



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:59 PM GMT

PDB ID : 4K2U
Title : Crystal structure of PfEBA-175 F1 in complex with R218 antibody Fab fragment
Authors : Tolia, N.H.
Deposited on : 2013-04-09
Resolution : 2.45 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
<http://wwpdb.org/validation/2016/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 : 1.7 (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

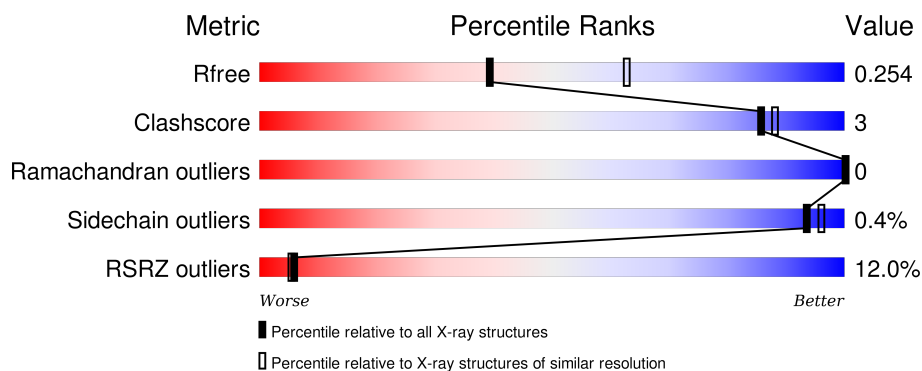
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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}	91344	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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 $\leq 5\%$. 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	297	<div> <div>11%</div> <div>72% 5% 23%</div> </div>
1	B	297	<div> <div>13%</div> <div>82% 13%</div> </div>
2	H	233	<div> <div>6%</div> <div>83% 6% 11%</div> </div>
2	I	233	<div> <div>7%</div> <div>85% 6% 8%</div> </div>
3	L	234	<div> <div>13%</div> <div>82% 7% 11%</div> </div>

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Mol	Chain	Length	Quality of chain
3	M	234	

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
4	SO4	I	301	-	-	-	X
4	SO4	I	303	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20975 atoms, of which 10201 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 Erythrocyte binding antigen 175.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	230	Total	C	H	N	O	S	0	0	0
			3869	1236	1919	345	353	16			
1	B	257	Total	C	H	N	O	S	0	0	0
			4313	1376	2144	376	398	19			

- Molecule 2 is a protein called Antibody Heavy Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	208	Total	C	H	N	O	S	0	0	0
			3143	1023	1544	257	314	5			
2	I	214	Total	C	H	N	O	S	0	0	0
			3235	1049	1589	267	324	6			

- Molecule 3 is a protein called Antibody Light Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	L	208	Total	C	H	N	O	S	0	0	0
			3146	1009	1526	273	332	6			
3	M	200	Total	C	H	N	O	S	0	0	0
			3038	970	1479	262	321	6			

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	I	1	Total	O	S	0	0
			5	4	1		
4	I	1	Total	O	S	0	0
			5	4	1		
4	I	1	Total	O	S	0	0
			5	4	1		
4	L	1	Total	O	S	0	0
			5	4	1		
4	L	1	Total	O	S	0	0
			5	4	1		
4	M	1	Total	O	S	0	0
			5	4	1		

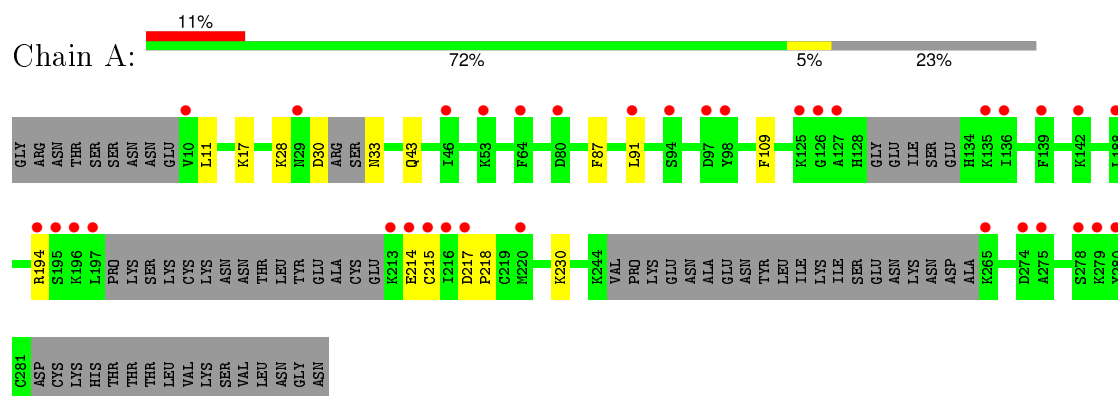
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	31	Total 31	O 31	0	0
5	B	46	Total 46	O 46	0	0
5	H	23	Total 23	O 23	0	0
5	I	36	Total 36	O 36	0	0
5	L	14	Total 14	O 14	0	0
5	M	21	Total 21	O 21	0	0

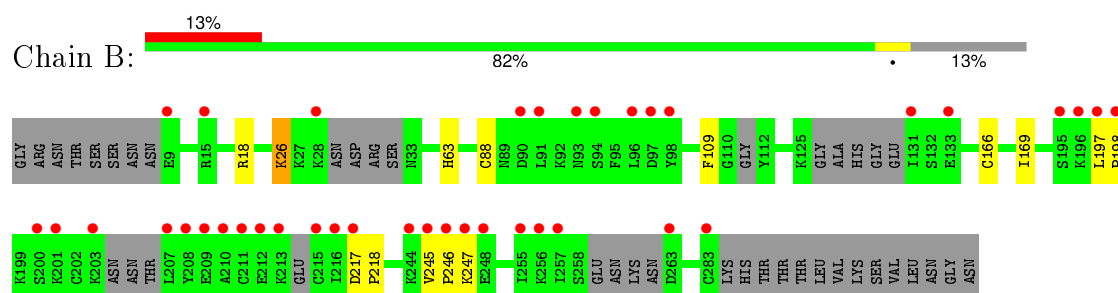
3 Residue-property plots [i](#)

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.

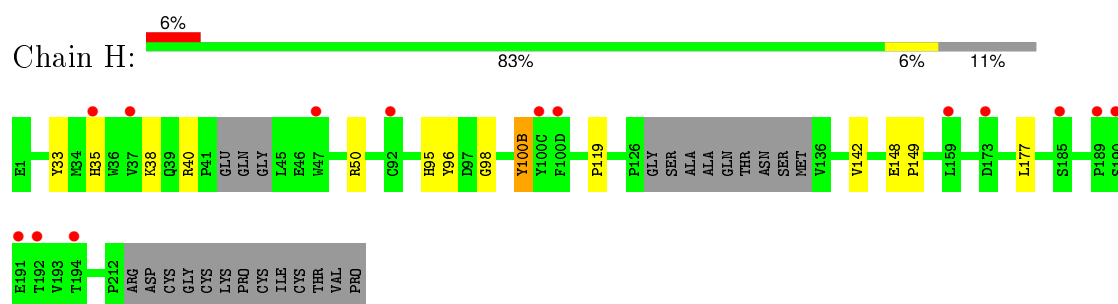
• Molecule 1: Erythrocyte binding antigen 175



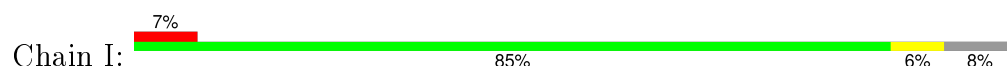
• Molecule 1: Erythrocyte binding antigen 175

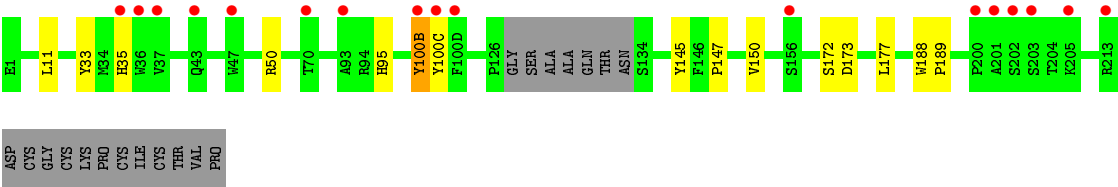


• Molecule 2: Antibody Heavy Chain

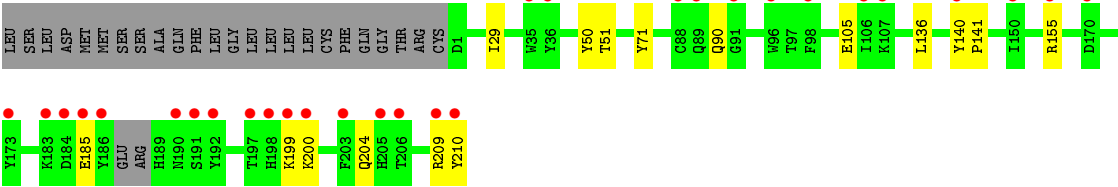
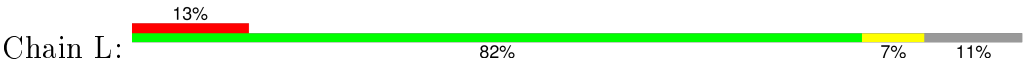


• Molecule 2: Antibody Heavy Chain

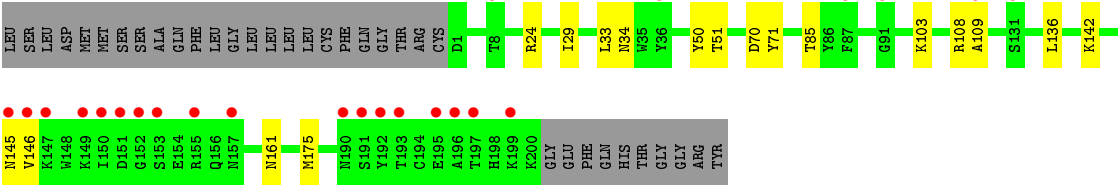
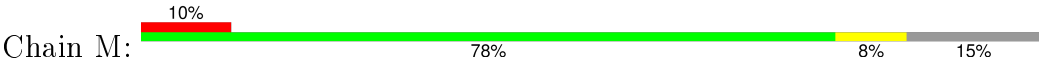




● Molecule 3: Antibody Light Chain



● Molecule 3: Antibody Light Chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	101.95Å 53.53Å 156.79Å 90.00° 91.18° 90.00°	Depositor
Resolution (Å)	29.79 – 2.45 29.79 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.4 (29.79-2.45) 99.5 (29.79-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.45Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.204 , 0.253 0.205 , 0.254	Depositor DCC
R_{free} test set	1996 reflections (3.19%)	DCC
Wilson B-factor (Å ²)	55.6	Xtriage
Anisotropy	0.572	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.1	EDS
Estimated twinning fraction	0.019 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 62644 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20975	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% 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, 0.375 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: SO4

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	0.22	0/1989	0.35	0/2654
1	B	0.22	0/2209	0.34	0/2947
2	H	0.23	0/1644	0.42	0/2251
2	I	0.23	0/1692	0.42	0/2315
3	L	0.22	0/1656	0.38	0/2245
3	M	0.23	0/1593	0.41	0/2162
All	All	0.22	0/10783	0.39	0/14574

There are no bond length outliers.

There are no bond angle outliers.

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	1950	1919	1926	11	0
1	B	2169	2144	2150	13	0
2	H	1599	1544	1551	8	0
2	I	1646	1589	1596	9	0
3	L	1620	1526	1533	8	0
3	M	1559	1479	1485	11	0
4	A	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	5	0	0	0	0
4	H	15	0	0	1	0
4	I	15	0	0	1	0
4	L	10	0	0	0	0
4	M	5	0	0	0	0
5	A	31	0	0	1	0
5	B	46	0	0	1	0
5	H	23	0	0	0	0
5	I	36	0	0	0	0
5	L	14	0	0	0	0
5	M	21	0	0	0	0
All	All	10774	10201	10241	58	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 3.

All (58) 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:M:108:ARG:NH1	3:M:109:ALA:O	1.98	0.97
1:A:30:ASP:OD2	1:A:33:ASN:N	2.17	0.77
1:A:194:ARG:NH2	5:A:423:HOH:O	2.24	0.70
3:L:155:ARG:NH2	3:L:185:GLU:OE2	2.33	0.62
1:B:245:VAL:HB	1:B:246:PRO:CD	2.34	0.58
3:M:145:ASN:OD1	3:M:146:VAL:N	2.37	0.57
3:L:29:ILE:HD11	3:L:71:TYR:CE1	2.39	0.57
2:H:100(B):TYR:OH	4:H:303:SO4:O4	2.17	0.57
1:A:217:ASP:N	1:A:218:PRO:HD2	2.19	0.57
2:H:38:LYS:HE2	2:H:40:ARG:HD2	1.87	0.57
1:B:88:CYS:SG	1:B:166:CYS:CB	2.93	0.56
3:M:24:ARG:NH1	3:M:70:ASP:OD1	2.38	0.56
2:I:100(B):TYR:OH	4:I:303:SO4:O3	2.07	0.54
1:B:18:ARG:NH2	5:B:405:HOH:O	2.42	0.53
2:I:11:LEU:HB2	2:I:147:PRO:HG3	1.91	0.52
2:H:33:TYR:HB2	2:H:95:HIS:HB2	1.92	0.52
1:B:245:VAL:HB	1:B:246:PRO:HD3	1.93	0.50
1:A:17:LYS:NZ	1:A:43:GLN:O	2.44	0.50
1:B:26:LYS:HD2	1:B:109:PHE:CE1	2.47	0.50
3:M:136:LEU:HD12	3:M:136:LEU:N	2.27	0.49
2:I:33:TYR:HB2	2:I:95:HIS:HB2	1.94	0.49
1:B:88:CYS:SG	1:B:166:CYS:HB2	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:209:ARG:HB3	3:L:210:TYR:HA	1.94	0.49
1:A:87:PHE:CE2	1:A:91:LEU:HD11	2.48	0.49
3:M:33:LEU:HD22	3:M:71:TYR:CB	2.42	0.48
2:I:177:LEU:C	2:I:177:LEU:HD12	2.34	0.47
1:B:217:ASP:N	1:B:218:PRO:HD2	2.30	0.47
1:B:197:LEU:HB3	1:B:198:PRO:HD3	1.97	0.47
1:A:11:LEU:HD23	1:B:63:HIS:NE2	2.31	0.46
3:L:140:TYR:CG	3:L:141:PRO:HA	2.51	0.46
1:B:26:LYS:HD2	1:B:109:PHE:CZ	2.51	0.46
2:H:119:PRO:HB2	2:H:142:VAL:HG13	1.98	0.45
2:H:177:LEU:C	2:H:177:LEU:HD12	2.37	0.45
1:A:214:GLU:O	1:A:215:CYS:HB3	2.16	0.45
1:A:217:ASP:N	1:A:218:PRO:CD	2.79	0.44
2:I:35:HIS:ND1	2:I:50:ARG:HB3	2.32	0.44
1:A:28:LYS:HG3	1:A:109:PHE:CE1	2.52	0.44
2:I:145:TYR:CE1	2:I:150:VAL:HG23	2.53	0.44
3:M:142:LYS:HG2	3:M:142:LYS:O	2.18	0.44
3:L:204:GLN:N	3:L:204:GLN:OE1	2.51	0.43
1:B:245:VAL:CB	1:B:246:PRO:CD	2.95	0.43
2:I:100(C):TYR:HB3	3:M:34:ASN:ND2	2.33	0.43
3:M:29:ILE:HD11	3:M:71:TYR:CE1	2.53	0.42
3:L:136:LEU:N	3:L:136:LEU:HD12	2.34	0.42
3:M:161:ASN:HB3	3:M:175:MET:HE3	2.02	0.42
2:I:172:SER:O	2:I:173:ASP:HB3	2.20	0.42
2:I:188:TRP:CD1	2:I:189:PRO:HA	2.54	0.42
1:A:230:LYS:NZ	4:A:302:SO4:O4	2.49	0.41
3:M:50:TYR:O	3:M:51:THR:HB	2.20	0.41
2:H:96:TYR:CE2	2:H:98:GLY:HA3	2.55	0.41
1:B:246:PRO:O	1:B:247:LYS:C	2.58	0.41
3:L:50:TYR:O	3:L:51:THR:HB	2.20	0.41
2:H:35:HIS:ND1	2:H:50:ARG:HB3	2.36	0.41
2:H:148:GLU:HB3	2:H:149:PRO:HA	2.02	0.41
1:B:169:ILE:O	1:B:169:ILE:HG23	2.20	0.41
3:M:85:THR:HG22	3:M:103:LYS:HA	2.03	0.41
3:L:199:LYS:HB3	3:L:200:LYS:HA	2.03	0.41
1:A:87:PHE:CZ	1:A:91:LEU:HD11	2.56	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	220/297 (74%)	212 (96%)	8 (4%)	0	100	100
1	B	243/297 (82%)	235 (97%)	8 (3%)	0	100	100
2	H	202/233 (87%)	197 (98%)	5 (2%)	0	100	100
2	I	210/233 (90%)	201 (96%)	9 (4%)	0	100	100
3	L	204/234 (87%)	188 (92%)	16 (8%)	0	100	100
3	M	198/234 (85%)	189 (96%)	9 (4%)	0	100	100
All	All	1277/1528 (84%)	1222 (96%)	55 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	217/278 (78%)	217 (100%)	0	100	100
1	B	244/278 (88%)	243 (100%)	1 (0%)	93	96
2	H	181/201 (90%)	180 (99%)	1 (1%)	90	94
2	I	186/201 (92%)	185 (100%)	1 (0%)	92	95
3	L	182/205 (89%)	180 (99%)	2 (1%)	80	88
3	M	177/205 (86%)	177 (100%)	0	100	100
All	All	1187/1368 (87%)	1182 (100%)	5 (0%)	93	96

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

Mol	Chain	Res	Type
1	B	26	LYS
2	H	100(B)	TYR
2	I	100(B)	TYR
3	L	90	GLN
3	L	105	GLU

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

12 ligands are 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	SO4	A	301	-	4,4,4	0.22	0	6,6,6	0.09	0
4	SO4	A	302	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	B	301	-	4,4,4	0.22	0	6,6,6	0.08	0
4	SO4	H	301	-	4,4,4	0.22	0	6,6,6	0.06	0
4	SO4	H	302	-	4,4,4	0.23	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	H	303	-	4,4,4	0.19	0	6,6,6	0.15	0
4	SO4	I	301	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	I	302	-	4,4,4	0.24	0	6,6,6	0.09	0
4	SO4	I	303	-	4,4,4	0.21	0	6,6,6	0.12	0
4	SO4	L	301	-	4,4,4	0.24	0	6,6,6	0.09	0
4	SO4	L	302	-	4,4,4	0.25	0	6,6,6	0.09	0
4	SO4	M	301	-	4,4,4	0.24	0	6,6,6	0.07	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	SO4	A	301	-	-	0/0/0/0	0/0/0/0
4	SO4	A	302	-	-	0/0/0/0	0/0/0/0
4	SO4	B	301	-	-	0/0/0/0	0/0/0/0
4	SO4	H	301	-	-	0/0/0/0	0/0/0/0
4	SO4	H	302	-	-	0/0/0/0	0/0/0/0
4	SO4	H	303	-	-	0/0/0/0	0/0/0/0
4	SO4	I	301	-	-	0/0/0/0	0/0/0/0
4	SO4	I	302	-	-	0/0/0/0	0/0/0/0
4	SO4	I	303	-	-	0/0/0/0	0/0/0/0
4	SO4	L	301	-	-	0/0/0/0	0/0/0/0
4	SO4	L	302	-	-	0/0/0/0	0/0/0/0
4	SO4	M	301	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	302	SO4	1	0
4	H	303	SO4	1	0
4	I	303	SO4	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, 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	230/297 (77%)	0.86	34 (14%)	3 3	51, 78, 153, 184	0
1	B	257/297 (86%)	0.91	39 (15%)	3 2	46, 72, 138, 166	0
2	H	208/233 (89%)	0.41	14 (6%)	21 22	48, 72, 112, 138	0
2	I	214/233 (91%)	0.54	17 (7%)	15 16	43, 67, 110, 136	0
3	L	208/234 (88%)	0.75	30 (14%)	3 3	51, 86, 142, 166	0
3	M	200/234 (85%)	0.75	24 (12%)	6 5	44, 78, 140, 159	0
All	All	1317/1528 (86%)	0.71	158 (11%)	6 5	43, 75, 139, 184	0

All (158) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	LEU	9.1
1	A	196	LYS	7.4
1	B	245	VAL	7.0
1	B	208	TYR	6.9
1	B	213	LYS	6.7
3	M	196	ALA	6.3
1	A	215	CYS	6.2
1	A	280	TYR	6.2
1	B	207	LEU	6.1
2	I	201	ALA	6.0
3	L	206	THR	5.9
1	A	135	LYS	5.9
1	B	211	CYS	5.7
3	M	149	LYS	5.4
1	B	246	PRO	5.4
1	B	210	ALA	5.2
3	L	200	LYS	5.1
3	M	197	THR	5.1
3	M	191	SER	4.9

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Mol	Chain	Res	Type	RSRZ
1	B	216	ILE	4.8
3	L	184	ASP	4.6
2	I	100(D)	PHE	4.6
1	B	283	CYS	4.6
1	A	98	TYR	4.6
1	B	94	SER	4.6
1	A	274	ASP	4.5
1	A	194	ARG	4.4
2	I	200	PRO	4.4
3	L	209	ARG	4.3
1	A	53	LYS	4.3
1	A	195	SER	4.2
1	A	125	LYS	4.0
3	L	185	GLU	4.0
1	A	136	ILE	4.0
3	M	195	GLU	3.9
3	L	210	TYR	3.9
3	M	36	TYR	3.9
1	A	188	LEU	3.8
1	B	93	ASN	3.8
3	L	190	ASN	3.7
3	M	146	VAL	3.7
1	B	212	GLU	3.7
1	B	247	LYS	3.7
3	L	183	LYS	3.7
3	M	150	ILE	3.6
3	L	88	CYS	3.6
2	I	205	LYS	3.5
3	L	203	PHE	3.5
2	I	213	ARG	3.5
1	B	133	GLU	3.5
1	B	215	CYS	3.5
3	L	192	TYR	3.4
1	B	98	TYR	3.4
2	H	100(D)	PHE	3.4
3	L	150	ILE	3.4
3	L	197	THR	3.4
1	A	142	LYS	3.3
1	B	197	LEU	3.3
2	H	191	GLU	3.3
1	A	279	LYS	3.2
1	B	196	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
3	L	186	TYR	3.1
3	M	192	TYR	3.1
1	A	214	GLU	3.1
3	M	152	GLY	3.1
1	B	255	ILE	3.1
2	I	203	SER	3.1
3	L	173	TYR	3.0
1	A	139	PHE	3.0
2	I	47	TRP	3.0
3	L	198	HIS	3.0
3	M	8	THR	3.0
1	A	265	LYS	3.0
3	L	35	TRP	3.0
3	M	193	THR	2.9
1	B	201	LYS	2.9
1	A	94	SER	2.9
1	B	209	GLU	2.9
1	B	131	ILE	2.9
2	I	100(C)	TYR	2.9
1	B	244	LYS	2.9
3	L	199	LYS	2.9
1	A	213	LYS	2.9
2	I	43	GLN	2.8
3	L	36	TYR	2.8
3	L	205	HIS	2.8
2	H	192	THR	2.7
1	B	248	GLU	2.7
1	A	126	GLY	2.7
3	L	191	SER	2.7
2	H	173	ASP	2.7
2	I	100(B)	TYR	2.7
3	M	190	ASN	2.7
3	M	147	LYS	2.7
2	H	185	SER	2.6
3	M	199	LYS	2.6
1	B	9	GLU	2.6
3	L	91	GLY	2.6
1	B	198	PRO	2.6
2	I	156	SER	2.6
3	L	155	ARG	2.6
2	H	37	VAL	2.6
2	I	35	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	90	ASP	2.6
1	B	217	ASP	2.6
1	A	216	ILE	2.5
2	I	36	TRP	2.5
1	A	46	ILE	2.5
2	H	47	TRP	2.5
3	M	91	GLY	2.5
3	M	87	PHE	2.5
3	M	131	SER	2.5
3	L	98	PHE	2.4
3	L	107	LYS	2.4
2	H	189	PRO	2.4
1	B	28	LYS	2.4
1	B	91	LEU	2.4
2	H	190	SER	2.4
1	A	275	ALA	2.4
1	A	97	ASP	2.4
2	H	194	THR	2.4
1	A	29	ASN	2.3
1	B	257	ILE	2.3
1	A	64	PHE	2.3
1	B	15	ARG	2.3
1	B	96	LEU	2.3
2	I	70	THR	2.3
3	M	157	ASN	2.3
1	A	278	SER	2.2
1	B	200	SER	2.2
1	B	256	LYS	2.2
1	B	263	ASP	2.2
3	L	96	TRP	2.2
3	L	170	ASP	2.2
1	A	10	VAL	2.2
3	M	109	ALA	2.2
2	I	202	SER	2.2
3	M	151	ASP	2.2
3	M	155	ARG	2.1
1	B	203	LYS	2.1
3	M	145	ASN	2.1
3	L	89	GLN	2.1
2	H	92	CYS	2.1
2	H	159	LEU	2.1
2	I	37	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
2	H	35	HIS	2.1
2	I	93	ALA	2.1
3	M	153	SER	2.1
1	B	97	ASP	2.1
1	A	220	MET	2.0
1	A	91	LEU	2.0
1	A	217	ASP	2.0
1	B	195	SER	2.0
2	H	100(C)	TYR	2.0
3	L	140	TYR	2.0
1	A	127	ALA	2.0
1	A	80	ASP	2.0
3	L	106	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
4	SO4	I	301	5/5	0.66	0.74	29.08	199,200,201,202	0
4	SO4	I	303	5/5	0.95	0.35	2.06	76,77,103,108	0
4	SO4	A	302	5/5	0.90	0.35	0.80	117,123,125,127	0
4	SO4	H	303	5/5	0.97	0.21	0.37	76,83,92,102	0
4	SO4	A	301	5/5	0.90	0.15	-0.52	113,117,123,128	0
4	SO4	H	301	5/5	0.97	0.11	-0.89	64,64,76,81	0
4	SO4	I	302	5/5	0.96	0.13	-1.07	80,81,84,87	0
4	SO4	L	301	5/5	0.96	0.12	-1.16	76,85,95,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	SO4	H	302	5/5	0.91	0.13	-1.39	136,137,138,138	0
4	SO4	M	301	5/5	0.97	0.11	-1.59	62,71,82,84	0
4	SO4	B	301	5/5	0.95	0.11	-	123,124,128,131	0
4	SO4	L	302	5/5	0.79	0.25	-	145,151,152,153	0

6.5 Other polymers [i](#)

There are no such residues in this entry.