



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2023 – 12:41 AM JST

PDB ID : 7E5W
Title : The structure of CcpA from Staphylococcus aureus
Authors : Yu, G.; Wei, X.
Deposited on : 2021-02-20
Resolution : 2.55 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 : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

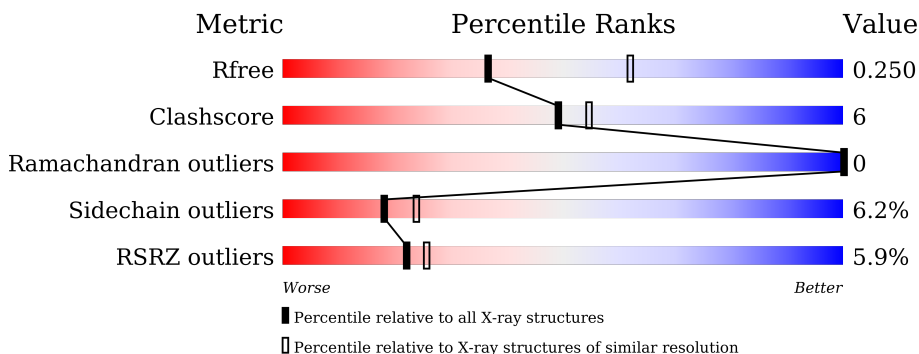
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	329	 3% 85% 12% ..
1	B	329	 6% 83% 14% ..
1	C	329	 9% 74% 21% ..

2 Entry composition [i](#)

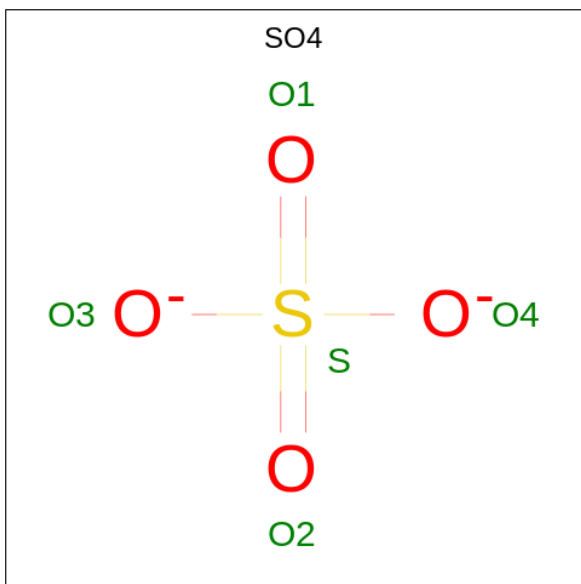
There are 3 unique types of molecules in this entry. The entry contains 7416 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Catabolite control protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	320	Total 2463	C 1542	N 420	O 490	S 11	0	0	0
1	B	319	Total 2454	C 1536	N 418	O 489	S 11	0	0	0
1	C	319	Total 2454	C 1536	N 418	O 489	S 11	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

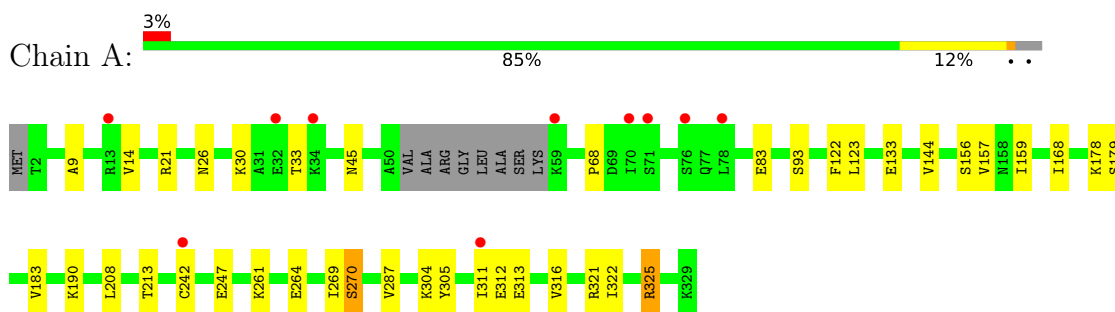
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	9	Total	O	0	0
			9	9		

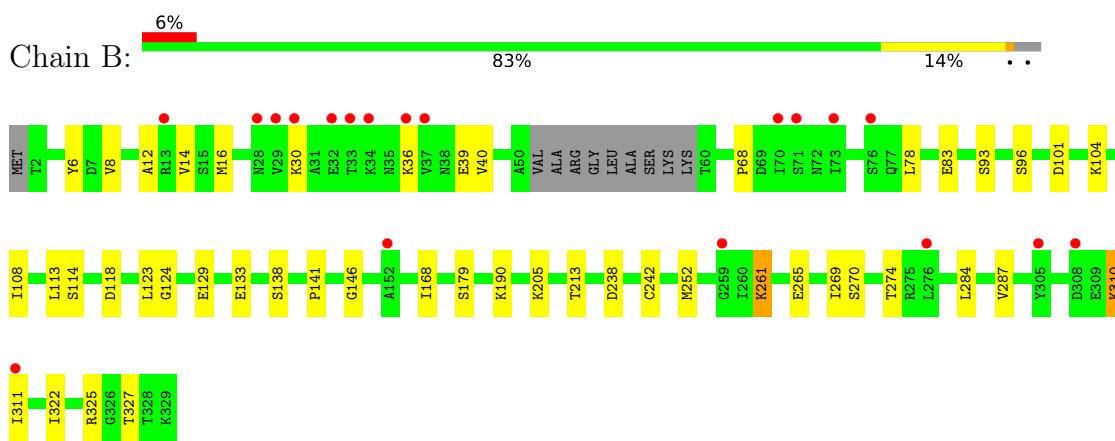
3 Residue-property plots [i](#)

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.

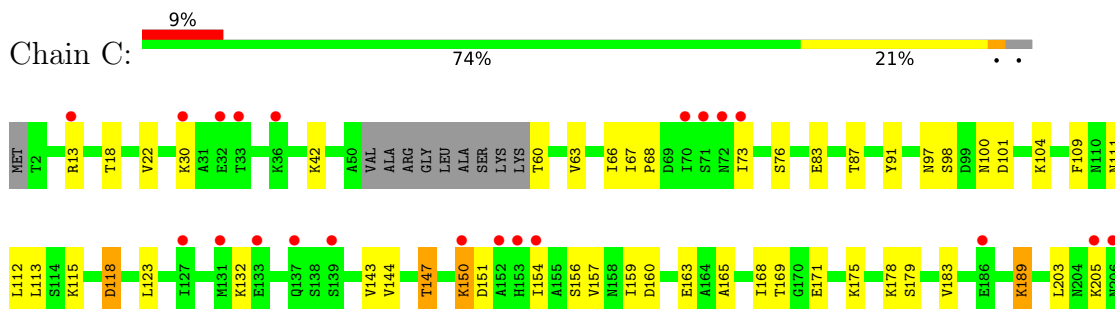
- Molecule 1: Catabolite control protein A

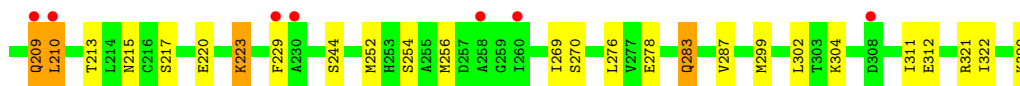


- Molecule 1: Catabolite control protein A



- Molecule 1: Catabolite control protein A





4 Data and refinement statistics i

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	179.29Å 179.29Å 173.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.26 – 2.55 42.26 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.26-2.55) 99.9 (42.26-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.51 (at 2.54Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.233 , 0.255 0.231 , 0.250	Depositor DCC
R_{free} test set	2318 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	59.3	Xtrriage
Anisotropy	0.271	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.010 for l,-k,h 0.009 for -h,-l,-k	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7416	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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: 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	0.50	0/2492	0.69	0/3364
1	B	0.51	1/2483 (0.0%)	0.67	0/3353
1	C	0.49	0/2483	0.64	0/3353
All	All	0.50	1/7458 (0.0%)	0.67	0/10070

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	242	CYS	CB-SG	-5.27	1.73	1.81

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	2463	0	2502	24	1
1	B	2454	0	2489	24	0
1	C	2454	0	2489	43	1
2	A	15	0	0	0	0
2	B	10	0	0	1	0
2	C	5	0	0	0	0
3	A	6	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	9	0	0	1	0
All	All	7416	0	7480	88	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 6.

All (88) 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:242:CYS:HB3	3:A:503:HOH:O	1.59	1.01
1:A:247:GLU:HB3	3:A:503:HOH:O	1.70	0.89
1:A:30:LYS:HD3	1:A:30:LYS:H	1.41	0.83
1:B:104:LYS:HE3	1:C:87:THR:HG21	1.67	0.76
1:B:96:SER:HB3	1:B:108:ILE:HD13	1.70	0.74
1:C:304:LYS:HE3	1:C:311:ILE:HD12	1.72	0.71
1:C:109:PHE:O	1:C:113:LEU:HD12	1.98	0.64
1:C:229:PHE:CD2	1:C:254:SER:HB3	2.32	0.63
1:A:68:PRO:HD3	1:A:123:LEU:O	2.00	0.61
1:C:160:ASP:OD2	1:C:163:GLU:HB2	2.01	0.60
1:C:109:PHE:CE1	1:C:113:LEU:HD11	2.37	0.60
1:A:122:PHE:HB2	1:A:144:VAL:HG12	1.83	0.59
1:A:30:LYS:HE2	1:A:33:THR:HG21	1.84	0.59
1:C:312:GLU:CD	1:C:312:GLU:H	2.06	0.59
1:C:67:ILE:HG22	1:C:123:LEU:HB2	1.84	0.58
1:C:171:GLU:HG3	1:C:175:LYS:HE3	1.86	0.57
1:C:111:ASN:OD1	1:C:115:LYS:NZ	2.37	0.57
1:C:252:MET:O	1:C:256:MET:HG3	2.04	0.57
1:A:168:ILE:HG13	1:A:322:ILE:HD13	1.88	0.56
1:B:68:PRO:HD3	1:B:123:LEU:O	2.05	0.56
1:B:168:ILE:HD11	1:B:287:VAL:HG22	1.89	0.54
1:C:101:ASP:HB3	1:C:104:LYS:HB2	1.88	0.54
1:C:83:GLU:O	1:C:87:THR:HG23	2.09	0.53
1:C:168:ILE:HG13	1:C:322:ILE:HD13	1.90	0.53
1:B:104:LYS:O	1:B:108:ILE:HG13	2.09	0.53
1:A:83:GLU:OE1	1:A:93:SER:OG	2.26	0.52
1:A:305:TYR:CZ	1:A:311:ILE:HD12	2.44	0.52
1:C:168:ILE:HD11	1:C:287:VAL:HG23	1.92	0.51
1:C:91:TYR:HD2	1:C:299:MET:HE1	1.75	0.51
1:B:168:ILE:HG13	1:B:322:ILE:HD13	1.92	0.51
1:B:274:THR:HG21	3:B:501:HOH:O	2.10	0.51
1:A:242:CYS:CB	3:A:503:HOH:O	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:ASN:O	1:A:45:ASN:ND2	2.44	0.50
1:A:213:THR:HB	1:B:213:THR:HB	1.93	0.50
1:C:144:VAL:HG13	1:C:147:THR:HG23	1.92	0.50
1:B:261:LYS:HB2	1:B:265:GLU:OE2	2.12	0.49
1:B:16:MET:HG3	2:B:401:SO4:O1	2.12	0.49
1:C:171:GLU:CG	1:C:175:LYS:HE3	2.42	0.49
1:A:304:LYS:HD3	1:A:311:ILE:HG12	1.95	0.49
1:C:109:PHE:CD1	1:C:113:LEU:HD11	2.47	0.49
1:A:264:GLU:OE1	1:A:264:GLU:N	2.39	0.47
1:C:118:ASP:OD1	1:C:118:ASP:N	2.48	0.47
1:A:312:GLU:HG2	1:A:313:GLU:N	2.30	0.46
1:C:209:GLN:H	1:C:209:GLN:HG3	1.51	0.46
1:C:304:LYS:HE3	1:C:311:ILE:CD1	2.43	0.46
1:C:189:LYS:HA	1:C:189:LYS:HD2	1.49	0.46
1:A:21:ARG:HD2	1:A:26:ASN:HD22	1.81	0.46
1:B:83:GLU:CD	1:B:93:SER:HG	2.20	0.45
1:B:179:SER:OG	1:B:238:ASP:N	2.44	0.45
1:B:284:LEU:HD12	1:B:327:THR:HG21	1.98	0.44
1:B:118:ASP:O	1:B:141:PRO:HD2	2.16	0.44
1:C:98:SER:C	1:C:100:ASN:N	2.71	0.44
1:A:157:VAL:HA	1:A:316:VAL:O	2.17	0.44
1:A:168:ILE:HD11	1:A:287:VAL:HG23	1.99	0.44
1:C:18:THR:O	1:C:22:VAL:HG23	2.18	0.44
1:C:151:ASP:O	1:C:154:ILE:HG13	2.18	0.44
1:A:144:VAL:O	1:A:156:SER:HA	2.18	0.44
1:C:68:PRO:HD3	1:C:123:LEU:O	2.18	0.43
1:C:132:LYS:HD2	1:C:150:LYS:HB3	2.00	0.43
1:C:91:TYR:CD2	1:C:299:MET:HE1	2.54	0.43
1:C:283:GLN:H	1:C:283:GLN:HG2	1.53	0.43
1:A:325:ARG:HE	1:A:325:ARG:HB3	1.44	0.43
1:A:261:LYS:HE3	1:A:264:GLU:OE1	2.19	0.42
1:C:144:VAL:HG13	1:C:147:THR:CG2	2.50	0.42
1:A:9:ALA:HB1	1:A:14:VAL:O	2.20	0.42
1:A:242:CYS:O	1:A:270:SER:HA	2.19	0.42
1:B:124:GLY:HA2	1:B:146:GLY:O	2.20	0.42
1:B:310:LYS:HD3	1:B:310:LYS:HA	1.54	0.42
1:C:143:VAL:HG23	1:C:302:LEU:HD13	2.02	0.42
1:C:203:LEU:HD23	1:C:203:LEU:HA	1.80	0.42
1:B:39:GLU:OE1	1:B:39:GLU:HA	2.21	0.41
1:C:63:VAL:HG21	1:C:299:MET:HE3	2.03	0.41
1:C:66:ILE:HD11	1:C:112:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:GLU:HG3	1:C:97:ASN:CG	2.41	0.41
1:B:12:ALA:HB3	1:B:14:VAL:HG22	2.03	0.41
1:C:150:LYS:HA	1:C:150:LYS:HD2	1.74	0.41
1:B:36:LYS:HE2	1:B:36:LYS:HB3	1.83	0.41
1:C:223:LYS:HE2	1:C:223:LYS:HB2	1.90	0.41
1:B:8:VAL:HG13	1:B:40:VAL:HB	2.03	0.41
1:C:73:ILE:HA	1:C:76:SER:OG	2.21	0.41
1:C:144:VAL:O	1:C:156:SER:HA	2.21	0.41
1:C:210:LEU:HD12	1:C:210:LEU:HA	1.91	0.40
1:A:178:LYS:HA	1:A:208:LEU:HD13	2.03	0.40
1:B:78:LEU:HD23	1:B:78:LEU:HA	1.91	0.40
1:B:113:LEU:HD11	1:B:138:SER:OG	2.22	0.40
1:C:165:ALA:O	1:C:169:THR:OG1	2.30	0.40
1:B:101:ASP:HB3	1:B:104:LYS:HB2	2.03	0.40
1:C:30:LYS:H	1:C:30:LYS:HG2	1.65	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)
1:A:45:ASN:ND2	1:C:171:GLU:OE2[4_555]	2.09	0.11

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	316/329 (96%)	309 (98%)	7 (2%)	0	100	100
1	B	315/329 (96%)	308 (98%)	7 (2%)	0	100	100
1	C	315/329 (96%)	301 (96%)	14 (4%)	0	100	100
All	All	946/987 (96%)	918 (97%)	28 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	275/281 (98%)	266 (97%)	9 (3%)	38	51
1	B	274/281 (98%)	260 (95%)	14 (5%)	24	32
1	C	274/281 (98%)	246 (90%)	28 (10%)	7	8
All	All	823/843 (98%)	772 (94%)	51 (6%)	18	24

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	133	GLU
1	A	159	ILE
1	A	179	SER
1	A	183	VAL
1	A	190	LYS
1	A	269	ILE
1	A	270	SER
1	A	321	ARG
1	A	325	ARG
1	B	6	TYR
1	B	30	LYS
1	B	114	SER
1	B	129	GLU
1	B	133	GLU
1	B	190	LYS
1	B	205	LYS
1	B	252	MET
1	B	261	LYS
1	B	269	ILE
1	B	270	SER
1	B	310	LYS
1	B	311	ILE
1	B	325	ARG

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Mol	Chain	Res	Type
1	C	13	ARG
1	C	42	LYS
1	C	60	THR
1	C	118	ASP
1	C	147	THR
1	C	150	LYS
1	C	157	VAL
1	C	159	ILE
1	C	178	LYS
1	C	179	SER
1	C	183	VAL
1	C	189	LYS
1	C	205	LYS
1	C	209	GLN
1	C	210	LEU
1	C	213	THR
1	C	215	ASN
1	C	217	SER
1	C	220	GLU
1	C	223	LYS
1	C	244	SER
1	C	269	ILE
1	C	270	SER
1	C	276	LEU
1	C	278	GLU
1	C	283	GLN
1	C	321	ARG
1	C	329	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	283	GLN
1	B	24	ASN
1	B	28	ASN
1	B	35	ASN
1	B	49	ASN
1	B	77	GLN
1	B	92	HIS
1	C	235	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](#)

6 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	$\# Z > 2$
2	SO4	B	402	-	4,4,4	0.14	0	6,6,6	0.23	0
2	SO4	A	401	-	4,4,4	0.15	0	6,6,6	0.19	0
2	SO4	A	403	-	4,4,4	0.44	0	6,6,6	0.06	0
2	SO4	A	402	-	4,4,4	0.16	0	6,6,6	0.28	0
2	SO4	B	401	-	4,4,4	0.12	0	6,6,6	0.22	0
2	SO4	C	401	-	4,4,4	0.16	0	6,6,6	0.24	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	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	320/329 (97%)	0.21	10 (3%) 49 56	37, 55, 78, 100	0
1	B	319/329 (96%)	0.31	19 (5%) 21 25	33, 55, 86, 110	0
1	C	319/329 (96%)	0.60	28 (8%) 10 11	43, 75, 104, 115	0
All	All	958/987 (97%)	0.38	57 (5%) 22 26	33, 62, 96, 115	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	210	LEU	8.1
1	B	37	VAL	4.9
1	C	154	ILE	4.7
1	C	209	GLN	4.6
1	B	32	GLU	4.5
1	C	137	GLN	4.1
1	C	13	ARG	4.0
1	B	29	VAL	3.6
1	A	76	SER	3.3
1	B	13	ARG	3.2
1	B	33	THR	3.2
1	B	36	LYS	3.2
1	C	152	ALA	3.0
1	C	230	ALA	3.0
1	C	260	ILE	2.9
1	C	30	LYS	2.9
1	A	13	ARG	2.8
1	B	30	LYS	2.8
1	C	73	ILE	2.8
1	C	206	ASN	2.8
1	C	127	ILE	2.8
1	B	259	GLY	2.8
1	C	131	MET	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	133	GLU	2.7
1	B	28	ASN	2.6
1	B	305	TYR	2.6
1	A	70	ILE	2.5
1	C	71	SER	2.5
1	C	72	ASN	2.5
1	A	242	CYS	2.5
1	C	36	LYS	2.5
1	B	70	ILE	2.4
1	C	70	ILE	2.4
1	C	186	GLU	2.4
1	B	311	ILE	2.3
1	B	73	ILE	2.3
1	B	308	ASP	2.3
1	C	308	ASP	2.3
1	A	34	LYS	2.2
1	B	152	ALA	2.2
1	A	71	SER	2.2
1	C	153	HIS	2.2
1	C	205	LYS	2.2
1	A	311	ILE	2.2
1	C	32	GLU	2.2
1	B	76	SER	2.1
1	C	150	LYS	2.1
1	C	229	PHE	2.1
1	A	59	LYS	2.1
1	C	33	THR	2.1
1	A	78	LEU	2.1
1	C	139	SER	2.1
1	B	71	SER	2.1
1	B	276	LEU	2.1
1	B	34	LYS	2.1
1	C	258	ALA	2.0
1	A	32	GLU	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
2	SO4	A	403	5/5	0.80	0.28	92,96,114,116	0
2	SO4	A	401	5/5	0.90	0.25	87,87,98,102	0
2	SO4	B	402	5/5	0.94	0.24	77,93,105,105	0
2	SO4	A	402	5/5	0.95	0.15	66,67,68,72	0
2	SO4	B	401	5/5	0.97	0.10	77,80,83,88	0
2	SO4	C	401	5/5	0.98	0.14	61,67,70,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.