



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 11:26 AM EDT

PDB ID : 2W9E / pdb_00002w9e
Title : Structure of ICSM 18 (anti-Prp therapeutic antibody) Fab fragment complexed with human Prp fragment 119-231
Authors : Antonyuk, S.V.; Trevitt, C.R.; Strange, R.W.; Jackson, G.S.; Sangar, D.; Batchelor, M.; Jones, S.; Georgiou, T.; Cooper, S.; Fraser, C.; Khalili-Shirazi, A.; Clarke, A.R.; Hasnain, S.S.; Collinge, J.
Deposited on : 2009-01-23
Resolution : 2.90 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

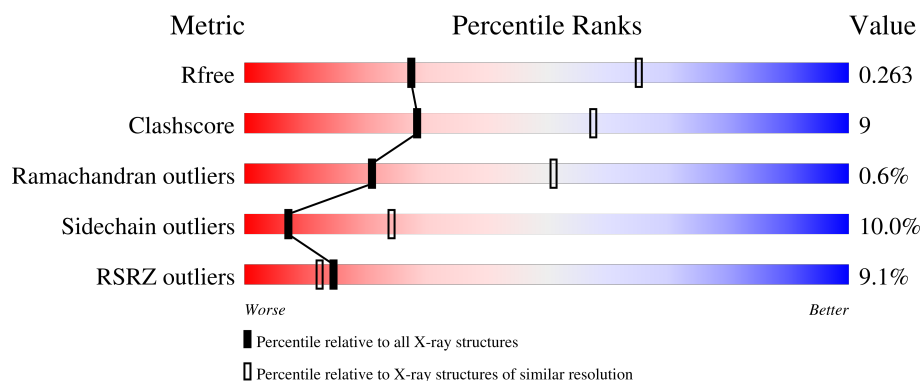
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	113	5% 67% 19% 12%
2	H	215	6% 73% 23% .
3	L	212	14% 78% 20% .

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4151 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 MAJOR PRION PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	99	Total	C	N	O	S	0	0	0
			828	512	144	163	9			

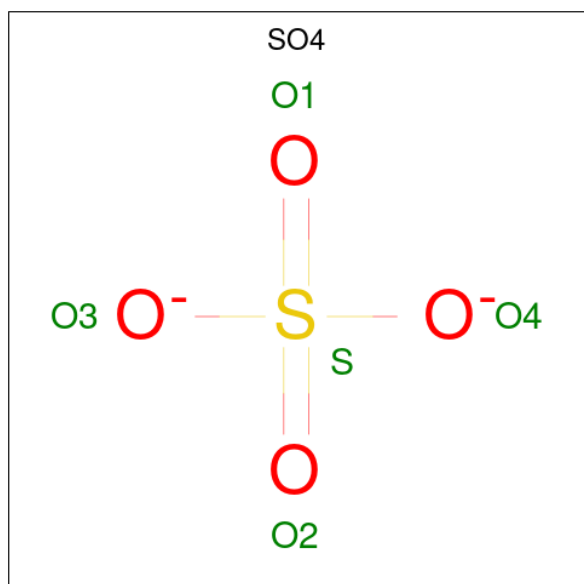
- Molecule 2 is a protein called ICSM 18-ANTI-PRP THERAPEUTIC FAB HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	215	Total	C	N	O	S	0	2	0
			1623	1029	263	326	5			

- Molecule 3 is a protein called ICSM 18-ANTI-PRP THERAPEUTIC FAB LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	6	0
			1653	1030	276	338	9			

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

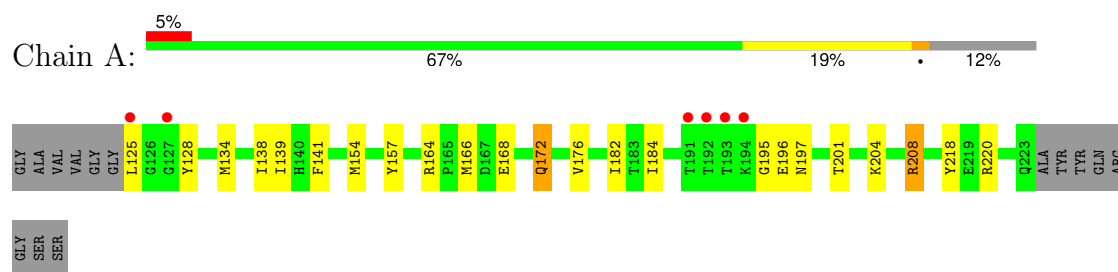
- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	4	Total	O		0	0
			4	4			
5	H	16	Total	O		0	0
			16	16			
5	L	22	Total	O		0	0
			22	22			

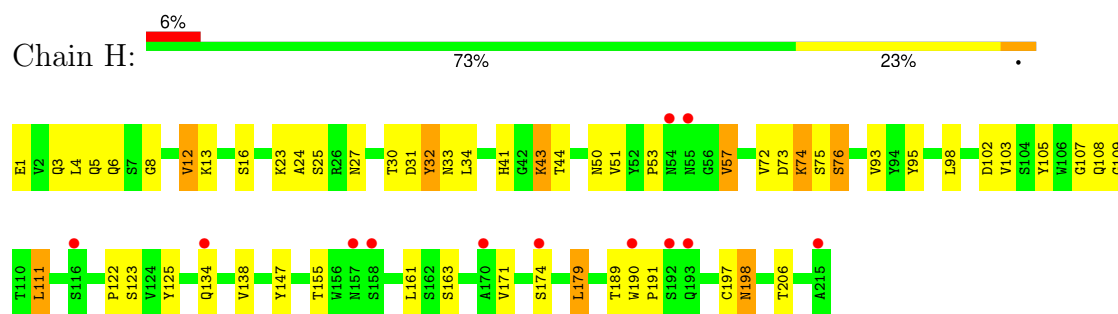
3 Residue-property plots [i](#)

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.

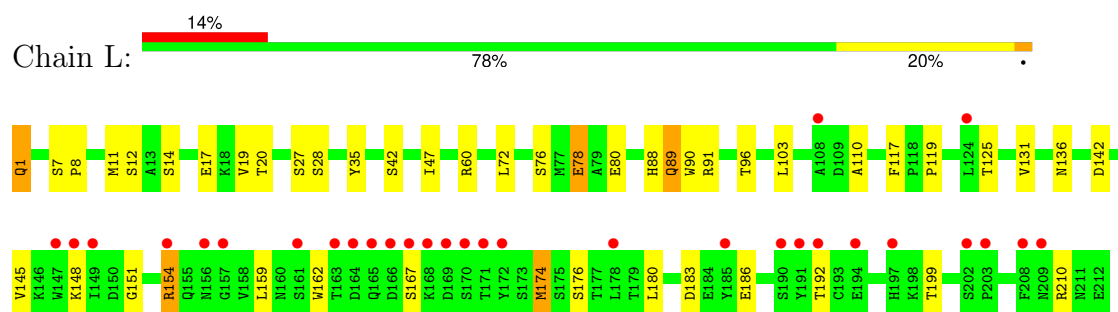
• Molecule 1: MAJOR PRION PROTEIN



• Molecule 2: ICSM 18-ANTI-PRP THERAPEUTIC FAB HEAVY CHAIN



• Molecule 3: ICSM 18-ANTI-PRP THERAPEUTIC FAB LIGHT CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	126.15Å 126.15Å 134.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.90 50.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (50.00-2.90) 97.5 (50.00-2.90)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.3.0037	Depositor
R, R_{free}	0.207 , 0.269 0.206 , 0.263	Depositor DCC
R_{free} test set	711 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	55.2	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 76.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4151	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% 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: 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	0.61	0/846	0.88	0/1141
2	H	0.59	0/1674	0.93	4/2296 (0.2%)
3	L	0.68	1/1712 (0.1%)	0.82	1/2323 (0.0%)
All	All	0.63	1/4232 (0.0%)	0.88	5/5760 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	151	GLY	C-N	13.94	1.53	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	23	LYS	N-CA-C	7.06	119.92	108.41
2	H	8	GLY	CA-C-N	5.57	125.75	119.90
2	H	8	GLY	C-N-CA	5.57	125.75	119.90
3	L	136	ASN	N-CA-C	5.56	118.47	109.40
2	H	57	VAL	N-CA-C	5.40	116.38	109.30

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	828	0	769	11	0
2	H	1623	0	1568	30	0
3	L	1653	0	1589	31	1
4	A	5	0	0	0	0
5	A	4	0	0	0	0
5	H	16	0	0	1	0
5	L	22	0	0	0	0
All	All	4151	0	3926	71	1

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 9.

All (71) 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:L:1:GLN:OE1	3:L:1:GLN:N	1.98	0.96
2:H:33:ASN:HD21	2:H:50:ASN:HD22	1.09	0.92
1:A:166:MET:HE1	1:A:218:TYR:CD1	2.07	0.90
2:H:122:PRO:HB3	2:H:147:TYR:HB3	1.58	0.86
2:H:6:GLN:NE2	2:H:109:GLY:H	1.82	0.77
2:H:33:ASN:ND2	2:H:50:ASN:HD22	1.83	0.76
3:L:148:LYS:HB2	3:L:192:THR:HB	1.68	0.75
1:A:166:MET:HE1	1:A:218:TYR:HD1	1.53	0.73
2:H:5:GLN:HG3	2:H:108:GLN:HE22	1.54	0.72
3:L:89:GLN:NE2	3:L:91:ARG:H	1.90	0.70
3:L:11:MET:CE	3:L:19:VAL:HG13	2.24	0.68
2:H:6:GLN:HE21	2:H:107:GLY:HA3	1.59	0.67
3:L:154:ARG:HG2	3:L:154:ARG:HH11	1.60	0.66
3:L:88:HIS:CE1	3:L:90:TRP:HE1	2.15	0.64
2:H:95:TYR:CE2	3:L:42:SER:HB2	2.33	0.64
3:L:162:TRP:HE1	3:L:174:MET:HE3	1.62	0.63
2:H:33:ASN:HD21	2:H:50:ASN:ND2	1.91	0.63
3:L:11:MET:HE3	3:L:19:VAL:HG13	1.81	0.60
3:L:11:MET:HE2	3:L:103:LEU:HD13	1.85	0.59
2:H:198:ASN:HD22	2:H:198:ASN:N	1.98	0.59
3:L:8:PRO:HG2	3:L:11:MET:HB2	1.85	0.59
2:H:43:LYS:HG3	2:H:44:THR:HG23	1.86	0.58
3:L:154:ARG:HG2	3:L:154:ARG:NH1	2.20	0.56
2:H:53:PRO:HB3	2:H:72:VAL:HG21	1.86	0.56
2:H:197:CYS:C	2:H:198:ASN:HD22	2.15	0.55
3:L:47:ILE:HD12	3:L:72[A]:LEU:HD13	1.89	0.54
2:H:122:PRO:CB	2:H:147:TYR:HB3	2.34	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:119:PRO:HD3	3:L:131:VAL:HG22	1.90	0.54
2:H:93:VAL:HG22	2:H:111:LEU:HD12	1.90	0.53
3:L:11:MET:HE1	3:L:19:VAL:HG13	1.90	0.53
2:H:134:GLN:HG3	2:H:134:GLN:O	2.09	0.51
3:L:162:TRP:CD1	3:L:174:MET:HG3	2.46	0.51
3:L:88:HIS:HD2	3:L:96:THR:O	1.94	0.50
1:A:172:GLN:O	1:A:176:VAL:HG23	2.12	0.50
3:L:162:TRP:NE1	3:L:174:MET:HE3	2.27	0.49
2:H:179:LEU:C	2:H:179:LEU:HD12	2.38	0.49
2:H:190:TRP:CD1	2:H:191:PRO:HA	2.48	0.49
1:A:139:ILE:HG21	1:A:208:ARG:HG2	1.95	0.48
2:H:31:ASP:O	2:H:32:TYR:HB3	2.14	0.48
3:L:159:LEU:O	3:L:176:SER:HA	2.14	0.47
3:L:1:GLN:N	3:L:1:GLN:CD	2.64	0.47
3:L:154:ARG:HH12	3:L:180:LEU:CD2	2.28	0.47
2:H:12:VAL:HG12	2:H:16:SER:HB2	1.95	0.46
3:L:60:ARG:HD2	3:L:76:SER:O	2.15	0.46
2:H:6:GLN:HE21	2:H:107:GLY:CA	2.27	0.46
2:H:123:SER:HB3	2:H:125:TYR:CZ	2.51	0.46
3:L:110:ALA:C	3:L:199:THR:HG21	2.40	0.46
2:H:74:LYS:C	2:H:76:SER:H	2.23	0.46
2:H:190:TRP:CG	2:H:191:PRO:HA	2.51	0.45
1:A:164:ARG:NH1	1:A:168:GLU:OE1	2.50	0.45
2:H:198:ASN:N	2:H:198:ASN:ND2	2.64	0.45
3:L:11:MET:CE	3:L:19:VAL:CG1	2.93	0.45
2:H:24:ALA:HB1	2:H:27:ASN:HB2	1.99	0.45
3:L:14:SER:O	3:L:17:GLU:HB2	2.16	0.45
3:L:11:MET:HE1	3:L:19:VAL:CG1	2.47	0.44
1:A:196:GLU:HG3	1:A:197:ASN:N	2.33	0.44
2:H:41:HIS:CD2	2:H:43:LYS:HG2	2.53	0.43
3:L:7:SER:HA	3:L:8:PRO:C	2.43	0.43
1:A:154:MET:HA	1:A:157:TYR:CD1	2.53	0.43
2:H:73:ASP:OD2	2:H:75:SER:HB2	2.19	0.42
1:A:134:MET:HE2	1:A:220:ARG:NH1	2.34	0.42
2:H:32:TYR:CZ	2:H:53:PRO:HG2	2.54	0.42
3:L:35:TYR:N	3:L:35:TYR:CD1	2.88	0.42
1:A:139:ILE:HG22	1:A:141:PHE:CZ	2.55	0.42
3:L:117:PHE:O	3:L:131:VAL:HG13	2.20	0.41
3:L:186:GLU:HA	3:L:210:ARG:NH2	2.35	0.41
1:A:128:TYR:CE2	1:A:182:ILE:HD13	2.55	0.41
2:H:1:GLU:N	2:H:105:TYR:OH	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:ILE:HD13	1:A:154:MET:HE1	2.02	0.41
2:H:111:LEU:HD23	5:H:2008:HOH:O	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:78:GLU:OE1	3:L:78:GLU:OE1[8_555]	1.94	0.26

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	97/113 (86%)	91 (94%)	5 (5%)	1 (1%)	12	39
2	H	215/215 (100%)	197 (92%)	16 (7%)	2 (1%)	14	41
3	L	216/212 (102%)	205 (95%)	11 (5%)	0	100	100
All	All	528/540 (98%)	493 (93%)	32 (6%)	3 (1%)	21	51

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	32	TYR
2	H	76	SER
1	A	195	GLY

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	93/101 (92%)	87 (94%)	6 (6%)	15	44
2	H	186/186 (100%)	160 (86%)	26 (14%)	3	11
3	L	191/185 (103%)	175 (92%)	16 (8%)	10	31
All	All	470/472 (100%)	422 (90%)	48 (10%)	7	23

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	LEU
1	A	172	GLN
1	A	184	ILE
1	A	201	THR
1	A	204	LYS
1	A	208	ARG
2	H	3	GLN
2	H	4	LEU
2	H	12	VAL
2	H	13	LYS
2	H	25	SER
2	H	30	THR
2	H	34	LEU
2	H	43	LYS
2	H	51	VAL
2	H	57	VAL
2	H	74	LYS
2	H	98[A]	LEU
2	H	98[B]	LEU
2	H	102	ASP
2	H	103	VAL
2	H	111	LEU
2	H	138	VAL
2	H	155	THR
2	H	161	LEU
2	H	163	SER
2	H	171	VAL
2	H	174	SER
2	H	179	LEU
2	H	189	THR
2	H	198	ASN

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Mol	Chain	Res	Type
2	H	206	THR
3	L	1	GLN
3	L	12	SER
3	L	20	THR
3	L	27	SER
3	L	28[A]	SER
3	L	28[B]	SER
3	L	78	GLU
3	L	80	GLU
3	L	89	GLN
3	L	125	THR
3	L	142	ASP
3	L	145	VAL
3	L	154	ARG
3	L	167	SER
3	L	174	MET
3	L	183	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	155	HIS
1	A	174	ASN
1	A	186	GLN
2	H	3	GLN
2	H	5	GLN
2	H	6	GLN
2	H	33	ASN
2	H	157	ASN
2	H	193	GLN
2	H	198	ASN
3	L	88	HIS
3	L	89	GLN
3	L	160	ASN

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 oligosaccharides 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	SO4	A	300	-	4,4,4	0.25	0	6,6,6	0.19	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.

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	99/113 (87%)	0.60	6 (6%) 27 21	30, 38, 57, 60	3 (3%)
2	H	215/215 (100%)	0.64	12 (5%) 30 23	21, 40, 49, 57	2 (0%)
3	L	212/212 (100%)	0.84	30 (14%) 6 5	25, 40, 50, 54	6 (2%)
All	All	526/540 (97%)	0.71	48 (9%) 15 12	21, 40, 51, 60	11 (2%)

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	193	THR	7.0
1	A	194	LYS	6.2
3	L	167	SER	5.8
3	L	170	SER	4.4
3	L	164	ASP	4.2
1	A	191	THR	4.1
2	H	116	SER	3.7
3	L	108	ALA	3.5
3	L	185	TYR	3.4
3	L	165	GLN	3.2
3	L	163	THR	3.1
3	L	190	SER	2.9
2	H	157	ASN	2.9
3	L	168	LYS	2.9
3	L	172	TYR	2.8
2	H	174	SER	2.7
3	L	191	TYR	2.6
3	L	161	SER	2.6
3	L	169	ASP	2.6
3	L	171	THR	2.6
1	A	127	GLY	2.5
3	L	203	PRO	2.5
2	H	215	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
2	H	192	SER	2.5
3	L	154	ARG	2.5
2	H	54	ASN	2.5
3	L	149	ILE	2.5
3	L	124	LEU	2.4
3	L	166	ASP	2.4
3	L	147	TRP	2.4
3	L	194	GLU	2.3
3	L	202	SER	2.3
2	H	193	GLN	2.3
3	L	156	ASN	2.2
1	A	192	THR	2.2
3	L	148	LYS	2.2
2	H	55	ASN	2.2
3	L	197	HIS	2.2
2	H	190	TRP	2.2
1	A	125	LEU	2.2
2	H	158	SER	2.2
3	L	192	THR	2.1
3	L	208	PHE	2.1
2	H	170	ALA	2.1
2	H	134	GLN	2.0
3	L	157	GLY	2.0
3	L	178	LEU	2.0
3	L	209	ASN	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
4	SO4	A	300	5/5	0.86	0.22	46,47,47,47	5

6.5 Other polymers [i](#)

There are no such residues in this entry.