



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2016 – 04:58 AM EDT

PDB ID : 5F8C
Title : Rv2258c-unbound
Authors : Im, H.N.; Suh, S.W.
Deposited on : 2015-12-09
Resolution : 1.83 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
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : rb-20027790

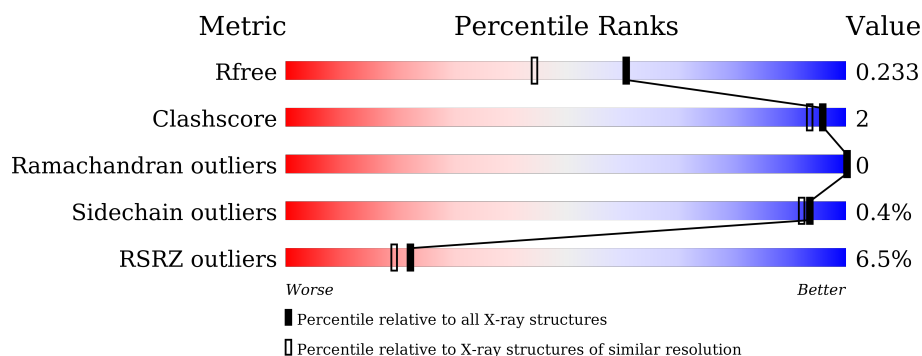
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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}	91344	2634 (1.86-1.82)
Clashscore	102246	2862 (1.86-1.82)
Ramachandran outliers	100387	2831 (1.86-1.82)
Sidechain outliers	100360	2832 (1.86-1.82)
RSRZ outliers	91569	2639 (1.86-1.82)

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	377	<div> <div>6%</div> <div> <div></div> <div>92%</div> <div>• 6%</div> </div> </div>
1	B	377	<div> <div>5%</div> <div> <div></div> <div>94%</div> <div>• •</div> </div> </div>
1	C	377	<div> <div>7%</div> <div> <div></div> <div>91%</div> <div>• 6%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	C	402	-	-	-	X
2	GOL	C	403	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8792 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 Methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	354	Total	C	N	O	S	0	0	0
			2657	1670	454	517	16			
1	B	363	Total	C	N	O	S	0	1	0
			2727	1711	470	530	16			
1	C	354	Total	C	N	O	S	0	1	0
			2665	1675	455	518	17			

There are 87 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	expression tag	UNP O53532
A	-14	GLY	-	expression tag	UNP O53532
A	-13	SER	-	expression tag	UNP O53532
A	-12	SER	-	expression tag	UNP O53532
A	-11	HIS	-	expression tag	UNP O53532
A	-10	HIS	-	expression tag	UNP O53532
A	-9	HIS	-	expression tag	UNP O53532
A	-8	HIS	-	expression tag	UNP O53532
A	-7	HIS	-	expression tag	UNP O53532
A	-6	HIS	-	expression tag	UNP O53532
A	-5	SER	-	expression tag	UNP O53532
A	-4	SER	-	expression tag	UNP O53532
A	-3	GLY	-	expression tag	UNP O53532
A	-2	LEU	-	expression tag	UNP O53532
A	-1	VAL	-	expression tag	UNP O53532
A	0	PRO	-	expression tag	UNP O53532
A	1	ARG	-	expression tag	UNP O53532
A	2	GLY	-	expression tag	UNP O53532
A	3	SER	-	expression tag	UNP O53532
A	4	HIS	-	expression tag	UNP O53532
A	5	MET	-	expression tag	UNP O53532
A	354	LEU	-	expression tag	UNP O53532
A	355	GLU	-	expression tag	UNP O53532

Continued on next page...

Continued from previous page...

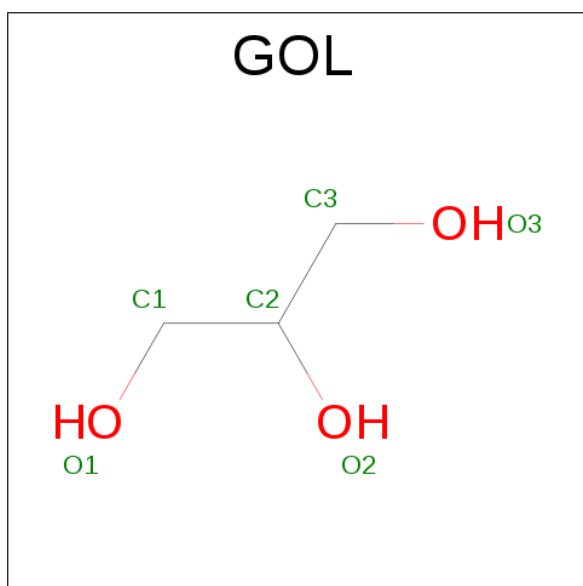
Chain	Residue	Modelled	Actual	Comment	Reference
A	356	HIS	-	expression tag	UNP O53532
A	357	HIS	-	expression tag	UNP O53532
A	358	HIS	-	expression tag	UNP O53532
A	359	HIS	-	expression tag	UNP O53532
A	360	HIS	-	expression tag	UNP O53532
A	361	HIS	-	expression tag	UNP O53532
B	-15	MET	-	expression tag	UNP O53532
B	-14	GLY	-	expression tag	UNP O53532
B	-13	SER	-	expression tag	UNP O53532
B	-12	SER	-	expression tag	UNP O53532
B	-11	HIS	-	expression tag	UNP O53532
B	-10	HIS	-	expression tag	UNP O53532
B	-9	HIS	-	expression tag	UNP O53532
B	-8	HIS	-	expression tag	UNP O53532
B	-7	HIS	-	expression tag	UNP O53532
B	-6	HIS	-	expression tag	UNP O53532
B	-5	SER	-	expression tag	UNP O53532
B	-4	SER	-	expression tag	UNP O53532
B	-3	GLY	-	expression tag	UNP O53532
B	-2	LEU	-	expression tag	UNP O53532
B	-1	VAL	-	expression tag	UNP O53532
B	0	PRO	-	expression tag	UNP O53532
B	1	ARG	-	expression tag	UNP O53532
B	2	GLY	-	expression tag	UNP O53532
B	3	SER	-	expression tag	UNP O53532
B	4	HIS	-	expression tag	UNP O53532
B	5	MET	-	expression tag	UNP O53532
B	354	LEU	-	expression tag	UNP O53532
B	355	GLU	-	expression tag	UNP O53532
B	356	HIS	-	expression tag	UNP O53532
B	357	HIS	-	expression tag	UNP O53532
B	358	HIS	-	expression tag	UNP O53532
B	359	HIS	-	expression tag	UNP O53532
B	360	HIS	-	expression tag	UNP O53532
B	361	HIS	-	expression tag	UNP O53532
C	-15	MET	-	expression tag	UNP O53532
C	-14	GLY	-	expression tag	UNP O53532
C	-13	SER	-	expression tag	UNP O53532
C	-12	SER	-	expression tag	UNP O53532
C	-11	HIS	-	expression tag	UNP O53532
C	-10	HIS	-	expression tag	UNP O53532
C	-9	HIS	-	expression tag	UNP O53532

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	HIS	-	expression tag	UNP O53532
C	-7	HIS	-	expression tag	UNP O53532
C	-6	HIS	-	expression tag	UNP O53532
C	-5	SER	-	expression tag	UNP O53532
C	-4	SER	-	expression tag	UNP O53532
C	-3	GLY	-	expression tag	UNP O53532
C	-2	LEU	-	expression tag	UNP O53532
C	-1	VAL	-	expression tag	UNP O53532
C	0	PRO	-	expression tag	UNP O53532
C	1	ARG	-	expression tag	UNP O53532
C	2	GLY	-	expression tag	UNP O53532
C	3	SER	-	expression tag	UNP O53532
C	4	HIS	-	expression tag	UNP O53532
C	5	MET	-	expression tag	UNP O53532
C	354	LEU	-	expression tag	UNP O53532
C	355	GLU	-	expression tag	UNP O53532
C	356	HIS	-	expression tag	UNP O53532
C	357	HIS	-	expression tag	UNP O53532
C	358	HIS	-	expression tag	UNP O53532
C	359	HIS	-	expression tag	UNP O53532
C	360	HIS	-	expression tag	UNP O53532
C	361	HIS	-	expression tag	UNP O53532

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	281	Total	O	0	0
			281	281		
3	B	212	Total	O	0	0
			212	212		
3	C	226	Total	O	0	0
			226	226		

- Molecule 1: Methyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	109.25Å 140.63Å 97.24Å 90.00° 98.56° 90.00°	Depositor
Resolution (Å)	27.25 – 1.83 27.07 – 1.83	Depositor EDS
% Data completeness (in resolution range)	99.8 (27.25-1.83) 99.8 (27.07-1.83)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.8.0124	Depositor
R, R_{free}	0.191 , 0.226 0.201 , 0.233	Depositor DCC
R_{free} test set	6387 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	28.4	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8792	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% 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: GOL, CSD

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	0.49	0/2696	0.69	0/3659
1	B	0.45	0/2767	0.64	0/3754
1	C	0.44	0/2704	0.66	0/3669
All	All	0.46	0/8167	0.66	0/11082

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	2657	0	2607	8	0
1	B	2727	0	2683	10	0
1	C	2665	0	2615	8	0
2	C	24	0	32	0	0
3	A	281	0	0	3	0
3	B	212	0	0	0	0
3	C	226	0	0	3	0
All	All	8792	0	7937	24	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 2.

All (24) 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:267:PRO:HG3	1:B:356:HIS:NE2	1.80	0.95
1:C:355:GLU:OE1	3:C:501:HOH:O	1.91	0.86
1:B:267:PRO:CG	1:B:356:HIS:NE2	2.43	0.82
1:C:356:HIS:ND1	3:C:502:HOH:O	2.19	0.74
1:A:356:HIS:NE2	3:A:401:HOH:O	2.23	0.68
1:A:356:HIS:CD2	3:A:401:HOH:O	2.49	0.65
1:B:249:HIS:NE2	1:B:302:CSD:OD2	2.27	0.65
1:A:301:HIS:HD2	1:A:302:CSD:OD2	1.83	0.61
1:A:354:LEU:HG	3:A:432:HOH:O	2.00	0.61
1:B:267:PRO:HB3	1:B:356:HIS:NE2	2.22	0.55
1:C:249:HIS:NE2	1:C:302:CSD:OD2	2.27	0.53
1:B:267:PRO:CG	1:B:356:HIS:CE1	2.91	0.53
1:B:267:PRO:CB	1:B:356:HIS:NE2	2.73	0.52
1:C:354:LEU:HD23	1:C:356:HIS:HB3	1.92	0.52
1:A:103:LEU:O	1:A:106:ILE:HG22	2.11	0.51
1:B:244:VAL:HG12	1:B:271:LEU:HD11	1.93	0.51
1:C:344:VAL:HG22	3:C:580:HOH:O	2.12	0.49
1:A:301:HIS:CD2	1:A:302:CSD:OD2	2.67	0.46
1:B:267:PRO:HB3	1:B:356:HIS:CD2	2.51	0.45
1:A:106:ILE:HD11	1:A:293:TYR:CE2	2.52	0.45
1:C:178:PHE:CE2	1:C:233:LEU:HD22	2.53	0.44
1:B:93:MET:CE	1:C:8:THR:HG22	2.48	0.44
1:A:250:ASP:OD1	1:A:302:CSD:OD1	2.37	0.43
1:B:93:MET:HE2	1:C:8:THR:HG22	2.01	0.41

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	351/377 (93%)	342 (97%)	9 (3%)	0	100	100
1	B	361/377 (96%)	352 (98%)	9 (2%)	0	100	100
1	C	352/377 (93%)	346 (98%)	6 (2%)	0	100	100
All	All	1064/1131 (94%)	1040 (98%)	24 (2%)	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	272/292 (93%)	272 (100%)	0	100	100
1	B	280/292 (96%)	278 (99%)	2 (1%)	88	84
1	C	273/292 (94%)	272 (100%)	1 (0%)	93	92
All	All	825/876 (94%)	822 (100%)	3 (0%)	93	92

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	109	PHE
1	B	250	ASP
1	C	318	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	301	HIS
1	B	356	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues are modelled in this entry.

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$
1	CSD	A	302	1	2,7,8	1.38	0	2,8,10	3.47	2 (100%)
1	CSD	B	302	1	2,7,8	1.46	0	2,8,10	2.15	2 (100%)
1	CSD	C	302	1	2,7,8	1.35	0	2,8,10	2.65	2 (100%)

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
1	CSD	A	302	1	-	0/2/6/8	0/0/0/0
1	CSD	B	302	1	-	0/2/6/8	0/0/0/0
1	CSD	C	302	1	-	0/2/6/8	0/0/0/0

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	302	CSD	O-C-CA	-2.32	119.51	125.72
1	A	302	CSD	O-C-CA	-2.28	119.61	125.72
1	B	302	CSD	O-C-CA	-2.18	119.87	125.72
1	B	302	CSD	OD1-SG-CB	2.12	108.92	105.43
1	C	302	CSD	OD1-SG-CB	2.94	110.27	105.43
1	A	302	CSD	OD1-SG-CB	4.35	112.59	105.43

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	302	CSD	3	0
1	B	302	CSD	1	0
1	C	302	CSD	1	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

4 ligands are modelled in this entry.

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	$\# Z > 2$
2	GOL	C	401	-	5,5,5	0.31	0	5,5,5	0.33	0
2	GOL	C	402	-	5,5,5	0.37	0	5,5,5	0.45	0
2	GOL	C	403	-	5,5,5	0.43	0	5,5,5	0.19	0
2	GOL	C	404	-	5,5,5	0.25	0	5,5,5	0.55	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
2	GOL	C	401	-	-	0/4/4/4	0/0/0/0
2	GOL	C	402	-	-	0/4/4/4	0/0/0/0
2	GOL	C	403	-	-	0/4/4/4	0/0/0/0
2	GOL	C	404	-	-	0/4/4/4	0/0/0/0

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

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	353/377 (93%)	0.22	23 (6%)	22 19	18, 27, 47, 84	0
1	B	362/377 (96%)	0.27	20 (5%)	29 26	23, 32, 54, 80	0
1	C	353/377 (93%)	0.27	26 (7%)	17 16	22, 32, 49, 70	0
All	All	1068/1131 (94%)	0.25	69 (6%)	22 19	18, 31, 51, 84	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	356	HIS	8.5
1	C	358	HIS	6.8
1	B	354	LEU	6.0
1	A	358	HIS	5.8
1	A	354	LEU	5.1
1	A	357	HIS	4.7
1	B	-6	HIS	4.7
1	B	333	THR	4.0
1	C	234	ASP	4.0
1	A	356	HIS	3.7
1	A	341	GLU	3.7
1	A	216	ALA	3.6
1	C	5	MET	3.6
1	B	5	MET	3.6
1	B	206	GLU	3.5
1	C	213	GLU	3.5
1	A	342	SER	3.4
1	C	354	LEU	3.4
1	B	27	LEU	3.3
1	C	356	HIS	3.3
1	B	210	ALA	3.3
1	A	217	ARG	3.2
1	A	242	ILE	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	4	HIS	3.0
1	B	30	VAL	3.0
1	A	213	GLU	3.0
1	B	65	TRP	3.0
1	C	27	LEU	2.9
1	A	100	PRO	2.9
1	A	221	ALA	2.9
1	C	216	ALA	2.9
1	A	109	PHE	2.7
1	B	213	GLU	2.7
1	B	209	ALA	2.7
1	C	217	ARG	2.7
1	C	310	ASP	2.7
1	C	206	GLU	2.7
1	B	26	ILE	2.6
1	A	148	MET	2.6
1	A	140	LYS	2.6
1	C	244	VAL	2.6
1	A	176	ALA	2.5
1	C	80	GLY	2.5
1	C	219	GLY	2.5
1	C	232	GLU	2.5
1	C	203	PHE	2.5
1	C	65	TRP	2.4
1	B	203	PHE	2.4
1	A	244	VAL	2.4
1	A	27	LEU	2.3
1	A	218	LEU	2.3
1	A	205	ASP	2.3
1	A	26	ILE	2.3
1	C	78	ASP	2.3
1	B	3	SER	2.2
1	C	26	ILE	2.2
1	B	205	ASP	2.2
1	C	25	ALA	2.1
1	C	10	GLU	2.1
1	B	247	ALA	2.1
1	C	79	ALA	2.1
1	C	272	LEU	2.1
1	A	271	LEU	2.1
1	B	2	GLY	2.1
1	C	97	ALA	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	209	ALA	2.1
1	C	122	ARG	2.0
1	A	206	GLU	2.0
1	B	219	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSD	B	302	8/9	0.98	0.07	-	27,30,39,39	0
1	CSD	A	302	8/9	0.96	0.09	-	20,22,32,37	0
1	CSD	C	302	8/9	0.95	0.07	-	26,29,37,37	0

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	GOL	C	402	6/6	0.92	0.14	6.56	31,39,45,50	0
2	GOL	C	403	6/6	0.92	0.11	2.64	32,37,43,48	0
2	GOL	C	404	6/6	0.92	0.12	0.35	46,50,51,56	0
2	GOL	C	401	6/6	0.94	0.09	-0.85	31,34,36,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.