



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2024 – 10:56 AM EDT

PDB ID : 2A1W
Title : Anti-cocaine antibody 7.5.21, crystal form I
Authors : Pozharski, E.; Hewagama, A.; Shanafelt, A.; Ringe, D.; Petsko, G.A.
Deposited on : 2005-06-21
Resolution : 2.70 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

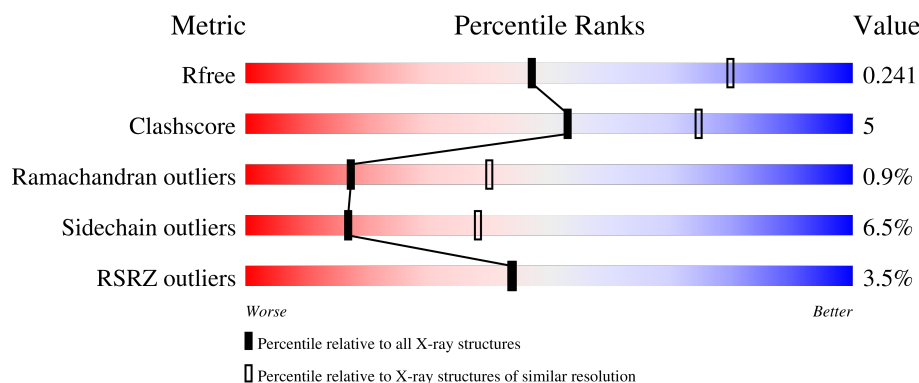
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	L	216	<div> <div>3%</div> <div>84%</div> <div>14%</div> <div>.</div> </div>
1	M	216	<div> <div>%</div> <div>85%</div> <div>12%</div> <div>.</div> </div>
2	H	225	<div> <div>4%</div> <div>81%</div> <div>16%</div> <div>.</div> </div>
2	I	225	<div> <div>6%</div> <div>83%</div> <div>15%</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6935 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 immunoglobulin light chain kappa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	216	Total	C	N	O	S	0	0	0
			1682	1052	288	335	7			
1	M	216	Total	C	N	O	S	0	0	0
			1682	1052	288	335	7			

- Molecule 2 is a protein called immunoglobulin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	225	Total	C	N	O	S	0	0	0
			1706	1078	286	334	8			
2	I	225	Total	C	N	O	S	0	0	0
			1706	1078	286	334	8			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

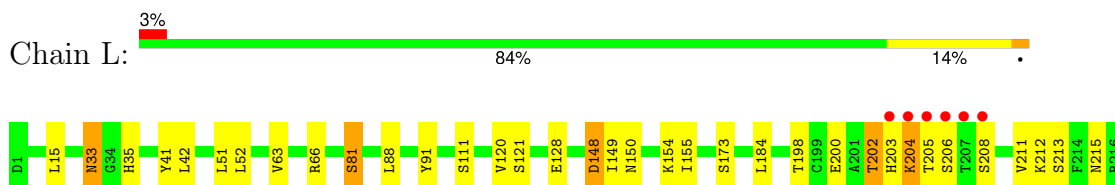
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	L	22	Total O 22 22	0	0
4	H	26	Total O 26 26	0	0
4	M	27	Total O 27 27	0	0
4	I	49	Total O 49 49	0	0

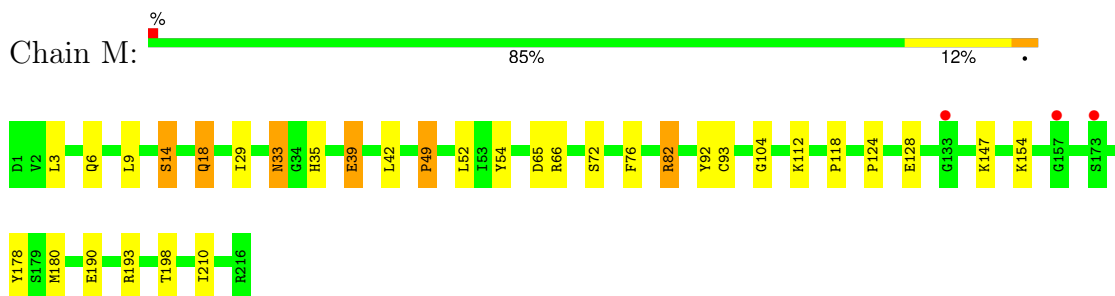
3 Residue-property plots [i](#)

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.

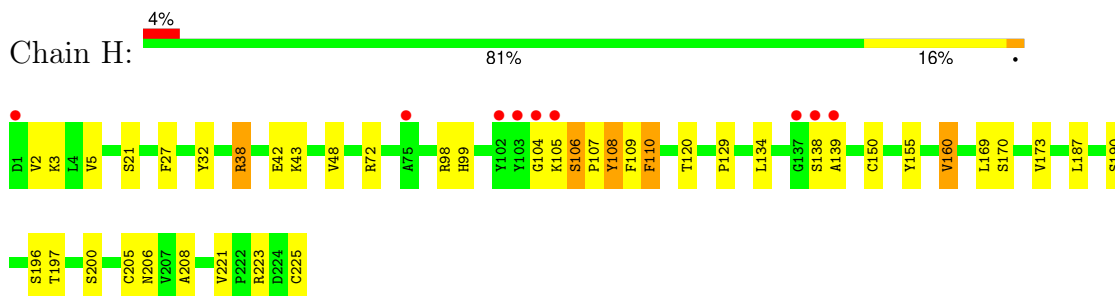
- Molecule 1: immunoglobulin light chain kappa



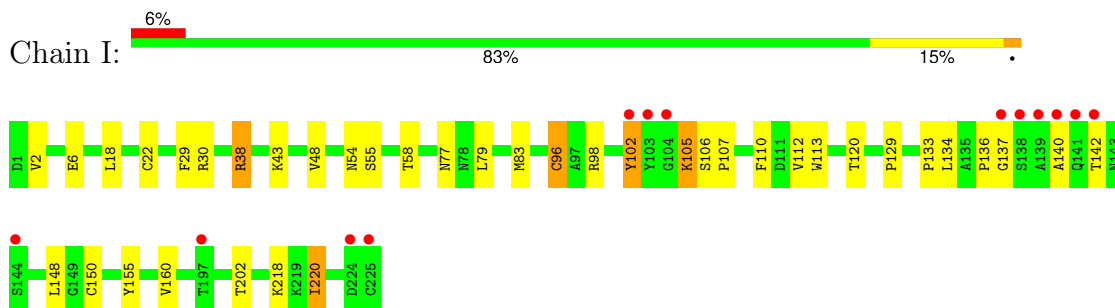
- Molecule 1: immunoglobulin light chain kappa



- Molecule 2: immunoglobulin heavy chain



- Molecule 2: immunoglobulin heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	178.60Å 58.40Å 98.10Å 90.00° 110.66° 90.00°	Depositor
Resolution (Å)	30.50 – 2.70 30.47 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.50-2.70) 99.8 (30.47-2.70)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.68Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.185 , 0.247 0.183 , 0.241	Depositor DCC
R_{free} test set	1334 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 48.8	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	0.94	EDS
Total number of atoms	6935	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 4.17% 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	L	0.43	0/1722	0.58	1/2333 (0.0%)
1	M	0.42	0/1722	0.57	0/2333
2	H	0.43	0/1752	0.59	0/2391
2	I	0.51	1/1752 (0.1%)	0.60	0/2391
All	All	0.45	1/6948 (0.0%)	0.59	1/9448 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	96	CYS	CB-SG	-7.84	1.69	1.82

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	204	LYS	N-CA-C	5.00	124.50	111.00

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	L	1682	0	1626	18	0
1	M	1682	0	1626	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	1706	0	1660	20	0
2	I	1706	0	1660	21	0
3	I	15	0	0	0	0
3	L	10	0	0	0	0
3	M	10	0	0	0	0
4	H	26	0	0	0	0
4	I	49	0	0	2	0
4	L	22	0	0	0	0
4	M	27	0	0	0	0
All	All	6935	0	6572	72	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 5.

All (72) 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:204:LYS:H	1:L:205:THR:HB	1.16	1.07
2:H:106:SER:HB3	2:I:105:LYS:HG2	1.60	0.82
2:H:105:LYS:HG3	2:H:107:PRO:HD3	1.65	0.79
1:L:204:LYS:N	1:L:205:THR:HB	1.97	0.79
2:I:102:TYR:HD2	2:I:102:TYR:H	1.32	0.78
1:L:203:HIS:HD2	1:L:206:SER:HB2	1.50	0.77
2:H:38:ARG:HG2	2:H:48:VAL:HG21	1.68	0.75
1:L:150:ASN:HB3	1:L:202:THR:HG22	1.69	0.74
2:I:38:ARG:HG2	2:I:48:VAL:CG1	2.19	0.71
2:I:2:VAL:HG11	2:I:112:VAL:HG21	1.77	0.65
2:H:42:GLU:O	2:H:43:LYS:HB2	2.00	0.61
2:H:99:HIS:HA	2:H:110:PHE:H	1.64	0.60
2:I:38:ARG:HG2	2:I:48:VAL:HG11	1.84	0.59
1:M:6:GLN:HE21	1:M:104:GLY:HA3	1.67	0.58
1:L:200:GLU:HG2	1:L:211:VAL:HG22	1.87	0.56
1:M:42:LEU:HB2	1:M:52:LEU:HD11	1.88	0.55
1:M:39:GLU:HB3	1:M:54:TYR:HA	1.89	0.55
1:L:203:HIS:HD2	1:L:206:SER:CB	2.19	0.54
2:I:18:LEU:HB3	2:I:83:MET:CE	2.36	0.54
1:L:203:HIS:HB3	1:L:206:SER:HB3	1.90	0.54
2:H:106:SER:N	2:H:107:PRO:HD3	2.22	0.53
1:M:18:GLN:H	1:M:18:GLN:HE21	1.56	0.53
2:I:18:LEU:HB3	2:I:83:MET:HE3	1.92	0.52
2:I:129:PRO:HB3	2:I:155:TYR:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:6:GLN:NE2	1:M:93:CYS:H	2.08	0.52
1:M:66:ARG:HB3	1:M:82:ARG:NH2	2.26	0.51
1:M:6:GLN:HE22	1:M:92:TYR:HA	1.76	0.51
2:H:38:ARG:HG2	2:H:48:VAL:CG2	2.37	0.50
2:H:105:LYS:HE3	2:H:107:PRO:HG3	1.93	0.50
2:I:54:ASN:O	2:I:55:SER:HB2	2.12	0.50
2:I:218:LYS:NZ	4:I:273:HOH:O	2.39	0.49
1:M:147:LYS:HD3	1:M:178:TYR:CD1	2.47	0.49
1:L:150:ASN:HB3	1:L:202:THR:CG2	2.42	0.49
1:L:41:TYR:OH	2:H:109:PHE:O	2.30	0.49
1:M:147:LYS:HD3	1:M:178:TYR:CE1	2.47	0.48
1:L:51:LEU:HD21	2:H:108:TYR:HB2	1.95	0.48
2:H:138:SER:HB3	2:H:223:ARG:O	2.13	0.48
2:H:105:LYS:HG3	2:H:106:SER:H	1.79	0.47
2:I:30:ARG:NH1	4:I:252:HOH:O	2.48	0.47
2:I:133:PRO:HD3	2:I:218:LYS:HE2	1.97	0.47
2:I:148:LEU:HB3	2:I:220:ILE:HD13	1.97	0.47
1:M:29:ILE:HD11	1:M:76:PHE:CE2	2.50	0.46
1:L:155:ILE:HD11	1:L:184:LEU:HD21	1.97	0.46
1:M:124:PRO:HG2	2:I:137:GLY:HA3	1.97	0.46
2:I:22:CYS:HB3	2:I:79:LEU:HB3	1.97	0.46
1:M:154:LYS:HB2	1:M:198:THR:OG1	2.17	0.44
2:H:106:SER:H	2:H:107:PRO:HD3	1.82	0.44
2:I:98:ARG:O	2:I:110:PHE:HA	2.18	0.44
1:M:49:PRO:HB2	2:I:113:TRP:CE2	2.53	0.44
1:L:66:ARG:HD2	1:L:81:SER:O	2.17	0.44
1:L:88:LEU:HD11	1:L:111:SER:HB3	1.99	0.43
1:L:33:ASN:HD22	1:L:35:HIS:H	1.66	0.43
2:H:104:GLY:HA2	2:H:105:LYS:HA	1.70	0.43
1:M:66:ARG:HD3	1:M:82:ARG:CZ	2.49	0.43
2:I:136:PRO:HB3	2:I:140:ALA:HB3	2.00	0.43
2:I:106:SER:HA	2:I:107:PRO:HD3	1.85	0.42
1:L:42:LEU:HD13	1:L:91:TYR:CZ	2.54	0.42
2:I:29:PHE:CD2	2:I:77:ASN:HA	2.55	0.42
1:L:52:LEU:HA	1:L:63:VAL:HG21	2.00	0.42
1:L:148:ASP:O	1:L:149:ILE:HG23	2.20	0.41
2:H:196:SER:O	2:H:200:SER:OG	2.38	0.41
1:M:14:SER:N	1:M:112:LYS:HE3	2.36	0.41
1:L:120:VAL:O	1:L:212:LYS:HE3	2.20	0.41
2:H:160:VAL:HG22	2:H:208:ALA:O	2.19	0.41
1:M:190:GLU:HG2	1:M:193:ARG:HH21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:32:TYR:O	2:H:72:ARG:NH2	2.52	0.41
2:H:2:VAL:HG13	2:H:27:PHE:CD1	2.56	0.41
1:M:118:PRO:HD2	1:M:210:ILE:HD12	2.03	0.41
2:I:6:GLU:HG3	2:I:96:CYS:HB2	2.03	0.41
2:H:129:PRO:HB3	2:H:155:TYR:HB3	2.03	0.41
2:H:170:SER:O	2:H:173:VAL:HG12	2.21	0.40
1:M:33:ASN:ND2	1:M:35:HIS:H	2.20	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	L	214/216 (99%)	198 (92%)	15 (7%)	1 (0%)	29	54
1	M	214/216 (99%)	201 (94%)	12 (6%)	1 (0%)	29	54
2	H	223/225 (99%)	206 (92%)	12 (5%)	5 (2%)	6	17
2	I	223/225 (99%)	208 (93%)	14 (6%)	1 (0%)	34	60
All	All	874/882 (99%)	813 (93%)	53 (6%)	8 (1%)	17	40

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	108	TYR
2	H	139	ALA
2	H	197	THR
2	I	142	THR
2	H	106	SER
2	H	110	PHE
1	L	208	SER
1	M	49	PRO

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	L	193/193 (100%)	181 (94%)	12 (6%)	18	40
1	M	193/193 (100%)	182 (94%)	11 (6%)	20	44
2	H	192/192 (100%)	176 (92%)	16 (8%)	11	25
2	I	192/192 (100%)	181 (94%)	11 (6%)	20	44
All	All	770/770 (100%)	720 (94%)	50 (6%)	17	38

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	15	LEU
1	L	33	ASN
1	L	81	SER
1	L	121	SER
1	L	128	GLU
1	L	148	ASP
1	L	154	LYS
1	L	173	SER
1	L	198	THR
1	L	202	THR
1	L	213	SER
1	L	215	ASN
2	H	3	LYS
2	H	5	VAL
2	H	21	SER
2	H	38	ARG
2	H	98	ARG
2	H	120	THR
2	H	134	LEU
2	H	150	CYS
2	H	160	VAL
2	H	169	LEU
2	H	187	LEU
2	H	190	SER

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Mol	Chain	Res	Type
2	H	205	CYS
2	H	206	ASN
2	H	221	VAL
2	H	225	CYS
1	M	3	LEU
1	M	9	LEU
1	M	14	SER
1	M	18	GLN
1	M	33	ASN
1	M	39	GLU
1	M	65	ASP
1	M	72	SER
1	M	82	ARG
1	M	128	GLU
1	M	180	MET
2	I	38	ARG
2	I	43	LYS
2	I	58	THR
2	I	102	TYR
2	I	105	LYS
2	I	120	THR
2	I	134	LEU
2	I	150	CYS
2	I	160	VAL
2	I	202	THR
2	I	220	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	33	ASN
1	L	166	ASN
1	L	203	HIS
1	L	215	ASN
2	H	77	ASN
1	M	6	GLN
1	M	18	GLN
1	M	33	ASN
1	M	35	HIS
1	M	166	ASN
2	I	77	ASN
2	I	78	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](#)

7 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	$\# Z > 2$
3	SO4	I	227	-	4,4,4	0.23	0	6,6,6	0.10	0
3	SO4	L	218	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	I	226	-	4,4,4	0.25	0	6,6,6	0.36	0
3	SO4	M	218	-	4,4,4	0.25	0	6,6,6	0.11	0
3	SO4	I	228	-	4,4,4	0.24	0	6,6,6	0.22	0
3	SO4	L	217	-	4,4,4	0.25	0	6,6,6	0.16	0
3	SO4	M	217	-	4,4,4	0.26	0	6,6,6	0.18	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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	L	216/216 (100%)	-0.17	6 (2%) 53 54	28, 38, 47, 60	0
1	M	216/216 (100%)	-0.08	3 (1%) 75 77	28, 40, 52, 57	0
2	H	225/225 (100%)	0.15	9 (4%) 38 37	30, 41, 58, 70	0
2	I	225/225 (100%)	0.12	13 (5%) 23 22	22, 35, 62, 69	0
All	All	882/882 (100%)	0.01	31 (3%) 44 44	22, 40, 56, 70	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	102	TYR	9.5
2	I	138	SER	8.4
1	L	205	THR	6.1
2	I	139	ALA	5.9
2	I	103	TYR	5.9
2	I	225	CYS	5.8
2	I	224	ASP	5.4
2	H	104	GLY	5.3
2	I	137	GLY	5.0
2	I	142	THR	4.7
2	H	102	TYR	3.9
2	H	139	ALA	3.7
1	L	206	SER	3.7
2	I	140	ALA	3.5
2	I	141	GLN	3.5
2	H	138	SER	3.3
1	L	203	HIS	3.2
2	H	103	TYR	3.2
2	H	75	ALA	3.2
1	L	204	LYS	3.2
1	L	208	SER	3.0

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Mol	Chain	Res	Type	RSRZ
2	H	105	LYS	2.9
1	M	157	GLY	2.8
2	H	137	GLY	2.5
1	M	173	SER	2.5
1	M	133	GLY	2.3
2	I	197	THR	2.2
2	H	1	ASP	2.2
2	I	144	SER	2.2
2	I	104	GLY	2.1
1	L	207	THR	2.1

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, 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(Å ²)	Q<0.9
3	SO4	M	218	5/5	0.85	0.22	48,48,48,49	5
3	SO4	L	218	5/5	0.95	0.16	42,42,43,43	5
3	SO4	M	217	5/5	0.98	0.15	45,46,46,47	0
3	SO4	L	217	5/5	0.98	0.12	40,40,41,41	0
3	SO4	I	228	5/5	0.98	0.08	25,25,25,26	5
3	SO4	I	226	5/5	0.99	0.08	37,37,38,38	0
3	SO4	I	227	5/5	1.00	0.07	25,25,25,25	5

6.5 Other polymers [i](#)

There are no such residues in this entry.