Full wwPDB X-ray Structure Validation Report (i)

Apr 27, 2024 – 10:09 pm BST

PDB ID	:	4UXF
Title	:	Crystal structure of the carboxy-terminal region of the bacteriophage T4 proximal long tail fibre protein gp34, P21 native crystal
Authors	:	Granell, M.; Alvira, S.; Garcia-Doval, C.; Singh, A.K.; van Raaij, M.J.
Deposited on	:	2014-08-22
Resolution	:	2.00 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

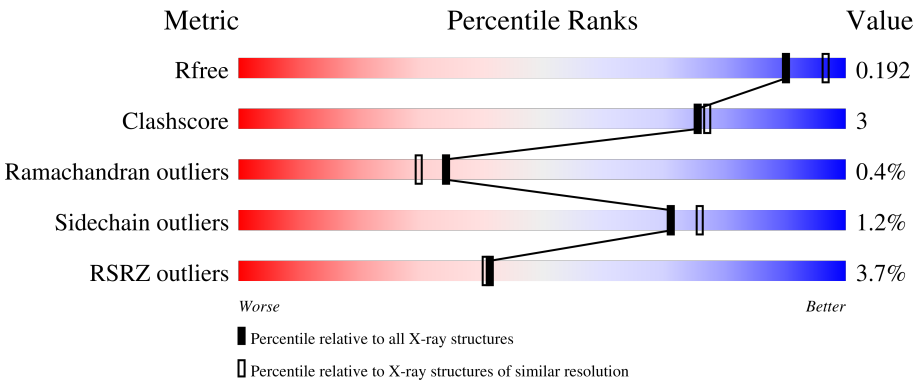
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	410	5% 91% 6% •
1	B	410	2% 90% 6% • •
1	C	410	4% 90% 6% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10873 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 LARGE TAIL FIBER PROTEIN P34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	397	3048	1903	537	602	6	0	2	0
			Total	C	N	O	S			
1	B	397	3059	1912	535	605	7	0	5	0
			Total	C	N	O	S			
1	C	396	3060	1915	537	600	8	0	7	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	880	MET	-	expression tag	UNP P18771
A	881	GLY	-	expression tag	UNP P18771
A	882	SER	-	expression tag	UNP P18771
A	883	SER	-	expression tag	UNP P18771
A	884	HIS	-	expression tag	UNP P18771
A	885	HIS	-	expression tag	UNP P18771
A	886	HIS	-	expression tag	UNP P18771
A	887	HIS	-	expression tag	UNP P18771
A	888	HIS	-	expression tag	UNP P18771
A	889	HIS	-	expression tag	UNP P18771
A	890	SER	-	expression tag	UNP P18771
A	891	GLN	-	expression tag	UNP P18771
A	892	ASP	-	expression tag	UNP P18771
A	893	PRO	-	expression tag	UNP P18771
B	880	MET	-	expression tag	UNP P18771
B	881	GLY	-	expression tag	UNP P18771
B	882	SER	-	expression tag	UNP P18771
B	883	SER	-	expression tag	UNP P18771
B	884	HIS	-	expression tag	UNP P18771
B	885	HIS	-	expression tag	UNP P18771
B	886	HIS	-	expression tag	UNP P18771
B	887	HIS	-	expression tag	UNP P18771
B	888	HIS	-	expression tag	UNP P18771

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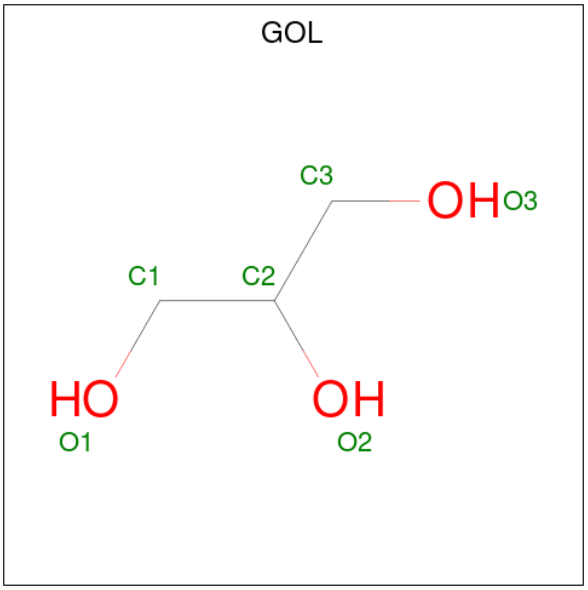
Chain	Residue	Modelled	Actual	Comment	Reference
B	889	HIS	-	expression tag	UNP P18771
B	890	SER	-	expression tag	UNP P18771
B	891	GLN	-	expression tag	UNP P18771
B	892	ASP	-	expression tag	UNP P18771
B	893	PRO	-	expression tag	UNP P18771
C	880	MET	-	expression tag	UNP P18771
C	881	GLY	-	expression tag	UNP P18771
C	882	SER	-	expression tag	UNP P18771
C	883	SER	-	expression tag	UNP P18771
C	884	HIS	-	expression tag	UNP P18771
C	885	HIS	-	expression tag	UNP P18771
C	886	HIS	-	expression tag	UNP P18771
C	887	HIS	-	expression tag	UNP P18771
C	888	HIS	-	expression tag	UNP P18771
C	889	HIS	-	expression tag	UNP P18771
C	890	SER	-	expression tag	UNP P18771
C	891	GLN	-	expression tag	UNP P18771
C	892	ASP	-	expression tag	UNP P18771
C	893	PRO	-	expression tag	UNP P18771

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



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

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

- Molecule 3 is water.

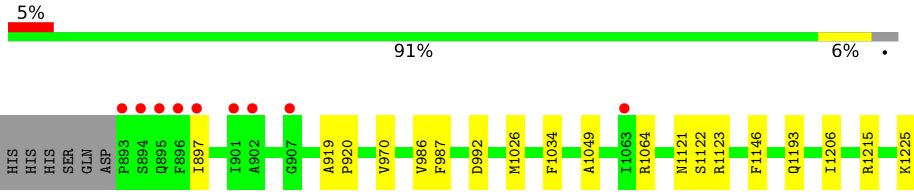
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	697	697	697	0	0
			Total	O		
3	B	578	578	578	0	0
			Total	O		
3	C	389	389	389	0	0

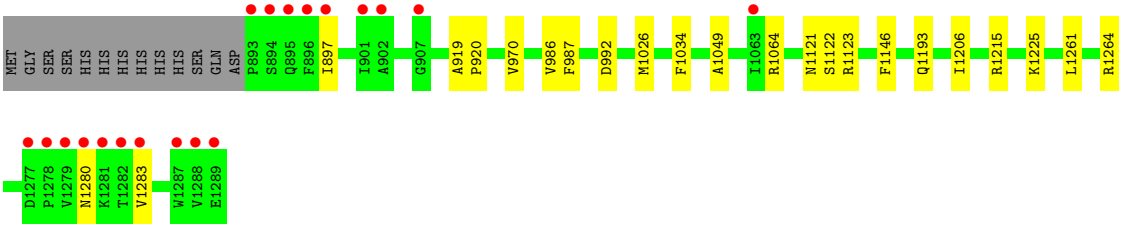
3 Residue-property plots (i)

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: LARGE TAIL FIBER PROTEIN P34

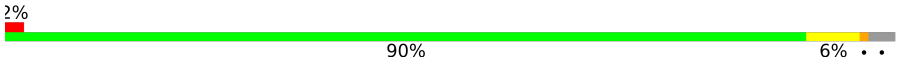
Chain A:

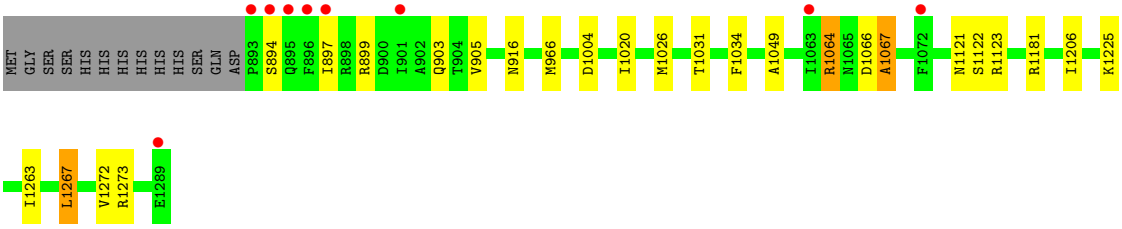




• Molecule 1: LARGE TAIL FIBER PROTEIN P34

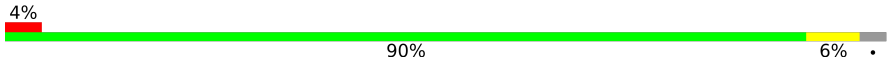
Chain B:

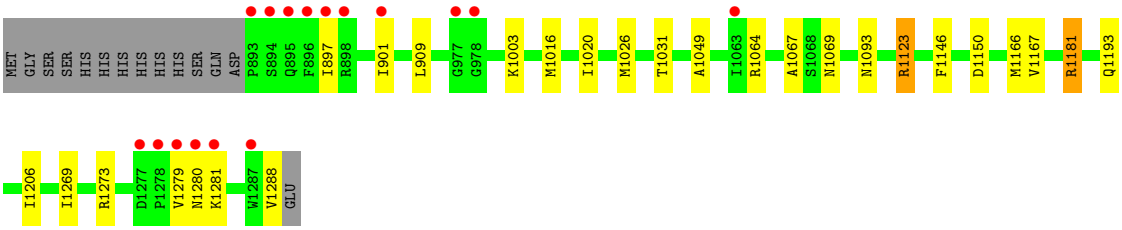




• Molecule 1: LARGE TAIL FIBER PROTEIN P34

Chain C:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	92.97Å 76.05Å 116.83Å 90.00° 99.12° 90.00°	Depositor
Resolution (Å)	115.41 – 2.00 29.56 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (115.41-2.00) 99.9 (29.56-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.90 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.146 , 0.187 0.156 , 0.192	Depositor DCC
R_{free} test set	2207 reflections (2.03%)	wwPDB-VP
Wilson B-factor (Å^2)	15.7	Xtriage
Anisotropy	0.393	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 67.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	10873	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% of the height of the origin peak. No significant pseudotranslation is detected.*

[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)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.66	0/3122	0.79	2/4244 (0.0%)
1	B	0.67	0/3144	0.82	3/4273 (0.1%)
1	C	0.66	0/3151	0.81	4/4285 (0.1%)
All	All	0.66	0/9417	0.81	9/12802 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	1181	ARG	NE-CZ-NH1	6.90	123.75	120.30
1	C	1150	ASP	CB-CG-OD1	6.38	124.04	118.30
1	B	1181	ARG	NE-CZ-NH1	5.90	123.25	120.30
1	A	992	ASP	CB-CG-OD2	5.77	123.50	118.30
1	B	1004	ASP	CB-CG-OD1	5.65	123.38	118.30
1	A	1215	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	C	1181	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	B	1064	ARG	NE-CZ-NH2	-5.17	117.72	120.30
1	C	1123	ARG	NE-CZ-NH1	5.08	122.84	120.30

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	3048	0	2949	25	0
1	B	3059	0	2963	28	0
1	C	3060	0	2977	30	0
2	A	12	0	16	0	0
2	B	12	0	16	0	0
2	C	18	0	24	0	0
3	A	697	0	0	1	0
3	B	578	0	0	4	0
3	C	389	0	0	3	0
All	All	10873	0	8945	57	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 3.

All (57) 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:1026[B]:MET:HE1	1:B:1026[B]:MET:CE	1.78	1.14
1:A:1026[B]:MET:CE	1:B:1026[B]:MET:HE1	1.80	1.11
1:A:1026[B]:MET:CE	1:C:1026[B]:MET:HE1	1.81	1.09
1:A:1026[B]:MET:HE1	1:C:1026[B]:MET:CE	1.85	1.06
1:B:1026[B]:MET:HE1	1:C:1026[B]:MET:HE1	1.03	1.00
1:B:1026[B]:MET:HE1	1:C:1026[B]:MET:CE	1.91	0.99
1:B:1026[B]:MET:CE	1:C:1026[B]:MET:HE1	1.94	0.97
1:A:1026[B]:MET:HE1	1:C:1026[B]:MET:HE1	0.95	0.95
1:A:1264[B]:ARG:HG2	1:A:1264[B]:ARG:HH11	1.31	0.91
1:C:1273[B]:ARG:HH11	1:C:1273[B]:ARG:HG3	1.41	0.83
1:A:1026[B]:MET:HE1	1:B:1026[B]:MET:HE1	0.88	0.82
1:A:1264[B]:ARG:HH11	1:A:1264[B]:ARG:CG	1.93	0.81
1:B:897:ILE:HD11	1:C:909:LEU:HD22	1.66	0.76
1:C:1273[B]:ARG:HH11	1:C:1273[B]:ARG:CG	1.99	0.75
1:A:1026[B]:MET:CE	1:C:1026[B]:MET:CE	2.55	0.74
3:B:2132:HOH:O	1:C:1016[B]:MET:HE1	1.88	0.72
3:A:2218:HOH:O	1:C:1031[A]:THR:HG22	1.92	0.70
1:B:1020:ILE:HB	1:C:1026[A]:MET:HG3	1.75	0.69
1:C:1273[B]:ARG:CG	1:C:1273[B]:ARG:NH1	2.57	0.67
1:A:1026[B]:MET:CE	1:B:1026[B]:MET:CE	2.54	0.63
1:B:897:ILE:HD12	1:B:905:VAL:HG22	1.83	0.61
1:A:1264[B]:ARG:CG	1:A:1264[B]:ARG:NH1	2.62	0.60
1:B:1031[B]:THR:HG22	3:B:2164:HOH:O	2.02	0.59
1:A:1026[A]:MET:HG3	1:C:1020:ILE:HB	1.88	0.56
1:A:1026[A]:MET:HE1	1:B:1034:PHE:CZ	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1283:VAL:HG13	1:B:1272:VAL:HG21	1.88	0.55
1:C:1166[B]:MET:HE3	3:C:2243:HOH:O	2.07	0.54
1:A:1206:ILE:HD12	1:A:1206:ILE:N	2.26	0.51
1:B:1273:ARG:NH1	3:B:2539:HOH:O	2.44	0.51
1:B:1026[B]:MET:CE	1:C:1026[B]:MET:CE	2.71	0.48
1:A:897:ILE:HD12	1:C:897:ILE:CG2	2.45	0.46
1:B:1206:ILE:HD12	1:B:1206:ILE:N	2.30	0.46
1:B:1066:ASP:O	1:B:1067:ALA:HB3	2.15	0.46
1:B:897:ILE:HG12	1:C:897:ILE:HD13	1.99	0.45
1:C:1167[B]:VAL:HG12	3:C:2266:HOH:O	2.17	0.44
1:A:1146:PHE:HA	1:A:1193:GLN:O	2.17	0.44
1:A:919:ALA:HB1	1:A:920:PRO:HD2	1.99	0.44
1:C:1206:ILE:N	1:C:1206:ILE:HD12	2.33	0.44
1:B:916:ASN:ND2	3:B:2031:HOH:O	2.47	0.43
1:B:897:ILE:HG23	1:C:897:ILE:HD13	2.00	0.43
1:B:1121:ASN:HA	1:B:1122:SER:HA	1.85	0.43
1:B:1263:ILE:HB	1:C:1269:ILE:HD13	2.00	0.43
1:C:1273[A]:ARG:NH1	3:C:2361:HOH:O	2.51	0.42
1:A:987:PHE:HB2	1:B:966:MET:SD	2.60	0.42
1:B:897:ILE:HD12	1:B:905:VAL:CG2	2.47	0.42
1:A:1034:PHE:CZ	1:C:1026[A]:MET:HE1	2.54	0.42
1:C:1166[B]:MET:HE2	1:C:1181:ARG:HA	2.02	0.42
1:A:970:VAL:HA	1:A:986:VAL:O	2.19	0.42
1:A:1121:ASN:HA	1:A:1122:SER:HA	1.86	0.42
1:A:1283:VAL:HG13	1:B:1272:VAL:CG2	2.48	0.41
1:B:899:ARG:HG2	1:C:897:ILE:HG13	2.01	0.41
1:C:1049:ALA:O	1:C:1064:ARG:HA	2.20	0.41
1:C:1069:ASN:OD1	1:C:1093:ASN:HA	2.20	0.41
1:B:1049:ALA:O	1:B:1064:ARG:HA	2.21	0.41
1:C:1146:PHE:HA	1:C:1193:GLN:O	2.21	0.41
1:A:1049:ALA:O	1:A:1064:ARG:HA	2.22	0.40
1:A:1261:LEU:HB3	1:B:1267:LEU:HD12	2.03	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	397/410 (97%)	385 (97%)	12 (3%)	0	100	100
1	B	400/410 (98%)	387 (97%)	11 (3%)	2 (0%)	29	23
1	C	401/410 (98%)	384 (96%)	14 (4%)	3 (1%)	22	16
All	All	1198/1230 (97%)	1156 (96%)	37 (3%)	5 (0%)	34	30

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	894	SER
1	C	1280	ASN
1	B	1067	ALA
1	C	1067	ALA
1	C	1279	VAL

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	333/343 (97%)	330 (99%)	3 (1%)	78	83
1	B	336/343 (98%)	332 (99%)	4 (1%)	71	76
1	C	337/343 (98%)	332 (98%)	5 (2%)	65	69
All	All	1006/1029 (98%)	994 (99%)	12 (1%)	71	76

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1123	ARG
1	A	1225	LYS
1	A	1280	ASN
1	B	903	GLN

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Mol	Chain	Res	Type
1	B	1123	ARG
1	B	1225	LYS
1	B	1267	LEU
1	C	901	ILE
1	C	1003	LYS
1	C	1123	ARG
1	C	1281	LYS
1	C	1288	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	914	GLN
1	B	916	ASN
1	B	1010	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

7 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	A	1390	-	5,5,5	0.41	0	5,5,5	0.18	0
2	GOL	C	1390	-	5,5,5	0.26	0	5,5,5	0.56	0
2	GOL	C	1391	-	5,5,5	0.27	0	5,5,5	0.45	0
2	GOL	B	1390	-	5,5,5	0.16	0	5,5,5	0.41	0
2	GOL	C	1389	-	5,5,5	0.34	0	5,5,5	0.40	0
2	GOL	A	1391	-	5,5,5	0.51	0	5,5,5	0.50	0
2	GOL	B	1391	-	5,5,5	0.37	0	5,5,5	0.24	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	A	1390	-	-	0/4/4/4	-
2	GOL	C	1390	-	-	2/4/4/4	-
2	GOL	C	1391	-	-	0/4/4/4	-
2	GOL	B	1390	-	-	0/4/4/4	-
2	GOL	C	1389	-	-	0/4/4/4	-
2	GOL	A	1391	-	-	0/4/4/4	-
2	GOL	B	1391	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1390	GOL	O1-C1-C2-C3
2	C	1390	GOL	O1-C1-C2-O2

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 (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	397/410 (96%)	-0.33	19 (4%)	30	29	10, 19, 63, 98	0
1	B	397/410 (96%)	-0.39	9 (2%)	60	59	11, 19, 52, 99	0
1	C	396/410 (96%)	-0.32	16 (4%)	38	37	11, 19, 61, 113	0
All	All	1190/1230 (96%)	-0.35	44 (3%)	41	41	10, 19, 59, 113	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1279	VAL	6.9
1	C	896	PHE	6.6
1	A	1279	VAL	6.4
1	C	1280	ASN	5.7
1	A	893	PRO	5.7
1	B	896	PHE	5.5
1	B	893	PRO	5.4
1	C	894	SER	5.1
1	A	896	PHE	5.1
1	C	893	PRO	4.9
1	C	1278	PRO	4.9
1	A	1289	GLU	4.2
1	A	1278	PRO	4.0
1	C	1281	LYS	3.8
1	A	895	GLN	3.8
1	C	895	GLN	3.7
1	B	894	SER	3.7
1	A	1281	LYS	3.4
1	A	894	SER	3.3
1	C	1277	ASP	3.1
1	B	1063	ILE	3.1
1	A	1288	VAL	3.1
1	B	897	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	1280	ASN	3.1
1	A	1287	TRP	2.9
1	A	1277	ASP	2.8
1	C	901	ILE	2.8
1	B	901	ILE	2.8
1	C	1287	TRP	2.5
1	A	1063	ILE	2.5
1	A	907	GLY	2.4
1	B	1289	GLU	2.4
1	B	895	GLN	2.3
1	C	978	GLY	2.3
1	A	902	ALA	2.3
1	A	901	ILE	2.3
1	C	977	GLY	2.3
1	C	898	ARG	2.3
1	C	897	ILE	2.2
1	B	1072	PHE	2.1
1	A	1283	VAL	2.1
1	C	1063	ILE	2.1
1	A	1282	THR	2.1
1	A	897	ILE	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
2	GOL	B	1391	6/6	0.92	0.12	28,33,37,40	0
2	GOL	A	1390	6/6	0.94	0.11	23,26,27,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GOL	C	1391	6/6	0.94	0.14	23,29,34,36	0
2	GOL	C	1389	6/6	0.95	0.14	23,27,28,29	0
2	GOL	A	1391	6/6	0.96	0.15	24,30,33,35	0
2	GOL	C	1390	6/6	0.97	0.15	23,24,26,26	0
2	GOL	B	1390	6/6	0.97	0.09	20,23,26,27	0

6.5 Other polymers (i)

There are no such residues in this entry.