



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 12:42 pm GMT

PDB ID : 3VMQ
Title : Crystal structure of Staphylococcus aureus membrane-bound transglycosylase:
Apoenzyme
Authors : Huang, C.Y.; Shih, H.W.; Lin, L.Y.; Tien, Y.W.; Cheng, T.J.R.; Cheng, W.C.;
Wong, C.H.; Ma, C.
Deposited on : 2011-12-15
Resolution : 2.52 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

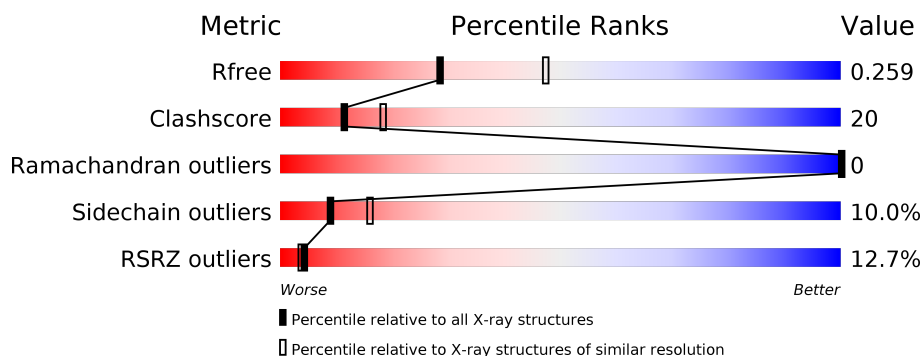
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.52 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}	100719	4636 (2.54-2.50)
Clashscore	112137	5382 (2.54-2.50)
Ramachandran outliers	110173	5282 (2.54-2.50)
Sidechain outliers	110143	5284 (2.54-2.50)
RSRZ outliers	101464	4669 (2.54-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	263	
1	B	263	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3650 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 Monofunctional glycosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1822	1156	313	346	7			
1	B	217	Total	C	N	O	S	0	0	0
			1781	1131	306	337	7			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	EXPRESSION TAG	UNP Q99T05
A	8	GLY	-	EXPRESSION TAG	UNP Q99T05
A	9	SER	-	EXPRESSION TAG	UNP Q99T05
A	10	SER	-	EXPRESSION TAG	UNP Q99T05
A	11	HIS	-	EXPRESSION TAG	UNP Q99T05
A	12	HIS	-	EXPRESSION TAG	UNP Q99T05
A	13	HIS	-	EXPRESSION TAG	UNP Q99T05
A	14	HIS	-	EXPRESSION TAG	UNP Q99T05
A	15	HIS	-	EXPRESSION TAG	UNP Q99T05
A	16	HIS	-	EXPRESSION TAG	UNP Q99T05
A	17	SER	-	EXPRESSION TAG	UNP Q99T05
A	18	SER	-	EXPRESSION TAG	UNP Q99T05
A	19	GLY	-	EXPRESSION TAG	UNP Q99T05
A	20	LEU	-	EXPRESSION TAG	UNP Q99T05
A	21	VAL	-	EXPRESSION TAG	UNP Q99T05
A	22	PRO	-	EXPRESSION TAG	UNP Q99T05
A	23	ARG	-	EXPRESSION TAG	UNP Q99T05
A	24	GLY	-	EXPRESSION TAG	UNP Q99T05
A	25	SER	-	EXPRESSION TAG	UNP Q99T05
A	26	HIS	-	EXPRESSION TAG	UNP Q99T05
A	27	MET	-	EXPRESSION TAG	UNP Q99T05
B	7	MET	-	EXPRESSION TAG	UNP Q99T05
B	8	GLY	-	EXPRESSION TAG	UNP Q99T05
B	9	SER	-	EXPRESSION TAG	UNP Q99T05
B	10	SER	-	EXPRESSION TAG	UNP Q99T05

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Chain	Residue	Modelled	Actual	Comment	Reference
B	11	HIS	-	EXPRESSION TAG	UNP Q99T05
B	12	HIS	-	EXPRESSION TAG	UNP Q99T05
B	13	HIS	-	EXPRESSION TAG	UNP Q99T05
B	14	HIS	-	EXPRESSION TAG	UNP Q99T05
B	15	HIS	-	EXPRESSION TAG	UNP Q99T05
B	16	HIS	-	EXPRESSION TAG	UNP Q99T05
B	17	SER	-	EXPRESSION TAG	UNP Q99T05
B	18	SER	-	EXPRESSION TAG	UNP Q99T05
B	19	GLY	-	EXPRESSION TAG	UNP Q99T05
B	20	LEU	-	EXPRESSION TAG	UNP Q99T05
B	21	VAL	-	EXPRESSION TAG	UNP Q99T05
B	22	PRO	-	EXPRESSION TAG	UNP Q99T05
B	23	ARG	-	EXPRESSION TAG	UNP Q99T05
B	24	GLY	-	EXPRESSION TAG	UNP Q99T05
B	25	SER	-	EXPRESSION TAG	UNP Q99T05
B	26	HIS	-	EXPRESSION TAG	UNP Q99T05
B	27	MET	-	EXPRESSION TAG	UNP Q99T05

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	33	Total O 33 33	0	0
3	B	13	Total O 13 13	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.68Å 67.41Å 152.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.08 – 2.52 30.08 – 2.52	Depositor EDS
% Data completeness (in resolution range)	89.8 (30.08-2.52) 97.4 (30.08-2.52)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.32 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.200 , 0.257 0.203 , 0.259	Depositor DCC
R_{free} test set	1200 reflections (5.11%)	DCC
Wilson B-factor (Å ²)	45.2	Xtriage
Anisotropy	0.885	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 69.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.031 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3650	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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

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

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	0.33	0/1854	0.50	0/2499
1	B	0.27	0/1812	0.43	0/2443
All	All	0.30	0/3666	0.47	0/4942

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

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	1822	0	1799	72	0
1	B	1781	0	1764	70	0
2	A	1	0	0	0	0
3	A	33	0	0	2	0
3	B	13	0	0	0	0
All	All	3650	0	3563	141	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 (141) 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:133:THR:HG22	1:A:136:GLN:HG3	1.55	0.88
1:A:113:LYS:HZ3	1:A:117:ARG:HE	1.18	0.86
1:A:41:ARG:HG2	1:A:41:ARG:HH11	1.42	0.84
1:A:41:ARG:CG	1:A:41:ARG:HH11	1.93	0.81
1:B:212:THR:H	1:B:215:GLN:NE2	1.83	0.76
1:A:113:LYS:HZ3	1:A:117:ARG:NE	1.85	0.75
1:A:56:LEU:O	1:A:60:ILE:HG13	1.88	0.73
1:A:112:LEU:O	1:A:116:THR:HG23	1.89	0.73
1:B:66:THR:HB	1:B:67:ARG:HG2	1.70	0.72
1:A:42:ILE:HD12	1:A:45:LYS:HD2	1.72	0.72
1:B:49:THR:O	1:B:52:ILE:HG13	1.90	0.71
1:B:48:LEU:O	1:B:52:ILE:HG23	1.91	0.70
1:A:67:ARG:HB3	1:A:68:ASP:C	2.12	0.69
1:A:61:MET:HA	1:A:61:MET:HE3	1.75	0.69
1:B:108:HIS:HD1	1:B:110:PHE:HE1	1.40	0.69
1:B:66:THR:HG22	1:B:162:ARG:NH1	2.08	0.69
1:A:225:ALA:HB1	1:A:229:TYR:CD2	2.28	0.68
1:B:49:THR:O	1:B:53:ILE:HG13	1.95	0.67
1:A:230:ASN:ND2	1:A:232:ASN:H	1.93	0.66
1:A:109:GLY:O	1:A:133:THR:HG21	1.97	0.65
1:B:135:THR:HG21	1:B:164:GLU:HG2	1.80	0.64
1:B:202:ASN:HD22	1:B:204:ASN:H	1.44	0.64
1:A:133:THR:HG22	1:A:136:GLN:CG	2.27	0.63
1:A:211:ILE:HG13	1:A:215:GLN:HE21	1.62	0.62
1:B:66:THR:CB	1:B:67:ARG:HG2	2.28	0.62
1:B:110:PHE:HB2	1:B:112:LEU:HD12	1.80	0.62
1:A:230:ASN:HD22	1:A:230:ASN:C	2.05	0.60
1:B:266:GLN:O	1:B:269:ARG:HB2	2.01	0.59
1:B:151:THR:HG22	1:B:155:LYS:HE3	1.84	0.59
1:B:225:ALA:HB1	1:B:229:TYR:CD2	2.37	0.59
1:B:181:TYR:CZ	1:B:183:GLY:HA2	2.38	0.59
1:A:45:LYS:HD3	1:A:46:ILE:HG23	1.85	0.58
1:A:46:ILE:HA	1:A:49:THR:HG22	1.85	0.58
1:A:65:SER:O	1:A:68:ASP:HB2	2.04	0.58
1:A:152:ARG:HA	1:A:155:LYS:HE2	1.84	0.58
1:B:67:ARG:HB3	1:B:68:ASP:C	2.24	0.57
1:B:199:THR:HG21	1:B:215:GLN:HE22	1.70	0.56
1:A:133:THR:CG2	1:A:136:GLN:H	2.19	0.56
1:A:133:THR:CG2	1:A:136:GLN:HG3	2.32	0.56
1:B:141:ASN:ND2	1:B:180:ILE:HG22	2.21	0.56
1:A:129:GLN:HG3	1:A:248:LYS:NZ	2.20	0.56
1:A:41:ARG:NH1	1:A:41:ARG:CG	2.61	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:LEU:HD12	1:B:43:LEU:H	1.70	0.55
1:A:60:ILE:O	1:A:64:LEU:HD22	2.07	0.55
1:B:50:ILE:O	1:B:54:ILE:HD13	2.07	0.55
1:B:45:LYS:NZ	1:B:45:LYS:HA	2.23	0.54
1:B:212:THR:H	1:B:215:GLN:HE21	1.52	0.53
1:A:230:ASN:HD22	1:A:232:ASN:H	1.56	0.53
1:B:246:LEU:HD23	1:B:249:MET:HE3	1.91	0.53
1:A:155:LYS:O	1:A:159:VAL:HG23	2.09	0.53
1:A:50:ILE:O	1:A:53:ILE:HG22	2.09	0.52
1:B:72:GLU:HG3	1:B:75:LYS:HD2	1.91	0.52
1:A:153:LYS:O	1:A:157:LEU:HD13	2.09	0.52
1:A:46:ILE:HD12	1:A:47:LEU:N	2.24	0.52
1:B:54:ILE:O	1:B:58:ILE:HG12	2.09	0.52
1:A:220:ALA:HB3	1:A:245:ASN:HD21	1.75	0.52
1:B:107:HIS:ND1	1:B:107:HIS:C	2.64	0.51
1:B:48:LEU:HD23	1:B:49:THR:N	2.26	0.51
1:A:106:ASN:N	1:A:106:ASN:HD22	2.07	0.51
1:B:110:PHE:CG	1:B:111:ASP:N	2.79	0.51
1:A:50:ILE:O	1:A:54:ILE:HG23	2.10	0.50
1:B:43:LEU:O	1:B:47:LEU:HD13	2.12	0.50
1:B:110:PHE:CD2	1:B:111:ASP:N	2.80	0.50
1:B:180:ILE:O	1:B:187:TYR:HA	2.11	0.50
1:B:150:PHE:O	1:B:154:VAL:HG23	2.12	0.49
1:B:43:LEU:HD12	1:B:43:LEU:N	2.27	0.49
1:B:153:LYS:HE2	1:B:153:LYS:HA	1.93	0.49
1:A:60:ILE:HG22	1:A:64:LEU:CD2	2.42	0.49
1:B:63:PHE:O	1:B:66:THR:O	2.30	0.49
1:A:180:ILE:O	1:A:187:TYR:HA	2.13	0.48
1:B:65:SER:O	1:B:68:ASP:HB2	2.13	0.48
1:A:66:THR:HG23	1:A:67:ARG:CZ	2.42	0.48
1:B:56:LEU:O	1:B:60:ILE:HG12	2.13	0.48
1:B:144:TYR:OH	1:B:152:ARG:HD2	2.13	0.48
1:B:66:THR:CA	1:B:67:ARG:HG2	2.43	0.48
1:B:189:LEU:HG	1:B:201:VAL:HG11	1.96	0.48
1:A:107:HIS:NE2	1:A:133:THR:OG1	2.46	0.47
1:A:113:LYS:NZ	1:A:117:ARG:HE	2.01	0.47
1:A:61:MET:CE	1:A:61:MET:HA	2.44	0.47
1:B:47:LEU:O	1:B:51:LEU:HD13	2.13	0.47
1:A:113:LYS:HZ1	1:A:117:ARG:HH11	1.62	0.47
1:B:53:ILE:O	1:B:57:PHE:HB2	2.15	0.47
1:B:202:ASN:ND2	1:B:204:ASN:H	2.12	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:ASN:HD22	1:A:231:ILE:N	2.13	0.46
1:A:230:ASN:HD21	1:A:232:ASN:HB2	1.79	0.46
1:B:202:ASN:C	1:B:202:ASN:HD22	2.19	0.46
1:B:41:ARG:HH22	1:B:45:LYS:HG2	1.81	0.46
1:B:42:ILE:O	1:B:46:ILE:HG22	2.16	0.46
1:B:113:LYS:O	1:B:117:ARG:HD2	2.16	0.46
1:B:41:ARG:HH22	1:B:45:LYS:CG	2.30	0.45
1:A:151:THR:O	1:A:155:LYS:HG2	2.16	0.45
1:A:69:ASN:O	1:A:72:GLU:HB2	2.16	0.45
1:A:133:THR:HG23	1:A:136:GLN:H	1.80	0.45
1:A:61:MET:HE1	1:A:64:LEU:HD23	1.98	0.45
1:A:202:ASN:HD21	1:A:204:ASN:HB2	1.81	0.45
1:B:54:ILE:HG22	1:B:55:ALA:N	2.30	0.45
1:A:106:ASN:ND2	1:A:106:ASN:N	2.65	0.45
1:A:65:SER:O	1:A:67:ARG:HA	2.17	0.44
1:B:144:TYR:HB3	1:B:145:ASP:H	1.57	0.44
1:B:217:ALA:HB2	1:B:249:MET:HE3	1.99	0.44
1:B:69:ASN:OD1	1:B:71:ASP:HB2	2.18	0.44
1:A:234:MET:HG2	1:A:238:PHE:CD2	2.53	0.43
1:A:67:ARG:HB3	1:A:69:ASN:N	2.33	0.43
1:B:108:HIS:ND1	1:B:110:PHE:HE1	2.13	0.43
1:A:133:THR:HG23	1:A:135:THR:N	2.33	0.43
1:B:45:LYS:HA	1:B:45:LYS:HZ3	1.83	0.43
1:B:50:ILE:HG13	1:B:51:LEU:N	2.33	0.43
1:B:62:TYR:C	1:B:62:TYR:CD1	2.91	0.43
1:B:50:ILE:HG13	1:B:51:LEU:HD12	2.00	0.43
1:A:47:LEU:O	1:A:51:LEU:HB2	2.19	0.43
1:B:180:ILE:HD12	1:B:223:VAL:HG21	2.02	0.42
1:B:73:LEU:HD12	1:B:73:LEU:HA	1.87	0.42
1:A:149:SER:H	1:A:152:ARG:HG3	1.83	0.42
1:A:189:LEU:HG	1:A:201:VAL:HG11	2.02	0.42
1:A:269:ARG:HB3	1:B:142:TYR:CE1	2.55	0.42
1:B:46:ILE:O	1:B:50:ILE:HG23	2.19	0.42
1:B:41:ARG:O	1:B:44:LEU:HG	2.20	0.42
1:B:66:THR:HA	1:B:67:ARG:HA	1.82	0.42
1:A:107:HIS:CE1	1:A:133:THR:OG1	2.73	0.41
1:A:51:LEU:O	1:A:54:ILE:HG12	2.19	0.41
1:A:61:MET:CE	1:A:64:LEU:HD23	2.50	0.41
1:A:142:TYR:HB2	3:A:274:HOH:O	2.20	0.41
1:A:66:THR:HA	1:A:67:ARG:HG3	2.01	0.41
1:B:221:SER:O	1:B:225:ALA:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:LEU:C	1:A:44:LEU:HD12	2.41	0.41
1:A:108:HIS:HD2	3:A:282:HOH:O	2.04	0.41
1:B:152:ARG:HA	1:B:152:ARG:HD3	1.79	0.41
1:A:60:ILE:HG22	1:A:64:LEU:HD22	2.02	0.41
1:A:203:LYS:O	1:A:210:HIS:HE1	2.04	0.41
1:A:50:ILE:HA	1:A:53:ILE:HG22	2.03	0.41
1:A:54:ILE:HG13	1:A:55:ALA:N	2.35	0.41
1:A:66:THR:HG23	1:A:67:ARG:HG3	2.02	0.40
1:B:62:TYR:O	1:B:66:THR:HG23	2.21	0.40
1:A:202:ASN:HD22	1:A:204:ASN:H	1.69	0.40
1:A:180:ILE:HD12	1:A:223:VAL:HG21	2.04	0.40
1:B:226:PRO:HB2	1:B:228:VAL:HG22	2.02	0.40
1:B:41:ARG:HG3	1:B:42:ILE:N	2.36	0.40
1:A:113:LYS:HZ1	1:A:117:ARG:NH1	2.19	0.40
1:B:96:PHE:CE2	1:B:220:ALA:HA	2.56	0.40
1:B:61:MET:O	1:B:65:SER:HB3	2.22	0.40
1:A:235:SER:O	1:A:239:THR:HG23	2.22	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	219/263 (83%)	205 (94%)	14 (6%)	0	100	100
1	B	213/263 (81%)	199 (93%)	14 (7%)	0	100	100
All	All	432/526 (82%)	404 (94%)	28 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	203/239 (85%)	186 (92%)	17 (8%)	13	23
1	B	199/239 (83%)	176 (88%)	23 (12%)	6	11
All	All	402/478 (84%)	362 (90%)	40 (10%)	9	16

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ARG
1	A	45	LYS
1	A	51	LEU
1	A	52	ILE
1	A	61	MET
1	A	64	LEU
1	A	73	LEU
1	A	74	ARG
1	A	119	LEU
1	A	122	THR
1	A	149	SER
1	A	177	LEU
1	A	180	ILE
1	A	202	ASN
1	A	230	ASN
1	A	238	PHE
1	A	242	VAL
1	B	42	ILE
1	B	46	ILE
1	B	56	LEU
1	B	57	PHE
1	B	65	SER
1	B	73	LEU
1	B	99	MET
1	B	107	HIS
1	B	113	LYS
1	B	115	THR

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Mol	Chain	Res	Type
1	B	117	ARG
1	B	140	LYS
1	B	144	TYR
1	B	147	ASP
1	B	148	ARG
1	B	152	ARG
1	B	153	LYS
1	B	155	LYS
1	B	156	GLU
1	B	170	ASN
1	B	200	THR
1	B	202	ASN
1	B	238	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	78	ASN
1	A	106	ASN
1	A	166	GLN
1	A	170	ASN
1	A	179	ASN
1	A	202	ASN
1	A	210	HIS
1	A	215	GLN
1	A	230	ASN
1	A	232	ASN
1	A	233	ASN
1	A	245	ASN
1	A	266	GLN
1	B	87	ASN
1	B	106	ASN
1	B	136	GLN
1	B	141	ASN
1	B	166	GLN
1	B	168	ASN
1	B	185	ASN
1	B	202	ASN
1	B	215	GLN
1	B	224	ASN
1	B	251	GLN

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Mol	Chain	Res	Type
1	B	268	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	223/263 (84%)	0.66	25 (11%) 6 5	32, 52, 147, 194	0
1	B	217/263 (82%)	0.87	31 (14%) 3 3	44, 84, 154, 201	0
All	All	440/526 (83%)	0.76	56 (12%) 4 4	32, 68, 153, 201	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	144	TYR	11.2
1	B	42	ILE	10.4
1	B	44	LEU	10.0
1	A	120	PHE	9.1
1	A	42	ILE	7.3
1	A	48	LEU	6.7
1	A	118	ALA	6.1
1	A	44	LEU	5.8
1	B	46	ILE	5.5
1	B	119	LEU	5.4
1	A	43	LEU	5.1
1	A	46	ILE	5.1
1	B	43	LEU	5.0
1	B	148	ARG	4.9
1	A	119	LEU	4.7
1	A	206	THR	4.6
1	B	67	ARG	4.5
1	A	41	ARG	4.5
1	B	152	ARG	4.5
1	B	118	ALA	4.0
1	A	45	LYS	3.8
1	B	228	VAL	3.8
1	B	150	PHE	3.7
1	B	145	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	108	HIS	3.5
1	A	122	THR	3.5
1	A	152	ARG	3.5
1	B	45	LYS	3.5
1	B	117	ARG	3.5
1	B	47	LEU	3.3
1	B	165	LYS	3.2
1	B	41	ARG	3.1
1	B	57	PHE	3.0
1	A	129	GLN	3.0
1	A	207	THR	2.9
1	B	60	ILE	2.9
1	A	208	MET	2.8
1	A	60	ILE	2.8
1	B	66	THR	2.6
1	A	63	PHE	2.6
1	A	67	ARG	2.6
1	B	63	PHE	2.6
1	B	176	TYR	2.5
1	B	68	ASP	2.5
1	B	161	HIS	2.5
1	B	146	ASN	2.5
1	B	112	LEU	2.5
1	A	96	PHE	2.3
1	A	57	PHE	2.3
1	A	97	ILE	2.2
1	B	53	ILE	2.2
1	B	96	PHE	2.1
1	A	98	SER	2.1
1	A	49	THR	2.1
1	A	151	THR	2.1
1	B	116	THR	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	MG	A	1	1/1	0.71	0.15	-0.59	100,100,100,100	0

6.5 Other polymers [i](#)

There are no such residues in this entry.