



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 10:53 PM UTC

PDB ID : 3VO9 / pdb_00003vo9
Title : Staphylococcus aureus FtsZ apo-form (SeMet)
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Deposited on : 2012-01-20
Resolution : 2.71 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
Mogul : 2022.3.0, CSD as543be (2022)
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

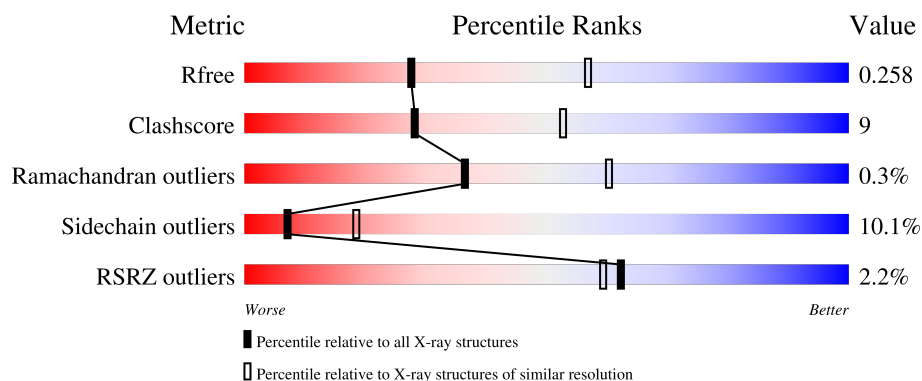
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	308	2% 74% 19% . .
1	B	308	3% 69% 24% . 5%
1	C	308	2% 80% 16% . .
1	D	308	2% 64% 25% 5% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8529 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 Cell division protein FtsZ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	Se	0	0	0
			2119	1315	357	436	11			
1	B	292	Total	C	N	O	Se	0	0	0
			2093	1298	354	430	11			
1	C	301	Total	C	N	O	Se	0	0	0
			2171	1344	372	444	11			
1	D	287	Total	C	N	O	Se	0	0	0
			2069	1284	350	424	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLY	-	expression tag	UNP P0A029
A	10	HIS	-	expression tag	UNP P0A029
A	11	MSE	-	expression tag	UNP P0A029
B	9	GLY	-	expression tag	UNP P0A029
B	10	HIS	-	expression tag	UNP P0A029
B	11	MSE	-	expression tag	UNP P0A029
C	9	GLY	-	expression tag	UNP P0A029
C	10	HIS	-	expression tag	UNP P0A029
C	11	MSE	-	expression tag	UNP P0A029
D	9	GLY	-	expression tag	UNP P0A029
D	10	HIS	-	expression tag	UNP P0A029
D	11	MSE	-	expression tag	UNP P0A029

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	29	Total	O	0	0
			29	29		
2	B	16	Total	O	0	0
			16	16		

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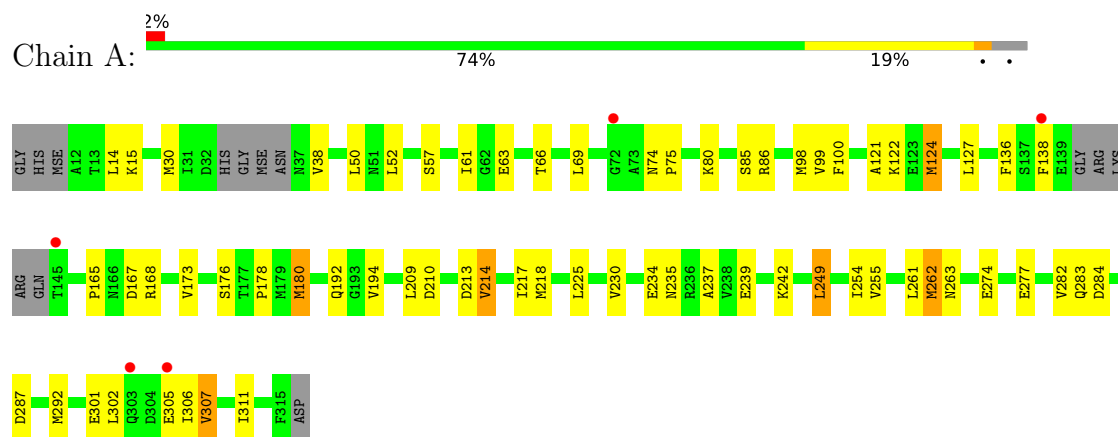
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	25	Total 25	O 25	0	0
2	D	7	Total 7	O 7	0	0

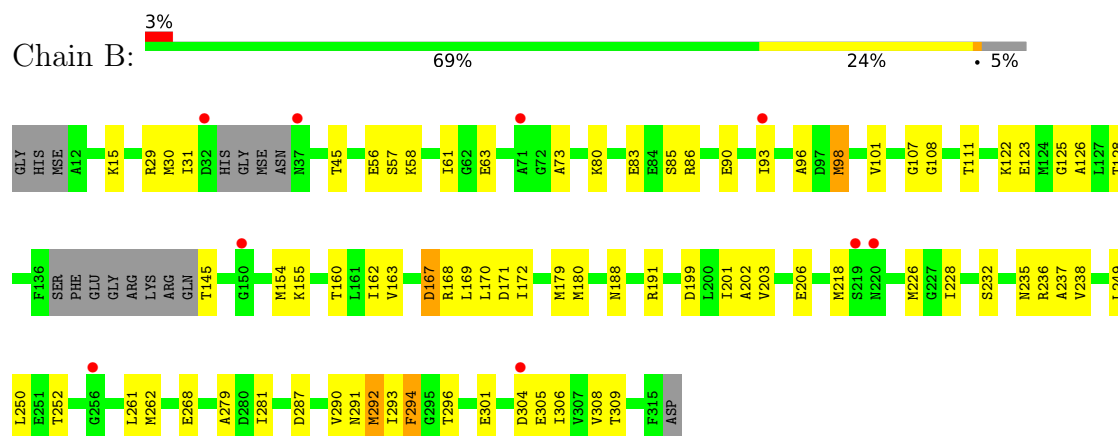
3 Residue-property plots [i](#)

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.

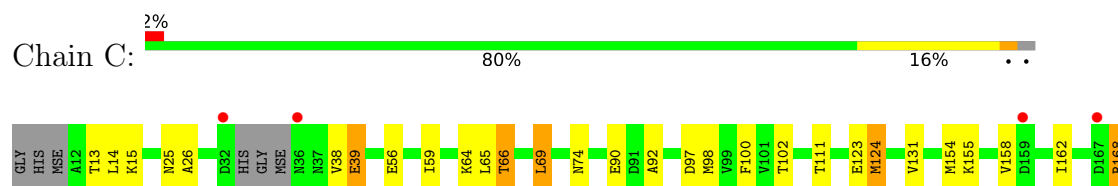
• Molecule 1: Cell division protein FtsZ

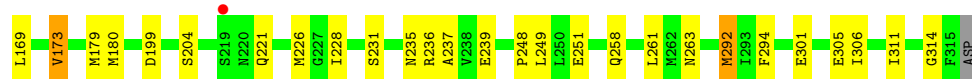


• Molecule 1: Cell division protein FtsZ

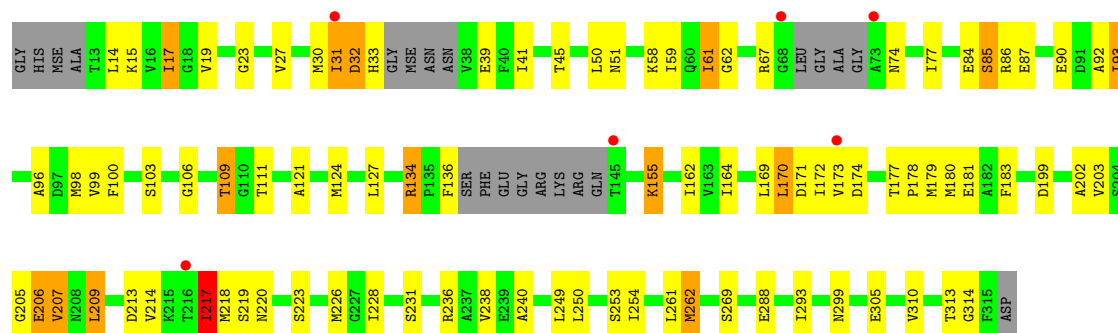


• Molecule 1: Cell division protein FtsZ





● Molecule 1: Cell division protein FtsZ



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.69Å 79.99Å 225.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.76 – 2.71 31.76 – 2.71	Depositor EDS
% Data completeness (in resolution range)	96.8 (31.76-2.71) 95.9 (31.76-2.71)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.99 (at 2.72Å)	Xtriage
Refinement program	PHENIX 1.7.2 _869	Depositor
R, R_{free}	0.227 , 0.272 0.215 , 0.258	Depositor DCC
R_{free} test set	1688 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.541	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8529	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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	0.75	0/2121	0.94	1/2846 (0.0%)
1	B	0.70	0/2094	0.97	0/2810
1	C	0.71	0/2174	0.97	3/2916 (0.1%)
1	D	0.70	0/2070	0.98	8/2776 (0.3%)
All	All	0.72	0/8459	0.96	12/11348 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	177	THR	CA-C-N	-7.43	110.55	119.84
1	D	177	THR	C-N-CA	-7.43	110.55	119.84
1	A	217	ILE	CB-CA-C	-7.01	102.54	112.22
1	D	299	ASN	CA-C-N	5.81	126.21	119.47
1	D	299	ASN	C-N-CA	5.81	126.21	119.47
1	D	99	VAL	N-CA-C	5.53	115.82	107.80
1	C	74	ASN	CA-C-N	5.37	124.83	119.24
1	C	74	ASN	C-N-CA	5.37	124.83	119.24
1	D	103	SER	N-CA-C	-5.31	106.67	112.72
1	C	292	MSE	N-CA-C	5.24	116.95	108.41
1	D	217	ILE	CB-CA-C	-5.13	105.14	112.22
1	D	162	ILE	N-CA-C	5.02	115.08	107.75

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	2119	0	2141	39	0
1	B	2093	0	2121	40	0
1	C	2171	0	2198	29	0
1	D	2069	0	2094	46	0
2	A	29	0	0	2	0
2	B	16	0	0	2	0
2	C	25	0	0	0	0
2	D	7	0	0	0	0
All	All	8529	0	8554	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 9.

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:D:93:ILE:HD11	1:D:124:MSE:HG3	1.58	0.86
1:C:90:GLU:HG2	1:C:124:MSE:HE1	1.59	0.84
1:B:98:MSE:SE	1:B:180:MSE:HG2	2.37	0.75
1:C:98:MSE:SE	1:C:180:MSE:HG2	2.37	0.74
1:D:15:LYS:HD2	1:D:96:ALA:HB2	1.73	0.71
1:B:261:LEU:HD23	1:B:293:ILE:HB	1.74	0.68
1:A:14:LEU:HD11	1:A:100:PHE:HD2	1.58	0.68
1:A:52:LEU:HD13	1:C:25:ASN:ND2	2.11	0.66
1:D:30:MSE:HE3	1:D:169:LEU:HG	1.77	0.66
1:D:262:MSE:HG3	1:D:310:VAL:HG22	1.77	0.66
1:B:86:ARG:NH1	1:B:90:GLU:OE2	2.29	0.65
1:B:294:PHE:CD2	1:B:294:PHE:C	2.75	0.65
1:B:287:ASP:HB2	1:B:290:VAL:HG23	1.78	0.64
1:D:203:VAL:HG11	1:D:249:LEU:HD23	1.79	0.64
1:C:292:MSE:HE2	1:C:294:PHE:CE1	2.35	0.62
1:D:288:GLU:H	1:D:288:GLU:CD	2.08	0.61
1:A:98:MSE:HE2	1:A:127:LEU:HD23	1.83	0.61
1:D:32:ASP:O	1:D:33:HIS:ND1	2.33	0.61
1:A:138:PHE:H	1:A:213:ASP:HB2	1.64	0.60
1:D:261:LEU:HD23	1:D:293:ILE:HB	1.83	0.59
1:A:214:VAL:HG13	1:A:218:MSE:HE2	1.86	0.58
1:C:168:ARG:HH11	1:C:168:ARG:HA	1.69	0.57
1:C:98:MSE:HE3	1:C:180:MSE:HE3	1.86	0.57
1:C:90:GLU:CG	1:C:124:MSE:HE1	2.32	0.57
1:B:203:VAL:HG21	1:B:249:LEU:HD23	1.86	0.57
1:A:30:MSE:HE3	1:A:173:VAL:HB	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:27:VAL:O	1:D:31:ILE:HG12	2.06	0.56
1:D:121:ALA:O	1:D:124:MSE:HB2	2.05	0.56
1:A:178:PRO:HB3	1:A:307:VAL:HG22	1.88	0.56
1:D:45:THR:OG1	1:D:109:THR:HG21	2.06	0.56
1:A:261:LEU:HB2	1:A:311:ILE:HB	1.89	0.55
1:D:61:ILE:HG22	1:D:85:SER:HB2	1.88	0.55
1:A:165:PRO:HG2	1:A:168:ARG:CG	2.37	0.55
1:C:38:VAL:HG21	1:C:173:VAL:HG22	1.88	0.55
1:C:258:GLN:HB2	1:C:314:GLY:HA3	1.89	0.54
1:B:30:MSE:HE2	1:B:169:LEU:HD11	1.90	0.54
1:B:279:ALA:HB2	1:B:294:PHE:CE1	2.42	0.54
1:C:226:MSE:HE3	1:C:228:ILE:HD11	1.90	0.53
1:A:225:LEU:HD22	1:A:249:LEU:HD23	1.90	0.53
1:B:30:MSE:HE2	1:B:169:LEU:HD21	1.91	0.53
1:D:209:LEU:HD11	1:D:249:LEU:HD22	1.90	0.52
1:B:101:VAL:HG12	1:B:154:MSE:HE1	1.92	0.52
1:D:30:MSE:HE3	1:D:169:LEU:CG	2.38	0.52
1:B:294:PHE:CZ	1:B:296:THR:OG1	2.62	0.51
1:D:50:LEU:HD11	1:D:59:ILE:O	2.10	0.51
1:B:80:LYS:NZ	1:B:83:GLU:OE2	2.38	0.51
1:D:136:PHE:HE2	1:D:217:ILE:HD11	1.75	0.51
1:C:102:THR:HB	1:C:131:VAL:HB	1.91	0.51
1:C:56:GLU:H	1:C:56:GLU:CD	2.18	0.50
1:B:226:MSE:HE3	1:B:228:ILE:HD11	1.92	0.50
1:C:15:LYS:NZ	1:C:39:GLU:HG2	2.27	0.50
1:A:167:ASP:OD1	1:A:167:ASP:N	2.45	0.50
1:D:50:LEU:HD22	1:D:58:LYS:HB3	1.93	0.50
1:B:236:ARG:NH1	1:B:304:ASP:O	2.44	0.49
1:A:274:GLU:O	1:A:277:GLU:HB2	2.13	0.49
1:B:98:MSE:SE	1:B:180:MSE:HE3	2.62	0.49
1:B:15:LYS:HE2	1:B:96:ALA:HB2	1.94	0.48
1:D:32:ASP:N	1:D:32:ASP:OD1	2.46	0.48
1:D:209:LEU:CD1	1:D:249:LEU:HD22	2.43	0.48
1:D:218:MSE:HE3	1:D:223:SER:HB2	1.96	0.48
1:A:283:GLN:HA	1:A:292:MSE:HE1	1.94	0.48
1:B:237:ALA:HA	1:B:306:ILE:HD11	1.96	0.48
1:D:106:GLY:H	1:D:134:ARG:HE	1.62	0.48
1:B:29:ARG:NH1	2:B:415:HOH:O	2.35	0.48
1:C:26:ALA:HB1	1:C:169:LEU:HD21	1.95	0.48
1:D:74:ASN:O	1:D:77:ILE:HG22	2.13	0.48
1:C:155:LYS:HZ3	1:C:199:ASP:HB2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:MSE:HE2	1:B:292:MSE:HB2	1.73	0.47
1:C:14:LEU:HD11	1:C:100:PHE:CE2	2.48	0.47
1:A:14:LEU:HD11	1:A:100:PHE:CD2	2.43	0.47
1:A:176:SER:O	1:A:180:MSE:HE2	2.14	0.47
1:A:209:LEU:HD23	1:A:209:LEU:HA	1.80	0.47
1:B:167:ASP:N	1:B:167:ASP:OD1	2.45	0.47
1:C:155:LYS:NZ	1:C:199:ASP:HB2	2.29	0.47
1:D:19:VAL:N	1:D:23:GLY:HA3	2.29	0.47
1:D:179:MSE:HE3	1:D:183:PHE:CZ	2.49	0.47
1:A:287:ASP:OD1	1:A:287:ASP:N	2.47	0.46
1:B:206:GLU:H	1:B:206:GLU:CD	2.22	0.46
1:D:164:ILE:HD11	1:D:169:LEU:HA	1.97	0.46
1:D:226:MSE:HE3	1:D:228:ILE:HD11	1.96	0.46
1:B:155:LYS:NZ	1:B:199:ASP:OD1	2.41	0.46
1:B:279:ALA:HB2	1:B:294:PHE:HE1	1.80	0.46
1:B:98:MSE:HB2	1:B:180:MSE:HE3	1.97	0.46
1:C:66:THR:O	1:C:69:LEU:HB2	2.16	0.46
1:A:192:GLN:HB2	1:A:194:VAL:HG23	1.98	0.45
1:B:122:LYS:O	1:B:125:GLY:N	2.41	0.45
1:B:238:VAL:HG13	1:B:281:ILE:HD11	1.98	0.45
1:D:178:PRO:O	1:D:181:GLU:HB2	2.17	0.45
1:A:301:GLU:HB2	1:D:51:ASN:HB3	1.97	0.45
1:D:231:SER:CB	1:D:240:ALA:HB2	2.47	0.45
1:A:237:ALA:HA	1:A:306:ILE:CD1	2.47	0.45
1:D:30:MSE:HE2	1:D:173:VAL:HG23	1.99	0.45
1:B:61:ILE:HG22	1:B:85:SER:HB2	1.99	0.45
1:C:248:PRO:HA	1:C:251:GLU:OE2	2.17	0.45
1:D:155:LYS:HE3	1:D:199:ASP:OD1	2.16	0.45
1:A:262:MSE:HG3	1:A:282:VAL:HG11	1.99	0.44
1:C:162:ILE:HD11	1:C:204:SER:HB2	2.00	0.44
1:C:261:LEU:HB2	1:C:311:ILE:HB	1.99	0.44
1:A:74:ASN:HB2	1:A:75:PRO:HD2	2.00	0.44
1:A:86:ARG:NH1	2:A:401:HOH:O	2.39	0.44
1:B:188:ASN:OD1	1:B:191:ARG:NH1	2.51	0.44
1:B:206:GLU:OE1	1:B:206:GLU:N	2.48	0.44
1:D:86:ARG:NH1	1:D:90:GLU:OE2	2.50	0.44
1:A:50:LEU:HD23	1:A:50:LEU:HA	1.83	0.43
1:A:61:ILE:HG22	1:A:85:SER:HB2	2.00	0.43
1:D:231:SER:HB3	1:D:240:ALA:HB2	1.99	0.43
1:A:263:ASN:HB2	2:A:418:HOH:O	2.17	0.43
1:C:154:MSE:O	1:C:158:VAL:HG22	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:ASN:O	1:C:239:GLU:HB2	2.18	0.43
1:B:162:ILE:HD12	1:B:202:ALA:O	2.18	0.43
1:D:313:THR:OG1	1:D:314:GLY:N	2.52	0.43
1:C:236:ARG:HG3	1:C:237:ALA:N	2.33	0.43
1:D:170:LEU:HD12	1:D:170:LEU:HA	1.79	0.43
1:A:165:PRO:HG2	1:A:168:ARG:HG2	2.00	0.43
1:A:210:ASP:HB3	1:A:213:ASP:OD2	2.19	0.43
1:B:262:MSE:HE2	1:B:308:VAL:HG13	2.00	0.43
1:B:30:MSE:HA	1:B:170:LEU:HD21	2.01	0.43
1:B:172:ILE:HG22	1:B:179:MSE:HE3	2.00	0.43
1:A:127:LEU:HD12	1:A:127:LEU:HA	1.84	0.42
1:B:168:ARG:NH1	1:B:171:ASP:OD2	2.52	0.42
1:B:126:ALA:O	1:B:128:THR:HG23	2.19	0.42
1:D:205:GLY:C	1:D:207:VAL:H	2.26	0.42
1:C:14:LEU:HD11	1:C:100:PHE:CD2	2.54	0.42
1:A:14:LEU:HD12	1:A:15:LYS:H	1.84	0.42
1:D:14:LEU:HD11	1:D:100:PHE:CE1	2.54	0.42
1:B:107:GLY:HA3	2:B:402:HOH:O	2.19	0.42
1:A:30:MSE:CE	1:A:173:VAL:HB	2.49	0.42
1:A:136:PHE:CZ	1:A:209:LEU:HD11	2.55	0.42
1:C:59:ILE:HD11	1:C:92:ALA:CB	2.50	0.41
1:C:59:ILE:HD11	1:C:92:ALA:HB2	2.01	0.41
1:D:59:ILE:HD11	1:D:92:ALA:HB2	2.01	0.41
1:A:121:ALA:HA	1:A:124:MSE:HG3	2.03	0.41
1:D:98:MSE:HE1	1:D:180:MSE:HB3	2.02	0.41
1:B:58:LYS:HB2	1:B:58:LYS:HE2	1.92	0.41
1:D:17:ILE:HG23	1:D:41:ILE:HB	2.02	0.41
1:A:235:ASN:O	1:A:239:GLU:HG3	2.20	0.41
1:A:80:LYS:HD3	1:A:80:LYS:HA	1.83	0.41
1:B:73:ALA:HB1	1:B:108:GLY:HA2	2.03	0.41
1:D:62:GLY:HA2	1:D:84:GLU:CD	2.45	0.41
1:D:218:MSE:CE	1:D:223:SER:HB2	2.51	0.41
1:A:98:MSE:CE	1:A:180:MSE:HG3	2.51	0.41
1:A:237:ALA:HA	1:A:306:ILE:HD11	2.03	0.41
1:B:232:SER:HB3	1:B:305:GLU:HG3	2.03	0.41
1:C:249:LEU:HA	1:C:249:LEU:HD23	1.79	0.40
1:D:98:MSE:HE2	1:D:127:LEU:HD23	2.03	0.40
1:A:230:VAL:HG22	1:A:307:VAL:HG13	2.02	0.40
1:D:202:ALA:HB2	1:D:226:MSE:HE2	2.03	0.40
1:A:165:PRO:HG2	1:A:168:ARG:HG3	2.03	0.40
1:B:201:ILE:HG12	1:B:218:MSE:SE	2.72	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:168:ARG:HA	1:C:168:ARG:HD2	1.94	0.40
1:D:171:ASP:HA	1:D:174:ASP:HB3	2.04	0.40
1:D:217:ILE:H	1:D:217:ILE:HG13	1.65	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	289/308 (94%)	280 (97%)	9 (3%)	0	100	100
1	B	286/308 (93%)	270 (94%)	15 (5%)	1 (0%)	36	60
1	C	297/308 (96%)	284 (96%)	13 (4%)	0	100	100
1	D	279/308 (91%)	254 (91%)	23 (8%)	2 (1%)	18	41
All	All	1151/1232 (93%)	1088 (94%)	60 (5%)	3 (0%)	36	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	206	GLU
1	B	291	ASN
1	D	220	ASN

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	223/220 (101%)	203 (91%)	20 (9%)	9	23
1	B	220/220 (100%)	199 (90%)	21 (10%)	8	20
1	C	228/220 (104%)	209 (92%)	19 (8%)	10	26
1	D	219/220 (100%)	189 (86%)	30 (14%)	3	9
All	All	890/880 (101%)	800 (90%)	90 (10%)	7	18

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	VAL
1	A	57	SER
1	A	63	GLU
1	A	66	THR
1	A	69	LEU
1	A	99	VAL
1	A	122	LYS
1	A	124	MSE
1	A	180	MSE
1	A	214	VAL
1	A	234	GLU
1	A	242	LYS
1	A	249	LEU
1	A	254	ILE
1	A	255	VAL
1	A	262	MSE
1	A	284	ASP
1	A	302	LEU
1	A	305	GLU
1	A	307	VAL
1	B	31	ILE
1	B	45	THR
1	B	56	GLU
1	B	57	SER
1	B	63	GLU
1	B	93	ILE
1	B	98	MSE
1	B	111	THR
1	B	123	GLU
1	B	145	THR
1	B	160	THR
1	B	163	VAL
1	B	167	ASP

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Mol	Chain	Res	Type
1	B	235	ASN
1	B	250	LEU
1	B	252	THR
1	B	268	GLU
1	B	292	MSE
1	B	294	PHE
1	B	301	GLU
1	B	309	THR
1	C	13	THR
1	C	39	GLU
1	C	64	LYS
1	C	65	LEU
1	C	66	THR
1	C	69	LEU
1	C	97	ASP
1	C	111	THR
1	C	123	GLU
1	C	124	MSE
1	C	168	ARG
1	C	173	VAL
1	C	179	MSE
1	C	221	GLN
1	C	231	SER
1	C	263	ASN
1	C	301	GLU
1	C	305	GLU
1	C	306	ILE
1	D	17	ILE
1	D	31	ILE
1	D	32	ASP
1	D	39	GLU
1	D	61	ILE
1	D	67	ARG
1	D	85	SER
1	D	87	GLU
1	D	93	ILE
1	D	109	THR
1	D	111	THR
1	D	134	ARG
1	D	155	LYS
1	D	170	LEU
1	D	172	ILE

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Mol	Chain	Res	Type
1	D	206	GLU
1	D	207	VAL
1	D	209	LEU
1	D	213	ASP
1	D	214	VAL
1	D	217	ILE
1	D	219	SER
1	D	236	ARG
1	D	238	VAL
1	D	250	LEU
1	D	253	SER
1	D	254	ILE
1	D	262	MSE
1	D	269	SER
1	D	305	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	263	ASN
1	B	25	ASN
1	C	24	ASN
1	C	195	GLN
1	D	192	GLN
1	D	299	ASN

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 oligosaccharides 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	284/308 (92%)	0.04	5 (1%) 67 65	27, 39, 64, 74	0
1	B	281/308 (91%)	0.18	9 (3%) 50 46	29, 45, 63, 80	0
1	C	290/308 (94%)	0.13	5 (1%) 69 67	28, 45, 66, 74	0
1	D	276/308 (89%)	0.47	6 (2%) 62 59	33, 56, 71, 78	0
All	All	1131/1232 (91%)	0.21	25 (2%) 62 59	27, 46, 68, 80	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	159	ASP	4.8
1	B	32	ASP	3.9
1	A	145	THR	3.9
1	B	37	ASN	3.8
1	C	219	SER	3.3
1	D	216	THR	3.1
1	D	73	ALA	2.8
1	B	93	ILE	2.6
1	A	303	GLN	2.6
1	B	219	SER	2.5
1	D	68	GLY	2.5
1	D	31	ILE	2.4
1	C	32	ASP	2.4
1	B	304	ASP	2.4
1	A	305	GLU	2.3
1	A	72	GLY	2.3
1	C	36	ASN	2.3
1	B	150	GLY	2.3
1	B	256	GLY	2.3
1	A	138	PHE	2.3
1	B	220	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	167	ASP	2.2
1	D	173	VAL	2.2
1	D	145	THR	2.1
1	B	71	ALA	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.