



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:15 AM UTC

PDB ID : 1K93 / pdb_00001k93
Title : Crystal structure of the adenylyl cyclase domain of anthrax edema factor (EF) in complex with calmodulin
Authors : Drum, C.L.; Yan, S.-Z.; Bard, J.; Shen, Y.-Q.; Lu, D.; Soelaiman, S.; Grabarek, Z.; Bohm, A.; Tang, W.-J.
Deposited on : 2001-10-26
Resolution : 2.95 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

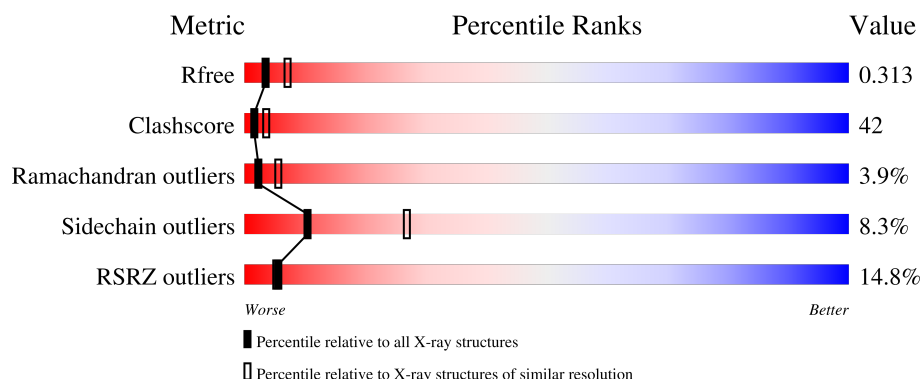
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

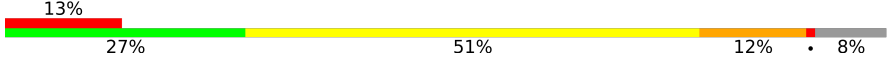
The reported resolution of this entry is 2.95 Å.

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	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	510	
1	B	510	
1	C	510	
2	D	144	
2	E	144	

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Mol	Chain	Length	Quality of chain
2	F	144	18% 33% 57% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15241 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 CALMODULIN-SENSITIVE ADENYLATE CYCLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	485	Total	C	N	O	S	65	0	0
			3952	2528	673	748	3			
1	B	467	Total	C	N	O	S	113	0	0
			3804	2437	644	720	3			
1	C	503	Total	C	N	O	S	166	0	0
			4094	2616	696	779	3			

- Molecule 2 is a protein called CALMODULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	143	Total	C	N	O	S	0	0	0
			1125	690	181	245	9			
2	E	143	Total	C	N	O	S	0	0	0
			1125	690	181	245	9			
2	F	143	Total	C	N	O	S	0	0	0
			1125	690	181	245	9			

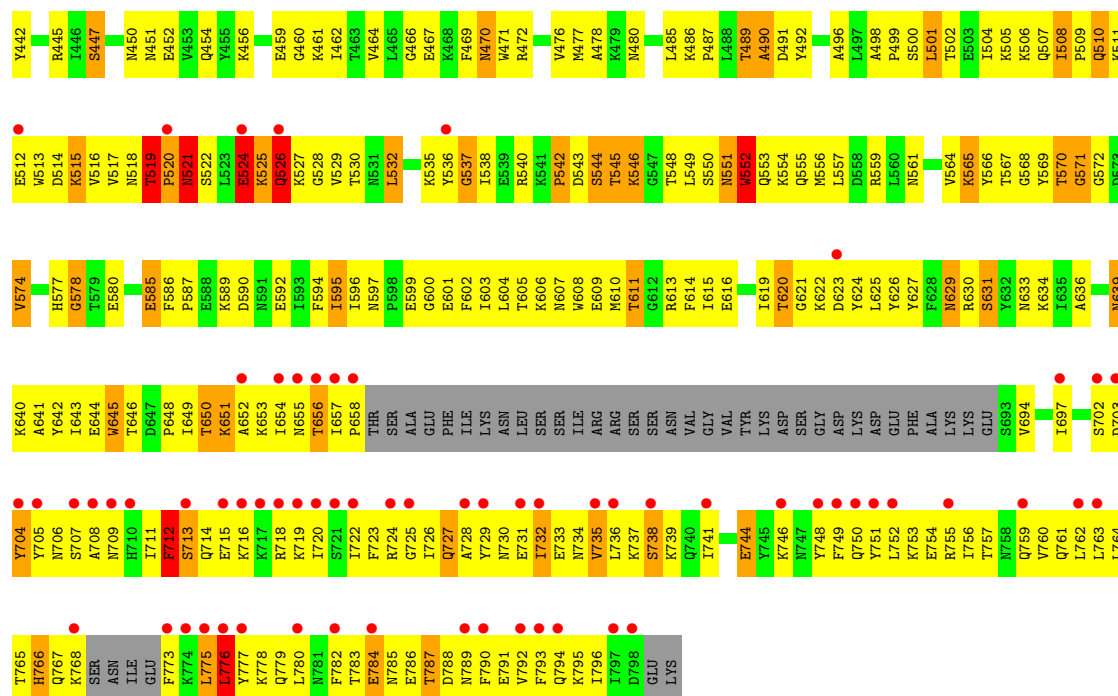
- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



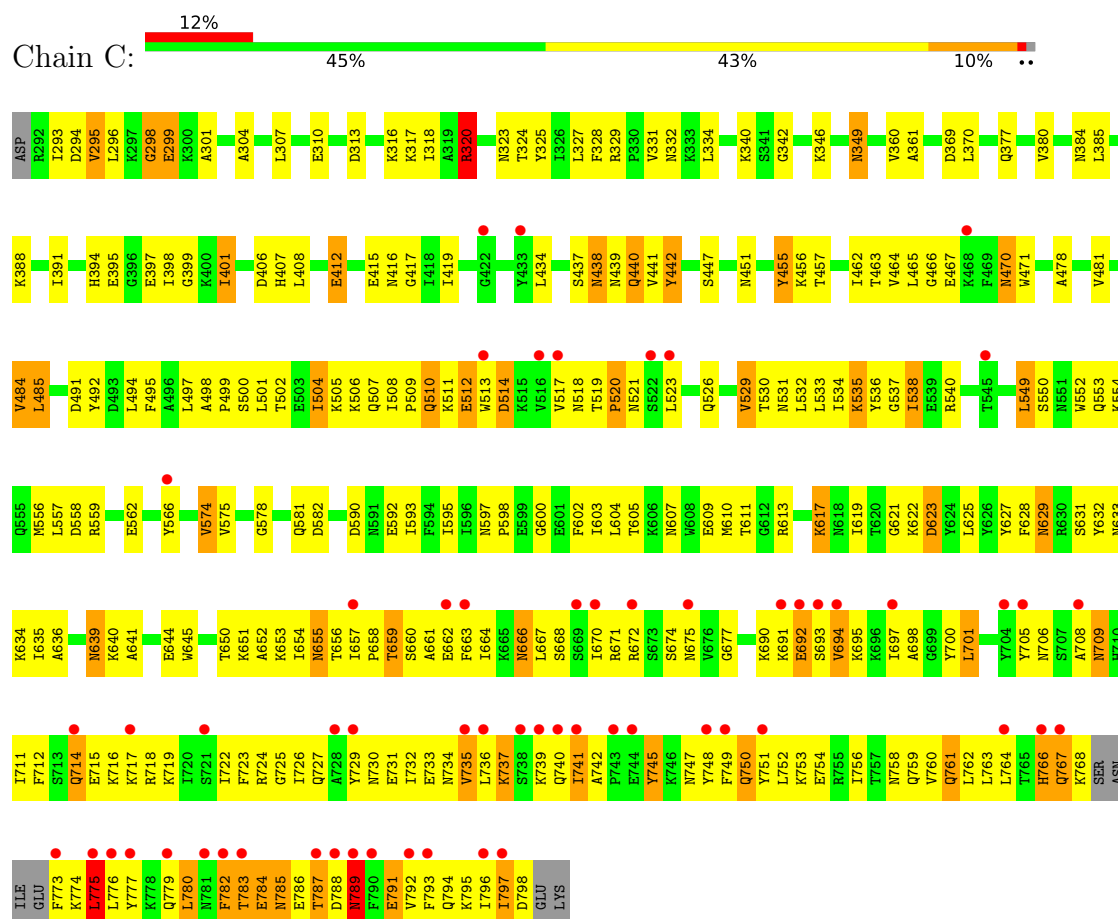
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

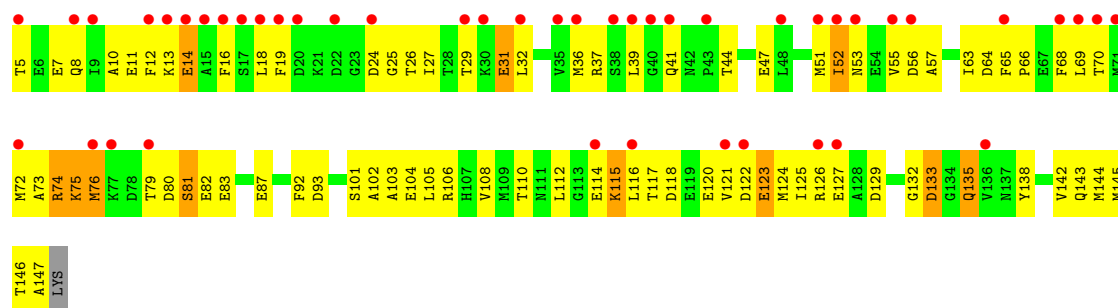
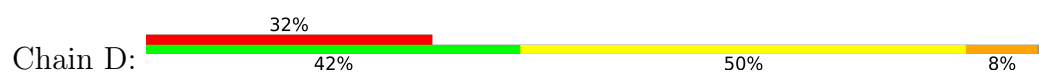
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	2	Total	Ca	0	0
			2	2		
4	E	2	Total	Ca	0	0
			2	2		
4	F	2	Total	Ca	0	0
			2	2		



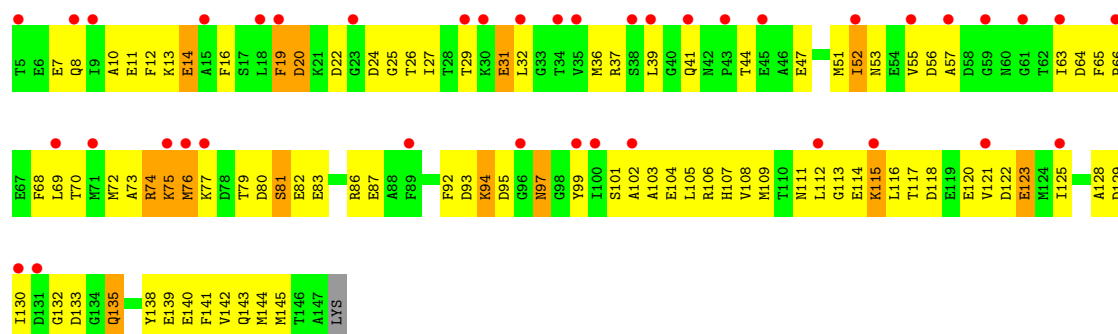
• Molecule 1: CALMODULIN-SENSITIVE ADENYLATE CYCLASE



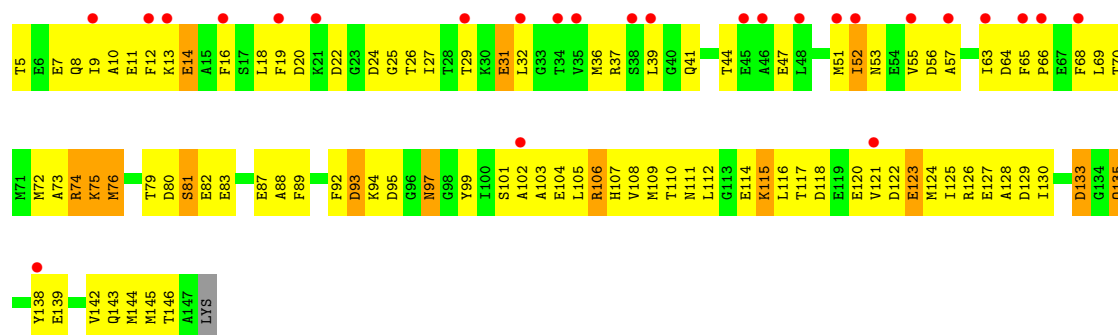
• Molecule 2: CALMODULIN



• Molecule 2: CALMODULIN



• Molecule 2: CALMODULIN



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	116.73Å 167.31Å 344.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.95 30.00 – 2.95	Depositor EDS
% Data completeness (in resolution range)	96.9 (30.00-2.95) 98.0 (30.00-2.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.45 (at 2.95Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.278 , 0.315 0.278 , 0.313	Depositor DCC
R_{free} test set	7056 reflections (10.10%)	wwPDB-VP
Wilson B-factor (Å ²)	83.2	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	15241	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% 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: CA, 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	0.72	2/4027 (0.0%)	1.25	51/5419 (0.9%)
1	B	0.82	7/3878 (0.2%)	1.30	48/5221 (0.9%)
1	C	0.68	4/4172 (0.1%)	1.17	37/5613 (0.7%)
2	D	0.53	0/1137	0.93	2/1527 (0.1%)
2	E	0.52	1/1137 (0.1%)	0.96	5/1527 (0.3%)
2	F	0.45	0/1137	0.98	6/1527 (0.4%)
All	All	0.69	14/15488 (0.1%)	1.18	149/20834 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	470	ASN	C-N	-8.30	1.21	1.33
1	B	525	LYS	C-O	7.41	1.33	1.24
1	B	522	SER	N-CA	6.28	1.54	1.45
1	C	784	GLU	CA-C	-6.01	1.44	1.52
1	B	354	SER	CB-OG	5.91	1.53	1.42

The worst 5 of 149 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	521	ASN	N-CA-C	20.18	134.91	111.71
1	C	785	ASN	CA-C-N	-19.41	102.36	123.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	785	ASN	C-N-CA	-19.41	102.36	123.13
1	A	785	ASN	N-CA-C	16.44	129.81	110.41
1	A	470	ASN	CA-C-N	-13.02	102.37	122.81

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	566	TYR	Sidechain
1	C	766	HIS	Mainchain

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	3952	0	3999	302	0
1	B	3804	0	3833	416	0
1	C	4094	0	4134	304	0
2	D	1125	0	1049	90	0
2	E	1125	0	1049	84	0
2	F	1125	0	1049	99	0
3	A	5	0	0	0	0
3	C	5	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
All	All	15241	0	15113	1242	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 42.

The worst 5 of 1242 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:616:GLU:HA	1:B:620:THR:HG22	1.31	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:PHE:HD1	1:B:477:MET:HE1	1.13	1.09
1:B:327:LEU:HD22	1:B:496:ALA:HB3	1.35	1.07
1:B:726:ILE:HA	1:B:729:TYR:HB2	1.35	1.03
2:F:19:PHE:HD1	2:F:19:PHE:O	1.42	1.02

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	479/510 (94%)	405 (85%)	63 (13%)	11 (2%)	5	14
1	B	461/510 (90%)	352 (76%)	81 (18%)	28 (6%)	1	2
1	C	499/510 (98%)	415 (83%)	66 (13%)	18 (4%)	2	6
2	D	141/144 (98%)	119 (84%)	17 (12%)	5 (4%)	3	7
2	E	141/144 (98%)	118 (84%)	18 (13%)	5 (4%)	3	7
2	F	141/144 (98%)	118 (84%)	18 (13%)	5 (4%)	3	7
All	All	1862/1962 (95%)	1527 (82%)	263 (14%)	72 (4%)	2	5

5 of 72 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	741	ILE
1	B	299	GLU
1	B	526	GLN
1	B	544	SER
1	B	571	GLY

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	433/455 (95%)	395 (91%)	38 (9%)	9	24
1	B	414/455 (91%)	375 (91%)	39 (9%)	8	22
1	C	448/455 (98%)	409 (91%)	39 (9%)	9	25
2	D	121/123 (98%)	114 (94%)	7 (6%)	18	41
2	E	121/123 (98%)	114 (94%)	7 (6%)	18	41
2	F	121/123 (98%)	113 (93%)	8 (7%)	15	37
All	All	1658/1734 (96%)	1520 (92%)	138 (8%)	10	27

5 of 138 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	797	ILE
2	D	75	LYS
2	F	14	GLU
1	B	437	SER
1	B	434	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 88 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	337	ASN
1	C	629	ASN
1	C	394	HIS
1	C	518	ASN
1	C	666	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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	C	1003	-	4,4,4	1.84	1 (25%)	6,6,6	1.04	0
3	SO4	A	1001	-	4,4,4	1.61	1 (25%)	6,6,6	0.49	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	SO4	O2-S	2.11	1.57	1.44
3	C	1003	SO4	O2-S	2.01	1.56	1.44

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 ⓘ

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(Å²)	Q<0.9
1	A	485/510 (95%)	0.60	36 (7%)	20	18	27, 70, 148, 169	16 (3%)
1	B	459/510 (90%)	0.77	67 (14%)	6	5	11, 68, 160, 167	12 (2%)
1	C	491/510 (96%)	0.77	60 (12%)	8	8	31, 72, 148, 169	19 (3%)
2	D	143/144 (99%)	1.61	46 (32%)	1	1	53, 145, 174, 176	0
2	E	143/144 (99%)	1.50	40 (27%)	1	1	55, 146, 174, 176	0
2	F	143/144 (99%)	1.29	26 (18%)	3	3	56, 146, 174, 176	0
All	All	1864/1962 (95%)	0.89	275 (14%)	5	5	11, 76, 168, 176	47 (2%)

The worst 5 of 275 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	697	ILE	30.4
2	D	76	MET	6.6
2	F	38	SER	6.5
1	C	675	ASN	6.4
1	B	705	TYR	5.9

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
4	CA	F	805	1/1	0.92	0.07	66,66,66,66	0
3	SO4	C	1003	5/5	0.96	0.07	51,51,55,56	0
4	CA	D	801	1/1	0.98	0.06	57,57,57,57	0
4	CA	D	802	1/1	0.98	0.04	61,61,61,61	0
4	CA	E	803	1/1	0.98	0.06	79,79,79,79	0
4	CA	E	804	1/1	0.98	0.05	81,81,81,81	0
3	SO4	A	1001	5/5	0.98	0.05	42,42,44,47	0
4	CA	F	806	1/1	0.98	0.05	79,79,79,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.