



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 10, 2022 – 03:09 pm GMT

PDB ID : 8B0U
Title : Structure of the CalpL/cA4 complex
Authors : Schneberger, N.; Hagelueken, G.
Deposited on : 2022-09-08
Resolution : 3.29 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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

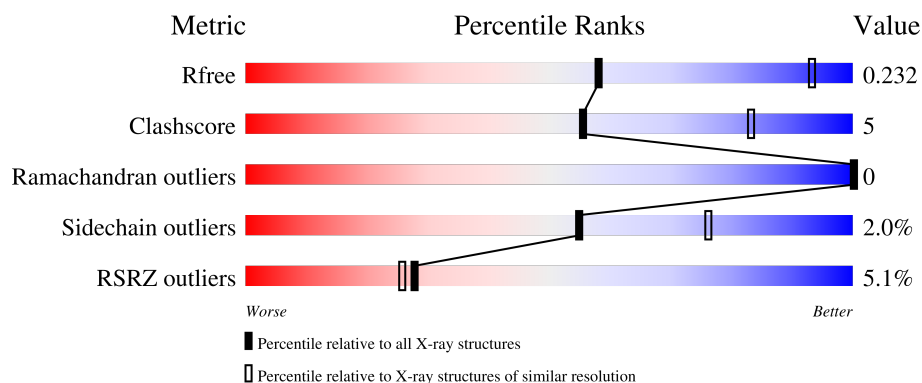
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.29 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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	496	<div> <div>7%</div> <div> <div></div> <div>86%</div> <div>14%</div> </div> </div>
1	B	496	<div> <div>4%</div> <div> <div></div> <div>84%</div> <div>15%</div> </div> </div>
2	C	76	<div> <div>0%</div> <div> <div></div> <div>78%</div> <div>22%</div> </div> </div>
2	D	76	<div> <div>3%</div> <div> <div></div> <div>84%</div> <div>16%</div> </div> </div>

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	GOL	D	301	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9441 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 SAVED domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	496	Total	C	N	O	S	0	0	0
			4078	2647	662	762	7			
1	B	496	Total	C	N	O	S	0	0	0
			4078	2647	662	762	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP B2V8L9
B	1	GLY	-	expression tag	UNP B2V8L9

- Molecule 2 is a protein called CalpT10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	76	Total	C	N	O	0	0	0
			618	400	94	124			
2	C	76	Total	C	N	O	0	0	0
			618	400	94	124			

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



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		

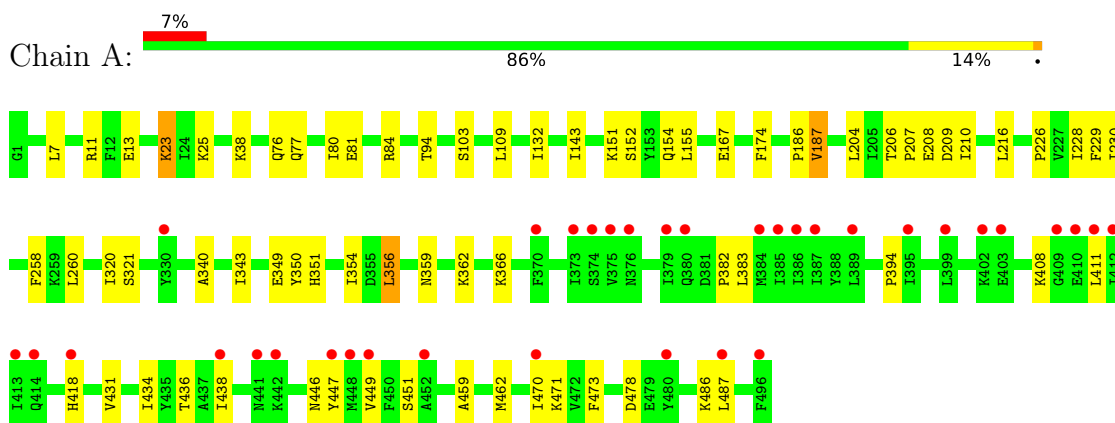
- Molecule 5 is water.

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

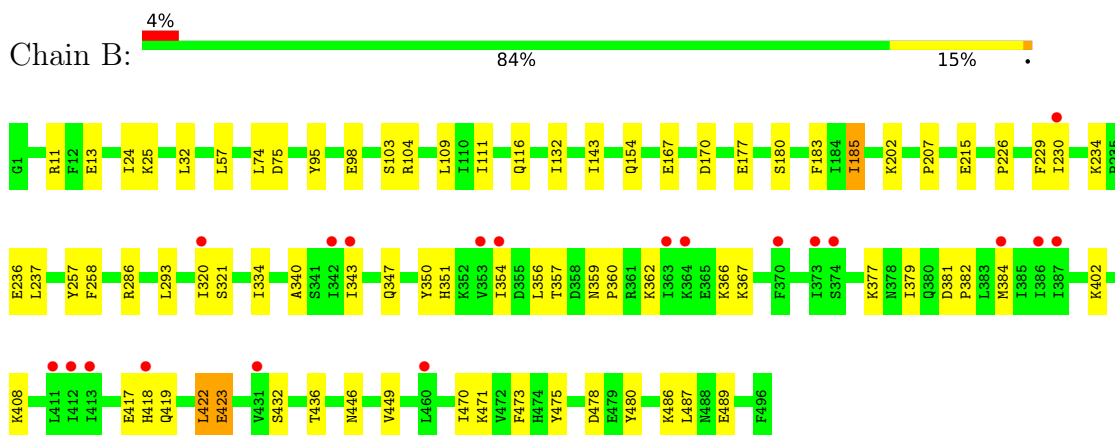
3 Residue-property plots

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.

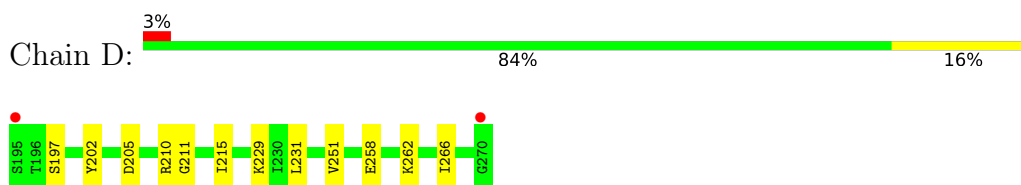
• Molecule 1: SAVED domain-containing protein



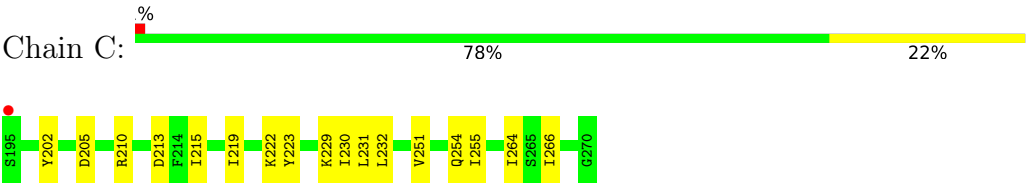
• Molecule 1: SAVED domain-containing protein



• Molecule 2: CalpT10



• Molecule 2: CalpT10



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.75Å 96.60Å 131.71Å 90.00° 98.19° 90.00°	Depositor
Resolution (Å)	49.31 – 3.29 49.31 – 3.29	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.31-3.29) 99.1 (49.31-3.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 3.33Å)	Xtriage
Refinement program		Depositor
R, R_{free}	0.195 , 0.230 0.198 , 0.232	Depositor DCC
R_{free} test set	1998 reflections (5.92%)	wwPDB-VP
Wilson B-factor (Å ²)	108.7	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	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	0.95	EDS
Total number of atoms	9441	wwPDB-VP
Average B, all atoms (Å ²)	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 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	0.24	0/4154	0.46	0/5602
1	B	0.25	0/4154	0.46	0/5602
2	C	0.25	0/627	0.49	0/845
2	D	0.25	0/627	0.48	0/845
All	All	0.25	0/9562	0.46	0/12894

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	4078	0	4198	41	0
1	B	4078	0	4198	44	0
2	C	618	0	627	12	0
2	D	618	0	627	7	0
3	A	20	0	0	1	0
3	B	15	0	0	1	0
4	D	12	0	16	0	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
All	All	9441	0	9666	98	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 (98) 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:B:382:PRO:HG2	1:B:408:LYS:H	1.38	0.88
1:B:11:ARG:NH1	1:B:13:GLU:OE2	2.17	0.77
1:A:11:ARG:NH1	1:A:13:GLU:OE2	2.18	0.77
1:A:94:THR:O	1:A:103:SER:HA	1.88	0.73
1:B:377:LYS:HD3	1:B:379:ILE:HD11	1.73	0.69
2:D:210:ARG:NH1	2:D:211:GLY:O	2.29	0.65
2:C:205:ASP:HB3	2:C:266:ILE:HD12	1.79	0.65
1:B:384:MET:HG2	1:B:402:LYS:HB2	1.80	0.63
1:A:359:ASN:HB3	1:A:362:LYS:HD3	1.82	0.61
1:B:286:ARG:NH2	1:B:489:GLU:OE2	2.28	0.61
1:B:95:TYR:HA	1:B:103:SER:HB2	1.82	0.60
1:B:177:GLU:HB2	1:B:185:ILE:HG12	1.84	0.60
1:B:367:LYS:H	1:B:436:THR:HG21	1.70	0.56
1:B:24:ILE:HD12	1:B:32:LEU:HD11	1.89	0.55
2:C:215:ILE:HG13	2:C:251:VAL:HB	1.88	0.55
1:A:449:VAL:HG12	1:A:473:PHE:HB2	1.89	0.54
1:A:206:THR:OG1	1:A:209:ASP:OD1	2.15	0.54
1:A:206:THR:OG1	1:A:208:GLU:HG3	2.07	0.54
1:B:470:ILE:HB	1:B:487:LEU:HD12	1.89	0.53
2:D:229:LYS:HE2	2:D:231:LEU:HD21	1.91	0.53
1:B:234:LYS:HD2	1:B:237:LEU:HD22	1.91	0.53
1:A:471:LYS:HE3	1:A:486:LYS:HE3	1.92	0.52
1:B:359:ASN:HB3	1:B:362:LYS:HD3	1.91	0.52
1:B:132:ILE:HD11	1:B:154:GLN:HG2	1.91	0.52
1:B:236:GLU:HG2	1:B:237:LEU:HD12	1.91	0.52
1:B:170:ASP:O	1:B:202:LYS:NZ	2.37	0.52
1:B:432:SER:O	1:B:436:THR:HG23	2.10	0.52
1:B:356:LEU:HB3	1:B:360:PRO:HA	1.91	0.51
1:A:349:GLU:HB2	1:A:351:HIS:CE1	2.46	0.51
1:B:167:GLU:N	1:B:167:GLU:OE1	2.44	0.51
1:A:167:GLU:OE1	1:A:167:GLU:N	2.44	0.50
2:C:219:ILE:HD12	2:C:266:ILE:HD11	1.93	0.50
2:C:229:LYS:HE2	2:C:231:LEU:HD21	1.92	0.50
1:A:383:LEU:HD21	1:A:411:LEU:HD13	1.95	0.49
1:A:351:HIS:H	1:A:351:HIS:CD2	2.31	0.49
1:B:215:GLU:HG3	1:B:257:TYR:HB3	1.94	0.48
1:A:470:ILE:HB	1:A:487:LEU:HD12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:GLN:HE22	1:B:180:SER:HB2	1.78	0.48
1:A:366:LYS:HB3	1:A:436:THR:HG23	1.94	0.48
1:A:382:PRO:HG2	1:A:408:LYS:H	1.79	0.48
1:A:226:PRO:HG2	1:A:258:PHE:CD1	2.49	0.47
1:B:449:VAL:HG12	1:B:473:PHE:HB2	1.95	0.47
1:A:25:LYS:HE3	2:D:202:TYR:HE2	1.79	0.47
1:A:77:GLN:O	1:A:81:GLU:HG3	2.14	0.47
1:B:57:LEU:HD11	1:B:111:ILE:HD11	1.97	0.47
1:B:293:LEU:HD22	1:B:334:ILE:HD12	1.96	0.47
2:C:210:ARG:HH12	2:C:254:GLN:HA	1.79	0.47
1:A:80:ILE:HD13	1:B:183:PHE:HB3	1.97	0.47
1:A:431:VAL:HG21	1:A:459:ALA:HB3	1.96	0.47
1:A:109:LEU:HB3	1:A:143:ILE:HG22	1.97	0.46
1:A:84:ARG:NH2	1:B:207:PRO:O	2.35	0.46
1:A:447:TYR:HD1	1:A:471:LYS:HB2	1.81	0.46
1:A:204:LEU:HD12	1:A:206:THR:HG22	1.98	0.46
1:A:230:ILE:HG22	1:A:321:SER:HB3	1.98	0.46
2:D:205:ASP:HB3	2:D:266:ILE:HD12	1.97	0.46
1:B:351:HIS:H	1:B:351:HIS:CD2	2.31	0.46
2:C:210:ARG:NH1	2:C:254:GLN:HA	2.31	0.46
1:B:226:PRO:HG2	1:B:258:PHE:CD1	2.51	0.45
1:A:228:ILE:HD12	1:A:260:LEU:HD21	1.98	0.45
2:D:215:ILE:HG13	2:D:251:VAL:HB	1.98	0.45
2:C:230:ILE:HD12	2:C:266:ILE:HG12	1.99	0.45
1:A:23:LYS:HE3	2:D:258:GLU:OE2	2.17	0.44
1:A:155:LEU:HG	1:A:174:PHE:HB3	1.99	0.44
1:B:109:LEU:HB3	1:B:143:ILE:HG22	1.99	0.44
1:B:381:ASP:HB3	1:B:382:PRO:HD3	2.00	0.44
1:B:359:ASN:ND2	1:B:362:LYS:HB3	2.32	0.44
1:A:152:SER:HB2	1:A:187:VAL:HG21	1.99	0.44
1:B:343:ILE:HB	1:B:354:ILE:HB	1.99	0.44
1:B:475:TYR:HB2	1:B:480:TYR:CE2	2.52	0.44
1:B:471:LYS:HE3	1:B:486:LYS:HE3	2.00	0.44
2:C:210:ARG:NH2	2:C:255:ILE:O	2.51	0.44
1:A:132:ILE:HD11	1:A:154:GLN:HG2	2.00	0.44
2:C:232:LEU:HD13	2:C:264:ILE:HG22	2.01	0.43
1:B:229:PHE:O	1:B:320:ILE:HA	2.19	0.43
1:B:340:ALA:HA	1:B:356:LEU:O	2.19	0.43
1:A:343:ILE:HB	1:A:354:ILE:HB	2.00	0.43
1:A:383:LEU:HD11	1:A:411:LEU:HB2	2.00	0.43
1:A:187:VAL:HG22	3:A:504:SO4:O4	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:LEU:HD21	1:A:38:LYS:HE3	2.01	0.43
2:C:222:LYS:HE3	2:C:223:TYR:CE2	2.54	0.42
1:A:229:PHE:O	1:A:320:ILE:HA	2.19	0.42
1:B:230:ILE:HG22	1:B:321:SER:HB3	2.00	0.42
1:B:422:LEU:HD22	1:B:422:LEU:H	1.84	0.42
1:A:394:PRO:HG3	1:A:451:SER:HB3	2.01	0.42
1:B:366:LYS:HB3	1:B:436:THR:HG22	2.01	0.42
1:A:343:ILE:HD11	1:A:462:MET:SD	2.60	0.42
1:B:104:ARG:NH2	3:B:503:SO4:O4	2.52	0.41
1:A:340:ALA:HA	1:A:356:LEU:O	2.21	0.41
2:D:258:GLU:O	2:D:262:LYS:HG3	2.21	0.41
1:A:434:ILE:O	1:A:438:ILE:HG12	2.21	0.41
1:B:75:ASP:OD2	1:B:116:GLN:NE2	2.54	0.41
1:B:423:GLU:H	1:B:423:GLU:HG3	1.73	0.41
2:C:213:ASP:N	2:C:213:ASP:OD1	2.54	0.41
1:B:340:ALA:HB1	1:B:357:THR:HA	2.03	0.40
1:B:25:LYS:HE3	2:C:202:TYR:CE2	2.56	0.40
1:B:475:TYR:HB2	1:B:480:TYR:CZ	2.57	0.40
1:A:186:PRO:HA	1:A:207:PRO:HG2	2.04	0.40
1:A:210:ILE:HD12	1:A:216:LEU:HB2	2.03	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	494/496 (100%)	480 (97%)	14 (3%)	0	100	100
1	B	494/496 (100%)	479 (97%)	15 (3%)	0	100	100
2	C	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
2	D	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
All	All	1136/1144 (99%)	1103 (97%)	33 (3%)	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	458/458 (100%)	450 (98%)	8 (2%)	60	78
1	B	458/458 (100%)	446 (97%)	12 (3%)	46	71
2	C	71/71 (100%)	71 (100%)	0	100	100
2	D	71/71 (100%)	70 (99%)	1 (1%)	67	82
All	All	1058/1058 (100%)	1037 (98%)	21 (2%)	55	76

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LYS
1	A	151	LYS
1	A	187	VAL
1	A	350	TYR
1	A	356	LEU
1	A	418	HIS
1	A	446	ASN
1	A	478	ASP
2	D	197	SER
1	B	74	LEU
1	B	98	GLU
1	B	185	ILE
1	B	347	GLN
1	B	350	TYR
1	B	417	GLU
1	B	418	HIS
1	B	419	GLN
1	B	422	LEU
1	B	423	GLU
1	B	446	ASN
1	B	478	ASP

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

Mol	Chain	Res	Type
2	C	198	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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	GOL	D	302	-	5,5,5	0.93	0	5,5,5	0.96	0
3	SO4	A	504	-	4,4,4	0.15	0	6,6,6	0.04	0
3	SO4	B	503	-	4,4,4	0.14	0	6,6,6	0.04	0
3	SO4	A	503	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	B	501	-	4,4,4	0.13	0	6,6,6	0.07	0
3	SO4	A	501	-	4,4,4	0.14	0	6,6,6	0.04	0
4	GOL	D	301	-	5,5,5	1.06	0	5,5,5	0.81	0
3	SO4	A	502	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	B	502	-	4,4,4	0.15	0	6,6,6	0.05	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	GOL	D	302	-	-	1/4/4/4	-
4	GOL	D	301	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	302	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	504	SO4	1	0
3	B	503	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	496/496 (100%)	0.42	35 (7%)	16 16	70, 124, 180, 203	0
1	B	496/496 (100%)	0.39	20 (4%)	38 36	62, 109, 166, 203	0
2	C	76/76 (100%)	0.40	1 (1%)	77 77	64, 83, 154, 189	0
2	D	76/76 (100%)	0.39	2 (2%)	56 53	71, 93, 170, 186	0
All	All	1144/1144 (100%)	0.40	58 (5%)	28 26	62, 113, 174, 203	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	195	SER	9.4
1	A	410	GLU	5.6
1	A	409	GLY	4.6
1	A	412	ILE	4.6
1	B	413	ILE	4.4
1	A	384	MET	3.8
1	A	386	ILE	3.7
1	B	354	ILE	3.7
1	A	442	LYS	3.6
1	A	447	TYR	3.6
1	A	449	VAL	3.4
1	A	376	ASN	3.4
1	A	452	ALA	3.4
1	A	385	ILE	3.3
1	A	413	ILE	3.3
1	B	384	MET	3.3
1	B	386	ILE	3.2
1	A	411	LEU	3.2
1	A	389	LEU	3.1
1	B	363	ILE	3.1
1	A	414	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	399	LEU	2.9
2	D	270	GLY	2.9
2	D	195	SER	2.8
1	A	373	ILE	2.8
1	A	470	ILE	2.7
1	B	411	LEU	2.7
1	B	412	ILE	2.7
1	A	387	ILE	2.7
1	A	441	ASN	2.7
1	A	448	MET	2.6
1	B	374	SER	2.6
1	A	480	TYR	2.6
1	B	460	LEU	2.5
1	A	379	ILE	2.5
1	B	343	ILE	2.5
1	A	418	HIS	2.5
1	B	373	ILE	2.5
1	B	342	ILE	2.4
1	B	320	ILE	2.4
1	B	431	VAL	2.4
1	B	387	ILE	2.4
1	B	370	PHE	2.4
1	B	353	VAL	2.4
1	A	438	ILE	2.4
1	A	370	PHE	2.4
1	A	380	GLN	2.3
1	A	395	ILE	2.3
1	B	418	HIS	2.3
1	B	364	LYS	2.2
1	A	403	GLU	2.2
1	B	230	ILE	2.1
1	A	330	TYR	2.1
1	A	375	VAL	2.1
1	A	402	LYS	2.1
1	A	487	LEU	2.1
1	A	496	PHE	2.1
1	A	374	SER	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 [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	503	5/5	0.76	0.21	172,173,178,202	0
4	GOL	D	301	6/6	0.78	0.51	70,104,110,111	0
4	GOL	D	302	6/6	0.80	0.17	90,97,125,127	0
3	SO4	A	502	5/5	0.88	0.16	102,113,158,166	0
3	SO4	A	504	5/5	0.88	0.42	122,142,148,259	0
3	SO4	B	503	5/5	0.90	0.29	141,141,177,177	0
3	SO4	A	501	5/5	0.94	0.12	108,116,136,139	0
3	SO4	B	502	5/5	0.96	0.15	119,123,125,130	0
3	SO4	B	501	5/5	0.97	0.19	85,92,108,124	0

6.5 Other polymers [i](#)

There are no such residues in this entry.