



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2024 – 06:18 PM EDT

PDB ID : 6RVM
Title : Cell division protein FtsZ from Staphylococcus aureus, apo form
Authors : Fernandez-Tornero, C.; Andreu, J.M.; Canosa-Valls, A.J.
Deposited on : 2019-05-31
Resolution : 2.15 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

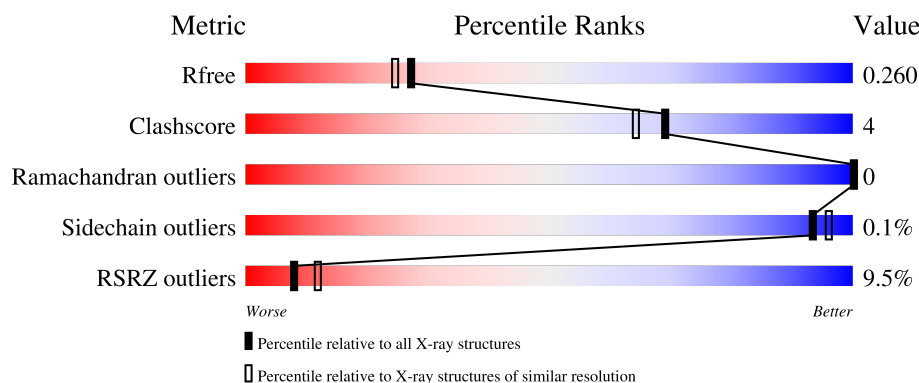
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	<div> <div>10%</div> <div>90%</div> <div>6%</div> </div>
1	B	308	<div> <div>11%</div> <div>84%</div> <div>9%</div> <div>7%</div> </div>
1	C	308	<div> <div>7%</div> <div>93%</div> <div>7%</div> </div>
1	D	308	<div> <div>8%</div> <div>91%</div> <div>8%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17422 atoms, of which 8705 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	296	Total	C	H	N	O	S	0	0	0
			4280	1316	2153	363	437	11			
1	B	287	Total	C	H	N	O	S	0	0	0
			4148	1278	2091	348	420	11			
1	C	306	Total	C	H	N	O	S	0	0	0
			4435	1366	2226	380	451	12			
1	D	303	Total	C	H	N	O	S	0	0	0
			4375	1351	2193	370	448	13			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	SER	-	expression tag	UNP P0A031
A	10	HIS	-	expression tag	UNP P0A031
A	11	MET	-	expression tag	UNP P0A031
B	9	SER	-	expression tag	UNP P0A031
B	10	HIS	-	expression tag	UNP P0A031
B	11	MET	-	expression tag	UNP P0A031
C	9	SER	-	expression tag	UNP P0A031
C	10	HIS	-	expression tag	UNP P0A031
C	11	MET	-	expression tag	UNP P0A031
D	9	SER	-	expression tag	UNP P0A031
D	10	HIS	-	expression tag	UNP P0A031
D	11	MET	-	expression tag	UNP P0A031

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C H O 13 3 7 3	0	0
3	A	1	Total C H O 14 3 8 3	0	0
3	A	1	Total C H O 11 3 5 3	0	0
3	B	1	Total C H O 13 3 7 3	0	0
3	C	1	Total C H O 14 3 8 3	0	0
3	D	1	Total C H O 13 3 7 3	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total Cl 3 3	0	0
4	C	3	Total Cl 3 3	0	0
4	D	3	Total Cl 3 3	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total Mg 1 1	0	0
5	D	1	Total Mg 1 1	0	0

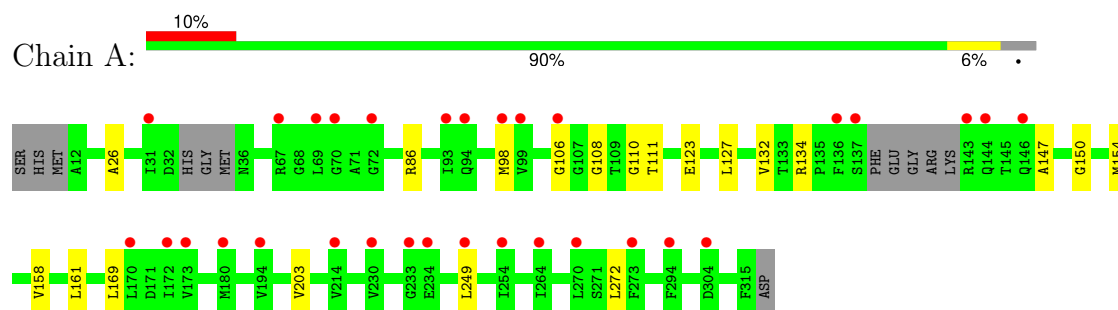
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	18	Total O 18 18	0	0
6	B	12	Total O 12 12	0	0
6	C	21	Total O 21 21	0	0
6	D	24	Total O 24 24	0	0

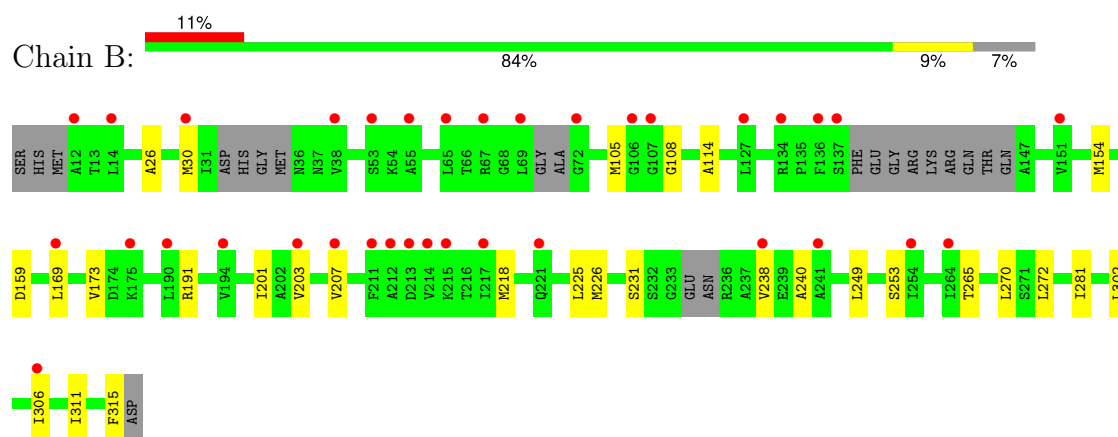
3 Residue-property plots [i](#)

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.

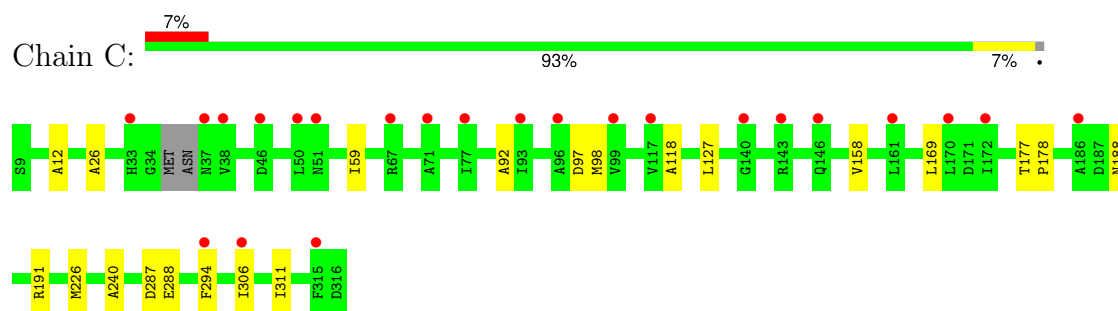
- Molecule 1: Cell division protein FtsZ



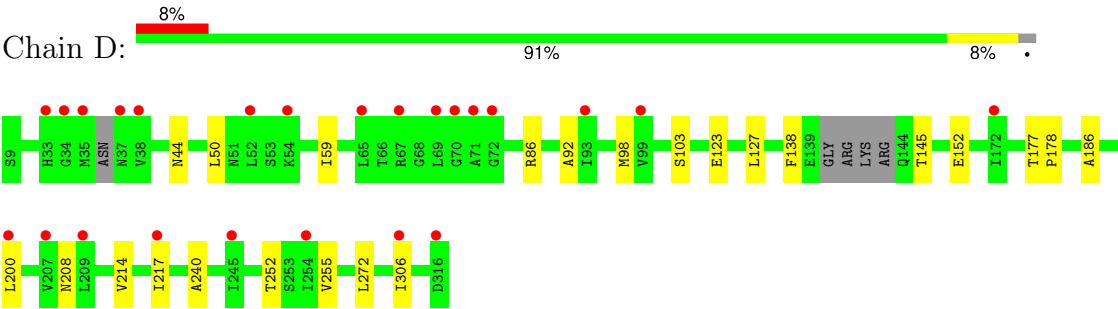
- Molecule 1: Cell division protein FtsZ



- 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	72.56Å 78.81Å 225.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.16 – 2.15 112.82 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.16-2.15) 99.8 (112.82-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.16Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.230 , 0.256 0.233 , 0.260	Depositor DCC
R_{free} test set	3530 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	59.0	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 47.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17422	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.96 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6106e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.25	0/2139	0.42	0/2888
1	B	0.25	0/2067	0.42	0/2788
1	C	0.25	0/2225	0.43	0/3002
1	D	0.25	0/2197	0.42	0/2965
All	All	0.25	0/8628	0.42	0/11643

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2127	2153	2153	13	0
1	B	2057	2091	2091	22	0
1	C	2209	2226	2227	13	0
1	D	2182	2193	2193	18	0
2	A	5	0	0	0	0
2	C	10	0	0	0	0
2	D	5	0	0	0	0
3	A	18	20	24	2	0
3	B	6	7	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	6	8	8	0	0
3	D	6	7	8	1	0
4	A	3	0	0	0	0
4	C	3	0	0	0	0
4	D	3	0	0	1	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	18	0	0	1	0
6	B	12	0	0	0	0
6	C	21	0	0	0	0
6	D	24	0	0	1	0
All	All	8717	8705	8712	64	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 4.

All (64) 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:B:225:LEU:HD13	1:B:249:LEU:HD21	1.65	0.78
1:B:238:VAL:HG13	1:B:281:ILE:HD11	1.66	0.77
1:B:159:ASP:OD1	1:B:191:ARG:NH2	2.27	0.66
1:C:59:ILE:HD11	1:C:92:ALA:CB	2.27	0.65
1:B:203:VAL:HG11	1:B:207:VAL:CG1	2.28	0.62
1:B:265:THR:HG22	1:B:302:LEU:CD1	2.29	0.62
1:B:225:LEU:HD13	1:B:249:LEU:CD2	2.30	0.61
1:B:265:THR:HG22	1:B:302:LEU:HD12	1.83	0.60
1:D:240:ALA:HB3	1:D:306:ILE:HD11	1.85	0.59
1:B:30:MET:SD	1:B:173:VAL:HG21	2.43	0.58
1:B:238:VAL:HG13	1:B:281:ILE:CD1	2.33	0.58
1:D:240:ALA:CB	1:D:306:ILE:HD11	2.34	0.58
1:D:252:THR:O	1:D:255:VAL:HG22	2.04	0.57
1:A:26:ALA:HB1	1:A:169:LEU:HD21	1.86	0.57
1:D:152:GLU:HA	1:D:217:ILE:HD11	1.85	0.57
1:A:111:THR:HG23	1:A:150:GLY:HA3	1.87	0.55
1:C:240:ALA:HB3	1:C:306:ILE:HD11	1.89	0.55
1:D:145:THR:HG22	6:D:515:HOH:O	2.07	0.55
1:A:272:LEU:HD22	1:B:272:LEU:HB3	1.91	0.53
1:C:287:ASP:OD1	1:C:288:GLU:N	2.42	0.53
1:B:203:VAL:HG11	1:B:207:VAL:HG11	1.91	0.51
1:C:98:MET:HE2	1:C:127:LEU:HD23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:ALA:CB	1:C:306:ILE:HD11	2.40	0.51
1:D:208:ASN:OD1	3:D:402:GOL:O3	2.27	0.50
1:B:225:LEU:HD22	1:B:249:LEU:HD21	1.94	0.50
1:D:98:MET:CE	1:D:127:LEU:HD23	2.42	0.48
1:C:12:ALA:HB1	1:C:97:ASP:CB	2.44	0.48
1:C:177:THR:HB	1:C:178:PRO:HD3	1.96	0.47
1:B:114:ALA:HB1	1:B:154:MET:HE1	1.97	0.47
1:C:98:MET:CE	1:C:127:LEU:HD23	2.44	0.47
1:C:226:MET:CE	1:C:311:ILE:HD11	2.44	0.47
1:A:203:VAL:HG21	1:A:249:LEU:HD23	1.98	0.46
1:B:26:ALA:HB1	1:B:169:LEU:HD22	1.98	0.46
1:C:188:ASN:OD1	1:C:191:ARG:NH2	2.48	0.46
1:B:26:ALA:HB1	1:B:169:LEU:CD2	2.46	0.45
1:D:214:VAL:O	1:D:217:ILE:HG22	2.16	0.45
1:A:98:MET:CE	1:A:127:LEU:HD23	2.47	0.45
1:C:294:PHE:CE2	1:D:272:LEU:HD21	2.52	0.45
1:D:59:ILE:HD11	1:D:92:ALA:CB	2.46	0.45
1:A:134:ARG:HE	1:A:147:ALA:HB2	1.82	0.44
1:B:270:LEU:HD13	1:B:306:ILE:HD13	2.00	0.44
1:D:44:ASN:HB3	1:D:50:LEU:HD13	1.99	0.44
1:A:106:GLY:O	6:A:501:HOH:O	2.21	0.44
1:A:86:ARG:NH2	1:A:123:GLU:OE1	2.51	0.44
1:B:231:SER:HB2	1:B:240:ALA:HB2	2.00	0.44
1:B:226:MET:HE2	1:B:311:ILE:HD11	2.00	0.43
1:B:226:MET:CE	1:B:311:ILE:HD11	2.48	0.43
1:B:201:ILE:HD12	1:B:218:MET:SD	2.58	0.43
1:D:98:MET:HE2	1:D:127:LEU:HD23	2.01	0.43
1:B:108:GLY:HA3	3:B:401:GOL:H2	2.01	0.42
1:C:118:ALA:HB1	1:C:158:VAL:HG12	2.01	0.42
1:D:177:THR:HB	1:D:178:PRO:HD3	2.01	0.42
1:A:108:GLY:H	3:A:404:GOL:C1	2.32	0.42
1:C:26:ALA:HB1	1:C:169:LEU:HD21	2.01	0.42
1:D:186:ALA:HB1	1:D:200:LEU:CD2	2.50	0.42
1:A:110:GLY:H	3:A:404:GOL:H31	1.85	0.42
1:D:138:PHE:CE2	1:D:217:ILE:HD12	2.55	0.42
1:B:253:SER:OG	1:B:315:PHE:HE1	2.02	0.41
1:A:108:GLY:O	1:A:111:THR:HB	2.21	0.41
1:D:86:ARG:NH2	1:D:123:GLU:OE1	2.49	0.41
1:A:154:MET:HE2	1:A:158:VAL:CG1	2.51	0.41
1:A:132:VAL:HG23	1:A:161:LEU:HD11	2.03	0.40
1:D:59:ILE:HD11	1:D:92:ALA:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:103:SER:O	4:D:405:CL:CL	2.77	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	290/308 (94%)	288 (99%)	2 (1%)	0	100	100
1	B	277/308 (90%)	271 (98%)	6 (2%)	0	100	100
1	C	302/308 (98%)	299 (99%)	3 (1%)	0	100	100
1	D	297/308 (96%)	295 (99%)	2 (1%)	0	100	100
All	All	1166/1232 (95%)	1153 (99%)	13 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	224/234 (96%)	224 (100%)	0	100	100
1	B	217/234 (93%)	216 (100%)	1 (0%)	88	92
1	C	232/234 (99%)	232 (100%)	0	100	100
1	D	230/234 (98%)	230 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	903/936 (96%)	902 (100%)	1 (0%)	93	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	105	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 21 ligands modelled in this entry, 11 are monoatomic - leaving 10 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	$\# Z > 2$
3	GOL	B	401	-	5,5,5	0.93	0	5,5,5	0.97	0
2	SO4	D	401	-	4,4,4	0.23	0	6,6,6	0.07	0
3	GOL	A	404	-	5,5,5	0.81	0	5,5,5	1.19	1 (20%)
2	SO4	C	402	-	4,4,4	0.23	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	403	-	5,5,5	0.89	0	5,5,5	0.94	0
2	SO4	A	401	-	4,4,4	0.25	0	6,6,6	0.10	0
3	GOL	D	402	-	5,5,5	0.95	0	5,5,5	1.06	0
3	GOL	A	402	-	5,5,5	0.91	0	5,5,5	1.00	0
2	SO4	C	401	-	4,4,4	0.24	0	6,6,6	0.08	0
3	GOL	C	403	-	5,5,5	0.88	0	5,5,5	0.97	0

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
3	GOL	B	401	-	-	2/4/4/4	-
3	GOL	A	404	-	-	2/4/4/4	-
3	GOL	A	403	-	-	0/4/4/4	-
3	GOL	D	402	-	-	0/4/4/4	-
3	GOL	A	402	-	-	1/4/4/4	-
3	GOL	C	403	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	404	GOL	C3-C2-C1	-2.17	103.83	111.80

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	GOL	O2-C2-C3-O3
3	A	404	GOL	O2-C2-C3-O3
3	B	401	GOL	O1-C1-C2-O2
3	A	402	GOL	O1-C1-C2-C3
3	A	404	GOL	C1-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	GOL	1	0
3	A	404	GOL	2	0
3	D	402	GOL	1	0

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

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	296/308 (96%)	0.81	31 (10%) 6 9	45, 64, 90, 108	0
1	B	287/308 (93%)	0.85	35 (12%) 4 6	44, 70, 97, 111	0
1	C	306/308 (99%)	0.73	23 (7%) 14 19	44, 63, 89, 104	0
1	D	303/308 (98%)	0.72	24 (7%) 12 17	41, 61, 90, 106	0
All	All	1192/1232 (96%)	0.77	113 (9%) 8 12	41, 65, 93, 111	0

All (113) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	144	GLN	7.8
1	B	136	PHE	7.3
1	A	172	ILE	6.2
1	D	69	LEU	6.1
1	A	106	GLY	5.5
1	D	71	ALA	5.4
1	A	72	GLY	5.3
1	D	72	GLY	5.3
1	D	34	GLY	4.8
1	C	71	ALA	4.6
1	C	38	VAL	4.5
1	B	72	GLY	4.4
1	D	70	GLY	4.3
1	D	33	HIS	4.1
1	B	106	GLY	3.9
1	A	234	GLU	3.8
1	B	137	SER	3.7
1	B	107	GLY	3.7
1	C	51	ASN	3.6
1	A	146	GLN	3.5
1	C	294	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	194	VAL	3.4
1	D	67	ARG	3.4
1	D	37	ASN	3.4
1	D	65	LEU	3.4
1	B	53	SER	3.4
1	A	137	SER	3.3
1	C	140	GLY	3.3
1	B	203	VAL	3.3
1	B	67	ARG	3.2
1	A	233	GLY	3.1
1	D	172	ILE	3.1
1	B	169	LEU	3.1
1	C	37	ASN	3.0
1	A	304	ASP	3.0
1	A	230	VAL	3.0
1	C	93	ILE	3.0
1	D	209	LEU	3.0
1	B	306	ILE	2.9
1	A	31	ILE	2.9
1	D	38	VAL	2.8
1	A	214	VAL	2.8
1	D	207	VAL	2.8
1	D	52	LEU	2.8
1	A	180	MET	2.7
1	A	98	MET	2.7
1	D	35	MET	2.7
1	B	69	LEU	2.7
1	B	207	VAL	2.7
1	B	65	LEU	2.7
1	A	254	ILE	2.7
1	D	306	ILE	2.7
1	D	54	LYS	2.6
1	B	211	PHE	2.6
1	C	50	LEU	2.6
1	B	254	ILE	2.6
1	B	127	LEU	2.6
1	C	143	ARG	2.6
1	C	172	ILE	2.6
1	A	67	ARG	2.6
1	A	143	ARG	2.6
1	B	264	ILE	2.6
1	A	136	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	77	ILE	2.5
1	B	213	ASP	2.5
1	B	38	VAL	2.5
1	A	270	LEU	2.4
1	B	134	ARG	2.4
1	C	46	ASP	2.4
1	B	221	GLN	2.4
1	B	190	LEU	2.4
1	A	99	VAL	2.4
1	B	30	MET	2.4
1	D	217	ILE	2.4
1	A	70	GLY	2.4
1	C	67	ARG	2.4
1	C	146	GLN	2.4
1	A	273	PHE	2.4
1	C	117	VAL	2.4
1	D	99	VAL	2.4
1	A	264	ILE	2.4
1	B	217	ILE	2.4
1	C	170	LEU	2.3
1	B	241	ALA	2.3
1	D	93	ILE	2.3
1	A	294	PHE	2.3
1	B	212	ALA	2.3
1	B	175	LYS	2.3
1	C	315	PHE	2.2
1	A	173	VAL	2.2
1	B	14	LEU	2.2
1	B	238	VAL	2.2
1	A	69	LEU	2.2
1	D	254	ILE	2.2
1	A	170	LEU	2.2
1	B	151	VAL	2.2
1	B	214	VAL	2.2
1	A	249	LEU	2.1
1	C	99	VAL	2.1
1	B	215	LYS	2.1
1	B	12	ALA	2.1
1	A	93	ILE	2.1
1	B	194	VAL	2.1
1	B	55	ALA	2.1
1	D	316	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	200	LEU	2.1
1	A	94	GLN	2.1
1	C	161	LEU	2.0
1	C	33	HIS	2.0
1	C	306	ILE	2.0
1	D	245	ILE	2.0
1	C	96	ALA	2.0
1	C	186	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 monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CL	D	404	1/1	0.24	0.32	112,112,112,112	0
4	CL	C	406	1/1	0.49	0.25	103,103,103,103	0
3	GOL	C	403	6/6	0.49	0.23	61,76,92,92	0
4	CL	A	407	1/1	0.54	0.17	110,110,110,110	0
4	CL	A	405	1/1	0.55	0.25	94,94,94,94	0
4	CL	C	405	1/1	0.59	0.17	105,105,105,105	0
3	GOL	A	403	6/6	0.72	0.25	78,94,99,102	0
4	CL	C	404	1/1	0.75	0.18	91,91,91,91	0
4	CL	A	406	1/1	0.75	0.34	76,76,76,76	0
3	GOL	D	402	6/6	0.79	0.20	69,84,96,101	0
4	CL	D	405	1/1	0.81	0.33	76,76,76,76	0
3	GOL	A	404	6/6	0.82	0.18	67,79,83,84	0
4	CL	D	403	1/1	0.84	0.13	85,85,85,85	0
3	GOL	B	401	6/6	0.85	0.12	67,81,92,103	0
3	GOL	A	402	6/6	0.85	0.21	75,90,103,113	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	MG	C	407	1/1	0.89	0.19	67,67,67,67	0
2	SO4	C	401	5/5	0.90	0.16	82,87,87,87	0
5	MG	D	406	1/1	0.91	0.10	72,72,72,72	0
2	SO4	D	401	5/5	0.92	0.11	87,88,96,98	0
2	SO4	A	401	5/5	0.92	0.15	64,66,77,88	0
2	SO4	C	402	5/5	0.93	0.09	82,84,96,101	0

6.5 Other polymers [i](#)

There are no such residues in this entry.