



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 10:02 PM UTC

PDB ID : 2GP1 / pdb_00002gp1
Title : Bacteriophage HK97 Prohead II crystal structure
Authors : Gertsman, I.; Gan, L.; Johnson, J.E.
Deposited on : 2006-04-15
Resolution : 5.20 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

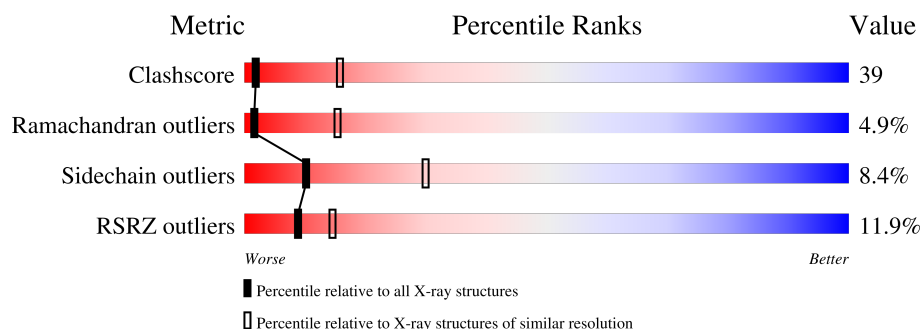
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.20 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1066 (6.38-4.00)
Ramachandran outliers	187476	1004 (6.46-3.94)
Sidechain outliers	187428	1006 (6.46-3.92)
RSRZ outliers	180081	1006 (6.38-4.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	282	11% 40% 38% 8% 10%
1	B	282	12% 50% 32% 5% 10%
1	C	282	8% 49% 34% 7% 10%
1	D	282	11% 43% 40% 6% 10%
1	E	282	12% 47% 35% 7% 10%
1	F	282	7% 45% 36% 7% 10%
1	G	282	13% 48% 34% 7% 10%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13797 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	0	0
			1971	1233	345	383	10			
1	B	254	Total	C	N	O	S	0	0	0
			1971	1233	345	383	10			
1	C	254	Total	C	N	O	S	0	0	0
			1971	1233	345	383	10			
1	D	254	Total	C	N	O	S	0	0	0
			1971	1233	345	383	10			
1	E	254	Total	C	N	O	S	0	0	0
			1971	1233	345	383	10			
1	F	254	Total	C	N	O	S	0	0	0
			1971	1233	345	383	10			
1	G	254	Total	C	N	O	S	0	0	0
			1971	1233	345	383	10			

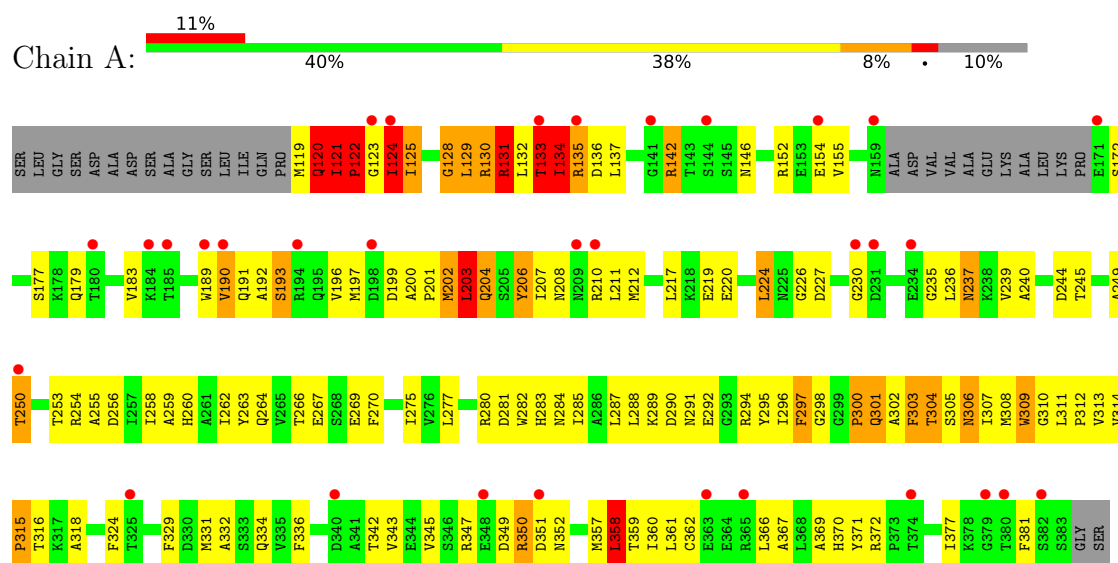
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	336	PHE	TRP	engineered mutation	UNP P49861
B	336	PHE	TRP	engineered mutation	UNP P49861
C	336	PHE	TRP	engineered mutation	UNP P49861
D	336	PHE	TRP	engineered mutation	UNP P49861
E	336	PHE	TRP	engineered mutation	UNP P49861
F	336	PHE	TRP	engineered mutation	UNP P49861
G	336	PHE	TRP	engineered mutation	UNP P49861

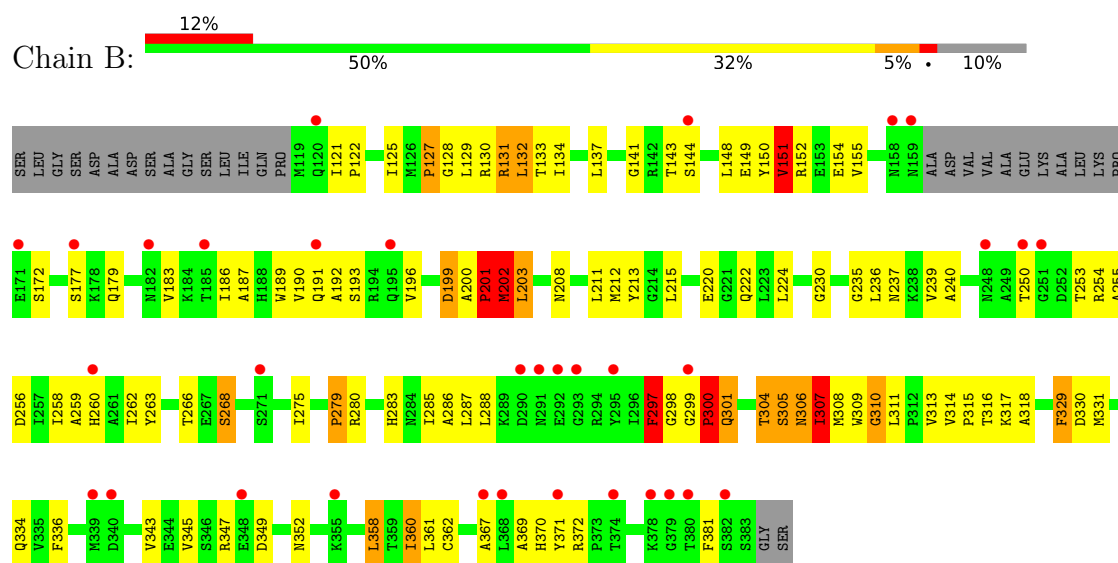
3 Residue-property plots

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

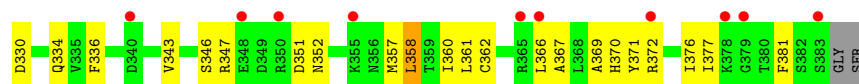
• Molecule 1: Major capsid protein



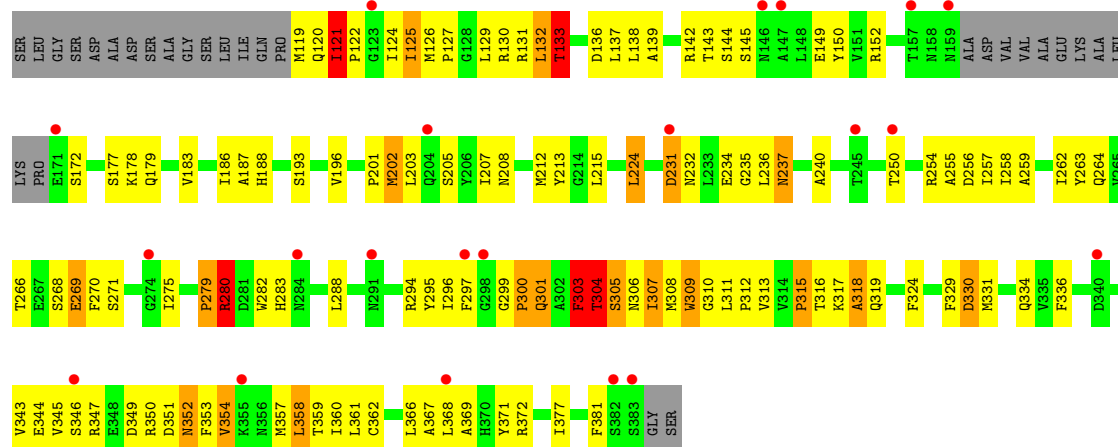
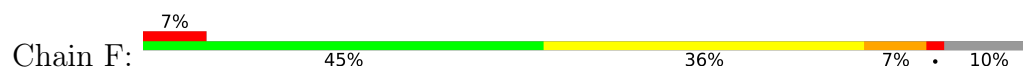
• Molecule 1: Major capsid protein



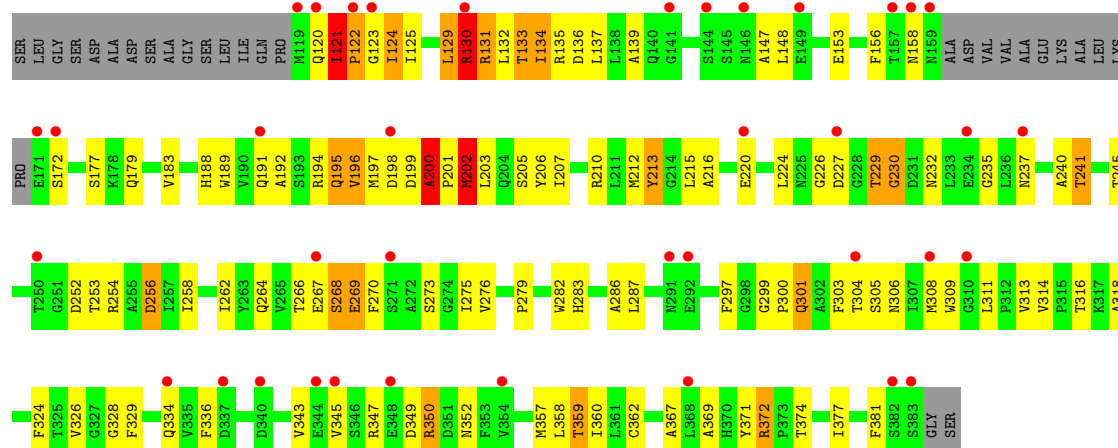
• Molecule 1: Major capsid protein



• Molecule 1: Major capsid protein



• Molecule 1: Major capsid protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	706.94Å 706.94Å 706.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 5.20 30.00 – 5.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-5.20) 83.8 (30.00-5.20)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 5.34Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.410 , (Not available) 0.371 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	124.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 111.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.076 for l,-k,h	Xtriage
F_o, F_c correlation	0.37	EDS
Total number of atoms	13797	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.84	13/2004 (0.6%)	1.17	20/2715 (0.7%)
1	B	0.44	0/2004	0.96	9/2715 (0.3%)
1	C	0.45	0/2004	0.94	9/2715 (0.3%)
1	D	0.44	0/2004	0.96	8/2715 (0.3%)
1	E	0.45	0/2004	0.96	11/2715 (0.4%)
1	F	0.91	2/2004 (0.1%)	1.06	15/2715 (0.6%)
1	G	0.47	1/2004 (0.0%)	0.98	10/2715 (0.4%)
All	All	0.60	16/14028 (0.1%)	1.01	82/19005 (0.4%)

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	1
1	G	0	1
All	All	0	2

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	231	ASP	C-N	-34.16	0.84	1.33
1	A	120	GLN	C-N	14.92	1.50	1.33
1	A	133	THR	N-CA	-11.63	1.31	1.46
1	F	280	ARG	N-CA	10.15	1.58	1.46
1	A	132	LEU	C-N	-9.17	1.20	1.33
1	A	131	ARG	CA-C	9.02	1.65	1.52
1	G	202	MET	SD-CE	8.70	2.01	1.79
1	A	128	GLY	N-CA	-7.93	1.37	1.45
1	A	120	GLN	CA-C	7.91	1.62	1.53
1	A	121	ILE	N-CA	6.95	1.55	1.46
1	A	131	ARG	C-N	6.62	1.43	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	132	LEU	N-CA	6.44	1.54	1.46
1	A	121	ILE	CA-C	-5.76	1.46	1.52
1	A	132	LEU	CA-C	-5.26	1.45	1.52
1	A	133	THR	C-N	-5.19	1.26	1.33
1	A	133	THR	CA-C	-5.08	1.46	1.52

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	318	ALA	N-CA-C	-14.90	95.03	111.28
1	A	122	PRO	CA-N-CD	-9.71	98.41	112.00
1	A	123	GLY	CA-C-N	9.60	139.26	121.97
1	A	123	GLY	C-N-CA	9.60	139.26	121.97
1	A	132	LEU	CA-C-N	-9.53	103.34	121.54
1	A	132	LEU	C-N-CA	-9.53	103.34	121.54
1	C	318	ALA	N-CA-C	-8.41	102.04	111.71
1	F	121	ILE	N-CA-C	8.28	117.05	107.77
1	E	197	MET	N-CA-C	8.11	122.28	112.38
1	A	122	PRO	CA-C-N	7.86	128.76	120.43
1	A	122	PRO	C-N-CA	7.86	128.76	120.43
1	A	296	ILE	N-CA-C	-7.80	102.17	110.36
1	A	123	GLY	O-C-N	7.71	129.56	122.77
1	A	204	GLN	N-CA-C	-7.55	102.98	111.14
1	B	202	MET	N-CA-C	7.37	126.50	110.80
1	F	133	THR	N-CA-C	7.29	126.33	110.80
1	A	358	LEU	N-CA-C	7.15	120.03	109.24
1	G	200	ALA	CA-C-N	-7.10	112.88	120.47
1	G	200	ALA	C-N-CA	-7.10	112.88	120.47
1	A	332	ALA	N-CA-C	6.68	118.56	111.28
1	E	199	ASP	N-CA-C	6.65	118.22	110.97
1	G	268	SER	N-CA-C	-6.53	105.61	113.97
1	D	134	ILE	N-CA-C	6.47	117.16	110.36
1	G	121	ILE	N-CA-C	6.41	114.49	108.15
1	E	121	ILE	N-CA-C	6.41	113.89	107.55
1	B	192	ALA	N-CA-C	6.37	116.97	108.38
1	D	121	ILE	N-CA-C	6.29	122.47	108.88
1	A	121	ILE	CB-CA-C	-6.27	99.95	111.36
1	F	237	ASN	N-CA-C	6.18	118.82	111.71
1	F	280	ARG	N-CA-CB	-6.16	101.13	110.07
1	G	134	ILE	N-CA-C	6.14	116.30	110.53
1	F	280	ARG	CA-C-O	-6.03	114.49	120.70
1	B	305	SER	N-CA-C	-6.01	106.60	112.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	304	THR	N-CA-C	-5.85	104.98	111.36
1	G	241	THR	N-CA-C	-5.66	100.45	109.96
1	B	203	LEU	N-CA-C	5.65	120.20	112.68
1	G	329	PHE	N-CA-C	5.64	117.88	111.11
1	A	120	GLN	CA-C-O	-5.64	115.58	122.41
1	B	240	ALA	N-CA-C	5.61	117.53	110.24
1	A	203	LEU	N-CA-C	-5.58	105.19	112.23
1	F	304	THR	N-CA-C	-5.53	99.03	110.80
1	E	314	VAL	N-CA-C	-5.49	102.71	108.15
1	G	235	GLY	N-CA-C	5.47	121.65	112.85
1	C	237	ASN	N-CA-C	5.44	118.71	111.75
1	F	303	PHE	N-CA-C	5.44	117.61	107.99
1	A	123	GLY	CA-C-O	5.42	126.08	120.98
1	F	138	LEU	N-CA-C	5.40	117.84	110.55
1	F	121	ILE	CA-C-N	5.39	125.29	119.85
1	F	121	ILE	C-N-CA	5.39	125.29	119.85
1	F	372	ARG	CA-C-N	5.38	125.03	119.05
1	F	372	ARG	C-N-CA	5.38	125.03	119.05
1	A	121	ILE	N-CA-CB	5.36	118.71	111.21
1	E	237	ASN	N-CA-C	5.36	119.31	112.34
1	C	372	ARG	CA-C-N	5.33	124.97	119.05
1	C	372	ARG	C-N-CA	5.33	124.97	119.05
1	C	126	MET	CA-C-N	5.33	126.50	119.84
1	C	126	MET	C-N-CA	5.33	126.50	119.84
1	A	237	ASN	N-CA-C	5.32	118.87	112.38
1	C	268	SER	N-CA-C	-5.30	105.95	112.90
1	B	131	ARG	N-CA-C	5.29	118.92	107.49
1	G	129	LEU	N-CA-C	-5.29	99.54	110.80
1	A	128	GLY	CA-C-N	5.25	131.57	121.54
1	A	128	GLY	C-N-CA	5.25	131.57	121.54
1	D	237	ASN	N-CA-C	5.25	118.79	112.38
1	B	372	ARG	CA-C-N	5.22	124.85	119.05
1	B	372	ARG	C-N-CA	5.22	124.85	119.05
1	D	285	ILE	N-CA-C	-5.21	106.61	111.45
1	C	300	PRO	N-CA-C	-5.21	106.75	113.57
1	D	372	ARG	CA-C-N	5.20	124.52	118.85
1	D	372	ARG	C-N-CA	5.20	124.52	118.85
1	C	200	ALA	N-CA-C	5.19	121.28	109.81
1	D	120	GLN	N-CA-C	5.16	117.90	109.59
1	E	228	GLY	N-CA-C	-5.11	108.61	114.69
1	F	240	ALA	N-CA-C	5.11	116.88	110.24
1	B	268	SER	N-CA-C	-5.08	107.08	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	268	SER	N-CA-C	-5.08	106.50	113.30
1	E	372	ARG	CA-C-N	5.05	124.66	119.05
1	E	372	ARG	C-N-CA	5.05	124.66	119.05
1	G	253	THR	N-CA-C	5.02	117.00	110.43
1	E	253	THR	N-CA-C	-5.01	103.79	110.55
1	F	231	ASP	O-C-N	-5.01	115.96	122.37
1	D	235	GLY	N-CA-C	5.00	119.72	112.82

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	TYR	Sidechain
1	G	213	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	1971	0	1937	231	0
1	B	1971	0	1938	153	0
1	C	1971	0	1938	179	0
1	D	1971	0	1937	188	0
1	E	1971	0	1938	202	0
1	F	1971	0	1936	212	0
1	G	1971	0	1938	131	0
All	All	13797	0	13562	1078	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 39.

All (1078) 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:280:ARG:HH22	1:B:262:ILE:CD1	1.21	1.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:279:PRO:CB	1:F:266:THR:HG21	1.51	1.39
1:A:280:ARG:NH2	1:B:262:ILE:HD13	1.37	1.37
1:C:279:PRO:CB	1:D:266:THR:HG21	1.55	1.36
1:D:202:MET:SD	1:E:143:THR:HA	1.71	1.30
1:A:280:ARG:NH2	1:B:262:ILE:CD1	1.88	1.30
1:A:134:ILE:O	1:A:136:ASP:N	1.65	1.28
1:F:231:ASP:C	1:F:232:ASN:CA	2.05	1.27
1:A:266:THR:HG21	1:F:279:PRO:CB	1.67	1.22
1:D:280:ARG:NH2	1:E:262:ILE:CD1	2.03	1.21
1:E:306:ASN:HB2	1:E:313:VAL:HB	1.20	1.18
1:E:279:PRO:HB2	1:F:266:THR:CG2	1.74	1.17
1:B:279:PRO:HB2	1:C:266:THR:HG21	1.21	1.17
1:F:231:ASP:O	1:F:232:ASN:N	1.77	1.17
1:F:231:ASP:CA	1:F:232:ASN:N	2.11	1.14
1:A:266:THR:HG21	1:F:279:PRO:CG	1.78	1.14
1:B:306:ASN:HB2	1:B:313:VAL:HB	1.27	1.10
1:D:306:ASN:HB2	1:D:313:VAL:HB	1.34	1.09
1:A:134:ILE:CG2	1:A:135:ARG:H	1.62	1.08
1:A:120:GLN:O	1:A:120:GLN:HG2	1.48	1.08
1:E:275:ILE:HB	1:E:313:VAL:HG22	1.34	1.07
1:A:121:ILE:O	1:A:121:ILE:HG22	1.26	1.05
1:A:134:ILE:HG22	1:A:135:ARG:N	1.64	1.05
1:C:279:PRO:HB2	1:D:266:THR:HG21	1.31	1.05
1:A:280:ARG:HA	1:B:310:GLY:HA3	1.38	1.05
1:A:121:ILE:O	1:A:121:ILE:CG2	2.03	1.03
1:D:280:ARG:HH22	1:E:262:ILE:CD1	1.65	1.02
1:C:306:ASN:HB2	1:C:313:VAL:HB	1.39	1.02
1:E:336:PHE:HE1	1:E:369:ALA:HB2	1.21	1.01
1:B:275:ILE:HB	1:B:313:VAL:HG22	1.41	1.00
1:D:280:ARG:HA	1:E:310:GLY:HA3	1.41	1.00
1:A:266:THR:CG2	1:F:279:PRO:HG2	1.92	1.00
1:C:279:PRO:HG2	1:C:317:LYS:HB3	1.41	0.99
1:E:197:MET:HG3	1:E:358:LEU:HD22	1.43	0.98
1:A:292:GLU:HA	1:C:294:ARG:HD2	1.40	0.98
1:A:129:LEU:O	1:A:130:ARG:HD3	1.63	0.97
1:E:279:PRO:CB	1:F:266:THR:CG2	2.37	0.97
1:A:280:ARG:HH22	1:B:262:ILE:HD11	1.28	0.97
1:F:345:VAL:HG22	1:F:360:ILE:HG23	1.46	0.97
1:D:280:ARG:NH2	1:E:262:ILE:HD13	1.79	0.96
1:D:280:ARG:HH22	1:E:262:ILE:HD12	1.29	0.96
1:A:134:ILE:HG22	1:A:135:ARG:H	0.79	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:279:PRO:CB	1:C:266:THR:HG21	1.96	0.96
1:E:196:VAL:HG22	1:F:149:GLU:HB3	1.45	0.95
1:D:206:TYR:CE1	1:E:141:GLY:HA3	2.02	0.95
1:E:131:ARG:HH22	1:E:317:LYS:HG2	1.31	0.94
1:F:201:PRO:HG2	1:F:202:MET:SD	2.06	0.94
1:A:125:ILE:CG2	1:A:212:MET:HG3	1.97	0.94
1:F:231:ASP:C	1:F:232:ASN:N	0.84	0.94
1:A:129:LEU:HD13	1:A:130:ARG:H	1.31	0.93
1:D:290:ASP:HB3	1:D:296:ILE:HD11	1.51	0.93
1:D:206:TYR:CZ	1:E:336:PHE:CE2	2.58	0.92
1:D:206:TYR:OH	1:E:336:PHE:CE2	2.21	0.92
1:C:279:PRO:CG	1:D:266:THR:HG21	2.01	0.90
1:G:286:ALA:HA	1:G:297:PHE:HZ	1.35	0.90
1:A:125:ILE:HG21	1:A:212:MET:HG3	1.54	0.90
1:A:266:THR:HG21	1:F:279:PRO:HG2	1.45	0.89
1:C:277:LEU:HD11	1:C:308:MET:HE1	1.51	0.89
1:E:336:PHE:HE1	1:E:369:ALA:CB	1.87	0.88
1:C:317:LYS:HB2	1:D:269:GLU:OE2	1.74	0.87
1:G:133:THR:CG2	1:G:314:VAL:HG13	2.05	0.87
1:C:280:ARG:CA	1:D:263:TYR:CE1	2.54	0.87
1:A:347:ARG:HG2	1:A:358:LEU:HG	1.57	0.87
1:D:196:VAL:HG13	1:D:203:LEU:HG	1.54	0.87
1:F:258:ILE:HB	1:F:309:TRP:CH2	2.09	0.87
1:G:224:LEU:HG	1:G:237:ASN:ND2	1.89	0.87
1:D:210:ARG:HH21	1:E:139:ALA:HB2	1.39	0.86
1:A:280:ARG:HH22	1:B:262:ILE:HD12	1.38	0.86
1:E:336:PHE:CE1	1:E:369:ALA:HB2	2.08	0.86
1:F:119:MET:SD	1:F:344:GLU:HA	2.15	0.86
1:E:317:LYS:HB3	1:F:269:GLU:HG3	1.57	0.86
1:F:279:PRO:HD2	1:F:317:LYS:HG2	1.58	0.86
1:C:317:LYS:HD2	1:D:269:GLU:HA	1.58	0.85
1:C:279:PRO:CG	1:C:317:LYS:HB3	2.06	0.85
1:E:198:ASP:HB2	1:E:347:ARG:HH22	1.40	0.85
1:E:196:VAL:HG23	1:F:178:LYS:HZ1	1.41	0.85
1:E:317:LYS:NZ	1:F:266:THR:HA	1.92	0.85
1:C:280:ARG:HA	1:D:263:TYR:CE1	2.08	0.85
1:D:206:TYR:OH	1:E:336:PHE:CD2	2.29	0.85
1:C:121:ILE:HB	1:C:122:PRO:HD3	1.58	0.85
1:A:133:THR:HG21	1:A:314:VAL:HG13	1.59	0.85
1:A:289:LYS:HA	1:A:295:TYR:HA	1.56	0.84
1:A:122:PRO:HB3	1:A:208:ASN:OD1	1.77	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:292:GLU:HA	1:F:294:ARG:HD2	1.57	0.84
1:E:196:VAL:HG23	1:F:178:LYS:NZ	1.93	0.83
1:E:317:LYS:HZ2	1:F:270:PHE:N	1.77	0.83
1:A:134:ILE:CD1	1:A:220:GLU:OE2	2.27	0.83
1:A:266:THR:HG21	1:F:279:PRO:HB3	1.60	0.83
1:F:119:MET:SD	1:F:121:ILE:HG12	2.19	0.83
1:G:199:ASP:O	1:G:201:PRO:HD3	1.78	0.83
1:D:280:ARG:HG2	1:E:310:GLY:C	2.03	0.83
1:C:279:PRO:HB3	1:D:266:THR:HG21	1.60	0.82
1:F:258:ILE:HB	1:F:309:TRP:HH2	1.42	0.82
1:G:133:THR:HG23	1:G:314:VAL:HG13	1.61	0.82
1:C:133:THR:HG21	1:C:316:THR:OG1	1.79	0.82
1:F:275:ILE:HB	1:F:313:VAL:HG12	1.61	0.82
1:E:275:ILE:HD12	1:E:308:MET:HB3	1.62	0.82
1:C:336:PHE:HZ	1:C:371:TYR:OH	1.61	0.81
1:A:190:VAL:HB	1:A:211:LEU:HD21	1.63	0.81
1:B:128:GLY:HA3	1:B:131:ARG:HB2	1.63	0.81
1:A:280:ARG:HG2	1:B:310:GLY:CA	2.11	0.81
1:F:231:ASP:O	1:F:232:ASN:CA	2.21	0.81
1:B:304:THR:HG23	1:B:305:SER:H	1.46	0.80
1:D:202:MET:SD	1:E:143:THR:CA	2.64	0.80
1:A:134:ILE:O	1:A:137:LEU:N	2.13	0.80
1:F:336:PHE:HZ	1:F:371:TYR:OH	1.65	0.80
1:A:134:ILE:HD12	1:A:220:GLU:OE2	1.82	0.80
1:D:202:MET:SD	1:D:203:LEU:N	2.55	0.80
1:D:210:ARG:HH21	1:E:139:ALA:CB	1.94	0.80
1:C:306:ASN:HD21	1:C:315:PRO:HD3	1.47	0.79
1:C:201:PRO:HG2	1:C:202:MET:SD	2.22	0.79
1:C:317:LYS:HD3	1:D:266:THR:HG23	1.62	0.79
1:A:336:PHE:HE1	1:A:369:ALA:HB3	1.46	0.79
1:A:131:ARG:HB3	1:A:304:THR:HG21	1.64	0.79
1:A:124:ILE:O	1:A:125:ILE:HD13	1.83	0.79
1:C:279:PRO:HG2	1:C:317:LYS:CB	2.13	0.79
1:F:133:THR:HG22	1:F:136:ASP:HB2	1.64	0.79
1:G:203:LEU:HG	1:G:206:TYR:HD2	1.48	0.78
1:A:122:PRO:HG2	1:A:343:VAL:O	1.82	0.78
1:B:300:PRO:HA	1:C:309:TRP:CZ3	2.17	0.78
1:F:305:SER:HB2	1:F:315:PRO:HD3	1.64	0.78
1:B:317:LYS:NZ	1:C:266:THR:HA	1.98	0.78
1:C:279:PRO:HG2	1:D:266:THR:CG2	2.14	0.77
1:D:280:ARG:HG2	1:E:310:GLY:CA	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:LEU:HD22	1:B:362:CYS:SG	2.25	0.77
1:A:129:LEU:CD1	1:A:130:ARG:H	1.96	0.77
1:A:129:LEU:C	1:A:130:ARG:HD3	2.09	0.76
1:G:229:THR:CG2	1:G:232:ASN:HD22	1.98	0.76
1:G:203:LEU:HA	1:G:206:TYR:HB3	1.67	0.76
1:B:187:ALA:HB1	1:B:361:LEU:HD11	1.65	0.76
1:A:134:ILE:HD12	1:A:220:GLU:CD	2.11	0.76
1:A:134:ILE:HG13	1:A:220:GLU:OE2	1.86	0.76
1:D:202:MET:HE2	1:E:144:SER:H	1.49	0.76
1:F:133:THR:O	1:F:137:LEU:HG	1.85	0.76
1:F:336:PHE:HZ	1:F:371:TYR:HH	1.32	0.75
1:A:134:ILE:C	1:A:136:ASP:N	2.40	0.75
1:A:336:PHE:HE1	1:A:369:ALA:CB	2.00	0.75
1:E:279:PRO:HB2	1:F:266:THR:HG21	0.77	0.75
1:E:317:LYS:HZ3	1:F:266:THR:HA	1.51	0.75
1:G:316:THR:HG22	1:G:318:ALA:H	1.50	0.75
1:G:125:ILE:HD12	1:G:125:ILE:H	1.51	0.75
1:A:301:GLN:HG2	1:A:302:ALA:H	1.50	0.74
1:A:134:ILE:O	1:A:135:ARG:C	2.29	0.74
1:B:317:LYS:HB3	1:C:269:GLU:HG3	1.69	0.74
1:E:211:LEU:HD21	1:E:360:ILE:HG23	1.68	0.74
1:A:196:VAL:HG12	1:A:203:LEU:HD22	1.68	0.74
1:D:137:LEU:HD11	1:D:314:VAL:HG21	1.69	0.74
1:E:200:ALA:HB3	1:E:203:LEU:HB2	1.69	0.74
1:G:254:ARG:HB3	1:G:381:PHE:CE2	2.24	0.73
1:E:134:ILE:HD13	1:E:224:LEU:HB2	1.70	0.73
1:C:186:ILE:HD12	1:C:366:LEU:HD12	1.70	0.73
1:G:197:MET:SD	1:G:207:ILE:HD13	2.28	0.73
1:C:279:PRO:HB2	1:D:266:THR:CG2	2.15	0.73
1:E:308:MET:C	1:E:310:GLY:H	1.96	0.73
1:D:258:ILE:O	1:D:262:ILE:HG13	1.88	0.73
1:B:183:VAL:HG22	1:B:367:ALA:HB2	1.71	0.72
1:G:254:ARG:HB3	1:G:381:PHE:HE2	1.53	0.72
1:B:215:LEU:HB2	1:B:362:CYS:SG	2.29	0.72
1:A:134:ILE:CG1	1:A:220:GLU:OE2	2.37	0.72
1:A:306:ASN:ND2	1:A:313:VAL:HB	2.04	0.72
1:B:306:ASN:OD1	1:B:315:PRO:HG3	1.90	0.72
1:G:121:ILE:HG22	1:G:124:ILE:HG12	1.70	0.72
1:E:301:GLN:HA	1:F:309:TRP:HA	1.72	0.72
1:F:258:ILE:O	1:F:262:ILE:HG13	1.89	0.72
1:E:193:SER:HB3	1:F:178:LYS:NZ	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ARG:CZ	1:D:290:ASP:HB2	2.21	0.71
1:F:352:ASN:HD21	1:F:359:THR:N	1.89	0.71
1:D:264:GLN:HB3	1:D:377:ILE:HD13	1.71	0.71
1:E:300:PRO:O	1:F:309:TRP:HB3	1.89	0.71
1:C:336:PHE:HZ	1:C:371:TYR:HH	1.34	0.71
1:G:229:THR:HG23	1:G:230:GLY:N	2.06	0.71
1:A:280:ARG:HD3	1:B:309:TRP:HB3	1.72	0.71
1:A:196:VAL:HG21	1:B:149:GLU:HB2	1.72	0.71
1:D:206:TYR:CZ	1:E:336:PHE:CD2	2.79	0.71
1:A:258:ILE:HG21	1:A:275:ILE:HD13	1.72	0.71
1:D:285:ILE:O	1:D:288:LEU:HB2	1.90	0.71
1:A:120:GLN:O	1:A:120:GLN:CG	2.28	0.71
1:B:316:THR:HG22	1:B:318:ALA:H	1.56	0.71
1:E:307:ILE:HG12	1:E:312:PRO:HA	1.73	0.70
1:B:125:ILE:O	1:B:127:PRO:HD3	1.91	0.70
1:C:279:PRO:CD	1:C:317:LYS:HB3	2.21	0.70
1:G:276:VAL:HG13	1:G:314:VAL:HG12	1.72	0.70
1:A:191:GLN:NE2	1:A:357:MET:HB3	2.06	0.70
1:A:280:ARG:HG2	1:B:310:GLY:HA3	1.71	0.70
1:D:275:ILE:HB	1:D:313:VAL:HG22	1.73	0.70
1:D:128:GLY:HA3	1:D:132:LEU:HD21	1.74	0.70
1:D:202:MET:SD	1:D:202:MET:C	2.74	0.70
1:E:279:PRO:CG	1:F:266:THR:HG21	2.21	0.70
1:F:224:LEU:HD13	1:F:237:ASN:ND2	2.06	0.70
1:F:126:MET:HE3	1:F:127:PRO:HD2	1.74	0.70
1:A:258:ILE:HD12	1:A:258:ILE:H	1.57	0.69
1:D:280:ARG:CA	1:E:310:GLY:HA3	2.18	0.69
1:C:279:PRO:CB	1:D:266:THR:CG2	2.51	0.69
1:C:244:ASP:OD1	1:C:246:SER:HB3	1.92	0.69
1:E:279:PRO:HG2	1:F:266:THR:HG23	1.73	0.69
1:E:306:ASN:ND2	1:E:315:PRO:HD3	2.07	0.69
1:A:347:ARG:H	1:A:359:THR:HB	1.56	0.69
1:A:134:ILE:HD12	1:A:220:GLU:CG	2.23	0.69
1:D:201:PRO:HD2	1:D:202:MET:HE3	1.74	0.69
1:E:133:THR:HG22	1:E:314:VAL:CG1	2.23	0.69
1:A:121:ILE:N	1:A:122:PRO:HD3	2.07	0.69
1:A:183:VAL:HG22	1:A:367:ALA:HB2	1.74	0.69
1:B:154:GLU:HG3	1:B:155:VAL:HG23	1.72	0.69
1:G:131:ARG:C	1:G:133:THR:H	2.00	0.69
1:E:198:ASP:HB2	1:E:347:ARG:NH2	2.07	0.69
1:F:119:MET:SD	1:F:343:VAL:O	2.51	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:ILE:HD12	1:B:220:GLU:HB3	1.75	0.68
1:C:279:PRO:CG	1:D:266:THR:CG2	2.71	0.68
1:D:200:ALA:HB1	1:D:204:GLN:HB2	1.74	0.68
1:G:336:PHE:HZ	1:G:371:TYR:HH	1.40	0.68
1:A:219:GLU:HG3	1:A:366:LEU:HD11	1.76	0.68
1:E:308:MET:HG3	1:E:309:TRP:HD1	1.58	0.68
1:E:131:ARG:HD2	1:E:133:THR:HG23	1.73	0.68
1:B:215:LEU:HD13	1:B:362:CYS:HB3	1.76	0.68
1:D:283:HIS:CE1	1:D:287:LEU:HD11	2.29	0.68
1:E:130:ARG:HG3	1:E:131:ARG:HG3	1.76	0.68
1:G:336:PHE:CE1	1:G:369:ALA:CB	2.77	0.68
1:A:258:ILE:O	1:A:262:ILE:HG13	1.94	0.68
1:C:258:ILE:O	1:C:262:ILE:HG13	1.94	0.68
1:D:280:ARG:HA	1:E:310:GLY:CA	2.20	0.68
1:E:286:ALA:HB1	1:E:299:GLY:H	1.56	0.68
1:F:231:ASP:O	1:F:232:ASN:HA	1.92	0.68
1:G:336:PHE:HE1	1:G:369:ALA:CB	2.06	0.68
1:A:280:ARG:NH2	1:B:262:ILE:HD11	1.93	0.68
1:D:336:PHE:HZ	1:D:371:TYR:HH	1.41	0.68
1:D:280:ARG:HH21	1:E:262:ILE:CD1	2.00	0.67
1:E:347:ARG:HG2	1:E:358:LEU:HD11	1.76	0.67
1:B:301:GLN:CD	1:B:301:GLN:H	2.02	0.67
1:E:275:ILE:O	1:E:313:VAL:HG13	1.95	0.67
1:A:285:ILE:O	1:A:288:LEU:HB2	1.94	0.67
1:B:280:ARG:NE	1:C:263:TYR:OH	2.26	0.67
1:F:187:ALA:HB1	1:F:361:LEU:HD11	1.77	0.67
1:B:152:ARG:HG2	1:B:179:GLN:HG3	1.77	0.67
1:B:345:VAL:HG22	1:B:360:ILE:HG23	1.76	0.67
1:E:131:ARG:NH2	1:E:317:LYS:HG2	2.07	0.67
1:F:307:ILE:HG23	1:F:310:GLY:HA2	1.76	0.67
1:G:227:ASP:HB3	1:G:229:THR:HG22	1.77	0.67
1:A:192:ALA:O	1:A:358:LEU:HD22	1.94	0.67
1:A:298:GLY:C	1:A:300:PRO:HD3	2.19	0.66
1:E:264:GLN:HB3	1:E:377:ILE:HD13	1.77	0.66
1:G:132:LEU:HD22	1:G:135:ARG:HB3	1.77	0.66
1:C:130:ARG:HG3	1:D:271:SER:HB2	1.76	0.66
1:C:280:ARG:N	1:D:263:TYR:CE1	2.63	0.66
1:C:317:LYS:HZ1	1:D:270:PHE:C	2.04	0.66
1:F:119:MET:HE3	1:F:345:VAL:HG23	1.76	0.66
1:F:119:MET:CE	1:F:345:VAL:HG23	2.26	0.66
1:G:192:ALA:O	1:G:358:LEU:HB2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:TYR:CE1	1:F:280:ARG:N	2.63	0.66
1:A:316:THR:HG22	1:A:318:ALA:H	1.59	0.66
1:G:229:THR:HG23	1:G:230:GLY:H	1.59	0.66
1:D:280:ARG:HH21	1:E:262:ILE:HD13	1.56	0.66
1:D:345:VAL:HG22	1:D:360:ILE:HG23	1.77	0.66
1:E:215:LEU:HD22	1:E:362:CYS:SG	2.36	0.66
1:G:345:VAL:HG22	1:G:360:ILE:HG23	1.77	0.66
1:B:307:ILE:HG22	1:B:310:GLY:C	2.20	0.66
1:C:306:ASN:ND2	1:C:315:PRO:HD3	2.11	0.66
1:C:317:LYS:HD3	1:D:266:THR:CG2	2.26	0.66
1:E:187:ALA:HB1	1:E:361:LEU:HD11	1.78	0.66
1:B:128:GLY:CA	1:B:131:ARG:HB2	2.26	0.65
1:F:282:TRP:CD1	1:F:305:SER:HG	2.13	0.65
1:A:259:ALA:HB2	1:A:309:TRP:HE1	1.59	0.65
1:A:260:HIS:ND1	1:F:283:HIS:NE2	2.44	0.65
1:D:206:TYR:CE1	1:E:141:GLY:CA	2.78	0.65
1:A:146:ASN:HD21	1:G:147:ALA:HB3	1.61	0.65
1:A:258:ILE:HD12	1:A:258:ILE:N	2.10	0.65
1:A:301:GLN:HG2	1:A:302:ALA:N	2.11	0.65
1:C:317:LYS:CD	1:D:266:THR:HG23	2.26	0.65
1:C:154:GLU:HG3	1:C:155:VAL:HG23	1.79	0.65
1:C:301:GLN:HB2	1:D:309:TRP:HA	1.77	0.65
1:F:183:VAL:HG22	1:F:367:ALA:HB2	1.79	0.65
1:C:131:ARG:HA	1:C:131:ARG:NE	2.12	0.65
1:D:154:GLU:HG3	1:D:155:VAL:HG23	1.79	0.65
1:D:202:MET:HE2	1:E:144:SER:N	2.11	0.65
1:D:280:ARG:NH2	1:E:262:ILE:HD11	2.08	0.65
1:A:129:LEU:HD13	1:A:130:ARG:N	2.07	0.64
1:A:134:ILE:C	1:A:136:ASP:H	2.00	0.64
1:A:202:MET:SD	1:B:143:THR:HA	2.37	0.64
1:C:301:GLN:C	1:C:303:PHE:H	2.05	0.64
1:A:191:GLN:HE22	1:A:357:MET:HB3	1.62	0.64
1:A:306:ASN:HD21	1:A:313:VAL:HB	1.61	0.64
1:C:306:ASN:HD21	1:C:315:PRO:CD	2.10	0.64
1:D:283:HIS:CE1	1:E:307:ILE:HB	2.31	0.64
1:G:336:PHE:CE1	1:G:369:ALA:HB2	2.33	0.64
1:A:202:MET:SD	1:A:203:LEU:N	2.70	0.64
1:B:317:LYS:HZ2	1:C:270:PHE:N	1.94	0.64
1:C:183:VAL:HG22	1:C:367:ALA:HB2	1.78	0.64
1:A:263:TYR:CZ	1:F:280:ARG:CA	2.81	0.64
1:A:292:GLU:HG2	1:A:294:ARG:NH2	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:197:MET:HE1	1:D:204:GLN:HE21	1.62	0.64
1:E:307:ILE:HG22	1:E:310:GLY:HA2	1.78	0.64
1:G:324:PHE:HB3	1:G:381:PHE:HE1	1.61	0.64
1:A:259:ALA:CB	1:A:309:TRP:HE1	2.11	0.64
1:A:280:ARG:CA	1:B:310:GLY:HA3	2.23	0.64
1:D:177:SER:HB2	1:D:179:GLN:HE21	1.63	0.64
1:E:197:MET:SD	1:E:207:ILE:HD13	2.38	0.64
1:G:207:ILE:HG21	1:G:360:ILE:HD13	1.80	0.64
1:D:133:THR:O	1:D:137:LEU:HG	1.97	0.64
1:D:280:ARG:NH2	1:E:262:ILE:HD12	1.95	0.64
1:D:229:THR:HG23	1:D:230:GLY:N	2.13	0.63
1:D:264:GLN:HB3	1:D:377:ILE:CD1	2.29	0.63
1:A:203:LEU:CD1	1:B:148:LEU:HD22	2.29	0.63
1:D:276:VAL:HG22	1:D:314:VAL:HB	1.80	0.63
1:C:130:ARG:NH2	1:C:131:ARG:HG2	2.13	0.63
1:G:188:HIS:CD2	1:G:362:CYS:HB3	2.34	0.63
1:E:307:ILE:HG22	1:E:310:GLY:C	2.24	0.63
1:F:353:PHE:HD2	1:G:359:THR:HG22	1.62	0.63
1:E:279:PRO:CG	1:F:266:THR:CG2	2.75	0.63
1:G:336:PHE:HB2	1:G:367:ALA:HB3	1.81	0.63
1:C:317:LYS:CB	1:D:269:GLU:OE2	2.46	0.63
1:E:307:ILE:HG22	1:E:310:GLY:CA	2.29	0.62
1:G:349:ASP:O	1:G:352:ASN:HB2	1.98	0.62
1:A:280:ARG:HD3	1:B:309:TRP:CB	2.28	0.62
1:A:294:ARG:NH2	1:D:290:ASP:HB2	2.14	0.62
1:F:282:TRP:CZ3	1:F:308:MET:SD	2.92	0.62
1:B:347:ARG:HD2	1:B:358:LEU:HD11	1.79	0.62
1:F:308:MET:HB3	1:F:313:VAL:HG11	1.81	0.62
1:A:190:VAL:HG12	1:A:360:ILE:HB	1.81	0.62
1:A:266:THR:HG21	1:F:279:PRO:HB2	1.75	0.62
1:C:125:ILE:HG22	1:C:126:MET:H	1.63	0.62
1:D:207:ILE:HG21	1:D:360:ILE:HD13	1.82	0.62
1:D:229:THR:HG23	1:D:232:ASN:HD22	1.64	0.62
1:G:343:VAL:HG22	1:G:362:CYS:SG	2.40	0.62
1:A:266:THR:CG2	1:F:279:PRO:CG	2.56	0.62
1:A:331:MET:HG3	1:A:372:ARG:NH2	2.14	0.62
1:E:211:LEU:HD23	1:E:343:VAL:HG13	1.81	0.62
1:F:125:ILE:O	1:F:127:PRO:HD3	2.00	0.62
1:F:282:TRP:HZ3	1:F:308:MET:SD	2.22	0.62
1:B:286:ALA:HB1	1:B:299:GLY:HA3	1.81	0.62
1:E:258:ILE:O	1:E:262:ILE:HG13	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:357:MET:O	1:F:358:LEU:HD13	1.99	0.62
1:A:134:ILE:HD12	1:A:220:GLU:HG2	1.82	0.62
1:E:130:ARG:HG2	1:F:271:SER:HB2	1.81	0.62
1:E:194:ARG:HA	1:E:358:LEU:HD13	1.81	0.62
1:B:201:PRO:O	1:B:202:MET:SD	2.57	0.61
1:B:150:TYR:O	1:B:151:VAL:HG13	2.01	0.61
1:B:317:LYS:HZ2	1:C:269:GLU:C	2.08	0.61
1:F:301:GLN:O	1:F:301:GLN:HG2	2.01	0.61
1:G:202:MET:HG2	1:G:203:LEU:HD13	1.82	0.61
1:G:286:ALA:HA	1:G:297:PHE:CZ	2.27	0.61
1:A:324:PHE:HB3	1:A:381:PHE:HE1	1.64	0.61
1:C:303:PHE:HZ	1:D:263:TYR:HB2	1.65	0.61
1:C:224:LEU:HD13	1:C:237:ASN:ND2	2.15	0.61
1:C:275:ILE:O	1:C:313:VAL:HG13	1.99	0.61
1:C:345:VAL:HG22	1:C:360:ILE:HG23	1.82	0.61
1:E:300:PRO:C	1:F:309:TRP:HB3	2.26	0.61
1:D:256:ASP:O	1:D:259:ALA:HB3	2.01	0.61
1:E:236:LEU:HD12	1:E:376:ILE:HD13	1.82	0.61
1:E:279:PRO:HG2	1:F:266:THR:CG2	2.31	0.61
1:G:156:PHE:CE2	1:G:158:ASN:HB2	2.36	0.61
1:G:197:MET:SD	1:G:207:ILE:CD1	2.89	0.60
1:A:199:ASP:C	1:A:201:PRO:HD3	2.26	0.60
1:C:275:ILE:HD12	1:C:313:VAL:HG22	1.82	0.60
1:D:206:TYR:CE2	1:E:336:PHE:CE2	2.89	0.60
1:D:294:ARG:HH11	1:F:299:GLY:HA2	1.64	0.60
1:E:130:ARG:HG2	1:F:271:SER:CB	2.31	0.60
1:A:267:GLU:HA	1:F:317:LYS:NZ	2.16	0.60
1:A:290:ASP:HB2	1:D:292:GLU:HG2	1.83	0.60
1:D:206:TYR:CE2	1:E:336:PHE:HE2	2.18	0.60
1:E:306:ASN:HB2	1:E:313:VAL:CB	2.13	0.60
1:G:336:PHE:HZ	1:G:371:TYR:OH	1.83	0.60
1:A:226:GLY:HA3	1:A:235:GLY:H	1.66	0.60
1:B:308:MET:HE2	1:B:309:TRP:HE1	1.65	0.60
1:E:305:SER:C	1:E:307:ILE:H	2.08	0.60
1:B:202:MET:HE2	1:C:143:THR:OG1	2.02	0.60
1:E:290:ASP:HB3	1:E:296:ILE:HD11	1.83	0.60
1:C:125:ILE:HG22	1:C:126:MET:N	2.17	0.60
1:D:316:THR:HG22	1:D:318:ALA:H	1.66	0.60
1:A:361:LEU:HG	1:A:362:CYS:H	1.67	0.60
1:C:133:THR:HG22	1:C:134:ILE:N	2.15	0.60
1:A:280:ARG:HH21	1:B:262:ILE:HD13	1.55	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:280:ARG:HG2	1:E:310:GLY:HA3	1.83	0.60
1:B:196:VAL:HB	1:B:203:LEU:HD22	1.83	0.60
1:E:264:GLN:HB3	1:E:377:ILE:CD1	2.32	0.60
1:B:349:ASP:O	1:B:352:ASN:HB2	2.02	0.59
1:A:280:ARG:HE	1:B:311:LEU:HG	1.67	0.59
1:C:210:ARG:HG3	1:C:210:ARG:HH11	1.67	0.59
1:D:134:ILE:HB	1:D:220:GLU:HG3	1.85	0.59
1:A:336:PHE:CE1	1:A:369:ALA:CB	2.85	0.59
1:B:258:ILE:HB	1:B:308:MET:HE1	1.84	0.59
1:E:360:ILE:O	1:E:360:ILE:HG22	2.02	0.59
1:A:292:GLU:C	1:C:294:ARG:HB3	2.28	0.59
1:B:224:LEU:HD13	1:B:237:ASN:ND2	2.18	0.59
1:B:317:LYS:HB3	1:C:269:GLU:OE2	2.03	0.59
1:D:206:TYR:HE1	1:E:141:GLY:C	2.11	0.59
1:A:142:ARG:O	1:F:202:MET:SD	2.61	0.59
1:D:152:ARG:HB2	1:D:371:TYR:O	2.03	0.59
1:B:224:LEU:HD13	1:B:237:ASN:HD22	1.67	0.59
1:C:280:ARG:N	1:D:263:TYR:HE1	2.01	0.59
1:E:301:GLN:HA	1:F:309:TRP:CA	2.33	0.59
1:E:317:LYS:HB3	1:F:269:GLU:CG	2.32	0.59
1:G:264:GLN:HB3	1:G:377:ILE:HD13	1.85	0.59
1:C:317:LYS:NZ	1:D:266:THR:HA	2.17	0.59
1:F:258:ILE:CD1	1:F:308:MET:HE1	2.33	0.59
1:A:266:THR:HG22	1:F:317:LYS:HG3	1.84	0.58
1:C:336:PHE:CZ	1:C:371:TYR:OH	2.45	0.58
1:F:224:LEU:HD13	1:F:237:ASN:HD22	1.66	0.58
1:F:258:ILE:HD13	1:F:308:MET:HE1	1.85	0.58
1:G:276:VAL:HG13	1:G:314:VAL:CG1	2.33	0.58
1:B:317:LYS:HZ1	1:C:266:THR:HA	1.65	0.58
1:C:290:ASP:HB3	1:C:296:ILE:HD11	1.85	0.58
1:G:282:TRP:CD2	1:G:313:VAL:HG11	2.38	0.58
1:F:275:ILE:HB	1:F:313:VAL:CG1	2.33	0.58
1:C:306:ASN:CB	1:C:313:VAL:HB	2.25	0.57
1:E:317:LYS:HZ2	1:F:269:GLU:C	2.12	0.57
1:E:306:ASN:ND2	1:E:306:ASN:H	2.02	0.57
1:F:361:LEU:HG	1:F:362:CYS:N	2.20	0.57
1:A:267:GLU:HA	1:F:317:LYS:CE	2.33	0.57
1:D:336:PHE:HE1	1:D:369:ALA:CB	2.17	0.57
1:E:131:ARG:HH22	1:E:317:LYS:CG	2.12	0.57
1:D:219:GLU:HG3	1:D:366:LEU:HD11	1.85	0.57
1:B:256:ASP:O	1:B:259:ALA:HB3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:THR:HG23	1:C:314:VAL:HG11	1.86	0.57
1:E:131:ARG:HD2	1:E:133:THR:CG2	2.34	0.57
1:G:275:ILE:O	1:G:314:VAL:HB	2.04	0.57
1:A:258:ILE:H	1:A:258:ILE:CD1	2.16	0.57
1:C:275:ILE:HB	1:C:313:VAL:HG22	1.87	0.57
1:C:279:PRO:CD	1:C:317:LYS:HA	2.34	0.57
1:D:133:THR:HB	1:D:314:VAL:HG13	1.86	0.57
1:F:255:ALA:HB1	1:F:309:TRP:HZ2	1.70	0.57
1:B:300:PRO:HA	1:C:309:TRP:HZ3	1.65	0.57
1:F:255:ALA:O	1:F:309:TRP:CH2	2.58	0.57
1:F:300:PRO:HG2	1:F:301:GLN:H	1.69	0.57
1:C:306:ASN:HB2	1:C:313:VAL:CB	2.26	0.57
1:G:252:ASP:HB2	1:G:256:ASP:CG	2.29	0.57
1:D:280:ARG:CZ	1:E:309:TRP:HB2	2.35	0.56
1:E:193:SER:HB3	1:F:178:LYS:HZ2	1.68	0.56
1:E:336:PHE:HB2	1:E:367:ALA:HB3	1.87	0.56
1:A:122:PRO:CG	1:A:343:VAL:O	2.50	0.56
1:A:134:ILE:O	1:A:136:ASP:CA	2.51	0.56
1:B:122:PRO:HD2	1:B:208:ASN:HD22	1.69	0.56
1:B:134:ILE:HD13	1:B:224:LEU:HB2	1.85	0.56
1:C:208:ASN:O	1:C:212:MET:HG2	2.05	0.56
1:E:317:LYS:HG3	1:F:269:GLU:C	2.30	0.56
1:B:137:LEU:HD11	1:B:314:VAL:HG21	1.88	0.56
1:C:244:ASP:HB2	1:C:264:GLN:HE22	1.71	0.56
1:C:306:ASN:HD22	1:C:313:VAL:C	2.13	0.56
1:F:224:LEU:O	1:F:237:ASN:HB2	2.05	0.56
1:G:229:THR:HG22	1:G:232:ASN:HD22	1.69	0.56
1:B:279:PRO:CB	1:C:266:THR:CG2	2.79	0.56
1:D:193:SER:OG	1:D:196:VAL:HG23	2.06	0.56
1:D:280:ARG:NH1	1:E:309:TRP:HB2	2.20	0.56
1:F:235:GLY:O	1:F:236:LEU:C	2.48	0.56
1:G:196:VAL:HG12	1:G:203:LEU:HD22	1.88	0.56
1:A:254:ARG:HB3	1:A:381:PHE:HE2	1.70	0.56
1:A:256:ASP:O	1:A:259:ALA:HB3	2.06	0.56
1:B:343:VAL:HG22	1:B:362:CYS:SG	2.46	0.56
1:E:317:LYS:HZ1	1:F:266:THR:HA	1.67	0.56
1:G:130:ARG:HA	1:G:130:ARG:NE	2.19	0.56
1:A:125:ILE:HG21	1:A:212:MET:CG	2.33	0.56
1:B:317:LYS:HZ3	1:C:266:THR:HA	1.71	0.56
1:C:264:GLN:HB3	1:C:377:ILE:HD13	1.87	0.56
1:D:203:LEU:HD12	1:D:203:LEU:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:189:TRP:HA	1:E:360:ILE:O	2.05	0.56
1:F:352:ASN:HD21	1:F:359:THR:H	1.54	0.56
1:A:177:SER:HB3	1:A:179:GLN:HE21	1.71	0.56
1:D:262:ILE:HD12	1:D:309:TRP:CD1	2.41	0.56
1:A:146:ASN:ND2	1:G:147:ALA:HB3	2.21	0.56
1:A:202:MET:HE2	1:B:144:SER:H	1.71	0.56
1:B:133:THR:O	1:B:137:LEU:HG	2.06	0.56
1:B:286:ALA:HB1	1:B:299:GLY:CA	2.36	0.56
1:A:263:TYR:CE1	1:F:280:ARG:CA	2.90	0.55
1:C:131:ARG:HD3	1:C:132:LEU:H	1.71	0.55
1:D:212:MET:HE1	1:D:341:ALA:O	2.06	0.55
1:E:211:LEU:CD2	1:E:360:ILE:HG23	2.36	0.55
1:C:256:ASP:O	1:C:259:ALA:HB3	2.06	0.55
1:D:229:THR:CG2	1:D:232:ASN:HD22	2.19	0.55
1:A:239:VAL:HG21	1:A:370:HIS:CG	2.41	0.55
1:A:331:MET:HG3	1:A:372:ARG:HH22	1.71	0.55
1:D:191:GLN:HA	1:D:358:LEU:O	2.07	0.55
1:D:229:THR:HG23	1:D:230:GLY:H	1.71	0.55
1:A:206:TYR:HE2	1:A:210:ARG:HD3	1.71	0.55
1:B:127:PRO:HG2	1:B:128:GLY:H	1.71	0.55
1:D:336:PHE:HZ	1:D:371:TYR:OH	1.89	0.55
1:E:306:ASN:H	1:E:306:ASN:HD22	1.54	0.55
1:C:254:ARG:HB3	1:C:381:PHE:CE2	2.42	0.55
1:C:308:MET:HB3	1:C:313:VAL:HG21	1.89	0.55
1:D:294:ARG:HH11	1:F:299:GLY:CA	2.18	0.55
1:G:139:ALA:HB3	1:G:334:GLN:HB3	1.88	0.55
1:A:308:MET:O	1:A:309:TRP:HB2	2.06	0.55
1:A:125:ILE:HG22	1:A:212:MET:HG3	1.87	0.55
1:A:352:ASN:CB	1:A:357:MET:HB2	2.36	0.55
1:C:134:ILE:O	1:C:138:LEU:HG	2.06	0.55
1:D:329:PHE:O	1:D:331:MET:N	2.40	0.55
1:A:192:ALA:H	1:A:358:LEU:HB3	1.71	0.55
1:C:210:ARG:NH1	1:D:372:ARG:NH2	2.55	0.55
1:D:258:ILE:HB	1:D:308:MET:HE1	1.87	0.55
1:E:280:ARG:HA	1:F:263:TYR:CE1	2.42	0.55
1:G:224:LEU:HG	1:G:237:ASN:HD21	1.69	0.55
1:A:134:ILE:CG2	1:A:135:ARG:N	2.36	0.54
1:E:124:ILE:HB	1:E:212:MET:HG3	1.89	0.54
1:E:224:LEU:HG	1:E:237:ASN:ND2	2.22	0.54
1:F:307:ILE:HG23	1:F:310:GLY:CA	2.37	0.54
1:G:314:VAL:HG12	1:G:314:VAL:O	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:ALA:HB1	1:A:309:TRP:CH2	2.42	0.54
1:A:262:ILE:HD12	1:A:309:TRP:CD1	2.43	0.54
1:C:279:PRO:HD2	1:C:317:LYS:HB3	1.89	0.54
1:A:193:SER:HB3	1:A:196:VAL:HG23	1.87	0.54
1:A:294:ARG:NH2	1:D:291:ASN:H	2.05	0.54
1:B:213:TYR:CD2	1:C:331:MET:HE1	2.42	0.54
1:B:307:ILE:HG22	1:B:310:GLY:O	2.08	0.54
1:C:279:PRO:HG2	1:C:317:LYS:CG	2.37	0.54
1:F:349:ASP:O	1:F:352:ASN:HB2	2.06	0.54
1:C:130:ARG:HG3	1:D:271:SER:CB	2.37	0.54
1:C:279:PRO:HD3	1:C:317:LYS:HA	1.88	0.54
1:E:286:ALA:O	1:E:298:GLY:HA2	2.08	0.54
1:G:300:PRO:O	1:G:301:GLN:HG3	2.07	0.54
1:A:291:ASN:HB2	1:D:292:GLU:OE2	2.08	0.54
1:A:361:LEU:HG	1:A:362:CYS:N	2.22	0.54
1:B:131:ARG:HD3	1:C:271:SER:OG	2.07	0.54
1:B:152:ARG:CG	1:B:179:GLN:HG3	2.37	0.54
1:E:280:ARG:NE	1:F:263:TYR:CE2	2.71	0.54
1:C:177:SER:HB2	1:C:179:GLN:HE21	1.73	0.54
1:C:244:ASP:CG	1:C:246:SER:HB3	2.32	0.54
1:D:336:PHE:HE1	1:D:369:ALA:HB3	1.72	0.54
1:E:150:TYR:O	1:E:178:LYS:HA	2.07	0.54
1:E:193:SER:HB3	1:F:178:LYS:HZ3	1.72	0.54
1:F:126:MET:HE2	1:F:129:LEU:HD11	1.90	0.54
1:B:258:ILE:HG21	1:B:275:ILE:HD13	1.88	0.54
1:B:336:PHE:HE1	1:B:369:ALA:HB3	1.72	0.54
1:F:122:PRO:HB3	1:F:124:ILE:HD13	1.89	0.54
1:C:244:ASP:HB2	1:C:264:GLN:NE2	2.23	0.54
1:F:133:THR:HG22	1:F:136:ASP:CB	2.38	0.54
1:G:206:TYR:CD1	1:G:206:TYR:C	2.84	0.54
1:A:226:GLY:HA3	1:A:235:GLY:N	2.22	0.54
1:C:223:LEU:O	1:C:236:LEU:HG	2.08	0.54
1:D:229:THR:CG2	1:D:232:ASN:ND2	2.71	0.54
1:F:152:ARG:HB2	1:F:371:TYR:O	2.08	0.54
1:C:301:GLN:CB	1:D:309:TRP:HA	2.37	0.53
1:A:200:ALA:HA	1:A:202:MET:HE1	1.90	0.53
1:E:196:VAL:HG22	1:F:149:GLU:CB	2.29	0.53
1:A:280:ARG:HH21	1:B:311:LEU:HD12	1.73	0.53
1:B:131:ARG:NH1	1:B:131:ARG:HA	2.23	0.53
1:B:258:ILE:O	1:B:262:ILE:HG13	2.07	0.53
1:B:263:TYR:O	1:B:266:THR:N	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:280:ARG:CA	1:F:263:TYR:CE1	2.91	0.53
1:G:258:ILE:HG21	1:G:275:ILE:HD13	1.89	0.53
1:A:202:MET:CE	1:B:144:SER:H	2.22	0.53
1:A:347:ARG:HG2	1:A:358:LEU:CG	2.36	0.53
1:B:301:GLN:HA	1:C:309:TRP:HA	1.90	0.53
1:C:121:ILE:HB	1:C:122:PRO:CD	2.35	0.53
1:E:186:ILE:HD12	1:E:366:LEU:HD12	1.90	0.53
1:A:313:VAL:HG12	1:A:314:VAL:N	2.24	0.53
1:B:254:ARG:HB3	1:B:381:PHE:CE2	2.44	0.53
1:C:336:PHE:HE1	1:C:369:ALA:HB3	1.74	0.53
1:A:292:GLU:HG2	1:A:294:ARG:CZ	2.38	0.53
1:G:203:LEU:HG	1:G:206:TYR:CD2	2.38	0.53
1:A:131:ARG:CB	1:A:304:THR:HG21	2.37	0.53
1:A:283:HIS:C	1:A:285:ILE:H	2.17	0.53
1:D:224:LEU:HG	1:D:237:ASN:ND2	2.24	0.53
1:G:270:PHE:HE1	1:G:372:ARG:CZ	2.22	0.53
1:A:203:LEU:HD13	1:B:148:LEU:HD22	1.91	0.53
1:B:300:PRO:HA	1:C:309:TRP:CE3	2.43	0.53
1:C:280:ARG:NE	1:D:263:TYR:HE2	2.07	0.53
1:G:189:TRP:HZ3	1:G:191:GLN:HE21	1.57	0.53
1:A:128:GLY:HA2	1:A:130:ARG:NH1	2.24	0.52
1:A:203:LEU:HD12	1:B:148:LEU:HD22	1.90	0.52
1:A:342:THR:HG22	1:A:343:VAL:N	2.24	0.52
1:C:275:ILE:HB	1:C:313:VAL:HG13	1.91	0.52
1:F:256:ASP:O	1:F:259:ALA:HB3	2.08	0.52
1:F:361:LEU:HG	1:F:362:CYS:H	1.74	0.52
1:C:317:LYS:HZ3	1:D:266:THR:HA	1.73	0.52
1:D:224:LEU:HD12	1:D:236:LEU:HB2	1.90	0.52
1:D:275:ILE:O	1:D:313:VAL:HG13	2.08	0.52
1:D:297:PHE:CE2	1:D:308:MET:HG3	2.44	0.52
1:F:275:ILE:CD1	1:F:308:MET:HE2	2.40	0.52
1:F:316:THR:C	1:F:318:ALA:H	2.14	0.52
1:E:336:PHE:HD1	1:E:367:ALA:O	1.91	0.52
1:A:154:GLU:HG3	1:A:155:VAL:HG23	1.91	0.52
1:C:317:LYS:NZ	1:D:270:PHE:O	2.42	0.52
1:D:270:PHE:CZ	1:D:372:ARG:CZ	2.93	0.52
1:E:308:MET:C	1:E:310:GLY:N	2.63	0.52
1:G:148:LEU:HD13	1:G:336:PHE:CD2	2.45	0.52
1:E:130:ARG:HH12	1:E:304:THR:HB	1.73	0.52
1:E:279:PRO:HG2	1:E:317:LYS:HD3	1.90	0.52
1:G:349:ASP:OD2	1:G:350:ARG:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:239:VAL:HG21	1:D:370:HIS:CG	2.45	0.52
1:D:307:ILE:HG22	1:D:310:GLY:HA2	1.92	0.52
1:F:126:MET:HG3	1:F:129:LEU:HD21	1.92	0.52
1:G:125:ILE:HD12	1:G:125:ILE:N	2.23	0.52
1:A:336:PHE:HD1	1:A:367:ALA:O	1.93	0.52
1:B:306:ASN:O	1:B:308:MET:N	2.42	0.52
1:E:317:LYS:HB3	1:F:269:GLU:OE2	2.09	0.52
1:F:275:ILE:HD13	1:F:308:MET:HE2	1.92	0.52
1:C:268:SER:O	1:C:269:GLU:HB2	2.09	0.52
1:C:275:ILE:HD13	1:C:308:MET:HE3	1.92	0.52
1:D:206:TYR:CE1	1:E:141:GLY:C	2.88	0.52
1:A:308:MET:C	1:A:310:GLY:H	2.18	0.51
1:G:202:MET:CG	1:G:203:LEU:H	2.23	0.51
1:G:299:GLY:O	1:G:303:PHE:HB2	2.11	0.51
1:A:260:HIS:O	1:A:263:TYR:HB3	2.10	0.51
1:B:235:GLY:O	1:B:236:LEU:C	2.53	0.51
1:B:254:ARG:HB3	1:B:381:PHE:HE2	1.75	0.51
1:G:122:PRO:HG2	1:G:123:GLY:H	1.75	0.51
1:A:152:ARG:HB2	1:A:371:TYR:O	2.10	0.51
1:B:336:PHE:HB2	1:B:367:ALA:HB3	1.92	0.51
1:C:258:ILE:N	1:C:258:ILE:HD12	2.25	0.51
1:F:132:LEU:O	1:F:133:THR:HG23	2.11	0.51
1:A:200:ALA:HA	1:A:202:MET:CE	2.40	0.51
1:A:263:TYR:HE1	1:F:279:PRO:HB2	1.75	0.51
1:E:139:ALA:O	1:E:334:GLN:HG3	2.11	0.51
1:C:275:ILE:HG23	1:C:326:VAL:HG22	1.92	0.51
1:D:191:GLN:OE1	1:D:357:MET:HE3	2.10	0.51
1:E:314:VAL:HG12	1:E:316:THR:OG1	2.11	0.51
1:A:262:ILE:HD12	1:A:309:TRP:HD1	1.76	0.51
1:A:280:ARG:HG2	1:B:310:GLY:N	2.24	0.51
1:E:133:THR:O	1:E:135:ARG:N	2.42	0.51
1:D:193:SER:HB3	1:E:178:LYS:HD3	1.91	0.51
1:F:275:ILE:HD12	1:F:313:VAL:CG1	2.41	0.51
1:F:275:ILE:CB	1:F:313:VAL:HG12	2.36	0.51
1:C:279:PRO:HG3	1:C:315:PRO:O	2.10	0.51
1:F:202:MET:HE2	1:F:203:LEU:N	2.26	0.51
1:G:124:ILE:HD12	1:G:212:MET:HE2	1.92	0.51
1:A:269:GLU:OE2	1:F:317:LYS:HB2	2.11	0.51
1:A:206:TYR:CE1	1:B:141:GLY:HA2	2.46	0.50
1:A:301:GLN:CG	1:A:302:ALA:H	2.21	0.50
1:B:283:HIS:O	1:B:286:ALA:HB3	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:134:ILE:CD1	1:E:316:THR:HG21	2.41	0.50
1:E:301:GLN:NE2	1:F:309:TRP:HD1	2.08	0.50
1:A:196:VAL:O	1:A:200:ALA:HB3	2.10	0.50
1:A:282:TRP:HA	1:A:285:ILE:HD12	1.93	0.50
1:D:119:MET:HG3	1:D:120:GLN:H	1.76	0.50
1:B:280:ARG:HB2	1:C:263:TYR:CE1	2.47	0.50
1:E:124:ILE:O	1:E:124:ILE:HG22	2.11	0.50
1:G:183:VAL:HG22	1:G:367:ALA:HB2	1.93	0.50
1:G:279:PRO:HD3	1:G:316:THR:O	2.12	0.50
1:A:129:LEU:CG	1:A:130:ARG:H	2.20	0.50
1:G:194:ARG:HD2	1:G:347:ARG:NH2	2.26	0.50
1:G:282:TRP:CE2	1:G:313:VAL:HG11	2.47	0.50
1:E:317:LYS:NZ	1:F:270:PHE:N	2.54	0.50
1:F:305:SER:HB3	1:F:313:VAL:HG23	1.94	0.50
1:G:139:ALA:HB3	1:G:334:GLN:CB	2.41	0.50
1:A:358:LEU:HD23	1:A:360:ILE:HG13	1.92	0.50
1:F:353:PHE:CD2	1:G:359:THR:HG22	2.46	0.50
1:G:206:TYR:CE1	1:G:210:ARG:HB2	2.47	0.50
1:A:263:TYR:CZ	1:F:280:ARG:HA	2.46	0.50
1:A:336:PHE:CE1	1:A:369:ALA:HB3	2.36	0.50
1:B:308:MET:HE2	1:B:309:TRP:NE1	2.27	0.50
1:E:307:ILE:CG2	1:E:310:GLY:C	2.84	0.50
1:E:336:PHE:CE1	1:E:369:ALA:CB	2.79	0.50
1:A:336:PHE:HB2	1:A:367:ALA:HB3	1.93	0.50
1:A:349:ASP:O	1:A:352:ASN:HB2	2.12	0.50
1:B:254:ARG:HB2	1:B:285:ILE:HG12	1.93	0.50
1:E:301:GLN:HG3	1:F:309:TRP:HA	1.93	0.50
1:F:305:SER:HB2	1:F:315:PRO:CD	2.37	0.50
1:G:148:LEU:CD1	1:G:336:PHE:CG	2.95	0.50
1:A:266:THR:CG2	1:F:279:PRO:CB	2.63	0.49
1:B:193:SER:O	1:B:358:LEU:HD22	2.12	0.49
1:C:317:LYS:CD	1:D:269:GLU:HA	2.38	0.49
1:D:259:ALA:CB	1:D:309:TRP:HE1	2.25	0.49
1:D:260:HIS:O	1:D:263:TYR:HB3	2.12	0.49
1:D:334:GLN:HE21	1:D:371:TYR:HE1	1.59	0.49
1:A:129:LEU:O	1:A:130:ARG:CD	2.49	0.49
1:A:203:LEU:HD21	1:A:207:ILE:HD11	1.92	0.49
1:B:208:ASN:O	1:B:212:MET:HG2	2.12	0.49
1:B:258:ILE:HD11	1:B:381:PHE:CZ	2.46	0.49
1:G:268:SER:O	1:G:269:GLU:HB2	2.12	0.49
1:C:194:ARG:HG3	1:C:347:ARG:HH12	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:263:TYR:O	1:C:266:THR:N	2.40	0.49
1:F:205:SER:HA	1:F:208:ASN:ND2	2.27	0.49
1:E:298:GLY:C	1:E:300:PRO:HD3	2.38	0.49
1:E:306:ASN:O	1:E:308:MET:N	2.46	0.49
1:E:352:ASN:HA	1:E:357:MET:HB3	1.93	0.49
1:G:266:THR:C	1:G:268:SER:H	2.20	0.49
1:B:308:MET:C	1:B:310:GLY:H	2.19	0.49
1:C:235:GLY:O	1:C:236:LEU:C	2.55	0.49
1:D:219:GLU:HG3	1:D:366:LEU:CD1	2.42	0.49
1:E:305:SER:C	1:E:307:ILE:N	2.71	0.49
1:G:357:MET:O	1:G:358:LEU:HD12	2.13	0.49
1:E:235:GLY:O	1:E:236:LEU:C	2.54	0.49
1:A:336:PHE:HZ	1:A:371:TYR:OH	1.95	0.49
1:D:135:ARG:HH12	1:D:335:VAL:HG11	1.76	0.49
1:D:280:ARG:NH1	1:E:309:TRP:CB	2.75	0.49
1:E:129:LEU:HB2	1:F:330:ASP:OD2	2.12	0.49
1:G:202:MET:HG2	1:G:203:LEU:H	1.78	0.49
1:B:304:THR:HG23	1:B:305:SER:N	2.22	0.49
1:B:329:PHE:C	1:B:331:MET:H	2.21	0.49
1:F:127:PRO:O	1:F:129:LEU:HD22	2.12	0.49
1:A:196:VAL:O	1:A:203:LEU:HD22	2.12	0.49
1:B:239:VAL:HG21	1:B:370:HIS:CG	2.48	0.49
1:E:147:ALA:C	1:E:148:LEU:HG	2.37	0.49
1:F:150:TYR:HE1	1:F:152:ARG:HB3	1.77	0.49
1:G:336:PHE:CE1	1:G:369:ALA:HB3	2.46	0.49
1:A:258:ILE:CG2	1:A:275:ILE:HD13	2.42	0.49
1:D:133:THR:CB	1:D:314:VAL:HG13	2.43	0.49
1:D:150:TYR:HE1	1:D:152:ARG:HD3	1.77	0.49
1:E:188:HIS:HD2	1:E:362:CYS:HB3	1.78	0.49
1:F:224:LEU:HD22	1:F:237:ASN:ND2	2.28	0.49
1:A:224:LEU:HD13	1:A:237:ASN:ND2	2.27	0.48
1:A:313:VAL:HG12	1:A:314:VAL:H	1.76	0.48
1:A:336:PHE:CE1	1:A:369:ALA:HB2	2.48	0.48
1:B:297:PHE:CG	1:B:298:GLY:N	2.80	0.48
1:E:202:MET:HG3	1:F:142:ARG:O	2.13	0.48
1:F:316:THR:C	1:F:318:ALA:N	2.71	0.48
1:B:308:MET:HG2	1:B:309:TRP:CD1	2.48	0.48
1:F:317:LYS:C	1:F:319:GLN:N	2.65	0.48
1:A:219:GLU:HG3	1:A:366:LEU:CD1	2.41	0.48
1:D:186:ILE:HD12	1:D:366:LEU:HD12	1.95	0.48
1:D:196:VAL:HG22	1:D:203:LEU:HD21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:296:ILE:HG22	1:E:297:PHE:HD1	1.77	0.48
1:F:119:MET:SD	1:F:121:ILE:CG1	2.98	0.48
1:E:279:PRO:HG2	1:E:317:LYS:CD	2.43	0.48
1:F:305:SER:HB3	1:F:313:VAL:O	2.13	0.48
1:D:200:ALA:N	1:D:201:PRO:HD3	2.29	0.48
1:E:275:ILE:CD1	1:E:308:MET:HB3	2.38	0.48
1:E:308:MET:CG	1:E:309:TRP:HD1	2.26	0.48
1:F:336:PHE:HB2	1:F:367:ALA:HB3	1.96	0.48
1:G:129:LEU:O	1:G:130:ARG:C	2.57	0.48
1:G:199:ASP:C	1:G:201:PRO:HD3	2.38	0.48
1:G:336:PHE:HE1	1:G:369:ALA:N	2.11	0.48
1:A:189:TRP:H	1:A:189:TRP:CD1	2.31	0.48
1:B:279:PRO:HG2	1:B:317:LYS:HD3	1.94	0.48
1:D:218:LYS:O	1:D:222:GLN:HG2	2.14	0.48
1:F:354:VAL:HG12	1:G:189:TRP:CG	2.47	0.48
1:G:148:LEU:HD11	1:G:336:PHE:CG	2.48	0.48
1:A:352:ASN:HB3	1:A:357:MET:HB2	1.96	0.48
1:D:292:GLU:HA	1:F:294:ARG:HH11	1.78	0.48
1:E:308:MET:SD	1:E:309:TRP:CD1	3.07	0.48
1:G:131:ARG:C	1:G:133:THR:N	2.71	0.48
1:G:191:GLN:HA	1:G:358:LEU:O	2.13	0.48
1:A:297:PHE:HD1	1:A:297:PHE:O	1.97	0.48
1:E:130:ARG:HG3	1:E:131:ARG:CG	2.43	0.48
1:E:314:VAL:C	1:E:316:THR:H	2.21	0.48
1:B:253:THR:OG1	1:B:255:ALA:HB3	2.13	0.48
1:B:317:LYS:NZ	1:C:270:PHE:O	2.47	0.48
1:C:193:SER:HB3	1:D:178:LYS:NZ	2.29	0.48
1:D:191:GLN:O	1:E:151:VAL:HG13	2.13	0.48
1:E:152:ARG:HA	1:E:371:TYR:O	2.14	0.48
1:G:216:ALA:O	1:G:220:GLU:HB2	2.14	0.48
1:F:288:LEU:O	1:F:296:ILE:HG12	2.14	0.47
1:F:352:ASN:ND2	1:F:359:THR:H	2.12	0.47
1:G:153:GLU:HB3	1:G:372:ARG:HD2	1.96	0.47
1:G:334:GLN:HG2	1:G:371:TYR:OH	2.14	0.47
1:G:270:PHE:HE1	1:G:372:ARG:NE	2.13	0.47
1:A:288:LEU:HB2	1:A:297:PHE:HE1	1.78	0.47
1:A:292:GLU:O	1:A:292:GLU:HG3	2.15	0.47
1:D:206:TYR:CZ	1:E:336:PHE:HE2	2.24	0.47
1:A:177:SER:HB3	1:A:179:GLN:NE2	2.29	0.47
1:F:177:SER:HB2	1:F:179:GLN:HE21	1.80	0.47
1:F:347:ARG:HD2	1:F:358:LEU:HD12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:ILE:C	1:A:125:ILE:HD13	2.39	0.47
1:A:206:TYR:CE2	1:B:334:GLN:OE1	2.68	0.47
1:A:235:GLY:O	1:A:236:LEU:C	2.57	0.47
1:C:200:ALA:HB1	1:C:204:GLN:HB2	1.94	0.47
1:C:279:PRO:CD	1:C:317:LYS:CA	2.92	0.47
1:D:139:ALA:O	1:D:334:GLN:HG3	2.14	0.47
1:B:133:THR:O	1:B:137:LEU:N	2.47	0.47
1:C:336:PHE:HE1	1:C:369:ALA:CB	2.27	0.47
1:E:190:VAL:O	1:E:360:ILE:HB	2.14	0.47
1:A:304:THR:HB	1:A:315:PRO:HD2	1.96	0.47
1:C:253:THR:HB	1:C:288:LEU:HD11	1.96	0.47
1:E:127:PRO:CB	1:E:132:LEU:HD21	2.45	0.47
1:E:133:THR:HG22	1:E:314:VAL:HG12	1.96	0.47
1:E:208:ASN:O	1:E:212:MET:HG2	2.14	0.47
1:G:133:THR:HG22	1:G:134:ILE:N	2.29	0.47
1:G:203:LEU:CA	1:G:206:TYR:HB3	2.40	0.47
1:G:229:THR:CG2	1:G:230:GLY:H	2.20	0.47
1:G:336:PHE:CZ	1:G:371:TYR:OH	2.63	0.47
1:C:133:THR:O	1:C:137:LEU:HG	2.15	0.47
1:C:306:ASN:O	1:C:313:VAL:N	2.43	0.47
1:F:279:PRO:CD	1:F:317:LYS:HG2	2.38	0.47
1:G:132:LEU:CD2	1:G:135:ARG:HB3	2.45	0.47
1:G:213:TYR:C	1:G:213:TYR:CD2	2.93	0.47
1:C:210:ARG:HH21	1:D:371:TYR:HB3	1.80	0.47
1:C:357:MET:O	1:C:358:LEU:HD12	2.15	0.47
1:A:289:LYS:CA	1:A:295:TYR:HA	2.37	0.47
1:E:343:VAL:HG22	1:E:362:CYS:SG	2.55	0.47
1:F:295:TYR:HB3	1:F:299:GLY:HA2	1.97	0.47
1:G:336:PHE:HE1	1:G:369:ALA:H	1.62	0.46
1:C:279:PRO:CD	1:C:317:LYS:CB	2.92	0.46
1:E:299:GLY:N	1:E:300:PRO:HD3	2.30	0.46
1:F:307:ILE:HG22	1:F:307:ILE:O	2.14	0.46
1:F:313:VAL:HG23	1:F:313:VAL:O	2.15	0.46
1:B:122:PRO:HD2	1:B:208:ASN:ND2	2.29	0.46
1:D:263:TYR:O	1:D:266:THR:N	2.39	0.46
1:C:258:ILE:HG21	1:C:308:MET:HE3	1.97	0.46
1:D:229:THR:HG23	1:D:232:ASN:ND2	2.31	0.46
1:F:207:ILE:HG21	1:F:360:ILE:HD13	1.97	0.46
1:F:215:LEU:HD12	1:F:362:CYS:SG	2.55	0.46
1:D:268:SER:O	1:D:269:GLU:HB2	2.15	0.46
1:F:130:ARG:O	1:F:131:ARG:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:308:MET:HE3	1:F:309:TRP:CH2	2.51	0.46
1:C:317:LYS:C	1:C:319:GLN:N	2.72	0.46
1:D:128:GLY:HA3	1:D:132:LEU:CD2	2.44	0.46
1:D:297:PHE:HE2	1:D:308:MET:HG3	1.80	0.46
1:E:130:ARG:NH1	1:E:304:THR:HB	2.30	0.46
1:E:134:ILE:HD12	1:E:220:GLU:HG3	1.96	0.46
1:E:286:ALA:HB1	1:E:299:GLY:N	2.28	0.46
1:E:346:SER:O	1:E:358:LEU:HG	2.15	0.46
1:A:263:TYR:O	1:A:266:THR:N	2.35	0.46
1:A:298:GLY:O	1:A:300:PRO:HD3	2.16	0.46
1:B:150:TYR:CG	1:B:151:VAL:N	2.84	0.46
1:B:199:ASP:O	1:B:200:ALA:C	2.59	0.46
1:C:152:ARG:HB2	1:C:371:TYR:O	2.15	0.46
1:D:206:TYR:CD1	1:E:142:ARG:O	2.69	0.46
1:D:229:THR:CG2	1:D:230:GLY:N	2.78	0.46
1:D:283:HIS:O	1:D:283:HIS:CD2	2.69	0.46
1:E:197:MET:HE1	1:E:207:ILE:HG21	1.97	0.46
1:C:125:ILE:CG2	1:C:126:MET:H	2.25	0.46
1:F:119:MET:HG2	1:F:121:ILE:HD13	1.98	0.46
1:G:283:HIS:O	1:G:287:LEU:HG	2.16	0.46
1:G:336:PHE:HE1	1:G:369:ALA:HB3	1.80	0.46
1:A:197:MET:SD	1:A:360:ILE:HD11	2.56	0.46
1:B:258:ILE:HD12	1:B:258:ILE:N	2.31	0.46
1:D:211:LEU:HB3	1:D:362:CYS:HB2	1.97	0.46
1:D:229:THR:CG2	1:D:230:GLY:H	2.28	0.46
1:F:186:ILE:HD12	1:F:366:LEU:HD12	1.96	0.46
1:A:189:TRP:HA	1:A:361:LEU:HA	1.98	0.45
1:A:201:PRO:O	1:A:204:GLN:HB3	2.16	0.45
1:B:329:PHE:O	1:B:331:MET:N	2.50	0.45
1:G:125:ILE:H	1:G:125:ILE:CD1	2.27	0.45
1:B:133:THR:HG21	1:B:314:VAL:HG13	1.97	0.45
1:C:177:SER:HB2	1:C:179:GLN:NE2	2.31	0.45
1:G:177:SER:HB2	1:G:179:GLN:HE21	1.81	0.45
1:G:196:VAL:CG1	1:G:203:LEU:HD22	2.45	0.45
1:C:301:GLN:C	1:C:303:PHE:N	2.74	0.45
1:D:235:GLY:O	1:D:236:LEU:C	2.57	0.45
1:D:294:ARG:NH1	1:F:295:TYR:HB2	2.31	0.45
1:G:129:LEU:O	1:G:131:ARG:N	2.49	0.45
1:G:139:ALA:O	1:G:334:GLN:HB2	2.15	0.45
1:G:195:GLN:H	1:G:195:GLN:NE2	2.15	0.45
1:A:270:PHE:CE2	1:F:213:TYR:CE2	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:134:ILE:HD11	1:E:224:LEU:HD22	1.97	0.45
1:D:357:MET:O	1:D:358:LEU:HD12	2.17	0.45
1:A:267:GLU:C	1:F:317:LYS:HZ1	2.24	0.45
1:D:201:PRO:HB2	1:E:144:SER:OG	2.16	0.45
1:D:254:ARG:HB3	1:D:381:PHE:HE2	1.82	0.45
1:E:263:TYR:O	1:E:266:THR:N	2.46	0.45
1:F:121:ILE:HA	1:F:122:PRO:HD3	1.70	0.45
1:F:139:ALA:O	1:F:334:GLN:HG3	2.16	0.45
1:E:197:MET:CE	1:E:207:ILE:HD13	2.46	0.45
1:F:142:ARG:NH1	1:F:142:ARG:HB3	2.31	0.45
1:F:336:PHE:CZ	1:F:371:TYR:OH	2.51	0.45
1:G:121:ILE:CG2	1:G:124:ILE:HG12	2.45	0.45
1:G:258:ILE:HB	1:G:308:MET:HE1	1.99	0.45
1:B:279:PRO:HG3	1:B:315:PRO:O	2.17	0.45
1:G:334:GLN:HG2	1:G:371:TYR:CE1	2.52	0.45
1:A:264:GLN:HG2	1:A:377:ILE:CD1	2.46	0.45
1:F:208:ASN:O	1:F:212:MET:HG2	2.17	0.45
1:A:189:TRP:H	1:A:189:TRP:HD1	1.65	0.45
1:B:317:LYS:HB3	1:C:269:GLU:CG	2.42	0.45
1:D:150:TYR:O	1:D:178:LYS:HA	2.17	0.45
1:E:317:LYS:HZ3	1:F:266:THR:CA	2.25	0.45
1:A:206:TYR:HE2	1:A:210:ARG:CD	2.30	0.44
1:B:317:LYS:HE2	1:C:266:THR:HG23	2.00	0.44
1:C:195:GLN:HG3	1:D:149:GLU:OE1	2.17	0.44
1:C:311:LEU:O	1:C:313:VAL:HG23	2.17	0.44
1:D:227:ASP:HB3	1:D:229:THR:HG22	1.99	0.44
1:E:149:GLU:HA	1:E:179:GLN:O	2.17	0.44
1:E:193:SER:HA	1:E:357:MET:HA	2.00	0.44
1:F:329:PHE:O	1:F:331:MET:N	2.49	0.44
1:B:200:ALA:HA	1:B:201:PRO:C	2.42	0.44
1:B:260:HIS:O	1:B:263:TYR:HB3	2.16	0.44
1:E:130:ARG:HE	1:E:130:ARG:C	2.25	0.44
1:E:137:LEU:HD11	1:E:314:VAL:HG21	1.98	0.44
1:E:196:VAL:HG23	1:F:178:LYS:HZ2	1.81	0.44
1:A:263:TYR:HE1	1:F:280:ARG:N	2.13	0.44
1:C:197:MET:HG2	1:C:358:LEU:HD21	1.98	0.44
1:G:308:MET:HE3	1:G:309:TRP:NE1	2.33	0.44
1:B:190:VAL:HG12	1:B:191:GLN:N	2.32	0.44
1:C:282:TRP:CZ3	1:C:308:MET:HB2	2.53	0.44
1:C:285:ILE:O	1:C:288:LEU:HB2	2.18	0.44
1:D:311:LEU:HA	1:D:312:PRO:HD3	1.89	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:150:TYR:CD1	1:E:151:VAL:N	2.86	0.44
1:E:183:VAL:HG22	1:E:367:ALA:HB2	1.99	0.44
1:E:254:ARG:HB3	1:E:381:PHE:CE2	2.53	0.44
1:C:279:PRO:HG2	1:D:266:THR:HG23	1.98	0.44
1:D:129:LEU:H	1:D:130:ARG:NH2	2.15	0.44
1:F:196:VAL:HG12	1:F:207:ILE:HD11	1.99	0.44
1:F:258:ILE:HG21	1:F:308:MET:HE1	2.00	0.44
1:A:152:ARG:CZ	1:A:179:GLN:HG3	2.47	0.44
1:A:281:ASP:O	1:A:285:ILE:HG13	2.17	0.44
1:A:342:THR:O	1:A:362:CYS:HA	2.18	0.44
1:A:343:VAL:HG13	1:A:361:LEU:O	2.17	0.44
1:B:121:ILE:HD12	1:B:122:PRO:HD2	1.99	0.44
1:B:297:PHE:O	1:B:300:PRO:HD2	2.17	0.44
1:C:239:VAL:HG21	1:C:370:HIS:CE1	2.53	0.44
1:E:192:ALA:O	1:E:357:MET:HA	2.17	0.44
1:F:143:THR:OG1	1:F:144:SER:N	2.49	0.44
1:B:317:LYS:HG3	1:C:269:GLU:C	2.43	0.44
1:B:345:VAL:HG22	1:B:360:ILE:CG2	2.43	0.44
1:D:130:ARG:HE	1:D:130:ARG:N	2.16	0.44
1:D:253:THR:OG1	1:D:255:ALA:HB3	2.18	0.44
1:E:317:LYS:NZ	1:F:270:PHE:O	2.49	0.44
1:A:249:ALA:O	1:A:250:THR:C	2.60	0.43
1:B:275:ILE:O	1:B:313:VAL:HA	2.18	0.43
1:D:306:ASN:CB	1:D:313:VAL:HB	2.25	0.43
1:F:353:PHE:HB3	1:G:349:ASP:OD1	2.18	0.43
1:B:305:SER:O	1:B:306:ASN:C	2.60	0.43
1:C:262:ILE:HD13	1:C:311:LEU:HD12	1.99	0.43
1:C:275:ILE:HD12	1:C:313:VAL:CG2	2.47	0.43
1:C:275:ILE:CD1	1:C:308:MET:HE3	2.48	0.43
1:F:275:ILE:HD12	1:F:313:VAL:HG12	2.00	0.43
1:F:361:LEU:CG	1:F:362:CYS:H	2.31	0.43
1:A:152:ARG:NE	1:A:179:GLN:HG3	2.33	0.43
1:D:201:PRO:HD2	1:D:202:MET:CE	2.45	0.43
1:C:196:VAL:HG13	1:C:207:ILE:HD11	2.00	0.43
1:C:268:SER:O	1:C:269:GLU:CB	2.67	0.43
1:D:121:ILE:HA	1:D:122:PRO:HD2	1.98	0.43
1:F:268:SER:O	1:F:269:GLU:HB2	2.18	0.43
1:G:199:ASP:O	1:G:200:ALA:HB3	2.18	0.43
1:A:258:ILE:HB	1:A:308:MET:HE1	2.01	0.43
1:G:202:MET:CG	1:G:203:LEU:N	2.80	0.43
1:B:308:MET:C	1:B:310:GLY:N	2.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:PHE:C	1:B:331:MET:N	2.77	0.43
1:D:119:MET:HB2	1:D:345:VAL:H	1.83	0.43
1:D:193:SER:HA	1:E:178:LYS:NZ	2.34	0.43
1:E:197:MET:HB2	1:E:347:ARG:HH21	1.84	0.43
1:E:256:ASP:O	1:E:259:ALA:HB3	2.18	0.43
1:B:211:LEU:HD13	1:B:343:VAL:CG1	2.49	0.43
1:G:137:LEU:HD11	1:G:314:VAL:HG21	2.00	0.43
1:G:220:GLU:OE1	1:G:316:THR:HG23	2.19	0.43
1:A:350:ARG:HB3	1:A:351:ASP:H	1.71	0.43
1:C:121:ILE:HG21	1:C:208:ASN:HD21	1.83	0.43
1:C:258:ILE:HG21	1:C:275:ILE:HD13	2.01	0.43
1:D:223:LEU:O	1:D:236:LEU:HG	2.19	0.43
1:F:336:PHE:HE1	1:F:369:ALA:CB	2.32	0.43
1:B:131:ARG:CD	1:C:271:SER:OG	2.67	0.43
1:B:224:LEU:CD1	1:B:237:ASN:ND2	2.81	0.43
1:C:279:PRO:HD3	1:C:317:LYS:CA	2.49	0.43
1:D:249:ALA:O	1:D:250:THR:C	2.62	0.43
1:D:324:PHE:HB3	1:D:381:PHE:HE1	1.83	0.43
1:E:134:ILE:HD12	1:E:220:GLU:CG	2.48	0.43
1:A:196:VAL:HG12	1:A:203:LEU:CD2	2.42	0.43
1:A:334:GLN:HE21	1:A:371:TYR:HE1	1.67	0.43
1:C:329:PHE:O	1:C:331:MET:N	2.52	0.43
1:E:224:LEU:HG	1:E:237:ASN:HD22	1.83	0.43
1:F:263:TYR:O	1:F:266:THR:N	2.39	0.43
1:F:361:LEU:CG	1:F:362:CYS:N	2.82	0.43
1:G:264:GLN:HB3	1:G:377:ILE:CD1	2.49	0.43
1:G:286:ALA:CA	1:G:297:PHE:HZ	2.19	0.43
1:A:245:THR:HG22	1:A:245:THR:O	2.19	0.42
1:B:189:TRP:CD1	1:B:189:TRP:H	2.37	0.42
1:E:213:TYR:HE2	1:F:270:PHE:HE2	1.66	0.42
1:F:258:ILE:HG21	1:F:275:ILE:HD13	2.01	0.42
1:F:303:PHE:HD2	1:F:303:PHE:HA	1.68	0.42
1:B:286:ALA:C	1:B:288:LEU:H	2.27	0.42
1:C:139:ALA:O	1:C:334:GLN:HG3	2.19	0.42
1:C:336:PHE:HD1	1:C:367:ALA:O	2.03	0.42
1:G:121:ILE:O	1:G:124:ILE:HD11	2.19	0.42
1:A:119:MET:HB2	1:A:345:VAL:O	2.20	0.42
1:A:303:PHE:C	1:A:305:SER:H	2.27	0.42
1:F:126:MET:HE2	1:F:129:LEU:CD1	2.49	0.42
1:F:308:MET:HB3	1:F:313:VAL:CG1	2.49	0.42
1:A:133:THR:HB	1:A:134:ILE:H	1.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:SER:HB3	1:A:196:VAL:CG2	2.50	0.42
1:A:199:ASP:O	1:A:201:PRO:HD3	2.19	0.42
1:C:336:PHE:HB2	1:C:367:ALA:HB3	2.00	0.42
1:G:282:TRP:CZ2	1:G:313:VAL:HG21	2.54	0.42
1:A:259:ALA:HB2	1:A:309:TRP:NE1	2.32	0.42
1:B:187:ALA:HB1	1:B:361:LEU:CD1	2.43	0.42
1:F:202:MET:HE2	1:F:203:LEU:HB2	2.00	0.42
1:F:354:VAL:HG12	1:G:189:TRP:CD2	2.55	0.42
1:D:141:GLY:O	1:D:336:PHE:HA	2.20	0.42
1:F:196:VAL:HG12	1:F:196:VAL:O	2.20	0.42
1:F:324:PHE:CD1	1:F:324:PHE:C	2.97	0.42
1:A:253:THR:O	1:A:256:ASP:HB2	2.20	0.42
1:A:266:THR:O	1:A:269:GLU:N	2.46	0.42
1:B:371:TYR:CD1	1:B:371:TYR:N	2.88	0.42
1:C:131:ARG:HD3	1:C:132:LEU:N	2.35	0.42
1:D:294:ARG:NH1	1:F:299:GLY:HA2	2.31	0.42
1:F:297:PHE:HZ	1:F:309:TRP:HE1	1.68	0.42
1:A:263:TYR:CE1	1:F:279:PRO:C	2.97	0.42
1:D:133:THR:HB	1:D:314:VAL:CG1	2.50	0.42
1:D:222:GLN:HB3	1:D:233:LEU:HB2	2.02	0.42
1:E:223:LEU:O	1:E:236:LEU:HD22	2.19	0.42
1:E:239:VAL:HG21	1:E:370:HIS:CG	2.54	0.42
1:E:357:MET:O	1:E:358:LEU:HD12	2.20	0.42
1:F:121:ILE:HA	1:F:121:ILE:HD12	1.79	0.42
1:F:336:PHE:HE1	1:F:369:ALA:HB3	1.85	0.42
1:G:137:LEU:CD1	1:G:314:VAL:HG21	2.50	0.42
1:A:253:THR:O	1:A:254:ARG:C	2.62	0.42
1:B:143:THR:OG1	1:B:144:SER:N	2.52	0.42
1:B:317:LYS:CE	1:C:266:THR:HG23	2.50	0.42
1:C:324:PHE:CZ	1:C:379:GLY:HA3	2.55	0.42
1:D:184:LYS:HG3	1:D:231:ASP:O	2.20	0.42
1:D:306:ASN:OD1	1:D:315:PRO:HG3	2.19	0.42
1:E:150:TYR:HD1	1:E:151:VAL:N	2.16	0.42
1:E:192:ALA:O	1:E:358:LEU:N	2.53	0.42
1:E:200:ALA:HA	1:E:201:PRO:HD3	1.75	0.42
1:E:311:LEU:HD23	1:E:311:LEU:HA	1.90	0.42
1:F:125:ILE:HG23	1:F:212:MET:HE3	2.02	0.42
1:A:270:PHE:CZ	1:F:213:TYR:CE2	3.07	0.42
1:B:211:LEU:HD13	1:B:343:VAL:HG11	2.02	0.42
1:C:275:ILE:H	1:C:313:VAL:HA	1.85	0.42
1:F:305:SER:OG	1:F:315:PRO:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:LYS:HG3	1:C:269:GLU:O	2.20	0.41
1:B:336:PHE:HE1	1:B:369:ALA:CB	2.33	0.41
1:C:254:ARG:O	1:C:258:ILE:HD13	2.19	0.41
1:D:195:GLN:H	1:D:195:GLN:CD	2.27	0.41
1:G:241:THR:OG1	1:G:374:THR:HA	2.20	0.41
1:A:202:MET:HG3	1:B:144:SER:OG	2.20	0.41
1:A:283:HIS:ND1	1:B:307:ILE:HB	2.35	0.41
1:B:308:MET:O	1:B:309:TRP:HB2	2.19	0.41
1:C:299:GLY:N	1:C:300:PRO:HD3	2.34	0.41
1:C:304:THR:O	1:C:305:SER:HB3	2.19	0.41
1:E:297:PHE:O	1:E:297:PHE:CG	2.72	0.41
1:G:275:ILE:HG12	1:G:326:VAL:HG22	2.01	0.41
1:A:202:MET:SD	1:B:143:THR:CA	3.07	0.41
1:C:120:GLN:HG2	1:C:121:ILE:N	2.36	0.41
1:C:254:ARG:HB3	1:C:381:PHE:HE2	1.82	0.41
1:E:192:ALA:HB3	1:E:358:LEU:HB3	2.02	0.41
1:G:224:LEU:C	1:G:226:GLY:H	2.28	0.41
1:G:308:MET:HE3	1:G:309:TRP:CD1	2.55	0.41
1:A:294:ARG:H	1:A:294:ARG:HG2	1.65	0.41
1:E:193:SER:CB	1:F:178:LYS:HZ3	2.32	0.41
1:F:264:GLN:HG2	1:F:377:ILE:CD1	2.51	0.41
1:D:210:ARG:NH1	1:D:213:TYR:HD2	2.19	0.41
1:D:255:ALA:HA	1:D:258:ILE:HD12	2.02	0.41
1:E:124:ILE:O	1:E:126:MET:N	2.53	0.41
1:E:137:LEU:HD21	1:E:314:VAL:HG21	2.01	0.41
1:G:316:THR:HG22	1:G:318:ALA:N	2.25	0.41
1:A:200:ALA:HB1	1:A:203:LEU:HB3	2.02	0.41
1:C:279:PRO:HG2	1:C:317:LYS:HG2	2.02	0.41
1:F:224:LEU:CD1	1:F:237:ASN:ND2	2.78	0.41
1:F:311:LEU:HA	1:F:312:PRO:HD3	1.96	0.41
1:G:273:SER:H	1:G:328:GLY:HA2	1.86	0.41
1:A:306:ASN:ND2	1:A:306:ASN:N	2.68	0.41
1:C:239:VAL:HG12	1:C:373:PRO:HB3	2.03	0.41
1:C:150:TYR:HE1	1:C:152:ARG:HB3	1.85	0.41
1:C:203:LEU:O	1:C:207:ILE:HG13	2.21	0.41
1:C:258:ILE:HD12	1:C:258:ILE:H	1.86	0.41
1:C:258:ILE:H	1:C:258:ILE:CD1	2.33	0.41
1:C:264:GLN:HB3	1:C:377:ILE:CD1	2.50	0.41
1:D:201:PRO:CD	1:D:202:MET:HE3	2.48	0.41
1:F:234:GLU:O	1:F:368:LEU:HD23	2.21	0.41
1:F:254:ARG:HB3	1:F:381:PHE:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:304:THR:O	1:F:305:SER:C	2.64	0.41
1:F:352:ASN:HA	1:F:357:MET:HB3	2.02	0.41
1:G:258:ILE:O	1:G:262:ILE:HG13	2.21	0.41
1:G:301:GLN:HE21	1:G:301:GLN:HB2	1.72	0.41
1:A:308:MET:C	1:A:310:GLY:N	2.79	0.41
1:A:329:PHE:C	1:A:331:MET:H	2.29	0.41
1:A:361:LEU:CG	1:A:362:CYS:H	2.33	0.41
1:B:133:THR:C	1:B:137:LEU:HG	2.46	0.41
1:B:199:ASP:HB3	1:B:201:PRO:HB2	2.03	0.41
1:C:275:ILE:O	1:C:313:VAL:CG1	2.69	0.41
1:D:275:ILE:HG23	1:D:326:VAL:HG22	2.03	0.41
1:E:266:THR:C	1:E:268:SER:H	2.28	0.41
1:F:231:ASP:N	1:F:232:ASN:N	2.65	0.41
1:G:183:VAL:HA	1:G:367:ALA:HB2	2.03	0.41
1:A:280:ARG:HD3	1:B:309:TRP:HB2	2.02	0.40
1:E:126:MET:HA	1:E:127:PRO:HD2	1.91	0.40
1:E:324:PHE:CD1	1:E:324:PHE:C	2.99	0.40
1:F:202:MET:SD	1:F:202:MET:N	2.94	0.40
1:F:257:ILE:C	1:F:259:ALA:N	2.79	0.40
1:F:306:ASN:HA	1:F:312:PRO:HA	2.02	0.40
1:F:311:LEU:O	1:F:313:VAL:HG13	2.21	0.40
1:A:119:MET:CB	1:A:345:VAL:O	2.69	0.40
1:A:239:VAL:HG21	1:A:370:HIS:CD2	2.56	0.40
1:A:303:PHE:O	1:A:304:THR:HG22	2.21	0.40
1:B:186:ILE:HD12	1:B:222:GLN:HG3	2.02	0.40
1:C:279:PRO:CG	1:C:317:LYS:CB	2.84	0.40
1:E:229:THR:HG22	1:E:232:ASN:HD22	1.86	0.40
1:F:119:MET:SD	1:F:343:VAL:C	3.03	0.40
1:F:308:MET:CB	1:F:313:VAL:HG11	2.50	0.40
1:A:311:LEU:HA	1:A:312:PRO:HD3	1.91	0.40
1:B:258:ILE:HG21	1:B:308:MET:SD	2.61	0.40
1:C:324:PHE:CD1	1:C:324:PHE:C	2.99	0.40
1:D:294:ARG:NH1	1:F:300:PRO:HD3	2.37	0.40
1:D:350:ARG:HB3	1:D:351:ASP:H	1.78	0.40
1:F:352:ASN:ND2	1:F:359:THR:N	2.62	0.40
1:A:244:ASP:HB2	1:A:264:GLN:NE2	2.37	0.40
1:B:262:ILE:HD13	1:B:311:LEU:HD12	2.04	0.40
1:B:371:TYR:N	1:B:371:TYR:HD1	2.19	0.40
1:C:345:VAL:HG13	1:C:360:ILE:HG12	2.03	0.40
1:D:143:THR:OG1	1:D:144:SER:N	2.54	0.40
1:F:295:TYR:CB	1:F:299:GLY:HA2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:350:ARG:HA	1:G:350:ARG:HB3	2.01	0.40
1:G:188:HIS:NE2	1:G:215:LEU:HB2	2.36	0.40
1:A:137:LEU:HD11	1:A:314:VAL:HG21	2.02	0.40
1:A:277:LEU:HD13	1:A:285:ILE:HD12	2.04	0.40
1:B:336:PHE:HD1	1:B:367:ALA:O	2.05	0.40
1:C:194:ARG:HG3	1:C:347:ARG:NH1	2.36	0.40
1:C:243:TYR:HA	1:C:264:GLN:OE1	2.20	0.40
1:C:260:HIS:O	1:C:263:TYR:HB3	2.22	0.40
1:F:224:LEU:HD11	1:F:319:GLN:HA	2.03	0.40
1:G:276:VAL:HG22	1:G:314:VAL:HG11	2.03	0.40
1:G:352:ASN:CG	1:G:357:MET:HB2	2.46	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 X-ray entries followed by that with respect to entries of similar resolution.

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	250/282 (89%)	198 (79%)	37 (15%)	15 (6%)	1	12
1	B	250/282 (89%)	201 (80%)	32 (13%)	17 (7%)	1	11
1	C	250/282 (89%)	212 (85%)	30 (12%)	8 (3%)	3	21
1	D	250/282 (89%)	205 (82%)	33 (13%)	12 (5%)	2	16
1	E	250/282 (89%)	206 (82%)	34 (14%)	10 (4%)	2	17
1	F	250/282 (89%)	201 (80%)	39 (16%)	10 (4%)	2	17
1	G	250/282 (89%)	200 (80%)	36 (14%)	14 (6%)	1	14
All	All	1750/1974 (89%)	1423 (81%)	241 (14%)	86 (5%)	1	15

All (86) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	PRO
1	A	124	ILE
1	A	135	ARG
1	A	193	SER
1	A	350	ARG
1	B	151	VAL
1	B	201	PRO
1	B	202	MET
1	B	306	ASN
1	C	127	PRO
1	D	229	THR
1	D	284	ASN
1	D	299	GLY
1	D	301	GLN
1	E	307	ILE
1	F	304	THR
1	F	307	ILE
1	G	130	ARG
1	G	200	ALA
1	G	229	THR
1	A	130	ARG
1	A	134	ILE
1	A	300	PRO
1	A	301	GLN
1	A	304	THR
1	B	127	PRO
1	B	300	PRO
1	C	269	GLU
1	D	130	ARG
1	D	230	GLY
1	D	306	ASN
1	D	330	ASP
1	E	125	ILE
1	E	230	GLY
1	F	330	ASP
1	G	133	THR
1	G	202	MET
1	G	350	ARG
1	B	132	LEU
1	B	199	ASP
1	B	230	GLY
1	B	297	PHE
1	B	301	GLN

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Mol	Chain	Res	Type
1	B	330	ASP
1	C	121	ILE
1	C	330	ASP
1	D	269	GLU
1	E	134	ILE
1	E	236	LEU
1	E	318	ALA
1	E	330	ASP
1	F	269	GLU
1	F	300	PRO
1	F	305	SER
1	F	352	ASN
1	G	122	PRO
1	G	230	GLY
1	G	240	ALA
1	G	267	GLU
1	G	269	GLU
1	A	227	ASP
1	A	240	ALA
1	A	284	ASN
1	B	287	LEU
1	B	304	THR
1	B	307	ILE
1	B	329	PHE
1	C	125	ILE
1	C	130	ARG
1	E	297	PHE
1	E	312	PRO
1	E	351	ASP
1	F	351	ASP
1	C	124	ILE
1	D	300	PRO
1	F	315	PRO
1	G	304	THR
1	B	310	GLY
1	D	127	PRO
1	F	309	TRP
1	G	305	SER
1	G	306	ASN
1	A	230	GLY
1	D	296	ILE
1	A	315	PRO

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Mol	Chain	Res	Type
1	C	312	PRO

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 X-ray entries followed by that with respect to entries of similar resolution.

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	211/231 (91%)	188 (89%)	23 (11%)	6	21
1	B	211/231 (91%)	195 (92%)	16 (8%)	12	32
1	C	205/231 (89%)	187 (91%)	18 (9%)	9	29
1	D	211/231 (91%)	198 (94%)	13 (6%)	16	38
1	E	211/231 (91%)	193 (92%)	18 (8%)	10	29
1	F	211/231 (91%)	192 (91%)	19 (9%)	9	28
1	G	211/231 (91%)	194 (92%)	17 (8%)	11	31
All	All	1471/1617 (91%)	1347 (92%)	124 (8%)	10	30

All (124) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	121	ILE
1	A	124	ILE
1	A	125	ILE
1	A	129	LEU
1	A	131	ARG
1	A	133	THR
1	A	134	ILE
1	A	142	ARG
1	A	172	SER
1	A	190	VAL
1	A	202	MET
1	A	203	LEU
1	A	217	LEU
1	A	224	LEU
1	A	250	THR

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Mol	Chain	Res	Type
1	A	287	LEU
1	A	297	PHE
1	A	303	PHE
1	A	306	ASN
1	A	307	ILE
1	A	309	TRP
1	A	358	LEU
1	B	129	LEU
1	B	130	ARG
1	B	132	LEU
1	B	151	VAL
1	B	172	SER
1	B	177	SER
1	B	201	PRO
1	B	202	MET
1	B	250	THR
1	B	268	SER
1	B	279	PRO
1	B	297	PHE
1	B	300	PRO
1	B	307	ILE
1	B	358	LEU
1	B	360	ILE
1	C	126	MET
1	C	129	LEU
1	C	131	ARG
1	C	172	SER
1	C	188	HIS
1	C	196	VAL
1	C	202	MET
1	C	210	ARG
1	C	224	LEU
1	C	234	GLU
1	C	250	THR
1	C	256	ASP
1	C	280	ARG
1	C	288	LEU
1	C	301	GLN
1	C	306	ASN
1	C	317	LYS
1	C	346	SER
1	D	130	ARG

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Mol	Chain	Res	Type
1	D	133	THR
1	D	172	SER
1	D	202	MET
1	D	210	ARG
1	D	215	LEU
1	D	250	THR
1	D	288	LEU
1	D	295	TYR
1	D	306	ASN
1	D	309	TRP
1	D	354	VAL
1	D	359	THR
1	E	126	MET
1	E	131	ARG
1	E	148	LEU
1	E	150	TYR
1	E	151	VAL
1	E	172	SER
1	E	188	HIS
1	E	202	MET
1	E	229	THR
1	E	236	LEU
1	E	239	VAL
1	E	250	THR
1	E	279	PRO
1	E	303	PHE
1	E	304	THR
1	E	305	SER
1	E	306	ASN
1	E	358	LEU
1	F	120	GLN
1	F	121	ILE
1	F	125	ILE
1	F	132	LEU
1	F	133	THR
1	F	145	SER
1	F	172	SER
1	F	188	HIS
1	F	193	SER
1	F	202	MET
1	F	224	LEU
1	F	250	THR

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Mol	Chain	Res	Type
1	F	279	PRO
1	F	280	ARG
1	F	301	GLN
1	F	303	PHE
1	F	346	SER
1	F	354	VAL
1	F	358	LEU
1	G	120	GLN
1	G	121	ILE
1	G	124	ILE
1	G	130	ARG
1	G	131	ARG
1	G	136	ASP
1	G	172	SER
1	G	195	GLN
1	G	196	VAL
1	G	198	ASP
1	G	205	SER
1	G	245	THR
1	G	256	ASP
1	G	301	GLN
1	G	311	LEU
1	G	359	THR
1	G	372	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	179	GLN
1	A	191	GLN
1	A	237	ASN
1	A	306	ASN
1	A	334	GLN
1	B	179	GLN
1	B	182	ASN
1	B	208	ASN
1	B	222	GLN
1	B	232	ASN
1	B	237	ASN
1	B	306	ASN
1	B	334	GLN

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Mol	Chain	Res	Type
1	C	179	GLN
1	C	208	ASN
1	C	225	ASN
1	C	306	ASN
1	D	179	GLN
1	D	204	GLN
1	D	208	ASN
1	D	222	GLN
1	D	232	ASN
1	D	283	HIS
1	D	291	ASN
1	D	301	GLN
1	D	334	GLN
1	E	188	HIS
1	E	204	GLN
1	E	208	ASN
1	E	222	GLN
1	E	232	ASN
1	E	237	ASN
1	E	306	ASN
1	F	179	GLN
1	F	191	GLN
1	F	208	ASN
1	F	222	GLN
1	F	237	ASN
1	F	301	GLN
1	F	334	GLN
1	F	352	ASN
1	G	179	GLN
1	G	195	GLN
1	G	232	ASN
1	G	301	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	231:ASP	C	232:ASN	N	0.84

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	254/282 (90%)	0.84	32 (12%) 8 14	47, 95, 95, 95	0
1	B	254/282 (90%)	0.90	33 (12%) 7 13	54, 114, 114, 114	0
1	C	254/282 (90%)	0.80	23 (9%) 15 19	57, 122, 122, 122	0
1	D	254/282 (90%)	0.85	30 (11%) 9 15	50, 103, 103, 103	0
1	E	254/282 (90%)	0.79	35 (13%) 6 13	54, 114, 114, 114	0
1	F	254/282 (90%)	0.76	21 (8%) 17 22	51, 104, 104, 104	0
1	G	254/282 (90%)	0.91	38 (14%) 5 12	61, 132, 132, 132	0
All	All	1778/1974 (90%)	0.84	212 (11%) 9 14	47, 114, 132, 132	0

All (212) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	171	GLU	13.2
1	A	340	ASP	9.2
1	B	191	GLN	6.3
1	A	250	THR	6.2
1	B	159	ASN	6.0
1	G	382	SER	6.0
1	D	383	SER	5.5
1	D	348	GLU	5.2
1	G	171	GLU	5.2
1	C	344	GLU	5.0
1	F	383	SER	5.0
1	B	355	LYS	4.9
1	A	171	GLU	4.6
1	B	348	GLU	4.6
1	B	382	SER	4.5
1	G	291	ASN	4.4
1	C	339	MET	4.4

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Mol	Chain	Res	Type	RSRZ
1	D	267	GLU	4.3
1	E	171	GLU	4.3
1	C	340	ASP	4.2
1	D	185	THR	4.2
1	C	159	ASN	4.1
1	G	191	GLN	4.1
1	B	291	ASN	4.1
1	F	382	SER	4.1
1	B	379	GLY	4.1
1	E	303	PHE	4.0
1	F	171	GLU	4.0
1	B	371	TYR	3.9
1	C	191	GLN	3.9
1	C	383	SER	3.9
1	G	383	SER	3.9
1	A	348	GLU	3.8
1	B	120	GLN	3.8
1	B	171	GLU	3.8
1	D	141	GLY	3.8
1	F	291	ASN	3.7
1	F	231	ASP	3.7
1	B	299	GLY	3.6
1	G	123	GLY	3.6
1	E	291	ASN	3.6
1	A	141	GLY	3.6
1	B	251	GLY	3.5
1	B	195	GLN	3.4
1	B	295	TYR	3.4
1	G	144	SER	3.4
1	G	159	ASN	3.4
1	A	184	LYS	3.3
1	B	340	ASP	3.3
1	F	368	LEU	3.3
1	C	267	GLU	3.2
1	E	250	THR	3.2
1	E	378	LYS	3.2
1	D	378	LYS	3.2
1	F	340	ASP	3.2
1	G	158	ASN	3.1
1	D	173	ASP	3.1
1	G	220	GLU	3.1
1	A	365	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	209	ASN	3.0
1	B	158	ASN	3.0
1	E	219	GLU	3.0
1	A	230	GLY	3.0
1	D	127	PRO	3.0
1	E	271	SER	3.0
1	G	348	GLU	3.0
1	A	194	ARG	3.0
1	D	153	GLU	2.9
1	F	346	SER	2.9
1	A	190	VAL	2.9
1	D	151	VAL	2.9
1	G	344	GLU	2.9
1	E	213	TYR	2.9
1	A	325	THR	2.9
1	G	354	VAL	2.9
1	B	248	ASN	2.9
1	E	230	GLY	2.9
1	C	231	ASP	2.9
1	G	340	ASP	2.9
1	E	292	GLU	2.9
1	B	271	SER	2.9
1	B	339	MET	2.8
1	A	234	GLU	2.8
1	E	372	ARG	2.8
1	F	159	ASN	2.8
1	C	368	LEU	2.8
1	D	303	PHE	2.8
1	A	382	SER	2.8
1	D	325	THR	2.8
1	B	378	LYS	2.8
1	E	234	GLU	2.8
1	G	267	GLU	2.8
1	E	366	LEU	2.8
1	D	344	GLU	2.8
1	D	209	ASN	2.7
1	A	123	GLY	2.7
1	G	122	PRO	2.7
1	B	380	THR	2.7
1	G	119	MET	2.7
1	C	119	MET	2.7
1	G	292	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	185	THR	2.7
1	D	158	ASN	2.6
1	D	222	GLN	2.6
1	D	351	ASP	2.6
1	B	182	ASN	2.6
1	F	355	LYS	2.6
1	D	346	SER	2.6
1	E	350	ARG	2.6
1	F	250	THR	2.6
1	E	149	GLU	2.6
1	E	210	ARG	2.6
1	E	379	GLY	2.6
1	D	254	ARG	2.6
1	G	157	THR	2.6
1	A	144	SER	2.5
1	F	298	GLY	2.5
1	E	348	GLU	2.5
1	C	346	SER	2.5
1	D	338	ARG	2.5
1	E	120	GLN	2.5
1	G	304	THR	2.5
1	C	291	ASN	2.5
1	E	211	LEU	2.5
1	A	374	THR	2.4
1	B	177	SER	2.4
1	A	198	ASP	2.4
1	C	350	ARG	2.4
1	F	146	ASN	2.4
1	D	154	GLU	2.4
1	B	290	ASP	2.4
1	B	292	GLU	2.4
1	G	334	GLN	2.4
1	E	119	MET	2.4
1	G	141	GLY	2.4
1	C	365	ARG	2.4
1	D	230	GLY	2.4
1	A	210	ARG	2.4
1	G	337	ASP	2.4
1	E	146	ASN	2.4
1	G	368	LEU	2.4
1	G	345	VAL	2.4
1	D	274	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	G	310	GLY	2.3
1	E	142	ARG	2.3
1	G	130	ARG	2.3
1	A	133	THR	2.3
1	E	173	ASP	2.3
1	E	383	SER	2.3
1	B	250	THR	2.3
1	B	368	LEU	2.3
1	B	185	THR	2.2
1	A	135	ARG	2.2
1	C	330	ASP	2.2
1	E	340	ASP	2.2
1	F	297	PHE	2.2
1	B	144	SER	2.2
1	A	154	GLU	2.2
1	G	237	ASN	2.2
1	B	293	GLY	2.2
1	G	308	MET	2.2
1	G	198	ASP	2.2
1	C	145	SER	2.2
1	F	204	GLN	2.2
1	E	295	TYR	2.2
1	D	174	ILE	2.2
1	A	189	TRP	2.2
1	A	231	ASP	2.1
1	A	379	GLY	2.1
1	D	159	ASN	2.1
1	G	250	THR	2.1
1	D	172	SER	2.1
1	G	149	GLU	2.1
1	G	234	GLU	2.1
1	F	147	ALA	2.1
1	B	260	HIS	2.1
1	A	380	THR	2.1
1	G	120	GLN	2.1
1	C	367	ALA	2.1
1	A	124	ILE	2.1
1	E	135	ARG	2.1
1	A	159	ASN	2.1
1	G	146	ASN	2.1
1	B	374	THR	2.1
1	B	367	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	225	ASN	2.1
1	D	250	THR	2.1
1	E	248	ASN	2.1
1	E	294	ARG	2.1
1	C	356	ASN	2.1
1	F	157	THR	2.1
1	D	171	GLU	2.1
1	E	269	GLU	2.1
1	C	194	ARG	2.0
1	F	123	GLY	2.0
1	A	180	THR	2.0
1	C	241	THR	2.0
1	F	284	ASN	2.0
1	C	351	ASP	2.0
1	D	192	ALA	2.0
1	E	293	GLY	2.0
1	G	227	ASP	2.0
1	F	245	THR	2.0
1	E	212	MET	2.0
1	E	365	ARG	2.0
1	F	274	GLY	2.0
1	A	351	ASP	2.0
1	D	326	VAL	2.0
1	A	363	GLU	2.0
1	E	355	LYS	2.0
1	G	172	SER	2.0
1	G	271	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.