1:Cv:54:THR:N	2.35	0.41
1:Gv:21:ILE:HD13	1:HM:92:LEU:HD23	2.02	0.41
2:Xu:830:THR:HG22	1:Fy:43:GLY:O	2.20	0.41
1:Ay:27:MET:HE1	1:Ay:48:VAL:HG12	2.03	0.41
1:Gy:84:VAL:HG13	1:Gy:88:VAL:HB	2.01	0.41
1:Cw:22:GLU:HG2	1:Cw:71:VAL:HG21	2.03	0.41
1:Fw:62:ARG:HH22	2:Xw:799:ASP:HB2	1.86	0.41
3:Pw:30:LYS:HE3	3:Pw:30:LYS:HB2	1.79	0.41
1:Cx:11:MET:HE3	1:Cx:79:HIS:HB3	2.02	0.41
1:BA:35:LEU:HD21	1:EA:91:ILE:HD13	2.03	0.41
1:CF:53:GLU:HG2	1:CF:54:THR:N	2.35	0.41
3:PI:15:ARG:HH21	3:PI:19:MET:HB3	1.86	0.41
1:DK:79:HIS:ND1	2:XM:820:SER:HB2	2.35	0.41
1:GK:85:HIS:ND1	1:GK:87:GLU:HG3	2.36	0.41
1:GN:85:HIS:HB3	1:GN:88:VAL:HG23	2.02	0.41
1:AL:7:ILE:HD11	1:DP:32:GLU:OE1	2.21	0.41
1:AL:41:VAL:HB	1:AL:45:TYR:HB2	2.02	0.41
1:CL:22:GLU:HG2	1:CL:71:VAL:HG21	2.03	0.41
1:AO:30:ALA:O	1:HV:82:ALA:HB3	2.21	0.41
2:XO:863:TYR:HD2	2:XO:869:GLY:CA	2.33	0.41
1:BS:18:VAL:HG22	1:ES:11:MET:HB3	2.02	0.41
1:BS:35:LEU:HD21	1:ES:91:ILE:HD13	2.03	0.41
1:FS:23:ALA:O	1:FS:27:MET:HG3	2.20	0.41
3:PS:53:VAL:HB	3:PS:74:ILE:HD13	2.03	0.41
1:ER:85:HIS:O	1:ER:89:GLU:HG2	2.21	0.41
1:BU:35:LEU:HD21	1:EU:91:ILE:HD13	2.03	0.41
1:CU:23:ALA:O	1:CU:27:MET:HG3	2.21	0.41
1:AX:62:ARG:HA	2:XX:724:ILE:HD11	2.02	0.41
3:PX:15:ARG:HH21	3:PX:19:MET:HB3	1.86	0.41
1:AV:68:CYS:SG	1:AV:75:LEU:HB2	2.61	0.41
1:AV:90:ASN:HD22	1:AV:90:ASN:HA	1.72	0.41
1:EW:85:HIS:O	1:EW:89:GLU:HG2	2.21	0.41
2:XV:843:LYS:HE3	2:XV:860:LEU:HD13	2.01	0.41
1:C2:53:GLU:HG2	1:C2:54:THR:N	2.35	0.41
2:X2:806:ILE:HD11	1:G1:62:ARG:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X2:822:ARG:HE	2:X2:822:ARG:HB2	1.70	0.41
2:X5:818:ASN:HA	2:X5:819:PRO:HD3	1.93	0.41
1:A3:68:CYS:SG	1:A3:75:LEU:HB2	2.61	0.41
1:C3:84:VAL:HG12	1:C3:88:VAL:HB	2.02	0.41
1:E4:41:VAL:HB	1:E4:45:TYR:HB2	2.01	0.41
3:P7:50:VAL:HG12	3:P7:76:ILE:HG12	2.01	0.41
1:F0:23:ALA:O	1:F0:27:MET:HG3	2.20	0.41
3:P0:13:THR:HG21	1:E8:55:GLY:HA2	2.03	0.41
1:Cb:53:GLU:HG2	1:Cb:54:THR:N	2.35	0.41
2:Xb:806:ILE:HD11	1:Ga:62:ARG:HA	2.02	0.41
2:Xa:713:ILE:CG2	1:Ht:80:ILE:CD1	2.80	0.41
1:Ae:27:MET:HE1	1:Ae:48:VAL:HG12	2.03	0.41
1:He:9:LEU:HD11	1:He:49:LEU:HD23	2.03	0.41
1:Ec:8:ALA:HB3	1:Ec:52:GLY:O	2.21	0.41
1:Fc:62:ARG:HH22	2:Xc:799:ASP:HB2	1.86	0.41
1:Hd:11:MET:HE3	1:Hd:11:MET:HB2	1.88	0.41
1:Bg:35:LEU:HD21	1:Eg:91:ILE:HD13	2.03	0.41
1:Dg:27:MET:HG2	1:Dg:60:ALA:O	2.20	0.41
2:Xf:727:THR:O	2:Xf:728:PRO:C	2.61	0.41
1:Aj:62:ARG:HA	2:Xj:724:ILE:HD11	2.02	0.41
1:Dj:49:LEU:HD13	1:Dj:93:PRO:HG3	2.03	0.41
1:Cl:9:LEU:HD11	1:Cl:49:LEU:HD23	2.02	0.41
1:Cl:23:ALA:O	1:Cl:27:MET:HG3	2.21	0.41
1:Fo:11:MET:HE3	1:Fo:11:MET:HB2	1.87	0.41
1:Am:68:CYS:SG	1:Am:75:LEU:HB2	2.61	0.41
1:Gm:9:LEU:HD11	1:Gm:49:LEU:HD23	2.03	0.41
3:Pm:14:ASN:HD21	3:Pn:76:ILE:CG1	2.32	0.41
1:Gn:88:VAL:HG21	1:Hn:25:ASP:HA	2.02	0.41
1:Gq:12:ILE:HG23	1:Gq:75:LEU:HD12	2.02	0.41
1:Hq:91:ILE:HD13	1:GB:35:LEU:CD2	2.36	0.41
1:Hp:35:LEU:CD1	1:Hp:48:VAL:HG13	2.50	0.41
1:Dt:65:ALA:O	1:Dt:66:ASP:C	2.62	0.41
1:Ft:23:ALA:O	1:Ft:27:MET:HG3	2.20	0.41
3:Pt:6:VAL:HA	3:Pt:27:VAL:HG12	2.01	0.41
3:Pr:16:ILE:HG23	3:Ps:42:ILE:HD11	2.03	0.41
1:Es:85:HIS:O	1:Es:89:GLU:HG2	2.21	0.41
1:Av:14:THR:HB	1:Av:19:PRO:HB2	2.02	0.41
1:Dv:15:ARG:HH21	2:Xx:825:ALA:HB3	1.85	0.41
3:Pu:6:VAL:HA	3:Pu:27:VAL:HG12	2.03	0.41
1:Hw:11:MET:HB3	1:Gz:18:VAL:HG22	2.03	0.41
1:CA:23:ALA:O	1:CA:27:MET:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Gz:27:MET:HE1	1:Gz:48:VAL:HG22	2.03	0.41
1:AB:57:VAL:HG12	1:AB:80:ILE:HG12	2.03	0.41
3:PC:6:VAL:HA	3:PC:27:VAL:HG12	2.02	0.41
1:DF:15:ARG:HE	2:XH:825:ALA:HB3	1.84	0.41
2:XF:806:ILE:HD11	1:GE:62:ARG:HA	2.02	0.41
2:XF:818:ASN:HA	2:XF:819:PRO:HD3	1.82	0.41
1:DE:61:VAL:O	1:DE:62:ARG:C	2.62	0.41
1:GI:84:VAL:CG1	1:GI:89:GLU:HG2	2.51	0.41
3:PI:22:LYS:HD3	3:PI:23:PRO:HD2	2.03	0.41
1:GH:40:PHE:CD1	1:Hx:41:VAL:HG13	2.56	0.41
1:AN:62:ARG:HA	2:XN:724:ILE:HD11	2.02	0.41
1:BN:70:ARG:HA	1:BN:70:ARG:HD3	1.91	0.41
1:BL:11:MET:HE3	1:BL:11:MET:HB2	1.99	0.41
3:PL:42:ILE:HD13	3:PL:42:ILE:HA	1.81	0.41
1:CP:61:VAL:CG1	1:CP:78:ALA:HB1	2.51	0.41
2:XP:832:ALA:HB1	1:BO:15:ARG:HG2	2.02	0.41
3:PP:68:PRO:HA	3:PO:57:ALA:HB1	2.02	0.41
2:XO:830:THR:HG22	1:FS:43:GLY:O	2.20	0.41
1:CR:11:MET:HE3	1:CR:79:HIS:HB3	2.02	0.41
1:GU:85:HIS:ND1	1:GU:87:GLU:HG3	2.36	0.41
2:XT:727:THR:O	2:XT:728:PRO:C	2.61	0.41
2:XT:830:THR:HG22	1:FX:43:GLY:O	2.20	0.41
1:FV:62:ARG:HH22	2:XV:799:ASP:HB2	1.86	0.41
1:H6:38:ARG:NH2	1:H6:97:GLN:HE21	2.18	0.41
2:Xm:790:LYS:HE2	2:Xm:790:LYS:HB2	1.45	0.41
3:P2:50:VAL:HG12	3:P2:76:ILE:HG12	2.02	0.41
1:F5:11:MET:HB2	1:F5:11:MET:HE3	1.87	0.41
1:G5:84:VAL:CG1	1:G5:89:GLU:HG2	2.51	0.41
1:A3:7:ILE:HD11	1:D7:32:GLU:OE1	2.21	0.41
1:D7:15:ARG:HH21	2:X9:825:ALA:HB3	1.85	0.41
1:A6:30:ALA:O	1:Hc:82:ALA:HB3	2.21	0.41
1:D8:32:GLU:OE2	1:Au:7:ILE:CD1	2.69	0.41
1:F8:9:LEU:HG	1:F8:11:MET:HG3	2.02	0.41
1:G8:9:LEU:HD11	1:G8:49:LEU:HD23	2.03	0.41
1:Cb:61:VAL:CG1	1:Cb:78:ALA:HB1	2.51	0.41
1:Ec:41:VAL:HB	1:Ec:45:TYR:HB2	2.03	0.41
3:Pc:14:ASN:HD21	3:Pd:76:ILE:HD12	1.85	0.41
1:Gd:40:PHE:CD1	1:H6:41:VAL:HG13	2.56	0.41
3:Pj:15:ARG:HH21	3:Pj:19:MET:HB3	1.86	0.41
1:Ah:7:ILE:HD11	1:DI:32:GLU:OE1	2.21	0.41
1:Dk:61:VAL:O	1:Dk:62:ARG:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Fn:11:MET:HE3	1:Fn:11:MET:HB2	1.90	0.41
1:Dq:79:HIS:ND1	2:Xs:820:SER:HB2	2.35	0.41
3:Pq:68:PRO:HA	3:Pp:57:ALA:HB1	2.02	0.41
1:At:27:MET:HE1	1:At:48:VAL:HG12	2.03	0.41
1:Dt:49:LEU:HD13	1:Dt:93:PRO:HG3	2.03	0.41
1:Du:61:VAL:O	1:Du:62:ARG:C	2.62	0.41
1:Dw:57:VAL:HG12	1:Dw:80:ILE:HG23	2.03	0.41
1:CA:61:VAL:CG1	1:CA:78:ALA:HB1	2.51	0.41
1:DA:81:ILE:HG21	1:DA:84:VAL:HG23	2.03	0.41
1:EC:85:HIS:O	1:EC:89:GLU:HG2	2.21	0.41
1:AF:14:THR:HB	1:AF:19:PRO:HB2	2.02	0.41
1:DF:15:ARG:HH21	2:XH:825:ALA:HB3	1.85	0.41
1:DI:49:LEU:HD13	1:DI:93:PRO:HG3	2.03	0.41
3:PI:50:VAL:HG12	3:PI:76:ILE:HG12	2.01	0.41
3:PG:14:ASN:HD21	3:PH:76:ILE:HD12	1.85	0.41
1:EH:85:HIS:O	1:EH:89:GLU:HG2	2.21	0.41
1:FH:9:LEU:HD11	1:FH:49:LEU:HD23	2.02	0.41
1:CK:23:ALA:O	1:CK:27:MET:HG3	2.21	0.41
3:PK:30:LYS:HE3	3:PK:30:LYS:HB2	1.94	0.41
3:PL:16:ILE:HG23	3:PM:42:ILE:HD11	2.03	0.41
1:DO:35:LEU:CD1	1:DO:48:VAL:HG13	2.47	0.41
1:GS:84:VAL:CG1	1:GS:89:GLU:HG2	2.51	0.41
1:AQ:68:CYS:SG	1:AQ:75:LEU:HB2	2.61	0.41
1:FQ:62:ARG:HH22	2:XQ:799:ASP:HB2	1.86	0.41
2:XR:843:LYS:HD2	2:XR:860:LEU:HD13	2.02	0.41
1:DU:94:LYS:HE3	1:DU:94:LYS:HB3	1.90	0.41
1:GX:85:HIS:HB3	1:GX:88:VAL:HG23	2.02	0.41
1:Hk:38:ARG:NH2	1:Hk:97:GLN:HE21	2.18	0.41
1:HO:38:ARG:NH2	1:HO:97:GLN:HE21	2.18	0.41
1:F2:94:LYS:HB2	1:F2:94:LYS:HE3	1.78	0.41
2:X2:727:THR:O	2:X2:728:PRO:C	2.58	0.41
3:P2:14:ASN:HD21	3:P1:76:ILE:CG1	2.34	0.41
2:X1:863:TYR:HD2	2:X1:869:GLY:CA	2.33	0.41
1:G5:25:ASP:HA	1:Hm:88:VAL:CG2	2.50	0.41
1:H5:41:VAL:HB	1:H5:45:TYR:HB2	2.03	0.41
1:D3:32:GLU:CD	1:A7:7:ILE:HD11	2.46	0.41
1:E3:11:MET:HE3	1:E3:11:MET:HB2	1.89	0.41
1:F3:62:ARG:HH22	2:X3:799:ASP:HB2	1.86	0.41
1:H3:81:ILE:HG21	1:G6:25:ASP:OD2	2.21	0.41
1:B7:94:LYS:HA	1:B7:94:LYS:HD3	1.98	0.41
1:C7:23:ALA:O	1:C7:27:MET:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X7:727:THR:O	2:X7:728:PRO:C	2.58	0.41
1:B0:18:VAL:HG22	1:E0:11:MET:HB3	2.02	0.41
1:D0:65:ALA:O	1:D0:66:ASP:C	2.62	0.41
1:G0:84:VAL:CG1	1:G0:89:GLU:HG2	2.51	0.41
1:A8:57:VAL:HG12	1:A8:80:ILE:HG12	2.03	0.41
1:A9:11:MET:HE3	1:A9:11:MET:HB2	1.92	0.41
1:A9:23:ALA:O	1:A9:27:MET:HG3	2.20	0.41
1:F9:9:LEU:HD11	1:F9:49:LEU:HD23	2.02	0.41
1:G9:88:VAL:HG21	1:H9:25:ASP:HA	2.02	0.41
1:H9:24:ALA:HB2	1:H9:48:VAL:HG11	2.03	0.41
2:X9:790:LYS:HB2	2:X9:790:LYS:HE2	1.96	0.41
1:Gb:27:MET:HE1	1:Gb:48:VAL:HG12	2.03	0.41
3:Pb:68:PRO:HA	3:Pa:57:ALA:HB1	2.02	0.41
1:Da:35:LEU:CD1	1:Da:48:VAL:HG13	2.47	0.41
1:Ea:62:ARG:HD3	2:Xd:869:GLY:HA2	2.03	0.41
1:Ha:35:LEU:CD1	1:Ha:48:VAL:HG13	2.50	0.41
1:Ae:11:MET:HE3	1:Ae:11:MET:HB2	2.00	0.41
1:He:41:VAL:HB	1:He:45:TYR:HB2	2.03	0.41
1:Ac:90:ASN:HD22	1:Ac:90:ASN:HA	1.72	0.41
1:Fc:9:LEU:HG	1:Fc:11:MET:HG3	2.02	0.41
1:Ed:85:HIS:O	1:Ed:89:GLU:HG2	2.21	0.41
1:Gd:6:GLY:N	1:Gd:34:ARG:HH12	2.19	0.41
2:Xd:843:LYS:HD2	2:Xd:860:LEU:HD13	2.02	0.41
1:Gg:27:MET:HE1	1:Gg:48:VAL:HG12	2.03	0.41
3:Pg:68:PRO:HA	3:Pf:57:ALA:HB1	2.03	0.41
1:Bf:17:LEU:O	1:Bf:21:ILE:HG12	2.21	0.41
1:Bj:35:LEU:HD21	1:Ej:91:ILE:HD13	2.03	0.41
1:Dj:23:ALA:O	1:Dj:27:MET:HG3	2.21	0.41
1:Fj:41:VAL:HB	1:Fj:45:TYR:HB2	2.03	0.41
1:Hj:9:LEU:HD11	1:Hj:49:LEU:HD23	2.03	0.41
1:Ah:68:CYS:SG	1:Ah:75:LEU:HB2	2.61	0.41
1:Fh:9:LEU:HG	1:Fh:11:MET:HG3	2.02	0.41
1:Gi:6:GLY:N	1:Gi:34:ARG:HH12	2.19	0.41
1:Hi:11:MET:HE3	1:Hi:11:MET:HB2	1.88	0.41
1:Di:11:MET:HE3	1:Di:79:HIS:HB3	2.03	0.41
1:Di:81:ILE:HG21	1:Di:84:VAL:HG23	2.03	0.41
3:Pi:53:VAL:HB	3:Pi:74:ILE:HD13	2.01	0.41
2:Xk:713:ILE:HG21	1:Hr:80:ILE:HD11	2.02	0.41
1:Do:49:LEU:HD13	1:Do:93:PRO:HG3	2.03	0.41
2:Xo:727:THR:O	2:Xo:728:PRO:C	2.61	0.41
1:Bm:94:LYS:HA	1:Bm:94:LYS:HD3	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:En:85:HIS:O	1:En:89:GLU:HG2	2.21	0.41
1:Cq:23:ALA:O	1:Cq:27:MET:HG3	2.21	0.41
1:Hq:88:VAL:CG2	1:GB:25:ASP:HA	2.48	0.41
2:Xq:727:THR:O	2:Xq:728:PRO:C	2.58	0.41
2:Xq:806:ILE:HD11	1:Gp:62:ARG:HA	2.02	0.41
1:Fp:18:VAL:O	1:Fp:19:PRO:C	2.62	0.41
2:Xp:713:ILE:HG23	1:HI:80:ILE:HD12	1.94	0.41
1:Ht:41:VAL:HB	1:Ht:45:TYR:HB2	2.03	0.41
1:Gs:88:VAL:HG21	1:Hs:25:ASP:HA	2.02	0.41
1:Hs:24:ALA:HB2	1:Hs:48:VAL:HG11	2.03	0.41
3:Ps:6:VAL:HA	3:Ps:27:VAL:HG12	2.02	0.41
1:Dv:27:MET:HG2	1:Dv:60:ALA:O	2.20	0.41
1:Au:11:MET:HE3	1:Au:11:MET:HB2	1.91	0.41
1:Bu:17:LEU:O	1:Bu:21:ILE:HG12	2.21	0.41
1:By:18:VAL:HG22	1:Ey:11:MET:HB3	2.02	0.41
1:Dy:49:LEU:HD13	1:Dy:93:PRO:HG3	2.03	0.41
1:Fy:65:ALA:O	1:Fy:66:ASP:C	2.61	0.41
1:Hy:7:ILE:H	1:Hy:7:ILE:HG13	1.80	0.41
1:Dw:32:GLU:CD	1:AA:7:ILE:HD11	2.46	0.41
1:Ew:41:VAL:HB	1:Ew:45:TYR:HB2	2.03	0.41
1:Gw:9:LEU:HD11	1:Gw:49:LEU:HD23	2.03	0.41
1:Ex:85:HIS:O	1:Ex:89:GLU:HG2	2.21	0.41
1:Gx:14:THR:HB	1:Gx:19:PRO:HB2	2.03	0.41
2:Xx:821:MET:HB3	2:Xx:821:MET:HE3	1.82	0.41
1:DA:11:MET:HE3	1:DA:79:HIS:HB3	2.03	0.41
3:PA:14:ASN:HD21	3:Pz:76:ILE:CG1	2.34	0.41
2:Xz:713:ILE:HG21	1:HG:80:ILE:HD11	2.02	0.41
2:Xz:821:MET:HG2	1:DD:78:ALA:HB3	2.03	0.41
1:DD:49:LEU:HD13	1:DD:93:PRO:HG3	2.03	0.41
1:GD:84:VAL:CG1	1:GD:89:GLU:HG2	2.51	0.41
1:HD:41:VAL:HB	1:HD:45:TYR:HB2	2.03	0.41
1:AB:41:VAL:HB	1:AB:45:TYR:HB2	2.02	0.41
1:GC:6:GLY:N	1:GC:34:ARG:HH12	2.19	0.41
1:HC:11:MET:HB3	1:GJ:18:VAL:HG22	2.03	0.41
2:XC:843:LYS:HD2	2:XC:860:LEU:HD13	2.02	0.41
3:PC:30:LYS:HE3	3:PC:30:LYS:HB2	1.74	0.41
1:AF:61:VAL:HG12	2:XF:724:ILE:HD12	2.03	0.41
1:BF:94:LYS:HA	1:BF:94:LYS:HD3	1.98	0.41
1:AE:23:ALA:O	1:AE:27:MET:HG3	2.21	0.41
1:BE:17:LEU:O	1:BE:21:ILE:HG12	2.21	0.41
1:BI:18:VAL:HG22	1:EI:11:MET:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:PH:6:VAL:HA	3:PH:27:VAL:HG12	2.02	0.41
1:CK:53:GLU:HG2	1:CK:54:THR:N	2.35	0.41
1:FK:94:LYS:HE3	1:FK:94:LYS:HB2	1.78	0.41
3:PK:14:ASN:HD21	3:PJ:76:ILE:CG1	2.34	0.41
1:DN:61:VAL:O	1:DN:62:ARG:C	2.63	0.41
1:HN:62:ARG:HA	2:XW:713:ILE:CD1	2.48	0.41
3:PN:22:LYS:HD3	3:PN:23:PRO:HD2	2.03	0.41
1:AL:68:CYS:SG	1:AL:75:LEU:HB2	2.61	0.41
1:FL:11:MET:HB2	1:FL:11:MET:HE3	1.81	0.41
1:GP:85:HIS:ND1	1:GP:87:GLU:HG3	2.36	0.41
3:PP:14:ASN:HD21	3:PO:76:ILE:CG1	2.34	0.41
1:BO:17:LEU:O	1:BO:21:ILE:HG12	2.21	0.41
1:HS:11:MET:HE3	1:HS:11:MET:HB2	1.89	0.41
1:EQ:41:VAL:HB	1:EQ:45:TYR:HB2	2.03	0.41
1:GR:6:GLY:N	1:GR:34:ARG:HH12	2.19	0.41
1:HR:24:ALA:HB2	1:HR:48:VAL:HG11	2.03	0.41
1:AU:14:THR:HB	1:AU:19:PRO:HB2	2.02	0.41
3:PU:14:ASN:HD21	3:PT:76:ILE:CG1	2.34	0.41
3:PU:50:VAL:HG12	3:PU:76:ILE:HG12	2.01	0.41
3:PU:68:PRO:HA	3:PT:57:ALA:HB1	2.02	0.41
1:AT:23:ALA:O	1:AT:27:MET:HG3	2.21	0.41
1:FX:65:ALA:O	1:FX:66:ASP:C	2.61	0.41
1:GX:27:MET:HG2	1:GX:60:ALA:O	2.21	0.41
1:HX:11:MET:HE3	1:HX:11:MET:HB2	1.89	0.41
1:AV:57:VAL:HG12	1:AV:80:ILE:HG12	2.03	0.41
1:GW:14:THR:HB	1:GW:19:PRO:HB2	2.03	0.41
1:HW:24:ALA:HB2	1:HW:48:VAL:HG11	2.03	0.41
3:PW:6:VAL:HA	3:PW:27:VAL:HG12	2.02	0.41
1:H2:51:ARG:HA	1:H2:51:ARG:HD2	1.95	0.41
1:A1:23:ALA:O	1:A1:27:MET:HG3	2.21	0.41
1:D5:49:LEU:HD13	1:D5:93:PRO:HG3	2.03	0.41
1:H3:11:MET:HB3	1:G6:18:VAL:HG22	2.03	0.41
1:D6:35:LEU:CD1	1:D6:48:VAL:HG13	2.47	0.41
3:P8:14:ASN:HD21	3:P9:76:ILE:HD12	1.85	0.41
1:Cb:23:ALA:O	1:Cb:27:MET:HG3	2.21	0.41
2:Xb:822:ARG:HE	2:Xb:822:ARG:HB2	1.70	0.41
2:Xa:821:MET:HG2	1:De:78:ALA:HB3	2.03	0.41
2:Xa:830:THR:HG22	1:Fe:43:GLY:O	2.20	0.41
1:Cc:94:LYS:HE3	1:Cc:94:LYS:HB3	1.79	0.41
1:Ec:11:MET:HE3	1:Ec:11:MET:HB2	1.89	0.41
1:Bf:72:GLY:CA	1:Ef:77:ALA:HB2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xf:830:THR:HG22	1:Fj:43:GLY:O	2.20	0.41
1:Bl:35:LEU:HD21	1:El:91:ILE:HD13	2.03	0.41
1:Cl:61:VAL:CG1	1:Cl:78:ALA:HB1	2.51	0.41
1:Dl:79:HIS:ND1	2:Xn:820:SER:HB2	2.35	0.41
3:Pl:68:PRO:HA	3:Pk:57:ALA:HB1	2.03	0.41
1:Ak:30:ALA:O	1:Hr:82:ALA:HB3	2.21	0.41
3:Po:15:ARG:HH21	3:Po:19:MET:HB3	1.86	0.41
3:Po:53:VAL:HB	3:Po:74:ILE:HD13	2.03	0.41
1:Am:57:VAL:HG12	1:Am:80:ILE:HG12	2.03	0.41
1:Bt:35:LEU:HD21	1:Et:91:ILE:HD13	2.03	0.41
1:Dt:23:ALA:O	1:Dt:27:MET:HG3	2.21	0.41
1:Ft:41:VAL:HB	1:Ft:45:TYR:HB2	2.03	0.41
3:Pt:22:LYS:HD3	3:Pt:23:PRO:HD2	2.03	0.41
1:Br:90:ASN:HD22	1:Fr:96:PRO:HG2	1.86	0.41
1:Gs:40:PHE:CD1	1:Hk:41:VAL:HG13	2.56	0.41
1:Gv:12:ILE:HG23	1:Gv:75:LEU:HD12	2.02	0.41
3:Py:13:THR:HG21	1:Ew:55:GLY:HA2	2.03	0.41
1:Cw:84:VAL:HG12	1:Cw:88:VAL:HB	2.02	0.41
1:DA:15:ARG:HH21	2:XC:825:ALA:HB3	1.85	0.41
3:PD:53:VAL:HB	3:PD:74:ILE:HD13	2.03	0.41
3:PB:22:LYS:HD3	3:PB:23:PRO:HD2	2.03	0.41
1:HC:80:ILE:O	2:XK:716:PRO:CD	2.65	0.41
1:GF:85:HIS:ND1	1:GF:87:GLU:HG3	2.36	0.41
1:DI:23:ALA:O	1:DI:27:MET:HG3	2.21	0.41
1:FI:41:VAL:HB	1:FI:45:TYR:HB2	2.03	0.41
2:XI:727:THR:O	2:XI:728:PRO:C	2.61	0.41
1:FG:62:ARG:HH22	2:XG:799:ASP:HB2	1.86	0.41
1:DK:81:ILE:HG21	1:DK:84:VAL:HG23	2.03	0.41
1:HN:9:LEU:HD11	1:HN:49:LEU:HD23	2.03	0.41
3:PN:13:THR:HG21	1:EL:55:GLY:HA2	2.03	0.41
1:HL:81:ILE:HG21	1:GO:25:ASP:OD2	2.21	0.41
2:XM:843:LYS:HD2	2:XM:860:LEU:HD13	2.02	0.41
1:GS:27:MET:HG2	1:GS:60:ALA:O	2.21	0.41
1:FQ:9:LEU:HG	1:FQ:11:MET:HG3	2.02	0.41
1:DU:11:MET:HE3	1:DU:79:HIS:HB3	2.03	0.41
1:ET:18:VAL:HB	1:ET:19:PRO:HD3	2.03	0.41
1:HX:41:VAL:HB	1:HX:45:TYR:HB2	2.03	0.41
1:Hf:35:LEU:CD1	1:Hf:48:VAL:HG13	2.50	0.41
1:G2:12:ILE:HG23	1:G2:75:LEU:HD12	2.02	0.40
1:F5:41:VAL:HB	1:F5:45:TYR:HB2	2.03	0.40
1:H5:9:LEU:HD11	1:H5:49:LEU:HD23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P5:15:ARG:HH21	3:P5:19:MET:HB3	1.86	0.40
3:P3:14:ASN:HD21	3:P4:76:ILE:HD12	1.85	0.40
1:E4:85:HIS:O	1:E4:89:GLU:HG2	2.21	0.40
1:A7:14:THR:HB	1:A7:19:PRO:HB2	2.02	0.40
1:A7:61:VAL:HG12	2:X7:724:ILE:HD12	2.03	0.40
2:X7:832:ALA:HB1	1:B6:15:ARG:HG2	2.02	0.40
1:B0:35:LEU:HD21	1:E0:91:ILE:HD13	2.03	0.40
1:F0:41:VAL:HB	1:F0:45:TYR:HB2	2.03	0.40
1:H0:9:LEU:HD11	1:H0:49:LEU:HD23	2.03	0.40
2:X0:727:THR:O	2:X0:728:PRO:C	2.61	0.40
1:A8:68:CYS:SG	1:A8:75:LEU:HB2	2.61	0.40
1:G8:77:ALA:HB2	1:H8:72:GLY:HA2	2.01	0.40
3:P8:16:ILE:HG23	3:P9:42:ILE:HD11	2.03	0.40
2:Xb:832:ALA:HB1	1:Ba:15:ARG:HG2	2.02	0.40
3:Pb:14:ASN:HD21	3:Pa:76:ILE:CG1	2.34	0.40
1:Ba:17:LEU:O	1:Ba:21:ILE:HG12	2.21	0.40
2:Xa:863:TYR:HD2	2:Xa:869:GLY:CA	2.33	0.40
1:De:32:GLU:HG3	1:AE:7:ILE:HD11	1.89	0.40
1:Ac:41:VAL:HB	1:Ac:45:TYR:HB2	2.02	0.40
1:Cg:61:VAL:CG1	1:Cg:78:ALA:HB1	2.51	0.40
2:Xg:784:ARG:HE	2:Xg:784:ARG:HB2	1.76	0.40
1:Aj:27:MET:HE1	1:Aj:48:VAL:HG12	2.03	0.40
1:Hj:41:VAL:HB	1:Hj:45:TYR:HB2	2.03	0.40
2:Xj:821:MET:HE3	2:Xj:821:MET:HB2	1.68	0.40
1:Bh:90:ASN:HD22	1:Fh:96:PRO:HG2	1.86	0.40
1:Dh:32:GLU:CD	1:Al:7:ILE:HD11	2.46	0.40
1:Gi:14:THR:HB	1:Gi:19:PRO:HB2	2.03	0.40
1:Cl:53:GLU:HG2	1:Cl:54:THR:N	2.35	0.40
1:Bk:85:HIS:HE2	1:Co:83:ARG:HH22	1.69	0.40
1:Ek:18:VAL:O	1:Ek:19:PRO:C	2.64	0.40
1:Do:65:ALA:O	1:Do:66:ASP:C	2.62	0.40
1:Am:35:LEU:HD21	1:Fm:91:ILE:HD13	2.04	0.40
1:Em:18:VAL:O	1:Em:19:PRO:C	2.64	0.40
2:Xn:843:LYS:HD2	2:Xn:860:LEU:HD13	2.02	0.40
1:Dq:11:MET:HE3	1:Dq:79:HIS:HB3	2.03	0.40
1:Hq:80:ILE:CD1	2:XD:713:ILE:CG2	2.99	0.40
1:At:62:ARG:HA	2:Xt:724:ILE:HD11	2.02	0.40
1:Gt:27:MET:HG2	1:Gt:60:ALA:O	2.22	0.40
1:Ar:35:LEU:HD21	1:Fr:91:ILE:HD13	2.03	0.40
1:Fr:9:LEU:HG	1:Fr:11:MET:HG3	2.02	0.40
1:Gs:14:THR:HB	1:Gs:19:PRO:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cv:23:ALA:O	1:Cv:27:MET:HG3	2.21	0.40
3:Pv:14:ASN:HD21	3:Pu:76:ILE:CG1	2.34	0.40
1:Dy:65:ALA:O	1:Dy:66:ASP:C	2.62	0.40
2:Xz:830:THR:HG22	1:FD:43:GLY:O	2.20	0.40
1:HD:9:LEU:HD11	1:HD:49:LEU:HD23	2.03	0.40
1:DF:11:MET:HE3	1:DF:79:HIS:HB3	2.03	0.40
1:FE:18:VAL:O	1:FE:19:PRO:C	2.62	0.40
1:CK:61:VAL:CG1	1:CK:78:ALA:HB1	2.51	0.40
2:XJ:821:MET:HG2	1:DN:78:ALA:HB3	2.03	0.40
2:XJ:830:THR:HG22	1:FN:43:GLY:O	2.20	0.40
1:FN:23:ALA:O	1:FN:27:MET:HG3	2.20	0.40
1:HN:41:VAL:HB	1:HN:45:TYR:HB2	2.03	0.40
3:PN:15:ARG:HH21	3:PN:19:MET:HB3	1.86	0.40
1:DL:57:VAL:HG12	1:DL:80:ILE:HG23	2.03	0.40
1:FL:9:LEU:HG	1:FL:11:MET:HG3	2.02	0.40
1:GM:6:GLY:N	1:GM:34:ARG:HH12	2.19	0.40
1:GM:14:THR:HB	1:GM:19:PRO:HB2	2.03	0.40
1:GP:27:MET:HE1	1:GP:48:VAL:HG12	2.03	0.40
3:PP:10:LEU:HD22	3:PP:10:LEU:HA	1.89	0.40
1:AO:23:ALA:O	1:AO:27:MET:HG3	2.21	0.40
1:AS:27:MET:HE1	1:AS:48:VAL:HG12	2.03	0.40
1:EV:41:VAL:HB	1:EV:45:TYR:HB2	2.03	0.40
1:Hf:94:LYS:HB2	1:Hf:94:LYS:HE2	1.87	0.40
1:A2:61:VAL:HG12	2:X2:724:ILE:HD12	2.03	0.40
3:P2:68:PRO:HA	3:P1:57:ALA:HB1	2.03	0.40
1:D1:61:VAL:O	1:D1:62:ARG:C	2.62	0.40
1:F1:11:MET:HE3	1:F1:11:MET:HB2	1.99	0.40
1:A5:62:ARG:HA	2:X5:724:ILE:HD11	2.02	0.40
1:D3:57:VAL:HG12	1:D3:80:ILE:HG23	2.03	0.40
1:G4:6:GLY:N	1:G4:34:ARG:HH12	2.19	0.40
1:G0:85:HIS:HB3	1:G0:88:VAL:HG23	2.02	0.40
2:X0:862:THR:CG2	2:X0:866:GLY:HA2	2.52	0.40
1:E8:41:VAL:HB	1:E8:45:TYR:HB2	2.03	0.40
1:E9:85:HIS:O	1:E9:89:GLU:HG2	2.21	0.40
1:H9:7:ILE:H	1:H9:7:ILE:HG13	1.57	0.40
3:Pb:10:LEU:HD22	3:Pb:10:LEU:HA	1.89	0.40
1:De:23:ALA:O	1:De:27:MET:HG3	2.21	0.40
1:He:88:VAL:HG21	1:GI:25:ASP:CA	2.50	0.40
1:Ac:68:CYS:SG	1:Ac:75:LEU:HB2	2.61	0.40
1:Fd:94:LYS:HB3	1:Fd:94:LYS:HE3	1.70	0.40
1:Gd:14:THR:HB	1:Gd:19:PRO:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Xj:727:THR:O	2:Xj:728:PRO:C	2.61	0.40
1:Ah:57:VAL:HG12	1:Ah:80:ILE:HG12	2.03	0.40
1:Eh:41:VAL:HB	1:Eh:45:TYR:HB2	2.03	0.40
1:Fh:62:ARG:HH22	2:Xh:799:ASP:HB2	1.86	0.40
1:Gh:9:LEU:HD11	1:Gh:49:LEU:HD23	2.03	0.40
1:Gl:27:MET:HE1	1:Gl:48:VAL:HG12	2.03	0.40
1:Hi:41:VAL:HB	1:Hi:45:TYR:O	2.22	0.40
1:Ek:18:VAL:HB	1:Ek:19:PRO:HD3	2.03	0.40
2:Xk:863:TYR:HD2	2:Xk:869:GLY:CA	2.33	0.40
3:Pk:6:VAL:HA	3:Pk:27:VAL:HG12	2.02	0.40
1:Do:23:ALA:O	1:Do:27:MET:HG3	2.21	0.40
1:Bq:70:ARG:HA	1:Bq:70:ARG:HD3	1.86	0.40
1:Ap:23:ALA:O	1:Ap:27:MET:HG3	2.21	0.40
1:Ar:11:MET:HE3	1:Ar:11:MET:HB2	2.01	0.40
1:Cr:22:GLU:HG2	1:Cr:71:VAL:HG21	2.03	0.40
1:Er:41:VAL:HB	1:Er:45:TYR:HB2	2.03	0.40
1:Cv:61:VAL:CG1	1:Cv:78:ALA:HB1	2.51	0.40
2:Xu:727:THR:O	2:Xu:728:PRO:C	2.61	0.40
1:Gy:81:ILE:HG21	1:Gy:84:VAL:HG23	2.01	0.40
1:Gy:84:VAL:CG1	1:Gy:89:GLU:HG2	2.51	0.40
3:Py:15:ARG:HH21	3:Py:19:MET:HB3	1.86	0.40
1:Gw:35:LEU:HD21	1:HH:91:ILE:HG21	2.01	0.40
1:Hw:53:GLU:HG3	1:AA:53:GLU:OE1	2.22	0.40
3:Pw:42:ILE:HD13	3:Pw:42:ILE:HA	1.81	0.40
1:BA:41:VAL:HB	1:BA:45:TYR:HB2	2.04	0.40
1:BA:94:LYS:HA	1:BA:94:LYS:HD3	1.98	0.40
1:Bz:17:LEU:O	1:Bz:21:ILE:HG12	2.21	0.40
3:PD:13:THR:HG21	1:EB:55:GLY:HA2	2.03	0.40
1:GC:80:ILE:CD1	2:XB:806:ILE:HG21	2.52	0.40
1:HC:24:ALA:HB2	1:HC:48:VAL:HG11	2.03	0.40
1:CF:61:VAL:CG1	1:CF:78:ALA:HB1	2.51	0.40
3:PF:14:ASN:HD21	3:PE:76:ILE:CG1	2.34	0.40
1:BE:94:LYS:HD3	1:BE:94:LYS:HA	1.70	0.40
1:GH:14:THR:HB	1:GH:19:PRO:HB2	2.03	0.40
1:EJ:62:ARG:HD3	2:XM:869:GLY:HA2	2.03	0.40
1:GN:27:MET:HG2	1:GN:60:ALA:O	2.22	0.40
1:GS:11:MET:HE3	1:GS:11:MET:HB2	1.98	0.40
1:GS:81:ILE:HG21	1:GS:84:VAL:HG23	2.01	0.40
1:HS:41:VAL:HB	1:HS:45:TYR:HB2	2.03	0.40
1:BQ:11:MET:HE3	1:BQ:11:MET:HB2	1.99	0.40
1:DU:15:ARG:HH21	2:XW:825:ALA:HB3	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FU:70:ARG:HD2	2:XW:844:PRO:HD3	2.04	0.40
3:PU:51:LEU:HD12	3:PU:51:LEU:HA	1.88	0.40
1:BT:17:LEU:O	1:BT:21:ILE:HG12	2.21	0.40
1:HX:7:ILE:H	1:HX:7:ILE:HG13	1.80	0.40
3:PX:13:THR:HG21	1:EV:55:GLY:HA2	2.03	0.40
2:XW:821:MET:HB3	2:XW:821:MET:HE3	1.82	0.40
2:XW:843:LYS:HD2	2:XW:860:LEU:HD13	2.02	0.40
2:X8:790:LYS:HE2	2:X8:790:LYS:HB2	1.45	0.40
2:Xr:790:LYS:HB2	2:Xr:790:LYS:HE2	1.45	0.40
1:Hu:35:LEU:CD1	1:Hu:48:VAL:HG13	2.50	0.40
1:HO:94:LYS:HE2	1:HO:94:LYS:HB2	1.87	0.40
2:X2:784:ARG:HE	2:X2:784:ARG:HB2	1.76	0.40
1:B1:17:LEU:O	1:B1:21:ILE:HG12	2.21	0.40
2:X1:821:MET:HG2	1:D5:78:ALA:HB3	2.03	0.40
3:P5:22:LYS:HD3	3:P5:23:PRO:HD2	2.03	0.40
1:C7:9:LEU:HD11	1:C7:49:LEU:HD23	2.02	0.40
1:C7:61:VAL:CG1	1:C7:78:ALA:HB1	2.51	0.40
1:H7:41:VAL:HB	1:H7:45:TYR:O	2.22	0.40
1:E6:18:VAL:HB	1:E6:19:PRO:HD3	2.03	0.40
1:F6:65:ALA:O	1:F6:66:ASP:C	2.64	0.40
1:Ab:61:VAL:HG12	2:Xb:724:ILE:HD12	2.03	0.40
3:Pb:37:VAL:HB	3:Pa:51:LEU:HD11	2.04	0.40
3:Pa:6:VAL:HA	3:Pa:27:VAL:HG12	2.03	0.40
3:Pd:6:VAL:HA	3:Pd:27:VAL:HG12	2.02	0.40
1:Dg:11:MET:HE3	1:Dg:79:HIS:HB3	2.03	0.40
1:Gg:12:ILE:HG23	1:Gg:75:LEU:HD12	2.02	0.40
3:Ph:22:LYS:HD3	3:Ph:23:PRO:HD2	2.03	0.40
1:Hi:88:VAL:HG21	1:GT:25:ASP:CA	2.49	0.40
1:Al:61:VAL:HG12	2:Xl:724:ILE:HD12	2.03	0.40
1:Bk:17:LEU:O	1:Bk:21:ILE:HG12	2.21	0.40
1:Go:84:VAL:CG1	1:Go:89:GLU:HG2	2.51	0.40
1:Go:85:HIS:HB3	1:Go:88:VAL:HG23	2.02	0.40
1:Ho:9:LEU:HD11	1:Ho:49:LEU:HD23	2.03	0.40
2:Xo:862:THR:CG2	2:Xo:866:GLY:HA2	2.52	0.40
1:Dm:57:VAL:HG12	1:Dm:80:ILE:HG23	2.03	0.40
1:Dn:32:GLU:HG3	1:AT:83:ARG:HH11	1.85	0.40
1:Gn:6:GLY:N	1:Gn:34:ARG:HH12	2.19	0.40
1:Gq:27:MET:HE1	1:Gq:48:VAL:HG12	2.03	0.40
1:Gq:85:HIS:ND1	1:Gq:87:GLU:HG3	2.36	0.40
1:Bp:17:LEU:O	1:Bp:21:ILE:HG12	2.21	0.40
3:Pt:13:THR:HG21	1:Er:55:GLY:HA2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Pt:15:ARG:HH21	3:Pt:19:MET:HB3	1.86	0.40
1:Gs:6:GLY:N	1:Gs:34:ARG:HH12	2.19	0.40
2:Xy:862:THR:CG2	2:Xy:866:GLY:HA2	2.52	0.40
1:Aw:57:VAL:HG12	1:Aw:80:ILE:HG12	2.03	0.40
1:Fw:9:LEU:HG	1:Fw:11:MET:HG3	2.02	0.40
3:Pw:22:LYS:HD3	3:Pw:23:PRO:HD2	2.03	0.40
1:Fx:9:LEU:HD11	1:Fx:49:LEU:HD23	2.02	0.40
1:CA:9:LEU:HD11	1:CA:49:LEU:HD23	2.02	0.40
1:HA:41:VAL:HB	1:HA:45:TYR:O	2.22	0.40
1:FD:65:ALA:O	1:FD:66:ASP:C	2.61	0.40
1:GD:27:MET:HG2	1:GD:60:ALA:O	2.21	0.40
1:GC:88:VAL:HG21	1:HC:25:ASP:HA	2.02	0.40
1:CF:23:ALA:O	1:CF:27:MET:HG3	2.21	0.40
1:GF:27:MET:HE1	1:GF:48:VAL:HG12	2.03	0.40
1:AI:27:MET:HE1	1:AI:48:VAL:HG12	2.03	0.40
1:CI:94:LYS:HB3	1:CI:94:LYS:HE3	1.73	0.40
1:DG:57:VAL:HG12	1:DG:80:ILE:HG23	2.03	0.40
1:HH:24:ALA:HB2	1:HH:48:VAL:HG11	2.03	0.40
2:XH:843:LYS:HD2	2:XH:860:LEU:HD13	2.02	0.40
1:BK:35:LEU:HD21	1:EK:91:ILE:HD13	2.03	0.40
1:DK:94:LYS:HE3	1:DK:94:LYS:HB3	1.90	0.40
1:GK:12:ILE:HG23	1:GK:75:LEU:HD12	2.02	0.40
1:HK:41:VAL:HB	1:HK:45:TYR:O	2.22	0.40
1:BJ:17:LEU:O	1:BJ:21:ILE:HG12	2.21	0.40
2:XJ:822:ARG:HE	2:XJ:822:ARG:HB3	1.73	0.40
3:PJ:6:VAL:HA	3:PJ:27:VAL:HG12	2.03	0.40
1:EM:85:HIS:O	1:EM:89:GLU:HG2	2.21	0.40
1:HM:24:ALA:HB2	1:HM:48:VAL:HG11	2.03	0.40
1:DO:61:VAL:O	1:DO:62:ARG:C	2.62	0.40
1:FO:18:VAL:O	1:FO:19:PRO:C	2.62	0.40
2:XO:821:MET:HG2	1:DS:78:ALA:HB3	2.03	0.40
2:XQ:806:ILE:HG21	1:GR:80:ILE:CD1	2.52	0.40
1:FT:18:VAL:O	1:FT:19:PRO:C	2.62	0.40
2:XX:862:THR:CG2	2:XX:866:GLY:HA2	2.52	0.40
1:DV:57:VAL:HG12	1:DV:80:ILE:HG23	2.03	0.40
1:EV:8:ALA:HB3	1:EV:52:GLY:O	2.21	0.40
1:FV:9:LEU:HG	1:FV:11:MET:HG3	2.02	0.40
1:GV:9:LEU:HD11	1:GV:49:LEU:HD23	2.03	0.40
1:G2:27:MET:HE1	1:G2:48:VAL:HG12	2.03	0.40
1:E1:18:VAL:O	1:E1:19:PRO:C	2.64	0.40
1:E1:62:ARG:HD3	2:X4:869:GLY:HA2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X5:821:MET:HE3	2:X5:821:MET:HB2	1.68	0.40
2:X5:862:THR:CG2	2:X5:866:GLY:HA2	2.52	0.40
1:A4:11:MET:HE3	1:A4:11:MET:HB2	1.92	0.40
1:G4:14:THR:HB	1:G4:19:PRO:HB2	2.03	0.40
3:P7:14:ASN:HD21	3:P6:76:ILE:CG1	2.34	0.40
3:P7:51:LEU:HD12	3:P7:51:LEU:HA	1.88	0.40
1:D6:61:VAL:O	1:D6:62:ARG:C	2.62	0.40
3:P6:30:LYS:HB2	3:P6:30:LYS:HE3	1.74	0.40
1:A0:94:LYS:HE2	1:A0:94:LYS:HB3	1.85	0.40
3:P0:15:ARG:HH21	3:P0:19:MET:HB3	1.86	0.40
3:P0:53:VAL:HB	3:P0:74:ILE:HD13	2.03	0.40
1:Hb:41:VAL:HB	1:Hb:45:TYR:O	2.22	0.40
2:Xb:801:SER:O	1:Ga:62:ARG:NH1	2.55	0.40
1:Ae:62:ARG:HA	2:Xe:724:ILE:HD11	2.02	0.40
1:Be:18:VAL:HG22	1:Ee:11:MET:HB3	2.02	0.40
1:Be:35:LEU:HD21	1:Ee:91:ILE:HD13	2.03	0.40
1:Ge:27:MET:HG2	1:Ge:60:ALA:O	2.21	0.40
1:Gd:88:VAL:HG21	1:Hd:25:ASP:HA	2.02	0.40
1:Ef:18:VAL:O	1:Ef:19:PRO:C	2.64	0.40
3:Pf:6:VAL:HA	3:Pf:27:VAL:HG12	2.03	0.40
2:Xj:818:ASN:HA	2:Xj:819:PRO:HD3	1.93	0.40
3:Pj:53:VAL:HB	3:Pj:74:ILE:HD13	2.03	0.40
1:Eh:18:VAL:O	1:Eh:19:PRO:C	2.64	0.40
1:Fi:11:MET:HE3	1:Fi:11:MET:HB2	1.90	0.40
3:Pm:30:LYS:HB2	3:Pm:30:LYS:HE3	1.79	0.40
1:Gn:80:ILE:CD1	2:Xm:806:ILE:HG21	2.52	0.40
3:Pq:37:VAL:HB	3:Pp:51:LEU:HD11	2.03	0.40
1:Ep:62:ARG:HD3	2:Xs:869:GLY:HA2	2.03	0.40
3:Pp:6:VAL:HA	3:Pp:27:VAL:HG12	2.03	0.40
1:Bt:70:ARG:HA	1:Bt:70:ARG:HD3	1.91	0.40
1:Hy:88:VAL:CG2	1:GF:25:ASP:HA	2.46	0.40
1:Aw:68:CYS:SG	1:Aw:75:LEU:HB2	2.61	0.40
1:AA:61:VAL:HG12	2:XA:724:ILE:HD12	2.04	0.40
1:FA:70:ARG:HD2	2:XC:844:PRO:HD3	2.04	0.40
3:PA:51:LEU:HA	3:PA:51:LEU:HD12	1.88	0.40
1:Ez:18:VAL:O	1:Ez:19:PRO:C	2.64	0.40
2:XD:862:THR:CG2	2:XD:866:GLY:HA2	2.52	0.40
1:BB:90:ASN:HD22	1:FB:96:PRO:HG2	1.87	0.40
1:DB:57:VAL:HG12	1:DB:80:ILE:HG23	2.03	0.40
1:FC:9:LEU:HD11	1:FC:49:LEU:HD23	2.02	0.40
2:XF:832:ALA:HB1	1:BE:15:ARG:HG2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:PG:22:LYS:HD3	3:PG:23:PRO:HD2	2.03	0.40
1:DK:11:MET:HE3	1:DK:79:HIS:HB3	2.03	0.40
3:PK:51:LEU:HA	3:PK:51:LEU:HD12	1.89	0.40
1:GJ:27:MET:HE1	1:GJ:48:VAL:HG22	2.03	0.40
1:AN:27:MET:HE1	1:AN:48:VAL:HG12	2.03	0.40
1:AL:35:LEU:HD21	1:FL:91:ILE:HD13	2.04	0.40
3:PP:37:VAL:HB	3:PO:51:LEU:HD11	2.04	0.40
2:XO:713:ILE:HG21	1:HV:80:ILE:HD11	2.02	0.40
3:PS:13:THR:HG21	1:EQ:55:GLY:HA2	2.03	0.40
1:HR:11:MET:HE3	1:HR:11:MET:HB2	1.88	0.40
3:PR:6:VAL:HA	3:PR:27:VAL:HG12	2.03	0.40
1:CU:53:GLU:HG2	1:CU:54:THR:N	2.35	0.40
1:DX:65:ALA:O	1:DX:66:ASP:C	2.62	0.40
1:Hk:94:LYS:HE2	1:Hk:94:LYS:HB2	1.87	0.40
1:B2:35:LEU:HD21	1:E2:91:ILE:HD13	2.03	0.40
1:B2:41:VAL:HB	1:B2:45:TYR:HB2	2.04	0.40
1:F1:65:ALA:O	1:F1:66:ASP:C	2.64	0.40
1:D5:23:ALA:O	1:D5:27:MET:HG3	2.21	0.40
1:G5:27:MET:HG2	1:G5:60:ALA:O	2.21	0.40
3:P5:53:VAL:HB	3:P5:74:ILE:HD13	2.03	0.40
1:B3:90:ASN:HD22	1:F3:96:PRO:HG2	1.86	0.40
1:C4:11:MET:HE3	1:C4:11:MET:HB2	1.89	0.40
1:B6:17:LEU:O	1:B6:21:ILE:HG12	2.21	0.40
1:B6:91:ILE:HD13	1:F6:35:LEU:HD21	2.04	0.40
1:E6:62:ARG:HD3	2:X9:869:GLY:HA2	2.03	0.40
1:G6:27:MET:HE1	1:G6:48:VAL:HG22	2.03	0.40
1:A0:38:ARG:CZ	1:A0:38:ARG:HB3	2.52	0.40
1:F0:18:VAL:HB	1:F0:19:PRO:HD3	2.04	0.40
1:Fa:65:ALA:O	1:Fa:66:ASP:C	2.64	0.40
1:Ha:88:VAL:HG21	1:Gr:25:ASP:CA	2.47	0.40
3:Pc:22:LYS:HD3	3:Pc:23:PRO:HD2	2.03	0.40
1:Bg:41:VAL:HB	1:Bg:45:TYR:HB2	2.04	0.40
1:Fg:70:ARG:HD2	2:Xi:844:PRO:HD3	2.04	0.40
1:Gg:11:MET:HE3	1:Gg:11:MET:HB2	2.00	0.40
1:Hg:77:ALA:HB2	1:GN:72:GLY:CA	2.52	0.40
2:Xg:801:SER:O	1:Gf:62:ARG:NH1	2.55	0.40
3:Pg:37:VAL:HB	3:Pf:51:LEU:HD11	2.03	0.40
1:Ef:62:ARG:HD3	2:Xi:869:GLY:HA2	2.03	0.40
1:Ff:18:VAL:O	1:Ff:19:PRO:C	2.62	0.40
1:Gf:27:MET:HE1	1:Gf:48:VAL:HG22	2.03	0.40
3:Pj:13:THR:HG21	1:Eh:55:GLY:HA2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Pj:22:LYS:HD3	3:Pj:23:PRO:HD2	2.03	0.40
1:Gi:35:LEU:CD2	1:Hi:91:ILE:HG21	2.52	0.40
1:Bl:41:VAL:HB	1:Bl:45:TYR:HB2	2.04	0.40
1:Bk:23:ALA:O	1:Bk:27:MET:HG3	2.22	0.40
1:Ao:94:LYS:HE2	1:Ao:94:LYS:HB3	1.85	0.40
3:Po:13:THR:HG21	1:Em:55:GLY:HA2	2.03	0.40
3:Po:22:LYS:HD3	3:Po:23:PRO:HD2	2.03	0.40
1:Hn:7:ILE:H	1:Hn:7:ILE:HG13	1.57	0.40
1:Bq:35:LEU:HD21	1:Eq:91:ILE:HD13	2.03	0.40
1:Hq:41:VAL:HB	1:Hq:45:TYR:O	2.22	0.40
2:Xq:801:SER:O	1:Gp:62:ARG:NH1	2.55	0.40
1:Ep:65:ALA:O	1:Ep:66:ASP:C	2.64	0.40
1:Gt:85:HIS:HB3	1:Gt:88:VAL:HG23	2.02	0.40
1:Ar:68:CYS:SG	1:Ar:75:LEU:HB2	2.61	0.40
2:Xs:843:LYS:HD2	2:Xs:860:LEU:HD13	2.02	0.40
1:Bv:35:LEU:HD21	1:Ev:91:ILE:HD13	2.03	0.40
1:Fy:11:MET:HE3	1:Fy:11:MET:HB2	1.87	0.40
1:Fy:41:VAL:HB	1:Fy:45:TYR:HB2	2.03	0.40
1:Gy:27:MET:HG2	1:Gy:60:ALA:O	2.21	0.40
1:Hy:9:LEU:HD11	1:Hy:49:LEU:HD23	2.03	0.40
1:Fw:11:MET:HE3	1:Fw:11:MET:HB2	1.81	0.40
1:Bz:91:ILE:HD13	1:Fz:35:LEU:HD21	2.04	0.40
1:Ez:65:ALA:O	1:Ez:66:ASP:C	2.64	0.40
1:FD:41:VAL:HB	1:FD:45:TYR:HB2	2.03	0.40
1:GD:11:MET:HE3	1:GD:11:MET:HB2	1.98	0.40
1:GB:11:MET:HE3	1:GB:11:MET:HB2	1.99	0.40
1:FF:70:ARG:HD2	2:XH:844:PRO:HD3	2.04	0.40
1:HE:35:LEU:CD1	1:HE:48:VAL:HG13	2.50	0.40
2:XI:819:PRO:HD2	1:DG:80:ILE:O	2.22	0.40
2:XL:806:ILE:HG21	1:GM:80:ILE:CD1	2.52	0.40
1:AM:9:LEU:HD11	1:AM:49:LEU:HD23	2.04	0.40
1:HS:12:ILE:HG23	1:HS:75:LEU:HD12	2.04	0.40
1:DQ:57:VAL:HG12	1:DQ:80:ILE:HG23	2.03	0.40
2:XU:832:ALA:HB1	1:BT:15:ARG:HG2	2.02	0.40
1:DT:61:VAL:O	1:DT:62:ARG:C	2.62	0.40
1:ET:65:ALA:O	1:ET:66:ASP:C	2.64	0.40
1:BX:65:ALA:O	1:BX:66:ASP:C	2.64	0.40
1:FX:41:VAL:HB	1:FX:45:TYR:HB2	2.03	0.40
2:XX:819:PRO:HD2	1:DV:80:ILE:O	2.22	0.40
3:PX:53:VAL:HB	3:PX:74:ILE:HD13	2.03	0.40
1:CV:84:VAL:HG12	1:CV:88:VAL:HB	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EV:18:VAL:O	1:EV:19:PRO:C	2.64	0.40
1:GW:6:GLY:N	1:GW:34:ARG:HH12	2.19	0.40
1:GW:40:PHE:CD1	1:HO:41:VAL:HG13	2.56	0.40
1:GW:90:ASN:HD22	1:HW:96:PRO:HG2	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A0	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	A1	90/98 (92%)	90 (100%)	0	0	100	100
1	A2	90/98 (92%)	90 (100%)	0	0	100	100
1	A3	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	A4	90/98 (92%)	90 (100%)	0	0	100	100
1	A5	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	A6	90/98 (92%)	90 (100%)	0	0	100	100
1	A7	90/98 (92%)	90 (100%)	0	0	100	100
1	A8	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	A9	90/98 (92%)	90 (100%)	0	0	100	100
1	AA	90/98 (92%)	90 (100%)	0	0	100	100
1	AB	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AC	90/98 (92%)	90 (100%)	0	0	100	100
1	AD	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AE	90/98 (92%)	90 (100%)	0	0	100	100
1	AF	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AG	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AH	90/98 (92%)	90 (100%)	0	0	100	100
1	AI	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AJ	90/98 (92%)	90 (100%)	0	0	100	100
1	AK	90/98 (92%)	90 (100%)	0	0	100	100
1	AL	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AM	90/98 (92%)	90 (100%)	0	0	100	100
1	AN	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AO	90/98 (92%)	90 (100%)	0	0	100	100
1	AP	90/98 (92%)	90 (100%)	0	0	100	100
1	AQ	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AR	90/98 (92%)	90 (100%)	0	0	100	100
1	AS	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AT	90/98 (92%)	90 (100%)	0	0	100	100
1	AU	90/98 (92%)	90 (100%)	0	0	100	100
1	AV	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	AW	90/98 (92%)	90 (100%)	0	0	100	100
1	AX	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Aa	90/98 (92%)	90 (100%)	0	0	100	100
1	Ab	90/98 (92%)	90 (100%)	0	0	100	100
1	Ac	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ad	90/98 (92%)	90 (100%)	0	0	100	100
1	Ae	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Af	90/98 (92%)	90 (100%)	0	0	100	100
1	Ag	90/98 (92%)	90 (100%)	0	0	100	100
1	Ah	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ai	90/98 (92%)	90 (100%)	0	0	100	100
1	Aj	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ak	90/98 (92%)	90 (100%)	0	0	100	100
1	Al	90/98 (92%)	90 (100%)	0	0	100	100
1	Am	90/98 (92%)	89 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	An	90/98 (92%)	90 (100%)	0	0	100	100
1	Ao	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ap	90/98 (92%)	90 (100%)	0	0	100	100
1	Aq	90/98 (92%)	90 (100%)	0	0	100	100
1	Ar	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	As	90/98 (92%)	90 (100%)	0	0	100	100
1	At	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Au	90/98 (92%)	90 (100%)	0	0	100	100
1	Av	90/98 (92%)	90 (100%)	0	0	100	100
1	Aw	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ax	90/98 (92%)	90 (100%)	0	0	100	100
1	Ay	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Az	90/98 (92%)	90 (100%)	0	0	100	100
1	B0	90/98 (92%)	90 (100%)	0	0	100	100
1	B1	90/98 (92%)	90 (100%)	0	0	100	100
1	B2	90/98 (92%)	90 (100%)	0	0	100	100
1	B3	90/98 (92%)	90 (100%)	0	0	100	100
1	B4	90/98 (92%)	90 (100%)	0	0	100	100
1	B5	90/98 (92%)	90 (100%)	0	0	100	100
1	B6	90/98 (92%)	90 (100%)	0	0	100	100
1	B7	90/98 (92%)	90 (100%)	0	0	100	100
1	B8	90/98 (92%)	90 (100%)	0	0	100	100
1	B9	90/98 (92%)	90 (100%)	0	0	100	100
1	BA	90/98 (92%)	90 (100%)	0	0	100	100
1	BB	90/98 (92%)	90 (100%)	0	0	100	100
1	BC	90/98 (92%)	90 (100%)	0	0	100	100
1	BD	90/98 (92%)	90 (100%)	0	0	100	100
1	BE	90/98 (92%)	90 (100%)	0	0	100	100
1	BF	90/98 (92%)	90 (100%)	0	0	100	100
1	BG	90/98 (92%)	90 (100%)	0	0	100	100
1	BH	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BI	90/98 (92%)	90 (100%)	0	0	100	100
1	BJ	90/98 (92%)	90 (100%)	0	0	100	100
1	BK	90/98 (92%)	90 (100%)	0	0	100	100
1	BL	90/98 (92%)	90 (100%)	0	0	100	100
1	BM	90/98 (92%)	90 (100%)	0	0	100	100
1	BN	90/98 (92%)	90 (100%)	0	0	100	100
1	BO	90/98 (92%)	90 (100%)	0	0	100	100
1	BP	90/98 (92%)	90 (100%)	0	0	100	100
1	BQ	90/98 (92%)	90 (100%)	0	0	100	100
1	BR	90/98 (92%)	90 (100%)	0	0	100	100
1	BS	90/98 (92%)	90 (100%)	0	0	100	100
1	BT	90/98 (92%)	90 (100%)	0	0	100	100
1	BU	90/98 (92%)	90 (100%)	0	0	100	100
1	BV	90/98 (92%)	90 (100%)	0	0	100	100
1	BW	90/98 (92%)	90 (100%)	0	0	100	100
1	BX	90/98 (92%)	90 (100%)	0	0	100	100
1	Ba	90/98 (92%)	90 (100%)	0	0	100	100
1	Bb	90/98 (92%)	90 (100%)	0	0	100	100
1	Bc	90/98 (92%)	90 (100%)	0	0	100	100
1	Bd	90/98 (92%)	90 (100%)	0	0	100	100
1	Be	90/98 (92%)	90 (100%)	0	0	100	100
1	Bf	90/98 (92%)	90 (100%)	0	0	100	100
1	Bg	90/98 (92%)	90 (100%)	0	0	100	100
1	Bh	90/98 (92%)	90 (100%)	0	0	100	100
1	Bi	90/98 (92%)	90 (100%)	0	0	100	100
1	Bj	90/98 (92%)	90 (100%)	0	0	100	100
1	Bk	90/98 (92%)	90 (100%)	0	0	100	100
1	Bl	90/98 (92%)	90 (100%)	0	0	100	100
1	Bm	90/98 (92%)	90 (100%)	0	0	100	100
1	Bn	90/98 (92%)	90 (100%)	0	0	100	100
1	Bo	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Bp	90/98 (92%)	90 (100%)	0	0	100	100
1	Bq	90/98 (92%)	90 (100%)	0	0	100	100
1	Br	90/98 (92%)	90 (100%)	0	0	100	100
1	Bs	90/98 (92%)	90 (100%)	0	0	100	100
1	Bt	90/98 (92%)	90 (100%)	0	0	100	100
1	Bu	90/98 (92%)	90 (100%)	0	0	100	100
1	Bv	90/98 (92%)	90 (100%)	0	0	100	100
1	Bw	90/98 (92%)	90 (100%)	0	0	100	100
1	Bx	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	By	90/98 (92%)	90 (100%)	0	0	100	100
1	Bz	90/98 (92%)	90 (100%)	0	0	100	100
1	C0	90/98 (92%)	90 (100%)	0	0	100	100
1	C1	90/98 (92%)	90 (100%)	0	0	100	100
1	C2	90/98 (92%)	90 (100%)	0	0	100	100
1	C3	90/98 (92%)	90 (100%)	0	0	100	100
1	C4	90/98 (92%)	90 (100%)	0	0	100	100
1	C5	90/98 (92%)	90 (100%)	0	0	100	100
1	C6	90/98 (92%)	90 (100%)	0	0	100	100
1	C7	90/98 (92%)	90 (100%)	0	0	100	100
1	C8	90/98 (92%)	90 (100%)	0	0	100	100
1	C9	90/98 (92%)	90 (100%)	0	0	100	100
1	CA	90/98 (92%)	90 (100%)	0	0	100	100
1	CB	90/98 (92%)	90 (100%)	0	0	100	100
1	CC	90/98 (92%)	90 (100%)	0	0	100	100
1	CD	90/98 (92%)	90 (100%)	0	0	100	100
1	CE	90/98 (92%)	90 (100%)	0	0	100	100
1	CF	90/98 (92%)	90 (100%)	0	0	100	100
1	CG	90/98 (92%)	90 (100%)	0	0	100	100
1	CH	90/98 (92%)	90 (100%)	0	0	100	100
1	CI	90/98 (92%)	90 (100%)	0	0	100	100
1	CJ	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CK	90/98 (92%)	90 (100%)	0	0	100	100
1	CL	90/98 (92%)	90 (100%)	0	0	100	100
1	CM	90/98 (92%)	90 (100%)	0	0	100	100
1	CN	90/98 (92%)	90 (100%)	0	0	100	100
1	CO	90/98 (92%)	90 (100%)	0	0	100	100
1	CP	90/98 (92%)	90 (100%)	0	0	100	100
1	CQ	90/98 (92%)	90 (100%)	0	0	100	100
1	CR	90/98 (92%)	90 (100%)	0	0	100	100
1	CS	90/98 (92%)	90 (100%)	0	0	100	100
1	CT	90/98 (92%)	90 (100%)	0	0	100	100
1	CU	90/98 (92%)	90 (100%)	0	0	100	100
1	CV	90/98 (92%)	90 (100%)	0	0	100	100
1	CW	90/98 (92%)	90 (100%)	0	0	100	100
1	CX	90/98 (92%)	90 (100%)	0	0	100	100
1	Ca	90/98 (92%)	90 (100%)	0	0	100	100
1	Cb	90/98 (92%)	90 (100%)	0	0	100	100
1	Cc	90/98 (92%)	90 (100%)	0	0	100	100
1	Cd	90/98 (92%)	90 (100%)	0	0	100	100
1	Ce	90/98 (92%)	90 (100%)	0	0	100	100
1	Cf	90/98 (92%)	90 (100%)	0	0	100	100
1	Cg	90/98 (92%)	90 (100%)	0	0	100	100
1	Ch	90/98 (92%)	90 (100%)	0	0	100	100
1	Ci	90/98 (92%)	90 (100%)	0	0	100	100
1	Cj	90/98 (92%)	90 (100%)	0	0	100	100
1	Ck	90/98 (92%)	90 (100%)	0	0	100	100
1	Cl	90/98 (92%)	90 (100%)	0	0	100	100
1	Cm	90/98 (92%)	90 (100%)	0	0	100	100
1	Cn	90/98 (92%)	90 (100%)	0	0	100	100
1	Co	90/98 (92%)	90 (100%)	0	0	100	100
1	Cp	90/98 (92%)	90 (100%)	0	0	100	100
1	Cq	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Cr	90/98 (92%)	90 (100%)	0	0	100	100
1	Cs	90/98 (92%)	90 (100%)	0	0	100	100
1	Ct	90/98 (92%)	90 (100%)	0	0	100	100
1	Cu	90/98 (92%)	90 (100%)	0	0	100	100
1	Cv	90/98 (92%)	90 (100%)	0	0	100	100
1	Cw	90/98 (92%)	90 (100%)	0	0	100	100
1	Cx	90/98 (92%)	90 (100%)	0	0	100	100
1	Cy	90/98 (92%)	90 (100%)	0	0	100	100
1	Cz	90/98 (92%)	90 (100%)	0	0	100	100
1	D0	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	D1	90/98 (92%)	90 (100%)	0	0	100	100
1	D2	90/98 (92%)	90 (100%)	0	0	100	100
1	D3	90/98 (92%)	90 (100%)	0	0	100	100
1	D4	90/98 (92%)	90 (100%)	0	0	100	100
1	D5	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	D6	90/98 (92%)	90 (100%)	0	0	100	100
1	D7	90/98 (92%)	90 (100%)	0	0	100	100
1	D8	90/98 (92%)	90 (100%)	0	0	100	100
1	D9	90/98 (92%)	90 (100%)	0	0	100	100
1	DA	90/98 (92%)	90 (100%)	0	0	100	100
1	DB	90/98 (92%)	90 (100%)	0	0	100	100
1	DC	90/98 (92%)	90 (100%)	0	0	100	100
1	DD	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	DE	90/98 (92%)	90 (100%)	0	0	100	100
1	DF	90/98 (92%)	90 (100%)	0	0	100	100
1	DG	90/98 (92%)	90 (100%)	0	0	100	100
1	DH	90/98 (92%)	90 (100%)	0	0	100	100
1	DI	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	DJ	90/98 (92%)	90 (100%)	0	0	100	100
1	DK	90/98 (92%)	90 (100%)	0	0	100	100
1	DL	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DM	90/98 (92%)	90 (100%)	0	0	100	100
1	DN	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	DO	90/98 (92%)	90 (100%)	0	0	100	100
1	DP	90/98 (92%)	90 (100%)	0	0	100	100
1	DQ	90/98 (92%)	90 (100%)	0	0	100	100
1	DR	90/98 (92%)	90 (100%)	0	0	100	100
1	DS	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	DT	90/98 (92%)	90 (100%)	0	0	100	100
1	DU	90/98 (92%)	90 (100%)	0	0	100	100
1	DV	90/98 (92%)	90 (100%)	0	0	100	100
1	DW	90/98 (92%)	90 (100%)	0	0	100	100
1	DX	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Da	90/98 (92%)	90 (100%)	0	0	100	100
1	Db	90/98 (92%)	90 (100%)	0	0	100	100
1	Dc	90/98 (92%)	90 (100%)	0	0	100	100
1	Dd	90/98 (92%)	90 (100%)	0	0	100	100
1	De	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Df	90/98 (92%)	90 (100%)	0	0	100	100
1	Dg	90/98 (92%)	90 (100%)	0	0	100	100
1	Dh	90/98 (92%)	90 (100%)	0	0	100	100
1	Di	90/98 (92%)	90 (100%)	0	0	100	100
1	Dj	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Dk	90/98 (92%)	90 (100%)	0	0	100	100
1	Dl	90/98 (92%)	90 (100%)	0	0	100	100
1	Dm	90/98 (92%)	90 (100%)	0	0	100	100
1	Dn	90/98 (92%)	90 (100%)	0	0	100	100
1	Do	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Dp	90/98 (92%)	90 (100%)	0	0	100	100
1	Dq	90/98 (92%)	90 (100%)	0	0	100	100
1	Dr	90/98 (92%)	90 (100%)	0	0	100	100
1	Ds	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Dt	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Du	90/98 (92%)	90 (100%)	0	0	100	100
1	Dv	90/98 (92%)	90 (100%)	0	0	100	100
1	Dw	90/98 (92%)	90 (100%)	0	0	100	100
1	Dx	90/98 (92%)	90 (100%)	0	0	100	100
1	Dy	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Dz	90/98 (92%)	90 (100%)	0	0	100	100
1	E0	90/98 (92%)	90 (100%)	0	0	100	100
1	E1	90/98 (92%)	90 (100%)	0	0	100	100
1	E2	90/98 (92%)	90 (100%)	0	0	100	100
1	E3	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	E4	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	E5	90/98 (92%)	90 (100%)	0	0	100	100
1	E6	90/98 (92%)	90 (100%)	0	0	100	100
1	E7	90/98 (92%)	90 (100%)	0	0	100	100
1	E8	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	E9	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	EA	90/98 (92%)	90 (100%)	0	0	100	100
1	EB	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	EC	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	ED	90/98 (92%)	90 (100%)	0	0	100	100
1	EE	90/98 (92%)	90 (100%)	0	0	100	100
1	EF	90/98 (92%)	90 (100%)	0	0	100	100
1	EG	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	EH	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	EI	90/98 (92%)	90 (100%)	0	0	100	100
1	EJ	90/98 (92%)	90 (100%)	0	0	100	100
1	EK	90/98 (92%)	90 (100%)	0	0	100	100
1	EL	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	EM	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	EN	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EO	90/98 (92%)	90 (100%)	0	0	100	100
1	EP	90/98 (92%)	90 (100%)	0	0	100	100
1	EQ	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	ER	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	ES	90/98 (92%)	90 (100%)	0	0	100	100
1	ET	90/98 (92%)	90 (100%)	0	0	100	100
1	EU	90/98 (92%)	90 (100%)	0	0	100	100
1	EV	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	EW	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	EX	90/98 (92%)	90 (100%)	0	0	100	100
1	Ea	90/98 (92%)	90 (100%)	0	0	100	100
1	Eb	90/98 (92%)	90 (100%)	0	0	100	100
1	Ec	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ed	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ee	90/98 (92%)	90 (100%)	0	0	100	100
1	Ef	90/98 (92%)	90 (100%)	0	0	100	100
1	Eg	90/98 (92%)	90 (100%)	0	0	100	100
1	Eh	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ei	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ej	90/98 (92%)	90 (100%)	0	0	100	100
1	Ek	90/98 (92%)	90 (100%)	0	0	100	100
1	El	90/98 (92%)	90 (100%)	0	0	100	100
1	Em	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	En	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Eo	90/98 (92%)	90 (100%)	0	0	100	100
1	Ep	90/98 (92%)	90 (100%)	0	0	100	100
1	Eq	90/98 (92%)	90 (100%)	0	0	100	100
1	Er	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Es	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Et	90/98 (92%)	90 (100%)	0	0	100	100
1	Eu	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ev	90/98 (92%)	90 (100%)	0	0	100	100
1	Ew	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ex	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Ey	90/98 (92%)	90 (100%)	0	0	100	100
1	Ez	90/98 (92%)	90 (100%)	0	0	100	100
1	F0	90/98 (92%)	90 (100%)	0	0	100	100
1	F1	90/98 (92%)	90 (100%)	0	0	100	100
1	F2	90/98 (92%)	90 (100%)	0	0	100	100
1	F3	90/98 (92%)	90 (100%)	0	0	100	100
1	F4	90/98 (92%)	90 (100%)	0	0	100	100
1	F5	90/98 (92%)	90 (100%)	0	0	100	100
1	F6	90/98 (92%)	90 (100%)	0	0	100	100
1	F7	90/98 (92%)	90 (100%)	0	0	100	100
1	F8	90/98 (92%)	90 (100%)	0	0	100	100
1	F9	90/98 (92%)	90 (100%)	0	0	100	100
1	FA	90/98 (92%)	90 (100%)	0	0	100	100
1	FB	90/98 (92%)	90 (100%)	0	0	100	100
1	FC	90/98 (92%)	90 (100%)	0	0	100	100
1	FD	90/98 (92%)	90 (100%)	0	0	100	100
1	FE	90/98 (92%)	90 (100%)	0	0	100	100
1	FF	90/98 (92%)	90 (100%)	0	0	100	100
1	FG	90/98 (92%)	90 (100%)	0	0	100	100
1	FH	90/98 (92%)	90 (100%)	0	0	100	100
1	FI	90/98 (92%)	90 (100%)	0	0	100	100
1	FJ	90/98 (92%)	90 (100%)	0	0	100	100
1	FK	90/98 (92%)	90 (100%)	0	0	100	100
1	FL	90/98 (92%)	90 (100%)	0	0	100	100
1	FM	90/98 (92%)	90 (100%)	0	0	100	100
1	FN	90/98 (92%)	90 (100%)	0	0	100	100
1	FO	90/98 (92%)	90 (100%)	0	0	100	100
1	FP	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	FQ	90/98 (92%)	90 (100%)	0	0	100	100
1	FR	90/98 (92%)	90 (100%)	0	0	100	100
1	FS	90/98 (92%)	90 (100%)	0	0	100	100
1	FT	90/98 (92%)	90 (100%)	0	0	100	100
1	FU	90/98 (92%)	90 (100%)	0	0	100	100
1	FV	90/98 (92%)	90 (100%)	0	0	100	100
1	FW	90/98 (92%)	90 (100%)	0	0	100	100
1	FX	90/98 (92%)	90 (100%)	0	0	100	100
1	Fa	90/98 (92%)	90 (100%)	0	0	100	100
1	Fb	90/98 (92%)	90 (100%)	0	0	100	100
1	Fc	90/98 (92%)	90 (100%)	0	0	100	100
1	Fd	90/98 (92%)	90 (100%)	0	0	100	100
1	Fe	90/98 (92%)	90 (100%)	0	0	100	100
1	Ff	90/98 (92%)	90 (100%)	0	0	100	100
1	Fg	90/98 (92%)	90 (100%)	0	0	100	100
1	Fh	90/98 (92%)	90 (100%)	0	0	100	100
1	Fi	90/98 (92%)	90 (100%)	0	0	100	100
1	Fj	90/98 (92%)	90 (100%)	0	0	100	100
1	Fk	90/98 (92%)	90 (100%)	0	0	100	100
1	Fl	90/98 (92%)	90 (100%)	0	0	100	100
1	Fm	90/98 (92%)	90 (100%)	0	0	100	100
1	Fn	90/98 (92%)	90 (100%)	0	0	100	100
1	Fo	90/98 (92%)	90 (100%)	0	0	100	100
1	Fp	90/98 (92%)	90 (100%)	0	0	100	100
1	Fq	90/98 (92%)	90 (100%)	0	0	100	100
1	Fr	90/98 (92%)	90 (100%)	0	0	100	100
1	Fs	90/98 (92%)	90 (100%)	0	0	100	100
1	Ft	90/98 (92%)	90 (100%)	0	0	100	100
1	Fu	90/98 (92%)	90 (100%)	0	0	100	100
1	Fv	90/98 (92%)	90 (100%)	0	0	100	100
1	Fw	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Fx	90/98 (92%)	90 (100%)	0	0	100	100
1	Fy	90/98 (92%)	90 (100%)	0	0	100	100
1	Fz	90/98 (92%)	90 (100%)	0	0	100	100
1	G0	90/98 (92%)	90 (100%)	0	0	100	100
1	G1	90/98 (92%)	90 (100%)	0	0	100	100
1	G2	90/98 (92%)	90 (100%)	0	0	100	100
1	G3	90/98 (92%)	90 (100%)	0	0	100	100
1	G4	90/98 (92%)	90 (100%)	0	0	100	100
1	G5	90/98 (92%)	90 (100%)	0	0	100	100
1	G6	90/98 (92%)	90 (100%)	0	0	100	100
1	G7	90/98 (92%)	90 (100%)	0	0	100	100
1	G8	90/98 (92%)	90 (100%)	0	0	100	100
1	G9	90/98 (92%)	90 (100%)	0	0	100	100
1	GA	90/98 (92%)	90 (100%)	0	0	100	100
1	GB	90/98 (92%)	90 (100%)	0	0	100	100
1	GC	90/98 (92%)	90 (100%)	0	0	100	100
1	GD	90/98 (92%)	90 (100%)	0	0	100	100
1	GE	90/98 (92%)	90 (100%)	0	0	100	100
1	GF	90/98 (92%)	90 (100%)	0	0	100	100
1	GG	90/98 (92%)	90 (100%)	0	0	100	100
1	GH	90/98 (92%)	90 (100%)	0	0	100	100
1	GI	90/98 (92%)	90 (100%)	0	0	100	100
1	GJ	90/98 (92%)	90 (100%)	0	0	100	100
1	GK	90/98 (92%)	90 (100%)	0	0	100	100
1	GL	90/98 (92%)	90 (100%)	0	0	100	100
1	GM	90/98 (92%)	90 (100%)	0	0	100	100
1	GN	90/98 (92%)	90 (100%)	0	0	100	100
1	GO	90/98 (92%)	90 (100%)	0	0	100	100
1	GP	90/98 (92%)	90 (100%)	0	0	100	100
1	GQ	90/98 (92%)	90 (100%)	0	0	100	100
1	GR	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GS	90/98 (92%)	90 (100%)	0	0	100	100
1	GT	90/98 (92%)	90 (100%)	0	0	100	100
1	GU	90/98 (92%)	90 (100%)	0	0	100	100
1	GV	90/98 (92%)	90 (100%)	0	0	100	100
1	GW	90/98 (92%)	90 (100%)	0	0	100	100
1	GX	90/98 (92%)	90 (100%)	0	0	100	100
1	Ga	90/98 (92%)	90 (100%)	0	0	100	100
1	Gb	90/98 (92%)	90 (100%)	0	0	100	100
1	Gc	90/98 (92%)	90 (100%)	0	0	100	100
1	Gd	90/98 (92%)	90 (100%)	0	0	100	100
1	Ge	90/98 (92%)	90 (100%)	0	0	100	100
1	Gf	90/98 (92%)	90 (100%)	0	0	100	100
1	Gg	90/98 (92%)	90 (100%)	0	0	100	100
1	Gh	90/98 (92%)	90 (100%)	0	0	100	100
1	Gi	90/98 (92%)	90 (100%)	0	0	100	100
1	Gj	90/98 (92%)	90 (100%)	0	0	100	100
1	Gk	90/98 (92%)	90 (100%)	0	0	100	100
1	Gl	90/98 (92%)	90 (100%)	0	0	100	100
1	Gm	90/98 (92%)	90 (100%)	0	0	100	100
1	Gn	90/98 (92%)	90 (100%)	0	0	100	100
1	Go	90/98 (92%)	90 (100%)	0	0	100	100
1	Gp	90/98 (92%)	90 (100%)	0	0	100	100
1	Gq	90/98 (92%)	90 (100%)	0	0	100	100
1	Gr	90/98 (92%)	90 (100%)	0	0	100	100
1	Gs	90/98 (92%)	90 (100%)	0	0	100	100
1	Gt	90/98 (92%)	90 (100%)	0	0	100	100
1	Gu	90/98 (92%)	90 (100%)	0	0	100	100
1	Gv	90/98 (92%)	90 (100%)	0	0	100	100
1	Gw	90/98 (92%)	90 (100%)	0	0	100	100
1	Gx	90/98 (92%)	90 (100%)	0	0	100	100
1	Gy	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Gz	90/98 (92%)	90 (100%)	0	0	100	100
1	H0	90/98 (92%)	90 (100%)	0	0	100	100
1	H1	90/98 (92%)	90 (100%)	0	0	100	100
1	H2	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	H3	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	H4	90/98 (92%)	90 (100%)	0	0	100	100
1	H5	90/98 (92%)	90 (100%)	0	0	100	100
1	H6	90/98 (92%)	90 (100%)	0	0	100	100
1	H7	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	H8	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	H9	90/98 (92%)	90 (100%)	0	0	100	100
1	HA	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HB	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HC	90/98 (92%)	90 (100%)	0	0	100	100
1	HD	90/98 (92%)	90 (100%)	0	0	100	100
1	HE	90/98 (92%)	90 (100%)	0	0	100	100
1	HF	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HG	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HH	90/98 (92%)	90 (100%)	0	0	100	100
1	HI	90/98 (92%)	90 (100%)	0	0	100	100
1	HJ	90/98 (92%)	90 (100%)	0	0	100	100
1	HK	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HL	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HM	90/98 (92%)	90 (100%)	0	0	100	100
1	HN	90/98 (92%)	90 (100%)	0	0	100	100
1	HO	90/98 (92%)	90 (100%)	0	0	100	100
1	HP	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HQ	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HR	90/98 (92%)	90 (100%)	0	0	100	100
1	HS	90/98 (92%)	90 (100%)	0	0	100	100
1	HT	90/98 (92%)	90 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	HU	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HV	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	HW	90/98 (92%)	90 (100%)	0	0	100	100
1	HX	90/98 (92%)	90 (100%)	0	0	100	100
1	Ha	90/98 (92%)	90 (100%)	0	0	100	100
1	Hb	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hc	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hd	90/98 (92%)	90 (100%)	0	0	100	100
1	He	90/98 (92%)	90 (100%)	0	0	100	100
1	Hf	90/98 (92%)	90 (100%)	0	0	100	100
1	Hg	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hh	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hi	90/98 (92%)	90 (100%)	0	0	100	100
1	Hj	90/98 (92%)	90 (100%)	0	0	100	100
1	Hk	90/98 (92%)	90 (100%)	0	0	100	100
1	Hl	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hm	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hn	90/98 (92%)	90 (100%)	0	0	100	100
1	Ho	90/98 (92%)	90 (100%)	0	0	100	100
1	Hp	90/98 (92%)	90 (100%)	0	0	100	100
1	Hq	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hr	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hs	90/98 (92%)	90 (100%)	0	0	100	100
1	Ht	90/98 (92%)	90 (100%)	0	0	100	100
1	Hu	90/98 (92%)	90 (100%)	0	0	100	100
1	Hv	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hw	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
1	Hx	90/98 (92%)	90 (100%)	0	0	100	100
1	Hy	90/98 (92%)	90 (100%)	0	0	100	100
1	Hz	90/98 (92%)	90 (100%)	0	0	100	100
2	X0	113/869 (13%)	109 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	X1	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	X2	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	X3	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	X4	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	X5	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	X6	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	X7	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	X8	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	X9	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XA	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	XB	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XC	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XD	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	XE	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XF	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	XG	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	XH	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XI	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	XJ	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XK	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	XL	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	XM	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XN	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	XO	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XP	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	XQ	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XR	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XS	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	XT	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XU	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	XV	113/869 (13%)	111 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	XW	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	XX	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	Xa	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xb	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	Xc	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	Xd	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xe	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	Xf	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xg	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	Xh	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xi	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xj	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	Xk	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xl	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	Xm	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xn	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xo	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	Xp	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xq	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	Xr	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xs	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xt	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	Xu	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xv	113/869 (13%)	110 (97%)	3 (3%)	0	100	100
2	Xw	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xx	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
2	Xy	113/869 (13%)	109 (96%)	4 (4%)	0	100	100
2	Xz	113/869 (13%)	111 (98%)	2 (2%)	0	100	100
3	P0	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	P1	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	P2	80/83 (96%)	76 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	P3	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	P4	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	P5	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	P6	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	P7	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	P8	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	P9	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PA	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	PB	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PC	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PD	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	PE	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PF	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	PG	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PH	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PI	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	PJ	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PK	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	PL	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PM	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PN	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	PO	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PP	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	PQ	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PR	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PS	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	PT	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PU	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	PV	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PW	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	PX	80/83 (96%)	78 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Pa	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pb	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	Pc	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pd	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pe	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	Pf	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pg	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	Ph	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pi	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pj	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	Pk	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pl	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	Pm	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pn	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Po	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	Pp	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pq	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	Pr	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Ps	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pt	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	Pu	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Pv	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
3	Pw	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Px	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
3	Py	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
3	Pz	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
All	All	54780/104160 (53%)	54428 (99%)	352 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A0	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	A1	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	A2	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	A3	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	A4	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	A5	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	A6	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	A7	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	A8	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	A9	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AA	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AB	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AC	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AD	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AE	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AF	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AG	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AH	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AI	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AJ	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AK	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AL	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AM	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AN	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AO	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AP	63/67 (94%)	62 (98%)	1 (2%)	55	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AQ	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AR	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AS	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AT	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AU	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AV	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	AW	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	AX	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Aa	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ab	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ac	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ad	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ae	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Af	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ag	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ah	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ai	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Aj	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ak	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Al	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Am	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	An	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ao	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ap	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Aq	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ar	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	As	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	At	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Au	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Av	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Aw	63/67 (94%)	62 (98%)	1 (2%)	55	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Ax	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ay	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Az	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	B0	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	B1	63/67 (94%)	63 (100%)	0	100	100
1	B2	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	B3	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	B4	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	B5	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	B6	63/67 (94%)	63 (100%)	0	100	100
1	B7	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	B8	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	B9	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BA	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	BB	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BC	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BD	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BE	63/67 (94%)	63 (100%)	0	100	100
1	BF	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	BG	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BH	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BI	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BJ	63/67 (94%)	63 (100%)	0	100	100
1	BK	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	BL	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BM	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BN	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BO	63/67 (94%)	63 (100%)	0	100	100
1	BP	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	BQ	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BR	63/67 (94%)	61 (97%)	2 (3%)	34	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BS	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BT	63/67 (94%)	63 (100%)	0	100	100
1	BU	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	BV	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BW	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	BX	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ba	63/67 (94%)	63 (100%)	0	100	100
1	Bb	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Bc	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bd	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Be	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bf	63/67 (94%)	63 (100%)	0	100	100
1	Bg	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Bh	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bi	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bj	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bk	63/67 (94%)	63 (100%)	0	100	100
1	Bl	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Bm	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bn	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bo	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bp	63/67 (94%)	63 (100%)	0	100	100
1	Bq	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Br	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bs	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bt	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bu	63/67 (94%)	63 (100%)	0	100	100
1	Bv	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Bw	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Bx	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	By	63/67 (94%)	61 (97%)	2 (3%)	34	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Bz	63/67 (94%)	63 (100%)	0	100	100
1	C0	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	C1	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	C2	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	C3	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	C4	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	C5	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	C6	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	C7	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	C8	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	C9	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CA	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CB	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CC	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CD	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	CE	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	CF	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CG	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CH	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CI	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	CJ	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	CK	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CL	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CM	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CN	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	CO	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	CP	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CQ	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CR	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CS	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	CT	63/67 (94%)	60 (95%)	3 (5%)	23	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CU	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CV	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CW	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	CX	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Ca	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cb	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cc	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cd	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ce	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cf	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cg	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ch	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ci	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cj	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Ck	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cl	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cm	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cn	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Co	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cp	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cq	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cr	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cs	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ct	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cu	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cv	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cw	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cx	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Cy	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Cz	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	D0	63/67 (94%)	60 (95%)	3 (5%)	23	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D1	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	D2	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	D3	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	D4	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	D5	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	D6	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	D7	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	D8	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	D9	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DA	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	DB	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	DC	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DD	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DE	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DF	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	DG	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	DH	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DI	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DJ	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DK	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	DL	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	DM	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DN	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DO	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DP	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	DQ	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	DR	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DS	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DT	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DU	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	DV	63/67 (94%)	62 (98%)	1 (2%)	55	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DW	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	DX	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Da	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Db	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Dc	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Dd	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	De	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Df	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dg	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Dh	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Di	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dj	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dk	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dl	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Dm	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Dn	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Do	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dp	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dq	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Dr	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ds	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dt	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Du	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dv	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Dw	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Dx	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dy	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Dz	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	E0	63/67 (94%)	63 (100%)	0	100	100
1	E1	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	E2	63/67 (94%)	62 (98%)	1 (2%)	55	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E3	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	E4	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	E5	63/67 (94%)	63 (100%)	0	100	100
1	E6	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	E7	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	E8	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	E9	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	EA	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	EB	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	EC	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	ED	63/67 (94%)	63 (100%)	0	100	100
1	EE	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	EF	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	EG	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	EH	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	EI	63/67 (94%)	63 (100%)	0	100	100
1	EJ	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	EK	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	EL	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	EM	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	EN	63/67 (94%)	63 (100%)	0	100	100
1	EO	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	EP	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	EQ	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	ER	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	ES	63/67 (94%)	63 (100%)	0	100	100
1	ET	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	EU	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	EV	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	EW	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	EX	63/67 (94%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Ea	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Eb	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ec	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Ed	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ee	63/67 (94%)	63 (100%)	0	100	100
1	Ef	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Eg	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Eh	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Ei	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ej	63/67 (94%)	63 (100%)	0	100	100
1	Ek	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	El	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Em	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	En	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Eo	63/67 (94%)	63 (100%)	0	100	100
1	Ep	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Eq	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Er	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Es	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Et	63/67 (94%)	63 (100%)	0	100	100
1	Eu	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ev	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ew	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Ex	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ey	63/67 (94%)	63 (100%)	0	100	100
1	Ez	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	F0	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	F1	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	F2	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	F3	63/67 (94%)	63 (100%)	0	100	100
1	F4	63/67 (94%)	60 (95%)	3 (5%)	23	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F5	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	F6	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	F7	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	F8	63/67 (94%)	63 (100%)	0	100	100
1	F9	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FA	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FB	63/67 (94%)	63 (100%)	0	100	100
1	FC	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FD	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	FE	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	FF	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FG	63/67 (94%)	63 (100%)	0	100	100
1	FH	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FI	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	FJ	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	FK	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FL	63/67 (94%)	63 (100%)	0	100	100
1	FM	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FN	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	FO	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	FP	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FQ	63/67 (94%)	63 (100%)	0	100	100
1	FR	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FS	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	FT	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	FU	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FV	63/67 (94%)	63 (100%)	0	100	100
1	FW	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	FX	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fa	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fb	63/67 (94%)	60 (95%)	3 (5%)	23	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Fc	63/67 (94%)	63 (100%)	0	100	100
1	Fd	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Fe	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ff	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fg	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Fh	63/67 (94%)	63 (100%)	0	100	100
1	Fi	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Fj	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fk	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fl	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Fm	63/67 (94%)	63 (100%)	0	100	100
1	Fn	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Fo	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fp	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fq	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Fr	63/67 (94%)	63 (100%)	0	100	100
1	Fs	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Ft	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fu	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fv	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Fw	63/67 (94%)	63 (100%)	0	100	100
1	Fx	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Fy	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Fz	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	G0	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	G1	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	G2	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	G3	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	G4	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	G5	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	G6	63/67 (94%)	60 (95%)	3 (5%)	23	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G7	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	G8	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	G9	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GA	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GB	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	GC	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GD	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	GE	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	GF	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GG	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	GH	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GI	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	GJ	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	GK	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GL	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	GM	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GN	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	GO	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	GP	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GQ	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	GR	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GS	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	GT	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	GU	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GV	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	GW	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	GX	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Ga	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gb	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Gc	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Gd	63/67 (94%)	61 (97%)	2 (3%)	34	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Ge	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gf	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gg	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Gh	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Gi	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Gj	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gk	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gl	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Gm	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Gn	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Go	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gp	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gq	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Gr	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Gs	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Gt	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gu	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gv	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Gw	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Gx	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Gy	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	Gz	63/67 (94%)	60 (95%)	3 (5%)	23	53
1	H0	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	H1	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	H2	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	H3	63/67 (94%)	63 (100%)	0	100	100
1	H4	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	H5	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	H6	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	H7	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	H8	63/67 (94%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H9	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HA	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HB	63/67 (94%)	63 (100%)	0	100	100
1	HC	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HD	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HE	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HF	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HG	63/67 (94%)	63 (100%)	0	100	100
1	HH	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HI	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HJ	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HK	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HL	63/67 (94%)	63 (100%)	0	100	100
1	HM	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HN	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HO	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HP	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HQ	63/67 (94%)	63 (100%)	0	100	100
1	HR	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HS	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HT	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HU	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	HV	63/67 (94%)	63 (100%)	0	100	100
1	HW	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	HX	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Ha	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Hb	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hc	63/67 (94%)	63 (100%)	0	100	100
1	Hd	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	He	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hf	63/67 (94%)	61 (97%)	2 (3%)	34	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Hg	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hh	63/67 (94%)	63 (100%)	0	100	100
1	Hi	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Hj	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hk	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Hl	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hm	63/67 (94%)	63 (100%)	0	100	100
1	Hn	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ho	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hp	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Hq	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hr	63/67 (94%)	63 (100%)	0	100	100
1	Hs	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Ht	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hu	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Hv	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hw	63/67 (94%)	63 (100%)	0	100	100
1	Hx	63/67 (94%)	61 (97%)	2 (3%)	34	67
1	Hy	63/67 (94%)	62 (98%)	1 (2%)	55	81
1	Hz	63/67 (94%)	61 (97%)	2 (3%)	34	67
2	X0	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	X1	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	X2	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	X3	91/702 (13%)	83 (91%)	8 (9%)	9	27
2	X4	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	X5	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	X6	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	X7	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	X8	91/702 (13%)	82 (90%)	9 (10%)	7	22
2	X9	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	XA	91/702 (13%)	86 (94%)	5 (6%)	19	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	XB	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	XC	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	XD	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	XE	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	XF	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	XG	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	XH	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	XI	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	XJ	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	XK	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	XL	91/702 (13%)	83 (91%)	8 (9%)	9	27
2	XM	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	XN	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	XO	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	XP	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	XQ	91/702 (13%)	83 (91%)	8 (9%)	9	27
2	XR	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	XS	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	XT	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	XU	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	XV	91/702 (13%)	83 (91%)	8 (9%)	9	27
2	XW	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	XX	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	Xa	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xb	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xc	91/702 (13%)	82 (90%)	9 (10%)	7	22
2	Xd	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	Xe	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	Xf	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xg	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xh	91/702 (13%)	83 (91%)	8 (9%)	9	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Xi	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	Xj	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	Xk	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xl	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xm	91/702 (13%)	83 (91%)	8 (9%)	9	27
2	Xn	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	Xo	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	Xp	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xq	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xr	91/702 (13%)	83 (91%)	8 (9%)	9	27
2	Xs	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	Xt	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	Xu	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xv	91/702 (13%)	86 (94%)	5 (6%)	19	47
2	Xw	91/702 (13%)	83 (91%)	8 (9%)	9	27
2	Xx	91/702 (13%)	81 (89%)	10 (11%)	6	18
2	Xy	91/702 (13%)	87 (96%)	4 (4%)	25	56
2	Xz	91/702 (13%)	86 (94%)	5 (6%)	19	47
3	P0	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	P1	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	P2	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	P3	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	P4	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	P5	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	P6	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	P7	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	P8	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	P9	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	PA	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PB	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PC	66/67 (98%)	63 (96%)	3 (4%)	24	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	PD	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	PE	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PF	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PG	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PH	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	PI	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	PJ	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PK	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PL	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PM	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	PN	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	PO	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PP	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PQ	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PR	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	PS	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	PT	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PU	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PV	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	PW	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	PX	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	Pa	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pb	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pc	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pd	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	Pe	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	Pf	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pg	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Ph	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pi	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	Pj	66/67 (98%)	65 (98%)	1 (2%)	57	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Pk	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pl	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pm	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pn	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	Po	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	Pp	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pq	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pr	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Ps	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	Pt	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	Pu	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pv	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Pw	66/67 (98%)	64 (97%)	2 (3%)	36	69
3	Px	66/67 (98%)	63 (96%)	3 (4%)	24	55
3	Py	66/67 (98%)	65 (98%)	1 (2%)	57	81
3	Pz	66/67 (98%)	64 (97%)	2 (3%)	36	69
All	All	39660/78300 (51%)	38286 (96%)	1374 (4%)	32	64

All (1374) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A2	7	ILE
1	B2	49	LEU
1	C2	53	GLU
1	C2	84	VAL
1	D2	53	GLU
1	D2	84	VAL
1	E2	48	VAL
1	F2	12	ILE
1	F2	75	LEU
1	F2	84	VAL
1	G2	32	GLU
1	G2	75	LEU
1	H2	75	LEU
2	X2	786	SER
2	X2	824	ASN

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Mol	Chain	Res	Type
2	X2	827	VAL
2	X2	852	SER
2	X2	861	ILE
3	P2	10	LEU
3	P2	28	TRP
1	A1	57	VAL
1	A1	84	VAL
1	C1	7	ILE
1	C1	48	VAL
1	C1	84	VAL
1	D1	32	GLU
1	D1	53	GLU
1	D1	84	VAL
1	E1	48	VAL
1	E1	66	ASP
1	F1	69	GLU
1	G1	12	ILE
1	G1	48	VAL
1	G1	84	VAL
2	X1	812	GLN
2	X1	821	MET
2	X1	852	SER
2	X1	862	THR
2	X1	863	TYR
3	P1	9	THR
3	P1	28	TRP
1	A5	7	ILE
1	A5	84	VAL
1	B5	7	ILE
1	B5	75	LEU
1	C5	7	ILE
1	C5	53	GLU
1	C5	83	ARG
1	D5	12	ILE
1	D5	53	GLU
1	D5	84	VAL
1	F5	84	VAL
1	G5	32	GLU
1	G5	75	LEU
1	G5	84	VAL
1	H5	7	ILE
2	X5	809	THR

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Mol	Chain	Res	Type
2	X5	827	VAL
2	X5	846	SER
2	X5	849	THR
3	P5	4	MET
1	A3	7	ILE
1	B3	75	LEU
1	B3	86	SER
1	C3	12	ILE
1	C3	38	ARG
1	D3	53	GLU
1	E3	75	LEU
1	E3	86	SER
1	E3	88	VAL
1	G3	75	LEU
2	X3	727	THR
2	X3	786	SER
2	X3	790	LYS
2	X3	802	VAL
2	X3	809	THR
2	X3	812	GLN
2	X3	838	VAL
2	X3	849	THR
3	P3	10	LEU
3	P3	28	TRP
1	A4	7	ILE
1	A4	84	VAL
1	B4	48	VAL
1	B4	75	LEU
1	C4	84	VAL
1	C4	86	SER
1	D4	48	VAL
1	D4	53	GLU
1	D4	84	VAL
1	E4	39	GLN
1	E4	75	LEU
1	F4	9	LEU
1	F4	48	VAL
1	F4	97	GLN
1	G4	7	ILE
1	G4	86	SER
1	H4	7	ILE
1	H4	39	GLN

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Mol	Chain	Res	Type
2	X4	729	GLU
2	X4	786	SER
2	X4	802	VAL
2	X4	812	GLN
2	X4	827	VAL
2	X4	838	VAL
2	X4	848	ILE
2	X4	849	THR
2	X4	852	SER
2	X4	862	THR
3	P4	9	THR
3	P4	10	LEU
3	P4	28	TRP
1	A7	7	ILE
1	B7	49	LEU
1	C7	53	GLU
1	C7	84	VAL
1	D7	53	GLU
1	D7	84	VAL
1	E7	48	VAL
1	F7	12	ILE
1	F7	75	LEU
1	F7	84	VAL
1	G7	32	GLU
1	G7	75	LEU
1	H7	75	LEU
2	X7	786	SER
2	X7	824	ASN
2	X7	827	VAL
2	X7	852	SER
2	X7	861	ILE
3	P7	10	LEU
3	P7	28	TRP
1	A6	57	VAL
1	A6	84	VAL
1	C6	7	ILE
1	C6	48	VAL
1	C6	84	VAL
1	D6	32	GLU
1	D6	53	GLU
1	D6	84	VAL
1	E6	48	VAL

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Mol	Chain	Res	Type
1	E6	66	ASP
1	F6	69	GLU
1	G6	12	ILE
1	G6	48	VAL
1	G6	84	VAL
2	X6	812	GLN
2	X6	821	MET
2	X6	852	SER
2	X6	862	THR
2	X6	863	TYR
3	P6	9	THR
3	P6	28	TRP
1	A0	7	ILE
1	A0	84	VAL
1	B0	7	ILE
1	B0	75	LEU
1	C0	7	ILE
1	C0	53	GLU
1	C0	83	ARG
1	D0	12	ILE
1	D0	53	GLU
1	D0	84	VAL
1	F0	84	VAL
1	G0	32	GLU
1	G0	75	LEU
1	G0	84	VAL
1	H0	7	ILE
2	X0	809	THR
2	X0	827	VAL
2	X0	846	SER
2	X0	849	THR
3	P0	4	MET
1	A8	7	ILE
1	B8	75	LEU
1	B8	86	SER
1	C8	12	ILE
1	C8	38	ARG
1	D8	53	GLU
1	E8	75	LEU
1	E8	86	SER
1	E8	88	VAL
1	G8	75	LEU

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Mol	Chain	Res	Type
3	P8	10	LEU
3	P8	28	TRP
1	A9	7	ILE
1	A9	84	VAL
1	B9	48	VAL
1	B9	75	LEU
1	C9	84	VAL
1	C9	86	SER
1	D9	48	VAL
1	D9	53	GLU
1	D9	84	VAL
1	E9	39	GLN
1	E9	75	LEU
1	F9	9	LEU
1	F9	48	VAL
1	F9	97	GLN
1	G9	7	ILE
1	G9	86	SER
1	H9	7	ILE
1	H9	39	GLN
2	X9	729	GLU
2	X9	786	SER
2	X9	802	VAL
2	X9	812	GLN
2	X9	827	VAL
2	X9	838	VAL
2	X9	848	ILE
2	X9	849	THR
2	X9	852	SER
2	X9	862	THR
3	P9	9	THR
3	P9	10	LEU
3	P9	28	TRP
1	Ab	7	ILE
1	Bb	49	LEU
1	Cb	53	GLU
1	Cb	84	VAL
1	Db	53	GLU
1	Db	84	VAL
1	Eb	48	VAL
1	Fb	12	ILE
1	Fb	75	LEU

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Mol	Chain	Res	Type
1	Fb	84	VAL
1	Gb	32	GLU
1	Gb	75	LEU
1	Hb	75	LEU
2	Xb	786	SER
2	Xb	824	ASN
2	Xb	827	VAL
2	Xb	852	SER
2	Xb	861	ILE
3	Pb	10	LEU
3	Pb	28	TRP
1	Aa	57	VAL
1	Aa	84	VAL
1	Ca	7	ILE
1	Ca	48	VAL
1	Ca	84	VAL
1	Da	32	GLU
1	Da	53	GLU
1	Da	84	VAL
1	Ea	48	VAL
1	Ea	66	ASP
1	Fa	69	GLU
1	Ga	12	ILE
1	Ga	48	VAL
1	Ga	84	VAL
1	Ha	7	ILE
1	Ha	38	ARG
2	Xa	812	GLN
2	Xa	821	MET
2	Xa	852	SER
2	Xa	862	THR
2	Xa	863	TYR
3	Pa	9	THR
3	Pa	28	TRP
1	Ae	7	ILE
1	Ae	84	VAL
1	Be	7	ILE
1	Be	75	LEU
1	Ce	7	ILE
1	Ce	53	GLU
1	Ce	83	ARG
1	De	12	ILE

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Mol	Chain	Res	Type
1	De	53	GLU
1	De	84	VAL
1	Fe	84	VAL
1	Ge	32	GLU
1	Ge	75	LEU
1	Ge	84	VAL
1	He	7	ILE
2	Xe	809	THR
2	Xe	827	VAL
2	Xe	846	SER
2	Xe	849	THR
3	Pe	4	MET
1	Ac	7	ILE
1	Bc	75	LEU
1	Bc	86	SER
1	Cc	12	ILE
1	Cc	38	ARG
1	Dc	53	GLU
1	Ec	75	LEU
1	Ec	86	SER
1	Ec	88	VAL
1	Gc	75	LEU
3	Pc	10	LEU
3	Pc	28	TRP
1	Ad	7	ILE
1	Ad	84	VAL
1	Bd	48	VAL
1	Bd	75	LEU
1	Cd	84	VAL
1	Cd	86	SER
1	Dd	48	VAL
1	Dd	53	GLU
1	Dd	84	VAL
1	Ed	39	GLN
1	Ed	75	LEU
1	Fd	9	LEU
1	Fd	48	VAL
1	Fd	97	GLN
1	Gd	7	ILE
1	Gd	86	SER
1	Hd	7	ILE
1	Hd	39	GLN

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Mol	Chain	Res	Type
2	Xd	729	GLU
2	Xd	786	SER
2	Xd	802	VAL
2	Xd	812	GLN
2	Xd	827	VAL
2	Xd	838	VAL
2	Xd	848	ILE
2	Xd	849	THR
2	Xd	852	SER
2	Xd	862	THR
3	Pd	9	THR
3	Pd	10	LEU
3	Pd	28	TRP
1	Ag	7	ILE
1	Bg	49	LEU
1	Cg	53	GLU
1	Cg	84	VAL
1	Dg	53	GLU
1	Dg	84	VAL
1	Eg	48	VAL
1	Fg	12	ILE
1	Fg	75	LEU
1	Fg	84	VAL
1	Gg	32	GLU
1	Gg	75	LEU
1	Hg	75	LEU
2	Xg	786	SER
2	Xg	824	ASN
2	Xg	827	VAL
2	Xg	852	SER
2	Xg	861	ILE
3	Pg	10	LEU
3	Pg	28	TRP
1	Af	57	VAL
1	Af	84	VAL
1	Cf	7	ILE
1	Cf	48	VAL
1	Cf	84	VAL
1	Df	32	GLU
1	Df	53	GLU
1	Df	84	VAL
1	Ef	48	VAL

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Mol	Chain	Res	Type
1	Ef	66	ASP
1	Ff	69	GLU
1	Gf	12	ILE
1	Gf	48	VAL
1	Gf	84	VAL
2	Xf	812	GLN
2	Xf	821	MET
2	Xf	852	SER
2	Xf	862	THR
2	Xf	863	TYR
3	Pf	9	THR
3	Pf	28	TRP
1	Aj	7	ILE
1	Aj	84	VAL
1	Bj	7	ILE
1	Bj	75	LEU
1	Cj	7	ILE
1	Cj	53	GLU
1	Cj	83	ARG
1	Dj	12	ILE
1	Dj	53	GLU
1	Dj	84	VAL
1	Fj	84	VAL
1	Gj	32	GLU
1	Gj	75	LEU
1	Gj	84	VAL
1	Hj	7	ILE
2	Xj	809	THR
2	Xj	827	VAL
2	Xj	846	SER
2	Xj	849	THR
3	Pj	4	MET
1	Ah	7	ILE
1	Bh	75	LEU
1	Bh	86	SER
1	Ch	12	ILE
1	Ch	38	ARG
1	Dh	53	GLU
1	Eh	75	LEU
1	Eh	86	SER
1	Eh	88	VAL
1	Gh	75	LEU

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Mol	Chain	Res	Type
2	Xh	727	THR
2	Xh	786	SER
2	Xh	790	LYS
2	Xh	802	VAL
2	Xh	809	THR
2	Xh	812	GLN
2	Xh	838	VAL
2	Xh	849	THR
3	Ph	10	LEU
3	Ph	28	TRP
1	Ai	7	ILE
1	Ai	84	VAL
1	Bi	48	VAL
1	Bi	75	LEU
1	Ci	84	VAL
1	Ci	86	SER
1	Di	48	VAL
1	Di	53	GLU
1	Di	84	VAL
1	Ei	39	GLN
1	Ei	75	LEU
1	Fi	9	LEU
1	Fi	48	VAL
1	Fi	97	GLN
1	Gi	7	ILE
1	Gi	86	SER
1	Hi	7	ILE
1	Hi	39	GLN
2	Xi	729	GLU
2	Xi	786	SER
2	Xi	802	VAL
2	Xi	812	GLN
2	Xi	827	VAL
2	Xi	838	VAL
2	Xi	848	ILE
2	Xi	849	THR
2	Xi	852	SER
2	Xi	862	THR
3	Pi	9	THR
3	Pi	10	LEU
3	Pi	28	TRP
1	Al	7	ILE

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Mol	Chain	Res	Type
1	Bl	49	LEU
1	Cl	53	GLU
1	Cl	84	VAL
1	Dl	53	GLU
1	Dl	84	VAL
1	El	48	VAL
1	Fl	12	ILE
1	Fl	75	LEU
1	Fl	84	VAL
1	Gl	32	GLU
1	Gl	75	LEU
1	Hl	75	LEU
2	Xl	786	SER
2	Xl	824	ASN
2	Xl	827	VAL
2	Xl	852	SER
2	Xl	861	ILE
3	Pl	10	LEU
3	Pl	28	TRP
1	Ak	57	VAL
1	Ak	84	VAL
1	Ck	7	ILE
1	Ck	48	VAL
1	Ck	84	VAL
1	Dk	32	GLU
1	Dk	53	GLU
1	Dk	84	VAL
1	Ek	48	VAL
1	Ek	66	ASP
1	Fk	69	GLU
1	Gk	12	ILE
1	Gk	48	VAL
1	Gk	84	VAL
2	Xk	812	GLN
2	Xk	821	MET
2	Xk	852	SER
2	Xk	862	THR
2	Xk	863	TYR
3	Pk	9	THR
3	Pk	28	TRP
1	Ao	7	ILE
1	Ao	84	VAL

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Mol	Chain	Res	Type
1	Bo	7	ILE
1	Bo	75	LEU
1	Co	7	ILE
1	Co	53	GLU
1	Co	83	ARG
1	Do	12	ILE
1	Do	53	GLU
1	Do	84	VAL
1	Fo	84	VAL
1	Go	32	GLU
1	Go	75	LEU
1	Go	84	VAL
1	Ho	7	ILE
2	Xo	809	THR
2	Xo	827	VAL
2	Xo	846	SER
2	Xo	849	THR
3	Po	4	MET
1	Am	7	ILE
1	Bm	75	LEU
1	Bm	86	SER
1	Cm	12	ILE
1	Cm	38	ARG
1	Dm	53	GLU
1	Em	75	LEU
1	Em	86	SER
1	Em	88	VAL
1	Gm	75	LEU
3	Pm	10	LEU
3	Pm	28	TRP
1	An	7	ILE
1	An	84	VAL
1	Bn	48	VAL
1	Bn	75	LEU
1	Cn	84	VAL
1	Cn	86	SER
1	Dn	48	VAL
1	Dn	53	GLU
1	Dn	84	VAL
1	En	39	GLN
1	En	75	LEU
1	Fn	9	LEU

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Mol	Chain	Res	Type
1	Fn	48	VAL
1	Fn	97	GLN
1	Gn	7	ILE
1	Gn	86	SER
1	Hn	7	ILE
1	Hn	39	GLN
2	Xn	729	GLU
2	Xn	786	SER
2	Xn	802	VAL
2	Xn	812	GLN
2	Xn	827	VAL
2	Xn	838	VAL
2	Xn	848	ILE
2	Xn	849	THR
2	Xn	852	SER
2	Xn	862	THR
3	Pn	9	THR
3	Pn	10	LEU
3	Pn	28	TRP
1	Aq	7	ILE
1	Bq	49	LEU
1	Cq	53	GLU
1	Cq	84	VAL
1	Dq	53	GLU
1	Dq	84	VAL
1	Eq	48	VAL
1	Fq	12	ILE
1	Fq	75	LEU
1	Fq	84	VAL
1	Gq	32	GLU
1	Gq	75	LEU
1	Hq	75	LEU
2	Xq	786	SER
2	Xq	824	ASN
2	Xq	827	VAL
2	Xq	852	SER
2	Xq	861	ILE
3	Pq	10	LEU
3	Pq	28	TRP
1	Ap	57	VAL
1	Ap	84	VAL
1	Cp	7	ILE

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Mol	Chain	Res	Type
1	Cp	48	VAL
1	Cp	84	VAL
1	Dp	32	GLU
1	Dp	53	GLU
1	Dp	84	VAL
1	Ep	48	VAL
1	Ep	66	ASP
1	Fp	69	GLU
1	Gp	12	ILE
1	Gp	48	VAL
1	Gp	84	VAL
1	Hp	7	ILE
1	Hp	38	ARG
2	Xp	812	GLN
2	Xp	821	MET
2	Xp	852	SER
2	Xp	862	THR
2	Xp	863	TYR
3	Pp	9	THR
3	Pp	28	TRP
1	At	7	ILE
1	At	84	VAL
1	Bt	7	ILE
1	Bt	75	LEU
1	Ct	7	ILE
1	Ct	53	GLU
1	Ct	83	ARG
1	Dt	12	ILE
1	Dt	53	GLU
1	Dt	84	VAL
1	Ft	84	VAL
1	Gt	32	GLU
1	Gt	75	LEU
1	Gt	84	VAL
1	Ht	7	ILE
2	Xt	809	THR
2	Xt	827	VAL
2	Xt	846	SER
2	Xt	849	THR
3	Pt	4	MET
1	Ar	7	ILE
1	Br	75	LEU

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Mol	Chain	Res	Type
1	Br	86	SER
1	Cr	12	ILE
1	Cr	38	ARG
1	Dr	53	GLU
1	Er	75	LEU
1	Er	86	SER
1	Er	88	VAL
1	Gr	75	LEU
3	Pr	10	LEU
3	Pr	28	TRP
1	As	7	ILE
1	As	84	VAL
1	Bs	48	VAL
1	Bs	75	LEU
1	Cs	84	VAL
1	Cs	86	SER
1	Ds	48	VAL
1	Ds	53	GLU
1	Ds	84	VAL
1	Es	39	GLN
1	Es	75	LEU
1	Fs	9	LEU
1	Fs	48	VAL
1	Fs	97	GLN
1	Gs	7	ILE
1	Gs	86	SER
1	Hs	7	ILE
1	Hs	39	GLN
2	Xs	729	GLU
2	Xs	786	SER
2	Xs	802	VAL
2	Xs	812	GLN
2	Xs	827	VAL
2	Xs	838	VAL
2	Xs	848	ILE
2	Xs	849	THR
2	Xs	852	SER
2	Xs	862	THR
3	Ps	9	THR
3	Ps	10	LEU
3	Ps	28	TRP
1	Av	7	ILE

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Mol	Chain	Res	Type
1	Bv	49	LEU
1	Cv	53	GLU
1	Cv	84	VAL
1	Dv	53	GLU
1	Dv	84	VAL
1	Ev	48	VAL
1	Fv	12	ILE
1	Fv	75	LEU
1	Fv	84	VAL
1	Gv	32	GLU
1	Gv	75	LEU
1	Hv	75	LEU
2	Xv	786	SER
2	Xv	824	ASN
2	Xv	827	VAL
2	Xv	852	SER
2	Xv	861	ILE
3	Pv	10	LEU
3	Pv	28	TRP
1	Au	57	VAL
1	Au	84	VAL
1	Cu	7	ILE
1	Cu	48	VAL
1	Cu	84	VAL
1	Du	32	GLU
1	Du	53	GLU
1	Du	84	VAL
1	Eu	48	VAL
1	Eu	66	ASP
1	Fu	69	GLU
1	Gu	12	ILE
1	Gu	48	VAL
1	Gu	84	VAL
2	Xu	812	GLN
2	Xu	821	MET
2	Xu	852	SER
2	Xu	862	THR
2	Xu	863	TYR
3	Pu	9	THR
3	Pu	28	TRP
1	Ay	7	ILE
1	Ay	84	VAL

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Mol	Chain	Res	Type
1	By	7	ILE
1	By	75	LEU
1	Cy	7	ILE
1	Cy	53	GLU
1	Cy	83	ARG
1	Dy	12	ILE
1	Dy	53	GLU
1	Dy	84	VAL
1	Fy	84	VAL
1	Gy	32	GLU
1	Gy	75	LEU
1	Gy	84	VAL
1	Hy	7	ILE
2	Xy	809	THR
2	Xy	827	VAL
2	Xy	846	SER
2	Xy	849	THR
3	Py	4	MET
1	Aw	7	ILE
1	Bw	75	LEU
1	Bw	86	SER
1	Cw	12	ILE
1	Cw	38	ARG
1	Dw	53	GLU
1	Ew	75	LEU
1	Ew	86	SER
1	Ew	88	VAL
1	Gw	75	LEU
2	Xw	727	THR
2	Xw	786	SER
2	Xw	790	LYS
2	Xw	802	VAL
2	Xw	809	THR
2	Xw	812	GLN
2	Xw	838	VAL
2	Xw	849	THR
3	Pw	10	LEU
3	Pw	28	TRP
1	Ax	7	ILE
1	Ax	84	VAL
1	Bx	48	VAL
1	Bx	75	LEU

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Mol	Chain	Res	Type
1	Cx	84	VAL
1	Cx	86	SER
1	Dx	48	VAL
1	Dx	53	GLU
1	Dx	84	VAL
1	Ex	39	GLN
1	Ex	75	LEU
1	Fx	9	LEU
1	Fx	48	VAL
1	Fx	97	GLN
1	Gx	7	ILE
1	Gx	86	SER
1	Hx	7	ILE
1	Hx	39	GLN
2	Xx	729	GLU
2	Xx	786	SER
2	Xx	802	VAL
2	Xx	812	GLN
2	Xx	827	VAL
2	Xx	838	VAL
2	Xx	848	ILE
2	Xx	849	THR
2	Xx	852	SER
2	Xx	862	THR
3	Px	9	THR
3	Px	10	LEU
3	Px	28	TRP
1	AA	7	ILE
1	BA	49	LEU
1	CA	53	GLU
1	CA	84	VAL
1	DA	53	GLU
1	DA	84	VAL
1	EA	48	VAL
1	FA	12	ILE
1	FA	75	LEU
1	FA	84	VAL
1	GA	32	GLU
1	GA	75	LEU
1	HA	75	LEU
2	XA	786	SER
2	XA	824	ASN

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Mol	Chain	Res	Type
2	XA	827	VAL
2	XA	852	SER
2	XA	861	ILE
3	PA	10	LEU
3	PA	28	TRP
1	Az	57	VAL
1	Az	84	VAL
1	Cz	7	ILE
1	Cz	48	VAL
1	Cz	84	VAL
1	Dz	32	GLU
1	Dz	53	GLU
1	Dz	84	VAL
1	Ez	48	VAL
1	Ez	66	ASP
1	Fz	69	GLU
1	Gz	12	ILE
1	Gz	48	VAL
1	Gz	84	VAL
2	Xz	812	GLN
2	Xz	821	MET
2	Xz	852	SER
2	Xz	862	THR
2	Xz	863	TYR
3	Pz	9	THR
3	Pz	28	TRP
1	AD	7	ILE
1	AD	84	VAL
1	BD	7	ILE
1	BD	75	LEU
1	CD	7	ILE
1	CD	53	GLU
1	CD	83	ARG
1	DD	12	ILE
1	DD	53	GLU
1	DD	84	VAL
1	FD	84	VAL
1	GD	32	GLU
1	GD	75	LEU
1	GD	84	VAL
1	HD	7	ILE
2	XD	809	THR

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Mol	Chain	Res	Type
2	XD	827	VAL
2	XD	846	SER
2	XD	849	THR
3	PD	4	MET
1	AB	7	ILE
1	BB	75	LEU
1	BB	86	SER
1	CB	12	ILE
1	CB	38	ARG
1	DB	53	GLU
1	EB	75	LEU
1	EB	86	SER
1	EB	88	VAL
1	GB	75	LEU
3	PB	10	LEU
3	PB	28	TRP
1	AC	7	ILE
1	AC	84	VAL
1	BC	48	VAL
1	BC	75	LEU
1	CC	84	VAL
1	CC	86	SER
1	DC	48	VAL
1	DC	53	GLU
1	DC	84	VAL
1	EC	39	GLN
1	EC	75	LEU
1	FC	9	LEU
1	FC	48	VAL
1	FC	97	GLN
1	GC	7	ILE
1	GC	86	SER
1	HC	7	ILE
1	HC	39	GLN
2	XC	729	GLU
2	XC	786	SER
2	XC	802	VAL
2	XC	812	GLN
2	XC	827	VAL
2	XC	838	VAL
2	XC	848	ILE
2	XC	849	THR

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Mol	Chain	Res	Type
2	XC	852	SER
2	XC	862	THR
3	PC	9	THR
3	PC	10	LEU
3	PC	28	TRP
1	AF	7	ILE
1	BF	49	LEU
1	CF	53	GLU
1	CF	84	VAL
1	DF	53	GLU
1	DF	84	VAL
1	EF	48	VAL
1	FF	12	ILE
1	FF	75	LEU
1	FF	84	VAL
1	GF	32	GLU
1	GF	75	LEU
1	HF	75	LEU
2	XF	786	SER
2	XF	824	ASN
2	XF	827	VAL
2	XF	852	SER
2	XF	861	ILE
3	PF	10	LEU
3	PF	28	TRP
1	AE	57	VAL
1	AE	84	VAL
1	CE	7	ILE
1	CE	48	VAL
1	CE	84	VAL
1	DE	32	GLU
1	DE	53	GLU
1	DE	84	VAL
1	EE	48	VAL
1	EE	66	ASP
1	FE	69	GLU
1	GE	12	ILE
1	GE	48	VAL
1	GE	84	VAL
1	HE	7	ILE
1	HE	38	ARG
2	XE	812	GLN

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Mol	Chain	Res	Type
2	XE	821	MET
2	XE	852	SER
2	XE	862	THR
2	XE	863	TYR
3	PE	9	THR
3	PE	28	TRP
1	AI	7	ILE
1	AI	84	VAL
1	BI	7	ILE
1	BI	75	LEU
1	CI	7	ILE
1	CI	53	GLU
1	CI	83	ARG
1	DI	12	ILE
1	DI	53	GLU
1	DI	84	VAL
1	FI	84	VAL
1	GI	32	GLU
1	GI	75	LEU
1	GI	84	VAL
1	HI	7	ILE
2	XI	809	THR
2	XI	827	VAL
2	XI	846	SER
2	XI	849	THR
3	PI	4	MET
1	AG	7	ILE
1	BG	75	LEU
1	BG	86	SER
1	CG	12	ILE
1	CG	38	ARG
1	DG	53	GLU
1	EG	75	LEU
1	EG	86	SER
1	EG	88	VAL
1	GG	75	LEU
3	PG	10	LEU
3	PG	28	TRP
1	AH	7	ILE
1	AH	84	VAL
1	BH	48	VAL
1	BH	75	LEU

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Mol	Chain	Res	Type
1	CH	84	VAL
1	CH	86	SER
1	DH	48	VAL
1	DH	53	GLU
1	DH	84	VAL
1	EH	39	GLN
1	EH	75	LEU
1	FH	9	LEU
1	FH	48	VAL
1	FH	97	GLN
1	GH	7	ILE
1	GH	86	SER
1	HH	7	ILE
1	HH	39	GLN
2	XH	729	GLU
2	XH	786	SER
2	XH	802	VAL
2	XH	812	GLN
2	XH	827	VAL
2	XH	838	VAL
2	XH	848	ILE
2	XH	849	THR
2	XH	852	SER
2	XH	862	THR
3	PH	9	THR
3	PH	10	LEU
3	PH	28	TRP
1	AK	7	ILE
1	BK	49	LEU
1	CK	53	GLU
1	CK	84	VAL
1	DK	53	GLU
1	DK	84	VAL
1	EK	48	VAL
1	FK	12	ILE
1	FK	75	LEU
1	FK	84	VAL
1	GK	32	GLU
1	GK	75	LEU
1	HK	75	LEU
2	XK	786	SER
2	XK	824	ASN

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Mol	Chain	Res	Type
2	XK	827	VAL
2	XK	852	SER
2	XK	861	ILE
3	PK	10	LEU
3	PK	28	TRP
1	AJ	57	VAL
1	AJ	84	VAL
1	CJ	7	ILE
1	CJ	48	VAL
1	CJ	84	VAL
1	DJ	32	GLU
1	DJ	53	GLU
1	DJ	84	VAL
1	EJ	48	VAL
1	EJ	66	ASP
1	FJ	69	GLU
1	GJ	12	ILE
1	GJ	48	VAL
1	GJ	84	VAL
1	HJ	7	ILE
1	HJ	38	ARG
2	XJ	812	GLN
2	XJ	821	MET
2	XJ	852	SER
2	XJ	862	THR
2	XJ	863	TYR
3	PJ	9	THR
3	PJ	28	TRP
1	AN	7	ILE
1	AN	84	VAL
1	BN	7	ILE
1	BN	75	LEU
1	CN	7	ILE
1	CN	53	GLU
1	CN	83	ARG
1	DN	12	ILE
1	DN	53	GLU
1	DN	84	VAL
1	FN	84	VAL
1	GN	32	GLU
1	GN	75	LEU
1	GN	84	VAL

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Mol	Chain	Res	Type
1	HN	7	ILE
2	XN	809	THR
2	XN	827	VAL
2	XN	846	SER
2	XN	849	THR
3	PN	4	MET
1	AL	7	ILE
1	BL	75	LEU
1	BL	86	SER
1	CL	12	ILE
1	CL	38	ARG
1	DL	53	GLU
1	EL	75	LEU
1	EL	86	SER
1	EL	88	VAL
1	GL	75	LEU
2	XL	727	THR
2	XL	786	SER
2	XL	790	LYS
2	XL	802	VAL
2	XL	809	THR
2	XL	812	GLN
2	XL	838	VAL
2	XL	849	THR
3	PL	10	LEU
3	PL	28	TRP
1	AM	7	ILE
1	AM	84	VAL
1	BM	48	VAL
1	BM	75	LEU
1	CM	84	VAL
1	CM	86	SER
1	DM	48	VAL
1	DM	53	GLU
1	DM	84	VAL
1	EM	39	GLN
1	EM	75	LEU
1	FM	9	LEU
1	FM	48	VAL
1	FM	97	GLN
1	GM	7	ILE
1	GM	86	SER

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Mol	Chain	Res	Type
1	HM	7	ILE
1	HM	39	GLN
2	XM	729	GLU
2	XM	786	SER
2	XM	802	VAL
2	XM	812	GLN
2	XM	827	VAL
2	XM	838	VAL
2	XM	848	ILE
2	XM	849	THR
2	XM	852	SER
2	XM	862	THR
3	PM	9	THR
3	PM	10	LEU
3	PM	28	TRP
1	AP	7	ILE
1	BP	49	LEU
1	CP	53	GLU
1	CP	84	VAL
1	DP	53	GLU
1	DP	84	VAL
1	EP	48	VAL
1	FP	12	ILE
1	FP	75	LEU
1	FP	84	VAL
1	GP	32	GLU
1	GP	75	LEU
1	HP	75	LEU
2	XP	786	SER
2	XP	824	ASN
2	XP	827	VAL
2	XP	852	SER
2	XP	861	ILE
3	PP	10	LEU
3	PP	28	TRP
1	AO	57	VAL
1	AO	84	VAL
1	CO	7	ILE
1	CO	48	VAL
1	CO	84	VAL
1	DO	32	GLU
1	DO	53	GLU

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Mol	Chain	Res	Type
1	DO	84	VAL
1	EO	48	VAL
1	EO	66	ASP
1	FO	69	GLU
1	GO	12	ILE
1	GO	48	VAL
1	GO	84	VAL
2	XO	812	GLN
2	XO	821	MET
2	XO	852	SER
2	XO	862	THR
2	XO	863	TYR
3	PO	9	THR
3	PO	28	TRP
1	AS	7	ILE
1	AS	84	VAL
1	BS	7	ILE
1	BS	75	LEU
1	CS	7	ILE
1	CS	53	GLU
1	CS	83	ARG
1	DS	12	ILE
1	DS	53	GLU
1	DS	84	VAL
1	FS	84	VAL
1	GS	32	GLU
1	GS	75	LEU
1	GS	84	VAL
1	HS	7	ILE
2	XS	809	THR
2	XS	827	VAL
2	XS	846	SER
2	XS	849	THR
3	PS	4	MET
1	AQ	7	ILE
1	BQ	75	LEU
1	BQ	86	SER
1	CQ	12	ILE
1	CQ	38	ARG
1	DQ	53	GLU
1	EQ	75	LEU
1	EQ	86	SER

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Mol	Chain	Res	Type
1	EQ	88	VAL
1	GQ	75	LEU
2	XQ	727	THR
2	XQ	786	SER
2	XQ	790	LYS
2	XQ	802	VAL
2	XQ	809	THR
2	XQ	812	GLN
2	XQ	838	VAL
2	XQ	849	THR
3	PQ	10	LEU
3	PQ	28	TRP
1	AR	7	ILE
1	AR	84	VAL
1	BR	48	VAL
1	BR	75	LEU
1	CR	84	VAL
1	CR	86	SER
1	DR	48	VAL
1	DR	53	GLU
1	DR	84	VAL
1	ER	39	GLN
1	ER	75	LEU
1	FR	9	LEU
1	FR	48	VAL
1	FR	97	GLN
1	GR	7	ILE
1	GR	86	SER
1	HR	7	ILE
1	HR	39	GLN
2	XR	729	GLU
2	XR	786	SER
2	XR	802	VAL
2	XR	812	GLN
2	XR	827	VAL
2	XR	838	VAL
2	XR	848	ILE
2	XR	849	THR
2	XR	852	SER
2	XR	862	THR
3	PR	9	THR
3	PR	10	LEU

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Mol	Chain	Res	Type
3	PR	28	TRP
1	AU	7	ILE
1	BU	49	LEU
1	CU	53	GLU
1	CU	84	VAL
1	DU	53	GLU
1	DU	84	VAL
1	EU	48	VAL
1	FU	12	ILE
1	FU	75	LEU
1	FU	84	VAL
1	GU	32	GLU
1	GU	75	LEU
1	HU	75	LEU
2	XU	786	SER
2	XU	824	ASN
2	XU	827	VAL
2	XU	852	SER
2	XU	861	ILE
3	PU	10	LEU
3	PU	28	TRP
1	AT	57	VAL
1	AT	84	VAL
1	CT	7	ILE
1	CT	48	VAL
1	CT	84	VAL
1	DT	32	GLU
1	DT	53	GLU
1	DT	84	VAL
1	ET	48	VAL
1	ET	66	ASP
1	FT	69	GLU
1	GT	12	ILE
1	GT	48	VAL
1	GT	84	VAL
1	HT	7	ILE
1	HT	38	ARG
2	XT	812	GLN
2	XT	821	MET
2	XT	852	SER
2	XT	862	THR
2	XT	863	TYR

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Mol	Chain	Res	Type
3	PT	9	THR
3	PT	28	TRP
1	AX	7	ILE
1	AX	84	VAL
1	BX	7	ILE
1	BX	75	LEU
1	CX	7	ILE
1	CX	53	GLU
1	CX	83	ARG
1	DX	12	ILE
1	DX	53	GLU
1	DX	84	VAL
1	FX	84	VAL
1	GX	32	GLU
1	GX	75	LEU
1	GX	84	VAL
1	HX	7	ILE
2	XX	809	THR
2	XX	827	VAL
2	XX	846	SER
2	XX	849	THR
3	PX	4	MET
1	AV	7	ILE
1	BV	75	LEU
1	BV	86	SER
1	CV	12	ILE
1	CV	38	ARG
1	DV	53	GLU
1	EV	75	LEU
1	EV	86	SER
1	EV	88	VAL
1	GV	75	LEU
3	PV	10	LEU
3	PV	28	TRP
1	AW	7	ILE
1	AW	84	VAL
1	BW	48	VAL
1	BW	75	LEU
1	CW	84	VAL
1	CW	86	SER
1	DW	48	VAL
1	DW	53	GLU

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Mol	Chain	Res	Type
1	DW	84	VAL
1	EW	39	GLN
1	EW	75	LEU
1	FW	9	LEU
1	FW	48	VAL
1	FW	97	GLN
1	GW	7	ILE
1	GW	86	SER
1	HW	7	ILE
1	HW	39	GLN
2	XW	729	GLU
2	XW	786	SER
2	XW	802	VAL
2	XW	812	GLN
2	XW	827	VAL
2	XW	838	VAL
2	XW	848	ILE
2	XW	849	THR
2	XW	852	SER
2	XW	862	THR
3	PW	9	THR
3	PW	10	LEU
3	PW	28	TRP
1	H1	7	ILE
1	H1	38	ARG
1	H6	7	ILE
1	H6	38	ARG
2	X8	712	ARG
2	X8	727	THR
2	X8	786	SER
2	X8	790	LYS
2	X8	802	VAL
2	X8	809	THR
2	X8	812	GLN
2	X8	838	VAL
2	X8	849	THR
2	Xc	712	ARG
2	Xc	727	THR
2	Xc	786	SER
2	Xc	790	LYS
2	Xc	802	VAL
2	Xc	809	THR

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Mol	Chain	Res	Type
2	Xc	812	GLN
2	Xc	838	VAL
2	Xc	849	THR
1	Hf	7	ILE
1	Hf	38	ARG
1	Hk	7	ILE
1	Hk	38	ARG
2	Xm	727	THR
2	Xm	786	SER
2	Xm	790	LYS
2	Xm	802	VAL
2	Xm	809	THR
2	Xm	812	GLN
2	Xm	838	VAL
2	Xm	849	THR
2	Xr	727	THR
2	Xr	786	SER
2	Xr	790	LYS
2	Xr	802	VAL
2	Xr	809	THR
2	Xr	812	GLN
2	Xr	838	VAL
2	Xr	849	THR
1	Hu	7	ILE
1	Hu	38	ARG
1	Hz	7	ILE
1	Hz	38	ARG
2	XB	712	ARG
2	XB	714	THR
2	XB	727	THR
2	XB	786	SER
2	XB	790	LYS
2	XB	802	VAL
2	XB	809	THR
2	XB	812	GLN
2	XB	838	VAL
2	XB	849	THR
2	XG	712	ARG
2	XG	713	ILE
2	XG	727	THR
2	XG	786	SER
2	XG	790	LYS

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Mol	Chain	Res	Type
2	XG	802	VAL
2	XG	809	THR
2	XG	812	GLN
2	XG	838	VAL
2	XG	849	THR
1	HO	7	ILE
1	HO	38	ARG
2	XV	727	THR
2	XV	786	SER
2	XV	790	LYS
2	XV	802	VAL
2	XV	809	THR
2	XV	812	GLN
2	XV	838	VAL
2	XV	849	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (439) such sidechains are listed below:

Mol	Chain	Res	Type
1	C2	90	ASN
1	D2	39	GLN
2	X2	794	HIS
1	A1	90	ASN
1	C1	90	ASN
1	E1	85	HIS
3	P1	14	ASN
1	A5	90	ASN
1	B5	85	HIS
1	C5	39	GLN
1	C5	90	ASN
1	D5	39	GLN
1	F5	97	GLN
2	X5	812	GLN
3	P5	36	GLN
1	A3	90	ASN
1	B3	90	ASN
1	C3	90	ASN
1	D3	39	GLN
1	D3	85	HIS
1	D3	90	ASN
1	H3	97	GLN
2	X3	812	GLN

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Mol	Chain	Res	Type
1	C4	39	GLN
1	C4	58	ASN
1	C4	90	ASN
1	D4	39	GLN
1	D4	90	ASN
1	E4	85	HIS
1	G4	90	ASN
1	H4	58	ASN
1	H4	97	GLN
2	X4	812	GLN
3	P4	14	ASN
1	A7	90	ASN
1	C7	90	ASN
1	D7	39	GLN
2	X7	794	HIS
1	A6	90	ASN
1	C6	90	ASN
1	E6	85	HIS
3	P6	14	ASN
1	A0	90	ASN
1	B0	85	HIS
1	C0	39	GLN
1	C0	90	ASN
1	D0	39	GLN
1	D0	79	HIS
1	F0	97	GLN
2	X0	812	GLN
3	P0	36	GLN
1	A8	90	ASN
1	B8	90	ASN
1	C8	90	ASN
1	D8	39	GLN
1	D8	85	HIS
1	D8	90	ASN
1	H8	97	GLN
1	C9	39	GLN
1	C9	58	ASN
1	C9	90	ASN
1	D9	39	GLN
1	D9	90	ASN
1	E9	85	HIS
1	G9	90	ASN

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Mol	Chain	Res	Type
1	H9	58	ASN
1	H9	97	GLN
2	X9	812	GLN
3	P9	14	ASN
1	Cb	90	ASN
1	Db	39	GLN
2	Xb	794	HIS
1	Aa	90	ASN
1	Ca	90	ASN
1	Ea	85	HIS
1	Ha	97	GLN
3	Pa	14	ASN
1	Ae	90	ASN
1	Be	85	HIS
1	Ce	39	GLN
1	Ce	90	ASN
1	De	39	GLN
1	De	79	HIS
1	Fe	97	GLN
2	Xe	812	GLN
3	Pe	36	GLN
1	Ac	90	ASN
1	Bc	90	ASN
1	Cc	90	ASN
1	Dc	39	GLN
1	Dc	85	HIS
1	Dc	90	ASN
1	Hc	97	GLN
3	Pc	36	GLN
1	Cd	39	GLN
1	Cd	58	ASN
1	Cd	90	ASN
1	Dd	39	GLN
1	Dd	90	ASN
1	Ed	85	HIS
1	Hd	58	ASN
1	Hd	97	GLN
2	Xd	812	GLN
3	Pd	14	ASN
1	Ag	90	ASN
1	Cg	90	ASN
1	Dg	39	GLN

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Mol	Chain	Res	Type
1	Eg	79	HIS
2	Xg	794	HIS
1	Af	90	ASN
1	Cf	90	ASN
1	Ef	85	HIS
3	Pf	14	ASN
1	Aj	90	ASN
1	Bj	85	HIS
1	Cj	39	GLN
1	Cj	90	ASN
1	Dj	39	GLN
1	Fj	97	GLN
2	Xj	812	GLN
3	Pj	36	GLN
1	Ah	90	ASN
1	Bh	90	ASN
1	Ch	90	ASN
1	Dh	39	GLN
1	Dh	85	HIS
1	Dh	90	ASN
1	Hh	97	GLN
2	Xh	812	GLN
1	Ci	39	GLN
1	Ci	58	ASN
1	Ci	90	ASN
1	Di	39	GLN
1	Di	90	ASN
1	Ei	85	HIS
1	Gi	90	ASN
1	Hi	58	ASN
1	Hi	97	GLN
2	Xi	812	GLN
3	Pi	14	ASN
1	Cl	90	ASN
1	Dl	39	GLN
2	Xl	794	HIS
1	Ak	90	ASN
1	Ck	90	ASN
1	Ek	85	HIS
3	Pk	14	ASN
1	Ao	90	ASN
1	Bo	85	HIS

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Mol	Chain	Res	Type
1	Co	39	GLN
1	Co	90	ASN
1	Do	39	GLN
1	Do	79	HIS
1	Fo	97	GLN
2	Xo	812	GLN
3	Po	36	GLN
1	Am	90	ASN
1	Bm	90	ASN
1	Cm	90	ASN
1	Dm	39	GLN
1	Dm	85	HIS
1	Dm	90	ASN
1	Hm	97	GLN
3	Pm	36	GLN
1	Cn	39	GLN
1	Cn	58	ASN
1	Cn	90	ASN
1	Dn	39	GLN
1	Dn	90	ASN
1	En	85	HIS
1	Hn	58	ASN
1	Hn	97	GLN
2	Xn	812	GLN
3	Pn	14	ASN
1	Cq	90	ASN
1	Dq	39	GLN
1	Ap	90	ASN
1	Cp	90	ASN
1	Ep	85	HIS
1	Hp	97	GLN
3	Pp	14	ASN
1	At	90	ASN
1	Bt	85	HIS
1	Ct	39	GLN
1	Ct	90	ASN
1	Dt	39	GLN
1	Ft	97	GLN
2	Xt	812	GLN
3	Pt	36	GLN
1	Ar	90	ASN
1	Br	90	ASN

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Mol	Chain	Res	Type
1	Cr	90	ASN
1	Dr	39	GLN
1	Dr	85	HIS
1	Dr	90	ASN
1	Hr	97	GLN
1	Cs	39	GLN
1	Cs	58	ASN
1	Cs	90	ASN
1	Ds	39	GLN
1	Ds	90	ASN
1	Es	85	HIS
1	Gs	90	ASN
1	Hs	58	ASN
1	Hs	97	GLN
2	Xs	812	GLN
3	Ps	14	ASN
1	Cv	90	ASN
1	Dv	39	GLN
1	Au	90	ASN
1	Cu	90	ASN
1	Eu	85	HIS
3	Pu	14	ASN
1	Ay	90	ASN
1	By	85	HIS
1	Cy	39	GLN
1	Cy	90	ASN
1	Dy	39	GLN
1	Dy	79	HIS
1	Fy	97	GLN
2	Xy	812	GLN
3	Py	36	GLN
1	Aw	90	ASN
1	Bw	90	ASN
1	Cw	90	ASN
1	Dw	39	GLN
1	Dw	85	HIS
1	Dw	90	ASN
1	Ew	97	GLN
1	Hw	97	GLN
2	Xw	812	GLN
3	Pw	36	GLN
1	Cx	39	GLN

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Mol	Chain	Res	Type
1	Cx	58	ASN
1	Cx	90	ASN
1	Dx	39	GLN
1	Dx	90	ASN
1	Ex	85	HIS
1	Gx	90	ASN
1	Hx	58	ASN
1	Hx	97	GLN
2	Xx	812	GLN
3	Px	14	ASN
1	AA	90	ASN
1	CA	90	ASN
1	DA	39	GLN
1	EA	79	HIS
2	XA	794	HIS
1	Az	90	ASN
1	Ez	85	HIS
3	Pz	14	ASN
1	AD	90	ASN
1	BD	85	HIS
1	CD	39	GLN
1	CD	90	ASN
1	DD	39	GLN
1	DD	79	HIS
1	FD	97	GLN
2	XD	812	GLN
3	PD	36	GLN
1	AB	90	ASN
1	BB	90	ASN
1	CB	90	ASN
1	DB	39	GLN
1	DB	85	HIS
1	DB	90	ASN
1	HB	97	GLN
3	PB	36	GLN
1	CC	39	GLN
1	CC	58	ASN
1	CC	90	ASN
1	DC	39	GLN
1	DC	90	ASN
1	EC	85	HIS
1	GC	90	ASN

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Mol	Chain	Res	Type
1	HC	58	ASN
1	HC	97	GLN
2	XC	812	GLN
3	PC	14	ASN
1	CF	90	ASN
1	DF	39	GLN
1	AE	90	ASN
1	CE	90	ASN
1	HE	97	GLN
3	PE	14	ASN
1	AI	90	ASN
1	BI	85	HIS
1	CI	39	GLN
1	CI	90	ASN
1	DI	39	GLN
1	DI	79	HIS
1	FI	97	GLN
1	HI	85	HIS
2	XI	812	GLN
3	PI	36	GLN
1	AG	90	ASN
1	BG	90	ASN
1	CG	90	ASN
1	DG	39	GLN
1	DG	85	HIS
1	DG	90	ASN
1	HG	97	GLN
3	PG	36	GLN
1	CH	39	GLN
1	CH	58	ASN
1	CH	90	ASN
1	DH	39	GLN
1	DH	90	ASN
1	EH	85	HIS
1	GH	90	ASN
1	HH	58	ASN
1	HH	97	GLN
2	XH	812	GLN
3	PH	14	ASN
1	AK	90	ASN
1	CK	90	ASN
1	DK	39	GLN

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Mol	Chain	Res	Type
2	XK	794	HIS
1	AJ	90	ASN
1	EJ	85	HIS
1	HJ	97	GLN
3	PJ	14	ASN
1	AN	90	ASN
1	BN	85	HIS
1	CN	39	GLN
1	CN	90	ASN
1	DN	39	GLN
1	FN	97	GLN
2	XN	812	GLN
3	PN	36	GLN
1	AL	90	ASN
1	BL	90	ASN
1	CL	90	ASN
1	DL	39	GLN
1	DL	85	HIS
1	DL	90	ASN
1	HL	97	GLN
2	XL	812	GLN
3	PL	36	GLN
1	CM	39	GLN
1	CM	58	ASN
1	CM	90	ASN
1	DM	39	GLN
1	DM	90	ASN
1	EM	85	HIS
1	GM	90	ASN
1	HM	58	ASN
1	HM	97	GLN
2	XM	812	GLN
3	PM	14	ASN
1	CP	90	ASN
1	DP	39	GLN
2	XP	794	HIS
1	AO	90	ASN
1	CO	90	ASN
1	EO	85	HIS
3	PO	14	ASN
3	PO	36	GLN
1	AS	90	ASN

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Mol	Chain	Res	Type
1	BS	85	HIS
1	CS	39	GLN
1	CS	90	ASN
1	DS	39	GLN
1	DS	79	HIS
1	FS	97	GLN
2	XS	812	GLN
3	PS	36	GLN
1	AQ	90	ASN
1	BQ	90	ASN
1	CQ	90	ASN
1	DQ	39	GLN
1	DQ	85	HIS
1	DQ	90	ASN
1	HQ	97	GLN
2	XQ	812	GLN
3	PQ	36	GLN
1	CR	39	GLN
1	CR	58	ASN
1	CR	90	ASN
1	DR	39	GLN
1	DR	90	ASN
1	ER	85	HIS
1	HR	58	ASN
1	HR	97	GLN
2	XR	812	GLN
3	PR	14	ASN
1	CU	90	ASN
1	DU	39	GLN
1	AT	90	ASN
1	CT	90	ASN
1	ET	85	HIS
1	HT	85	HIS
1	HT	97	GLN
3	PT	14	ASN
1	AX	90	ASN
1	BX	85	HIS
1	CX	39	GLN
1	CX	90	ASN
1	DX	39	GLN
1	DX	79	HIS
1	FX	97	GLN

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Mol	Chain	Res	Type
2	XX	812	GLN
3	PX	36	GLN
1	AV	90	ASN
1	BV	90	ASN
1	CV	90	ASN
1	DV	39	GLN
1	DV	85	HIS
1	DV	90	ASN
1	HV	97	GLN
3	PV	36	GLN
1	CW	39	GLN
1	CW	58	ASN
1	CW	90	ASN
1	DW	39	GLN
1	DW	90	ASN
1	EW	85	HIS
1	GW	90	ASN
1	HW	58	ASN
1	HW	97	GLN
2	XW	812	GLN
3	PW	14	ASN
1	H1	85	HIS
1	H1	97	GLN
1	H6	97	GLN
2	X8	812	GLN
2	Xc	812	GLN
1	Hf	97	GLN
1	Hk	85	HIS
1	Hk	97	GLN
2	Xm	812	GLN
2	Xr	812	GLN
1	Hu	85	HIS
1	Hu	97	GLN
1	Hv	97	GLN
2	XB	812	GLN
2	XG	812	GLN
1	HO	97	GLN
2	XV	812	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

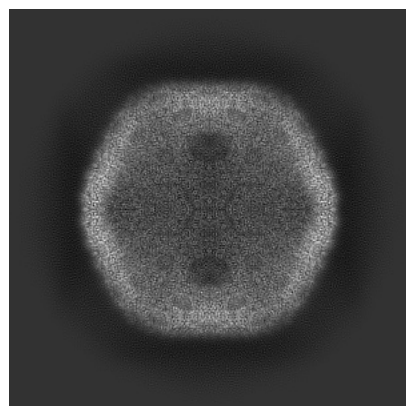
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62530. These allow visual inspection of the internal detail of the map and identification of artifacts.

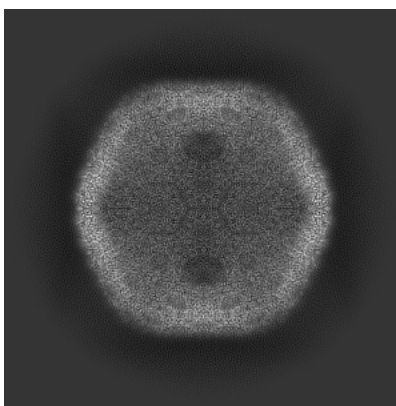
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

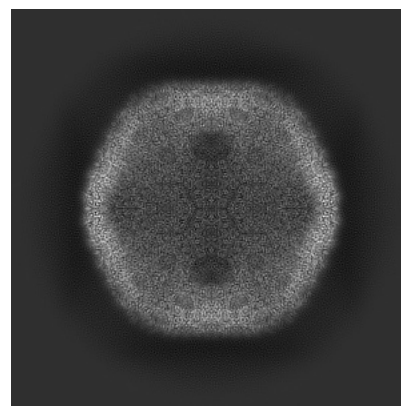
6.1.1 Primary map



X

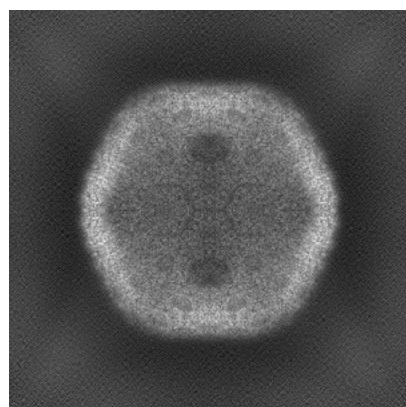


Y

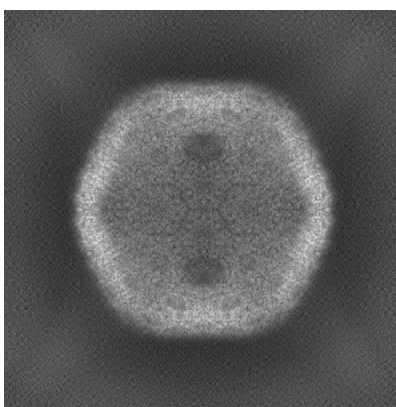


Z

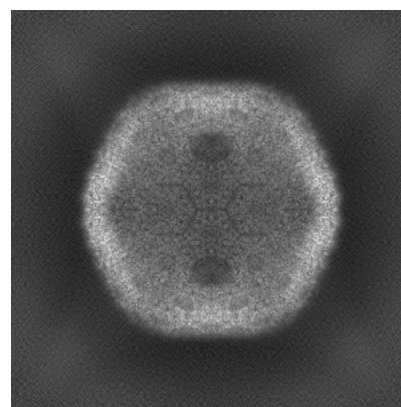
6.1.2 Raw map



X



Y

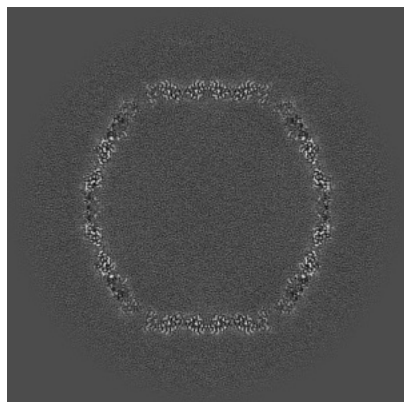


Z

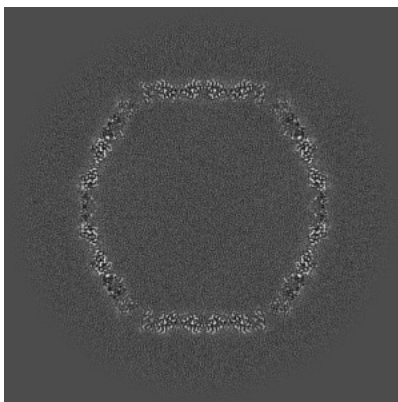
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

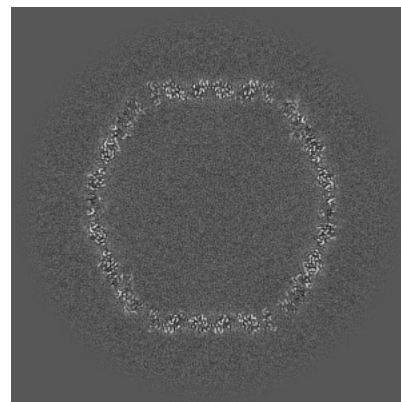
6.2.1 Primary map



X Index: 250

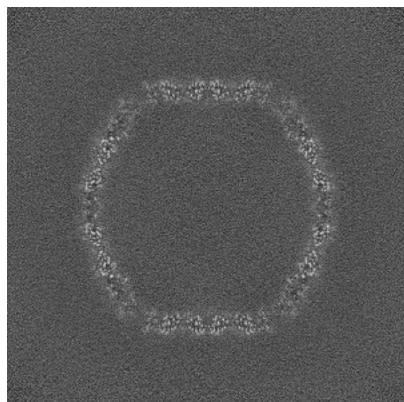


Y Index: 250

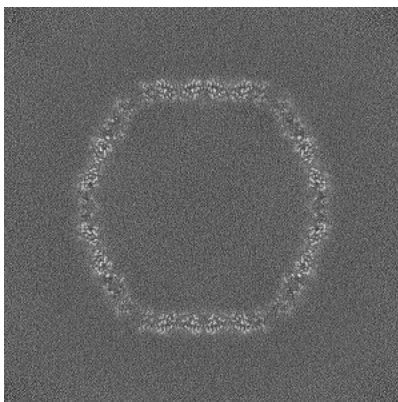


Z Index: 250

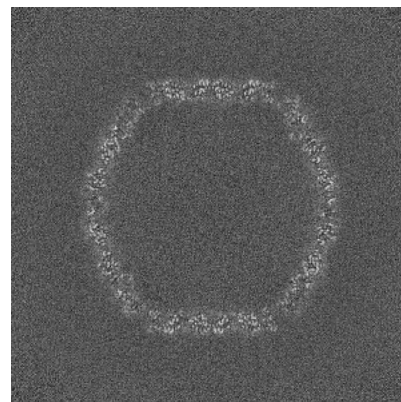
6.2.2 Raw map



X Index: 250



Y Index: 250

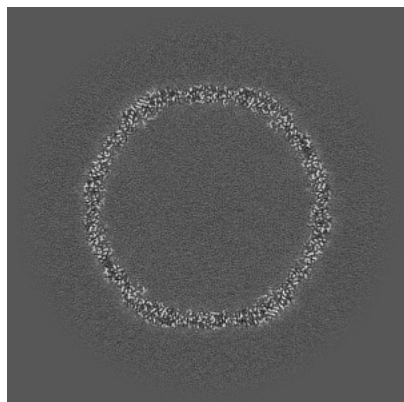


Z Index: 250

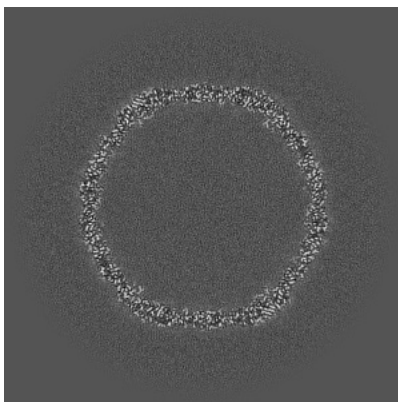
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

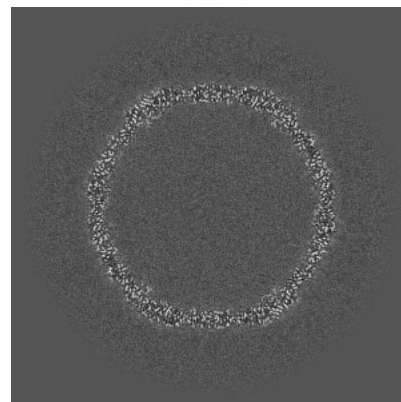
6.3.1 Primary map



X Index: 287

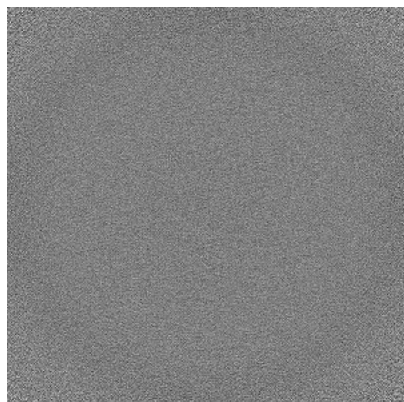


Y Index: 287

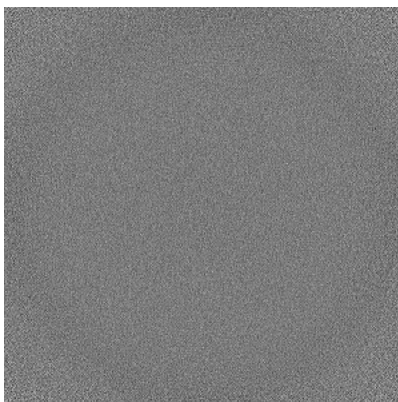


Z Index: 286

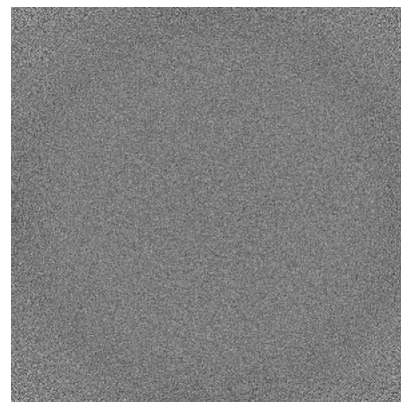
6.3.2 Raw map



X Index: 0



Y Index: 0

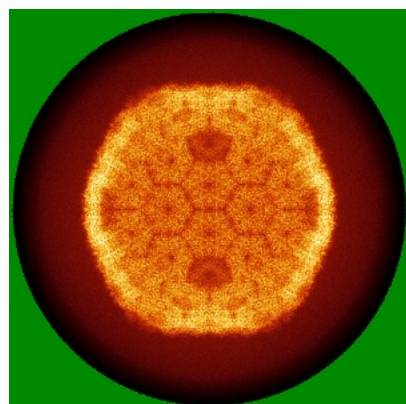


Z Index: 499

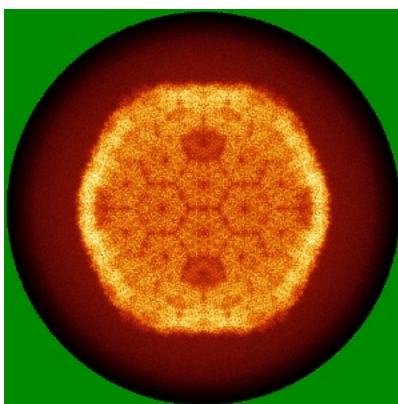
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

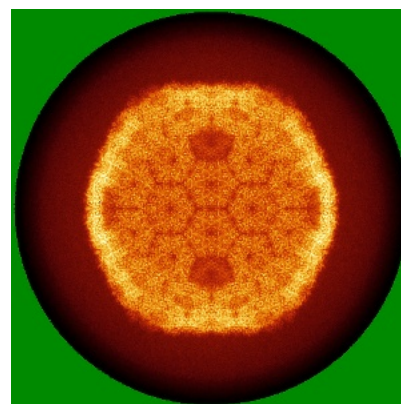
6.4.1 Primary map



X

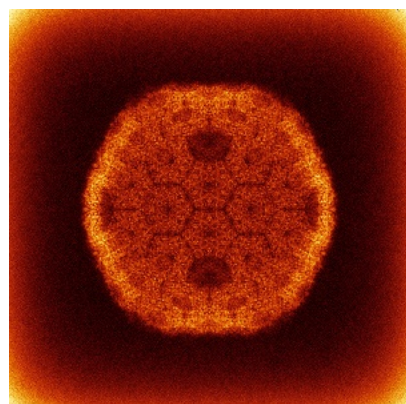


Y

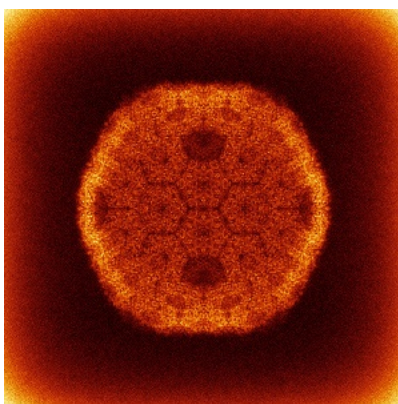


Z

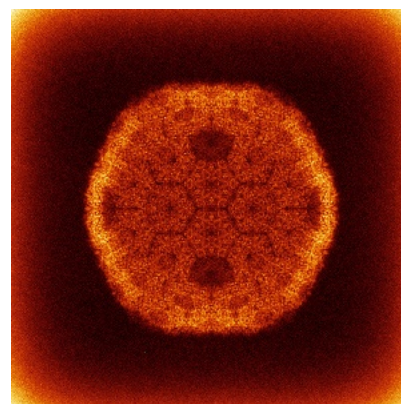
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



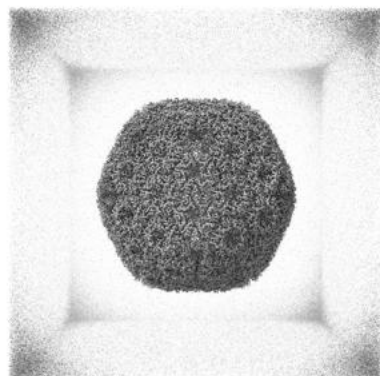
Y



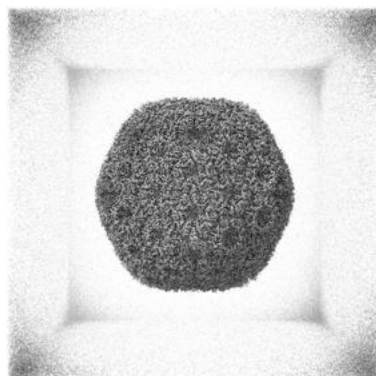
Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

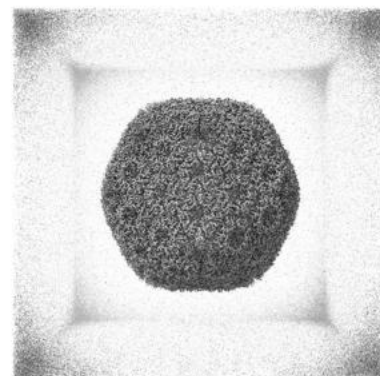
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

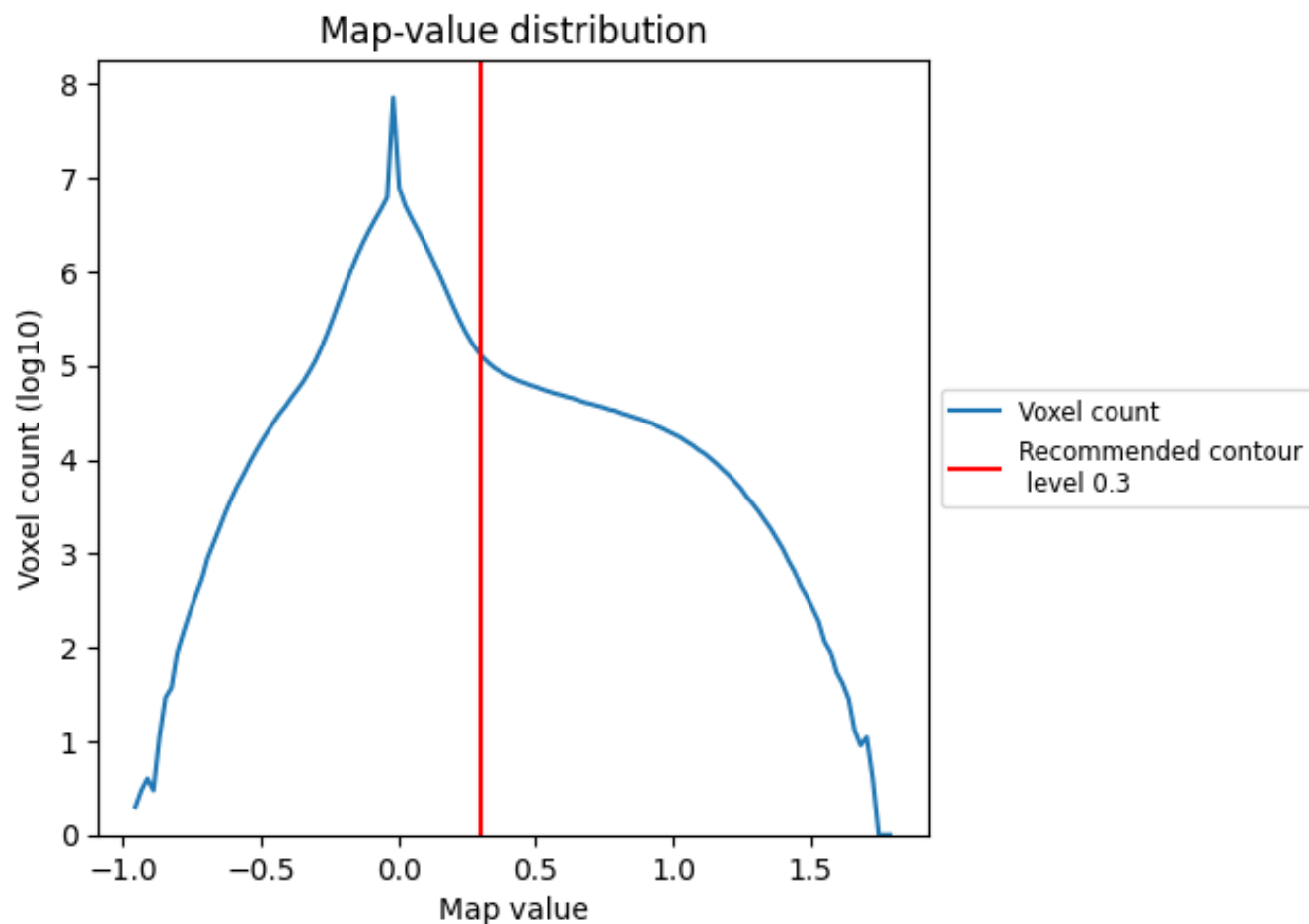
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

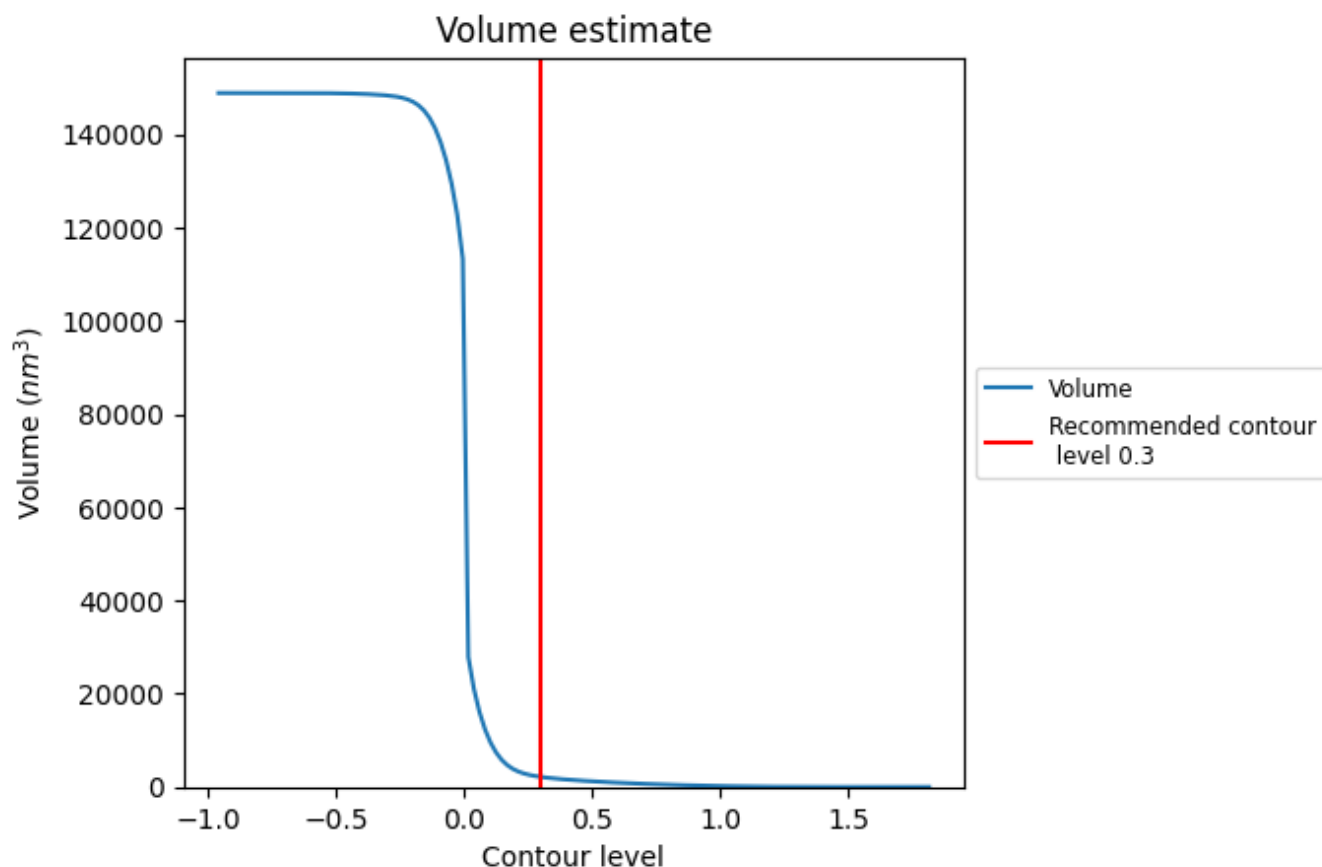
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

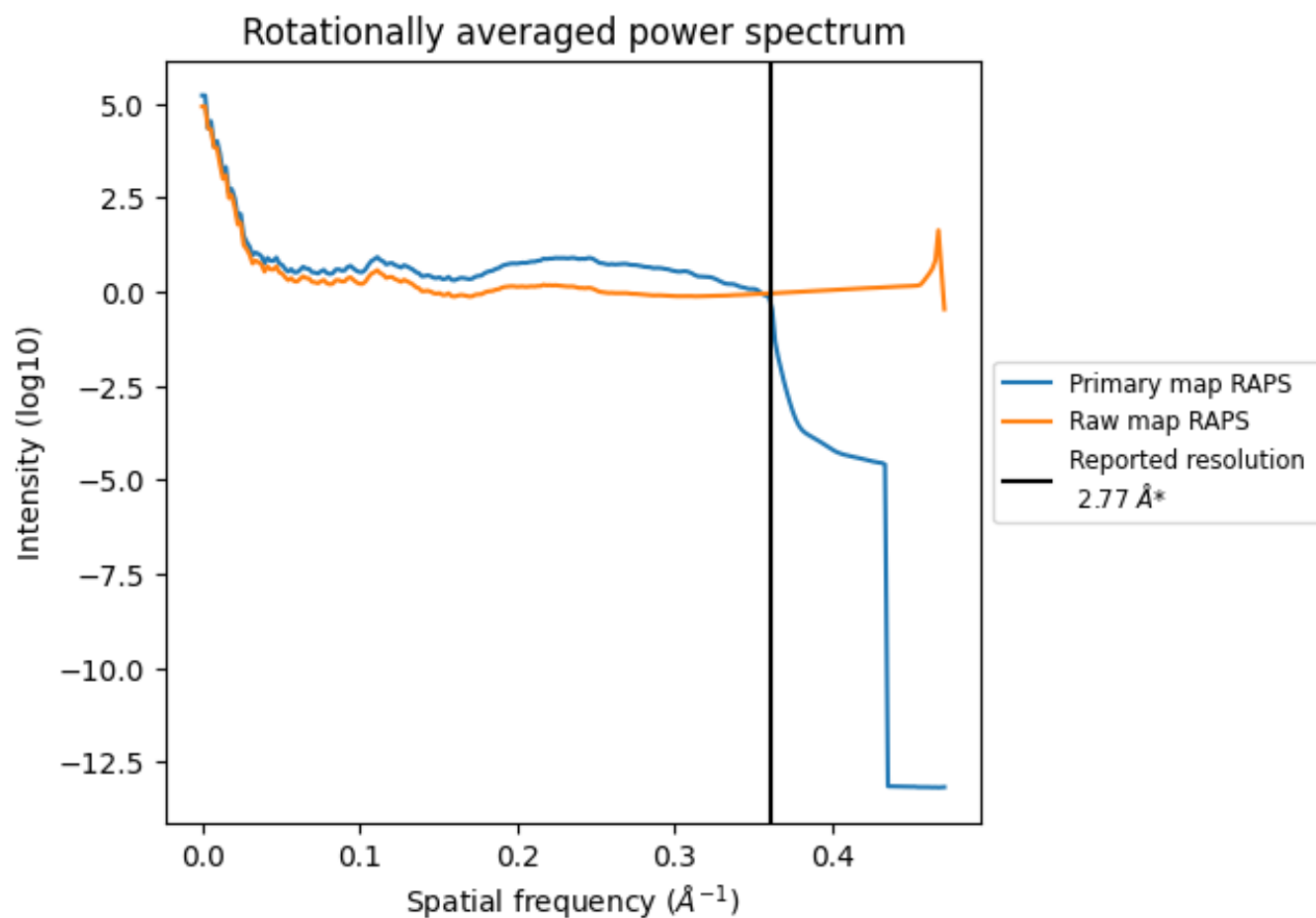
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2152 nm³; this corresponds to an approximate mass of 1944 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

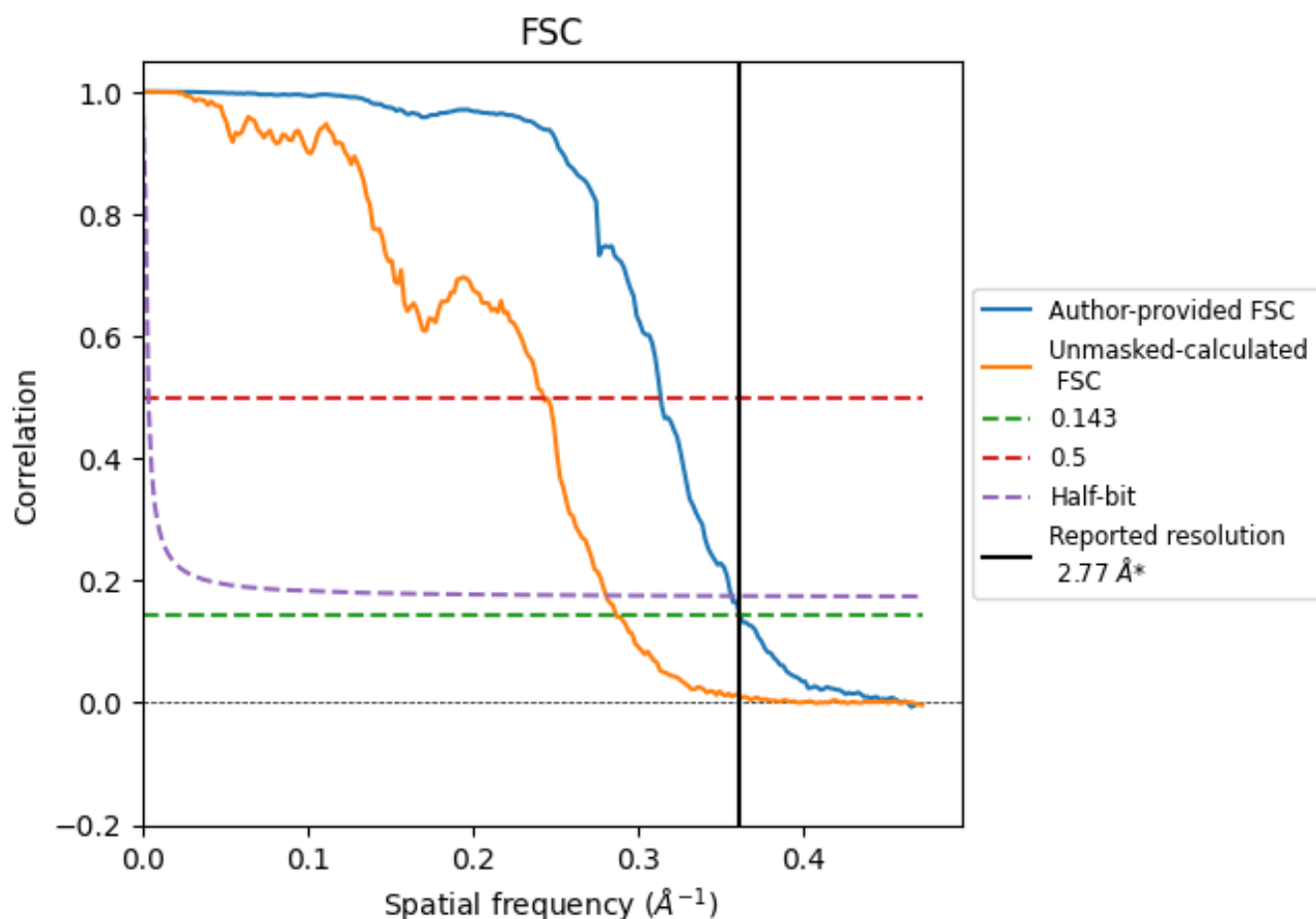


*Reported resolution corresponds to spatial frequency of 0.361 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.361 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

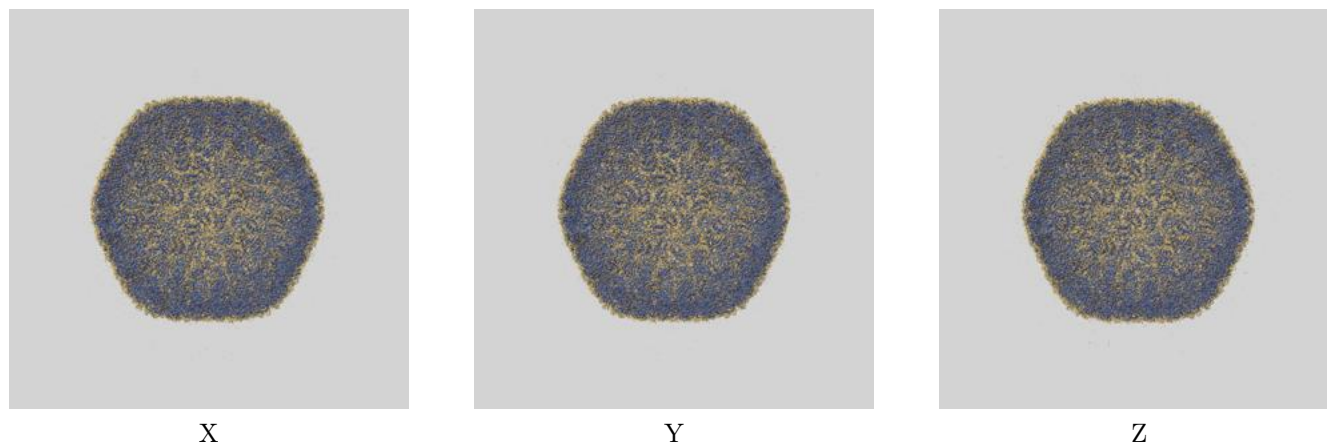
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.77	-	-
Author-provided FSC curve	2.77	3.19	2.81
Unmasked-calculated*	3.49	4.12	3.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.49 differs from the reported value 2.77 by more than 10 %

9 Map-model fit [i](#)

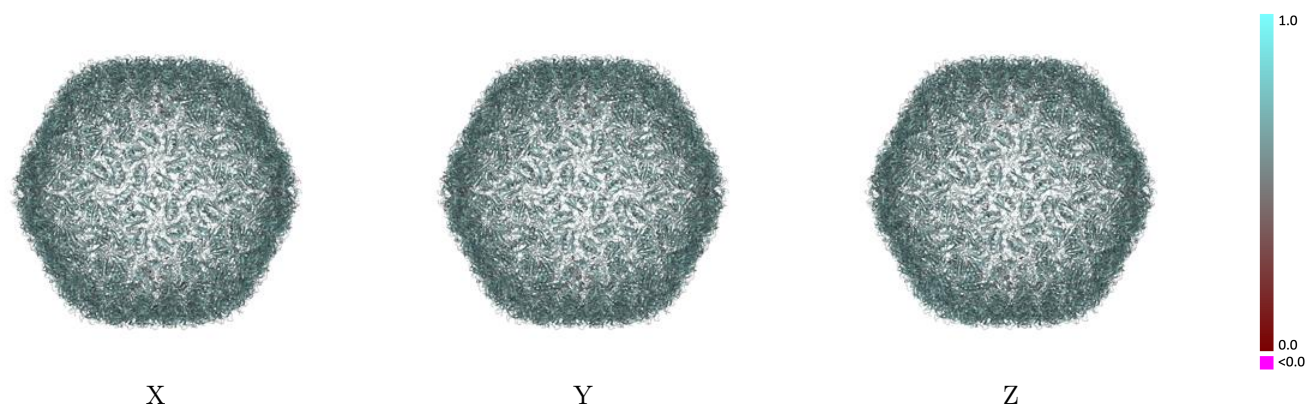
This section contains information regarding the fit between EMDB map EMD-62530 and PDB model 9LY8. Per-residue inclusion information can be found in section [3](#) on page [56](#).

9.1 Map-model overlay [i](#)



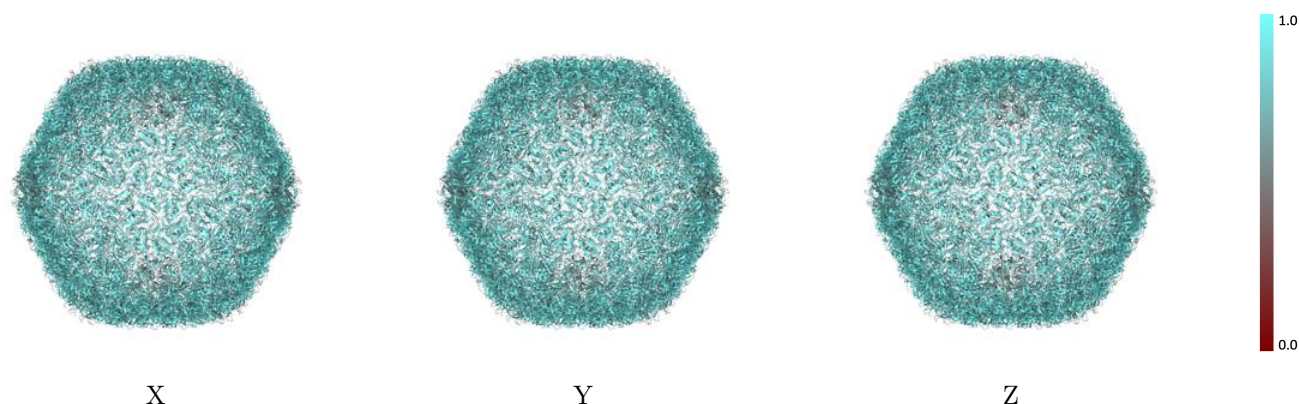
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



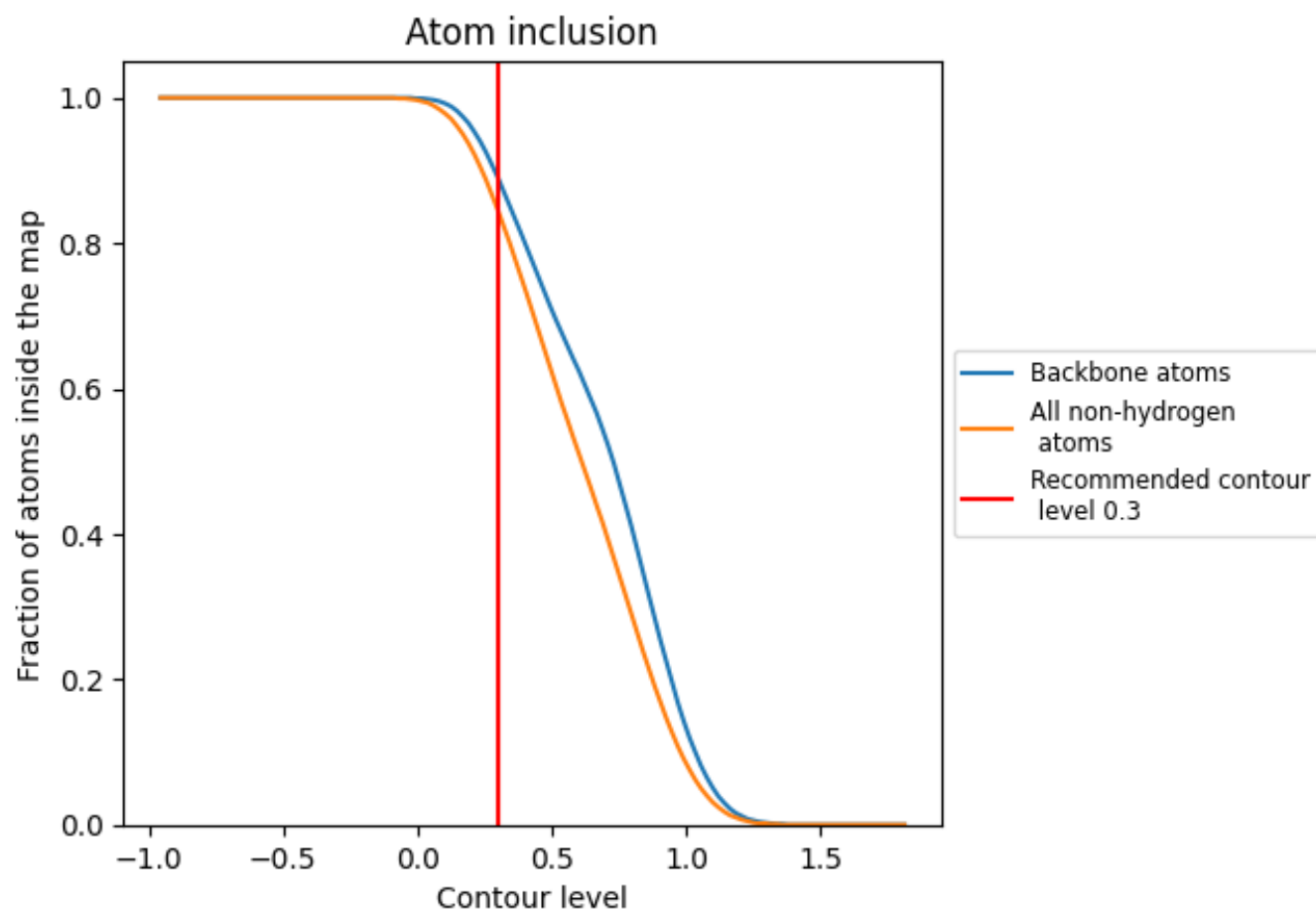
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8450	 0.5950
A0	 0.8830	 0.6030
A1	 0.9030	 0.6320
A2	 0.9000	 0.6330
A3	 0.8910	 0.6280
A4	 0.8860	 0.6270
A5	 0.9000	 0.6260
A6	 0.8810	 0.6050
A7	 0.8640	 0.5980
A8	 0.8810	 0.6100
A9	 0.8910	 0.6040
AA	 0.8810	 0.6130
AB	 0.8880	 0.6060
AC	 0.8920	 0.6090
AD	 0.8830	 0.6060
AE	 0.8810	 0.6020
AF	 0.8890	 0.6110
AG	 0.8810	 0.6080
AH	 0.8880	 0.6060
AI	 0.8890	 0.6130
AJ	 0.8890	 0.6030
AK	 0.8860	 0.6140
AL	 0.8740	 0.6070
AM	 0.8800	 0.6050
AN	 0.8880	 0.6090
AO	 0.8860	 0.6050
AP	 0.8800	 0.6010
AQ	 0.8970	 0.6090
AR	 0.8780	 0.6040
AS	 0.8850	 0.6070
AT	 0.8740	 0.5970
AU	 0.8850	 0.6010
AV	 0.8800	 0.5980
AW	 0.8810	 0.6030
AX	 0.8850	 0.6020



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Chain	Atom inclusion	Q-score
Aa	 0.8720	 0.6010
Ab	 0.8850	 0.6050
Ac	 0.8800	 0.6100
Ad	 0.8860	 0.5990
Ae	 0.8770	 0.6070
Af	 0.8850	 0.6060
Ag	 0.8860	 0.6010
Ah	 0.8810	 0.6090
Ai	 0.8880	 0.6060
Aj	 0.8830	 0.6040
Ak	 0.8750	 0.5970
Al	 0.8800	 0.6010
Am	 0.8750	 0.6030
An	 0.8850	 0.6040
Ao	 0.8880	 0.6100
Ap	 0.8750	 0.6000
Aq	 0.8750	 0.6030
Ar	 0.8810	 0.6030
As	 0.8780	 0.6070
At	 0.8720	 0.5970
Au	 0.8860	 0.6030
Av	 0.8830	 0.6090
Aw	 0.8910	 0.6090
Ax	 0.8890	 0.6020
Ay	 0.8920	 0.6020
Az	 0.8910	 0.6150
B0	 0.8750	 0.5950
B1	 0.9050	 0.6260
B2	 0.8880	 0.6260
B3	 0.8860	 0.6250
B4	 0.8950	 0.6280
B5	 0.8940	 0.6260
B6	 0.8640	 0.6000
B7	 0.8800	 0.6020
B8	 0.8770	 0.6020
B9	 0.8610	 0.5950
BA	 0.8890	 0.6010
BB	 0.8800	 0.6030
BC	 0.8830	 0.6030
BD	 0.8810	 0.6090
BE	 0.8800	 0.5940
BF	 0.8580	 0.5980

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Chain	Atom inclusion	Q-score
BG	 0.8550	 0.5930
BH	 0.8720	 0.5970
BI	 0.8770	 0.5970
BJ	 0.8750	 0.5910
BK	 0.8780	 0.5920
BL	 0.8720	 0.5990
BM	 0.8720	 0.6020
BN	 0.8880	 0.5940
BO	 0.8800	 0.6050
BP	 0.8640	 0.5980
BQ	 0.8830	 0.5950
BR	 0.8640	 0.5970
BS	 0.8720	 0.5950
BT	 0.8630	 0.5940
BU	 0.8690	 0.5990
BV	 0.8710	 0.6000
BW	 0.8690	 0.5970
BX	 0.8810	 0.5930
Ba	 0.8600	 0.5940
Bb	 0.8750	 0.5950
Bc	 0.8890	 0.5880
Bd	 0.8690	 0.5990
Be	 0.8780	 0.5980
Bf	 0.8720	 0.5910
Bg	 0.8600	 0.5920
Bh	 0.8800	 0.6020
Bi	 0.8850	 0.5970
Bj	 0.8740	 0.5970
Bk	 0.8850	 0.5990
Bl	 0.8880	 0.6080
Bm	 0.8860	 0.6030
Bn	 0.8710	 0.6030
Bo	 0.8670	 0.5990
Bp	 0.8800	 0.5980
Bq	 0.8670	 0.5920
Br	 0.8800	 0.5990
Bs	 0.8690	 0.5990
Bt	 0.8720	 0.5990
Bu	 0.8780	 0.6020
Bv	 0.8780	 0.6020
Bw	 0.8890	 0.6020
Bx	 0.8810	 0.5980

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Chain	Atom inclusion	Q-score
By	 0.8600	 0.5990
Bz	 0.8880	 0.6000
C0	 0.8880	 0.6000
C1	 0.9020	 0.6270
C2	 0.9080	 0.6300
C3	 0.9020	 0.6220
C4	 0.9020	 0.6270
C5	 0.9170	 0.6310
C6	 0.8720	 0.6040
C7	 0.8770	 0.6040
C8	 0.8970	 0.6070
C9	 0.8890	 0.6050
CA	 0.8890	 0.6110
CB	 0.9000	 0.6110
CC	 0.8950	 0.6130
CD	 0.9060	 0.6110
CE	 0.8720	 0.6080
CF	 0.8860	 0.6090
CG	 0.8860	 0.6070
CH	 0.8660	 0.6060
CI	 0.8770	 0.5960
CJ	 0.8800	 0.6070
CK	 0.8810	 0.6030
CL	 0.8800	 0.6060
CM	 0.8690	 0.6040
CN	 0.8970	 0.6080
CO	 0.8810	 0.6020
CP	 0.8670	 0.5970
CQ	 0.9060	 0.6080
CR	 0.8830	 0.6030
CS	 0.8880	 0.6040
CT	 0.8750	 0.6040
CU	 0.8940	 0.6080
CV	 0.8850	 0.5990
CW	 0.8830	 0.6030
CX	 0.8880	 0.6070
Ca	 0.8660	 0.6040
Cb	 0.8810	 0.6080
Cc	 0.8750	 0.6000
Cd	 0.8880	 0.6050
Ce	 0.8890	 0.6070
Cf	 0.8770	 0.6100

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Chain	Atom inclusion	Q-score
Cg	 0.8950	 0.6120
Ch	 0.8880	 0.6040
Ci	 0.8920	 0.6090
Cj	 0.8890	 0.5990
Ck	 0.8710	 0.6020
Cl	 0.8920	 0.6090
Cm	 0.8890	 0.6050
Cn	 0.8910	 0.6110
Co	 0.8740	 0.6020
Cp	 0.8750	 0.6030
Cq	 0.8970	 0.6030
Cr	 0.8720	 0.5970
Cs	 0.8860	 0.6090
Ct	 0.8860	 0.6000
Cu	 0.8860	 0.6100
Cv	 0.8750	 0.6000
Cw	 0.9020	 0.6060
Cx	 0.8910	 0.6100
Cy	 0.8860	 0.5980
Cz	 0.8880	 0.6160
D0	 0.8810	 0.6030
D1	 0.8940	 0.6300
D2	 0.8990	 0.6260
D3	 0.8950	 0.6280
D4	 0.8950	 0.6240
D5	 0.8950	 0.6280
D6	 0.8850	 0.5990
D7	 0.8800	 0.6050
D8	 0.8740	 0.5990
D9	 0.8770	 0.6000
DA	 0.8950	 0.6120
DB	 0.8940	 0.6140
DC	 0.8630	 0.5980
DD	 0.8740	 0.6050
DE	 0.8880	 0.6120
DF	 0.8950	 0.6070
DG	 0.8880	 0.6100
DH	 0.8880	 0.6010
DI	 0.8780	 0.6000
DJ	 0.8750	 0.6020
DK	 0.8850	 0.6120
DL	 0.8800	 0.6100

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Chain	Atom inclusion	Q-score
DM	 0.8640	 0.6050
DN	 0.8780	 0.6030
DO	 0.8750	 0.6080
DP	 0.8610	 0.6010
DQ	 0.8860	 0.6030
DR	 0.8800	 0.6050
DS	 0.8850	 0.6030
DT	 0.8750	 0.6100
DU	 0.8800	 0.6010
DV	 0.8720	 0.5960
DW	 0.8780	 0.6030
DX	 0.8890	 0.6090
Da	 0.8770	 0.6070
Db	 0.8830	 0.6100
Dc	 0.8720	 0.5980
Dd	 0.8810	 0.5960
De	 0.8670	 0.6050
Df	 0.8750	 0.6030
Dg	 0.8780	 0.6060
Dh	 0.8890	 0.6020
Di	 0.8800	 0.6050
Dj	 0.8740	 0.6010
Dk	 0.8720	 0.6100
Dl	 0.9000	 0.6070
Dm	 0.8710	 0.6060
Dn	 0.8850	 0.6000
Do	 0.8770	 0.6040
Dp	 0.8830	 0.6020
Dq	 0.8780	 0.6050
Dr	 0.8950	 0.6060
Ds	 0.8890	 0.6020
Dt	 0.8710	 0.5950
Du	 0.8860	 0.6060
Dv	 0.8750	 0.6040
Dw	 0.8880	 0.6060
Dx	 0.8850	 0.5980
Dy	 0.8810	 0.6050
Dz	 0.8850	 0.6120
E0	 0.8890	 0.6010
E1	 0.9080	 0.6310
E2	 0.9020	 0.6260
E3	 0.8990	 0.6260

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Chain	Atom inclusion	Q-score
E4	 0.9020	 0.6270
E5	 0.8970	 0.6250
E6	 0.8860	 0.6030
E7	 0.8800	 0.5960
E8	 0.8920	 0.5970
E9	 0.8810	 0.5990
EA	 0.8910	 0.6130
EB	 0.8810	 0.6010
EC	 0.8890	 0.6080
ED	 0.8880	 0.6120
EE	 0.8890	 0.6030
EF	 0.8880	 0.6000
EG	 0.8750	 0.5980
EH	 0.9050	 0.6050
EI	 0.8860	 0.6080
EJ	 0.8970	 0.6010
EK	 0.8950	 0.6030
EL	 0.8800	 0.5990
EM	 0.8800	 0.6030
EN	 0.8940	 0.6030
EO	 0.8800	 0.5950
EP	 0.8920	 0.5950
EQ	 0.8850	 0.6010
ER	 0.8810	 0.5960
ES	 0.9020	 0.6070
ET	 0.8910	 0.6070
EU	 0.8690	 0.5990
EV	 0.8910	 0.6040
EW	 0.8910	 0.6020
EX	 0.8810	 0.6050
Ea	 0.8740	 0.6000
Eb	 0.8720	 0.6040
Ec	 0.8810	 0.5950
Ed	 0.8780	 0.5920
Ee	 0.8780	 0.6010
Ef	 0.8750	 0.5970
Eg	 0.8570	 0.5960
Eh	 0.8750	 0.6050
Ei	 0.8770	 0.5940
Ej	 0.8800	 0.6050
Ek	 0.8800	 0.5940
El	 0.8800	 0.6080

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Chain	Atom inclusion	Q-score
Em	 0.8990	 0.6070
En	 0.8850	 0.6000
Eo	 0.8780	 0.6080
Ep	 0.8780	 0.6050
Eq	 0.8810	 0.5930
Er	 0.8710	 0.5940
Es	 0.8910	 0.6010
Et	 0.8830	 0.6020
Eu	 0.8690	 0.6000
Ev	 0.8860	 0.5990
Ew	 0.8800	 0.6060
Ex	 0.8830	 0.6060
Ey	 0.8770	 0.6050
Ez	 0.8860	 0.6100
F0	 0.8880	 0.6040
F1	 0.9130	 0.6320
F2	 0.9030	 0.6290
F3	 0.9030	 0.6280
F4	 0.9020	 0.6270
F5	 0.9020	 0.6280
F6	 0.8810	 0.6030
F7	 0.8850	 0.6090
F8	 0.9030	 0.6110
F9	 0.8800	 0.6090
FA	 0.8910	 0.6140
FB	 0.8940	 0.6090
FC	 0.8830	 0.6100
FD	 0.8890	 0.6100
FE	 0.8970	 0.6130
FF	 0.8850	 0.5970
FG	 0.8850	 0.6110
FH	 0.8920	 0.6100
FI	 0.8810	 0.6090
FJ	 0.8910	 0.6090
FK	 0.8950	 0.6070
FL	 0.8850	 0.6050
FM	 0.8810	 0.6150
FN	 0.8950	 0.6130
FO	 0.8950	 0.6050
FP	 0.8750	 0.6050
FQ	 0.8880	 0.6060
FR	 0.8780	 0.6090

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Chain	Atom inclusion	Q-score
FS	 0.8890	 0.6040
FT	 0.8920	 0.6170
FU	 0.8950	 0.6100
FV	 0.8850	 0.6000
FW	 0.8920	 0.6070
FX	 0.8860	 0.6120
Fa	 0.8740	 0.6060
Fb	 0.8740	 0.6010
Fc	 0.8780	 0.6040
Fd	 0.8880	 0.6050
Fe	 0.8800	 0.6060
Ff	 0.8920	 0.6110
Fg	 0.9020	 0.6110
Fh	 0.8810	 0.6030
Fi	 0.8770	 0.6030
Fj	 0.8910	 0.6110
Fk	 0.8910	 0.6090
Fl	 0.8860	 0.6120
Fm	 0.8910	 0.6070
Fn	 0.8780	 0.6110
Fo	 0.8780	 0.6040
Fp	 0.8810	 0.6020
Fq	 0.9000	 0.6130
Fr	 0.8940	 0.6040
Fs	 0.8830	 0.6050
Ft	 0.8800	 0.6120
Fu	 0.8810	 0.6080
Fv	 0.8950	 0.6110
Fw	 0.8970	 0.6060
Fx	 0.8850	 0.6010
Fy	 0.8800	 0.6140
Fz	 0.8830	 0.6070
G0	 0.8920	 0.6060
G1	 0.9060	 0.6300
G2	 0.8970	 0.6220
G3	 0.8830	 0.6260
G4	 0.9030	 0.6310
G5	 0.9030	 0.6270
G6	 0.8890	 0.6050
G7	 0.8800	 0.5990
G8	 0.8800	 0.6070
G9	 0.8950	 0.6020

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Chain	Atom inclusion	Q-score
GA	 0.9020	 0.6100
GB	 0.8830	 0.6030
GC	 0.8740	 0.6080
GD	 0.8850	 0.6050
GE	 0.8830	 0.5960
GF	 0.8740	 0.6020
GG	 0.8890	 0.6000
GH	 0.8990	 0.6080
GI	 0.8830	 0.6040
GJ	 0.8720	 0.6060
GK	 0.8810	 0.6020
GL	 0.8690	 0.5990
GM	 0.8860	 0.6050
GN	 0.8920	 0.6050
GO	 0.8910	 0.5990
GP	 0.8770	 0.6000
GQ	 0.8860	 0.6020
GR	 0.8990	 0.6010
GS	 0.8780	 0.6080
GT	 0.8690	 0.6010
GU	 0.8890	 0.5980
GV	 0.8750	 0.6000
GW	 0.8780	 0.6010
GX	 0.8830	 0.6040
Ga	 0.8670	 0.5960
Gb	 0.8770	 0.6040
Gc	 0.8800	 0.6010
Gd	 0.9000	 0.6010
Ge	 0.8830	 0.5980
Gf	 0.8740	 0.5960
Gg	 0.8860	 0.5990
Gh	 0.8810	 0.6030
Gi	 0.8780	 0.6020
Gj	 0.8850	 0.6070
Gk	 0.8890	 0.6070
Gl	 0.8800	 0.6030
Gm	 0.9020	 0.6000
Gn	 0.8880	 0.6070
Go	 0.8920	 0.6010
Gp	 0.8950	 0.5960
Gq	 0.8780	 0.5950
Gr	 0.8610	 0.6000

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Chain	Atom inclusion	Q-score
Gs	 0.8940	 0.6100
Gt	 0.8770	 0.5960
Gu	 0.8860	 0.6050
Gv	 0.8800	 0.6040
Gw	 0.8740	 0.5930
Gx	 0.8810	 0.6020
Gy	 0.8800	 0.6040
Gz	 0.9030	 0.6110
H0	 0.8550	 0.5970
H1	 0.8890	 0.6280
H2	 0.8880	 0.6250
H3	 0.8830	 0.6220
H4	 0.8910	 0.6240
H5	 0.8910	 0.6250
H6	 0.8800	 0.6060
H7	 0.8690	 0.5980
H8	 0.8770	 0.6070
H9	 0.8770	 0.6060
HA	 0.8750	 0.6070
HB	 0.8770	 0.6110
HC	 0.8750	 0.6060
HD	 0.8740	 0.6060
HE	 0.8740	 0.6050
HF	 0.8710	 0.6050
HG	 0.8750	 0.6100
HH	 0.8690	 0.6040
HI	 0.8570	 0.5970
HJ	 0.8660	 0.6030
HK	 0.8630	 0.6070
HL	 0.8640	 0.6080
HM	 0.8720	 0.6090
HN	 0.8670	 0.6010
HO	 0.8710	 0.6060
HP	 0.8720	 0.5970
HQ	 0.8800	 0.6050
HR	 0.8640	 0.6000
HS	 0.8770	 0.5970
HT	 0.8780	 0.6100
HU	 0.8580	 0.5950
HV	 0.8570	 0.6010
HW	 0.8580	 0.6100
HX	 0.8690	 0.5910

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Chain	Atom inclusion	Q-score
Ha	 0.8530	 0.6030
Hb	 0.8720	 0.6020
Hc	 0.8880	 0.6090
Hd	 0.8550	 0.6000
He	 0.8640	 0.6020
Hf	 0.8670	 0.6030
Hg	 0.8910	 0.6010
Hh	 0.8710	 0.6040
Hi	 0.8710	 0.6010
Hj	 0.8690	 0.6040
Hk	 0.8670	 0.6080
Hl	 0.8830	 0.6070
Hm	 0.8810	 0.6030
Hz	 0.8660	 0.6080
Ho	 0.8810	 0.6000
Hp	 0.8690	 0.6030
Hq	 0.8550	 0.5960
Hr	 0.8740	 0.6070
Hs	 0.8630	 0.6010
Ht	 0.8610	 0.6000
Hu	 0.8770	 0.6080
Hv	 0.8660	 0.5950
Hw	 0.8850	 0.6080
Hx	 0.8720	 0.6070
Hy	 0.8710	 0.5950
Hx	 0.8850	 0.6070
P0	 0.6690	 0.5690
P1	 0.7130	 0.6130
P2	 0.7160	 0.6050
P3	 0.6880	 0.6000
P4	 0.6910	 0.5720
P5	 0.7040	 0.6030
P6	 0.6790	 0.5680
P7	 0.6730	 0.5660
P8	 0.6810	 0.5600
P9	 0.6960	 0.5690
PA	 0.6830	 0.5720
PB	 0.7080	 0.5660
PC	 0.6830	 0.5650
PD	 0.6910	 0.5640
PE	 0.6880	 0.5620
PF	 0.6960	 0.5760

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Chain	Atom inclusion	Q-score
PG	 0.6830	 0.5660
PH	 0.6760	 0.5750
PI	 0.6830	 0.5690
PJ	 0.6590	 0.5640
PK	 0.6960	 0.5710
PL	 0.6560	 0.5530
PM	 0.6830	 0.5590
PN	 0.6760	 0.5610
PO	 0.6660	 0.5580
PP	 0.6480	 0.5580
PQ	 0.6810	 0.5560
PR	 0.6790	 0.5580
PS	 0.6860	 0.5700
PT	 0.6640	 0.5670
PU	 0.6990	 0.5600
PV	 0.6840	 0.5540
PW	 0.6940	 0.5670
PX	 0.6930	 0.5680
Pa	 0.6510	 0.5580
Pb	 0.6540	 0.5640
Pc	 0.6630	 0.5540
Pd	 0.6680	 0.5670
Pe	 0.6630	 0.5630
Pf	 0.6730	 0.5660
Pg	 0.6910	 0.5700
Ph	 0.6590	 0.5610
Pi	 0.6960	 0.5780
Pj	 0.6710	 0.5660
Pk	 0.6740	 0.5660
Pl	 0.6840	 0.5550
Pm	 0.6790	 0.5660
Pn	 0.6890	 0.5580
Po	 0.6810	 0.5720
Pp	 0.6630	 0.5690
Pq	 0.6680	 0.5640
Pr	 0.6610	 0.5660
Ps	 0.6610	 0.5570
Pt	 0.6540	 0.5530
Pu	 0.6910	 0.5790
Pv	 0.7130	 0.5710
Pw	 0.6990	 0.5670
Px	 0.7090	 0.5650

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Chain	Atom inclusion	Q-score
Py	 0.6860	 0.5670
Pz	 0.6840	 0.5700
X0	 0.7260	 0.5480
X1	 0.7640	 0.5970
X2	 0.7750	 0.5890
X3	 0.7540	 0.5890
X4	 0.7610	 0.5970
X5	 0.7760	 0.5930
X6	 0.7240	 0.5530
X7	 0.7480	 0.5430
X8	 0.7370	 0.5420
X9	 0.7460	 0.5510
XA	 0.7540	 0.5610
XB	 0.7270	 0.5550
XC	 0.7370	 0.5540
XD	 0.7300	 0.5520
XE	 0.7260	 0.5500
XF	 0.7250	 0.5350
XG	 0.7400	 0.5520
XH	 0.7380	 0.5490
XI	 0.7300	 0.5460
XJ	 0.7190	 0.5540
XK	 0.7330	 0.5530
XL	 0.7250	 0.5460
XM	 0.7240	 0.5480
XN	 0.7200	 0.5520
XO	 0.7180	 0.5480
XP	 0.7250	 0.5470
XQ	 0.7330	 0.5510
XR	 0.7320	 0.5530
XS	 0.7270	 0.5410
XT	 0.7340	 0.5580
XU	 0.7450	 0.5520
XV	 0.7320	 0.5440
XW	 0.7290	 0.5480
XX	 0.7290	 0.5560
Xa	 0.7310	 0.5480
Xb	 0.7180	 0.5280
Xc	 0.7360	 0.5430
Xd	 0.7330	 0.5560
Xe	 0.7260	 0.5470
Xf	 0.7360	 0.5510

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Chain	Atom inclusion	Q-score
Xg	 0.7450	 0.5440
Xh	 0.7320	 0.5500
Xi	 0.7290	 0.5550
Xj	 0.7400	 0.5490
Xk	 0.7290	 0.5560
Xl	 0.7320	 0.5510
Xm	 0.7550	 0.5450
Xn	 0.7490	 0.5650
Xo	 0.7390	 0.5490
Xp	 0.7300	 0.5470
Xq	 0.7270	 0.5420
Xr	 0.7310	 0.5390
Xs	 0.7290	 0.5420
Xt	 0.7240	 0.5450
Xu	 0.7380	 0.5590
Xv	 0.7440	 0.5540
Xw	 0.7460	 0.5570
Xx	 0.7240	 0.5540
Xy	 0.7420	 0.5450
Xz	 0.7570	 0.5600