



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:12 PM UTC

PDB ID : 3AJA / pdb_00003aja
Title : Crystal Structure of MSMEG_6394
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Deposited on : 2010-05-27
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

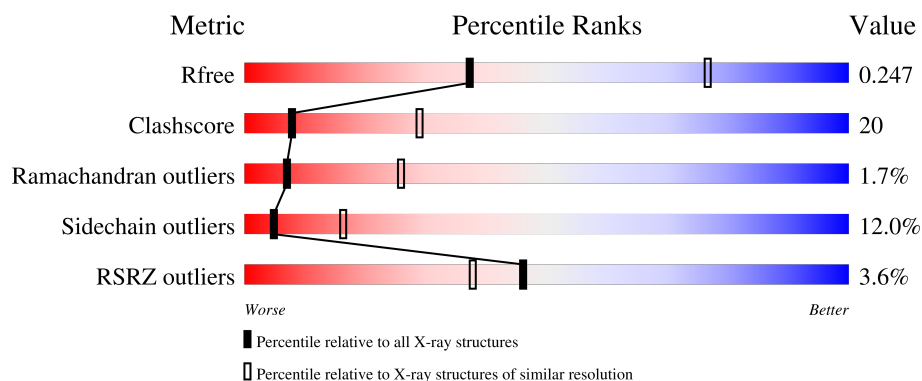
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	302	5% 53% 25% 8% 14%
1	B	302	% 51% 28% 7% 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3956 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 Putative uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			1952	1219	334	386	13			
1	B	264	Total	C	N	O	S	0	0	0
			1972	1230	338	391	13			

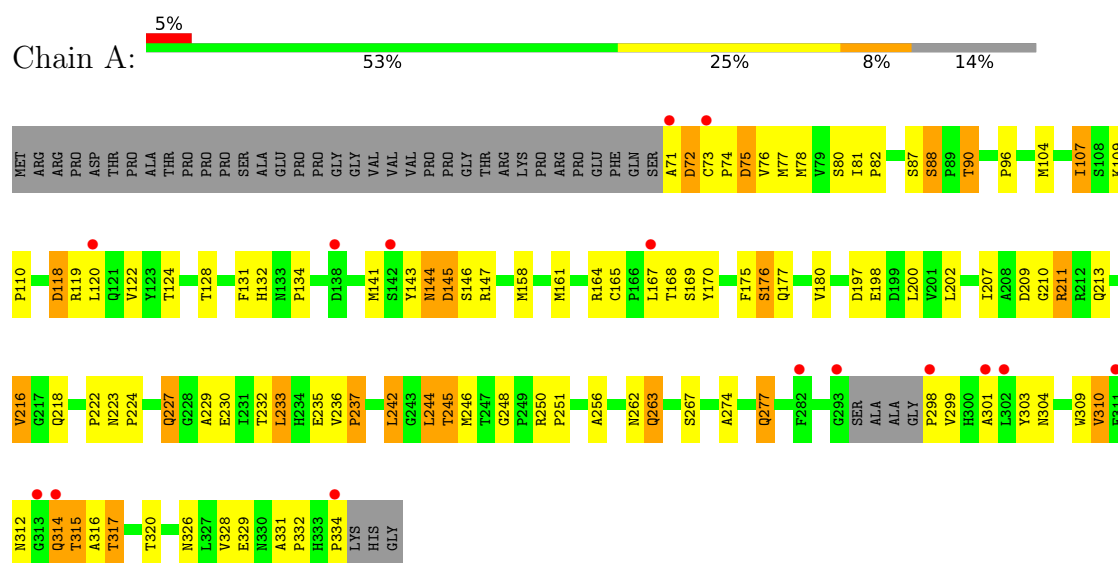
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	14	Total	O	0	0
			14	14		
2	B	18	Total	O	0	0
			18	18		

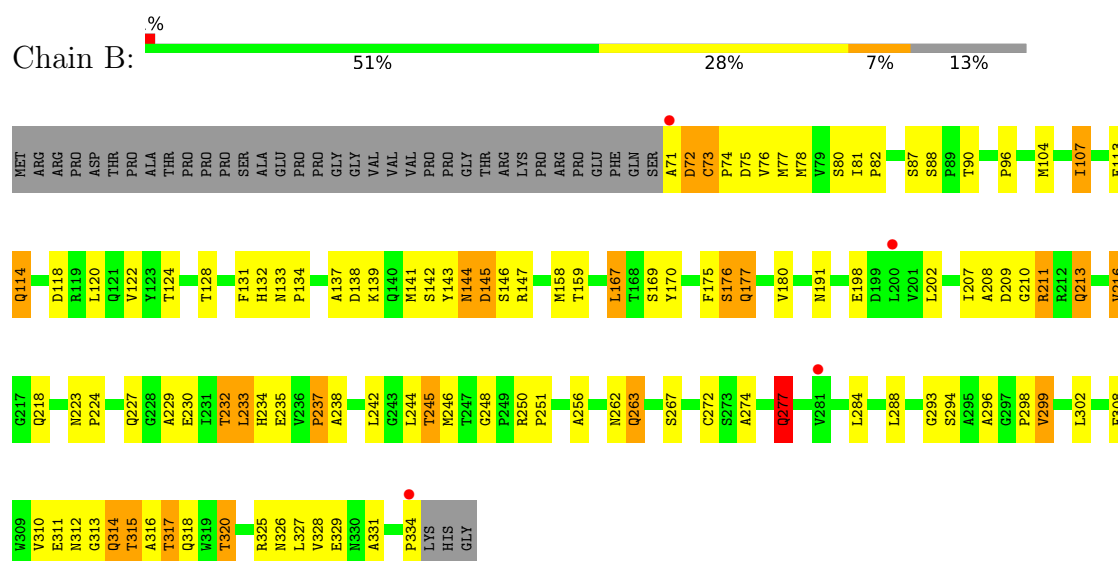
3 Residue-property plots [i](#)

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: Putative uncharacterized protein



• Molecule 1: Putative uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	130.43Å 130.43Å 209.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.17 – 2.90 29.17 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.17-2.90) 88.3 (29.17-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.80 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.213 , 0.250 0.210 , 0.247	Depositor DCC
R_{free} test set	932 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	94.7	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 82.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3956	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.82	7/2000 (0.3%)	0.98	3/2732 (0.1%)
1	B	0.87	12/2021 (0.6%)	1.00	6/2763 (0.2%)
All	All	0.84	19/4021 (0.5%)	0.99	9/5495 (0.2%)

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	277	GLN	CD-OE1	6.10	1.35	1.23
1	B	213	GLN	CD-OE1	5.74	1.34	1.23
1	A	144	ASN	CG-OD1	5.70	1.34	1.23
1	B	144	ASN	CG-OD1	5.61	1.34	1.23
1	A	277	GLN	CD-OE1	5.59	1.34	1.23
1	B	234	HIS	ND1-CE1	5.52	1.38	1.32
1	A	262	ASN	CG-OD1	5.39	1.33	1.23
1	B	114	GLN	CD-OE1	5.39	1.33	1.23
1	B	318	GLN	CD-OE1	5.35	1.33	1.23
1	A	132	HIS	ND1-CE1	5.34	1.37	1.32
1	A	223	ASN	CG-ND2	-5.33	1.22	1.33
1	B	191	ASN	CG-OD1	5.27	1.33	1.23
1	B	263	GLN	CD-OE1	5.19	1.33	1.23
1	B	262	ASN	CG-OD1	5.18	1.33	1.23
1	B	132	HIS	ND1-CE1	5.13	1.37	1.32
1	A	227	GLN	CD-OE1	5.10	1.33	1.23
1	B	223	ASN	CG-ND2	-5.07	1.22	1.33
1	B	177	GLN	CD-OE1	5.02	1.33	1.23
1	A	263	GLN	CD-OE1	5.01	1.33	1.23

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	234	HIS	CB-CG-CD2	-6.74	122.44	131.20
1	A	132	HIS	CB-CG-CD2	-6.65	122.56	131.20
1	B	132	HIS	CB-CG-CD2	-6.56	122.67	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	312	ASN	N-CA-C	6.11	120.06	112.24
1	B	234	HIS	CB-CG-ND1	5.82	131.44	122.70
1	A	132	HIS	CB-CG-ND1	5.70	131.25	122.70
1	B	139	LYS	N-CA-C	-5.58	107.06	112.97
1	B	132	HIS	CB-CG-ND1	5.55	131.03	122.70
1	B	296	ALA	N-CA-C	-5.28	102.57	110.23

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	1952	0	1863	78	0
1	B	1972	0	1881	74	0
2	A	14	0	0	1	0
2	B	18	0	0	4	0
All	All	3956	0	3744	152	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 20.

All (152) 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:73:CYS:HB2	1:A:74:PRO:CD	1.71	1.20
1:A:141:MET:HE3	1:A:146:SER:HA	1.30	1.13
1:A:75:ASP:O	1:A:168:THR:HG23	1.51	1.11
1:A:73:CYS:HB2	1:A:74:PRO:HD3	1.27	1.06
1:B:141:MET:HE3	1:B:146:SER:HA	1.35	1.05
1:B:316:ALA:O	1:B:320:THR:HG22	1.57	1.04
1:A:316:ALA:O	1:A:320:THR:HG22	1.64	0.96
1:A:73:CYS:CB	1:A:74:PRO:CD	2.43	0.94
1:B:141:MET:CE	1:B:146:SER:HA	1.98	0.93
1:A:141:MET:CE	1:A:146:SER:HA	1.97	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:MET:HE3	1:A:146:SER:CA	2.05	0.87
1:A:315:THR:HG22	1:A:317:THR:H	1.39	0.86
1:A:71:ALA:O	1:A:72:ASP:HB2	1.78	0.83
1:B:71:ALA:O	1:B:72:ASP:HB2	1.77	0.83
1:A:315:THR:HG23	1:A:316:ALA:N	1.93	0.82
1:A:73:CYS:CB	1:A:74:PRO:HD2	2.09	0.82
1:A:315:THR:CG2	1:A:316:ALA:N	2.45	0.79
1:A:73:CYS:HB2	1:A:74:PRO:HD2	1.61	0.78
1:B:141:MET:HE3	1:B:146:SER:CA	2.13	0.78
1:B:72:ASP:O	2:B:25:HOH:O	2.00	0.78
1:B:142:SER:HB2	1:B:145:ASP:OD1	1.83	0.78
1:A:315:THR:HG23	1:A:316:ALA:H	1.49	0.78
1:A:77:MET:HE2	1:A:170:TYR:HE1	1.49	0.77
1:B:71:ALA:O	1:B:72:ASP:CB	2.33	0.76
1:A:209:ASP:OD2	1:A:250:ARG:NH2	2.18	0.76
1:B:311:GLU:O	1:B:312:ASN:C	2.30	0.75
1:B:77:MET:HE2	1:B:170:TYR:HE1	1.51	0.75
1:B:80:SER:HB3	1:B:124:THR:HG22	1.69	0.74
1:A:80:SER:HB3	1:A:124:THR:HG22	1.70	0.73
1:B:209:ASP:OD2	1:B:250:ARG:NH2	2.22	0.72
1:A:73:CYS:SG	1:A:74:PRO:HD2	2.31	0.70
1:A:77:MET:HE2	1:A:170:TYR:CE1	2.29	0.68
1:B:75:ASP:OD1	1:B:334:PRO:HD2	1.95	0.67
1:A:71:ALA:HB2	1:A:334:PRO:O	1.96	0.66
1:B:315:THR:HG22	1:B:317:THR:H	1.60	0.65
1:B:77:MET:HE2	1:B:170:TYR:CE1	2.30	0.65
1:B:138:ASP:HA	2:B:2:HOH:O	1.96	0.65
1:A:75:ASP:O	1:A:168:THR:CG2	2.39	0.63
1:A:104:MET:HE1	1:A:207:ILE:HD12	1.79	0.63
1:A:71:ALA:O	1:A:72:ASP:CB	2.46	0.63
1:A:315:THR:CG2	1:A:317:THR:H	2.12	0.62
1:A:304:ASN:HA	1:A:315:THR:HG21	1.82	0.61
1:B:107:ILE:HD12	1:B:320:THR:HG23	1.82	0.61
1:A:145:ASP:OD1	1:A:145:ASP:N	2.30	0.60
1:B:229:ALA:O	1:B:233:LEU:HB2	2.01	0.60
1:B:73:CYS:HB2	1:B:74:PRO:HD2	1.83	0.59
1:A:107:ILE:HD12	1:A:320:THR:HG23	1.83	0.59
1:A:315:THR:HG22	1:A:317:THR:N	2.17	0.58
1:B:277:GLN:CD	1:B:277:GLN:H	2.12	0.57
1:B:143:TYR:HE2	1:B:147:ARG:NH2	2.02	0.57
1:A:210:GLY:O	1:A:230:GLU:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:SER:HB3	1:A:202:LEU:HD13	1.85	0.57
1:B:104:MET:HE3	1:B:175:PHE:HB2	1.86	0.56
1:B:104:MET:HA	1:B:104:MET:HE2	1.88	0.56
1:B:316:ALA:O	1:B:320:THR:CG2	2.45	0.56
1:A:224:PRO:HG3	1:A:267:SER:HA	1.88	0.55
1:B:227:GLN:OE1	1:B:232:THR:HG22	2.06	0.55
1:A:143:TYR:HE2	1:A:147:ARG:NH2	2.04	0.55
1:A:298:PRO:O	1:A:301:ALA:N	2.40	0.55
1:B:233:LEU:HB3	1:B:246:MET:HG3	1.89	0.54
1:B:302:LEU:HD12	1:B:308:PHE:HE2	1.72	0.54
1:B:311:GLU:HG3	1:B:312:ASN:N	2.22	0.53
1:B:169:SER:HB3	1:B:202:LEU:HD13	1.91	0.53
1:B:224:PRO:HG3	1:B:267:SER:HA	1.91	0.53
1:B:96:PRO:HG3	1:B:124:THR:OG1	2.09	0.53
1:B:104:MET:HE1	1:B:207:ILE:HD12	1.90	0.53
1:A:202:LEU:HD21	1:A:331:ALA:HB2	1.91	0.52
1:A:310:VAL:HG23	1:A:314:GLN:O	2.09	0.52
1:B:73:CYS:HB2	1:B:74:PRO:CD	2.40	0.52
1:A:277:GLN:H	1:A:277:GLN:CD	2.19	0.51
1:A:213:GLN:HB2	1:A:216:VAL:CG1	2.41	0.51
1:B:71:ALA:HB2	1:B:334:PRO:O	2.11	0.51
1:A:76:VAL:HG11	1:A:328:VAL:HG13	1.93	0.51
1:A:104:MET:HE3	1:A:175:PHE:HB2	1.93	0.51
1:A:145:ASP:O	1:A:146:SER:C	2.54	0.51
1:A:222:PRO:HD2	1:A:309:TRP:CD1	2.46	0.50
1:B:213:GLN:HB2	1:B:216:VAL:CG1	2.41	0.50
1:B:311:GLU:O	1:B:313:GLY:N	2.44	0.50
1:B:134:PRO:HG2	1:B:242:LEU:HG	1.94	0.49
1:A:96:PRO:HG3	1:A:124:THR:OG1	2.12	0.49
1:A:198:GLU:HG3	1:A:256:ALA:HB3	1.94	0.49
1:B:198:GLU:HG3	1:B:256:ALA:HB3	1.94	0.49
1:A:161:MET:HA	1:A:164:ARG:NH1	2.28	0.49
1:B:143:TYR:CE2	1:B:147:ARG:NH2	2.81	0.49
1:A:131:PHE:CD1	1:A:143:TYR:CD1	3.01	0.49
1:A:144:ASN:HD21	1:A:245:THR:CG2	2.25	0.49
1:B:78:MET:HB2	1:B:120:LEU:HD11	1.94	0.48
1:B:211:ARG:HD3	1:B:248:GLY:O	2.13	0.48
1:A:227:GLN:OE1	1:A:232:THR:HG22	2.12	0.48
1:A:232:THR:HG21	1:A:274:ALA:O	2.13	0.48
1:B:76:VAL:HG11	1:B:328:VAL:HG13	1.95	0.47
1:A:197:ASP:HB2	1:A:200:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:TYR:O	1:A:315:THR:HG23	2.14	0.47
1:B:137:ALA:C	2:B:2:HOH:O	2.57	0.47
1:B:128:THR:HB	1:B:141:MET:HE2	1.96	0.47
1:B:232:THR:HG21	1:B:274:ALA:O	2.14	0.47
1:B:211:ARG:HD2	1:B:250:ARG:HG3	1.97	0.47
1:B:114:GLN:HE22	1:B:325:ARG:HG3	1.80	0.47
1:B:144:ASN:HD21	1:B:245:THR:CG2	2.28	0.47
1:A:71:ALA:N	1:A:334:PRO:C	2.73	0.46
1:A:74:PRO:HD2	1:A:165:CYS:SG	2.55	0.46
1:A:82:PRO:HG2	1:A:87:SER:HB2	1.97	0.46
1:A:128:THR:HB	1:A:141:MET:HE2	1.96	0.46
1:B:202:LEU:HB3	1:B:327:LEU:HD23	1.97	0.46
1:A:78:MET:HB2	1:A:120:LEU:HD11	1.97	0.46
1:A:74:PRO:HA	1:A:118:ASP:O	2.16	0.46
1:A:134:PRO:HG2	1:A:242:LEU:HG	1.97	0.46
1:B:237:PRO:O	1:B:238:ALA:C	2.59	0.45
1:B:114:GLN:NE2	1:B:325:ARG:HG3	2.32	0.45
1:B:202:LEU:HD21	1:B:331:ALA:HB2	1.99	0.45
1:A:176:SER:OG	1:A:177:GLN:N	2.40	0.44
1:A:229:ALA:O	1:A:233:LEU:HB2	2.17	0.44
1:B:131:PHE:CD1	1:B:143:TYR:CD1	3.05	0.44
1:B:82:PRO:HG2	1:B:87:SER:HB2	1.99	0.44
1:B:250:ARG:HA	1:B:251:PRO:HD3	1.80	0.44
1:A:75:ASP:OD1	1:A:119:ARG:HD2	2.17	0.44
1:A:76:VAL:HG13	1:A:120:LEU:HD13	2.00	0.44
1:A:250:ARG:HA	1:A:251:PRO:HD3	1.84	0.44
1:A:75:ASP:HB2	1:A:119:ARG:O	2.18	0.44
1:A:211:ARG:HD3	1:A:248:GLY:O	2.17	0.44
1:A:104:MET:CE	1:A:207:ILE:HD12	2.47	0.44
1:B:315:THR:CG2	1:B:317:THR:H	2.28	0.44
1:A:118:ASP:OD1	1:A:118:ASP:N	2.51	0.43
1:B:311:GLU:C	1:B:313:GLY:N	2.75	0.43
1:A:143:TYR:CE2	1:A:147:ARG:NH2	2.86	0.43
1:B:73:CYS:SG	1:B:167:LEU:HD21	2.59	0.43
1:A:77:MET:HE1	1:A:158:MET:HA	1.99	0.43
1:B:210:GLY:O	1:B:230:GLU:HB2	2.18	0.43
1:A:218:GLN:HA	1:A:218:GLN:OE1	2.19	0.42
1:A:332:PRO:HD2	2:A:26:HOH:O	2.18	0.42
1:B:134:PRO:HD2	1:B:288:LEU:CD2	2.49	0.42
1:B:144:ASN:HD21	1:B:245:THR:HG23	1.84	0.42
1:A:109:LYS:HB2	1:A:110:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:PRO:O	1:B:299:VAL:C	2.62	0.42
1:A:233:LEU:HB3	1:A:246:MET:HG3	2.01	0.41
1:A:143:TYR:HB3	1:A:244:LEU:HB3	2.02	0.41
1:B:72:ASP:N	2:B:31:HOH:O	2.50	0.41
1:B:227:GLN:HG3	1:B:232:THR:CG2	2.50	0.41
1:B:208:ALA:HA	1:B:272:CYS:SG	2.61	0.41
1:B:314:GLN:H	1:B:314:GLN:HG2	1.46	0.41
1:A:236:VAL:HA	1:A:237:PRO:HD3	1.80	0.41
1:A:303:TYR:O	1:A:315:THR:CG2	2.69	0.41
1:B:176:SER:OG	1:B:177:GLN:N	2.50	0.41
1:B:118:ASP:OD1	1:B:118:ASP:N	2.54	0.41
1:B:133:ASN:OD1	1:B:133:ASN:C	2.63	0.41
1:B:293:GLY:O	1:B:294:SER:C	2.63	0.41
1:B:73:CYS:CB	1:B:74:PRO:CD	2.98	0.40
1:B:77:MET:HE1	1:B:158:MET:HA	2.03	0.40
1:B:218:GLN:HA	1:B:218:GLN:OE1	2.20	0.40
1:A:88:SER:C	1:A:90:THR:H	2.30	0.40
1:B:76:VAL:HG13	1:B:120:LEU:HD13	2.02	0.40
1:A:144:ASN:HD21	1:A:245:THR:HG23	1.86	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	256/302 (85%)	239 (93%)	12 (5%)	5 (2%)	6	22
1	B	262/302 (87%)	239 (91%)	19 (7%)	4 (2%)	8	28
All	All	518/604 (86%)	478 (92%)	31 (6%)	9 (2%)	7	26

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	ASP
1	B	72	ASP
1	A	176	SER
1	A	75	ASP
1	B	176	SER
1	A	237	PRO
1	B	237	PRO
1	B	299	VAL
1	A	299	VAL

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	212/245 (86%)	189 (89%)	23 (11%)	6	21
1	B	213/245 (87%)	185 (87%)	28 (13%)	4	13
All	All	425/490 (87%)	374 (88%)	51 (12%)	5	16

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

Mol	Chain	Res	Type
1	A	81	ILE
1	A	88	SER
1	A	90	THR
1	A	107	ILE
1	A	118	ASP
1	A	122	VAL
1	A	145	ASP
1	A	167	LEU
1	A	180	VAL
1	A	211	ARG
1	A	216	VAL
1	A	233	LEU
1	A	235	GLU
1	A	242	LEU
1	A	244	LEU

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Mol	Chain	Res	Type
1	A	245	THR
1	A	263	GLN
1	A	310	VAL
1	A	314	GLN
1	A	315	THR
1	A	317	THR
1	A	326	ASN
1	A	329	GLU
1	B	73	CYS
1	B	81	ILE
1	B	88	SER
1	B	90	THR
1	B	107	ILE
1	B	113	GLU
1	B	122	VAL
1	B	145	ASP
1	B	159	THR
1	B	167	LEU
1	B	180	VAL
1	B	211	ARG
1	B	216	VAL
1	B	232	THR
1	B	233	LEU
1	B	235	GLU
1	B	244	LEU
1	B	245	THR
1	B	263	GLN
1	B	277	GLN
1	B	284	LEU
1	B	310	VAL
1	B	314	GLN
1	B	315	THR
1	B	317	THR
1	B	320	THR
1	B	326	ASN
1	B	329	GLU

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

Mol	Chain	Res	Type
1	A	114	GLN
1	A	263	GLN

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Mol	Chain	Res	Type
1	A	304	ASN
1	A	314	GLN
1	A	326	ASN
1	A	330	ASN
1	B	177	GLN
1	B	326	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	260/302 (86%)	0.11	15 (5%) 29 22	82, 101, 133, 162	0
1	B	264/302 (87%)	-0.10	4 (1%) 72 64	76, 97, 140, 174	0
All	All	524/604 (86%)	0.01	19 (3%) 46 38	76, 99, 138, 174	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	71	ALA	5.3
1	A	71	ALA	5.1
1	A	313	GLY	3.5
1	A	142	SER	2.9
1	A	334	PRO	2.8
1	A	73	CYS	2.6
1	A	302	LEU	2.5
1	B	334	PRO	2.5
1	A	167	LEU	2.4
1	A	314	GLN	2.3
1	A	293	GLY	2.2
1	B	200	LEU	2.1
1	A	311	GLU	2.1
1	A	120	LEU	2.1
1	A	301	ALA	2.1
1	A	298	PRO	2.1
1	A	138	ASP	2.1
1	A	282	PHE	2.0
1	B	281	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.