



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:45 PM UTC

PDB ID : 8VAN / pdb_00008van
EMDB ID : EMD-43096
Title : Structure of the E. coli clamp loader bound to the beta clamp in an Initial-Binding conformation
Authors : Landeck, J.T.; Pajak, J.; Kelch, B.A.
Deposited on : 2023-12-11
Resolution : 7.70 Å(reported)
Based on initial models : 3GLF, 2POL

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

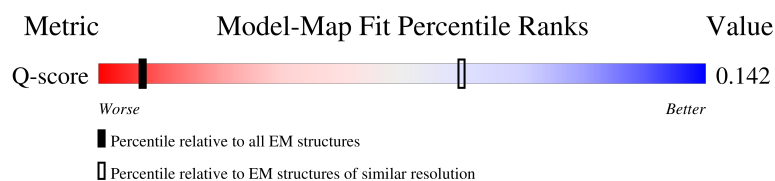
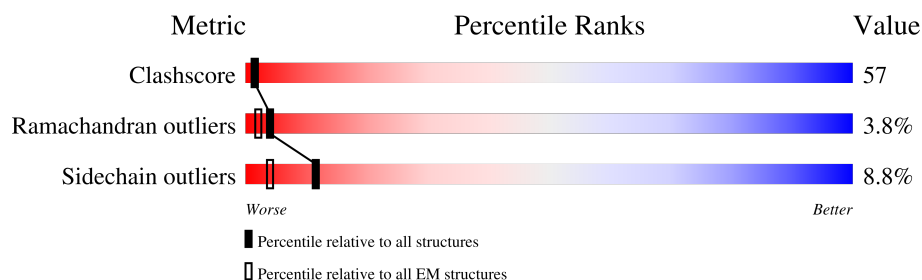
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.70 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	384 (7.20 - 8.20)

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	A	343	
2	B	376	
2	C	376	
2	D	376	

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Mol	Chain	Length	Quality of chain
3	E	337	
4	F	369	
4	G	369	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19433 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 DNA polymerase III subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	343	Total	C	N	O	S	0	0
			2726	1728	493	495	10		

- Molecule 2 is a protein called DNA polymerase III subunit tau.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	360	Total	C	N	O	S	0	0
			2796	1757	505	518	16		
2	C	365	Total	C	N	O	S	0	0
			2835	1783	513	523	16		
2	D	359	Total	C	N	O	S	0	0
			2786	1752	503	516	15		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	expression tag	UNP P06710
B	-1	PRO	-	expression tag	UNP P06710
B	0	HIS	-	expression tag	UNP P06710
C	-2	GLY	-	expression tag	UNP P06710
C	-1	PRO	-	expression tag	UNP P06710
C	0	HIS	-	expression tag	UNP P06710
D	-2	GLY	-	expression tag	UNP P06710
D	-1	PRO	-	expression tag	UNP P06710
D	0	HIS	-	expression tag	UNP P06710

- Molecule 3 is a protein called DNA polymerase III subunit delta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	334	Total	C	N	O	S	0	0
			2602	1655	468	466	13		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP P28631
E	-1	PRO	-	expression tag	UNP P28631
E	0	HIS	-	expression tag	UNP P28631

- Molecule 4 is a protein called Beta sliding clamp.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	366	Total	C	N	O	S	0	0
			2844	1786	498	541	19		
4	G	366	Total	C	N	O	S	0	0
			2844	1786	498	541	19		

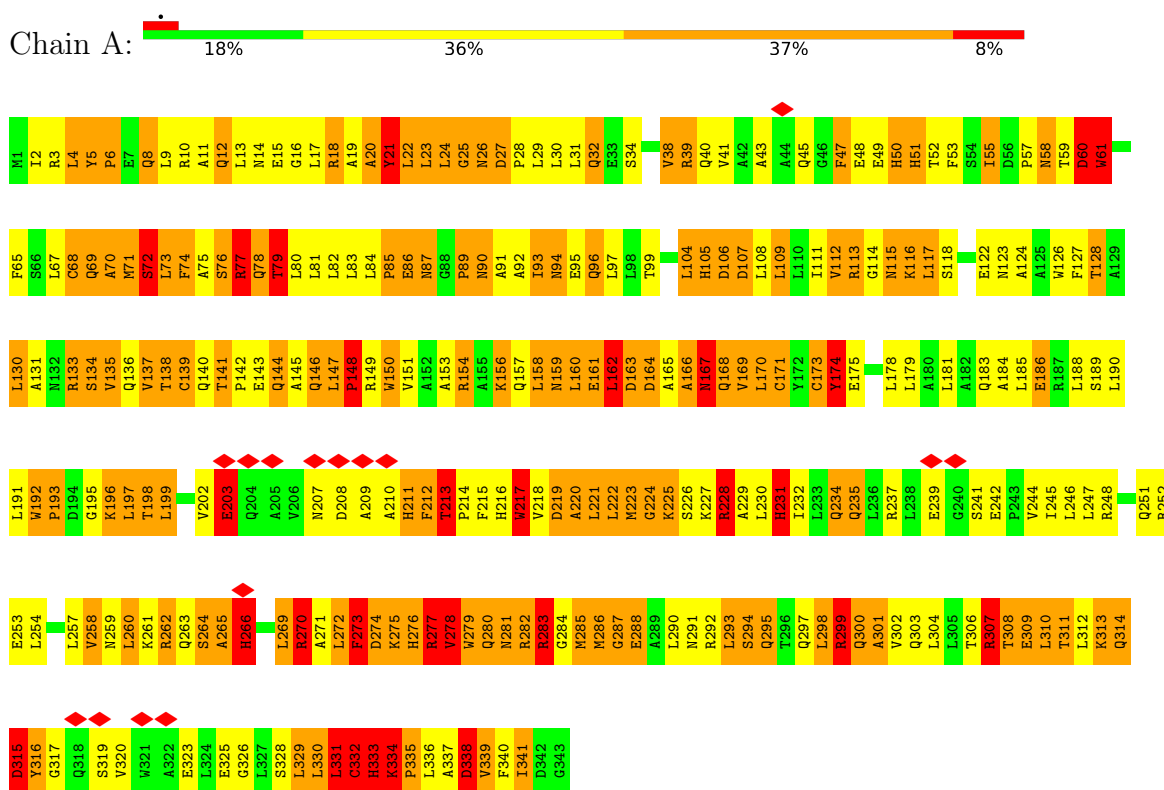
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-2	GLY	-	expression tag	UNP C3SLM2
F	-1	PRO	-	expression tag	UNP C3SLM2
F	0	HIS	-	expression tag	UNP C3SLM2
G	-2	GLY	-	expression tag	UNP C3SLM2
G	-1	PRO	-	expression tag	UNP C3SLM2
G	0	HIS	-	expression tag	UNP C3SLM2

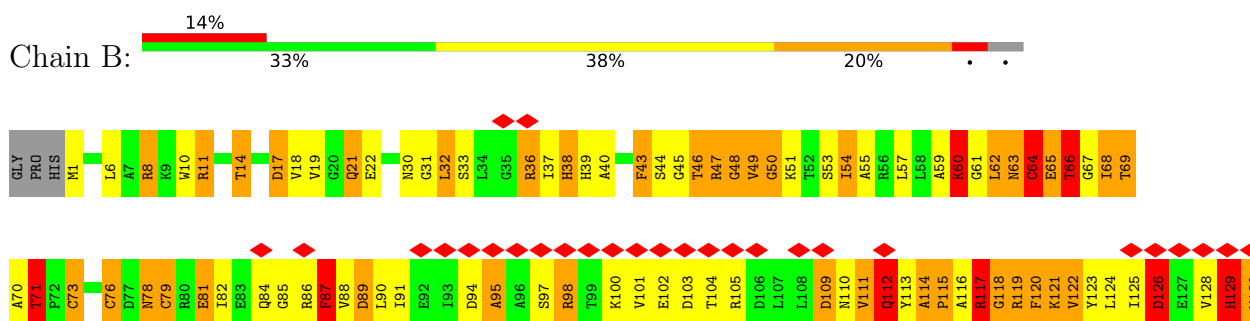
3 Residue-property plots

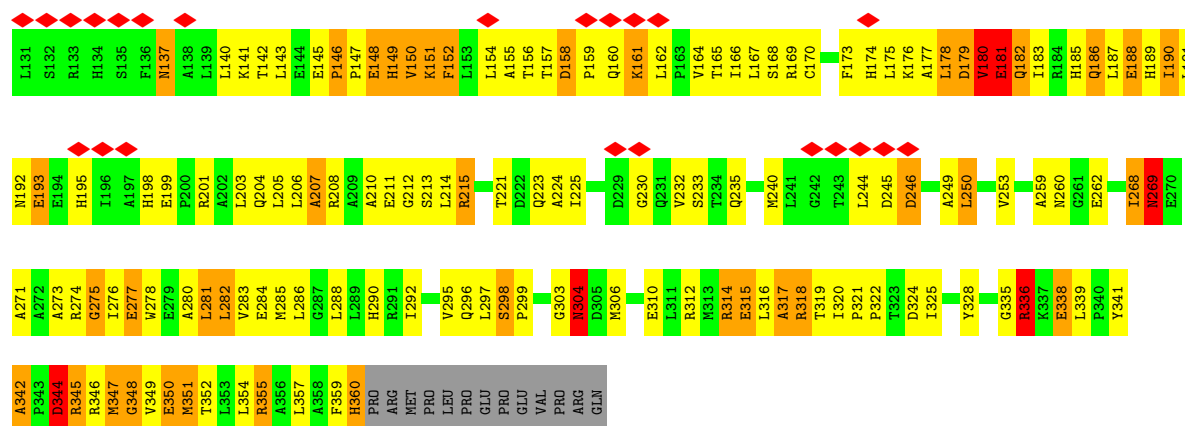
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA polymerase III subunit delta

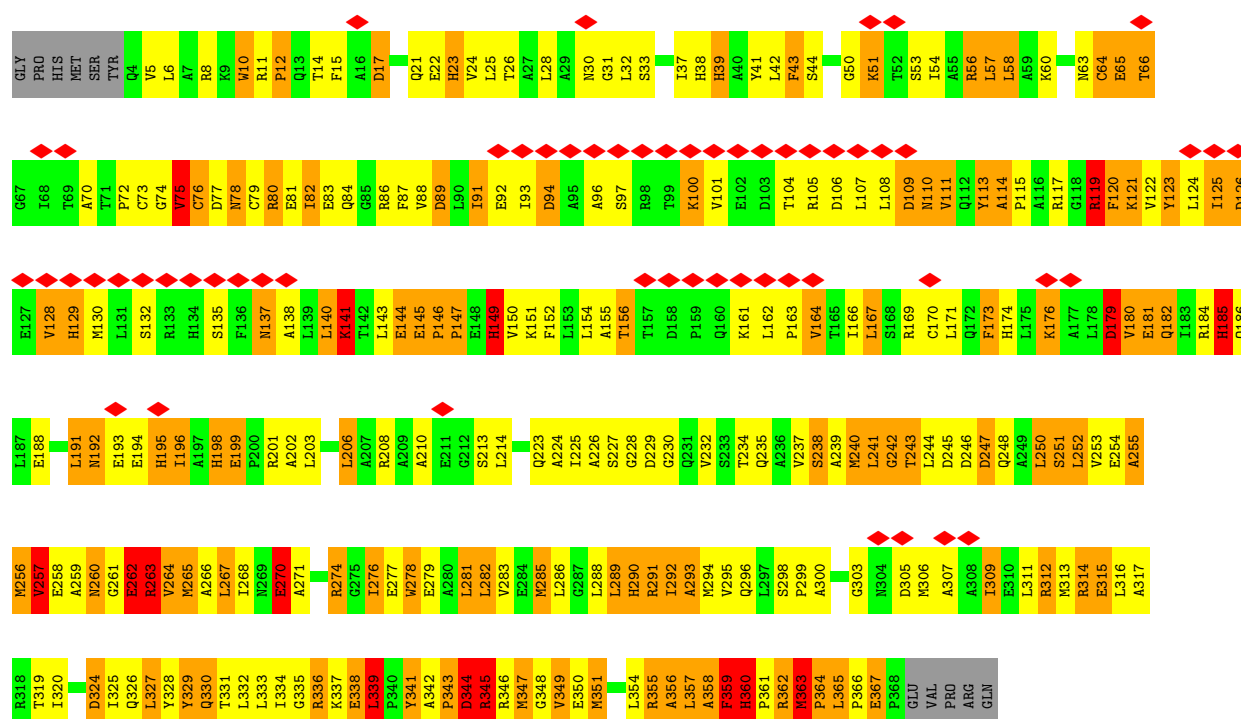


• Molecule 2: DNA polymerase III subunit tau

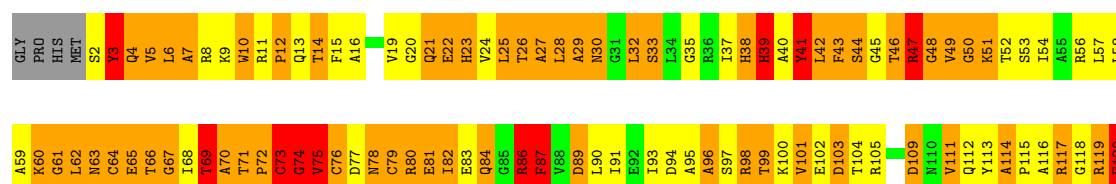


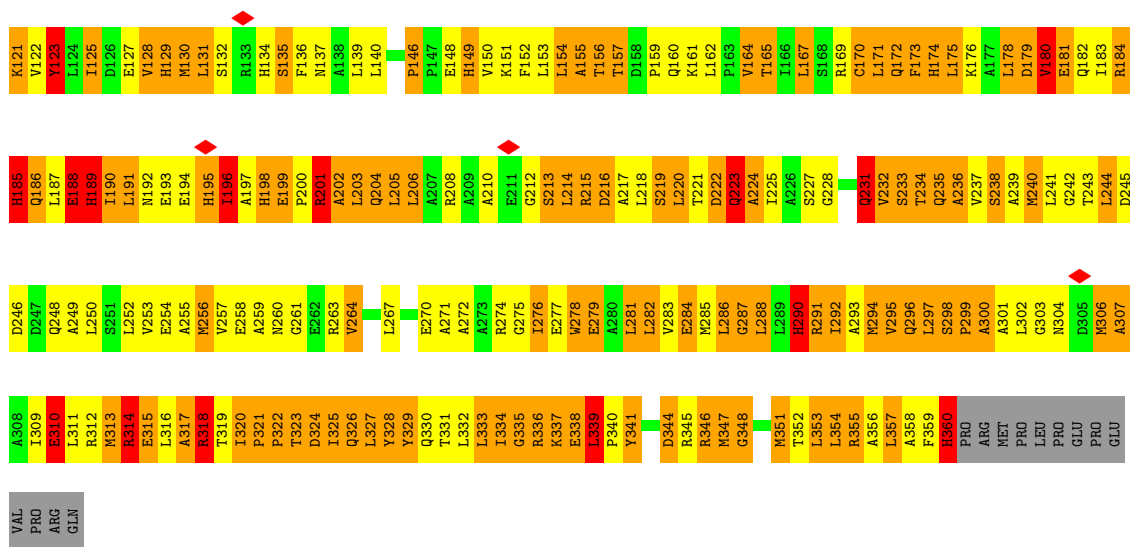


• Molecule 2: DNA polymerase III subunit tau

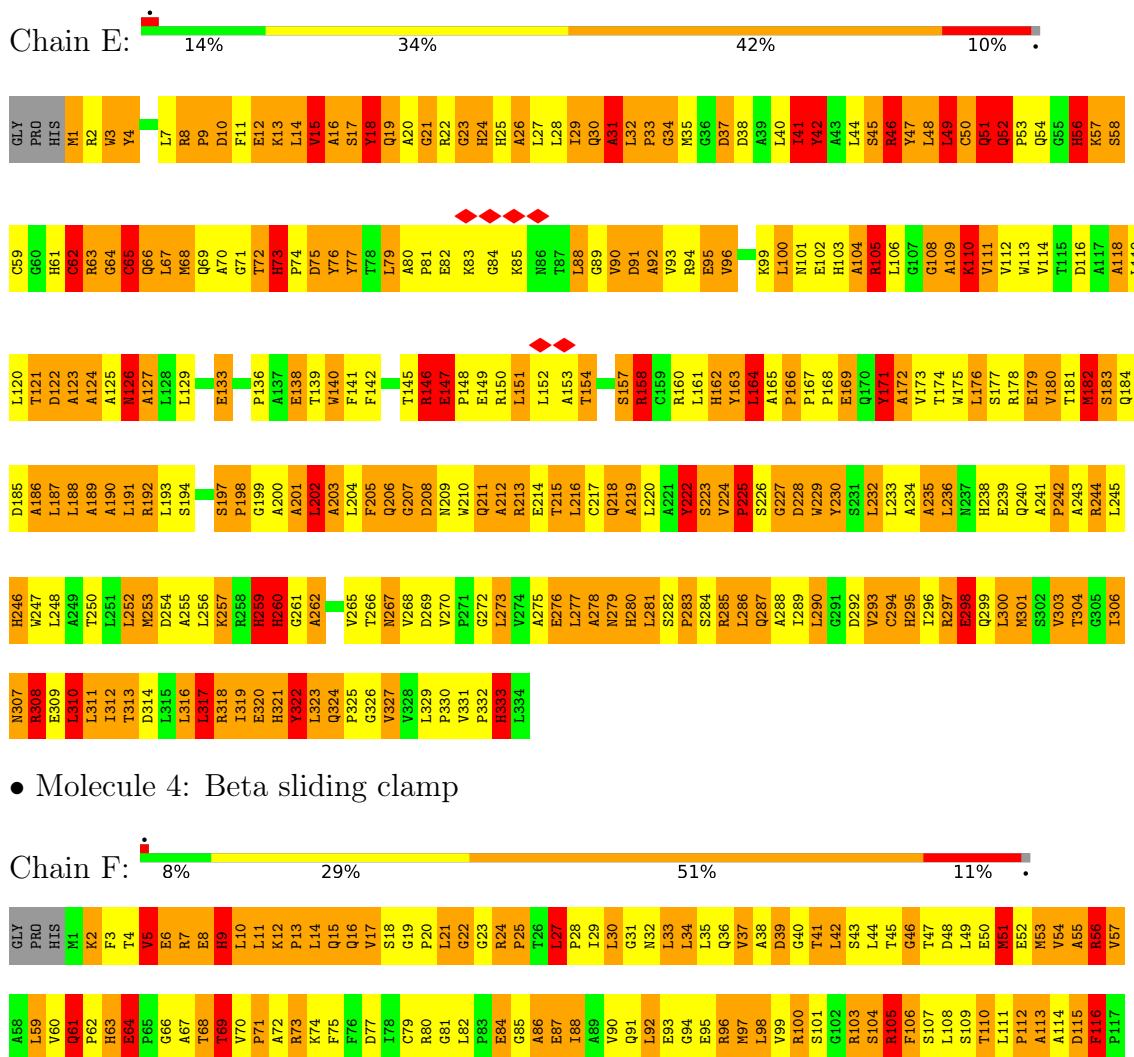


• Molecule 2: DNA polymerase III subunit tau

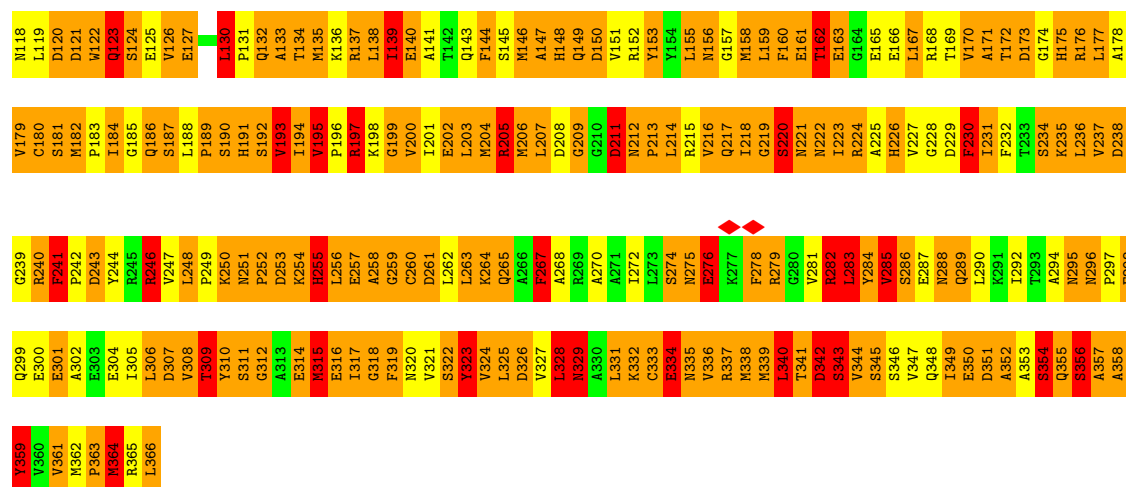




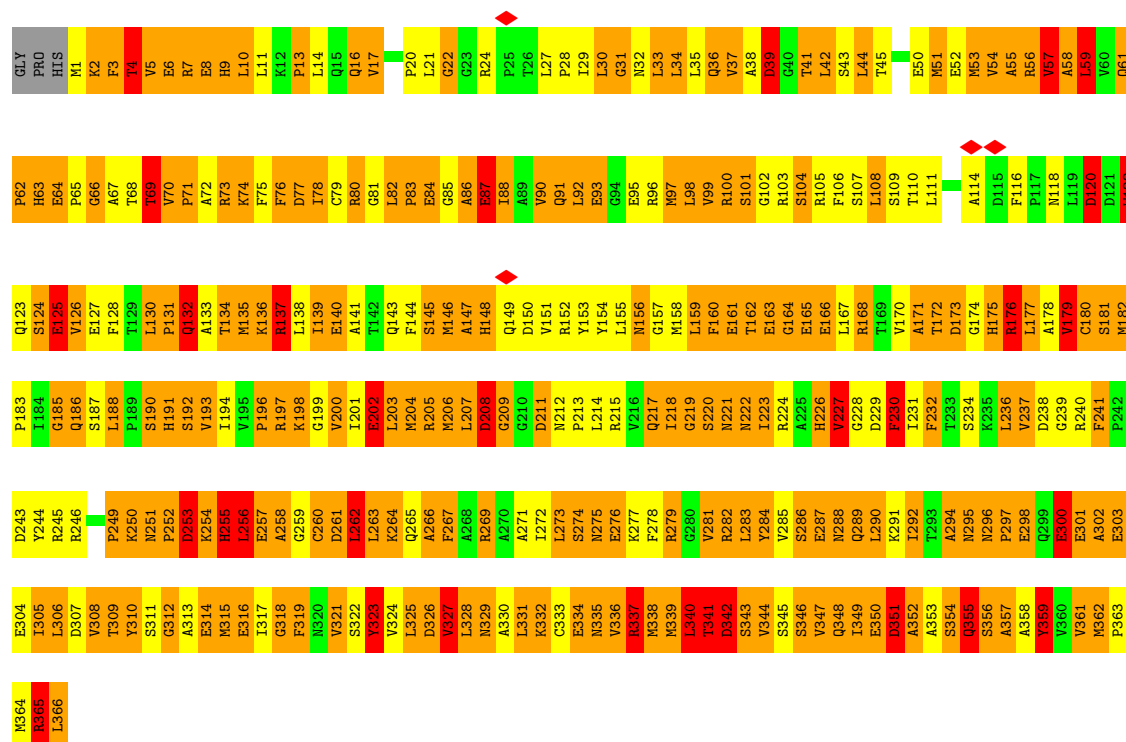
• Molecule 3: DNA polymerase III subunit delta'



• Molecule 4: Beta sliding clamp



● Molecule 4: Beta sliding clamp



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	44484	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.8	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.050	Depositor
Minimum map value	-0.238	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.084	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	261.0, 261.0, 261.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87, 0.87, 0.87	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	A	2.54	199/2775 (7.2%)	2.53	230/3769 (6.1%)
2	B	2.13	100/2840 (3.5%)	2.32	178/3848 (4.6%)
2	C	2.28	134/2882 (4.6%)	2.51	218/3908 (5.6%)
2	D	2.58	220/2830 (7.8%)	2.65	251/3835 (6.5%)
3	E	2.68	218/2667 (8.2%)	2.77	272/3639 (7.5%)
4	F	3.10	350/2893 (12.1%)	2.78	304/3915 (7.8%)
4	G	2.95	313/2893 (10.8%)	2.70	290/3915 (7.4%)
All	All	2.63	1534/19780 (7.8%)	2.61	1743/26829 (6.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	16
2	B	0	9
2	C	0	8
2	D	0	12
3	E	0	16
4	F	0	14
4	G	0	8
All	All	0	83

All (1534) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	221	ASN	CA-C	-22.16	1.37	1.52
4	G	354	SER	CA-C	-15.06	1.36	1.53
4	F	257	GLU	CA-C	-14.62	1.35	1.52
4	F	122	TRP	CA-C	-14.36	1.34	1.52
2	C	364	PRO	CA-C	-14.31	1.39	1.53
4	G	355	GLN	N-CA	-14.05	1.29	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	355	GLN	CA-C	-13.44	1.38	1.52
3	E	166	PRO	CA-C	-13.30	1.44	1.51
4	G	219	GLY	CA-C	-13.28	1.40	1.51
4	F	222	ASN	CA-C	-13.03	1.36	1.52
4	G	262	LEU	CA-C	-12.87	1.36	1.52
4	F	336	VAL	N-CA	-12.62	1.31	1.46
4	F	56	ARG	CA-C	-12.61	1.37	1.52
4	F	338	MET	CA-C	-12.52	1.37	1.52
4	G	338	MET	CA-C	-12.44	1.37	1.52
3	E	267	ASN	CA-C	-12.39	1.40	1.53
4	F	146	MET	CA-C	-12.16	1.37	1.52
3	E	319	ILE	CA-C	-12.13	1.38	1.52
4	F	337	ARG	CA-C	-12.04	1.38	1.52
3	E	280	HIS	CA-C	-12.03	1.36	1.52
4	G	356	SER	N-CA	-11.89	1.30	1.46
2	D	25	LEU	CA-C	-11.82	1.38	1.52
4	G	349	ILE	CA-C	-11.77	1.38	1.52
4	F	6	GLU	CA-C	-11.75	1.39	1.52
2	D	321	PRO	CA-C	-11.74	1.45	1.51
2	C	77	ASP	CA-C	-11.72	1.40	1.52
1	A	313	LYS	CA-C	-11.70	1.36	1.52
4	G	222	ASN	N-CA	-11.34	1.32	1.46
4	F	308	VAL	N-CA	-11.32	1.34	1.46
3	E	18	TYR	CA-C	-11.27	1.38	1.52
2	D	322	PRO	CA-C	-11.25	1.35	1.52
4	F	42	LEU	N-CA	-11.23	1.32	1.46
4	G	318	GLY	CA-C	-11.22	1.42	1.51
4	F	41	THR	CA-C	-11.07	1.39	1.52
4	F	230	PHE	CA-C	-11.05	1.38	1.53
1	A	282	ARG	CA-C	-11.04	1.37	1.52
3	E	281	LEU	CA-C	-11.03	1.39	1.52
3	E	229	TRP	CA-C	-11.01	1.38	1.52
2	D	291	ARG	CA-C	-11.00	1.38	1.52
1	A	278	VAL	CA-C	-10.99	1.38	1.52
4	F	121	ASP	CA-C	-10.96	1.39	1.52
4	F	335	ASN	CA-C	-10.95	1.39	1.52
1	A	276	HIS	CA-C	-10.94	1.47	1.52
4	F	223	ILE	N-CA	-10.89	1.33	1.46
4	F	358	ALA	CA-C	-10.88	1.39	1.52
4	G	336	VAL	N-CA	-10.86	1.33	1.46
4	G	230	PHE	CA-C	-10.74	1.38	1.53
4	G	134	THR	CA-C	-10.72	1.38	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	148	HIS	CA-C	-10.69	1.39	1.52
2	D	21	GLN	CA-C	-10.63	1.39	1.53
2	D	64	CYS	CA-C	-10.62	1.39	1.52
2	D	43	PHE	CA-C	-10.59	1.39	1.52
4	F	256	LEU	CA-C	-10.58	1.38	1.52
2	D	323	THR	N-CA	-10.54	1.33	1.46
1	A	293	LEU	CA-C	-10.48	1.39	1.52
4	F	340	LEU	CA-C	-10.48	1.38	1.53
4	F	289	GLN	CA-C	-10.45	1.40	1.52
4	G	70	VAL	CA-C	-10.44	1.44	1.52
3	E	16	ALA	CA-C	-10.43	1.39	1.52
1	A	115	ASN	CA-C	-10.37	1.40	1.52
4	F	251	ASN	CA-C	-10.36	1.40	1.52
4	G	335	ASN	CA-C	-10.35	1.40	1.52
4	G	97	MET	CA-C	-10.34	1.40	1.52
3	E	14	LEU	CA-C	-10.33	1.39	1.52
2	C	347	MET	CA-C	-10.33	1.39	1.52
4	G	350	GLU	CA-C	-10.30	1.39	1.52
4	F	189	PRO	CA-C	-10.29	1.41	1.52
4	F	350	GLU	CA-C	-10.29	1.39	1.52
4	F	97	MET	CA-C	-10.27	1.40	1.52
4	F	54	VAL	CA-C	-10.27	1.40	1.52
2	D	234	THR	CA-C	-10.25	1.39	1.52
4	F	192	SER	CA-C	-10.23	1.39	1.52
1	A	279	TRP	CA-C	-10.23	1.40	1.52
2	D	22	GLU	CA-C	-10.22	1.39	1.52
1	A	270	ARG	CA-C	-10.19	1.39	1.52
3	E	47	TYR	CA-C	-10.19	1.42	1.53
2	B	344	ASP	CA-C	-10.18	1.39	1.52
4	G	42	LEU	CA-C	-10.15	1.40	1.52
4	G	53	MET	CA-C	-10.12	1.42	1.53
4	F	10	LEU	N-CA	-10.02	1.33	1.46
2	D	120	PHE	CA-C	-9.97	1.39	1.52
3	E	281	LEU	N-CA	-9.96	1.33	1.46
4	F	349	ILE	CA-CB	-9.96	1.42	1.54
2	C	320	ILE	CA-C	-9.96	1.43	1.52
4	G	55	ALA	CA-C	-9.95	1.40	1.52
4	G	223	ILE	N-CA	-9.95	1.34	1.46
4	F	336	VAL	CA-C	-9.94	1.41	1.52
4	F	87	GLU	CA-C	-9.94	1.40	1.52
2	D	314	ARG	CA-C	-9.91	1.39	1.52
4	G	160	PHE	CA-C	-9.90	1.41	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	173	PHE	CA-C	-9.87	1.40	1.52
4	G	257	GLU	CA-C	-9.86	1.40	1.52
4	F	123	GLN	N-CA	-9.86	1.33	1.46
4	G	310	TYR	CA-C	-9.85	1.41	1.52
4	G	356	SER	CA-C	-9.83	1.39	1.52
3	E	110	LYS	CA-C	-9.80	1.40	1.52
4	F	55	ALA	CA-C	-9.77	1.40	1.52
4	G	36	GLN	N-CA	-9.77	1.33	1.46
4	G	59	LEU	CA-C	-9.73	1.39	1.52
4	G	290	LEU	N-CA	-9.71	1.33	1.46
1	A	78	GLN	CA-C	-9.70	1.40	1.52
2	D	63	ASN	CA-C	-9.68	1.41	1.53
4	F	9	HIS	CA-C	-9.66	1.39	1.52
4	G	57	VAL	CA-C	-9.64	1.40	1.52
4	G	340	LEU	CA-C	-9.64	1.40	1.52
3	E	303	VAL	CA-C	-9.62	1.41	1.52
4	G	337	ARG	N-CA	-9.62	1.34	1.46
3	E	109	ALA	CA-C	-9.57	1.40	1.53
4	F	337	ARG	N-CA	-9.57	1.34	1.46
4	F	349	ILE	N-CA	-9.54	1.35	1.46
4	G	350	GLU	N-CA	-9.54	1.33	1.45
4	G	348	GLN	CA-C	-9.51	1.41	1.52
4	G	182	MET	CA-C	-9.50	1.41	1.52
3	E	93	VAL	N-CA	-9.50	1.35	1.46
4	F	42	LEU	CA-C	-9.46	1.42	1.53
2	C	366	PRO	CA-C	-9.42	1.41	1.52
4	G	218	ILE	CA-C	-9.41	1.42	1.52
2	D	220	LEU	CA-C	-9.41	1.40	1.52
4	G	63	HIS	CA-C	-9.41	1.41	1.52
4	G	96	ARG	CA-C	-9.40	1.42	1.52
4	F	91	GLN	CA-C	-9.39	1.41	1.52
3	E	320	GLU	N-CA	-9.37	1.34	1.46
3	E	147	GLU	N-CA	-9.36	1.36	1.45
4	G	35	LEU	CA-C	-9.36	1.41	1.52
2	B	345	ARG	N-CA	-9.36	1.34	1.46
2	B	276	ILE	CA-C	-9.33	1.41	1.52
4	G	231	ILE	N-CA	-9.32	1.35	1.46
4	G	161	GLU	CA-C	-9.32	1.41	1.52
3	E	279	ASN	N-CA	-9.31	1.35	1.46
1	A	312	LEU	N-CA	-9.30	1.35	1.46
2	B	342	ALA	CA-C	-9.28	1.42	1.52
4	F	308	VAL	CA-C	-9.27	1.41	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	122	TRP	N-CA	-9.26	1.34	1.45
1	A	196	LYS	CA-C	-9.24	1.41	1.52
2	B	151	LYS	CA-C	-9.24	1.41	1.52
4	F	348	GLN	CA-C	-9.23	1.41	1.52
3	E	76	TYR	N-CA	-9.23	1.34	1.46
4	G	193	VAL	CA-C	-9.21	1.41	1.52
4	F	64	GLU	CA-C	-9.20	1.44	1.52
2	D	184	ARG	CA-C	-9.19	1.41	1.52
2	B	120	PHE	CA-C	-9.16	1.41	1.52
4	F	329	ASN	N-CA	-9.15	1.35	1.46
4	G	167	LEU	N-CA	-9.15	1.34	1.46
4	F	202	GLU	CA-C	-9.13	1.41	1.52
4	F	105	ARG	CA-C	-9.13	1.41	1.52
4	F	157	GLY	N-CA	-9.12	1.34	1.45
2	B	78	ASN	CA-C	-9.10	1.41	1.52
4	F	37	VAL	CA-C	-9.09	1.41	1.52
4	G	263	LEU	N-CA	-9.05	1.35	1.46
3	E	181	THR	CA-C	-9.04	1.41	1.52
4	F	38	ALA	CA-C	-9.03	1.41	1.52
1	A	25	GLY	CA-C	-9.02	1.42	1.52
4	F	230	PHE	N-CA	-9.02	1.35	1.46
4	F	288	ASN	N-CA	-9.02	1.34	1.46
3	E	46	ARG	CA-C	-9.01	1.40	1.52
3	E	216	LEU	N-CA	-9.01	1.35	1.46
4	F	359	TYR	CA-C	-9.00	1.42	1.52
4	G	44	LEU	CA-C	-8.99	1.40	1.52
4	G	342	ASP	CA-C	-8.97	1.41	1.52
4	G	191	HIS	CA-C	-8.96	1.41	1.52
4	G	54	VAL	CA-C	-8.95	1.41	1.52
4	F	124	SER	N-CA	-8.94	1.34	1.46
4	G	181	SER	CA-C	-8.94	1.41	1.52
2	C	80	ARG	CA-C	-8.90	1.41	1.52
4	F	274	SER	CA-C	-8.89	1.42	1.52
4	G	349	ILE	N-CA	-8.89	1.35	1.46
4	F	25	PRO	CA-C	-8.88	1.41	1.52
4	G	193	VAL	N-CA	-8.88	1.34	1.46
3	E	164	LEU	CA-C	-8.87	1.40	1.52
4	F	180	CYS	CA-C	-8.87	1.42	1.52
2	D	26	THR	CA-C	-8.85	1.41	1.52
4	F	219	GLY	CA-C	-8.82	1.39	1.51
4	F	96	ARG	CA-C	-8.81	1.41	1.52
4	F	309	THR	CA-C	-8.81	1.41	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	222	ASN	N-CA	-8.78	1.34	1.45
2	B	62	LEU	CA-C	-8.78	1.40	1.52
4	G	98	LEU	CA-C	-8.78	1.42	1.52
4	G	287	GLU	CA-C	-8.77	1.41	1.52
1	A	273	PHE	CA-C	-8.77	1.40	1.52
4	F	71	PRO	CA-C	-8.75	1.42	1.52
3	E	277	LEU	CA-C	-8.74	1.41	1.52
3	E	318	ARG	N-CA	-8.74	1.35	1.46
4	F	236	LEU	CA-C	-8.72	1.41	1.52
4	F	354	SER	CA-C	-8.72	1.41	1.52
4	F	334	GLU	N-CA	-8.72	1.37	1.46
4	G	55	ALA	N-CA	-8.71	1.35	1.45
2	D	276	ILE	CA-C	-8.69	1.40	1.52
4	G	357	ALA	CA-C	-8.69	1.41	1.52
2	D	188	GLU	CA-C	-8.68	1.41	1.52
1	A	311	THR	CA-C	-8.68	1.41	1.52
2	C	292	ILE	CA-C	-8.67	1.42	1.52
4	G	42	LEU	N-CA	-8.67	1.35	1.45
2	D	199	GLU	CA-C	-8.65	1.42	1.52
2	C	291	ARG	CA-C	-8.65	1.41	1.52
1	A	192	TRP	CA-C	-8.65	1.41	1.52
1	A	167	ASN	CA-C	-8.65	1.42	1.52
2	B	203	LEU	CA-C	-8.63	1.42	1.52
2	C	365	LEU	CA-C	-8.63	1.42	1.52
2	D	311	LEU	CA-C	-8.63	1.41	1.52
4	F	22	GLY	CA-C	-8.63	1.42	1.52
1	A	286	MET	N-CA	-8.62	1.34	1.46
2	D	81	GLU	CA-C	-8.60	1.40	1.52
4	F	188	LEU	CA-C	-8.60	1.42	1.52
4	F	163	GLU	CA-C	-8.59	1.42	1.52
2	D	27	ALA	CA-C	-8.58	1.40	1.52
4	F	35	LEU	CA-C	-8.57	1.42	1.52
3	E	13	LYS	CA-C	-8.57	1.41	1.52
2	C	367	GLU	CA-C	-8.57	1.41	1.52
4	F	349	ILE	CA-C	-8.57	1.43	1.52
4	G	310	TYR	N-CA	-8.54	1.35	1.46
4	F	36	GLN	CA-C	-8.54	1.43	1.52
4	G	37	VAL	CA-C	-8.54	1.43	1.52
4	F	97	MET	N-CA	-8.53	1.35	1.46
3	E	208	ASP	CA-C	-8.52	1.37	1.52
2	C	330	GLN	N-CA	-8.52	1.35	1.46
4	G	5	VAL	CA-C	-8.51	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	42	LEU	CA-C	-8.47	1.44	1.53
4	G	255	HIS	CA-C	-8.44	1.42	1.52
3	E	232	LEU	CA-C	-8.44	1.40	1.52
4	G	311	SER	CA-C	-8.43	1.42	1.52
4	G	41	THR	CA-C	-8.43	1.41	1.53
3	E	223	SER	CA-C	-8.42	1.42	1.52
4	F	328	LEU	CA-C	-8.41	1.42	1.52
4	F	337	ARG	CA-CB	-8.41	1.40	1.53
2	C	364	PRO	N-CA	-8.40	1.39	1.46
2	D	65	GLU	CA-C	-8.40	1.41	1.52
3	E	73	HIS	N-CA	-8.40	1.32	1.46
4	G	122	TRP	CA-C	-8.39	1.42	1.52
2	C	81	GLU	CA-C	-8.39	1.41	1.52
2	B	119	ARG	CA-C	-8.38	1.42	1.52
4	G	349	ILE	CA-CB	-8.37	1.43	1.54
4	G	202	GLU	CA-C	-8.36	1.41	1.52
4	G	337	ARG	CA-C	-8.35	1.42	1.52
4	G	352	ALA	N-CA	-8.35	1.35	1.46
4	G	163	GLU	CA-C	-8.34	1.42	1.52
1	A	147	LEU	N-CA	-8.32	1.38	1.46
2	D	80	ARG	CA-C	-8.32	1.41	1.52
4	G	96	ARG	N-CA	-8.31	1.36	1.46
3	E	140	TRP	CA-C	-8.30	1.42	1.52
4	F	296	ASN	CA-C	-8.30	1.44	1.52
4	G	286	SER	CA-C	-8.29	1.42	1.52
4	G	90	VAL	CA-C	-8.29	1.42	1.52
4	G	63	HIS	N-CA	-8.29	1.35	1.46
3	E	320	GLU	CA-C	-8.29	1.41	1.52
4	F	55	ALA	N-CA	-8.28	1.35	1.45
4	G	161	GLU	N-CA	-8.28	1.36	1.46
2	C	143	LEU	CA-C	-8.28	1.42	1.52
4	F	175	HIS	CA-C	-8.28	1.42	1.52
4	G	249	PRO	CA-C	-8.27	1.40	1.52
2	D	288	LEU	CA-C	-8.27	1.42	1.52
1	A	71	MET	CA-C	-8.27	1.42	1.52
2	D	317	ALA	CA-C	-8.26	1.42	1.52
3	E	147	GLU	CA-C	-8.26	1.43	1.52
4	G	219	GLY	N-CA	-8.26	1.36	1.45
2	D	201	ARG	CA-C	-8.24	1.42	1.52
4	F	240	ARG	CA-C	-8.23	1.42	1.52
2	C	314	ARG	CA-C	-8.23	1.42	1.52
3	E	31	ALA	CA-C	-8.22	1.41	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	332	CYS	CA-C	-8.21	1.42	1.52
4	F	353	ALA	CA-C	-8.21	1.44	1.53
2	D	76	CYS	N-CA	-8.20	1.35	1.46
3	E	32	LEU	CA-C	-8.19	1.42	1.52
4	F	181	SER	N-CA	-8.19	1.35	1.45
1	A	116	LYS	CA-C	-8.18	1.42	1.52
2	D	221	THR	N-CA	-8.14	1.36	1.46
1	A	283	ARG	N-CA	-8.12	1.36	1.46
4	F	84	GLU	CA-C	-8.10	1.42	1.53
2	C	262	GLU	CA-C	-8.10	1.43	1.52
1	A	253	GLU	CA-C	-8.10	1.41	1.52
3	E	110	LYS	N-CA	-8.09	1.36	1.45
2	B	63	ASN	CA-C	-8.09	1.42	1.53
4	G	73	ARG	CA-C	-8.06	1.42	1.52
4	G	336	VAL	CA-C	-8.05	1.42	1.52
1	A	79	THR	CA-C	-8.05	1.42	1.52
4	F	218	ILE	CA-C	-8.05	1.42	1.52
3	E	14	LEU	N-CA	-8.04	1.36	1.46
1	A	310	LEU	CA-C	-8.04	1.41	1.52
4	F	345	SER	CA-C	-8.03	1.42	1.52
2	B	151	LYS	N-CA	-8.02	1.35	1.46
4	F	36	GLN	N-CA	-8.02	1.37	1.46
2	B	91	ILE	CA-C	-8.02	1.43	1.52
2	B	150	VAL	CA-C	-8.01	1.43	1.52
4	F	253	ASP	CA-C	-7.99	1.42	1.52
1	A	70	ALA	CA-C	-7.98	1.42	1.52
1	A	333	HIS	N-CA	-7.97	1.35	1.46
2	C	357	LEU	CA-C	-7.97	1.42	1.52
3	E	224	VAL	CA-C	-7.96	1.44	1.52
4	G	175	HIS	CA-C	-7.96	1.43	1.52
3	E	296	ILE	CA-C	-7.95	1.42	1.52
2	C	341	TYR	CA-C	-7.94	1.41	1.52
1	A	78	GLN	N-CA	-7.93	1.35	1.45
2	D	41	TYR	CA-C	-7.93	1.43	1.52
4	G	8	GLU	CA-C	-7.92	1.42	1.52
1	A	315	ASP	CA-C	-7.92	1.41	1.52
4	F	98	LEU	N-CA	-7.92	1.36	1.46
1	A	270	ARG	N-CA	-7.91	1.35	1.46
4	F	301	GLU	CA-C	-7.90	1.43	1.52
4	G	311	SER	N-CA	-7.90	1.36	1.45
2	D	320	ILE	N-CA	-7.89	1.38	1.46
2	D	134	HIS	CA-C	-7.88	1.42	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	175	LEU	CA-C	-7.88	1.43	1.52
3	E	111	VAL	N-CA	-7.88	1.36	1.46
3	E	310	LEU	CA-C	-7.88	1.42	1.52
3	E	278	ALA	CA-C	-7.87	1.42	1.52
2	C	252	LEU	CA-C	-7.87	1.42	1.52
4	F	345	SER	N-CA	-7.85	1.35	1.45
2	B	282	LEU	CA-C	-7.85	1.42	1.52
2	C	76	CYS	CA-C	-7.84	1.46	1.53
2	C	320	ILE	N-CA	-7.83	1.39	1.46
4	F	158	MET	CA-C	-7.82	1.43	1.52
4	G	56	ARG	N-CA	-7.82	1.35	1.45
4	G	201	ILE	N-CA	-7.82	1.37	1.46
4	G	135	MET	N-CA	-7.82	1.36	1.46
2	B	64	CYS	CA-C	-7.81	1.42	1.53
2	C	358	ALA	CA-C	-7.80	1.41	1.52
2	D	76	CYS	CA-C	-7.80	1.42	1.52
1	A	4	LEU	CA-C	-7.80	1.43	1.52
4	G	162	THR	CA-C	-7.79	1.42	1.52
4	F	5	VAL	CA-C	-7.79	1.42	1.52
2	C	367	GLU	N-CA	-7.79	1.33	1.46
1	A	198	THR	N-CA	-7.78	1.36	1.46
3	E	73	HIS	CB-CG	-7.78	1.39	1.50
2	C	22	GLU	CA-C	-7.78	1.42	1.52
4	G	43	SER	CA-C	-7.77	1.43	1.52
4	F	169	THR	CA-C	-7.77	1.43	1.52
3	E	260	HIS	CA-C	-7.77	1.43	1.53
3	E	29	ILE	CA-C	-7.76	1.44	1.52
3	E	298	GLU	CA-C	-7.74	1.43	1.52
1	A	173	CYS	CA-C	-7.74	1.42	1.52
4	F	124	SER	CA-C	-7.74	1.43	1.52
4	F	156	ASN	CA-C	-7.73	1.43	1.53
3	E	229	TRP	NE1-CE2	-7.72	1.28	1.37
2	D	171	LEU	CA-C	-7.72	1.42	1.52
3	E	19	GLN	CA-C	-7.72	1.41	1.52
4	G	331	LEU	N-CA	-7.71	1.36	1.46
1	A	251	GLN	CA-C	-7.70	1.42	1.52
1	A	133	ARG	CA-C	-7.69	1.42	1.52
4	G	341	THR	CA-C	-7.69	1.43	1.52
2	D	279	GLU	CA-C	-7.68	1.43	1.52
3	E	215	THR	CA-C	-7.68	1.43	1.52
4	G	82	LEU	CA-C	-7.67	1.43	1.53
4	F	32	ASN	CA-C	-7.66	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	191	HIS	CA-C	-7.65	1.42	1.52
2	C	329	TYR	CA-C	-7.64	1.42	1.52
4	F	170	VAL	CA-C	-7.64	1.43	1.52
4	F	350	GLU	N-CA	-7.64	1.36	1.45
4	G	253	ASP	CA-C	-7.64	1.42	1.52
4	G	137	ARG	CA-C	-7.63	1.42	1.52
2	D	146	PRO	CA-C	-7.63	1.45	1.52
2	C	320	ILE	CA-CB	-7.62	1.47	1.54
4	F	315	MET	CA-C	-7.62	1.43	1.52
2	D	310	GLU	CA-C	-7.61	1.42	1.52
4	G	192	SER	CA-C	-7.61	1.42	1.52
3	E	48	LEU	CA-C	-7.60	1.42	1.52
3	E	20	ALA	CA-C	-7.60	1.42	1.52
4	G	136	LYS	N-CA	-7.60	1.37	1.46
1	A	106	ASP	CA-C	-7.59	1.42	1.52
2	C	263	ARG	CA-C	-7.59	1.43	1.52
2	D	98	ARG	CA-C	-7.58	1.43	1.52
2	D	28	LEU	N-CA	-7.58	1.36	1.46
4	F	18	SER	CA-C	-7.58	1.43	1.52
4	F	294	ALA	CA-C	-7.58	1.43	1.52
4	F	15	GLN	CA-C	-7.57	1.44	1.52
2	D	69	THR	CA-C	-7.57	1.43	1.52
4	G	254	LYS	CA-C	-7.56	1.43	1.52
2	C	145	GLU	N-CA	-7.56	1.39	1.46
4	G	45	THR	CA-C	-7.56	1.43	1.52
3	E	96	VAL	CA-C	-7.55	1.43	1.52
2	C	78	ASN	CA-C	-7.54	1.43	1.52
3	E	206	GLN	N-CA	-7.53	1.36	1.45
4	F	255	HIS	CA-C	-7.53	1.43	1.52
1	A	50	HIS	CA-C	-7.52	1.43	1.52
2	C	247	ASP	CA-C	-7.52	1.42	1.52
2	C	262	GLU	N-CA	-7.52	1.36	1.46
4	F	336	VAL	CA-CB	-7.52	1.44	1.54
3	E	311	LEU	N-CA	-7.51	1.37	1.46
2	D	64	CYS	N-CA	-7.51	1.36	1.46
4	G	328	LEU	CA-C	-7.50	1.43	1.52
3	E	75	ASP	CA-C	-7.49	1.43	1.52
4	F	267	PHE	CA-C	-7.47	1.43	1.52
1	A	108	LEU	CA-C	-7.47	1.43	1.53
3	E	47	TYR	N-CA	-7.46	1.36	1.46
3	E	205	PHE	CA-C	-7.46	1.42	1.52
4	G	92	LEU	CA-C	-7.46	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	201	ILE	CA-CB	-7.46	1.46	1.54
2	C	348	GLY	CA-C	-7.46	1.44	1.52
4	G	162	THR	N-CA	-7.46	1.36	1.46
4	G	74	LYS	CA-C	-7.45	1.43	1.52
2	D	235	GLN	N-CA	-7.45	1.37	1.46
4	F	193	VAL	CA-C	-7.45	1.43	1.52
4	G	91	GLN	CA-C	-7.44	1.43	1.52
3	E	257	LYS	CA-C	-7.44	1.43	1.52
2	D	325	ILE	CA-C	-7.43	1.44	1.52
1	A	156	LYS	CA-C	-7.42	1.42	1.52
2	B	120	PHE	N-CA	-7.42	1.36	1.46
4	F	207	LEU	CA-C	-7.41	1.43	1.52
3	E	189	ALA	CA-C	-7.41	1.42	1.52
4	G	43	SER	N-CA	-7.41	1.37	1.45
1	A	329	LEU	N-CA	-7.40	1.36	1.45
4	G	56	ARG	CA-C	-7.40	1.43	1.52
2	D	339	LEU	N-CA	-7.39	1.39	1.46
4	F	322	SER	CA-C	-7.39	1.42	1.52
4	F	92	LEU	CA-C	-7.39	1.43	1.52
2	B	190	ILE	CA-C	-7.39	1.43	1.52
4	G	274	SER	CA-C	-7.38	1.43	1.52
4	F	316	GLU	CA-C	-7.38	1.43	1.52
3	E	187	LEU	CA-C	-7.37	1.43	1.52
4	F	16	GLN	CA-C	-7.37	1.43	1.52
1	A	150	TRP	N-CA	-7.37	1.37	1.46
3	E	15	VAL	CA-C	-7.36	1.42	1.52
4	F	161	GLU	CA-C	-7.35	1.43	1.52
4	G	207	LEU	CA-C	-7.35	1.43	1.52
4	G	267	PHE	CA-C	-7.35	1.42	1.52
2	D	90	LEU	N-CA	-7.35	1.36	1.46
2	C	300	ALA	N-CA	-7.34	1.36	1.46
2	D	324	ASP	CA-C	-7.33	1.42	1.52
4	F	361	VAL	CA-C	-7.33	1.43	1.52
1	A	246	LEU	CA-C	-7.32	1.43	1.52
2	C	338	GLU	CA-C	-7.32	1.42	1.52
2	C	362	ARG	N-CA	-7.32	1.36	1.46
2	D	77	ASP	CA-C	-7.31	1.43	1.52
3	E	322	TYR	CA-C	-7.31	1.42	1.52
4	F	7	ARG	N-CA	-7.31	1.36	1.46
4	F	258	ALA	CA-C	-7.30	1.43	1.52
1	A	312	LEU	CA-C	-7.30	1.43	1.52
1	A	93	ILE	N-CA	-7.29	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	89	ASP	CA-C	-7.29	1.42	1.52
2	B	342	ALA	C-N	-7.28	1.26	1.34
4	G	57	VAL	N-CA	-7.28	1.37	1.46
4	G	186	GLN	N-CA	-7.28	1.36	1.45
2	D	10	TRP	CA-C	-7.27	1.43	1.52
2	D	76	CYS	C-N	-7.27	1.24	1.33
4	G	308	VAL	CA-C	-7.27	1.43	1.52
4	F	290	LEU	N-CA	-7.27	1.37	1.46
1	A	16	GLY	CA-C	-7.27	1.43	1.51
2	C	332	LEU	CA-C	-7.25	1.43	1.52
2	C	363	MET	CA-C	-7.25	1.44	1.52
4	G	341	THR	N-CA	-7.24	1.37	1.46
3	E	228	ASP	C-N	-7.23	1.23	1.33
4	G	359	TYR	CA-C	-7.22	1.43	1.52
4	F	262	LEU	CA-C	-7.22	1.43	1.52
4	F	338	MET	N-CA	-7.22	1.37	1.46
2	B	193	GLU	CA-C	-7.21	1.42	1.52
4	F	82	LEU	CA-C	-7.21	1.44	1.53
4	F	54	VAL	N-CA	-7.20	1.38	1.46
3	E	17	SER	N-CA	-7.20	1.37	1.46
1	A	10	ARG	CA-C	-7.20	1.43	1.52
1	A	144	GLN	CA-C	-7.20	1.43	1.52
2	B	179	ASP	CA-C	-7.20	1.44	1.52
2	B	276	ILE	N-CA	-7.19	1.37	1.46
1	A	161	GLU	CA-C	-7.18	1.43	1.52
3	E	90	VAL	CA-C	-7.18	1.42	1.52
4	G	345	SER	CA-C	-7.17	1.43	1.52
2	C	339	LEU	N-CA	-7.17	1.39	1.46
4	G	36	GLN	CA-C	-7.17	1.43	1.52
2	C	282	LEU	CA-C	-7.17	1.43	1.52
3	E	208	ASP	C-O	-7.17	1.13	1.24
4	F	283	LEU	CA-C	-7.17	1.44	1.52
3	E	33	PRO	N-CA	-7.16	1.38	1.47
4	G	17	VAL	N-CA	-7.16	1.37	1.46
1	A	14	ASN	CA-C	-7.16	1.43	1.52
4	F	275	ASN	N-CA	-7.15	1.36	1.46
4	F	264	LYS	CA-C	-7.15	1.43	1.52
3	E	309	GLU	CA-C	-7.14	1.43	1.52
2	B	233	SER	CA-C	-7.14	1.43	1.52
4	G	295	ASN	CA-C	-7.13	1.44	1.52
4	G	203	LEU	CA-C	-7.13	1.43	1.52
4	F	75	PHE	N-CA	-7.12	1.37	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	315	MET	N-CA	-7.12	1.36	1.46
2	D	153	LEU	CA-C	-7.12	1.43	1.52
4	F	66	GLY	CA-C	-7.12	1.43	1.52
1	A	77	ARG	CA-C	-7.11	1.43	1.52
4	F	127	GLU	CA-C	-7.11	1.44	1.52
2	C	356	ALA	CA-C	-7.10	1.43	1.52
3	E	287	GLN	N-CA	-7.10	1.37	1.46
4	F	130	LEU	CA-C	-7.10	1.45	1.53
2	B	245	ASP	C-N	7.10	1.43	1.33
3	E	67	LEU	CA-C	-7.10	1.42	1.52
3	E	49	LEU	CA-C	-7.09	1.42	1.52
4	G	132	GLN	N-CA	-7.09	1.37	1.46
4	F	44	LEU	CA-C	-7.09	1.44	1.52
2	D	162	LEU	N-CA	-7.09	1.36	1.46
1	A	340	PHE	CA-C	-7.08	1.44	1.52
2	D	313	MET	CA-C	-7.08	1.43	1.52
4	G	180	CYS	CA-C	-7.08	1.44	1.52
3	E	308	ARG	CA-C	-7.08	1.44	1.52
4	F	17	VAL	CA-CB	-7.08	1.44	1.54
4	G	323	TYR	CA-C	-7.07	1.43	1.52
4	G	353	ALA	CA-C	-7.07	1.42	1.52
2	C	213	SER	CA-C	-7.06	1.44	1.52
4	G	200	VAL	CA-C	-7.06	1.42	1.52
2	C	294	MET	CA-C	-7.06	1.43	1.52
4	G	217	GLN	CA-C	-7.06	1.43	1.52
2	C	56	ARG	CA-C	-7.05	1.43	1.52
1	A	291	ASN	CA-C	-7.05	1.43	1.52
4	F	268	ALA	N-CA	-7.04	1.38	1.46
1	A	149	ARG	CA-C	-7.04	1.43	1.52
1	A	272	LEU	CA-C	-7.04	1.43	1.52
3	E	4	TYR	CA-C	-7.04	1.44	1.52
3	E	222	TYR	N-CA	-7.04	1.37	1.46
4	G	54	VAL	CA-CB	-7.04	1.45	1.54
4	G	44	LEU	N-CA	-7.04	1.37	1.46
4	F	201	ILE	CA-CB	-7.04	1.46	1.54
2	D	297	LEU	CA-C	-7.03	1.43	1.52
1	A	17	LEU	CA-C	-7.03	1.44	1.52
2	D	292	ILE	CA-CB	-7.03	1.46	1.54
4	F	257	GLU	N-CA	-7.02	1.37	1.45
4	G	124	SER	CA-C	-7.02	1.43	1.52
3	E	180	VAL	CA-C	-7.02	1.43	1.52
4	G	84	GLU	CA-C	-7.02	1.43	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	139	THR	CA-C	-7.01	1.44	1.52
4	G	152	ARG	CA-CB	7.01	1.62	1.53
4	G	348	GLN	N-CA	-7.00	1.37	1.46
3	E	317	LEU	CA-C	-7.00	1.43	1.52
1	A	23	LEU	CA-C	-7.00	1.44	1.52
4	F	8	GLU	CA-C	-7.00	1.42	1.52
1	A	269	LEU	CA-C	-6.99	1.43	1.52
2	C	289	LEU	CA-C	-6.98	1.43	1.52
2	D	196	ILE	CA-C	-6.98	1.43	1.52
4	F	162	THR	CA-C	-6.98	1.44	1.52
2	D	353	LEU	CA-C	-6.98	1.43	1.52
4	F	300	GLU	CA-C	-6.96	1.44	1.52
1	A	258	VAL	CA-C	-6.96	1.44	1.52
4	G	258	ALA	CA-C	-6.96	1.44	1.52
4	F	176	ARG	N-CA	-6.96	1.37	1.46
4	G	93	GLU	CA-C	-6.95	1.44	1.52
2	B	69	THR	CA-C	-6.95	1.44	1.52
3	E	284	SER	CA-C	-6.95	1.43	1.52
4	G	339	MET	CA-C	-6.95	1.44	1.53
2	B	274	ARG	CA-C	-6.95	1.44	1.53
2	D	315	GLU	CA-C	-6.95	1.44	1.52
3	E	24	HIS	N-CA	-6.95	1.37	1.46
2	D	72	PRO	CA-CB	-6.94	1.44	1.53
3	E	102	GLU	CA-C	-6.94	1.44	1.52
4	G	185	GLY	CA-C	-6.94	1.40	1.51
3	E	56	HIS	N-CA	-6.93	1.37	1.46
2	B	149	HIS	CA-C	-6.93	1.43	1.52
4	F	256	LEU	N-CA	-6.93	1.37	1.46
4	G	227	VAL	CA-CB	-6.93	1.48	1.55
2	C	203	LEU	CA-C	-6.93	1.44	1.52
2	D	131	LEU	CA-C	-6.93	1.44	1.52
2	C	144	GLU	CA-C	-6.92	1.43	1.52
4	G	64	GLU	N-CA	-6.92	1.40	1.45
2	D	130	MET	CA-C	-6.92	1.43	1.52
4	F	356	SER	N-CA	-6.91	1.37	1.46
2	D	84	GLN	CA-C	-6.91	1.44	1.52
1	A	158	LEU	CA-C	-6.90	1.43	1.52
2	C	75	VAL	CA-C	-6.90	1.43	1.52
4	G	362	MET	CA-C	-6.90	1.44	1.52
3	E	297	ARG	N-CA	-6.89	1.38	1.46
4	F	312	GLY	CA-C	-6.89	1.41	1.52
4	F	88	ILE	N-CA	-6.88	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	354	SER	N-CA	-6.88	1.37	1.46
1	A	77	ARG	N-CA	-6.87	1.37	1.45
4	G	86	ALA	N-CA	-6.87	1.37	1.46
2	D	8	ARG	CA-C	-6.87	1.44	1.52
4	F	104	SER	N-CA	-6.87	1.38	1.46
3	E	188	LEU	N-CA	-6.87	1.38	1.46
4	F	57	VAL	CA-C	-6.87	1.43	1.52
4	F	221	ASN	N-CA	-6.86	1.39	1.46
4	G	339	MET	N-CA	-6.86	1.37	1.46
1	A	25	GLY	N-CA	-6.86	1.38	1.45
4	G	105	ARG	CA-C	-6.85	1.44	1.52
1	A	171	CYS	CA-C	-6.85	1.44	1.52
2	C	359	PHE	N-CA	-6.84	1.37	1.46
2	B	262	GLU	CA-C	-6.84	1.43	1.52
4	F	190	SER	N-CA	-6.84	1.37	1.46
4	F	53	MET	CA-C	-6.84	1.44	1.52
2	C	315	GLU	N-CA	-6.83	1.38	1.46
4	F	359	TYR	N-CA	-6.83	1.38	1.46
4	G	87	GLU	CA-C	-6.82	1.44	1.52
4	F	332	LYS	N-CA	-6.81	1.38	1.46
2	C	250	LEU	CA-C	-6.81	1.44	1.52
4	F	222	ASN	C-N	-6.81	1.24	1.33
2	B	121	LYS	N-CA	-6.80	1.37	1.46
2	D	181	GLU	N-CA	-6.80	1.38	1.46
4	F	59	LEU	N-CA	-6.80	1.38	1.46
4	G	72	ALA	CA-C	-6.79	1.44	1.52
4	G	97	MET	N-CA	-6.78	1.38	1.46
4	G	198	LYS	CA-C	-6.78	1.44	1.52
4	F	300	GLU	N-CA	-6.77	1.38	1.46
4	F	107	SER	CA-C	-6.77	1.45	1.52
1	A	106	ASP	N-CA	-6.77	1.37	1.46
3	E	321	HIS	CB-CG	-6.77	1.40	1.50
2	D	26	THR	N-CA	-6.76	1.38	1.46
3	E	267	ASN	N-CA	-6.76	1.38	1.46
4	F	254	LYS	CA-C	-6.76	1.44	1.52
2	D	189	HIS	N-CA	-6.76	1.38	1.46
2	D	42	LEU	CA-C	-6.76	1.44	1.52
4	F	201	ILE	N-CA	-6.75	1.38	1.46
4	F	132	GLN	N-CA	-6.75	1.37	1.46
3	E	192	ARG	CA-C	-6.75	1.44	1.52
4	F	341	THR	N-CA	-6.75	1.37	1.45
3	E	138	GLU	CA-C	-6.75	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	14	ASN	N-CA	-6.74	1.38	1.46
4	G	230	PHE	N-CA	-6.74	1.36	1.45
4	G	351	ASP	N-CA	-6.74	1.37	1.46
4	F	139	ILE	CA-C	-6.73	1.44	1.52
2	D	187	LEU	CA-C	-6.72	1.44	1.52
2	D	277	GLU	N-CA	-6.72	1.37	1.46
2	C	258	GLU	N-CA	-6.71	1.37	1.46
4	F	314	GLU	CA-C	-6.71	1.44	1.52
1	A	24	LEU	CA-C	-6.71	1.44	1.52
4	F	126	VAL	CA-C	-6.71	1.44	1.52
2	D	174	HIS	N-CA	-6.71	1.38	1.46
4	G	145	SER	CA-C	-6.71	1.46	1.53
4	G	194	ILE	CA-C	-6.70	1.44	1.52
4	G	222	ASN	CA-C	-6.70	1.44	1.52
4	G	99	VAL	CA-C	-6.69	1.44	1.52
2	D	294	MET	CA-C	-6.69	1.44	1.52
1	A	79	THR	N-CA	-6.69	1.37	1.45
2	D	336	ARG	CA-C	-6.69	1.44	1.52
3	E	93	VAL	CA-CB	-6.69	1.47	1.54
2	D	170	CYS	CA-C	-6.68	1.44	1.52
3	E	306	ILE	CA-CB	-6.68	1.46	1.54
1	A	303	GLN	N-CA	-6.67	1.37	1.46
3	E	51	GLN	N-CA	-6.67	1.37	1.46
1	A	283	ARG	CA-CB	-6.67	1.42	1.53
1	A	20	ALA	CA-C	-6.67	1.44	1.53
1	A	170	LEU	N-CA	-6.67	1.37	1.46
2	C	194	GLU	CA-C	-6.66	1.44	1.53
2	C	281	LEU	N-CA	-6.66	1.38	1.46
4	G	135	MET	CA-C	-6.66	1.43	1.52
4	F	240	ARG	N-CA	-6.66	1.37	1.46
2	D	200	PRO	CA-C	-6.66	1.42	1.52
4	F	203	LEU	CA-C	-6.65	1.44	1.52
4	G	156	ASN	CA-C	-6.65	1.43	1.52
4	F	263	LEU	N-CA	-6.64	1.38	1.46
1	A	90	ASN	CA-C	-6.64	1.43	1.53
4	G	276	GLU	CA-C	-6.64	1.43	1.52
4	G	291	LYS	N-CA	-6.64	1.37	1.46
4	G	313	ALA	CA-C	-6.63	1.44	1.52
2	C	198	HIS	N-CA	-6.63	1.38	1.46
2	D	351	MET	CA-C	-6.63	1.44	1.52
1	A	264	SER	CA-C	-6.63	1.44	1.52
1	A	131	ALA	CA-C	-6.62	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	309	THR	N-CA	-6.62	1.37	1.46
2	B	344	ASP	N-CA	-6.62	1.37	1.46
4	G	258	ALA	N-CA	-6.62	1.37	1.45
2	B	90	LEU	N-CA	-6.62	1.38	1.46
2	D	295	VAL	N-CA	-6.61	1.38	1.46
2	C	299	PRO	CA-C	-6.61	1.46	1.53
4	F	110	THR	CA-C	-6.61	1.44	1.52
3	E	206	GLN	CA-C	-6.60	1.43	1.53
1	A	60	ASP	N-CA	-6.60	1.37	1.46
1	A	3	ARG	CA-C	-6.60	1.44	1.52
2	D	94	ASP	CA-CB	6.60	1.61	1.53
2	D	298	SER	N-CA	-6.60	1.36	1.46
4	F	160	PHE	CA-C	-6.59	1.44	1.52
4	G	329	ASN	N-CA	-6.59	1.37	1.46
1	A	242	GLU	CA-C	-6.59	1.45	1.53
4	F	310	TYR	N-CA	-6.59	1.37	1.45
2	D	82	ILE	CA-C	-6.58	1.44	1.52
3	E	225	PRO	CA-C	-6.58	1.43	1.52
4	F	67	ALA	CA-C	-6.58	1.44	1.52
4	G	62	PRO	CA-C	-6.58	1.43	1.52
2	B	60	LYS	CA-C	-6.57	1.44	1.52
4	F	166	GLU	CA-C	-6.56	1.44	1.52
4	G	75	PHE	N-CA	-6.56	1.38	1.46
3	E	223	SER	N-CA	-6.56	1.38	1.46
2	D	62	LEU	CA-C	-6.56	1.44	1.52
2	D	185	HIS	N-CA	-6.56	1.38	1.46
4	F	323	TYR	N-CA	-6.56	1.38	1.46
1	A	313	LYS	N-CA	-6.55	1.37	1.46
4	F	176	ARG	CA-C	-6.55	1.44	1.52
2	D	101	VAL	CA-C	-6.54	1.44	1.52
2	B	118	GLY	CA-C	-6.54	1.43	1.52
2	D	48	GLY	CA-C	-6.54	1.44	1.51
3	E	185	ASP	CA-C	-6.54	1.43	1.52
2	C	196	ILE	CA-C	-6.53	1.44	1.52
3	E	282	SER	N-CA	-6.53	1.38	1.45
4	F	140	GLU	N-CA	-6.53	1.38	1.46
1	A	225	LYS	CA-C	-6.52	1.44	1.52
1	A	293	LEU	N-CA	-6.52	1.38	1.46
1	A	276	HIS	N-CA	-6.52	1.38	1.45
3	E	229	TRP	N-CA	-6.52	1.37	1.46
4	F	43	SER	CA-C	-6.52	1.44	1.52
4	G	283	LEU	CA-C	-6.52	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	75	VAL	C-N	-6.51	1.25	1.33
1	A	333	HIS	CA-C	-6.50	1.44	1.52
1	A	12	GLN	CA-C	-6.50	1.43	1.52
2	D	160	GLN	CA-C	-6.50	1.44	1.52
3	E	300	LEU	CA-C	-6.50	1.43	1.52
2	C	201	ARG	CA-C	-6.50	1.44	1.52
1	A	271	ALA	N-CA	-6.49	1.38	1.46
4	F	108	LEU	CA-C	-6.49	1.44	1.53
2	C	359	PHE	CA-C	-6.49	1.44	1.52
3	E	301	MET	N-CA	-6.49	1.38	1.46
4	F	195	VAL	CA-C	-6.48	1.47	1.52
4	F	57	VAL	N-CA	-6.48	1.38	1.46
4	F	342	ASP	N-CA	-6.48	1.37	1.46
4	G	64	GLU	CA-C	-6.48	1.45	1.52
4	F	299	GLN	CA-C	-6.48	1.45	1.53
2	B	316	LEU	CA-C	-6.48	1.44	1.52
2	B	318	ARG	CA-C	-6.48	1.43	1.52
1	A	280	GLN	N-CA	-6.47	1.38	1.46
3	E	294	CYS	C-O	-6.47	1.16	1.24
1	A	277	ARG	CA-C	-6.47	1.45	1.52
2	C	251	SER	N-CA	-6.47	1.38	1.46
2	D	198	HIS	CA-C	-6.47	1.44	1.53
4	F	316	GLU	N-CA	-6.47	1.38	1.46
3	E	285	ARG	N-CA	-6.46	1.37	1.46
4	F	331	LEU	N-CA	-6.46	1.38	1.46
4	G	177	LEU	N-CA	-6.46	1.37	1.45
4	G	176	ARG	CA-C	-6.46	1.44	1.52
2	B	213	SER	CA-C	-6.45	1.44	1.52
4	G	331	LEU	CA-C	-6.45	1.45	1.52
2	B	47	ARG	N-CA	-6.45	1.37	1.46
3	E	111	VAL	CA-C	-6.44	1.44	1.52
3	E	182	MET	N-CA	-6.44	1.37	1.46
1	A	114	GLY	CA-C	-6.44	1.43	1.52
4	F	237	VAL	CA-C	-6.44	1.44	1.52
4	G	357	ALA	N-CA	-6.44	1.38	1.46
4	F	86	ALA	CA-C	-6.43	1.44	1.52
4	F	134	THR	CA-C	-6.43	1.44	1.52
1	A	168	GLN	CA-C	-6.43	1.44	1.52
4	F	216	VAL	CA-C	-6.43	1.44	1.52
2	B	186	GLN	CA-C	-6.43	1.44	1.52
2	D	216	ASP	CA-C	-6.43	1.44	1.52
4	F	234	SER	CA-C	-6.42	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	147	PRO	CA-C	-6.41	1.44	1.52
4	G	197	ARG	N-CA	-6.41	1.38	1.46
4	G	221	ASN	CA-C	-6.41	1.44	1.52
2	B	317	ALA	CA-C	-6.41	1.44	1.52
3	E	297	ARG	CA-C	-6.41	1.44	1.52
4	G	176	ARG	N-CA	-6.40	1.38	1.46
2	D	316	LEU	N-CA	-6.40	1.38	1.46
4	F	217	GLN	N-CA	-6.40	1.38	1.46
4	F	317	ILE	N-CA	-6.40	1.39	1.46
2	D	72	PRO	CA-C	-6.39	1.43	1.52
2	C	81	GLU	N-CA	-6.39	1.38	1.46
4	F	12	LYS	C-N	-6.39	1.26	1.34
4	F	74	LYS	CA-C	-6.39	1.44	1.52
4	G	131	PRO	CA-C	-6.39	1.44	1.52
1	A	271	ALA	CA-C	-6.39	1.44	1.52
4	G	125	GLU	CA-C	-6.39	1.44	1.53
1	A	245	ILE	CA-C	-6.38	1.43	1.52
3	E	12	GLU	CA-C	-6.38	1.44	1.52
4	G	73	ARG	N-CA	-6.38	1.38	1.46
4	F	162	THR	N-CA	-6.36	1.38	1.46
1	A	197	LEU	CA-C	-6.36	1.44	1.52
2	D	327	LEU	CA-C	-6.36	1.44	1.52
3	E	198	PRO	CA-C	-6.35	1.46	1.52
2	C	140	LEU	CA-C	-6.35	1.44	1.52
4	G	322	SER	CA-C	-6.35	1.44	1.52
1	A	105	HIS	CA-C	-6.35	1.44	1.53
3	E	50	CYS	CA-C	-6.35	1.43	1.52
2	C	254	GLU	N-CA	-6.34	1.38	1.46
2	D	65	GLU	N-CA	-6.34	1.39	1.46
4	F	333	CYS	CA-C	-6.34	1.44	1.52
3	E	169	GLU	CA-C	-6.33	1.44	1.52
4	F	17	VAL	CA-C	-6.33	1.42	1.52
2	C	327	LEU	CA-C	-6.33	1.44	1.52
2	D	296	GLN	CA-C	-6.33	1.44	1.52
1	A	217	TRP	N-CA	-6.33	1.38	1.46
3	E	42	TYR	N-CA	-6.32	1.38	1.46
2	D	154	LEU	CA-C	-6.32	1.44	1.52
4	F	138	LEU	N-CA	-6.32	1.38	1.46
2	D	239	ALA	CA-C	-6.32	1.44	1.52
3	E	15	VAL	N-CA	-6.32	1.38	1.46
4	G	17	VAL	CA-C	-6.32	1.44	1.53
1	A	28	PRO	CA-C	-6.32	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	212	PHE	CA-C	-6.32	1.45	1.53
4	G	164	GLY	CA-C	-6.31	1.43	1.52
3	E	24	HIS	CA-C	-6.31	1.44	1.52
4	G	238	ASP	N-CA	-6.31	1.38	1.46
2	B	63	ASN	N-CA	-6.31	1.38	1.46
2	C	179	ASP	CA-C	-6.31	1.44	1.52
2	C	198	HIS	CA-C	-6.31	1.45	1.52
2	C	319	THR	CA-C	-6.30	1.44	1.52
1	A	294	SER	N-CA	-6.30	1.38	1.46
2	B	157	THR	N-CA	-6.30	1.40	1.46
2	C	290	HIS	N-CA	-6.30	1.38	1.46
3	E	41	ILE	CA-C	-6.30	1.44	1.52
1	A	38	VAL	CA-C	-6.30	1.45	1.52
2	C	181	GLU	CA-C	-6.29	1.44	1.52
3	E	230	TYR	N-CA	-6.29	1.38	1.46
1	A	18	ARG	CA-C	-6.29	1.44	1.52
4	G	352	ALA	CA-C	-6.29	1.44	1.52
1	A	254	LEU	N-CA	-6.28	1.38	1.46
2	D	199	GLU	N-CA	-6.28	1.37	1.46
3	E	320	GLU	C-O	-6.28	1.16	1.24
4	G	109	SER	N-CA	-6.28	1.38	1.45
3	E	272	GLY	CA-C	-6.27	1.45	1.52
4	F	172	THR	CA-C	-6.27	1.45	1.52
1	A	71	MET	N-CA	-6.26	1.38	1.45
4	G	334	GLU	CA-C	-6.26	1.44	1.52
1	A	116	LYS	N-CA	-6.26	1.38	1.46
1	A	237	ARG	CA-C	-6.26	1.45	1.52
3	E	63	ARG	N-CA	-6.25	1.38	1.46
4	F	236	LEU	N-CA	-6.25	1.38	1.46
4	G	351	ASP	CA-C	-6.25	1.44	1.52
1	A	55	ILE	CA-C	-6.25	1.44	1.52
2	D	121	LYS	N-CA	-6.25	1.38	1.46
2	B	348	GLY	CA-C	-6.24	1.45	1.52
4	G	86	ALA	CA-C	-6.24	1.45	1.52
2	B	158	ASP	C-N	-6.24	1.28	1.33
4	F	363	PRO	CA-C	-6.24	1.45	1.52
2	B	33	SER	CA-C	-6.24	1.45	1.52
4	F	170	VAL	N-CA	-6.24	1.38	1.46
2	D	23	HIS	CA-C	-6.23	1.44	1.52
4	F	355	GLN	CA-C	-6.23	1.44	1.52
4	F	179	VAL	CA-C	-6.22	1.45	1.52
4	F	249	PRO	CA-C	-6.22	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	347	VAL	CA-C	-6.22	1.45	1.52
4	F	93	GLU	N-CA	-6.22	1.38	1.46
3	E	201	ALA	CA-C	-6.21	1.44	1.52
2	D	78	ASN	CA-C	-6.21	1.45	1.52
4	F	34	LEU	CA-C	-6.21	1.45	1.52
2	D	214	LEU	CA-C	-6.20	1.44	1.52
1	A	316	TYR	CA-C	-6.20	1.45	1.53
4	F	308	VAL	CA-CB	-6.20	1.46	1.55
3	E	23	GLY	CA-C	-6.20	1.43	1.51
3	E	186	ALA	N-CA	-6.19	1.38	1.46
2	D	290	HIS	CB-CG	-6.19	1.41	1.50
2	C	357	LEU	N-CA	-6.19	1.38	1.46
3	E	17	SER	CA-C	-6.18	1.44	1.52
4	F	310	TYR	CA-C	-6.18	1.45	1.52
3	E	287	GLN	CA-C	-6.17	1.45	1.52
4	F	251	ASN	C-N	-6.17	1.26	1.34
4	G	303	GLU	CA-C	-6.17	1.44	1.52
2	C	188	GLU	CA-C	-6.17	1.45	1.52
2	D	42	LEU	N-CA	-6.17	1.39	1.46
3	E	183	SER	CA-C	-6.17	1.44	1.52
2	D	204	GLN	N-CA	-6.17	1.39	1.46
4	G	16	GLN	CA-C	-6.17	1.44	1.52
2	C	355	ARG	CA-C	-6.16	1.45	1.52
2	D	164	VAL	CA-C	-6.16	1.44	1.52
4	F	124	SER	CA-CB	-6.16	1.44	1.53
4	F	255	HIS	N-CA	-6.16	1.37	1.45
4	G	237	VAL	CA-C	-6.16	1.44	1.52
4	F	206	MET	N-CA	-6.16	1.39	1.46
4	F	349	ILE	C-N	-6.16	1.25	1.33
2	C	94	ASP	C-N	6.16	1.41	1.33
2	D	175	LEU	N-CA	-6.16	1.38	1.46
3	E	171	TYR	N-CA	-6.15	1.38	1.46
2	D	231	GLN	CA-C	-6.15	1.44	1.52
2	C	339	LEU	CA-C	-6.15	1.44	1.52
2	C	357	LEU	C-O	-6.15	1.16	1.24
4	F	171	ALA	CA-C	-6.15	1.45	1.52
1	A	135	VAL	CA-C	-6.14	1.45	1.52
4	F	344	VAL	CA-C	-6.14	1.45	1.52
2	D	114	ALA	CA-C	-6.14	1.44	1.52
4	F	11	LEU	N-CA	-6.14	1.39	1.46
2	B	182	GLN	CA-C	-6.14	1.44	1.52
2	D	165	THR	N-CA	-6.14	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	60	LYS	N-CA	-6.13	1.39	1.46
3	E	294	CYS	N-CA	-6.13	1.39	1.46
4	F	296	ASN	N-CA	-6.13	1.40	1.45
2	C	324	ASP	N-CA	-6.13	1.39	1.46
4	G	289	GLN	N-CA	-6.13	1.38	1.46
2	B	87	PHE	N-CA	-6.12	1.38	1.46
4	G	186	GLN	CA-C	-6.12	1.45	1.52
4	F	159	LEU	N-CA	-6.12	1.38	1.46
4	F	259	GLY	CA-C	-6.12	1.42	1.52
4	F	341	THR	C-N	-6.12	1.25	1.33
2	D	156	THR	N-CA	-6.12	1.38	1.46
4	F	189	PRO	N-CA	-6.12	1.39	1.47
2	C	266	ALA	N-CA	-6.12	1.39	1.46
4	G	315	MET	CA-C	-6.12	1.44	1.52
2	D	223	GLN	N-CA	-6.11	1.39	1.46
4	G	108	LEU	CA-C	-6.11	1.44	1.53
2	D	319	THR	CA-C	-6.10	1.44	1.52
3	E	286	LEU	CA-C	-6.10	1.44	1.52
4	G	79	CYS	CA-C	-6.10	1.45	1.52
3	E	288	ALA	CA-C	-6.10	1.44	1.52
3	E	139	THR	N-CA	-6.10	1.38	1.46
4	F	254	LYS	N-CA	-6.10	1.38	1.45
3	E	62	CYS	CA-C	-6.09	1.44	1.52
3	E	9	PRO	CA-C	-6.09	1.42	1.52
1	A	160	LEU	CA-C	-6.09	1.44	1.53
4	G	166	GLU	CA-C	-6.09	1.44	1.53
4	G	178	ALA	N-CA	-6.09	1.39	1.46
4	G	139	ILE	CA-C	-6.08	1.44	1.52
3	E	309	GLU	N-CA	-6.08	1.39	1.46
2	C	82	ILE	CA-C	-6.08	1.45	1.52
2	D	203	LEU	CA-C	-6.08	1.45	1.52
4	F	39	ASP	N-CA	-6.08	1.39	1.47
2	B	87	PHE	CA-C	-6.08	1.45	1.52
4	F	328	LEU	C-N	-6.08	1.25	1.33
4	F	147	ALA	N-CA	-6.07	1.37	1.45
2	D	244	LEU	CA-C	-6.07	1.45	1.52
4	G	298	GLU	N-CA	-6.07	1.38	1.46
4	G	78	ILE	CA-CB	-6.07	1.47	1.54
4	G	236	LEU	CA-C	-6.07	1.44	1.52
4	G	256	LEU	CA-C	-6.07	1.44	1.53
4	G	83	PRO	CA-C	-6.06	1.45	1.52
4	G	124	SER	N-CA	-6.06	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	314	GLN	N-CA	-6.06	1.38	1.45
4	F	10	LEU	CA-C	-6.06	1.44	1.52
2	B	277	GLU	N-CA	-6.05	1.38	1.46
4	G	140	GLU	CA-C	-6.05	1.45	1.52
4	F	171	ALA	N-CA	-6.05	1.38	1.45
1	A	188	LEU	CA-C	-6.04	1.44	1.52
2	D	191	LEU	CA-C	-6.04	1.44	1.52
3	E	168	PRO	CA-C	-6.04	1.45	1.52
1	A	281	ASN	N-CA	-6.03	1.38	1.46
4	F	99	VAL	CA-C	-6.03	1.45	1.52
2	D	354	LEU	CA-C	-6.02	1.45	1.52
4	G	301	GLU	N-CA	-6.02	1.38	1.46
3	E	293	VAL	CA-C	-6.02	1.45	1.52
3	E	318	ARG	CA-C	-6.01	1.44	1.52
4	G	3	PHE	CA-C	-6.01	1.45	1.52
4	G	78	ILE	N-CA	-6.01	1.39	1.46
4	G	324	VAL	CA-C	-6.01	1.45	1.52
1	A	270	ARG	CA-CB	-6.01	1.43	1.53
3	E	207	GLY	CA-C	-6.01	1.43	1.51
1	A	146	GLN	CA-C	-6.00	1.44	1.52
4	G	309	THR	CA-C	-6.00	1.45	1.52
1	A	159	ASN	N-CA	-6.00	1.38	1.46
3	E	259	HIS	CE1-NE2	-6.00	1.26	1.32
1	A	292	ARG	N-CA	-5.99	1.38	1.46
4	F	2	LYS	CA-C	-5.99	1.45	1.52
1	A	308	THR	CA-C	-5.99	1.45	1.52
2	B	81	GLU	CA-C	-5.99	1.45	1.52
4	G	125	GLU	N-CA	-5.99	1.37	1.45
3	E	219	ALA	CA-C	-5.98	1.45	1.52
4	G	250	LYS	N-CA	-5.98	1.39	1.46
4	F	37	VAL	CA-CB	-5.98	1.47	1.54
2	D	161	LYS	CA-C	-5.97	1.46	1.53
1	A	229	ALA	N-CA	-5.97	1.39	1.46
3	E	182	MET	CA-C	-5.97	1.44	1.52
2	D	224	ALA	CA-C	-5.97	1.45	1.52
4	F	187	SER	CA-C	-5.97	1.44	1.52
2	D	315	GLU	N-CA	-5.97	1.39	1.46
4	G	88	ILE	N-CA	-5.96	1.39	1.46
2	B	122	VAL	N-CA	-5.96	1.38	1.46
4	G	222	ASN	C-N	-5.96	1.25	1.33
2	C	192	ASN	N-CA	-5.96	1.38	1.46
4	F	55	ALA	CA-CB	-5.96	1.39	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	9	HIS	CB-CG	-5.96	1.41	1.50
4	G	173	ASP	CA-C	-5.96	1.44	1.52
4	G	223	ILE	CA-C	-5.95	1.45	1.52
4	G	308	VAL	CA-CB	-5.95	1.46	1.54
4	F	9	HIS	CB-CG	-5.95	1.41	1.50
2	D	6	LEU	N-CA	-5.94	1.38	1.46
2	D	172	GLN	CA-C	-5.94	1.45	1.52
1	A	277	ARG	N-CA	-5.94	1.39	1.46
3	E	66	GLN	CA-C	-5.94	1.45	1.52
4	G	285	VAL	CA-C	-5.94	1.45	1.52
2	B	46	THR	CA-C	-5.93	1.45	1.52
4	F	311	SER	CA-C	-5.93	1.45	1.52
2	D	155	ALA	CA-C	-5.93	1.45	1.52
2	D	278	TRP	N-CA	-5.93	1.39	1.46
2	D	334	ILE	CA-CB	-5.93	1.47	1.54
2	B	150	VAL	N-CA	-5.93	1.39	1.46
3	E	303	VAL	CA-CB	-5.92	1.47	1.54
4	G	127	GLU	N-CA	-5.92	1.39	1.46
3	E	327	VAL	CA-C	-5.92	1.45	1.52
2	C	191	LEU	CA-C	-5.92	1.44	1.52
3	E	74	PRO	CA-C	-5.92	1.44	1.52
4	F	30	LEU	CA-C	-5.92	1.45	1.52
4	F	346	SER	N-CA	-5.92	1.37	1.45
2	B	232	VAL	CA-C	-5.92	1.47	1.53
2	D	99	THR	CA-C	-5.92	1.44	1.52
4	F	284	TYR	N-CA	-5.92	1.39	1.46
4	G	289	GLN	CA-C	-5.92	1.44	1.52
1	A	248	ARG	CA-C	-5.92	1.45	1.52
3	E	283	PRO	N-CA	-5.92	1.39	1.47
4	G	9	HIS	CA-C	-5.91	1.45	1.52
2	D	198	HIS	CB-CG	-5.91	1.41	1.50
4	F	91	GLN	N-CA	-5.91	1.39	1.46
2	C	283	VAL	N-CA	-5.91	1.39	1.46
4	F	43	SER	N-CA	-5.91	1.39	1.45
3	E	88	LEU	CA-C	-5.91	1.45	1.52
4	G	220	SER	N-CA	-5.91	1.39	1.46
2	B	164	VAL	CA-C	-5.91	1.45	1.52
4	F	100	ARG	N-CA	-5.91	1.39	1.46
4	G	181	SER	N-CA	-5.91	1.38	1.46
2	B	315	GLU	CA-C	-5.90	1.44	1.52
4	G	177	LEU	CA-C	-5.90	1.45	1.52
4	F	16	GLN	N-CA	-5.89	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	327	VAL	N-CA	-5.89	1.38	1.46
4	G	357	ALA	CA-CB	-5.89	1.45	1.53
1	A	244	VAL	CA-C	-5.89	1.45	1.52
2	D	90	LEU	CA-C	-5.89	1.45	1.52
2	B	121	LYS	CA-C	-5.88	1.45	1.52
2	C	311	LEU	CA-C	-5.88	1.45	1.52
4	F	2	LYS	N-CA	-5.88	1.39	1.46
2	D	172	GLN	N-CA	-5.88	1.39	1.46
2	D	291	ARG	CA-CB	-5.88	1.44	1.53
4	F	265	GLN	CA-C	-5.88	1.45	1.52
4	G	317	ILE	CA-C	-5.88	1.45	1.52
4	G	29	ILE	CA-C	-5.87	1.45	1.52
1	A	55	ILE	N-CA	-5.87	1.38	1.46
4	G	33	LEU	CA-C	-5.87	1.45	1.52
2	D	59	ALA	CA-C	-5.87	1.45	1.52
4	G	39	ASP	CA-C	-5.87	1.45	1.52
3	E	111	VAL	CA-CB	-5.87	1.46	1.54
1	A	260	LEU	CA-C	-5.86	1.44	1.52
1	A	265	ALA	N-CA	-5.86	1.38	1.46
4	F	27	LEU	N-CA	-5.86	1.38	1.45
4	G	246	ARG	NE-CZ	5.86	1.39	1.33
4	F	123	GLN	CA-C	-5.86	1.45	1.52
4	F	158	MET	N-CA	-5.86	1.39	1.45
1	A	13	LEU	N-CA	-5.86	1.39	1.46
4	F	93	GLU	CA-C	-5.86	1.45	1.53
4	G	346	SER	N-CA	-5.86	1.38	1.46
1	A	248	ARG	N-CA	-5.85	1.39	1.46
4	F	231	ILE	N-CA	-5.85	1.39	1.46
4	F	348	GLN	N-CA	-5.85	1.39	1.46
2	B	158	ASP	N-CA	-5.85	1.41	1.46
4	F	350	GLU	CA-CB	-5.85	1.42	1.54
2	D	291	ARG	N-CA	-5.84	1.39	1.46
3	E	316	LEU	CA-C	-5.84	1.45	1.52
4	F	17	VAL	N-CA	-5.84	1.38	1.46
1	A	331	LEU	CA-C	-5.83	1.46	1.52
2	D	135	SER	N-CA	-5.83	1.39	1.46
2	B	180	VAL	N-CA	-5.83	1.40	1.46
3	E	262	ALA	CA-C	-5.83	1.45	1.52
4	F	109	SER	N-CA	-5.83	1.39	1.46
2	B	273	ALA	CA-C	-5.83	1.45	1.52
3	E	299	GLN	CA-C	-5.83	1.44	1.52
2	D	22	GLU	N-CA	-5.83	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	306	ILE	CA-C	-5.83	1.45	1.52
3	E	282	SER	C-N	-5.82	1.26	1.34
4	F	260	CYS	CA-C	-5.82	1.45	1.52
3	E	273	LEU	N-CA	-5.82	1.39	1.46
1	A	313	LYS	C-N	-5.82	1.25	1.33
2	C	39	HIS	CB-CG	5.81	1.58	1.50
2	C	186	GLN	CA-C	-5.81	1.45	1.52
2	C	264	VAL	N-CA	-5.81	1.39	1.46
2	C	334	ILE	CA-C	-5.81	1.45	1.52
3	E	94	ARG	C-N	-5.81	1.26	1.33
3	E	236	LEU	CA-C	-5.81	1.45	1.52
2	D	313	MET	N-CA	-5.81	1.39	1.46
3	E	3	TRP	N-CA	-5.80	1.38	1.46
2	B	274	ARG	N-CA	-5.80	1.39	1.46
3	E	309	GLU	CA-CB	-5.80	1.44	1.53
4	F	32	ASN	N-CA	-5.80	1.38	1.45
4	G	136	LYS	CA-CB	-5.80	1.44	1.53
2	C	234	THR	CA-C	-5.80	1.45	1.52
2	B	245	ASP	CA-C	5.79	1.59	1.52
3	E	2	ARG	CA-C	-5.79	1.45	1.52
3	E	307	ASN	N-CA	-5.79	1.39	1.46
2	D	167	LEU	CA-C	-5.79	1.45	1.52
4	G	84	GLU	N-CA	-5.79	1.38	1.45
2	C	185	HIS	CB-CG	-5.78	1.42	1.50
4	F	276	GLU	CA-C	-5.78	1.45	1.52
1	A	336	LEU	N-CA	-5.78	1.38	1.46
3	E	226	SER	CA-C	-5.78	1.44	1.52
1	A	89	PRO	CA-C	-5.78	1.45	1.52
2	D	190	ILE	N-CA	-5.78	1.39	1.46
2	C	214	LEU	N-CA	-5.78	1.39	1.46
2	C	293	ALA	N-CA	-5.78	1.39	1.46
4	F	324	VAL	CA-C	-5.78	1.44	1.52
4	F	339	MET	CA-C	-5.78	1.46	1.52
1	A	138	THR	CA-C	-5.77	1.45	1.52
4	F	326	ASP	CA-C	-5.77	1.45	1.52
4	F	205	ARG	CA-C	-5.77	1.44	1.52
4	G	10	LEU	N-CA	-5.77	1.38	1.46
2	D	23	HIS	N-CA	-5.76	1.39	1.46
2	D	70	ALA	CA-C	-5.76	1.44	1.52
2	D	174	HIS	CA-C	-5.75	1.45	1.52
2	D	321	PRO	C-N	-5.75	1.26	1.33
4	F	212	ASN	CA-C	-5.75	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	353	ALA	N-CA	-5.75	1.38	1.46
4	G	347	VAL	CA-CB	-5.75	1.47	1.54
3	E	76	TYR	CA-C	-5.75	1.45	1.52
2	D	197	ALA	CA-C	-5.75	1.45	1.52
2	D	66	THR	N-CA	-5.74	1.33	1.46
2	B	152	PHE	N-CA	-5.74	1.39	1.46
4	F	56	ARG	N-CA	-5.74	1.38	1.45
1	A	69	GLN	CA-C	-5.73	1.46	1.53
1	A	306	THR	CA-C	-5.73	1.45	1.52
3	E	228	ASP	N-CA	-5.73	1.39	1.46
2	C	360	HIS	CB-CG	-5.73	1.42	1.50
4	G	326	ASP	CA-C	-5.73	1.45	1.52
3	E	33	PRO	CA-C	-5.73	1.43	1.52
4	F	338	MET	CA-CB	-5.73	1.43	1.53
1	A	262	ARG	CA-C	-5.72	1.45	1.52
4	F	133	ALA	CA-C	-5.72	1.45	1.52
2	D	32	LEU	CA-C	-5.72	1.45	1.52
4	G	305	ILE	N-CA	-5.72	1.39	1.46
4	G	163	GLU	N-CA	-5.72	1.39	1.46
4	G	199	GLY	CA-C	-5.71	1.45	1.51
3	E	122	ASP	CA-C	-5.71	1.45	1.52
3	E	136	PRO	CA-C	-5.71	1.46	1.52
2	C	120	PHE	CA-C	-5.71	1.45	1.52
2	D	215	ARG	CA-C	-5.71	1.45	1.52
2	D	155	ALA	N-CA	-5.70	1.38	1.46
2	D	254	GLU	N-CA	-5.70	1.39	1.46
2	D	277	GLU	CA-C	-5.70	1.44	1.52
1	A	168	GLN	N-CA	-5.70	1.39	1.46
4	F	301	GLU	N-CA	-5.70	1.38	1.45
4	G	337	ARG	CA-CB	-5.70	1.43	1.53
2	C	367	GLU	C-N	-5.70	1.25	1.34
3	E	140	TRP	N-CA	-5.70	1.39	1.46
2	D	333	LEU	CA-C	-5.69	1.45	1.52
3	E	116	ASP	CA-C	-5.69	1.47	1.53
4	F	343	SER	CA-C	-5.69	1.45	1.52
2	D	339	LEU	CA-C	-5.68	1.45	1.52
4	F	352	ALA	N-CA	-5.68	1.39	1.46
2	C	270	GLU	CA-C	-5.68	1.45	1.52
3	E	45	SER	CA-C	-5.67	1.45	1.52
4	F	331	LEU	CA-C	-5.67	1.45	1.52
2	B	205	LEU	CA-C	-5.67	1.45	1.52
2	C	298	SER	CA-C	-5.67	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	237	VAL	CA-C	-5.67	1.45	1.52
3	E	296	ILE	CA-CB	-5.67	1.47	1.54
2	B	207	ALA	CA-C	-5.67	1.45	1.52
2	B	344	ASP	C-N	-5.66	1.26	1.34
4	G	159	LEU	CA-C	-5.65	1.45	1.52
2	D	30	ASN	CA-C	-5.65	1.45	1.52
4	G	327	VAL	N-CA	-5.65	1.38	1.46
2	D	213	SER	CA-C	-5.65	1.45	1.52
4	G	290	LEU	CA-C	-5.65	1.45	1.52
1	A	124	ALA	CA-C	-5.65	1.45	1.52
1	A	145	ALA	N-CA	-5.65	1.39	1.46
3	E	65	CYS	CA-C	-5.65	1.45	1.52
3	E	228	ASP	CA-C	-5.64	1.46	1.52
1	A	221	LEU	N-CA	5.64	1.53	1.46
4	F	29	ILE	CA-C	-5.64	1.45	1.52
2	D	197	ALA	N-CA	-5.64	1.38	1.46
2	C	366	PRO	N-CA	-5.64	1.40	1.47
3	E	292	ASP	N-CA	-5.64	1.39	1.46
4	G	362	MET	N-CA	-5.63	1.39	1.45
4	F	172	THR	N-CA	-5.63	1.39	1.46
2	D	256	MET	CA-C	-5.63	1.45	1.52
2	C	195	HIS	CA-C	-5.62	1.45	1.52
4	F	334	GLU	CA-C	-5.62	1.47	1.53
2	C	234	THR	N-CA	-5.62	1.39	1.46
4	F	163	GLU	N-CA	-5.62	1.39	1.46
1	A	32	GLN	CA-C	-5.62	1.45	1.52
4	F	106	PHE	N-CA	-5.62	1.38	1.45
1	A	292	ARG	CA-C	-5.62	1.45	1.52
4	F	282	ARG	CA-C	-5.62	1.45	1.52
4	F	364	MET	CA-C	-5.61	1.46	1.52
4	G	76	PHE	N-CA	-5.61	1.39	1.46
2	D	286	LEU	CA-C	-5.61	1.45	1.52
4	G	300	GLU	CA-C	-5.61	1.45	1.52
1	A	8	GLN	CA-C	-5.61	1.45	1.52
4	F	14	LEU	CA-C	-5.61	1.44	1.52
4	G	273	LEU	CA-C	-5.60	1.45	1.52
4	F	304	GLU	CA-C	-5.60	1.45	1.52
4	F	258	ALA	N-CA	-5.60	1.38	1.46
1	A	284	GLY	CA-C	-5.60	1.45	1.52
2	C	363	MET	C-N	-5.60	1.26	1.33
2	D	216	ASP	N-CA	-5.60	1.39	1.46
1	A	226	SER	CA-C	-5.59	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	90	VAL	CA-C	-5.59	1.46	1.52
4	F	278	PHE	CA-CB	5.59	1.62	1.53
1	A	190	LEU	CA-C	-5.59	1.45	1.52
2	D	74	GLY	CA-C	-5.59	1.44	1.51
4	G	152	ARG	CD-NE	5.58	1.54	1.46
4	F	186	GLN	CA-C	-5.58	1.45	1.52
4	F	325	LEU	CA-C	-5.58	1.45	1.52
1	A	94	ASN	CA-C	-5.58	1.45	1.52
4	G	67	ALA	CA-C	-5.58	1.46	1.52
4	G	146	MET	CA-C	-5.58	1.46	1.52
2	B	317	ALA	N-CA	-5.58	1.39	1.46
2	D	235	GLN	CA-C	-5.58	1.45	1.52
3	E	95	GLU	N-CA	-5.58	1.39	1.46
3	E	162	HIS	N-CA	-5.58	1.39	1.46
2	D	287	GLY	CA-C	-5.57	1.45	1.52
2	C	247	ASP	N-CA	-5.57	1.39	1.46
3	E	91	ASP	N-CA	-5.57	1.39	1.46
4	F	66	GLY	N-CA	-5.57	1.39	1.45
2	C	303	GLY	C-N	5.57	1.41	1.33
3	E	99	LYS	CA-C	-5.57	1.45	1.52
2	C	257	VAL	CA-C	-5.56	1.45	1.52
3	E	57	LYS	CA-C	-5.56	1.45	1.52
3	E	227	GLY	CA-C	-5.56	1.43	1.51
4	F	223	ILE	CA-C	-5.56	1.45	1.52
4	G	53	MET	CA-CB	-5.56	1.44	1.52
1	A	269	LEU	N-CA	-5.55	1.39	1.46
1	A	329	LEU	C-O	-5.55	1.17	1.23
4	F	340	LEU	N-CA	-5.55	1.39	1.45
2	D	328	TYR	CA-C	-5.55	1.45	1.52
4	F	57	VAL	CA-CB	-5.55	1.47	1.54
4	G	213	PRO	CA-C	-5.55	1.46	1.52
4	F	104	SER	CA-C	-5.55	1.46	1.52
4	F	159	LEU	CA-C	-5.55	1.46	1.53
4	G	301	GLU	CA-C	-5.55	1.45	1.52
4	G	91	GLN	N-CA	-5.54	1.39	1.46
2	D	120	PHE	N-CA	-5.54	1.39	1.46
1	A	298	LEU	N-CA	-5.54	1.39	1.46
2	D	198	HIS	N-CA	-5.53	1.39	1.46
4	F	288	ASN	CA-C	-5.53	1.45	1.52
2	B	122	VAL	CA-C	-5.53	1.45	1.52
4	F	351	ASP	N-CA	-5.53	1.38	1.45
4	G	300	GLU	N-CA	-5.53	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	260	HIS	CB-CG	-5.53	1.42	1.50
4	F	190	SER	CA-C	-5.53	1.45	1.52
3	E	165	ALA	C-N	-5.52	1.28	1.33
3	E	124	ALA	CA-C	-5.52	1.45	1.52
4	F	63	HIS	CA-C	-5.52	1.45	1.52
2	B	268	ILE	CA-C	-5.52	1.45	1.52
4	F	92	LEU	N-CA	-5.52	1.39	1.46
4	F	204	MET	N-CA	-5.51	1.39	1.46
4	G	255	HIS	N-CA	-5.51	1.39	1.46
3	E	141	PHE	CA-C	-5.50	1.46	1.52
4	F	41	THR	N-CA	-5.50	1.39	1.45
4	G	95	GLU	CA-C	-5.50	1.46	1.53
4	G	194	ILE	CA-CB	-5.50	1.47	1.54
1	A	109	LEU	N-CA	-5.50	1.39	1.46
4	G	53	MET	N-CA	-5.50	1.40	1.46
4	F	135	MET	CA-C	-5.50	1.46	1.52
1	A	220	ALA	CA-CB	-5.49	1.44	1.53
2	D	358	ALA	N-CA	-5.49	1.39	1.46
4	F	100	ARG	CA-C	-5.49	1.46	1.52
2	B	111	VAL	CA-CB	-5.49	1.47	1.54
2	D	233	SER	N-CA	-5.49	1.39	1.45
4	F	317	ILE	CA-C	-5.48	1.46	1.52
1	A	96	GLN	CA-C	-5.48	1.45	1.52
1	A	150	TRP	CA-C	-5.48	1.45	1.52
2	B	181	GLU	N-CA	-5.48	1.39	1.46
3	E	252	LEU	CA-C	-5.48	1.45	1.52
4	F	265	GLN	N-CA	-5.48	1.39	1.46
1	A	148	PRO	CA-C	-5.48	1.44	1.52
4	G	6	GLU	N-CA	-5.48	1.39	1.46
2	C	182	GLN	CA-C	-5.48	1.45	1.52
3	E	197	SER	CA-C	-5.48	1.45	1.52
2	D	173	PHE	N-CA	-5.47	1.39	1.46
4	G	80	ARG	N-CA	-5.47	1.39	1.46
2	D	232	VAL	CA-C	-5.47	1.46	1.52
4	F	134	THR	N-CA	-5.47	1.39	1.46
4	G	312	GLY	N-CA	-5.47	1.37	1.45
3	E	198	PRO	N-CA	-5.47	1.41	1.46
4	F	191	HIS	N-CA	-5.47	1.39	1.46
1	A	72	SER	N-CA	-5.46	1.39	1.46
2	B	187	LEU	CA-C	-5.46	1.46	1.52
4	F	21	LEU	CA-C	-5.46	1.45	1.52
4	F	27	LEU	C-N	-5.46	1.26	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	104	SER	N-CA	-5.46	1.39	1.46
4	F	51	MET	N-CA	-5.45	1.39	1.46
4	F	302	ALA	N-CA	-5.45	1.39	1.46
2	D	214	LEU	N-CA	-5.45	1.39	1.46
4	G	324	VAL	N-CA	-5.45	1.40	1.46
3	E	22	ARG	CA-C	-5.45	1.46	1.52
4	G	281	VAL	CA-CB	-5.45	1.48	1.54
2	D	49	VAL	CA-C	-5.45	1.46	1.52
1	A	47	PHE	N-CA	-5.44	1.40	1.46
1	A	169	VAL	CA-C	-5.44	1.45	1.52
2	D	37	ILE	CA-C	-5.44	1.45	1.52
4	G	100	ARG	N-CA	-5.44	1.39	1.46
4	G	205	ARG	CA-C	-5.44	1.45	1.52
2	C	355	ARG	N-CA	-5.43	1.39	1.46
2	B	221	THR	CA-C	-5.43	1.45	1.52
1	A	137	VAL	CA-CB	-5.43	1.47	1.54
4	F	231	ILE	CA-CB	-5.43	1.47	1.54
2	B	79	CYS	N-CA	-5.42	1.39	1.46
2	D	281	LEU	N-CA	-5.42	1.39	1.46
4	G	71	PRO	CA-C	-5.42	1.46	1.52
1	A	257	LEU	CA-C	-5.42	1.45	1.52
2	D	283	VAL	CA-CB	-5.42	1.47	1.54
1	A	226	SER	N-CA	-5.41	1.38	1.46
2	C	345	ARG	CA-C	-5.41	1.45	1.52
2	B	359	PHE	CA-C	-5.41	1.45	1.52
3	E	92	ALA	CA-C	-5.41	1.45	1.52
4	G	229	ASP	CA-C	-5.41	1.44	1.52
1	A	288	GLU	N-CA	-5.41	1.40	1.46
1	A	329	LEU	CA-C	-5.41	1.45	1.52
2	B	250	LEU	CA-C	-5.41	1.46	1.52
1	A	92	ALA	CA-C	-5.40	1.45	1.52
2	D	100	LYS	N-CA	-5.40	1.39	1.46
2	B	324	ASP	CA-C	-5.40	1.45	1.52
4	G	314	GLU	CA-C	-5.39	1.45	1.52
3	E	77	TYR	CA-C	-5.39	1.46	1.52
2	D	360	HIS	CB-CG	-5.39	1.42	1.50
2	D	186	GLN	CA-C	-5.38	1.45	1.52
2	B	48	GLY	CA-C	-5.37	1.43	1.51
3	E	116	ASP	N-CA	-5.37	1.39	1.46
1	A	117	LEU	CA-C	-5.37	1.45	1.53
2	D	225	ILE	CA-CB	-5.37	1.47	1.54
4	F	156	ASN	C-N	-5.37	1.26	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	73	CYS	CA-C	-5.37	1.46	1.52
2	D	26	THR	C-O	-5.37	1.17	1.24
3	E	146	ARG	CA-C	-5.37	1.45	1.52
4	F	121	ASP	N-CA	-5.37	1.39	1.46
2	D	29	ALA	CA-C	-5.36	1.46	1.52
4	F	335	ASN	C-N	-5.36	1.25	1.33
4	G	307	ASP	CA-C	-5.36	1.45	1.52
4	G	197	ARG	CA-C	-5.35	1.45	1.52
1	A	154	ARG	N-CA	-5.35	1.39	1.46
2	B	112	GLN	CA-CB	5.35	1.62	1.53
4	F	323	TYR	CA-C	-5.35	1.45	1.52
2	B	275	GLY	CA-C	-5.35	1.44	1.51
4	F	226	HIS	CA-C	-5.35	1.47	1.53
1	A	282	ARG	CA-CB	-5.35	1.44	1.53
3	E	278	ALA	N-CA	-5.35	1.39	1.46
2	D	96	ALA	N-CA	-5.34	1.39	1.46
2	D	290	HIS	N-CA	-5.34	1.40	1.46
2	D	311	LEU	N-CA	-5.34	1.39	1.46
2	C	155	ALA	CA-C	-5.34	1.46	1.52
4	G	308	VAL	N-CA	-5.34	1.40	1.46
2	C	364	PRO	CA-CB	-5.33	1.45	1.54
3	E	108	GLY	N-CA	-5.33	1.39	1.45
4	G	346	SER	CA-C	-5.33	1.46	1.52
1	A	191	LEU	CA-C	-5.33	1.45	1.52
4	F	235	LYS	N-CA	-5.33	1.39	1.45
4	F	46	GLY	N-CA	-5.33	1.37	1.45
4	F	307	ASP	C-N	-5.33	1.27	1.33
4	F	73	ARG	CA-C	-5.33	1.46	1.53
3	E	151	LEU	C-N	5.33	1.41	1.33
4	G	254	LYS	N-CA	-5.33	1.39	1.46
4	F	357	ALA	CA-C	-5.32	1.46	1.52
3	E	285	ARG	CA-C	-5.32	1.45	1.52
4	G	22	GLY	CA-C	-5.32	1.45	1.52
1	A	239	GLU	CA-CB	5.32	1.62	1.53
2	D	263	ARG	CA-C	-5.32	1.45	1.52
3	E	19	GLN	N-CA	-5.32	1.39	1.46
3	E	294	CYS	CA-C	-5.32	1.46	1.52
2	C	292	ILE	CA-CB	-5.31	1.48	1.54
4	F	238	ASP	CA-C	-5.31	1.45	1.53
4	G	107	SER	N-CA	-5.31	1.40	1.46
3	E	232	LEU	N-CA	-5.31	1.39	1.46
1	A	181	LEU	CA-C	-5.31	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	295	ASN	N-CA	-5.31	1.39	1.45
2	B	79	CYS	CA-C	-5.30	1.45	1.52
4	F	203	LEU	N-CA	-5.30	1.40	1.46
4	G	292	ILE	CA-C	-5.30	1.46	1.52
4	G	30	LEU	N-CA	-5.30	1.40	1.46
4	F	84	GLU	N-CA	-5.30	1.38	1.45
2	B	170	CYS	CA-C	-5.30	1.46	1.52
3	E	323	LEU	CA-C	-5.29	1.45	1.52
2	C	156	THR	CA-C	-5.29	1.46	1.52
2	D	99	THR	N-CA	-5.29	1.39	1.46
2	D	60	LYS	CA-C	-5.29	1.46	1.52
1	A	166	ALA	N-CA	-5.29	1.39	1.46
4	F	257	GLU	C-N	-5.28	1.27	1.33
2	C	362	ARG	CA-C	-5.28	1.45	1.52
2	B	269	ASN	N-CA	-5.28	1.39	1.46
1	A	209	ALA	C-N	5.28	1.40	1.33
4	F	70	VAL	CA-C	-5.28	1.47	1.52
4	G	34	LEU	CA-C	-5.28	1.46	1.52
1	A	184	ALA	CA-C	-5.27	1.46	1.52
2	C	39	HIS	ND1-CE1	5.27	1.37	1.32
4	G	365	ARG	CA-C	-5.27	1.45	1.52
2	D	204	GLN	CA-C	-5.27	1.46	1.52
2	D	292	ILE	N-CA	-5.27	1.40	1.46
4	F	261	ASP	N-CA	-5.27	1.39	1.46
3	E	234	ALA	N-CA	-5.26	1.40	1.46
1	A	278	VAL	N-CA	-5.26	1.39	1.46
2	C	185	HIS	N-CA	-5.26	1.40	1.46
2	D	12	PRO	CA-C	-5.25	1.45	1.52
4	F	181	SER	CA-C	-5.25	1.46	1.52
2	D	358	ALA	CA-C	-5.25	1.45	1.52
4	G	203	LEU	CA-CB	-5.25	1.45	1.53
2	C	113	TYR	CA-C	-5.25	1.46	1.52
3	E	48	LEU	N-CA	-5.25	1.39	1.46
1	A	259	ASN	N-CA	-5.24	1.39	1.46
2	C	300	ALA	CA-C	-5.24	1.45	1.52
3	E	129	LEU	CA-C	-5.24	1.46	1.52
2	D	232	VAL	CA-CB	-5.24	1.48	1.54
3	E	72	THR	CA-C	-5.24	1.45	1.52
2	C	154	LEU	CA-C	-5.24	1.46	1.52
2	D	264	VAL	N-CA	-5.24	1.40	1.46
4	G	179	VAL	CA-C	-5.24	1.45	1.52
1	A	174	TYR	CA-C	-5.24	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	295	VAL	CA-CB	-5.24	1.47	1.54
4	G	302	ALA	CA-C	-5.23	1.46	1.52
4	G	305	ILE	CA-C	-5.23	1.46	1.52
3	E	306	ILE	N-CA	-5.23	1.39	1.46
4	F	201	ILE	CA-C	-5.23	1.46	1.52
1	A	40	GLN	CA-C	-5.22	1.46	1.52
3	E	224	VAL	N-CA	-5.22	1.40	1.46
4	F	184	ILE	CA-C	-5.22	1.47	1.52
4	F	267	PHE	CB-CG	-5.22	1.38	1.50
4	F	325	LEU	N-CA	-5.22	1.39	1.46
2	C	343	PRO	CA-C	-5.22	1.46	1.52
2	D	178	LEU	CA-C	-5.22	1.46	1.52
2	D	22	GLU	C-O	-5.22	1.18	1.24
4	G	297	PRO	CA-C	-5.21	1.44	1.52
2	C	348	GLY	N-CA	-5.21	1.39	1.45
2	C	335	GLY	CA-C	-5.21	1.46	1.51
2	D	318	ARG	N-CA	-5.21	1.39	1.46
4	G	187	SER	N-CA	-5.21	1.39	1.46
2	D	63	ASN	N-CA	-5.21	1.40	1.46
2	B	198	HIS	CA-C	-5.21	1.46	1.52
3	E	18	TYR	N-CA	-5.21	1.40	1.46
4	F	24	ARG	N-CA	-5.21	1.38	1.46
4	F	149	GLN	CA-C	-5.21	1.46	1.52
2	B	11	ARG	CA-C	-5.20	1.46	1.52
2	D	325	ILE	N-CA	-5.20	1.39	1.46
4	G	328	LEU	C-N	-5.20	1.26	1.33
1	A	286	MET	CA-C	-5.20	1.45	1.52
3	E	152	LEU	CA-CB	5.20	1.61	1.53
4	G	70	VAL	CA-CB	-5.20	1.50	1.55
1	A	4	LEU	N-CA	-5.20	1.39	1.45
2	B	281	LEU	N-CA	-5.19	1.39	1.46
2	C	196	ILE	N-CA	-5.19	1.40	1.46
2	C	344	ASP	N-CA	-5.19	1.39	1.46
4	G	168	ARG	N-CA	-5.19	1.39	1.46
3	E	102	GLU	N-CA	-5.19	1.40	1.46
4	F	115	ASP	CA-C	-5.19	1.46	1.52
4	G	291	LYS	CA-C	-5.19	1.46	1.52
4	F	168	ARG	CA-C	-5.18	1.46	1.52
4	G	167	LEU	CA-C	-5.18	1.46	1.52
4	F	118	ASN	CA-C	5.18	1.59	1.52
4	G	136	LYS	CA-C	-5.18	1.46	1.52
2	D	71	THR	CA-C	-5.18	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	296	ASN	N-CA	-5.18	1.37	1.46
4	F	177	LEU	CA-C	-5.18	1.46	1.52
2	C	281	LEU	CA-C	-5.18	1.46	1.52
1	A	228	ARG	CA-C	-5.17	1.46	1.52
2	C	337	LYS	CA-C	-5.17	1.45	1.52
2	B	123	TYR	CA-C	-5.17	1.46	1.52
2	B	156	THR	CA-C	-5.17	1.46	1.53
2	D	204	GLN	CA-CB	-5.17	1.45	1.53
2	B	68	ILE	N-CA	-5.17	1.39	1.46
2	B	160	GLN	CA-C	-5.17	1.45	1.52
3	E	216	LEU	CA-C	-5.17	1.46	1.52
2	D	44	SER	CA-C	-5.16	1.46	1.52
1	A	310	LEU	N-CA	-5.16	1.39	1.46
2	D	329	TYR	N-CA	-5.16	1.40	1.46
2	B	73	CYS	N-CA	-5.16	1.40	1.46
2	C	8	ARG	CA-C	-5.16	1.46	1.52
2	C	337	LYS	N-CA	-5.16	1.39	1.46
4	F	216	VAL	N-CA	-5.16	1.40	1.46
2	D	320	ILE	CA-CB	-5.15	1.48	1.54
1	A	330	LEU	CA-C	-5.15	1.45	1.52
4	F	231	ILE	CA-C	-5.15	1.46	1.52
4	G	57	VAL	CA-CB	-5.15	1.47	1.54
2	B	320	ILE	CA-C	-5.15	1.47	1.52
2	C	199	GLU	CA-C	-5.15	1.47	1.52
4	G	343	SER	CA-C	-5.15	1.45	1.52
4	G	52	GLU	CA-C	-5.15	1.46	1.52
2	D	180	VAL	CA-C	-5.14	1.46	1.52
3	E	266	THR	CA-C	-5.14	1.45	1.52
3	E	297	ARG	C-O	-5.14	1.18	1.24
4	G	168	ARG	CA-C	-5.14	1.46	1.52
4	F	302	ALA	CA-C	-5.14	1.46	1.52
1	A	223	MET	N-CA	-5.14	1.40	1.46
2	C	75	VAL	N-CA	-5.14	1.40	1.46
2	D	194	GLU	N-CA	-5.13	1.39	1.46
3	E	283	PRO	CA-C	-5.13	1.44	1.52
2	D	357	LEU	CA-C	-5.13	1.45	1.52
2	D	195	HIS	CA-C	-5.13	1.46	1.52
4	F	60	VAL	CA-C	-5.13	1.44	1.52
4	G	250	LYS	CA-C	-5.13	1.46	1.52
4	F	246	ARG	N-CA	-5.12	1.39	1.46
1	A	178	LEU	CA-C	-5.12	1.46	1.52
2	D	237	VAL	N-CA	-5.12	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	38	ASP	CA-C	-5.12	1.46	1.52
4	F	306	LEU	CA-C	-5.12	1.45	1.52
4	G	172	THR	CA-C	-5.12	1.46	1.52
1	A	24	LEU	N-CA	-5.12	1.39	1.46
4	F	341	THR	CA-C	-5.12	1.46	1.53
4	G	69	THR	CA-C	-5.12	1.47	1.52
3	E	290	LEU	N-CA	-5.12	1.40	1.46
1	A	219	ASP	CA-C	-5.12	1.46	1.52
3	E	181	THR	N-CA	-5.12	1.39	1.46
1	A	53	PHE	CA-C	-5.11	1.46	1.52
2	D	13	GLN	N-CA	-5.11	1.39	1.46
4	F	105	ARG	N-CA	-5.11	1.40	1.45
2	B	244	LEU	C-N	5.11	1.40	1.33
4	G	264	LYS	CA-C	-5.11	1.46	1.52
2	B	188	GLU	CA-C	-5.10	1.46	1.52
3	E	161	LEU	CA-C	-5.10	1.46	1.52
4	F	349	ILE	C-O	-5.10	1.18	1.24
4	F	220	SER	N-CA	-5.10	1.40	1.46
3	E	242	PRO	CA-C	-5.10	1.44	1.52
4	F	351	ASP	CA-C	-5.10	1.46	1.53
3	E	253	MET	N-CA	-5.09	1.39	1.46
4	G	35	LEU	N-CA	-5.09	1.39	1.46
2	D	287	GLY	N-CA	-5.09	1.39	1.45
4	F	192	SER	N-CA	-5.09	1.39	1.45
3	E	226	SER	N-CA	-5.09	1.39	1.46
4	G	178	ALA	CA-C	-5.09	1.46	1.52
1	A	273	PHE	C-O	-5.09	1.17	1.24
2	D	238	SER	CA-C	-5.09	1.46	1.52
4	G	66	GLY	CA-C	-5.09	1.44	1.51
1	A	166	ALA	CA-C	-5.08	1.45	1.52
2	D	236	ALA	CA-C	-5.08	1.45	1.52
4	F	178	ALA	CA-C	-5.08	1.46	1.52
4	G	211	ASP	CA-C	-5.08	1.46	1.52
1	A	22	LEU	N-CA	-5.08	1.39	1.46
1	A	13	LEU	CA-C	-5.08	1.46	1.52
4	G	45	THR	N-CA	-5.08	1.39	1.46
4	G	304	GLU	CA-C	-5.08	1.46	1.52
2	C	93	ILE	C-N	5.08	1.40	1.33
1	A	115	ASN	N-CA	-5.07	1.39	1.45
3	E	202	LEU	CA-C	-5.07	1.45	1.52
1	A	234	GLN	CA-C	-5.07	1.46	1.52
4	G	172	THR	N-CA	-5.07	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	178	LEU	CA-C	-5.07	1.46	1.52
4	G	296	ASN	CA-C	-5.07	1.45	1.52
1	A	130	LEU	CA-C	-5.07	1.45	1.52
4	F	167	LEU	N-CA	-5.07	1.39	1.46
2	D	345	ARG	CA-C	-5.06	1.46	1.52
2	B	198	HIS	N-CA	-5.06	1.40	1.46
4	G	77	ASP	CA-C	-5.06	1.46	1.52
4	F	137	ARG	CA-C	-5.06	1.46	1.52
4	G	347	VAL	N-CA	-5.06	1.40	1.46
4	F	250	LYS	CA-C	-5.05	1.45	1.52
2	C	10	TRP	CA-C	-5.05	1.44	1.52
2	D	338	GLU	CA-C	-5.05	1.45	1.52
4	F	45	THR	CA-C	-5.05	1.46	1.52
4	G	99	VAL	N-CA	-5.05	1.40	1.46
4	G	241	PHE	CA-C	-5.05	1.48	1.52
2	D	291	ARG	C-O	-5.05	1.18	1.24
2	D	322	PRO	N-CA	-5.05	1.41	1.47
4	F	197	ARG	N-CA	-5.04	1.40	1.46
1	A	247	LEU	CA-C	-5.04	1.46	1.52
1	A	246	LEU	N-CA	-5.04	1.40	1.46
2	B	283	VAL	N-CA	-5.04	1.39	1.46
2	D	256	MET	N-CA	-5.04	1.40	1.46
4	G	288	ASN	CA-C	-5.04	1.46	1.52
1	A	80	LEU	N-CA	-5.04	1.40	1.46
2	C	43	PHE	N-CA	-5.04	1.40	1.46
2	C	111	VAL	CA-CB	-5.04	1.48	1.54
4	G	275	ASN	N-CA	-5.04	1.39	1.46
1	A	6	PRO	CA-C	-5.03	1.44	1.52
1	A	22	LEU	CA-C	-5.03	1.46	1.53
1	A	235	GLN	N-CA	-5.03	1.40	1.46
3	E	227	GLY	N-CA	-5.03	1.38	1.45
1	A	26	ASN	CA-C	-5.03	1.45	1.52
1	A	245	ILE	N-CA	-5.03	1.39	1.46
2	D	123	TYR	CA-C	-5.03	1.46	1.52
4	F	220	SER	CA-C	-5.03	1.45	1.52
1	A	107	ASP	N-CA	-5.02	1.39	1.46
2	D	21	GLN	C-N	-5.02	1.27	1.33
2	D	89	ASP	CA-C	-5.02	1.46	1.52
1	A	279	TRP	C-N	-5.02	1.27	1.33
4	F	195	VAL	N-CA	-5.02	1.41	1.46
2	C	271	ALA	N-CA	-5.02	1.40	1.46
2	D	270	GLU	CA-C	-5.02	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	314	ASP	CA-C	-5.02	1.46	1.52
4	F	147	ALA	CA-CB	-5.02	1.45	1.53
4	G	204	MET	CA-C	-5.02	1.46	1.52
2	B	213	SER	N-CA	-5.01	1.39	1.46
2	D	300	ALA	CA-C	-5.01	1.46	1.52
4	G	194	ILE	N-CA	-5.01	1.40	1.46
1	A	107	ASP	CA-C	-5.01	1.46	1.52
4	G	126	VAL	N-CA	-5.01	1.40	1.46
4	F	98	LEU	CA-C	-5.01	1.46	1.52
2	C	104	THR	CA-C	-5.00	1.46	1.52
2	D	337	LYS	N-CA	-5.00	1.40	1.46
4	F	79	CYS	CA-C	-5.00	1.46	1.52
2	B	328	TYR	CA-C	-5.00	1.46	1.52
2	C	117	ARG	CA-C	-5.00	1.46	1.52
3	E	243	ALA	CA-C	-5.00	1.46	1.52
4	G	294	ALA	CA-C	-5.00	1.46	1.52

All (1743) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	367	GLU	N-CA-C	-18.53	84.74	110.31
3	E	22	ARG	N-CA-C	-16.41	91.72	112.72
4	G	160	PHE	CA-CB-CG	-15.57	98.23	113.80
4	F	157	GLY	N-CA-C	-15.02	88.85	110.63
3	E	267	ASN	CA-CB-CG	-14.93	97.67	112.60
4	F	148	HIS	CA-CB-CG	-14.67	99.13	113.80
2	D	76	CYS	N-CA-C	-14.66	85.59	108.76
4	G	296	ASN	N-CA-C	-13.92	89.44	109.62
3	E	208	ASP	CA-CB-CG	-13.68	98.92	112.60
4	G	222	ASN	N-CA-C	-13.67	88.64	108.60
4	G	151	VAL	N-CA-C	-13.32	97.83	113.42
2	B	120	PHE	CA-CB-CG	-13.23	100.57	113.80
3	E	95	GLU	N-CA-C	13.21	125.20	111.07
2	B	246	ASP	CA-CB-CG	13.01	125.61	112.60
2	C	362	ARG	N-CA-C	-12.95	83.22	110.80
3	E	205	PHE	CA-CB-CG	-12.68	101.12	113.80
4	F	38	ALA	N-CA-C	-12.38	86.19	108.48
4	G	124	SER	N-CA-C	-12.25	88.79	109.24
1	A	167	ASN	CA-CB-CG	12.24	124.84	112.60
2	C	247	ASP	CA-CB-CG	-12.23	100.37	112.60
4	F	222	ASN	CA-CB-CG	-12.04	100.56	112.60
4	F	279	ARG	CA-C-N	12.02	131.80	120.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	279	ARG	C-N-CA	12.02	131.80	120.98
4	G	251	ASN	CA-CB-CG	-11.90	100.70	112.60
4	G	230	PHE	CA-CB-CG	-11.82	101.98	113.80
4	G	356	SER	N-CA-C	-11.65	85.98	110.80
2	C	254	GLU	N-CA-C	-11.54	98.78	111.36
4	F	184	ILE	N-CA-C	-11.53	102.43	112.12
1	A	314	GLN	N-CA-C	-11.53	99.44	114.31
4	G	163	GLU	N-CA-C	-11.53	89.73	108.52
2	D	94	ASP	CA-CB-CG	11.46	124.06	112.60
2	D	325	ILE	N-CA-C	-11.44	101.97	111.81
3	E	322	TYR	N-CA-C	11.39	124.81	111.71
2	D	64	CYS	N-CA-C	-11.36	91.13	109.76
4	G	193	VAL	N-CA-C	-11.33	87.58	107.18
3	E	56	HIS	CA-CB-CG	-11.26	102.54	113.80
3	E	236	LEU	CB-CA-C	-11.23	90.20	109.07
4	G	161	GLU	CB-CG-CD	-11.17	93.61	112.60
3	E	262	ALA	CA-C-N	11.06	135.10	120.28
3	E	262	ALA	C-N-CA	11.06	135.10	120.28
3	E	222	TYR	N-CA-C	-11.06	99.62	113.55
1	A	224	GLY	N-CA-C	-11.05	99.37	114.95
3	E	73	HIS	CA-CB-CG	-11.00	102.80	113.80
2	B	8	ARG	N-CA-C	-10.95	102.14	114.62
2	B	151	LYS	N-CA-C	-10.94	90.96	109.24
4	F	180	CYS	N-CA-C	-10.95	92.27	109.23
2	B	129	HIS	CA-CB-CG	10.92	124.72	113.80
2	C	309	ILE	CA-C-N	10.91	135.27	120.54
2	C	309	ILE	C-N-CA	10.91	135.27	120.54
1	A	212	PHE	CA-CB-CG	-10.91	102.89	113.80
4	G	305	ILE	N-CA-C	-10.90	93.34	108.27
4	G	75	PHE	CA-CB-CG	-10.87	102.93	113.80
4	F	341	THR	N-CA-C	-10.85	93.79	110.17
4	F	278	PHE	CA-CB-CG	10.83	124.63	113.80
4	G	39	ASP	N-CA-C	-10.82	87.76	110.80
2	D	39	HIS	N-CA-C	-10.71	100.94	112.93
2	C	43	PHE	CA-CB-CG	-10.57	103.23	113.80
4	F	336	VAL	N-CA-C	-10.56	93.27	108.48
2	D	77	ASP	CA-CB-CG	-10.49	102.11	112.60
3	E	62	CYS	N-CA-CB	10.45	128.15	110.49
4	F	223	ILE	N-CA-C	-10.45	92.98	108.45
2	C	39	HIS	CA-CB-CG	10.34	124.14	113.80
2	B	276	ILE	N-CA-C	-10.32	94.85	108.06
3	E	91	ASP	CA-CB-CG	-10.31	102.29	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	43	PHE	CA-CB-CG	-10.28	103.52	113.80
2	B	360	HIS	CA-CB-CG	-10.26	103.55	113.80
1	A	332	CYS	N-CA-C	-10.24	99.81	110.97
1	A	221	LEU	N-CA-C	10.23	122.43	111.28
2	D	4	GLN	N-CA-C	10.21	123.52	110.24
3	E	111	VAL	N-CA-C	-10.21	93.34	108.45
4	F	181	SER	N-CA-C	-10.20	93.94	109.14
2	C	17	ASP	CA-CB-CG	10.20	122.80	112.60
2	B	65	GLU	N-CA-C	-10.14	101.16	112.72
3	E	234	ALA	N-CA-C	10.14	122.34	111.28
1	A	115	ASN	CA-CB-CG	-10.08	102.52	112.60
3	E	222	TYR	CB-CG-CD2	-10.03	105.76	120.80
2	D	157	THR	N-CA-C	-9.99	95.56	111.04
1	A	279	TRP	CA-C-N	9.97	135.77	120.82
1	A	279	TRP	C-N-CA	9.97	135.77	120.82
2	C	77	ASP	CA-CB-CG	-9.97	102.63	112.60
4	G	84	GLU	CB-CG-CD	-9.95	95.69	112.60
2	D	297	LEU	N-CA-CB	9.94	124.42	110.01
4	F	333	CYS	N-CA-CB	9.90	127.22	110.49
1	A	5	TYR	N-CA-C	-9.88	96.27	110.40
4	F	261	ASP	N-CA-C	9.88	122.12	111.36
1	A	55	ILE	N-CA-C	-9.85	93.19	107.77
1	A	273	PHE	CA-CB-CG	-9.85	103.95	113.80
3	E	313	THR	N-CA-C	9.84	121.60	111.07
3	E	280	HIS	CA-CB-CG	-9.84	103.96	113.80
4	G	295	ASN	CA-CB-CG	-9.79	102.81	112.60
2	C	255	ALA	N-CA-C	9.78	121.53	111.07
1	A	186	GLU	N-CA-C	9.77	121.52	111.07
4	F	115	ASP	N-CA-C	-9.76	94.42	108.96
4	F	253	ASP	CA-CB-CG	9.76	122.36	112.60
2	D	174	HIS	CA-CB-CG	-9.73	104.07	113.80
1	A	211	HIS	N-CA-C	9.73	123.58	110.35
2	C	210	ALA	N-CA-C	9.73	122.89	111.71
2	D	320	ILE	CB-CA-C	9.72	120.78	110.37
4	G	332	LYS	N-CA-C	-9.72	101.42	113.38
4	F	119	LEU	N-CA-C	9.72	123.67	110.55
4	F	36	GLN	CB-CG-CD	-9.71	96.09	112.60
3	E	329	LEU	CB-CA-C	-9.71	97.72	110.34
4	F	221	ASN	CA-CB-CG	-9.70	102.90	112.60
4	G	336	VAL	N-CA-C	-9.70	94.01	108.17
2	D	49	VAL	N-CA-C	-9.65	101.35	110.42
3	E	123	ALA	N-CA-C	-9.65	99.82	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	213	ARG	N-CA-C	-9.65	100.45	110.97
2	C	239	ALA	N-CA-C	9.60	121.50	111.14
3	E	260	HIS	CA-CB-CG	-9.57	104.23	113.80
2	B	157	THR	N-CA-C	-9.54	97.64	112.99
4	F	335	ASN	CA-C-O	9.51	130.97	120.70
4	F	335	ASN	N-CA-C	-9.48	93.94	109.40
4	F	207	LEU	N-CA-C	-9.48	100.95	111.28
4	G	57	VAL	N-CA-C	-9.48	94.42	108.45
4	G	187	SER	N-CA-C	-9.47	100.29	112.23
4	F	259	GLY	CA-C-N	9.46	133.31	120.54
4	F	259	GLY	C-N-CA	9.46	133.31	120.54
3	E	208	ASP	CB-CA-C	-9.44	92.90	110.36
4	G	194	ILE	N-CA-C	-9.43	93.81	107.77
4	G	274	SER	N-CA-C	-9.41	96.30	110.14
2	B	342	ALA	N-CA-C	-9.41	95.67	109.50
2	C	81	GLU	CB-CG-CD	-9.38	96.66	112.60
4	G	354	SER	N-CA-C	-9.38	95.13	108.07
2	D	155	ALA	N-CA-C	-9.37	93.14	109.06
2	B	87	PHE	CA-CB-CG	-9.35	104.45	113.80
4	G	274	SER	N-CA-CB	9.34	124.61	110.70
2	C	97	SER	N-CA-C	-9.33	101.59	113.72
4	G	56	ARG	N-CA-C	-9.32	95.24	109.41
3	E	33	PRO	N-CA-C	-9.28	101.74	114.27
4	F	156	ASN	CA-CB-CG	-9.27	103.33	112.60
2	D	65	GLU	N-CA-C	-9.26	102.10	112.57
3	E	73	HIS	CB-CA-C	9.26	124.41	109.41
2	C	330	GLN	N-CA-C	9.25	121.44	111.36
4	F	255	HIS	N-CA-C	-9.24	95.36	109.41
4	F	261	ASP	CB-CA-C	9.24	126.56	110.85
2	D	78	ASN	N-CA-C	-9.21	99.36	111.24
3	E	309	GLU	CB-CG-CD	-9.17	97.01	112.60
4	F	326	ASP	CB-CA-C	-9.16	96.50	110.88
1	A	271	ALA	N-CA-C	-9.15	101.38	111.36
2	D	76	CYS	N-CA-CB	9.15	127.41	111.39
4	F	193	VAL	N-CA-C	-9.13	96.29	108.35
4	G	133	ALA	N-CA-C	9.12	121.22	111.28
2	D	156	THR	N-CA-C	-9.10	94.88	108.79
1	A	75	ALA	N-CA-C	9.09	122.10	111.02
4	F	75	PHE	N-CA-CB	-9.08	96.69	110.13
4	G	134	THR	N-CA-C	-9.08	102.71	113.88
1	A	242	GLU	CB-CG-CD	-9.06	97.20	112.60
3	E	91	ASP	CA-C-N	9.04	132.74	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	91	ASP	C-N-CA	9.04	132.74	120.54
2	C	347	MET	CA-C-N	9.03	129.78	119.94
2	C	347	MET	C-N-CA	9.03	129.78	119.94
4	G	140	GLU	CB-CA-C	-9.03	96.70	110.88
1	A	231	HIS	CA-CB-CG	-9.01	104.79	113.80
1	A	123	ASN	N-CA-C	-9.00	102.45	113.97
4	F	350	GLU	N-CA-C	-8.99	95.66	109.24
4	G	238	ASP	N-CA-C	-8.99	94.25	108.90
1	A	25	GLY	N-CA-C	-8.98	97.79	110.63
3	E	322	TYR	CA-CB-CG	-8.97	97.76	113.90
4	F	9	HIS	CA-CB-CG	-8.95	104.85	113.80
4	F	345	SER	N-CA-C	-8.95	96.12	109.81
4	G	197	ARG	N-CA-C	-8.95	102.28	113.55
2	C	307	ALA	N-CA-C	-8.94	101.69	114.12
2	C	192	ASN	CA-CB-CG	-8.92	103.68	112.60
4	F	351	ASP	CA-CB-CG	8.91	121.52	112.60
4	F	122	TRP	N-CA-C	-8.91	95.00	108.99
3	E	118	ALA	N-CA-C	-8.90	101.58	111.28
1	A	73	LEU	N-CA-C	-8.88	102.57	113.50
2	B	113	TYR	CA-C-N	8.88	134.18	120.68
2	B	113	TYR	C-N-CA	8.88	134.18	120.68
3	E	319	ILE	CB-CA-C	-8.87	100.40	112.02
2	D	137	ASN	CA-CB-CG	-8.86	103.74	112.60
2	C	343	PRO	N-CA-C	-8.85	102.23	114.80
3	E	182	MET	N-CA-C	-8.85	91.95	110.80
4	G	219	GLY	N-CA-C	-8.84	96.97	111.38
1	A	237	ARG	N-CA-C	8.83	120.83	111.03
4	G	239	GLY	N-CA-C	-8.83	97.93	111.00
1	A	168	GLN	CB-CG-CD	-8.83	97.59	112.60
3	E	122	ASP	N-CA-C	8.83	122.06	111.82
2	D	245	ASP	N-CA-C	-8.82	102.43	113.02
2	B	179	ASP	CA-CB-CG	-8.81	103.79	112.60
2	D	306	MET	CA-C-N	8.81	132.44	120.54
2	D	306	MET	C-N-CA	8.81	132.44	120.54
2	B	342	ALA	N-CA-CB	8.78	125.75	109.68
4	F	251	ASN	CA-CB-CG	-8.76	103.84	112.60
2	C	309	ILE	N-CA-C	-8.76	102.60	111.88
4	F	192	SER	N-CA-C	-8.73	95.28	108.99
4	G	231	ILE	N-CA-C	-8.72	94.78	107.78
4	F	220	SER	N-CA-C	-8.71	103.77	114.75
4	G	7	ARG	CA-C-N	8.70	131.76	120.44
4	G	7	ARG	C-N-CA	8.70	131.76	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	48	GLU	CB-CG-CD	-8.70	97.81	112.60
4	F	237	VAL	N-CA-C	-8.70	95.75	108.71
2	C	58	LEU	CA-C-N	8.67	132.25	120.54
2	C	58	LEU	C-N-CA	8.67	132.25	120.54
4	F	162	THR	N-CA-C	-8.67	95.12	109.07
2	B	152	PHE	CA-CB-CG	-8.66	105.14	113.80
4	G	261	ASP	N-CA-C	8.65	121.50	111.11
2	B	348	GLY	N-CA-C	-8.65	102.47	112.50
1	A	4	LEU	N-CA-C	-8.65	96.18	109.24
2	D	345	ARG	CA-C-N	8.63	132.21	120.38
2	D	345	ARG	C-N-CA	8.63	132.21	120.38
3	E	229	TRP	CB-CG-CD2	-8.62	114.73	126.80
4	G	37	VAL	N-CA-C	-8.62	93.78	106.88
2	D	282	LEU	N-CA-C	8.60	120.65	111.28
4	G	331	LEU	N-CA-C	-8.60	95.29	108.96
2	D	116	ALA	N-CA-C	-8.59	102.51	113.16
4	G	353	ALA	CA-C-N	-8.59	109.52	122.23
4	G	353	ALA	C-N-CA	-8.59	109.52	122.23
4	G	204	MET	N-CA-C	-8.59	101.92	111.28
2	C	145	GLU	CB-CG-CD	-8.58	98.02	112.60
4	F	37	VAL	CA-CB-CG2	-8.58	95.82	110.40
4	F	251	ASN	N-CA-CB	8.57	125.39	110.05
2	B	156	THR	N-CA-C	-8.55	96.95	108.24
3	E	114	VAL	N-CA-CB	8.55	120.03	110.72
2	C	229	ASP	CA-CB-CG	-8.54	104.06	112.60
4	F	329	ASN	N-CA-CB	-8.53	97.57	110.12
4	F	160	PHE	CA-CB-CG	-8.53	105.28	113.80
3	E	121	THR	N-CA-CB	8.49	123.62	110.46
2	C	336	ARG	N-CA-C	8.48	121.59	111.33
1	A	227	LYS	N-CA-C	-8.47	103.54	114.04
2	C	78	ASN	CA-CB-CG	-8.46	104.14	112.60
4	G	96	ARG	N-CA-C	-8.46	92.90	107.61
1	A	277	ARG	N-CA-C	-8.44	95.31	108.14
3	E	228	ASP	CA-CB-CG	-8.43	104.17	112.60
2	C	137	ASN	CA-CB-CG	-8.42	104.18	112.60
2	D	290	HIS	CA-CB-CG	-8.41	105.39	113.80
2	C	186	GLN	N-CA-C	8.41	120.36	111.03
3	E	268	VAL	N-CA-C	-8.39	104.41	112.29
4	F	148	HIS	O-C-N	8.38	131.84	122.11
4	F	243	ASP	CA-C-N	8.36	133.98	120.60
4	F	243	ASP	C-N-CA	8.36	133.98	120.60
4	G	8	GLU	CB-CG-CD	-8.35	98.40	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	275	ASN	CA-CB-CG	-8.35	104.25	112.60
2	C	351	MET	CG-SD-CE	-8.33	82.58	100.90
4	F	21	LEU	CA-C-N	8.33	129.18	119.94
4	F	21	LEU	C-N-CA	8.33	129.18	119.94
4	F	213	PRO	N-CA-C	-8.31	95.36	112.47
3	E	38	ASP	CA-CB-CG	-8.29	104.31	112.60
4	G	151	VAL	CB-CA-C	8.29	119.91	110.88
2	C	235	GLN	CB-CG-CD	8.27	126.66	112.60
3	E	191	LEU	CA-C-N	8.27	131.37	120.28
3	E	191	LEU	C-N-CA	8.27	131.37	120.28
4	G	273	LEU	N-CA-C	-8.27	99.48	111.30
3	E	64	GLY	CA-C-N	8.25	131.67	120.54
3	E	64	GLY	C-N-CA	8.25	131.67	120.54
2	B	245	ASP	N-CA-C	8.24	122.84	108.75
4	F	27	LEU	CA-C-N	8.23	127.80	119.24
4	F	27	LEU	C-N-CA	8.23	127.80	119.24
2	B	199	GLU	N-CA-C	-8.23	97.80	109.24
2	C	38	HIS	N-CA-C	-8.23	98.04	110.14
4	F	66	GLY	N-CA-C	-8.22	99.47	110.74
4	F	257	GLU	CA-CB-CG	-8.22	97.66	114.10
4	F	335	ASN	CB-CA-C	-8.22	93.67	109.37
3	E	3	TRP	CB-CG-CD2	-8.21	115.30	126.80
2	D	49	VAL	CB-CA-C	-8.21	101.28	111.87
1	A	55	ILE	CB-CA-C	8.20	121.50	110.42
2	C	366	PRO	N-CA-CB	8.20	110.58	103.36
4	G	296	ASN	CA-CB-CG	-8.20	104.41	112.60
4	G	337	ARG	N-CA-C	-8.19	96.40	109.59
2	C	192	ASN	N-CA-C	-8.19	101.07	112.45
4	G	43	SER	N-CA-C	-8.19	96.99	110.17
4	F	219	GLY	N-CA-C	-8.18	93.80	113.18
4	G	59	LEU	N-CA-C	-8.18	96.09	108.52
2	B	148	GLU	N-CA-C	8.16	120.17	111.28
3	E	84	GLY	N-CA-C	-8.15	104.30	114.16
3	E	267	ASN	N-CA-C	-8.14	93.63	107.23
4	G	149	GLN	N-CA-CB	8.14	124.25	110.49
4	F	194	ILE	CA-C-O	8.14	129.46	120.59
4	G	36	GLN	N-CA-C	-8.13	94.29	108.69
4	G	288	ASN	CA-CB-CG	-8.13	104.47	112.60
4	G	341	THR	N-CA-C	-8.13	93.79	108.02
2	B	221	THR	N-CA-C	-8.12	102.51	111.36
2	C	347	MET	CB-CA-C	-8.11	97.06	110.85
4	F	6	GLU	N-CA-C	-8.11	97.05	109.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	171	ALA	N-CA-C	-8.11	96.65	109.23
2	D	347	MET	CA-CB-CG	8.10	130.29	114.10
2	B	274	ARG	N-CA-C	-8.08	90.81	107.70
2	D	199	GLU	CA-C-N	8.08	127.64	119.24
2	D	199	GLU	C-N-CA	8.08	127.64	119.24
1	A	276	HIS	CA-C-O	8.07	124.37	119.77
1	A	61	TRP	CB-CG-CD2	-8.07	115.50	126.80
2	B	181	GLU	CB-CG-CD	-8.07	98.88	112.60
1	A	316	TYR	CA-CB-CG	-8.07	99.38	113.90
3	E	94	ARG	O-C-N	-8.06	113.57	122.12
3	E	244	ARG	CA-C-N	8.06	131.08	120.28
3	E	244	ARG	C-N-CA	8.06	131.08	120.28
1	A	145	ALA	N-CA-C	8.05	119.68	111.07
4	G	160	PHE	CB-CA-C	-8.05	98.47	110.62
3	E	47	TYR	N-CA-CB	-8.02	95.91	110.27
4	F	32	ASN	N-CA-C	-8.01	97.10	109.52
4	F	338	MET	CA-C-N	-8.01	110.83	122.44
4	F	338	MET	C-N-CA	-8.01	110.83	122.44
2	B	344	ASP	N-CA-C	-8.00	93.76	110.80
4	F	155	LEU	CA-C-N	8.00	135.09	123.17
4	F	155	LEU	C-N-CA	8.00	135.09	123.17
4	G	257	GLU	CA-CB-CG	-8.00	98.10	114.10
2	C	276	ILE	CA-C-N	8.00	132.82	120.75
2	C	276	ILE	C-N-CA	8.00	132.82	120.75
4	F	217	GLN	N-CA-C	-7.99	95.00	108.26
2	D	173	PHE	N-CA-C	-7.99	94.04	108.02
4	F	267	PHE	CB-CA-C	-7.99	97.53	110.79
2	D	14	THR	CA-C-N	7.98	131.31	120.38
2	D	14	THR	C-N-CA	7.98	131.31	120.38
2	B	49	VAL	N-CA-C	-7.98	103.63	112.80
4	G	98	LEU	N-CA-C	-7.97	97.79	110.14
3	E	198	PRO	N-CA-C	-7.96	98.47	111.77
4	F	329	ASN	OD1-CG-ND2	-7.96	114.64	122.60
2	D	277	GLU	CB-CG-CD	-7.96	99.07	112.60
2	D	120	PHE	N-CA-C	-7.95	93.86	110.80
4	G	127	GLU	N-CA-C	-7.95	94.46	108.13
4	F	99	VAL	N-CA-C	-7.94	96.28	107.80
3	E	116	ASP	N-CA-C	-7.94	93.71	107.20
2	C	277	GLU	N-CA-CB	-7.93	98.39	110.04
1	A	159	ASN	CA-CB-CG	-7.90	104.70	112.60
2	D	123	TYR	CA-CB-CG	-7.90	99.67	113.90
2	D	204	GLN	CB-CG-CD	-7.88	99.20	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	96	ARG	N-CA-C	-7.87	96.56	109.40
2	B	351	MET	N-CA-C	-7.87	102.64	111.14
4	F	295	ASN	N-CA-C	-7.87	98.81	110.46
4	G	153	TYR	N-CA-C	7.87	121.38	108.08
2	D	6	LEU	N-CA-CB	-7.86	99.00	110.40
2	B	78	ASN	N-CA-CB	7.86	121.40	110.01
2	D	254	GLU	CB-CG-CD	-7.85	99.25	112.60
2	D	303	GLY	N-CA-C	-7.85	94.58	113.18
1	A	113	ARG	N-CA-C	-7.85	98.26	110.42
4	F	201	ILE	N-CA-C	7.85	117.95	110.42
2	B	347	MET	CB-CA-C	-7.84	97.52	110.85
4	F	252	PRO	N-CA-C	-7.84	103.29	114.18
4	F	308	VAL	CA-C-O	7.84	129.29	121.45
4	G	324	VAL	N-CA-C	7.84	117.90	110.30
2	B	359	PHE	CB-CA-C	-7.83	98.41	111.02
3	E	153	ALA	N-CA-C	7.83	119.81	111.28
2	C	114	ALA	N-CA-C	-7.83	100.21	110.39
3	E	23	GLY	CA-C-N	7.83	132.56	120.75
3	E	23	GLY	C-N-CA	7.83	132.56	120.75
2	C	258	GLU	N-CA-C	-7.82	104.17	112.93
2	D	351	MET	CB-CA-C	-7.82	97.55	110.85
2	D	296	GLN	CB-CA-C	-7.82	98.54	110.90
2	D	298	SER	N-CA-C	-7.82	92.53	109.81
2	C	91	ILE	CA-C-N	7.82	131.84	120.82
2	C	91	ILE	C-N-CA	7.82	131.84	120.82
4	G	146	MET	N-CA-C	-7.81	98.03	110.14
4	F	92	LEU	N-CA-C	-7.80	96.50	109.46
2	D	10	TRP	CB-CG-CD2	-7.80	115.88	126.80
4	F	59	LEU	N-CA-CB	-7.79	98.74	110.90
1	A	333	HIS	CB-CA-C	7.77	125.89	110.42
4	F	335	ASN	N-CA-CB	7.77	124.35	110.83
4	G	336	VAL	CA-C-O	7.77	128.90	120.43
3	E	163	TYR	CA-CB-CG	7.76	127.87	113.90
4	G	319	PHE	CA-CB-CG	-7.76	106.04	113.80
4	G	229	ASP	N-CA-CB	7.75	121.26	110.56
4	F	342	ASP	CA-CB-CG	-7.75	104.86	112.60
1	A	333	HIS	N-CA-C	-7.74	94.31	110.80
4	G	335	ASN	N-CA-CB	7.74	122.93	110.77
2	B	70	ALA	N-CA-C	-7.73	103.43	113.17
4	F	221	ASN	N-CA-C	-7.73	99.27	111.02
4	F	332	LYS	N-CA-C	-7.72	96.70	108.67
2	C	77	ASP	N-CA-C	-7.72	102.84	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	262	ARG	CB-CA-C	-7.72	97.73	110.85
3	E	206	GLN	N-CA-C	-7.71	99.10	110.52
3	E	101	ASN	CA-CB-CG	-7.71	104.89	112.60
4	G	338	MET	N-CA-CB	7.71	123.10	110.69
2	D	75	VAL	CA-C-O	7.71	130.07	121.13
4	G	42	LEU	N-CA-C	-7.69	97.50	108.96
4	G	79	CYS	CB-CA-C	-7.68	98.82	110.88
2	B	174	HIS	CA-CB-CG	-7.66	106.14	113.80
2	C	277	GLU	CB-CG-CD	7.66	125.62	112.60
4	F	97	MET	N-CA-C	-7.66	96.03	108.52
2	D	16	ALA	N-CA-C	7.66	119.62	111.28
3	E	119	LEU	N-CA-C	7.65	122.30	113.19
4	F	351	ASP	N-CA-C	-7.63	100.43	110.43
4	G	145	SER	N-CA-C	-7.63	98.28	109.11
2	C	170	CYS	N-CA-C	7.63	120.99	110.24
4	G	263	LEU	N-CA-CB	-7.63	98.91	110.12
2	D	63	ASN	N-CA-C	-7.62	100.07	111.81
4	F	274	SER	N-CA-C	-7.62	97.81	109.85
2	D	242	GLY	CA-C-N	7.60	131.51	120.71
2	D	242	GLY	C-N-CA	7.60	131.51	120.71
4	G	355	GLN	N-CA-C	-7.59	94.40	107.61
4	G	289	GLN	CB-CG-CD	-7.59	99.69	112.60
4	F	258	ALA	N-CA-C	-7.58	96.03	108.07
2	D	358	ALA	N-CA-C	-7.56	103.00	112.90
2	C	51	LYS	CA-C-N	7.55	130.72	120.44
2	C	51	LYS	C-N-CA	7.55	130.72	120.44
4	F	37	VAL	N-CA-C	-7.55	96.67	108.23
4	G	351	ASP	N-CA-C	-7.55	99.10	110.28
3	E	205	PHE	CB-CA-C	-7.55	95.22	109.72
4	F	348	GLN	N-CA-CB	7.55	121.60	110.35
4	F	261	ASP	CA-CB-CG	-7.54	105.06	112.60
3	E	152	LEU	N-CA-CB	7.54	122.70	110.41
3	E	276	GLU	CB-CG-CD	-7.53	99.80	112.60
1	A	24	LEU	N-CA-C	-7.53	96.97	109.24
2	D	296	GLN	CB-CG-CD	-7.53	99.80	112.60
1	A	264	SER	N-CA-CB	7.53	122.28	110.84
4	F	37	VAL	N-CA-CB	7.52	119.58	111.00
2	C	305	ASP	N-CA-C	-7.51	103.23	113.30
4	F	91	GLN	CB-CG-CD	-7.51	99.83	112.60
4	G	70	VAL	N-CA-C	-7.51	99.50	107.84
2	C	234	THR	CA-C-O	-7.49	112.61	120.55
4	F	306	LEU	N-CA-CB	7.49	123.16	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	217	TRP	N-CA-CB	-7.49	99.06	110.07
4	F	318	GLY	N-CA-C	-7.49	101.06	112.89
3	E	278	ALA	N-CA-C	-7.49	103.20	111.36
1	A	198	THR	N-CA-C	-7.48	96.89	108.42
4	F	201	ILE	N-CA-CB	-7.48	101.80	110.55
4	G	254	LYS	N-CA-C	-7.48	97.39	109.96
4	F	281	VAL	CB-CA-C	7.46	120.49	110.42
1	A	314	GLN	N-CA-CB	-7.46	100.98	110.90
1	A	338	ASP	CA-C-N	7.45	132.72	123.10
1	A	338	ASP	C-N-CA	7.45	132.72	123.10
1	A	302	VAL	CB-CA-C	-7.45	100.61	112.16
2	C	132	SER	CA-C-N	7.44	131.25	120.38
2	C	132	SER	C-N-CA	7.44	131.25	120.38
4	G	191	HIS	N-CA-C	-7.44	97.77	109.07
4	G	306	LEU	N-CA-C	-7.43	99.08	108.45
3	E	66	GLN	N-CA-CB	7.43	121.28	110.20
4	G	153	TYR	CB-CA-C	-7.42	108.02	116.63
2	B	221	THR	N-CA-CB	7.41	121.13	110.16
4	F	84	GLU	CA-CB-CG	-7.41	99.28	114.10
4	F	122	TRP	CA-C-O	7.41	129.29	120.99
4	G	230	PHE	N-CA-C	-7.41	99.29	109.95
2	D	63	ASN	N-CA-CB	7.39	122.05	111.25
4	F	148	HIS	N-CA-C	-7.39	101.70	111.24
3	E	182	MET	N-CA-CB	7.38	122.97	110.49
1	A	277	ARG	NE-CZ-NH2	-7.38	112.56	119.20
2	D	26	THR	N-CA-C	-7.38	103.31	111.36
3	E	141	PHE	CA-CB-CG	-7.38	106.42	113.80
4	G	147	ALA	N-CA-C	-7.38	97.41	108.99
1	A	282	ARG	CA-CB-CG	-7.38	99.35	114.10
2	D	105	ARG	N-CA-C	7.37	119.01	110.97
1	A	59	THR	CA-C-N	7.36	135.60	121.54
1	A	59	THR	C-N-CA	7.36	135.60	121.54
1	A	222	LEU	N-CA-C	7.36	119.94	111.11
2	B	338	GLU	CB-CA-C	-7.35	95.38	110.38
2	D	233	SER	N-CA-C	-7.35	98.00	108.96
3	E	203	ALA	CA-C-N	7.34	130.44	120.38
3	E	203	ALA	C-N-CA	7.34	130.44	120.38
2	B	347	MET	CA-C-N	7.34	128.09	119.94
2	B	347	MET	C-N-CA	7.34	128.09	119.94
3	E	289	ILE	N-CA-C	7.34	118.11	110.62
1	A	329	LEU	N-CA-C	-7.33	104.59	113.97
4	F	218	ILE	N-CA-C	-7.33	97.79	108.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	62	CYS	CA-C-N	7.32	130.09	120.28
3	E	62	CYS	C-N-CA	7.32	130.09	120.28
3	E	68	MET	N-CA-C	-7.32	103.31	112.90
4	F	12	LYS	CA-C-O	7.31	125.89	118.73
1	A	285	MET	CA-C-O	7.30	128.37	119.97
2	D	66	THR	N-CA-C	-7.30	93.42	108.53
2	D	76	CYS	CA-C-N	7.29	130.39	120.54
2	D	76	CYS	C-N-CA	7.29	130.39	120.54
2	D	5	VAL	CA-C-O	7.29	128.72	121.72
4	F	57	VAL	N-CA-C	-7.29	98.29	108.27
3	E	188	LEU	N-CA-C	7.28	119.00	111.14
1	A	93	ILE	CA-C-N	7.28	130.36	120.54
1	A	93	ILE	C-N-CA	7.28	130.36	120.54
2	D	100	LYS	CA-C-N	7.27	130.75	120.42
2	D	100	LYS	C-N-CA	7.27	130.75	120.42
1	A	139	CYS	CA-C-N	7.26	131.71	120.75
1	A	139	CYS	C-N-CA	7.26	131.71	120.75
2	C	162	LEU	N-CA-C	7.26	118.79	109.65
4	G	267	PHE	CB-CA-C	-7.26	98.34	110.68
3	E	57	LYS	N-CA-C	-7.25	98.04	109.07
3	E	166	PRO	CA-C-O	-7.25	115.68	120.90
4	F	317	ILE	CB-CA-C	7.25	121.43	110.62
3	E	239	GLU	N-CA-C	-7.25	103.41	111.82
4	F	222	ASN	N-CA-C	-7.25	98.29	109.52
3	E	324	GLN	CA-C-N	7.24	128.22	120.11
3	E	324	GLN	C-N-CA	7.24	128.22	120.11
4	F	159	LEU	N-CA-CB	7.24	120.34	110.57
4	G	329	ASN	N-CA-CB	-7.23	99.16	110.30
4	F	98	LEU	N-CA-C	-7.23	97.46	108.96
4	G	266	ALA	CA-C-N	7.23	130.28	120.38
4	G	266	ALA	C-N-CA	7.23	130.28	120.38
3	E	192	ARG	NE-CZ-NH2	7.21	125.69	119.20
3	E	70	ALA	N-CA-C	-7.21	103.15	112.23
2	B	112	GLN	N-CA-CB	7.21	122.67	110.49
3	E	108	GLY	N-CA-C	-7.20	101.08	112.61
1	A	40	GLN	CB-CG-CD	-7.20	100.36	112.60
2	D	89	ASP	CB-CA-C	-7.20	98.44	110.68
1	A	270	ARG	N-CA-C	7.20	126.13	110.80
3	E	176	LEU	CA-C-N	7.18	131.22	120.31
3	E	176	LEU	C-N-CA	7.18	131.22	120.31
4	F	9	HIS	CB-CG-CD2	-7.18	121.87	131.20
2	D	245	ASP	CA-CB-CG	7.18	119.78	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	285	MET	N-CA-C	7.17	119.10	111.28
2	C	313	MET	N-CA-C	7.17	118.74	111.07
4	F	75	PHE	CA-CB-CG	-7.16	106.64	113.80
4	F	296	ASN	CA-CB-CG	7.16	119.76	112.60
4	G	262	LEU	N-CA-C	-7.16	103.41	111.14
2	B	14	THR	N-CA-C	-7.16	98.43	109.24
3	E	58	SER	N-CA-C	-7.15	104.03	112.89
1	A	90	ASN	CA-CB-CG	-7.14	105.46	112.60
4	F	289	GLN	N-CA-CB	7.14	121.33	110.70
2	B	122	VAL	N-CA-C	-7.13	97.21	107.77
2	D	76	CYS	CA-C-O	7.13	128.73	120.89
2	D	320	ILE	CA-C-N	7.13	124.86	119.66
2	D	320	ILE	C-N-CA	7.13	124.86	119.66
4	F	130	LEU	CB-CA-C	-7.12	98.23	109.42
2	C	179	ASP	N-CA-CB	7.12	120.51	110.04
4	G	339	MET	CG-SD-CE	-7.12	85.23	100.90
4	F	64	GLU	N-CA-C	-7.12	97.03	109.48
3	E	104	ALA	N-CA-C	-7.11	99.95	110.48
2	C	303	GLY	CA-C-N	7.11	133.50	122.49
2	C	303	GLY	C-N-CA	7.11	133.50	122.49
4	G	101	SER	N-CA-C	-7.11	95.91	108.13
4	F	176	ARG	NE-CZ-NH2	-7.10	112.81	119.20
4	G	67	ALA	N-CA-C	-7.10	97.65	109.07
2	C	256	MET	CG-SD-CE	-7.09	85.31	100.90
1	A	295	GLN	N-CA-C	7.09	120.82	111.75
4	F	352	ALA	N-CA-C	-7.09	102.75	111.40
2	D	196	ILE	N-CA-CB	7.08	122.03	110.13
2	B	54	ILE	N-CA-C	7.08	117.18	110.53
4	G	97	MET	N-CA-C	-7.07	96.99	108.52
4	G	352	ALA	N-CA-C	-7.07	103.32	112.23
1	A	278	VAL	N-CA-CB	7.07	122.89	111.23
3	E	92	ALA	CA-C-O	7.07	128.46	120.90
4	F	314	GLU	CB-CG-CD	-7.07	100.59	112.60
2	B	105	ARG	CA-C-N	7.07	130.06	120.38
2	B	105	ARG	C-N-CA	7.07	130.06	120.38
3	E	122	ASP	CB-CA-C	-7.06	97.11	110.67
4	G	325	LEU	CA-C-N	7.06	130.06	120.38
4	G	325	LEU	C-N-CA	7.06	130.06	120.38
1	A	294	SER	N-CA-C	-7.05	97.76	109.46
1	A	207	ASN	CA-CB-CG	7.04	119.64	112.60
1	A	21	TYR	CA-C-N	7.04	132.64	122.85
1	A	21	TYR	C-N-CA	7.04	132.64	122.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	350	GLU	N-CA-C	-7.03	98.66	109.14
4	F	116	PHE	N-CA-C	-7.03	94.27	109.81
4	G	328	LEU	CA-C-O	7.03	128.00	120.55
3	E	157	SER	N-CA-C	-7.02	103.56	111.07
2	C	100	LYS	CA-C-N	7.01	130.07	120.46
2	C	100	LYS	C-N-CA	7.01	130.07	120.46
4	F	10	LEU	N-CA-C	-7.00	103.40	112.23
4	G	63	HIS	N-CA-C	-7.00	98.08	108.79
4	F	148	HIS	CA-C-N	7.00	133.80	122.81
4	F	148	HIS	C-N-CA	7.00	133.80	122.81
4	F	6	GLU	CA-CB-CG	-6.99	100.11	114.10
1	A	279	TRP	CB-CA-C	-6.98	97.28	109.64
4	G	252	PRO	N-CA-C	-6.98	98.09	112.47
1	A	291	ASN	N-CA-C	-6.97	104.92	113.50
2	B	198	HIS	CA-CB-CG	6.97	120.77	113.80
4	F	206	MET	CG-SD-CE	-6.97	85.57	100.90
4	G	284	TYR	CA-CB-CG	-6.97	101.36	113.90
2	B	11	ARG	N-CA-C	-6.96	102.12	110.13
4	G	75	PHE	N-CA-CB	-6.96	99.86	110.16
2	C	107	LEU	CA-C-N	6.95	129.59	120.28
2	C	107	LEU	C-N-CA	6.95	129.59	120.28
2	C	111	VAL	CA-C-O	6.95	128.21	120.85
2	D	292	ILE	N-CA-CB	-6.94	102.81	110.51
2	C	206	LEU	CA-C-N	6.93	130.50	120.38
2	C	206	LEU	C-N-CA	6.93	130.50	120.38
2	C	156	THR	N-CA-C	-6.93	96.21	108.13
1	A	317	GLY	N-CA-C	-6.92	97.82	111.31
4	G	322	SER	N-CA-CB	6.92	120.29	110.12
4	G	335	ASN	N-CA-C	-6.91	97.00	108.34
2	D	348	GLY	N-CA-C	6.91	122.62	113.37
1	A	300	GLN	CB-CG-CD	-6.90	100.86	112.60
4	F	264	LYS	CB-CA-C	-6.90	99.12	110.85
2	D	291	ARG	N-CA-C	6.90	118.45	111.07
4	G	272	ILE	N-CA-C	6.89	117.65	110.62
2	C	119	ARG	N-CA-C	-6.89	104.88	113.28
3	E	158	ARG	NE-CZ-NH1	6.89	128.39	121.50
1	A	332	CYS	O-C-N	6.88	129.19	122.03
2	D	321	PRO	CA-C-N	6.88	126.40	119.24
2	D	321	PRO	C-N-CA	6.88	126.40	119.24
4	G	351	ASP	CA-CB-CG	6.88	119.48	112.60
4	F	274	SER	CB-CA-C	-6.88	96.32	109.66
3	E	186	ALA	N-CA-C	-6.88	103.89	112.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	11	ARG	N-CA-CB	6.88	117.26	109.49
4	F	230	PHE	CA-CB-CG	-6.87	106.93	113.80
2	D	277	GLU	CA-C-N	6.87	129.79	120.44
2	D	277	GLU	C-N-CA	6.87	129.79	120.44
3	E	297	ARG	CA-C-O	-6.87	113.27	120.55
2	C	338	GLU	CB-CA-C	-6.87	97.70	109.65
2	D	103	ASP	N-CA-C	-6.87	103.87	111.36
2	D	128	VAL	CA-C-N	6.87	131.12	120.82
2	D	128	VAL	C-N-CA	6.87	131.12	120.82
4	F	256	LEU	N-CA-CB	6.86	122.08	110.49
4	F	207	LEU	N-CA-CB	6.86	120.20	110.12
2	C	75	VAL	N-CA-C	-6.85	98.02	107.75
3	E	294	CYS	N-CA-C	-6.85	103.74	111.14
3	E	49	LEU	CA-C-O	6.85	127.29	119.27
3	E	140	TRP	N-CA-C	-6.85	97.11	108.34
4	F	126	VAL	N-CA-C	-6.85	98.25	108.46
2	D	102	GLU	CB-CG-CD	-6.85	100.96	112.60
2	D	335	GLY	CA-C-N	6.84	129.45	120.28
2	D	335	GLY	C-N-CA	6.84	129.45	120.28
2	D	136	PHE	CA-CB-CG	-6.84	106.96	113.80
1	A	141	THR	CA-C-N	6.84	126.80	119.76
1	A	141	THR	C-N-CA	6.84	126.80	119.76
2	C	75	VAL	N-CA-CB	6.83	122.24	110.96
4	F	50	GLU	CB-CG-CD	-6.83	100.99	112.60
3	E	122	ASP	CA-CB-CG	-6.83	105.77	112.60
3	E	61	HIS	CA-CB-CG	-6.82	106.98	113.80
3	E	298	GLU	CB-CA-C	-6.82	100.18	110.88
2	C	196	ILE	N-CA-C	-6.81	98.94	108.27
2	D	109	ASP	N-CA-C	6.81	119.57	111.33
4	F	82	LEU	N-CA-CB	6.80	120.04	110.11
3	E	15	VAL	CB-CA-C	-6.80	101.24	112.26
1	A	213	THR	CA-C-N	6.80	127.35	119.47
1	A	213	THR	C-N-CA	6.80	127.35	119.47
2	D	338	GLU	CB-CG-CD	-6.80	101.05	112.60
3	E	168	PRO	CA-C-N	6.79	129.68	120.38
3	E	168	PRO	C-N-CA	6.79	129.68	120.38
4	F	182	MET	CG-SD-CE	-6.78	85.98	100.90
2	D	190	ILE	N-CA-C	6.78	116.88	110.30
3	E	95	GLU	CB-CG-CD	-6.77	101.08	112.60
4	F	200	VAL	CB-CA-C	-6.77	103.01	112.14
4	G	148	HIS	CA-C-N	6.77	134.46	121.54
4	G	148	HIS	C-N-CA	6.77	134.46	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	82	LEU	CD1-CG-CD2	6.76	125.68	110.80
1	A	106	ASP	N-CA-C	-6.76	99.01	109.76
2	B	306	MET	CG-SD-CE	-6.75	86.06	100.90
2	B	76	CYS	CB-CA-C	-6.73	100.11	110.88
4	G	276	GLU	CA-CB-CG	-6.73	100.64	114.10
2	C	125	ILE	CB-CA-C	-6.72	104.19	111.59
1	A	114	GLY	CA-C-O	6.72	125.55	120.91
2	B	117	ARG	CA-C-N	6.71	128.92	122.27
2	B	117	ARG	C-N-CA	6.71	128.92	122.27
4	F	60	VAL	N-CA-C	-6.71	106.11	113.43
3	E	42	TYR	N-CA-CB	-6.71	99.97	110.30
4	F	112	PRO	N-CA-C	-6.70	100.69	111.14
2	C	146	PRO	CA-C-N	6.70	127.61	120.11
2	C	146	PRO	C-N-CA	6.70	127.61	120.11
2	D	179	ASP	CA-C-N	6.70	129.24	120.60
2	D	179	ASP	C-N-CA	6.70	129.24	120.60
3	E	50	CYS	N-CA-C	-6.69	104.86	113.16
1	A	338	ASP	CA-CB-CG	6.69	119.29	112.60
1	A	104	LEU	CA-C-N	6.68	131.63	122.07
1	A	104	LEU	C-N-CA	6.68	131.63	122.07
3	E	112	VAL	N-CA-C	-6.68	96.01	107.24
4	F	259	GLY	O-C-N	6.67	127.36	122.62
2	D	240	MET	N-CA-CB	6.67	120.06	110.06
2	C	278	TRP	CB-CA-C	-6.66	96.28	109.67
4	F	96	ARG	CA-C-O	6.66	127.90	120.70
3	E	1	MET	CG-SD-CE	6.66	115.55	100.90
2	B	315	GLU	CB-CG-CD	-6.65	101.29	112.60
1	A	292	ARG	N-CA-C	-6.64	103.21	112.45
3	E	267	ASN	OD1-CG-ND2	6.64	129.24	122.60
4	G	289	GLN	N-CA-C	-6.64	96.65	110.80
2	D	307	ALA	N-CA-C	6.64	119.08	111.11
4	G	180	CYS	N-CA-C	-6.64	99.36	109.85
2	D	194	GLU	CA-C-N	6.64	129.50	120.54
2	D	194	GLU	C-N-CA	6.64	129.50	120.54
4	G	185	GLY	N-CA-C	-6.64	101.47	110.43
2	D	234	THR	O-C-N	6.63	130.19	122.17
1	A	274	ASP	CA-CB-CG	-6.63	105.97	112.60
2	B	31	GLY	CA-C-N	6.63	129.16	120.28
2	B	31	GLY	C-N-CA	6.63	129.16	120.28
1	A	276	HIS	N-CA-C	-6.62	97.97	108.30
3	E	236	LEU	N-CA-CB	-6.62	101.47	110.67
2	C	235	GLN	CB-CA-C	-6.62	100.49	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	366	PRO	O-C-N	6.62	130.51	123.10
2	C	126	ASP	CA-CB-CG	6.62	119.22	112.60
2	D	84	GLN	N-CA-C	-6.62	99.36	109.41
4	F	319	PHE	CB-CA-C	-6.62	98.05	110.16
4	F	60	VAL	CB-CA-C	-6.60	102.59	110.84
4	F	13	PRO	CB-CA-C	-6.60	102.04	111.68
4	F	191	HIS	N-CA-C	-6.60	96.75	110.80
4	G	222	ASN	CA-C-O	6.59	128.36	121.38
1	A	288	GLU	N-CA-C	6.59	118.12	111.07
2	D	347	MET	CB-CA-C	6.58	121.72	110.79
4	G	206	MET	CG-SD-CE	-6.58	86.42	100.90
1	A	237	ARG	CB-CA-C	-6.58	100.75	110.95
2	C	341	TYR	CA-CB-CG	-6.58	102.06	113.90
2	D	346	ARG	N-CA-CB	-6.58	100.19	110.06
4	G	345	SER	N-CA-C	-6.58	98.72	108.79
4	F	324	VAL	N-CA-C	6.58	119.31	111.09
1	A	57	PRO	CA-C-N	6.58	130.49	120.82
1	A	57	PRO	C-N-CA	6.58	130.49	120.82
2	C	226	ALA	N-CA-C	6.57	120.51	112.23
2	D	44	SER	N-CA-C	-6.57	97.56	108.34
2	B	81	GLU	CB-CG-CD	-6.57	101.43	112.60
1	A	74	PHE	CA-C-N	6.57	129.92	120.79
1	A	74	PHE	C-N-CA	6.57	129.92	120.79
2	D	29	ALA	N-CA-C	-6.57	104.04	111.07
4	F	54	VAL	N-CA-C	-6.56	99.03	108.48
2	B	21	GLN	CB-CG-CD	-6.56	101.45	112.60
2	C	156	THR	CA-C-N	6.55	129.36	120.38
2	C	156	THR	C-N-CA	6.55	129.36	120.38
3	E	62	CYS	CB-CA-C	-6.55	97.39	110.42
4	F	113	ALA	CB-CA-C	-6.54	98.46	109.65
3	E	37	ASP	N-CA-CB	-6.54	100.14	110.22
2	D	10	TRP	CB-CG-CD1	6.54	136.71	126.90
3	E	164	LEU	N-CA-CB	6.53	121.52	110.49
2	D	188	GLU	N-CA-C	-6.52	104.17	111.28
1	A	160	LEU	N-CA-C	-6.51	102.40	110.41
1	A	199	LEU	CA-C-N	6.51	125.74	118.97
1	A	199	LEU	C-N-CA	6.51	125.74	118.97
4	G	64	GLU	N-CA-C	-6.51	97.76	109.09
4	G	188	LEU	N-CA-CB	6.50	121.95	110.37
3	E	110	LYS	N-CA-C	-6.50	100.34	110.42
1	A	164	ASP	N-CA-C	-6.50	105.17	113.23
2	C	173	PHE	CA-CB-CG	-6.50	107.30	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	139	LEU	N-CA-C	6.50	119.19	111.71
4	G	6	GLU	CB-CG-CD	-6.50	101.55	112.60
4	F	262	LEU	CA-C-N	6.50	129.52	120.29
4	F	262	LEU	C-N-CA	6.50	129.52	120.29
4	F	214	LEU	N-CA-C	-6.50	98.14	108.73
4	G	120	ASP	N-CA-CB	6.49	119.58	110.04
2	B	338	GLU	N-CA-CB	6.49	120.29	110.30
1	A	105	HIS	N-CA-C	-6.48	102.72	111.54
2	D	216	ASP	CA-CB-CG	-6.48	106.12	112.60
4	G	140	GLU	CB-CG-CD	-6.47	101.60	112.60
4	G	265	GLN	CB-CA-C	-6.47	101.00	110.96
3	E	4	TYR	N-CA-C	-6.47	95.52	109.81
4	G	256	LEU	N-CA-C	-6.47	97.82	108.49
4	F	213	PRO	CA-C-N	-6.47	114.17	122.77
4	F	213	PRO	C-N-CA	-6.47	114.17	122.77
2	C	42	LEU	CB-CA-C	-6.46	102.95	111.42
2	C	203	LEU	N-CA-CB	6.46	119.38	110.01
2	D	25	LEU	CB-CA-C	-6.46	100.69	110.90
2	C	30	ASN	N-CA-C	6.45	118.86	111.11
4	G	157	GLY	N-CA-C	-6.45	102.05	112.31
1	A	279	TRP	N-CA-CB	6.45	120.24	109.92
4	F	38	ALA	N-CA-CB	6.45	121.42	110.71
1	A	58	ASN	N-CA-CB	6.45	120.23	109.92
1	A	75	ALA	CA-C-N	6.45	133.85	121.54
1	A	75	ALA	C-N-CA	6.45	133.85	121.54
1	A	216	HIS	CA-C-O	6.45	127.59	120.63
1	A	203	GLU	N-CA-C	6.44	118.38	111.36
2	B	341	TYR	N-CA-C	-6.44	105.06	113.17
2	B	91	ILE	N-CA-CB	6.43	120.00	111.25
2	B	109	ASP	N-CA-CB	6.43	121.26	110.32
2	C	263	ARG	N-CA-CB	6.43	119.33	110.01
4	F	276	GLU	N-CA-C	-6.42	105.60	113.50
2	D	56	ARG	NE-CZ-NH2	6.42	124.98	119.20
4	F	209	GLY	CA-C-N	6.42	129.80	120.11
4	F	209	GLY	C-N-CA	6.42	129.80	120.11
2	D	338	GLU	N-CA-C	6.42	120.72	113.02
4	G	191	HIS	N-CA-CB	6.42	122.38	111.66
2	D	173	PHE	N-CA-CB	6.41	120.78	110.65
4	F	93	GLU	N-CA-C	-6.41	92.80	107.48
4	G	246	ARG	NE-CZ-NH2	6.41	124.97	119.20
1	A	208	ASP	N-CA-C	-6.41	105.04	112.92
2	B	199	GLU	CB-CG-CD	-6.41	101.71	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	344	ASP	N-CA-C	-6.40	99.87	110.17
3	E	180	VAL	N-CA-CB	6.40	121.85	111.36
4	G	229	ASP	CB-CA-C	-6.40	99.74	110.81
2	B	341	TYR	CA-C-N	6.39	129.24	120.67
2	B	341	TYR	C-N-CA	6.39	129.24	120.67
2	C	80	ARG	CB-CA-C	-6.39	100.84	110.88
2	D	306	MET	N-CA-C	-6.39	102.74	111.56
4	G	341	THR	CA-C-N	6.39	130.98	121.72
4	G	341	THR	C-N-CA	6.39	130.98	121.72
4	F	47	THR	N-CA-C	-6.39	100.52	110.42
2	B	282	LEU	CB-CA-C	-6.39	100.19	110.79
4	G	366	LEU	N-CA-C	-6.39	93.12	111.00
2	B	44	SER	N-CA-C	-6.38	99.42	108.23
2	C	164	VAL	N-CA-C	6.38	117.13	110.62
4	G	90	VAL	CB-CA-C	-6.38	99.70	111.18
1	A	281	ASN	N-CA-CB	-6.37	100.49	110.30
3	E	37	ASP	CA-C-N	6.37	128.72	120.44
3	E	37	ASP	C-N-CA	6.37	128.72	120.44
2	C	50	GLY	CA-C-N	6.37	129.10	120.38
2	C	50	GLY	C-N-CA	6.37	129.10	120.38
2	C	80	ARG	CA-C-N	6.37	129.13	120.54
2	C	80	ARG	C-N-CA	6.37	129.13	120.54
1	A	325	GLU	CA-C-N	6.36	127.00	119.94
1	A	325	GLU	C-N-CA	6.36	127.00	119.94
3	E	303	VAL	CA-CB-CG2	-6.36	99.59	110.40
1	A	258	VAL	CB-CA-C	-6.36	103.83	111.97
4	F	357	ALA	CA-C-O	6.36	128.86	120.15
2	D	304	ASN	N-CA-CB	6.35	119.31	109.97
4	F	182	MET	N-CA-C	-6.35	95.77	109.81
2	B	114	ALA	CA-C-N	6.35	127.78	119.84
2	B	114	ALA	C-N-CA	6.35	127.78	119.84
4	F	359	TYR	N-CA-C	-6.35	97.71	108.26
4	G	150	ASP	CA-CB-CG	6.35	118.95	112.60
1	A	141	THR	N-CA-C	6.35	119.51	110.24
4	G	356	SER	CB-CA-C	6.35	123.05	110.42
2	C	330	GLN	CB-CG-CD	-6.34	101.82	112.60
2	B	152	PHE	N-CA-C	-6.34	98.07	108.41
4	G	82	LEU	N-CA-C	-6.34	101.54	110.29
1	A	265	ALA	N-CA-C	-6.34	97.30	110.80
2	B	206	LEU	CA-C-N	6.34	129.06	120.44
2	B	206	LEU	C-N-CA	6.34	129.06	120.44
3	E	312	ILE	CA-CB-CG1	6.34	121.17	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	167	PRO	CA-C-N	6.33	126.35	119.89
3	E	167	PRO	C-N-CA	6.33	126.35	119.89
2	D	279	GLU	N-CA-C	6.33	117.84	111.07
3	E	229	TRP	N-CA-C	-6.32	105.72	113.50
4	F	55	ALA	N-CA-C	-6.32	99.51	109.50
2	B	321	PRO	CA-C-N	6.32	126.01	119.56
2	B	321	PRO	C-N-CA	6.32	126.01	119.56
4	G	295	ASN	N-CA-C	-6.32	99.43	109.23
3	E	133	GLU	N-CA-C	-6.31	101.26	111.04
1	A	329	LEU	N-CA-CB	-6.31	101.90	110.67
4	G	92	LEU	N-CA-C	-6.30	98.46	108.73
3	E	192	ARG	CB-CA-C	-6.30	100.33	110.79
1	A	87	ASN	N-CA-CB	-6.30	101.39	110.65
1	A	293	LEU	CA-C-N	6.30	131.07	122.19
1	A	293	LEU	C-N-CA	6.30	131.07	122.19
2	D	231	GLN	CB-CG-CD	-6.30	101.90	112.60
2	D	101	VAL	N-CA-C	-6.29	104.36	110.72
4	F	301	GLU	CB-CG-CD	-6.29	101.90	112.60
1	A	21	TYR	N-CA-C	-6.29	97.44	108.20
2	B	110	ASN	CB-CA-C	-6.29	99.93	110.56
4	F	53	MET	CG-SD-CE	-6.29	87.06	100.90
4	F	52	GLU	CB-CG-CD	-6.29	101.91	112.60
4	F	132	GLN	CB-CG-CD	-6.29	101.91	112.60
3	E	299	GLN	CB-CG-CD	-6.28	101.92	112.60
1	A	225	LYS	O-C-N	6.28	131.02	122.48
3	E	260	HIS	N-CA-CB	6.28	121.19	111.39
4	G	162	THR	N-CA-C	-6.28	99.65	109.25
2	B	299	PRO	N-CA-C	-6.27	105.36	113.57
4	F	329	ASN	CA-CB-CG	6.27	118.87	112.60
4	G	114	ALA	N-CA-C	6.26	118.19	111.36
2	B	38	HIS	N-CA-CB	-6.26	100.90	110.42
3	E	151	LEU	CB-CA-C	-6.26	99.22	110.36
3	E	92	ALA	N-CA-CB	6.25	119.26	109.94
4	G	155	LEU	N-CA-C	-6.25	104.36	112.68
4	F	275	ASN	N-CA-CB	-6.25	99.93	110.49
3	E	34	GLY	N-CA-C	-6.25	106.92	114.66
4	F	81	GLY	N-CA-C	-6.25	106.60	114.16
4	F	106	PHE	CA-CB-CG	-6.24	107.56	113.80
4	F	6	GLU	N-CA-CB	6.24	120.84	110.85
4	F	68	THR	N-CA-C	-6.24	99.95	108.38
2	B	17	ASP	CA-CB-CG	6.24	118.83	112.60
2	D	167	LEU	CA-C-N	6.22	129.24	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	167	LEU	C-N-CA	6.22	129.24	120.28
3	E	37	ASP	N-CA-C	6.22	118.87	111.71
3	E	126	ASN	N-CA-C	-6.22	104.41	111.07
3	E	172	ALA	CA-C-N	6.22	128.31	120.72
3	E	172	ALA	C-N-CA	6.22	128.31	120.72
2	C	267	LEU	N-CA-C	-6.21	105.19	112.89
4	F	241	PHE	CA-C-N	6.21	127.61	119.84
4	F	241	PHE	C-N-CA	6.21	127.61	119.84
2	C	306	MET	N-CA-C	-6.21	97.95	108.26
2	B	100	LYS	N-CA-C	-6.21	100.80	110.42
1	A	281	ASN	CA-CB-CG	6.21	118.81	112.60
2	B	97	SER	N-CA-C	-6.21	104.52	113.21
2	D	79	CYS	N-CA-C	6.21	118.84	111.33
2	D	111	VAL	CA-C-N	6.21	129.41	120.79
2	D	111	VAL	C-N-CA	6.21	129.41	120.79
4	F	32	ASN	CA-CB-CG	-6.20	106.40	112.60
4	G	38	ALA	N-CA-C	-6.20	103.83	111.33
1	A	298	LEU	CB-CA-C	6.19	121.07	110.79
4	F	224	ARG	NE-CZ-NH2	-6.19	113.63	119.20
2	C	242	GLY	O-C-N	-6.19	117.50	122.51
4	G	241	PHE	CA-CB-CG	-6.19	107.61	113.80
2	D	23	HIS	N-CA-C	-6.18	103.69	111.11
4	G	361	VAL	N-CA-C	-6.18	99.78	108.80
3	E	73	HIS	N-CA-C	-6.17	101.88	109.65
3	E	127	ALA	N-CA-C	6.17	118.79	111.33
3	E	229	TRP	N-CA-CB	-6.17	101.46	110.53
2	D	321	PRO	O-C-N	6.17	124.15	121.31
4	G	58	ALA	O-C-N	-6.17	115.44	123.02
4	F	119	LEU	CB-CA-C	-6.16	97.50	109.76
4	G	202	GLU	CB-CA-C	-6.16	99.23	110.63
1	A	26	ASN	CA-CB-CG	-6.16	106.44	112.60
4	G	338	MET	CB-CA-C	-6.16	98.29	109.38
4	F	309	THR	N-CA-C	-6.15	96.31	107.75
4	G	44	LEU	N-CA-C	-6.15	97.70	110.80
2	C	367	GLU	CA-CB-CG	-6.14	101.81	114.10
4	F	69	THR	N-CA-C	-6.14	98.59	108.55
4	F	350	GLU	O-C-N	6.14	130.60	123.17
2	C	39	HIS	CA-C-N	6.14	131.19	122.72
2	C	39	HIS	C-N-CA	6.14	131.19	122.72
2	C	329	TYR	CA-C-O	6.14	127.03	119.97
3	E	15	VAL	N-CA-CB	-6.14	99.66	110.77
2	C	42	LEU	N-CA-CB	6.14	120.79	110.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	228	ASP	CA-C-O	6.14	126.96	120.33
4	F	109	SER	N-CA-C	-6.13	99.24	109.24
1	A	217	TRP	CB-CG-CD1	-6.13	117.71	126.90
2	B	104	THR	N-CA-C	-6.13	105.83	113.55
4	F	338	MET	CA-C-O	-6.13	114.22	120.71
3	E	282	SER	CA-C-N	6.12	125.85	119.05
3	E	282	SER	C-N-CA	6.12	125.85	119.05
4	F	101	SER	N-CA-C	-6.12	97.76	110.80
2	D	136	PHE	N-CA-C	6.12	118.48	111.02
3	E	125	ALA	CA-C-N	6.11	128.39	120.44
3	E	125	ALA	C-N-CA	6.11	128.39	120.44
4	G	6	GLU	N-CA-C	-6.11	98.56	108.52
4	F	70	VAL	N-CA-C	-6.11	102.11	109.01
4	F	209	GLY	N-CA-C	-6.11	98.70	113.18
4	G	4	THR	N-CA-C	-6.11	101.42	110.46
3	E	129	LEU	CB-CA-C	-6.11	100.65	110.79
4	F	207	LEU	CB-CA-C	-6.11	100.66	110.79
2	D	294	MET	CG-SD-CE	-6.10	87.47	100.90
2	B	347	MET	CG-SD-CE	-6.10	87.48	100.90
2	D	203	LEU	N-CA-CB	6.10	118.85	110.01
3	E	85	LYS	N-CA-C	-6.10	97.82	110.80
2	D	3	TYR	CA-C-N	6.09	129.78	120.82
2	D	3	TYR	C-N-CA	6.09	129.78	120.82
4	F	238	ASP	N-CA-C	-6.09	101.44	110.46
4	G	237	VAL	N-CA-C	-6.09	99.61	108.87
2	D	51	LYS	N-CA-C	-6.09	104.92	112.90
2	C	101	VAL	CA-C-N	6.09	129.27	120.38
2	C	101	VAL	C-N-CA	6.09	129.27	120.38
2	C	257	VAL	CB-CA-C	-6.09	103.92	112.14
2	D	7	ALA	CA-C-N	6.09	128.35	120.44
2	D	7	ALA	C-N-CA	6.09	128.35	120.44
4	F	33	LEU	N-CA-C	-6.09	99.73	109.96
4	F	59	LEU	CB-CA-C	-6.08	101.74	110.62
4	G	201	ILE	CA-C-O	-6.08	114.78	121.29
3	E	202	LEU	N-CA-C	6.08	118.70	111.71
2	C	246	ASP	CA-C-N	6.08	128.71	120.38
2	C	246	ASP	C-N-CA	6.08	128.71	120.38
1	A	3	ARG	N-CA-C	-6.08	99.50	109.40
2	D	240	MET	N-CA-C	-6.08	103.98	111.33
2	B	59	ALA	CA-C-N	6.08	128.70	120.44
2	B	59	ALA	C-N-CA	6.08	128.70	120.44
3	E	12	GLU	N-CA-C	6.07	118.68	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	167	LEU	CA-C-N	6.07	129.02	120.28
2	C	167	LEU	C-N-CA	6.07	129.02	120.28
2	D	319	THR	N-CA-C	-6.07	105.71	113.23
2	C	257	VAL	O-C-N	6.06	127.75	121.87
2	D	213	SER	N-CA-CB	6.06	120.86	110.68
3	E	179	GLU	CB-CG-CD	6.06	122.91	112.60
2	D	274	ARG	N-CA-C	-6.06	105.53	113.17
3	E	201	ALA	N-CA-C	6.06	118.66	111.33
2	D	93	ILE	N-CA-C	6.06	116.57	108.27
1	A	190	LEU	CB-CA-C	-6.05	101.37	110.88
3	E	323	LEU	N-CA-C	-6.05	104.75	111.71
4	G	105	ARG	N-CA-C	-6.05	99.94	108.96
3	E	301	MET	N-CA-C	-6.05	106.03	113.41
3	E	26	ALA	N-CA-CB	6.05	118.67	110.38
2	B	190	ILE	CB-CA-C	-6.05	103.97	112.14
1	A	83	LEU	N-CA-C	-6.04	99.43	109.46
2	C	228	GLY	N-CA-C	-6.04	102.26	112.77
1	A	134	SER	N-CA-CB	-6.04	101.25	110.49
2	B	78	ASN	CA-CB-CG	-6.04	106.56	112.60
2	D	162	LEU	CA-C-N	6.04	127.39	119.84
2	D	162	LEU	C-N-CA	6.04	127.39	119.84
4	G	163	GLU	CB-CG-CD	-6.03	102.34	112.60
4	G	199	GLY	O-C-N	6.03	128.10	122.13
4	G	291	LYS	N-CA-C	-6.03	99.23	108.76
1	A	210	ALA	N-CA-C	6.03	118.10	107.61
1	A	326	GLY	CA-C-N	6.03	128.85	120.29
1	A	326	GLY	C-N-CA	6.03	128.85	120.29
4	F	356	SER	CA-C-N	-6.03	112.66	121.76
4	F	356	SER	C-N-CA	-6.03	112.66	121.76
4	F	51	MET	N-CA-C	-6.02	97.97	110.80
4	G	54	VAL	CA-CB-CG2	-6.02	100.16	110.40
4	F	260	CYS	N-CA-C	-6.02	103.89	111.11
4	F	15	GLN	OE1-CD-NE2	6.02	128.62	122.60
2	D	190	ILE	CA-C-N	6.01	129.16	120.38
2	D	190	ILE	C-N-CA	6.01	129.16	120.38
4	F	161	GLU	CB-CG-CD	-6.01	102.38	112.60
3	E	226	SER	N-CA-C	-6.01	105.44	112.89
4	G	41	THR	N-CA-C	-6.01	100.27	109.65
3	E	50	CYS	CA-CB-SG	-6.01	100.58	114.40
2	D	185	HIS	N-CA-CB	-6.00	101.00	109.94
4	F	14	LEU	N-CA-C	-6.00	105.22	112.54
2	D	23	HIS	CA-C-O	-6.00	114.48	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	241	PHE	CB-CA-C	6.00	118.17	108.87
4	F	139	ILE	CB-CA-C	-6.00	104.05	112.14
1	A	234	GLN	N-CA-C	-5.99	104.75	111.28
2	C	266	ALA	N-CA-C	5.99	117.48	111.07
2	B	112	GLN	N-CA-C	-5.99	98.04	110.80
2	D	164	VAL	CB-CA-C	-5.99	103.95	112.22
2	D	296	GLN	N-CA-CB	5.99	118.75	110.07
2	D	189	HIS	CB-CG-CD2	-5.98	123.42	131.20
1	A	221	LEU	N-CA-CB	-5.98	101.33	110.12
2	B	173	PHE	CB-CA-C	-5.97	100.40	110.19
3	E	22	ARG	N-CA-CB	5.97	120.83	110.44
2	D	290	HIS	CB-CA-C	5.97	120.33	110.90
3	E	91	ASP	CB-CA-C	5.97	120.70	110.79
4	F	173	ASP	N-CA-C	-5.97	105.73	114.39
1	A	118	SER	N-CA-C	-5.97	102.50	110.55
3	E	173	VAL	N-CA-CB	5.97	117.39	110.65
2	C	182	GLN	CA-C-N	5.96	128.08	120.56
2	C	182	GLN	C-N-CA	5.96	128.08	120.56
4	G	326	ASP	CB-CA-C	-5.96	100.54	110.68
2	D	13	GLN	N-CA-C	-5.96	98.10	110.80
1	A	216	HIS	N-CA-CB	-5.96	101.12	110.06
2	C	66	THR	N-CA-C	-5.96	103.72	111.71
2	C	300	ALA	N-CA-C	-5.96	99.35	108.76
3	E	94	ARG	CA-C-O	5.95	127.06	120.63
4	F	336	VAL	CG1-CB-CG2	5.95	123.89	110.80
4	F	338	MET	CA-CB-CG	-5.95	102.20	114.10
4	G	111	LEU	N-CA-C	-5.95	101.34	110.32
2	B	224	ALA	CA-C-N	5.94	128.05	120.56
2	B	224	ALA	C-N-CA	5.94	128.05	120.56
2	D	219	SER	N-CA-C	5.94	117.43	111.07
3	E	24	HIS	N-CA-C	-5.94	102.27	110.35
1	A	339	VAL	N-CA-C	-5.94	99.92	108.53
4	F	61	GLN	N-CA-C	-5.94	101.57	110.24
1	A	316	TYR	CB-CG-CD1	-5.93	111.90	120.80
3	E	326	GLY	CA-C-N	5.93	132.65	121.97
3	E	326	GLY	C-N-CA	5.93	132.65	121.97
1	A	27	ASP	CA-CB-CG	-5.93	106.67	112.60
4	G	114	ALA	CB-CA-C	-5.93	100.77	110.85
4	G	91	GLN	CB-CG-CD	-5.93	102.52	112.60
2	D	74	GLY	CA-C-N	5.92	128.51	120.63
2	D	74	GLY	C-N-CA	5.92	128.51	120.63
2	C	241	LEU	N-CA-CB	5.92	119.67	110.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	172	GLN	CB-CG-CD	-5.92	102.54	112.60
4	F	290	LEU	N-CA-C	-5.92	97.95	108.13
2	C	89	ASP	CA-C-N	5.92	130.59	121.19
2	C	89	ASP	C-N-CA	5.92	130.59	121.19
4	F	338	MET	CB-CA-C	-5.92	98.73	109.38
2	D	313	MET	CG-SD-CE	-5.91	87.89	100.90
3	E	295	HIS	CA-CB-CG	-5.91	107.89	113.80
4	F	108	LEU	N-CA-C	-5.91	101.71	110.46
4	G	192	SER	N-CA-CB	5.91	119.22	109.88
3	E	154	THR	N-CA-C	-5.91	104.84	111.28
4	F	167	LEU	N-CA-C	-5.91	100.08	109.59
2	B	347	MET	N-CA-CB	5.90	118.90	110.16
2	B	6	LEU	CB-CA-C	-5.90	100.23	110.09
1	A	226	SER	N-CA-C	-5.90	105.74	113.17
2	C	348	GLY	N-CA-C	-5.90	105.35	112.49
1	A	319	SER	N-CA-C	-5.89	104.58	113.89
3	E	208	ASP	N-CA-C	-5.89	106.14	113.15
4	F	139	ILE	N-CA-CB	5.89	118.55	110.54
4	G	207	LEU	CB-CA-C	-5.89	96.48	109.56
2	D	353	LEU	N-CA-C	5.88	118.48	111.71
4	G	159	LEU	CB-CA-C	-5.88	100.09	109.80
2	D	310	GLU	CB-CA-C	-5.88	101.02	110.79
3	E	47	TYR	CA-C-N	5.88	128.97	120.38
3	E	47	TYR	C-N-CA	5.88	128.97	120.38
3	E	121	THR	CA-C-N	5.88	129.25	120.31
3	E	121	THR	C-N-CA	5.88	129.25	120.31
4	F	157	GLY	CA-C-O	5.88	127.87	121.87
4	G	99	VAL	N-CA-C	-5.88	99.75	108.45
4	G	290	LEU	N-CA-C	-5.88	99.37	108.42
4	G	173	ASP	N-CA-C	-5.87	106.08	113.72
4	G	152	ARG	CB-CG-CD	5.87	124.81	111.30
1	A	220	ALA	CB-CA-C	-5.87	101.05	110.79
1	A	196	LYS	N-CA-CB	5.87	119.76	110.55
4	G	108	LEU	N-CA-CB	5.87	119.56	110.46
4	G	251	ASN	CB-CA-C	5.87	121.73	110.17
4	F	203	LEU	CB-CA-C	-5.87	101.05	110.79
4	F	207	LEU	CD1-CG-CD2	-5.86	97.91	110.80
1	A	170	LEU	CB-CA-C	5.86	121.41	110.70
1	A	220	ALA	O-C-N	5.86	128.33	122.12
2	C	235	GLN	N-CA-C	5.85	117.33	111.07
2	D	194	GLU	CB-CG-CD	-5.85	102.65	112.60
2	B	274	ARG	CA-C-N	5.85	132.87	121.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	274	ARG	C-N-CA	5.85	132.87	121.41
4	F	9	HIS	CA-C-O	5.85	126.69	119.79
4	F	175	HIS	CA-CB-CG	-5.85	107.95	113.80
4	F	317	ILE	N-CA-C	-5.85	100.06	108.48
4	F	25	PRO	O-C-N	5.84	130.26	123.01
4	G	211	ASP	N-CA-C	-5.84	98.36	110.80
2	C	260	ASN	OD1-CG-ND2	-5.84	116.76	122.60
4	G	262	LEU	CB-CA-C	-5.84	101.68	110.90
4	F	135	MET	CG-SD-CE	-5.83	88.07	100.90
2	D	351	MET	CG-SD-CE	-5.83	88.07	100.90
1	A	61	TRP	CB-CG-CD1	5.83	135.64	126.90
2	B	290	HIS	CE1-NE2-CD2	-5.83	103.17	109.00
2	D	43	PHE	CA-C-N	-5.83	114.56	122.77
2	D	43	PHE	C-N-CA	-5.83	114.56	122.77
3	E	19	GLN	CB-CG-CD	-5.82	102.71	112.60
4	F	246	ARG	CD-NE-CZ	-5.82	116.25	124.40
1	A	210	ALA	CA-C-N	5.82	129.53	120.75
1	A	210	ALA	C-N-CA	5.82	129.53	120.75
2	C	140	LEU	O-C-N	5.82	128.06	122.07
3	E	20	ALA	N-CA-C	-5.81	106.23	113.38
1	A	264	SER	CA-C-O	5.81	126.61	120.33
4	G	241	PHE	N-CA-C	-5.81	96.00	107.91
2	B	145	GLU	CB-CA-C	5.81	118.26	110.13
2	D	32	LEU	N-CA-C	5.81	118.08	111.11
1	A	311	THR	CB-CA-C	-5.80	99.89	110.63
4	F	308	VAL	N-CA-C	-5.80	99.44	108.44
2	B	45	GLY	CA-C-N	5.80	129.96	121.31
2	B	45	GLY	C-N-CA	5.80	129.96	121.31
4	G	76	PHE	CA-C-N	5.80	128.33	120.38
4	G	76	PHE	C-N-CA	5.80	128.33	120.38
2	D	73	CYS	CA-C-N	5.80	132.77	121.41
2	D	73	CYS	C-N-CA	5.80	132.77	121.41
3	E	4	TYR	N-CA-CB	5.80	120.69	110.37
2	C	25	LEU	CA-C-N	5.79	127.97	120.44
2	C	25	LEU	C-N-CA	5.79	127.97	120.44
3	E	3	TRP	CB-CG-CD1	5.79	135.59	126.90
4	F	196	PRO	CA-C-N	5.79	128.36	120.54
4	F	196	PRO	C-N-CA	5.79	128.36	120.54
4	G	292	ILE	N-CA-C	-5.79	100.70	108.35
2	C	277	GLU	N-CA-C	5.79	118.22	110.35
2	C	294	MET	CB-CA-C	-5.79	101.02	110.85
4	G	104	SER	N-CA-CB	-5.78	101.38	110.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	HIS	CA-CB-CG	5.78	119.58	113.80
1	A	214	PRO	CA-C-N	5.78	128.02	120.28
1	A	214	PRO	C-N-CA	5.78	128.02	120.28
2	B	78	ASN	CB-CA-C	-5.78	101.81	110.88
4	G	80	ARG	N-CA-C	5.78	117.58	111.28
4	F	263	LEU	N-CA-CB	-5.77	101.61	110.16
3	E	182	MET	CA-C-N	5.77	132.56	121.54
3	E	182	MET	C-N-CA	5.77	132.56	121.54
4	F	114	ALA	N-CA-C	-5.77	105.62	114.16
4	F	48	ASP	N-CA-C	-5.77	98.52	110.80
4	G	232	PHE	N-CA-C	-5.77	99.78	109.07
4	F	235	LYS	N-CA-C	-5.76	102.39	110.35
2	C	171	LEU	CA-C-N	5.76	129.05	120.87
2	C	171	LEU	C-N-CA	5.76	129.05	120.87
2	C	149	HIS	CA-CB-CG	-5.76	108.04	113.80
3	E	294	CYS	CA-CB-SG	-5.76	101.15	114.40
1	A	50	HIS	N-CA-C	-5.76	98.50	108.69
4	G	61	GLN	CA-C-N	5.76	127.04	119.84
4	G	61	GLN	C-N-CA	5.76	127.04	119.84
1	A	90	ASN	N-CA-C	-5.75	100.87	109.96
2	D	87	PHE	N-CA-CB	5.75	120.21	110.49
4	F	188	LEU	O-C-N	5.75	127.68	121.12
1	A	307	ARG	CB-CA-C	-5.75	101.61	110.81
2	C	195	HIS	CA-CB-CG	-5.75	108.05	113.80
4	F	261	ASP	N-CA-CB	-5.75	101.65	110.16
2	D	174	HIS	N-CA-C	-5.75	99.82	108.96
2	D	228	GLY	CA-C-N	5.75	130.56	122.46
2	D	228	GLY	C-N-CA	5.75	130.56	122.46
2	D	234	THR	N-CA-C	-5.75	104.39	111.40
1	A	59	THR	O-C-N	5.74	128.20	122.12
1	A	58	ASN	CA-C-N	5.74	128.24	120.38
1	A	58	ASN	C-N-CA	5.74	128.24	120.38
4	F	329	ASN	CB-CG-OD1	5.74	132.27	120.80
4	F	241	PHE	CA-CB-CG	5.73	119.53	113.80
2	B	283	VAL	N-CA-C	-5.73	103.76	111.44
2	D	128	VAL	N-CA-C	5.73	118.22	111.05
4	G	54	VAL	CB-CA-C	-5.73	104.02	110.96
4	F	111	LEU	N-CA-C	-5.73	102.94	110.39
4	F	319	PHE	N-CA-CB	5.73	121.41	111.39
4	G	66	GLY	N-CA-C	-5.73	99.60	113.18
3	E	317	LEU	N-CA-CB	-5.72	101.71	110.12
2	D	35	GLY	N-CA-C	-5.72	108.22	115.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	147	GLU	N-CA-C	-5.72	101.62	108.25
4	F	257	GLU	N-CA-C	-5.72	100.86	109.95
2	B	169	ARG	N-CA-C	5.71	118.28	111.71
2	D	202	ALA	CA-C-N	5.71	127.87	120.44
2	D	202	ALA	C-N-CA	5.71	127.87	120.44
2	C	238	SER	CA-C-N	5.71	128.21	120.44
2	C	238	SER	C-N-CA	5.71	128.21	120.44
2	C	143	LEU	N-CA-C	5.71	117.50	111.28
4	G	342	ASP	N-CA-C	-5.71	100.52	109.25
2	B	235	GLN	CB-CG-CD	-5.71	102.90	112.60
4	G	221	ASN	CA-CB-CG	5.71	118.31	112.60
1	A	57	PRO	N-CA-C	-5.70	105.95	113.65
1	A	43	ALA	CB-CA-C	-5.70	101.33	110.79
2	D	205	LEU	N-CA-CB	5.70	119.07	109.78
4	F	13	PRO	N-CA-CB	-5.70	98.04	103.51
4	F	137	ARG	NE-CZ-NH2	-5.70	114.07	119.20
4	F	211	ASP	CA-CB-CG	-5.70	106.90	112.60
3	E	244	ARG	N-CA-C	-5.69	105.06	112.23
3	E	109	ALA	N-CA-C	-5.69	103.19	110.53
4	F	180	CYS	N-CA-CB	5.69	122.12	111.53
2	B	260	ASN	CA-CB-CG	-5.69	106.91	112.60
4	F	199	GLY	CA-C-N	5.69	128.25	120.46
4	F	199	GLY	C-N-CA	5.69	128.25	120.46
4	G	8	GLU	CB-CA-C	-5.68	101.95	110.88
4	G	109	SER	N-CA-C	-5.68	102.05	110.46
2	D	91	ILE	CA-C-N	5.68	132.30	122.64
2	D	91	ILE	C-N-CA	5.68	132.30	122.64
3	E	68	MET	CB-CA-C	-5.68	98.25	109.67
4	G	317	ILE	N-CA-C	-5.68	99.60	108.81
2	D	282	LEU	CB-CA-C	-5.68	101.36	110.79
1	A	82	LEU	N-CA-CB	5.68	119.46	110.55
2	D	299	PRO	N-CA-C	-5.67	100.78	112.47
2	D	67	GLY	O-C-N	5.67	129.31	122.67
4	G	261	ASP	N-CA-CB	-5.67	101.49	109.94
2	D	11	ARG	CA-C-N	5.67	126.92	119.84
2	D	11	ARG	C-N-CA	5.67	126.92	119.84
2	C	176	LYS	CA-C-N	5.66	130.44	120.87
2	C	176	LYS	C-N-CA	5.66	130.44	120.87
4	F	226	HIS	CA-CB-CG	-5.66	108.14	113.80
2	C	64	CYS	N-CA-C	-5.66	98.74	110.80
2	C	265	MET	CG-SD-CE	5.66	113.34	100.90
3	E	308	ARG	CB-CA-C	-5.65	101.97	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	266	HIS	ND1-CE1-NE2	5.65	114.05	108.40
2	C	303	GLY	N-CA-C	5.65	121.80	112.30
2	C	344	ASP	CA-C-N	5.65	128.12	120.38
2	C	344	ASP	C-N-CA	5.65	128.12	120.38
4	G	93	GLU	N-CA-C	-5.65	99.05	108.32
4	G	265	GLN	N-CA-CB	5.65	118.16	109.91
2	B	43	PHE	N-CA-CB	5.65	120.35	111.20
2	C	366	PRO	CA-C-O	5.65	127.47	121.03
1	A	278	VAL	N-CA-C	-5.65	97.59	109.34
2	B	47	ARG	NE-CZ-NH1	-5.65	115.85	121.50
2	D	37	ILE	N-CA-C	-5.65	99.51	107.75
3	E	83	LYS	CB-CA-C	-5.65	99.02	109.29
4	G	37	VAL	CB-CA-C	-5.64	104.08	111.81
2	B	101	VAL	CA-C-N	5.64	128.41	120.28
2	B	101	VAL	C-N-CA	5.64	128.41	120.28
4	G	343	SER	N-CA-C	-5.64	98.78	110.80
2	B	188	GLU	CB-CG-CD	-5.64	103.01	112.60
4	F	82	LEU	N-CA-C	-5.64	102.30	110.08
2	D	185	HIS	CB-CG-CD2	-5.64	123.87	131.20
3	E	242	PRO	CB-CA-C	-5.63	102.84	112.64
4	G	269	ARG	N-CA-C	5.63	117.87	111.11
1	A	96	GLN	CB-CG-CD	-5.63	103.03	112.60
2	B	143	LEU	CA-C-N	5.63	127.76	120.44
2	B	143	LEU	C-N-CA	5.63	127.76	120.44
1	A	282	ARG	CG-CD-NE	-5.63	99.62	112.00
2	D	60	LYS	CA-C-O	-5.63	114.59	120.55
4	F	336	VAL	CA-CB-CG2	-5.63	100.83	110.40
2	D	311	LEU	N-CA-C	-5.62	105.23	111.36
2	D	291	ARG	CG-CD-NE	-5.62	99.63	112.00
3	E	292	ASP	CA-CB-CG	-5.62	106.98	112.60
4	F	175	HIS	N-CA-C	-5.62	108.21	114.62
4	F	204	MET	N-CA-C	-5.62	105.30	111.82
2	B	262	GLU	N-CA-C	-5.62	106.41	113.72
4	F	343	SER	CB-CA-C	-5.62	99.23	110.42
4	F	355	GLN	N-CA-C	-5.62	103.85	111.55
3	E	218	GLN	N-CA-C	5.62	117.09	110.97
1	A	136	GLN	N-CA-C	-5.61	100.09	109.24
2	C	329	TYR	N-CA-C	-5.61	105.31	111.82
2	C	57	LEU	N-CA-C	5.61	117.40	111.28
2	D	43	PHE	N-CA-C	-5.61	99.38	108.52
3	E	30	GLN	CB-CG-CD	-5.61	103.06	112.60
3	E	203	ALA	N-CA-C	5.61	118.33	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	212	ASN	N-CA-C	-5.61	100.78	109.87
2	B	173	PHE	N-CA-CB	5.61	119.36	110.55
4	G	160	PHE	N-CA-CB	5.61	119.37	110.84
2	C	163	PRO	CA-C-N	5.61	128.14	120.46
2	C	163	PRO	C-N-CA	5.61	128.14	120.46
4	F	224	ARG	NH1-CZ-NH2	5.61	126.59	119.30
4	F	282	ARG	CD-NE-CZ	-5.61	116.55	124.40
2	C	360	HIS	CA-C-O	-5.60	114.51	120.23
2	D	94	ASP	N-CA-CB	5.60	119.62	110.37
3	E	3	TRP	N-CA-C	-5.60	101.34	110.20
4	G	230	PHE	CB-CA-C	-5.60	100.78	111.48
1	A	170	LEU	N-CA-CB	-5.60	101.85	110.20
1	A	183	GLN	CB-CA-C	-5.60	99.92	110.67
4	F	356	SER	N-CA-C	-5.60	98.88	110.80
1	A	245	ILE	CB-CA-C	-5.60	103.19	112.26
2	C	195	HIS	CE1-NE2-CD2	-5.59	103.41	109.00
2	B	271	ALA	N-CA-C	-5.59	105.33	111.82
2	C	358	ALA	CA-C-N	5.59	132.67	122.50
2	C	358	ALA	C-N-CA	5.59	132.67	122.50
2	D	102	GLU	CB-CA-C	-5.58	101.19	110.68
2	D	331	THR	CB-CA-C	-5.58	101.87	110.81
1	A	51	HIS	N-CA-C	-5.58	100.81	109.24
1	A	76	SER	N-CA-C	5.58	122.69	110.80
1	A	143	GLU	CA-C-N	5.58	128.03	120.38
1	A	143	GLU	C-N-CA	5.58	128.03	120.38
2	C	331	THR	N-CA-C	-5.58	105.20	111.28
4	F	222	ASN	OD1-CG-ND2	-5.58	117.02	122.60
4	G	39	ASP	N-CA-CB	5.58	119.92	110.49
4	G	125	GLU	N-CA-CB	-5.58	102.46	110.44
2	D	172	GLN	N-CA-C	-5.58	99.43	108.52
1	A	153	ALA	N-CA-C	-5.58	104.83	111.69
4	G	147	ALA	N-CA-CB	5.58	121.89	111.52
2	B	336	ARG	CB-CA-C	5.57	120.16	110.68
4	G	182	MET	N-CA-CB	5.57	119.52	110.05
2	D	114	ALA	N-CA-C	-5.57	101.91	110.32
4	F	262	LEU	O-C-N	5.57	128.03	122.12
2	C	188	GLU	CB-CG-CD	-5.57	103.13	112.60
4	G	355	GLN	CA-C-O	5.56	127.77	120.15
2	D	227	SER	CB-CA-C	-5.56	101.16	110.56
4	G	355	GLN	CB-CA-C	5.56	118.52	110.79
2	B	47	ARG	NE-CZ-NH2	5.56	124.20	119.20
2	D	140	LEU	CA-C-N	5.56	127.99	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	140	LEU	C-N-CA	5.56	127.99	120.38
1	A	78	GLN	N-CA-C	-5.55	100.97	109.41
2	C	182	GLN	CB-CG-CD	-5.55	103.16	112.60
1	A	85	PRO	CA-C-N	5.55	132.15	121.54
1	A	85	PRO	C-N-CA	5.55	132.15	121.54
4	F	159	LEU	CB-CA-C	-5.55	103.37	112.03
4	G	137	ARG	CA-C-N	5.55	127.72	120.28
4	G	137	ARG	C-N-CA	5.55	127.72	120.28
3	E	279	ASN	CA-C-N	-5.55	113.89	122.49
3	E	279	ASN	C-N-CA	-5.55	113.89	122.49
2	B	260	ASN	N-CA-CB	5.55	119.22	110.23
3	E	331	VAL	N-CA-C	-5.55	96.90	108.88
4	G	176	ARG	N-CA-C	-5.55	98.98	110.80
1	A	258	VAL	CA-CB-CG1	5.54	119.83	110.40
2	C	292	ILE	N-CA-C	-5.54	105.10	110.42
4	G	226	HIS	CE1-NE2-CD2	-5.54	103.46	109.00
4	F	191	HIS	N-CA-CB	5.54	119.86	110.49
4	G	186	GLN	N-CA-C	-5.54	100.99	109.41
2	D	315	GLU	N-CA-CB	-5.54	101.98	110.01
4	F	166	GLU	CA-C-O	5.54	126.95	120.80
1	A	251	GLN	N-CA-C	-5.54	105.33	111.36
2	B	90	LEU	N-CA-C	-5.54	100.22	109.24
4	G	302	ALA	N-CA-C	-5.54	100.94	109.52
2	C	256	MET	N-CA-CB	5.53	118.25	110.12
2	D	313	MET	N-CA-C	5.53	117.75	111.11
2	B	260	ASN	OD1-CG-ND2	5.53	128.13	122.60
2	B	85	GLY	CA-C-N	5.53	132.10	121.54
2	B	85	GLY	C-N-CA	5.53	132.10	121.54
2	D	313	MET	CA-C-N	5.53	128.00	120.54
2	D	313	MET	C-N-CA	5.53	128.00	120.54
1	A	299	ARG	N-CA-C	5.53	116.98	111.07
2	C	151	LYS	N-CA-CB	5.52	119.96	110.68
2	C	80	ARG	CG-CD-NE	-5.52	99.85	112.00
1	A	334	LYS	O-C-N	-5.52	114.97	121.32
1	A	331	LEU	CA-C-N	5.52	127.94	120.65
1	A	331	LEU	C-N-CA	5.52	127.94	120.65
2	B	98	ARG	N-CA-C	-5.52	104.97	112.26
2	C	224	ALA	CA-C-N	5.52	128.31	120.53
2	C	224	ALA	C-N-CA	5.52	128.31	120.53
1	A	293	LEU	O-C-N	5.51	130.08	123.13
2	B	342	ALA	CB-CA-C	-5.51	100.57	109.67
2	D	87	PHE	CA-CB-CG	-5.51	108.29	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	LEU	CB-CA-C	-5.50	101.66	110.79
3	E	273	LEU	N-CA-CB	-5.50	102.03	110.12
4	F	160	PHE	CB-CA-C	-5.50	102.08	110.88
2	B	118	GLY	N-CA-C	-5.50	104.16	112.41
4	G	316	GLU	CB-CG-CD	-5.50	103.25	112.60
2	B	168	SER	N-CA-C	-5.50	105.29	111.28
3	E	168	PRO	N-CA-CB	5.50	107.94	103.32
4	F	239	GLY	N-CA-C	-5.50	102.60	110.46
4	F	285	VAL	N-CA-C	5.50	115.46	106.72
3	E	279	ASN	N-CA-C	5.50	117.27	111.28
2	D	25	LEU	CA-C-N	5.49	128.09	120.29
2	D	25	LEU	C-N-CA	5.49	128.09	120.29
2	D	30	ASN	CB-CA-C	-5.49	102.26	110.88
4	G	341	THR	OG1-CB-CG2	5.49	120.29	109.30
1	A	173	CYS	CB-CA-C	-5.49	98.41	109.55
2	B	109	ASP	CA-CB-CG	5.49	118.09	112.60
2	D	326	GLN	CB-CG-CD	-5.49	103.27	112.60
4	G	255	HIS	N-CA-C	-5.49	99.58	108.52
2	D	184	ARG	N-CA-CB	5.48	117.96	110.01
4	G	173	ASP	CB-CA-C	-5.48	100.35	109.55
3	E	324	GLN	CG-CD-NE2	5.48	124.61	116.40
2	D	117	ARG	O-C-N	-5.47	115.31	122.59
2	D	359	PHE	N-CA-C	-5.47	106.10	112.89
2	B	137	ASN	N-CA-CB	5.47	118.76	110.28
4	G	204	MET	CA-C-N	5.47	128.16	120.28
4	G	204	MET	C-N-CA	5.47	128.16	120.28
4	G	287	GLU	CA-CB-CG	-5.47	103.15	114.10
3	E	223	SER	CB-CA-C	-5.47	101.56	110.85
3	E	199	GLY	N-CA-C	-5.46	100.23	113.18
4	F	348	GLN	OE1-CD-NE2	5.46	128.06	122.60
3	E	310	LEU	N-CA-C	-5.45	105.33	111.28
1	A	275	LYS	N-CA-C	-5.45	105.89	112.54
2	D	59	ALA	N-CA-C	5.45	116.90	111.07
4	G	297	PRO	O-C-N	5.45	128.07	122.18
1	A	231	HIS	CB-CG-CD2	-5.45	124.12	131.20
2	D	63	ASN	CA-CB-CG	-5.45	107.15	112.60
2	D	190	ILE	CB-CA-C	5.45	118.62	111.81
4	G	294	ALA	N-CA-CB	5.45	120.40	111.08
3	E	211	GLN	N-CA-C	-5.45	104.99	111.69
1	A	5	TYR	CA-C-N	5.45	125.53	119.32
1	A	5	TYR	C-N-CA	5.45	125.53	119.32
2	D	103	ASP	N-CA-CB	-5.45	102.10	110.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	50	GLU	CB-CG-CD	-5.45	103.34	112.60
3	E	73	HIS	N-CA-CB	-5.44	101.14	110.01
4	G	349	ILE	N-CA-C	-5.44	100.35	108.46
1	A	338	ASP	CB-CA-C	5.44	121.25	110.42
4	F	120	ASP	CA-C-N	5.44	130.00	122.77
4	F	120	ASP	C-N-CA	5.44	130.00	122.77
2	B	126	ASP	CA-C-N	5.44	131.05	122.78
2	B	126	ASP	C-N-CA	5.44	131.05	122.78
2	B	260	ASN	N-CA-C	-5.44	100.82	109.96
2	C	92	GLU	CB-CG-CD	5.44	121.85	112.60
2	D	146	PRO	CB-CA-C	-5.44	104.28	110.92
3	E	208	ASP	N-CA-CB	5.44	118.83	110.46
4	F	274	SER	CA-C-N	5.44	131.93	121.54
4	F	274	SER	C-N-CA	5.44	131.93	121.54
3	E	114	VAL	CA-C-N	5.44	127.51	120.44
3	E	114	VAL	C-N-CA	5.44	127.51	120.44
3	E	319	ILE	CA-CB-CG1	-5.44	101.16	110.40
2	B	123	TYR	N-CA-C	-5.43	98.37	107.99
2	D	23	HIS	CE1-NE2-CD2	-5.43	103.56	109.00
2	D	284	GLU	N-CA-C	5.43	117.20	111.28
3	E	10	ASP	CA-C-N	5.43	128.34	120.79
3	E	10	ASP	C-N-CA	5.43	128.34	120.79
2	D	227	SER	N-CA-CB	-5.43	102.63	110.56
1	A	174	TYR	N-CA-C	-5.43	103.54	111.30
1	A	229	ALA	N-CA-C	-5.43	105.37	111.28
2	B	141	LYS	N-CA-C	5.43	117.90	111.33
2	C	355	ARG	CA-C-N	5.43	127.81	120.38
2	C	355	ARG	C-N-CA	5.43	127.81	120.38
2	D	222	ASP	CA-C-O	5.42	126.52	120.82
1	A	20	ALA	CA-C-N	-5.42	115.79	122.84
1	A	20	ALA	C-N-CA	-5.42	115.79	122.84
2	C	121	LYS	N-CA-C	-5.42	101.63	110.20
2	C	94	ASP	CA-CB-CG	5.42	118.02	112.60
4	G	238	ASP	CA-CB-CG	-5.42	107.18	112.60
2	D	134	HIS	CA-CB-CG	-5.42	108.38	113.80
4	F	140	GLU	CB-CA-C	-5.42	102.34	110.90
1	A	222	LEU	CA-C-O	5.42	126.69	120.90
3	E	54	GLN	CA-C-N	5.41	126.09	120.03
3	E	54	GLN	C-N-CA	5.41	126.09	120.03
2	B	145	GLU	N-CA-C	-5.41	97.58	109.11
4	F	122	TRP	CA-CB-CG	5.41	123.88	113.60
2	D	81	GLU	CB-CG-CD	-5.41	103.41	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	37	VAL	N-CA-CB	5.41	118.09	111.60
2	C	180	VAL	CB-CA-C	-5.41	104.84	112.14
2	D	67	GLY	CA-C-N	5.40	130.14	123.12
2	D	67	GLY	C-N-CA	5.40	130.14	123.12
2	D	87	PHE	N-CA-C	-5.40	99.30	110.80
4	G	198	LYS	CB-CA-C	-5.40	101.72	110.79
2	D	47	ARG	CD-NE-CZ	-5.39	116.85	124.40
4	F	248	LEU	CA-C-N	5.39	126.58	119.84
4	F	248	LEU	C-N-CA	5.39	126.58	119.84
4	G	139	ILE	N-CA-C	-5.39	105.12	111.00
4	G	282	ARG	CB-CA-C	-5.39	100.40	109.72
4	G	265	GLN	CA-C-N	5.39	127.81	120.54
4	G	265	GLN	C-N-CA	5.39	127.81	120.54
2	C	349	VAL	N-CA-C	-5.38	105.47	110.53
2	B	335	GLY	CA-C-N	5.38	127.75	120.38
2	B	335	GLY	C-N-CA	5.38	127.75	120.38
2	C	44	SER	N-CA-C	-5.38	101.23	109.41
2	D	129	HIS	CE1-NE2-CD2	-5.38	103.62	109.00
4	G	260	CYS	CA-C-N	5.38	127.80	120.54
4	G	260	CYS	C-N-CA	5.38	127.80	120.54
2	B	319	THR	N-CA-C	-5.37	106.31	112.92
2	D	189	HIS	CB-CG-ND1	5.37	130.76	122.70
3	E	246	HIS	N-CA-C	5.37	117.22	111.36
1	A	225	LYS	CA-C-N	5.37	131.40	122.54
1	A	225	LYS	C-N-CA	5.37	131.40	122.54
4	F	106	PHE	N-CA-C	-5.37	100.91	109.23
4	G	100	ARG	N-CA-C	-5.37	99.19	108.69
3	E	318	ARG	N-CA-CB	-5.37	101.96	110.28
2	C	263	ARG	CB-CA-C	-5.37	102.45	110.88
3	E	21	GLY	N-CA-C	-5.37	104.10	113.76
3	E	100	LEU	N-CA-C	-5.37	106.51	113.16
2	B	354	LEU	N-CA-C	-5.36	106.24	112.89
4	F	146	MET	CA-C-N	-5.36	110.06	121.32
4	F	146	MET	C-N-CA	-5.36	110.06	121.32
1	A	38	VAL	N-CA-C	-5.36	105.39	110.42
2	B	91	ILE	N-CA-C	-5.36	100.67	108.17
3	E	301	MET	CG-SD-CE	-5.36	89.12	100.90
4	G	231	ILE	CB-CA-C	5.35	117.40	110.12
2	C	305	ASP	N-CA-CB	5.35	118.69	110.61
3	E	317	LEU	CA-C-O	5.35	126.22	120.55
2	D	42	LEU	N-CA-C	-5.34	98.94	108.13
1	A	264	SER	CA-C-N	5.34	131.74	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	264	SER	C-N-CA	5.34	131.74	121.54
3	E	124	ALA	CB-CA-C	-5.34	101.92	110.79
3	E	298	GLU	N-CA-C	5.34	116.79	111.07
2	B	89	ASP	CA-C-N	-5.34	115.35	122.72
2	B	89	ASP	C-N-CA	-5.34	115.35	122.72
2	D	328	TYR	N-CA-C	-5.34	105.38	111.14
4	F	348	GLN	CB-CA-C	-5.34	102.23	111.30
2	B	344	ASP	N-CA-CB	5.33	119.50	110.49
2	B	348	GLY	CA-C-N	5.33	127.28	120.56
2	B	348	GLY	C-N-CA	5.33	127.28	120.56
3	E	189	ALA	N-CA-CB	5.33	118.06	110.06
4	F	67	ALA	N-CA-C	-5.33	100.81	108.60
4	G	330	ALA	CA-C-O	5.33	125.53	119.18
2	D	324	ASP	CB-CA-C	-5.33	99.30	110.17
4	F	84	GLU	N-CA-C	5.33	117.41	110.43
4	G	191	HIS	CE1-NE2-CD2	-5.33	103.67	109.00
3	E	75	ASP	O-C-N	5.33	127.56	122.07
4	F	319	PHE	CA-CB-CG	-5.33	108.47	113.80
2	C	22	GLU	CB-CG-CD	-5.33	103.55	112.60
4	G	186	GLN	CA-C-O	5.33	127.76	121.58
4	G	353	ALA	CB-CA-C	-5.32	98.86	109.99
3	E	189	ALA	O-C-N	5.32	127.76	122.12
4	G	24	ARG	CA-C-N	5.32	125.13	119.28
4	G	24	ARG	C-N-CA	5.32	125.13	119.28
4	F	305	ILE	N-CA-C	-5.32	100.82	108.48
4	G	104	SER	N-CA-C	-5.32	101.02	109.59
1	A	211	HIS	CE1-NE2-CD2	-5.32	103.68	109.00
2	B	101	VAL	N-CA-C	5.32	116.05	110.62
4	F	130	LEU	N-CA-C	5.32	116.58	109.83
2	C	203	LEU	CB-CA-C	-5.32	102.53	110.88
4	F	14	LEU	N-CA-CB	5.32	119.22	110.39
1	A	105	HIS	CE1-NE2-CD2	-5.32	103.69	109.00
3	E	50	CYS	CA-C-N	5.32	131.69	121.54
3	E	50	CYS	C-N-CA	5.32	131.69	121.54
4	G	318	GLY	N-CA-C	-5.31	102.72	111.38
2	C	362	ARG	CB-CA-C	5.31	120.99	110.42
2	D	314	ARG	CA-C-N	5.31	127.35	120.44
2	D	314	ARG	C-N-CA	5.31	127.35	120.44
2	C	262	GLU	N-CA-C	-5.30	105.63	112.68
2	D	344	ASP	O-C-N	-5.30	117.00	123.10
4	G	219	GLY	CA-C-N	5.30	127.92	120.28
4	G	219	GLY	C-N-CA	5.30	127.92	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	273	PHE	CB-CG-CD2	-5.30	111.69	120.70
4	G	194	ILE	N-CA-CB	5.30	119.03	111.82
2	C	193	GLU	N-CA-C	5.30	116.74	111.07
4	F	366	LEU	N-CA-CB	5.30	119.51	110.50
3	E	65	CYS	N-CA-CB	5.30	117.83	109.94
4	G	35	LEU	CB-CA-C	-5.30	100.38	109.65
3	E	215	THR	CA-C-O	5.29	126.38	120.82
4	G	286	SER	N-CA-CB	5.29	117.83	109.83
2	B	84	GLN	N-CA-C	-5.29	102.07	109.69
2	B	43	PHE	CA-CB-CG	-5.29	108.51	113.80
3	E	33	PRO	CA-C-N	5.29	130.05	120.79
3	E	33	PRO	C-N-CA	5.29	130.05	120.79
4	F	355	GLN	CA-C-N	5.29	131.65	121.54
4	F	355	GLN	C-N-CA	5.29	131.65	121.54
2	C	334	ILE	N-CA-CB	5.29	117.73	110.54
3	E	248	LEU	N-CA-C	5.28	117.04	111.28
4	F	302	ALA	N-CA-C	-5.28	100.42	109.24
2	B	149	HIS	CE1-NE2-CD2	-5.28	103.72	109.00
2	D	120	PHE	N-CA-CB	5.28	119.41	110.49
2	B	191	LEU	N-CA-C	-5.28	106.35	112.89
4	F	48	ASP	CA-C-N	5.28	131.62	121.54
4	F	48	ASP	C-N-CA	5.28	131.62	121.54
4	G	229	ASP	N-CA-C	-5.28	107.02	112.93
2	C	186	GLN	CA-C-N	5.28	128.08	120.38
2	C	186	GLN	C-N-CA	5.28	128.08	120.38
2	D	21	GLN	CA-C-N	5.28	127.35	120.28
2	D	21	GLN	C-N-CA	5.28	127.35	120.28
4	G	77	ASP	CA-CB-CG	-5.28	107.32	112.60
2	D	239	ALA	N-CA-CB	5.27	117.71	110.07
4	G	209	GLY	N-CA-C	-5.27	100.69	113.18
4	F	298	GLU	CB-CG-CD	-5.27	103.64	112.60
1	A	51	HIS	CE1-NE2-CD2	-5.27	103.73	109.00
2	B	32	LEU	N-CA-C	5.26	117.02	111.28
2	C	213	SER	N-CA-C	-5.26	98.81	108.02
2	B	245	ASP	CA-CB-CG	5.26	117.86	112.60
4	F	355	GLN	CB-CG-CD	-5.26	103.66	112.60
2	B	350	GLU	CA-C-N	5.25	127.59	120.44
2	B	350	GLU	C-N-CA	5.25	127.59	120.44
2	C	254	GLU	CA-C-N	-5.25	113.61	120.44
2	C	254	GLU	C-N-CA	-5.25	113.61	120.44
2	D	164	VAL	CA-C-N	5.25	127.84	120.28
2	D	164	VAL	C-N-CA	5.25	127.84	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	254	LYS	N-CA-C	-5.25	103.09	110.50
2	D	96	ALA	CA-C-N	5.25	128.05	120.38
2	D	96	ALA	C-N-CA	5.25	128.05	120.38
4	G	177	LEU	N-CA-C	-5.25	101.31	109.24
3	E	267	ASN	CB-CG-OD1	-5.25	110.30	120.80
3	E	174	THR	CA-C-N	5.25	127.31	120.28
3	E	174	THR	C-N-CA	5.25	127.31	120.28
2	C	335	GLY	N-CA-C	-5.25	106.29	112.64
1	A	30	LEU	N-CA-C	5.24	117.08	111.36
4	G	139	ILE	CA-C-O	-5.24	115.10	120.71
2	B	166	ILE	CB-CA-C	-5.24	103.77	112.26
2	C	125	ILE	CA-C-O	-5.24	115.64	121.98
4	F	260	CYS	CA-C-N	5.24	127.73	120.29
4	F	260	CYS	C-N-CA	5.24	127.73	120.29
2	B	119	ARG	CB-CA-C	-5.24	101.64	110.64
2	D	154	LEU	N-CA-CB	5.24	119.16	110.52
3	E	235	ALA	CA-C-N	5.24	130.70	122.11
3	E	235	ALA	C-N-CA	5.24	130.70	122.11
1	A	320	VAL	CA-C-N	5.23	127.60	120.54
1	A	320	VAL	C-N-CA	5.23	127.60	120.54
2	C	199	GLU	CA-C-N	5.23	125.54	119.47
2	C	199	GLU	C-N-CA	5.23	125.54	119.47
3	E	260	HIS	N-CA-C	-5.23	104.49	111.87
4	F	18	SER	N-CA-CB	5.23	117.87	110.13
4	G	128	PHE	N-CA-CB	5.23	119.41	110.57
4	G	267	PHE	CA-CB-CG	-5.23	108.57	113.80
3	E	93	VAL	N-CA-CB	-5.23	105.13	110.62
3	E	296	ILE	CB-CA-C	-5.23	105.00	112.22
4	G	181	SER	N-CA-C	-5.23	99.43	108.69
2	D	222	ASP	CA-C-N	5.23	127.29	120.28
2	D	222	ASP	C-N-CA	5.23	127.29	120.28
1	A	223	MET	CG-SD-CE	5.22	112.39	100.90
3	E	166	PRO	N-CA-CB	5.22	106.11	103.19
4	F	274	SER	N-CA-CB	5.22	119.66	111.20
3	E	181	THR	N-CA-C	-5.22	100.67	109.07
4	F	281	VAL	N-CA-C	-5.22	100.05	107.77
4	G	220	SER	CA-C-N	5.21	131.50	121.54
4	G	220	SER	C-N-CA	5.21	131.50	121.54
2	D	277	GLU	N-CA-C	5.21	117.73	109.96
2	C	240	MET	N-CA-C	-5.21	106.19	112.54
2	D	223	GLN	N-CA-CB	-5.21	102.47	110.12
3	E	52	GLN	O-C-N	-5.21	115.33	121.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	66	THR	CA-C-N	5.20	131.61	121.41
2	B	66	THR	C-N-CA	5.20	131.61	121.41
3	E	222	TYR	CB-CG-CD1	5.20	128.60	120.80
4	G	338	MET	CA-CB-CG	-5.20	103.70	114.10
2	B	206	LEU	N-CA-CB	-5.20	102.22	110.28
3	E	66	GLN	N-CA-C	-5.20	105.30	111.69
2	C	11	ARG	CA-C-N	5.20	125.48	119.92
2	C	11	ARG	C-N-CA	5.20	125.48	119.92
3	E	252	LEU	CB-CA-C	-5.20	101.02	110.63
4	F	60	VAL	N-CA-CB	-5.20	106.50	112.21
4	F	272	ILE	CA-C-N	5.20	131.46	121.54
4	F	272	ILE	C-N-CA	5.20	131.46	121.54
4	F	349	ILE	CA-CB-CG2	-5.19	101.67	110.50
2	B	179	ASP	CA-C-N	5.19	127.30	120.60
2	B	179	ASP	C-N-CA	5.19	127.30	120.60
3	E	121	THR	CA-CB-OG1	5.19	117.39	109.60
4	F	226	HIS	CB-CG-CD2	-5.19	124.45	131.20
2	D	304	ASN	CB-CA-C	-5.19	100.78	109.65
2	D	22	GLU	CA-C-N	5.19	127.54	120.54
2	D	22	GLU	C-N-CA	5.19	127.54	120.54
2	C	41	TYR	CA-CB-CG	-5.18	104.57	113.90
2	B	22	GLU	N-CA-C	5.18	117.67	111.71
2	B	328	TYR	CA-C-N	5.18	127.18	120.44
2	B	328	TYR	C-N-CA	5.18	127.18	120.44
3	E	17	SER	CB-CA-C	5.18	119.39	110.79
1	A	111	ILE	N-CA-C	-5.18	98.54	107.24
2	C	347	MET	O-C-N	5.18	128.05	122.15
2	D	61	GLY	CA-C-O	-5.18	114.81	120.40
4	G	57	VAL	CA-CB-CG1	5.18	119.20	110.40
2	B	69	THR	N-CA-C	-5.18	101.44	109.72
4	G	222	ASN	CA-C-N	5.18	131.11	122.57
4	G	222	ASN	C-N-CA	5.18	131.11	122.57
2	C	338	GLU	CB-CG-CD	-5.17	103.80	112.60
2	D	175	LEU	N-CA-C	-5.17	100.08	108.41
4	G	9	HIS	CE1-NE2-CD2	-5.17	103.83	109.00
2	C	128	VAL	CB-CA-C	5.17	117.40	110.42
1	A	315	ASP	CA-CB-CG	-5.17	107.43	112.60
2	C	65	GLU	N-CA-C	-5.17	104.78	111.71
3	E	285	ARG	N-CA-C	-5.17	106.12	112.90
4	F	12	LYS	O-C-N	-5.17	115.88	120.48
4	G	124	SER	CA-C-O	5.17	126.61	120.66
1	A	271	ALA	O-C-N	5.17	128.04	122.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	330	LEU	N-CA-C	-5.17	106.13	112.90
2	D	263	ARG	NE-CZ-NH2	-5.17	114.55	119.20
2	D	42	LEU	N-CA-CB	5.16	119.11	110.59
4	G	59	LEU	CB-CA-C	-5.16	101.68	109.99
1	A	333	HIS	CE1-NE2-CD2	-5.16	103.84	109.00
2	B	130	MET	CA-C-N	5.16	128.54	120.75
2	B	130	MET	C-N-CA	5.16	128.54	120.75
2	D	181	GLU	N-CA-CB	-5.16	102.54	110.12
3	E	308	ARG	CG-CD-NE	-5.16	100.65	112.00
4	G	261	ASP	CA-C-N	5.16	127.46	120.44
4	G	261	ASP	C-N-CA	5.16	127.46	120.44
4	G	150	ASP	CA-C-O	5.16	126.56	120.58
3	E	287	GLN	N-CA-C	-5.15	105.11	111.40
1	A	124	ALA	N-CA-CB	5.15	117.53	109.85
1	A	301	ALA	N-CA-C	-5.15	105.58	111.14
4	G	273	LEU	CA-C-O	-5.15	115.26	121.34
1	A	174	TYR	CA-CB-CG	-5.14	104.64	113.90
2	D	291	ARG	NE-CZ-NH1	-5.14	116.36	121.50
2	B	89	ASP	N-CA-CB	5.14	119.04	110.41
4	F	255	HIS	CB-CG-CD2	-5.14	124.52	131.20
4	G	249	PRO	N-CA-CB	5.14	108.64	103.25
4	G	339	MET	CB-CA-C	5.13	119.85	111.23
4	G	279	ARG	N-CA-C	-5.13	105.86	113.40
2	D	38	HIS	N-CA-C	-5.13	101.91	110.17
2	D	336	ARG	CB-CA-C	-5.13	102.28	110.79
2	C	135	SER	CA-C-N	5.13	127.10	120.44
2	C	135	SER	C-N-CA	5.13	127.10	120.44
1	A	65	PHE	CB-CA-C	-5.12	102.77	110.92
2	B	50	GLY	N-CA-C	-5.12	101.03	113.18
2	B	315	GLU	N-CA-CB	-5.12	103.00	110.53
2	C	257	VAL	CA-CB-CG1	5.12	119.11	110.40
3	E	49	LEU	CD1-CG-CD2	5.12	122.07	110.80
3	E	174	THR	N-CA-CB	5.12	117.74	110.06
4	F	17	VAL	CA-CB-CG2	-5.12	101.69	110.40
1	A	309	GLU	CA-C-O	5.12	125.88	120.10
1	A	335	PRO	CB-CA-C	-5.12	104.58	111.85
2	B	167	LEU	CA-C-N	5.12	127.14	120.28
2	B	167	LEU	C-N-CA	5.12	127.14	120.28
2	B	204	GLN	CB-CG-CD	-5.12	103.90	112.60
2	B	89	ASP	CB-CA-C	-5.12	99.77	109.95
2	C	80	ARG	CA-CB-CG	-5.11	103.87	114.10
2	C	179	ASP	CB-CA-C	-5.11	100.47	109.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	194	GLU	N-CA-C	-5.11	97.66	107.57
4	G	31	GLY	N-CA-C	-5.11	101.07	113.18
1	A	241	SER	N-CA-CB	5.11	117.99	109.56
2	C	23	HIS	CE1-NE2-CD2	-5.11	103.89	109.00
3	E	333	HIS	CE1-NE2-CD2	-5.11	103.89	109.00
4	G	106	PHE	N-CA-C	-5.10	100.98	108.79
4	F	334	GLU	CA-C-N	-5.10	115.29	122.94
4	F	334	GLU	C-N-CA	-5.10	115.29	122.94
2	D	10	TRP	CB-CA-C	5.10	119.34	110.72
4	F	205	ARG	N-CA-C	5.10	117.58	111.71
2	D	345	ARG	CB-CA-C	-5.10	102.18	110.85
1	A	219	ASP	CA-CB-CG	-5.10	107.50	112.60
4	G	341	THR	CA-CB-CG2	-5.10	101.84	110.50
2	B	71	THR	CA-C-N	5.09	125.03	119.78
2	B	71	THR	C-N-CA	5.09	125.03	119.78
3	E	234	ALA	CB-CA-C	-5.09	102.33	110.79
1	A	285	MET	N-CA-C	-5.09	105.91	111.82
2	C	58	LEU	N-CA-CB	5.09	117.34	109.91
3	E	218	GLN	CB-CG-CD	5.09	121.25	112.60
4	F	87	GLU	CB-CG-CD	-5.09	103.95	112.60
4	G	16	GLN	O-C-N	5.09	128.00	122.20
2	C	299	PRO	N-CA-C	-5.09	105.61	112.48
4	G	81	GLY	N-CA-C	-5.09	108.35	114.66
2	D	314	ARG	O-C-N	5.08	127.38	122.09
2	B	146	PRO	CA-C-O	-5.08	113.19	120.56
2	C	316	LEU	CB-CA-C	5.08	120.03	110.63
3	E	73	HIS	CE1-NE2-CD2	-5.08	103.92	109.00
4	G	226	HIS	N-CA-CB	-5.08	102.79	110.77
2	D	77	ASP	N-CA-C	-5.08	105.02	111.11
3	E	190	ALA	CA-C-N	5.08	127.04	120.44
3	E	190	ALA	C-N-CA	5.08	127.04	120.44
4	F	215	ARG	CG-CD-NE	-5.08	100.83	112.00
1	A	287	GLY	CA-C-N	5.08	127.04	120.44
1	A	287	GLY	C-N-CA	5.08	127.04	120.44
4	F	122	TRP	CB-CG-CD1	-5.08	119.28	126.90
4	G	124	SER	N-CA-CB	5.08	120.19	111.00
4	G	108	LEU	CB-CA-C	-5.08	101.67	110.45
2	B	102	GLU	N-CA-C	5.07	117.55	111.71
4	F	189	PRO	O-C-N	5.07	128.51	122.98
4	G	338	MET	N-CA-C	-5.07	101.42	109.59
2	B	113	TYR	N-CA-CB	5.07	118.95	110.59
1	A	266	HIS	CE1-NE2-CD2	-5.07	103.93	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	THR	CA-C-N	5.07	127.32	120.38
1	A	99	THR	C-N-CA	5.07	127.32	120.38
1	A	158	LEU	CB-CA-C	-5.07	100.89	110.01
2	C	111	VAL	N-CA-C	-5.07	105.60	110.72
1	A	154	ARG	CD-NE-CZ	-5.06	117.31	124.40
3	E	225	PRO	N-CA-C	-5.06	102.04	112.47
4	F	44	LEU	N-CA-C	-5.06	101.90	109.95
2	B	66	THR	N-CA-CB	5.06	120.22	110.90
2	C	110	ASN	CA-CB-CG	-5.06	107.54	112.60
3	E	24	HIS	CE1-NE2-CD2	-5.06	103.94	109.00
4	G	221	ASN	CA-C-O	5.06	127.74	120.51
2	C	360	HIS	CA-C-N	5.06	126.16	119.84
2	C	360	HIS	C-N-CA	5.06	126.16	119.84
4	G	88	ILE	CB-CA-C	5.06	116.69	111.23
4	G	133	ALA	CB-CA-C	-5.06	102.40	110.79
3	E	303	VAL	N-CA-CB	5.05	116.61	110.95
4	F	69	THR	N-CA-CB	5.05	119.94	110.99
4	F	214	LEU	CA-C-N	-5.05	114.20	121.42
4	F	214	LEU	C-N-CA	-5.05	114.20	121.42
2	C	319	THR	CA-CB-CG2	-5.05	101.92	110.50
3	E	75	ASP	N-CA-CB	5.05	117.33	110.01
2	C	181	GLU	CB-CA-C	-5.05	102.27	110.85
1	A	150	TRP	O-C-N	5.05	127.27	122.07
3	E	212	ALA	N-CA-C	-5.05	105.97	111.82
4	G	237	VAL	N-CA-CB	5.05	117.52	110.56
4	G	174	GLY	N-CA-C	-5.04	108.36	115.32
3	E	147	GLU	CA-C-N	5.04	125.32	119.47
3	E	147	GLU	C-N-CA	5.04	125.32	119.47
4	F	309	THR	CA-CB-CG2	-5.04	101.93	110.50
4	G	193	VAL	CB-CA-C	5.04	116.16	110.41
1	A	279	TRP	O-C-N	5.04	129.27	122.82
3	E	158	ARG	NH1-CZ-NH2	-5.04	112.75	119.30
2	C	12	PRO	CA-C-O	-5.04	115.66	121.95
2	C	130	MET	CA-C-N	5.04	128.35	120.75
2	C	130	MET	C-N-CA	5.04	128.35	120.75
4	F	205	ARG	CB-CA-C	-5.04	101.31	110.63
4	G	61	GLN	N-CA-C	5.04	115.76	109.57
1	A	341	ILE	N-CA-CB	5.03	118.24	110.14
2	B	176	LYS	N-CA-C	5.03	117.77	110.17
2	B	359	PHE	N-CA-C	-5.03	106.45	112.59
4	G	116	PHE	CA-C-N	5.03	124.72	119.64
4	G	116	PHE	C-N-CA	5.03	124.72	119.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	97	SER	CA-C-N	5.03	129.02	121.72
2	C	97	SER	C-N-CA	5.03	129.02	121.72
4	G	5	VAL	N-CA-CB	5.03	120.11	112.06
4	G	303	GLU	CB-CG-CD	-5.03	104.05	112.60
2	C	88	VAL	CB-CA-C	-5.03	105.45	112.04
2	B	150	VAL	CA-CB-CG2	5.03	118.95	110.40
4	G	336	VAL	N-CA-CB	-5.03	103.44	111.58
2	C	109	ASP	N-CA-C	5.03	118.67	112.54
4	F	86	ALA	N-CA-CB	5.03	117.85	109.56
4	G	287	GLU	O-C-N	5.03	129.05	122.87
3	E	152	LEU	CA-C-N	5.02	127.01	120.28
3	E	152	LEU	C-N-CA	5.02	127.01	120.28
1	A	228	ARG	CA-C-O	5.02	125.74	120.42
3	E	69	GLN	N-CA-CB	5.02	117.59	110.16
3	E	300	LEU	N-CA-C	-5.02	106.41	112.54
2	B	38	HIS	CB-CA-C	-5.02	101.02	110.51
3	E	227	GLY	N-CA-C	-5.02	106.14	114.48
4	F	212	ASN	N-CA-C	-5.02	100.79	109.58
2	B	304	ASN	N-CA-C	5.02	118.18	111.75
3	E	22	ARG	CB-CA-C	-5.02	102.14	110.37
4	F	148	HIS	CE1-NE2-CD2	-5.02	103.98	109.00
3	E	19	GLN	CA-C-N	-5.02	113.58	122.26
3	E	19	GLN	C-N-CA	-5.02	113.58	122.26
4	F	146	MET	N-CA-CB	5.02	118.05	109.87
4	G	287	GLU	CB-CG-CD	-5.02	104.07	112.60
2	C	210	ALA	CB-CA-C	-5.01	101.35	110.63
1	A	78	GLN	CB-CG-CD	-5.01	104.08	112.60
2	C	26	THR	N-CA-C	-5.01	105.71	111.07
4	G	83	PRO	N-CA-CB	5.01	107.53	103.32
1	A	335	PRO	N-CA-CB	5.01	108.49	103.48
3	E	206	GLN	CA-CB-CG	-5.01	104.08	114.10
4	G	238	ASP	CB-CA-C	5.01	118.88	109.71
4	F	100	ARG	NE-CZ-NH2	-5.01	114.69	119.20
4	G	221	ASN	N-CA-C	-5.01	100.14	110.80
3	E	61	HIS	N-CA-C	-5.00	102.66	110.42
1	A	112	VAL	N-CA-C	-5.00	99.97	107.37
1	A	283	ARG	CG-CD-NE	-5.00	101.00	112.00
2	D	78	ASN	CB-CA-C	-5.00	102.61	110.86
3	E	329	LEU	N-CA-CB	5.00	118.93	110.43
3	E	330	PRO	CA-C-N	5.00	131.38	122.13
3	E	330	PRO	C-N-CA	5.00	131.38	122.13

There are no chirality outliers.

All (83) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	174	TYR	Sidechain
1	A	21	TYR	Sidechain
1	A	228	ARG	Sidechain
1	A	231	HIS	Sidechain
1	A	252	ARG	Sidechain
1	A	266	HIS	Sidechain
1	A	270	ARG	Sidechain
1	A	273	PHE	Sidechain
1	A	277	ARG	Sidechain
1	A	283	ARG	Sidechain
1	A	299	ARG	Sidechain
1	A	307	ARG	Sidechain
1	A	316	TYR	Sidechain
1	A	333	HIS	Sidechain
1	A	39	ARG	Sidechain
1	A	77	ARG	Sidechain
2	B	11	ARG	Sidechain
2	B	137	ASN	Peptide
2	B	201	ARG	Sidechain
2	B	215	ARG	Sidechain
2	B	314	ARG	Sidechain,Mainchain
2	B	336	ARG	Sidechain
2	B	355	ARG	Sidechain
2	B	87	PHE	Sidechain
2	C	119	ARG	Sidechain
2	C	123	TYR	Sidechain
2	C	185	HIS	Sidechain
2	C	263	ARG	Sidechain
2	C	274	ARG	Sidechain
2	C	312	ARG	Sidechain
2	C	345	ARG	Sidechain
2	C	359	PHE	Sidechain
2	D	123	TYR	Sidechain
2	D	169	ARG	Sidechain
2	D	201	ARG	Sidechain
2	D	208	ARG	Sidechain
2	D	290	HIS	Sidechain
2	D	3	TYR	Sidechain
2	D	314	ARG	Sidechain
2	D	328	TYR	Sidechain
2	D	355	ARG	Sidechain
2	D	360	HIS	Sidechain

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Mol	Chain	Res	Type	Group
2	D	41	TYR	Sidechain
2	D	47	ARG	Sidechain
3	E	105	ARG	Sidechain
3	E	146	ARG	Sidechain
3	E	158	ARG	Sidechain
3	E	163	TYR	Sidechain
3	E	171	TYR	Sidechain
3	E	18	TYR	Sidechain
3	E	222	TYR	Sidechain
3	E	259	HIS	Sidechain
3	E	260	HIS	Sidechain
3	E	308	ARG	Sidechain
3	E	322	TYR	Sidechain
3	E	42	TYR	Sidechain
3	E	46	ARG	Sidechain
3	E	73	HIS	Sidechain
3	E	77	TYR	Sidechain
3	E	8	ARG	Sidechain
4	F	105	ARG	Sidechain
4	F	197	ARG	Sidechain
4	F	205	ARG	Sidechain
4	F	230	PHE	Sidechain
4	F	241	PHE	Sidechain
4	F	244	TYR	Sidechain
4	F	246	ARG	Sidechain
4	F	267	PHE	Sidechain
4	F	282	ARG	Sidechain
4	F	284	TYR	Sidechain
4	F	323	TYR	Sidechain
4	F	359	TYR	Sidechain
4	F	56	ARG	Sidechain
4	F	9	HIS	Sidechain
4	G	137	ARG	Sidechain
4	G	230	PHE	Sidechain
4	G	240	ARG	Sidechain
4	G	244	TYR	Sidechain
4	G	255	HIS	Sidechain
4	G	323	TYR	Sidechain
4	G	337	ARG	Sidechain
4	G	359	TYR	Sidechain

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	A	2726	0	2779	323	0
2	B	2796	0	2846	172	0
2	C	2835	0	2889	239	0
2	D	2786	0	2832	370	0
3	E	2602	0	2607	440	0
4	F	2844	0	2861	463	0
4	G	2844	0	2861	367	0
All	All	19433	0	19675	2240	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 57.

All (2240) 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)
1:A:73:LEU:HD11	4:F:176:ARG:C	1.48	1.38
1:A:73:LEU:CD2	4:F:177:LEU:HB2	1.65	1.26
1:A:73:LEU:HD21	4:F:177:LEU:CB	1.77	1.14
1:A:73:LEU:HD13	4:F:172:THR:OG1	1.49	1.10
1:A:73:LEU:CD1	4:F:176:ARG:C	2.24	1.09
1:A:73:LEU:HD22	4:F:177:LEU:HB2	1.32	1.07
1:A:73:LEU:CD2	4:F:177:LEU:CB	2.31	1.06
1:A:73:LEU:HD21	4:F:177:LEU:HB3	1.37	1.02
4:F:354:SER:HA	4:F:357:ALA:HB3	1.41	1.00
2:D:295:VAL:HG11	2:D:314:ARG:HA	1.44	0.97
1:A:72:SER:OG	4:F:362:MET:SD	2.21	0.97
1:A:73:LEU:HD13	4:F:172:THR:HG1	1.26	0.94
1:A:73:LEU:HD11	4:F:177:LEU:N	1.84	0.91
4:G:207:LEU:HD21	4:G:214:LEU:HB2	1.51	0.90
3:E:146:ARG:HB3	3:E:150:ARG:HE	1.38	0.89
3:E:33:PRO:HD3	3:E:146:ARG:HA	1.55	0.89
4:F:193:VAL:HG21	4:F:236:LEU:HD13	1.59	0.84
2:D:99:THR:HG22	2:D:130:MET:HE3	1.60	0.83
2:B:129:HIS:CD2	2:B:158:ASP:HB3	2.13	0.83
2:B:286:LEU:HD13	2:B:336:ARG:HH11	1.44	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:17:VAL:HA	4:G:53:MET:HB3	1.60	0.82
1:A:73:LEU:CD1	4:F:176:ARG:O	2.27	0.81
1:A:263:GLN:HA	1:A:266:HIS:CE1	2.15	0.81
2:D:201:ARG:HG2	2:D:234:THR:HG23	1.60	0.81
1:A:220:ALA:HB1	1:A:228:ARG:HG3	1.62	0.81
4:F:121:ASP:HA	4:F:224:ARG:HH22	1.45	0.81
1:A:300:GLN:HE21	1:A:330:LEU:HD11	1.45	0.81
4:F:53:MET:CE	4:F:230:PHE:HB3	2.11	0.81
4:G:206:MET:HB3	4:G:227:VAL:HB	1.62	0.81
2:D:121:LYS:H	2:D:149:HIS:HB2	1.44	0.80
4:G:132:GLN:HB3	4:G:207:LEU:HD22	1.62	0.80
1:A:73:LEU:HD12	4:F:175:HIS:N	1.97	0.79
2:C:357:LEU:O	2:C:364:PRO:HA	1.82	0.79
3:E:229:TRP:HD1	3:E:320:GLU:HG2	1.45	0.79
4:F:193:VAL:HG23	4:F:238:ASP:CG	2.07	0.79
1:A:69:GLN:HE21	4:F:362:MET:CE	1.96	0.79
4:F:122:TRP:CE3	4:F:222:ASN:HB2	2.17	0.79
1:A:220:ALA:CB	1:A:228:ARG:HG3	2.13	0.78
4:G:77:ASP:HA	4:G:80:ARG:HE	1.46	0.78
2:D:67:GLY:HA2	2:D:119:ARG:HH12	1.48	0.78
2:C:15:PHE:CD1	2:C:72:PRO:HA	2.18	0.78
1:A:73:LEU:HD12	4:F:176:ARG:N	1.99	0.78
2:B:315:GLU:HA	2:B:318:ARG:HE	1.48	0.78
2:C:347:MET:SD	2:D:287:GLY:HA2	2.23	0.78
2:D:201:ARG:CG	2:D:234:THR:HG23	2.14	0.77
1:A:220:ALA:HA	1:A:223:MET:SD	2.25	0.77
2:B:292:ILE:HG23	2:B:317:ALA:HA	1.65	0.77
2:D:25:LEU:HD23	2:D:54:ILE:HD11	1.67	0.77
1:A:73:LEU:HD23	4:F:247:VAL:HG21	1.67	0.77
3:E:118:ALA:HB1	3:E:150:ARG:HB3	1.67	0.77
2:D:21:GLN:HA	2:D:23:HIS:CE1	2.19	0.77
2:D:122:VAL:HG22	2:D:151:LYS:HG3	1.66	0.77
4:F:100:ARG:HH11	4:F:105:ARG:HG2	1.47	0.77
2:D:23:HIS:CD2	2:D:24:VAL:HG23	2.21	0.76
1:A:330:LEU:O	1:A:333:HIS:CE1	2.38	0.76
2:B:259:ALA:HB2	2:B:360:HIS:HA	1.65	0.76
3:E:176:LEU:HD11	3:E:202:LEU:HA	1.68	0.76
4:F:317:ILE:HD12	4:F:343:SER:HA	1.68	0.76
4:G:132:GLN:CB	4:G:207:LEU:HD22	2.16	0.76
1:A:269:LEU:H	1:A:269:LEU:HD22	1.51	0.76
3:E:212:ALA:HA	3:E:215:THR:OG1	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:121:ASP:HA	4:F:224:ARG:NH2	2.01	0.75
3:E:75:ASP:HB3	3:E:110:LYS:HA	1.67	0.74
4:G:9:HIS:CG	4:G:57:VAL:HG13	2.22	0.74
3:E:31:ALA:HB1	3:E:35:MET:SD	2.27	0.74
4:G:9:HIS:CD2	4:G:57:VAL:HG13	2.23	0.74
4:G:258:ALA:HB2	4:G:308:VAL:HG22	1.70	0.74
1:A:78:GLN:H	1:A:107:ASP:HA	1.53	0.74
2:C:364:PRO:HG2	2:C:367:GLU:CD	2.13	0.74
4:F:146:MET:CA	4:F:171:ALA:HB1	2.19	0.73
1:A:73:LEU:HD22	4:F:177:LEU:CD1	2.18	0.73
4:G:3:PHE:HB3	4:G:63:HIS:HA	1.71	0.73
3:E:48:LEU:HD22	3:E:140:TRP:CG	2.23	0.73
3:E:180:VAL:HG21	3:E:205:PHE:CD2	2.23	0.73
2:D:3:TYR:HB2	3:E:21:GLY:HA2	1.71	0.73
3:E:10:ASP:HA	3:E:162:HIS:CE1	2.24	0.73
4:F:103:ARG:HE	4:G:305:ILE:HB	1.54	0.73
2:C:191:LEU:HD22	2:C:196:ILE:HB	1.70	0.73
1:A:154:ARG:HA	1:A:157:GLN:HG2	1.70	0.73
3:E:11:PHE:CD1	3:E:56:HIS:HE1	2.06	0.73
4:F:137:ARG:HE	4:F:332:LYS:HE3	1.53	0.73
1:A:77:ARG:HE	1:A:107:ASP:H	1.35	0.73
2:D:288:LEU:HA	2:D:306:MET:SD	2.29	0.73
3:E:297:ARG:O	3:E:301:MET:HG2	1.89	0.73
3:E:227:GLY:HA2	3:E:323:LEU:CD1	2.19	0.72
3:E:18:TYR:HB2	3:E:52:GLN:HE22	1.55	0.72
4:G:3:PHE:CB	4:G:63:HIS:HA	2.20	0.72
4:G:296:ASN:HD21	4:G:298:GLU:HB3	1.55	0.72
2:D:120:PHE:HD1	2:D:149:HIS:HA	1.55	0.72
4:G:162:THR:H	4:G:190:SER:HB3	1.55	0.72
3:E:32:LEU:H	3:E:35:MET:HE3	1.55	0.72
4:F:56:ARG:H	4:F:229:ASP:HB3	1.55	0.71
4:G:181:SER:O	4:G:356:SER:HA	1.90	0.71
2:D:2:SER:CA	3:E:25:HIS:HB3	2.20	0.71
3:E:180:VAL:HG11	3:E:205:PHE:HB2	1.72	0.71
4:G:82:LEU:HD13	4:G:101:SER:HB3	1.72	0.71
2:C:255:ALA:HB2	2:C:263:ARG:NE	2.06	0.71
3:E:90:VAL:HA	3:E:124:ALA:HA	1.70	0.71
3:E:48:LEU:O	3:E:109:ALA:HB3	1.91	0.71
2:C:75:VAL:H	2:C:79:CYS:HB2	1.56	0.71
1:A:73:LEU:HD11	4:F:176:ARG:CA	2.21	0.70
4:G:203:LEU:HD21	4:G:232:PHE:CD1	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:227:SER:HA	2:D:27:ALA:CB	2.21	0.70
1:A:73:LEU:HD22	4:F:177:LEU:CB	2.08	0.70
3:E:295:HIS:HA	3:E:298:GLU:HG2	1.74	0.70
1:A:272:LEU:HD21	1:A:273:PHE:CZ	2.26	0.70
1:A:231:HIS:CE1	1:A:235:GLN:HE21	2.10	0.70
4:F:59:LEU:HD21	4:F:63:HIS:HB3	1.74	0.70
2:D:114:ALA:HB2	4:G:366:LEU:HD21	1.73	0.70
3:E:229:TRP:CD1	3:E:320:GLU:HG2	2.26	0.70
4:F:202:GLU:HB2	4:F:205:ARG:HH21	1.57	0.70
3:E:14:LEU:HD22	3:E:27:LEU:HD13	1.74	0.70
4:F:256:LEU:HB3	4:F:338:MET:SD	2.31	0.70
4:G:177:LEU:HD21	4:G:179:VAL:HG13	1.74	0.70
1:A:148:PRO:HB3	1:A:167:ASN:HD21	1.57	0.70
3:E:146:ARG:HD2	3:E:150:ARG:HH21	1.55	0.70
4:G:206:MET:O	4:G:207:LEU:HD23	1.92	0.69
3:E:14:LEU:HD21	3:E:162:HIS:CD2	2.27	0.69
2:C:114:ALA:HA	2:C:149:HIS:CD2	2.27	0.69
1:A:166:ALA:HA	1:A:199:LEU:HD13	1.74	0.69
4:F:255:HIS:CG	4:F:256:LEU:N	2.60	0.69
1:A:23:LEU:HD22	1:A:34:SER:HB3	1.73	0.69
1:A:73:LEU:HD23	4:F:247:VAL:CG2	2.23	0.69
3:E:118:ALA:CB	3:E:150:ARG:HB3	2.22	0.69
3:E:182:MET:SD	3:E:205:PHE:CD1	2.85	0.69
3:E:224:VAL:HA	3:E:229:TRP:CZ2	2.27	0.69
4:F:337:ARG:HH12	4:F:352:ALA:HA	1.57	0.69
4:G:193:VAL:HG21	4:G:218:ILE:HG13	1.73	0.69
1:A:234:GLN:HE21	2:B:303:GLY:HA3	1.58	0.69
1:A:333:HIS:HB3	1:A:338:ASP:H	1.59	0.68
2:C:359:PHE:CE1	2:D:323:THR:HA	2.28	0.68
3:E:48:LEU:HD13	3:E:142:PHE:CZ	2.28	0.68
4:G:256:LEU:HG	4:G:338:MET:HE3	1.75	0.68
4:G:260:CYS:HB3	4:G:334:GLU:HA	1.76	0.68
1:A:189:SER:HA	1:A:195:GLY:HA2	1.75	0.68
4:F:182:MET:HA	4:F:355:GLN:HB2	1.75	0.68
3:E:281:LEU:HA	3:E:285:ARG:HE	1.58	0.68
1:A:297:GLN:HB2	1:A:333:HIS:CE1	2.28	0.68
2:C:244:LEU:HD13	2:C:274:ARG:HH11	1.58	0.68
2:C:199:GLU:HG3	2:C:202:ALA:H	1.59	0.68
1:A:73:LEU:CD1	4:F:176:ARG:N	2.56	0.68
2:C:225:ILE:HG23	2:C:230:GLY:HA2	1.76	0.68
3:E:33:PRO:CD	3:E:146:ARG:HA	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:146:MET:HA	4:F:171:ALA:HB1	1.76	0.68
4:F:159:LEU:CD1	4:F:240:ARG:HA	2.24	0.68
4:F:321:VAL:O	4:F:324:VAL:HG22	1.93	0.68
1:A:77:ARG:HA	1:A:107:ASP:HA	1.75	0.67
2:D:2:SER:HA	3:E:25:HIS:HB3	1.75	0.67
2:D:310:GLU:HG3	2:D:314:ARG:HD3	1.76	0.67
4:F:317:ILE:CD1	4:F:343:SER:HA	2.24	0.67
4:G:193:VAL:HA	4:G:236:LEU:HD22	1.77	0.67
2:B:69:THR:HB	2:B:71:THR:H	1.59	0.67
2:D:210:ALA:HB1	2:D:217:ALA:HB2	1.77	0.67
4:G:331:LEU:HD11	4:G:333:CYS:HB3	1.75	0.67
2:D:99:THR:CG2	2:D:130:MET:HE3	2.25	0.67
3:E:191:LEU:CD1	3:E:201:ALA:HB2	2.25	0.67
4:G:357:ALA:HB1	4:G:359:TYR:CE2	2.30	0.67
3:E:48:LEU:HD22	3:E:140:TRP:CD2	2.30	0.67
4:F:121:ASP:CA	4:F:224:ARG:HH22	2.07	0.67
3:E:25:HIS:HA	3:E:140:TRP:CZ3	2.30	0.67
3:E:92:ALA:HA	3:E:95:GLU:OE2	1.95	0.67
4:F:357:ALA:HB1	4:F:359:TYR:CZ	2.29	0.67
4:F:223:ILE:HB	4:F:236:LEU:HD11	1.77	0.66
4:F:254:LYS:HB2	4:F:340:LEU:HB2	1.77	0.66
4:G:315:MET:HA	4:G:342:ASP:CB	2.25	0.66
1:A:270:ARG:HA	1:A:273:PHE:CD2	2.31	0.66
4:F:8:GLU:HA	4:F:11:LEU:HB2	1.77	0.66
4:G:92:LEU:HA	4:G:97:MET:SD	2.36	0.66
1:A:331:LEU:O	1:A:333:HIS:CD2	2.48	0.66
2:C:355:ARG:HG3	2:C:359:PHE:CE2	2.30	0.66
2:B:111:VAL:HG11	2:B:147:PRO:HG2	1.77	0.66
3:E:49:LEU:HD21	3:E:73:HIS:CE1	2.31	0.66
4:G:245:ARG:HA	4:G:245:ARG:HE	1.61	0.66
2:C:289:LEU:HD13	2:C:329:TYR:CA	2.25	0.66
4:G:31:GLY:CA	4:G:73:ARG:HH12	2.08	0.66
1:A:192:TRP:HB2	1:A:195:GLY:H	1.60	0.66
2:C:358:ALA:HB3	2:D:326:GLN:HG3	1.78	0.66
2:D:256:MET:HG2	2:D:357:LEU:HA	1.78	0.66
3:E:11:PHE:CD1	3:E:56:HIS:CE1	2.83	0.66
3:E:33:PRO:HA	3:E:37:ASP:HB2	1.76	0.66
4:F:135:MET:HG3	4:F:207:LEU:HD12	1.78	0.66
4:F:259:GLY:HA2	4:F:334:GLU:OE1	1.96	0.66
3:E:49:LEU:HD22	3:E:68:MET:HG3	1.78	0.65
2:B:73:CYS:HB3	2:B:76:CYS:SG	2.37	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:51:MET:HB2	4:F:232:PHE:CE2	2.32	0.65
1:A:273:PHE:CD2	1:A:283:ARG:HA	2.31	0.65
2:B:64:CYS:HB3	2:B:79:CYS:SG	2.36	0.65
2:D:346:ARG:HH22	3:E:192:ARG:HD2	1.60	0.65
3:E:33:PRO:HD3	3:E:146:ARG:CA	2.25	0.65
3:E:140:TRP:HB3	3:E:142:PHE:CZ	2.31	0.65
1:A:158:LEU:HD13	1:A:185:LEU:HD13	1.78	0.65
2:C:15:PHE:CE1	2:C:57:LEU:HB3	2.32	0.65
2:D:261:GLY:HA2	2:D:357:LEU:HD21	1.78	0.65
3:E:31:ALA:HB1	3:E:35:MET:CG	2.26	0.65
4:F:6:GLU:OE2	4:F:9:HIS:CE1	2.50	0.65
4:G:191:HIS:CD2	4:G:218:ILE:HG12	2.32	0.65
4:F:12:LYS:HZ2	4:F:16:GLN:HG3	1.59	0.65
4:F:162:THR:O	4:F:190:SER:HA	1.96	0.65
4:G:206:MET:HB3	4:G:227:VAL:CB	2.25	0.65
2:D:62:LEU:HD23	2:D:68:ILE:HG22	1.78	0.65
2:D:79:CYS:HA	2:D:82:ILE:HD12	1.79	0.65
4:G:5:VAL:HA	4:G:59:LEU:HD12	1.79	0.65
2:D:195:HIS:CD2	2:D:196:ILE:H	2.15	0.65
3:E:27:LEU:HA	3:E:160:ARG:O	1.98	0.64
3:E:278:ALA:HA	3:E:286:LEU:HD11	1.79	0.64
4:F:53:MET:HE1	4:F:230:PHE:HB3	1.78	0.64
4:G:9:HIS:CE1	4:G:58:ALA:O	2.50	0.64
4:F:212:ASN:HB3	4:F:227:VAL:HG13	1.78	0.64
3:E:18:TYR:CG	3:E:140:TRP:CZ3	2.85	0.64
4:F:255:HIS:CE1	4:F:257:GLU:H	2.14	0.64
2:D:121:LYS:O	2:D:150:VAL:HA	1.97	0.64
2:D:224:ALA:HA	2:D:240:MET:SD	2.37	0.64
2:D:296:GLN:HG2	2:D:317:ALA:O	1.96	0.64
3:E:47:TYR:HE2	3:E:52:GLN:HE21	1.44	0.64
4:G:78:ILE:HG21	4:G:99:VAL:HG11	1.79	0.64
4:F:24:ARG:HH22	4:F:73:ARG:HG2	1.62	0.64
2:C:252:LEU:O	2:C:255:ALA:HB3	1.97	0.64
2:D:7:ALA:HA	2:D:218:LEU:HD13	1.80	0.64
2:C:179:ASP:HB2	2:C:182:GLN:H	1.62	0.64
2:D:39:HIS:HB2	2:D:151:LYS:HA	1.80	0.64
4:F:254:LYS:HD3	4:F:315:MET:HE2	1.80	0.64
4:G:357:ALA:HB1	4:G:359:TYR:CZ	2.32	0.64
3:E:3:TRP:HA	3:E:7:LEU:HD12	1.80	0.64
4:F:122:TRP:NE1	4:F:219:GLY:HA3	2.12	0.64
4:F:137:ARG:HE	4:F:332:LYS:CE	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:SER:HA	1:A:195:GLY:CA	2.28	0.64
1:A:231:HIS:C	1:A:231:HIS:CD2	2.76	0.64
2:C:341:TYR:HB2	2:D:333:LEU:CD1	2.28	0.64
4:F:150:ASP:CG	4:F:155:LEU:HD12	2.23	0.64
2:C:338:GLU:HB3	2:D:333:LEU:HD21	1.79	0.63
2:C:358:ALA:HB1	2:D:322:PRO:HB2	1.79	0.63
3:E:35:MET:SD	3:E:166:PRO:HA	2.38	0.63
4:F:124:SER:CB	4:F:217:GLN:HB3	2.28	0.63
4:F:354:SER:CA	4:F:357:ALA:HB3	2.22	0.63
3:E:158:ARG:H	3:E:158:ARG:HD2	1.64	0.63
3:E:25:HIS:HA	3:E:140:TRP:CE3	2.33	0.63
2:C:111:VAL:O	2:C:150:VAL:HG21	1.97	0.63
2:D:42:LEU:HD21	2:D:159:PRO:HB3	1.79	0.63
2:D:298:SER:HB2	2:D:301:ALA:H	1.62	0.63
3:E:88:LEU:HB3	3:E:120:LEU:HA	1.80	0.63
4:F:317:ILE:HA	4:F:343:SER:HB2	1.81	0.63
4:G:131:PRO:O	4:G:135:MET:HB2	1.99	0.63
2:D:324:ASP:HA	2:D:327:LEU:HD12	1.79	0.63
1:A:314:GLN:CD	3:E:303:VAL:HG22	2.24	0.63
3:E:254:ASP:HB3	3:E:265:VAL:HG12	1.81	0.63
4:G:146:MET:HB3	4:G:156:ASN:HA	1.80	0.63
1:A:61:TRP:HE1	1:A:93:ILE:HA	1.64	0.63
3:E:280:HIS:HB2	3:E:281:LEU:HD12	1.81	0.63
4:F:59:LEU:HD21	4:F:63:HIS:CB	2.28	0.63
4:F:132:GLN:O	4:F:135:MET:HB3	1.98	0.63
4:G:137:ARG:HH11	4:G:357:ALA:CB	2.12	0.63
4:G:254:LYS:HZ1	4:G:342:ASP:CG	2.07	0.63
2:D:14:THR:CA	2:D:57:LEU:HD21	2.29	0.63
1:A:273:PHE:HB3	1:A:278:VAL:HB	1.81	0.63
4:F:121:ASP:HA	4:F:224:ARG:CZ	2.29	0.63
4:G:146:MET:CB	4:G:156:ASN:HA	2.29	0.63
3:E:203:ALA:HA	3:E:206:GLN:OE1	1.99	0.62
4:F:276:GLU:OE1	4:F:276:GLU:HA	1.98	0.62
4:G:351:ASP:HB2	4:G:354:SER:H	1.64	0.62
1:A:171:CYS:O	1:A:175:GLU:HA	1.99	0.62
2:D:96:ALA:HA	2:D:130:MET:HG3	1.81	0.62
3:E:67:LEU:C	3:E:73:HIS:HB2	2.24	0.62
3:E:180:VAL:HG21	3:E:205:PHE:CG	2.34	0.62
3:E:241:ALA:HB3	3:E:242:PRO:HD3	1.82	0.62
3:E:252:LEU:HB2	3:E:290:LEU:HD13	1.81	0.62
2:C:278:TRP:HB3	2:C:349:VAL:HG21	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:131:LEU:HB3	2:D:135:SER:CB	2.29	0.62
2:D:249:ALA:CB	2:D:284:GLU:HG3	2.30	0.62
3:E:32:LEU:HB3	3:E:34:GLY:H	1.64	0.62
3:E:216:LEU:HD13	3:E:235:ALA:HB3	1.82	0.62
4:F:13:PRO:HG2	4:F:57:VAL:CG2	2.29	0.62
1:A:334:LYS:HZ3	1:A:338:ASP:CG	2.07	0.62
2:C:365:LEU:O	2:C:367:GLU:HG2	2.00	0.62
4:G:132:GLN:HG3	4:G:209:GLY:C	2.24	0.62
2:B:339:LEU:HB3	2:B:345:ARG:HE	1.62	0.62
2:D:60:LYS:HB2	2:D:72:PRO:CB	2.29	0.62
2:D:338:GLU:HA	2:D:341:TYR:CE2	2.34	0.62
3:E:27:LEU:HD11	3:E:162:HIS:CB	2.30	0.62
2:D:297:LEU:HD12	2:D:298:SER:N	2.15	0.62
2:D:64:CYS:HA	2:D:79:CYS:SG	2.40	0.62
2:D:348:GLY:HA2	2:D:351:MET:SD	2.40	0.62
3:E:109:ALA:HA	3:E:138:GLU:HB3	1.82	0.62
4:F:123:GLN:OE1	4:F:123:GLN:HA	1.99	0.62
1:A:72:SER:OG	4:F:362:MET:CG	2.47	0.62
1:A:273:PHE:CE1	1:A:286:MET:HG3	2.35	0.62
3:E:244:ARG:HA	3:E:247:TRP:CD2	2.34	0.62
4:F:11:LEU:HA	4:F:14:LEU:HB2	1.82	0.62
4:G:22:GLY:HA2	4:G:30:LEU:HB3	1.80	0.62
4:F:218:ILE:HG22	4:F:219:GLY:O	2.00	0.61
4:G:159:LEU:HB2	4:G:241:PHE:CB	2.30	0.61
2:D:4:GLN:HE21	2:D:5:VAL:HG22	1.65	0.61
4:F:13:PRO:HB3	4:F:55:ALA:HB3	1.81	0.61
4:F:121:ASP:HA	4:F:224:ARG:NH1	2.15	0.61
4:G:191:HIS:CD2	4:G:218:ILE:O	2.53	0.61
2:B:180:VAL:O	2:B:207:ALA:HB1	2.00	0.61
2:C:60:LYS:HD2	2:C:73:CYS:C	2.25	0.61
3:E:229:TRP:CD1	3:E:320:GLU:CG	2.84	0.61
4:G:6:GLU:CG	4:G:9:HIS:HB2	2.30	0.61
2:C:227:SER:HA	2:D:27:ALA:HB1	1.81	0.61
1:A:211:HIS:CD2	1:A:213:THR:HA	2.36	0.61
1:A:329:LEU:HB3	1:A:334:LYS:NZ	2.16	0.61
4:F:87:GLU:HA	4:F:87:GLU:OE2	2.00	0.61
1:A:223:MET:HA	1:A:288:GLU:CD	2.26	0.61
4:G:14:LEU:HA	4:G:44:LEU:HD21	1.82	0.61
2:C:282:LEU:HA	2:C:285:MET:HE3	1.82	0.61
2:C:341:TYR:HB2	2:D:333:LEU:HD12	1.81	0.61
2:D:3:TYR:CD1	3:E:21:GLY:O	2.54	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:154:LEU:HD12	2:D:170:CYS:SG	2.40	0.61
2:D:338:GLU:HA	2:D:341:TYR:CZ	2.35	0.61
4:G:7:ARG:CZ	4:G:84:GLU:HB3	2.30	0.61
4:G:42:LEU:O	4:G:56:ARG:HA	2.00	0.61
4:G:148:HIS:CE1	4:G:156:ASN:HB2	2.36	0.61
4:G:274:SER:HA	4:G:294:ALA:HB1	1.83	0.61
3:E:46:ARG:HE	3:E:65:CYS:HB2	1.66	0.61
3:E:176:LEU:CD1	3:E:202:LEU:HA	2.30	0.61
3:E:179:GLU:CD	3:E:202:LEU:HD23	2.25	0.61
4:F:144:PHE:CE2	4:F:176:ARG:HD2	2.35	0.61
4:G:254:LYS:HB3	4:G:310:TYR:CE1	2.35	0.61
1:A:148:PRO:CB	1:A:167:ASN:HD21	2.14	0.61
3:E:17:SER:CB	3:E:23:GLY:HA3	2.31	0.61
3:E:24:HIS:CE1	3:E:26:ALA:HB3	2.36	0.61
4:F:243:ASP:H	4:F:246:ARG:NH2	1.99	0.61
2:B:19:VAL:HG21	2:B:185:HIS:CD2	2.36	0.61
3:E:46:ARG:HA	3:E:68:MET:HE1	1.82	0.60
1:A:18:ARG:HA	1:A:133:ARG:O	2.00	0.60
1:A:47:PHE:CE2	1:A:77:ARG:HB3	2.36	0.60
2:D:184:ARG:HD3	2:D:204:GLN:HG2	1.82	0.60
3:E:48:LEU:HG	3:E:52:GLN:HG2	1.83	0.60
4:F:22:GLY:HA2	4:F:72:ALA:HB3	1.83	0.60
1:A:73:LEU:CD2	4:F:247:VAL:HG21	2.31	0.60
3:E:82:GLU:CG	3:E:92:ALA:HB2	2.31	0.60
3:E:89:GLY:C	3:E:124:ALA:HB2	2.25	0.60
3:E:14:LEU:HD13	3:E:27:LEU:HD21	1.81	0.60
3:E:176:LEU:O	3:E:179:GLU:HG2	2.02	0.60
3:E:187:LEU:HA	3:E:205:PHE:CZ	2.36	0.60
3:E:213:ARG:HA	3:E:247:TRP:CE3	2.36	0.60
3:E:255:ALA:HB2	3:E:277:LEU:HB2	1.84	0.60
4:F:54:VAL:O	4:F:230:PHE:HA	2.01	0.60
4:F:150:ASP:OD2	4:F:155:LEU:HD12	2.01	0.60
4:G:31:GLY:HA2	4:G:73:ARG:HH12	1.64	0.60
4:G:84:GLU:C	4:G:86:ALA:H	2.07	0.60
2:D:298:SER:CB	2:D:301:ALA:H	2.15	0.60
4:F:121:ASP:HA	4:F:224:ARG:HH12	1.65	0.60
4:G:137:ARG:HA	4:G:332:LYS:HD2	1.83	0.60
1:A:269:LEU:C	1:A:270:ARG:HG2	2.26	0.60
2:C:355:ARG:HG3	2:C:359:PHE:CD2	2.37	0.60
3:E:81:PRO:HA	3:E:88:LEU:HA	1.82	0.60
3:E:208:ASP:HA	3:E:211:GLN:CD	2.25	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:213:ARG:HD2	3:E:247:TRP:HB3	1.83	0.60
4:F:24:ARG:HA	4:F:31:GLY:HA3	1.83	0.60
4:F:315:MET:SD	4:F:342:ASP:HA	2.40	0.60
4:G:16:GLN:HG3	4:G:230:PHE:CE2	2.37	0.60
1:A:269:LEU:HB3	1:A:287:GLY:HA3	1.83	0.60
3:E:45:SER:HA	3:E:111:VAL:HG11	1.84	0.60
4:F:161:GLU:HA	4:F:192:SER:HA	1.84	0.60
1:A:73:LEU:HB2	4:F:174:GLY:C	2.27	0.60
1:A:199:LEU:HA	1:A:202:VAL:HG12	1.84	0.60
2:B:54:ILE:HG13	2:B:175:LEU:HD11	1.82	0.60
2:D:307:ALA:HA	2:D:310:GLU:HB2	1.83	0.60
3:E:244:ARG:HG2	3:E:247:TRP:CH2	2.36	0.60
3:E:316:LEU:O	3:E:320:GLU:HG3	2.02	0.60
4:F:182:MET:HA	4:F:355:GLN:CB	2.32	0.60
4:G:219:GLY:H	4:G:223:ILE:HG22	1.67	0.60
1:A:158:LEU:CD2	1:A:185:LEU:HB3	2.31	0.60
2:B:63:ASN:CB	2:B:118:GLY:HA3	2.32	0.60
1:A:295:GLN:HA	1:A:298:LEU:HD23	1.83	0.60
3:E:259:HIS:NE2	3:E:286:LEU:HD12	2.16	0.60
3:E:318:ARG:HA	3:E:321:HIS:HB2	1.83	0.60
2:C:57:LEU:HA	2:C:60:LYS:HZ2	1.66	0.59
3:E:90:VAL:HG13	3:E:91:ASP:OD2	2.02	0.59
4:F:21:LEU:HD21	4:F:46:GLY:HA2	1.82	0.59
3:E:47:TYR:HA	3:E:59:CYS:SG	2.42	0.59
1:A:225:LYS:NZ	1:A:228:ARG:HG2	2.17	0.59
2:D:64:CYS:C	2:D:66:THR:H	2.09	0.59
2:D:115:PRO:HB2	2:D:118:GLY:H	1.67	0.59
2:D:339:LEU:O	2:D:348:GLY:HA3	2.02	0.59
3:E:223:SER:HA	3:E:228:ASP:O	2.02	0.59
4:F:256:LEU:HD11	4:F:308:VAL:HG11	1.83	0.59
4:G:1:MET:N	4:G:66:GLY:HA3	2.17	0.59
3:E:180:VAL:HG11	3:E:205:PHE:CB	2.32	0.59
4:F:137:ARG:HG2	4:F:182:MET:HE2	1.84	0.59
1:A:51:HIS:HE1	1:A:78:GLN:HB2	1.67	0.59
3:E:209:ASN:O	3:E:213:ARG:N	2.32	0.59
4:F:135:MET:HG3	4:F:207:LEU:CD1	2.32	0.59
4:G:315:MET:HA	4:G:342:ASP:HB3	1.84	0.59
4:F:132:GLN:HG3	4:F:214:LEU:HD11	1.84	0.59
4:G:82:LEU:CD1	4:G:101:SER:HB3	2.33	0.59
4:G:120:ASP:HA	4:G:122:TRP:CZ2	2.38	0.59
4:G:257:GLU:HG2	4:G:337:ARG:HA	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:SER:HG	4:F:362:MET:CG	2.15	0.59
2:B:82:ILE:HD11	2:B:87:PHE:CD2	2.38	0.59
2:D:75:VAL:HA	2:D:80:ARG:CD	2.32	0.59
2:C:351:MET:SD	2:D:290:HIS:HA	2.43	0.59
4:F:126:VAL:HG22	4:F:191:HIS:HE1	1.68	0.59
1:A:223:MET:HA	1:A:288:GLU:OE1	2.03	0.59
2:D:172:GLN:HB3	2:D:174:HIS:CE1	2.38	0.59
3:E:276:GLU:HA	3:E:279:ASN:CB	2.33	0.59
4:F:130:LEU:HB3	4:F:132:GLN:H	1.68	0.59
3:E:246:HIS:HB2	3:E:297:ARG:NH1	2.18	0.59
4:F:5:VAL:HG11	4:F:57:VAL:HG11	1.85	0.59
4:G:135:MET:HB3	4:G:207:LEU:HD13	1.85	0.59
2:C:289:LEU:HD13	2:C:329:TYR:HA	1.84	0.58
4:F:159:LEU:HD22	4:F:241:PHE:H	1.68	0.58
4:G:191:HIS:CD2	4:G:218:ILE:HG23	2.38	0.58
2:B:63:ASN:HB3	2:B:87:PHE:CE2	2.37	0.58
2:B:63:ASN:O	2:B:78:ASN:HB3	2.04	0.58
2:B:339:LEU:HD22	2:B:345:ARG:HA	1.84	0.58
2:D:172:GLN:CB	2:D:174:HIS:CE1	2.86	0.58
4:F:267:PHE:HB2	4:F:325:LEU:HD11	1.83	0.58
2:B:10:TRP:CD2	2:B:190:ILE:HG21	2.38	0.58
2:B:351:MET:HE2	2:C:329:TYR:CG	2.39	0.58
2:C:121:LYS:HG2	2:C:123:TYR:CZ	2.38	0.58
3:E:228:ASP:OD1	3:E:230:TYR:HB3	2.02	0.58
4:F:16:GLN:HB3	4:F:53:MET:HE3	1.85	0.58
4:G:202:GLU:O	4:G:205:ARG:HB2	2.03	0.58
4:G:286:SER:HA	4:G:314:GLU:OE1	2.03	0.58
1:A:144:GLN:HA	1:A:175:GLU:CD	2.28	0.58
1:A:273:PHE:HD2	1:A:283:ARG:CA	2.16	0.58
1:A:273:PHE:HB2	1:A:283:ARG:HD2	1.84	0.58
2:C:12:PRO:HA	2:C:17:ASP:HB3	1.83	0.58
2:D:75:VAL:HG23	2:D:80:ARG:CG	2.33	0.58
4:F:17:VAL:HG21	4:F:55:ALA:CB	2.34	0.58
2:B:249:ALA:HB1	2:B:285:MET:HG2	1.85	0.58
2:D:22:GLU:OE2	2:D:25:LEU:HD12	2.03	0.58
4:F:147:ALA:HB1	4:F:149:GLN:O	2.02	0.58
4:G:82:LEU:HD13	4:G:101:SER:CB	2.33	0.58
4:G:93:GLU:OE2	4:G:98:LEU:HD13	2.04	0.58
2:B:65:GLU:CD	2:B:78:ASN:H	2.11	0.58
4:F:135:MET:CG	4:F:207:LEU:HD12	2.34	0.58
4:F:282:ARG:HB3	4:F:316:GLU:OE1	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:277:GLU:HG2	2:B:280:ALA:H	1.69	0.58
2:C:265:MET:HE2	2:D:301:ALA:O	2.04	0.58
2:D:120:PHE:CD1	2:D:149:HIS:HA	2.37	0.58
4:F:122:TRP:CE2	4:F:219:GLY:HA3	2.38	0.58
4:G:17:VAL:HG13	4:G:53:MET:O	2.04	0.58
4:G:348:GLN:C	4:G:349:ILE:HG13	2.29	0.58
1:A:18:ARG:HB2	1:A:21:TYR:CE2	2.38	0.58
1:A:24:LEU:HD22	1:A:115:ASN:O	2.04	0.58
1:A:163:ASP:OD2	1:A:199:LEU:HB2	2.04	0.58
3:E:10:ASP:CA	3:E:162:HIS:CE1	2.87	0.58
3:E:186:ALA:HB1	3:E:210:TRP:CD1	2.38	0.58
4:F:258:ALA:C	4:F:335:ASN:HD22	2.12	0.58
4:F:276:GLU:CG	4:F:298:GLU:OE1	2.51	0.58
4:F:340:LEU:N	4:F:340:LEU:HD12	2.19	0.58
4:G:192:SER:O	4:G:220:SER:HA	2.04	0.58
4:G:282:ARG:HA	4:G:318:GLY:HA3	1.84	0.58
2:B:183:ILE:HD11	2:B:211:GLU:HA	1.86	0.58
2:D:164:VAL:HG23	2:D:165:THR:HG23	1.85	0.58
3:E:250:THR:HA	3:E:253:MET:HE2	1.84	0.58
4:G:361:VAL:HG22	4:G:362:MET:H	1.68	0.58
1:A:264:SER:HB3	1:A:290:LEU:HD13	1.86	0.57
4:G:132:GLN:O	4:G:136:LYS:HB2	2.04	0.57
1:A:25:GLY:HA3	1:A:139:CYS:H	1.68	0.57
3:E:49:LEU:HB3	3:E:68:MET:SD	2.43	0.57
3:E:73:HIS:HB3	3:E:76:TYR:CB	2.34	0.57
3:E:204:LEU:O	3:E:210:TRP:HB2	2.04	0.57
4:G:144:PHE:CZ	4:G:327:VAL:HG12	2.39	0.57
2:B:62:LEU:HD22	2:B:120:PHE:CD2	2.39	0.57
2:C:279:GLU:OE2	2:C:336:ARG:HA	2.03	0.57
4:F:25:PRO:HD2	4:F:31:GLY:HA2	1.87	0.57
4:G:8:GLU:HA	4:G:11:LEU:HB2	1.86	0.57
4:G:139:ILE:O	4:G:143:GLN:HG3	2.05	0.57
1:A:55:ILE:HG12	1:A:93:ILE:HG23	1.85	0.57
1:A:273:PHE:HB3	1:A:283:ARG:HG2	1.86	0.57
1:A:311:THR:HA	1:A:315:ASP:OD2	2.03	0.57
3:E:190:ALA:HB1	3:E:204:LEU:CD1	2.33	0.57
4:F:351:ASP:HB3	4:F:354:SER:CA	2.34	0.57
4:G:254:LYS:HB3	4:G:310:TYR:HE1	1.68	0.57
1:A:273:PHE:CD2	1:A:283:ARG:O	2.57	0.57
2:C:256:MET:SD	2:C:356:ALA:HB3	2.44	0.57
3:E:32:LEU:HA	3:E:146:ARG:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:259:HIS:CD2	3:E:286:LEU:HD12	2.39	0.57
3:E:276:GLU:HA	3:E:279:ASN:HB2	1.86	0.57
4:F:251:ASN:HB3	4:F:253:ASP:OD1	2.04	0.57
3:E:33:PRO:HA	3:E:37:ASP:CB	2.34	0.57
3:E:256:LEU:HD21	3:E:286:LEU:HB2	1.86	0.57
4:F:145:SER:HB3	4:F:172:THR:HA	1.86	0.57
4:G:148:HIS:CE1	4:G:156:ASN:CB	2.88	0.57
2:C:32:LEU:HD13	2:C:70:ALA:HA	1.86	0.57
3:E:147:GLU:HA	3:E:147:GLU:OE2	2.03	0.57
4:G:215:ARG:HD3	4:G:226:HIS:HB2	1.86	0.57
3:E:210:TRP:HA	3:E:213:ARG:HB3	1.87	0.57
3:E:238:HIS:H	3:E:241:ALA:HB2	1.69	0.57
4:F:6:GLU:O	4:F:10:LEU:HB2	2.04	0.57
4:F:267:PHE:CB	4:F:325:LEU:HD11	2.34	0.57
2:C:23:HIS:CE1	2:C:24:VAL:HG23	2.40	0.56
2:D:205:LEU:HD13	2:D:238:SER:HA	1.86	0.56
3:E:176:LEU:HD22	3:E:201:ALA:HB1	1.87	0.56
3:E:230:TYR:CE1	3:E:313:THR:HG23	2.39	0.56
4:F:122:TRP:CZ2	4:F:124:SER:HA	2.40	0.56
4:F:163:GLU:HA	4:F:190:SER:OG	2.05	0.56
4:G:154:TYR:CD1	4:G:237:VAL:HG21	2.40	0.56
1:A:217:TRP:O	1:A:220:ALA:HB3	2.05	0.56
2:B:65:GLU:HB2	2:B:76:CYS:SG	2.45	0.56
2:D:111:VAL:HB	2:D:150:VAL:CG2	2.36	0.56
3:E:81:PRO:HA	3:E:88:LEU:HB2	1.87	0.56
4:F:12:LYS:HD2	4:F:16:GLN:HG2	1.86	0.56
4:F:133:ALA:HA	4:F:136:LYS:CE	2.35	0.56
1:A:70:ALA:HB1	4:F:175:HIS:ND1	2.21	0.56
2:C:252:LEU:HA	2:C:267:LEU:HD12	1.88	0.56
2:D:2:SER:HA	3:E:25:HIS:CB	2.35	0.56
3:E:12:GLU:HA	3:E:56:HIS:CE1	2.40	0.56
3:E:51:GLN:HB2	3:E:108:GLY:HA2	1.87	0.56
3:E:80:ALA:O	3:E:88:LEU:HD13	2.05	0.56
4:F:159:LEU:HD11	4:F:240:ARG:HA	1.86	0.56
4:F:255:HIS:HB2	4:F:339:MET:HE1	1.86	0.56
4:G:41:THR:HB	4:G:56:ARG:HB2	1.87	0.56
4:G:154:TYR:O	4:G:241:PHE:CZ	2.58	0.56
2:D:252:LEU:HD21	2:D:267:LEU:HD23	1.88	0.56
3:E:175:TRP:CZ3	3:E:198:PRO:HB2	2.40	0.56
2:B:64:CYS:CB	2:B:79:CYS:SG	2.94	0.56
3:E:15:VAL:HG23	3:E:44:LEU:HD23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:103:HIS:CG	3:E:104:ALA:H	2.24	0.56
3:E:229:TRP:CD1	3:E:229:TRP:N	2.69	0.56
4:F:228:GLY:C	4:F:230:PHE:H	2.14	0.56
4:G:137:ARG:HH11	4:G:357:ALA:HB2	1.69	0.56
1:A:297:GLN:CD	1:A:333:HIS:CD2	2.84	0.56
1:A:329:LEU:HB3	1:A:334:LYS:HZ1	1.71	0.56
2:C:179:ASP:CG	2:C:182:GLN:HE21	2.13	0.56
2:D:42:LEU:HA	2:D:154:LEU:HB2	1.88	0.56
3:E:49:LEU:HD11	3:E:76:TYR:HB2	1.87	0.56
3:E:310:LEU:HG	3:E:311:LEU:HD12	1.88	0.56
4:G:6:GLU:HG3	4:G:9:HIS:HB2	1.87	0.56
4:G:22:GLY:CA	4:G:30:LEU:HB3	2.36	0.56
2:C:252:LEU:HD12	2:C:267:LEU:CB	2.35	0.56
2:C:358:ALA:HB3	2:D:326:GLN:CG	2.35	0.56
2:C:365:LEU:H	2:C:365:LEU:HD22	1.70	0.56
2:D:80:ARG:NE	2:D:80:ARG:HA	2.21	0.56
3:E:27:LEU:HD11	3:E:162:HIS:HB2	1.87	0.56
3:E:259:HIS:CD2	3:E:283:PRO:HB3	2.40	0.56
4:F:55:ALA:HB1	4:F:230:PHE:HE1	1.71	0.56
4:F:274:SER:C	4:F:296:ASN:HB3	2.29	0.56
2:B:64:CYS:HB2	2:B:66:THR:H	1.71	0.56
2:B:111:VAL:HG11	2:B:147:PRO:CG	2.36	0.56
2:B:142:THR:O	2:B:146:PRO:HA	2.06	0.56
2:D:74:GLY:C	2:D:80:ARG:HH11	2.14	0.56
2:D:244:LEU:HD21	2:D:276:ILE:HG21	1.86	0.56
4:F:39:ASP:CG	4:F:40:GLY:H	2.13	0.56
4:G:264:LYS:HE2	4:G:328:LEU:HB3	1.86	0.56
2:B:98:ARG:HA	2:B:103:ASP:HB3	1.88	0.56
2:B:178:LEU:HB3	2:B:183:ILE:HG13	1.87	0.56
3:E:332:PRO:O	3:E:333:HIS:CG	2.59	0.56
4:F:207:LEU:HD23	4:F:208:ASP:O	2.06	0.56
4:G:36:GLN:O	4:G:42:LEU:HA	2.06	0.56
4:F:21:LEU:CD2	4:F:46:GLY:HA2	2.36	0.56
4:F:217:GLN:CD	4:F:226:HIS:HE1	2.14	0.56
4:F:260:CYS:HB2	4:F:334:GLU:O	2.06	0.56
2:B:38:HIS:HD2	2:B:40:ALA:H	1.52	0.55
3:E:256:LEU:HD11	3:E:287:GLN:HA	1.88	0.55
4:F:315:MET:HG2	4:F:342:ASP:HA	1.88	0.55
2:D:10:TRP:HA	2:D:10:TRP:CE3	2.40	0.55
3:E:16:ALA:HA	3:E:19:GLN:OE1	2.07	0.55
4:F:15:GLN:HG3	4:F:16:GLN:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:237:VAL:HG12	4:F:238:ASP:O	2.06	0.55
1:A:217:TRP:HB2	1:A:232:ILE:HB	1.89	0.55
3:E:18:TYR:HB3	3:E:140:TRP:CH2	2.41	0.55
3:E:216:LEU:HA	3:E:235:ALA:HB1	1.87	0.55
4:F:98:LEU:HD13	4:F:105:ARG:NH2	2.20	0.55
4:F:224:ARG:HG2	4:F:226:HIS:CE1	2.41	0.55
4:G:20:PRO:HG3	4:G:53:MET:HE2	1.87	0.55
1:A:163:ASP:CB	1:A:198:THR:HA	2.37	0.55
1:A:262:ARG:HH22	3:E:317:LEU:CD1	2.20	0.55
1:A:273:PHE:CB	1:A:278:VAL:HB	2.36	0.55
1:A:333:HIS:ND1	1:A:339:VAL:HB	2.22	0.55
2:D:64:CYS:SG	2:D:73:CYS:HB2	2.46	0.55
2:D:287:GLY:C	2:D:306:MET:HE1	2.31	0.55
3:E:50:CYS:SG	3:E:65:CYS:N	2.79	0.55
4:F:77:ASP:CG	4:F:80:ARG:HH21	2.13	0.55
2:D:290:HIS:C	2:D:290:HIS:CD2	2.83	0.55
3:E:7:LEU:O	3:E:40:LEU:HD13	2.06	0.55
3:E:193:LEU:HD11	3:E:247:TRP:HA	1.89	0.55
1:A:71:MET:O	4:F:362:MET:HE2	2.07	0.55
1:A:77:ARG:NE	1:A:107:ASP:H	2.03	0.55
2:B:62:LEU:O	2:B:119:ARG:HD3	2.07	0.55
2:D:148:GLU:O	2:D:150:VAL:N	2.34	0.55
2:D:334:ILE:HG22	2:D:338:GLU:OE2	2.05	0.55
3:E:24:HIS:CE1	3:E:26:ALA:CB	2.89	0.55
4:G:78:ILE:CG2	4:G:99:VAL:HG11	2.37	0.55
1:A:199:LEU:HD12	1:A:203:GLU:OE1	2.06	0.55
1:A:333:HIS:CB	1:A:337:ALA:HA	2.36	0.55
2:D:23:HIS:O	2:D:27:ALA:HB2	2.06	0.55
4:F:354:SER:HB2	4:F:357:ALA:H	1.72	0.55
4:G:16:GLN:HB2	4:G:230:PHE:CE1	2.41	0.55
1:A:78:GLN:HG3	1:A:107:ASP:HB3	1.88	0.55
1:A:142:PRO:HA	1:A:146:GLN:HE21	1.72	0.55
2:C:265:MET:O	2:C:265:MET:HE3	2.07	0.55
3:E:32:LEU:HD21	3:E:200:ALA:HB2	1.88	0.55
4:G:1:MET:H3	4:G:66:GLY:HA3	1.71	0.55
4:G:255:HIS:O	4:G:255:HIS:CG	2.58	0.55
2:C:199:GLU:CG	2:C:202:ALA:H	2.20	0.55
2:D:32:LEU:HD11	2:D:58:LEU:HA	1.89	0.55
2:D:41:TYR:HB3	2:D:43:PHE:CZ	2.42	0.55
4:F:251:ASN:N	4:F:341:THR:HG23	2.22	0.55
1:A:144:GLN:HA	1:A:175:GLU:OE1	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:149:HIS:CD2	2:B:150:VAL:HG13	2.42	0.55
2:D:24:VAL:HA	2:D:27:ALA:HB3	1.89	0.55
3:E:179:GLU:OE1	3:E:202:LEU:HD23	2.06	0.55
4:F:17:VAL:HG21	4:F:55:ALA:HB3	1.89	0.55
4:F:354:SER:HA	4:F:357:ALA:CB	2.26	0.55
4:G:37:VAL:HG12	4:G:39:ASP:HA	1.89	0.55
4:G:206:MET:CB	4:G:227:VAL:HG21	2.37	0.55
2:D:76:CYS:HB2	2:D:79:CYS:H	1.72	0.54
2:D:296:GLN:OE1	2:D:322:PRO:HA	2.06	0.54
3:E:46:ARG:O	3:E:50:CYS:SG	2.64	0.54
4:F:255:HIS:HE1	4:F:309:THR:HB	1.72	0.54
4:F:341:THR:HG22	4:F:342:ASP:OD2	2.08	0.54
4:G:130:LEU:HD11	4:G:185:GLY:HA2	1.89	0.54
1:A:47:PHE:CD2	1:A:77:ARG:HB3	2.42	0.54
2:B:65:GLU:HG2	2:B:78:ASN:CG	2.32	0.54
2:B:149:HIS:CE1	2:B:150:VAL:HG13	2.42	0.54
2:D:51:LYS:HA	2:D:175:LEU:CD1	2.37	0.54
2:D:61:GLY:HA2	2:D:64:CYS:HB2	1.90	0.54
2:D:191:LEU:HD23	2:D:198:HIS:HB2	1.89	0.54
2:D:257:VAL:HA	2:D:360:HIS:CD2	2.42	0.54
2:D:295:VAL:HG23	2:D:302:LEU:HD21	1.89	0.54
2:D:357:LEU:HA	2:D:360:HIS:O	2.06	0.54
3:E:12:GLU:HG2	3:E:56:HIS:CD2	2.42	0.54
1:A:162:LEU:HA	1:A:197:LEU:HB2	1.89	0.54
1:A:274:ASP:OD1	1:A:283:ARG:HD3	2.08	0.54
2:D:191:LEU:HG	2:D:198:HIS:CB	2.37	0.54
2:D:198:HIS:HD2	2:D:203:LEU:CD1	2.20	0.54
2:D:206:LEU:HD12	2:D:241:LEU:HD11	1.89	0.54
2:D:255:ALA:HA	2:D:258:GLU:CD	2.32	0.54
3:E:4:TYR:H	3:E:7:LEU:HD12	1.72	0.54
3:E:92:ALA:CA	3:E:95:GLU:OE2	2.54	0.54
4:F:317:ILE:HD12	4:F:343:SER:CA	2.37	0.54
1:A:32:GLN:HA	1:A:113:ARG:NH1	2.23	0.54
2:B:129:HIS:CB	2:B:161:LYS:HB2	2.38	0.54
2:D:250:LEU:HD13	2:D:288:LEU:HD13	1.88	0.54
3:E:51:GLN:HA	3:E:109:ALA:H	1.72	0.54
3:E:73:HIS:HB3	3:E:76:TYR:HB2	1.90	0.54
4:F:13:PRO:HB3	4:F:55:ALA:CB	2.38	0.54
4:G:340:LEU:HB3	4:G:347:VAL:HG13	1.89	0.54
2:B:149:HIS:CG	2:B:150:VAL:N	2.75	0.54
2:C:149:HIS:CD2	2:C:150:VAL:HG23	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:341:TYR:CD1	2:D:337:LYS:HA	2.42	0.54
2:D:355:ARG:HD2	3:E:333:HIS:CE1	2.42	0.54
3:E:14:LEU:O	3:E:18:TYR:CG	2.60	0.54
4:F:17:VAL:CG2	4:F:55:ALA:HB2	2.38	0.54
4:F:148:HIS:O	4:F:156:ASN:HB3	2.07	0.54
4:G:217:GLN:O	4:G:223:ILE:HA	2.07	0.54
1:A:164:ASP:HA	1:A:167:ASN:HB3	1.90	0.54
1:A:211:HIS:CG	1:A:212:PHE:N	2.76	0.54
1:A:299:ARG:CZ	3:E:320:GLU:HB3	2.37	0.54
2:C:10:TRP:HA	2:C:10:TRP:CE3	2.41	0.54
2:C:259:ALA:HA	2:C:357:LEU:CD2	2.38	0.54
2:D:2:SER:O	3:E:140:TRP:CH2	2.61	0.54
2:D:95:ALA:O	2:D:130:MET:HB2	2.08	0.54
3:E:109:ALA:HB1	3:E:138:GLU:O	2.07	0.54
4:F:365:ARG:N	4:F:365:ARG:HD2	2.23	0.54
3:E:227:GLY:HA2	3:E:323:LEU:HD11	1.90	0.54
4:F:12:LYS:NZ	4:F:16:GLN:HG3	2.23	0.54
4:F:328:LEU:HB3	4:F:329:ASN:OD1	2.07	0.54
4:G:350:GLU:HB2	4:G:355:GLN:CD	2.33	0.54
1:A:47:PHE:CE2	1:A:109:LEU:HB2	2.43	0.54
2:D:98:ARG:HD3	2:D:103:ASP:HB3	1.90	0.54
2:D:172:GLN:HB2	2:D:174:HIS:NE2	2.23	0.54
4:F:104:SER:HA	4:G:303:GLU:O	2.08	0.54
1:A:219:ASP:OD1	1:A:285:MET:HG3	2.08	0.54
2:B:46:THR:O	2:B:49:VAL:HG22	2.08	0.54
3:E:30:GLN:HG3	3:E:148:PRO:HD3	1.90	0.54
3:E:133:GLU:CD	3:E:158:ARG:HH21	2.16	0.54
4:F:103:ARG:HH11	4:G:305:ILE:HG22	1.71	0.54
4:F:137:ARG:HA	4:F:332:LYS:NZ	2.23	0.54
4:F:158:MET:SD	4:F:171:ALA:HB2	2.48	0.54
4:F:229:ASP:HB2	4:F:230:PHE:CZ	2.43	0.54
4:F:251:ASN:H	4:F:341:THR:HG23	1.71	0.54
4:G:135:MET:O	4:G:139:ILE:HG13	2.08	0.54
4:G:275:ASN:HD21	4:G:278:PHE:H	1.56	0.54
2:D:38:HIS:CE1	2:D:40:ALA:HB3	2.43	0.53
3:E:177:SER:HB3	3:E:184:GLN:HE22	1.72	0.53
4:F:7:ARG:HB2	4:F:88:ILE:HD11	1.89	0.53
4:F:138:LEU:CD2	4:F:182:MET:HG2	2.39	0.53
4:F:354:SER:HB3	4:F:357:ALA:O	2.07	0.53
1:A:69:GLN:HE21	4:F:362:MET:HE2	1.70	0.53
1:A:263:GLN:HA	1:A:266:HIS:HE1	1.70	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:240:MET:HE1	2:D:27:ALA:HB2	1.89	0.53
4:F:137:ARG:HG2	4:F:182:MET:CE	2.39	0.53
4:G:215:ARG:CD	4:G:226:HIS:HB2	2.39	0.53
1:A:122:GLU:HA	1:A:127:PHE:CD2	2.44	0.53
1:A:231:HIS:HE1	1:A:235:GLN:HE21	1.51	0.53
1:A:261:LYS:HE2	1:A:290:LEU:O	2.08	0.53
3:E:191:LEU:HD12	3:E:201:ALA:HB2	1.89	0.53
3:E:241:ALA:HB3	3:E:308:ARG:HH11	1.74	0.53
4:G:83:PRO:O	4:G:86:ALA:HB3	2.09	0.53
1:A:73:LEU:HD13	4:F:176:ARG:O	2.04	0.53
2:C:262:GLU:N	2:C:262:GLU:CD	2.66	0.53
2:D:131:LEU:HB3	2:D:135:SER:HB2	1.89	0.53
2:D:201:ARG:HD2	2:D:205:LEU:HD21	1.90	0.53
2:D:287:GLY:HA3	2:D:306:MET:HE1	1.89	0.53
4:F:97:MET:HB2	4:F:110:THR:HG21	1.91	0.53
4:G:6:GLU:HB3	4:G:9:HIS:CB	2.38	0.53
4:G:53:MET:SD	4:G:206:MET:HE3	2.49	0.53
4:G:266:ALA:HA	4:G:269:ARG:HE	1.74	0.53
4:G:283:LEU:O	4:G:316:GLU:HA	2.08	0.53
3:E:48:LEU:CD2	3:E:140:TRP:CD2	2.91	0.53
4:F:122:TRP:CH2	4:F:124:SER:HB2	2.44	0.53
4:F:224:ARG:CZ	4:F:224:ARG:HB2	2.38	0.53
4:G:37:VAL:HA	4:G:42:LEU:HB3	1.89	0.53
4:G:202:GLU:O	4:G:206:MET:HG2	2.08	0.53
1:A:334:LYS:HG2	1:A:338:ASP:HB3	1.90	0.53
2:B:30:ASN:HB3	2:B:36:ARG:HH11	1.72	0.53
2:C:252:LEU:HD12	2:C:267:LEU:HB2	1.89	0.53
2:D:236:ALA:O	2:D:240:MET:HB2	2.08	0.53
3:E:18:TYR:N	3:E:18:TYR:CD1	2.75	0.53
3:E:207:GLY:C	3:E:209:ASN:H	2.15	0.53
4:G:8:GLU:C	4:G:11:LEU:H	2.17	0.53
1:A:220:ALA:HB1	1:A:228:ARG:CG	2.36	0.53
2:B:63:ASN:HB3	2:B:118:GLY:HA3	1.91	0.53
2:D:191:LEU:CD2	2:D:198:HIS:HA	2.38	0.53
3:E:222:TYR:OH	3:E:228:ASP:HB3	2.08	0.53
4:F:2:LYS:O	4:F:37:VAL:HG21	2.09	0.53
4:F:6:GLU:CD	4:F:9:HIS:CG	2.87	0.53
4:G:139:ILE:CD1	4:G:204:MET:HA	2.39	0.53
2:D:42:LEU:HD11	2:D:156:THR:CG2	2.39	0.53
2:D:146:PRO:HB3	2:D:152:PHE:CE2	2.43	0.53
3:E:79:LEU:HD22	3:E:96:VAL:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:81:PRO:HA	3:E:88:LEU:CA	2.38	0.53
4:G:132:GLN:HA	4:G:207:LEU:HD13	1.91	0.53
4:G:135:MET:CG	4:G:207:LEU:HD11	2.38	0.53
4:G:165:GLU:HA	4:G:186:GLN:C	2.34	0.53
4:G:340:LEU:HD13	4:G:342:ASP:CA	2.39	0.53
1:A:231:HIS:HE1	1:A:235:GLN:NE2	2.07	0.53
1:A:314:GLN:HB2	3:E:303:VAL:HG13	1.90	0.53
1:A:328:SER:O	1:A:332:CYS:HB2	2.08	0.53
2:B:61:GLY:O	2:B:68:ILE:HA	2.08	0.53
2:C:360:HIS:C	2:C:362:ARG:H	2.17	0.53
3:E:202:LEU:O	3:E:202:LEU:HD22	2.09	0.53
3:E:246:HIS:HB2	3:E:297:ARG:HH11	1.74	0.53
4:F:267:PHE:HB3	4:F:325:LEU:HD21	1.91	0.53
4:F:276:GLU:OE1	4:F:276:GLU:CA	2.56	0.53
4:G:7:ARG:CG	4:G:88:ILE:HD11	2.39	0.53
2:C:144:GLU:HA	2:C:169:ARG:CZ	2.39	0.53
4:F:13:PRO:HG2	4:F:57:VAL:HG22	1.90	0.53
1:A:6:PRO:HD3	1:A:138:THR:O	2.09	0.52
1:A:333:HIS:HB2	1:A:337:ALA:HA	1.90	0.52
2:B:87:PHE:CZ	2:B:117:ARG:HB2	2.45	0.52
2:D:19:VAL:HG13	2:D:178:LEU:HD22	1.89	0.52
2:D:97:SER:HA	3:E:127:ALA:HB2	1.91	0.52
3:E:46:ARG:HA	3:E:68:MET:CE	2.39	0.52
3:E:49:LEU:HA	3:E:111:VAL:HG23	1.91	0.52
4:F:146:MET:HE2	4:F:197:ARG:NH1	2.23	0.52
1:A:220:ALA:HB2	1:A:228:ARG:HG3	1.90	0.52
2:B:189:HIS:CE1	2:B:190:ILE:HG12	2.44	0.52
2:D:272:ALA:C	2:D:275:GLY:H	2.17	0.52
3:E:190:ALA:HB1	3:E:204:LEU:HD12	1.92	0.52
3:E:223:SER:CA	3:E:228:ASP:O	2.58	0.52
4:F:220:SER:C	4:F:236:LEU:HD12	2.33	0.52
4:G:2:LYS:HA	4:G:90:VAL:O	2.10	0.52
4:G:5:VAL:HA	4:G:59:LEU:CD1	2.38	0.52
1:A:270:ARG:N	1:A:273:PHE:CE2	2.73	0.52
2:D:3:TYR:HB2	3:E:21:GLY:CA	2.39	0.52
2:D:24:VAL:HG13	2:D:173:PHE:HB3	1.90	0.52
2:D:172:GLN:HB2	2:D:174:HIS:CE1	2.45	0.52
2:D:196:ILE:HB	2:D:231:GLN:HA	1.90	0.52
2:D:261:GLY:HA2	2:D:357:LEU:CD2	2.38	0.52
3:E:32:LEU:HA	3:E:146:ARG:HA	1.91	0.52
1:A:234:GLN:HG2	2:B:304:ASN:OD1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:227:SER:O	2:D:27:ALA:HA	2.09	0.52
2:D:15:PHE:HA	2:D:57:LEU:HD11	1.91	0.52
2:D:190:ILE:HA	2:D:193:GLU:OE2	2.09	0.52
4:F:34:LEU:HA	4:F:69:THR:HG22	1.90	0.52
4:F:132:GLN:HG2	4:F:207:LEU:HD21	1.92	0.52
4:G:250:LYS:O	4:G:341:THR:HG21	2.09	0.52
4:G:337:ARG:CZ	4:G:337:ARG:HB3	2.39	0.52
1:A:69:GLN:HE21	4:F:362:MET:HE1	1.71	0.52
1:A:138:THR:HG23	1:A:140:GLN:HG2	1.91	0.52
1:A:333:HIS:HA	1:A:338:ASP:O	2.09	0.52
2:C:28:LEU:HD22	2:C:58:LEU:HD13	1.92	0.52
3:E:15:VAL:HG12	3:E:19:GLN:OE1	2.09	0.52
4:F:257:GLU:HG2	4:F:337:ARG:HA	1.91	0.52
2:C:250:LEU:CD2	2:C:312:ARG:HE	2.23	0.52
2:C:259:ALA:HA	2:C:357:LEU:HD21	1.91	0.52
2:C:292:ILE:CG2	2:C:317:ALA:HA	2.40	0.52
4:F:103:ARG:NH1	4:G:305:ILE:HG22	2.25	0.52
4:F:259:GLY:O	4:F:263:LEU:HB2	2.10	0.52
4:G:264:LYS:HB2	4:G:328:LEU:HD13	1.91	0.52
2:B:63:ASN:HA	2:B:119:ARG:H	1.74	0.52
2:B:87:PHE:CZ	2:B:117:ARG:CB	2.92	0.52
2:D:271:ALA:HB1	2:D:276:ILE:HB	1.90	0.52
2:D:295:VAL:CG1	2:D:314:ARG:HA	2.28	0.52
4:F:5:VAL:HG12	4:F:6:GLU:H	1.75	0.52
4:F:132:GLN:CG	4:F:214:LEU:HD11	2.39	0.52
4:G:59:LEU:HD12	4:G:61:GLN:HB2	1.92	0.52
4:G:132:GLN:HB2	4:G:207:LEU:HB3	1.92	0.52
3:E:32:LEU:HD13	3:E:35:MET:CE	2.39	0.52
3:E:45:SER:CA	3:E:111:VAL:HG11	2.40	0.52
3:E:294:CYS:O	3:E:298:GLU:OE2	2.27	0.52
4:F:53:MET:SD	4:F:230:PHE:HB3	2.49	0.52
4:G:255:HIS:O	4:G:255:HIS:CD2	2.62	0.52
1:A:223:MET:HA	1:A:288:GLU:OE2	2.10	0.52
2:C:292:ILE:HG23	2:C:317:ALA:HA	1.91	0.52
2:D:60:LYS:CB	2:D:72:PRO:HB2	2.39	0.52
2:D:179:ASP:H	2:D:182:GLN:HE21	1.58	0.52
2:D:276:ILE:O	2:D:278:TRP:CE2	2.63	0.52
3:E:118:ALA:CB	3:E:150:ARG:CB	2.88	0.52
4:F:206:MET:SD	4:F:232:PHE:CB	2.98	0.52
4:G:16:GLN:HE21	4:G:206:MET:HE1	1.75	0.52
4:G:37:VAL:HG12	4:G:39:ASP:CA	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:130:LEU:CD1	4:G:185:GLY:HA2	2.40	0.52
1:A:47:PHE:HB3	1:A:79:THR:OG1	2.10	0.52
1:A:73:LEU:CD1	4:F:177:LEU:HB2	2.40	0.51
1:A:309:GLU:OE1	3:E:306:ILE:HD12	2.10	0.51
3:E:175:TRP:CE3	3:E:198:PRO:HB2	2.45	0.51
4:F:3:PHE:CB	4:F:59:LEU:HD21	2.40	0.51
4:F:7:ARG:HD3	4:F:84:GLU:HA	1.91	0.51
4:F:126:VAL:CG2	4:F:191:HIS:HE1	2.23	0.51
4:F:137:ARG:HH22	4:F:141:ALA:HB2	1.74	0.51
4:G:191:HIS:HD2	4:G:218:ILE:HG12	1.74	0.51
1:A:32:GLN:HE22	2:B:165:THR:HG23	1.74	0.51
2:B:39:HIS:CE1	2:B:147:PRO:O	2.63	0.51
2:B:269:ASN:CA	2:B:346:ARG:HH21	2.24	0.51
2:B:278:TRP:CE2	2:B:346:ARG:HB2	2.45	0.51
2:C:84:GLN:CB	2:C:86:ARG:HG2	2.39	0.51
2:C:346:ARG:O	2:C:350:GLU:HG3	2.11	0.51
2:D:121:LYS:HG3	2:D:123:TYR:CZ	2.46	0.51
3:E:145:THR:HG21	3:E:151:LEU:HG	1.92	0.51
3:E:222:TYR:CE1	3:E:223:SER:HA	2.45	0.51
3:E:244:ARG:HA	3:E:247:TRP:CE3	2.45	0.51
4:F:207:LEU:O	4:F:214:LEU:HD21	2.11	0.51
4:G:6:GLU:HB3	4:G:9:HIS:HB2	1.92	0.51
4:G:264:LYS:HE2	4:G:328:LEU:CB	2.39	0.51
2:B:63:ASN:HA	2:B:118:GLY:CA	2.40	0.51
2:C:341:TYR:CE1	2:D:337:LYS:HA	2.46	0.51
2:D:112:GLN:HG3	2:D:113:TYR:N	2.24	0.51
3:E:11:PHE:CG	3:E:56:HIS:CE1	2.98	0.51
3:E:18:TYR:CB	3:E:140:TRP:CZ3	2.93	0.51
3:E:27:LEU:CD1	3:E:162:HIS:HB2	2.40	0.51
4:F:8:GLU:C	4:F:11:LEU:H	2.18	0.51
4:G:166:GLU:HA	4:G:183:PRO:O	2.11	0.51
1:A:51:HIS:HE1	1:A:78:GLN:CB	2.22	0.51
1:A:269:LEU:H	1:A:269:LEU:CD2	2.21	0.51
1:A:277:ARG:HE	1:A:278:VAL:H	1.57	0.51
1:A:334:LYS:HB3	1:A:335:PRO:HD2	1.91	0.51
2:B:286:LEU:CD1	2:B:336:ARG:HH11	2.17	0.51
2:C:12:PRO:HA	2:C:17:ASP:CB	2.40	0.51
2:D:46:THR:HB	2:D:49:VAL:HG23	1.92	0.51
3:E:48:LEU:HD23	3:E:52:GLN:CG	2.41	0.51
3:E:176:LEU:HA	3:E:179:GLU:OE1	2.09	0.51
3:E:233:LEU:HD12	3:E:312:ILE:CG2	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:17:VAL:HG23	4:F:55:ALA:HB2	1.91	0.51
4:G:256:LEU:HD13	4:G:310:TYR:CG	2.46	0.51
4:G:350:GLU:HB2	4:G:355:GLN:NE2	2.25	0.51
1:A:61:TRP:CD1	1:A:96:GLN:HB2	2.45	0.51
1:A:73:LEU:HD22	4:F:177:LEU:HD13	1.91	0.51
1:A:162:LEU:HD13	1:A:163:ASP:O	2.11	0.51
1:A:262:ARG:HH22	3:E:317:LEU:HD13	1.75	0.51
3:E:14:LEU:HB3	3:E:18:TYR:CE2	2.46	0.51
3:E:68:MET:HE3	3:E:76:TYR:CE1	2.46	0.51
3:E:245:LEU:HD13	3:E:297:ARG:CA	2.40	0.51
4:F:16:GLN:HB3	4:F:53:MET:HG2	1.92	0.51
4:F:17:VAL:CG2	4:F:55:ALA:CB	2.88	0.51
4:F:130:LEU:O	4:F:213:PRO:HA	2.11	0.51
1:A:278:VAL:HG21	1:A:286:MET:HG2	1.92	0.51
1:A:333:HIS:HB3	1:A:338:ASP:N	2.24	0.51
2:B:94:ASP:O	2:B:125:ILE:HG23	2.11	0.51
2:D:78:ASN:O	2:D:82:ILE:HG13	2.11	0.51
2:D:295:VAL:CG2	2:D:302:LEU:HD21	2.40	0.51
4:G:132:GLN:CA	4:G:207:LEU:HD22	2.40	0.51
4:G:365:ARG:C	4:G:366:LEU:HD22	2.36	0.51
1:A:270:ARG:CB	1:A:283:ARG:HB3	2.40	0.51
2:B:347:MET:SD	2:C:290:HIS:CD2	3.04	0.51
2:D:199:GLU:HG3	2:D:202:ALA:H	1.75	0.51
3:E:18:TYR:HB2	3:E:52:GLN:NE2	2.24	0.51
4:F:13:PRO:HA	4:F:55:ALA:CB	2.40	0.51
4:F:252:PRO:O	4:F:339:MET:HE3	2.10	0.51
1:A:22:LEU:HA	1:A:112:VAL:O	2.11	0.51
1:A:104:LEU:HB2	1:A:106:ASP:HB2	1.92	0.51
1:A:171:CYS:O	1:A:175:GLU:CA	2.59	0.51
2:C:250:LEU:HD23	2:C:309:ILE:HG21	1.93	0.51
2:C:288:LEU:HA	2:C:291:ARG:HE	1.75	0.51
2:C:358:ALA:CB	2:D:326:GLN:CG	2.89	0.51
2:D:205:LEU:HD13	2:D:238:SER:CA	2.40	0.51
3:E:11:PHE:CE1	3:E:44:LEU:HA	2.46	0.51
3:E:17:SER:C	3:E:23:GLY:HA3	2.36	0.51
3:E:18:TYR:CD1	3:E:140:TRP:CZ3	2.98	0.51
3:E:320:GLU:O	3:E:324:GLN:HG2	2.11	0.51
4:G:163:GLU:OE1	4:G:168:ARG:CB	2.59	0.51
4:G:257:GLU:OE1	4:G:352:ALA:HB1	2.11	0.51
1:A:301:ALA:HA	1:A:330:LEU:HD23	1.93	0.51
1:A:313:LYS:HB3	3:E:304:THR:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:87:PHE:CE2	2:B:117:ARG:HB2	2.46	0.51
2:D:188:GLU:OE1	2:D:203:LEU:HD13	2.10	0.51
2:D:199:GLU:HG2	2:D:233:SER:C	2.36	0.51
3:E:227:GLY:HA2	3:E:229:TRP:HE1	1.76	0.51
4:F:22:GLY:C	4:F:24:ARG:H	2.18	0.51
4:F:86:ALA:O	4:F:88:ILE:HG13	2.11	0.51
4:F:176:ARG:HB3	4:F:361:VAL:HG12	1.93	0.51
4:G:176:ARG:HB3	4:G:361:VAL:HG23	1.93	0.51
1:A:147:LEU:O	1:A:151:VAL:HG23	2.10	0.51
2:C:156:THR:HG21	2:C:161:LYS:HB2	1.93	0.51
2:D:279:GLU:OE2	2:D:282:LEU:HD12	2.10	0.51
2:D:292:ILE:HG12	2:D:313:MET:HA	1.92	0.51
3:E:49:LEU:HD22	3:E:68:MET:CG	2.41	0.51
3:E:145:THR:HB	3:E:147:GLU:O	2.11	0.51
4:G:10:LEU:HA	4:G:57:VAL:CG2	2.41	0.51
4:G:249:PRO:HA	4:G:346:SER:HB2	1.92	0.51
4:G:251:ASN:HB3	4:G:253:ASP:OD2	2.11	0.51
1:A:77:ARG:HH12	1:A:105:HIS:CD2	2.29	0.50
1:A:158:LEU:C	1:A:160:LEU:H	2.18	0.50
3:E:17:SER:HB2	3:E:23:GLY:CA	2.41	0.50
3:E:71:GLY:C	3:E:73:HIS:H	2.17	0.50
3:E:259:HIS:NE2	3:E:278:ALA:HA	2.26	0.50
4:F:133:ALA:HA	4:F:136:LYS:HE3	1.93	0.50
4:F:159:LEU:HD13	4:F:240:ARG:HA	1.92	0.50
4:G:143:GLN:HG2	4:G:204:MET:HE1	1.93	0.50
1:A:158:LEU:HD21	1:A:185:LEU:HB3	1.93	0.50
1:A:223:MET:HG2	1:A:285:MET:SD	2.52	0.50
2:C:358:ALA:C	2:C:364:PRO:HB3	2.36	0.50
2:D:41:TYR:CE2	2:D:58:LEU:HD21	2.46	0.50
3:E:210:TRP:O	3:E:213:ARG:HB3	2.11	0.50
3:E:332:PRO:O	3:E:333:HIS:CD2	2.65	0.50
4:G:331:LEU:CD1	4:G:333:CYS:HB3	2.40	0.50
1:A:49:GLU:O	1:A:78:GLN:HA	2.11	0.50
1:A:84:LEU:HD22	1:A:89:PRO:HD3	1.93	0.50
2:D:75:VAL:HG23	2:D:80:ARG:HG3	1.93	0.50
3:E:63:ARG:HA	3:E:66:GLN:HG2	1.92	0.50
3:E:81:PRO:HA	3:E:88:LEU:CB	2.42	0.50
4:F:56:ARG:HB2	4:F:229:ASP:CG	2.36	0.50
4:F:137:ARG:HH22	4:F:141:ALA:CB	2.24	0.50
4:G:132:GLN:HG3	4:G:209:GLY:O	2.11	0.50
1:A:29:LEU:HD13	1:A:179:LEU:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:GLN:OE1	1:A:333:HIS:CD2	2.64	0.50
2:B:62:LEU:HB3	2:B:120:PHE:HD2	1.77	0.50
2:C:367:GLU:HA	2:D:322:PRO:HD3	1.93	0.50
2:D:111:VAL:HB	2:D:150:VAL:HG22	1.94	0.50
2:D:276:ILE:O	2:D:278:TRP:CD2	2.65	0.50
3:E:230:TYR:HA	3:E:316:LEU:HD13	1.92	0.50
4:F:126:VAL:HG22	4:F:191:HIS:CE1	2.46	0.50
4:G:146:MET:SD	4:G:171:ALA:HB1	2.52	0.50
1:A:91:ALA:HA	1:A:95:GLU:OE1	2.11	0.50
1:A:304:LEU:O	1:A:307:ARG:HB3	2.12	0.50
2:B:249:ALA:O	2:B:253:VAL:HG23	2.12	0.50
2:C:15:PHE:CD1	2:C:57:LEU:HD13	2.46	0.50
2:C:333:LEU:O	2:C:336:ARG:HB2	2.12	0.50
2:D:214:LEU:O	2:D:218:LEU:HG	2.10	0.50
2:D:315:GLU:HA	2:D:318:ARG:CZ	2.41	0.50
3:E:236:LEU:O	3:E:241:ALA:HA	2.12	0.50
3:E:242:PRO:HB3	3:E:297:ARG:HG3	1.93	0.50
4:G:147:ALA:HB2	4:G:173:ASP:HA	1.93	0.50
2:B:109:ASP:O	2:B:112:GLN:HG2	2.11	0.50
2:B:268:ILE:HD13	2:B:350:GLU:HB2	1.93	0.50
2:C:359:PHE:CZ	2:D:326:GLN:HB2	2.47	0.50
2:D:146:PRO:HB3	2:D:152:PHE:HE2	1.77	0.50
2:D:287:GLY:CA	2:D:306:MET:HE1	2.41	0.50
4:F:307:ASP:O	4:F:308:VAL:HG13	2.11	0.50
4:G:186:GLN:HB3	4:G:188:LEU:H	1.77	0.50
4:G:339:MET:HG2	4:G:350:GLU:OE1	2.11	0.50
1:A:225:LYS:HZ3	1:A:228:ARG:HG2	1.76	0.50
2:B:49:VAL:CG2	2:B:175:LEU:HD13	2.42	0.50
2:D:195:HIS:CG	2:D:196:ILE:N	2.79	0.50
2:D:249:ALA:HB1	2:D:285:MET:HG3	1.92	0.50
4:F:115:ASP:O	4:F:116:PHE:CB	2.60	0.50
4:F:193:VAL:HG13	4:F:236:LEU:HD22	1.94	0.50
4:G:222:ASN:HA	4:G:234:SER:O	2.12	0.50
1:A:95:GLU:CD	1:A:95:GLU:N	2.70	0.50
1:A:215:PHE:HA	1:A:218:VAL:HG12	1.92	0.50
1:A:270:ARG:CA	1:A:273:PHE:CD2	2.94	0.50
2:B:67:GLY:HA2	2:B:119:ARG:HE	1.77	0.50
2:D:60:LYS:CE	2:D:83:GLU:OE1	2.59	0.50
2:D:183:ILE:HD11	2:D:212:GLY:HA2	1.93	0.50
3:E:10:ASP:O	3:E:14:LEU:HG	2.12	0.50
4:F:331:LEU:HD21	4:F:351:ASP:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:36:GLN:HG3	4:G:63:HIS:CE1	2.46	0.50
4:G:260:CYS:SG	4:G:328:LEU:O	2.69	0.50
4:G:290:LEU:HD21	4:G:292:ILE:HG13	1.94	0.50
1:A:55:ILE:CG2	1:A:85:PRO:HD3	2.42	0.50
1:A:225:LYS:HE2	1:A:228:ARG:HB2	1.94	0.50
3:E:14:LEU:HD22	3:E:27:LEU:CD1	2.41	0.50
4:F:12:LYS:NZ	4:F:230:PHE:CD2	2.80	0.50
4:F:96:ARG:CZ	4:G:300:GLU:H	2.24	0.50
4:G:146:MET:HE3	4:G:156:ASN:O	2.12	0.50
1:A:166:ALA:O	1:A:170:LEU:HG	2.11	0.49
2:B:345:ARG:O	2:B:349:VAL:HG23	2.12	0.49
2:C:21:GLN:NE2	2:C:23:HIS:CE1	2.80	0.49
2:C:56:ARG:O	2:C:60:LYS:HB3	2.12	0.49
2:D:32:LEU:HB3	2:D:70:ALA:HA	1.93	0.49
2:D:60:LYS:HB2	2:D:72:PRO:HB3	1.92	0.49
3:E:24:HIS:ND1	3:E:26:ALA:HB3	2.27	0.49
3:E:48:LEU:CD2	3:E:140:TRP:CG	2.95	0.49
3:E:146:ARG:C	3:E:146:ARG:HD3	2.37	0.49
3:E:223:SER:OG	3:E:232:LEU:HD21	2.12	0.49
4:F:176:ARG:CB	4:F:361:VAL:HG12	2.42	0.49
4:F:255:HIS:CE1	4:F:309:THR:O	2.65	0.49
4:G:245:ARG:HE	4:G:245:ARG:CA	2.24	0.49
4:G:249:PRO:HB3	4:G:346:SER:O	2.12	0.49
4:G:340:LEU:HD13	4:G:342:ASP:HA	1.93	0.49
1:A:225:LYS:HB3	1:A:228:ARG:HB3	1.94	0.49
1:A:334:LYS:CG	1:A:338:ASP:HB3	2.42	0.49
2:C:105:ARG:HA	2:C:108:LEU:HD12	1.94	0.49
3:E:15:VAL:HG11	3:E:56:HIS:ND1	2.27	0.49
3:E:18:TYR:CG	3:E:140:TRP:CE3	3.00	0.49
3:E:188:LEU:HA	3:E:191:LEU:HB3	1.95	0.49
3:E:191:LEU:HD13	3:E:201:ALA:HB2	1.92	0.49
4:F:122:TRP:CZ2	4:F:124:SER:CB	2.96	0.49
4:F:193:VAL:HG23	4:F:238:ASP:OD2	2.13	0.49
2:B:98:ARG:HA	2:B:103:ASP:CB	2.42	0.49
2:D:290:HIS:HB2	2:D:329:TYR:CE1	2.47	0.49
2:D:291:ARG:CB	2:D:313:MET:SD	3.01	0.49
2:D:320:ILE:O	2:D:325:ILE:HD11	2.12	0.49
3:E:8:ARG:HD2	3:E:12:GLU:OE1	2.12	0.49
4:F:256:LEU:HD23	4:F:256:LEU:C	2.37	0.49
4:G:17:VAL:HG22	4:G:53:MET:O	2.12	0.49
4:G:206:MET:CB	4:G:227:VAL:CG2	2.90	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:255:HIS:CD2	4:G:255:HIS:H	2.30	0.49
2:C:288:LEU:HG	2:C:291:ARG:HH21	1.77	0.49
2:C:357:LEU:C	2:C:359:PHE:H	2.21	0.49
2:C:358:ALA:CB	2:D:322:PRO:HB2	2.42	0.49
2:D:60:LYS:HB2	2:D:72:PRO:HB2	1.95	0.49
2:D:181:GLU:O	2:D:185:HIS:HB3	2.12	0.49
2:D:302:LEU:HD12	2:D:302:LEU:H	1.78	0.49
3:E:146:ARG:HB3	3:E:150:ARG:NE	2.18	0.49
3:E:223:SER:HB3	3:E:229:TRP:HA	1.95	0.49
3:E:244:ARG:HD3	3:E:247:TRP:CZ3	2.46	0.49
4:F:34:LEU:HB2	4:F:116:PHE:CD2	2.47	0.49
4:F:295:ASN:HA	4:F:301:GLU:HG2	1.92	0.49
4:G:55:ALA:HB2	4:G:230:PHE:CE1	2.48	0.49
4:G:144:PHE:CD1	4:G:144:PHE:C	2.91	0.49
4:G:271:ALA:HB2	4:G:321:VAL:HG11	1.94	0.49
4:G:287:GLU:C	4:G:289:GLN:H	2.20	0.49
2:C:240:MET:HE1	2:D:27:ALA:CB	2.43	0.49
2:C:315:GLU:C	2:C:315:GLU:CD	2.80	0.49
2:D:185:HIS:CG	2:D:186:GLN:N	2.80	0.49
4:F:125:GLU:OE1	4:F:191:HIS:CE1	2.65	0.49
4:F:256:LEU:HD12	4:F:310:TYR:HD1	1.77	0.49
4:F:344:VAL:O	4:F:362:MET:HE1	2.12	0.49
4:G:123:GLN:HA	4:G:224:ARG:HD3	1.95	0.49
4:G:355:GLN:NE2	4:G:355:GLN:HA	2.19	0.49
1:A:20:ALA:O	1:A:134:SER:HB3	2.13	0.49
1:A:219:ASP:CG	1:A:223:MET:HE3	2.37	0.49
2:C:261:GLY:HA2	2:C:264:VAL:CG2	2.42	0.49
2:C:293:ALA:HB2	2:C:325:ILE:HG21	1.95	0.49
2:D:291:ARG:HB2	2:D:313:MET:SD	2.53	0.49
3:E:73:HIS:CE1	3:E:75:ASP:HB2	2.47	0.49
4:F:122:TRP:CD2	4:F:222:ASN:HB2	2.47	0.49
4:F:260:CYS:HB3	4:F:261:ASP:OD2	2.12	0.49
4:F:320:ASN:OD1	4:F:323:TYR:CD1	2.66	0.49
4:G:123:GLN:HA	4:G:224:ARG:CD	2.42	0.49
4:G:144:PHE:CE1	4:G:327:VAL:HG12	2.48	0.49
1:A:158:LEU:HD22	1:A:185:LEU:HB3	1.94	0.49
2:B:314:ARG:HG2	2:B:314:ARG:HH21	1.77	0.49
2:C:256:MET:HG3	2:C:357:LEU:HD21	1.93	0.49
2:C:351:MET:HB2	2:D:290:HIS:CD2	2.48	0.49
3:E:10:ASP:HB3	3:E:162:HIS:CE1	2.47	0.49
3:E:11:PHE:CD1	3:E:44:LEU:HG	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:12:GLU:HA	3:E:56:HIS:ND1	2.27	0.49
3:E:210:TRP:CH2	3:E:213:ARG:HD3	2.48	0.49
4:F:51:MET:HG2	4:F:198:LYS:HG2	1.95	0.49
4:F:243:ASP:H	4:F:246:ARG:HH21	1.60	0.49
4:F:315:MET:SD	4:F:342:ASP:O	2.70	0.49
4:G:135:MET:HG3	4:G:207:LEU:HD11	1.95	0.49
1:A:261:LYS:HD3	1:A:293:LEU:O	2.12	0.49
4:F:151:VAL:C	4:F:153:TYR:H	2.21	0.49
4:G:4:THR:HB	4:G:61:GLN:HB3	1.95	0.49
4:G:206:MET:HB3	4:G:227:VAL:CG2	2.42	0.49
4:G:350:GLU:HG2	4:G:351:ASP:O	2.12	0.49
1:A:94:ASN:O	1:A:126:TRP:HB3	2.13	0.49
1:A:273:PHE:O	1:A:277:ARG:C	2.56	0.49
1:A:295:GLN:HA	1:A:298:LEU:HB3	1.95	0.49
2:B:269:ASN:HA	2:B:346:ARG:HH21	1.77	0.49
2:C:39:HIS:CD2	2:C:146:PRO:HG3	2.48	0.49
2:C:252:LEU:HA	2:C:267:LEU:CD1	2.43	0.49
2:C:261:GLY:CA	2:C:264:VAL:HG22	2.43	0.49
2:C:289:LEU:CD1	2:C:329:TYR:HA	2.43	0.49
4:F:3:PHE:HA	4:F:63:HIS:HA	1.95	0.49
4:F:92:LEU:HD11	4:F:94:GLY:O	2.13	0.49
4:F:202:GLU:HA	4:F:205:ARG:HE	1.78	0.49
4:G:273:LEU:HD22	4:G:300:GLU:HB3	1.95	0.49
1:A:274:ASP:CG	1:A:283:ARG:HD3	2.38	0.49
2:C:245:ASP:O	2:C:248:GLN:HG2	2.13	0.49
2:C:255:ALA:HA	2:C:260:ASN:OD1	2.12	0.49
2:D:47:ARG:HG2	2:D:215:ARG:HD2	1.95	0.49
3:E:242:PRO:HG2	3:E:301:MET:SD	2.53	0.49
3:E:255:ALA:CB	3:E:277:LEU:HB2	2.42	0.49
4:F:33:LEU:O	4:F:69:THR:HA	2.13	0.49
4:F:159:LEU:HD11	4:F:192:SER:HB3	1.95	0.49
4:F:308:VAL:HG23	4:F:310:TYR:HB2	1.94	0.49
4:G:190:SER:HA	4:G:218:ILE:HD13	1.95	0.49
4:G:223:ILE:HG23	4:G:236:LEU:HD11	1.94	0.49
2:B:250:LEU:HA	2:B:288:LEU:HD13	1.95	0.48
2:D:299:PRO:HB2	2:D:314:ARG:HE	1.78	0.48
3:E:229:TRP:CD2	3:E:319:ILE:HG21	2.47	0.48
3:E:259:HIS:CE1	3:E:283:PRO:HD3	2.47	0.48
4:F:174:GLY:C	4:F:175:HIS:CD2	2.91	0.48
2:B:183:ILE:CD1	2:B:211:GLU:HA	2.42	0.48
2:C:367:GLU:OE2	2:D:322:PRO:HD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:21:GLN:CD	2:D:21:GLN:N	2.71	0.48
2:D:310:GLU:HG3	2:D:314:ARG:CD	2.43	0.48
3:E:90:VAL:HB	3:E:123:ALA:C	2.38	0.48
4:F:125:GLU:HG2	4:F:218:ILE:O	2.12	0.48
4:F:275:ASN:HA	4:F:296:ASN:HA	1.96	0.48
4:F:308:VAL:CG2	4:F:310:TYR:HB2	2.43	0.48
4:G:3:PHE:HA	4:G:63:HIS:HA	1.94	0.48
4:G:139:ILE:HD13	4:G:204:MET:HA	1.95	0.48
4:G:256:LEU:HD13	4:G:310:TYR:HB2	1.94	0.48
1:A:41:VAL:O	1:A:45:GLN:HG3	2.13	0.48
2:B:351:MET:HE3	2:C:326:GLN:OE1	2.13	0.48
2:C:164:VAL:HA	2:C:167:LEU:HB3	1.95	0.48
2:D:95:ALA:HB1	2:D:131:LEU:HG	1.96	0.48
3:E:15:VAL:HG13	3:E:47:TYR:CE2	2.48	0.48
3:E:147:GLU:H	3:E:150:ARG:HG2	1.78	0.48
4:F:254:LYS:CD	4:F:315:MET:HE2	2.44	0.48
4:F:285:VAL:O	4:F:314:GLU:HB3	2.14	0.48
4:F:296:ASN:HB2	4:F:297:PRO:HD2	1.94	0.48
4:G:92:LEU:CA	4:G:97:MET:SD	3.00	0.48
1:A:280:GLN:CA	1:A:283:ARG:HG3	2.43	0.48
1:A:300:GLN:NE2	1:A:330:LEU:HD11	2.23	0.48
2:B:89:ASP:OD2	2:B:115:PRO:HB3	2.13	0.48
2:C:248:GLN:HG3	2:C:274:ARG:NH1	2.28	0.48
2:C:350:GLU:HB3	2:D:290:HIS:NE2	2.28	0.48
2:C:365:LEU:HB2	2:D:322:PRO:HG3	1.95	0.48
2:D:191:LEU:HD21	2:D:198:HIS:HA	1.94	0.48
2:D:335:GLY:HA3	2:D:352:THR:HG23	1.94	0.48
3:E:30:GLN:HG2	3:E:31:ALA:N	2.29	0.48
3:E:75:ASP:HA	3:E:105:ARG:NH2	2.28	0.48
3:E:229:TRP:HD1	3:E:320:GLU:CG	2.17	0.48
4:G:3:PHE:HA	4:G:62:PRO:O	2.13	0.48
4:G:145:SER:O	4:G:172:THR:N	2.47	0.48
4:G:55:ALA:HB2	4:G:230:PHE:HE1	1.78	0.48
4:G:124:SER:O	4:G:217:GLN:HB3	2.14	0.48
4:G:340:LEU:CB	4:G:347:VAL:HG22	2.43	0.48
1:A:224:GLY:HA3	1:A:335:PRO:HA	1.96	0.48
2:C:89:ASP:HB2	2:C:122:VAL:HG22	1.93	0.48
2:C:364:PRO:HG2	2:C:367:GLU:OE2	2.13	0.48
2:D:96:ALA:C	3:E:126:ASN:HB3	2.38	0.48
2:D:259:ALA:C	2:D:357:LEU:HD11	2.38	0.48
3:E:4:TYR:H	3:E:7:LEU:CD1	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:82:GLU:HG2	3:E:92:ALA:HB2	1.94	0.48
4:F:103:ARG:HE	4:G:305:ILE:CB	2.24	0.48
4:F:132:GLN:HE22	4:F:209:GLY:C	2.21	0.48
4:F:176:ARG:HD3	4:F:323:TYR:CE1	2.48	0.48
4:G:355:GLN:NE2	4:G:358:ALA:HB2	2.29	0.48
1:A:158:LEU:HD21	1:A:185:LEU:CB	2.44	0.48
1:A:270:ARG:HA	1:A:273:PHE:H	1.78	0.48
1:A:329:LEU:O	1:A:338:ASP:O	2.31	0.48
2:C:149:HIS:CD2	2:C:149:HIS:C	2.92	0.48
2:C:181:GLU:OE1	2:C:185:HIS:HB2	2.13	0.48
2:C:355:ARG:HD3	2:D:330:GLN:OE1	2.13	0.48
3:E:76:TYR:HE1	3:E:113:TRP:HE1	1.62	0.48
4:F:256:LEU:HD12	4:F:310:TYR:CD1	2.49	0.48
1:A:218:VAL:O	1:A:221:LEU:HB3	2.14	0.48
2:C:357:LEU:HD23	2:C:360:HIS:CG	2.49	0.48
2:D:4:GLN:NE2	2:D:5:VAL:HG22	2.28	0.48
3:E:176:LEU:HD12	3:E:179:GLU:OE1	2.14	0.48
4:F:16:GLN:HB3	4:F:53:MET:CG	2.43	0.48
4:F:97:MET:SD	4:F:110:THR:HG21	2.53	0.48
4:F:180:CYS:HA	4:F:357:ALA:HA	1.94	0.48
4:F:358:ALA:C	4:F:359:TYR:CG	2.92	0.48
4:G:2:LYS:HB2	4:G:64:GLU:CD	2.39	0.48
4:G:254:LYS:NZ	4:G:312:GLY:HA3	2.28	0.48
1:A:71:MET:SD	4:F:175:HIS:CE1	3.07	0.48
2:B:259:ALA:HB2	2:B:360:HIS:CA	2.40	0.48
2:B:339:LEU:HB2	2:B:345:ARG:HH21	1.78	0.48
2:C:15:PHE:CE1	2:C:72:PRO:HA	2.48	0.48
2:C:278:TRP:CD1	2:C:345:ARG:HB2	2.49	0.48
3:E:51:GLN:O	3:E:52:GLN:HB2	2.14	0.48
3:E:208:ASP:O	3:E:212:ALA:N	2.40	0.48
4:F:138:LEU:HD21	4:F:182:MET:HG2	1.95	0.48
4:F:282:ARG:HH21	4:F:318:GLY:N	2.12	0.48
4:G:161:GLU:HA	4:G:190:SER:CB	2.44	0.48
1:A:47:PHE:CE2	1:A:77:ARG:CB	2.96	0.48
2:C:192:ASN:O	2:C:195:HIS:CE1	2.67	0.48
2:D:15:PHE:CE2	2:D:28:LEU:HD23	2.49	0.48
4:F:315:MET:CG	4:F:342:ASP:HA	2.44	0.48
4:G:132:GLN:H	4:G:132:GLN:CD	2.21	0.48
2:B:38:HIS:CD2	2:B:40:ALA:O	2.67	0.47
2:B:82:ILE:CD1	2:B:87:PHE:CD2	2.97	0.47
2:C:362:ARG:HB3	2:C:363:MET:SD	2.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:294:MET:HB2	2:D:302:LEU:HD23	1.96	0.47
2:D:297:LEU:HD12	2:D:298:SER:H	1.79	0.47
3:E:49:LEU:CA	3:E:111:VAL:HG23	2.43	0.47
4:F:17:VAL:HG13	4:F:46:GLY:N	2.28	0.47
4:F:146:MET:N	4:F:171:ALA:HB1	2.29	0.47
4:F:173:ASP:OD1	4:F:176:ARG:HG3	2.14	0.47
4:F:286:SER:HA	4:F:314:GLU:CD	2.39	0.47
1:A:310:LEU:CD2	3:E:303:VAL:HG21	2.43	0.47
2:D:95:ALA:HB3	2:D:128:VAL:HA	1.96	0.47
2:D:202:ALA:HA	2:D:205:LEU:HB2	1.96	0.47
2:D:252:LEU:CD2	2:D:264:VAL:HA	2.44	0.47
2:D:352:THR:CA	2:D:355:ARG:HH21	2.27	0.47
4:F:103:ARG:HH11	4:G:305:ILE:CG2	2.27	0.47
4:F:319:PHE:N	4:F:364:MET:O	2.47	0.47
4:F:351:ASP:HB2	4:F:359:TYR:HE2	1.78	0.47
4:F:357:ALA:HB1	4:F:359:TYR:OH	2.15	0.47
4:G:74:LYS:HB2	4:G:108:LEU:HD23	1.96	0.47
4:G:207:LEU:HD11	4:G:214:LEU:HD13	1.94	0.47
1:A:332:CYS:HB3	1:A:334:LYS:O	2.14	0.47
2:B:120:PHE:CD1	2:B:151:LYS:NZ	2.83	0.47
2:C:363:MET:SD	2:C:363:MET:N	2.88	0.47
2:D:96:ALA:HA	2:D:130:MET:CG	2.44	0.47
3:E:45:SER:CB	3:E:111:VAL:HG11	2.43	0.47
3:E:214:GLU:HA	3:E:217:CYS:SG	2.54	0.47
4:F:7:ARG:CB	4:F:88:ILE:HD11	2.45	0.47
4:F:221:ASN:O	4:F:235:LYS:HA	2.14	0.47
4:G:228:GLY:C	4:G:230:PHE:H	2.21	0.47
4:G:259:GLY:HA2	4:G:334:GLU:O	2.14	0.47
1:A:163:ASP:HB2	1:A:198:THR:HA	1.94	0.47
1:A:219:ASP:CG	1:A:285:MET:HG3	2.39	0.47
1:A:219:ASP:O	1:A:223:MET:SD	2.73	0.47
2:B:322:PRO:HA	2:B:325:ILE:CG1	2.44	0.47
2:C:31:GLY:O	2:C:37:ILE:HG23	2.15	0.47
2:C:356:ALA:O	2:C:360:HIS:HA	2.13	0.47
2:D:3:TYR:CG	3:E:21:GLY:O	2.68	0.47
2:D:38:HIS:O	2:D:41:TYR:CE2	2.67	0.47
2:D:296:GLN:CG	2:D:317:ALA:O	2.62	0.47
3:E:242:PRO:CG	3:E:301:MET:SD	3.02	0.47
3:E:245:LEU:CD1	3:E:297:ARG:HA	2.44	0.47
4:F:68:THR:HA	4:F:112:PRO:HA	1.95	0.47
4:G:37:VAL:HG13	4:G:59:LEU:HD21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:137:ARG:HB2	4:G:332:LYS:CD	2.44	0.47
1:A:279:TRP:O	1:A:283:ARG:HG3	2.14	0.47
2:C:268:ILE:HG22	2:C:346:ARG:HH21	1.79	0.47
2:C:278:TRP:CE2	2:C:346:ARG:HB2	2.49	0.47
2:D:45:GLY:O	2:D:157:THR:HA	2.15	0.47
2:D:74:GLY:O	2:D:79:CYS:CB	2.62	0.47
2:D:112:GLN:OE1	4:G:364:MET:HE3	2.15	0.47
2:D:291:ARG:O	2:D:294:MET:HB2	2.14	0.47
3:E:27:LEU:HD11	3:E:162:HIS:HB3	1.96	0.47
3:E:236:LEU:HA	3:E:244:ARG:CB	2.45	0.47
4:G:13:PRO:HB3	4:G:55:ALA:CB	2.44	0.47
1:A:275:LYS:HE3	1:A:276:HIS:HE1	1.80	0.47
2:B:8:ARG:HD3	2:C:145:GLU:HB3	1.97	0.47
2:C:74:GLY:CA	2:C:83:GLU:OE1	2.63	0.47
2:C:282:LEU:HA	2:C:285:MET:CE	2.43	0.47
2:C:351:MET:HG2	2:D:329:TYR:CD1	2.49	0.47
2:D:64:CYS:SG	2:D:79:CYS:SG	3.10	0.47
2:D:114:ALA:HB2	4:G:366:LEU:CD2	2.42	0.47
2:D:125:ILE:H	2:D:125:ILE:HD12	1.79	0.47
3:E:73:HIS:O	3:E:76:TYR:HB3	2.14	0.47
4:F:251:ASN:OD1	4:F:341:THR:HA	2.13	0.47
4:F:358:ALA:O	4:F:359:TYR:CD1	2.68	0.47
4:G:91:GLN:HB2	4:G:100:ARG:HH12	1.80	0.47
4:G:125:GLU:OE2	4:G:191:HIS:CE1	2.68	0.47
1:A:18:ARG:CG	1:A:21:TYR:CE2	2.98	0.47
1:A:169:VAL:O	1:A:173:CYS:SG	2.73	0.47
1:A:225:LYS:CB	1:A:228:ARG:HB3	2.45	0.47
1:A:272:LEU:HD23	1:A:273:PHE:H	1.80	0.47
1:A:333:HIS:O	1:A:337:ALA:C	2.58	0.47
2:B:177:ALA:HA	2:B:212:GLY:HA2	1.96	0.47
2:B:339:LEU:HD13	2:B:345:ARG:HB3	1.96	0.47
2:C:362:ARG:CB	2:C:363:MET:SD	3.03	0.47
3:E:307:ASN:HB3	3:E:310:LEU:HB3	1.96	0.47
4:F:6:GLU:OE2	4:F:9:HIS:CD2	2.68	0.47
4:F:97:MET:HB2	4:F:110:THR:CG2	2.45	0.47
4:F:126:VAL:CG2	4:F:191:HIS:CE1	2.98	0.47
4:F:338:MET:O	4:F:339:MET:SD	2.73	0.47
4:G:8:GLU:OE1	4:G:85:GLY:HA2	2.15	0.47
1:A:61:TRP:CE3	1:A:61:TRP:HA	2.49	0.47
2:B:87:PHE:CZ	2:B:117:ARG:HB3	2.50	0.47
2:C:198:HIS:HA	2:C:232:VAL:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:343:PRO:HB3	2:D:286:LEU:HB2	1.97	0.47
2:D:43:PHE:HB2	2:D:155:ALA:HA	1.97	0.47
2:D:63:ASN:HB3	2:D:78:ASN:HD22	1.80	0.47
2:D:188:GLU:CG	2:D:203:LEU:HD13	2.44	0.47
3:E:14:LEU:HB3	3:E:18:TYR:CZ	2.50	0.47
3:E:18:TYR:CA	3:E:140:TRP:CH2	2.98	0.47
4:F:20:PRO:C	4:F:21:LEU:HD12	2.39	0.47
4:F:331:LEU:HG	4:F:333:CYS:HB3	1.96	0.47
4:G:54:VAL:O	4:G:230:PHE:HA	2.15	0.47
4:G:87:GLU:OE1	4:G:87:GLU:HA	2.10	0.47
4:G:256:LEU:HD22	4:G:310:TYR:CD1	2.50	0.47
4:G:256:LEU:CG	4:G:338:MET:HE3	2.43	0.47
4:G:283:LEU:HD12	4:G:318:GLY:HA2	1.96	0.47
4:G:350:GLU:HB2	4:G:355:GLN:OE1	2.14	0.47
2:B:73:CYS:HB2	2:B:79:CYS:SG	2.55	0.47
2:C:256:MET:O	2:C:360:HIS:CE1	2.68	0.47
4:G:350:GLU:HA	4:G:357:ALA:O	2.15	0.47
1:A:11:ALA:O	1:A:15:GLU:HG3	2.15	0.47
1:A:167:ASN:HD22	1:A:168:GLN:N	2.13	0.47
2:C:199:GLU:HG2	2:C:202:ALA:CB	2.45	0.47
2:D:14:THR:HA	2:D:57:LEU:HD21	1.96	0.47
2:D:123:TYR:HB2	2:D:151:LYS:O	2.15	0.47
2:D:210:ALA:CB	2:D:217:ALA:HB2	2.44	0.47
3:E:3:TRP:HA	3:E:7:LEU:CD1	2.43	0.47
3:E:32:LEU:H	3:E:32:LEU:HD12	1.79	0.47
3:E:49:LEU:CD1	3:E:76:TYR:HB2	2.44	0.47
3:E:220:LEU:C	3:E:222:TYR:H	2.23	0.47
3:E:245:LEU:CD1	3:E:300:LEU:HD12	2.45	0.47
4:F:3:PHE:CB	4:F:59:LEU:CD2	2.93	0.47
4:F:192:SER:O	4:F:238:ASP:OD1	2.33	0.47
4:F:206:MET:SD	4:F:232:PHE:HB3	2.55	0.47
4:G:163:GLU:OE1	4:G:168:ARG:HB3	2.15	0.47
1:A:217:TRP:CD1	1:A:217:TRP:C	2.91	0.46
2:B:48:GLY:HA3	2:B:215:ARG:H	1.79	0.46
2:B:282:LEU:HD21	2:B:349:VAL:HG22	1.97	0.46
2:C:238:SER:HB2	2:C:243:THR:O	2.16	0.46
2:C:292:ILE:HG23	2:C:317:ALA:CA	2.45	0.46
2:D:42:LEU:N	2:D:171:LEU:O	2.48	0.46
2:D:151:LYS:HB3	2:D:151:LYS:HE3	1.72	0.46
3:E:229:TRP:O	3:E:316:LEU:HD22	2.15	0.46
3:E:233:LEU:CD1	3:E:312:ILE:HB	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:137:ARG:HA	4:F:332:LYS:CE	2.45	0.46
4:F:310:TYR:CG	4:F:311:SER:N	2.82	0.46
4:G:7:ARG:CD	4:G:84:GLU:HA	2.45	0.46
2:C:115:PRO:HB3	2:C:120:PHE:C	2.40	0.46
2:C:191:LEU:O	2:C:195:HIS:HA	2.14	0.46
2:C:357:LEU:O	2:C:360:HIS:HB2	2.15	0.46
2:D:26:THR:O	2:D:30:ASN:CG	2.58	0.46
2:D:81:GLU:HA	2:D:84:GLN:OE1	2.15	0.46
2:D:148:GLU:O	2:D:149:HIS:CG	2.69	0.46
2:D:298:SER:C	2:D:300:ALA:H	2.24	0.46
3:E:10:ASP:CB	3:E:162:HIS:CE1	2.98	0.46
4:F:115:ASP:O	4:F:116:PHE:HB2	2.15	0.46
4:G:53:MET:CE	4:G:206:MET:CE	2.93	0.46
4:G:310:TYR:CE1	4:G:312:GLY:O	2.68	0.46
2:B:62:LEU:O	2:B:119:ARG:HB2	2.15	0.46
2:B:344:ASP:OD2	2:B:346:ARG:HB3	2.15	0.46
2:D:2:SER:O	2:D:3:TYR:CB	2.63	0.46
2:D:14:THR:HA	2:D:57:LEU:CD2	2.45	0.46
2:D:21:GLN:O	2:D:24:VAL:HB	2.15	0.46
2:D:112:GLN:CG	2:D:113:TYR:N	2.78	0.46
2:D:290:HIS:CE1	2:D:291:ARG:NE	2.83	0.46
3:E:15:VAL:HG13	3:E:47:TYR:CZ	2.49	0.46
3:E:30:GLN:CA	3:E:148:PRO:HD3	2.45	0.46
3:E:68:MET:HG2	3:E:76:TYR:CD1	2.50	0.46
3:E:303:VAL:HB	3:E:306:ILE:HB	1.96	0.46
4:F:161:GLU:O	4:F:167:LEU:HD12	2.15	0.46
4:F:212:ASN:O	4:F:214:LEU:CD2	2.63	0.46
1:A:78:GLN:H	1:A:107:ASP:CA	2.25	0.46
2:B:63:ASN:HD22	2:B:82:ILE:HD11	1.80	0.46
2:C:82:ILE:HG13	2:C:87:PHE:CG	2.50	0.46
3:E:204:LEU:HB3	3:E:210:TRP:CE3	2.50	0.46
4:F:53:MET:HE1	4:F:206:MET:SD	2.54	0.46
4:F:144:PHE:CZ	4:F:176:ARG:HB2	2.50	0.46
4:F:264:LYS:HA	4:F:328:LEU:CD2	2.45	0.46
4:G:3:PHE:HB3	4:G:63:HIS:ND1	2.31	0.46
4:G:20:PRO:CG	4:G:53:MET:HB2	2.46	0.46
4:G:53:MET:HG3	4:G:230:PHE:CD1	2.50	0.46
2:B:60:LYS:CA	2:B:82:ILE:HG21	2.45	0.46
2:C:244:LEU:CD2	2:C:274:ARG:HD3	2.45	0.46
2:C:357:LEU:HD23	2:C:360:HIS:CD2	2.50	0.46
2:D:220:LEU:HA	2:D:223:GLN:OE1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:321:HIS:O	3:E:324:GLN:HB2	2.16	0.46
4:F:21:LEU:CD2	4:F:46:GLY:CA	2.94	0.46
4:F:24:ARG:HH12	4:F:72:ALA:HB3	1.81	0.46
4:F:55:ALA:HA	4:F:230:PHE:CD1	2.51	0.46
4:F:341:THR:H	4:F:347:VAL:HG12	1.80	0.46
1:A:47:PHE:CD2	1:A:77:ARG:CB	2.99	0.46
2:B:183:ILE:HD13	2:B:210:ALA:O	2.15	0.46
2:C:65:GLU:HG3	2:C:76:CYS:SG	2.56	0.46
2:C:358:ALA:C	2:C:364:PRO:CB	2.88	0.46
2:D:21:GLN:CA	2:D:23:HIS:CE1	2.94	0.46
2:D:75:VAL:HG23	2:D:80:ARG:HG2	1.96	0.46
2:D:188:GLU:HG3	2:D:203:LEU:HD13	1.97	0.46
2:D:295:VAL:HG21	2:D:313:MET:HB3	1.97	0.46
3:E:90:VAL:HG13	3:E:91:ASP:CG	2.41	0.46
3:E:176:LEU:HD23	3:E:187:LEU:HB3	1.98	0.46
3:E:177:SER:CB	3:E:184:GLN:HE22	2.29	0.46
4:F:42:LEU:HB2	4:F:59:LEU:HD22	1.98	0.46
4:F:193:VAL:HG23	4:F:238:ASP:HA	1.97	0.46
1:A:158:LEU:HD13	1:A:185:LEU:CD1	2.45	0.46
1:A:163:ASP:HB3	1:A:198:THR:HA	1.96	0.46
2:B:147:PRO:O	2:B:150:VAL:HG22	2.15	0.46
2:D:292:ILE:HG23	2:D:317:ALA:CA	2.45	0.46
4:F:140:GLU:OE1	4:F:332:LYS:HE2	2.16	0.46
4:G:73:ARG:O	4:G:77:ASP:CG	2.58	0.46
4:G:159:LEU:HG	4:G:160:PHE:N	2.31	0.46
2:B:62:LEU:HB3	2:B:120:PHE:CD2	2.50	0.46
2:C:23:HIS:ND1	2:C:24:VAL:HG23	2.31	0.46
2:D:3:TYR:CZ	2:D:4:GLN:O	2.69	0.46
2:D:89:ASP:OD1	2:D:118:GLY:HA3	2.15	0.46
3:E:7:LEU:HB3	3:E:40:LEU:HB2	1.98	0.46
3:E:90:VAL:HA	3:E:124:ALA:CA	2.43	0.46
4:F:3:PHE:HB3	4:F:59:LEU:CD2	2.46	0.46
4:F:286:SER:HB2	4:F:288:ASN:OD1	2.15	0.46
4:G:181:SER:HB3	4:G:356:SER:HA	1.98	0.46
4:G:286:SER:HB2	4:G:289:GLN:HB2	1.97	0.46
1:A:217:TRP:HB2	1:A:232:ILE:CG2	2.45	0.46
1:A:297:GLN:OE1	1:A:333:HIS:CG	2.69	0.46
2:B:68:ILE:HD11	2:B:119:ARG:HB2	1.98	0.46
2:B:73:CYS:O	2:B:79:CYS:HB2	2.16	0.46
2:D:51:LYS:HA	2:D:175:LEU:HD11	1.97	0.46
2:D:75:VAL:CG2	2:D:80:ARG:HG2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:51:GLN:OE1	3:E:109:ALA:N	2.48	0.46
3:E:82:GLU:OE2	3:E:89:GLY:C	2.59	0.46
3:E:140:TRP:CB	3:E:142:PHE:CZ	2.99	0.46
3:E:318:ARG:O	3:E:321:HIS:CB	2.64	0.46
4:F:223:ILE:HG21	4:F:236:LEU:HD21	1.98	0.46
4:F:334:GLU:C	4:F:334:GLU:CD	2.84	0.46
4:G:207:LEU:CD2	4:G:214:LEU:HB2	2.35	0.46
1:A:50:HIS:CD2	1:A:50:HIS:O	2.69	0.46
1:A:234:GLN:HG2	2:B:304:ASN:CG	2.41	0.46
2:B:188:GLU:O	2:B:192:ASN:HB2	2.16	0.46
2:B:295:VAL:HG11	2:B:314:ARG:HA	1.98	0.46
2:C:324:ASP:O	2:C:328:TYR:CD2	2.70	0.46
2:D:188:GLU:O	2:D:192:ASN:CG	2.59	0.46
2:D:198:HIS:HD2	2:D:203:LEU:HD12	1.81	0.46
2:D:201:ARG:HG2	2:D:234:THR:CG2	2.38	0.46
3:E:154:THR:O	3:E:158:ARG:HD2	2.16	0.46
3:E:209:ASN:HA	3:E:247:TRP:CH2	2.51	0.46
3:E:250:THR:O	3:E:254:ASP:CG	2.59	0.46
4:F:156:ASN:O	4:F:197:ARG:HB2	2.15	0.46
4:G:7:ARG:CZ	4:G:80:ARG:HA	2.46	0.46
2:B:76:CYS:HB2	2:B:79:CYS:SG	2.55	0.45
2:B:177:ALA:CA	2:B:212:GLY:HA2	2.46	0.45
2:D:42:LEU:HB3	2:D:172:GLN:HA	1.98	0.45
2:D:246:ASP:HB3	2:D:248:GLN:OE1	2.15	0.45
2:D:295:VAL:HB	2:D:317:ALA:HB2	1.97	0.45
3:E:42:TYR:CD1	3:E:113:TRP:CZ2	3.03	0.45
4:F:4:THR:O	4:F:59:LEU:CD1	2.64	0.45
4:G:70:VAL:HG12	4:G:110:THR:HA	1.98	0.45
4:G:91:GLN:HB3	4:G:93:GLU:OE1	2.16	0.45
4:G:135:MET:CG	4:G:207:LEU:CD1	2.94	0.45
4:G:166:GLU:HG2	4:G:183:PRO:HA	1.97	0.45
4:G:257:GLU:OE1	4:G:352:ALA:CB	2.65	0.45
4:G:325:LEU:O	4:G:329:ASN:CG	2.59	0.45
4:G:340:LEU:HB3	4:G:347:VAL:CG1	2.45	0.45
1:A:73:LEU:HD12	4:F:175:HIS:C	2.40	0.45
2:B:115:PRO:HG3	2:B:121:LYS:N	2.32	0.45
2:B:148:GLU:OE2	2:B:151:LYS:NZ	2.49	0.45
2:C:53:SER:O	2:C:57:LEU:HG	2.16	0.45
2:C:110:ASN:HA	2:C:113:TYR:CD2	2.52	0.45
2:C:252:LEU:CD1	2:C:267:LEU:HB2	2.46	0.45
2:C:328:TYR:CE1	2:C:360:HIS:CD2	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:341:TYR:CG	2:D:337:LYS:HB2	2.51	0.45
2:D:60:LYS:HA	2:D:82:ILE:HD12	1.98	0.45
2:D:291:ARG:O	2:D:295:VAL:N	2.48	0.45
3:E:67:LEU:HB2	3:E:73:HIS:HD2	1.80	0.45
3:E:169:GLU:H	3:E:169:GLU:CD	2.24	0.45
4:F:106:PHE:CE1	4:G:302:ALA:HB1	2.51	0.45
4:F:147:ALA:O	4:F:156:ASN:HA	2.15	0.45
4:F:165:GLU:HB3	4:F:185:GLY:HA2	1.98	0.45
4:G:44:LEU:HD12	4:G:44:LEU:HA	1.74	0.45
4:G:143:GLN:HA	4:G:158:MET:CE	2.46	0.45
1:A:70:ALA:HB2	4:F:364:MET:SD	2.55	0.45
2:B:43:PHE:HB2	2:B:155:ALA:HA	1.97	0.45
2:B:65:GLU:C	2:B:76:CYS:SG	2.99	0.45
2:B:249:ALA:HB2	2:B:284:GLU:CD	2.42	0.45
2:B:292:ILE:CG2	2:B:317:ALA:HA	2.41	0.45
2:B:351:MET:HE2	2:C:329:TYR:CB	2.46	0.45
2:C:15:PHE:HA	2:C:57:LEU:HD13	1.99	0.45
2:C:206:LEU:HD11	2:C:232:VAL:CG1	2.45	0.45
2:C:244:LEU:HD13	2:C:274:ARG:NH1	2.30	0.45
2:C:244:LEU:HD22	2:C:274:ARG:HD3	1.99	0.45
2:D:74:GLY:O	2:D:79:CYS:HB3	2.16	0.45
2:D:159:PRO:HB2	2:D:167:LEU:HD21	1.97	0.45
3:E:46:ARG:N	3:E:68:MET:HE1	2.31	0.45
3:E:49:LEU:C	3:E:49:LEU:HD23	2.41	0.45
3:E:208:ASP:O	3:E:212:ALA:CB	2.64	0.45
4:F:199:GLY:HA2	4:F:232:PHE:CZ	2.52	0.45
4:F:251:ASN:HB2	4:F:340:LEU:O	2.15	0.45
4:F:254:LYS:HA	4:F:312:GLY:HA3	1.99	0.45
4:F:340:LEU:HB3	4:F:341:THR:O	2.16	0.45
4:G:3:PHE:CA	4:G:63:HIS:HA	2.46	0.45
4:G:5:VAL:HG12	4:G:59:LEU:CD1	2.46	0.45
4:G:61:GLN:CD	4:G:87:GLU:OE2	2.60	0.45
4:G:159:LEU:HB2	4:G:241:PHE:CG	2.51	0.45
4:G:251:ASN:O	4:G:341:THR:HG23	2.17	0.45
1:A:219:ASP:OD2	1:A:285:MET:HG3	2.17	0.45
2:B:88:VAL:HG11	2:B:116:ALA:HB3	1.99	0.45
2:B:296:GLN:HG3	2:B:317:ALA:HB1	1.98	0.45
2:C:6:LEU:O	2:C:10:TRP:CD1	2.69	0.45
2:C:60:LYS:HD3	2:C:83:GLU:OE1	2.16	0.45
2:D:259:ALA:O	2:D:357:LEU:HD11	2.17	0.45
2:D:339:LEU:N	2:D:340:PRO:CD	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:49:LEU:HD13	3:E:68:MET:HG2	1.98	0.45
3:E:207:GLY:C	3:E:209:ASN:N	2.73	0.45
3:E:318:ARG:O	3:E:321:HIS:HB3	2.17	0.45
4:F:6:GLU:HG3	4:F:87:GLU:OE2	2.16	0.45
4:F:8:GLU:OE2	4:F:11:LEU:HD22	2.17	0.45
4:F:122:TRP:CE3	4:F:122:TRP:N	2.85	0.45
4:F:148:HIS:CD2	4:F:148:HIS:H	2.35	0.45
4:F:317:ILE:HD12	4:F:343:SER:N	2.31	0.45
4:G:20:PRO:HG2	4:G:53:MET:HB2	1.98	0.45
4:G:71:PRO:HB2	4:G:74:LYS:HG3	1.98	0.45
4:G:137:ARG:HA	4:G:140:GLU:CD	2.41	0.45
4:G:193:VAL:HG22	4:G:223:ILE:CG2	2.46	0.45
4:G:254:LYS:HB2	4:G:340:LEU:CD1	2.46	0.45
1:A:27:ASP:OD2	1:A:29:LEU:HB3	2.17	0.45
1:A:77:ARG:CA	1:A:107:ASP:HA	2.44	0.45
1:A:156:LYS:C	1:A:159:ASN:H	2.25	0.45
2:B:55:ALA:HB1	2:B:124:LEU:HD13	1.98	0.45
2:C:355:ARG:O	2:C:359:PHE:CG	2.70	0.45
2:D:60:LYS:O	2:D:64:CYS:CA	2.65	0.45
2:D:64:CYS:SG	2:D:66:THR:OG1	2.73	0.45
3:E:12:GLU:CG	3:E:56:HIS:CD2	3.00	0.45
4:F:222:ASN:ND2	4:F:235:LYS:HG2	2.32	0.45
4:F:261:ASP:HA	4:F:264:LYS:CB	2.47	0.45
4:G:154:TYR:O	4:G:241:PHE:CE2	2.70	0.45
4:G:337:ARG:CZ	4:G:337:ARG:CB	2.95	0.45
2:C:343:PRO:HA	2:D:336:ARG:HH12	1.80	0.45
2:D:24:VAL:HG21	2:D:175:LEU:HA	1.97	0.45
3:E:32:LEU:HD13	3:E:197:SER:HB3	1.98	0.45
3:E:49:LEU:HD11	3:E:76:TYR:N	2.32	0.45
3:E:68:MET:HE3	3:E:76:TYR:CD1	2.52	0.45
3:E:73:HIS:ND1	3:E:75:ASP:HB2	2.32	0.45
3:E:189:ALA:CB	3:E:269:ASP:OD2	2.64	0.45
3:E:245:LEU:HD13	3:E:297:ARG:HA	1.97	0.45
4:F:68:THR:HA	4:F:113:ALA:H	1.81	0.45
4:F:138:LEU:HG	4:F:182:MET:HG2	1.98	0.45
4:F:279:ARG:HB3	4:F:321:VAL:HG12	1.98	0.45
4:F:286:SER:C	4:F:288:ASN:H	2.25	0.45
4:G:158:MET:HA	4:G:241:PHE:CZ	2.51	0.45
4:G:175:HIS:C	4:G:362:MET:HE2	2.42	0.45
1:A:160:LEU:C	1:A:160:LEU:HD12	2.42	0.45
1:A:272:LEU:HG	1:A:273:PHE:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:261:GLY:HA2	2:C:264:VAL:HG22	1.99	0.45
2:C:358:ALA:HB1	2:D:322:PRO:C	2.42	0.45
2:D:23:HIS:HE1	2:D:176:LYS:HG2	1.82	0.45
2:D:122:VAL:HG22	2:D:151:LYS:CG	2.44	0.45
2:D:127:GLU:HB3	2:D:129:HIS:HE1	1.82	0.45
3:E:57:LYS:HB3	3:E:59:CYS:H	1.82	0.45
3:E:122:ASP:O	3:E:126:ASN:HB2	2.17	0.45
3:E:145:THR:HB	3:E:150:ARG:HB2	1.99	0.45
3:E:235:ALA:O	3:E:244:ARG:HD3	2.17	0.45
4:F:120:ASP:O	4:F:222:ASN:CB	2.65	0.45
4:F:195:VAL:HG12	4:F:236:LEU:CD2	2.46	0.45
4:F:206:MET:HA	4:F:208:ASP:OD1	2.16	0.45
4:F:264:LYS:HB2	4:F:328:LEU:HD23	1.99	0.45
4:F:337:ARG:CZ	4:F:350:GLU:HG3	2.47	0.45
4:G:57:VAL:HG12	4:G:59:LEU:HB3	1.99	0.45
4:G:215:ARG:HB2	4:G:226:HIS:HD2	1.82	0.45
4:G:276:GLU:CD	4:G:296:ASN:CG	2.84	0.45
1:A:150:TRP:CH2	1:A:154:ARG:HG2	2.52	0.45
2:B:76:CYS:CB	2:B:79:CYS:SG	3.05	0.45
2:C:250:LEU:HD23	2:C:312:ARG:HH21	1.82	0.45
2:C:265:MET:HB3	2:D:301:ALA:O	2.16	0.45
2:D:101:VAL:HG22	2:D:132:SER:OG	2.17	0.45
3:E:29:ILE:HD13	3:E:162:HIS:O	2.17	0.45
3:E:276:GLU:HA	3:E:279:ASN:HB3	1.99	0.45
4:F:13:PRO:CB	4:F:55:ALA:CB	2.95	0.45
4:F:161:GLU:HA	4:F:191:HIS:O	2.17	0.45
4:F:254:LYS:O	4:F:339:MET:HA	2.17	0.45
4:F:286:SER:HB2	4:F:289:GLN:HB2	1.99	0.45
1:A:270:ARG:N	1:A:272:LEU:CD2	2.80	0.45
1:A:273:PHE:CE2	1:A:283:ARG:O	2.70	0.45
2:C:251:SER:O	2:C:263:ARG:NH2	2.50	0.45
2:C:252:LEU:HD12	2:C:267:LEU:HB3	1.99	0.45
2:D:6:LEU:O	2:D:9:LYS:HB3	2.16	0.45
4:F:106:PHE:HE1	4:G:302:ALA:HB1	1.81	0.45
4:F:147:ALA:CB	4:F:150:ASP:OD2	2.65	0.45
4:F:222:ASN:HD21	4:F:235:LYS:HG2	1.82	0.45
4:F:285:VAL:HG22	4:F:310:TYR:CG	2.52	0.45
4:G:21:LEU:HD22	4:G:33:LEU:HD21	1.99	0.45
4:G:53:MET:SD	4:G:232:PHE:HB2	2.57	0.45
4:G:143:GLN:HA	4:G:158:MET:HE2	1.98	0.45
1:A:18:ARG:CA	1:A:133:ARG:O	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:10:TRP:O	2:B:18:VAL:HG22	2.17	0.45
2:D:33:SER:HB3	2:D:70:ALA:HB2	1.99	0.45
2:D:295:VAL:HG22	2:D:314:ARG:NH1	2.32	0.45
4:F:160:PHE:HB2	4:F:193:VAL:HG12	1.99	0.45
4:F:176:ARG:HD3	4:F:323:TYR:CD1	2.52	0.45
4:F:337:ARG:NH2	4:F:350:GLU:HG3	2.32	0.45
1:A:77:ARG:CZ	1:A:106:ASP:HA	2.47	0.44
1:A:142:PRO:HA	1:A:146:GLN:NE2	2.31	0.44
1:A:279:TRP:H	1:A:282:ARG:HH21	1.63	0.44
2:B:150:VAL:CG2	2:B:152:PHE:CE2	3.00	0.44
2:C:57:LEU:HD22	2:C:60:LYS:HZ1	1.82	0.44
2:D:184:ARG:CD	2:D:204:GLN:HG2	2.45	0.44
2:D:300:ALA:N	2:D:302:LEU:HD12	2.33	0.44
3:E:15:VAL:HG13	3:E:47:TYR:OH	2.16	0.44
3:E:169:GLU:HA	3:E:172:ALA:HB3	1.99	0.44
4:F:203:LEU:O	4:F:207:LEU:N	2.50	0.44
4:F:257:GLU:HA	4:F:336:VAL:O	2.16	0.44
4:G:32:ASN:HB3	4:G:69:THR:HG22	1.98	0.44
1:A:308:THR:HA	1:A:323:GLU:OE1	2.17	0.44
2:C:342:ALA:C	2:C:344:ASP:H	2.26	0.44
2:D:20:GLY:C	2:D:22:GLU:OE1	2.59	0.44
2:D:64:CYS:SG	2:D:76:CYS:SG	3.13	0.44
2:D:179:ASP:H	2:D:182:GLN:NE2	2.14	0.44
3:E:49:LEU:HD21	3:E:73:HIS:ND1	2.32	0.44
4:F:21:LEU:HA	4:F:25:PRO:CD	2.48	0.44
4:F:27:LEU:HA	4:F:28:PRO:HD3	1.79	0.44
4:F:84:GLU:C	4:F:86:ALA:H	2.23	0.44
4:F:138:LEU:CG	4:F:182:MET:HG2	2.48	0.44
4:F:202:GLU:HB3	4:F:232:PHE:CE2	2.52	0.44
4:F:251:ASN:OD1	4:F:254:LYS:NZ	2.51	0.44
4:G:168:ARG:CZ	4:G:181:SER:HB2	2.46	0.44
4:G:262:LEU:HB3	4:G:306:LEU:HD21	1.99	0.44
1:A:263:GLN:CA	1:A:266:HIS:CE1	2.95	0.44
2:B:225:ILE:HG23	2:B:230:GLY:HA2	1.99	0.44
2:C:75:VAL:C	2:C:76:CYS:SG	3.01	0.44
2:C:279:GLU:CG	2:C:282:LEU:HD12	2.48	0.44
2:C:279:GLU:CG	2:C:339:LEU:HD22	2.47	0.44
2:D:292:ILE:HG23	2:D:317:ALA:N	2.32	0.44
3:E:31:ALA:CB	3:E:35:MET:SD	3.03	0.44
3:E:45:SER:HB2	3:E:113:TRP:CD1	2.52	0.44
3:E:223:SER:CB	3:E:228:ASP:O	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:224:VAL:HB	3:E:225:PRO:CD	2.47	0.44
3:E:281:LEU:HA	3:E:285:ARG:NE	2.29	0.44
4:F:252:PRO:O	4:F:339:MET:HB3	2.17	0.44
4:F:283:LEU:O	4:F:316:GLU:HA	2.18	0.44
4:G:82:LEU:HD22	4:G:101:SER:HB3	2.00	0.44
4:G:137:ARG:HH11	4:G:357:ALA:HB3	1.81	0.44
1:A:97:LEU:HB3	1:A:126:TRP:HB2	1.99	0.44
1:A:270:ARG:HH11	1:A:283:ARG:HE	1.64	0.44
2:B:129:HIS:HB3	2:B:161:LYS:HB2	2.00	0.44
2:B:268:ILE:HG23	2:B:346:ARG:NH2	2.32	0.44
2:C:14:THR:HG22	2:C:73:CYS:HA	1.99	0.44
2:C:328:TYR:CE1	2:C:361:PRO:CD	3.01	0.44
2:D:291:ARG:CG	2:D:306:MET:SD	3.06	0.44
2:D:354:LEU:CD2	3:E:260:HIS:CD2	3.01	0.44
3:E:18:TYR:HB3	3:E:140:TRP:CZ3	2.52	0.44
3:E:18:TYR:CB	3:E:140:TRP:CH2	3.01	0.44
3:E:68:MET:C	3:E:71:GLY:H	2.25	0.44
3:E:250:THR:HB	3:E:267:ASN:OD1	2.17	0.44
4:G:53:MET:SD	4:G:230:PHE:HB3	2.57	0.44
4:G:53:MET:HE3	4:G:206:MET:CE	2.48	0.44
4:G:274:SER:C	4:G:296:ASN:HA	2.42	0.44
1:A:22:LEU:HD23	1:A:112:VAL:HB	2.00	0.44
1:A:260:LEU:O	1:A:264:SER:HB3	2.17	0.44
2:B:114:ALA:O	2:B:121:LYS:HE2	2.17	0.44
2:C:282:LEU:HB2	2:C:336:ARG:HD3	1.99	0.44
2:D:61:GLY:O	2:D:68:ILE:HA	2.18	0.44
2:D:189:HIS:ND1	2:D:190:ILE:HG13	2.32	0.44
2:D:191:LEU:CG	2:D:198:HIS:HA	2.48	0.44
2:D:291:ARG:HB3	2:D:313:MET:SD	2.58	0.44
3:E:146:ARG:HH11	3:E:147:GLU:HG2	1.82	0.44
3:E:187:LEU:HA	3:E:205:PHE:HZ	1.82	0.44
3:E:240:GLN:O	3:E:244:ARG:HG3	2.18	0.44
3:E:322:TYR:CE1	3:E:327:VAL:HG12	2.53	0.44
4:F:2:LYS:O	4:F:63:HIS:HA	2.17	0.44
4:F:6:GLU:OE2	4:F:9:HIS:CG	2.70	0.44
4:F:150:ASP:CB	4:F:155:LEU:HB2	2.47	0.44
4:F:295:ASN:CG	4:F:296:ASN:N	2.76	0.44
4:G:156:ASN:HB2	4:G:197:ARG:HB3	1.98	0.44
4:G:279:ARG:O	4:G:321:VAL:HG12	2.18	0.44
1:A:18:ARG:HB2	1:A:21:TYR:CD2	2.52	0.44
1:A:274:ASP:OD1	1:A:278:VAL:O	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:LEU:C	1:A:333:HIS:CD2	2.95	0.44
2:B:19:VAL:HG22	2:B:186:GLN:HA	1.99	0.44
2:B:149:HIS:NE2	2:B:150:VAL:HG13	2.32	0.44
2:B:352:THR:HA	2:B:355:ARG:HH21	1.82	0.44
2:C:345:ARG:O	2:C:349:VAL:HG23	2.18	0.44
2:D:97:SER:OG	3:E:127:ALA:HA	2.18	0.44
2:D:120:PHE:HD1	2:D:120:PHE:HA	1.71	0.44
2:D:199:GLU:HG2	2:D:234:THR:N	2.31	0.44
4:F:122:TRP:CZ2	4:F:124:SER:HB2	2.53	0.44
4:F:182:MET:SD	4:F:355:GLN:HG2	2.58	0.44
4:F:193:VAL:HG13	4:F:195:VAL:HG12	2.00	0.44
4:F:285:VAL:O	4:F:314:GLU:CB	2.66	0.44
4:F:306:LEU:HA	4:G:103:ARG:HH11	1.82	0.44
4:G:37:VAL:O	4:G:63:HIS:CG	2.71	0.44
4:G:68:THR:OG1	4:G:110:THR:HG23	2.18	0.44
4:G:130:LEU:HD22	4:G:130:LEU:N	2.33	0.44
4:G:284:TYR:C	4:G:314:GLU:OE2	2.60	0.44
1:A:61:TRP:NE1	1:A:93:ILE:HA	2.32	0.44
2:B:121:LYS:CB	2:B:150:VAL:HA	2.48	0.44
2:B:338:GLU:O	2:B:342:ALA:N	2.51	0.44
2:C:261:GLY:C	2:C:264:VAL:HG22	2.43	0.44
2:D:257:VAL:HG13	2:D:360:HIS:CD2	2.52	0.44
2:D:290:HIS:HE1	2:D:291:ARG:CZ	2.29	0.44
3:E:51:GLN:HA	3:E:51:GLN:OE1	2.17	0.44
3:E:229:TRP:HB3	3:E:316:LEU:HD22	2.00	0.44
3:E:273:LEU:HA	3:E:276:GLU:OE2	2.17	0.44
4:G:179:VAL:O	4:G:358:ALA:O	2.35	0.44
4:G:319:PHE:CD1	4:G:319:PHE:C	2.96	0.44
1:A:55:ILE:HD12	1:A:55:ILE:HA	1.88	0.44
1:A:148:PRO:HA	1:A:171:CYS:SG	2.58	0.44
2:B:121:LYS:HB2	2:B:150:VAL:HA	2.00	0.44
2:C:355:ARG:HA	2:D:326:GLN:HG3	2.00	0.44
2:C:355:ARG:HH11	2:D:330:GLN:CG	2.31	0.44
2:D:65:GLU:CG	2:D:78:ASN:CG	2.91	0.44
2:D:195:HIS:CG	2:D:196:ILE:H	2.36	0.44
2:D:219:SER:HB3	3:E:157:SER:O	2.17	0.44
3:E:186:ALA:HB1	3:E:210:TRP:NE1	2.33	0.44
4:G:41:THR:HA	4:G:57:VAL:O	2.17	0.44
4:G:51:MET:SD	4:G:198:LYS:HB2	2.57	0.44
1:A:270:ARG:HB2	1:A:283:ARG:HB3	1.99	0.44
1:A:277:ARG:NE	1:A:277:ARG:HA	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:278:TRP:HA	2:B:278:TRP:CE3	2.53	0.44
2:C:223:GLN:HE22	2:D:172:GLN:NE2	2.16	0.44
2:C:247:ASP:HA	2:C:312:ARG:NH2	2.32	0.44
2:C:358:ALA:O	2:D:323:THR:CG2	2.66	0.44
2:D:63:ASN:O	2:D:78:ASN:CB	2.66	0.44
2:D:63:ASN:O	2:D:78:ASN:HB2	2.18	0.44
2:D:75:VAL:HA	2:D:80:ARG:HD3	2.00	0.44
2:D:292:ILE:HG13	2:D:313:MET:SD	2.58	0.44
3:E:10:ASP:HA	3:E:162:HIS:HE1	1.78	0.44
4:F:159:LEU:HD12	4:F:159:LEU:HA	1.77	0.44
4:F:270:ALA:HB2	4:F:292:ILE:HD12	1.99	0.44
4:G:333:CYS:SG	4:G:335:ASN:O	2.75	0.44
2:B:49:VAL:HG23	2:B:175:LEU:HD13	1.99	0.43
2:D:60:LYS:HA	2:D:82:ILE:CD1	2.47	0.43
2:D:86:ARG:O	2:D:87:PHE:HB2	2.18	0.43
2:D:295:VAL:HA	2:D:299:PRO:HA	1.99	0.43
2:D:296:GLN:HE22	2:D:322:PRO:N	2.16	0.43
3:E:278:ALA:HA	3:E:286:LEU:CD1	2.48	0.43
4:F:177:LEU:HD21	4:F:179:VAL:HG23	2.00	0.43
4:F:255:HIS:HA	4:F:339:MET:SD	2.57	0.43
4:F:256:LEU:HB2	4:F:310:TYR:HD1	1.83	0.43
4:F:317:ILE:HA	4:F:343:SER:CB	2.45	0.43
4:G:73:ARG:O	4:G:76:PHE:HB3	2.18	0.43
4:G:339:MET:HG2	4:G:350:GLU:CD	2.43	0.43
1:A:52:THR:HA	1:A:81:LEU:HB3	1.99	0.43
1:A:73:LEU:HD22	4:F:177:LEU:HD12	1.96	0.43
1:A:270:ARG:O	1:A:283:ARG:HD2	2.18	0.43
1:A:272:LEU:HD23	1:A:272:LEU:N	2.33	0.43
1:A:273:PHE:HD2	1:A:283:ARG:HA	1.71	0.43
2:B:64:CYS:HA	2:B:79:CYS:SG	2.58	0.43
2:C:82:ILE:HG13	2:C:87:PHE:HB2	2.00	0.43
2:C:360:HIS:ND1	2:C:362:ARG:HB2	2.33	0.43
2:D:15:PHE:HA	2:D:57:LEU:CD1	2.47	0.43
2:D:121:LYS:HG2	2:D:123:TYR:OH	2.18	0.43
3:E:194:SER:OG	3:E:201:ALA:HA	2.18	0.43
4:F:24:ARG:HD3	4:F:31:GLY:HA3	2.00	0.43
4:F:56:ARG:HB2	4:F:229:ASP:OD2	2.18	0.43
4:F:132:GLN:NE2	4:F:212:ASN:H	2.16	0.43
4:F:320:ASN:OD1	4:F:323:TYR:N	2.51	0.43
4:G:16:GLN:O	4:G:53:MET:HG2	2.18	0.43
1:A:47:PHE:HA	1:A:77:ARG:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:GLN:OE1	1:A:96:GLN:HA	2.18	0.43
2:B:223:GLN:HB3	2:B:240:MET:SD	2.58	0.43
2:B:339:LEU:O	2:B:342:ALA:HB3	2.18	0.43
2:B:357:LEU:HA	2:B:360:HIS:O	2.18	0.43
2:C:255:ALA:HB2	2:C:263:ARG:HE	1.81	0.43
2:C:338:GLU:HB3	2:D:333:LEU:CD2	2.48	0.43
2:D:188:GLU:HA	2:D:203:LEU:HD13	2.00	0.43
3:E:46:ARG:CA	3:E:68:MET:HE1	2.47	0.43
3:E:300:LEU:HD13	3:E:308:ARG:NH1	2.33	0.43
4:F:3:PHE:CG	4:F:42:LEU:HD22	2.53	0.43
4:G:6:GLU:CB	4:G:9:HIS:HB2	2.47	0.43
4:G:102:GLY:C	4:G:104:SER:H	2.26	0.43
4:G:175:HIS:HB2	4:G:323:TYR:CE2	2.53	0.43
1:A:12:GLN:HA	1:A:15:GLU:HG3	1.99	0.43
1:A:12:GLN:CB	1:A:135:VAL:HG21	2.48	0.43
1:A:158:LEU:HD12	1:A:158:LEU:N	2.33	0.43
2:B:60:LYS:HD3	2:B:79:CYS:HB3	2.00	0.43
2:C:84:GLN:HB3	2:C:86:ARG:HG2	2.00	0.43
2:C:358:ALA:HA	2:C:365:LEU:HD22	2.00	0.43
2:D:32:LEU:HG	2:D:58:LEU:CD1	2.47	0.43
2:D:298:SER:HB2	2:D:301:ALA:N	2.32	0.43
3:E:211:GLN:H	3:E:211:GLN:HG3	1.66	0.43
4:F:8:GLU:HG2	4:F:85:GLY:HA2	2.00	0.43
4:F:55:ALA:HB1	4:F:230:PHE:CE1	2.51	0.43
4:F:279:ARG:HD3	4:F:279:ARG:HA	1.87	0.43
4:G:139:ILE:HG22	4:G:204:MET:SD	2.59	0.43
4:G:336:VAL:HG23	4:G:350:GLU:O	2.18	0.43
1:A:150:TRP:C	1:A:150:TRP:CD2	2.95	0.43
2:B:94:ASP:CG	2:B:95:ALA:H	2.26	0.43
2:C:292:ILE:HG23	2:C:317:ALA:N	2.33	0.43
2:D:241:LEU:C	2:D:243:THR:H	2.25	0.43
3:E:19:GLN:HG3	3:E:52:GLN:NE2	2.33	0.43
3:E:149:GLU:HB2	3:E:150:ARG:NH1	2.34	0.43
3:E:245:LEU:HD11	3:E:300:LEU:HD12	2.01	0.43
3:E:254:ASP:HB3	3:E:265:VAL:CG1	2.46	0.43
4:F:145:SER:O	4:F:172:THR:C	2.61	0.43
4:F:217:GLN:OE1	4:F:226:HIS:CE1	2.72	0.43
4:G:315:MET:HB2	4:G:340:LEU:HD22	1.99	0.43
1:A:50:HIS:O	1:A:50:HIS:CG	2.71	0.43
1:A:223:MET:SD	1:A:225:LYS:HD3	2.58	0.43
2:B:129:HIS:HB2	2:B:161:LYS:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:137:ASN:HA	2:C:140:LEU:HG	2.00	0.43
2:C:279:GLU:HG2	2:C:339:LEU:HD22	1.99	0.43
2:C:360:HIS:HB3	2:C:363:MET:N	2.33	0.43
2:D:48:GLY:HA2	2:D:52:THR:OG1	2.19	0.43
2:D:332:LEU:HD21	2:D:356:ALA:CB	2.49	0.43
3:E:32:LEU:HG	3:E:146:ARG:CD	2.48	0.43
3:E:49:LEU:HD23	3:E:50:CYS:HA	2.00	0.43
3:E:180:VAL:HG23	3:E:187:LEU:HD21	2.01	0.43
3:E:224:VAL:HG22	3:E:229:TRP:CH2	2.53	0.43
4:F:3:PHE:HB3	4:F:59:LEU:HD21	1.99	0.43
4:F:27:LEU:O	4:F:30:LEU:HB2	2.19	0.43
4:G:256:LEU:CD2	4:G:310:TYR:CD1	3.02	0.43
1:A:9:LEU:HD21	1:A:38:VAL:HG23	1.99	0.43
1:A:196:LYS:HD3	1:A:196:LYS:HA	1.82	0.43
2:D:292:ILE:CG2	2:D:317:ALA:HA	2.48	0.43
3:E:18:TYR:HA	3:E:140:TRP:CH2	2.53	0.43
3:E:32:LEU:HD13	3:E:35:MET:HE2	1.98	0.43
4:F:343:SER:O	4:F:363:PRO:HG2	2.18	0.43
4:G:8:GLU:HG3	4:G:85:GLY:H	1.82	0.43
4:G:44:LEU:O	4:G:54:VAL:HA	2.19	0.43
4:G:137:ARG:HE	4:G:332:LYS:CG	2.31	0.43
4:G:145:SER:OG	4:G:176:ARG:HD2	2.18	0.43
4:G:211:ASP:CG	4:G:228:GLY:H	2.27	0.43
4:G:259:GLY:O	4:G:263:LEU:HB2	2.18	0.43
2:B:78:ASN:HA	2:B:81:GLU:OE1	2.19	0.43
2:C:250:LEU:HG	2:C:312:ARG:CZ	2.49	0.43
2:C:341:TYR:CD1	2:D:337:LYS:HB2	2.54	0.43
2:C:364:PRO:C	2:C:365:LEU:O	2.61	0.43
2:D:154:LEU:CD1	2:D:170:CYS:SG	3.07	0.43
2:D:322:PRO:O	2:D:326:GLN:HG2	2.19	0.43
3:E:31:ALA:HB2	3:E:164:LEU:O	2.19	0.43
3:E:240:GLN:O	3:E:241:ALA:C	2.60	0.43
4:F:61:GLN:H	4:F:61:GLN:HG3	1.61	0.43
4:F:95:GLU:OE1	4:F:112:PRO:HD3	2.19	0.43
4:F:254:LYS:HG2	4:F:312:GLY:HA3	2.00	0.43
4:G:132:GLN:HA	4:G:135:MET:HB3	2.00	0.43
4:G:132:GLN:CG	4:G:209:GLY:H	2.32	0.43
4:G:257:GLU:CD	4:G:337:ARG:HB2	2.43	0.43
4:G:295:ASN:OD1	4:G:301:GLU:HB3	2.19	0.43
4:G:337:ARG:HB3	4:G:350:GLU:OE1	2.18	0.43
1:A:68:CYS:SG	1:A:70:ALA:HB2	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:VAL:O	1:A:283:ARG:HG2	2.19	0.43
2:D:14:THR:C	2:D:57:LEU:HD21	2.44	0.43
2:D:111:VAL:HB	2:D:150:VAL:HG21	1.99	0.43
3:E:31:ALA:CA	3:E:164:LEU:O	2.67	0.43
3:E:71:GLY:C	3:E:73:HIS:N	2.77	0.43
4:F:136:LYS:HB3	4:F:204:MET:HE1	2.00	0.43
4:F:148:HIS:HA	4:F:197:ARG:NH1	2.34	0.43
4:G:135:MET:HG3	4:G:207:LEU:CD1	2.49	0.43
4:G:154:TYR:CE1	4:G:237:VAL:HG21	2.53	0.43
4:G:218:ILE:HA	4:G:223:ILE:HG22	2.01	0.43
1:A:5:TYR:HB3	1:A:8:GLN:OE1	2.19	0.43
1:A:270:ARG:HB3	1:A:283:ARG:HB3	1.99	0.43
2:C:174:HIS:CD2	2:C:176:LYS:HG2	2.54	0.43
2:C:360:HIS:HB3	2:C:363:MET:H	1.84	0.43
2:D:4:GLN:HG3	2:D:5:VAL:O	2.19	0.43
2:D:65:GLU:HG3	2:D:78:ASN:OD1	2.19	0.43
3:E:68:MET:HG2	3:E:76:TYR:HB2	2.00	0.43
4:F:13:PRO:CA	4:F:55:ALA:CB	2.96	0.43
4:F:200:VAL:O	4:F:203:LEU:HB3	2.19	0.43
4:F:223:ILE:HG22	4:F:236:LEU:HG	2.00	0.43
4:F:255:HIS:HB2	4:F:339:MET:CE	2.49	0.43
4:F:256:LEU:HD21	4:F:258:ALA:HB2	2.01	0.43
4:G:82:LEU:HA	4:G:82:LEU:HD23	1.76	0.43
1:A:73:LEU:HD12	4:F:175:HIS:H	1.79	0.42
1:A:78:GLN:N	1:A:107:ASP:HA	2.28	0.42
1:A:116:LYS:HD3	1:A:116:LYS:HA	1.85	0.42
1:A:192:TRP:HB3	1:A:193:PRO:HD2	2.01	0.42
1:A:211:HIS:CD2	1:A:213:THR:CA	3.02	0.42
1:A:220:ALA:O	1:A:225:LYS:HB2	2.19	0.42
1:A:228:ARG:HE	1:A:232:ILE:CG1	2.31	0.42
1:A:273:PHE:CZ	1:A:287:GLY:HA2	2.54	0.42
1:A:331:LEU:C	1:A:331:LEU:HD13	2.44	0.42
2:B:62:LEU:O	2:B:119:ARG:CD	2.67	0.42
2:B:62:LEU:HD13	2:B:120:PHE:CB	2.49	0.42
2:B:149:HIS:CD2	2:B:150:VAL:CG1	3.01	0.42
2:C:63:ASN:CB	2:C:119:ARG:H	2.32	0.42
2:C:75:VAL:O	2:C:76:CYS:SG	2.73	0.42
2:C:111:VAL:HG22	2:C:152:PHE:CE2	2.54	0.42
2:C:184:ARG:NH2	2:C:185:HIS:HA	2.34	0.42
2:C:278:TRP:CD1	2:C:345:ARG:CB	3.02	0.42
2:C:347:MET:SD	2:D:287:GLY:CA	2.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:235:GLN:HA	2:D:238:SER:OG	2.19	0.42
3:E:28:LEU:HD22	3:E:151:LEU:HD12	2.00	0.42
3:E:75:ASP:HB3	3:E:110:LYS:CA	2.45	0.42
3:E:236:LEU:HA	3:E:244:ARG:HB3	2.01	0.42
3:E:300:LEU:HD22	3:E:308:ARG:HG3	2.01	0.42
4:F:21:LEU:CD2	4:F:30:LEU:O	2.67	0.42
4:F:68:THR:CA	4:F:113:ALA:H	2.32	0.42
4:F:206:MET:SD	4:F:232:PHE:HB2	2.59	0.42
4:F:296:ASN:ND2	4:F:298:GLU:CD	2.77	0.42
4:G:159:LEU:HB2	4:G:241:PHE:HB2	1.99	0.42
1:A:231:HIS:CE1	1:A:235:GLN:HG2	2.54	0.42
2:B:47:ARG:HA	2:B:51:LYS:HZ2	1.83	0.42
2:C:80:ARG:O	2:C:83:GLU:HG2	2.19	0.42
2:C:89:ASP:HB3	2:C:122:VAL:H	1.83	0.42
2:C:121:LYS:HG2	2:C:123:TYR:CE1	2.54	0.42
2:C:138:ALA:HA	2:C:141:LYS:HE3	2.02	0.42
2:C:237:VAL:O	2:C:241:LEU:HG	2.19	0.42
3:E:31:ALA:HB2	3:E:164:LEU:HG	2.01	0.42
3:E:46:ARG:CB	3:E:58:SER:O	2.67	0.42
3:E:63:ARG:HA	3:E:66:GLN:CG	2.49	0.42
4:F:202:GLU:CG	4:F:232:PHE:CD2	3.02	0.42
4:F:337:ARG:CZ	4:F:337:ARG:HB3	2.49	0.42
4:G:275:ASN:HA	4:G:297:PRO:CD	2.48	0.42
1:A:39:ARG:HH22	1:A:81:LEU:HB2	1.84	0.42
2:B:50:GLY:CA	2:B:53:SER:OG	2.68	0.42
2:C:140:LEU:HA	2:C:166:ILE:HG21	2.01	0.42
2:C:267:LEU:HA	2:C:270:GLU:HB3	1.99	0.42
2:C:278:TRP:CZ2	2:C:346:ARG:HB2	2.54	0.42
2:D:199:GLU:HB3	2:D:232:VAL:HG12	2.00	0.42
2:D:344:ASP:O	2:D:347:MET:HB3	2.19	0.42
3:E:228:ASP:HA	3:E:320:GLU:OE1	2.19	0.42
4:F:211:ASP:CG	4:F:211:ASP:O	2.59	0.42
4:F:365:ARG:N	4:F:365:ARG:CD	2.82	0.42
4:G:132:GLN:HB3	4:G:207:LEU:CD2	2.41	0.42
4:G:146:MET:HA	4:G:156:ASN:HA	2.01	0.42
4:G:255:HIS:HA	4:G:338:MET:O	2.18	0.42
4:G:358:ALA:C	4:G:359:TYR:CG	2.98	0.42
1:A:90:ASN:H	1:A:93:ILE:HD12	1.85	0.42
1:A:273:PHE:CD1	1:A:286:MET:HG3	2.54	0.42
2:B:48:GLY:HA2	2:B:215:ARG:HB2	2.02	0.42
2:B:63:ASN:HA	2:B:119:ARG:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:181:GLU:HG3	2:B:182:GLN:N	2.34	0.42
2:D:258:GLU:HB2	2:D:260:ASN:CB	2.49	0.42
4:F:2:LYS:HB3	4:F:64:GLU:HB3	2.01	0.42
4:F:256:LEU:HD23	4:F:257:GLU:C	2.44	0.42
4:F:287:GLU:OE1	4:F:310:TYR:CD2	2.72	0.42
4:F:331:LEU:CD2	4:F:333:CYS:SG	3.07	0.42
4:G:37:VAL:HG12	4:G:39:ASP:N	2.33	0.42
4:G:53:MET:SD	4:G:230:PHE:CB	3.08	0.42
4:G:256:LEU:HD21	4:G:310:TYR:CE1	2.54	0.42
1:A:274:ASP:OD1	1:A:277:ARG:NH2	2.52	0.42
1:A:281:ASN:ND2	1:A:282:ARG:HG3	2.35	0.42
2:B:39:HIS:CE1	2:B:150:VAL:HG23	2.54	0.42
2:B:178:LEU:H	2:B:212:GLY:CA	2.32	0.42
2:B:179:ASP:H	2:B:182:GLN:CD	2.28	0.42
2:D:281:LEU:O	2:D:285:MET:SD	2.78	0.42
3:E:64:GLY:O	3:E:68:MET:HG3	2.20	0.42
3:E:230:TYR:HE1	3:E:313:THR:HG23	1.84	0.42
3:E:294:CYS:O	3:E:297:ARG:N	2.53	0.42
4:F:318:GLY:HA3	4:F:365:ARG:HA	2.01	0.42
4:F:325:LEU:O	4:F:329:ASN:CG	2.62	0.42
1:A:4:LEU:CD2	1:A:9:LEU:HA	2.49	0.42
1:A:117:LEU:HB2	1:A:122:GLU:HG3	2.01	0.42
1:A:261:LYS:HE3	1:A:294:SER:HA	2.01	0.42
2:B:49:VAL:HG23	2:B:51:LYS:HA	2.00	0.42
2:C:111:VAL:HG12	2:C:147:PRO:HG2	2.00	0.42
2:C:347:MET:O	2:C:351:MET:HB2	2.19	0.42
2:D:5:VAL:HA	2:D:222:ASP:OD2	2.19	0.42
3:E:47:TYR:CD2	3:E:52:GLN:HA	2.54	0.42
3:E:49:LEU:HD22	3:E:68:MET:SD	2.58	0.42
3:E:100:LEU:HD23	3:E:105:ARG:HH12	1.85	0.42
3:E:229:TRP:CE2	3:E:319:ILE:HG21	2.55	0.42
4:G:84:GLU:C	4:G:86:ALA:N	2.74	0.42
4:G:281:VAL:HG13	4:G:283:LEU:HD11	2.01	0.42
1:A:5:TYR:CG	1:A:6:PRO:HD2	2.54	0.42
1:A:74:PHE:HD2	4:F:174:GLY:HA2	1.85	0.42
1:A:165:ALA:HA	1:A:168:GLN:NE2	2.34	0.42
1:A:273:PHE:HB3	1:A:278:VAL:CB	2.48	0.42
2:B:61:GLY:HA2	2:B:64:CYS:SG	2.60	0.42
2:B:111:VAL:HG22	2:B:150:VAL:HG11	2.02	0.42
2:C:358:ALA:O	2:D:323:THR:HG22	2.20	0.42
2:D:180:VAL:HG13	2:D:181:GLU:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:35:MET:HE1	3:E:166:PRO:CA	2.50	0.42
3:E:41:ILE:HG22	3:E:113:TRP:CE3	2.54	0.42
3:E:49:LEU:HA	3:E:109:ALA:O	2.20	0.42
3:E:118:ALA:HB1	3:E:150:ARG:CB	2.44	0.42
3:E:220:LEU:CD1	3:E:224:VAL:HG23	2.50	0.42
4:F:162:THR:C	4:F:190:SER:HA	2.44	0.42
4:F:265:GLN:OE1	4:F:265:GLN:O	2.38	0.42
4:G:148:HIS:CE1	4:G:156:ASN:HB3	2.55	0.42
4:G:200:VAL:HA	4:G:203:LEU:HD12	2.02	0.42
4:G:351:ASP:OD1	4:G:351:ASP:N	2.52	0.42
1:A:25:GLY:HA3	1:A:139:CYS:HB2	2.02	0.42
2:B:312:ARG:HA	2:B:312:ARG:HE	1.85	0.42
2:C:252:LEU:CA	2:C:267:LEU:CD1	2.97	0.42
2:D:50:GLY:HA2	2:D:53:SER:HB2	2.02	0.42
2:D:148:GLU:O	2:D:150:VAL:HG23	2.19	0.42
2:D:219:SER:CB	3:E:157:SER:O	2.67	0.42
2:D:335:GLY:O	2:D:339:LEU:N	2.53	0.42
4:G:3:PHE:CD1	4:G:37:VAL:HG23	2.54	0.42
4:G:197:ARG:HG2	4:G:198:LYS:N	2.35	0.42
1:A:60:ASP:O	1:A:61:TRP:HB2	2.20	0.42
1:A:163:ASP:CG	1:A:165:ALA:HB3	2.45	0.42
1:A:164:ASP:OD1	1:A:167:ASN:HB3	2.19	0.42
1:A:228:ARG:HG2	1:A:228:ARG:HH11	1.84	0.42
1:A:273:PHE:HD2	1:A:283:ARG:C	2.28	0.42
1:A:273:PHE:CE2	1:A:287:GLY:CA	3.03	0.42
2:B:32:LEU:HA	2:B:37:ILE:CG2	2.50	0.42
2:B:63:ASN:ND2	2:B:89:ASP:HB2	2.35	0.42
2:B:126:ASP:CB	2:B:155:ALA:HB3	2.50	0.42
2:C:358:ALA:O	2:C:364:PRO:CB	2.68	0.42
2:D:2:SER:CB	3:E:25:HIS:HB3	2.50	0.42
2:D:64:CYS:SG	2:D:72:PRO:O	2.77	0.42
2:D:312:ARG:HA	2:D:315:GLU:OE2	2.20	0.42
2:D:320:ILE:HG22	2:D:324:ASP:HB2	2.02	0.42
3:E:177:SER:HB3	3:E:187:LEU:CD1	2.50	0.42
3:E:216:LEU:HD13	3:E:235:ALA:CB	2.49	0.42
4:F:11:LEU:O	4:F:14:LEU:HB2	2.20	0.42
4:F:192:SER:CB	4:F:240:ARG:HB3	2.50	0.42
4:F:255:HIS:HB3	4:F:311:SER:HB3	2.02	0.42
1:A:282:ARG:O	1:A:286:MET:HB2	2.20	0.42
2:B:18:VAL:CG1	2:B:214:LEU:CD2	2.98	0.42
2:B:344:ASP:O	2:B:348:GLY:N	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:65:GLU:OE2	2:D:65:GLU:HA	2.14	0.42
2:D:191:LEU:HG	2:D:198:HIS:HB3	2.01	0.42
3:E:30:GLN:O	3:E:147:GLU:HA	2.19	0.42
3:E:177:SER:HA	3:E:187:LEU:CD1	2.50	0.42
4:F:21:LEU:HD23	4:F:30:LEU:O	2.20	0.42
4:F:194:ILE:O	4:F:237:VAL:O	2.38	0.42
4:F:310:TYR:HE1	4:F:340:LEU:HD13	1.84	0.42
4:F:340:LEU:N	4:F:340:LEU:CD1	2.83	0.42
4:G:192:SER:O	4:G:236:LEU:HD13	2.20	0.42
1:A:77:ARG:HA	1:A:107:ASP:OD1	2.20	0.41
1:A:222:LEU:HB2	1:A:285:MET:HB3	2.01	0.41
1:A:231:HIS:CE1	1:A:235:GLN:NE2	2.81	0.41
1:A:278:VAL:HG12	1:A:283:ARG:HG2	2.02	0.41
2:C:125:ILE:HG22	2:C:126:ASP:N	2.35	0.41
2:C:257:VAL:C	2:C:259:ALA:H	2.28	0.41
2:C:359:PHE:CE1	2:D:323:THR:CA	3.02	0.41
2:D:60:LYS:HB3	2:D:72:PRO:HB2	2.02	0.41
2:D:216:ASP:O	2:D:217:ALA:C	2.61	0.41
3:E:29:ILE:HB	3:E:37:ASP:OD1	2.19	0.41
3:E:59:CYS:HB3	3:E:65:CYS:HB3	2.02	0.41
3:E:73:HIS:HB3	3:E:76:TYR:HB3	2.01	0.41
3:E:300:LEU:HD23	3:E:300:LEU:HA	1.88	0.41
4:F:22:GLY:C	4:F:24:ARG:N	2.78	0.41
4:F:53:MET:CE	4:F:206:MET:SD	3.08	0.41
4:F:120:ASP:HB3	4:F:222:ASN:CG	2.45	0.41
4:F:202:GLU:HG2	4:F:232:PHE:CD2	2.54	0.41
4:F:216:VAL:C	4:F:217:GLN:CG	2.93	0.41
4:F:236:LEU:HA	4:F:236:LEU:HD23	1.75	0.41
4:G:125:GLU:OE1	4:G:219:GLY:CA	2.68	0.41
1:A:161:GLU:CD	1:A:161:GLU:N	2.76	0.41
1:A:273:PHE:CD2	1:A:286:MET:HB3	2.54	0.41
1:A:293:LEU:HD22	1:A:331:LEU:O	2.20	0.41
2:B:60:LYS:N	2:B:82:ILE:HG21	2.36	0.41
2:B:120:PHE:O	2:B:122:VAL:HG23	2.19	0.41
2:B:193:GLU:C	2:B:195:HIS:H	2.28	0.41
3:E:30:GLN:CB	3:E:148:PRO:HD3	2.51	0.41
3:E:32:LEU:CD1	3:E:35:MET:HE3	2.50	0.41
3:E:219:ALA:C	3:E:232:LEU:HD21	2.45	0.41
3:E:224:VAL:HG12	3:E:280:HIS:ND1	2.35	0.41
3:E:303:VAL:HG11	3:E:306:ILE:HD13	2.02	0.41
4:F:10:LEU:HA	4:F:10:LEU:HD12	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:328:LEU:CB	4:F:329:ASN:OD1	2.68	0.41
4:G:90:VAL:O	4:G:90:VAL:HG23	2.20	0.41
1:A:51:HIS:CE1	1:A:78:GLN:CB	3.02	0.41
2:C:192:ASN:O	2:C:195:HIS:CD2	2.73	0.41
2:C:250:LEU:HG	2:C:312:ARG:NE	2.35	0.41
2:C:260:ASN:CB	2:C:263:ARG:HB2	2.50	0.41
2:C:327:LEU:O	2:C:330:GLN:HB3	2.20	0.41
2:D:352:THR:HA	2:D:355:ARG:HH21	1.85	0.41
3:E:171:TYR:CZ	3:E:175:TRP:HB2	2.55	0.41
3:E:325:PRO:C	3:E:327:VAL:H	2.27	0.41
4:F:160:PHE:O	4:F:192:SER:HA	2.20	0.41
4:F:184:ILE:CG2	4:F:186:GLN:HG3	2.51	0.41
4:G:125:GLU:CD	4:G:219:GLY:HA2	2.46	0.41
4:G:253:ASP:HA	4:G:339:MET:HE3	2.02	0.41
4:G:256:LEU:HB3	4:G:308:VAL:HG11	2.02	0.41
4:G:256:LEU:HB2	4:G:338:MET:HB2	2.02	0.41
1:A:26:ASN:HA	1:A:31:LEU:HD11	2.02	0.41
1:A:279:TRP:CB	1:A:281:ASN:OD1	2.68	0.41
2:B:65:GLU:HG3	2:B:78:ASN:HB2	2.02	0.41
2:B:125:ILE:O	2:B:154:LEU:HA	2.20	0.41
2:B:128:VAL:O	2:B:162:LEU:HD11	2.20	0.41
2:B:177:ALA:HB1	2:B:212:GLY:HA2	2.01	0.41
2:D:2:SER:C	3:E:25:HIS:HB3	2.43	0.41
2:D:23:HIS:CE1	2:D:176:LYS:HG2	2.55	0.41
3:E:32:LEU:CD2	3:E:200:ALA:HB2	2.51	0.41
3:E:33:PRO:CD	3:E:34:GLY:H	2.32	0.41
3:E:219:ALA:O	3:E:222:TYR:HB3	2.21	0.41
4:F:136:LYS:HA	4:F:139:ILE:HB	2.02	0.41
4:F:138:LEU:HG	4:F:182:MET:CG	2.50	0.41
4:F:181:SER:C	4:F:355:GLN:O	2.63	0.41
4:F:222:ASN:HA	4:F:234:SER:O	2.20	0.41
4:G:16:GLN:HG3	4:G:230:PHE:CZ	2.56	0.41
4:G:71:PRO:HB3	4:G:73:ARG:HH21	1.85	0.41
4:G:254:LYS:O	4:G:339:MET:HA	2.20	0.41
4:G:275:ASN:OD1	4:G:277:LYS:HE2	2.19	0.41
4:G:296:ASN:ND2	4:G:298:GLU:HB3	2.28	0.41
4:G:310:TYR:OH	4:G:342:ASP:HB3	2.21	0.41
1:A:51:HIS:CE1	1:A:78:GLN:HB2	2.52	0.41
1:A:279:TRP:O	1:A:283:ARG:CG	2.68	0.41
1:A:299:ARG:NH1	3:E:320:GLU:HB3	2.35	0.41
2:B:297:LEU:O	2:B:298:SER:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:166:ILE:HG22	2:C:169:ARG:HH12	1.85	0.41
2:C:278:TRP:CD2	2:C:346:ARG:HA	2.56	0.41
2:C:286:LEU:CD2	2:C:329:TYR:O	2.69	0.41
2:D:3:TYR:CD1	2:D:3:TYR:C	2.94	0.41
3:E:9:PRO:HA	3:E:12:GLU:OE2	2.20	0.41
3:E:166:PRO:HB3	3:E:197:SER:HA	2.02	0.41
3:E:244:ARG:CD	3:E:247:TRP:CZ3	3.03	0.41
4:F:340:LEU:HA	4:F:347:VAL:HG12	2.01	0.41
4:G:206:MET:HB2	4:G:227:VAL:HG21	2.01	0.41
2:B:314:ARG:O	2:B:318:ARG:HG3	2.21	0.41
2:C:78:ASN:O	2:C:82:ILE:HG13	2.21	0.41
2:D:3:TYR:CD1	2:D:4:GLN:N	2.88	0.41
2:D:75:VAL:HA	2:D:80:ARG:HG2	2.03	0.41
2:D:255:ALA:O	2:D:260:ASN:HB3	2.21	0.41
2:D:321:PRO:HA	2:D:322:PRO:HD3	1.86	0.41
3:E:48:LEU:HD23	3:E:52:GLN:CD	2.46	0.41
3:E:176:LEU:O	3:E:180:VAL:HG22	2.20	0.41
4:F:130:LEU:HD23	4:F:131:PRO:HD2	2.03	0.41
4:G:6:GLU:HA	4:G:87:GLU:OE1	2.21	0.41
1:A:55:ILE:HG22	1:A:85:PRO:HD3	2.03	0.41
1:A:158:LEU:HD12	1:A:158:LEU:H	1.86	0.41
2:B:269:ASN:HA	2:B:346:ARG:NH2	2.35	0.41
2:C:129:HIS:HB2	2:C:161:LYS:HE2	2.01	0.41
2:C:227:SER:HA	2:D:27:ALA:CA	2.50	0.41
2:D:23:HIS:O	2:D:27:ALA:CB	2.67	0.41
2:D:198:HIS:HD2	2:D:203:LEU:HD11	1.84	0.41
2:D:339:LEU:HG	2:D:340:PRO:N	2.35	0.41
3:E:18:TYR:O	3:E:140:TRP:CH2	2.74	0.41
3:E:50:CYS:HB2	3:E:53:PRO:HD3	2.02	0.41
3:E:229:TRP:HE1	3:E:323:LEU:HD11	1.86	0.41
4:F:5:VAL:HG21	4:F:10:LEU:HD13	2.01	0.41
4:F:223:ILE:HG22	4:F:234:SER:O	2.21	0.41
4:F:253:ASP:CG	4:F:254:LYS:N	2.79	0.41
4:F:354:SER:C	4:F:356:SER:N	2.79	0.41
4:G:193:VAL:CG2	4:G:223:ILE:CG2	2.99	0.41
4:G:331:LEU:HD12	4:G:331:LEU:HA	1.78	0.41
1:A:170:LEU:HD22	1:A:174:TYR:HE2	1.85	0.41
1:A:220:ALA:O	1:A:223:MET:HB2	2.21	0.41
1:A:272:LEU:HD23	1:A:272:LEU:H	1.86	0.41
1:A:273:PHE:HB3	1:A:278:VAL:CG1	2.51	0.41
2:B:277:GLU:O	2:B:281:LEU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:180:VAL:O	2:C:184:ARG:HB2	2.21	0.41
2:D:6:LEU:O	2:D:10:TRP:CD1	2.74	0.41
2:D:293:ALA:O	2:D:296:GLN:HB2	2.20	0.41
3:E:1:MET:N	3:E:33:PRO:O	2.48	0.41
3:E:30:GLN:HG3	3:E:147:GLU:OE2	2.21	0.41
3:E:32:LEU:HD12	3:E:147:GLU:OE1	2.21	0.41
3:E:121:THR:O	3:E:124:ALA:HB3	2.20	0.41
3:E:169:GLU:CD	3:E:169:GLU:N	2.78	0.41
3:E:242:PRO:HG3	3:E:301:MET:SD	2.61	0.41
4:F:59:LEU:HD11	4:F:61:GLN:O	2.21	0.41
4:F:122:TRP:HE1	4:F:219:GLY:HA3	1.82	0.41
4:F:152:ARG:HB2	4:F:155:LEU:CD1	2.50	0.41
4:G:146:MET:HE3	4:G:197:ARG:HA	2.03	0.41
4:G:176:ARG:O	4:G:176:ARG:HG3	2.21	0.41
4:G:206:MET:HG3	4:G:227:VAL:CG2	2.50	0.41
4:G:355:GLN:HE21	4:G:358:ALA:HB2	1.86	0.41
1:A:9:LEU:HD13	1:A:137:VAL:CG2	2.51	0.41
1:A:55:ILE:HG12	1:A:93:ILE:CG2	2.50	0.41
1:A:160:LEU:H	1:A:160:LEU:HG	1.71	0.41
1:A:270:ARG:HA	1:A:273:PHE:HB2	2.02	0.41
1:A:309:GLU:HG2	3:E:310:LEU:CD2	2.51	0.41
2:B:60:LYS:O	2:B:64:CYS:N	2.54	0.41
2:C:64:CYS:SG	2:C:79:CYS:SG	3.16	0.41
2:C:65:GLU:HB2	2:C:76:CYS:HB2	2.03	0.41
2:C:265:MET:CB	2:D:301:ALA:HB1	2.51	0.41
2:C:293:ALA:HA	2:C:296:GLN:OE1	2.21	0.41
2:C:295:VAL:HG11	2:C:314:ARG:HA	2.02	0.41
2:C:341:TYR:CD2	2:C:341:TYR:N	2.88	0.41
2:C:365:LEU:HD13	2:C:365:LEU:HA	1.77	0.41
2:D:23:HIS:H	2:D:23:HIS:HD1	1.69	0.41
2:D:41:TYR:CE1	2:D:171:LEU:HD12	2.56	0.41
2:D:69:THR:CB	2:D:73:CYS:SG	3.09	0.41
2:D:293:ALA:HB2	2:D:325:ILE:CG2	2.51	0.41
2:D:299:PRO:O	2:D:314:ARG:NH2	2.54	0.41
3:E:7:LEU:HA	3:E:10:ASP:OD2	2.20	0.41
3:E:10:ASP:HA	3:E:162:HIS:NE2	2.36	0.41
3:E:14:LEU:O	3:E:18:TYR:CD2	2.73	0.41
3:E:14:LEU:HD11	3:E:162:HIS:CG	2.55	0.41
3:E:29:ILE:HA	3:E:162:HIS:O	2.21	0.41
3:E:31:ALA:N	3:E:164:LEU:O	2.54	0.41
3:E:42:TYR:HB2	3:E:113:TRP:CH2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:46:ARG:HA	3:E:68:MET:SD	2.61	0.41
3:E:62:CYS:HB2	3:E:65:CYS:H	1.85	0.41
3:E:67:LEU:O	3:E:73:HIS:HB2	2.21	0.41
3:E:118:ALA:CA	3:E:150:ARG:HB3	2.51	0.41
3:E:118:ALA:HA	3:E:150:ARG:HB3	2.03	0.41
3:E:213:ARG:O	3:E:217:CYS:SG	2.75	0.41
3:E:318:ARG:HG2	3:E:322:TYR:CE2	2.55	0.41
4:F:12:LYS:HB3	4:F:13:PRO:HD3	2.02	0.41
4:F:21:LEU:HD11	4:F:46:GLY:C	2.46	0.41
4:F:182:MET:HB3	4:F:182:MET:HE3	1.93	0.41
4:F:193:VAL:CG2	4:F:238:ASP:HA	2.51	0.41
4:F:206:MET:O	4:F:227:VAL:HG21	2.21	0.41
4:F:250:LYS:H	4:F:345:SER:HB3	1.86	0.41
4:F:257:GLU:CG	4:F:337:ARG:HA	2.51	0.41
4:F:264:LYS:HG3	4:F:325:LEU:HD12	2.02	0.41
4:F:282:ARG:HH21	4:F:318:GLY:H	1.68	0.41
4:F:323:TYR:HA	4:F:326:ASP:OD2	2.20	0.41
4:G:141:ALA:O	4:G:144:PHE:CE2	2.74	0.41
4:G:158:MET:CA	4:G:241:PHE:CE2	3.04	0.41
4:G:162:THR:HB	4:G:164:GLY:O	2.20	0.41
4:G:180:CYS:HA	4:G:356:SER:O	2.20	0.41
4:G:193:VAL:CG1	4:G:223:ILE:HG21	2.51	0.41
4:G:254:LYS:HB2	4:G:340:LEU:HG	2.03	0.41
4:G:318:GLY:O	4:G:363:PRO:HA	2.20	0.41
1:A:192:TRP:HB3	1:A:193:PRO:CD	2.51	0.41
1:A:211:HIS:CD2	1:A:213:THR:N	2.89	0.41
2:B:48:GLY:O	2:B:214:LEU:HB3	2.21	0.41
2:B:119:ARG:N	2:B:119:ARG:HD2	2.36	0.41
2:C:84:GLN:HB2	2:C:86:ARG:HG2	2.03	0.41
2:C:111:VAL:HG12	2:C:147:PRO:CG	2.51	0.41
2:C:279:GLU:OE2	2:C:339:LEU:HB2	2.20	0.41
2:C:324:ASP:HB3	2:C:328:TYR:CE2	2.56	0.41
2:D:57:LEU:HA	2:D:57:LEU:HD23	1.88	0.41
2:D:62:LEU:C	2:D:64:CYS:H	2.29	0.41
2:D:123:TYR:CD2	2:D:150:VAL:HG13	2.56	0.41
2:D:296:GLN:HG2	2:D:317:ALA:C	2.45	0.41
3:E:30:GLN:HA	3:E:148:PRO:HD3	2.03	0.41
3:E:41:ILE:CG2	3:E:113:TRP:CE3	3.04	0.41
3:E:316:LEU:O	3:E:320:GLU:CG	2.69	0.41
4:F:41:THR:HG22	4:F:42:LEU:N	2.36	0.41
4:F:140:GLU:OE1	4:F:332:LYS:CE	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:192:SER:HB2	4:F:240:ARG:HB3	2.02	0.41
4:F:328:LEU:HA	4:F:328:LEU:HD12	1.84	0.41
4:G:90:VAL:HG21	4:G:97:MET:HE1	2.03	0.41
4:G:143:GLN:O	4:G:146:MET:HG2	2.21	0.41
4:G:250:LYS:O	4:G:341:THR:CG2	2.69	0.41
1:A:20:ALA:CB	1:A:130:LEU:HD22	2.52	0.40
1:A:87:ASN:O	1:A:117:LEU:HA	2.21	0.40
1:A:269:LEU:C	1:A:270:ARG:CG	2.93	0.40
2:B:120:PHE:CE1	2:B:148:GLU:OE2	2.74	0.40
2:C:79:CYS:HA	2:C:82:ILE:HD12	2.03	0.40
2:D:99:THR:HA	2:D:131:LEU:HA	2.02	0.40
3:E:46:ARG:HB3	3:E:58:SER:O	2.20	0.40
3:E:257:LYS:HB3	3:E:262:ALA:HB3	2.03	0.40
3:E:320:GLU:O	3:E:324:GLN:NE2	2.47	0.40
4:G:249:PRO:HD2	4:G:252:PRO:HB3	2.02	0.40
4:G:288:ASN:HA	4:G:308:VAL:O	2.21	0.40
1:A:84:LEU:HD22	1:A:89:PRO:HG3	2.02	0.40
2:C:265:MET:SD	2:D:302:LEU:HA	2.61	0.40
2:C:281:LEU:O	2:C:285:MET:HG3	2.20	0.40
2:C:351:MET:HG2	2:D:329:TYR:CE1	2.56	0.40
2:D:69:THR:HB	2:D:71:THR:O	2.21	0.40
2:D:258:GLU:HB2	2:D:260:ASN:HB3	2.04	0.40
2:D:290:HIS:NE2	2:D:294:MET:HG3	2.36	0.40
3:E:32:LEU:HB2	3:E:35:MET:H	1.87	0.40
3:E:177:SER:HA	3:E:187:LEU:HD11	2.02	0.40
3:E:275:ALA:O	3:E:279:ASN:HB2	2.21	0.40
4:F:4:THR:O	4:F:61:GLN:HB2	2.21	0.40
4:F:51:MET:CE	4:F:202:GLU:HG2	2.51	0.40
4:F:103:ARG:HB2	4:G:305:ILE:HB	2.03	0.40
4:F:143:GLN:HA	4:F:158:MET:HE1	2.03	0.40
4:F:220:SER:O	4:F:236:LEU:HB2	2.21	0.40
4:F:285:VAL:O	4:F:285:VAL:HG22	2.21	0.40
4:F:333:CYS:SG	4:F:336:VAL:HB	2.62	0.40
4:G:219:GLY:O	4:G:236:LEU:HD11	2.21	0.40
4:G:333:CYS:SG	4:G:351:ASP:CB	3.09	0.40
4:G:344:VAL:H	4:G:344:VAL:HG23	1.63	0.40
1:A:45:GLN:O	1:A:47:PHE:CD1	2.74	0.40
1:A:163:ASP:CG	1:A:166:ALA:H	2.29	0.40
2:C:43:PHE:CD1	2:C:173:PHE:HB2	2.56	0.40
2:D:198:HIS:CD2	2:D:203:LEU:HD11	2.56	0.40
2:D:332:LEU:HD21	2:D:356:ALA:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:135:MET:O	4:F:139:ILE:HG12	2.21	0.40
4:F:202:GLU:CB	4:F:205:ARG:HH21	2.31	0.40
4:F:228:GLY:C	4:F:230:PHE:N	2.77	0.40
4:F:255:HIS:NE2	4:F:257:GLU:N	2.70	0.40
4:G:57:VAL:CG1	4:G:59:LEU:HB3	2.52	0.40
4:G:137:ARG:HA	4:G:140:GLU:OE1	2.21	0.40
4:G:139:ILE:HD12	4:G:207:LEU:HD12	2.02	0.40
1:A:219:ASP:OD1	1:A:222:LEU:HD12	2.22	0.40
2:B:115:PRO:HG3	2:B:121:LYS:H	1.86	0.40
2:B:159:PRO:HA	2:B:162:LEU:HD13	2.04	0.40
2:B:310:GLU:O	2:B:314:ARG:HB2	2.21	0.40
2:C:238:SER:O	2:C:242:GLY:N	2.54	0.40
2:C:354:LEU:O	2:C:358:ALA:HB2	2.21	0.40
2:D:121:LYS:HG3	2:D:123:TYR:CE2	2.56	0.40
3:E:14:LEU:HD22	3:E:18:TYR:OH	2.22	0.40
4:F:127:GLU:HG2	4:F:217:GLN:HA	2.01	0.40
4:F:220:SER:N	4:F:236:LEU:HD12	2.36	0.40
4:F:254:LYS:HA	4:F:311:SER:O	2.21	0.40
4:F:331:LEU:HD11	4:F:351:ASP:CG	2.47	0.40
4:G:8:GLU:O	4:G:11:LEU:HB3	2.22	0.40
4:G:53:MET:CE	4:G:206:MET:HE3	2.51	0.40
4:G:139:ILE:HD12	4:G:204:MET:HA	2.03	0.40
4:G:267:PHE:CB	4:G:325:LEU:HD21	2.52	0.40
4:G:319:PHE:HA	4:G:364:MET:SD	2.61	0.40
1:A:228:ARG:HE	1:A:232:ILE:HG12	1.86	0.40
2:B:64:CYS:O	2:B:119:ARG:CZ	2.69	0.40
2:B:322:PRO:O	2:B:325:ILE:HB	2.21	0.40
2:C:106:ASP:HA	2:C:109:ASP:OD2	2.22	0.40
2:D:29:ALA:O	2:D:70:ALA:HA	2.22	0.40
2:D:39:HIS:O	2:D:152:PHE:N	2.55	0.40
2:D:202:ALA:HA	2:D:205:LEU:CG	2.51	0.40
2:D:291:ARG:HD3	2:D:291:ARG:HA	1.72	0.40
2:D:292:ILE:O	2:D:295:VAL:HB	2.21	0.40
2:D:306:MET:HB2	2:D:313:MET:SD	2.62	0.40
3:E:50:CYS:O	3:E:51:GLN:CB	2.70	0.40
3:E:59:CYS:HB3	3:E:65:CYS:CB	2.51	0.40
3:E:171:TYR:HE1	3:E:178:ARG:HH12	1.67	0.40
3:E:250:THR:CB	3:E:267:ASN:OD1	2.70	0.40
3:E:295:HIS:O	3:E:298:GLU:HB2	2.21	0.40
4:F:12:LYS:O	4:F:15:GLN:CG	2.70	0.40
4:F:24:ARG:NH1	4:F:72:ALA:H	2.19	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:132:GLN:HA	4:F:214:LEU:HD11	2.04	0.40
4:F:137:ARG:NE	4:F:332:LYS:HE3	2.29	0.40
4:F:225:ALA:O	4:F:231:ILE:HG23	2.21	0.40
4:G:136:LYS:CD	4:G:208:ASP:HA	2.51	0.40
4:G:331:LEU:CG	4:G:333:CYS:HB3	2.52	0.40
4:G:348:GLN:CG	4:G:349:ILE:N	2.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	A	341/343 (99%)	295 (86%)	26 (8%)	20 (6%)	1	13
2	B	358/376 (95%)	323 (90%)	24 (7%)	11 (3%)	3	22
2	C	363/376 (96%)	331 (91%)	24 (7%)	8 (2%)	5	29
2	D	357/376 (95%)	313 (88%)	34 (10%)	10 (3%)	4	24
3	E	332/337 (98%)	291 (88%)	26 (8%)	15 (4%)	2	17
4	F	364/369 (99%)	308 (85%)	41 (11%)	15 (4%)	2	18
4	G	364/369 (99%)	297 (82%)	53 (15%)	14 (4%)	2	19
All	All	2479/2546 (97%)	2158 (87%)	228 (9%)	93 (4%)	4	19

All (93) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	SER
1	A	76	SER
1	A	213	THR
1	A	265	ALA
1	A	270	ARG

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Mol	Chain	Res	Type
1	A	278	VAL
1	A	338	ASP
2	B	112	GLN
2	B	129	HIS
2	C	129	HIS
2	D	3	TYR
2	D	87	PHE
3	E	51	GLN
3	E	62	CYS
3	E	182	MET
3	E	183	SER
3	E	270	VAL
4	F	49	LEU
4	F	51	MET
4	F	116	PHE
4	F	153	TYR
4	F	248	LEU
4	F	343	SER
4	G	39	ASP
4	G	126	VAL
4	G	208	ASP
4	G	243	ASP
4	G	343	SER
4	G	344	VAL
1	A	68	CYS
1	A	128	THR
1	A	162	LEU
1	A	333	HIS
2	B	21	GLN
2	C	33	SER
2	C	91	ILE
2	C	96	ALA
2	C	344	ASP
2	D	74	GLY
2	D	86	ARG
2	D	120	PHE
2	D	149	HIS
3	E	333	HIS
4	F	103	ARG
4	G	2	LYS
4	G	196	PRO
1	A	266	HIS

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Mol	Chain	Res	Type
2	B	117	ARG
2	D	50	GLY
2	D	117	ARG
3	E	31	ALA
3	E	72	THR
3	E	106	LEU
3	E	164	LEU
4	F	23	GLY
4	F	150	ASP
4	F	211	ASP
4	F	242	PRO
4	G	28	PRO
4	G	118	ASN
4	G	253	ASP
1	A	67	LEU
2	B	17	ASP
2	B	95	ALA
2	B	115	PRO
2	B	275	GLY
2	C	5	VAL
2	C	149	HIS
2	D	231	GLN
3	E	52	GLN
3	E	56	HIS
3	E	261	GLY
4	F	187	SER
4	G	365	ARG
1	A	19	ALA
1	A	60	ASP
1	A	86	GLU
1	A	193	PRO
2	B	36	ARG
2	B	298	SER
2	D	47	ARG
4	F	278	PHE
4	G	65	PRO
1	A	61	TRP
1	A	163	ASP
2	B	86	ARG
2	C	141	LYS
3	E	79	LEU
4	F	183	PRO

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Mol	Chain	Res	Type
4	G	176	ARG
3	E	225	PRO
4	F	19	GLY
1	A	334	LYS

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	A	291/291 (100%)	272 (94%)	19 (6%)	15	37
2	B	296/312 (95%)	277 (94%)	19 (6%)	16	37
2	C	301/312 (96%)	280 (93%)	21 (7%)	14	35
2	D	294/312 (94%)	266 (90%)	28 (10%)	8	25
3	E	270/272 (99%)	251 (93%)	19 (7%)	14	35
4	F	313/315 (99%)	277 (88%)	36 (12%)	5	18
4	G	313/315 (99%)	272 (87%)	41 (13%)	4	15
All	All	2078/2129 (98%)	1895 (91%)	183 (9%)	11	28

All (183) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	58	ASN
1	A	79	THR
1	A	86	GLU
1	A	128	THR
1	A	141	THR
1	A	148	PRO
1	A	162	LEU
1	A	167	ASN
1	A	186	GLU
1	A	203	GLU
1	A	217	TRP
1	A	228	ARG

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Mol	Chain	Res	Type
1	A	258	VAL
1	A	315	ASP
1	A	331	LEU
1	A	332	CYS
1	A	338	ASP
1	A	341	ILE
2	B	1	MET
2	B	14	THR
2	B	57	LEU
2	B	60	LYS
2	B	64	CYS
2	B	66	THR
2	B	71	THR
2	B	126	ASP
2	B	129	HIS
2	B	130	MET
2	B	140	LEU
2	B	161	LYS
2	B	180	VAL
2	B	181	GLU
2	B	208	ARG
2	B	246	ASP
2	B	269	ASN
2	B	304	ASN
2	B	344	ASP
2	C	51	LYS
2	C	54	ILE
2	C	66	THR
2	C	75	VAL
2	C	94	ASP
2	C	100	LYS
2	C	124	LEU
2	C	128	VAL
2	C	141	LYS
2	C	179	ASP
2	C	208	ARG
2	C	243	THR
2	C	253	VAL
2	C	257	VAL
2	C	262	GLU
2	C	270	GLU
2	C	276	ILE

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Mol	Chain	Res	Type
2	C	339	LEU
2	C	344	ASP
2	C	360	HIS
2	C	363	MET
2	D	12	PRO
2	D	33	SER
2	D	39	HIS
2	D	44	SER
2	D	46	THR
2	D	69	THR
2	D	73	CYS
2	D	75	VAL
2	D	86	ARG
2	D	104	THR
2	D	109	ASP
2	D	119	ARG
2	D	125	ILE
2	D	180	VAL
2	D	185	HIS
2	D	188	GLU
2	D	189	HIS
2	D	196	ILE
2	D	206	LEU
2	D	213	SER
2	D	223	GLN
2	D	253	VAL
2	D	309	ILE
2	D	310	GLU
2	D	318	ARG
2	D	339	LEU
2	D	341	TYR
2	D	353	LEU
3	E	13	LYS
3	E	15	VAL
3	E	41	ILE
3	E	49	LEU
3	E	51	GLN
3	E	65	CYS
3	E	105	ARG
3	E	110	LYS
3	E	126	ASN
3	E	147	GLU

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Mol	Chain	Res	Type
3	E	158	ARG
3	E	202	LEU
3	E	218	GLN
3	E	222	TYR
3	E	293	VAL
3	E	298	GLU
3	E	304	THR
3	E	310	LEU
3	E	317	LEU
4	F	5	VAL
4	F	27	LEU
4	F	61	GLN
4	F	62	PRO
4	F	64	GLU
4	F	69	THR
4	F	71	PRO
4	F	123	GLN
4	F	130	LEU
4	F	134	THR
4	F	139	ILE
4	F	144	PHE
4	F	162	THR
4	F	170	VAL
4	F	189	PRO
4	F	193	VAL
4	F	195	VAL
4	F	220	SER
4	F	255	HIS
4	F	276	GLU
4	F	283	LEU
4	F	285	VAL
4	F	286	SER
4	F	309	THR
4	F	315	MET
4	F	322	SER
4	F	328	LEU
4	F	329	ASN
4	F	334	GLU
4	F	340	LEU
4	F	342	ASP
4	F	349	ILE
4	F	354	SER

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Mol	Chain	Res	Type
4	F	356	SER
4	F	364	MET
4	F	366	LEU
4	G	4	THR
4	G	13	PRO
4	G	27	LEU
4	G	34	LEU
4	G	51	MET
4	G	57	VAL
4	G	59	LEU
4	G	69	THR
4	G	87	GLU
4	G	120	ASP
4	G	122	TRP
4	G	125	GLU
4	G	130	LEU
4	G	132	GLN
4	G	134	THR
4	G	138	LEU
4	G	165	GLU
4	G	170	VAL
4	G	176	ARG
4	G	179	VAL
4	G	182	MET
4	G	190	SER
4	G	196	PRO
4	G	202	GLU
4	G	208	ASP
4	G	221	ASN
4	G	227	VAL
4	G	253	ASP
4	G	256	LEU
4	G	261	ASP
4	G	262	LEU
4	G	300	GLU
4	G	309	THR
4	G	321	VAL
4	G	326	ASP
4	G	327	VAL
4	G	340	LEU
4	G	341	THR
4	G	342	ASP

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Mol	Chain	Res	Type
4	G	351	ASP
4	G	355	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	50	HIS
1	A	51	HIS
1	A	69	GLN
1	A	78	GLN
1	A	105	HIS
1	A	144	GLN
1	A	146	GLN
1	A	157	GLN
1	A	167	ASN
1	A	168	GLN
1	A	231	HIS
1	A	234	GLN
1	A	235	GLN
1	A	266	HIS
1	A	276	HIS
1	A	300	GLN
1	A	333	HIS
2	B	38	HIS
2	B	112	GLN
2	B	172	GLN
2	B	174	HIS
2	B	248	GLN
2	B	326	GLN
2	C	21	GLN
2	C	23	HIS
2	C	129	HIS
2	C	149	HIS
2	C	174	HIS
2	C	182	GLN
2	C	189	HIS
2	C	223	GLN
2	C	235	GLN
2	C	269	ASN
2	D	4	GLN
2	D	78	ASN

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Mol	Chain	Res	Type
2	D	182	GLN
2	D	186	GLN
2	D	195	HIS
2	D	198	HIS
2	D	204	GLN
3	E	52	GLN
3	E	54	GLN
3	E	61	HIS
3	E	162	HIS
3	E	295	HIS
3	E	321	HIS
4	F	148	HIS
4	F	149	GLN
4	F	217	GLN
4	F	226	HIS
4	F	335	ASN
4	F	348	GLN
4	G	15	GLN
4	G	16	GLN
4	G	61	GLN
4	G	118	ASN
4	G	149	GLN
4	G	191	HIS
4	G	226	HIS
4	G	265	GLN
4	G	275	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43096. These allow visual inspection of the internal detail of the map and identification of artifacts.

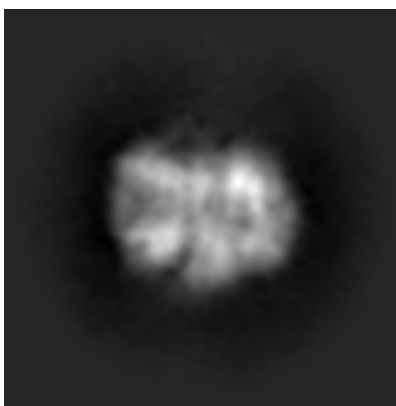
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

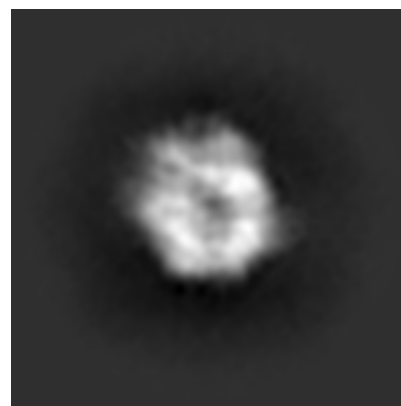
6.1.1 Primary map



X

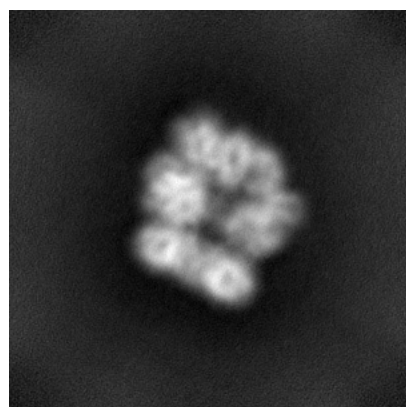


Y

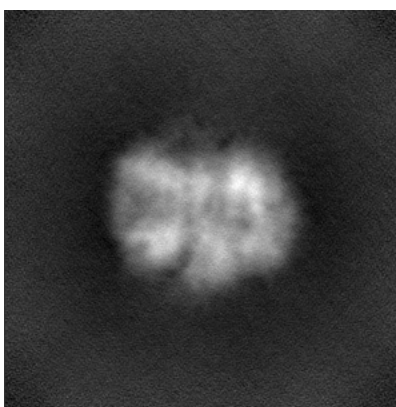


Z

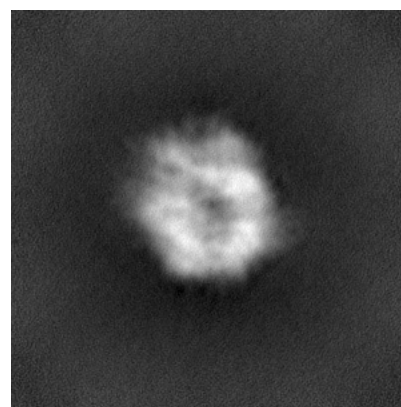
6.1.2 Raw map



X



Y

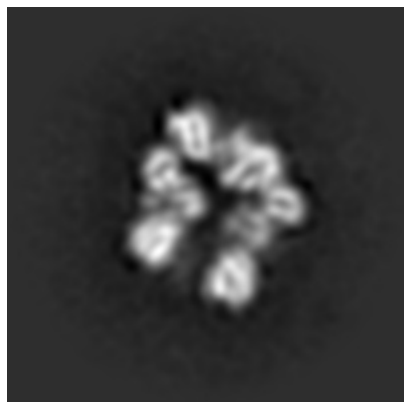


Z

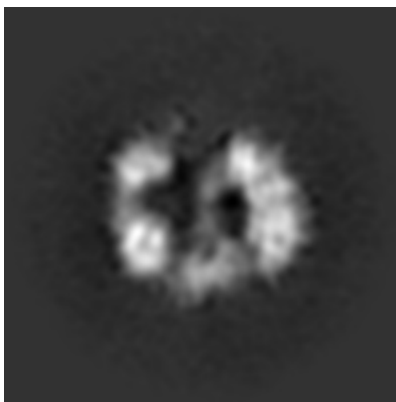
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150

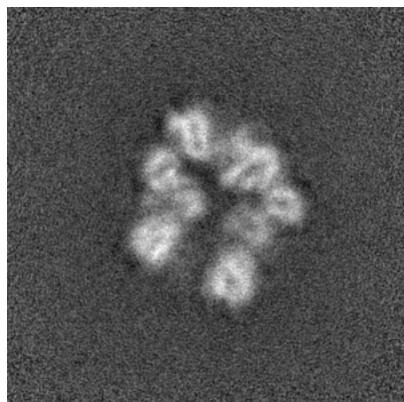


Y Index: 150

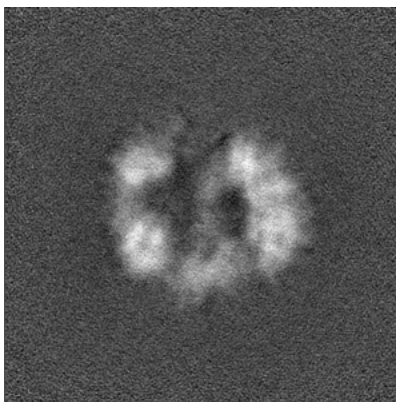


Z Index: 150

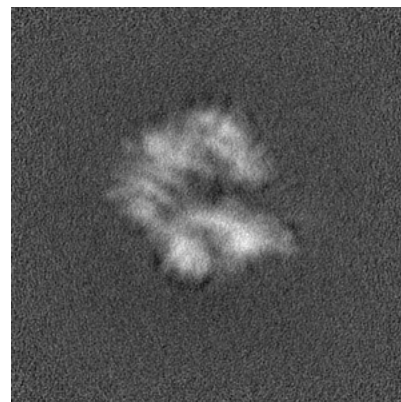
6.2.2 Raw map



X Index: 150



Y Index: 150

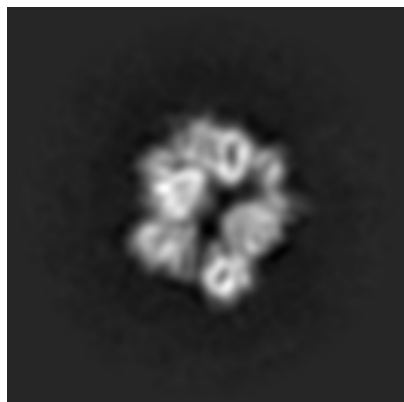


Z Index: 150

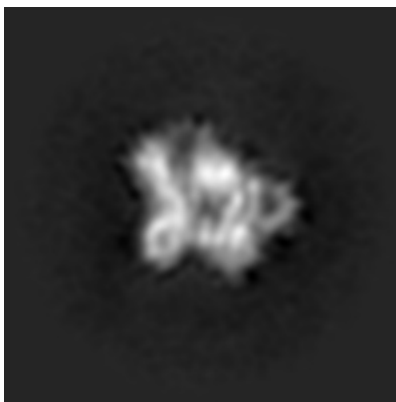
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

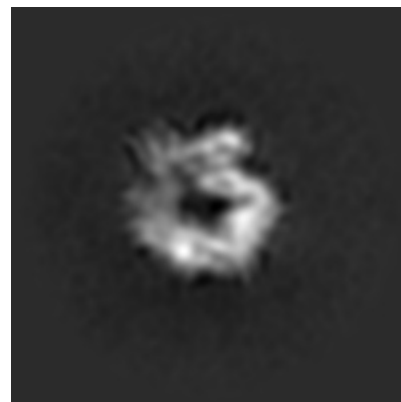
6.3.1 Primary map



X Index: 170

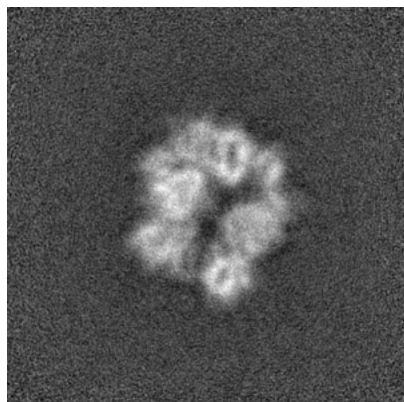


Y Index: 122

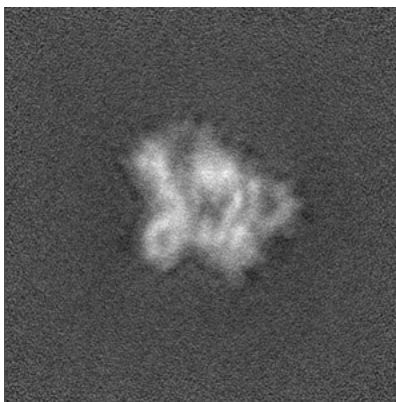


Z Index: 173

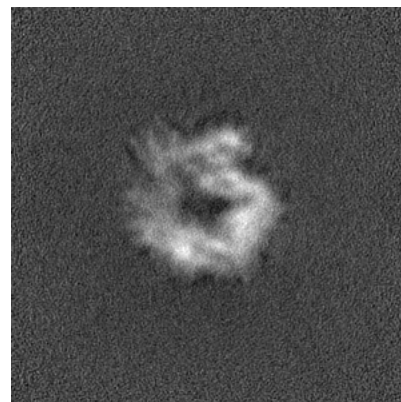
6.3.2 Raw map



X Index: 169



Y Index: 122

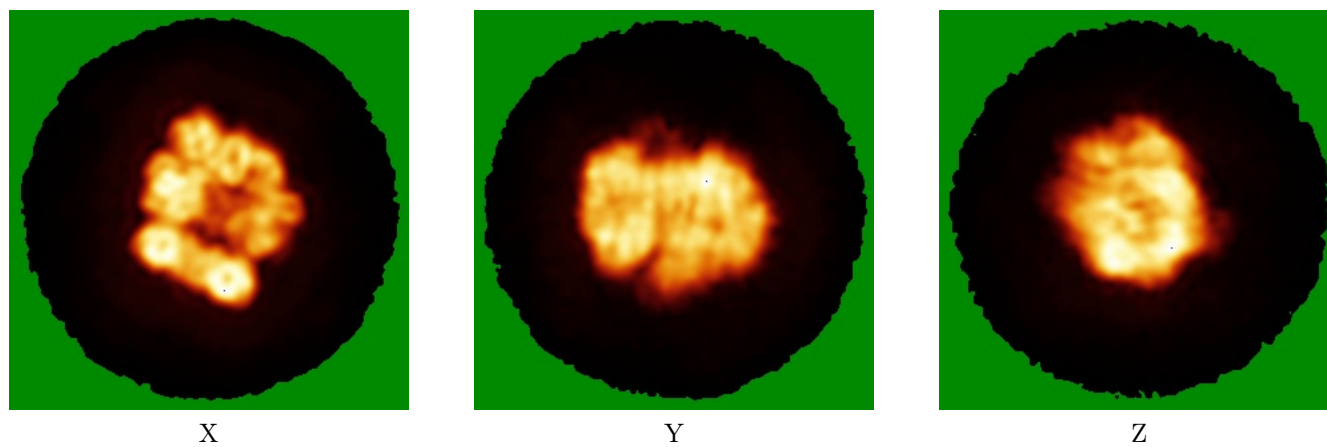


Z Index: 173

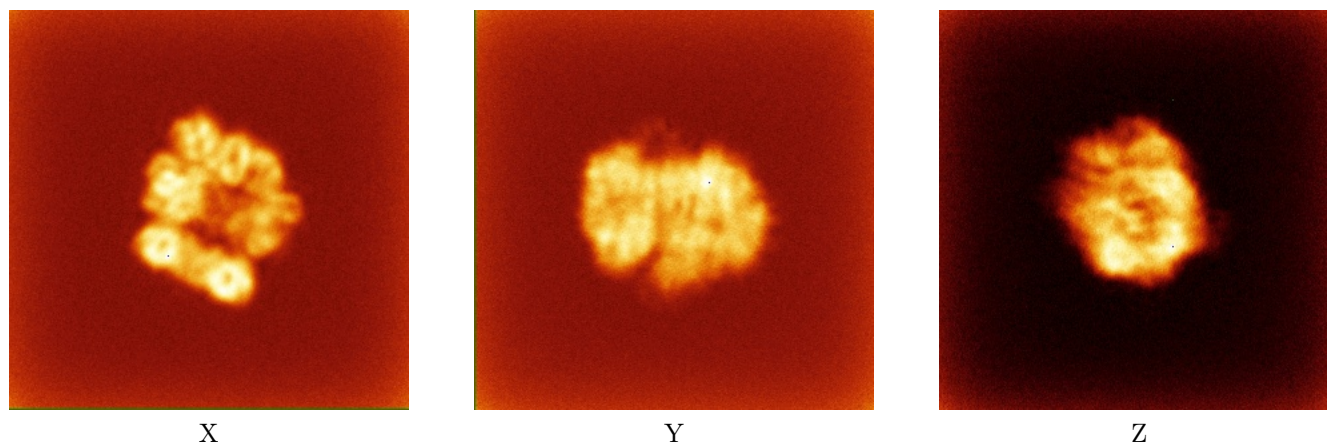
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

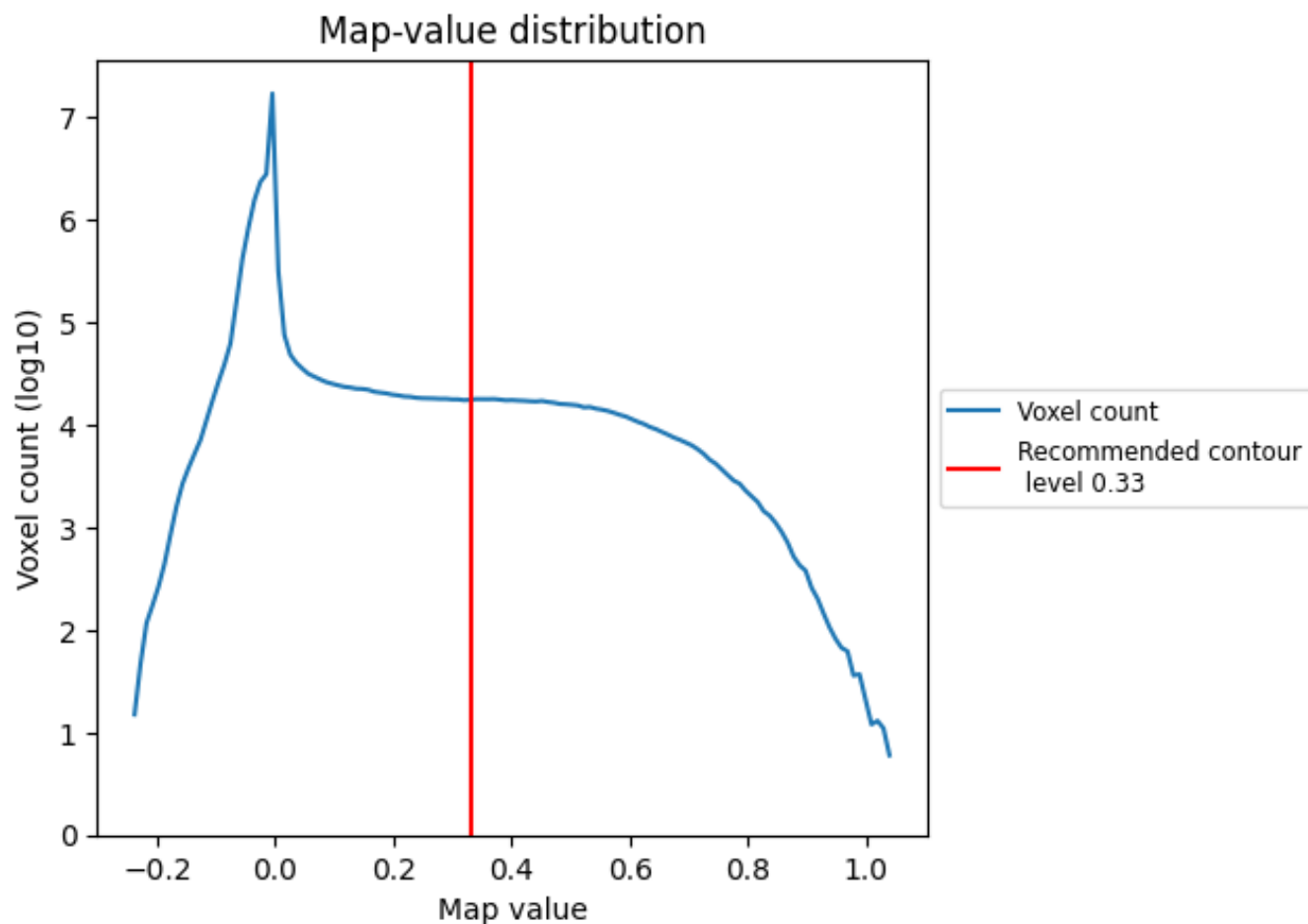
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

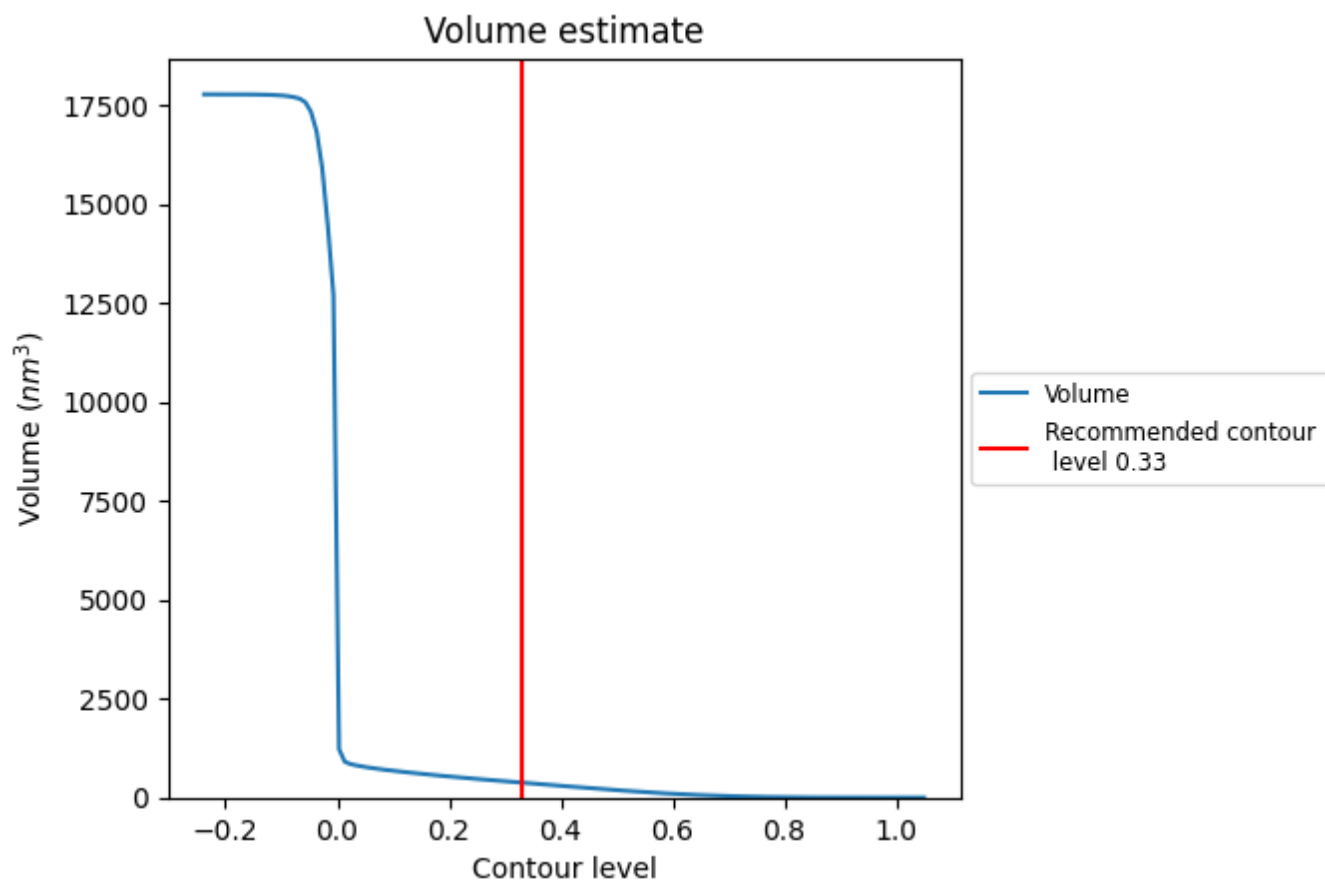
This section contains the results of statistical analysis of the map.

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.

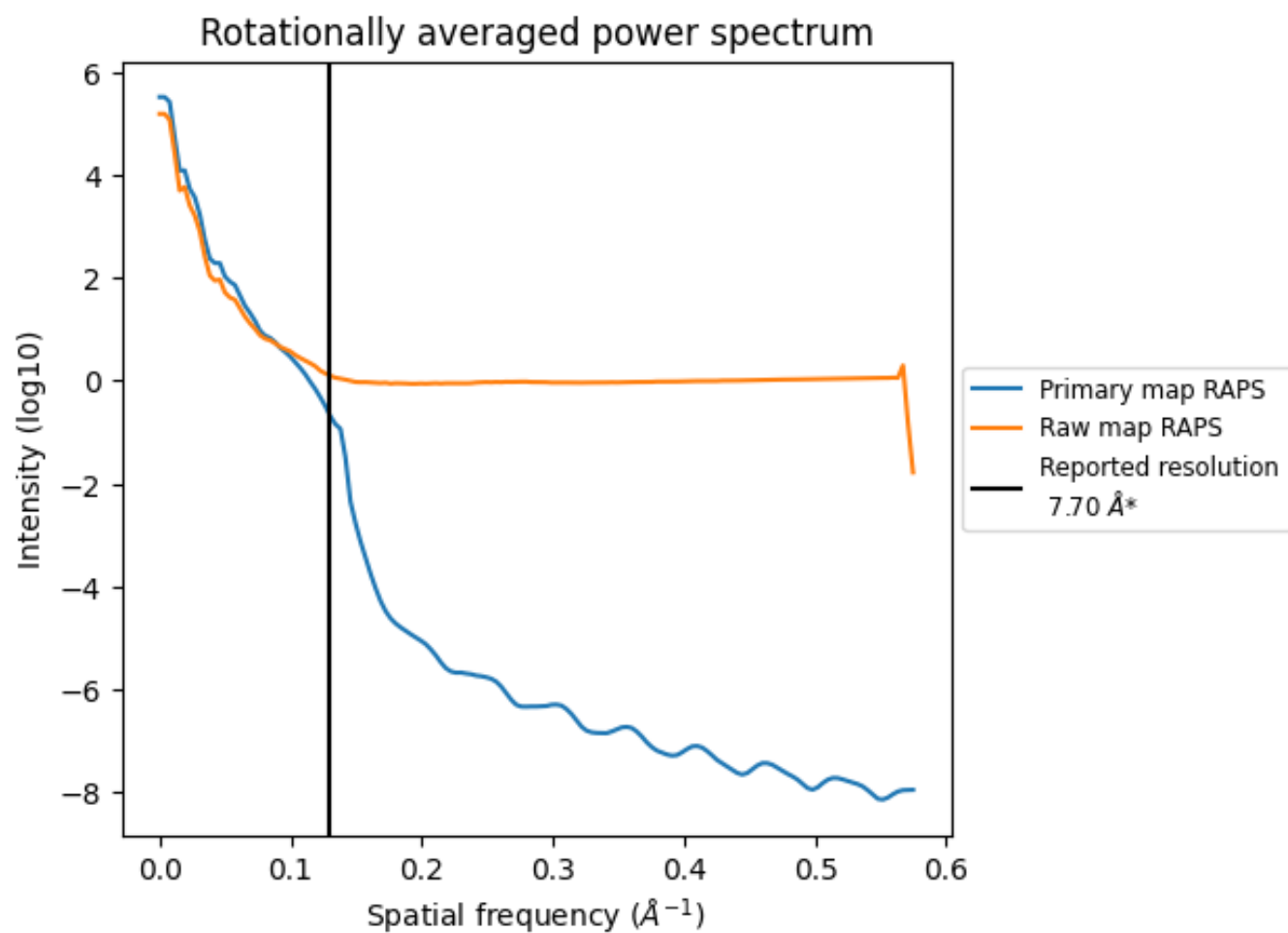
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 378 nm³; this corresponds to an approximate mass of 341 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 ⓘ

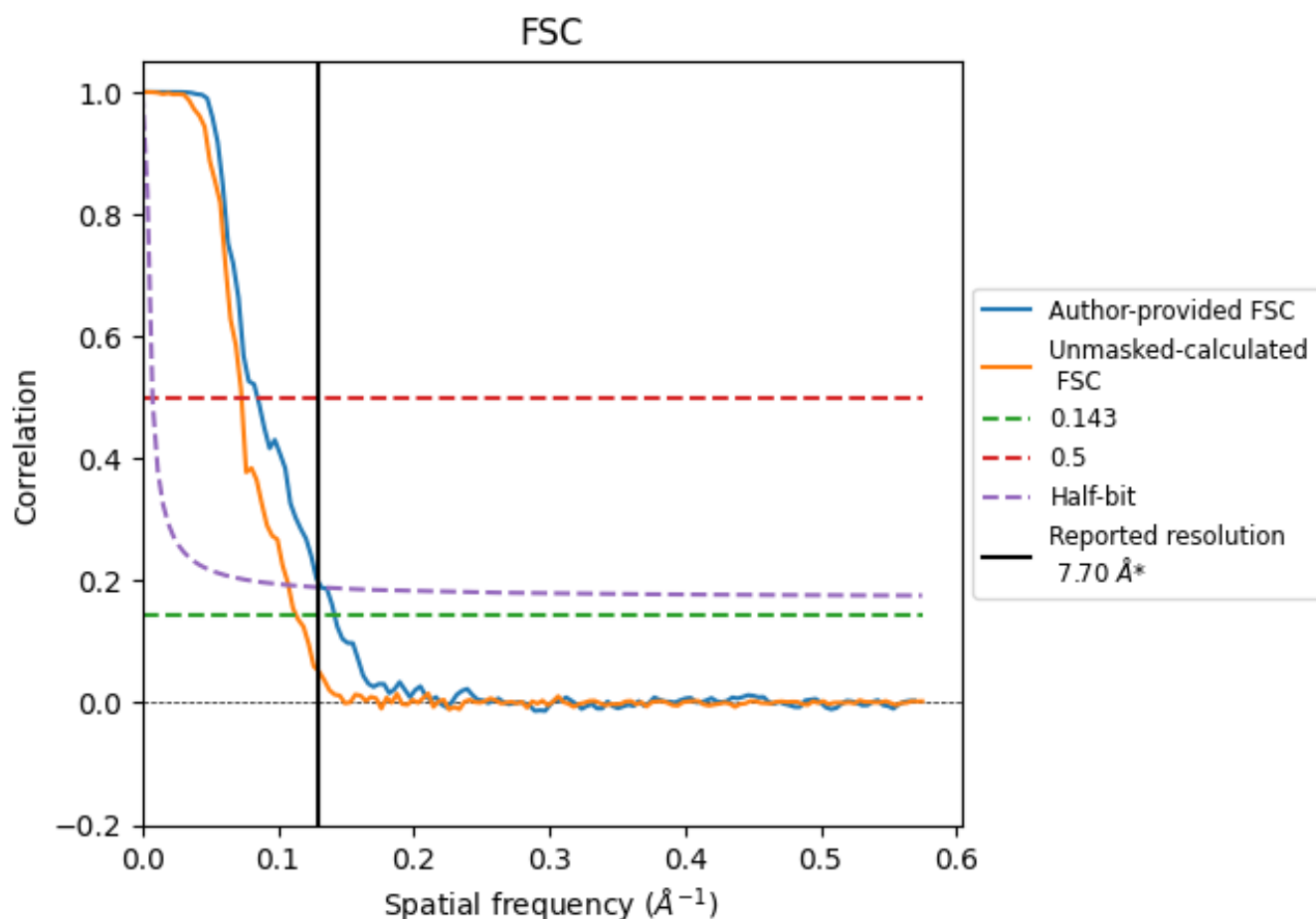


*Reported resolution corresponds to spatial frequency of 0.130 Å⁻¹

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 0.130 Å⁻¹

8.2 Resolution estimates [i](#)

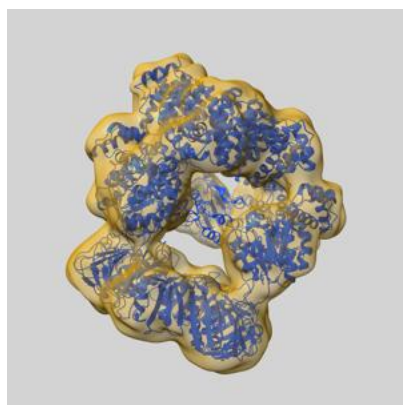
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.70	-	-
Author-provided FSC curve	7.05	11.78	7.56
Unmasked-calculated*	8.81	13.66	9.29

*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 8.81 differs from the reported value 7.7 by more than 10 %

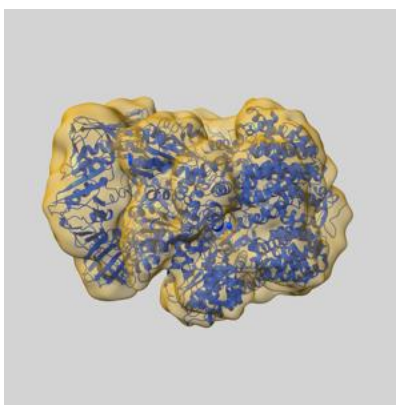
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43096 and PDB model 8VAN. Per-residue inclusion information can be found in section 3 on page 6.

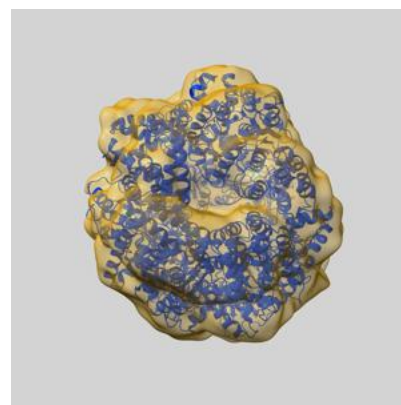
9.1 Map-model overlay [i](#)



X



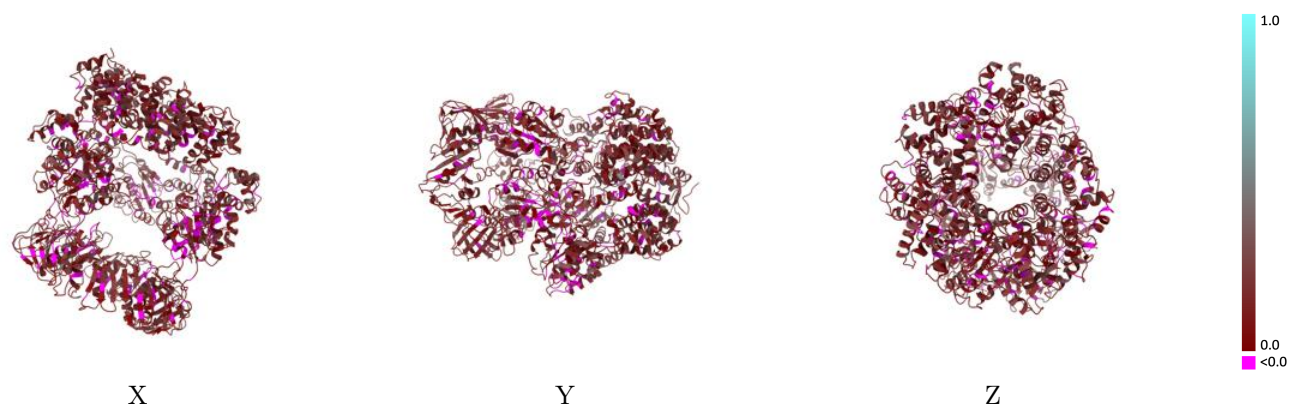
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.33 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](#)

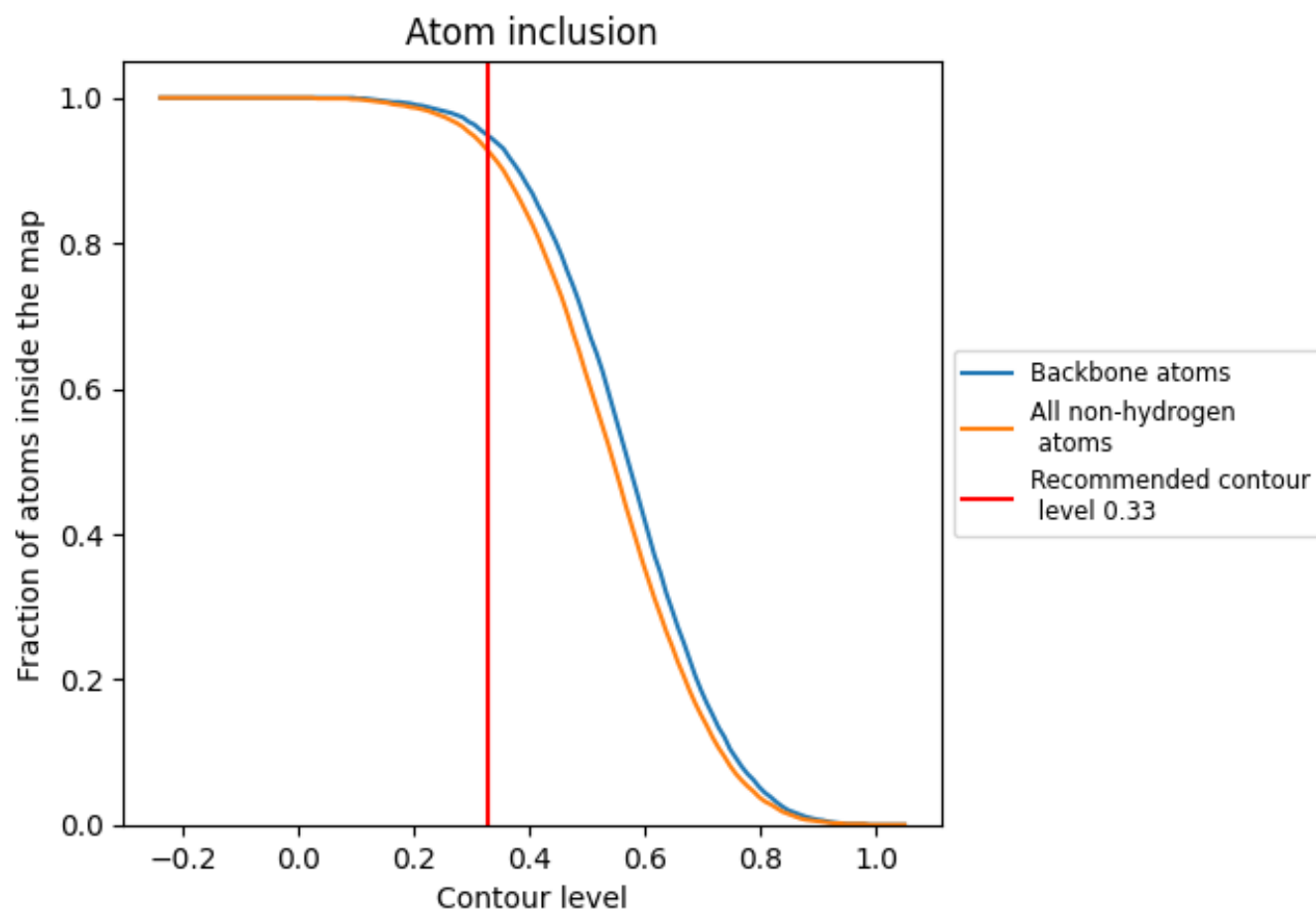


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9260	0.1420
A	0.9320	0.1460
B	0.8370	0.1280
C	0.8030	0.1320
D	0.9720	0.1470
E	0.9780	0.1450
F	0.9860	0.1540
G	0.9730	0.1460

1.0

0.0

<0.0