



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 3, 2017 – 07:37 PM EDT

PDB ID : 1QM4
Title : METHIONINE ADENOSYLTRANSFERASE COMPLEXED WITH A L-METHIONINE ANALOGOUS
Authors : Gonzalez, B.; Pajares, M.A.; Hermoso, J.A.; Sanz-Aparicio, J.
Deposited on : unknown
Resolution : 2.66 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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

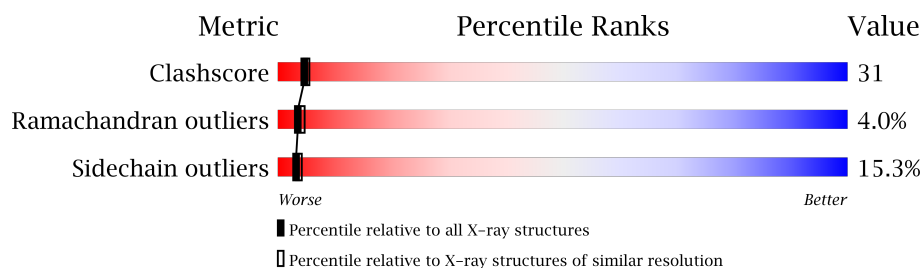
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.66 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	112137	1026 (2.68-2.64)
Ramachandran outliers	110173	1010 (2.68-2.64)
Sidechain outliers	110143	1010 (2.68-2.64)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	396	
1	B	396	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	401	-	X	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5918 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.

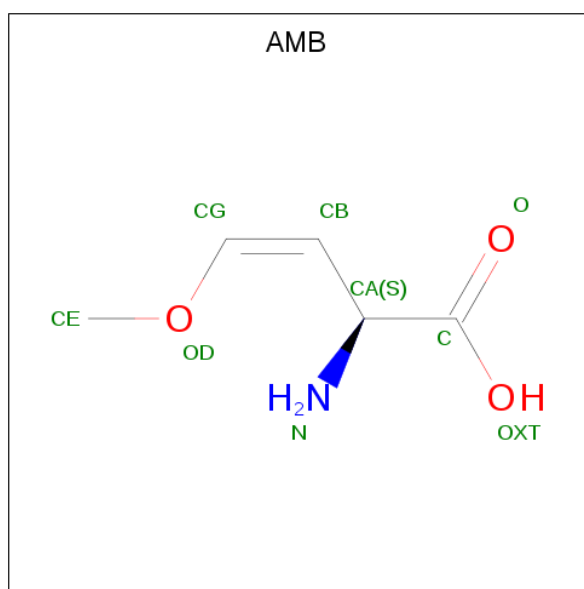
- Molecule 1 is a protein called METHIONINE ADENOSYLTRANSFERASE, ALPHA FORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	0	0
			2846	1803	491	536	16			
1	B	368	Total	C	N	O	S	0	0	0
			2846	1803	491	536	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASP	deletion	UNP P13444
B	?	-	ASP	deletion	UNP P13444

- Molecule 2 is L-2-AMINO-4-METHOXY-CIS-BUT-3-ENOIC ACID (three-letter code: AMB) (formula: C₅H₉NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			9	5	1	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		

- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	K	0	0
			1	1		
5	A	2	Total	K	0	0
			2	2		

- Molecule 6 is water.

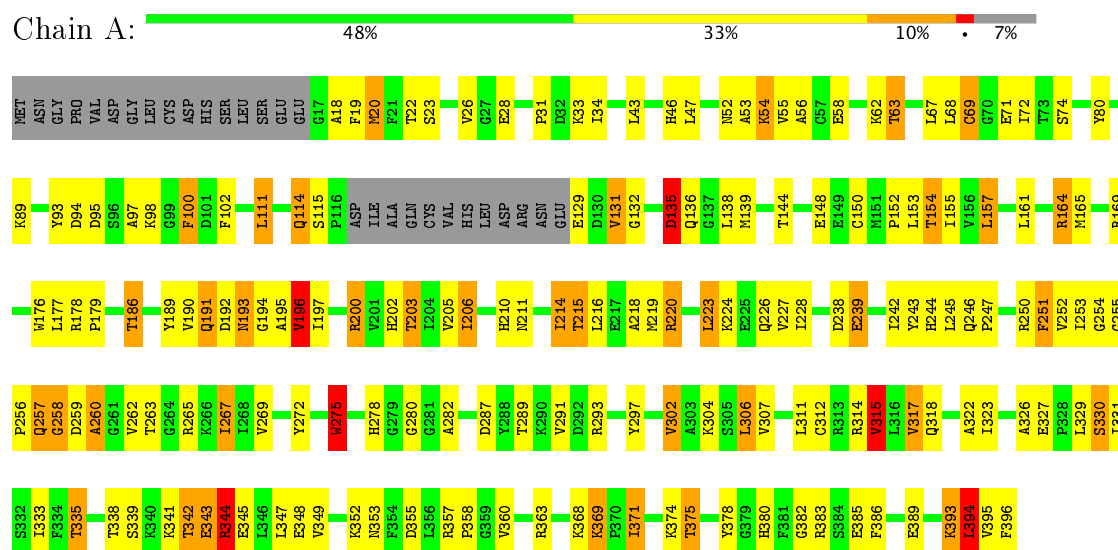
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	104	Total 104	O 104	0	0
6	B	93	Total 93	O 93	0	0

3 Residue-property plots

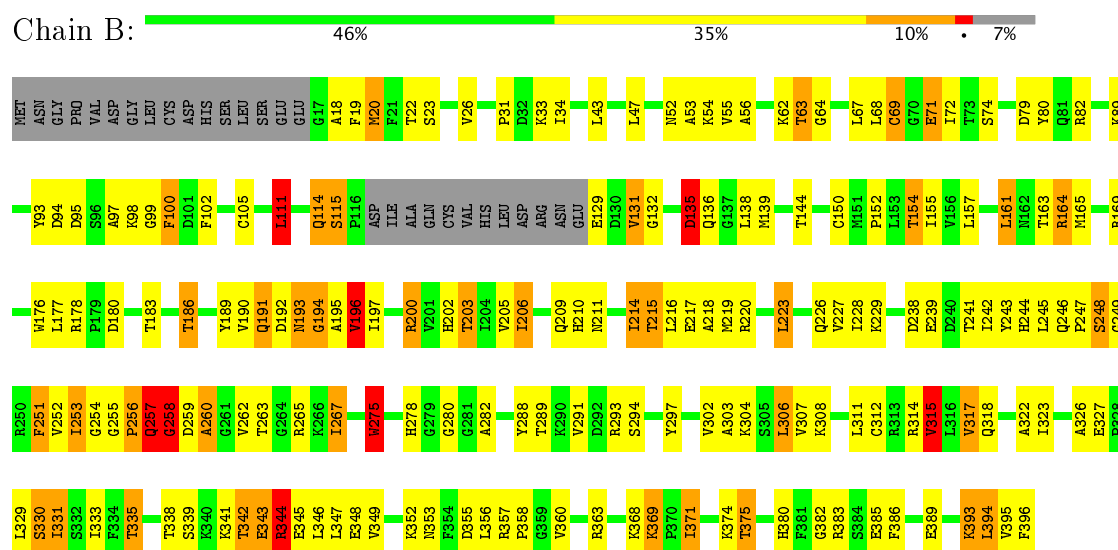
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

Note EDS was not executed.

• Molecule 1: METHIONINE ADENOSYLTRANSFERASE, ALPHA FORM



• Molecule 1: METHIONINE ADENOSYLTRANSFERASE, ALPHA FORM



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	115.20 Å 115.20 Å 159.98 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.66	Depositor
% Data completeness (in resolution range)	84.3 (10.00-2.66)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.230 , 0.290	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5918	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, AMB, K, SO4

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	0.79	1/2901 (0.0%)	1.02	14/3926 (0.4%)
1	B	0.78	2/2901 (0.1%)	1.04	14/3926 (0.4%)
All	All	0.79	3/5802 (0.1%)	1.03	28/7852 (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	B	0	2
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	69	CYS	CB-SG	-5.98	1.72	1.81
1	B	69	CYS	CB-SG	-5.21	1.73	1.81
1	B	258	GLY	CA-C	5.01	1.59	1.51

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	196	VAL	N-CA-C	8.15	133.00	111.00
1	A	344	ARG	NE-CZ-NH2	8.12	124.36	120.30
1	B	344	ARG	NE-CZ-NH2	8.08	124.34	120.30
1	B	196	VAL	N-CA-C	7.87	132.26	111.00
1	B	257	GLN	N-CA-C	-7.79	89.96	111.00
1	B	169	ARG	NE-CZ-NH1	7.16	123.88	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	169	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	B	315	VAL	CB-CA-C	-6.37	99.29	111.40
1	A	315	VAL	CB-CA-C	-6.16	99.70	111.40
1	A	111	LEU	CA-CB-CG	6.11	129.36	115.30
1	A	344	ARG	O-C-N	5.75	131.91	122.70
1	B	220	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	A	335	THR	N-CA-C	-5.66	95.72	111.00
1	A	169	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	A	238	ASP	N-CA-CB	-5.59	100.54	110.60
1	B	335	THR	N-CA-C	-5.57	95.95	111.00
1	A	200	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	B	200	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	B	111	LEU	CA-CB-CG	5.39	127.71	115.30
1	A	250	ARG	NE-CZ-NH1	-5.37	117.61	120.30
1	A	200	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	A	275	TRP	N-CA-C	5.25	125.16	111.00
1	A	179	PRO	N-CA-C	5.18	125.56	112.10
1	B	275	TRP	N-CA-C	5.09	124.73	111.00
1	A	220	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	B	257	GLN	CA-C-O	-5.08	109.44	120.10
1	B	194	GLY	N-CA-C	-5.05	100.47	113.10
1	B	200	ARG	NE-CZ-NH2	-5.01	117.79	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	272	TYR	Sidechain
1	B	257	GLN	Mainchain
1	B	258	GLY	Mainchain

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	2846	0	2852	179	0
1	B	2846	0	2852	183	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	9	0	8	0	0
3	A	10	0	0	0	0
3	B	5	0	0	0	0
4	A	2	0	0	0	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
6	A	104	0	0	4	0
6	B	93	0	0	7	0
All	All	5918	0	5712	356	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 31.

All (356) 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:341:LYS:O	1:A:342:THR:HG22	1.56	1.04
1:B:341:LYS:O	1:B:342:THR:HG22	1.58	1.03
1:A:344:ARG:NE	1:A:347:LEU:HD23	1.71	1.03
1:B:344:ARG:NE	1:B:347:LEU:HD23	1.75	1.01
1:A:262:VAL:HG11	1:B:262:VAL:HG11	1.43	1.00
1:A:267:ILE:HD11	1:A:282:ALA:HA	1.50	0.92
1:B:267:ILE:HD11	1:B:282:ALA:HA	1.54	0.87
1:A:278:HIS:HD2	1:A:280:GLY:H	1.24	0.86
1:B:202:HIS:ND1	1:B:203:THR:HG22	1.95	0.81
1:B:278:HIS:HD2	1:B:280:GLY:H	1.25	0.81
1:A:203:THR:HB	1:A:242:ILE:HB	1.63	0.80
1:A:344:ARG:CD	1:A:347:LEU:HD23	2.11	0.79
1:B:333:ILE:O	1:B:343:GLU:HG2	1.82	0.79
1:A:63:THR:OG1	1:A:257:GLN:CG	2.29	0.79
1:B:393:LYS:O	1:B:394:LEU:HB2	1.81	0.79
1:A:257:GLN:O	1:A:260:ALA:N	2.16	0.79
1:B:203:THR:HB	1:B:242:ILE:HB	1.63	0.79
1:B:34:ILE:HD11	1:B:256:PRO:HG3	1.65	0.79
1:B:341:LYS:O	1:B:342:THR:CG2	2.32	0.78
1:A:202:HIS:ND1	1:A:203:THR:HG22	1.99	0.78
1:A:257:GLN:O	1:A:259:ASP:N	2.17	0.78
1:A:333:ILE:O	1:A:343:GLU:HG2	1.84	0.77
1:A:63:THR:OG1	1:A:257:GLN:HG2	1.85	0.77
1:B:215:THR:HG21	6:B:557:HOH:O	1.84	0.77
1:B:335:THR:HG22	1:B:338:THR:H	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:SER:HB2	6:B:543:HOH:O	1.86	0.76
1:A:341:LYS:O	1:A:342:THR:CG2	2.32	0.76
1:A:393:LYS:O	1:A:394:LEU:HB2	1.84	0.76
1:B:135:ASP:HA	1:B:323:ILE:HD12	1.66	0.76
1:B:329:LEU:O	1:B:330:SER:HB3	1.85	0.76
1:A:342:THR:O	1:A:345:GLU:HB2	1.86	0.76
1:B:100:PHE:CD2	1:B:256:PRO:HG2	2.21	0.76
1:B:165:MET:HE1	1:B:206:ILE:HD11	1.68	0.75
1:A:148:GLU:HB2	6:A:521:HOH:O	1.88	0.73
1:A:342:THR:O	1:A:342:THR:HG23	1.87	0.73
1:A:135:ASP:HA	1:A:323:ILE:HD12	1.71	0.72
1:A:329:LEU:O	1:A:330:SER:HB3	1.90	0.72
1:B:342:THR:HG23	1:B:342:THR:O	1.89	0.72
1:A:95:ASP:HB2	1:A:98:LYS:HD2	1.72	0.72
1:A:335:THR:HG22	1:A:338:THR:H	1.54	0.71
1:B:95:ASP:HB2	1:B:98:LYS:HD2	1.72	0.71
1:A:31:PRO:HG3	1:A:256:PRO:HA	1.73	0.70
1:A:293:ARG:HH21	1:A:375:THR:HG21	1.58	0.68
1:B:344:ARG:CD	1:B:347:LEU:HD23	2.23	0.68
1:A:342:THR:O	1:A:342:THR:CG2	2.42	0.68
1:B:375:THR:HG23	1:B:380:HIS:NE2	2.08	0.68
1:A:375:THR:HG23	1:A:380:HIS:NE2	2.09	0.67
1:B:93:TYR:OH	1:B:256:PRO:HD3	1.95	0.67
1:B:210:HIS:CE1	1:B:251:PHE:H	2.13	0.67
1:B:312:CYS:SG	1:B:315:VAL:HG22	2.36	0.66
1:B:165:MET:CE	1:B:206:ILE:HD11	2.26	0.66
1:B:342:THR:O	1:B:345:GLU:HB2	1.95	0.66
1:A:69:CYS:SG	1:B:62:LYS:HE2	2.36	0.66
1:B:342:THR:HG22	1:B:345:GLU:HB2	1.78	0.66
1:B:293:ARG:HH21	1:B:375:THR:HG21	1.60	0.65
1:B:342:THR:O	1:B:342:THR:CG2	2.44	0.65
1:B:205:VAL:HG22	1:B:244:HIS:HB2	1.78	0.65
1:B:152:PRO:HB2	1:B:155:ILE:HG22	1.79	0.64
1:B:262:VAL:HG13	6:B:545:HOH:O	1.96	0.64
1:A:342:THR:HG22	1:A:345:GLU:HB2	1.79	0.64
1:A:63:THR:OG1	1:A:257:GLN:HG3	1.97	0.64
1:A:23:SER:HB2	1:A:154:THR:HG23	1.79	0.64
1:B:34:ILE:CD1	1:B:256:PRO:HG3	2.28	0.64
1:B:31:PRO:HG3	1:B:256:PRO:HA	1.79	0.64
1:A:257:GLN:C	1:A:259:ASP:N	2.48	0.63
1:A:210:HIS:CE1	1:A:251:PHE:H	2.17	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:ARG:HG2	1:B:227:VAL:HB	1.80	0.63
1:B:329:LEU:HG	1:B:329:LEU:O	1.98	0.63
1:A:223:LEU:HD23	1:A:245:LEU:HB3	1.80	0.62
1:A:22:THR:OG1	1:A:186:THR:HB	2.00	0.62
1:A:56:ALA:H	1:A:72:ILE:HG22	1.64	0.61
1:A:97:ALA:O	1:A:253:ILE:HD12	2.00	0.61
1:B:97:ALA:O	1:B:253:ILE:HG23	2.00	0.61
1:B:56:ALA:H	1:B:72:ILE:HG22	1.64	0.61
1:B:333:ILE:O	1:B:343:GLU:CG	2.48	0.61
1:A:267:ILE:HG23	1:A:278:HIS:CE1	2.35	0.61
1:B:23:SER:HB2	1:B:154:THR:HG23	1.81	0.61
1:A:23:SER:CB	1:A:154:THR:HG23	2.31	0.61
1:A:100:PHE:CD2	1:A:256:PRO:HG2	2.35	0.61
1:B:99:GLY:HA3	1:B:255:GLY:HA3	1.81	0.61
1:A:165:MET:CE	1:A:206:ILE:HD11	2.31	0.61
1:A:312:CYS:SG	1:A:315:VAL:HG22	2.42	0.60
1:B:335:THR:HG21	1:B:339:SER:N	2.17	0.60
1:B:278:HIS:CD2	1:B:280:GLY:H	2.14	0.60
1:A:164:ARG:HG2	1:A:227:VAL:HB	1.83	0.60
1:B:100:PHE:HD2	1:B:256:PRO:HG2	1.66	0.60
1:B:297:TYR:OH	1:B:380:HIS:HD2	1.84	0.60
1:B:215:THR:HG23	1:B:218:ALA:CB	2.31	0.60
1:A:345:GLU:O	1:A:349:VAL:HG23	2.02	0.60
1:A:348:GLU:HG3	1:A:352:LYS:HE2	1.84	0.60
1:B:223:LEU:HD23	1:B:245:LEU:HB3	1.83	0.59
1:B:345:GLU:O	1:B:349:VAL:HG23	2.02	0.59
1:B:210:HIS:CD2	1:B:252:VAL:HG22	2.38	0.59
1:A:136:GLN:NE2	1:A:323:ILE:H	2.00	0.59
1:B:267:ILE:HG23	1:B:278:HIS:CE1	2.37	0.59
1:A:297:TYR:OH	1:A:380:HIS:HD2	1.84	0.59
1:B:348:GLU:HG3	1:B:352:LYS:HE2	1.83	0.59
1:B:214:ILE:HD12	1:B:219:MET:HG3	1.84	0.59
1:A:165:MET:HE1	1:A:206:ILE:HD11	1.83	0.59
1:B:371:ILE:O	1:B:374:LYS:HG2	2.03	0.59
1:A:355:ASP:OD2	1:A:360:VAL:HG21	2.03	0.58
1:A:353:ASN:HD22	1:A:394:LEU:HD22	1.68	0.58
1:A:152:PRO:HB2	1:A:155:ILE:HG22	1.84	0.58
1:B:369:LYS:O	1:B:371:ILE:HD13	2.02	0.58
1:A:329:LEU:HG	1:A:329:LEU:O	2.01	0.58
1:B:23:SER:CB	1:B:154:THR:HG23	2.32	0.58
1:A:344:ARG:HD2	1:A:347:LEU:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:ILE:HB	1:A:374:LYS:HE3	1.86	0.57
1:A:278:HIS:CD2	1:A:280:GLY:H	2.13	0.57
1:A:194:GLY:O	1:A:195:ALA:HB2	2.04	0.57
1:A:31:PRO:HG3	1:A:256:PRO:CA	2.35	0.57
1:B:348:GLU:O	1:B:352:LYS:HG3	2.05	0.57
1:B:251:PHE:CE1	1:B:254:GLY:HA3	2.40	0.57
1:B:252:VAL:HG12	1:B:253:ILE:HD13	1.87	0.57
1:B:195:ALA:CB	1:B:314:ARG:HD3	2.35	0.56
1:A:195:ALA:CB	1:A:314:ARG:HD3	2.35	0.56
1:A:62:LYS:HE2	1:B:69:CYS:SG	2.45	0.56
1:B:63:THR:OG1	1:B:257:GLN:HB2	2.05	0.56
1:A:136:GLN:NE2	1:A:322:ALA:HA	2.20	0.56
1:A:371:ILE:O	1:A:374:LYS:HG2	2.04	0.56
1:A:333:ILE:O	1:A:343:GLU:CG	2.52	0.56
1:A:214:ILE:HD12	1:A:219:MET:HG3	1.87	0.56
1:A:348:GLU:O	1:A:352:LYS:HG3	2.04	0.56
1:A:369:LYS:O	1:A:371:ILE:HD13	2.06	0.56
1:B:341:LYS:O	1:B:342:THR:CB	2.52	0.56
1:B:371:ILE:HB	1:B:374:LYS:HE3	1.85	0.56
1:A:335:THR:HG21	1:A:339:SER:N	2.21	0.56
1:A:52:ASN:ND2	1:A:368:LYS:HE2	2.21	0.56
1:A:196:VAL:HG12	1:A:196:VAL:O	2.06	0.55
1:A:178:ARG:HH12	1:A:253:ILE:HD13	1.70	0.55
1:A:344:ARG:CD	1:A:347:LEU:CD2	2.83	0.55
1:B:342:THR:CG2	1:B:345:GLU:HB2	2.36	0.55
1:A:252:VAL:HG12	1:A:253:ILE:HD13	1.89	0.55
1:B:252:VAL:HG12	1:B:253:ILE:CD1	2.36	0.55
1:A:205:VAL:HG22	1:A:244:HIS:HB2	1.89	0.55
1:B:52:ASN:ND2	1:B:368:LYS:HE2	2.22	0.55
1:A:97:ALA:O	1:A:253:ILE:HG23	2.05	0.55
1:A:342:THR:CG2	1:A:345:GLU:HB2	2.36	0.55
1:B:94:ASP:OD1	1:B:98:LYS:NZ	2.39	0.55
1:B:228:ILE:HG21	1:B:243:TYR:HE2	1.72	0.54
1:B:194:GLY:O	1:B:195:ALA:HB2	2.05	0.54
1:A:374:LYS:HG3	1:A:386:PHE:HE1	1.73	0.54
1:A:215:THR:HG23	1:A:218:ALA:CB	2.38	0.54
1:B:97:ALA:O	1:B:253:ILE:HD12	2.07	0.54
1:B:355:ASP:OD2	1:B:360:VAL:HG21	2.07	0.54
1:A:89:LYS:HD2	1:A:102:PHE:CZ	2.43	0.54
1:B:93:TYR:HB3	1:B:100:PHE:HB3	1.90	0.53
1:A:341:LYS:O	1:A:342:THR:CB	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:ILE:CD1	1:A:218:ALA:HB3	2.38	0.53
1:B:136:GLN:NE2	1:B:323:ILE:H	2.07	0.53
1:A:257:GLN:C	1:A:259:ASP:H	2.13	0.53
1:A:93:TYR:HB3	1:A:100:PHE:HB3	1.89	0.52
1:B:26:VAL:CG2	1:B:33:LYS:HD3	2.39	0.52
1:B:374:LYS:HG3	1:B:386:PHE:HE1	1.74	0.52
1:B:176:TRP:CZ3	1:B:219:MET:HE2	2.44	0.52
1:B:22:THR:OG1	1:B:186:THR:HB	2.10	0.52
1:B:353:ASN:HD22	1:B:394:LEU:HD22	1.73	0.52
1:A:257:GLN:O	1:A:258:GLY:C	2.47	0.52
1:B:257:GLN:HB3	6:B:549:HOH:O	2.10	0.51
1:A:192:ASP:HB2	1:A:197:ILE:HD12	1.92	0.51
1:A:97:ALA:HB1	1:A:253:ILE:HD12	1.92	0.51
1:A:138:LEU:HD11	1:A:318:GLN:CG	2.39	0.51
1:B:189:TYR:CD2	1:B:196:VAL:HG13	2.45	0.51
1:B:178:ARG:HH12	1:B:253:ILE:HD13	1.74	0.51
1:B:192:ASP:HB2	1:B:197:ILE:HD12	1.92	0.51
1:B:163:THR:HG22	6:B:524:HOH:O	2.11	0.51
1:B:23:SER:OG	1:B:154:THR:HG23	2.10	0.51
1:A:72:ILE:CD1	1:A:111:LEU:HD11	2.41	0.51
1:B:89:LYS:HD2	1:B:102:PHE:CZ	2.45	0.51
1:A:23:SER:OG	1:A:154:THR:HG23	2.10	0.51
1:A:138:LEU:HD11	1:A:318:GLN:HG2	1.93	0.50
1:A:178:ARG:NE	1:A:211:ASN:OD1	2.43	0.50
1:A:34:ILE:HD11	1:A:256:PRO:CG	2.41	0.50
1:B:257:GLN:C	1:B:259:ASP:N	2.65	0.50
1:B:53:ALA:HB1	1:B:74:SER:HB2	1.92	0.50
1:A:267:ILE:HD11	1:A:282:ALA:CA	2.33	0.50
1:A:34:ILE:HD11	1:A:256:PRO:HG3	1.93	0.50
1:B:176:TRP:CE3	1:B:219:MET:HE3	2.46	0.50
1:A:228:ILE:HG21	1:A:243:TYR:HE2	1.75	0.50
1:B:176:TRP:CZ3	1:B:219:MET:CE	2.94	0.50
1:B:136:GLN:NE2	1:B:322:ALA:HA	2.27	0.50
1:B:344:ARG:HD2	1:B:347:LEU:HB3	1.94	0.50
1:B:196:VAL:HG12	1:B:196:VAL:O	2.11	0.50
1:B:138:LEU:HD11	1:B:318:GLN:HG2	1.93	0.49
1:B:383:ARG:O	1:B:389:GLU:HG3	2.12	0.49
1:A:214:ILE:HD13	1:A:218:ALA:HB3	1.94	0.49
1:B:72:ILE:CD1	1:B:111:LEU:HD11	2.42	0.49
1:A:20:MET:HE1	1:A:202:HIS:CD2	2.47	0.49
1:A:258:GLY:C	1:A:260:ALA:H	2.14	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:GLU:HA	1:A:357:ARG:HG2	1.94	0.49
1:B:100:PHE:HE2	1:B:256:PRO:HB2	1.76	0.49
1:A:239:GLU:HB2	6:A:565:HOH:O	2.12	0.49
1:B:327:GLU:HA	1:B:357:ARG:HG2	1.93	0.49
1:A:191:GLN:N	1:A:191:GLN:HE21	2.10	0.49
1:B:214:ILE:CD1	1:B:218:ALA:HB3	2.43	0.49
1:B:219:MET:HE1	1:B:246:GLN:NE2	2.27	0.49
1:A:192:ASP:O	1:A:194:GLY:N	2.46	0.49
1:B:216:LEU:HD21	1:B:249:GLY:HA2	1.94	0.49
1:B:214:ILE:HD13	1:B:215:THR:N	2.27	0.49
1:B:374:LYS:HD2	1:B:385:GLU:OE2	2.13	0.49
1:B:195:ALA:HB3	1:B:314:ARG:HD3	1.95	0.49
1:B:229:LYS:HG2	6:B:580:HOH:O	2.13	0.48
1:A:251:PHE:CE1	1:A:254:GLY:HA3	2.48	0.48
1:B:306:LEU:HD12	1:B:394:LEU:HD11	1.95	0.48
1:B:164:ARG:NH1	1:B:226:GLN:O	2.45	0.48
1:A:214:ILE:HD12	1:A:219:MET:CG	2.43	0.48
1:B:192:ASP:O	1:B:194:GLY:N	2.47	0.48
1:A:152:PRO:HB3	1:A:275:TRP:CE3	2.49	0.48
1:B:152:PRO:HB3	1:B:275:TRP:CE3	2.48	0.48
1:A:136:GLN:HE21	1:A:323:ILE:H	1.62	0.48
1:B:311:LEU:CD2	1:B:341:LYS:HD2	2.43	0.48
1:A:89:LYS:HD2	1:A:102:PHE:CE2	2.48	0.47
1:B:72:ILE:HD11	1:B:80:TYR:OH	2.14	0.47
1:A:297:TYR:OH	1:A:380:HIS:CD2	2.66	0.47
1:A:94:ASP:OD1	1:A:98:LYS:NZ	2.45	0.47
1:B:191:GLN:N	1:B:191:GLN:HE21	2.13	0.47
1:B:31:PRO:HG3	1:B:256:PRO:CA	2.44	0.47
1:A:93:TYR:HB3	1:A:100:PHE:O	2.14	0.47
1:A:306:LEU:HD12	1:A:394:LEU:HD11	1.96	0.47
1:B:144:THR:O	1:B:150:CYS:HA	2.14	0.47
1:B:178:ARG:NE	1:B:211:ASN:OD1	2.48	0.47
1:B:375:THR:HG23	1:B:380:HIS:CD2	2.50	0.47
1:A:342:THR:HG22	1:A:345:GLU:CB	2.43	0.47
1:A:58:GLU:CD	1:B:259:ASP:O	2.54	0.47
1:B:297:TYR:OH	1:B:380:HIS:CD2	2.67	0.46
1:B:349:VAL:HG13	1:B:396:PHE:HA	1.98	0.46
1:B:52:ASN:HA	1:B:288:TYR:OH	2.15	0.46
1:B:214:ILE:HD12	1:B:219:MET:CG	2.45	0.46
1:A:344:ARG:HE	1:A:347:LEU:HD23	1.69	0.46
1:B:348:GLU:HA	1:B:348:GLU:OE1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:MET:HE1	1:A:246:GLN:NE2	2.31	0.46
1:A:53:ALA:HB1	1:A:74:SER:HB2	1.97	0.46
1:A:93:TYR:CZ	1:A:256:PRO:HG3	2.50	0.46
1:B:259:ASP:O	1:B:260:ALA:HB3	2.15	0.46
1:A:262:VAL:HG12	1:A:263:THR:N	2.31	0.46
1:A:26:VAL:CG2	1:A:33:LYS:HD3	2.45	0.46
1:A:210:HIS:ND1	1:A:219:MET:HE1	2.31	0.46
1:A:210:HIS:CD2	1:A:252:VAL:HG22	2.51	0.46
1:B:138:LEU:HD11	1:B:318:GLN:CG	2.46	0.46
1:B:382:GLY:H	1:B:389:GLU:CD	2.20	0.46
1:A:176:TRP:CZ3	1:A:177:LEU:HD13	2.51	0.46
1:B:217:GLU:CD	6:B:514:HOH:O	2.54	0.46
1:B:43:LEU:HD13	1:B:55:VAL:HB	1.98	0.46
1:A:195:ALA:HB1	1:A:314:ARG:HD3	1.98	0.45
1:B:395:VAL:CG1	1:B:395:VAL:O	2.63	0.45
1:A:153:LEU:HG	1:A:157:LEU:HD22	1.98	0.45
1:B:215:THR:HG23	1:B:218:ALA:HB2	1.98	0.45
1:A:349:VAL:HG13	1:A:396:PHE:HA	1.97	0.45
1:B:344:ARG:HE	1:B:347:LEU:HD23	1.74	0.45
1:A:219:MET:CE	1:A:246:GLN:HE21	2.29	0.45
1:B:89:LYS:HD2	1:B:102:PHE:CE2	2.51	0.45
1:A:129:GLU:HG3	1:A:363:ARG:NH2	2.32	0.45
1:B:194:GLY:CA	1:B:338:THR:HG22	2.47	0.45
1:B:219:MET:CE	1:B:246:GLN:HE21	2.30	0.45
1:A:132:GLY:HA2	1:A:326:ALA:HA	1.97	0.45
1:A:97:ALA:HB1	1:A:253:ILE:CD1	2.47	0.45
1:B:34:ILE:CD1	1:B:256:PRO:CG	2.95	0.45
1:A:311:LEU:CD2	1:A:341:LYS:HD2	2.47	0.44
1:A:348:GLU:HA	1:A:348:GLU:OE1	2.17	0.44
1:A:375:THR:HG23	1:A:380:HIS:CD2	2.53	0.44
1:A:344:ARG:HA	1:A:344:ARG:HD2	1.49	0.44
1:B:293:ARG:NH2	1:B:375:THR:HG21	2.31	0.44
1:B:395:VAL:HG12	1:B:395:VAL:O	2.16	0.44
1:A:93:TYR:OH	1:A:256:PRO:HG3	2.17	0.44
1:A:34:ILE:HD12	1:A:256:PRO:CB	2.47	0.44
1:B:93:TYR:HB3	1:B:100:PHE:O	2.17	0.44
1:B:165:MET:HB3	1:B:177:LEU:HD21	1.99	0.44
1:A:194:GLY:CA	1:A:338:THR:HG22	2.47	0.44
1:A:28:GLU:HG3	1:A:378:TYR:OH	2.17	0.44
1:B:304:LYS:NZ	1:B:389:GLU:HB3	2.32	0.44
1:B:238:ASP:HB3	1:B:241:THR:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:ASP:OD2	1:B:251:PHE:HZ	2.01	0.44
1:B:342:THR:HG22	1:B:345:GLU:CB	2.46	0.44
1:A:144:THR:O	1:A:150:CYS:HA	2.17	0.44
1:A:138:LEU:HD22	1:B:22:THR:H	1.82	0.44
1:B:294:SER:O	1:B:297:TYR:HB2	2.18	0.44
1:B:344:ARG:HD2	1:B:344:ARG:HA	1.53	0.44
1:A:189:TYR:CD2	1:A:196:VAL:HG13	2.52	0.44
1:A:251:PHE:CD1	1:A:254:GLY:HA3	2.53	0.43
1:A:252:VAL:C	1:A:254:GLY:H	2.21	0.43
1:B:114:GLN:HB3	1:B:115:SER:H	1.66	0.43
1:A:195:ALA:HB3	1:A:314:ARG:HD3	1.99	0.43
1:A:374:LYS:HD2	1:A:385:GLU:OE2	2.17	0.43
1:B:209:GLN:HA	1:B:251:PHE:O	2.19	0.43
1:B:165:MET:O	1:B:177:LEU:HD23	2.18	0.43
1:B:132:GLY:HA2	1:B:326:ALA:HA	2.00	0.43
1:B:333:ILE:HB	1:B:343:GLU:HG3	2.00	0.43
1:B:344:ARG:CD	1:B:347:LEU:CD2	2.94	0.43
1:B:161:LEU:O	1:B:165:MET:HG3	2.19	0.43
1:B:215:THR:HG23	1:B:218:ALA:H	1.83	0.43
1:B:195:ALA:HB1	1:B:314:ARG:HD3	1.99	0.43
1:A:220:ARG:HG2	1:A:245:LEU:HB2	1.99	0.43
1:A:322:ALA:HB2	1:A:329:LEU:HD22	2.00	0.43
1:A:333:ILE:HB	1:A:343:GLU:HG3	1.99	0.43
1:A:382:GLY:H	1:A:389:GLU:CD	2.22	0.43
1:A:100:PHE:HD2	1:A:256:PRO:HG2	1.78	0.43
1:B:215:THR:HG23	1:B:218:ALA:HB3	2.01	0.43
1:A:216:LEU:HA	1:A:216:LEU:HD12	1.86	0.43
1:A:224:LYS:HE3	6:A:552:HOH:O	2.18	0.43
1:A:302:VAL:HG22	1:A:317:VAL:HG11	2.01	0.43
1:B:303:ALA:HB2	1:B:317:VAL:CG1	2.49	0.43
1:A:135:ASP:O	1:A:136:GLN:C	2.58	0.42
1:A:374:LYS:HG3	1:A:386:PHE:CE1	2.52	0.42
1:B:346:LEU:HD23	1:B:346:LEU:HA	1.78	0.42
1:A:259:ASP:O	1:A:260:ALA:HB2	2.19	0.42
1:A:43:LEU:HD13	1:A:55:VAL:HB	2.01	0.42
1:B:129:GLU:HG3	1:B:363:ARG:NH2	2.33	0.42
1:A:20:MET:HE3	1:A:20:MET:HB3	1.65	0.42
1:A:374:LYS:O	1:A:383:ARG:NH2	2.52	0.42
1:B:246:GLN:N	1:B:247:PRO:HD3	2.33	0.42
1:B:19:PHE:CD1	1:B:191:GLN:NE2	2.88	0.42
1:B:331:ILE:HD11	1:B:333:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:TRP:CE3	1:A:219:MET:HE3	2.54	0.42
1:A:176:TRP:CZ3	1:A:219:MET:CE	3.03	0.42
1:A:176:TRP:CZ3	1:A:219:MET:HE2	2.55	0.42
1:A:71:GLU:OE2	1:A:114:GLN:NE2	2.53	0.42
1:A:215:THR:HG23	1:A:218:ALA:HB2	2.02	0.42
1:A:252:VAL:HG12	1:A:253:ILE:CD1	2.49	0.42
1:B:374:LYS:HG3	1:B:386:PHE:CE1	2.54	0.42
1:A:192:ASP:O	1:A:193:ASN:C	2.57	0.42
1:A:246:GLN:N	1:A:247:PRO:HD3	2.34	0.42
1:A:253:ILE:HG22	1:A:253:ILE:O	2.19	0.42
1:A:46:HIS:HD1	1:A:74:SER:CB	2.32	0.42
1:B:251:PHE:CD1	1:B:251:PHE:C	2.93	0.42
1:A:262:VAL:CG1	1:B:262:VAL:HG11	2.31	0.42
1:A:395:VAL:CG1	1:A:395:VAL:O	2.68	0.41
1:B:262:VAL:HG12	1:B:263:THR:N	2.35	0.41
1:A:54:LYS:HA	1:A:287:ASP:OD2	2.20	0.41
1:B:293:ARG:HH21	1:B:375:THR:CG2	2.31	0.41
1:B:71:GLU:OE2	1:B:114:GLN:NE2	2.53	0.41
1:B:304:LYS:O	1:B:308:LYS:HB2	2.20	0.41
1:A:93:TYR:CB	1:A:100:PHE:HB3	2.50	0.41
1:A:165:MET:HB3	1:A:177:LEU:HD21	2.02	0.41
1:A:194:GLY:C	1:A:338:THR:HG22	2.41	0.41
1:B:252:VAL:C	1:B:254:GLY:H	2.24	0.41
1:A:304:LYS:NZ	1:A:389:GLU:HB3	2.36	0.41
1:A:293:ARG:NH2	1:A:375:THR:HG21	2.31	0.41
1:B:267:ILE:HD11	1:B:282:ALA:CA	2.37	0.41
1:B:180:ASP:H	1:B:209:GLN:HE21	1.68	0.41
1:B:251:PHE:CD1	1:B:254:GLY:HA3	2.56	0.41
1:A:114:GLN:N	1:A:114:GLN:HE21	2.19	0.40
1:A:72:ILE:HD11	1:A:80:TYR:OH	2.20	0.40
1:B:161:LEU:HD23	1:B:183:THR:HG23	2.03	0.40
1:B:219:MET:CE	1:B:246:GLN:NE2	2.83	0.40
1:A:19:PHE:CD2	1:A:191:GLN:NE2	2.90	0.40
1:B:114:GLN:HE21	1:B:114:GLN:N	2.19	0.40
1:B:192:ASP:O	1:B:193:ASN:C	2.58	0.40
1:B:19:PHE:HD1	1:B:191:GLN:HE22	1.69	0.40
1:A:164:ARG:NH1	1:A:226:GLN:O	2.51	0.40
1:A:194:GLY:HA3	6:A:514:HOH:O	2.20	0.40
1:A:215:THR:HG23	1:A:218:ALA:H	1.87	0.40
1:B:154:THR:CG2	1:B:155:ILE:N	2.84	0.40
1:B:20:MET:HE1	1:B:202:HIS:CD2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:393:LYS:O	1:B:394:LEU:CB	2.59	0.40
1:B:64:GLY:HA2	1:B:105:CYS:HB2	2.04	0.40
1:B:79:ASP:O	1:B:82:ARG:HB3	2.22	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	364/396 (92%)	314 (86%)	36 (10%)	14 (4%)	4	4
1	B	364/396 (92%)	310 (85%)	39 (11%)	15 (4%)	3	4
All	All	728/792 (92%)	624 (86%)	75 (10%)	29 (4%)	3	4

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ALA
1	A	193	ASN
1	B	18	ALA
1	B	193	ASN
1	B	258	GLY
1	A	196	VAL
1	A	258	GLY
1	A	344	ARG
1	B	196	VAL
1	B	344	ARG
1	A	63	THR
1	A	115	SER
1	A	330	SER
1	B	63	THR
1	B	115	SER

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Mol	Chain	Res	Type
1	B	135	ASP
1	B	330	SER
1	A	135	ASP
1	B	256	PRO
1	B	342	THR
1	A	131	VAL
1	A	260	ALA
1	A	342	THR
1	B	131	VAL
1	B	260	ALA
1	A	394	LEU
1	B	356	LEU
1	A	255	GLY
1	B	253	ILE

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	307/332 (92%)	261 (85%)	46 (15%)	3	4
1	B	307/332 (92%)	259 (84%)	48 (16%)	3	3
All	All	614/664 (92%)	520 (85%)	94 (15%)	3	4

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	MET
1	A	47	LEU
1	A	54	LYS
1	A	67	LEU
1	A	68	LEU
1	A	100	PHE
1	A	114	GLN
1	A	131	VAL
1	A	135	ASP

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Mol	Chain	Res	Type
1	A	139	MET
1	A	154	THR
1	A	157	LEU
1	A	161	LEU
1	A	164	ARG
1	A	186	THR
1	A	190	VAL
1	A	191	GLN
1	A	200	ARG
1	A	203	THR
1	A	206	ILE
1	A	214	ILE
1	A	215	THR
1	A	223	LEU
1	A	239	GLU
1	A	251	PHE
1	A	257	GLN
1	A	265	ARG
1	A	267	ILE
1	A	269	VAL
1	A	275	TRP
1	A	289	THR
1	A	291	VAL
1	A	302	VAL
1	A	306	LEU
1	A	307	VAL
1	A	315	VAL
1	A	317	VAL
1	A	331	ILE
1	A	343	GLU
1	A	344	ARG
1	A	358	PRO
1	A	369	LYS
1	A	371	ILE
1	A	375	THR
1	A	393	LYS
1	A	394	LEU
1	B	20	MET
1	B	47	LEU
1	B	54	LYS
1	B	67	LEU
1	B	68	LEU

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Mol	Chain	Res	Type
1	B	71	GLU
1	B	100	PHE
1	B	111	LEU
1	B	114	GLN
1	B	131	VAL
1	B	135	ASP
1	B	139	MET
1	B	154	THR
1	B	157	LEU
1	B	161	LEU
1	B	164	ARG
1	B	186	THR
1	B	190	VAL
1	B	191	GLN
1	B	200	ARG
1	B	203	THR
1	B	206	ILE
1	B	214	ILE
1	B	215	THR
1	B	223	LEU
1	B	239	GLU
1	B	248	SER
1	B	251	PHE
1	B	257	GLN
1	B	265	ARG
1	B	267	ILE
1	B	275	TRP
1	B	289	THR
1	B	291	VAL
1	B	302	VAL
1	B	306	LEU
1	B	307	VAL
1	B	315	VAL
1	B	317	VAL
1	B	331	ILE
1	B	343	GLU
1	B	344	ARG
1	B	358	PRO
1	B	369	LYS
1	B	371	ILE
1	B	375	THR
1	B	393	LYS

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Mol	Chain	Res	Type
1	B	394	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	113	GLN
1	A	114	GLN
1	A	136	GLN
1	A	159	HIS
1	A	162	ASN
1	A	191	GLN
1	A	209	GLN
1	A	210	HIS
1	A	278	HIS
1	A	318	GLN
1	A	380	HIS
1	B	52	ASN
1	B	113	GLN
1	B	114	GLN
1	B	136	GLN
1	B	159	HIS
1	B	162	ASN
1	B	191	GLN
1	B	209	GLN
1	B	210	HIS
1	B	278	HIS
1	B	318	GLN
1	B	380	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	AMB	A	401	4	2,8,8	1.58	1 (50%)	1,9,9	1.50	0
3	SO4	A	402	4	4,4,4	1.41	1 (25%)	6,6,6	2.18	2 (33%)
3	SO4	A	403	5	4,4,4	2.20	1 (25%)	6,6,6	1.74	2 (33%)
3	SO4	B	401	5	4,4,4	1.10	0	6,6,6	1.77	4 (66%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AMB	A	401	4	-	0/3/8/8	0/0/0/0
3	SO4	A	402	4	-	0/0/0/0	0/0/0/0
3	SO4	A	403	5	-	0/0/0/0	0/0/0/0
3	SO4	B	401	5	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	SO4	O1-S	2.13	1.57	1.45
2	A	401	AMB	CG-CB	2.23	1.43	1.30
3	A	403	SO4	O1-S	3.81	1.66	1.45

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	403	SO4	O3-S-O1	-3.08	92.29	109.26
3	A	402	SO4	O3-S-O1	-2.71	94.32	109.26
3	B	401	SO4	O3-S-O1	-2.32	96.45	109.26
3	B	401	SO4	O4-S-O1	-2.03	98.04	109.26
3	B	401	SO4	O4-S-O2	2.00	120.29	109.26
3	B	401	SO4	O3-S-O2	2.23	121.57	109.26
3	A	403	SO4	O2-S-O1	2.49	127.07	109.64
3	A	402	SO4	O4-S-O2	3.67	129.48	109.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.