



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:25 PM UTC

PDB ID : 7LFA / pdb_00007lfa
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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

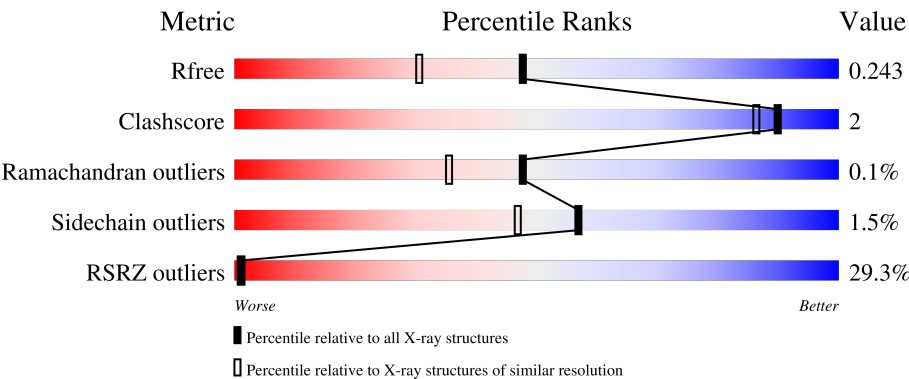
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 1.86 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}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (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	63% 68%28%
1	C	130	71% 72%5%23%
2	B	223	17% 94%..
2	H	223	19% 96%..
3	D	215	12% 91%6%..

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Mol	Chain	Length	Quality of chain
3	L	215	13% 95%

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 (CCD ID: 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 (CCD ID: 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.

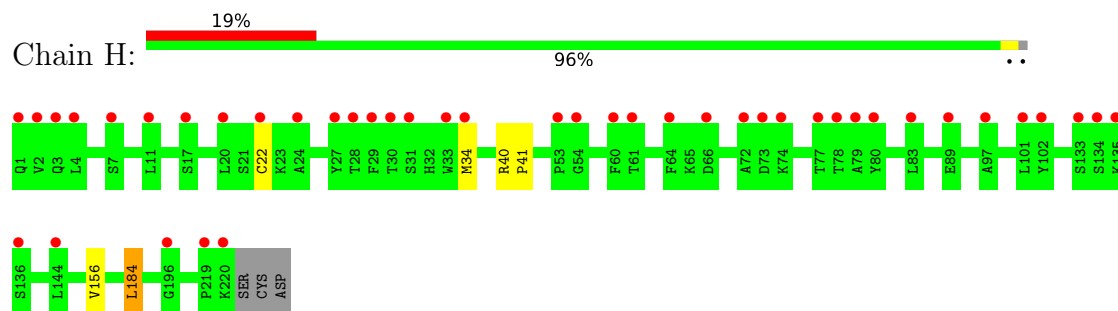
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	O	0	0
			3	3		
6	B	104	Total	O	0	0
			104	104		
6	C	2	Total	O	0	0
			2	2		
6	D	88	Total	O	0	0
			88	88		
6	H	104	Total	O	0	0
			104	104		

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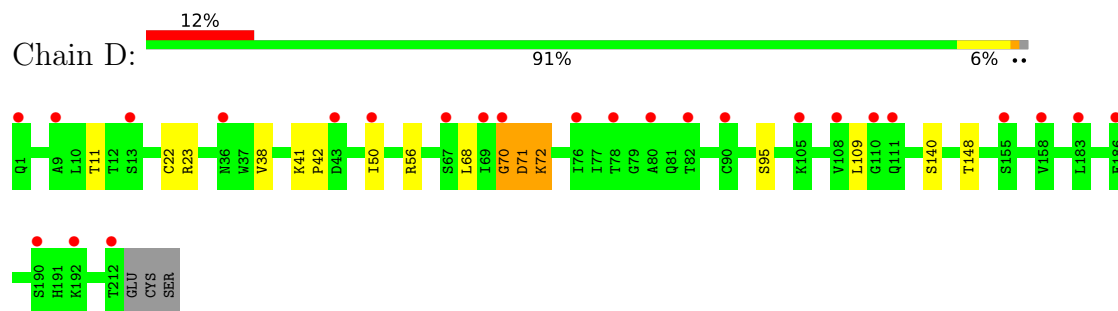
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	L	85	Total	O	0	0
			85	85		

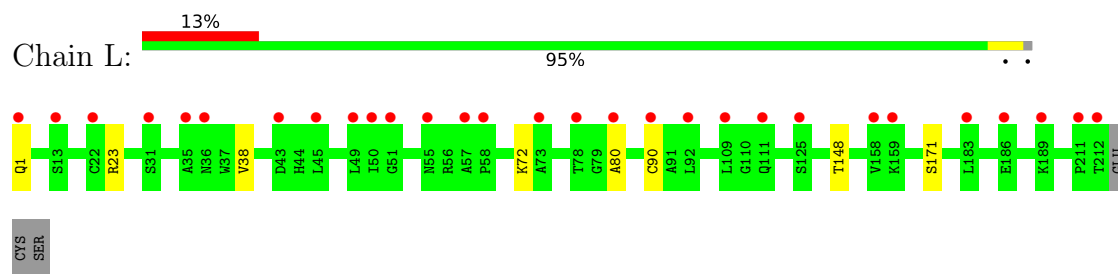
- Molecule 2: Fab 3B6 heavy chain



- 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 0.212 , 0.243	Depositor DCC
R_{free} test set	4044 reflections (2.69%)	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 , 48.2	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 [i](#)

5.1 Standard geometry [i](#)

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	0.41	0/710	0.82	0/966
1	C	0.38	0/700	0.81	0/957
2	B	0.73	0/1697	0.84	0/2312
2	H	0.71	0/1713	0.84	0/2334
3	D	0.72	1/1610 (0.1%)	0.86	3/2203 (0.1%)
3	L	0.73	0/1614	0.88	1/2208 (0.0%)
All	All	0.68	1/8044 (0.0%)	0.85	4/10980 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	68	LEU	C-O	-5.28	1.17	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	72	LYS	N-CA-C	5.64	117.81	109.69
3	D	70	GLY	N-CA-C	-5.60	99.91	113.18
3	D	140	SER	N-CA-C	5.06	116.88	109.24
3	L	80	ALA	N-CA-C	5.02	117.32	110.24

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	698	613	613	2	0
1	C	689	549	549	4	0
2	B	1654	1602	1605	9	0
2	H	1664	1613	1622	3	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
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
2:B:184:LEU:C	2:B:184:LEU:HD12	2.31	0.56
1:C:145:PRO:O	1:C:149:SER:OG	2.28	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:HE2	2:B:96:CYS:HB2	1.94	0.48
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:23:ARG:HH11	3:L:72:LYS:HE3	1.81	0.46
2:B:34:MET:HE2	2:B:96:CYS:SG	2.58	0.43
1:A:136:TYR:C	1:A:136:TYR:CD1	2.97	0.43
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:H:22:CYS:SG	2:H:34:MET:HE2	2.60	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: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
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%)	24	13
3	L	210/215 (98%)	204 (97%)	6 (3%)	0	100	100
All	All	1048/1136 (92%)	1017 (97%)	30 (3%)	1 (0%)	48	35

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%)	32	17
1	C	51/114 (45%)	50 (98%)	1 (2%)	48	36
2	B	182/187 (97%)	181 (100%)	1 (0%)	81	77
2	H	184/187 (98%)	183 (100%)	1 (0%)	81	77
3	D	171/175 (98%)	168 (98%)	3 (2%)	51	40
3	L	172/175 (98%)	168 (98%)	4 (2%)	44	30
All	All	819/952 (86%)	807 (98%)	12 (2%)	57	47

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

Mol	Chain	Res	Type
1	A	134	GLN
1	A	141	LEU
2	B	184	LEU
1	C	134	GLN
3	D	38	VAL
3	D	95	SER
3	D	148	THR
2	H	184	LEU
3	L	38	VAL
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 (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	82	GLN
1	C	134	GLN
1	C	135	GLN
1	C	138	ASN
2	H	177	GLN

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Mol	Chain	Res	Type
3	L	1	GLN
3	L	187	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	0.60	0	5,5,5	0.43	0
4	GOL	B	301	-	5,5,5	0.14	0	5,5,5	0.58	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
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(Å ²)	Q<0.9
1	A	94/130 (72%)	3.53	82 (87%) 0 0	58, 113, 149, 162	0
1	C	100/130 (76%)	4.25	92 (92%) 0 0	58, 127, 169, 202	0
2	B	220/223 (98%)	0.91	39 (17%) 4 3	22, 38, 75, 85	0
2	H	220/223 (98%)	1.11	43 (19%) 3 2	17, 42, 81, 99	2 (0%)
3	D	212/215 (98%)	0.87	25 (11%) 9 8	25, 43, 67, 102	0
3	L	212/215 (98%)	1.00	29 (13%) 6 6	21, 42, 64, 101	0
All	All	1058/1136 (93%)	1.51	310 (29%) 1 1	17, 46, 137, 202	2 (0%)

All (310) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	212	THR	8.9
1	C	97	PHE	8.2
1	C	165	VAL	8.2
1	C	139	TRP	8.0
1	A	97	PHE	7.8
1	C	152	GLU	7.7
1	C	168	VAL	7.7
1	A	79	VAL	7.5
1	A	75	PHE	7.4
1	A	140	PHE	7.4
1	A	155	ILE	7.4
1	A	74	TYR	7.3
1	A	66	ILE	7.3
1	C	147	LEU	6.9
1	C	111	LEU	6.8
1	C	114	ALA	6.7
1	C	118	LEU	6.7
1	C	108	ALA	6.6
1	C	144	PHE	6.4

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Mol	Chain	Res	Type	RSRZ
1	C	70	ASP	6.4
1	C	74	TYR	6.4
1	C	98	VAL	6.3
3	D	212	THR	6.2
1	A	104	PRO	6.0
1	C	105	ARG	6.0
1	C	75	PHE	6.0
1	A	118	LEU	5.9
1	C	90	ASP	5.8
1	C	87	LEU	5.8
1	C	79	VAL	5.8
1	C	115	LEU	5.7
1	C	93	ALA	5.7
1	C	146	ARG	5.6
1	A	103	LEU	5.6
1	C	76	LYS	5.6
1	A	67	PHE	5.6
1	A	159	ARG	5.5
3	L	1	GLN	5.5
1	C	106	ASN	5.4
1	C	140	PHE	5.4
1	C	72	ILE	5.4
1	A	123	ILE	5.4
1	C	81	THR	5.3
1	C	158	LEU	5.2
1	C	148	LYS	5.1
2	B	196	GLY	5.0
2	H	133	SER	5.0
1	C	100	ALA	4.9
1	C	88	LEU	4.9
1	A	106	ASN	4.9
1	A	77	GLU	4.9
1	A	108	ALA	4.9
1	A	158	LEU	4.9
1	A	146	ARG	4.9
1	C	156	ARG	4.8
1	C	135	GLN	4.8
1	C	92	GLU	4.8
1	C	99	ALA	4.8
1	C	101	ALA	4.8
1	C	155	ILE	4.8
1	C	103	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	87	LEU	4.7
1	C	84	LEU	4.7
1	A	90	ASP	4.7
1	C	120	ARG	4.7
1	A	94	TRP	4.6
1	A	84	LEU	4.6
2	B	1	GLN	4.5
1	C	151	LEU	4.5
1	A	115	LEU	4.4
3	D	78	THR	4.4
2	H	3	GLN	4.3
1	C	141	LEU	4.3
1	A	73	LYS	4.3
1	A	76	LYS	4.3
1	C	110	GLU	4.3
2	B	135	LYS	4.2
1	C	107	GLU	4.2
1	C	161	LEU	4.2
1	C	113	LYS	4.2
1	C	129	TRP	4.2
1	A	107	GLU	4.2
2	H	136	SER	4.1
1	A	99	ALA	4.1
1	C	71	ALA	4.1
1	C	89	THR	4.1
1	A	78	LYS	4.1
1	A	88	LEU	4.1
2	B	60	PHE	4.1
1	C	153	ASP	4.1
1	C	86	LEU	4.1
1	C	119	ALA	4.0
1	C	157	ARG	4.0
1	C	160	ALA	4.0
2	H	53	PRO	4.0
1	A	89	THR	4.0
2	H	220	LYS	4.0
1	C	104	PRO	4.0
1	A	151	LEU	4.0
1	C	78	LYS	4.0
1	C	85	LEU	4.0
2	H	31	SER	3.9
2	H	196	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	141	LEU	3.8
1	A	101	ALA	3.8
1	A	119	ALA	3.8
1	A	98	VAL	3.8
1	A	85	LEU	3.8
1	C	162	ALA	3.8
1	C	163	ASP	3.8
1	A	92	GLU	3.8
2	B	220	LYS	3.8
3	D	50	ILE	3.8
1	C	131	ASP	3.7
1	C	124	MET	3.7
1	C	145	PRO	3.7
2	B	137	THR	3.7
3	L	186	GLU	3.7
1	C	95	ASN	3.7
1	C	123	ILE	3.7
1	C	137	ARG	3.7
1	C	121	GLN	3.7
1	A	68	ILE	3.7
1	A	124	MET	3.7
1	A	139	TRP	3.7
2	H	80	TYR	3.7
2	B	66	ASP	3.6
1	A	72	ILE	3.6
2	H	7	SER	3.6
1	C	159	ARG	3.6
1	C	164	GLY	3.6
1	C	142	LYS	3.6
2	H	2	VAL	3.6
1	A	129	TRP	3.5
1	C	69	GLU	3.5
2	H	60	PHE	3.5
1	A	93	ALA	3.5
2	H	101	LEU	3.5
3	D	183	LEU	3.5
1	A	116	ASP	3.5
1	C	134	GLN	3.4
1	A	133	GLY	3.4
1	A	110	GLU	3.4
2	B	78	THR	3.4
1	C	94	TRP	3.3

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Mol	Chain	Res	Type	RSRZ
2	H	30	THR	3.3
1	A	112	ARG	3.3
1	A	136	TYR	3.3
1	C	109	ASP	3.3
1	C	133	GLY	3.3
2	H	134	SER	3.3
2	H	4	LEU	3.2
1	A	134	GLN	3.2
1	A	105	ARG	3.2
1	A	91	ASN	3.2
1	A	71	ALA	3.2
1	A	81	THR	3.2
1	A	121	GLN	3.1
3	L	211	PRO	3.1
1	A	153	ASP	3.1
2	H	135	LYS	3.1
3	L	36	ASN	3.1
2	H	78	THR	3.1
1	A	95	ASN	3.1
1	A	109	ASP	3.1
1	C	117	ASN	3.1
2	H	219	PRO	3.1
1	A	111	LEU	3.0
2	H	20	LEU	3.0
1	C	136	TYR	3.0
2	B	102	TYR	3.0
1	A	69	GLU	3.0
3	D	105	LYS	3.0
3	D	70	GLY	3.0
1	C	82	GLN	2.9
2	B	43	GLN	2.9
2	B	134	SER	2.9
1	A	96	GLY	2.9
2	H	28	THR	2.9
1	A	144	PHE	2.9
1	C	80	SER	2.9
1	C	102	GLU	2.9
2	B	24	ALA	2.9
3	L	73	ALA	2.8
1	C	166	GLN	2.8
3	L	111	GLN	2.8
1	C	73	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	27	TYR	2.8
1	A	122	MET	2.8
2	B	84	SER	2.8
2	H	24	ALA	2.8
1	A	82	GLN	2.8
1	A	120	ARG	2.8
1	A	150	GLU	2.8
1	A	149	SER	2.8
3	L	22	CYS	2.8
1	C	77	GLU	2.8
3	L	109	LEU	2.8
2	H	72	ALA	2.7
2	B	65	LYS	2.7
2	H	27	TYR	2.7
2	H	97	ALA	2.7
3	L	57	ALA	2.7
3	L	50	ILE	2.7
1	A	137	ARG	2.7
2	B	101	LEU	2.7
1	A	102	GLU	2.7
2	B	89	GLU	2.7
3	D	43	ASP	2.6
2	H	64	PHE	2.6
1	A	148	LYS	2.6
2	B	74	LYS	2.6
1	C	143	GLU	2.6
2	B	29	PHE	2.6
3	D	1	GLN	2.6
3	L	43	ASP	2.6
1	C	150	GLU	2.6
2	B	75	SER	2.6
2	B	52	TYR	2.6
1	A	86	LEU	2.6
1	A	125	LYS	2.6
1	A	100	ALA	2.6
1	A	117	ASN	2.6
1	A	156	ARG	2.5
2	B	26	GLY	2.5
2	B	68	ALA	2.5
2	B	3	GLN	2.5
2	H	1	GLN	2.5
3	D	90	CYS	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	108	TYR	2.5
3	L	183	LEU	2.5
3	D	69	ILE	2.5
1	C	83	ASN	2.5
1	C	154	ASN	2.5
2	H	77	THR	2.5
2	H	102	TYR	2.4
3	L	55	ASN	2.4
2	B	61	THR	2.4
1	A	131	ASP	2.4
1	A	80	SER	2.4
3	L	92	LEU	2.4
2	B	79	ALA	2.4
2	B	22	CYS	2.4
2	B	136	SER	2.4
2	H	74	LYS	2.4
1	C	116	ASP	2.4
1	C	112	ARG	2.4
3	D	186	GLU	2.4
2	H	61	THR	2.3
2	H	34	MET	2.3
2	H	54	GLY	2.3
1	A	135	GLN	2.3
3	D	111	GLN	2.3
2	H	79	ALA	2.3
3	D	76	ILE	2.3
3	L	58	PRO	2.3
2	B	80	TYR	2.3
3	L	189	LYS	2.3
3	L	35	ALA	2.3
3	D	110	GLY	2.3
1	C	132	LYS	2.3
2	B	37	LEU	2.3
1	A	145	PRO	2.2
2	H	33	TRP	2.2
1	C	122	MET	2.2
2	B	96	CYS	2.2
2	H	22	CYS	2.2
2	H	83	LEU	2.2
3	D	13	SER	2.2
3	L	13	SER	2.2
3	L	80	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
3	D	36	ASN	2.2
2	B	138	SER	2.2
3	L	90	CYS	2.2
1	C	96	GLY	2.2
3	L	51	GLY	2.2
2	B	131	ALA	2.2
1	A	157	ARG	2.2
2	H	29	PHE	2.1
2	H	89	GLU	2.1
2	B	62	GLN	2.1
1	A	70	ASP	2.1
3	D	155	SER	2.1
3	D	190	SER	2.1
3	L	45	LEU	2.1
3	L	49	LEU	2.1
1	A	142	LYS	2.1
2	H	17	SER	2.1
3	L	31	SER	2.1
3	D	9	ALA	2.1
3	D	80	ALA	2.1
2	B	51	ILE	2.1
2	H	73	ASP	2.1
3	D	67	SER	2.1
2	H	66	ASP	2.1
1	A	113	LYS	2.0
3	D	192	LYS	2.0
3	L	159	LYS	2.0
2	B	5	GLN	2.0
3	D	158	VAL	2.0
3	L	158	VAL	2.0
2	H	11	LEU	2.0
2	H	144	LEU	2.0
2	B	72	ALA	2.0
1	C	149	SER	2.0
2	B	133	SER	2.0
3	L	125	SER	2.0
3	D	82	THR	2.0
3	L	78	THR	2.0
3	D	108	VAL	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
5	CL	L	301	1/1	0.78	0.20	67,67,67,67	0
4	GOL	H	301	6/6	0.80	0.15	22,35,49,53	0
4	GOL	B	301	6/6	0.93	0.14	24,32,44,47	0
5	CL	D	301	1/1	0.95	0.18	57,57,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.