



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 11, 2016 – 01:09 PM EDT

PDB ID : 5DMI
Title : Structure of the extracellular domain of the CD40 in complex with CHI220 FAB
Authors : Sheriff, S.
Deposited on : 2015-09-08
Resolution : 3.69 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
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) : rb-20027790

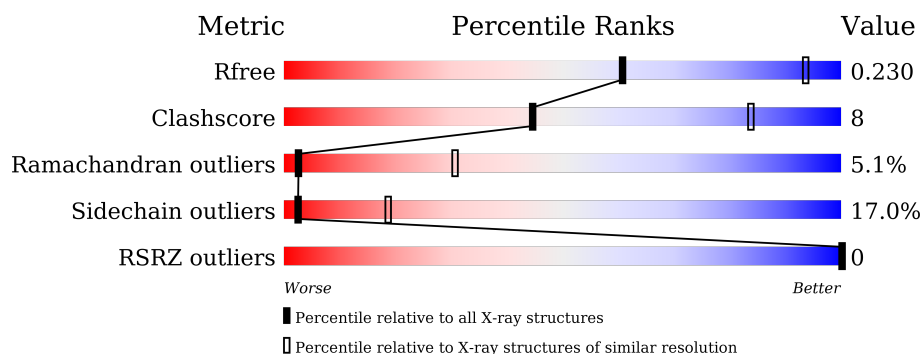
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.69 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	1101 (3.90-3.50)
Clashscore	102246	1224 (3.90-3.50)
Ramachandran outliers	100387	1172 (3.90-3.50)
Sidechain outliers	100360	1170 (3.90-3.50)
RSRZ outliers	91569	1108 (3.90-3.50)

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	183	<div> <div>29%</div> <div>19%</div> <div>5%</div> <div>46%</div> </div>
2	H	223	<div> <div>74%</div> <div>23%</div> <div>..</div> </div>
3	L	213	<div> <div>69%</div> <div>27%</div> <div>.</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4012 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 Tumor necrosis factor receptor superfamily member 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	98	Total	C	N	O	S	0	0	0
			698	421	123	140	14			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	ASP	ASN	SEE REMARK 999	UNP P25942
A	180	ASP	ASN	SEE REMARK 999	UNP P25942
A	194	ASP	-	expression tag	UNP P25942
A	195	PRO	-	expression tag	UNP P25942
A	196	GLY	-	expression tag	UNP P25942
A	197	GLY	-	expression tag	UNP P25942
A	198	GLY	-	expression tag	UNP P25942
A	199	GLY	-	expression tag	UNP P25942
A	200	GLY	-	expression tag	UNP P25942
A	201	ARG	-	expression tag	UNP P25942
A	202	LEU	-	expression tag	UNP P25942
A	203	VAL	-	expression tag	UNP P25942
A	204	PRO	-	expression tag	UNP P25942
A	205	ARG	-	expression tag	UNP P25942

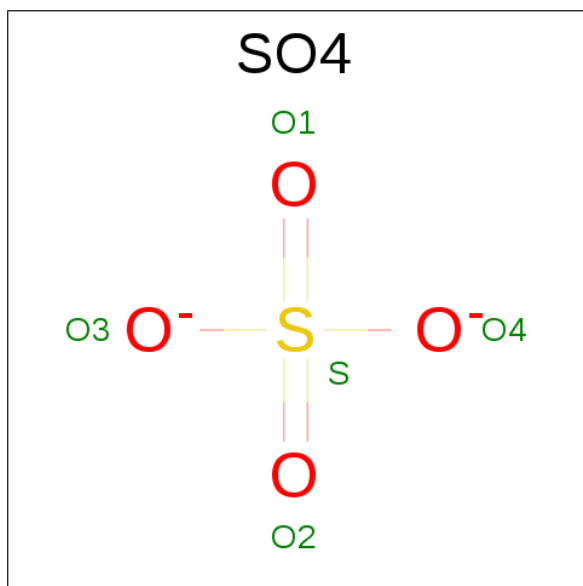
- Molecule 2 is a protein called Chi220 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	223	Total	C	N	O	S	0	0	0
			1663	1060	274	323	6			

- Molecule 3 is a protein called Chi220 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	0	0
			1640	1027	278	331	4			

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



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

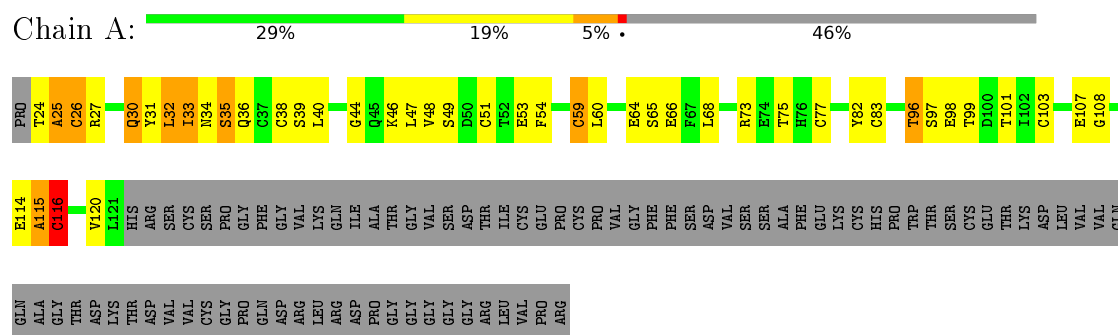
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	1	Total	O		
			1	1	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: Tumor necrosis factor receptor superfamily member 5



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	201.15Å 201.15Å 63.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.64 – 3.69 142.24 – 3.69	Depositor EDS
% Data completeness (in resolution range)	99.8 (32.64-3.69) 100.0 (142.24-3.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.25	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.53 (at 3.67Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.168 , 0.207 0.187 , 0.230	Depositor DCC
R_{free} test set	734 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 71.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4012	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% 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	0.63	0/710	0.97	1/969 (0.1%)
2	H	0.51	0/1707	0.81	0/2332
3	L	0.49	0/1679	0.78	0/2280
All	All	0.52	0/4096	0.83	1/5581 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	32	LEU	N-CA-C	-7.40	91.01	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	A	698	0	583	18	0
2	H	1663	0	1598	25	0
3	L	1640	0	1579	20	0
4	H	5	0	0	0	0
4	L	5	0	0	0	0
5	L	1	0	0	0	0
All	All	4012	0	3760	61	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 8.

All (61) 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)
2:H:95:SER:HA	2:H:96:GLY:O	1.64	0.96
2:H:35:GLN:HG2	2:H:50:TRP:HB3	1.58	0.83
1:A:32:LEU:HG	1:A:73:ARG:NH2	1.98	0.78
1:A:46:LYS:O	1:A:59:CYS:HA	1.87	0.74
3:L:47:LEU:HA	3:L:58:ILE:HG13	1.72	0.71
3:L:113:PRO:HD3	3:L:198:HIS:ND1	2.08	0.68
1:A:115:ALA:HA	1:A:116:CYS:HB2	1.78	0.65
2:H:11:LEU:HD23	2:H:116:THR:HG22	1.81	0.63
3:L:120:PRO:HD3	3:L:132:VAL:HG22	1.80	0.61
3:L:10:THR:HG23	3:L:103:LYS:HB3	1.83	0.60
1:A:64:GLU:O	1:A:65:SER:HB3	2.01	0.60
1:A:32:LEU:HG	1:A:73:ARG:HH21	1.68	0.59
3:L:163:VAL:HG22	3:L:175:LEU:HD12	1.85	0.59
1:A:36:GLN:OE1	1:A:53:GLU:HA	2.03	0.58
2:H:87:THR:HG23	2:H:110:THR:HA	1.87	0.57
2:H:35:GLN:CG	2:H:50:TRP:HB3	2.33	0.57
3:L:37:GLN:HB2	3:L:47:LEU:HD11	1.87	0.57
2:H:35:GLN:HG2	2:H:50:TRP:CB	2.33	0.55
2:H:35:GLN:HG3	2:H:50:TRP:HB2	1.88	0.55
1:A:48:VAL:HG11	1:A:60:LEU:HG	1.89	0.54
2:H:154:VAL:HG22	2:H:210:VAL:HG13	1.89	0.54
1:A:66:GLU:HB3	1:A:77:CYS:HB2	1.89	0.54
2:H:176:ALA:HA	2:H:187:LEU:HB3	1.90	0.53
2:H:35:GLN:CG	2:H:50:TRP:CB	2.86	0.53
3:L:166:GLN:HE21	3:L:171:SER:HB3	1.75	0.52
1:A:26:CYS:SG	1:A:33:ILE:HB	2.51	0.50
2:H:11:LEU:HB2	2:H:149:PRO:HG3	1.93	0.50
1:A:24:THR:HG22	1:A:25:ALA:H	1.77	0.50
3:L:83:VAL:HB	3:L:106:ILE:HG12	1.94	0.50
3:L:90:HIS:CD2	3:L:97:THR:H	2.31	0.49
1:A:32:LEU:HD22	1:A:38:CYS:HB2	1.95	0.49
1:A:32:LEU:HD12	1:A:40:LEU:HD23	1.95	0.48
3:L:35:TRP:HB2	3:L:48:ILE:HB	1.96	0.48
1:A:96:THR:HB	1:A:98:GLU:H	1.80	0.46
2:H:153:THR:HB	2:H:211:ASN:HB3	1.98	0.45
2:H:128:SER:HA	2:H:200:LEU:HD12	1.99	0.45
2:H:51:ILE:HD12	2:H:57:PRO:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:35:GLN:HB2	2:H:93:VAL:HG23	1.98	0.45
1:A:25:ALA:O	1:A:26:CYS:HB2	2.17	0.45
2:H:176:ALA:HB2	2:H:187:LEU:HD23	1.99	0.45
3:L:193:ALA:HB2	3:L:208:SER:HB3	1.99	0.44
2:H:123:PRO:HD2	3:L:121:SER:HB3	1.99	0.44
1:A:44:GLY:HA2	1:A:97:SER:O	2.17	0.44
1:A:115:ALA:HA	1:A:116:CYS:CB	2.46	0.44
3:L:80:PRO:HA	3:L:106:ILE:HG13	2.00	0.44
2:H:22:CYS:O	2:H:77:THR:HA	2.18	0.44
2:H:38:GLN:HG3	2:H:90:TYR:CE1	2.53	0.44
1:A:30:GLN:HA	1:A:39:SER:HA	2.00	0.43
2:H:59:TYR:CE1	2:H:68:ALA:HA	2.54	0.43
2:H:66:ARG:HD2	2:H:82(A):SER:O	2.19	0.43
1:A:30:GLN:O	1:A:38:CYS:O	2.37	0.42
3:L:7:SER:H	3:L:24:ARG:NH1	2.16	0.42
3:L:134:CYS:HB2	3:L:148:TRP:CZ2	2.55	0.42
2:H:226:GLU:HA	2:H:227:PRO:HD3	1.94	0.41
3:L:14:THR:HA	3:L:107:LYS:HB2	2.01	0.41
2:H:157:TRP:CH2	2:H:208:CYS:HB3	2.55	0.41
2:H:56:VAL:HA	2:H:57:PRO:HD3	1.93	0.41
3:L:166:GLN:NE2	3:L:171:SER:HB3	2.36	0.41
3:L:197:THR:HG23	3:L:204:PRO:HG3	2.03	0.41
3:L:81:GLU:C	3:L:83:VAL:H	2.24	0.41
2:H:100(A):ASP:C	3:L:96:TRP:HH2	2.24	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	A	96/183 (52%)	75 (78%)	10 (10%)	11 (12%)	0 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	221/223 (99%)	194 (88%)	18 (8%)	9 (4%)	3	37
3	L	211/213 (99%)	189 (90%)	15 (7%)	7 (3%)	5	44
All	All	528/619 (85%)	458 (87%)	43 (8%)	27 (5%)	2	31

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	GLU
1	A	116	CYS
2	H	43	LYS
2	H	96	GLY
1	A	26	CYS
1	A	59	CYS
1	A	82	TYR
2	H	100(A)	ASP
2	H	100(B)	LEU
2	H	146	ASP
2	H	225	VAL
3	L	78	VAL
3	L	93	SER
3	L	102	THR
3	L	138	ASN
1	A	25	ALA
2	H	95	SER
1	A	35	SER
1	A	83	CYS
1	A	115	ALA
2	H	226	GLU
3	L	171	SER
1	A	31	TYR
1	A	108	GLY
3	L	82	ASP
3	L	92	HIS
2	H	151	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	A	73/162 (45%)	55 (75%)	18 (25%)	1	6
2	H	179/187 (96%)	155 (87%)	24 (13%)	5	31
3	L	188/189 (100%)	155 (82%)	33 (18%)	2	16
All	All	440/538 (82%)	365 (83%)	75 (17%)	2	19

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ARG
1	A	30	GLN
1	A	33	ILE
1	A	34	ASN
1	A	35	SER
1	A	47	LEU
1	A	49	SER
1	A	51	CYS
1	A	54	PHE
1	A	68	LEU
1	A	75	THR
1	A	96	THR
1	A	99	THR
1	A	101	THR
1	A	103	CYS
1	A	107	GLU
1	A	116	CYS
1	A	120	VAL
2	H	1	GLN
2	H	32	THR
2	H	51	ILE
2	H	60	VAL
2	H	70	SER
2	H	71	LEU
2	H	81	GLN
2	H	84	ASN
2	H	85	GLU
2	H	94	ARG
2	H	95	SER
2	H	100(B)	LEU
2	H	115	SER

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Mol	Chain	Res	Type
2	H	116	THR
2	H	145	LYS
2	H	150	GLU
2	H	152	VAL
2	H	168	SER
2	H	178	LEU
2	H	188	SER
2	H	192	THR
2	H	203	THR
2	H	209	ASN
2	H	226	GLU
3	L	1	ASP
3	L	2	ILE
3	L	5	THR
3	L	7	SER
3	L	10	THR
3	L	14	THR
3	L	18	ARG
3	L	19	VAL
3	L	24	ARG
3	L	26	SER
3	L	39	LYS
3	L	60	SER
3	L	61	ARG
3	L	67	SER
3	L	70	ASP
3	L	72	THR
3	L	77	SER
3	L	81	GLU
3	L	85	ILE
3	L	89	GLN
3	L	97	THR
3	L	104	LEU
3	L	110	VAL
3	L	121	SER
3	L	122	ASP
3	L	124	GLN
3	L	125	LEU
3	L	168	SER
3	L	176	SER
3	L	182	SER
3	L	187	GLU

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Mol	Chain	Res	Type
3	L	191	VAL
3	L	211	ARG

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

Mol	Chain	Res	Type
3	L	166	GLN

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](#)

2 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	H	301	-	4,4,4	0.16	0	6,6,6	0.12	0
4	SO4	L	301	-	4,4,4	0.15	0	6,6,6	0.19	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	H	301	-	-	0/0/0/0	0/0/0/0
4	SO4	L	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.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	98/183 (53%)	0.16	0 100 100	20, 49, 81, 85	0
2	H	223/223 (100%)	0.30	0 100 100	13, 32, 64, 96	0
3	L	213/213 (100%)	0.26	0 100 100	22, 46, 65, 80	0
All	All	534/619 (86%)	0.26	0 100 100	13, 43, 72, 96	0

There are no RSRZ outliers to report.

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	L	301	5/5	0.91	0.40	-	102,103,103,103	0
4	SO4	H	301	5/5	0.94	0.14	-	102,102,103,104	0

6.5 Other polymers

There are no such residues in this entry.