



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:03 PM EDT

PDB ID : 7E5W / pdb_00007e5w
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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

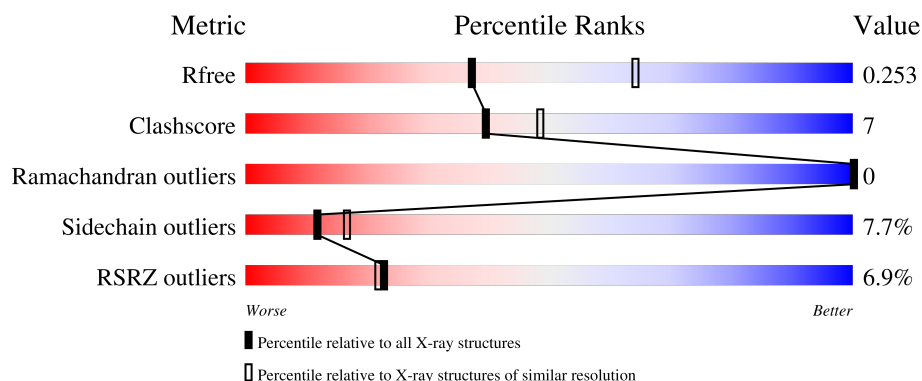
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

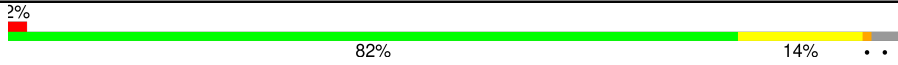
The reported resolution of this entry is 2.55 Å.

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}	180053	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	
1	B	329	
1	C	329	

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
1	A	320	Total	C	N	O	S	0	0	0
			2463	1542	420	490	11			
1	B	319	Total	C	N	O	S	0	0	0
			2454	1536	418	489	11			
1	C	319	Total	C	N	O	S	0	0	0
			2454	1536	418	489	11			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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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		

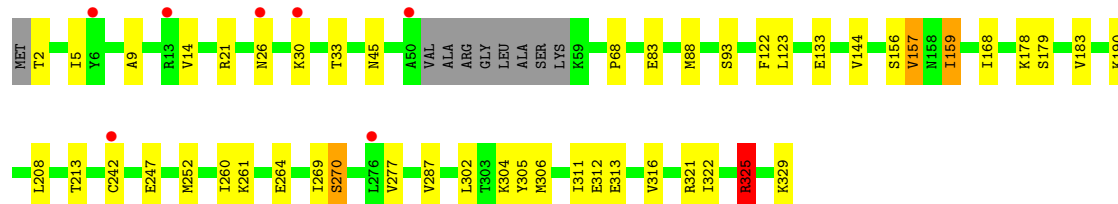
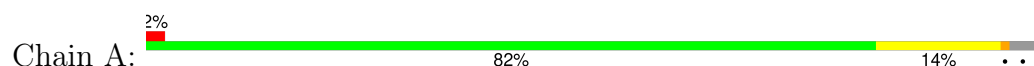
- Molecule 3 is water.

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

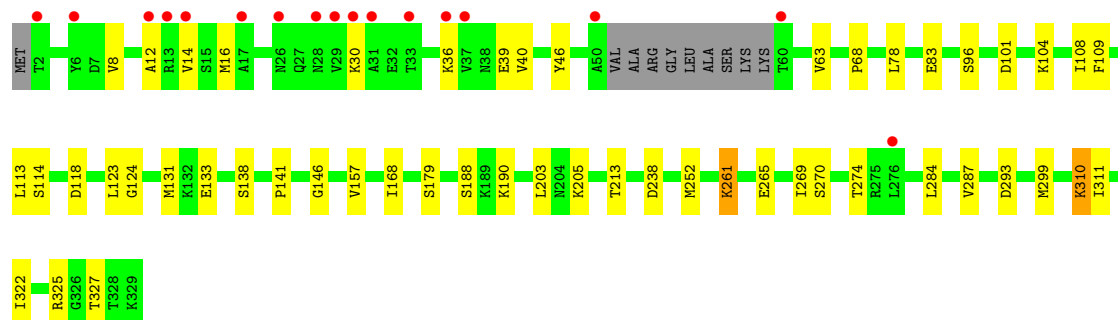
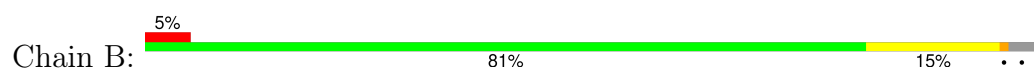
3 Residue-property plots [i](#)

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.

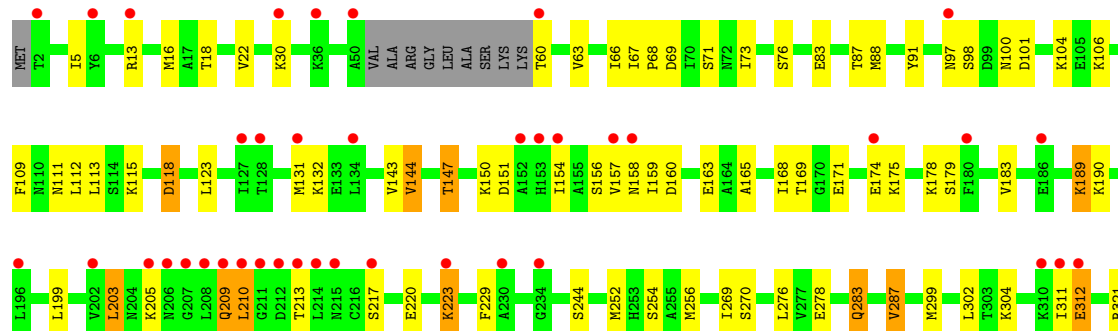
• Molecule 1: Catabolite control protein A

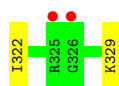


• Molecule 1: Catabolite control protein A



• Molecule 1: Catabolite control protein A





4 Data and refinement statistics

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)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.233 , 0.255 0.235 , 0.253	Depositor DCC
R_{free} test set	2318 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	59.3	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for l,-k,h 0.009 for -h,-l,-k	Xtriage
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

Xtriage'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	0.62	0/2492	0.91	3/3364 (0.1%)
1	B	0.63	0/2483	0.89	0/3353
1	C	0.59	0/2483	0.85	0/3353
All	All	0.61	0/7458	0.88	3/10070 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	159	ILE	N-CA-C	-6.36	100.68	109.46
1	A	325	ARG	CA-C-N	-5.70	117.26	123.30
1	A	325	ARG	C-N-CA	-5.70	117.26	123.30

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	28	1
1	B	2454	0	2489	26	0
1	C	2454	0	2489	49	1
2	A	15	0	0	0	0
2	B	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	5	0	0	0	0
3	A	6	0	0	3	0
3	B	9	0	0	1	0
All	All	7416	0	7480	100	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 7.

All (100) 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:63:VAL:HG21	1:C:299:MET:HE1	1.77	0.65
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:C:312:GLU:CD	1:C:312:GLU:H	2.06	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:C:91:TYR:CD2	1:C:299:MET:HE2	2.37	0.59
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: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:A:88:MET:HA	1:A:88:MET:HE2	1.86	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:C:69:ASP:CG	1:C:71:SER:HG	2.16	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:TYR:CZ	1:A:311:ILE:HD12	2.44	0.52
1:A:302:LEU:HG	1:A:306:MET:HE2	1.92	0.52
1:C:168:ILE:HD11	1:C:287:VAL:HG23	1.92	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
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:91:TYR:HD2	1:C:299:MET:HE2	1.75	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:88:MET:HE3	1:C:88:MET:HB3	1.63	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:B:83:GLU:HG3	1:C:97:ASN:CG	2.41	0.46
1:C:98:SER:C	1:C:100:ASN:N	2.71	0.46
1:A:21:ARG:HD2	1:A:26:ASN:HD22	1.81	0.46
1:C:91:TYR:CE2	1:C:299:MET:HE2	2.51	0.45
1:B:179:SER:OG	1:B:238:ASP:N	2.44	0.45
1:C:106:LYS:HA	1:C:131:MET:HE1	1.98	0.45
1:B:284:LEU:HD12	1:B:327:THR:HG21	1.98	0.44
1:B:63:VAL:HG21	1:B:299:MET:HE1	2.00	0.44
1:B:118:ASP:O	1:B:141:PRO:HD2	2.16	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:98:SER:C	1:C:100:ASN:H	2.26	0.43
1:A:312:GLU:H	1:A:312:GLU:CD	2.25	0.43
1:C:283:GLN:H	1:C:283:GLN:HG2	1.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:MET:HE2	1:A:252:MET:HB3	1.86	0.43
1:C:5:ILE:CG2	1:C:16:MET:HE3	2.48	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:B:46:TYR:OH	1:B:293:ASP:OD1	2.33	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:66:ILE:HD11	1:C:112:LEU:HD12	2.02	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:B:109:PHE:HB2	1:B:131:MET:HE1	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

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	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

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%)	260 (94%)	15 (6%)	19	29
1	B	274/281 (98%)	259 (94%)	15 (6%)	19	29
1	C	274/281 (98%)	241 (88%)	33 (12%)	5	5
All	All	823/843 (98%)	760 (92%)	63 (8%)	12	17

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	5	ILE
1	A	133	GLU
1	A	157	VAL
1	A	159	ILE

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Mol	Chain	Res	Type
1	A	179	SER
1	A	183	VAL
1	A	190	LYS
1	A	260	ILE
1	A	269	ILE
1	A	270	SER
1	A	277	VAL
1	A	321	ARG
1	A	325	ARG
1	A	329	LYS
1	B	30	LYS
1	B	114	SER
1	B	133	GLU
1	B	157	VAL
1	B	188	SER
1	B	190	LYS
1	B	203	LEU
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
1	C	13	ARG
1	C	60	THR
1	C	118	ASP
1	C	144	VAL
1	C	147	THR
1	C	157	VAL
1	C	158	ASN
1	C	159	ILE
1	C	174	GLU
1	C	178	LYS
1	C	179	SER
1	C	183	VAL
1	C	189	LYS
1	C	190	LYS
1	C	199	LEU
1	C	203	LEU
1	C	205	LYS

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Mol	Chain	Res	Type
1	C	209	GLN
1	C	210	LEU
1	C	213	THR
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	287	VAL
1	C	312	GLU
1	C	321	ARG
1	C	329	LYS

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

Mol	Chain	Res	Type
1	A	45	ASN
1	A	49	ASN
1	A	283	GLN
1	B	28	ASN
1	B	35	ASN
1	B	77	GLN
1	B	92	HIS
1	B	111	ASN
1	B	187	HIS
1	C	49	ASN
1	C	235	ASN
1	C	315	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	401	-	4,4,4	0.23	0	6,6,6	0.21	0
2	SO4	C	401	-	4,4,4	0.27	0	6,6,6	0.19	0
2	SO4	A	401	-	4,4,4	0.27	0	6,6,6	0.19	0
2	SO4	A	402	-	4,4,4	0.28	0	6,6,6	0.29	0
2	SO4	B	402	-	4,4,4	0.25	0	6,6,6	0.24	0
2	SO4	A	403	-	4,4,4	0.38	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.

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

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%)	0.24	7 (2%) 62 63	37, 55, 78, 100	0
1	B	319/329 (96%)	0.33	17 (5%) 32 31	33, 55, 86, 110	0
1	C	319/329 (96%)	0.97	42 (13%) 7 6	43, 75, 104, 115	0
All	All	958/987 (97%)	0.51	66 (6%) 23 22	33, 62, 96, 115	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	210	LEU	7.8
1	C	209	GLN	4.6
1	C	206	ASN	4.3
1	B	31	ALA	4.1
1	C	13	ARG	4.0
1	C	205	LYS	3.8
1	B	30	LYS	3.5
1	B	14	VAL	3.3
1	B	6	TYR	3.3
1	A	50	ALA	3.3
1	C	211	GLY	3.2
1	C	97	ASN	3.2
1	C	50	ALA	3.2
1	C	6	TYR	3.2
1	C	30	LYS	3.2
1	B	36	LYS	3.1
1	C	186	GLU	3.1
1	B	13	ARG	3.1
1	A	13	ARG	3.0
1	C	230	ALA	3.0
1	C	215	ASN	3.0
1	C	208	LEU	3.0
1	C	174	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	37	VAL	2.9
1	C	310	LYS	2.8
1	B	17	ALA	2.7
1	A	276	LEU	2.7
1	B	276	LEU	2.7
1	B	60	THR	2.7
1	C	223	LYS	2.7
1	A	6	TYR	2.7
1	A	30	LYS	2.6
1	C	128	THR	2.6
1	C	213	THR	2.6
1	C	214	LEU	2.5
1	C	154	ILE	2.5
1	B	12	ALA	2.5
1	C	127	ILE	2.4
1	C	60	THR	2.4
1	C	312	GLU	2.4
1	C	212	ASP	2.3
1	B	33	THR	2.3
1	C	158	ASN	2.3
1	C	217	SER	2.3
1	B	2	THR	2.3
1	C	152	ALA	2.2
1	B	26	ASN	2.2
1	B	50	ALA	2.2
1	C	157	VAL	2.2
1	C	131	MET	2.2
1	A	242	CYS	2.2
1	C	326	GLY	2.2
1	C	36	LYS	2.2
1	C	153	HIS	2.1
1	C	2	THR	2.1
1	C	207	GLY	2.1
1	C	234	GLY	2.1
1	C	180	PHE	2.1
1	C	202	VAL	2.1
1	C	196	LEU	2.1
1	C	325	ARG	2.1
1	B	29	VAL	2.0
1	C	134	LEU	2.0
1	A	26	ASN	2.0
1	B	28	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	311	ILE	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	SO4	A	403	5/5	0.61	0.13	92,96,114,116	0
2	SO4	A	401	5/5	0.80	0.21	87,87,98,102	0
2	SO4	B	402	5/5	0.83	0.09	77,93,105,105	0
2	SO4	B	401	5/5	0.88	0.15	77,80,83,88	0
2	SO4	A	402	5/5	0.94	0.11	66,67,68,72	0
2	SO4	C	401	5/5	0.94	0.14	61,67,70,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.