



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2017 – 05:00 PM EDT

PDB ID : 5N1V  
Title : Crystal structure of the protein kinase CK2 catalytic subunit in complex with pyrazolo-pyrimidine macrocyclic ligand  
Authors : Robb, G.; Ferguson, A.; Hargreaves, D.  
Deposited on : 2017-02-06  
Resolution : 2.52 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029077  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029077

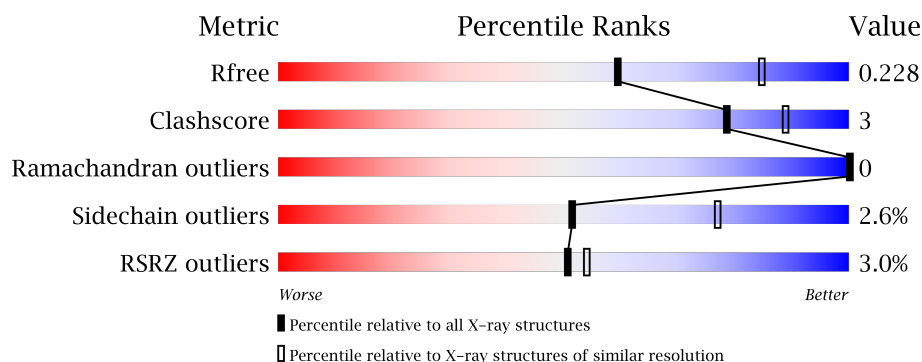
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.52 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))
$R_{free}$	100719	4636 (2.54-2.50)
Clashscore	112137	5382 (2.54-2.50)
Ramachandran outliers	110173	5282 (2.54-2.50)
Sidechain outliers	110143	5284 (2.54-2.50)
RSRZ outliers	101464	4669 (2.54-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	342	<div> <div>3%</div> <div>88%</div> <div>8%</div> <div>•</div> </div>
1	B	342	<div> <div>3%</div> <div>86%</div> <div>11%</div> <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
2	SO4	A	401	-	-	-	X
2	SO4	A	404	-	-	-	X
2	SO4	B	401	-	-	-	X
3	EDO	A	406	-	-	-	X
3	EDO	A	409	-	-	-	X
3	EDO	A	410	-	-	-	X
3	EDO	B	404	-	-	-	X
3	EDO	B	407	-	-	-	X
3	EDO	B	409	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5922 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.

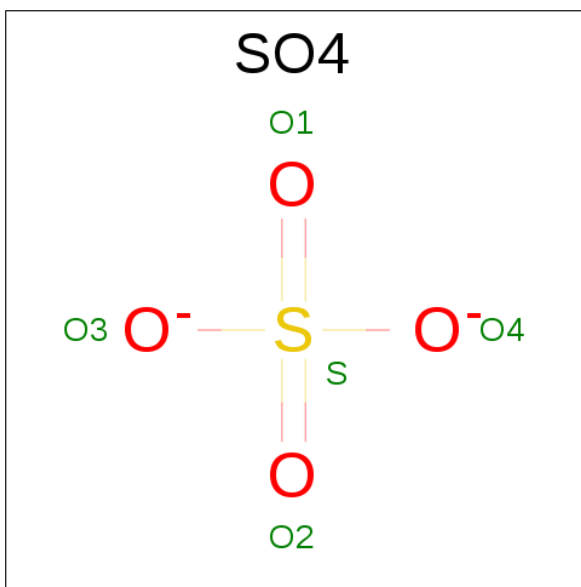
- Molecule 1 is a protein called Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	2	0
			2809	1799	497	502	11			
1	B	331	Total	C	N	O	S	0	1	0
			2801	1794	494	502	11			

There are 12 discrepancies between the modelled and reference sequences:

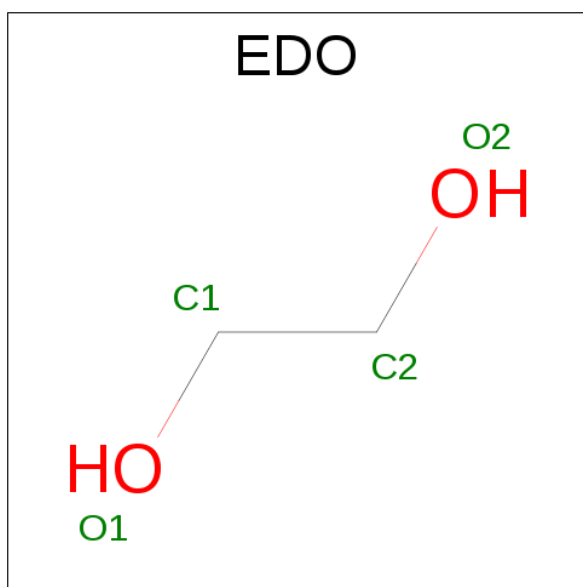
Chain	Residue	Modelled	Actual	Comment	Reference
A	337	HIS	-	expression tag	UNP P68400
A	338	HIS	-	expression tag	UNP P68400
A	339	HIS	-	expression tag	UNP P68400
A	340	HIS	-	expression tag	UNP P68400
A	341	HIS	-	expression tag	UNP P68400
A	342	HIS	-	expression tag	UNP P68400
B	337	HIS	-	expression tag	UNP P68400
B	338	HIS	-	expression tag	UNP P68400
B	339	HIS	-	expression tag	UNP P68400
B	340	HIS	-	expression tag	UNP P68400
B	341	HIS	-	expression tag	UNP P68400
B	342	HIS	-	expression tag	UNP P68400

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



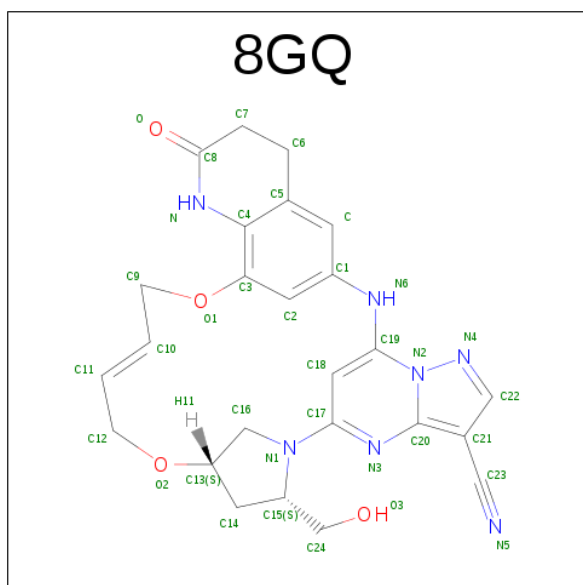
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 4 is pyrazolo-pyrimidine macrocycle (three-letter code: 8GQ) (formula:  $C_{25}H_{25}N_7O_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			36	25	7	4		
4	B	1	Total	C	N	O	0	0
			36	25	7	4		

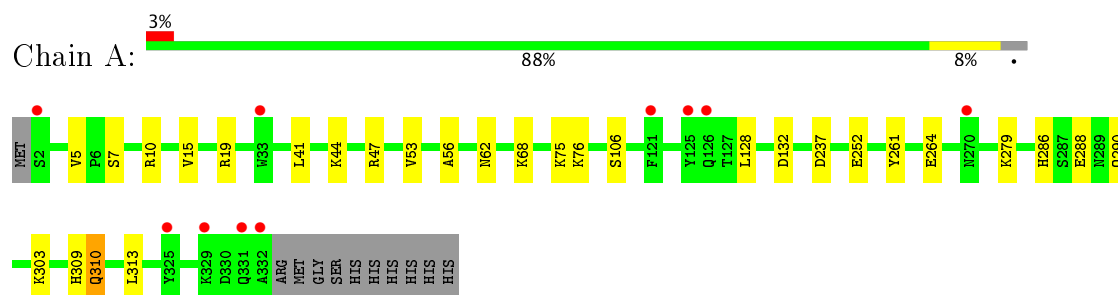
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	66	Total	O	0	0
			66	66		
5	B	75	Total	O	0	0
			75	75		

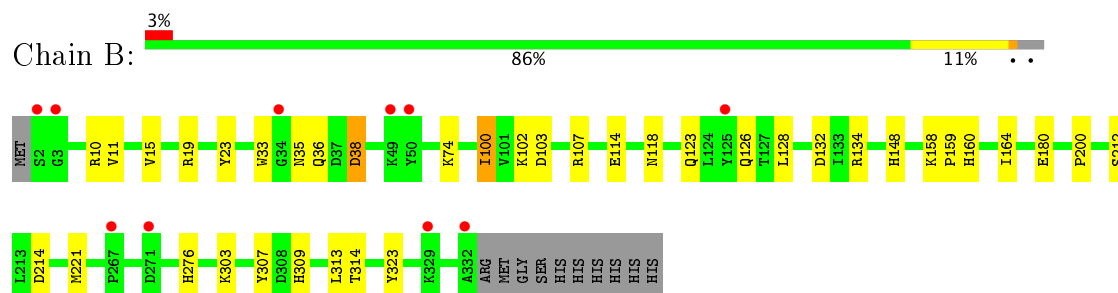
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Casein kinase II subunit alpha



#### • Molecule 1: Casein kinase II subunit alpha





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.77Å 128.77Å 125.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.05 – 2.52 90.05 – 2.52	Depositor EDS
% Data completeness (in resolution range)	100.0 (91.05-2.52) 100.0 (90.05-2.52)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, $R_{free}$	0.187 , 0.229 0.189 , 0.228	Depositor DCC
$R_{free}$ test set	1655 reflections (4.77%)	DCC
Wilson B-factor (Å <sup>2</sup> )	52.1	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 49.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k 0.000 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5922	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 32.12 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 9.9029e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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: 8GQ, EDO, 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	0.48	0/2890	0.67	0/3908
1	B	0.48	0/2879	0.67	0/3894
All	All	0.48	0/5769	0.67	0/7802

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

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	2809	0	2761	14	0
1	B	2801	0	2748	23	0
2	A	25	0	0	0	0
2	B	10	0	0	0	0
3	A	28	0	42	4	0
3	B	36	0	54	8	0
4	A	36	0	0	0	0
4	B	36	0	0	0	0
5	A	66	0	0	0	0
5	B	75	0	0	0	0
All	All	5922	0	5605	37	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 3.

All (37) 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:310:GLN:HA	3:A:409:EDO:H21	1.53	0.91
1:B:10:ARG:H	3:B:407:EDO:H22	1.53	0.73
1:A:53:VAL:HG22	1:A:68:LYS:HG2	1.72	0.72
1:B:35:ASN:O	1:B:38:ASP:HB2	2.00	0.62
1:B:314:THR:HA	3:B:409:EDO:H12	1.81	0.60
1:B:33:TRP:CZ3	1:B:100:ILE:HD11	2.37	0.58
1:B:10:ARG:N	3:B:407:EDO:H22	2.19	0.57
1:B:36:GLN:HG2	3:B:408:EDO:H12	1.87	0.56
1:A:279:LYS:HZ1	3:A:412:EDO:H11	1.72	0.54
1:B:276:HIS:HD2	3:B:405:EDO:H22	1.73	0.54
1:B:159:PRO:HD3	1:B:221:MET:HG2	1.89	0.53
1:A:128:LEU:HD22	1:A:132:ASP:HB3	1.91	0.52
1:A:7:SER:OG	1:A:309:HIS:HE1	1.93	0.52
1:B:36:GLN:HG3	1:B:103:ASP:HA	1.90	0.52
1:B:148:HIS:HD2	3:B:409:EDO:O2	1.94	0.50
1:A:10:ARG:HE	3:A:409:EDO:H22	1.78	0.49
1:B:303:LYS:HB3	1:B:313:LEU:HG	1.96	0.47
1:A:44:LYS:HE2	1:A:47:ARG:HG2	1.96	0.46
1:B:148:HIS:HE1	1:B:214:ASP:OD2	1.98	0.46
1:A:75:LYS:HD2	3:A:411:EDO:H21	1.97	0.46
1:A:303:LYS:HB3	1:A:313:LEU:HG	1.98	0.46
1:A:5:VAL:HB	1:A:261:TYR:HA	1.99	0.45
1:B:19[B]:ARG:HD2	1:B:23:TYR:CG	2.51	0.45
1:A:15:VAL:O	1:A:19[A]:ARG:HG3	2.17	0.44
1:B:11:VAL:HG21	3:B:409:EDO:H21	1.99	0.44
1:B:134:ARG:HG2	1:B:323:TYR:CZ	2.53	0.44
1:A:286:HIS:CE1	1:A:288:GLU:HG2	2.53	0.44
1:B:123:GLN:O	1:B:126:GLN:HG2	2.18	0.43
1:B:128:LEU:HD22	1:B:132:ASP:HB3	1.99	0.43
1:B:158:LYS:HE3	1:B:160:HIS:HB3	1.99	0.43
1:B:118:ASN:HA	1:B:164:ILE:O	2.18	0.43
1:A:41:LEU:HD23	1:A:56:ALA:HB2	2.00	0.43
1:B:276:HIS:HD2	3:B:405:EDO:C2	2.32	0.42
1:A:261:TYR:OH	1:A:310:GLN:HG3	2.20	0.41
1:B:212:SER:OG	1:B:309:HIS:HB2	2.20	0.41
1:B:134:ARG:HD3	1:B:323:TYR:O	2.20	0.41
1:B:200:PRO:HG2	1:B:307:TYR:HA	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	331/342 (97%)	322 (97%)	9 (3%)	0	100	100
1	B	330/342 (96%)	316 (96%)	14 (4%)	0	100	100
All	All	661/684 (97%)	638 (96%)	23 (4%)	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	306/314 (98%)	298 (97%)	8 (3%)	51	77
1	B	305/314 (97%)	297 (97%)	8 (3%)	51	77
All	All	611/628 (97%)	595 (97%)	16 (3%)	51	77

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	76	LYS
1	A	106	SER
1	A	237	ASP
1	A	252	GLU

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Mol	Chain	Res	Type
1	A	264	GLU
1	A	290	GLN
1	A	310	GLN
1	B	15	VAL
1	B	38	ASP
1	B	74	LYS
1	B	100	ILE
1	B	102	LYS
1	B	107	ARG
1	B	114	GLU
1	B	180	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	160	HIS
1	A	309	HIS
1	A	310	GLN
1	B	16	ASN
1	B	126	GLN
1	B	148	HIS
1	B	186	GLN
1	B	234	HIS
1	B	276	HIS
1	B	310	GLN

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

25 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	A	401	-	4,4,4	0.25	0	6,6,6	0.38	0
2	SO4	A	402	-	4,4,4	0.21	0	6,6,6	0.16	0
2	SO4	A	403	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	A	404	-	4,4,4	0.22	0	6,6,6	0.09	0
2	SO4	A	405	-	4,4,4	0.20	0	6,6,6	0.14	0
3	EDO	A	406	-	3,3,3	0.53	0	2,2,2	0.26	0
3	EDO	A	407	-	3,3,3	0.55	0	2,2,2	0.38	0
3	EDO	A	408	-	3,3,3	0.62	0	2,2,2	0.14	0
3	EDO	A	409	-	3,3,3	0.82	0	2,2,2	0.32	0
3	EDO	A	410	-	3,3,3	0.56	0	2,2,2	0.47	0
3	EDO	A	411	-	3,3,3	0.70	0	2,2,2	0.22	0
3	EDO	A	412	-	3,3,3	0.66	0	2,2,2	0.16	0
4	8GQ	A	413	-	35,41,41	0.60	1 (2%)	44,59,59	1.17	1 (2%)
2	SO4	B	401	-	4,4,4	0.16	0	6,6,6	0.28	0
2	SO4	B	402	-	4,4,4	0.19	0	6,6,6	0.08	0
3	EDO	B	403	-	3,3,3	0.70	0	2,2,2	0.16	0
3	EDO	B	404	-	3,3,3	0.46	0	2,2,2	0.66	0
3	EDO	B	405	-	3,3,3	0.58	0	2,2,2	0.26	0
3	EDO	B	406	-	3,3,3	0.63	0	2,2,2	0.15	0
3	EDO	B	407	-	3,3,3	0.83	0	2,2,2	0.49	0
3	EDO	B	408	-	3,3,3	0.42	0	2,2,2	0.63	0
3	EDO	B	409	-	3,3,3	0.42	0	2,2,2	0.54	0
3	EDO	B	410	-	3,3,3	0.64	0	2,2,2	0.31	0
3	EDO	B	411	-	3,3,3	0.68	0	2,2,2	0.10	0
4	8GQ	B	412	-	35,41,41	0.54	1 (2%)	44,59,59	1.25	1 (2%)

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
2	SO4	A	401	-	-	0/0/0/0	0/0/0/0
2	SO4	A	402	-	-	0/0/0/0	0/0/0/0
2	SO4	A	403	-	-	0/0/0/0	0/0/0/0
2	SO4	A	404	-	-	0/0/0/0	0/0/0/0
2	SO4	A	405	-	-	0/0/0/0	0/0/0/0
3	EDO	A	406	-	-	0/1/1/1	0/0/0/0
3	EDO	A	407	-	-	0/1/1/1	0/0/0/0
3	EDO	A	408	-	-	0/1/1/1	0/0/0/0
3	EDO	A	409	-	-	0/1/1/1	0/0/0/0
3	EDO	A	410	-	-	0/1/1/1	0/0/0/0
3	EDO	A	411	-	-	0/1/1/1	0/0/0/0
3	EDO	A	412	-	-	0/1/1/1	0/0/0/0
4	8GQ	A	413	-	-	0/19/42/42	0/2/6/6
2	SO4	B	401	-	-	0/0/0/0	0/0/0/0
2	SO4	B	402	-	-	0/0/0/0	0/0/0/0
3	EDO	B	403	-	-	0/1/1/1	0/0/0/0
3	EDO	B	404	-	-	0/1/1/1	0/0/0/0
3	EDO	B	405	-	-	0/1/1/1	0/0/0/0
3	EDO	B	406	-	-	0/1/1/1	0/0/0/0
3	EDO	B	407	-	-	0/1/1/1	0/0/0/0
3	EDO	B	408	-	-	0/1/1/1	0/0/0/0
3	EDO	B	409	-	-	0/1/1/1	0/0/0/0
3	EDO	B	410	-	-	0/1/1/1	0/0/0/0
3	EDO	B	411	-	-	0/1/1/1	0/0/0/0
4	8GQ	B	412	-	-	0/19/42/42	0/2/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	412	8GQ	C17-N3	2.37	1.35	1.32
4	A	413	8GQ	C17-N3	2.74	1.36	1.32

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	413	8GQ	N6-C19-N2	6.28	119.33	113.84
4	B	412	8GQ	N6-C19-N2	6.74	119.73	113.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	409	EDO	2	0
3	A	411	EDO	1	0
3	A	412	EDO	1	0
3	B	405	EDO	2	0
3	B	407	EDO	2	0
3	B	408	EDO	1	0
3	B	409	EDO	3	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	331/342 (96%)	0.02	10 (3%) 51 54	33, 51, 91, 109	0
1	B	331/342 (96%)	0.14	10 (3%) 51 54	34, 54, 94, 110	0
All	All	662/684 (96%)	0.08	20 (3%) 51 54	33, 52, 92, 110	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	50	TYR	4.4
1	B	2	SER	3.9
1	B	3	GLY	3.5
1	B	332	ALA	3.4
1	A	125	TYR	3.2
1	B	34	GLY	2.8
1	A	2	SER	2.8
1	B	267	PRO	2.6
1	A	33	TRP	2.6
1	A	329	LYS	2.6
1	A	332	ALA	2.5
1	A	126	GLN	2.4
1	A	270	ASN	2.4
1	B	49	LYS	2.4
1	A	121	PHE	2.2
1	B	329	LYS	2.2
1	A	331	GLN	2.1
1	A	325	TYR	2.1
1	B	125	TYR	2.0
1	B	271	ASP	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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	EDO	A	409	4/4	0.84	0.51	16.51	55,56,58,59	0
2	SO4	A	404	5/5	0.84	0.41	13.67	133,134,134,135	0
3	EDO	B	407	4/4	0.85	0.40	12.80	49,56,59,61	0
3	EDO	A	410	4/4	0.94	0.35	9.54	48,50,51,52	0
3	EDO	B	404	4/4	0.85	0.34	7.88	76,77,78,80	0
3	EDO	B	409	4/4	0.97	0.28	4.82	44,46,49,49	0
3	EDO	A	406	4/4	0.92	0.20	4.20	67,68,68,69	0
2	SO4	B	401	5/5	0.95	0.24	3.68	75,77,79,79	0
2	SO4	A	401	5/5	0.95	0.24	2.73	78,79,80,80	0
3	EDO	B	408	4/4	0.90	0.23	1.73	56,59,59,64	0
3	EDO	B	411	4/4	0.78	0.29	1.70	78,78,79,79	0
3	EDO	A	407	4/4	0.93	0.21	1.55	56,58,63,69	0
3	EDO	A	408	4/4	0.90	0.18	1.03	65,65,66,67	0
3	EDO	B	403	4/4	0.91	0.18	0.26	49,52,56,59	0
4	8GQ	B	412	36/36	0.96	0.16	-0.15	40,53,79,84	0
4	8GQ	A	413	36/36	0.94	0.15	-0.16	37,55,79,82	0
3	EDO	B	405	4/4	0.89	0.15	-0.16	75,75,76,76	0
2	SO4	B	402	5/5	0.91	0.30	-	137,137,138,138	0
3	EDO	A	412	4/4	0.83	0.18	-	65,67,68,69	0
3	EDO	B	410	4/4	0.88	0.27	-	86,88,89,89	0
3	EDO	A	411	4/4	0.80	0.42	-	64,66,68,68	0
2	SO4	A	405	5/5	0.89	0.21	-	126,126,127,128	0
2	SO4	A	403	5/5	0.89	0.23	-	122,122,122,123	0
2	SO4	A	402	5/5	0.92	0.18	-	103,103,104,105	0
3	EDO	B	406	4/4	0.85	0.30	-	75,77,77,78	0

## 6.5 Other polymers

There are no such residues in this entry.