WORLDWIDE PDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:49 PM GMT

PDB ID	:	4AMK
Title	:	Fab fragment of antiporphrin antibody 13g10
Authors	:	Mahy, J.P.; Golinelli-Pimpaneau, B.
Deposited on	:	2012-03-12
Resolution	:	2.05 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
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)	:	trunk26865

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 2.05 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		0.273
Clashscore		23
Ramachandran outliers		1.4%
Sidechain outliers		4.5%
RSRZ outliers		19.0%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
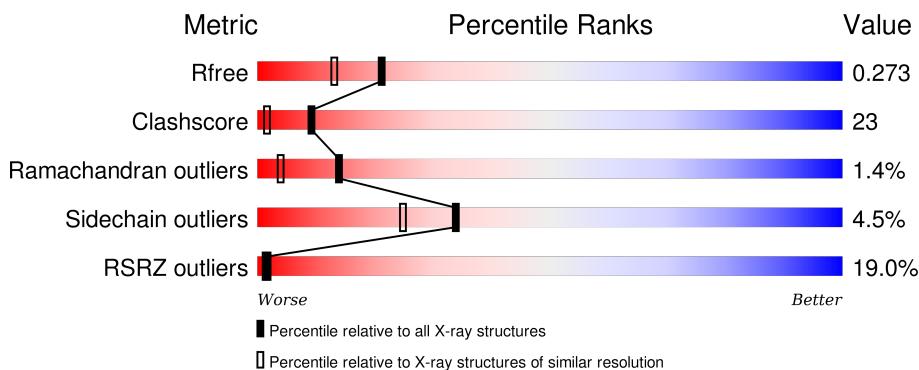
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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 <=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	H	217	21% — 64% / 30% / 5% ·
2	L	212	17% — 65% / 33% ·
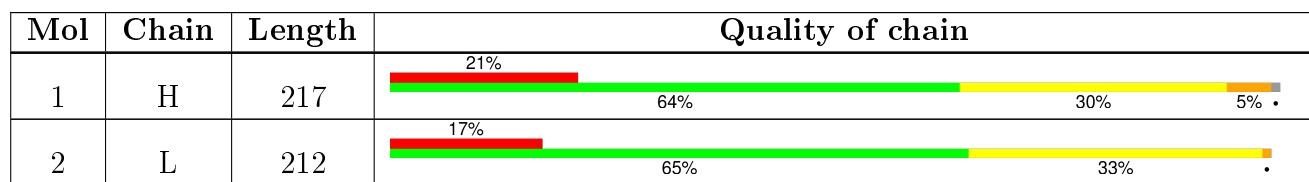
The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	H	1219	-	X	-	-
3	GOL	L	1212	-	X	-	X
3	GOL	L	1213	-	X	-	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3424 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 FAB13G10, HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	215	Total	C	N	O	S	0	3	0
			1613	1017	265	321	10			

- Molecule 2 is a protein called FAB13G10, LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	211	Total	C	N	O	S	0	3	1
			1604	1002	272	324	6			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).
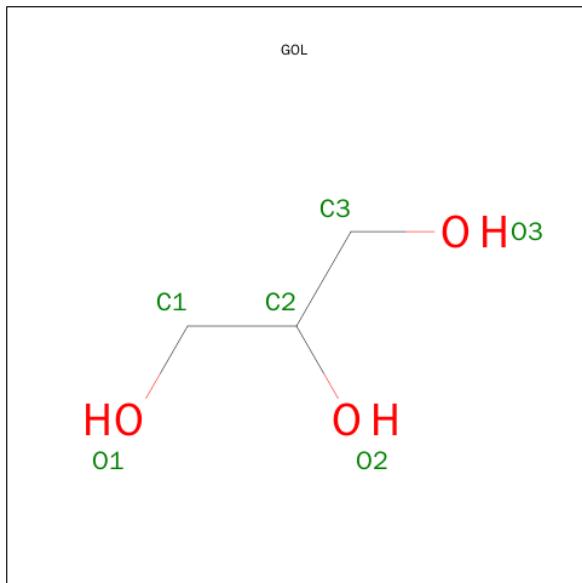
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	C	O	0	0
			6	3	3		
3	L	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	1	Total 1	Mg 1	0	0

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	91	Total 91	O 91	0	0
5	L	97	Total 97	O 97	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: FAB13G10, HEAVY CHAIN
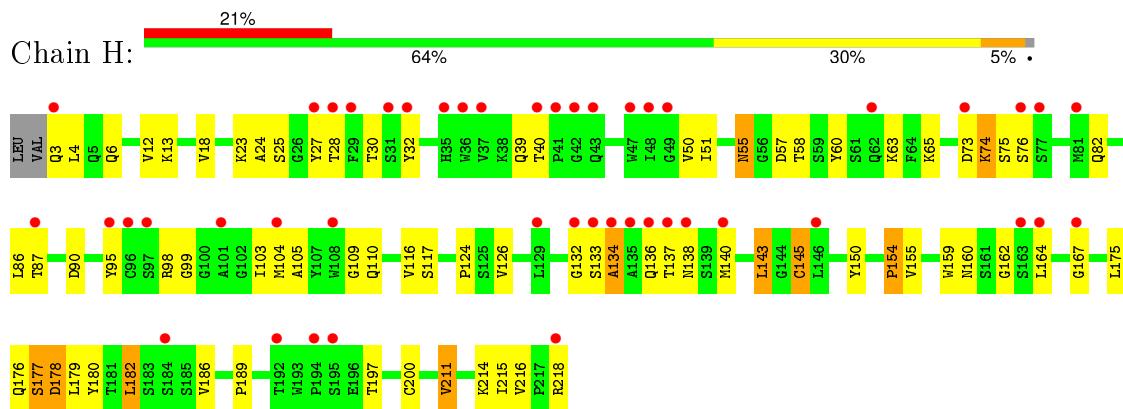
- Molecule 2: FAB13G10, LIGHT CHAIN
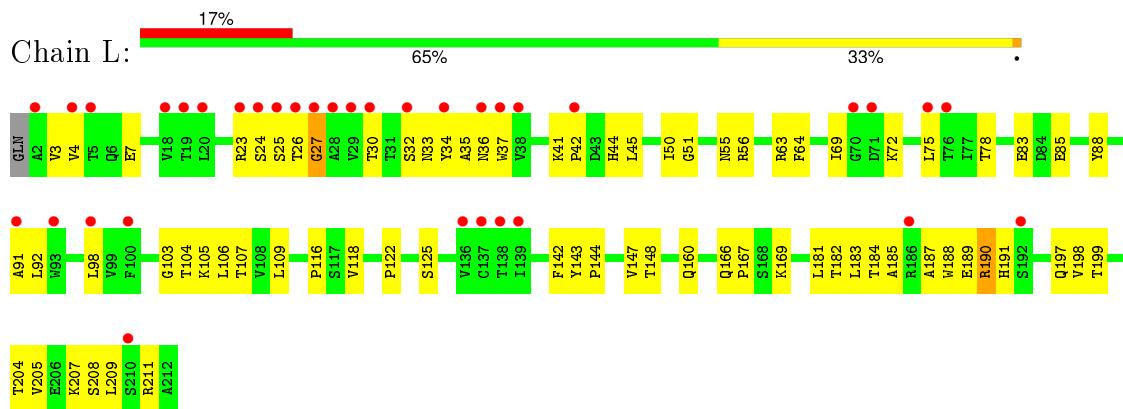
4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	55.80Å 62.75Å 113.50Å 90.00° 91.65° 90.00°	Depositor
Resolution (Å)	20.00 – 2.05 24.75 – 2.01	Depositor EDS
% Data completeness (in resolution range)	93.9 (20.00-2.05) 93.0 (24.75-2.01)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.39 (at 2.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.224 , 0.275 0.225 , 0.273	Depositor DCC
R_{free} test set	1116 reflections (5.05%)	DCC
Wilson B-factor (Å^2)	41.1	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 63.2	EDS
Estimated twinning fraction	0.034 for -h,-k,l	Xtriage
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Outliers	0 of 24276 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3424	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.83% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, 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	H	0.39	0/1655	0.71	1/2259 (0.0%)
2	L	0.44	0/1640	0.71	0/2241
All	All	0.41	0/3295	0.71	1/4500 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	145	CYS	CA-CB-SG	5.75	124.35	114.00

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	H	1613	0	1574	88	0
2	L	1604	0	1549	73	0
3	H	6	0	4	0	0
3	L	12	0	8	0	0
4	L	1	0	0	0	0
5	H	91	0	0	7	0
5	L	97	0	0	10	0
All	All	3424	0	3135	146	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 23.

All (146) 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:H:3:GLN:O	1:H:24:ALA:HA	1.47	1.12
1:H:12:VAL:HG11	1:H:86:LEU:HD12	1.43	0.98
1:H:74:LYS:H	1:H:74:LYS:HD3	1.30	0.96
1:H:3:GLN:HA	1:H:25:SER:H	1.34	0.90
1:H:3:GLN:O	1:H:4:LEU:HD23	1.70	0.90
1:H:134:ALA:HB3	2:L:209:LEU:HA	1.65	0.77
1:H:110[B]:GLN:HG3	5:H:2044:HOH:O	1.85	0.77
1:H:160:ASN:HD22	1:H:164:LEU:HD13	1.51	0.76
1:H:3:GLN:HA	1:H:25:SER:N	2.01	0.75
1:H:13:LYS:HD3	1:H:13:LYS:H	1.51	0.75
1:H:40:THR:HG22	5:H:2014:HOH:O	1.88	0.74
1:H:124:PRO:HB3	1:H:150:TYR:HB3	1.69	0.72
1:H:103:ILE:HG12	2:L:51:GLY:HA3	1.72	0.69
1:H:104[A]:MET:H	2:L:36:ASN:HD21	1.39	0.69
1:H:13:LYS:HD3	1:H:13:LYS:N	2.08	0.68
1:H:132:GLY:HA3	1:H:218:ARG:HD3	1.75	0.68
1:H:58:THR:HG21	1:H:60:TYR:CZ	2.29	0.68
1:H:104[B]:MET:H	2:L:36:ASN:HD21	1.39	0.67
2:L:4:VAL:HG22	2:L:92:LEU:HD12	1.76	0.67
1:H:110[B]:GLN:NE2	5:H:2002:HOH:O	2.27	0.66
2:L:56:ARG:HG3	2:L:56:ARG:HH11	1.61	0.66
1:H:160:ASN:HD22	1:H:164:LEU:CD1	2.09	0.65
1:H:103:ILE:HD11	2:L:55:ASN:CB	2.27	0.64
2:L:197:GLN:HE21	2:L:204:THR:HG21	1.63	0.64
1:H:176:GLN:O	1:H:177:SER:HB2	1.97	0.64
2:L:187:ALA:HA	2:L:190:ARG:NH1	2.14	0.63
1:H:65:LYS:NZ	5:H:2029:HOH:O	2.26	0.62
1:H:13:LYS:CD	1:H:13:LYS:H	2.11	0.62
2:L:27:GLY:HA2	5:L:2014:HOH:O	1.99	0.61
2:L:116:PRO:HB3	2:L:142:PHE:HB3	1.83	0.61
1:H:197:THR:HG23	1:H:214:LYS:HE2	1.84	0.60
1:H:3:GLN:HG2	1:H:4:LEU:N	2.15	0.60
1:H:103:ILE:HD11	2:L:55:ASN:HB3	1.83	0.60
1:H:73:ASP:OD1	1:H:75:SER:HB3	2.01	0.60
1:H:87:THR:HG22	1:H:90:ASP:OD2	2.03	0.59
2:L:45:LEU:HD12	2:L:45:LEU:O	2.02	0.58
1:H:95:TYR:OH	2:L:44:HIS:HB3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:162:GLY:HA2	5:H:2072:HOH:O	2.04	0.58
1:H:104[A]:MET:H	2:L:36:ASN:ND2	2.02	0.57
1:H:182:LEU:C	1:H:182:LEU:HD23	2.24	0.57
1:H:104[B]:MET:H	2:L:36:ASN:ND2	2.02	0.57
1:H:58:THR:CG2	1:H:60:TYR:CE1	2.88	0.57
1:H:197:THR:CG2	1:H:214:LYS:HE2	2.35	0.56
2:L:3:VAL:O	2:L:25:SER:HB2	2.06	0.56
2:L:23:ARG:CG	2:L:72:LYS:HD3	2.36	0.56
1:H:137:THR:O	1:H:137:THR:HG23	2.05	0.56
1:H:39[A]:GLN:NE2	1:H:95:TYR:OH	2.37	0.56
2:L:45:LEU:HD12	5:L:2022:HOH:O	2.07	0.55
1:H:3:GLN:HG2	1:H:4:LEU:H	1.71	0.54
1:H:74:LYS:N	1:H:74:LYS:HD3	2.12	0.54
2:L:56:ARG:HG3	2:L:56:ARG:NH1	2.23	0.54
2:L:118:VAL:O	2:L:207[B]:LYS:HE3	2.08	0.54
1:H:63:LYS:HG2	1:H:63:LYS:O	2.08	0.53
2:L:69:ILE:O	2:L:69:ILE:HG23	2.08	0.53
2:L:50:ILE:HD13	2:L:56:ARG:HA	1.92	0.52
2:L:24:SER:O	2:L:26:THR:N	2.36	0.52
1:H:218:ARG:HG3	1:H:218:ARG:HH11	1.74	0.51
1:H:24:ALA:HB1	1:H:27:TYR:CE1	2.46	0.51
1:H:58:THR:HG22	1:H:60:TYR:CE1	2.45	0.51
1:H:39[A]:GLN:HE21	1:H:95:TYR:HE2	1.59	0.51
1:H:39[A]:GLN:HE22	2:L:44:HIS:HD2	1.57	0.51
2:L:185:ALA:O	2:L:188:TRP:HB3	2.11	0.51
1:H:58:THR:HG21	1:H:60:TYR:CE1	2.45	0.50
2:L:189:GLU:HA	2:L:211:ARG:NE	2.26	0.50
1:H:3:GLN:C	1:H:4:LEU:HD23	2.31	0.50
2:L:190:ARG:HH11	2:L:190:ARG:HB2	1.76	0.50
2:L:181:LEU:HG	2:L:183:LEU:HD21	1.93	0.50
1:H:55:ASN:HD21	1:H:57:ASP:CG	2.13	0.50
2:L:184:THR:HG22	5:L:2070:HOH:O	2.11	0.50
2:L:147:VAL:CG2	2:L:198:VAL:HG13	2.42	0.50
2:L:148:THR:OG1	2:L:199:THR:HB	2.12	0.49
2:L:56:ARG:NH1	2:L:64:PHE:O	2.45	0.49
1:H:18:VAL:CG1	1:H:86:LEU:HD11	2.43	0.49
1:H:110[B]:GLN:HG2	1:H:110[B]:GLN:O	2.12	0.49
1:H:103:ILE:HG12	2:L:51:GLY:CA	2.40	0.49
1:H:6:GLN:HE21	1:H:109:GLY:HA3	1.77	0.49
1:H:132:GLY:CA	1:H:218:ARG:HB3	2.43	0.49
1:H:39[A]:GLN:HE22	2:L:44:HIS:CD2	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:23:ARG:HG3	2:L:72:LYS:HD3	1.93	0.49
1:H:103:ILE:HD11	2:L:55:ASN:HB2	1.94	0.49
1:H:32:TYR:HB3	1:H:99:GLY:O	2.13	0.49
1:H:134:ALA:O	2:L:208:SER:O	2.31	0.48
2:L:147:VAL:HG21	2:L:198:VAL:CG1	2.43	0.48
1:H:133:SER:O	1:H:134:ALA:C	2.52	0.48
1:H:27:TYR:CE2	1:H:98:ARG:HD2	2.49	0.48
1:H:73:ASP:CG	1:H:76:SER:H	2.18	0.47
1:H:140:MET:CE	1:H:189:PRO:HA	2.44	0.47
1:H:55:ASN:ND2	1:H:57:ASP:OD2	2.44	0.47
2:L:41:LYS:HB2	2:L:45:LEU:HD11	1.96	0.47
2:L:143:TYR:HA	2:L:144:PRO:C	2.35	0.47
2:L:122:PRO:HB3	2:L:209:LEU:HD22	1.97	0.47
1:H:164:LEU:HD23	1:H:186:VAL:HG21	1.97	0.47
2:L:169:LYS:NZ	5:L:2053:HOH:O	2.34	0.46
2:L:24:SER:C	2:L:26:THR:H	2.15	0.46
1:H:159:TRP:CZ3	1:H:200:CYS:HB3	2.51	0.46
1:H:140:MET:HE2	1:H:189:PRO:HA	1.97	0.46
2:L:41:LYS:HE2	2:L:42:PRO:HD2	1.98	0.46
2:L:88:TYR:O	2:L:103:GLY:HA2	2.16	0.46
1:H:178:ASP:O	1:H:179:LEU:HD23	2.16	0.46
2:L:63:ARG:HB2	2:L:78:THR:O	2.15	0.45
2:L:191:HIS:O	2:L:211:ARG:NE	2.45	0.45
2:L:167:PRO:HG3	5:L:2076:HOH:O	2.15	0.45
1:H:4:LEU:HA	1:H:23:LYS:O	2.17	0.45
2:L:147:VAL:CG2	2:L:198:VAL:CG1	2.94	0.45
1:H:18:VAL:HG12	1:H:86:LEU:HD11	1.98	0.45
2:L:85:GLU:HG3	2:L:107:THR:HA	1.99	0.45
1:H:50:VAL:HG22	1:H:51:ILE:N	2.32	0.45
2:L:211:ARG:HH11	2:L:211:ARG:HG2	1.81	0.45
1:H:175:LEU:HD13	1:H:180:TYR:CE2	2.51	0.45
2:L:205:VAL:O	2:L:205:VAL:HG13	2.17	0.45
1:H:167:GLY:O	1:H:186:VAL:HA	2.17	0.45
1:H:12:VAL:O	1:H:116:VAL:HA	2.17	0.45
2:L:33:ASN:O	2:L:34:TYR:C	2.55	0.45
2:L:182:THR:O	2:L:183:LEU:HD23	2.16	0.44
1:H:143:LEU:HG	1:H:215:ILE:HG21	1.99	0.44
2:L:30:THR:C	2:L:32:SER:H	2.21	0.44
2:L:37:TRP:CD2	2:L:75:LEU:HB2	2.52	0.44
2:L:83:GLU:HG2	5:L:2050:HOH:O	2.17	0.43
2:L:7:GLU:O	2:L:104:THR:OG1	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:82:GLN:NE2	5:H:2006:HOH:O	2.45	0.43
2:L:105:LYS:HE2	5:L:2020:HOH:O	2.18	0.43
1:H:218:ARG:HG3	1:H:218:ARG:NH1	2.32	0.43
1:H:132:GLY:HA3	1:H:218:ARG:HB3	1.99	0.43
1:H:95:TYR:HH	2:L:44:HIS:HB3	1.83	0.43
2:L:45:LEU:CD1	5:L:2022:HOH:O	2.64	0.43
2:L:3:VAL:O	2:L:25:SER:CB	2.68	0.42
1:H:63:LYS:CG	1:H:63:LYS:O	2.67	0.42
1:H:117:SER:OG	1:H:178:ASP:OD1	2.28	0.42
2:L:160:GLN:NE2	5:L:2083:HOH:O	2.53	0.42
1:H:3:GLN:N	1:H:25:SER:HB3	2.35	0.41
2:L:34:TYR:N	2:L:34:TYR:CD1	2.87	0.41
1:H:132:GLY:HA3	1:H:218:ARG:CD	2.47	0.41
2:L:85:GLU:HG3	2:L:106:LEU:O	2.20	0.41
2:L:34:TYR:O	2:L:35:ALA:C	2.59	0.41
2:L:91:ALA:HB1	2:L:98:LEU:HD11	2.03	0.41
1:H:12:VAL:HG21	1:H:18:VAL:HB	2.02	0.41
1:H:124:PRO:CB	1:H:150:TYR:HB3	2.45	0.41
1:H:13:LYS:HB2	1:H:13:LYS:HE2	1.82	0.41
1:H:160:ASN:ND2	1:H:164:LEU:HD13	2.28	0.41
2:L:23:ARG:HG2	2:L:72:LYS:HD3	2.02	0.41
2:L:24:SER:C	2:L:26:THR:N	2.73	0.41
2:L:41:LYS:HB2	2:L:45:LEU:CD1	2.51	0.41
2:L:41:LYS:NZ	5:L:2027:HOH:O	2.54	0.41
2:L:143:TYR:HA	2:L:144:PRO:O	2.21	0.41
1:H:105:ALA:HB3	5:H:2038:HOH:O	2.20	0.40
1:H:126:VAL:HG21	1:H:211:VAL:CG2	2.51	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	H	216/217 (100%)	198 (92%)	14 (6%)	4 (2%)	10	2
2	L	212/212 (100%)	197 (93%)	13 (6%)	2 (1%)	21	10
All	All	428/429 (100%)	395 (92%)	27 (6%)	6 (1%)	14	4

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	134	ALA
1	H	136	GLN
1	H	177	SER
2	L	109	LEU
2	L	27	GLY
1	H	154	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	H	182/182 (100%)	169 (93%)	13 (7%)	18	10
2	L	179/179 (100%)	176 (98%)	3 (2%)	68	65
All	All	361/361 (100%)	345 (96%)	16 (4%)	34	26

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	28	THR
1	H	30	THR
1	H	55	ASN
1	H	74	LYS
1	H	138	ASN
1	H	143	LEU
1	H	145	CYS
1	H	154	PRO
1	H	155	VAL
1	H	178	ASP

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Mol	Chain	Res	Type
1	H	182	LEU
1	H	211	VAL
1	H	216	VAL
2	L	125	SER
2	L	166	GLN
2	L	190	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	6	GLN
1	H	160	ASN
1	H	176	GLN
2	L	33	ASN
2	L	36	ASN
2	L	44	HIS
2	L	97	HIS
2	L	111	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)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	$\#\|Z\| > 2$
3	GOL	H	1219	-	5,5,5	4.76	5 (100%)	5,5,5	5.68	3 (60%)
3	GOL	L	1212	-	5,5,5	4.81	5 (100%)	5,5,5	5.62	3 (60%)
3	GOL	L	1213	-	5,5,5	4.78	5 (100%)	5,5,5	5.73	3 (60%)

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
3	GOL	H	1219	-	-	0/4/4/4	0/0/0/0
3	GOL	L	1212	-	-	0/4/4/4	0/0/0/0
3	GOL	L	1213	-	-	0/4/4/4	0/0/0/0

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	1212	GOL	C3-C2	-8.23	1.20	1.52
3	L	1213	GOL	C3-C2	-8.08	1.21	1.52
3	H	1219	GOL	C3-C2	-8.01	1.21	1.52
3	L	1212	GOL	C1-C2	-3.38	1.39	1.52
3	H	1219	GOL	C1-C2	-3.16	1.40	1.52
3	L	1213	GOL	C1-C2	-2.97	1.41	1.52
3	L	1213	GOL	O2-C2	-2.94	1.34	1.43
3	H	1219	GOL	O2-C2	-2.84	1.35	1.43
3	L	1212	GOL	O2-C2	-2.79	1.35	1.43
3	L	1212	GOL	O3-C3	3.19	1.56	1.42
3	H	1219	GOL	O3-C3	3.24	1.56	1.42
3	L	1213	GOL	O3-C3	3.29	1.56	1.42
3	L	1212	GOL	O1-C1	4.27	1.60	1.42
3	H	1219	GOL	O1-C1	4.51	1.61	1.42
3	L	1213	GOL	O1-C1	4.52	1.61	1.42

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	L	1212	GOL	O1-C1-C2	2.96	124.52	110.18
3	H	1219	GOL	O1-C1-C2	3.11	125.25	110.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	L	1213	GOL	O1-C1-C2	3.25	125.92	110.18
3	H	1219	GOL	O2-C2-C3	6.58	138.83	108.65
3	L	1213	GOL	O2-C2-C3	6.59	138.89	108.65
3	L	1212	GOL	O2-C2-C3	6.63	139.06	108.65
3	L	1212	GOL	O3-C3-C2	10.23	159.81	110.18
3	H	1219	GOL	O3-C3-C2	10.40	160.61	110.18
3	L	1213	GOL	O3-C3-C2	10.46	160.90	110.18

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 (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	H	215/217 (99%)	0.99	46 (21%)	1	1	28, 49, 74, 99	0
2	L	211/212 (99%)	0.69	35 (16%)	2	2	30, 46, 66, 89	0
All	All	426/429 (99%)	0.84	81 (19%)	2	1	28, 46, 71, 99	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	134	ALA	8.3
1	H	3	GLN	7.6
2	L	27	GLY	5.6
1	H	136	GLN	4.5
1	H	37	VAL	4.5
2	L	25	SER	4.5
2	L	71	ASP	4.4
1	H	36	TRP	4.3
1	H	133	SER	4.3
2	L	26	THR	3.9
1	H	138	ASN	3.8
2	L	100	PHE	3.8
2	L	34	TYR	3.8
1	H	104[A]	MET	3.5
1	H	41	PRO	3.5
2	L	75	LEU	3.4
1	H	62	GLN	3.3
1	H	87	THR	3.3
1	H	137	THR	3.3
2	L	2	ALA	3.2
1	H	27	TYR	3.2
2	L	23	ARG	3.2
2	L	28	ALA	3.2
1	H	218	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
2	L	20	LEU	3.1
1	H	28	THR	3.1
1	H	32	TYR	3.1
1	H	129	LEU	3.1
2	L	38	VAL	3.0
1	H	195	SER	3.0
1	H	192	THR	3.0
2	L	137	CYS	2.9
2	L	37	TRP	2.9
1	H	132	GLY	2.9
2	L	24	SER	2.9
1	H	47	TRP	2.8
2	L	98	LEU	2.8
2	L	4	VAL	2.8
1	H	49	GLY	2.8
1	H	48	ILE	2.8
1	H	135	ALA	2.7
2	L	70	GLY	2.7
1	H	43	GLN	2.7
1	H	164	LEU	2.7
1	H	35	HIS	2.7
2	L	136	VAL	2.6
1	H	42	GLY	2.6
2	L	32	SER	2.6
2	L	36	ASN	2.5
1	H	81	MET	2.5
2	L	186	ARG	2.5
2	L	18	VAL	2.5
2	L	138	THR	2.5
2	L	91	ALA	2.4
1	H	77	SER	2.4
1	H	146	LEU	2.4
1	H	96	CYS	2.4
2	L	29	VAL	2.4
1	H	163	SER	2.3
2	L	19	THR	2.3
2	L	76	THR	2.3
1	H	73	ASP	2.3
1	H	101	ALA	2.3
1	H	97	SER	2.3
2	L	192	SER	2.2
1	H	194	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	140	MET	2.1
2	L	42	PRO	2.1
1	H	31	SER	2.1
2	L	30	THR	2.1
1	H	108	TRP	2.1
1	H	95	TYR	2.1
1	H	40	THR	2.1
2	L	93	TRP	2.1
1	H	167	GLY	2.1
2	L	210	SER	2.1
1	H	29	PHE	2.1
1	H	184	SER	2.0
2	L	5	THR	2.0
1	H	76	SER	2.0
2	L	139	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 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
3	GOL	L	1212	6/6	0.67	0.37	6.23	68,78,83,87	0
3	GOL	H	1219	6/6	0.85	0.26	0.69	66,72,75,82	0
4	MG	L	1214	1/1	0.96	0.17	-	45,45,45,45	0
3	GOL	L	1213	6/6	0.60	0.38	-	73,77,78,78	0

6.5 Other polymers (i)

There are no such residues in this entry.