



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2023 – 07:09 AM JST

PDB ID : 6L7M
Title : Characterization and structural analysis of a thermostable zearalenone-degrading enzyme
Authors : Wei, X.H.; Meng, G.
Deposited on : 2019-11-01
Resolution : 2.40 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

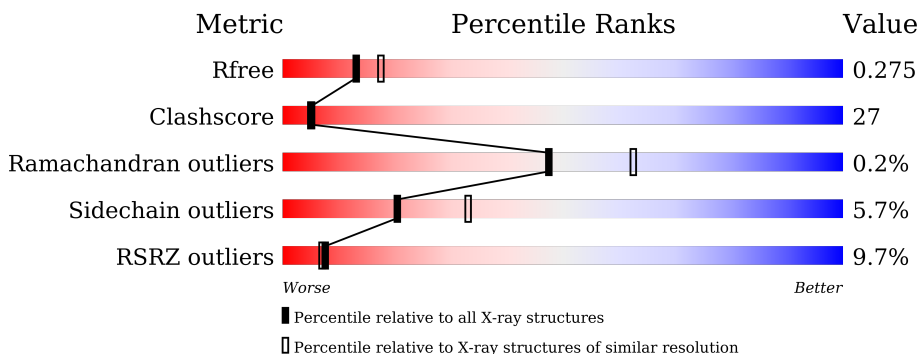
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	267	
1	B	267	
1	C	267	
1	D	267	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8947 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 AB hydrolase-1 domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	267	2092	1335	353	387	17	0	0	0
1	B	267	2092	1335	353	387	17	0	0	0
1	C	267	2092	1335	353	387	17	0	0	0
1	D	267	2092	1335	353	387	17	0	0	0

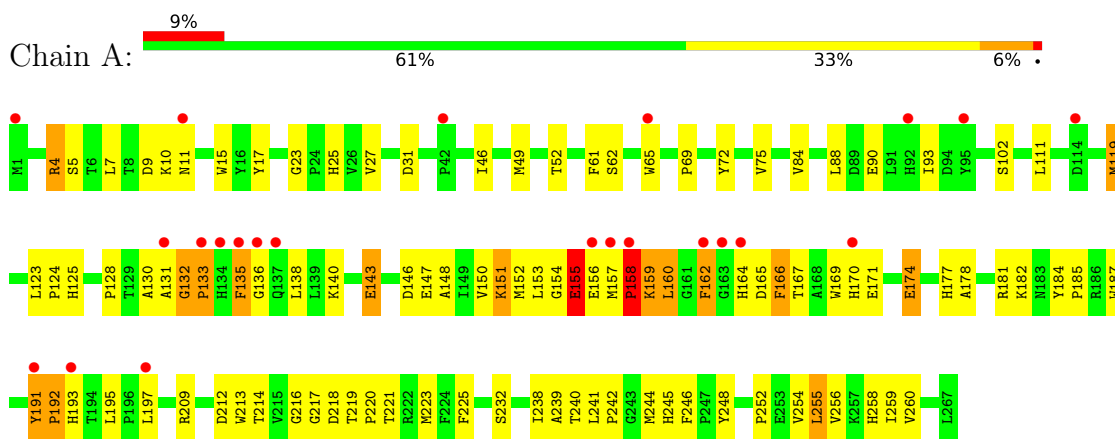
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	163	Total 163	O 163	0	0
2	B	154	Total 154	O 154	0	0
2	C	125	Total 125	O 125	0	0
2	D	137	Total 137	O 137	0	0

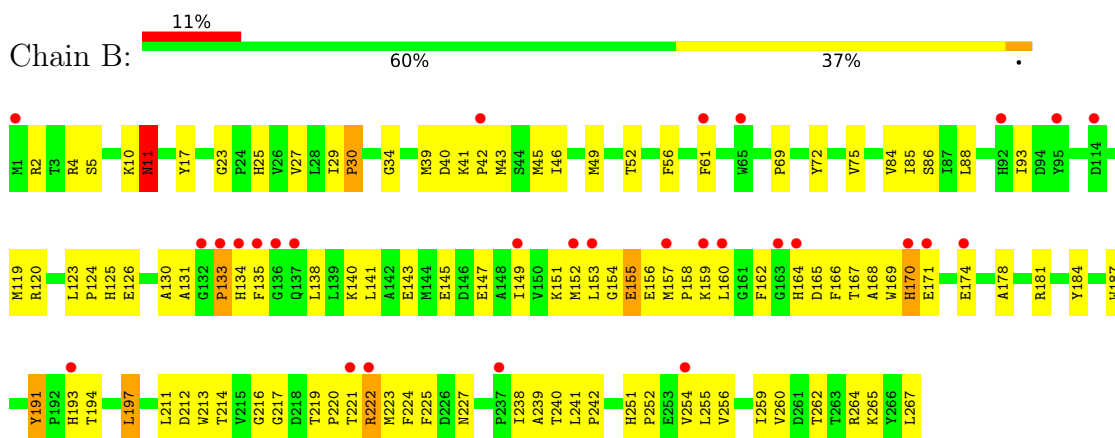
3 Residue-property plots [i](#)

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

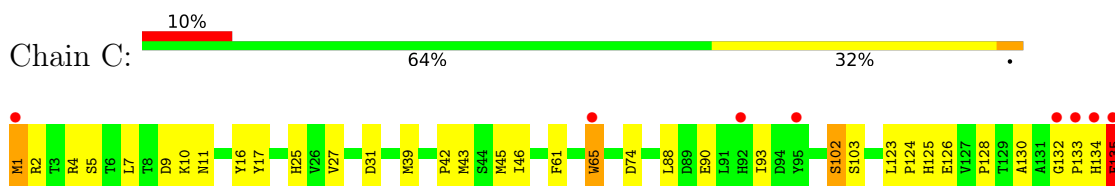
- Molecule 1: AB hydrolase-1 domain-containing protein

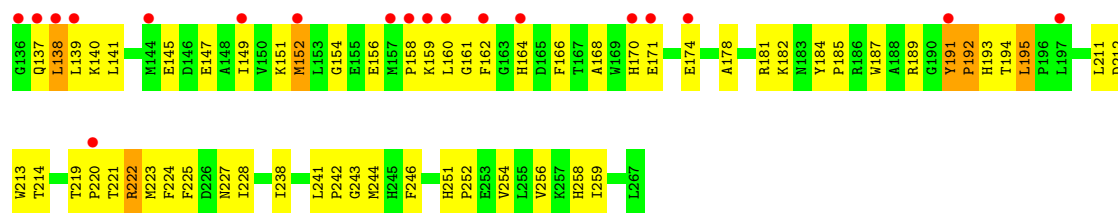


- Molecule 1: AB hydrolase-1 domain-containing protein

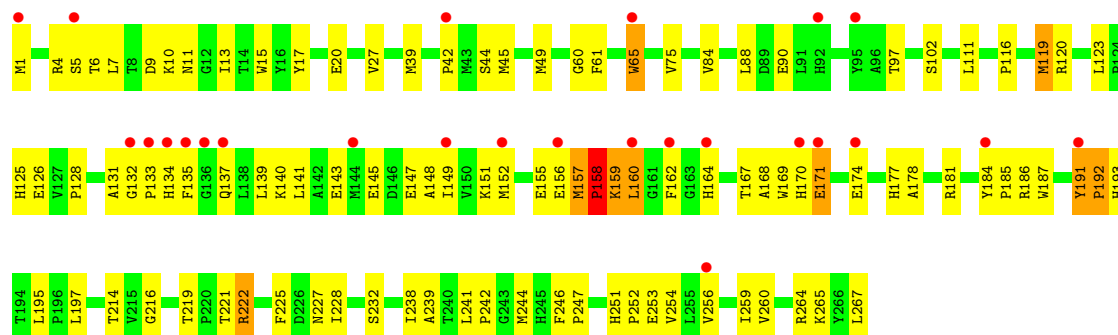


- Molecule 1: AB hydrolase-1 domain-containing protein





● Molecule 1: AB hydrolase-1 domain-containing protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.01Å 116.32Å 130.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.79 – 2.40 49.74 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.79-2.40) 99.9 (49.74-2.40)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.77 (at 2.39Å)	Xtrriage
Refinement program	REFMAC ccp4 7.0.077	Depositor
R, R_{free}	0.248 , 0.275 0.248 , 0.275	Depositor DCC
R_{free} test set	2975 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	15.9	Xtrriage
Anisotropy	0.052	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	8947	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.72	6/2156 (0.3%)	0.80	6/2931 (0.2%)
1	B	0.58	3/2156 (0.1%)	0.75	6/2931 (0.2%)
1	C	0.58	4/2156 (0.2%)	0.68	4/2931 (0.1%)
1	D	0.69	5/2156 (0.2%)	0.83	5/2931 (0.2%)
All	All	0.65	18/8624 (0.2%)	0.77	21/11724 (0.2%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	192	PRO	N-CA	14.10	1.71	1.47
1	A	192	PRO	N-CA	13.99	1.71	1.47
1	C	192	PRO	N-CA	13.78	1.70	1.47
1	A	133	PRO	N-CA	13.66	1.70	1.47
1	B	30	PRO	N-CA	11.67	1.67	1.47
1	D	158	PRO	C-O	-11.30	1.00	1.23
1	A	158	PRO	N-CA	11.18	1.66	1.47
1	D	158	PRO	N-CA	10.95	1.65	1.47
1	C	195	LEU	C-N	7.75	1.49	1.34
1	A	191	TYR	C-N	6.27	1.46	1.34
1	D	157	MET	C-N	6.21	1.46	1.34
1	B	29	ILE	C-N	6.20	1.46	1.34
1	A	132	GLY	C-N	6.02	1.45	1.34
1	A	158	PRO	C-O	-5.82	1.11	1.23
1	D	191	TYR	C-N	5.79	1.45	1.34
1	C	191	TYR	C-N	5.57	1.44	1.34
1	C	243	GLY	C-O	-5.33	1.15	1.23
1	B	191	TYR	C-N	5.29	1.44	1.34

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	158	PRO	CA-N-CD	-21.47	81.44	111.50
1	A	158	PRO	CA-N-CD	-12.10	94.56	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	192	PRO	CA-N-CD	-9.62	98.03	111.50
1	A	133	PRO	CA-N-CD	-8.89	99.06	111.50
1	A	158	PRO	N-CD-CG	8.60	116.10	103.20
1	C	192	PRO	CA-N-CD	-7.92	100.41	111.50
1	C	193	HIS	CB-CA-C	-7.03	96.35	110.40
1	D	158	PRO	N-CD-CG	6.97	113.66	103.20
1	D	192	PRO	CA-N-CD	-6.93	101.80	111.50
1	B	133	PRO	C-N-CA	6.24	137.29	121.70
1	B	191	TYR	O-C-N	-6.22	109.28	121.10
1	A	155	GLU	CB-CG-CD	5.97	130.31	114.20
1	B	155	GLU	CB-CG-CD	5.54	129.16	114.20
1	B	135	PHE	CB-CA-C	-5.52	99.36	110.40
1	D	191	TYR	CA-C-N	5.48	132.44	117.10
1	D	191	TYR	O-C-N	-5.48	110.69	121.10
1	A	166	PHE	CB-CA-C	5.45	121.29	110.40
1	C	135	PHE	CB-CA-C	5.43	121.26	110.40
1	C	191	TYR	O-C-N	-5.23	111.17	121.10
1	B	11	ASN	CB-CA-C	5.16	120.72	110.40
1	B	191	TYR	CA-C-N	5.03	131.18	117.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2092	0	2030	146	0
1	B	2092	0	2030	131	0
1	C	2092	0	2030	128	0
1	D	2092	0	2030	105	0
2	A	163	0	0	5	0
2	B	154	0	0	5	0
2	C	125	0	0	0	0
2	D	137	0	0	4	0
All	All	8947	0	8120	441	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 27.

All (441) 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:C:192:PRO:CA	1:C:192:PRO:N	1.70	1.46
1:A:192:PRO:N	1:A:192:PRO:CA	1.71	1.40
1:A:133:PRO:CA	1:A:133:PRO:N	1.70	1.38
1:C:130:ALA:HB3	1:C:133:PRO:CG	1.52	1.37
1:D:192:PRO:N	1:D:192:PRO:CA	1.71	1.37
1:C:219:THR:HG23	1:C:223:MET:CE	1.69	1.20
1:C:130:ALA:HB3	1:C:133:PRO:CD	1.73	1.17
1:A:164:HIS:HB2	1:A:244:MET:CE	1.76	1.15
1:C:130:ALA:CB	1:C:133:PRO:HG3	1.75	1.15
1:B:154:GLY:O	1:B:158:PRO:HD3	1.50	1.11
1:C:219:THR:HG23	1:C:223:MET:HE3	1.09	1.07
1:A:174:GLU:HG3	1:B:178:ALA:HA	1.15	1.07
1:A:130:ALA:HB3	1:A:133:PRO:HG2	1.32	1.07
1:C:178:ALA:HA	1:D:174:GLU:HG3	1.36	1.07
1:C:164:HIS:HB2	1:C:244:MET:HE2	1.39	1.04
1:C:130:ALA:HB3	1:C:133:PRO:HG3	1.03	1.02
1:A:158:PRO:HA	1:A:162:PHE:CE1	1.94	1.01
1:C:170:HIS:HE1	1:D:152:MET:HA	1.24	0.99
1:C:170:HIS:NE2	1:D:155:GLU:HB2	1.76	0.99
1:B:222:ARG:HH21	1:B:222:ARG:HG3	1.26	0.98
1:C:130:ALA:CB	1:C:133:PRO:CD	2.45	0.94
1:A:164:HIS:HB2	1:A:244:MET:HE3	1.50	0.92
1:C:130:ALA:CB	1:C:133:PRO:CG	2.38	0.92
1:A:174:GLU:HG3	1:B:178:ALA:CA	2.01	0.90
1:B:134:HIS:CD2	1:B:223:MET:SD	2.65	0.89
1:A:170:HIS:NE2	1:B:155:GLU:HB2	1.86	0.89
1:C:154:GLY:O	1:C:158:PRO:HD3	1.71	0.89
1:C:130:ALA:HB3	1:C:133:PRO:HD3	1.55	0.86
1:A:162:PHE:O	1:A:244:MET:HB2	1.76	0.85
1:A:152:MET:HA	1:B:170:HIS:HE1	1.40	0.85
1:C:139:LEU:HD13	1:C:187:TRP:HH2	1.41	0.85
1:A:159:LYS:H	1:A:159:LYS:HD2	1.42	0.84
1:B:134:HIS:HE2	1:B:162:PHE:HE1	1.23	0.84
1:D:151:LYS:HD2	1:D:181:ARG:HD3	1.59	0.84
1:C:130:ALA:C	1:C:133:PRO:HD2	1.97	0.84
1:A:164:HIS:HB2	1:A:244:MET:HE2	1.55	0.84
1:C:170:HIS:CE1	1:D:152:MET:HA	2.12	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:159:LYS:HD3	1:D:169:TRP:CD1	2.14	0.83
1:B:159:LYS:HD3	1:B:169:TRP:CD1	2.14	0.82
1:C:219:THR:CG2	1:C:223:MET:CE	2.57	0.81
1:C:170:HIS:NE2	1:D:155:GLU:CB	2.43	0.81
1:C:156:GLU:HB3	1:D:170:HIS:NE2	1.96	0.80
1:C:178:ALA:CA	1:D:174:GLU:HG3	2.12	0.80
1:C:219:THR:CG2	1:C:223:MET:HE3	2.04	0.79
1:C:132:GLY:N	1:C:133:PRO:HD2	1.97	0.79
1:A:130:ALA:O	1:A:133:PRO:HD2	1.83	0.78
1:A:164:HIS:CB	1:A:244:MET:HE2	2.14	0.78
1:C:130:ALA:CB	1:C:133:PRO:HD3	2.13	0.77
1:A:152:MET:HA	1:B:170:HIS:CE1	2.20	0.76
1:A:153:LEU:O	1:A:157:MET:HG3	1.86	0.76
1:A:7:LEU:HD23	1:A:90:GLU:HG2	1.66	0.76
1:C:174:GLU:HG3	1:D:178:ALA:HA	1.68	0.75
1:B:134:HIS:NE2	1:B:162:PHE:HE1	1.84	0.75
1:C:74:ASP:HA	1:C:194:THR:HG21	1.66	0.75
1:A:155:GLU:HB3	1:B:170:HIS:NE2	2.01	0.75
1:D:155:GLU:HG2	1:D:184:TYR:HE2	1.52	0.75
1:B:238:ILE:HG13	1:D:225:PHE:HZ	1.50	0.74
1:A:155:GLU:O	1:A:159:LYS:HE3	1.87	0.74
1:A:214:THR:HB	1:A:241:LEU:HD22	1.71	0.73
1:B:2:ARG:CZ	1:B:43:MET:HE3	2.20	0.72
1:B:134:HIS:HD2	1:B:223:MET:SD	2.12	0.72
1:C:228:ILE:HA	1:C:238:ILE:HD13	1.70	0.71
1:C:132:GLY:N	1:C:133:PRO:CD	2.54	0.71
1:A:170:HIS:CE1	1:B:152:MET:HA	2.26	0.71
1:C:27:VAL:HG21	1:C:88:LEU:HD11	1.73	0.71
1:A:225:PHE:HZ	1:C:238:ILE:HG12	1.54	0.70
1:C:7:LEU:HD23	1:C:90:GLU:HG2	1.71	0.70
1:C:1:MET:SD	1:C:2:ARG:N	2.64	0.70
1:C:147:GLU:OE1	1:C:189:ARG:NH1	2.25	0.70
1:A:164:HIS:CB	1:A:244:MET:CE	2.62	0.70
1:C:164:HIS:CB	1:C:244:MET:HE2	2.19	0.70
1:A:9:ASP:OD2	1:A:15:TRP:NE1	2.25	0.69
1:A:84:VAL:O	1:A:88:LEU:HB2	1.93	0.69
1:A:155:GLU:HB3	1:B:170:HIS:CD2	2.27	0.69
1:A:218:ASP:HA	1:C:220:PRO:HB3	1.75	0.69
1:B:41:LYS:HE2	1:B:171:GLU:OE1	1.94	0.68
1:D:131:ALA:HB1	1:D:140:LYS:HD2	1.75	0.68
1:C:219:THR:HG23	1:C:223:MET:HE2	1.69	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:GLY:N	1:A:133:PRO:HD3	2.08	0.68
1:A:159:LYS:HD2	1:A:159:LYS:N	2.08	0.68
1:B:46:ILE:HG12	1:B:256:VAL:HG13	1.75	0.68
1:A:125:HIS:CE1	1:A:241:LEU:HD21	2.28	0.68
1:B:49:MET:HG3	1:B:260:VAL:HG21	1.74	0.68
1:A:191:TYR:O	1:A:195:LEU:HD23	1.95	0.67
1:A:221:THR:HG22	1:C:221:THR:HA	1.77	0.67
1:B:222:ARG:HG3	1:B:222:ARG:NH2	1.98	0.67
1:A:154:GLY:O	1:A:158:PRO:HD3	1.95	0.67
1:D:228:ILE:HA	1:D:238:ILE:HD13	1.77	0.67
1:A:170:HIS:NE2	1:B:155:GLU:CB	2.58	0.66
1:C:139:LEU:HD13	1:C:187:TRP:CH2	2.28	0.66
1:A:221:THR:HG23	1:C:219:THR:O	1.95	0.66
1:B:40:ASP:HA	1:B:43:MET:CE	2.26	0.66
1:D:27:VAL:HG21	1:D:88:LEU:HD21	1.77	0.66
1:A:162:PHE:HB2	1:A:245:HIS:HB2	1.79	0.65
1:C:222:ARG:HH11	1:C:222:ARG:CG	2.10	0.65
1:A:158:PRO:HD2	1:A:159:LYS:HD2	1.78	0.65
1:B:221:THR:HA	1:D:221:THR:HG22	1.79	0.65
1:A:155:GLU:OE2	1:A:159:LYS:CE	2.45	0.65
1:B:120:ARG:NH2	2:B:303:HOH:O	2.28	0.64
1:B:264:ARG:NH1	2:B:304:HOH:O	2.29	0.64
1:A:170:HIS:HE1	1:B:152:MET:HA	1.61	0.64
1:C:147:GLU:O	1:C:151:LYS:HG3	1.98	0.64
1:D:159:LYS:HG3	2:D:303:HOH:O	1.96	0.64
1:A:148:ALA:HA	1:A:151:LYS:HD2	1.78	0.64
1:A:242:PRO:HG2	1:A:254:VAL:HG11	1.79	0.64
1:C:159:LYS:HE3	1:C:166:PHE:CG	2.33	0.64
1:D:159:LYS:HZ2	1:D:169:TRP:HE1	1.46	0.64
1:B:159:LYS:HD2	1:B:166:PHE:HE1	1.63	0.63
1:C:170:HIS:HE1	1:D:152:MET:CA	2.06	0.63
1:A:135:PHE:CE2	1:A:157:MET:SD	2.92	0.63
1:C:135:PHE:HB2	1:C:223:MET:SD	2.39	0.63
1:D:45:MET:HB2	1:D:256:VAL:HG11	1.80	0.63
1:C:222:ARG:HH11	1:C:222:ARG:HG2	1.64	0.62
1:B:154:GLY:O	1:B:158:PRO:CD	2.38	0.62
1:A:130:ALA:CB	1:A:133:PRO:HG2	2.20	0.62
1:D:148:ALA:O	1:D:152:MET:HG3	1.99	0.62
1:C:130:ALA:CA	1:C:133:PRO:CG	2.77	0.62
1:C:151:LYS:HD2	1:C:181:ARG:HD3	1.82	0.62
1:A:159:LYS:H	1:A:159:LYS:CD	2.09	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:GLU:HB3	1:D:170:HIS:CE1	2.34	0.61
1:C:139:LEU:HB2	1:C:192:PRO:HB3	1.81	0.61
1:D:9:ASP:OD2	1:D:11:ASN:ND2	2.30	0.61
1:A:178:ALA:HA	1:B:174:GLU:HB3	1.82	0.61
1:B:159:LYS:HD3	1:B:169:TRP:NE1	2.15	0.60
1:A:135:PHE:HE2	1:A:157:MET:SD	2.23	0.60
1:A:152:MET:CA	1:B:170:HIS:HE1	2.13	0.60
1:A:5:SER:HB3	1:A:17:TYR:CZ	2.37	0.60
1:A:174:GLU:HB2	1:B:181:ARG:HD3	1.84	0.60
1:D:260:VAL:O	1:D:264:ARG:HG3	2.02	0.59
1:A:46:ILE:HG12	1:A:256:VAL:HG23	1.85	0.59
1:C:168:ALA:O	1:C:171:GLU:HG3	2.03	0.59
1:D:241:LEU:HD11	1:D:247:PRO:HB2	1.84	0.59
1:D:267:LEU:HD22	2:D:418:HOH:O	2.02	0.59
1:B:45:MET:HB2	1:B:256:VAL:HG21	1.84	0.59
1:B:223:MET:HG2	1:B:224:PHE:CE2	2.38	0.59
1:A:181:ARG:HB2	1:B:174:GLU:CG	2.33	0.59
1:A:187:TRP:O	1:A:192:PRO:HD2	2.03	0.58
1:A:209:ARG:NH2	2:A:305:HOH:O	2.35	0.58
1:C:174:GLU:CG	1:D:178:ALA:HA	2.34	0.58
1:A:131:ALA:C	1:A:133:PRO:HD3	2.24	0.58
1:C:130:ALA:C	1:C:133:PRO:CD	2.72	0.58
1:D:123:LEU:HD22	1:D:259:ILE:HD13	1.85	0.58
1:A:143:GLU:HG2	1:A:193:HIS:CE1	2.38	0.58
1:B:130:ALA:HB3	1:B:133:PRO:HG3	1.86	0.58
1:C:102:SER:OG	1:C:103:SER:N	2.37	0.57
1:D:20:GLU:OE2	1:D:44:SER:HA	2.04	0.57
1:C:159:LYS:HE3	1:C:166:PHE:CD1	2.38	0.57
1:B:216:GLY:O	1:D:221:THR:OG1	2.21	0.57
1:B:221:THR:OG1	1:D:216:GLY:O	2.23	0.57
1:A:238:ILE:HG13	1:C:225:PHE:HZ	1.68	0.57
1:B:134:HIS:NE2	1:B:162:PHE:CE1	2.65	0.57
1:A:217:GLY:HA2	1:A:240:THR:CG2	2.35	0.57
1:C:174:GLU:HG2	1:D:177:HIS:O	2.05	0.57
1:D:252:PRO:O	1:D:256:VAL:HG13	2.05	0.56
1:B:40:ASP:HA	1:B:43:MET:HE2	1.86	0.56
1:B:131:ALA:HB1	1:B:140:LYS:HD2	1.87	0.56
1:C:102:SER:HA	1:C:128:PRO:HD3	1.87	0.56
1:C:132:GLY:H	1:C:133:PRO:HD2	1.68	0.56
1:D:241:LEU:HD11	1:D:247:PRO:CB	2.36	0.56
1:C:130:ALA:CA	1:C:133:PRO:HG3	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:GLY:H	1:C:133:PRO:CD	2.17	0.56
1:C:151:LYS:HB3	1:C:181:ARG:HD3	1.87	0.56
1:D:147:GLU:O	1:D:151:LYS:HG3	2.05	0.56
1:D:151:LYS:HD2	1:D:181:ARG:CD	2.35	0.56
1:A:216:GLY:O	1:C:221:THR:OG1	2.24	0.55
1:B:155:GLU:CG	1:B:184:TYR:CE2	2.89	0.55
1:C:61:PHE:HE2	1:C:191:TYR:CE1	2.24	0.55
1:B:11:ASN:OD1	1:B:11:ASN:N	2.35	0.55
1:A:135:PHE:CE2	1:A:157:MET:HB3	2.41	0.55
1:D:5:SER:HB2	1:D:17:TYR:CZ	2.42	0.55
1:A:9:ASP:OD2	1:A:15:TRP:CD1	2.60	0.55
1:A:187:TRP:CD1	1:A:191:TYR:HB2	2.42	0.55
1:C:242:PRO:HB2	1:C:254:VAL:HG11	1.88	0.55
1:B:154:GLY:O	1:B:157:MET:HG3	2.07	0.55
1:B:168:ALA:HA	1:B:171:GLU:HB3	1.89	0.55
1:B:221:THR:HG22	1:D:221:THR:HA	1.89	0.54
1:C:151:LYS:HD2	1:C:181:ARG:CD	2.37	0.54
1:A:132:GLY:N	1:A:133:PRO:CD	2.70	0.54
1:A:155:GLU:CB	1:B:170:HIS:NE2	2.70	0.54
1:B:138:LEU:HB3	1:B:141:LEU:HD23	1.90	0.54
1:D:49:MET:HG3	1:D:260:VAL:HG21	1.88	0.54
1:D:155:GLU:HG2	1:D:184:TYR:CE2	2.38	0.54
1:B:159:LYS:O	1:B:164:HIS:CD2	2.60	0.54
1:C:134:HIS:NE2	1:C:162:PHE:HZ	2.05	0.54
1:A:155:GLU:HG2	1:A:184:TYR:CE2	2.43	0.54
1:D:251:HIS:HB3	1:D:254:VAL:HG22	1.89	0.54
1:A:124:PRO:HD2	1:A:212:ASP:O	2.08	0.54
1:C:7:LEU:CD2	1:C:90:GLU:HG2	2.38	0.54
1:C:126:GLU:HB3	1:C:224:PHE:CE2	2.43	0.54
1:D:61:PHE:HE2	1:D:191:TYR:CE1	2.25	0.54
1:C:181:ARG:HG2	1:D:174:GLU:HB2	1.89	0.54
1:C:4:ARG:HD3	1:C:16:TYR:HE1	1.72	0.54
1:D:145:GLU:HB3	1:D:149:ILE:CG2	2.38	0.54
1:B:251:HIS:HB3	1:B:254:VAL:HG22	1.91	0.53
1:D:160:LEU:O	1:D:164:HIS:CD2	2.61	0.53
1:A:174:GLU:CB	1:B:181:ARG:HB2	2.39	0.53
1:C:181:ARG:HG2	1:D:174:GLU:CB	2.38	0.53
1:C:135:PHE:HB2	1:C:223:MET:HG3	1.90	0.53
1:D:187:TRP:CD1	1:D:191:TYR:HB2	2.44	0.53
1:A:162:PHE:HB2	1:A:245:HIS:CB	2.39	0.52
1:B:197:LEU:H	1:B:197:LEU:HD23	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:LEU:HB3	1:D:119:MET:CE	2.40	0.52
1:A:138:LEU:HD22	1:A:140:LYS:HB2	1.92	0.52
1:B:84:VAL:O	1:B:88:LEU:HG	2.09	0.52
1:B:265:LYS:HE2	1:B:265:LYS:HA	1.92	0.52
1:C:135:PHE:O	1:C:162:PHE:HE1	1.93	0.52
1:B:5:SER:HB3	1:B:17:TYR:CZ	2.45	0.51
1:D:143:GLU:HG2	1:D:193:HIS:NE2	2.25	0.51
1:D:167:THR:HA	1:D:170:HIS:CE1	2.45	0.51
1:B:155:GLU:HG2	1:B:184:TYR:CE2	2.45	0.51
1:B:39:MET:O	1:B:43:MET:HE2	2.11	0.51
1:C:151:LYS:CB	1:C:181:ARG:HD3	2.40	0.51
1:B:220:PRO:HD2	1:B:223:MET:HE2	1.92	0.51
1:D:116:PRO:HA	1:D:119:MET:SD	2.51	0.51
1:B:165:ASP:OD1	1:B:167:THR:HG22	2.10	0.50
1:A:174:GLU:HB2	1:B:181:ARG:CG	2.42	0.50
1:B:147:GLU:O	1:B:151:LYS:HE3	2.11	0.50
1:A:158:PRO:HG2	1:A:159:LYS:HD2	1.93	0.50
1:B:222:ARG:HH21	1:B:222:ARG:CG	2.12	0.50
1:C:25:HIS:CE1	1:C:93:ILE:HG12	2.47	0.50
1:B:217:GLY:HA2	1:B:240:THR:CG2	2.41	0.50
1:C:214:THR:HB	1:C:241:LEU:HD22	1.93	0.50
1:C:219:THR:CG2	1:C:223:MET:HE2	2.35	0.50
1:C:138:LEU:HD13	1:C:141:LEU:HG	1.92	0.50
1:D:7:LEU:HD13	1:D:90:GLU:HG2	1.94	0.50
1:C:166:PHE:HZ	1:D:159:LYS:HE2	1.77	0.49
1:B:145:GLU:HB3	1:B:149:ILE:HG23	1.94	0.49
1:B:25:HIS:CE1	1:B:93:ILE:HG12	2.47	0.49
1:B:217:GLY:HA2	1:B:240:THR:HG21	1.94	0.49
1:A:170:HIS:CE1	1:B:155:GLU:HB2	2.44	0.49
1:B:130:ALA:HB3	1:B:133:PRO:HD3	1.94	0.49
1:C:149:ILE:HA	1:C:152:MET:HG3	1.93	0.49
1:D:7:LEU:HD22	1:D:90:GLU:HG2	1.95	0.49
1:A:221:THR:HA	1:C:221:THR:HG22	1.94	0.49
1:B:40:ASP:HA	1:B:43:MET:HE1	1.94	0.49
1:C:2:ARG:HD2	1:C:43:MET:HE1	1.94	0.49
1:C:130:ALA:H	1:C:133:PRO:HG2	1.78	0.49
1:D:61:PHE:CE2	1:D:191:TYR:CE1	3.01	0.49
1:B:130:ALA:HB3	1:B:133:PRO:CG	2.43	0.49
1:C:135:PHE:HB2	1:C:223:MET:CG	2.43	0.49
1:C:145:GLU:HB3	1:C:149:ILE:HG23	1.94	0.48
1:D:61:PHE:HE2	1:D:191:TYR:CZ	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:158:PRO:HA	1:D:162:PHE:HB2	1.95	0.48
1:B:221:THR:HG23	1:D:219:THR:O	2.13	0.48
1:D:84:VAL:O	1:D:88:LEU:HD13	2.13	0.48
1:D:214:THR:HA	1:D:239:ALA:O	2.13	0.48
1:A:135:PHE:C	1:A:135:PHE:CD1	2.86	0.48
1:C:168:ALA:HA	1:C:171:GLU:HG3	1.94	0.48
1:B:242:PRO:HB2	1:B:254:VAL:HG21	1.95	0.48
1:B:160:LEU:HA	1:B:164:HIS:CG	2.48	0.48
1:C:125:HIS:CE1	1:C:241:LEU:HD21	2.49	0.48
1:D:170:HIS:HA	1:D:177:HIS:NE2	2.28	0.48
1:A:220:PRO:HG2	1:A:223:MET:HE3	1.96	0.48
1:A:102:SER:HB2	1:A:245:HIS:NE2	2.28	0.48
1:A:174:GLU:HG2	1:B:181:ARG:HB2	1.95	0.48
1:B:252:PRO:O	1:B:256:VAL:HG23	2.14	0.48
1:C:151:LYS:HG2	1:C:185:PRO:HD3	1.94	0.48
1:C:166:PHE:O	1:C:170:HIS:HB3	2.13	0.48
1:D:168:ALA:O	1:D:171:GLU:HG3	2.13	0.48
1:A:147:GLU:HG2	1:A:185:PRO:CB	2.44	0.48
1:A:177:HIS:O	1:B:174:GLU:HG3	2.13	0.47
1:C:251:HIS:HB3	1:C:254:VAL:HG12	1.96	0.47
1:A:151:LYS:HD3	1:A:181:ARG:CD	2.45	0.47
1:A:164:HIS:ND1	1:A:244:MET:HE2	2.29	0.47
1:A:174:GLU:HB2	1:B:181:ARG:CD	2.43	0.47
1:A:23:GLY:O	1:A:52:THR:HG22	2.14	0.47
1:A:155:GLU:OE2	1:A:159:LYS:HE2	2.12	0.47
1:B:61:PHE:HE2	1:B:191:TYR:CE1	2.32	0.47
1:C:162:PHE:HB3	1:C:246:PHE:CE2	2.50	0.47
1:C:65:TRP:CZ3	1:C:182:LYS:HB3	2.50	0.47
1:A:169:TRP:HZ3	1:A:246:PHE:CE2	2.33	0.47
1:A:171:GLU:HB3	2:A:324:HOH:O	2.15	0.47
1:A:5:SER:HB3	1:A:17:TYR:CE1	2.49	0.47
1:A:174:GLU:CG	1:B:181:ARG:HB2	2.44	0.47
1:B:213:TRP:O	1:B:238:ILE:HD12	2.14	0.47
1:C:45:MET:HE1	1:C:252:PRO:HB2	1.96	0.47
1:D:159:LYS:NZ	1:D:169:TRP:HE1	2.11	0.47
1:D:253:GLU:O	1:D:256:VAL:HG22	2.15	0.47
1:A:166:PHE:CZ	1:B:159:LYS:HE2	2.50	0.47
1:A:181:ARG:HB2	1:B:174:GLU:HG3	1.97	0.47
1:B:143:GLU:HG2	1:B:193:HIS:CE1	2.49	0.47
1:D:132:GLY:N	1:D:133:PRO:HD3	2.30	0.47
1:A:11:ASN:ND2	2:A:310:HOH:O	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:MET:O	1:A:156:GLU:HB3	2.15	0.47
1:C:181:ARG:HB3	1:D:174:GLU:HB2	1.97	0.47
1:C:45:MET:HB2	1:C:256:VAL:HG11	1.97	0.46
1:C:181:ARG:CB	1:D:174:GLU:HB2	2.45	0.46
1:A:241:LEU:HD23	1:A:241:LEU:H	1.81	0.46
1:B:147:GLU:C	1:B:151:LYS:HE3	2.36	0.46
1:C:61:PHE:CE2	1:C:191:TYR:CE1	3.04	0.46
1:A:158:PRO:HB2	1:A:169:TRP:CH2	2.50	0.46
1:B:159:LYS:HD2	1:B:166:PHE:CE1	2.48	0.46
1:B:267:LEU:N	2:B:313:HOH:O	2.49	0.46
1:C:187:TRP:O	1:C:192:PRO:HD2	2.15	0.46
1:D:242:PRO:HB2	1:D:254:VAL:HG21	1.97	0.46
1:B:126:GLU:HB3	1:B:224:PHE:CE2	2.50	0.46
1:B:240:THR:HG21	1:D:222:ARG:HB2	1.96	0.46
1:C:156:GLU:CB	1:D:170:HIS:CE1	2.99	0.46
1:A:214:THR:HA	1:A:239:ALA:O	2.16	0.46
1:B:155:GLU:HG3	1:B:184:TYR:CE2	2.50	0.46
1:C:159:LYS:HD3	1:C:160:LEU:HD22	1.96	0.46
1:C:123:LEU:HD23	1:C:258:HIS:CE1	2.49	0.46
1:D:102:SER:HA	1:D:128:PRO:HD3	1.98	0.46
1:A:165:ASP:OD1	1:A:167:THR:HG22	2.16	0.46
1:B:152:MET:HE3	2:B:302:HOH:O	2.14	0.46
1:A:62:SER:O	1:A:65:TRP:HB2	2.15	0.46
1:A:181:ARG:HG2	1:B:174:GLU:HB2	1.97	0.46
1:A:27:VAL:HG21	1:A:88:LEU:HD11	1.97	0.45
1:A:61:PHE:HE2	1:A:191:TYR:CE1	2.34	0.45
1:C:46:ILE:HG13	1:C:256:VAL:HG12	1.98	0.45
1:A:102:SER:HA	1:A:128:PRO:HD3	1.99	0.45
1:A:151:LYS:HD3	1:A:181:ARG:HD3	1.97	0.45
1:A:155:GLU:OE2	1:A:159:LYS:HE3	2.16	0.45
1:C:152:MET:HE3	1:D:171:GLU:HB3	1.98	0.45
1:B:225:PHE:HZ	1:D:238:ILE:HG12	1.81	0.45
1:D:119:MET:HB3	1:D:119:MET:HE3	1.34	0.45
1:C:5:SER:HB3	1:C:17:TYR:CZ	2.52	0.45
1:A:167:THR:O	1:A:171:GLU:HB2	2.15	0.45
1:A:217:GLY:HA2	1:A:240:THR:HG21	1.98	0.45
1:B:166:PHE:O	1:B:170:HIS:HB3	2.15	0.45
1:C:130:ALA:N	1:C:133:PRO:CG	2.80	0.45
1:B:85:ILE:HA	1:B:88:LEU:HD12	1.98	0.45
1:C:124:PRO:HG3	1:C:211:LEU:HD11	1.99	0.45
1:A:49:MET:HG3	1:A:260:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:PRO:O	1:B:223:MET:O	2.35	0.45
1:B:10:LYS:HE3	1:B:86:SER:OG	2.17	0.45
1:D:134:HIS:HB2	1:D:139:LEU:HD21	1.98	0.45
1:D:61:PHE:HE1	1:D:186:ARG:HB3	1.82	0.45
1:D:147:GLU:C	1:D:151:LYS:HE2	2.38	0.45
1:D:157:MET:HB3	2:D:335:HOH:O	2.16	0.45
1:B:219:THR:O	1:D:221:THR:HG23	2.17	0.44
1:C:213:TRP:O	1:C:238:ILE:HA	2.18	0.44
1:D:75:VAL:O	1:D:195:LEU:HD22	2.18	0.44
1:D:160:LEU:O	1:D:164:HIS:NE2	2.50	0.44
1:B:151:LYS:HG2	1:B:181:ARG:O	2.17	0.44
1:C:130:ALA:O	1:C:133:PRO:HD2	2.15	0.44
1:A:174:GLU:CG	1:B:178:ALA:HA	2.11	0.44
1:B:123:LEU:HD21	1:B:262:THR:HG21	1.98	0.44
1:C:124:PRO:HD2	1:C:212:ASP:O	2.17	0.44
1:C:138:LEU:HD23	1:C:138:LEU:HA	1.74	0.44
1:A:111:LEU:HB3	1:A:119:MET:SD	2.56	0.44
1:A:191:TYR:HA	1:A:195:LEU:HD23	1.99	0.44
1:B:126:GLU:HB3	1:B:224:PHE:CZ	2.53	0.44
1:C:228:ILE:HA	1:C:238:ILE:CD1	2.42	0.44
1:D:120:ARG:HD3	1:D:267:LEU:HA	1.98	0.44
1:D:125:HIS:CD2	1:D:126:GLU:HG3	2.52	0.44
1:D:160:LEU:H	1:D:160:LEU:HD23	1.83	0.44
1:B:30:PRO:HG2	1:B:56:PHE:O	2.18	0.44
1:C:138:LEU:HD22	1:C:140:LYS:HG2	1.98	0.44
1:A:158:PRO:CD	1:A:159:LYS:HD2	2.47	0.44
1:D:145:GLU:HB3	1:D:149:ILE:HG23	2.00	0.43
1:A:135:PHE:CZ	1:A:157:MET:HB3	2.54	0.43
1:A:164:HIS:CG	1:A:244:MET:HE2	2.54	0.43
1:C:134:HIS:CE1	1:C:139:LEU:HD11	2.54	0.43
1:C:139:LEU:CB	1:C:192:PRO:HB3	2.47	0.43
1:C:170:HIS:CD2	1:D:155:GLU:HB3	2.53	0.43
1:A:31:ASP:OD1	1:A:246:PHE:HE1	2.00	0.43
1:A:240:THR:HG21	1:C:222:ARG:CG	2.48	0.43
1:B:168:ALA:O	1:B:171:GLU:HB3	2.18	0.43
1:D:151:LYS:HG2	1:D:185:PRO:HD3	2.00	0.43
1:D:187:TRP:CD1	1:D:191:TYR:CG	3.07	0.43
1:A:7:LEU:CD2	1:A:90:GLU:HG2	2.43	0.43
1:B:193:HIS:HB2	2:B:383:HOH:O	2.17	0.43
1:C:39:MET:C	1:C:42:PRO:HD2	2.39	0.43
1:D:152:MET:O	1:D:156:GLU:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:GLU:HG3	1:D:157:MET:SD	2.59	0.43
1:C:9:ASP:OD2	1:C:11:ASN:ND2	2.32	0.43
1:C:130:ALA:N	1:C:133:PRO:HG3	2.34	0.43
1:A:152:MET:HG2	1:B:170:HIS:CE1	2.54	0.43
1:A:252:PRO:O	1:A:256:VAL:HG12	2.19	0.43
1:C:161:GLY:C	1:C:162:PHE:HD1	2.22	0.43
1:B:124:PRO:HG3	1:B:211:LEU:HD11	2.01	0.43
1:D:162:PHE:HB3	1:D:246:PHE:CE2	2.54	0.43
1:A:75:VAL:O	1:A:195:LEU:HD22	2.19	0.42
1:B:158:PRO:HD2	1:B:159:LYS:H	1.84	0.42
1:C:222:ARG:CG	1:C:222:ARG:NH1	2.72	0.42
1:D:97:THR:OG1	1:D:120:ARG:NH1	2.52	0.42
1:A:123:LEU:HD22	1:A:259:ILE:HD13	2.01	0.42
1:A:213:TRP:O	1:A:238:ILE:HD12	2.18	0.42
1:B:153:LEU:HA	1:B:156:GLU:HG2	2.01	0.42
1:D:9:ASP:OD1	1:D:13:ILE:HB	2.19	0.42
1:D:4:ARG:NH2	2:D:316:HOH:O	2.44	0.42
1:A:135:PHE:HB2	1:A:162:PHE:HE2	1.85	0.42
1:A:166:PHE:O	1:A:170:HIS:HB3	2.19	0.42
1:D:159:LYS:HD3	1:D:169:TRP:NE1	2.34	0.42
1:B:45:MET:CB	1:B:256:VAL:HG11	2.49	0.42
1:B:125:HIS:CE1	1:B:241:LEU:HD11	2.54	0.42
1:A:69:PRO:HA	1:A:72:TYR:CZ	2.55	0.42
1:B:255:LEU:O	1:B:259:ILE:HG12	2.20	0.42
1:C:46:ILE:HD11	1:C:259:ILE:HD12	2.01	0.42
1:A:174:GLU:OE2	1:B:174:GLU:OE2	2.38	0.42
1:B:125:HIS:CD2	1:B:126:GLU:HG3	2.55	0.42
1:B:155:GLU:HG2	1:B:184:TYR:CZ	2.55	0.42
1:D:111:LEU:HB3	1:D:119:MET:HE1	2.01	0.42
1:A:90:GLU:OE2	2:A:301:HOH:O	2.21	0.41
1:C:159:LYS:HE2	1:C:160:LEU:CD1	2.50	0.41
1:B:124:PRO:HD2	1:B:212:ASP:O	2.19	0.41
1:B:140:LYS:HE3	1:B:193:HIS:HA	2.02	0.41
1:A:155:GLU:HG2	1:A:184:TYR:HE2	1.84	0.41
1:D:162:PHE:C	1:D:244:MET:HE3	2.40	0.41
1:A:65:TRP:CH2	1:A:182:LYS:HB3	2.55	0.41
1:A:159:LYS:HZ2	1:B:166:PHE:HZ	1.68	0.41
1:A:174:GLU:HB2	1:B:181:ARG:HB2	2.02	0.41
1:C:221:THR:O	1:C:225:PHE:HB2	2.21	0.41
1:A:123:LEU:HD23	1:A:258:HIS:NE2	2.35	0.41
1:A:159:LYS:HG2	1:A:166:PHE:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:PRO:HB2	1:B:34:GLY:HA2	2.02	0.41
1:D:251:HIS:HB3	1:D:254:VAL:CG2	2.51	0.41
1:A:159:LYS:HZ2	1:A:166:PHE:HE1	1.67	0.41
1:B:27:VAL:HG11	1:B:88:LEU:HD21	2.02	0.41
1:A:219:THR:O	1:C:220:PRO:HA	2.21	0.41
1:D:167:THR:HA	1:D:170:HIS:NE2	2.36	0.41
1:A:75:VAL:HB	1:A:195:LEU:HD21	2.03	0.41
1:A:162:PHE:CB	1:A:245:HIS:HB2	2.48	0.41
1:A:254:VAL:HG23	2:A:342:HOH:O	2.21	0.41
1:C:181:ARG:HA	1:C:184:TYR:CD2	2.56	0.41
1:A:31:ASP:CG	1:A:246:PHE:HE1	2.23	0.41
1:A:164:HIS:CB	1:A:244:MET:HE3	2.37	0.41
1:B:39:MET:C	1:B:42:PRO:HD2	2.41	0.41
1:D:60:GLY:C	1:D:65:TRP:HA	2.42	0.41
1:B:130:ALA:HB3	1:B:133:PRO:CD	2.51	0.40
1:D:6:THR:HA	1:D:15:TRP:O	2.22	0.40
1:A:4:ARG:O	1:A:4:ARG:HD3	2.22	0.40
1:A:158:PRO:CB	1:A:162:PHE:HE1	2.34	0.40
1:B:214:THR:HA	1:B:239:ALA:O	2.22	0.40
1:A:150:VAL:HG11	1:A:185:PRO:HA	2.04	0.40
1:A:158:PRO:CB	1:A:162:PHE:CE1	3.04	0.40
1:A:159:LYS:N	1:A:159:LYS:CD	2.72	0.40
1:D:39:MET:C	1:D:42:PRO:HD2	2.41	0.40
1:A:25:HIS:CE1	1:A:93:ILE:HG12	2.56	0.40
1:A:248:TYR:N	1:A:255:LEU:HD13	2.37	0.40
1:B:23:GLY:O	1:B:52:THR:HG22	2.21	0.40
1:B:69:PRO:HA	1:B:72:TYR:CZ	2.56	0.40
1:B:75:VAL:N	1:B:194:THR:HG21	2.37	0.40
1:B:159:LYS:HZ2	1:B:169:TRP:HE1	1.69	0.40
1:B:238:ILE:HG13	1:D:225:PHE:CZ	2.41	0.40
1:C:164:HIS:CD2	1:C:244:MET:CE	3.05	0.40
1:A:160:LEU:HD23	1:A:164:HIS:CE1	2.57	0.40
1:B:143:GLU:H	1:B:143:GLU:HG3	1.64	0.40
1:B:187:TRP:CD1	1:B:191:TYR:HB2	2.57	0.40
1:D:164:HIS:HD2	1:D:244:MET:CE	2.34	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	265/267 (99%)	248 (94%)	16 (6%)	1 (0%)	34	48
1	B	265/267 (99%)	252 (95%)	13 (5%)	0	100	100
1	C	265/267 (99%)	253 (96%)	12 (4%)	0	100	100
1	D	265/267 (99%)	251 (95%)	13 (5%)	1 (0%)	34	48
All	All	1060/1068 (99%)	1004 (95%)	54 (5%)	2 (0%)	47	62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	GLY
1	D	158	PRO

5.3.2 Protein sidechains [i](#)

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	223/223 (100%)	207 (93%)	16 (7%)	14	23
1	B	223/223 (100%)	216 (97%)	7 (3%)	40	60
1	C	223/223 (100%)	211 (95%)	12 (5%)	22	36
1	D	223/223 (100%)	207 (93%)	16 (7%)	14	23
All	All	892/892 (100%)	841 (94%)	51 (6%)	20	33

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	A	10	LYS
1	A	119	MET
1	A	135	PHE
1	A	143	GLU
1	A	146	ASP
1	A	151	LYS
1	A	155	GLU
1	A	158	PRO
1	A	159	LYS
1	A	160	LEU
1	A	162	PHE
1	A	174	GLU
1	A	197	LEU
1	A	232	SER
1	A	255	LEU
1	B	4	ARG
1	B	11	ASN
1	B	119	MET
1	B	170	HIS
1	B	197	LEU
1	B	222	ARG
1	B	227	ASN
1	C	1	MET
1	C	10	LYS
1	C	31	ASP
1	C	65	TRP
1	C	102	SER
1	C	135	PHE
1	C	137	GLN
1	C	138	LEU
1	C	152	MET
1	C	195	LEU
1	C	222	ARG
1	C	227	ASN
1	D	1	MET
1	D	10	LYS
1	D	65	TRP
1	D	119	MET
1	D	135	PHE
1	D	137	GLN
1	D	141	LEU
1	D	158	PRO

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Mol	Chain	Res	Type
1	D	159	LYS
1	D	160	LEU
1	D	171	GLU
1	D	197	LEU
1	D	222	ARG
1	D	227	ASN
1	D	232	SER
1	D	265	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	164	HIS
1	C	137	GLN
1	C	164	HIS
1	D	164	HIS

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 monosaccharides 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

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	267/267 (100%)	0.43	23 (8%) 10 9	5, 15, 42, 86	0
1	B	267/267 (100%)	0.53	29 (10%) 5 5	7, 17, 40, 115	0
1	C	267/267 (100%)	0.61	27 (10%) 7 6	5, 16, 41, 96	0
1	D	267/267 (100%)	0.56	25 (9%) 8 7	6, 17, 42, 98	0
All	All	1068/1068 (100%)	0.53	104 (9%) 7 7	5, 16, 42, 115	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	134	HIS	15.3
1	D	135	PHE	13.0
1	D	133	PRO	12.1
1	C	132	GLY	11.3
1	B	136	GLY	11.1
1	B	137	GLN	11.0
1	A	133	PRO	10.5
1	B	134	HIS	10.5
1	B	135	PHE	9.3
1	C	137	GLN	8.9
1	A	137	GLN	8.6
1	A	135	PHE	8.3
1	D	134	HIS	8.0
1	C	135	PHE	7.2
1	C	92	HIS	7.2
1	D	136	GLY	7.0
1	D	137	GLN	6.8
1	B	132	GLY	6.4
1	C	136	GLY	6.3
1	D	132	GLY	5.9
1	A	136	GLY	5.8

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Mol	Chain	Res	Type	RSRZ
1	C	133	PRO	5.7
1	C	1	MET	5.1
1	B	133	PRO	4.8
1	A	134	HIS	4.7
1	A	164	HIS	4.6
1	A	65	TRP	4.5
1	D	162	PHE	4.5
1	B	171	GLU	4.4
1	D	1	MET	4.3
1	D	65	TRP	4.1
1	A	170	HIS	4.0
1	A	157	MET	3.9
1	C	65	TRP	3.9
1	B	1	MET	3.9
1	C	139	LEU	3.7
1	C	95	TYR	3.7
1	C	149	ILE	3.6
1	A	197	LEU	3.6
1	A	1	MET	3.5
1	C	160	LEU	3.5
1	B	163	GLY	3.5
1	D	164	HIS	3.5
1	D	92	HIS	3.4
1	C	191	TYR	3.3
1	A	162	PHE	3.3
1	C	138	LEU	3.3
1	C	164	HIS	3.2
1	D	171	GLU	3.2
1	B	65	TRP	3.1
1	B	42	PRO	3.1
1	D	160	LEU	3.1
1	D	184	TYR	3.1
1	A	131	ALA	3.1
1	A	95	TYR	3.0
1	D	191	TYR	3.0
1	A	163	GLY	3.0
1	C	170	HIS	2.9
1	B	164	HIS	2.9
1	B	160	LEU	2.9
1	D	95	TYR	2.9
1	B	170	HIS	2.8
1	A	114	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	237	PRO	2.7
1	A	92	HIS	2.7
1	A	42	PRO	2.7
1	B	95	TYR	2.7
1	B	92	HIS	2.6
1	C	159	LYS	2.6
1	A	156	GLU	2.6
1	B	152	MET	2.5
1	B	174	GLU	2.5
1	B	114	ASP	2.4
1	C	158	PRO	2.4
1	D	42	PRO	2.4
1	C	197	LEU	2.4
1	B	149	ILE	2.4
1	C	152	MET	2.4
1	D	170	HIS	2.4
1	D	5	SER	2.4
1	B	193	HIS	2.3
1	B	222	ARG	2.3
1	B	157	MET	2.3
1	C	144	MET	2.3
1	D	149	ILE	2.3
1	A	193	HIS	2.3
1	D	256	VAL	2.3
1	D	152	MET	2.3
1	C	174	GLU	2.3
1	B	221	THR	2.2
1	B	153	LEU	2.2
1	C	220	PRO	2.2
1	C	171	GLU	2.2
1	D	174	GLU	2.2
1	B	254	VAL	2.2
1	C	162	PHE	2.1
1	A	191	TYR	2.1
1	A	11	ASN	2.1
1	A	158	PRO	2.1
1	C	157	MET	2.1
1	B	61	PHE	2.1
1	D	144	MET	2.0
1	D	156	GLU	2.0
1	B	159	LYS	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 monosaccharides 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.