



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2017 – 06:53 PM EDT

PDB ID : 5H2T
Title : Structure of trehalose synthase
Authors : Wang, D.; Huang, H.; Zhou, J.; Jiang, L.
Deposited on : unknown
Resolution : 2.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

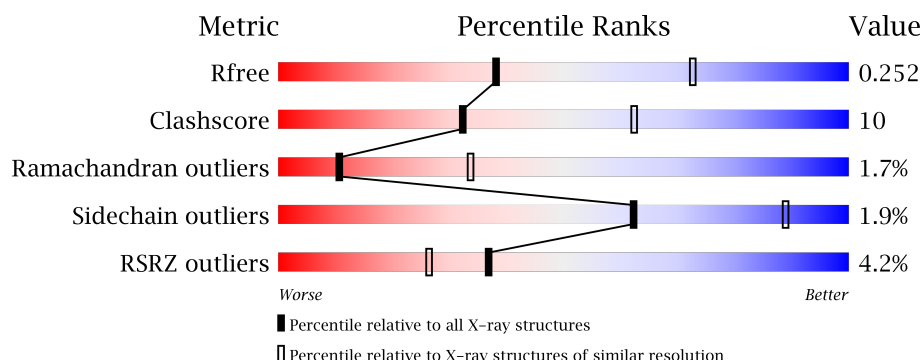
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
R_{free}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	601	<div> <div>0.1%</div> <div> <div></div> <div>75%</div> <div>15%</div> <div>9%</div> </div> </div>
1	B	601	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>15%</div> <div>9%</div> </div> </div>
1	C	601	<div> <div>2%</div> <div> <div></div> <div>70%</div> <div>19%</div> <div>9%</div> </div> </div>
1	D	601	<div> <div>4%</div> <div> <div></div> <div>72%</div> <div>16%</div> <div>9%</div> </div> </div>
1	E	601	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>19%</div> <div>9%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	601	<div><div></div><div>5%</div><div>67%</div><div>20%</div><div>•</div><div>9%</div></div>
1	G	601	<div><div></div><div>3%</div><div>71%</div><div>18%</div><div>•</div><div>9%</div></div>
1	H	601	<div><div></div><div>10%</div><div>61%</div><div>24%</div><div>• •</div><div>11%</div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 35620 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.

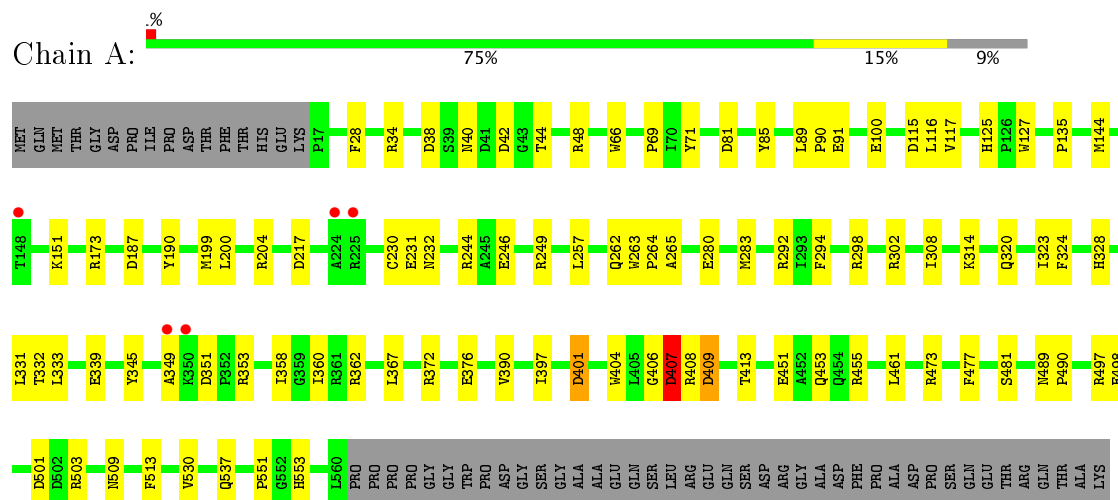
- Molecule 1 is a protein called Trehalose synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	544	Total	C	N	O	S	0	0	0
			4462	2858	763	818	23			
1	B	544	Total	C	N	O	S	0	0	0
			4462	2858	763	818	23			
1	C	544	Total	C	N	O	S	0	0	0
			4462	2858	763	818	23			
1	D	544	Total	C	N	O	S	0	0	0
			4462	2858	763	818	23			
1	E	544	Total	C	N	O	S	0	0	0
			4462	2858	763	818	23			
1	F	544	Total	C	N	O	S	0	0	0
			4462	2858	763	818	23			
1	G	544	Total	C	N	O	S	0	0	0
			4462	2858	763	818	23			
1	H	536	Total	C	N	O	S	0	0	0
			4386	2810	748	805	23			

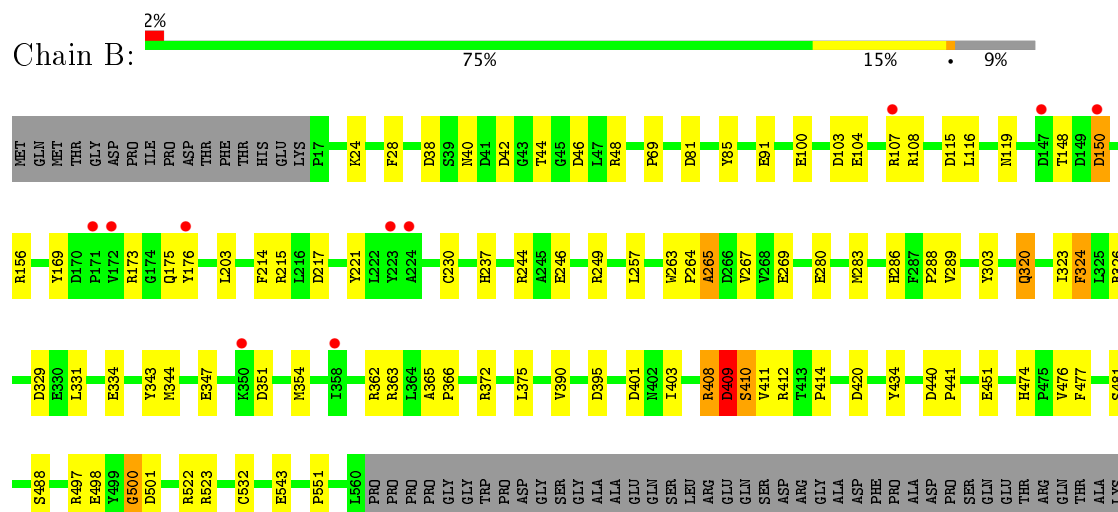
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Trehalose synthase

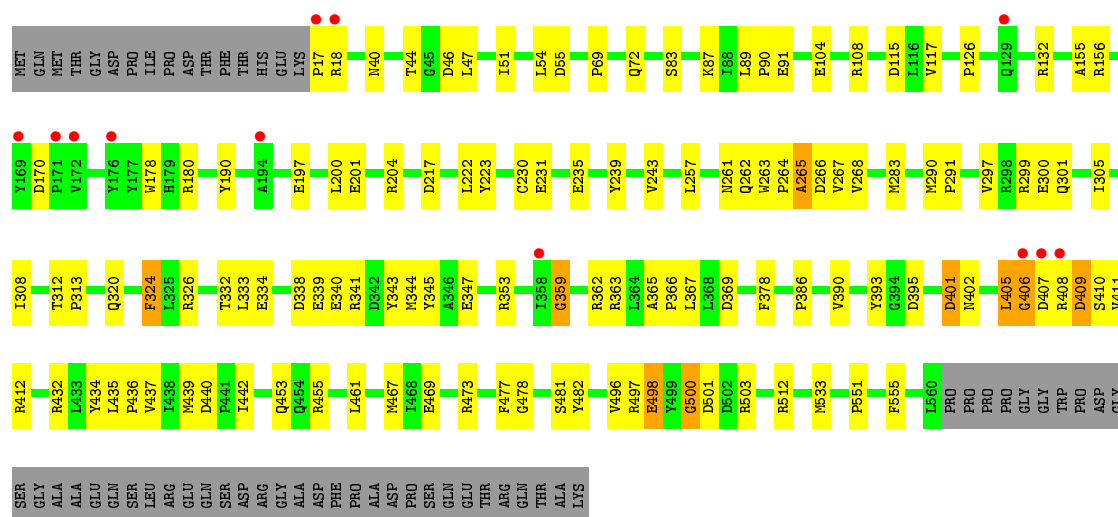


• Molecule 1: Trehalose synthase

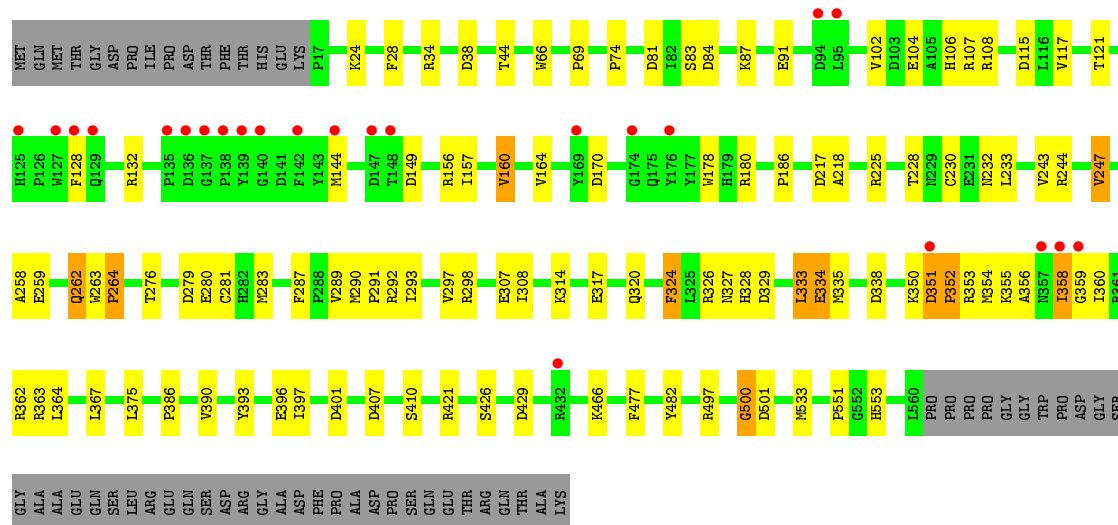
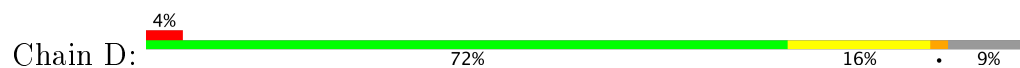


• Molecule 1: Trehalose synthase

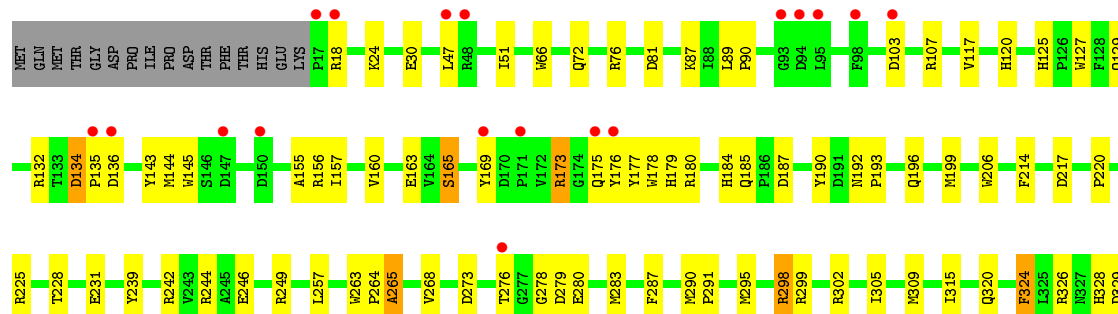


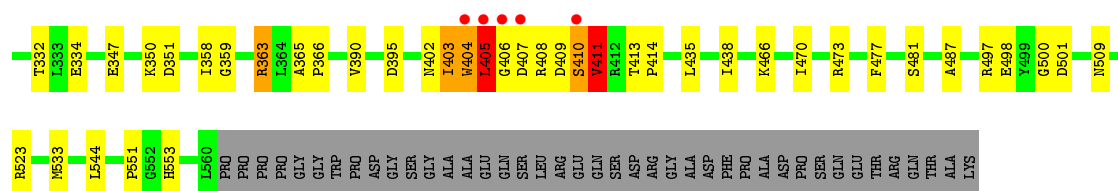


• Molecule 1: Trehalose synthase

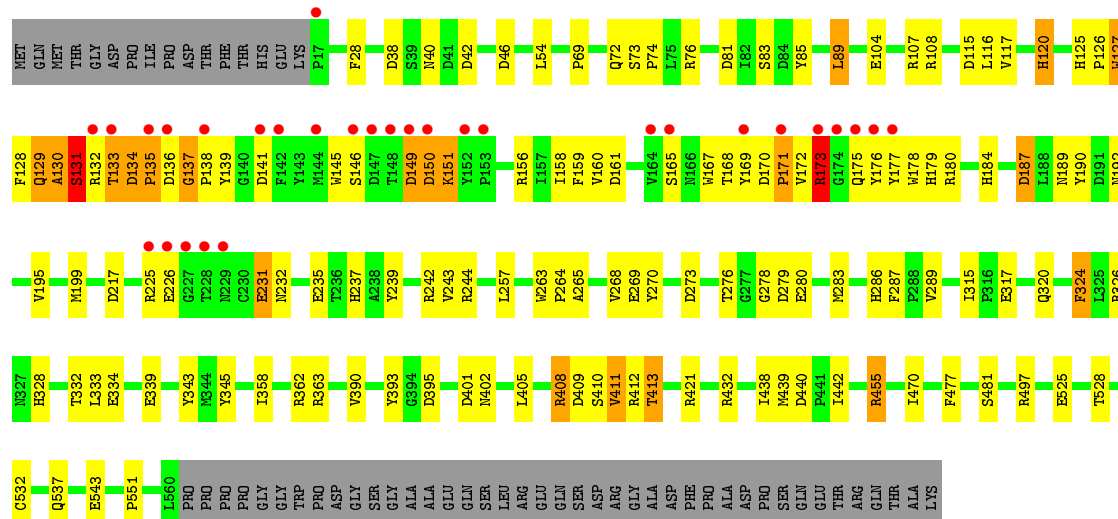


• Molecule 1: Trehalose synthase

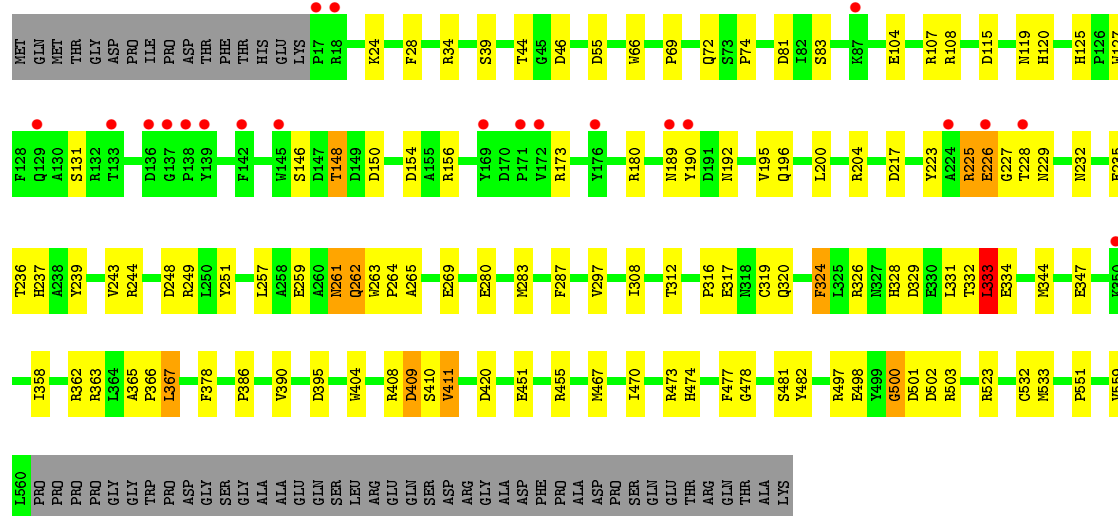




• Molecule 1: Trehalose synthase

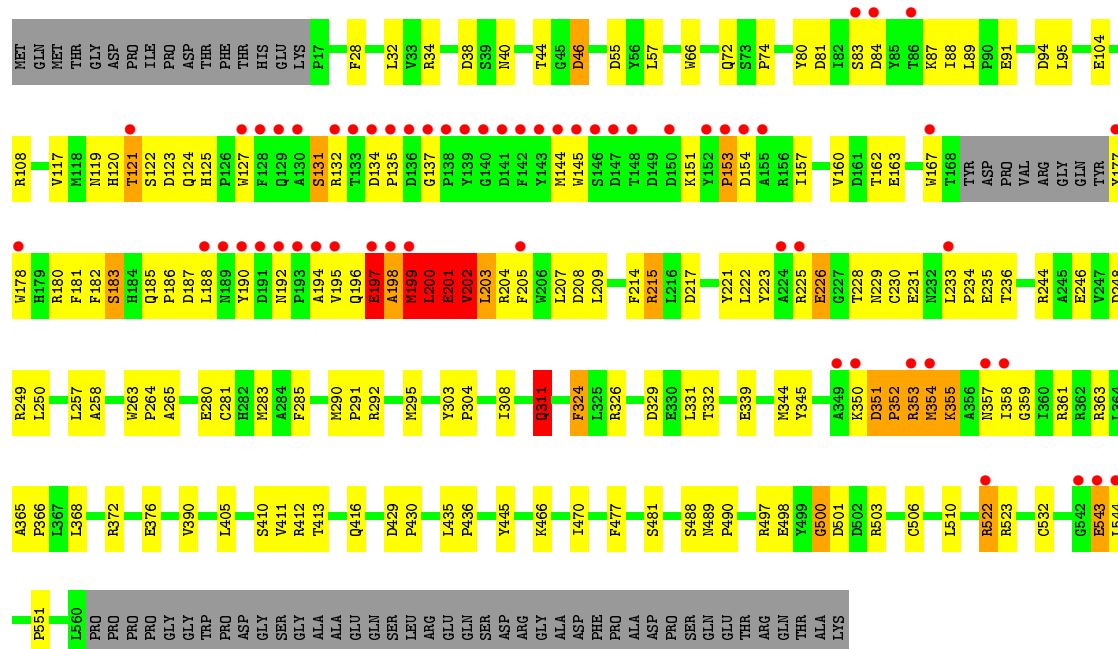


• Molecule 1: Trehalose synthase



• Molecule 1: Trehalose synthase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	248.76Å 133.12Å 211.78Å 90.00° 112.54° 90.00°	Depositor
Resolution (Å)	43.57 – 2.80 49.18 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (43.57-2.80) 99.2 (49.18-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.10.1-2155	Depositor
R, R_{free}	0.205 , 0.252 0.205 , 0.252	Depositor DCC
R_{free} test set	7737 reflections (4.95%)	DCC
Wilson B-factor (Å ²)	46.0	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 32.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	35620	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.17% 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	0.65	0/4599	0.69	1/6269 (0.0%)
1	B	0.63	1/4599 (0.0%)	0.68	2/6269 (0.0%)
1	C	0.59	0/4599	0.67	1/6269 (0.0%)
1	D	0.59	0/4599	0.69	1/6269 (0.0%)
1	E	0.59	0/4599	0.69	4/6269 (0.1%)
1	F	0.61	0/4599	0.76	6/6269 (0.1%)
1	G	0.59	1/4599 (0.0%)	0.70	4/6269 (0.1%)
1	H	0.61	1/4519 (0.0%)	0.78	6/6159 (0.1%)
All	All	0.61	3/36712 (0.0%)	0.71	25/50042 (0.0%)

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	D	0	2
1	E	0	2
1	F	0	2
1	G	0	2
1	H	0	9
All	All	0	18

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	404	TRP	CD2-CE2	7.18	1.50	1.41
1	H	506	CYS	CB-SG	-5.55	1.72	1.81
1	B	532	CYS	CB-SG	-5.33	1.73	1.81

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	200	LEU	CA-CB-CG	11.07	140.76	115.30
1	G	333	LEU	CA-CB-CG	9.66	137.52	115.30
1	G	404	TRP	CG-CD2-CE3	7.93	141.03	133.90
1	H	311	GLN	CA-CB-CG	6.89	128.57	113.40
1	F	89	LEU	CA-CB-CG	6.70	130.70	115.30
1	H	201	GLU	N-CA-C	-6.67	92.99	111.00
1	E	134	ASP	CB-CG-OD1	6.06	123.75	118.30
1	H	197	GLU	CA-CB-CG	5.91	126.39	113.40
1	G	404	TRP	CD1-CG-CD2	5.76	110.91	106.30
1	C	359	GLY	N-CA-C	-5.57	99.17	113.10
1	H	510	LEU	CA-CB-CG	-5.54	102.56	115.30
1	B	409	ASP	N-CA-C	-5.50	96.14	111.00
1	F	408	ARG	N-CA-C	-5.49	96.19	111.00
1	A	332	THR	N-CA-C	-5.46	96.25	111.00
1	E	363	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	F	411	VAL	N-CA-C	-5.38	96.47	111.00
1	E	411	VAL	N-CA-C	-5.34	96.58	111.00
1	F	173	ARG	CB-CG-CD	5.34	125.48	111.60
1	B	408	ARG	N-CA-C	-5.30	96.70	111.00
1	F	137	GLY	C-N-CD	-5.25	109.05	120.60
1	G	404	TRP	CE2-CD2-CG	-5.23	103.12	107.30
1	D	333	LEU	CB-CA-C	5.19	120.07	110.20
1	H	202	VAL	CA-C-N	-5.18	105.80	117.20
1	F	131	SER	N-CA-C	5.14	124.87	111.00
1	E	405	LEU	CA-CB-CG	5.13	127.10	115.30

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	407	ASP	Peptide
1	D	351	ASP	Peptide
1	D	352	PRO	Peptide
1	E	165	SER	Peptide
1	E	410	SER	Peptide
1	F	131	SER	Peptide
1	F	149	ASP	Peptide
1	G	225	ARG	Peptide
1	G	333	LEU	Peptide
1	H	131	SER	Peptide
1	H	196	GLN	Peptide
1	H	199	MET	Peptide
1	H	200	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	H	202	VAL	Peptide
1	H	350	LYS	Peptide
1	H	352	PRO	Peptide
1	H	353	ARG	Peptide
1	H	543	GLU	Peptide

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	4462	0	4252	59	0
1	B	4462	0	4252	64	0
1	C	4462	0	4252	81	0
1	D	4462	0	4252	78	0
1	E	4462	0	4252	90	0
1	F	4462	0	4252	114	0
1	G	4462	0	4252	79	0
1	H	4386	0	4178	141	0
All	All	35620	0	33942	692	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 10.

All (692) 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:D:356:ALA:HB1	1:D:360:ILE:H	0.99	1.13
1:D:334:GLU:N	1:D:358:ILE:O	1.99	0.94
1:D:356:ALA:HB1	1:D:360:ILE:N	1.83	0.94
1:H:201:GLU:O	1:H:204:ARG:N	2.04	0.91
1:A:125:HIS:HD2	1:A:127:TRP:H	1.20	0.90
1:F:133:THR:HG23	1:F:134:ASP:HA	1.54	0.90
1:D:352:PRO:HA	1:D:354:MET:HG2	1.56	0.87
1:E:196:GLN:OE1	1:E:242:ARG:NH1	2.07	0.87
1:D:333:LEU:HB3	1:D:359:GLY:H	1.40	0.85
1:G:332:THR:HG23	1:G:334:GLU:H	1.38	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:477:PHE:O	1:D:497:ARG:NH2	2.10	0.85
1:F:137:GLY:N	1:F:139:TYR:H	1.76	0.84
1:E:407:ASP:OD1	1:E:410:SER:N	2.09	0.83
1:A:232:ASN:ND2	1:A:262:GLN:HE22	1.76	0.83
1:B:119:ASN:HD21	1:B:221:TYR:HB2	1.43	0.82
1:H:197:GLU:O	1:H:200:LEU:N	2.09	0.82
1:F:137:GLY:H	1:F:139:TYR:H	1.28	0.82
1:G:477:PHE:O	1:G:497:ARG:NH2	2.12	0.82
1:C:551:PRO:HG3	1:E:551:PRO:HG3	1.61	0.82
1:C:72:GLN:HG3	1:C:87:LYS:HD3	1.62	0.81
1:B:119:ASN:ND2	1:B:221:TYR:HB2	1.94	0.81
1:A:372:ARG:NH1	1:A:376:GLU:OE2	2.13	0.81
1:F:170:ASP:HB2	1:F:173:ARG:HG3	1.63	0.80
1:F:332:THR:O	1:F:334:GLU:N	2.15	0.80
1:C:156:ARG:O	1:C:180:ARG:NH1	2.15	0.80
1:H:355:LYS:N	1:H:357:ASN:OD1	2.14	0.80
1:E:477:PHE:O	1:E:497:ARG:NH2	2.15	0.79
1:H:226:GLU:H	1:H:228:THR:H	1.28	0.78
1:B:551:PRO:HG3	1:D:551:PRO:HG3	1.66	0.77
1:F:117:VAL:HG11	1:F:120:HIS:CE1	2.19	0.77
1:H:522:ARG:HH22	1:H:544:LEU:HA	1.50	0.77
1:H:225:ARG:HG2	1:H:233:LEU:HD13	1.66	0.76
1:C:477:PHE:O	1:C:497:ARG:NH2	2.18	0.76
1:F:131:SER:HB3	1:F:173:ARG:HB3	1.67	0.76
1:B:363:ARG:HG3	1:B:395:ASP:OD1	1.86	0.76
1:F:551:PRO:HG3	1:G:551:PRO:HG3	1.68	0.76
1:H:200:LEU:O	1:H:201:GLU:HG3	1.87	0.75
1:B:477:PHE:O	1:B:497:ARG:NH2	2.19	0.75
1:F:165:SER:OG	1:F:167:TRP:O	2.05	0.75
1:F:363:ARG:HG2	1:F:395:ASP:OD1	1.87	0.74
1:F:455:ARG:HG3	1:F:455:ARG:HH11	1.51	0.74
1:A:498:GLU:OE2	1:A:503:ARG:NH1	2.20	0.73
1:A:246:GLU:OE2	1:A:249:ARG:NH1	2.22	0.73
1:G:244:ARG:HD3	1:G:280:GLU:O	1.88	0.73
1:E:470:ILE:HD13	1:E:473:ARG:HH21	1.54	0.73
1:C:406:GLY:O	1:C:407:ASP:HB3	1.89	0.72
1:C:408:ARG:O	1:C:409:ASP:HB2	1.89	0.72
1:F:170:ASP:N	1:F:170:ASP:OD1	2.19	0.72
1:G:226:GLU:O	1:G:228:THR:HG23	1.90	0.71
1:H:351:ASP:HB3	1:H:352:PRO:HA	1.72	0.71
1:H:498:GLU:OE2	1:H:523:ARG:NH2	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:332:THR:O	1:C:334:GLU:N	2.23	0.71
1:A:477:PHE:O	1:A:497:ARG:NH2	2.24	0.71
1:F:477:PHE:O	1:F:497:ARG:NH2	2.24	0.70
1:G:55:ASP:OD1	1:G:108:ARG:NH2	2.22	0.70
1:F:283:MET:HG2	1:F:320:GLN:HB3	1.72	0.70
1:F:156:ARG:O	1:F:180:ARG:NH1	2.24	0.70
1:H:83:SER:O	1:H:125:HIS:ND1	2.25	0.70
1:B:409:ASP:O	1:B:411:VAL:N	2.21	0.70
1:D:356:ALA:CB	1:D:360:ILE:H	1.93	0.69
1:F:409:ASP:O	1:F:410:SER:OG	2.06	0.69
1:C:362:ARG:HB2	1:C:367:LEU:HD13	1.73	0.69
1:E:72:GLN:HG3	1:E:87:LYS:HD3	1.75	0.69
1:E:184:HIS:HD2	1:E:185:GLN:HG3	1.58	0.69
1:F:40:ASN:ND2	1:F:42:ASP:OD1	2.26	0.69
1:G:328:HIS:NE2	1:G:358:ILE:O	2.25	0.69
1:A:551:PRO:HG3	1:H:551:PRO:HG3	1.74	0.69
1:A:406:GLY:O	1:A:408:ARG:N	2.25	0.68
1:E:156:ARG:O	1:E:180:ARG:NH1	2.27	0.68
1:C:467:MET:HE3	1:C:555:PHE:HZ	1.59	0.68
1:G:232:ASN:OD1	1:G:262:GLN:NE2	2.27	0.68
1:H:40:ASN:ND2	1:H:46:ASP:OD1	2.27	0.68
1:D:232:ASN:ND2	1:D:262:GLN:OE1	2.27	0.68
1:E:407:ASP:OD1	1:E:409:ASP:N	2.27	0.67
1:F:276:THR:HG23	1:F:278:GLY:H	1.59	0.67
1:C:353:ARG:NH1	1:C:369:ASP:OD2	2.28	0.67
1:H:372:ARG:NH1	1:H:376:GLU:OE2	2.27	0.67
1:C:363:ARG:HG2	1:C:395:ASP:OD1	1.94	0.67
1:H:200:LEU:HB3	1:H:202:VAL:N	2.10	0.67
1:E:405:LEU:HD23	1:E:435:LEU:HD22	1.77	0.67
1:F:128:PHE:O	1:F:130:ALA:N	2.28	0.66
1:F:104:GLU:OE1	1:F:108:ARG:NH1	2.27	0.66
1:E:145:TRP:CH2	1:E:173:ARG:HD3	2.30	0.66
1:H:229:ASN:O	1:H:231:GLU:N	2.29	0.66
1:F:130:ALA:HA	1:F:132:ARG:H	1.58	0.66
1:H:120:HIS:CD2	1:H:185:GLN:HB3	2.30	0.66
1:H:498:GLU:HG2	1:H:503:ARG:HG2	1.78	0.66
1:G:473:ARG:O	1:G:474:HIS:HD2	1.79	0.66
1:C:132:ARG:HD2	1:C:170:ASP:OD2	1.95	0.66
1:H:198:ALA:C	1:H:200:LEU:N	2.50	0.66
1:H:470:ILE:HD13	1:H:532:CYS:HB3	1.78	0.66
1:C:266:ASP:OD1	1:C:341:ARG:NH1	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:72:GLN:HA	1:F:89:LEU:HD13	1.77	0.65
1:E:295:MET:SD	1:E:298:ARG:NH1	2.69	0.65
1:H:500:GLY:O	1:H:501:ASP:HB2	1.96	0.65
1:H:257:LEU:HG	1:H:283:MET:HB2	1.77	0.65
1:B:498:GLU:OE2	1:B:523:ARG:NH1	2.30	0.65
1:C:409:ASP:HA	1:C:412:ARG:HB2	1.79	0.65
1:E:332:THR:O	1:E:334:GLU:N	2.30	0.65
1:D:354:MET:HG3	1:D:355:LYS:N	2.12	0.65
1:F:180:ARG:NH2	1:F:231:GLU:OE1	2.29	0.65
1:G:287:PHE:CE1	1:G:329:ASP:HB3	2.32	0.65
1:G:320:GLN:NE2	1:G:478:GLY:O	2.28	0.65
1:H:188:LEU:HD13	1:H:199:MET:HE3	1.77	0.65
1:D:156:ARG:O	1:D:180:ARG:NH1	2.30	0.64
1:H:194:ALA:C	1:H:197:GLU:HB3	2.16	0.64
1:A:44:THR:HG21	1:A:91:GLU:HG2	1.78	0.64
1:E:276:THR:HG21	1:E:279:ASP:HB3	1.78	0.64
1:H:95:LEU:HD23	1:H:205:PHE:HZ	1.61	0.64
1:B:40:ASN:ND2	1:B:42:ASP:OD1	2.31	0.64
1:D:354:MET:HG3	1:D:355:LYS:HG3	1.79	0.64
1:D:355:LYS:HD2	1:D:362:ARG:HG3	1.80	0.64
1:G:237:HIS:CE1	1:G:269:GLU:HG2	2.33	0.64
1:H:203:LEU:HD12	1:H:203:LEU:H	1.63	0.64
1:E:163:GLU:HG3	1:E:165:SER:HB3	1.79	0.64
1:F:363:ARG:NH1	1:F:393:TYR:O	2.31	0.63
1:C:104:GLU:OE1	1:C:108:ARG:NH1	2.31	0.63
1:H:95:LEU:HD23	1:H:205:PHE:CZ	2.34	0.63
1:B:522:ARG:HD3	1:B:543:GLU:HG3	1.80	0.63
1:E:295:MET:SD	1:E:298:ARG:NH2	2.72	0.63
1:E:283:MET:HG2	1:E:320:GLN:HB3	1.79	0.63
1:H:74:PRO:HD3	1:H:83:SER:OG	1.98	0.63
1:E:276:THR:HG23	1:E:278:GLY:H	1.64	0.63
1:F:273:ASP:O	1:F:276:THR:HG22	1.99	0.63
1:H:354:MET:HG3	1:H:357:ASN:OD1	1.98	0.62
1:D:334:GLU:H	1:D:358:ILE:C	2.02	0.62
1:H:477:PHE:O	1:H:497:ARG:NH2	2.33	0.62
1:H:134:ASP:HB3	1:H:137:GLY:HA3	1.82	0.62
1:D:132:ARG:HD2	1:D:170:ASP:OD2	1.99	0.62
1:B:173:ARG:NE	1:B:175:GLN:OE1	2.31	0.62
1:F:339:GLU:HG2	1:F:345:TYR:CZ	2.34	0.62
1:H:522:ARG:HH22	1:H:544:LEU:CA	2.12	0.62
1:F:131:SER:CB	1:F:173:ARG:HB3	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:156:ARG:O	1:G:180:ARG:NH2	2.29	0.62
1:A:360:ILE:HA	1:A:407:ASP:HB2	1.82	0.61
1:C:407:ASP:O	1:C:408:ARG:HG2	2.01	0.61
1:F:125:HIS:HD1	1:F:126:PRO:HD2	1.65	0.61
1:F:232:ASN:OD1	1:F:270:TYR:OH	2.11	0.61
1:F:328:HIS:NE2	1:F:358:ILE:O	2.33	0.61
1:G:263:TRP:CD2	1:G:264:PRO:HD2	2.35	0.61
1:D:28:PHE:HB2	1:D:390:VAL:HG22	1.83	0.61
1:E:145:TRP:HB3	1:E:175:GLN:NE2	2.15	0.61
1:E:328:HIS:NE2	1:E:358:ILE:O	2.33	0.61
1:H:225:ARG:O	1:H:228:THR:OG1	2.17	0.61
1:E:403:ILE:O	1:E:405:LEU:N	2.30	0.61
1:F:130:ALA:HA	1:F:132:ARG:N	2.15	0.61
1:A:257:LEU:HG	1:A:283:MET:HB2	1.82	0.60
1:H:190:TYR:HA	1:H:195:VAL:HG21	1.83	0.60
1:F:192:ASN:O	1:F:195:VAL:HG22	2.00	0.60
1:F:117:VAL:HA	1:F:217:ASP:HB2	1.81	0.60
1:E:295:MET:SD	1:E:298:ARG:CZ	2.90	0.60
1:A:190:TYR:OH	1:A:199:MET:HG3	2.01	0.60
1:C:55:ASP:OD1	1:C:108:ARG:NH2	2.29	0.60
1:D:355:LYS:HE3	1:D:367:LEU:HD23	1.83	0.60
1:E:134:ASP:HB2	1:E:136:ASP:OD1	2.02	0.60
1:H:339:GLU:HG3	1:H:345:TYR:CD2	2.36	0.60
1:F:40:ASN:N	1:F:40:ASN:OD1	2.34	0.60
1:C:434:TYR:O	1:C:435:LEU:HD12	2.02	0.60
1:D:354:MET:HG3	1:D:355:LYS:H	1.67	0.60
1:G:333:LEU:HD13	1:G:334:GLU:HG3	1.84	0.60
1:A:231:GLU:HB3	1:A:232:ASN:HD22	1.66	0.60
1:B:286:HIS:O	1:B:289:VAL:HG12	2.01	0.59
1:E:363:ARG:HG2	1:E:395:ASP:OD1	2.01	0.59
1:H:522:ARG:HH12	1:H:544:LEU:C	2.06	0.59
1:E:135:PRO:HB3	1:E:173:ARG:HH12	1.66	0.59
1:F:408:ARG:O	1:F:409:ASP:HB2	2.03	0.59
1:A:283:MET:HG2	1:A:320:GLN:HB3	1.84	0.59
1:D:283:MET:HG2	1:D:320:GLN:HB3	1.85	0.59
1:G:244:ARG:NH1	1:G:248:ASP:OD2	2.36	0.59
1:D:328:HIS:CE1	1:D:356:ALA:HB3	2.38	0.58
1:D:421:ARG:NH1	1:G:451:GLU:OE2	2.22	0.58
1:E:407:ASP:C	1:E:409:ASP:H	2.04	0.58
1:G:470:ILE:HD13	1:G:532:CYS:HB3	1.85	0.58
1:H:151:LYS:NZ	1:H:226:GLU:OE1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:329:ASP:OD1	1:G:332:THR:HG22	2.04	0.58
1:B:169:TYR:HB2	1:B:176:TYR:CE1	2.38	0.58
1:D:24:LYS:NZ	1:D:317:GLU:O	2.26	0.58
1:E:225:ARG:O	1:E:228:THR:HG22	2.04	0.58
1:F:362:ARG:HD2	1:F:401:ASP:OD2	2.04	0.58
1:B:362:ARG:CZ	1:B:403:ILE:HD11	2.32	0.58
1:C:261:ASN:ND2	1:C:261:ASN:O	2.37	0.58
1:F:76:ARG:HD3	1:F:184:HIS:CD2	2.38	0.58
1:D:333:LEU:HB3	1:D:359:GLY:N	2.15	0.58
1:E:298:ARG:NH2	1:E:351:ASP:HB2	2.18	0.58
1:G:72:GLN:HG3	1:G:83:SER:HB2	1.85	0.58
1:A:232:ASN:HD21	1:A:262:GLN:HE22	1.49	0.58
1:G:257:LEU:HG	1:G:283:MET:HB2	1.86	0.58
1:H:292:ARG:NH1	1:H:308:ILE:HG23	2.19	0.57
1:B:148:THR:OG1	1:B:150:ASP:OD2	2.18	0.57
1:C:339:GLU:HG2	1:C:345:TYR:CE2	2.39	0.57
1:D:351:ASP:C	1:D:353:ARG:H	2.07	0.57
1:H:326:ARG:HB2	1:H:361:ARG:NH1	2.19	0.57
1:F:150:ASP:OD1	1:F:151:LYS:N	2.28	0.57
1:G:473:ARG:O	1:G:474:HIS:CD2	2.58	0.57
1:B:451:GLU:OE2	1:F:421:ARG:NH1	2.31	0.57
1:C:500:GLY:O	1:C:501:ASP:HB2	2.05	0.57
1:H:203:LEU:O	1:H:207:LEU:HB2	2.05	0.57
1:H:263:TRP:CD2	1:H:264:PRO:HD2	2.38	0.57
1:A:125:HIS:CD2	1:A:127:TRP:H	2.11	0.57
1:B:103:ASP:HB3	1:B:107:ARG:NH1	2.19	0.57
1:B:257:LEU:HG	1:B:283:MET:HB2	1.86	0.57
1:E:145:TRP:HB3	1:E:175:GLN:HE21	1.69	0.57
1:G:498:GLU:OE2	1:G:523:ARG:NH2	2.38	0.57
1:D:74:PRO:HD3	1:D:83:SER:OG	2.04	0.57
1:E:324:PHE:CD1	1:E:326:ARG:HG2	2.40	0.56
1:E:302:ARG:NH2	1:E:487:ALA:O	2.37	0.56
1:F:244:ARG:HD2	1:F:280:GLU:O	2.05	0.56
1:A:408:ARG:O	1:A:409:ASP:HB2	2.04	0.56
1:B:263:TRP:CD2	1:B:264:PRO:HD2	2.40	0.56
1:G:363:ARG:HG2	1:G:395:ASP:OD1	2.05	0.56
1:H:246:GLU:OE2	1:H:249:ARG:NH2	2.27	0.56
1:H:38:ASP:OD1	1:H:40:ASN:ND2	2.38	0.56
1:E:129:GLN:OE1	1:E:132:ARG:NE	2.36	0.56
1:G:225:ARG:HE	1:G:235:GLU:HG2	1.70	0.56
1:H:201:GLU:O	1:H:204:ARG:HG3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:168:THR:HG23	1:F:179:HIS:NE2	2.20	0.56
1:G:362:ARG:HB2	1:G:367:LEU:HD13	1.87	0.56
1:F:257:LEU:HG	1:F:283:MET:HB2	1.88	0.56
1:H:87:LYS:HD2	1:H:87:LYS:N	2.20	0.56
1:D:364:LEU:HG	1:D:375:LEU:HD23	1.86	0.56
1:D:500:GLY:O	1:D:501:ASP:HB2	2.05	0.56
1:F:263:TRP:CD2	1:F:264:PRO:HD2	2.41	0.56
1:A:292:ARG:HG3	1:A:308:ILE:HG12	1.88	0.56
1:C:320:GLN:NE2	1:C:478:GLY:O	2.35	0.56
1:E:402:ASN:ND2	1:E:405:LEU:HD11	2.20	0.56
1:A:44:THR:HG21	1:A:91:GLU:CG	2.36	0.55
1:F:409:ASP:HA	1:F:412:ARG:HB2	1.88	0.55
1:H:119:ASN:ND2	1:H:187:ASP:OD1	2.39	0.55
1:C:469:GLU:OE2	1:C:473:ARG:NH1	2.39	0.55
1:F:170:ASP:HB2	1:F:173:ARG:CG	2.36	0.55
1:F:402:ASN:O	1:F:410:SER:HB2	2.06	0.55
1:H:329:ASP:OD1	1:H:332:THR:OG1	2.20	0.55
1:D:225:ARG:O	1:D:228:THR:HG22	2.06	0.55
1:H:84:ASP:CG	1:H:87:LYS:HD3	2.27	0.55
1:A:481:SER:O	1:A:497:ARG:HD2	2.07	0.55
1:B:244:ARG:HD2	1:B:280:GLU:O	2.06	0.55
1:C:362:ARG:HD2	1:C:401:ASP:OD2	2.06	0.55
1:D:149:ASP:OD2	1:F:169:TYR:OH	2.25	0.55
1:B:156:ARG:NH2	1:B:334:GLU:OE1	2.40	0.55
1:F:134:ASP:N	1:F:135:PRO:CD	2.70	0.55
1:F:146:SER:O	1:F:175:GLN:HB2	2.07	0.55
1:E:103:ASP:HB3	1:E:107:ARG:HH21	1.72	0.54
1:E:145:TRP:CZ2	1:E:173:ARG:HD3	2.42	0.54
1:F:76:ARG:HD3	1:F:184:HIS:CG	2.42	0.54
1:H:104:GLU:OE1	1:H:108:ARG:NH1	2.39	0.54
1:A:48:ARG:NH2	1:A:100:GLU:OE1	2.38	0.54
1:D:421:ARG:NH2	1:G:420:ASP:OD2	2.35	0.54
1:H:311:GLN:HA	1:H:311:GLN:HE21	1.72	0.54
1:C:498:GLU:HB3	1:C:503:ARG:HG2	1.90	0.54
1:E:405:LEU:HD22	1:E:405:LEU:O	2.08	0.54
1:F:470:ILE:HD13	1:F:532:CYS:HB3	1.89	0.54
1:C:69:PRO:HD3	1:C:115:ASP:HB2	1.89	0.54
1:D:218:ALA:N	1:D:259:GLU:OE1	2.30	0.54
1:F:76:ARG:HG2	1:F:184:HIS:CE1	2.41	0.54
1:H:324:PHE:CD1	1:H:326:ARG:HG2	2.43	0.54
1:D:66:TRP:CD1	1:D:66:TRP:C	2.81	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:358:ILE:H	1:D:359:GLY:HA3	1.72	0.54
1:F:286:HIS:O	1:F:289:VAL:HG12	2.07	0.54
1:H:163:GLU:OE2	1:H:183:SER:N	2.40	0.54
1:B:500:GLY:O	1:B:501:ASP:HB2	2.08	0.53
1:C:338:ASP:OD2	1:C:341:ARG:NH2	2.31	0.53
1:F:190:TYR:OH	1:F:199:MET:HG3	2.07	0.53
1:F:481:SER:O	1:F:497:ARG:HD2	2.08	0.53
1:G:467:MET:HE2	1:G:533:MET:SD	2.47	0.53
1:C:363:ARG:NH1	1:C:393:TYR:O	2.42	0.53
1:D:69:PRO:HD3	1:D:115:ASP:HB2	1.91	0.53
1:D:363:ARG:NH1	1:D:393:TYR:O	2.42	0.53
1:F:239:TYR:O	1:F:243:VAL:HG23	2.09	0.53
1:B:40:ASN:OD1	1:B:40:ASN:N	2.41	0.53
1:D:324:PHE:CD1	1:D:326:ARG:HG2	2.44	0.53
1:E:144:MET:HB2	1:E:178:TRP:HB3	1.90	0.53
1:E:268:VAL:HG23	1:E:315:ILE:HG22	1.91	0.53
1:C:44:THR:HG21	1:C:91:GLU:CG	2.39	0.53
1:F:28:PHE:HB2	1:F:390:VAL:HG22	1.91	0.53
1:B:104:GLU:OE1	1:B:108:ARG:NH1	2.41	0.53
1:C:263:TRP:CD2	1:C:264:PRO:HD2	2.44	0.53
1:H:215:ARG:HD2	1:H:285:PHE:CE2	2.44	0.53
1:A:328:HIS:NE2	1:A:358:ILE:O	2.41	0.52
1:H:162:THR:HG22	1:H:163:GLU:HG3	1.91	0.52
1:H:192:ASN:OD1	1:H:194:ALA:N	2.36	0.52
1:E:246:GLU:OE2	1:E:249:ARG:NH1	2.42	0.52
1:D:44:THR:HG21	1:D:91:GLU:OE1	2.09	0.52
1:D:81:ASP:N	1:D:81:ASP:OD1	2.40	0.52
1:F:525:GLU:OE2	1:F:543:GLU:HG2	2.08	0.52
1:G:74:PRO:HD3	1:G:83:SER:OG	2.10	0.52
1:B:38:ASP:OD1	1:B:40:ASN:OD1	2.26	0.52
1:F:156:ARG:HH21	1:F:158:ILE:HA	1.74	0.52
1:A:263:TRP:CD2	1:A:264:PRO:HD2	2.44	0.52
1:A:362:ARG:HB2	1:A:367:LEU:HD13	1.92	0.52
1:D:358:ILE:H	1:D:359:GLY:CA	2.23	0.52
1:B:289:VAL:HG11	1:B:323:ILE:HG22	1.91	0.52
1:G:474:HIS:CE1	1:G:559:VAL:HG21	2.45	0.52
1:B:408:ARG:O	1:B:409:ASP:HB3	2.10	0.51
1:E:120:HIS:CD2	1:E:185:GLN:HB3	2.46	0.51
1:H:34:ARG:HG3	1:H:44:THR:HG23	1.93	0.51
1:D:34:ARG:HG3	1:D:44:THR:HG23	1.92	0.51
1:D:429:ASP:OD1	1:G:455:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:PRO:HD3	1:B:115:ASP:HB2	1.92	0.51
1:B:362:ARG:NH2	1:B:403:ILE:HD11	2.25	0.51
1:C:440:ASP:OD2	1:C:442:ILE:N	2.32	0.51
1:G:261:ASN:C	1:G:262:GLN:HG2	2.30	0.51
1:C:44:THR:HG21	1:C:91:GLU:HG2	1.92	0.51
1:C:200:LEU:O	1:C:204:ARG:HG3	2.10	0.51
1:C:434:TYR:CD2	1:C:435:LEU:HD13	2.45	0.51
1:D:355:LYS:HE3	1:D:367:LEU:CD2	2.41	0.51
1:E:470:ILE:HD13	1:E:473:ARG:NH2	2.25	0.51
1:F:117:VAL:HG11	1:F:120:HIS:HE1	1.72	0.51
1:F:276:THR:HG21	1:F:279:ASP:HB3	1.93	0.51
1:G:190:TYR:O	1:G:196:GLN:NE2	2.44	0.51
1:H:353:ARG:NH2	1:H:368:LEU:HA	2.25	0.51
1:H:95:LEU:N	1:H:95:LEU:HD12	2.25	0.51
1:E:117:VAL:HA	1:E:217:ASP:HB2	1.92	0.51
1:H:200:LEU:HG	1:H:202:VAL:HA	1.91	0.51
1:E:498:GLU:OE2	1:E:523:ARG:NH1	2.44	0.51
1:F:137:GLY:N	1:F:139:TYR:N	2.54	0.51
1:A:81:ASP:OD1	1:A:81:ASP:N	2.44	0.51
1:H:351:ASP:HB3	1:H:354:MET:O	2.10	0.51
1:H:66:TRP:CZ3	1:H:390:VAL:HG11	2.45	0.51
1:D:102:VAL:O	1:D:106:HIS:ND1	2.43	0.50
1:H:104:GLU:CD	1:H:108:ARG:HH12	2.14	0.50
1:H:80:TYR:CD1	1:H:331:LEU:HD21	2.46	0.50
1:D:117:VAL:HA	1:D:217:ASP:HB2	1.92	0.50
1:E:184:HIS:CD2	1:E:185:GLN:HG3	2.42	0.50
1:F:170:ASP:HB2	1:F:173:ARG:HE	1.76	0.50
1:G:232:ASN:CG	1:G:262:GLN:HE22	2.13	0.50
1:C:324:PHE:CD1	1:C:326:ARG:HG2	2.46	0.50
1:D:263:TRP:CD2	1:D:264:PRO:HD2	2.46	0.50
1:D:359:GLY:O	1:D:407:ASP:HB3	2.11	0.50
1:H:203:LEU:HB3	1:H:207:LEU:HD12	1.93	0.50
1:C:257:LEU:HG	1:C:283:MET:HB2	1.92	0.50
1:F:69:PRO:HD3	1:F:115:ASP:HB2	1.93	0.50
1:H:351:ASP:HB3	1:H:352:PRO:CA	2.41	0.50
1:C:17:PRO:C	1:C:18:ARG:HG3	2.32	0.50
1:G:196:GLN:O	1:G:200:LEU:HD13	2.11	0.50
1:C:339:GLU:HG2	1:C:345:TYR:CZ	2.46	0.50
1:G:259:GLU:HG3	1:G:331:LEU:HD13	1.93	0.50
1:E:481:SER:O	1:E:497:ARG:HD2	2.11	0.50
1:F:440:ASP:OD1	1:F:442:ILE:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:132:ARG:CB	1:E:173:ARG:HG3	2.42	0.49
1:F:137:GLY:H	1:F:139:TYR:N	2.03	0.49
1:H:121:THR:HG22	1:H:122:SER:O	2.11	0.49
1:F:413:THR:HG21	1:F:438:ILE:HG13	1.94	0.49
1:H:215:ARG:HD2	1:H:285:PHE:HE2	1.77	0.49
1:E:257:LEU:HG	1:E:283:MET:HB2	1.94	0.49
1:E:404:TRP:CD1	1:H:436:PRO:HD3	2.48	0.49
1:F:129:GLN:O	1:F:132:ARG:HG3	2.12	0.49
1:B:362:ARG:HD2	1:B:401:ASP:OD2	2.13	0.49
1:E:135:PRO:HB3	1:E:173:ARG:NH1	2.27	0.49
1:F:324:PHE:CD1	1:F:326:ARG:HG2	2.47	0.49
1:H:201:GLU:HB3	1:H:204:ARG:HG2	1.93	0.49
1:E:239:TYR:O	1:E:242:ARG:HB2	2.12	0.49
1:H:199:MET:O	1:H:201:GLU:N	2.43	0.49
1:F:405:LEU:HB2	1:F:410:SER:HB3	1.95	0.49
1:A:28:PHE:HB2	1:A:390:VAL:HG22	1.95	0.49
1:F:190:TYR:HA	1:F:195:VAL:HG21	1.94	0.49
1:G:200:LEU:O	1:G:204:ARG:HG3	2.13	0.49
1:H:235:GLU:N	1:H:235:GLU:OE1	2.37	0.49
1:H:498:GLU:CD	1:H:523:ARG:HH21	2.16	0.48
1:A:360:ILE:HG23	1:A:407:ASP:HA	1.95	0.48
1:E:273:ASP:O	1:E:276:THR:HG22	2.13	0.48
1:G:28:PHE:HB2	1:G:390:VAL:HG22	1.94	0.48
1:H:132:ARG:HG3	1:H:135:PRO:HG3	1.95	0.48
1:H:200:LEU:HB3	1:H:201:GLU:C	2.34	0.48
1:H:88:ILE:HG22	1:H:95:LEU:HD12	1.95	0.48
1:G:125:HIS:HD2	1:G:127:TRP:HB2	1.77	0.48
1:E:298:ARG:HH11	1:E:299:ARG:HH21	1.62	0.48
1:H:223:TYR:HD2	1:H:236:THR:HG22	1.78	0.48
1:H:32:LEU:HD22	1:H:412:ARG:HB3	1.95	0.48
1:A:244:ARG:HD2	1:A:280:GLU:O	2.12	0.48
1:B:40:ASN:ND2	1:B:42:ASP:CG	2.67	0.48
1:E:169:TYR:HA	1:E:176:TYR:HA	1.96	0.48
1:G:498:GLU:OE1	1:G:523:ARG:NH1	2.40	0.48
1:H:416:GLN:HG2	1:H:445:TYR:HB3	1.95	0.48
1:A:530:VAL:HG22	1:A:537:GLN:HG2	1.94	0.48
1:F:74:PRO:HD3	1:F:83:SER:OG	2.13	0.48
1:G:217:ASP:HB3	1:G:331:LEU:HD21	1.96	0.48
1:H:258:ALA:HB2	1:H:281:CYS:SG	2.53	0.48
1:D:329:ASP:O	1:D:333:LEU:HA	2.14	0.48
1:D:386:PRO:HA	1:D:497:ARG:NH2	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:287:PHE:CE1	1:G:324:PHE:HZ	2.32	0.48
1:G:500:GLY:O	1:G:501:ASP:HB2	2.13	0.48
1:E:190:TYR:OH	1:E:199:MET:HG2	2.14	0.48
1:H:292:ARG:HG3	1:H:308:ILE:HG12	1.96	0.48
1:D:243:VAL:O	1:D:247:VAL:HG13	2.14	0.47
1:E:81:ASP:OD1	1:E:81:ASP:N	2.44	0.47
1:F:127:TRP:O	1:F:128:PHE:C	2.53	0.47
1:F:129:GLN:HE22	1:F:173:ARG:NH1	2.12	0.47
1:A:298:ARG:NH1	1:A:351:ASP:OD2	2.47	0.47
1:B:420:ASP:OD1	1:F:421:ARG:HB2	2.14	0.47
1:B:217:ASP:HB3	1:B:331:LEU:HD21	1.95	0.47
1:F:83:SER:O	1:F:126:PRO:HD2	2.13	0.47
1:F:179:HIS:HA	1:F:187:ASP:OD1	2.13	0.47
1:G:189:ASN:O	1:G:195:VAL:HG21	2.14	0.47
1:H:481:SER:O	1:H:497:ARG:HD2	2.14	0.47
1:B:409:ASP:C	1:B:411:VAL:H	2.11	0.47
1:C:362:ARG:CB	1:C:367:LEU:HD13	2.43	0.47
1:H:197:GLU:HG3	1:H:198:ALA:H	1.80	0.47
1:H:326:ARG:HB2	1:H:361:ARG:HH12	1.78	0.47
1:D:104:GLU:HG3	1:D:108:ARG:NH1	2.30	0.47
1:D:263:TRP:CG	1:D:264:PRO:HD2	2.49	0.47
1:G:474:HIS:CE1	1:G:559:VAL:CG2	2.98	0.47
1:H:167:TRP:CZ3	1:H:177:TYR:O	2.67	0.47
1:A:66:TRP:CD1	1:A:66:TRP:C	2.87	0.47
1:D:121:THR:O	1:D:186:PRO:HD2	2.15	0.47
1:E:134:ASP:HA	1:E:135:PRO:HD2	1.81	0.47
1:E:305:ILE:O	1:E:309:MET:HG2	2.15	0.47
1:B:351:ASP:HB3	1:B:354:MET:HB3	1.97	0.47
1:C:155:ALA:HB1	1:C:180:ARG:NH1	2.29	0.47
1:D:244:ARG:HD2	1:D:280:GLU:O	2.15	0.47
1:E:407:ASP:C	1:E:409:ASP:N	2.68	0.47
1:H:28:PHE:HB2	1:H:390:VAL:HG22	1.97	0.47
1:C:299:ARG:NH2	1:C:301:GLN:OE1	2.48	0.47
1:F:189:ASN:O	1:F:195:VAL:HG21	2.15	0.47
1:A:362:ARG:HD2	1:A:401:ASP:OD2	2.14	0.47
1:F:40:ASN:OD1	1:F:46:ASP:OD2	2.33	0.47
1:H:365:ALA:HB3	1:H:366:PRO:HD3	1.97	0.47
1:A:404:TRP:CD1	1:C:436:PRO:HD3	2.50	0.46
1:H:199:MET:O	1:H:202:VAL:HG23	2.15	0.46
1:C:197:GLU:O	1:C:201:GLU:HB2	2.14	0.46
1:F:145:TRP:CZ3	1:F:177:TYR:HB3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:163:GLU:OE1	1:H:182:PHE:HA	2.15	0.46
1:H:225:ARG:HH21	1:H:234:PRO:HD2	1.80	0.46
1:E:298:ARG:CZ	1:E:351:ASP:HB2	2.46	0.46
1:G:239:TYR:O	1:G:243:VAL:HG23	2.15	0.46
1:H:190:TYR:OH	1:H:199:MET:HG2	2.15	0.46
1:H:244:ARG:HD3	1:H:280:GLU:O	2.15	0.46
1:H:72:GLN:HA	1:H:89:LEU:HD13	1.96	0.46
1:D:144:MET:HB2	1:D:178:TRP:HB3	1.97	0.46
1:A:513:PHE:HE1	1:H:466:LYS:NZ	2.14	0.46
1:A:117:VAL:HA	1:A:217:ASP:HB2	1.97	0.46
1:C:239:TYR:O	1:C:243:VAL:HG23	2.15	0.46
1:D:358:ILE:N	1:D:359:GLY:CA	2.79	0.46
1:D:421:ARG:HB2	1:G:420:ASP:OD1	2.15	0.46
1:H:81:ASP:OD1	1:H:81:ASP:N	2.48	0.46
1:C:117:VAL:HA	1:C:217:ASP:HB2	1.98	0.46
1:C:47:LEU:O	1:C:51:ILE:HG13	2.16	0.46
1:G:131:SER:O	1:G:173:ARG:NH1	2.47	0.46
1:H:119:ASN:ND2	1:H:221:TYR:HB2	2.31	0.46
1:B:324:PHE:CD1	1:B:326:ARG:HG2	2.50	0.46
1:C:324:PHE:HB3	1:C:390:VAL:HB	1.98	0.46
1:F:146:SER:O	1:F:176:TYR:N	2.49	0.45
1:A:397:ILE:HG22	1:A:461:LEU:HB2	1.97	0.45
1:F:128:PHE:O	1:F:129:GLN:C	2.54	0.45
1:F:167:TRP:CE2	1:F:178:TRP:HE3	2.34	0.45
1:F:237:HIS:CE1	1:F:269:GLU:HB3	2.51	0.45
1:A:367:LEU:HA	1:A:367:LEU:HD12	1.68	0.45
1:B:24:LYS:HG2	1:B:320:GLN:HG2	1.97	0.45
1:C:402:ASN:HB3	1:C:405:LEU:HD22	1.98	0.45
1:E:413:THR:HG23	1:E:414:PRO:HD2	1.97	0.45
1:H:357:ASN:O	1:H:357:ASN:ND2	2.50	0.45
1:E:413:THR:HG21	1:E:438:ILE:HG13	1.98	0.45
1:G:154:ASP:HB2	1:G:228:THR:O	2.16	0.45
1:G:69:PRO:HD3	1:G:115:ASP:HB2	1.98	0.45
1:D:396:GLU:HG2	1:D:397:ILE:HG23	1.99	0.45
1:G:498:GLU:OE2	1:G:503:ARG:NH1	2.50	0.45
1:B:246:GLU:OE2	1:B:249:ARG:NH1	2.50	0.45
1:C:300:GLU:OE2	1:C:512:ARG:NH1	2.48	0.45
1:C:453:GLN:HB3	1:C:461:LEU:HB3	1.99	0.45
1:G:237:HIS:NE2	1:G:269:GLU:HG2	2.32	0.45
1:G:308:ILE:O	1:G:312:THR:OG1	2.23	0.45
1:H:358:ILE:HD13	1:H:358:ILE:HA	1.88	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:128:PHE:CE2	1:D:132:ARG:HD3	2.52	0.45
1:F:136:ASP:HB2	1:F:137:GLY:C	2.37	0.45
1:F:171:PRO:HD2	1:F:173:ARG:NH2	2.31	0.45
1:F:268:VAL:HG23	1:F:315:ILE:HG22	1.98	0.45
1:F:279:ASP:OD1	1:F:279:ASP:N	2.50	0.45
1:F:362:ARG:HH11	1:F:401:ASP:CG	2.20	0.45
1:C:235:GLU:OE1	1:C:235:GLU:N	2.44	0.45
1:C:408:ARG:HG2	1:C:408:ARG:HH11	1.81	0.45
1:E:466:LYS:NZ	1:E:533:MET:O	2.24	0.45
1:F:128:PHE:C	1:F:130:ALA:N	2.67	0.45
1:F:134:ASP:C	1:F:134:ASP:OD1	2.56	0.45
1:H:200:LEU:HD12	1:H:204:ARG:HG3	1.99	0.45
1:H:117:VAL:HA	1:H:217:ASP:HB2	1.98	0.45
1:C:83:SER:O	1:C:126:PRO:HD2	2.17	0.45
1:G:473:ARG:C	1:G:474:HIS:CD2	2.91	0.45
1:H:290:MET:HB3	1:H:291:PRO:HD3	1.99	0.45
1:H:470:ILE:HG21	1:H:532:CYS:HB3	1.99	0.45
1:B:215:ARG:HD3	1:B:217:ASP:OD1	2.18	0.44
1:D:289:VAL:O	1:D:293:ILE:HG13	2.17	0.44
1:H:55:ASP:OD1	1:H:55:ASP:N	2.49	0.44
1:G:223:TYR:H	1:G:236:THR:HG22	1.82	0.44
1:H:522:ARG:CZ	1:H:543:GLU:HG2	2.47	0.44
1:B:48:ARG:NH1	1:B:100:GLU:OE2	2.46	0.44
1:E:157:ILE:O	1:E:160:VAL:HG22	2.17	0.44
1:A:69:PRO:HD3	1:A:115:ASP:HB2	1.99	0.44
1:B:237:HIS:CE1	1:B:269:GLU:HB3	2.53	0.44
1:D:298:ARG:NH2	1:D:350:LYS:O	2.50	0.44
1:E:407:ASP:OD1	1:E:408:ARG:N	2.49	0.44
1:G:192:ASN:O	1:G:195:VAL:HG22	2.18	0.44
1:G:409:ASP:C	1:G:411:VAL:N	2.69	0.44
1:D:355:LYS:HE2	1:D:355:LYS:HB2	1.48	0.44
1:E:145:TRP:CZ3	1:E:177:TYR:HB3	2.52	0.44
1:F:402:ASN:C	1:F:410:SER:HB2	2.37	0.44
1:H:40:ASN:HD22	1:H:46:ASP:CG	2.20	0.44
1:A:151:LYS:HB2	1:A:151:LYS:HE3	1.63	0.44
1:A:217:ASP:HB3	1:A:331:LEU:HD21	1.99	0.44
1:B:265:ALA:H	1:B:267:VAL:H	1.65	0.44
1:B:344:MET:HE1	1:B:347:GLU:HG3	2.00	0.44
1:B:409:ASP:HA	1:B:412:ARG:HD2	2.00	0.44
1:H:95:LEU:H	1:H:95:LEU:HD12	1.82	0.44
1:D:466:LYS:HD3	1:D:533:MET:CE	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:297:VAL:HG13	1:D:553:HIS:HE1	1.83	0.44
1:F:171:PRO:O	1:F:173:ARG:N	2.43	0.44
1:F:38:ASP:OD1	1:F:40:ASN:OD1	2.35	0.44
1:H:203:LEU:HG	1:H:214:PHE:CE1	2.53	0.44
1:A:89:LEU:HA	1:A:90:PRO:HD3	1.84	0.44
1:C:408:ARG:NH1	1:C:408:ARG:HG2	2.32	0.44
1:E:509:ASN:O	1:E:553:HIS:HA	2.18	0.44
1:H:125:HIS:HD2	1:H:127:TRP:HB2	1.82	0.44
1:C:40:ASN:N	1:C:40:ASN:OD1	2.50	0.44
1:E:30:GLU:OE1	1:E:326:ARG:NH2	2.38	0.44
1:E:359:GLY:HA3	1:E:408:ARG:NH1	2.33	0.44
1:F:125:HIS:ND1	1:F:126:PRO:HD2	2.30	0.44
1:G:386:PRO:HG3	1:G:482:TYR:HB2	1.99	0.44
1:H:295:MET:HG2	1:H:344:MET:SD	2.58	0.44
1:A:349:ALA:C	1:A:351:ASP:H	2.20	0.43
1:B:474:HIS:HB3	1:B:476:VAL:HG12	1.99	0.43
1:A:200:LEU:O	1:A:204:ARG:HG3	2.18	0.43
1:H:66:TRP:HZ3	1:H:390:VAL:HG11	1.82	0.43
1:C:405:LEU:O	1:C:406:GLY:O	2.37	0.43
1:E:324:PHE:HB3	1:E:390:VAL:HB	1.99	0.43
1:F:133:THR:CG2	1:F:134:ASP:HA	2.36	0.43
1:H:123:ASP:OD1	1:H:124:GLN:NE2	2.44	0.43
1:H:354:MET:HG3	1:H:357:ASN:CG	2.38	0.43
1:B:303:TYR:HD2	1:B:343:TYR:HH	1.67	0.43
1:B:40:ASN:OD1	1:B:46:ASP:OD2	2.36	0.43
1:E:244:ARG:HD3	1:E:280:GLU:O	2.19	0.43
1:E:24:LYS:HA	1:E:320:GLN:HE21	1.82	0.43
1:F:190:TYR:HA	1:F:195:VAL:CG2	2.49	0.43
1:F:528:THR:HG21	1:F:537:GLN:OE1	2.18	0.43
1:G:228:THR:HB	1:G:229:ASN:H	1.51	0.43
1:H:363:ARG:HG3	1:H:411:VAL:CG2	2.49	0.43
1:C:290:MET:HB3	1:C:291:PRO:HD3	2.01	0.43
1:D:132:ARG:NH1	1:D:170:ASP:OD1	2.52	0.43
1:D:327:ASN:O	1:D:335:MET:HG3	2.18	0.43
1:G:104:GLU:HA	1:G:107:ARG:HD2	2.01	0.43
1:H:192:ASN:O	1:H:195:VAL:HG22	2.18	0.43
1:A:38:ASP:OD1	1:A:40:ASN:OD1	2.36	0.43
1:C:496:VAL:HG12	1:C:498:GLU:HG2	2.01	0.43
1:E:179:HIS:HA	1:E:187:ASP:OD1	2.19	0.43
1:F:235:GLU:N	1:F:235:GLU:OE1	2.48	0.43
1:H:303:TYR:HB2	1:H:304:PRO:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:354:MET:C	1:H:357:ASN:OD1	2.56	0.43
1:H:429:ASP:OD1	1:H:430:PRO:HD2	2.19	0.43
1:G:324:PHE:CD1	1:G:326:ARG:HG2	2.54	0.43
1:H:416:GLN:HE21	1:H:445:TYR:CA	2.31	0.43
1:H:91:GLU:HG2	1:H:91:GLU:H	1.39	0.43
1:D:290:MET:HB3	1:D:291:PRO:HD3	2.00	0.43
1:H:88:ILE:HG21	1:H:94:ASP:HA	2.01	0.43
1:A:333:LEU:HD21	1:A:408:ARG:HB2	2.00	0.43
1:A:509:ASN:O	1:A:553:HIS:HA	2.17	0.43
1:B:409:ASP:O	1:B:410:SER:HB3	2.19	0.43
1:B:85:TYR:HD1	1:B:116:LEU:HD11	1.84	0.43
1:C:408:ARG:O	1:C:409:ASP:CB	2.63	0.43
1:D:287:PHE:CE1	1:D:324:PHE:HZ	2.36	0.43
1:E:89:LEU:HA	1:E:90:PRO:HD3	1.83	0.43
1:F:54:LEU:HA	1:F:54:LEU:HD23	1.84	0.43
1:G:365:ALA:HB3	1:G:366:PRO:HD3	2.01	0.43
1:G:498:GLU:CD	1:G:523:ARG:HH22	2.22	0.43
1:B:103:ASP:HB3	1:B:107:ARG:HH12	1.83	0.42
1:B:203:LEU:HD22	1:B:214:PHE:CE1	2.54	0.42
1:C:437:VAL:O	1:C:439:MET:HG3	2.19	0.42
1:E:47:LEU:O	1:E:51:ILE:HG13	2.18	0.42
1:F:81:ASP:N	1:F:81:ASP:OD1	2.52	0.42
1:B:414:PRO:HG3	1:B:434:TYR:CE1	2.55	0.42
1:C:305:ILE:O	1:C:308:ILE:HG13	2.19	0.42
1:D:276:THR:HG21	1:D:279:ASP:HB3	2.00	0.42
1:E:365:ALA:HB3	1:E:366:PRO:HD3	2.01	0.42
1:E:402:ASN:C	1:E:403:ILE:O	2.57	0.42
1:H:204:ARG:O	1:H:208:ASP:N	2.43	0.42
1:B:286:HIS:CE1	1:B:288:PRO:HG2	2.54	0.42
1:E:143:TYR:HD1	1:E:187:ASP:O	2.02	0.42
1:F:134:ASP:N	1:F:135:PRO:HD3	2.33	0.42
1:H:205:PHE:O	1:H:209:LEU:HG	2.18	0.42
1:A:308:ILE:H	1:A:308:ILE:HG13	1.64	0.42
1:C:54:LEU:HA	1:C:54:LEU:HD23	1.91	0.42
1:D:228:THR:HG21	1:D:233:LEU:HD21	2.01	0.42
1:F:409:ASP:O	1:F:410:SER:CB	2.67	0.42
1:A:339:GLU:HG3	1:A:345:TYR:CD2	2.54	0.42
1:A:40:ASN:ND2	1:A:42:ASP:CG	2.73	0.42
1:B:481:SER:O	1:B:497:ARG:HD2	2.19	0.42
1:C:367:LEU:HA	1:C:367:LEU:HD12	1.91	0.42
1:E:220:PRO:O	1:E:231:GLU:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:473:ARG:HE	1:A:473:ARG:HB2	1.67	0.42
1:C:200:LEU:HD21	1:C:243:VAL:HG22	2.02	0.42
1:F:151:LYS:HG3	1:F:167:TRP:HZ2	1.85	0.42
1:F:287:PHE:CE1	1:F:324:PHE:HZ	2.37	0.42
1:H:132:ARG:HG2	1:H:132:ARG:O	2.20	0.42
1:H:324:PHE:CE1	1:H:326:ARG:HG2	2.55	0.42
1:E:406:GLY:N	1:E:407:ASP:HA	2.35	0.42
1:E:66:TRP:C	1:E:66:TRP:CD1	2.93	0.42
1:G:119:ASN:HD22	1:G:120:HIS:HD2	1.66	0.42
1:H:489:ASN:HA	1:H:490:PRO:HD3	1.77	0.42
1:B:329:ASP:OD1	1:B:331:LEU:N	2.49	0.42
1:B:522:ARG:CD	1:B:543:GLU:HG3	2.47	0.42
1:C:340:GLU:HG2	1:C:341:ARG:HG3	2.00	0.42
1:D:157:ILE:O	1:D:160:VAL:HG22	2.19	0.42
1:D:84:ASP:OD2	1:D:87:LYS:HG3	2.20	0.42
1:E:155:ALA:HB1	1:E:180:ARG:NH1	2.34	0.42
1:D:228:THR:HG23	1:D:230:CYS:H	1.85	0.42
1:D:386:PRO:HG3	1:D:482:TYR:HB2	2.01	0.42
1:F:167:TRP:CH2	1:F:178:TRP:HB2	2.55	0.42
1:G:474:HIS:HE1	1:G:559:VAL:HG21	1.85	0.42
1:C:312:THR:HA	1:C:313:PRO:HD3	1.91	0.42
1:E:76:ARG:HB3	1:E:184:HIS:CE1	2.55	0.42
1:G:148:THR:HG23	1:G:150:ASP:OD1	2.20	0.42
1:H:180:ARG:HA	1:H:180:ARG:HD2	1.87	0.42
1:H:84:ASP:OD2	1:H:87:LYS:HD3	2.20	0.42
1:C:386:PRO:HG3	1:C:482:TYR:HB2	2.01	0.41
1:E:347:GLU:HA	1:E:350:LYS:HE2	2.01	0.41
1:G:204:ARG:HB3	1:G:251:TYR:OH	2.20	0.41
1:H:127:TRP:HZ3	1:H:199:MET:HE2	1.84	0.41
1:A:397:ILE:HB	1:A:453:GLN:HG3	2.02	0.41
1:B:115:ASP:OD1	1:B:215:ARG:HD2	2.20	0.41
1:D:258:ALA:HB2	1:D:281:CYS:SG	2.60	0.41
1:E:265:ALA:O	1:E:268:VAL:HG12	2.21	0.41
1:G:481:SER:O	1:G:497:ARG:HD2	2.19	0.41
1:H:200:LEU:O	1:H:201:GLU:CG	2.63	0.41
1:H:88:ILE:HG22	1:H:95:LEU:CD1	2.50	0.41
1:A:135:PRO:HG3	1:A:173:ARG:HD2	2.01	0.41
1:C:178:TRP:CZ2	1:C:180:ARG:HD3	2.55	0.41
1:C:265:ALA:O	1:C:268:VAL:HG12	2.21	0.41
1:G:217:ASP:HA	1:G:259:GLU:HB3	2.02	0.41
1:B:365:ALA:HB3	1:B:366:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:467:MET:HE2	1:C:533:MET:SD	2.60	0.41
1:E:206:TRP:HB2	1:E:214:PHE:HZ	1.84	0.41
1:H:153:PRO:HB2	1:H:154:ASP:H	1.72	0.41
1:H:66:TRP:CD1	1:H:66:TRP:C	2.94	0.41
1:D:38:ASP:HB3	1:D:426:SER:HB2	2.02	0.41
1:F:159:PHE:C	1:F:161:ASP:H	2.24	0.41
1:H:194:ALA:CA	1:H:197:GLU:HB3	2.51	0.41
1:B:44:THR:HG21	1:B:91:GLU:HB2	2.02	0.41
1:C:297:VAL:HG21	1:C:378:PHE:CE1	2.55	0.41
1:D:292:ARG:HH12	1:D:307:GLU:HB3	1.86	0.41
1:D:283:MET:HA	1:D:320:GLN:O	2.21	0.41
1:E:263:TRP:CD2	1:E:264:PRO:HD2	2.56	0.41
1:F:137:GLY:CA	1:F:139:TYR:H	2.31	0.41
1:G:344:MET:HE1	1:G:347:GLU:HG3	2.02	0.41
1:G:81:ASP:OD1	1:G:81:ASP:N	2.49	0.41
1:H:488:SER:O	1:H:490:PRO:HD3	2.21	0.41
1:A:144:MET:HE3	1:A:187:ASP:HB3	2.02	0.41
1:A:451:GLU:OE2	1:A:455:ARG:NH1	2.54	0.41
1:E:192:ASN:HA	1:E:193:PRO:HD3	1.95	0.41
1:E:290:MET:HB3	1:E:291:PRO:HD3	2.02	0.41
1:F:73:SER:H	1:F:89:LEU:HD13	1.86	0.41
1:G:297:VAL:HG21	1:G:378:PHE:CE1	2.56	0.41
1:G:500:GLY:C	1:G:502:ASP:H	2.24	0.41
1:G:66:TRP:CZ3	1:G:390:VAL:HG11	2.56	0.41
1:H:194:ALA:HA	1:H:197:GLU:HB3	2.02	0.41
1:H:57:LEU:HA	1:H:57:LEU:HD23	1.84	0.41
1:B:440:ASP:HA	1:B:441:PRO:HD3	1.97	0.41
1:G:24:LYS:NZ	1:G:317:GLU:O	2.40	0.41
1:A:323:ILE:HG21	1:A:323:ILE:HD13	1.74	0.41
1:B:48:ARG:NH2	1:B:100:GLU:OE1	2.49	0.41
1:B:372:ARG:HA	1:B:375:LEU:HD12	2.03	0.41
1:C:481:SER:O	1:C:497:ARG:HD2	2.20	0.41
1:C:89:LEU:HA	1:C:90:PRO:HD3	1.83	0.41
1:F:85:TYR:HD1	1:F:116:LEU:HD11	1.86	0.41
1:H:181:PHE:HB3	1:H:182:PHE:H	1.76	0.41
1:B:28:PHE:HB2	1:B:390:VAL:HG22	2.03	0.41
1:C:222:LEU:HD23	1:C:222:LEU:HA	1.88	0.41
1:C:190:TYR:HB3	1:C:223:TYR:CZ	2.56	0.41
1:F:126:PRO:C	1:F:127:TRP:O	2.55	0.41
1:D:292:ARG:HG3	1:D:308:ILE:HG12	2.03	0.40
1:E:125:HIS:CD2	1:E:127:TRP:H	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:151:LYS:CG	1:F:167:TRP:CZ2	3.04	0.40
1:G:146:SER:C	1:G:148:THR:H	2.25	0.40
1:H:222:LEU:HB2	1:H:236:THR:HG22	2.03	0.40
1:H:405:LEU:HD13	1:H:435:LEU:HD22	2.03	0.40
1:A:489:ASN:HA	1:A:490:PRO:HD3	1.88	0.40
1:C:344:MET:HE1	1:C:347:GLU:HG3	2.03	0.40
1:C:40:ASN:OD1	1:C:46:ASP:OD1	2.40	0.40
1:G:192:ASN:O	1:G:196:GLN:HG3	2.21	0.40
1:H:144:MET:O	1:H:177:TYR:O	2.39	0.40
1:A:85:TYR:HD1	1:A:116:LEU:HD11	1.86	0.40
1:E:287:PHE:CE1	1:E:329:ASP:HB3	2.56	0.40
1:F:125:HIS:CD2	1:F:127:TRP:HB2	2.55	0.40
1:G:316:PRO:HB2	1:G:319:CYS:SG	2.61	0.40
1:G:34:ARG:HG3	1:G:44:THR:HG23	2.03	0.40
1:H:157:ILE:O	1:H:160:VAL:HG12	2.21	0.40
1:H:363:ARG:HG3	1:H:411:VAL:HG23	2.02	0.40
1:C:200:LEU:HA	1:C:200:LEU:HD23	1.90	0.40
1:C:231:GLU:OE1	1:C:262:GLN:NE2	2.54	0.40
1:C:365:ALA:HB3	1:C:366:PRO:HD3	2.04	0.40
1:A:71:TYR:CZ	1:A:116:LEU:HD13	2.57	0.40
1:A:294:PHE:O	1:A:298:ARG:HG2	2.21	0.40
1:B:408:ARG:HG2	1:B:409:ASP:H	1.86	0.40
1:B:81:ASP:N	1:B:81:ASP:OD1	2.51	0.40
1:C:265:ALA:H	1:C:267:VAL:H	1.68	0.40
1:F:129:GLN:HE22	1:F:173:ARG:HH12	1.68	0.40
1:H:121:THR:O	1:H:186:PRO:HD2	2.21	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	542/601 (90%)	521 (96%)	17 (3%)	4 (1%)	25	59
1	B	542/601 (90%)	522 (96%)	15 (3%)	5 (1%)	20	52
1	C	542/601 (90%)	513 (95%)	21 (4%)	8 (2%)	12	37
1	D	542/601 (90%)	516 (95%)	21 (4%)	5 (1%)	20	52
1	E	542/601 (90%)	515 (95%)	21 (4%)	6 (1%)	17	47
1	F	542/601 (90%)	496 (92%)	26 (5%)	20 (4%)	4	13
1	G	542/601 (90%)	518 (96%)	16 (3%)	8 (2%)	12	37
1	H	532/601 (88%)	491 (92%)	24 (4%)	17 (3%)	5	16
All	All	4326/4808 (90%)	4092 (95%)	161 (4%)	73 (2%)	11	34

All (73) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	265	ALA
1	A	407	ASP
1	B	150	ASP
1	D	358	ILE
1	E	403	ILE
1	E	411	VAL
1	F	127	TRP
1	F	129	GLN
1	F	131	SER
1	F	149	ASP
1	F	150	ASP
1	F	151	LYS
1	G	226	GLU
1	G	261	ASN
1	G	265	ALA
1	H	153	PRO
1	H	178	TRP
1	H	197	GLU
1	H	198	ALA
1	H	201	GLU
1	H	203	LEU
1	H	230	CYS
1	H	354	MET
1	H	355	LYS
1	H	410	SER
1	A	409	ASP
1	B	265	ALA

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Mol	Chain	Res	Type
1	B	500	GLY
1	C	265	ALA
1	C	333	LEU
1	C	406	GLY
1	D	410	SER
1	E	18	ARG
1	E	265	ALA
1	F	160	VAL
1	F	172	VAL
1	F	265	ALA
1	F	333	LEU
1	G	409	ASP
1	G	410	SER
1	G	500	GLY
1	H	265	ALA
1	H	351	ASP
1	H	500	GLY
1	C	230	CYS
1	C	409	ASP
1	C	410	SER
1	E	500	GLY
1	F	135	PRO
1	F	141	ASP
1	F	187	ASP
1	F	225	ARG
1	G	227	GLY
1	G	408	ARG
1	H	226	GLU
1	B	230	CYS
1	B	409	ASP
1	C	359	GLY
1	D	334	GLU
1	F	173	ARG
1	F	226	GLU
1	H	183	SER
1	H	200	LEU
1	H	359	GLY
1	E	404	TRP
1	F	130	ALA
1	F	138	PRO
1	A	230	CYS
1	F	171	PRO

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Mol	Chain	Res	Type
1	D	500	GLY
1	F	134	ASP
1	C	500	GLY
1	D	264	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	476/522 (91%)	468 (98%)	8 (2%)	66	90
1	B	476/522 (91%)	472 (99%)	4 (1%)	85	96
1	C	476/522 (91%)	468 (98%)	8 (2%)	66	90
1	D	476/522 (91%)	467 (98%)	9 (2%)	62	89
1	E	476/522 (91%)	469 (98%)	7 (2%)	70	92
1	F	476/522 (91%)	462 (97%)	14 (3%)	48	81
1	G	476/522 (91%)	467 (98%)	9 (2%)	62	89
1	H	468/522 (90%)	455 (97%)	13 (3%)	49	82
All	All	3800/4176 (91%)	3728 (98%)	72 (2%)	62	89

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	ARG
1	A	302	ARG
1	A	314	LYS
1	A	324	PHE
1	A	353	ARG
1	A	401	ASP
1	A	413	THR
1	A	501	ASP
1	B	320	GLN
1	B	324	PHE
1	B	410	SER

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Mol	Chain	Res	Type
1	B	488	SER
1	C	324	PHE
1	C	343	TYR
1	C	401	ASP
1	C	405	LEU
1	C	411	VAL
1	C	432	ARG
1	C	455	ARG
1	C	498	GLU
1	D	107	ARG
1	D	160	VAL
1	D	164	VAL
1	D	247	VAL
1	D	262	GLN
1	D	314	LYS
1	D	324	PHE
1	D	338	ASP
1	D	401	ASP
1	E	173	ARG
1	E	298	ARG
1	E	324	PHE
1	E	405	LEU
1	E	411	VAL
1	E	501	ASP
1	E	544	LEU
1	F	107	ARG
1	F	120	HIS
1	F	133	THR
1	F	173	ARG
1	F	231	GLU
1	F	242	ARG
1	F	317	GLU
1	F	324	PHE
1	F	343	TYR
1	F	411	VAL
1	F	413	THR
1	F	432	ARG
1	F	439	MET
1	F	455	ARG
1	G	39	SER
1	G	46	ASP
1	G	148	THR

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Mol	Chain	Res	Type
1	G	249	ARG
1	G	262	GLN
1	G	324	PHE
1	G	333	LEU
1	G	367	LEU
1	G	411	VAL
1	H	46	ASP
1	H	121	THR
1	H	131	SER
1	H	145	TRP
1	H	199	MET
1	H	200	LEU
1	H	215	ARG
1	H	248	ASP
1	H	250	LEU
1	H	311	GLN
1	H	324	PHE
1	H	413	THR
1	H	522	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	125	HIS
1	A	232	ASN
1	B	119	ASN
1	D	119	ASN
1	D	553	HIS
1	E	175	GLN
1	E	184	HIS
1	E	416	GLN
1	F	129	GLN
1	F	166	ASN
1	F	184	HIS
1	G	119	ASN
1	G	262	GLN
1	G	474	HIS
1	H	120	HIS
1	H	311	GLN
1	H	416	GLN
1	H	446	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	544/601 (90%)	-0.31	5 (0%) 84 79	13, 24, 43, 71	0
1	B	544/601 (90%)	-0.25	10 (1%) 69 60	12, 25, 48, 72	0
1	C	544/601 (90%)	-0.22	12 (2%) 62 52	14, 31, 51, 102	0
1	D	544/601 (90%)	0.03	24 (4%) 35 25	15, 34, 54, 71	0
1	E	544/601 (90%)	-0.01	23 (4%) 37 26	15, 34, 68, 94	0
1	F	544/601 (90%)	0.07	30 (5%) 26 17	14, 31, 87, 103	0
1	G	544/601 (90%)	-0.07	21 (3%) 40 29	15, 36, 63, 87	0
1	H	536/601 (89%)	0.36	58 (10%) 6 3	16, 38, 80, 95	0
All	All	4344/4808 (90%)	-0.05	183 (4%) 37 26	12, 30, 65, 103	0

All (183) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	349	ALA	14.4
1	F	169	TYR	10.5
1	H	138	PRO	8.3
1	F	228	THR	8.1
1	D	358	ILE	7.9
1	F	227	GLY	6.5
1	D	357	ASN	6.4
1	H	225	ARG	6.2
1	H	139	TYR	5.9
1	F	138	PRO	5.8
1	F	153	PRO	5.6
1	F	174	GLY	5.5
1	H	198	ALA	5.2
1	C	406	GLY	5.2
1	H	133	THR	5.1
1	E	406	GLY	5.1

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Mol	Chain	Res	Type	RSRZ
1	H	177	TYR	5.1
1	F	149	ASP	5.0
1	H	145	TRP	4.9
1	H	199	MET	4.8
1	G	136	ASP	4.7
1	F	136	ASP	4.7
1	H	137	GLY	4.7
1	H	143	TYR	4.7
1	A	350	LYS	4.6
1	H	144	MET	4.6
1	H	543	GLU	4.5
1	H	189	ASN	4.4
1	H	135	PRO	4.4
1	H	141	ASP	4.4
1	H	142	PHE	4.4
1	H	190	TYR	4.3
1	H	194	ALA	4.3
1	E	136	ASP	4.2
1	C	407	ASP	4.1
1	H	155	ALA	4.0
1	B	172	VAL	3.9
1	H	136	ASP	3.9
1	E	169	TYR	3.9
1	F	135	PRO	3.8
1	H	350	LYS	3.8
1	H	542	GLY	3.7
1	G	228	THR	3.7
1	D	139	TYR	3.6
1	D	359	GLY	3.6
1	E	410	SER	3.6
1	C	358	ILE	3.6
1	H	130	ALA	3.6
1	D	138	PRO	3.6
1	F	152	TYR	3.6
1	F	148	THR	3.6
1	F	133	THR	3.5
1	E	405	LEU	3.5
1	H	128	PHE	3.5
1	F	147	ASP	3.5
1	D	147	ASP	3.5
1	H	193	PRO	3.4
1	H	140	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	H	146	SER	3.4
1	F	226	GLU	3.4
1	H	147	ASP	3.3
1	D	176	TYR	3.3
1	H	353	ARG	3.3
1	H	154	ASP	3.3
1	H	191	ASP	3.3
1	D	135	PRO	3.3
1	C	169	TYR	3.2
1	G	169	TYR	3.2
1	E	407	ASP	3.2
1	H	153	PRO	3.2
1	G	171	PRO	3.2
1	H	167	TRP	3.1
1	F	175	GLN	3.1
1	H	522	ARG	3.1
1	G	17	PRO	3.1
1	G	224	ALA	3.1
1	F	225	ARG	3.0
1	F	146	SER	3.0
1	F	141	ASP	3.0
1	B	350	LYS	3.0
1	D	136	ASP	3.0
1	H	358	ILE	3.0
1	G	172	VAL	3.0
1	H	195	VAL	3.0
1	B	150	ASP	2.9
1	C	17	PRO	2.9
1	D	169	TYR	2.9
1	E	176	TYR	2.9
1	H	134	ASP	2.9
1	E	171	PRO	2.9
1	C	18	ARG	2.8
1	H	233	LEU	2.8
1	G	189	ASN	2.8
1	G	142	PHE	2.8
1	F	173	ARG	2.8
1	H	544	LEU	2.8
1	H	132	ARG	2.8
1	G	138	PRO	2.7
1	F	165	SER	2.7
1	D	140	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	F	171	PRO	2.7
1	E	18	ARG	2.7
1	A	224	ALA	2.7
1	F	177	TYR	2.7
1	H	83	SER	2.7
1	H	129	GLN	2.7
1	E	47	LEU	2.7
1	H	127	TRP	2.7
1	E	276	THR	2.7
1	E	147	ASP	2.7
1	D	137	GLY	2.6
1	F	150	ASP	2.6
1	H	178	TRP	2.6
1	H	224	ALA	2.6
1	H	152	TYR	2.6
1	B	171	PRO	2.6
1	B	224	ALA	2.6
1	C	194	ALA	2.6
1	F	144	MET	2.6
1	D	127	TRP	2.5
1	A	225	ARG	2.5
1	G	137	GLY	2.5
1	H	188	LEU	2.4
1	G	18	ARG	2.4
1	D	129	GLN	2.4
1	H	357	ASN	2.4
1	E	48	ARG	2.4
1	H	148	THR	2.4
1	H	205	PHE	2.4
1	G	129	GLN	2.4
1	E	103	ASP	2.4
1	G	133	THR	2.3
1	G	350	LYS	2.3
1	B	176	TYR	2.3
1	B	147	ASP	2.3
1	H	192	ASN	2.3
1	D	351	ASP	2.3
1	D	174	GLY	2.3
1	C	172	VAL	2.3
1	D	432	ARG	2.3
1	F	132	ARG	2.3
1	C	171	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	95	LEU	2.3
1	G	139	TYR	2.3
1	A	349	ALA	2.3
1	D	94	ASP	2.2
1	E	17	PRO	2.2
1	E	150	ASP	2.2
1	F	142	PHE	2.2
1	D	142	PHE	2.2
1	B	107	ARG	2.2
1	B	358	ILE	2.2
1	F	164	VAL	2.2
1	E	135	PRO	2.2
1	H	121	THR	2.2
1	F	176	TYR	2.1
1	D	144	MET	2.1
1	G	190	TYR	2.1
1	D	125	HIS	2.1
1	D	128	PHE	2.1
1	C	408	ARG	2.1
1	A	148	THR	2.1
1	H	86	THR	2.1
1	F	229	ASN	2.1
1	C	176	TYR	2.1
1	B	223	TYR	2.1
1	F	17	PRO	2.1
1	E	175	GLN	2.1
1	E	404	TRP	2.1
1	H	354	MET	2.1
1	D	148	THR	2.1
1	G	176	TYR	2.1
1	G	145	TRP	2.1
1	G	226	GLU	2.1
1	E	93	GLY	2.0
1	E	94	ASP	2.0
1	E	95	LEU	2.0
1	H	84	ASP	2.0
1	C	129	GLN	2.0
1	G	87	LYS	2.0
1	H	150	ASP	2.0
1	E	98	PHE	2.0
1	H	197	GLU	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 carbohydrates 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.