Full wwPDB X-ray Structure Validation Report (i)

May 26, 2020 – 08:29 am BST

PDB ID	:	2FYW
Title	:	Crystal Structure of a Conserved Protein of Unknown Function from Streptococcus pneumoniae
Authors	:	Nocek, B.; Hatzos, C.; Abdullah, J.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2006-02-08
Resolution	:	2.40 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 (i) symbol.

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

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	Percentile Ranks	Value
Rfree		0.258
Clashscore		9
Ramachandran outliers		0.3%
Sidechain outliers		5.6%
RSRZ outliers		0

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
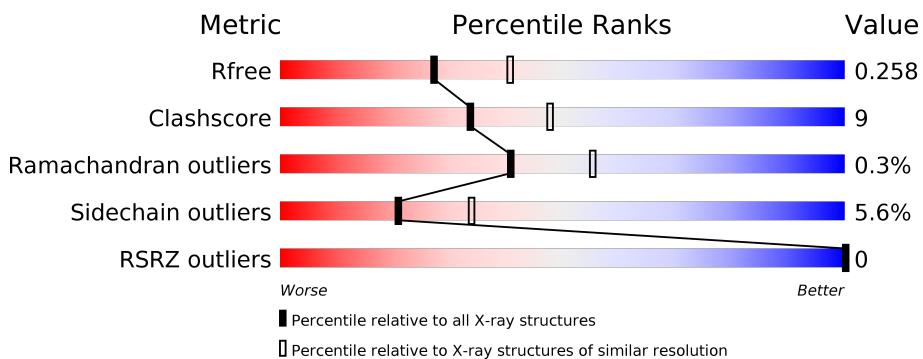
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 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 <=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	267	79% 18% •
1	B	267	80% 18% •
1	C	267	80% 17% •
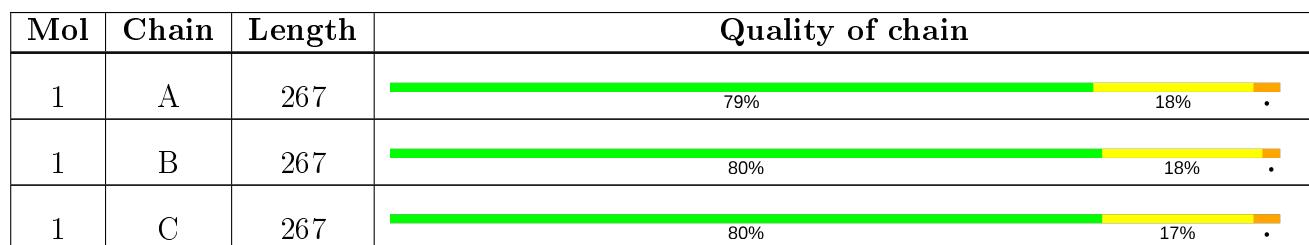
2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6575 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 conserved hypothetical protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	267	Total 2131	C 1357	N 356	O 409	S 3	Se 6	0	4	0
1	B	267	Total 2124	C 1353	N 356	O 406	S 3	Se 6	0	3	0
1	C	266	Total 2123	C 1353	N 352	O 409	S 3	Se 6	4	4	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ASN	-	CLONING ARTIFACT	GB 14973101
A	0	ALA	-	CLONING ARTIFACT	GB 14973101
A	1	MSE	MET	MODIFIED RESIDUE	GB 14973101
A	20	MSE	MET	MODIFIED RESIDUE	GB 14973101
A	40	MSE	MET	MODIFIED RESIDUE	GB 14973101
A	116	MSE	MET	MODIFIED RESIDUE	GB 14973101
A	163	MSE	MET	MODIFIED RESIDUE	GB 14973101
A	213	MSE	MET	MODIFIED RESIDUE	GB 14973101
B	-1	ASN	-	CLONING ARTIFACT	GB 14973101
B	0	ALA	-	CLONING ARTIFACT	GB 14973101
B	1	MSE	MET	MODIFIED RESIDUE	GB 14973101
B	20	MSE	MET	MODIFIED RESIDUE	GB 14973101
B	40	MSE	MET	MODIFIED RESIDUE	GB 14973101
B	116	MSE	MET	MODIFIED RESIDUE	GB 14973101
B	163	MSE	MET	MODIFIED RESIDUE	GB 14973101
B	213	MSE	MET	MODIFIED RESIDUE	GB 14973101
C	-1	ASN	-	CLONING ARTIFACT	GB 14973101
C	0	ALA	-	CLONING ARTIFACT	GB 14973101
C	1	MSE	MET	MODIFIED RESIDUE	GB 14973101
C	20	MSE	MET	MODIFIED RESIDUE	GB 14973101
C	40	MSE	MET	MODIFIED RESIDUE	GB 14973101
C	116	MSE	MET	MODIFIED RESIDUE	GB 14973101
C	163	MSE	MET	MODIFIED RESIDUE	GB 14973101

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Chain	Residue	Modelled	Actual	Comment	Reference
C	213	MSE	MET	MODIFIED RESIDUE	GB 14973101

- Molecule 2 is water.

| Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	72	Total O 72 72	0	0
2	B	61	Total O 61 61	0	0
2	C	64	Total O 64 64	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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: conserved hypothetical protein
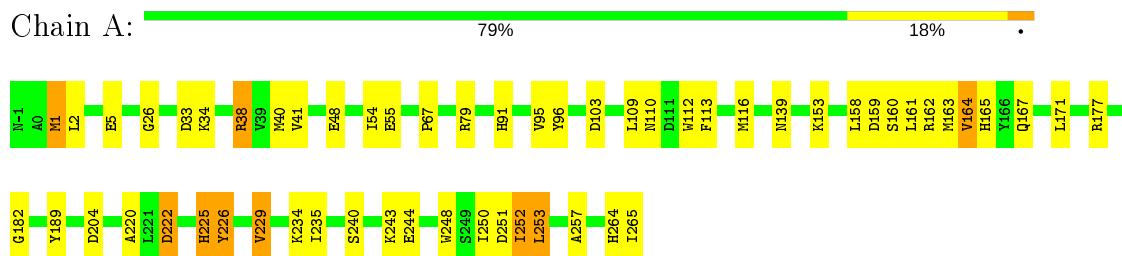
Chain A:

- Molecule 1: conserved hypothetical protein

Chain B:

- Molecule 1: conserved hypothetical protein

Chain C:
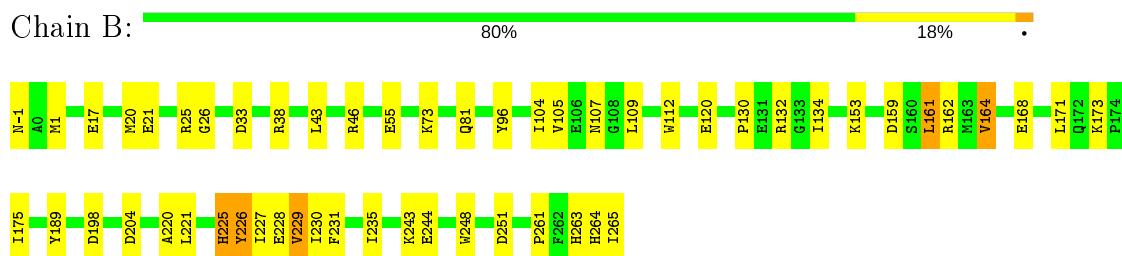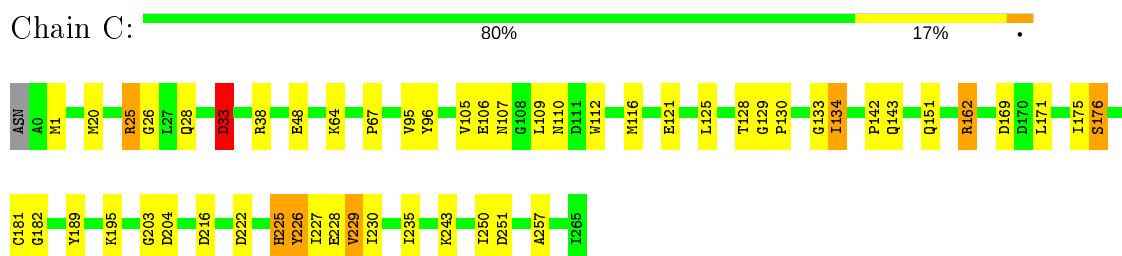
4   Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	96.48Å 167.02Å 122.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.40 34.47 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.00-2.40) 99.4 (34.47-2.30)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.92 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.200 , 0.259 0.207 , 0.258	Depositor DCC
R_{free} test set	2204 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	36.4	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 12.5	EDS
L-test for twinning [2]	$< |L| > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.146 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.176 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6575	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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)

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	0.89	0/2169	0.82	1/2932 (0.0%)
1	B	0.89	0/2162	0.82	1/2922 (0.0%)
1	C	0.89	2/2161 (0.1%)	0.82	2/2921 (0.1%)
All	All	0.89	2/6492 (0.0%)	0.82	4/8775 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	181	CYS	CB-SG	-6.42	1.71	1.82
1	C	121	GLU	CB-CG	5.93	1.63	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	222	ASP	CB-CG-OD1	6.21	123.88	118.30
1	C	33	ASP	CB-CG-OD2	5.81	123.53	118.30
1	B	33	ASP	CB-CG-OD2	5.79	123.51	118.30
1	C	216	ASP	CB-CG-OD1	5.78	123.50	118.30

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	2131	0	2074	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2124	0	2072	33	0
1	C	2123	0	2064	36	0
2	A	72	0	0	7	0
2	B	61	0	0	4	0
2	C	64	0	0	4	0
All	All	6575	0	6210	108	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 (108) 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:C:105:VAL:HB	2:C:287:HOH:O	1.62	0.97
1:C:110:ASN:HD21	1:C:182:GLY:H	1.13	0.94
1:A:1:MSE:HE2	1:A:5:GLU:HG3	1.48	0.91
1:A:34:LYS:HE2	2:A:310:HOH:O	1.71	0.88
1:A:160:SER:HA	2:A:280:HOH:O	1.79	0.83
1:C:20:MSE:HE2	1:C:134:ILE:HD13	1.61	0.82
1:A:110:ASN:HD21	1:A:182:GLY:H	1.30	0.79
1:B:265:ILE:HA	2:B:325:HOH:O	1.83	0.78
1:A:264:HIS:HB3	1:A:265:ILE:HD12	1.66	0.77
1:A:33:ASP:OD1	2:A:276:HOH:O	2.03	0.75
1:A:225:HIS:HB3	2:A:278:HOH:O	1.87	0.74
1:A:234:LYS:HE2	2:A:328:HOH:O	1.90	0.71
1:C:110:ASN:ND2	1:C:182:GLY:H	1.89	0.70
1:A:109:LEU:HA	1:A:112:TRP:CE3	2.29	0.67
1:C:112:TRP:C	1:C:116:MSE:HE3	2.15	0.66
1:A:48:GLU:HG2	1:A:257:ALA:HB1	1.77	0.65
1:C:226:TYR:O	1:C:229:VAL:HG22	1.97	0.63
1:C:112:TRP:O	1:C:116:MSE:HE3	1.98	0.63
1:A:226:TYR:O	1:A:229:VAL:HG22	1.99	0.62
1:C:227:ILE:O	1:C:230:ILE:HG12	2.00	0.62
1:B:43:LEU:HD11	1:B:228:GLU:HG3	1.82	0.61
1:A:161:LEU:H	1:B:265:ILE:HG13	1.64	0.61
1:C:33:ASP:HB3	2:C:281:HOH:O	2.00	0.60
1:A:163:MSE:HE1	1:A:171:LEU:CD2	2.32	0.60
1:A:67:PRO:HG3	1:A:95:VAL:HG11	1.84	0.60
1:A:79:ARG:HG2	1:A:79:ARG:HH11	1.66	0.58
1:A:2:LEU:O	1:A:5:GLU:HG2	2.04	0.58
1:A:160:SER:HA	1:B:265:ILE:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:231:PHE:CE1	1:B:235:ILE:HD12	2.40	0.57
1:C:67:PRO:HG3	1:C:95:VAL:HG11	1.86	0.56
1:B:227:ILE:O	1:B:230:ILE:HG12	2.06	0.56
1:C:203:GLY:O	1:C:204:ASP:HB3	2.06	0.56
1:C:20:MSE:CE	1:C:134:ILE:HD13	2.33	0.56
1:C:25:ARG:HH11	1:C:25:ARG:HG2	1.70	0.55
1:C:38:ARG:HG2	1:C:251:ASP:HB2	1.87	0.55
1:A:34:LYS:HB2	2:A:282:HOH:O	2.06	0.55
1:B:168:GLU:O	1:B:171:LEU:HB2	2.08	0.54
1:B:107:ASN:HB3	2:B:307:HOH:O	2.08	0.54
1:A:161:LEU:H	1:B:265:ILE:CG1	2.21	0.53
1:C:48[B]:GLU:HB2	2:C:300:HOH:O	2.09	0.52
1:C:143:GLN:HE22	1:C:151:GLN:NE2	2.07	0.52
1:B:26:GLY:HA2	1:B:96:TYR:CE1	2.45	0.51
1:C:225:HIS:O	1:C:228:GLU:HG2	2.10	0.51
1:C:112:TRP:HH2	1:C:235:ILE:CD1	2.24	0.51
1:C:129:GLY:HA2	2:C:312:HOH:O	2.10	0.51
1:B:109:LEU:HA	1:B:112:TRP:CE3	2.46	0.51
1:C:162:ARG:HB2	1:C:222:ASP:HB3	1.93	0.51
1:A:240:SER:O	1:A:244:GLU:HG2	2.11	0.50
1:A:103:ASP:OD1	1:A:109:LEU:HD23	2.12	0.50
1:C:64:LYS:HE3	1:C:109:LEU:HD22	1.94	0.50
1:A:243:LYS:HA	1:A:248:TRP:HB2	1.92	0.50
1:B:38:ARG:HG2	1:B:251:ASP:HB2	1.94	0.49
1:A:162:ARG:HB3	1:A:222:ASP:HB3	1.94	0.49
1:A:1:MSE:CE	1:A:5:GLU:HG3	2.32	0.49
1:B:226:TYR:O	1:B:229:VAL:HG22	2.13	0.49
1:A:41:VAL:HG11	1:A:235:ILE:HB	1.95	0.49
1:A:153:LYS:HZ1	1:B:265:ILE:HD13	1.78	0.49
1:B:46:ARG:HH12	1:B:81:GLN:HE22	1.61	0.49
1:C:112:TRP:HB3	1:C:116:MSE:CE	2.43	0.48
1:C:26:GLY:HA2	1:C:96:TYR:CE1	2.48	0.48
1:B:161:LEU:HD21	1:B:221:LEU:HD22	1.96	0.47
1:A:265:ILE:HG23	1:B:153:LYS:HD2	1.95	0.47
1:B:225:HIS:O	1:B:228:GLU:HG2	2.15	0.47
1:A:113:PHE:HA	1:A:116:MSE:HE3	1.98	0.46
1:B:1:MSE:HE1	1:B:248:TRP:CE2	2.50	0.46
1:B:17:GLU:HA	1:B:25[B]:ARG:HH21	1.80	0.46
1:C:107:ASN:O	1:C:112:TRP:NE1	2.49	0.45
1:A:165:HIS:CD2	1:B:263:HIS:HD2	2.35	0.45
1:A:113:PHE:HD1	1:A:116:MSE:CE	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:MSE:HG3	1:B:104:ILE:HD11	1.99	0.45
1:B:204:ASP:O	1:B:204:ASP:CG	2.56	0.45
1:C:20:MSE:HE2	1:C:134:ILE:CD1	2.40	0.45
1:A:112:TRP:O	1:A:116:MSE:HG3	2.17	0.44
1:C:48[B]:GLU:HB3	1:C:257:ALA:HB1	1.99	0.44
1:B:231:PHE:CD1	1:B:235:ILE:HD12	2.51	0.44
1:C:28:GLN:OE1	1:C:67:PRO:HD2	2.18	0.44
1:C:142:PRO:HG3	1:C:176:SER:HB2	1.99	0.44
1:B:175:ILE:HG23	1:B:198:ASP:HB2	2.00	0.44
1:A:48:GLU:HG2	1:A:257:ALA:CB	2.44	0.43
1:C:128:THR:OG1	1:C:133:GLY:HA2	2.18	0.43
1:C:25:ARG:NH1	1:C:25:ARG:HG2	2.32	0.43
1:A:164:VAL:HA	1:B:261:PRO:O	2.19	0.43
1:A:139:ASN:HD21	1:A:177:ARG:HD2	1.84	0.43
1:B:132:ARG:HD3	2:B:275:HOH:O	2.19	0.43
1:C:1:MSE:HE3	1:C:1:MSE:HB2	1.81	0.43
1:A:163:MSE:HE1	1:A:171:LEU:HD22	1.99	0.42
1:A:26:GLY:HA2	1:A:96:TYR:CE1	2.53	0.42
1:A:264:HIS:CE1	1:B:162:ARG:HE	2.37	0.42
1:A:162:ARG:HE	1:B:264:HIS:HE1	1.66	0.42
1:A:164:VAL:HG22	1:A:220:ALA:HB3	2.01	0.42
1:C:125:LEU:O	1:C:195:LYS:HE3	2.20	0.42
1:A:250:ILE:HD11	1:A:252:ILE:HD11	2.02	0.42
1:A:153:LYS:HA	1:A:158:LEU:HD12	2.02	0.42
1:B:244:GLU:HA	2:B:303:HOH:O	2.20	0.41
1:A:204:ASP:CG	1:A:204:ASP:O	2.59	0.41
1:A:38:ARG:HG3	1:A:251:ASP:HB2	2.03	0.41
1:C:225:HIS:O	1:C:228:GLU:CG	2.69	0.41
1:B:164:VAL:CG1	1:B:220:ALA:HB3	2.51	0.41
1:A:165:HIS:ND1	1:A:167:GLN:O	2.53	0.41
1:A:40:MSE:HA	1:A:253:LEU:O	2.20	0.41
1:C:105:VAL:HG22	1:C:106:GLU:N	2.36	0.41
1:C:142:PRO:HA	1:C:175:ILE:O	2.21	0.40
1:C:243:LYS:HE3	1:C:250:ILE:O	2.21	0.40
1:A:164:VAL:CG2	1:A:220:ALA:HB3	2.52	0.40
1:A:160:SER:CB	2:A:280:HOH:O	2.69	0.40
1:A:161:LEU:O	1:B:265:ILE:N	2.46	0.40
1:A:54:ILE:HG12	1:A:91:HIS:CG	2.57	0.40
1:A:162:ARG:HE	1:B:264:HIS:CE1	2.40	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	267/267 (100%)	259 (97%)	8 (3%)	0	100	100
1	B	266/267 (100%)	258 (97%)	7 (3%)	1 (0%)	34	48
1	C	266/267 (100%)	254 (96%)	11 (4%)	1 (0%)	34	48
All	All	799/801 (100%)	771 (96%)	26 (3%)	2 (0%)	41	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	130	PRO
1	B	130	PRO

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	230/222 (104%)	219 (95%)	11 (5%)	25	41
1	B	229/222 (103%)	213 (93%)	16 (7%)	15	24
1	C	229/222 (103%)	218 (95%)	11 (5%)	25	41
All	All	688/666 (103%)	650 (94%)	38 (6%)	21	35

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MSE

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Mol	Chain	Res	Type
1	A	38	ARG
1	A	55	GLU
1	A	159	ASP
1	A	164	VAL
1	A	189	TYR
1	A	225	HIS
1	A	226	TYR
1	A	229	VAL
1	A	252	ILE
1	A	253	LEU
1	B	-1	ASN
1	B	21	GLU
1	B	55	GLU
1	B	73	LYS
1	B	105	VAL
1	B	120	GLU
1	B	134	ILE
1	B	159	ASP
1	B	161	LEU
1	B	164	VAL
1	B	173	LYS
1	B	189	TYR
1	B	225	HIS
1	B	226	TYR
1	B	229	VAL
1	B	243	LYS
1	C	25	ARG
1	C	33	ASP
1	C	134	ILE
1	C	162	ARG
1	C	169	ASP
1	C	171	LEU
1	C	176	SER
1	C	189	TYR
1	C	225	HIS
1	C	226	TYR
1	C	229	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	GLN

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Mol	Chain	Res	Type
1	A	110	ASN
1	A	139	ASN
1	A	211	GLN
1	A	264	HIS
1	B	81	GLN
1	B	139	ASN
1	B	211	GLN
1	B	256	GLN
1	B	263	HIS
1	B	264	HIS
1	C	82	ASN
1	C	110	ASN
1	C	151	GLN
1	C	241	GLN

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)

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	261/267 (97%)	-0.40	0	100	100	21, 31, 44, 53	0
1	B	261/267 (97%)	-0.41	0	100	100	21, 31, 44, 53	0
1	C	260/267 (97%)	-0.44	0	100	100	20, 31, 45, 54	1 (0%)
All	All	782/801 (97%)	-0.42	0	100	100	20, 31, 45, 54	1 (0%)

There are no RSRZ outliers to report.

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.