Full wwPDB X-ray Structure Validation Report (i)

Aug 28, 2023 – 06:36 AM EDT

PDB ID	:	3L5W
Title	:	Crystal structure of the complex between IL-13 and C836 FAB
Authors	:	Teplyakov, A.; Obmolova, G.; Malia, T.; Gilliland, G.L.
Deposited on	:	2009-12-22
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 (1)) were used in the production of this report:

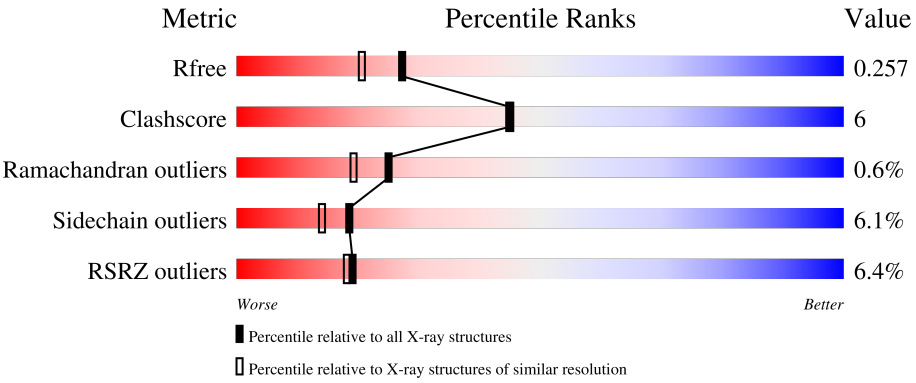
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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	214	2% 81% 16% ·
1	L	214	% 81% 17% ·
2	B	230	6% 83% 12% ·
2	H	230	5% 79% 16% · ·
3	I	113	10% 72% 16% · 11%

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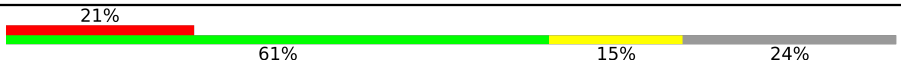
Mol	Chain	Length	Quality of chain
3	J	113	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8510 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 C836 LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	213	Total	C	N	O	S	0	0	0
			1646	1035	271	335	5			
1	A	213	Total	C	N	O	S	0	0	0
			1646	1035	271	335	5			

- Molecule 2 is a protein called C836 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	223	Total	C	N	O	S	0	1	0
			1680	1070	274	330	6			
2	B	221	Total	C	N	O	S	0	0	0
			1664	1060	272	326	6			

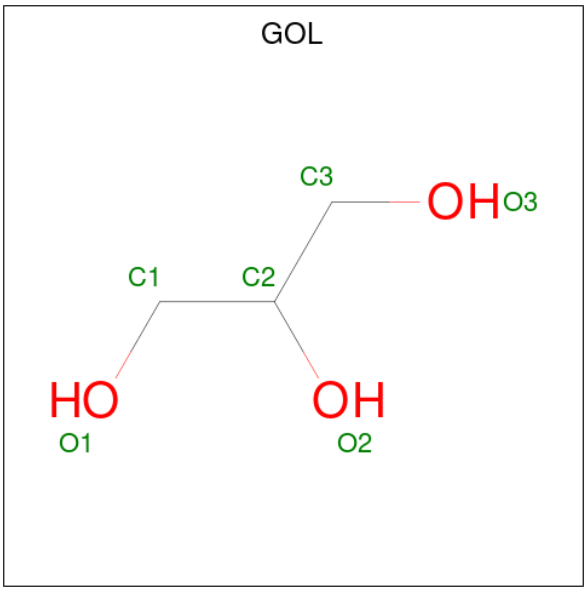
- Molecule 3 is a protein called Interleukin-13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	101	Total	C	N	O	S	0	0	0
			775	491	134	143	7			
3	J	86	Total	C	N	O	S	0	0	0
			667	425	113	122	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	1	MET	-	expression tag	UNP P35225
J	1	MET	-	expression tag	UNP P35225

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

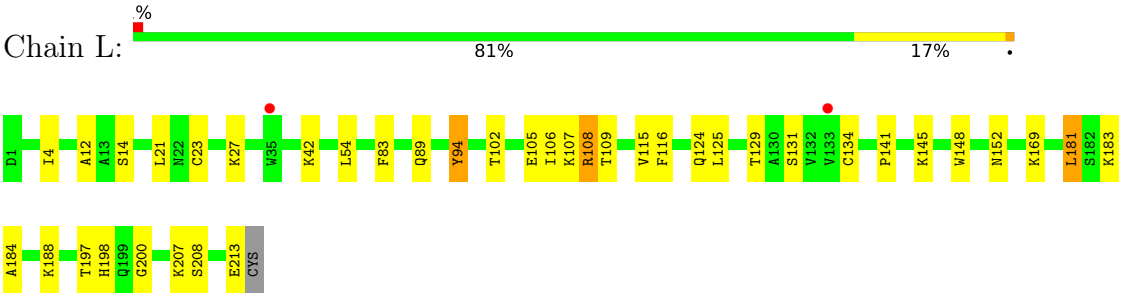
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	99	Total O 99 99	0	0
5	H	97	Total O 97 97	0	0
5	I	37	Total O 37 37	0	0
5	A	93	Total O 93 93	0	0
5	B	96	Total O 96 96	0	0
5	J	4	Total O 4 4	0	0

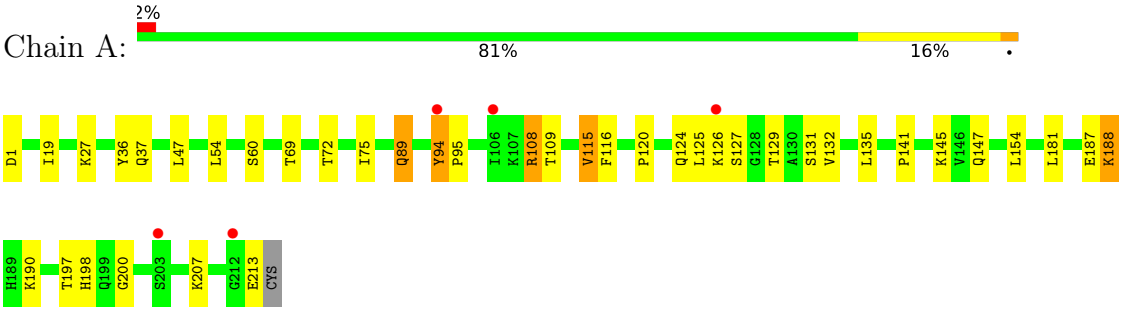
3 Residue-property plots (i)

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.

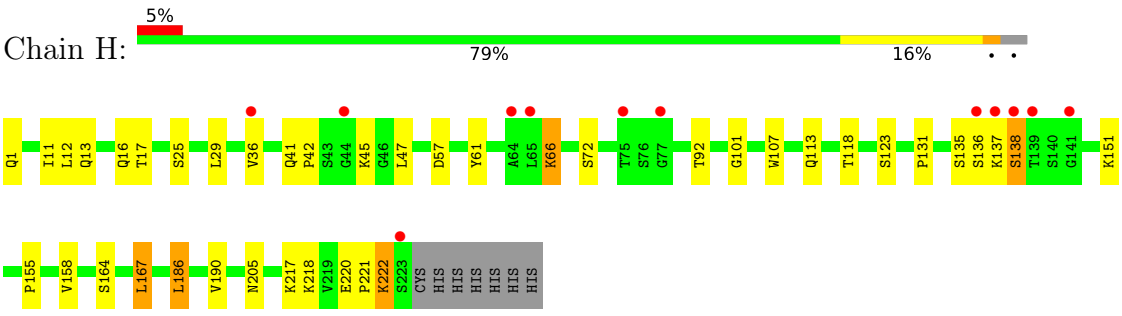
• Molecule 1: C836 LIGHT CHAIN



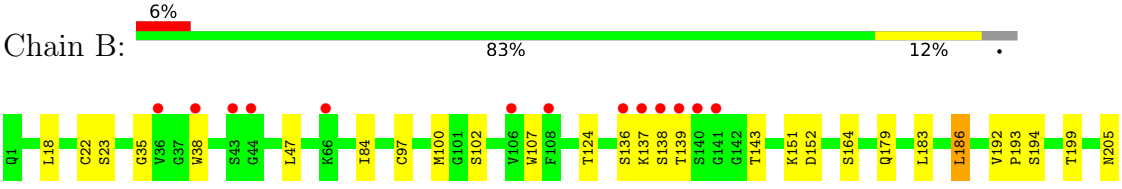
• Molecule 1: C836 LIGHT CHAIN

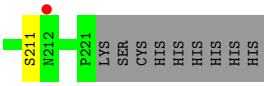


• Molecule 2: C836 HEAVY CHAIN



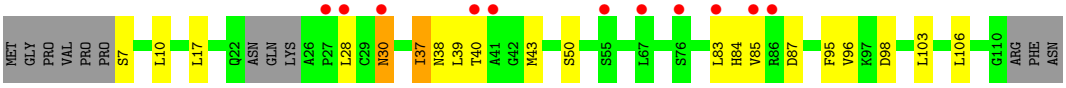
• Molecule 2: C836 HEAVY CHAIN





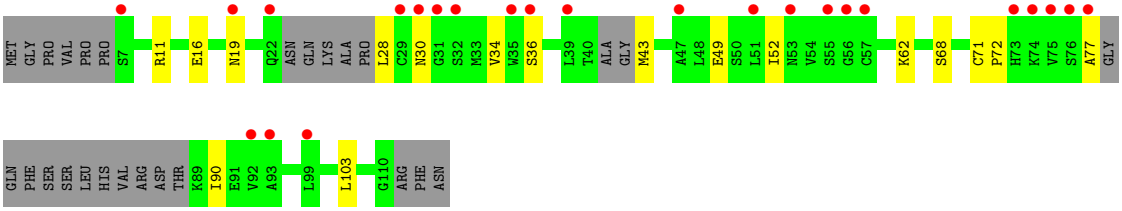
• Molecule 3: Interleukin-13

Chain I:



• Molecule 3: Interleukin-13

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	76.62Å 65.56Å 118.74Å 90.00° 107.02° 90.00°	Depositor
Resolution (Å)	15.00 – 2.00 19.76 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.7 (15.00-2.00) 99.6 (19.76-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.48 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.205 , 0.253 0.211 , 0.257	Depositor DCC
R_{free} test set	3818 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	41.2	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 44.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8510	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.31 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.9561e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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	0.58	0/1683	0.70	0/2282
1	L	0.56	0/1683	0.67	1/2282 (0.0%)
2	B	0.56	1/1709 (0.1%)	0.67	1/2334 (0.0%)
2	H	0.56	0/1729	0.71	1/2362 (0.0%)
3	I	0.52	0/785	0.63	0/1056
3	J	0.44	0/672	0.58	0/899
All	All	0.55	1/8261 (0.0%)	0.68	3/11215 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	97	CYS	CB-SG	-5.20	1.73	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	186	LEU	CA-CB-CG	6.90	131.17	115.30
1	L	181	LEU	CA-CB-CG	6.52	130.29	115.30
2	B	186	LEU	CA-CB-CG	5.18	127.22	115.30

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	1646	0	1596	27	0
1	L	1646	0	1596	28	0
2	B	1664	0	1633	17	0
2	H	1680	0	1641	29	0
3	I	775	0	793	11	0
3	J	667	0	690	4	0
4	A	6	0	8	1	0
5	A	93	0	0	2	0
5	B	96	0	0	0	0
5	H	97	0	0	0	0
5	I	37	0	0	0	0
5	J	4	0	0	0	0
5	L	99	0	0	1	0
All	All	8510	0	7957	104	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 6.

All (104) 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:L:116:PHE:HD2	2:H:138:SER:HA	1.35	0.89
2:B:164:SER:H	2:B:205:ASN:HD21	1.21	0.89
1:A:116:PHE:HD2	2:B:138:SER:HA	1.38	0.88
2:H:164:SER:H	2:H:205:ASN:HD21	1.29	0.80
1:L:207:LYS:HA	2:H:137:LYS:HE3	1.66	0.76
1:L:116:PHE:HD2	2:H:138:SER:CA	1.99	0.76
1:L:116:PHE:CD2	2:H:138:SER:HA	2.22	0.74
1:A:108:ARG:HD3	1:A:109:THR:O	1.87	0.73
3:I:37:ILE:HD11	3:I:95:PHE:CZ	2.24	0.73
1:A:94:TYR:H	1:A:94:TYR:HD1	1.34	0.72
3:I:38:ASN:OD1	3:I:40:THR:HG22	1.92	0.70
2:B:151:LYS:HE2	2:B:179:GLN:HE22	1.57	0.68
1:A:198:HIS:CD2	1:A:200:GLY:H	2.12	0.67
1:L:208:SER:H	2:H:137:LYS:HE2	1.60	0.66
3:I:84:HIS:HB3	3:I:87:ASP:HB2	1.77	0.66
1:A:116:PHE:CD2	2:B:138:SER:HA	2.28	0.66
2:H:221:PRO:O	2:H:222:LYS:HB2	1.97	0.64
3:I:37:ILE:HD11	3:I:95:PHE:HZ	1.63	0.62
1:L:115:VAL:HG13	1:L:207:LYS:HE2	1.82	0.62
1:L:208:SER:H	2:H:137:LYS:CE	2.13	0.60
1:A:116:PHE:HD2	2:B:138:SER:CA	2.11	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:52:ILE:HG23	3:J:77:ALA:HB2	1.82	0.60
1:A:94:TYR:CD1	1:A:94:TYR:N	2.58	0.58
1:A:115:VAL:HG22	1:A:207:LYS:CG	2.34	0.57
1:A:198:HIS:HD2	1:A:200:GLY:H	1.50	0.57
2:B:18:LEU:HD23	2:B:84:ILE:HD12	1.87	0.56
2:B:164:SER:N	2:B:205:ASN:HD21	1.98	0.56
1:L:198:HIS:CD2	1:L:200:GLY:H	2.24	0.56
1:A:115:VAL:HG22	1:A:207:LYS:HG3	1.89	0.55
2:H:29:LEU:HD11	2:H:36:VAL:HG23	1.88	0.55
2:H:42:PRO:HB2	2:H:45:LYS:HD3	1.88	0.54
1:L:83:PHE:CG	1:L:106:ILE:HG12	2.43	0.54
2:H:16:GLN:HG3	2:H:17:THR:H	1.74	0.53
1:A:141:PRO:O	1:A:198:HIS:HE1	1.91	0.53
1:L:42:LYS:C	2:H:113:GLN:HE22	2.13	0.52
2:H:16:GLN:HG3	2:H:17:THR:N	2.24	0.52
2:B:136:SER:HA	2:B:139:THR:HB	1.91	0.52
3:J:36:SER:HB3	3:J:90:ILE:HG12	1.91	0.52
4:A:1001:GOL:H32	2:B:47:LEU:HD12	1.93	0.51
1:L:108:ARG:HD3	1:L:109:THR:O	2.11	0.51
2:H:131:PRO:HD3	2:H:217:LYS:HE2	1.92	0.51
1:L:12:ALA:HB1	1:L:107:LYS:HG3	1.93	0.50
2:H:138:SER:OG	2:H:138:SER:O	2.30	0.50
1:L:141:PRO:O	1:L:198:HIS:HE1	1.93	0.50
2:H:11:ILE:HB	2:H:155:PRO:HG3	1.94	0.50
2:B:139:THR:HG23	2:B:194:SER:OG	2.12	0.49
3:I:7:SER:HB3	3:I:10:LEU:HB3	1.94	0.49
1:L:108:ARG:CD	1:L:109:THR:O	2.61	0.48
3:I:37:ILE:HD13	3:I:39:LEU:CD2	2.43	0.48
1:L:207:LYS:CA	2:H:137:LYS:HE3	2.41	0.48
1:A:120:PRO:HD3	1:A:132:VAL:HG22	1.95	0.48
1:L:208:SER:O	2:H:137:LYS:HG2	2.15	0.47
2:H:218:LYS:HE2	2:H:220:GLU:HG2	1.95	0.47
2:B:192:VAL:HB	2:B:193:PRO:HD2	1.96	0.47
1:A:197:THR:HG23	5:A:275:HOH:O	2.15	0.47
1:L:83:PHE:CD2	1:L:106:ILE:HG12	2.50	0.47
2:B:35:GLY:HA3	2:B:100:MET:HE2	1.95	0.47
1:A:115:VAL:HG22	1:A:207:LYS:HG2	1.98	0.46
2:H:135:SER:OG	2:H:136:SER:N	2.48	0.46
1:A:54:LEU:HD11	1:A:60:SER:HA	1.96	0.46
1:L:124:GLN:HG2	1:L:129:THR:O	2.16	0.45
1:L:197:THR:HG23	5:L:248:HOH:O	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:37:ILE:HD11	3:I:95:PHE:CE2	2.52	0.45
1:A:125:LEU:C	1:A:127:SER:H	2.20	0.45
1:A:124:GLN:HE22	1:A:131:SER:H	1.65	0.45
2:H:167:LEU:HD23	2:H:190:VAL:HG21	1.99	0.45
1:A:124:GLN:NE2	1:A:131:SER:H	2.14	0.45
3:I:43:MET:SD	3:I:103:LEU:HD23	2.56	0.45
2:B:124:THR:HG22	2:B:211:SER:HB3	1.98	0.44
2:H:41:GLN:HB2	2:H:47:LEU:HD23	1.98	0.44
2:B:152:ASP:HB3	2:B:183:LEU:HD13	1.99	0.44
1:A:147:GLN:HG2	1:A:154:LEU:HD13	1.99	0.44
2:B:102:SER:HB2	2:B:107:TRP:CH2	2.53	0.44
1:A:19:ILE:HD11	1:A:75:ILE:HD12	1.99	0.44
2:H:218:LYS:HE2	2:H:220:GLU:CG	2.47	0.43
2:H:164:SER:N	2:H:205:ASN:HD21	2.06	0.43
1:L:134:CYS:HB2	1:L:148:TRP:CZ2	2.54	0.43
1:L:124:GLN:NE2	1:L:131:SER:H	2.16	0.43
2:H:61:TYR:HB2	2:H:66:LYS:HD2	2.01	0.43
1:A:1:ASP:HB2	5:A:418:HOH:O	2.19	0.43
2:H:135:SER:OG	2:H:137:LYS:N	2.52	0.42
3:I:17:LEU:HD22	3:I:96:VAL:HG13	2.01	0.42
1:A:188:LYS:O	1:A:188:LYS:HG3	2.19	0.42
1:L:12:ALA:HA	1:L:105:GLU:O	2.19	0.42
2:H:11:ILE:HA	2:H:118:THR:O	2.20	0.42
2:H:92:THR:HG23	2:H:118:THR:HA	2.02	0.42
1:L:145:LYS:HB3	1:L:197:THR:OG1	2.19	0.42
3:I:37:ILE:HD13	3:I:39:LEU:HD23	2.02	0.42
3:I:39:LEU:O	3:I:43:MET:HB2	2.18	0.42
1:A:36:TYR:OH	1:A:89:GLN:NE2	2.53	0.42
1:L:21:LEU:HD22	1:L:102:THR:HG21	2.02	0.42
1:L:184:ALA:O	1:L:188:LYS:HG3	2.19	0.41
1:A:37:GLN:HB2	1:A:47:LEU:HD11	2.01	0.41
1:A:147:GLN:HG2	1:A:154:LEU:CD1	2.50	0.41
1:L:125:LEU:O	1:L:183:LYS:HD2	2.20	0.41
2:B:22:CYS:HB2	2:B:38:TRP:CZ2	2.56	0.41
3:J:16:GLU:OE1	3:J:62:LYS:HD3	2.21	0.41
2:H:101:GLY:HA3	2:H:107:TRP:CZ3	2.56	0.41
2:B:139:THR:HG22	2:B:139:THR:O	2.21	0.41
1:L:4:ILE:CG2	1:L:23:CYS:SG	3.09	0.41
1:L:94:TYR:CD2	1:L:94:TYR:C	2.95	0.41
3:J:71:CYS:HA	3:J:72:PRO:HD3	1.81	0.41
1:A:115:VAL:HA	1:A:135:LEU:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:TYR:HA	1:A:95:PRO:C	2.41	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	211/214 (99%)	204 (97%)	6 (3%)	1 (0%)	29 23
1	L	211/214 (99%)	204 (97%)	7 (3%)	0	100 100
2	B	219/230 (95%)	211 (96%)	8 (4%)	0	100 100
2	H	222/230 (96%)	209 (94%)	11 (5%)	2 (1%)	17 11
3	I	97/113 (86%)	90 (93%)	5 (5%)	2 (2%)	7 2
3	J	78/113 (69%)	70 (90%)	7 (9%)	1 (1%)	12 6
All	All	1038/1114 (93%)	988 (95%)	44 (4%)	6 (1%)	25 19

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	222	LYS
1	A	126	LYS
3	J	30	ASN
2	H	66	LYS
3	I	30	ASN
3	I	28	LEU

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	187/188 (100%)	173 (92%)	14 (8%)	13 9
1	L	187/188 (100%)	177 (95%)	10 (5%)	22 18
2	B	189/198 (96%)	184 (97%)	5 (3%)	46 48
2	H	190/198 (96%)	178 (94%)	12 (6%)	18 13
3	I	87/98 (89%)	80 (92%)	7 (8%)	12 7
3	J	76/98 (78%)	68 (90%)	8 (10%)	7 4
All	All	916/968 (95%)	860 (94%)	56 (6%)	18 14

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	14	SER
1	L	27	LYS
1	L	54	LEU
1	L	89	GLN
1	L	94	TYR
1	L	108	ARG
1	L	152	ASN
1	L	169	LYS
1	L	181	LEU
1	L	213	GLU
2	H	1	GLN
2	H	12	LEU
2	H	13	GLN
2	H	25	SER
2	H	57	ASP
2	H	72	SER
2	H	123	SER
2	H	138	SER
2	H	151	LYS
2	H	158	VAL
2	H	167	LEU
2	H	186	LEU
3	I	30	ASN
3	I	37	ILE
3	I	50	SER
3	I	83	LEU

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Mol	Chain	Res	Type
3	I	85	VAL
3	I	98	ASP
3	I	106	LEU
1	A	27	LYS
1	A	69	THR
1	A	72	THR
1	A	89	GLN
1	A	94	TYR
1	A	108	ARG
1	A	115	VAL
1	A	129	THR
1	A	145	LYS
1	A	181	LEU
1	A	187	GLU
1	A	188	LYS
1	A	190	LYS
1	A	213	GLU
2	B	23	SER
2	B	137	LYS
2	B	143	THR
2	B	186	LEU
2	B	199	THR
3	J	11	ARG
3	J	19	ASN
3	J	28	LEU
3	J	34	VAL
3	J	43	MET
3	J	49	GLU
3	J	68	SER
3	J	103	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	89	GLN
1	L	124	GLN
1	L	198	HIS
2	H	13	GLN
2	H	113	GLN
2	H	179	GLN
2	H	200	GLN
2	H	205	ASN

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Mol	Chain	Res	Type
3	I	22	GLN
3	I	64	GLN
3	I	84	HIS
3	I	94	GLN
1	A	89	GLN
1	A	91	HIS
1	A	124	GLN
1	A	138	ASN
1	A	152	ASN
1	A	198	HIS
2	B	1	GLN
2	B	13	GLN
2	B	41	GLN
2	B	179	GLN
2	B	205	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)

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	$\#\|Z\| > 2$
4	GOL	A	1001	-	5,5,5	0.35	0	5,5,5	0.43	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
4	GOL	A	1001	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1001	GOL	O1-C1-C2-C3
4	A	1001	GOL	O1-C1-C2-O2
4	A	1001	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001	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	213/214 (99%)	0.02	5 (2%) 60 59	34, 44, 70, 92	0
1	L	213/214 (99%)	-0.03	2 (0%) 84 83	28, 43, 64, 83	0
2	B	221/230 (96%)	0.09	14 (6%) 20 19	32, 42, 70, 101	0
2	H	223/230 (96%)	0.15	12 (5%) 25 24	31, 45, 73, 90	0
3	I	101/113 (89%)	0.43	11 (10%) 5 5	34, 51, 78, 101	0
3	J	86/113 (76%)	1.37	24 (27%) 0 0	44, 77, 113, 118	0
All	All	1057/1114 (94%)	0.20	68 (6%) 19 18	28, 46, 83, 118	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	138	SER	6.9
2	H	138	SER	6.5
3	J	35	TRP	5.9
3	J	39	LEU	5.9
2	B	136	SER	5.6
3	J	55	SER	5.5
2	H	75	THR	5.4
3	J	75	VAL	5.3
3	I	83	LEU	5.3
3	J	30	ASN	4.7
2	H	136	SER	4.3
2	B	141	GLY	4.2
3	J	51	LEU	3.9
2	B	140	SER	3.9
3	I	85	VAL	3.8
3	I	40	THR	3.8
3	J	76	SER	3.8
3	J	77	ALA	3.8
2	B	139	THR	3.8

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Mol	Chain	Res	Type	RSRZ
2	H	139	THR	3.7
3	J	32	SER	3.7
3	J	74	LYS	3.7
2	H	36	VAL	3.6
3	I	55	SER	3.5
3	J	73	HIS	3.5
3	I	86	ARG	3.4
2	B	66	LYS	3.4
2	H	64	ALA	3.4
3	J	57	CYS	3.3
2	H	44	GLY	3.2
1	A	94	TYR	3.2
3	I	30	ASN	3.2
1	A	203	SER	3.1
2	B	36	VAL	3.1
3	J	31	GLY	3.1
2	B	106	VAL	3.0
3	J	7	SER	3.0
3	J	47	ALA	2.8
2	H	141	GLY	2.8
2	H	65	LEU	2.7
3	I	27	PRO	2.7
3	J	92	VAL	2.6
3	J	19	ASN	2.5
2	B	108	PHE	2.4
1	A	126	LYS	2.4
1	L	35	TRP	2.4
2	B	212	ASN	2.4
3	J	99	LEU	2.4
2	H	137	LYS	2.4
3	I	28	LEU	2.4
3	J	53	ASN	2.3
2	B	44	GLY	2.3
3	J	36	SER	2.3
1	L	133	VAL	2.3
2	B	137	LYS	2.3
3	I	76	SER	2.3
3	J	29	CYS	2.3
2	H	223	SER	2.2
3	J	56	GLY	2.2
1	A	106	ILE	2.2
3	J	93	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	38	TRP	2.1
2	H	77	GLY	2.1
1	A	212	GLY	2.1
2	B	43	SER	2.1
3	J	22	GLN	2.1
3	I	41	ALA	2.0
3	I	67	LEU	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, 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
4	GOL	A	1001	6/6	0.95	0.10	44,51,61,70	0

6.5 Other polymers (i)

There are no such residues in this entry.