



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 9, 2022 – 10:07 AM EST

PDB ID : 7LFA
Title : Fab 3B6 bound to ApoL1 NTD
Authors : Ultsch, M.; Kirchhofer, D.
Deposited on : 2021-01-15
Resolution : 1.86 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.26
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) : 2.26

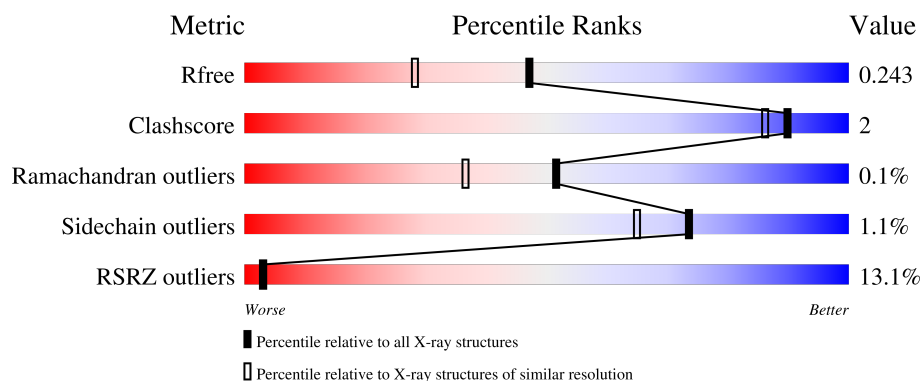
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	130	<div> <div>45%</div> <div>69%</div> <div>28%</div> </div>
1	C	130	<div> <div>49%</div> <div>72%</div> <div>5%</div> <div>23%</div> </div>
2	B	223	<div> <div>2%</div> <div>93%</div> <div>6%</div> </div>
2	H	223	<div> <div>4%</div> <div>95%</div> <div>5%</div> </div>
3	D	215	<div> <div>0%</div> <div>93%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
3	L	215	<div><div>%</div><div><div></div></div><div>96%</div><div><div></div></div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15677 atoms, of which 7426 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 Apolipoprotein L1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	94	Total	C	H	N	O	S	0	0	0
			1311	440	613	129	127	2			
1	C	100	Total	C	H	N	O	S	0	0	0
			1238	425	549	127	135	2			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	43	MET	-	initiating methionine	UNP O14791
A	44	ASP	-	expression tag	UNP O14791
A	45	TYR	-	expression tag	UNP O14791
A	46	LYS	-	expression tag	UNP O14791
A	47	ASP	-	expression tag	UNP O14791
A	48	ASP	-	expression tag	UNP O14791
A	49	ASP	-	expression tag	UNP O14791
A	50	ASP	-	expression tag	UNP O14791
A	51	LYS	-	expression tag	UNP O14791
A	52	GLY	-	expression tag	UNP O14791
A	53	GLU	-	expression tag	UNP O14791
A	54	ASN	-	expression tag	UNP O14791
A	55	LEU	-	expression tag	UNP O14791
A	56	TYR	-	expression tag	UNP O14791
A	57	PHE	-	expression tag	UNP O14791
A	58	GLN	-	expression tag	UNP O14791
A	59	GLY	-	expression tag	UNP O14791
A	60	SER	-	expression tag	UNP O14791
C	43	MET	-	initiating methionine	UNP O14791
C	44	ASP	-	expression tag	UNP O14791
C	45	TYR	-	expression tag	UNP O14791
C	46	LYS	-	expression tag	UNP O14791
C	47	ASP	-	expression tag	UNP O14791
C	48	ASP	-	expression tag	UNP O14791
C	49	ASP	-	expression tag	UNP O14791

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Chain	Residue	Modelled	Actual	Comment	Reference
C	50	ASP	-	expression tag	UNP O14791
C	51	LYS	-	expression tag	UNP O14791
C	52	GLY	-	expression tag	UNP O14791
C	53	GLU	-	expression tag	UNP O14791
C	54	ASN	-	expression tag	UNP O14791
C	55	LEU	-	expression tag	UNP O14791
C	56	TYR	-	expression tag	UNP O14791
C	57	PHE	-	expression tag	UNP O14791
C	58	GLN	-	expression tag	UNP O14791
C	59	GLY	-	expression tag	UNP O14791
C	60	SER	-	expression tag	UNP O14791

- Molecule 2 is a protein called Fab 3B6 heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	220	Total	C	H	N	O	S	0	0	0
			3256	1049	1602	271	328	6			
2	H	220	Total	C	H	N	O	S	0	2	0
			3277	1057	1613	272	329	6			

- Molecule 3 is a protein called Fab 3B6 light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	D	212	Total	C	H	N	O	S	0	0	0
			3087	992	1516	260	315	4			
3	L	212	Total	C	H	N	O	S	0	0	0
			3092	994	1517	261	316	4			

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			14	3	8	3		
4	H	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Cl	0	0
			1	1		
5	L	1	Total	Cl	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	O	0	0
			3	3		
6	B	104	Total	O	0	0
			104	104		
6	C	2	Total	O	0	0
			2	2		
6	D	88	Total	O	0	0
			88	88		
6	H	104	Total	O	0	0
			104	104		

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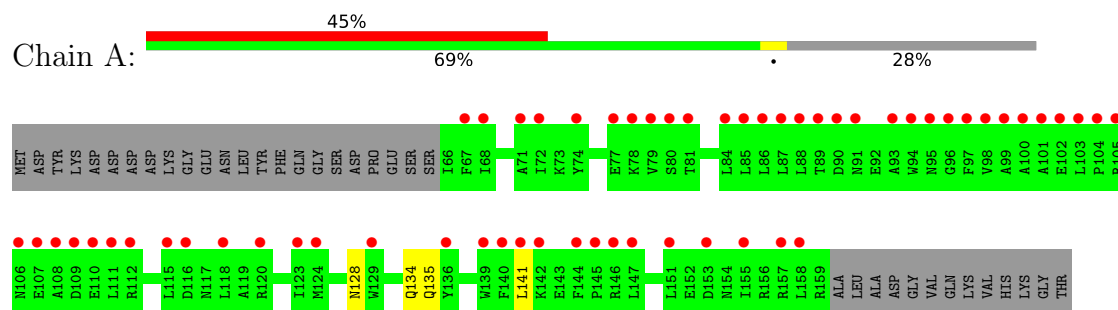
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	L	85	Total	O	0	0
			85	85		

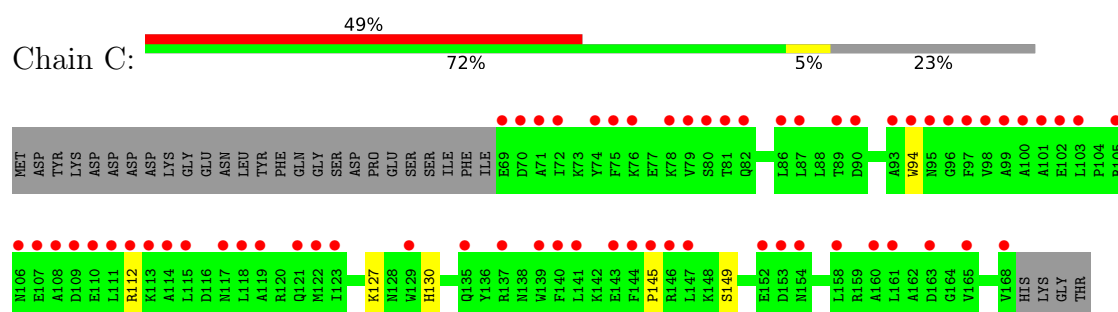
3 Residue-property plots [i](#)

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.

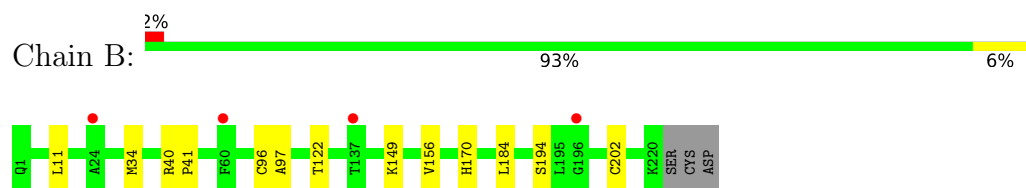
- Molecule 1: Apolipoprotein L1



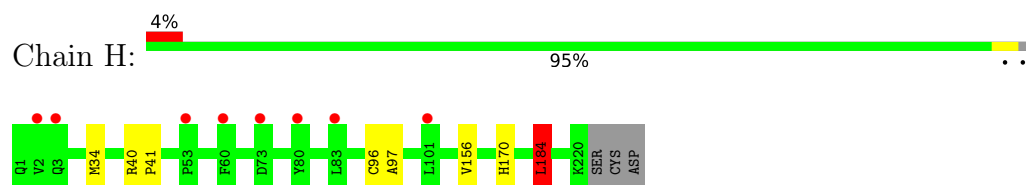
- Molecule 1: Apolipoprotein L1



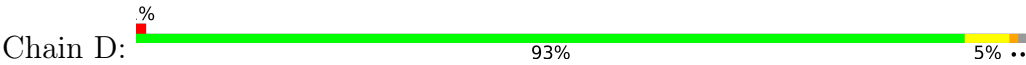
- Molecule 2: Fab 3B6 heavy chain



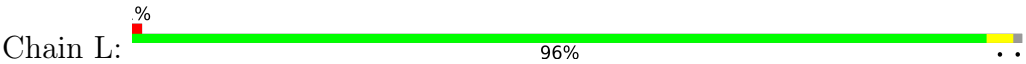
- Molecule 2: Fab 3B6 heavy chain



- Molecule 3: Fab 3B6 light chain



● Molecule 3: Fab 3B6 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	52.75Å 71.87Å 123.44Å 80.16° 85.05° 90.16°	Depositor
Resolution (Å)	70.80 – 1.86 70.80 – 1.86	Depositor EDS
% Data completeness (in resolution range)	55.0 (70.80-1.86) 55.0 (70.80-1.86)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 1.86Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.205 , 0.242 0.211 , 0.243	Depositor DCC
R_{free} test set	4035 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15677	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CL

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	0.31	0/710	0.45	0/966
1	C	0.28	0/700	0.45	0/957
2	B	0.61	1/1697 (0.1%)	0.66	0/2312
2	H	0.58	0/1713	0.65	1/2334 (0.0%)
3	D	0.57	0/1610	0.65	1/2203 (0.0%)
3	L	0.56	0/1614	0.66	0/2208
All	All	0.54	1/8044 (0.0%)	0.63	2/10980 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	202	CYS	CB-SG	-5.28	1.73	1.81

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	184	LEU	CA-CB-CG	5.41	127.74	115.30
3	D	70	GLY	N-CA-C	-5.28	99.91	113.10

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	698	613	613	1	0
1	C	689	549	549	4	0
2	B	1654	1602	1605	9	0
2	H	1664	1613	1622	4	0
3	D	1571	1516	1528	8	0
3	L	1575	1517	1534	2	0
4	B	6	8	8	0	0
4	H	6	8	8	0	0
5	D	1	0	0	0	0
5	L	1	0	0	0	0
6	A	3	0	0	0	0
6	B	104	0	0	2	0
6	C	2	0	0	0	0
6	D	88	0	0	0	0
6	H	104	0	0	0	0
6	L	85	0	0	1	0
All	All	8251	7426	7467	28	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (28) 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)
3:D:23:ARG:NH1	3:D:71:ASP:OD1	2.14	0.79
3:D:70:GLY:HA3	3:D:71:ASP:HB3	1.75	0.69
2:B:34:MET:HE2	2:B:96:CYS:HB2	1.82	0.59
2:H:34:MET:HE2	2:H:96:CYS:HB2	1.87	0.56
3:D:70:GLY:CA	3:D:71:ASP:CB	2.83	0.56
2:H:156:VAL:CG2	2:H:184:LEU:HD13	2.35	0.56
3:D:70:GLY:HA3	3:D:71:ASP:CB	2.35	0.56
1:C:145:PRO:O	1:C:149:SER:OG	2.28	0.51
2:B:184:LEU:C	2:B:184:LEU:HD12	2.31	0.51
2:B:156:VAL:CG2	2:B:184:LEU:HD21	2.40	0.51
3:D:22:CYS:O	3:D:72:LYS:HB3	2.13	0.49
2:B:34:MET:CE	2:B:96:CYS:HB2	2.44	0.48
1:C:127:LYS:HA	1:C:130:HIS:CD2	2.49	0.47
3:D:50:ILE:HD13	3:D:56:ARG:HA	1.95	0.47
1:C:127:LYS:HA	1:C:130:HIS:CG	2.50	0.46
1:A:128:ASN:HB3	1:A:135:GLN:HG2	1.97	0.46
2:B:149:LYS:NZ	6:B:410:HOH:O	2.48	0.46
3:L:23:ARG:HH11	3:L:72:LYS:HE3	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:ARG:HB3	2:B:41:PRO:HD2	2.01	0.42
3:D:41:LYS:HB3	3:D:42:PRO:HD2	2.01	0.42
1:C:94:TRP:CD1	1:C:112:ARG:NH1	2.88	0.42
2:B:194:SER:HB3	6:B:493:HOH:O	2.20	0.41
3:D:11:THR:CG2	3:D:109:LEU:HG	2.50	0.41
2:H:34:MET:HE3	2:H:97:ALA:N	2.35	0.41
2:B:11:LEU:CD2	2:B:122:THR:HG22	2.51	0.41
2:H:40:ARG:HB3	2:H:41:PRO:HD2	2.04	0.40
2:B:34:MET:HE3	2:B:97:ALA:N	2.37	0.40
3:L:1:GLN:NE2	6:L:413:HOH:O	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	92/130 (71%)	91 (99%)	1 (1%)	0	100	100
1	C	98/130 (75%)	96 (98%)	2 (2%)	0	100	100
2	B	218/223 (98%)	212 (97%)	6 (3%)	0	100	100
2	H	220/223 (99%)	213 (97%)	7 (3%)	0	100	100
3	D	210/215 (98%)	201 (96%)	8 (4%)	1 (0%)	29	15
3	L	210/215 (98%)	204 (97%)	6 (3%)	0	100	100
All	All	1048/1136 (92%)	1017 (97%)	30 (3%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	71	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	59/114 (52%)	57 (97%)	2 (3%)	37	19
1	C	51/114 (45%)	51 (100%)	0	100	100
2	B	182/187 (97%)	181 (100%)	1 (0%)	88	86
2	H	184/187 (98%)	182 (99%)	2 (1%)	73	65
3	D	171/175 (98%)	170 (99%)	1 (1%)	86	83
3	L	172/175 (98%)	169 (98%)	3 (2%)	60	47
All	All	819/952 (86%)	810 (99%)	9 (1%)	73	65

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	GLN
1	A	141	LEU
2	B	170	HIS
3	D	148	THR
2	H	170	HIS
2	H	184	LEU
3	L	90	CYS
3	L	148	THR
3	L	171	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	L	1	GLN

5.3.3 RNA ⓘ

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
4	GOL	H	301	-	5,5,5	0.57	0	5,5,5	0.40	0
4	GOL	B	301	-	5,5,5	0.14	0	5,5,5	0.53	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	H	301	-	-	4/4/4/4	-
4	GOL	B	301	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	301	GOL	O1-C1-C2-C3
4	H	301	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
4	H	301	GOL	O1-C1-C2-O2
4	H	301	GOL	O2-C2-C3-O3

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å²)	Q<0.9
1	A	94/130 (72%)	2.92	59 (62%)	0	0	52, 104, 141, 154	0
1	C	100/130 (76%)	3.06	64 (64%)	0	0	52, 116, 159, 190	0
2	B	220/223 (98%)	0.46	4 (1%)	68	68	20, 35, 68, 77	0
2	H	220/223 (98%)	0.63	8 (3%)	42	40	24, 38, 74, 88	0
3	D	212/215 (98%)	0.30	2 (0%)	84	84	23, 40, 60, 93	0
3	L	212/215 (98%)	0.31	2 (0%)	84	84	21, 38, 59, 92	0
All	All	1058/1136 (93%)	0.90	139 (13%)	3	3	20, 43, 126, 190	0

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	139	TRP	10.7
1	A	79	VAL	9.7
1	C	98	VAL	9.5
1	A	94	TRP	8.6
1	C	111	LEU	8.5
1	C	146	ARG	8.5
1	C	114	ALA	7.9
1	A	140	PHE	7.4
1	A	101	ALA	7.1
1	C	144	PHE	6.9
1	A	155	ILE	6.7
1	A	99	ALA	6.5
1	A	97	PHE	6.4
1	C	115	LEU	6.4
1	C	87	LEU	6.3
1	A	98	VAL	6.2
1	C	74	TYR	6.0
1	C	101	ALA	5.8
1	A	104	PRO	5.7

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Mol	Chain	Res	Type	RSRZ
1	C	100	ALA	5.7
1	A	103	LEU	5.6
1	C	71	ALA	5.5
1	C	93	ALA	5.5
1	A	89	THR	5.4
1	A	74	TYR	5.3
1	C	118	LEU	5.2
1	A	100	ALA	5.2
1	C	145	PRO	5.2
2	H	53	PRO	5.2
1	C	72	ILE	5.2
1	A	85	LEU	5.0
1	A	87	LEU	4.9
1	A	88	LEU	4.9
1	C	75	PHE	4.9
1	A	96	GLY	4.9
1	A	95	ASN	4.7
1	A	158	LEU	4.7
1	C	70	ASP	4.7
1	C	94	TRP	4.6
1	A	78	LYS	4.6
1	C	99	ALA	4.5
1	C	110	GLU	4.5
1	A	93	ALA	4.5
1	C	106	ASN	4.3
1	A	67	PHE	4.3
1	A	147	LEU	4.3
1	A	115	LEU	4.2
1	C	102	GLU	4.2
1	A	72	ILE	4.2
1	A	116	ASP	4.1
1	C	152	GLU	4.1
1	C	79	VAL	4.1
1	C	140	PHE	4.1
1	C	76	LYS	4.0
1	A	123	ILE	4.0
1	C	119	ALA	4.0
1	C	108	ALA	4.0
1	C	107	GLU	3.9
1	C	161	LEU	3.9
1	C	97	PHE	3.9
1	C	141	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	118	LEU	3.8
1	C	147	LEU	3.8
1	A	146	ARG	3.7
1	C	153	ASP	3.6
1	A	80	SER	3.5
1	A	141	LEU	3.5
1	A	144	PHE	3.5
1	C	165	VAL	3.5
2	H	80	TYR	3.4
1	A	107	GLU	3.4
1	A	124	MET	3.4
1	C	129	TRP	3.3
1	C	113	LYS	3.3
3	L	1	GLN	3.3
1	A	111	LEU	3.2
1	A	102	GLU	3.2
1	C	69	GLU	3.2
1	A	112	ARG	3.2
1	A	84	LEU	3.1
1	A	139	TRP	3.1
1	C	81	THR	3.0
1	A	120	ARG	3.0
1	C	86	LEU	3.0
1	C	123	ILE	3.0
1	A	105	ARG	3.0
1	A	129	TRP	3.0
1	C	160	ALA	3.0
1	C	80	SER	2.9
1	C	112	ARG	2.9
1	C	168	VAL	2.9
1	A	109	ASP	2.9
1	A	91	ASN	2.8
1	C	154	ASN	2.8
1	C	121	GLN	2.8
2	H	60	PHE	2.8
1	C	109	ASP	2.8
1	C	105	ARG	2.8
1	C	78	LYS	2.7
3	D	212	THR	2.7
1	C	82	GLN	2.7
1	A	142	LYS	2.7
1	C	137	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	90	ASP	2.7
1	A	106	ASN	2.7
1	A	86	LEU	2.6
1	C	103	LEU	2.6
2	B	196	GLY	2.6
1	C	143	GLU	2.6
1	A	145	PRO	2.5
1	A	153	ASP	2.5
1	A	157	ARG	2.5
1	C	96	GLY	2.5
1	C	122	MET	2.5
2	H	2	VAL	2.4
2	H	73	ASP	2.4
1	A	68	ILE	2.4
1	A	77	GLU	2.3
1	A	136	TYR	2.3
1	A	81	THR	2.2
1	C	95	ASN	2.2
1	C	117	ASN	2.2
1	A	90	ASP	2.2
1	A	110	GLU	2.2
3	L	212	THR	2.2
2	B	60	PHE	2.2
1	A	151	LEU	2.2
1	C	135	GLN	2.2
3	D	183	LEU	2.1
1	A	108	ALA	2.1
1	C	89	THR	2.1
1	A	71	ALA	2.1
2	H	101	LEU	2.1
1	C	163	ASP	2.1
2	H	3	GLN	2.1
2	H	83	LEU	2.1
2	B	137	THR	2.0
2	B	24	ALA	2.0
1	C	158	LEU	2.0

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

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(\AA^2)	Q<0.9
4	GOL	H	301	6/6	0.85	0.15	22,35,49,53	0
5	CL	L	301	1/1	0.88	0.15	67,67,67,67	0
4	GOL	B	301	6/6	0.90	0.14	24,32,44,47	0
5	CL	D	301	1/1	0.94	0.20	57,57,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.