Full wwPDB X-ray Structure Validation Report (i)

Jun 26, 2024 – 12:59 AM EDT

PDB ID	:	6SUA
Title	:	Structure of the high affinity engineered lipocalin C1B12 in complex with the mouse CD98 heavy chain ectodomain
Authors	:	Schiefner, A.; Deuschle, F.-C.; Skerra, A.
Deposited on	:	2019-09-13
Resolution	:	2.75 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 (i) 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 (i)) were used in the production of this report:

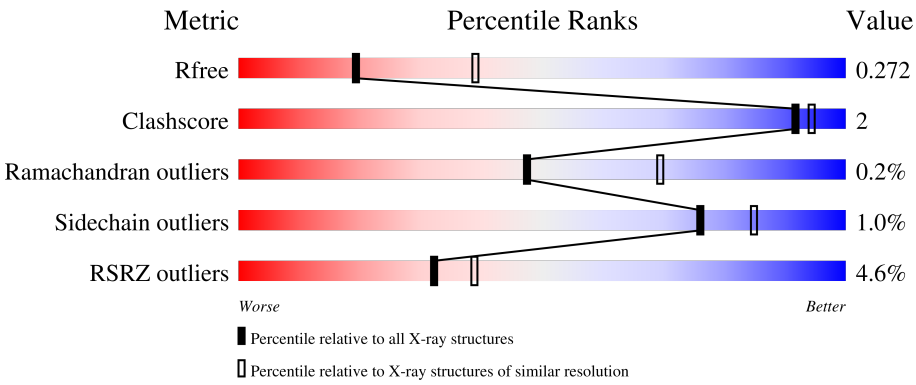
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 <=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	186	6% 87% 6% 6%
1	C	186	8% 88% 6% 6%
2	B	434	3% 93% · ·
2	D	434	3% 92% · ·

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9630 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 Neutrophil gelatinase-associated lipocalin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	174	1416	916	237	259	4	0	0	0
1	C	174	1416	916	237	259	4	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	HIS	GLN	engineered mutation	UNP P80188
A	40	GLY	ALA	engineered mutation	UNP P80188
A	41	ASN	ILE	engineered mutation	UNP P80188
A	49	LEU	GLN	engineered mutation	UNP P80188
A	68	ASP	SER	engineered mutation	UNP P80188
A	72	ILE	ARG	engineered mutation	UNP P80188
A	73	ASP	LYS	engineered mutation	UNP P80188
A	77	HIS	ASP	engineered mutation	UNP P80188
A	79	LEU	TRP	engineered mutation	UNP P80188
A	81	ASN	ARG	engineered mutation	UNP P80188
A	87	SER	CYS	engineered mutation	UNP P80188
A	96	SER	ASN	engineered mutation	UNP P80188
A	100	THR	TYR	engineered mutation	UNP P80188
A	101	LEU	PRO	engineered mutation	UNP P80188
A	103	SER	LEU	engineered mutation	UNP P80188
A	106	ARG	TYR	engineered mutation	UNP P80188
A	125	TRP	LYS	engineered mutation	UNP P80188
A	127	HIS	SER	engineered mutation	UNP P80188
A	132	TRP	TYR	engineered mutation	UNP P80188
A	134	TYR	LYS	engineered mutation	UNP P80188
A	179	SER	-	expression tag	UNP P80188
A	180	ALA	-	expression tag	UNP P80188
A	181	HIS	-	expression tag	UNP P80188
A	182	HIS	-	expression tag	UNP P80188
A	183	HIS	-	expression tag	UNP P80188

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Chain	Residue	Modelled	Actual	Comment	Reference
A	184	HIS	-	expression tag	UNP P80188
A	185	HIS	-	expression tag	UNP P80188
A	186	HIS	-	expression tag	UNP P80188
C	28	HIS	GLN	engineered mutation	UNP P80188
C	40	GLY	ALA	engineered mutation	UNP P80188
C	41	ASN	ILE	engineered mutation	UNP P80188
C	49	LEU	GLN	engineered mutation	UNP P80188
C	68	ASP	SER	engineered mutation	UNP P80188
C	72	ILE	ARG	engineered mutation	UNP P80188
C	73	ASP	LYS	engineered mutation	UNP P80188
C	77	HIS	ASP	engineered mutation	UNP P80188
C	79	LEU	TRP	engineered mutation	UNP P80188
C	81	ASN	ARG	engineered mutation	UNP P80188
C	87	SER	CYS	engineered mutation	UNP P80188
C	96	SER	ASN	engineered mutation	UNP P80188
C	100	THR	TYR	engineered mutation	UNP P80188
C	101	LEU	PRO	engineered mutation	UNP P80188
C	103	SER	LEU	engineered mutation	UNP P80188
C	106	ARG	TYR	engineered mutation	UNP P80188
C	125	TRP	LYS	engineered mutation	UNP P80188
C	127	HIS	SER	engineered mutation	UNP P80188
C	132	TRP	TYR	engineered mutation	UNP P80188
C	134	TYR	LYS	engineered mutation	UNP P80188
C	179	SER	-	expression tag	UNP P80188
C	180	ALA	-	expression tag	UNP P80188
C	181	HIS	-	expression tag	UNP P80188
C	182	HIS	-	expression tag	UNP P80188
C	183	HIS	-	expression tag	UNP P80188
C	184	HIS	-	expression tag	UNP P80188
C	185	HIS	-	expression tag	UNP P80188
C	186	HIS	-	expression tag	UNP P80188

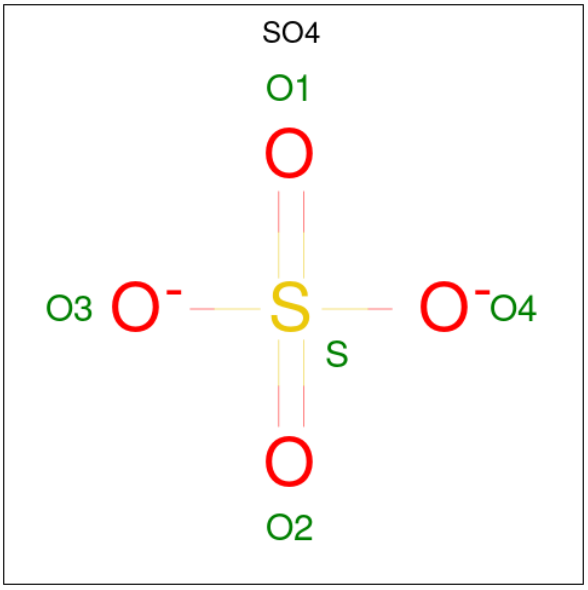
- Molecule 2 is a protein called 4F2 cell-surface antigen heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	419	3296	2098	569	624	5	0	0	0
			Total	C	N	O	S			
2	D	419	3296	2098	569	624	5	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	93	ALA	-	expression tag	UNP P10852
B	94	SER	-	expression tag	UNP P10852
B	95	TRP	-	expression tag	UNP P10852
B	96	SER	-	expression tag	UNP P10852
B	97	HIS	-	expression tag	UNP P10852
B	98	PRO	-	expression tag	UNP P10852
B	99	GLN	-	expression tag	UNP P10852
B	100	PHE	-	expression tag	UNP P10852
B	101	GLU	-	expression tag	UNP P10852
B	102	LYS	-	expression tag	UNP P10852
B	103	GLY	-	expression tag	UNP P10852
B	104	ALA	-	expression tag	UNP P10852
D	93	ALA	-	expression tag	UNP P10852
D	94	SER	-	expression tag	UNP P10852
D	95	TRP	-	expression tag	UNP P10852
D	96	SER	-	expression tag	UNP P10852
D	97	HIS	-	expression tag	UNP P10852
D	98	PRO	-	expression tag	UNP P10852
D	99	GLN	-	expression tag	UNP P10852
D	100	PHE	-	expression tag	UNP P10852
D	101	GLU	-	expression tag	UNP P10852
D	102	LYS	-	expression tag	UNP P10852
D	103	GLY	-	expression tag	UNP P10852
D	104	ALA	-	expression tag	UNP P10852

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	A	1	5	4	1	0	0
3	B	1	5	4	1	0	0
3	B	1	5	4	1	0	0
3	B	1	5	4	1	0	0
3	B	1	5	4	1	0	0
3	B	1	5	4	1	0	0
3	C	1	5	4	1	0	0
3	D	1	5	4	1	0	0
3	D	1	5	4	1	0	0
3	D	1	5	4	1	0	0
3	D	1	5	4	1	0	0
3	D	1	5	4	1	0	0

- Molecule 4 is water.

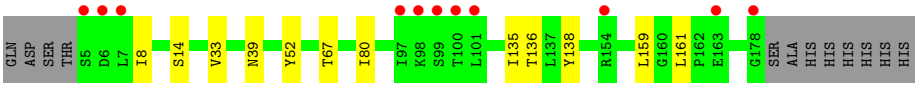
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	16	16	16	0	0
4	B	50	50	50	0	0
4	C	10	10	10	0	0
4	D	70	70	70	0	0

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.

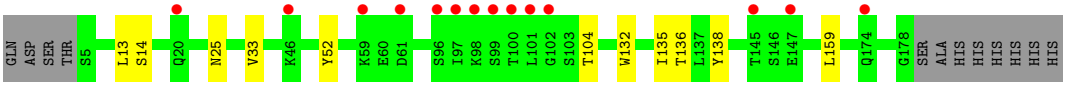
• Molecule 1: Neutrophil gelatinase-associated lipocalin

Chain A:



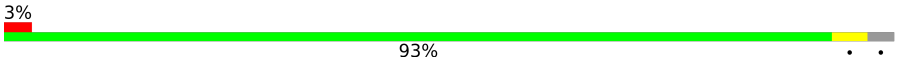
• Molecule 1: Neutrophil gelatinase-associated lipocalin

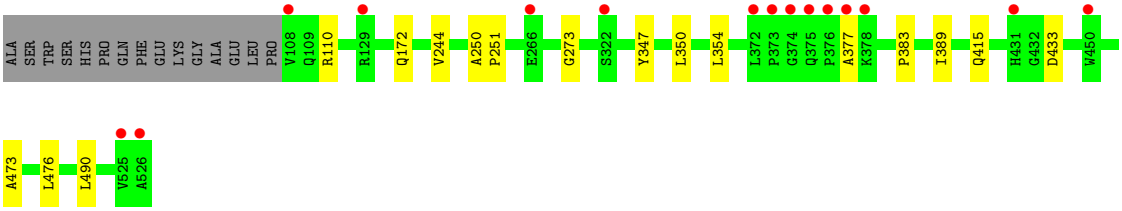
Chain C:



• Molecule 2: 4F2 cell-surface antigen heavy chain

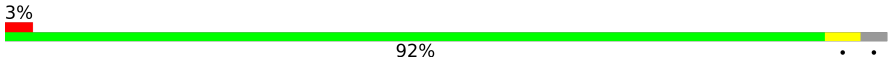
Chain B:

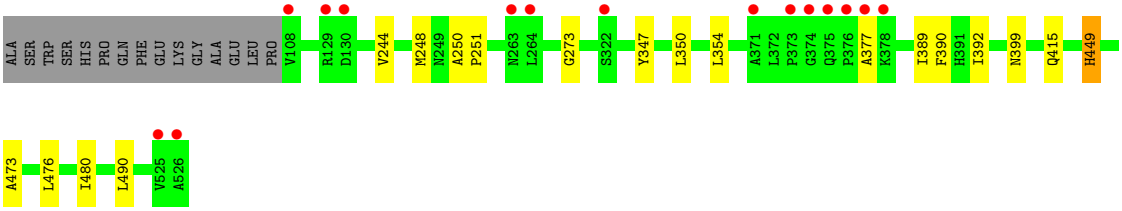




• Molecule 2: 4F2 cell-surface antigen heavy chain

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	105.04Å 107.74Å 133.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.71 – 2.75 34.69 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.1 (34.71-2.75) 99.2 (34.69-2.75)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.44 (at 2.76Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.220 , 0.271 0.224 , 0.272	Depositor DCC
R_{free} test set	1961 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	42.7	Xtriage
Anisotropy	0.552	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 33.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.069 for k,h,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	9630	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 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	0.64	0/1455	0.71	0/1974
1	C	0.64	0/1455	0.71	0/1974
2	B	0.65	0/3369	0.70	0/4572
2	D	0.65	0/3369	0.71	0/4572
All	All	0.65	0/9648	0.71	0/13092

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	1416	0	1395	8	0
1	C	1416	0	1395	6	0
2	B	3296	0	3287	7	0
2	D	3296	0	3287	10	0
3	A	5	0	0	0	0
3	B	25	0	0	0	0
3	C	5	0	0	0	0
3	D	25	0	0	0	0
4	A	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	50	0	0	0	0
4	C	10	0	0	0	0
4	D	70	0	0	0	0
All	All	9630	0	9364	30	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 (30) 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:A:8:ILE:HG23	1:A:39:ASN:HB2	1.72	0.72
2:D:449:HIS:CE1	2:D:480:ILE:HD11	2.39	0.57
1:A:67:THR:HG23	1:A:80:ILE:CD1	2.39	0.53
1:A:33:VAL:HG21	1:A:52:TYR:CE2	2.44	0.52
2:D:390:PHE:O	2:D:392:ILE:HD12	2.08	0.52
1:C:33:VAL:HG21	1:C:52:TYR:CE2	2.45	0.52
1:A:135:ILE:HD11	1:A:159:LEU:HD12	1.93	0.50
1:A:67:THR:HG23	1:A:80:ILE:HD13	1.94	0.50
1:A:8:ILE:HD11	1:A:161:LEU:HD23	1.93	0.49
1:C:135:ILE:HD11	1:C:159:LEU:HD12	1.95	0.48
2:D:415:GLN:HG3	2:D:490:LEU:HD11	1.95	0.47
2:B:415:GLN:HG3	2:B:490:LEU:HD11	1.98	0.45
2:D:473:ALA:HB1	2:D:476:LEU:HD12	1.98	0.45
2:B:383:PRO:HB3	2:B:389:ILE:HG22	1.98	0.45
1:C:136:THR:HG21	1:C:138:TYR:CE1	2.52	0.45
2:B:383:PRO:CB	2:B:389:ILE:HG22	2.47	0.44
2:D:244:VAL:HG22	2:D:273:GLY:O	2.17	0.44
2:B:244:VAL:HG22	2:B:273:GLY:O	2.18	0.43
1:A:136:THR:HG21	1:A:138:TYR:CE1	2.53	0.43
1:A:33:VAL:HG21	1:A:52:TYR:CZ	2.53	0.43
1:C:132:TRP:CZ2	2:D:399:ASN:HB3	2.54	0.43
1:C:33:VAL:HG21	1:C:52:TYR:CZ	2.54	0.43
2:D:250:ALA:N	2:D:251:PRO:CD	2.82	0.42
1:C:13:LEU:CD1	1:C:104:THR:CG2	2.98	0.42
2:B:473:ALA:HB1	2:B:476:LEU:HD12	2.01	0.41
2:B:250:ALA:N	2:B:251:PRO:CD	2.83	0.41
2:D:389:ILE:HD11	2:D:392:ILE:HD13	2.03	0.41
2:B:350:LEU:HD11	2:B:354:LEU:HD11	2.03	0.40
2:D:250:ALA:HB3	2:D:251:PRO:HD3	2.02	0.40
2:D:350:LEU:HD11	2:D:354:LEU:HD11	2.03	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	172/186 (92%)	163 (95%)	9 (5%)	0	100	100
1	C	172/186 (92%)	163 (95%)	9 (5%)	0	100	100
2	B	417/434 (96%)	403 (97%)	13 (3%)	1 (0%)	47	69
2	D	417/434 (96%)	403 (97%)	13 (3%)	1 (0%)	47	69
All	All	1178/1240 (95%)	1132 (96%)	44 (4%)	2 (0%)	47	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	377	ALA
2	D	377	ALA

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	159/170 (94%)	158 (99%)	1 (1%)	86	90
1	C	159/170 (94%)	157 (99%)	2 (1%)	69	81
2	B	362/374 (97%)	358 (99%)	4 (1%)	73	84
2	D	362/374 (97%)	359 (99%)	3 (1%)	81	88
All	All	1042/1088 (96%)	1032 (99%)	10 (1%)	76	85

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	SER
2	B	110	ARG
2	B	172	GLN
2	B	347	TYR
2	B	433	ASP
1	C	14	SER
1	C	25	ASN
2	D	248	MET
2	D	347	TYR
2	D	449	HIS

Sometimes 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 monosaccharides 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	$\#\|Z\| > 2$
3	SO4	D	602	-	4,4,4	0.38	0	6,6,6	0.06	0
3	SO4	B	601	-	4,4,4	0.38	0	6,6,6	0.05	0
3	SO4	D	601	-	4,4,4	0.36	0	6,6,6	0.07	0
3	SO4	B	603	-	4,4,4	0.39	0	6,6,6	0.06	0
3	SO4	A	201	-	4,4,4	0.37	0	6,6,6	0.07	0
3	SO4	B	605	-	4,4,4	0.37	0	6,6,6	0.05	0
3	SO4	B	602	-	4,4,4	0.39	0	6,6,6	0.07	0
3	SO4	B	604	-	4,4,4	0.39	0	6,6,6	0.04	0
3	SO4	C	201	-	4,4,4	0.38	0	6,6,6	0.08	0
3	SO4	D	605	-	4,4,4	0.38	0	6,6,6	0.06	0
3	SO4	D	604	-	4,4,4	0.37	0	6,6,6	0.07	0
3	SO4	D	603	-	4,4,4	0.39	0	6,6,6	0.07	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	174/186 (93%)	0.39	11 (6%)	20	24	33, 52, 91, 122	0
1	C	174/186 (93%)	0.55	14 (8%)	12	15	34, 58, 93, 123	0
2	B	419/434 (96%)	0.15	15 (3%)	42	51	25, 39, 73, 143	0
2	D	419/434 (96%)	0.12	15 (3%)	42	51	23, 38, 69, 131	0
All	All	1186/1240 (95%)	0.23	55 (4%)	32	39	23, 44, 78, 143	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	374	GLY	8.5
2	B	375	GLN	7.9
1	C	100	THR	7.8
2	B	377	ALA	7.4
2	D	108	VAL	7.3
2	B	376	PRO	7.0
1	A	98	LYS	6.8
1	C	99	SER	6.6
2	D	377	ALA	6.0
1	C	102	GLY	5.9
2	D	526	ALA	5.5
2	D	374	GLY	5.4
2	D	375	GLN	4.9
1	A	99	SER	4.7
1	A	5	SER	4.7
1	C	98	LYS	4.7
2	D	376	PRO	4.4
1	C	101	LEU	4.3
2	D	322	SER	4.2
2	D	373	PRO	4.1
2	B	373	PRO	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	101	LEU	3.7
2	B	526	ALA	3.5
2	B	129	ARG	3.1
2	B	378	LYS	3.1
1	C	147	GLU	3.0
1	A	100	THR	3.0
2	B	372	LEU	2.9
1	A	154	ARG	2.8
1	A	7	LEU	2.8
2	D	263	ASN	2.7
1	A	97	ILE	2.7
2	D	525	VAL	2.7
2	B	108	VAL	2.6
1	A	6	ASP	2.6
2	D	264	LEU	2.6
2	B	266	GLU	2.6
2	D	130	ASP	2.5
1	A	163	GLU	2.4
1	C	59	LYS	2.4
1	C	97	ILE	2.4
2	B	322	SER	2.4
2	D	378	LYS	2.4
1	A	178	GLY	2.3
2	B	525	VAL	2.3
2	B	431	HIS	2.3
1	C	61	ASP	2.3
1	C	145	THR	2.2
1	C	96	SER	2.2
2	D	129	ARG	2.2
1	C	46	LYS	2.2
2	B	450	TRP	2.1
2	D	371	ALA	2.1
1	C	20	GLN	2.0
1	C	174	GLN	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 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	A	201	5/5	0.88	0.20	70,74,76,77	0
3	SO4	D	605	5/5	0.88	0.36	84,85,85,85	0
3	SO4	B	602	5/5	0.90	0.18	59,60,62,65	0
3	SO4	B	605	5/5	0.92	0.33	77,78,80,81	0
3	SO4	B	604	5/5	0.93	0.32	87,91,94,96	0
3	SO4	C	201	5/5	0.94	0.20	70,71,73,73	0
3	SO4	D	604	5/5	0.95	0.13	63,64,65,66	0
3	SO4	B	603	5/5	0.96	0.13	68,71,73,74	0
3	SO4	D	603	5/5	0.97	0.09	52,53,55,55	0
3	SO4	D	602	5/5	0.98	0.13	58,59,61,61	0
3	SO4	B	601	5/5	0.99	0.08	32,33,34,34	0
3	SO4	D	601	5/5	0.99	0.09	27,27,29,29	0

6.5 Other polymers (i)

There are no such residues in this entry.