



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 10:10 PM GMT

PDB ID : 1A2O
Title : STRUCTURAL BASIS FOR METHYLESTERASE CHEB REGULATION
BY A PHOSPHORYLATION-ACTIVATEDDOMAIN
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Deposited on : 1998-01-06
Resolution : 2.40 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

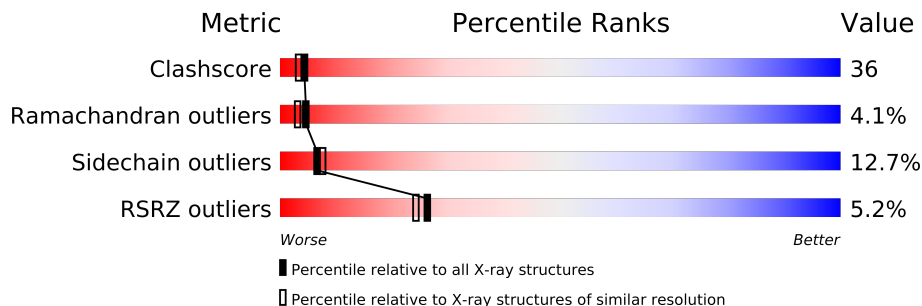
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance



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))
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	349	
1	B	349	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5615 atoms, of which 0 are hydrogen and 0 are deuterium.

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 CHEB METHYLESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	0	0	0
			2602	1633	465	481	23			
1	B	347	Total	C	N	O	S	0	0	0
			2602	1633	465	481	23			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	221	Total	O	0	0
			221	221		
2	B	190	Total	O	0	0
			190	190		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	163.83Å 100.46Å 53.12Å 90.00° 98.63° 90.00°	Depositor
Resolution (Å)	10.00 – 2.40 14.98 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.9 (10.00-2.40) 97.4 (14.98-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.93 (at 2.20Å)	Xtriage
Refinement program	REFMAC, X-PLOR	Depositor
R, R_{free}	0.222 , (Not available) 0.231 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	30.2	Xtriage
Anisotropy	0.495	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 73.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 41964 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5615	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.53	0/2645	1.36	31/3577 (0.9%)
1	B	0.52	0/2645	1.30	18/3577 (0.5%)
All	All	0.52	0/5290	1.33	49/7154 (0.7%)

There are no bond length outliers.

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	128	ARG	NE-CZ-NH1	15.51	128.05	120.30
1	A	172	ARG	NE-CZ-NH2	-12.73	113.94	120.30
1	A	219	ARG	NE-CZ-NH1	10.88	125.74	120.30
1	B	145	THR	C-N-CA	10.64	148.31	121.70
1	B	172	ARG	NE-CZ-NH2	10.01	125.30	120.30
1	A	172	ARG	NE-CZ-NH1	9.44	125.02	120.30
1	B	257	ARG	NE-CZ-NH2	-8.88	115.86	120.30
1	B	261	ASP	CB-CG-OD1	8.58	126.02	118.30
1	A	128	ARG	CD-NE-CZ	8.45	135.43	123.60
1	B	238	ARG	NE-CZ-NH2	-8.29	116.16	120.30
1	B	243	TYR	CB-CG-CD2	-7.65	116.41	121.00
1	A	197	ARG	NE-CZ-NH1	7.62	124.11	120.30
1	A	197	ARG	NE-CZ-NH2	-7.50	116.55	120.30
1	A	255	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	A	219	ARG	NE-CZ-NH2	-7.33	116.64	120.30
1	A	257	ARG	CA-C-O	-7.23	104.91	120.10
1	B	172	ARG	NE-CZ-NH1	-7.21	116.69	120.30
1	A	128	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	A	257	ARG	NE-CZ-NH1	6.94	123.77	120.30
1	B	238	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	A	67	PHE	CB-CG-CD1	6.78	125.54	120.80
1	A	42	ARG	NE-CZ-NH1	6.67	123.64	120.30
1	A	172	ARG	CD-NE-CZ	6.63	132.89	123.60
1	B	43	ASP	CB-CG-OD2	6.59	124.23	118.30
1	B	113	ARG	NE-CZ-NH1	-6.39	117.11	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	ARG	CD-NE-CZ	6.33	132.47	123.60
1	A	42	ARG	NE-CZ-NH2	-6.31	117.14	120.30
1	A	329	ASP	CB-CG-OD1	-6.31	112.62	118.30
1	A	255	ARG	NH1-CZ-NH2	5.85	125.83	119.40
1	B	146	THR	N-CA-C	5.85	126.79	111.00
1	B	122	MET	CA-CB-CG	5.77	123.11	113.30
1	A	5	ARG	NE-CZ-NH1	5.65	123.13	120.30
1	B	148	LYS	C-N-CA	5.65	135.81	121.70
1	A	16	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	A	5	ARG	NE-CZ-NH2	-5.53	117.53	120.30
1	A	255	ARG	NE-CZ-NH1	-5.48	117.56	120.30
1	B	147	LEU	N-CA-CB	-5.48	99.45	110.40
1	A	91	GLU	OE1-CD-OE2	-5.44	116.77	123.30
1	A	111	GLY	N-CA-C	-5.40	99.61	113.10
1	B	37	ASP	CB-CG-OD1	5.40	123.16	118.30
1	A	67	PHE	CA-CB-CG	5.38	126.81	113.90
1	B	255	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	218	GLU	OE1-CD-OE2	-5.37	116.86	123.30
1	A	156	GLU	OE1-CD-OE2	-5.27	116.97	123.30
1	A	67	PHE	N-CA-CB	5.24	120.03	110.60
1	B	63	ASP	CB-CG-OD1	5.18	122.96	118.30
1	B	112	ILE	N-CA-C	5.08	124.70	111.00
1	A	180	LEU	CA-CB-CG	5.04	126.88	115.30
1	A	258	PRO	N-CD-CG	5.02	110.74	103.20

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2602	0	2686	183	0
1	B	2602	0	2685	196	0
2	A	221	0	0	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	190	0	0	11	0
All	All	5615	0	5371	379	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 36.

All (379) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:319:ILE:HG13	2:A:547:HOH:O	1.40	1.20
1:A:85:LEU:HD11	1:A:108:PRO:HD3	1.21	1.19
1:A:85:LEU:N	1:A:85:LEU:HD22	1.55	1.17
1:B:147:LEU:HD22	1:B:338:LEU:HD23	1.26	1.16
1:B:157:LYS:HZ1	1:B:345:GLN:HG2	1.09	1.14
1:B:109:GLN:NE2	1:B:112:ILE:HG13	1.66	1.11
1:B:147:LEU:HD11	1:B:178:LEU:HD23	1.32	1.07
1:B:147:LEU:HD22	1:B:338:LEU:CD2	1.85	1.06
1:B:110:LEU:O	1:B:110:LEU:HD12	1.55	1.06
1:B:42:ARG:HD3	2:B:506:HOH:O	1.56	1.05
1:A:144:PRO:HB2	1:A:146:THR:OG1	1.56	1.05
1:A:109:GLN:HE22	1:A:110:LEU:HB2	1.24	1.01
1:A:22:ILE:HG13	1:A:23:ILE:N	1.74	1.00
1:A:147:LEU:HD12	1:A:338:LEU:HD22	1.40	1.00
1:B:157:LYS:NZ	1:B:345:GLN:HG2	1.77	0.99
1:A:88:LYS:HA	1:A:88:LYS:HE3	1.41	0.99
1:B:147:LEU:CD2	1:B:338:LEU:CD2	2.40	0.98
1:B:147:LEU:HD21	1:B:338:LEU:HB2	1.46	0.97
1:B:109:GLN:HE21	1:B:112:ILE:HG13	1.26	0.97
1:B:147:LEU:CD1	1:B:178:LEU:HA	1.95	0.96
1:B:147:LEU:HD13	1:B:147:LEU:O	1.67	0.95
1:A:109:GLN:NE2	1:A:110:LEU:HB2	1.80	0.95
1:A:10:ASP:OD2	1:A:15:MET:HG2	1.66	0.94
1:B:149:ALA:HA	2:B:509:HOH:O	1.67	0.94
1:B:110:LEU:O	1:B:110:LEU:CD1	2.15	0.94
1:B:65:LEU:HD12	1:B:99:LEU:HD23	1.51	0.92
1:B:257:ARG:HB3	1:B:258:PRO:HD3	1.50	0.92
1:A:147:LEU:HD11	1:A:178:LEU:HD23	1.53	0.91
1:B:167:GLY:O	1:B:171:ILE:HG23	1.70	0.91
1:B:108:PRO:HG3	1:B:122:MET:CE	2.00	0.91
1:B:147:LEU:O	1:B:177:PRO:O	1.90	0.90
1:A:94:LEU:O	1:A:98:GLU:HG2	1.71	0.89
1:A:5:ARG:HB3	1:A:32:VAL:HG21	1.56	0.88
1:A:22:ILE:HD11	1:A:123:ILE:HG21	1.55	0.87

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:119:TYR:CE1	1:B:123:ILE:HD11	2.10	0.87
1:B:22:ILE:HD13	1:B:23:ILE:N	1.89	0.87
1:A:4:ILE:HD11	1:A:132:ARG:NH2	1.90	0.86
1:A:85:LEU:HD22	1:A:85:LEU:H	1.42	0.85
1:A:300:TRP:CD1	1:A:340:LYS:HG3	2.11	0.85
1:A:65:LEU:O	1:A:69:GLU:HB2	1.75	0.85
1:A:7:LEU:HB3	2:A:535:HOH:O	1.76	0.85
1:B:147:LEU:HD21	1:B:338:LEU:CB	2.07	0.84
1:B:111:GLY:C	1:B:112:ILE:HG12	1.97	0.83
1:A:147:LEU:HD21	1:A:334:SER:OG	1.79	0.82
1:A:238:ARG:HD3	2:A:549:HOH:O	1.80	0.82
1:B:147:LEU:CD1	1:B:178:LEU:HD23	2.08	0.81
1:B:112:ILE:HG22	1:B:113:ARG:H	1.45	0.81
1:A:107:LYS:HD2	1:A:107:LYS:O	1.79	0.81
1:B:147:LEU:CD2	1:B:338:LEU:HD22	2.10	0.81
1:A:85:LEU:HD21	1:A:108:PRO:HA	1.60	0.80
1:A:85:LEU:N	1:A:85:LEU:CD2	2.32	0.80
1:B:145:THR:O	1:B:148:LYS:CE	2.29	0.80
1:B:147:LEU:CD2	1:B:338:LEU:HD23	2.07	0.80
1:A:108:PRO:O	1:A:109:GLN:HB3	1.82	0.80
1:B:55:LEU:HD13	1:B:57:VAL:CG2	2.11	0.80
1:A:147:LEU:HD12	1:A:338:LEU:CD2	2.12	0.79
1:B:158:LEU:HD11	1:B:186:ILE:HD13	1.63	0.78
1:A:55:LEU:HD12	1:A:81:MET:HE1	1.65	0.78
1:B:106:THR:O	1:B:108:PRO:HD3	1.84	0.77
1:B:61:ARG:NE	1:B:61:ARG:HA	2.00	0.77
1:B:147:LEU:CD2	1:B:338:LEU:CB	2.62	0.76
1:B:158:LEU:HD11	1:B:186:ILE:CD1	2.16	0.76
1:B:147:LEU:HD11	1:B:178:LEU:HA	1.67	0.76
1:A:22:ILE:HD11	1:A:123:ILE:CG2	2.16	0.75
1:A:84:SER:C	1:A:85:LEU:HD22	2.05	0.75
1:A:192:PRO:HG3	2:A:417:HOH:O	1.86	0.75
1:A:53:LEU:HD12	1:A:79:VAL:HG13	1.68	0.74
1:B:147:LEU:O	1:B:147:LEU:CD1	2.35	0.74
1:A:85:LEU:HD21	1:A:108:PRO:CA	2.16	0.74
1:A:91:GLU:HB2	2:A:502:HOH:O	1.86	0.74
1:A:17:GLN:OE1	2:A:437:HOH:O	2.06	0.73
1:B:171:ILE:HD11	1:B:203:LEU:CD1	2.18	0.73
1:B:153:LEU:HD12	1:B:183:PRO:HG3	1.70	0.72
1:B:69:GLU:O	1:B:73:ARG:HB2	1.89	0.72
1:A:61:ARG:O	1:A:62:MET:C	2.28	0.72
1:B:147:LEU:HD21	1:B:338:LEU:CD2	2.17	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:257:ARG:HB3	1:B:258:PRO:CD	2.19	0.72
1:B:108:PRO:HG3	1:B:122:MET:HE1	1.71	0.72
1:A:88:LYS:HA	1:A:88:LYS:CE	2.16	0.72
1:B:135:ILE:N	1:B:135:ILE:HD13	2.04	0.72
1:A:37:ASP:HB2	1:A:38:PRO:HD2	1.70	0.72
1:B:147:LEU:HD21	1:B:338:LEU:HD22	1.70	0.71
1:B:7:LEU:O	1:B:53:LEU:HD22	1.90	0.71
1:A:85:LEU:CD1	1:A:108:PRO:HD3	2.11	0.71
1:A:221:LEU:HB3	1:A:222:PRO:HD2	1.73	0.71
1:A:69:GLU:O	1:A:73:ARG:HG3	1.89	0.70
1:A:88:LYS:HE2	1:A:91:GLU:HB3	1.73	0.70
1:B:85:LEU:H	1:B:85:LEU:HD22	1.57	0.70
1:B:147:LEU:HD11	1:B:178:LEU:CD2	2.16	0.70
1:A:147:LEU:H	1:A:147:LEU:HD23	1.56	0.70
1:A:5:ARG:HB3	1:A:32:VAL:CG2	2.22	0.69
1:A:62:MET:HG2	2:A:512:HOH:O	1.92	0.69
1:B:95:ARG:HD3	1:B:202:ARG:HH22	1.58	0.69
1:B:158:LEU:CD1	1:B:186:ILE:HD13	2.22	0.69
1:B:20:THR:HG22	1:B:31:MET:HG2	1.74	0.69
1:A:45:ILE:HG21	1:A:77:MET:CE	2.22	0.69
1:A:11:ASP:HB2	1:A:59:MET:HG2	1.75	0.68
1:A:45:ILE:CG2	1:A:77:MET:HE1	2.24	0.68
1:A:55:LEU:HD12	1:A:81:MET:CE	2.24	0.67
1:B:235:GLU:HB2	1:B:266:SER:OG	1.92	0.67
1:B:257:ARG:O	1:B:259:SER:N	2.28	0.67
1:B:41:ALA:O	1:B:45:ILE:HG13	1.95	0.67
1:B:292:LEU:O	1:B:296:GLN:HG2	1.95	0.67
1:A:147:LEU:CD1	1:A:178:LEU:HD23	2.25	0.67
1:B:110:LEU:C	1:B:110:LEU:HD12	2.15	0.66
1:A:310:VAL:HG22	1:A:311:VAL:HG23	1.77	0.66
1:B:161:ILE:HG12	1:B:278:VAL:HB	1.76	0.66
1:B:32:VAL:HG22	1:B:48:PHE:CD2	2.31	0.66
1:A:281:THR:H	1:A:304:GLN:NE2	1.93	0.66
1:A:147:LEU:CD2	1:A:177:PRO:HB2	2.26	0.66
1:B:153:LEU:HD22	1:B:345:GLN:HG3	1.78	0.65
1:B:22:ILE:HD13	1:B:23:ILE:H	1.56	0.65
1:A:10:ASP:OD2	1:A:15:MET:CG	2.43	0.64
1:B:147:LEU:HD13	1:B:147:LEU:C	2.17	0.64
1:B:62:MET:HB3	2:B:507:HOH:O	1.97	0.64
1:A:110:LEU:C	1:A:112:ILE:H	2.00	0.63
1:A:39:LEU:CD1	1:A:42:ARG:HH21	2.12	0.63
1:A:110:LEU:HG	1:A:111:GLY:H	1.64	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:7:LEU:HD21	1:B:44:LEU:HB2	1.82	0.62
1:B:147:LEU:HD23	1:B:335:GLN:HA	1.79	0.62
1:B:135:ILE:CD1	1:B:135:ILE:H	2.12	0.62
1:B:108:PRO:O	1:B:109:GLN:O	2.18	0.62
1:B:147:LEU:CD2	1:B:338:LEU:HB2	2.22	0.62
1:A:128:ARG:O	1:A:132:ARG:HD2	2.00	0.62
1:B:171:ILE:HD11	1:B:203:LEU:HD11	1.81	0.61
1:A:77:MET:HE2	2:A:524:HOH:O	2.01	0.61
1:B:171:ILE:HD11	1:B:203:LEU:HD13	1.83	0.61
1:B:16:ARG:O	1:B:20:THR:HG23	2.01	0.61
1:B:73:ARG:HH22	1:B:140:PRO:HG2	1.67	0.60
1:B:135:ILE:CD1	1:B:135:ILE:N	2.64	0.60
1:A:147:LEU:C	1:A:148:LYS:HG2	2.22	0.60
1:A:2:SER:HA	1:A:28:ASP:C	2.21	0.60
1:A:321:MET:HG3	2:A:369:HOH:O	2.01	0.60
1:A:147:LEU:HD21	1:A:177:PRO:HB2	1.82	0.60
1:B:61:ARG:NH1	1:B:62:MET:HG2	2.16	0.60
1:B:147:LEU:HD12	1:B:178:LEU:HA	1.83	0.60
1:A:53:LEU:CD1	1:A:79:VAL:HG13	2.32	0.60
1:B:216:ASP:HB2	1:B:247:ILE:HB	1.84	0.60
1:A:45:ILE:HG21	1:A:77:MET:HE1	1.82	0.60
1:A:301:THR:OG1	1:A:324:VAL:HA	2.02	0.59
1:B:112:ILE:CG2	1:B:113:ARG:H	2.07	0.59
1:A:3:LYS:NZ	1:A:28:ASP:HB2	2.17	0.59
1:A:39:LEU:HD13	1:A:42:ARG:HH21	1.67	0.59
1:B:205:LYS:HD3	2:B:459:HOH:O	2.01	0.59
1:A:328:VAL:HG12	1:A:329:ASP:O	2.03	0.59
1:A:283:MET:HE2	2:A:553:HOH:O	2.01	0.59
1:A:55:LEU:CD1	1:A:81:MET:CE	2.81	0.59
1:B:119:TYR:CZ	1:B:123:ILE:HD11	2.38	0.59
1:A:55:LEU:CD1	1:A:81:MET:HE3	2.33	0.58
1:A:88:LYS:CE	1:A:91:GLU:HB3	2.33	0.58
1:B:145:THR:O	1:B:148:LYS:HE3	2.03	0.58
1:A:95:ARG:HD2	1:A:202:ARG:HH22	1.68	0.58
1:B:61:ARG:HA	1:B:61:ARG:HE	1.67	0.58
1:A:85:LEU:HD13	1:A:85:LEU:H	1.67	0.58
1:B:57:VAL:HG13	1:B:64:GLY:HA3	1.85	0.57
1:A:183:PRO:HG2	1:A:341:ILE:HG21	1.87	0.57
1:B:147:LEU:HD12	1:B:177:PRO:C	2.24	0.57
1:B:233:HIS:CE1	1:B:257:ARG:O	2.58	0.57
1:A:37:ASP:OD1	1:A:39:LEU:HB2	2.05	0.57
1:A:10:ASP:CG	1:A:15:MET:HG2	2.25	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:37:ASP:HB2	1:B:38:PRO:CD	2.35	0.57
1:A:84:SER:O	1:A:85:LEU:C	2.43	0.56
1:B:157:LYS:HZ1	1:B:345:GLN:HA	1.69	0.56
1:A:45:ILE:CG2	1:A:77:MET:CE	2.83	0.56
1:A:319:ILE:CG1	2:A:547:HOH:O	2.20	0.56
1:A:147:LEU:O	1:A:148:LYS:HG2	2.05	0.56
1:A:303:ALA:HB3	1:A:319:ILE:HD11	1.87	0.56
1:B:122:MET:O	1:B:125:GLU:HG3	2.06	0.56
1:A:22:ILE:HG13	1:A:23:ILE:H	1.70	0.56
1:A:176:GLN:HB3	1:A:177:PRO:HD3	1.87	0.56
1:B:157:LYS:HZ1	1:B:345:GLN:CG	1.99	0.55
1:A:55:LEU:HB3	1:A:81:MET:HE3	1.89	0.55
1:A:74:LEU:O	1:A:75:ARG:HB2	2.05	0.55
1:A:328:VAL:CG1	1:A:332:GLN:HB2	2.36	0.55
1:A:32:VAL:O	1:A:33:ALA:HB2	2.06	0.55
1:B:100:GLY:O	1:B:138:HIS:NE2	2.39	0.54
1:B:147:LEU:C	1:B:148:LYS:CG	2.76	0.54
1:B:97:LEU:HA	1:B:101:ALA:HB3	1.90	0.54
1:B:10:ASP:O	1:B:36:PRO:HA	2.07	0.54
1:A:192:PRO:CG	2:A:417:HOH:O	2.51	0.54
1:A:95:ARG:NH2	2:A:475:HOH:O	2.39	0.54
1:A:312:PHE:O	1:A:315:PRO:HD2	2.08	0.54
1:B:106:THR:O	1:B:108:PRO:CD	2.56	0.54
1:B:45:ILE:HD13	1:B:77:MET:HE3	1.90	0.54
1:B:119:TYR:O	1:B:123:ILE:HD12	2.08	0.54
1:A:71:LEU:HD22	1:A:71:LEU:O	2.08	0.54
1:B:147:LEU:HG	1:B:334:SER:OG	2.08	0.54
1:B:108:PRO:HG3	1:B:122:MET:HE3	1.88	0.54
1:A:55:LEU:HD13	1:A:81:MET:HE3	1.88	0.54
1:B:2:SER:HB3	2:B:424:HOH:O	2.06	0.54
1:B:145:THR:O	1:B:148:LYS:CD	2.55	0.54
1:A:190:HIS:NE2	1:A:286:ASP:OD2	2.41	0.54
1:A:150:GLY:N	2:A:364:HOH:O	2.41	0.53
1:A:3:LYS:HE2	1:A:132:ARG:NH2	2.24	0.53
1:A:147:LEU:HD11	1:A:178:LEU:CD2	2.34	0.53
1:B:89:GLY:O	1:B:90:SER:CB	2.55	0.53
1:B:231:ASP:C	1:B:257:ARG:HG2	2.29	0.53
1:A:346:ALA:HB2	2:A:488:HOH:O	2.09	0.53
1:B:112:ILE:HG22	1:B:113:ARG:N	2.20	0.53
1:A:16:ARG:O	1:A:20:THR:HG23	2.08	0.53
1:B:147:LEU:CD2	1:B:338:LEU:HB3	2.38	0.53
1:B:62:MET:O	1:B:63:ASP:O	2.27	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:110:LEU:C	1:A:112:ILE:N	2.62	0.53
1:B:145:THR:O	1:B:148:LYS:HE2	2.08	0.53
1:A:64:GLY:O	1:A:68:LEU:HB3	2.09	0.52
1:A:145:THR:OG1	1:A:146:THR:N	2.42	0.52
1:A:4:ILE:HD11	1:A:132:ARG:HH21	1.71	0.52
1:B:61:ARG:O	1:B:62:MET:HB2	2.08	0.52
1:B:254:ASN:OD1	1:B:261:ASP:OD2	2.25	0.52
1:B:157:LYS:NZ	1:B:345:GLN:HA	2.25	0.52
1:A:58:GLU:HG2	1:A:58:GLU:O	2.10	0.52
1:B:32:VAL:HG22	1:B:48:PHE:HD2	1.72	0.52
1:A:147:LEU:O	1:A:177:PRO:O	2.28	0.52
1:A:3:LYS:HE2	1:A:132:ARG:HH21	1.75	0.51
1:B:147:LEU:O	1:B:148:LYS:HG2	2.09	0.51
1:B:44:LEU:N	1:B:44:LEU:HD23	2.25	0.51
1:B:95:ARG:O	1:B:99:LEU:HB2	2.11	0.51
1:A:113:ARG:HA	1:A:113:ARG:HE	1.75	0.51
1:B:84:SER:O	1:B:86:THR:N	2.44	0.51
1:A:84:SER:O	1:A:86:THR:N	2.43	0.51
1:B:193:PRO:HG3	1:B:231:ASP:HB2	1.93	0.51
1:A:119:TYR:CZ	1:A:123:ILE:HD11	2.45	0.51
1:B:232:LYS:HD3	1:B:249:ASP:OD2	2.10	0.51
1:A:47:LYS:HG2	1:A:48:PHE:CD2	2.46	0.51
1:B:19:MET:O	1:B:22:ILE:HD13	2.11	0.51
1:A:215:GLU:HG2	1:A:218:GLU:OE2	2.10	0.51
1:B:238:ARG:NH2	2:B:378:HOH:O	2.44	0.50
1:A:32:VAL:HG11	1:A:48:PHE:HB3	1.92	0.50
1:B:18:ILE:HD13	1:B:18:ILE:N	2.27	0.50
1:B:10:ASP:HB3	1:B:16:ARG:HG3	1.92	0.50
1:A:269:LYS:HE2	1:A:270:HIS:CE1	2.47	0.50
1:B:65:LEU:CD1	1:B:99:LEU:HD23	2.32	0.50
1:A:6:VAL:HG22	1:A:31:MET:SD	2.51	0.50
1:B:17:GLN:O	1:B:20:THR:OG1	2.28	0.50
1:B:2:SER:HA	1:B:29:MET:N	2.26	0.50
1:A:109:GLN:OE1	1:A:112:ILE:HG21	2.11	0.50
1:B:62:MET:O	1:B:63:ASP:C	2.49	0.50
1:A:255:ARG:HA	1:A:255:ARG:NE	2.26	0.49
1:A:171:ILE:O	1:A:174:VAL:HG22	2.12	0.49
1:A:18:ILE:O	1:A:22:ILE:HG23	2.13	0.49
1:A:321:MET:CG	2:A:369:HOH:O	2.60	0.49
1:A:53:LEU:HD12	1:A:79:VAL:CG1	2.40	0.49
1:A:95:ARG:HD2	1:A:202:ARG:NH2	2.26	0.49
1:B:119:TYR:CD1	1:B:123:ILE:HD11	2.48	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:2:SER:HA	1:A:28:ASP:CA	2.43	0.48
1:A:64:GLY:O	1:A:68:LEU:CB	2.61	0.48
1:B:145:THR:OG1	1:B:146:THR:N	2.45	0.48
1:B:42:ARG:HG3	1:B:43:ASP:N	2.28	0.48
1:A:110:LEU:HG	1:A:111:GLY:N	2.29	0.48
1:B:233:HIS:ND1	1:B:262:VAL:HG21	2.28	0.48
1:A:319:ILE:HD13	1:A:324:VAL:HG11	1.96	0.48
1:B:147:LEU:HD13	1:B:179:PRO:HD3	1.95	0.48
1:A:84:SER:CA	1:A:85:LEU:HD22	2.44	0.47
1:B:110:LEU:O	1:B:110:LEU:HD13	2.11	0.47
1:B:135:ILE:H	1:B:135:ILE:HD13	1.70	0.47
1:A:57:VAL:HG23	2:A:501:HOH:O	2.13	0.47
1:B:55:LEU:HD13	1:B:57:VAL:HG22	1.93	0.47
1:A:153:LEU:HD12	1:A:183:PRO:HG3	1.96	0.47
1:B:135:ILE:HA	1:B:138:HIS:HB3	1.96	0.47
1:A:188:THR:HG23	1:A:258:PRO:HB2	1.96	0.47
1:A:109:GLN:CD	1:A:110:LEU:HB2	2.35	0.47
1:A:16:ARG:NH1	1:A:36:PRO:HB3	2.29	0.47
1:B:74:LEU:C	1:B:76:PRO:HD3	2.33	0.47
1:A:233:HIS:CE1	1:A:262:VAL:HG21	2.49	0.47
1:A:32:VAL:CG1	1:A:48:PHE:HB3	2.44	0.47
1:B:344:GLY:O	1:B:345:GLN:HB2	2.14	0.47
1:A:281:THR:H	1:A:304:GLN:HE22	1.63	0.47
1:A:253:VAL:HG12	1:A:254:ASN:OD1	2.15	0.46
1:B:95:ARG:CD	1:B:202:ARG:HH22	2.28	0.46
1:B:61:ARG:CA	1:B:61:ARG:NE	2.75	0.46
1:A:310:VAL:CG2	1:A:311:VAL:HG23	2.43	0.46
1:A:16:ARG:CZ	1:A:36:PRO:HB3	2.45	0.46
1:A:319:ILE:HD12	1:A:327:VAL:HG22	1.98	0.46
1:B:42:ARG:HG3	1:B:43:ASP:OD1	2.16	0.46
1:B:45:ILE:HD13	1:B:77:MET:CE	2.44	0.46
1:A:2:SER:HA	1:A:28:ASP:HA	1.97	0.46
1:A:215:GLU:O	1:A:218:GLU:HG2	2.16	0.46
1:A:319:ILE:CD1	1:A:324:VAL:HG11	2.46	0.46
1:B:107:LYS:O	1:B:108:PRO:C	2.54	0.46
1:A:16:ARG:NH2	1:A:36:PRO:HB3	2.31	0.46
1:B:255:ARG:HA	1:B:255:ARG:HD3	1.80	0.46
1:A:16:ARG:O	1:A:20:THR:CG2	2.64	0.46
1:A:45:ILE:HG23	1:A:77:MET:HE1	1.97	0.46
1:A:269:LYS:HD3	2:A:545:HOH:O	2.16	0.46
1:B:255:ARG:CD	1:B:255:ARG:N	2.79	0.46
1:A:103:ASP:OD2	1:A:126:LYS:NZ	2.48	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:72:MET:HG3	1:B:100:GLY:HA3	1.98	0.46
1:A:107:LYS:O	1:A:107:LYS:CD	2.59	0.45
1:B:32:VAL:CG2	1:B:48:PHE:HD2	2.28	0.45
1:A:85:LEU:CD2	1:A:85:LEU:H	2.10	0.45
1:B:38:PRO:HB3	1:B:67:PHE:HB2	1.98	0.45
1:B:195:PHE:HD2	2:B:521:HOH:O	1.99	0.45
1:A:228:ALA:HA	1:A:229:PRO:HD3	1.75	0.45
1:B:197:ARG:NH1	1:B:201:GLU:OE1	2.49	0.45
1:B:172:ARG:HG3	1:B:203:LEU:HD23	1.99	0.45
1:B:49:ASN:N	1:B:50:PRO:HD3	2.31	0.45
1:A:317:GLU:O	1:A:321:MET:HG3	2.17	0.45
1:B:90:SER:HA	1:B:195:PHE:CE2	2.51	0.45
1:B:113:ARG:N	1:B:113:ARG:HD2	2.32	0.44
1:B:257:ARG:CB	1:B:258:PRO:CD	2.91	0.44
1:B:60:PRO:HB2	1:B:61:ARG:H	1.61	0.44
1:A:253:VAL:O	1:A:254:ASN:HB2	2.17	0.44
1:B:316:ARG:HA	1:B:319:ILE:HD12	1.99	0.44
1:B:54:THR:HA	1:B:80:VAL:O	2.17	0.44
1:B:257:ARG:O	1:B:258:PRO:C	2.55	0.44
1:B:135:ILE:O	1:B:138:HIS:HB3	2.16	0.44
1:A:135:ILE:N	1:A:135:ILE:HD12	2.33	0.44
1:B:27:SER:O	1:B:28:ASP:HB3	2.17	0.44
1:B:6:VAL:HA	1:B:52:VAL:O	2.17	0.44
1:B:110:LEU:C	1:B:110:LEU:CD1	2.82	0.44
1:A:340:LYS:HD3	1:A:340:LYS:HA	1.78	0.44
1:A:122:MET:HE2	1:A:122:MET:HA	1.98	0.44
1:A:85:LEU:CD1	1:A:106:THR:HB	2.47	0.44
1:B:101:ALA:O	1:B:138:HIS:HE1	2.01	0.44
1:B:232:LYS:N	1:B:257:ARG:HG2	2.33	0.44
1:A:73:ARG:NH1	1:A:73:ARG:HG2	2.33	0.44
1:A:147:LEU:HD23	1:A:177:PRO:HB2	2.00	0.44
1:A:176:GLN:N	1:A:177:PRO:CD	2.81	0.43
1:B:61:ARG:HB2	2:B:423:HOH:O	2.18	0.43
1:A:283:MET:CE	2:A:553:HOH:O	2.64	0.43
1:B:71:LEU:CD2	1:B:75:ARG:O	2.66	0.43
1:B:168:THR:HG22	1:B:169:GLU:N	2.33	0.43
1:B:112:ILE:CG2	1:B:113:ARG:N	2.79	0.43
1:B:19:MET:O	1:B:22:ILE:CD1	2.65	0.43
1:A:300:TRP:NE1	1:A:340:LYS:HG3	2.33	0.43
1:A:73:ARG:HH11	1:A:73:ARG:HG2	1.83	0.43
1:A:319:ILE:CD1	1:A:327:VAL:HG22	2.48	0.43
1:A:10:ASP:OD2	1:A:15:MET:SD	2.77	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:344:GLY:O	1:B:345:GLN:CB	2.67	0.43
1:A:132:ARG:HD2	1:A:132:ARG:N	2.33	0.43
1:A:221:LEU:CB	1:A:222:PRO:HD2	2.44	0.43
1:A:143:ALA:HB2	1:A:172:ARG:NH2	2.34	0.43
1:A:121:GLU:O	1:A:125:GLU:HG2	2.18	0.43
1:B:108:PRO:HG3	1:B:122:MET:SD	2.59	0.42
1:B:3:LYS:HA	2:B:460:HOH:O	2.19	0.42
1:B:39:LEU:HA	1:B:39:LEU:HD12	1.82	0.42
1:B:273:ARG:HB3	1:B:298:GLY:HA3	2.02	0.42
1:B:179:PRO:HD2	1:B:182:SER:OG	2.19	0.42
1:A:191:MET:HG2	1:A:192:PRO:HD2	2.02	0.42
1:B:37:ASP:HB2	1:B:38:PRO:HD2	2.01	0.42
1:A:238:ARG:HB3	1:A:238:ARG:HE	1.75	0.42
1:A:157:LYS:HD3	1:A:157:LYS:N	2.35	0.42
1:B:258:PRO:HD2	2:B:368:HOH:O	2.19	0.42
1:A:156:GLU:OE2	1:A:238:ARG:NH1	2.52	0.42
1:A:278:VAL:HA	1:A:302:ILE:O	2.18	0.42
1:B:190:HIS:HA	2:B:368:HOH:O	2.20	0.42
1:A:1:MET:HG2	1:A:27:SER:O	2.20	0.42
1:B:269:LYS:HE3	1:B:269:LYS:HB2	1.89	0.41
1:B:147:LEU:HD23	1:B:338:LEU:HB3	2.00	0.41
1:B:73:ARG:HH22	1:B:140:PRO:CG	2.32	0.41
1:A:39:LEU:HA	1:A:39:LEU:HD13	1.77	0.41
1:B:143:ALA:HA	1:B:173:HIS:CD2	2.55	0.41
1:B:280:LEU:HB3	1:B:304:GLN:NE2	2.36	0.41
1:B:292:LEU:CD2	1:B:321:MET:HE2	2.50	0.41
1:B:328:VAL:CG1	1:B:332:GLN:HB3	2.51	0.41
1:A:197:ARG:NH1	1:A:201:GLU:OE1	2.52	0.41
1:A:85:LEU:HD21	1:A:108:PRO:CB	2.50	0.41
1:B:70:LYS:HA	1:B:70:LYS:HD2	1.46	0.41
1:B:147:LEU:HD21	1:B:338:LEU:CG	2.50	0.41
1:A:69:GLU:HG2	1:A:99:LEU:HD21	2.01	0.41
1:A:7:LEU:CD1	1:A:7:LEU:C	2.89	0.41
1:B:55:LEU:HA	1:B:55:LEU:HD23	1.82	0.41
1:B:137:ALA:HB1	1:B:308:SER:O	2.20	0.41
1:A:109:GLN:CD	1:A:109:GLN:C	2.78	0.41
1:B:233:HIS:ND1	1:B:257:ARG:O	2.54	0.40
1:A:2:SER:N	1:A:27:SER:O	2.54	0.40
1:B:100:GLY:O	1:B:138:HIS:CE1	2.75	0.40
1:B:1:MET:O	1:B:2:SER:C	2.57	0.40
1:A:86:THR:O	1:A:89:GLY:N	2.54	0.40
1:A:5:ARG:HG3	2:A:433:HOH:O	2.20	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:312:PHE:O	1:A:313:GLY:C	2.59	0.40
1:B:55:LEU:HD13	1:B:57:VAL:HG21	2.00	0.40
1:B:71:LEU:HD22	1:B:75:ARG:O	2.22	0.40
1:B:164:SER:HB3	1:B:282:GLY:CA	2.51	0.40
1:B:43:ASP:O	1:B:47:LYS:HG3	2.22	0.40
1:B:95:ARG:HD3	1:B:202:ARG:NH2	2.33	0.40
1:B:291:MET:HG2	1:B:323:GLY:O	2.21	0.40
1:B:65:LEU:HA	1:B:65:LEU:HD13	1.73	0.40
1:B:158:LEU:HD11	1:B:186:ILE:HD11	1.97	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	345/349 (99%)	320 (93%)	15 (4%)	10 (3%)	7	6
1	B	345/349 (99%)	300 (87%)	27 (8%)	18 (5%)	3	1
All	All	690/698 (99%)	620 (90%)	42 (6%)	28 (4%)	4	3

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	LEU
1	A	108	PRO
1	B	25	SER
1	B	63	ASP
1	B	109	GLN
1	B	112	ILE
1	B	146	THR
1	A	60	PRO
1	A	62	MET
1	A	87	GLY
1	A	146	THR

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Mol	Chain	Res	Type
1	B	28	ASP
1	B	60	PRO
1	B	90	SER
1	B	281	THR
1	B	345	GLN
1	A	86	THR
1	B	61	ARG
1	B	85	LEU
1	B	108	PRO
1	B	149	ALA
1	B	2	SER
1	A	61	ARG
1	B	257	ARG
1	A	164	SER
1	B	258	PRO
1	B	344	GLY
1	A	75	ARG

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	280/282 (99%)	246 (88%)	34 (12%)	7	9
1	B	280/282 (99%)	243 (87%)	37 (13%)	6	7
All	All	560/564 (99%)	489 (87%)	71 (13%)	6	7

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	5	ARG
1	A	6	VAL
1	A	7	LEU
1	A	12	SER
1	A	14	LEU
1	A	20	THR
1	A	21	GLU

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Mol	Chain	Res	Type
1	A	22	ILE
1	A	39	LEU
1	A	55	LEU
1	A	57	VAL
1	A	61	ARG
1	A	62	MET
1	A	66	ASP
1	A	67	PHE
1	A	69	GLU
1	A	71	LEU
1	A	81	MET
1	A	84	SER
1	A	85	LEU
1	A	88	LYS
1	A	99	LEU
1	A	107	LYS
1	A	113	ARG
1	A	121	GLU
1	A	132	ARG
1	A	146	THR
1	A	168	THR
1	A	180	LEU
1	A	197	ARG
1	A	235	GLU
1	A	255	ARG
1	A	325	SER
1	B	3	LYS
1	B	6	VAL
1	B	7	LEU
1	B	12	SER
1	B	14	LEU
1	B	22	ILE
1	B	25	SER
1	B	46	LYS
1	B	53	LEU
1	B	55	LEU
1	B	59	MET
1	B	65	LEU
1	B	70	LYS
1	B	73	ARG
1	B	85	LEU
1	B	102	ILE

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Mol	Chain	Res	Type
1	B	106	THR
1	B	107	LYS
1	B	112	ILE
1	B	120	SER
1	B	135	ILE
1	B	146	THR
1	B	147	LEU
1	B	148	LYS
1	B	158	LEU
1	B	168	THR
1	B	171	ILE
1	B	180	LEU
1	B	185	VAL
1	B	186	ILE
1	B	202	ARG
1	B	238	ARG
1	B	239	SER
1	B	255	ARG
1	B	296	GLN
1	B	310	VAL
1	B	345	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	242	ASN
1	A	304	GLN
1	B	109	GLN
1	B	176	GLN
1	B	254	ASN
1	B	270	HIS
1	B	296	GLN
1	B	304	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 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	347/349 (99%)	-0.20	16 (4%) 31 29	6, 20, 54, 60	0
1	B	347/349 (99%)	-0.11	20 (5%) 22 20	6, 23, 50, 60	0
All	All	694/698 (99%)	-0.15	36 (5%) 26 24	6, 22, 52, 60	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	347	ILE	6.9
1	B	346	ALA	6.4
1	B	112	ILE	6.1
1	A	110	LEU	5.5
1	B	111	GLY	5.5
1	A	347	ILE	5.3
1	A	146	THR	4.5
1	A	2	SER	4.3
1	B	1	MET	4.1
1	A	111	GLY	4.0
1	A	1	MET	3.9
1	B	2	SER	3.9
1	B	113	ARG	3.6
1	A	115	GLY	3.5
1	B	74	LEU	3.4
1	B	345	GLN	3.4
1	B	110	LEU	3.4
1	A	84	SER	3.2
1	B	147	LEU	3.2
1	B	62	MET	3.0
1	A	59	MET	2.9
1	B	108	PRO	2.9
1	A	61	ARG	2.8
1	B	114	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	60	PRO	2.6
1	B	146	THR	2.6
1	A	109	GLN	2.6
1	A	108	PRO	2.5
1	A	345	GLN	2.4
1	B	61	ARG	2.4
1	A	60	PRO	2.2
1	B	75	ARG	2.2
1	B	239	SER	2.1
1	A	85	LEU	2.1
1	A	346	ALA	2.1
1	B	149	ALA	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.