Full wwPDB X-ray Structure Validation Report (i)

Nov 20, 2023 – 12:14 AM JST

PDB ID	:	7CAZ
Title	:	Crystal structure of bacterial reductase
Authors	:	Kim, Y.; Lee, W.C.
Deposited on	:	2020-06-10
Resolution	:	1.79 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:

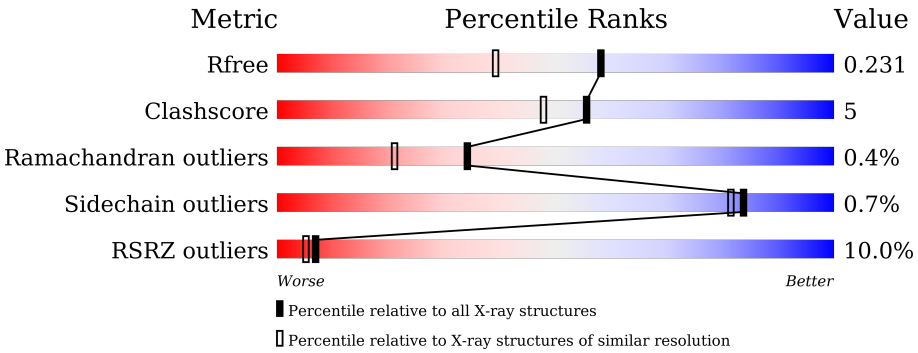
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.79 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	244	7% 86% 11%
1	B	244	9% 87% 10%
1	C	244	12% 90% 8%
1	D	244	11% 88% 9%

2 Entry composition

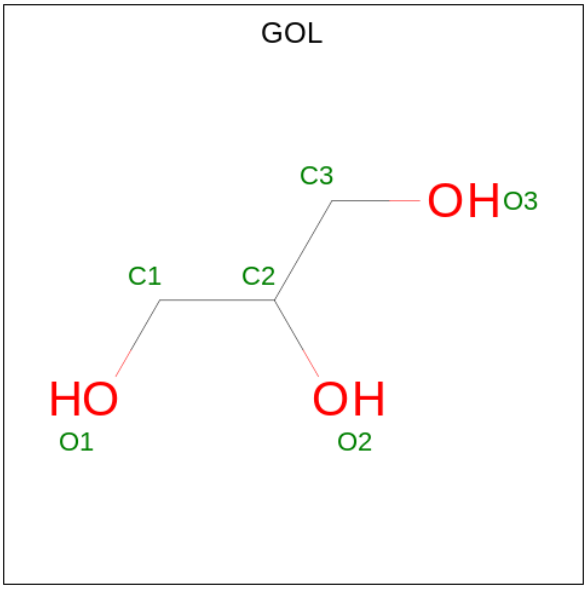
There are 3 unique types of molecules in this entry. The entry contains 7766 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 3-oxoacyl-[acyl-carrier-protein] reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	0	0	0
			1800	1125	320	349	6			
1	B	240	Total	C	N	O	S	0	1	0
			1806	1129	320	351	6			
1	C	242	Total	C	N	O	S	0	1	0
			1824	1139	323	356	6			
1	D	240	Total	C	N	O	S	0	1	0
			1803	1127	320	350	6			

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



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

- Molecule 3 is water.

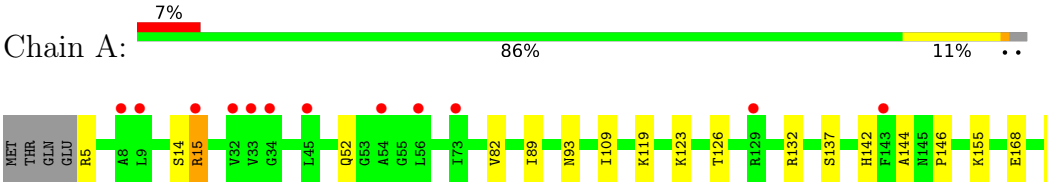
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	134	Total O 134 134	0	0
3	B	138	Total O 138 138	0	0
3	C	121	Total O 121 121	0	0
3	D	134	Total O 134 134	0	0

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.

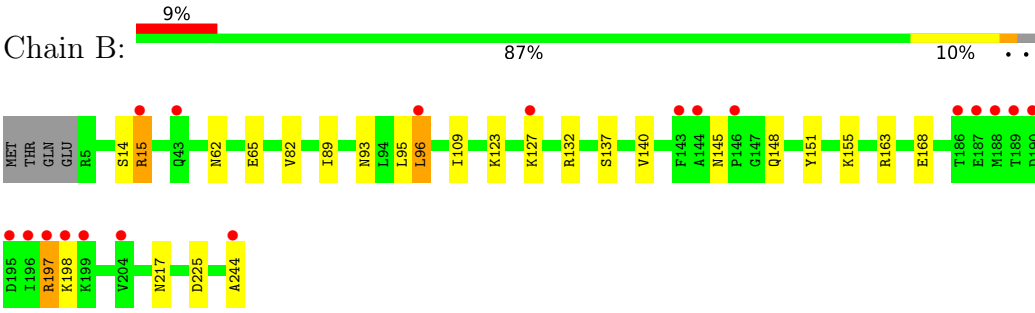
• Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase

Chain A:



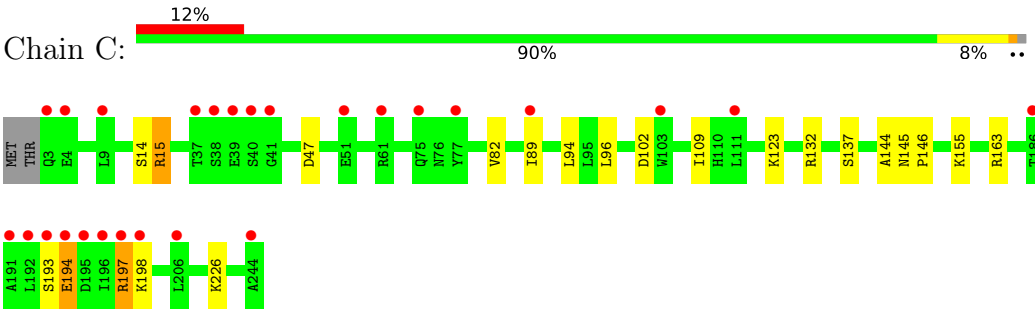
• Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase

Chain B:



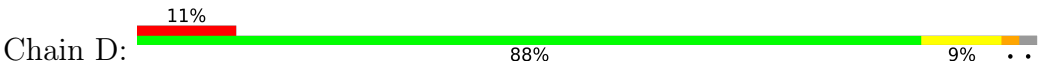
• Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase

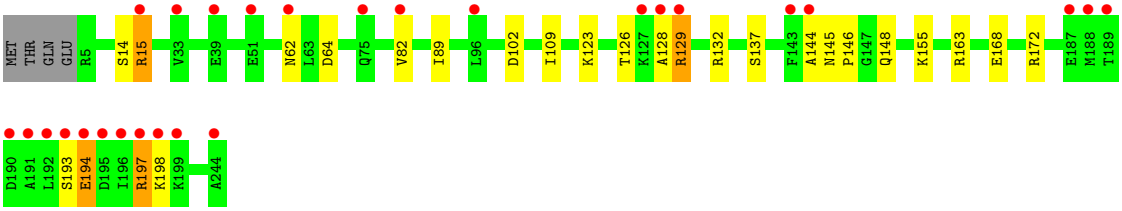
Chain C:



• Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase

Chain D:




MET
THR
GLN
GLU
R5
S14
R15
V38
E39
E51
N62
L63
D64
Q75
V82
I89
L96
D102
I109
K123
T126
K127
A128
R129
R132
S137
F143
A144
N145
P146
G147
Q148
K155
R163
E168
R172
E187
M188
T189
D190
A191
L192
S193
E194
D195
I196
R197
K198
K199
A244

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	78.61Å 100.04Å 120.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.91 – 1.79 19.91 – 1.79	Depositor EDS
% Data completeness (in resolution range)	96.9 (19.91-1.79) 88.5 (19.91-1.79)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.11 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.207 , 0.229 0.207 , 0.231	Depositor DCC
R_{free} test set	1928 reflections (2.26%)	wwPDB-VP
Wilson B-factor (Å^2)	19.8	Xtriage
Anisotropy	0.499	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 45.7	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	0.94	EDS
Total number of atoms	7766	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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

5.1 Standard geometry

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	0.47	0/1822	0.68	3/2460 (0.1%)
1	B	0.48	0/1831	0.71	5/2472 (0.2%)
1	C	0.48	0/1849	0.69	3/2496 (0.1%)
1	D	0.48	0/1828	0.68	3/2468 (0.1%)
All	All	0.48	0/7330	0.69	14/9896 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	15	ARG	NE-CZ-NH1	-8.11	116.24	120.30
1	C	15	ARG	NE-CZ-NH1	-8.09	116.25	120.30
1	A	15	ARG	NE-CZ-NH1	-8.06	116.27	120.30
1	D	15	ARG	NE-CZ-NH1	-8.01	116.30	120.30
1	C	198	LYS	CD-CE-NZ	7.90	129.88	111.70
1	B	198	LYS	CD-CE-NZ	7.90	129.87	111.70
1	D	198	LYS	CD-CE-NZ	7.88	129.84	111.70
1	A	198	LYS	CD-CE-NZ	7.87	129.79	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	96	LEU	CA-CB-CG	7.42	132.38	115.30
1	A	197	ARG	CG-CD-NE	7.41	127.35	111.80
1	B	197	ARG	CG-CD-NE	7.41	127.35	111.80
1	D	197	ARG	CG-CD-NE	7.40	127.34	111.80
1	C	197	ARG	CG-CD-NE	7.39	127.32	111.80
1	B	95	LEU	C-N-CA	-5.88	106.99	121.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	193	SER	Peptide
1	B	193	SER	Peptide
1	C	193	SER	Peptide
1	D	193	SER	Peptide

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	1800	0	1820	25	1
1	B	1806	0	1826	22	0
1	C	1824	0	1840	17	0
1	D	1803	0	1825	19	1
2	A	6	0	8	1	0
3	A	134	0	0	8	0
3	B	138	0	0	8	0
3	C	121	0	0	4	0
3	D	134	0	0	4	0
All	All	7766	0	7319	74	1

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 5.

All (74) 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:244:ALA:OXT	3:B:301:HOH:O	1.84	0.95
1:D:64:ASP:OD2	3:D:301:HOH:O	2.02	0.77
1:C:102:ASP:OD1	3:C:301:HOH:O	2.05	0.73
1:D:102:ASP:OD1	3:D:302:HOH:O	2.05	0.73
1:B:151:TYR:OH	3:B:302:HOH:O	2.09	0.69
1:D:64:ASP:OD2	3:D:304:HOH:O	2.11	0.69
1:D:126:THR:O	3:D:303:HOH:O	2.10	0.68
1:B:225:ASP:O	3:B:303:HOH:O	2.12	0.67
1:C:123:LYS:NZ	3:C:304:HOH:O	2.26	0.67
1:D:145:ASN:OD1	1:D:148:GLN:OE1	2.13	0.66
1:A:183:PHE:HA	2:A:301:GOL:H12	1.78	0.66
1:B:148:GLN:OE1	3:B:304:HOH:O	2.13	0.65
1:A:173:GLN:OE1	3:A:401:HOH:O	2.15	0.65
1:B:140:VAL:HG22	3:B:304:HOH:O	1.95	0.64
1:C:145:ASN:HB2	1:C:146:PRO:HD2	1.81	0.61
1:D:14:SER:C	1:D:15:ARG:HG3	2.21	0.61
1:A:14:SER:C	1:A:15:ARG:HG3	2.21	0.60
1:B:14:SER:C	1:B:15:ARG:HG3	2.21	0.59
1:A:225:ASP:O	3:A:402:HOH:O	2.16	0.59
1:C:47:ASP:OD2	3:C:302:HOH:O	2.17	0.59
1:C:14:SER:C	1:C:15:ARG:HG3	2.21	0.58
1:B:127:LYS:HG2	3:B:427:HOH:O	2.04	0.57
1:A:93:ASN:HB2	3:A:406:HOH:O	2.05	0.57
1:A:144:ALA:HB2	1:B:163:ARG:HB3	1.86	0.57
1:A:5:ARG:NH1	1:A:52:GLN:HG2	2.21	0.56
1:A:202:ASP:OD1	3:A:403:HOH:O	2.18	0.56
1:B:93:ASN:HB2	3:B:310:HOH:O	2.07	0.54
1:D:126:THR:HG23	1:D:172:ARG:HD2	1.90	0.52
1:D:145:ASN:HB2	1:D:146:PRO:HD2	1.91	0.52
1:C:194:GLU:HA	1:C:197:ARG:NH1	2.25	0.51
1:D:194:GLU:HA	1:D:197:ARG:NH1	2.25	0.51
1:A:194:GLU:HA	1:A:197:ARG:NH1	2.25	0.51
1:A:146:PRO:CB	1:B:168[A]:GLU:HG2	2.40	0.51
1:C:145:ASN:N	1:C:145:ASN:OD1	2.44	0.51
1:B:194:GLU:HA	1:B:197:ARG:NH1	2.25	0.50
1:A:142:HIS:ND1	3:A:409:HOH:O	2.34	0.50
1:A:173:GLN:O	3:A:404:HOH:O	2.19	0.50
1:C:144:ALA:HB2	1:D:163:ARG:HB3	1.93	0.49
1:A:146:PRO:HB3	1:B:168[A]:GLU:HG2	1.94	0.49
1:C:163:ARG:HB3	1:D:144:ALA:HB2	1.95	0.49
1:B:145:ASN:HB2	3:B:304:HOH:O	2.13	0.48
1:D:145:ASN:OD1	1:D:145:ASN:N	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:ASP:OD1	3:C:303:HOH:O	2.19	0.48
1:B:62:ASN:OD1	1:B:65:GLU:HG3	2.14	0.47
1:B:217:ASN:CG	1:C:226:LYS:HD3	2.35	0.46
1:A:126:THR:HG23	1:A:172:ARG:HD2	1.98	0.45
1:D:14:SER:C	1:D:15:ARG:CG	2.86	0.45
1:A:5:ARG:HH12	1:A:52:GLN:HG2	1.83	0.44
1:A:119:LYS:HG3	1:B:96:LEU:HD23	2.00	0.44
1:A:144:ALA:HA	3:A:460:HOH:O	2.17	0.44
1:C:194:GLU:HA	1:C:197:ARG:HH12	1.83	0.44
1:A:194:GLU:HA	1:A:197:ARG:HH12	1.83	0.44
1:B:194:GLU:HA	1:B:197:ARG:HH12	1.83	0.44
1:D:128:ALA:O	1:D:129:ARG:HB2	2.18	0.44
1:B:89:ILE:HG21	1:B:109:ILE:HD13	2.01	0.43
1:B:14:SER:C	1:B:15:ARG:CG	2.86	0.43
1:C:94:LEU:HD22	1:D:168:GLU:HG2	1.99	0.43
1:D:194:GLU:HA	1:D:197:ARG:HH12	1.83	0.43
1:C:14:SER:C	1:C:15:ARG:CG	2.86	0.42
1:A:168:GLU:OE2	3:A:405:HOH:O	2.20	0.42
1:C:89:ILE:HG21	1:C:109:ILE:HD13	2.01	0.42
1:B:137:SER:HA	1:B:155:LYS:HD2	2.02	0.42
1:C:137:SER:HA	1:C:155:LYS:HD2	2.02	0.42
1:A:89:ILE:HG21	1:A:109:ILE:HD13	2.01	0.42
1:D:89:ILE:HG21	1:D:109:ILE:HD13	2.01	0.41
1:A:186:THR:OG1	1:A:188:MET:HB3	2.20	0.41
1:C:82:VAL:HG22	1:C:132:ARG:HB2	2.03	0.41
1:A:14:SER:C	1:A:15:ARG:CG	2.86	0.41
1:B:82:VAL:HG22	1:B:132:ARG:HB2	2.03	0.41
1:A:119:LYS:CG	1:B:96:LEU:HD23	2.51	0.41
1:D:82:VAL:HG22	1:D:132:ARG:HB2	2.03	0.41
1:A:137:SER:HA	1:A:155:LYS:HD2	2.02	0.40
1:D:137:SER:HA	1:D:155:LYS:HD2	2.02	0.40
1:A:82:VAL:HG22	1:A:132:ARG:HB2	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:ARG:NH1	1:D:62:ASN:ND2[2_555]	1.80	0.40

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	238/244 (98%)	231 (97%)	6 (2%)	1 (0%)	34	21
1	B	239/244 (98%)	231 (97%)	7 (3%)	1 (0%)	34	21
1	C	241/244 (99%)	233 (97%)	7 (3%)	1 (0%)	34	21
1	D	239/244 (98%)	232 (97%)	6 (2%)	1 (0%)	34	21
All	All	957/976 (98%)	927 (97%)	26 (3%)	4 (0%)	34	21

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	194	GLU
1	B	194	GLU
1	C	194	GLU
1	D	194	GLU

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	188/192 (98%)	187 (100%)	1 (0%)	88	87
1	B	189/192 (98%)	188 (100%)	1 (0%)	88	87
1	C	191/192 (100%)	190 (100%)	1 (0%)	88	87
1	D	189/192 (98%)	187 (99%)	2 (1%)	73	68
All	All	757/768 (99%)	752 (99%)	5 (1%)	84	81

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	123	LYS
1	B	123	LYS
1	C	96	LEU
1	D	123	LYS
1	D	129	ARG

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

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)

1 ligand is 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	301	-	5,5,5	1.19	0	5,5,5	0.90	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	301	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	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, 95^{th} 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	240/244 (98%)	0.61	16 (6%) 17 14	16, 23, 58, 94	0
1	B	240/244 (98%)	0.81	23 (9%) 8 6	16, 23, 58, 94	0
1	C	242/244 (99%)	0.83	30 (12%) 4 3	16, 23, 64, 94	0
1	D	240/244 (98%)	0.69	27 (11%) 5 3	16, 23, 61, 94	0
All	All	962/976 (98%)	0.74	96 (9%) 7 5	16, 23, 61, 94	0

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	191	ALA	15.3
1	C	196	ILE	10.9
1	C	191	ALA	9.7
1	B	188	MET	8.7
1	B	192	LEU	8.5
1	B	193	SER	8.5
1	B	196	ILE	8.2
1	C	188	MET	8.1
1	C	193	SER	7.1
1	B	187	GLU	6.2
1	B	194	GLU	5.9
1	D	195	ASP	5.8
1	D	191	ALA	5.6
1	D	187	GLU	5.6
1	D	192	LEU	5.3
1	B	190	ASP	5.3
1	C	192	LEU	5.3
1	C	4	GLU	5.1
1	D	196	ILE	5.1
1	D	193	SER	5.0
1	B	198	LYS	4.9

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Mol	Chain	Res	Type	RSRZ
1	C	195	ASP	4.9
1	C	186	THR	4.9
1	B	195	ASP	4.8
1	C	194	GLU	4.8
1	D	188	MET	4.7
1	C	187	GLU	4.6
1	C	3	GLN	4.3
1	C	189	THR	4.2
1	B	96	LEU	4.0
1	A	33	VAL	4.0
1	A	194	GLU	3.8
1	C	197	ARG	3.7
1	D	129	ARG	3.3
1	B	186	THR	3.3
1	D	190	ASP	3.3
1	B	197	ARG	3.3
1	D	198	LYS	3.2
1	A	32	VAL	3.2
1	B	189	THR	3.1
1	D	62	ASN	3.1
1	A	56	LEU	3.1
1	C	190	ASP	3.1
1	B	15	ARG	3.0
1	D	144	ALA	2.9
1	C	61	ARG	2.9
1	C	39	GLU	2.9
1	C	51	GLU	2.9
1	D	194	GLU	2.9
1	A	45	LEU	2.9
1	D	51	GLU	2.8
1	A	54	ALA	2.8
1	C	198	LYS	2.8
1	D	96	LEU	2.8
1	A	143	PHE	2.8
1	A	129	ARG	2.7
1	A	191	ALA	2.7
1	D	143	PHE	2.7
1	B	143	PHE	2.7
1	A	188	MET	2.6
1	C	40	SER	2.6
1	C	37	THR	2.6
1	B	144	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	39	GLU	2.5
1	C	9	LEU	2.5
1	C	89	ILE	2.5
1	D	199	LYS	2.5
1	D	128	ALA	2.4
1	D	189	THR	2.4
1	D	15	ARG	2.3
1	D	127	LYS	2.3
1	A	73	ILE	2.3
1	A	15	ARG	2.3
1	C	244	ALA	2.3
1	D	244	ALA	2.2
1	C	206	LEU	2.2
1	A	196	ILE	2.2
1	B	146	PRO	2.2
1	C	75	GLN	2.2
1	D	75	GLN	2.2
1	D	82	VAL	2.1
1	B	127	LYS	2.1
1	B	199	LYS	2.1
1	A	34	GLY	2.1
1	D	197	ARG	2.1
1	C	38	SER	2.1
1	B	244	ALA	2.1
1	C	77	TYR	2.1
1	D	33	VAL	2.1
1	A	8	ALA	2.1
1	C	111	LEU	2.1
1	A	9	LEU	2.1
1	C	41	GLY	2.0
1	B	204	VAL	2.0
1	B	43	GLN	2.0
1	C	103	TRP	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

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, 95^{th} 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	A	301	6/6	0.80	0.17	41,49,74,81	0

6.5 Other polymers

There are no such residues in this entry.