



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 02:01 pm BST

PDB ID : 6RGY  
Title : Revisiting pH-gated conformational switch. Complex HK853-RR468 pH 7.5  
Authors : Mideros-Mora, C.; Casino, P.; Marina, A.  
Deposited on : 2019-04-18  
Resolution : 2.20 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
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) : 2.11

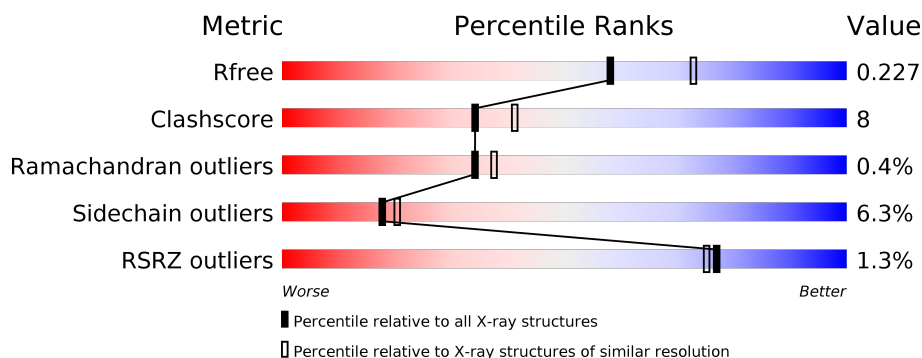
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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	258	<div> <div>3%</div> <div> <div></div> <div>79%</div> <div>10%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	258	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>12%</div> <div>•</div> <div>9%</div> </div> </div>
2	C	122	<div> <div></div> <div> <div>84%</div> <div>11%</div> <div>••</div> </div> </div>
2	D	122	<div> <div></div> <div> <div>86%</div> <div>11%</div> <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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SO4	C	204	-	-	X	-
4	SO4	D	203	-	-	X	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5990 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.

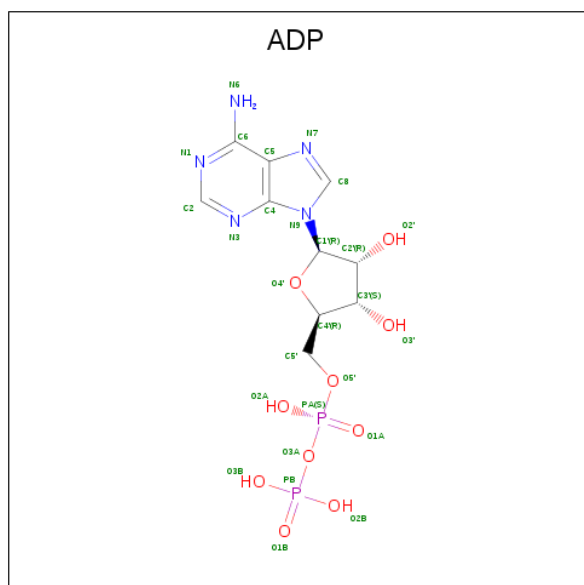
- Molecule 1 is a protein called Osmosensitive K<sup>+</sup> channel histidine kinase KdpD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	236	Total	C	N	O	S	0	1	0
			1822	1167	309	343	3			
1	B	236	Total	C	N	O	S	0	2	0
			1844	1178	311	352	3			

- Molecule 2 is a protein called Response regulator.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
2	C	120	Total	Be	C	F	N	O	S	0	0	0
			940	1	605	3	153	174	4			
2	D	121	Total	Be	C	F	N	O	S	0	0	0
			948	1	609	3	151	180	4			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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



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

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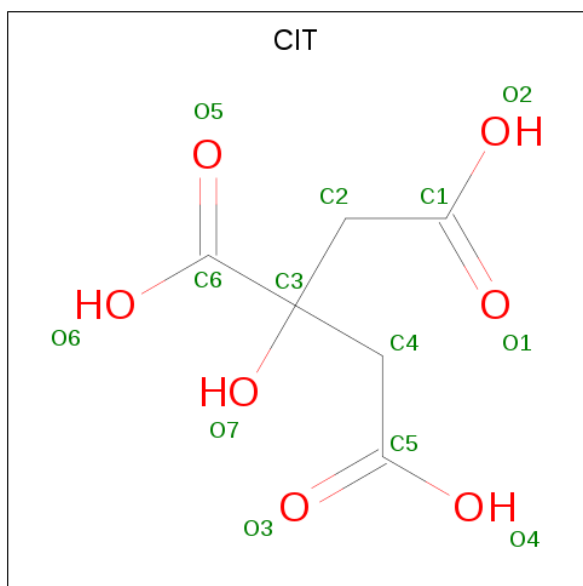
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		

- Molecule 6 is CITRIC ACID (three-letter code: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			13	6	7		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	93	Total	O	0	0
			93	93		

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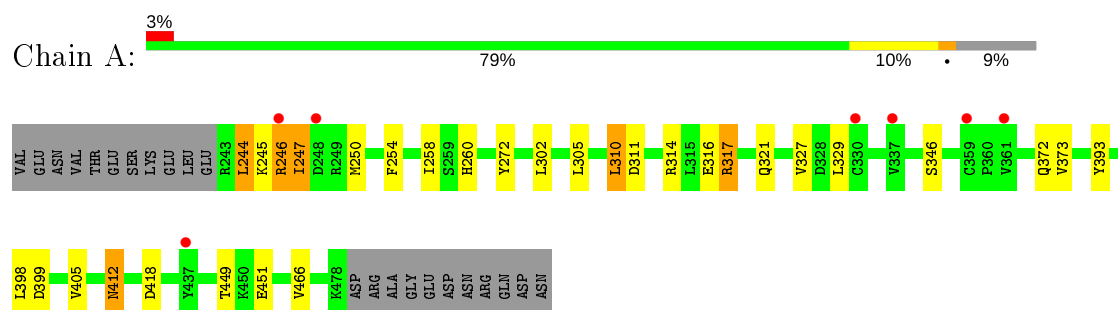
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	86	Total 86	O 86	0	0
7	C	57	Total 57	O 57	0	0
7	D	66	Total 66	O 66	0	0

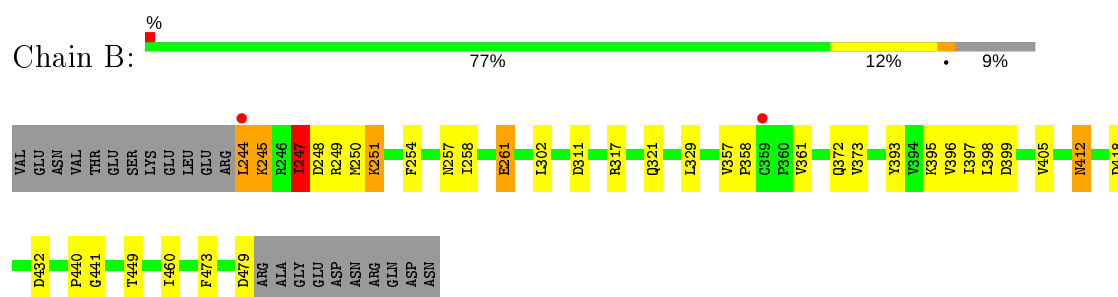
### 3 Residue-property plots [i](#)

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.

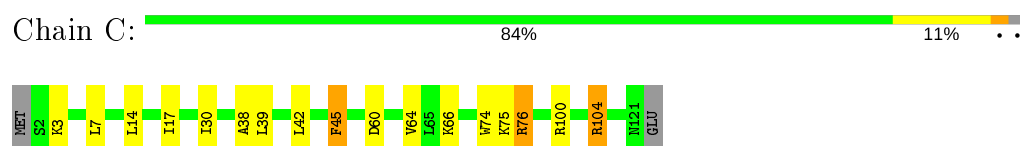
- Molecule 1: Osmosensitive K<sup>+</sup> channel histidine kinase KdpD



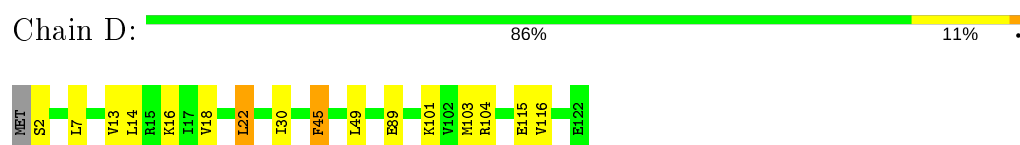
- Molecule 1: Osmosensitive K<sup>+</sup> channel histidine kinase KdpD



- Molecule 2: Response regulator



- Molecule 2: Response regulator





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.47Å 92.71Å 174.52Å 90.00° 93.39° 90.00°	Depositor
Resolution (Å)	87.11 – 2.20 87.11 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (87.11-2.20) 99.7 (87.11-2.20)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.26 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.186 , 0.227 0.195 , 0.227	Depositor DCC
$R_{free}$ test set	2793 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.4	Xtriage
Anisotropy	0.451	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 46.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5990	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.97% of the height of the origin peak. No significant pseudotranslation is detected.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CIT, SO4, ADP, BFD

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	0.96	0/1857	0.89	0/2526
1	B	0.94	0/1881	0.92	0/2555
2	C	0.97	0/940	0.93	0/1264
2	D	0.98	0/948	0.93	0/1274
All	All	0.96	0/5626	0.91	0/7619

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	1822	0	1790	39	0
1	B	1844	0	1828	28	0
2	C	940	0	975	17	0
2	D	948	0	974	12	0
3	A	27	0	12	0	0
3	B	27	0	12	0	0
4	A	15	0	0	1	0
4	B	15	0	0	0	0
4	C	15	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	20	0	0	3	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	D	13	0	5	0	0
7	A	93	0	0	1	0
7	B	86	0	0	1	0
7	C	57	0	0	3	0
7	D	66	0	0	1	0
All	All	5990	0	5596	95	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 8.

All (95) 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)
2:C:76:ARG:HG2	2:C:76:ARG:HH11	1.25	0.97
1:A:247:ILE:HG23	1:A:250:MET:H	1.27	0.96
1:A:310:LEU:HD13	1:A:314:ARG:NH2	1.82	0.94
1:A:246:ARG:NH2	1:A:246:ARG:HB2	1.81	0.94
1:A:246:ARG:CZ	1:A:246:ARG:HB2	2.00	0.90
2:C:74:TRP:O	2:C:76:ARG:N	2.10	0.83
1:A:247:ILE:HG23	1:A:250:MET:N	1.95	0.82
2:C:76:ARG:HG2	2:C:76:ARG:NH1	1.94	0.81
1:A:254:PHE:CZ	1:A:258:ILE:HD11	2.19	0.76
1:A:246:ARG:HG3	1:A:247:ILE:H	1.52	0.74
1:B:248:ASP:OD1	1:B:251:LYS:NZ	2.21	0.71
1:A:310:LEU:HD13	1:A:314:ARG:HH22	1.53	0.71
2:D:104:ARG:CZ	4:D:203:SO4:O2	2.39	0.70
1:A:247:ILE:HG22	1:A:250:MET:CG	2.20	0.70
1:B:261[A]:GLU:HG2	1:B:440:PRO:HB2	1.73	0.70
1:B:329:LEU:CD2	1:B:405:VAL:HG11	2.22	0.70
1:B:261[A]:GLU:CG	1:B:440:PRO:HB2	2.22	0.69
1:A:247:ILE:CG2	1:A:250:MET:HG3	2.23	0.68
1:B:247:ILE:CG2	1:B:250:MET:H	2.08	0.67
1:A:246:ARG:HG3	1:A:247:ILE:N	2.09	0.67
1:B:244:LEU:O	1:B:245:LYS:HB2	1.94	0.67
1:A:310:LEU:HD13	1:A:314:ARG:CZ	2.25	0.66
1:B:247:ILE:HG23	1:B:250:MET:H	1.62	0.65
1:B:247:ILE:HG23	1:B:249:ARG:N	2.12	0.65
1:B:254:PHE:CZ	1:B:258:ILE:HD11	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:373:VAL:HG13	1:B:449:THR:HG23	1.79	0.64
1:A:412:ASN:H	1:A:412:ASN:HD22	1.47	0.62
2:C:76:ARG:CG	2:C:76:ARG:HH11	2.07	0.62
1:A:310:LEU:HD11	1:A:314:ARG:NH1	2.17	0.60
1:A:329:LEU:CD2	1:A:405:VAL:HG11	2.33	0.58
2:D:18:VAL:HG12	2:D:22:LEU:HD22	1.86	0.58
1:A:316:GLU:OE2	1:A:316:GLU:HA	2.03	0.58
1:A:247:ILE:HG22	1:A:250:MET:HB2	1.86	0.57
1:B:395:LYS:HE3	1:B:397:ILE:HD11	1.86	0.57
2:D:103:MET:HE1	2:D:115:GLU:HG3	1.85	0.57
1:B:412:ASN:HD22	1:B:412:ASN:H	1.55	0.55
1:A:247:ILE:HG22	1:A:250:MET:CB	2.36	0.55
1:A:393:TYR:H	1:A:412:ASN:HD21	1.54	0.54
1:A:311:ASP:OD2	1:A:372:GLN:NE2	2.40	0.54
1:A:244:LEU:HD12	1:A:244:LEU:N	2.22	0.54
1:A:317:ARG:HD3	7:A:645:HOH:O	2.06	0.54
2:D:13:VAL:HG23	4:D:204:SO4:O3	2.08	0.53
1:B:361:VAL:HG11	1:B:398:LEU:HD21	1.91	0.53
1:A:310:LEU:HD11	1:A:314:ARG:HH12	1.74	0.53
1:B:247:ILE:HG23	1:B:249:ARG:H	1.72	0.53
1:A:329:LEU:HD23	1:A:405:VAL:HG11	1.91	0.53
1:A:247:ILE:HG22	1:A:250:MET:HG3	1.85	0.53
1:A:246:ARG:CG	1:A:247:ILE:N	2.71	0.52
1:A:310:LEU:CD1	1:A:314:ARG:NH1	2.73	0.52
1:A:244:LEU:N	1:A:244:LEU:CD1	2.73	0.52
2:C:38:ALA:O	2:C:42:LEU:HD22	2.10	0.52
2:C:74:TRP:C	2:C:76:ARG:H	2.13	0.52
1:B:247:ILE:HG22	1:B:250:MET:HB2	1.91	0.51
2:C:30:ILE:N	2:C:30:ILE:HD12	2.26	0.51
1:B:393:TYR:H	1:B:412:ASN:HD21	1.59	0.51
1:A:398:LEU:HD23	1:A:399:ASP:N	2.26	0.50
2:C:76:ARG:CD	7:C:331:HOH:O	2.60	0.50
2:C:30:ILE:HD13	2:C:45:PHE:CE2	2.47	0.50
1:B:247:ILE:HG22	1:B:250:MET:CB	2.43	0.49
1:A:247:ILE:CG2	1:A:250:MET:CG	2.85	0.49
1:B:398:LEU:HD23	1:B:399:ASP:N	2.27	0.49
1:B:329:LEU:HD22	1:B:405:VAL:HG11	1.94	0.48
1:B:244:LEU:HD13	1:B:244:LEU:HA	1.77	0.47
1:B:311:ASP:OD2	1:B:372:GLN:NE2	2.48	0.47
1:B:257:ASN:HB3	1:B:441:GLY:O	2.14	0.47
2:C:104:ARG:HG3	4:C:204:SO4:O2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:LEU:CD1	1:A:314:ARG:CZ	2.93	0.46
2:C:104:ARG:HD3	7:C:345:HOH:O	2.16	0.46
1:B:247:ILE:CG2	1:B:250:MET:N	2.78	0.45
2:D:104:ARG:NH2	4:D:203:SO4:O2	2.50	0.45
2:D:16:LYS:NZ	7:D:304:HOH:O	2.50	0.45
2:C:14:LEU:HD13	2:C:14:LEU:C	2.38	0.44
1:A:373:VAL:HG13	1:A:449:THR:HG23	1.99	0.44
1:A:260:HIS:NE2	4:A:502:SO4:O2	2.50	0.44
2:D:103:MET:CE	2:D:115:GLU:HG3	2.46	0.44
1:B:357:VAL:HG22	1:B:358:PRO:HD2	1.98	0.44
1:B:460:ILE:HA	1:B:473:PHE:O	2.18	0.43
2:C:39:LEU:HA	2:C:42:LEU:HD23	2.00	0.43
1:A:451:GLU:HA	1:A:451:GLU:OE1	2.18	0.43
2:C:76:ARG:HD3	7:C:331:HOH:O	2.19	0.43
1:B:317:ARG:NH2	7:B:605:HOH:O	2.51	0.43
2:C:60:ASP:O	2:C:64:VAL:HG23	2.18	0.43
1:B:247:ILE:HG22	1:B:250:MET:H	1.83	0.43
2:C:104:ARG:NH2	4:C:204:SO4:O1	2.52	0.43
1:A:272:TYR:CE1	2:C:17:ILE:HB	2.54	0.42
2:D:103:MET:HE1	2:D:115:GLU:CG	2.50	0.42
2:D:49:LEU:CD2	2:D:116:VAL:HG13	2.50	0.42
2:D:30:ILE:HD13	2:D:45:PHE:CE2	2.54	0.42
1:A:247:ILE:CG2	1:A:250:MET:HB2	2.50	0.42
1:A:247:ILE:CG2	1:A:250:MET:CB	2.97	0.41
2:D:30:ILE:HD12	2:D:30:ILE:N	2.36	0.41
2:D:14:LEU:HD13	2:D:14:LEU:C	2.41	0.41
1:A:310:LEU:HA	1:A:310:LEU:HD23	1.94	0.40
1:A:412:ASN:N	1:A:412:ASN:HD22	2.11	0.40
1:B:247:ILE:HG22	1:B:250:MET:CG	2.51	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	235/258 (91%)	229 (97%)	6 (3%)	0	100	100
1	B	236/258 (92%)	227 (96%)	7 (3%)	2 (1%)	19	19
2	C	117/122 (96%)	112 (96%)	4 (3%)	1 (1%)	17	16
2	D	118/122 (97%)	114 (97%)	4 (3%)	0	100	100
All	All	706/760 (93%)	682 (97%)	21 (3%)	3 (0%)	34	37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	75	LYS
1	B	245	LYS
1	B	247	ILE

### 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	194/232 (84%)	180 (93%)	14 (7%)	14	15
1	B	201/232 (87%)	189 (94%)	12 (6%)	19	22
2	C	103/109 (94%)	96 (93%)	7 (7%)	16	17
2	D	104/109 (95%)	98 (94%)	6 (6%)	20	23
All	All	602/682 (88%)	563 (94%)	39 (6%)	18	19

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	244	LEU
1	A	245	LYS
1	A	246	ARG
1	A	247	ILE
1	A	302	LEU
1	A	305	LEU
1	A	310	LEU
1	A	317	ARG

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Mol	Chain	Res	Type
1	A	321	GLN
1	A	327	VAL
1	A	346	SER
1	A	412	ASN
1	A	418	ASP
1	A	466	VAL
1	B	244	LEU
1	B	247	ILE
1	B	251	LYS
1	B	261[A]	GLU
1	B	261[B]	GLU
1	B	302	LEU
1	B	321	GLN
1	B	396	VAL
1	B	412	ASN
1	B	418	ASP
1	B	432	ASP
1	B	479	ASP
2	C	3	LYS
2	C	7	LEU
2	C	45	PHE
2	C	66	LYS
2	C	76	ARG
2	C	100	ARG
2	C	104	ARG
2	D	2	SER
2	D	7	LEU
2	D	22	LEU
2	D	45	PHE
2	D	89	GLU
2	D	101	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	380	ASN
1	A	412	ASN
1	B	380	ASN
1	B	412	ASN
2	C	111	GLN
2	D	111	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	BFD	D	53	2,5	8,11,12	4.32	3 (37%)	3,15,17	2.02	1 (33%)
2	BFD	C	53	2,5	8,11,12	4.63	3 (37%)	3,15,17	2.23	1 (33%)

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	BFD	D	53	2,5	-	2/5/11/13	-
2	BFD	C	53	2,5	-	2/5/11/13	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	53	BFD	F3-BE	7.86	1.73	1.54
2	D	53	BFD	F3-BE	7.47	1.72	1.54
2	C	53	BFD	F2-BE	7.27	1.71	1.54
2	C	53	BFD	F1-BE	7.27	1.71	1.54
2	D	53	BFD	F2-BE	6.92	1.71	1.54
2	D	53	BFD	F1-BE	6.40	1.69	1.54

All (2) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	53	BFD	OD2-CG-CB	-3.80	116.33	124.73
2	D	53	BFD	OD2-CG-CB	-3.32	117.39	124.73

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	53	BFD	CA-CB-CG-OD2
2	C	53	BFD	CA-CB-CG-OD2
2	C	53	BFD	CA-CB-CG-OD1
2	D	53	BFD	CA-CB-CG-OD1

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 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
4	SO4	B	502	-	4,4,4	0.31	0	6,6,6	0.59	0
6	CIT	D	206	-	3,12,12	0.21	0	3,17,17	1.77	1 (33%)
4	SO4	C	202	-	4,4,4	0.45	0	6,6,6	0.39	0
3	ADP	A	501	-	24,29,29	1.38	4 (16%)	29,45,45	1.79	10 (34%)
4	SO4	D	204	-	4,4,4	0.49	0	6,6,6	0.69	0
4	SO4	A	503	-	4,4,4	0.38	0	6,6,6	0.69	0
4	SO4	D	203	-	4,4,4	0.34	0	6,6,6	0.46	0
4	SO4	C	203	-	4,4,4	0.42	0	6,6,6	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	ADP	B	501	-	24,29,29	1.69	5 (20%)	29,45,45	1.94	9 (31%)
4	SO4	C	204	-	4,4,4	0.32	0	6,6,6	0.74	0
4	SO4	A	502	-	4,4,4	0.50	0	6,6,6	0.24	0
4	SO4	B	504	-	4,4,4	0.43	0	6,6,6	0.34	0
4	SO4	B	503	-	4,4,4	0.49	0	6,6,6	0.13	0
4	SO4	D	205	-	4,4,4	0.56	0	6,6,6	0.38	0
4	SO4	D	202	-	4,4,4	0.45	0	6,6,6	0.38	0
4	SO4	A	504	-	4,4,4	0.45	0	6,6,6	0.34	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
6	CIT	D	206	-	-	4/6/16/16	-
3	ADP	B	501	-	-	3/12/32/32	0/3/3/3
3	ADP	A	501	-	-	2/12/32/32	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	ADP	C2'-C1'	-5.75	1.45	1.53
3	A	501	ADP	C2'-C1'	-5.07	1.46	1.53
3	B	501	ADP	O4'-C1'	-2.62	1.37	1.41
3	A	501	ADP	C2-N1	2.27	1.38	1.33
3	A	501	ADP	C5-N7	-2.18	1.31	1.39
3	B	501	ADP	C5-N7	-2.16	1.31	1.39
3	B	501	ADP	C5-C4	2.14	1.46	1.40
3	A	501	ADP	C5-C4	2.06	1.46	1.40
3	B	501	ADP	PB-O1B	-2.06	1.43	1.50

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	ADP	C1'-N9-C4	-4.81	118.19	126.64
3	A	501	ADP	O3A-PB-O1B	-3.66	90.91	111.19
3	A	501	ADP	C1'-N9-C4	-3.64	120.25	126.64
3	A	501	ADP	N6-C6-N1	3.52	125.88	118.57
3	B	501	ADP	O2B-PB-O1B	3.38	123.93	110.68
3	B	501	ADP	N3-C2-N1	-3.32	123.49	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	ADP	O3B-PB-O1B	2.91	122.06	110.68
3	B	501	ADP	C3'-C2'-C1'	2.90	105.35	100.98
3	B	501	ADP	O2A-PA-O1A	2.78	126.00	112.24
3	B	501	ADP	O3A-PB-O1B	-2.76	95.90	111.19
3	A	501	ADP	C2-N1-C6	2.66	123.30	118.75
3	A	501	ADP	O2A-PA-O1A	2.65	125.33	112.24
3	B	501	ADP	C2-N1-C6	2.63	123.25	118.75
3	A	501	ADP	O4'-C1'-C2'	2.57	110.69	106.93
3	A	501	ADP	O3B-PB-O2B	2.37	116.70	107.64
3	B	501	ADP	N6-C6-N1	2.33	123.41	118.57
3	A	501	ADP	N3-C2-N1	-2.20	125.24	128.68
3	A	501	ADP	C5-C6-N1	-2.18	115.42	120.35
3	B	501	ADP	O3B-PB-O2B	2.16	115.89	107.64
6	D	206	CIT	C4-C3-C2	2.10	114.94	109.33

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	206	CIT	O7-C3-C4-C5
6	D	206	CIT	C6-C3-C4-C5
3	B	501	ADP	PA-O3A-PB-O2B
3	A	501	ADP	PA-O3A-PB-O3B
6	D	206	CIT	C2-C3-C4-C5
3	B	501	ADP	PA-O3A-PB-O3B
6	D	206	CIT	C1-C2-C3-C6
3	A	501	ADP	PA-O3A-PB-O2B
3	B	501	ADP	PA-O3A-PB-O1B

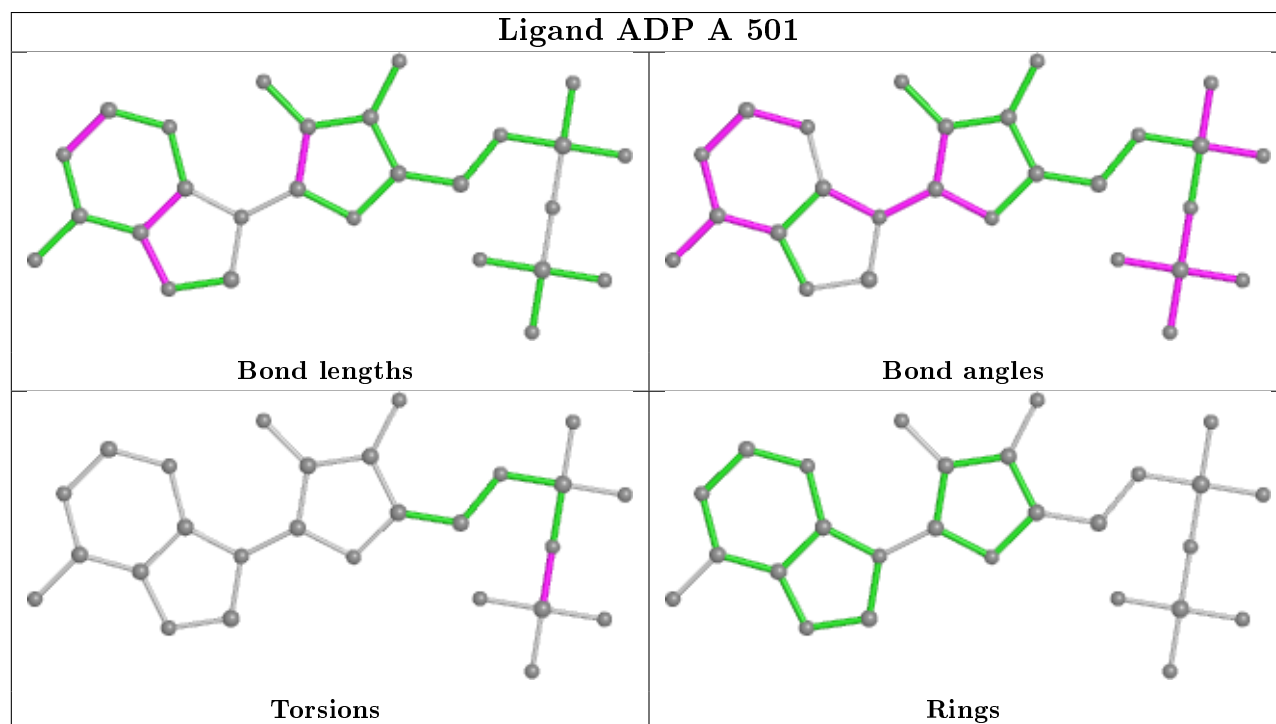
There are no ring outliers.

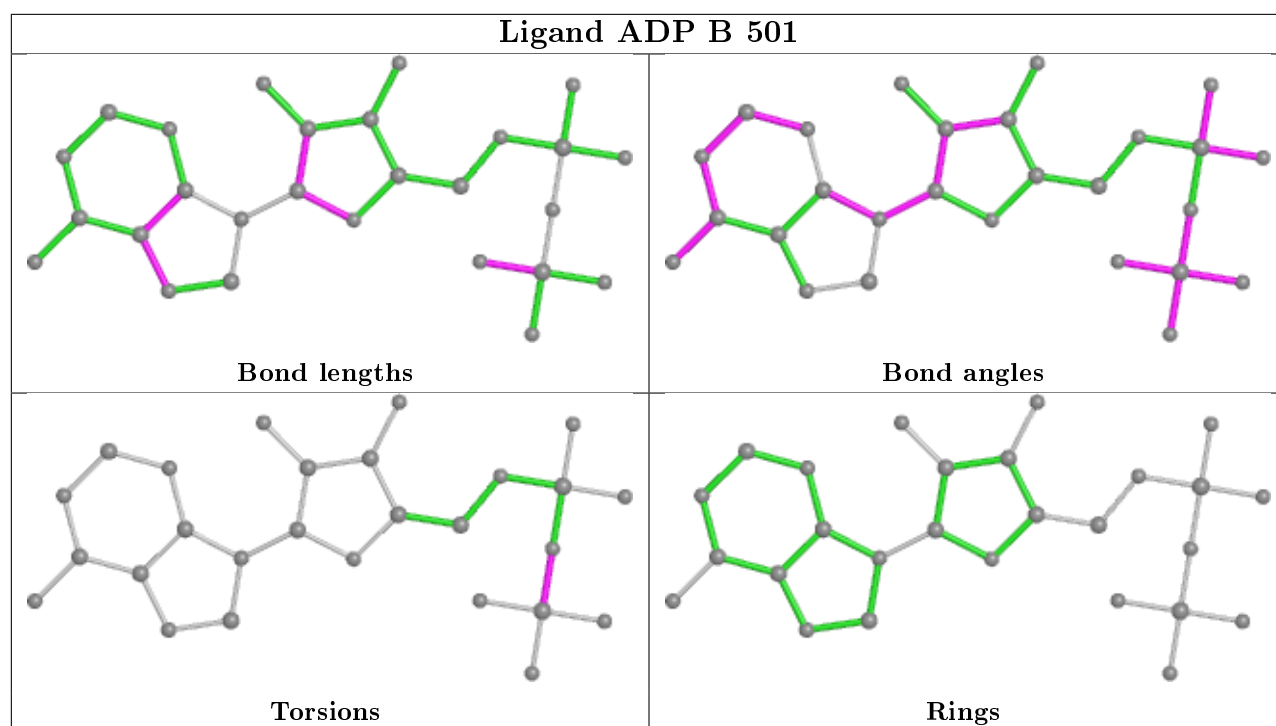
4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	204	SO4	1	0
4	D	203	SO4	2	0
4	C	204	SO4	2	0
4	A	502	SO4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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	236/258 (91%)	0.16	7 (2%) 50 48	28, 57, 99, 130	5 (2%)
1	B	236/258 (91%)	0.13	2 (0%) 86 85	29, 56, 95, 120	7 (2%)
2	C	119/122 (97%)	-0.04	0 100 100	32, 52, 91, 104	0
2	D	120/122 (98%)	0.02	0 100 100	35, 53, 96, 110	0
All	All	711/760 (93%)	0.09	9 (1%) 77 75	28, 55, 97, 130	12 (1%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	359	CYS	3.6
1	B	244	LEU	3.4
1	A	337	VAL	3.3
1	A	330	CYS	2.9
1	A	361	VAL	2.4
1	A	246	ARG	2.2
1	A	248	ASP	2.1
1	B	359	CYS	2.1
1	A	437	TYR	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains

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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	BFD	D	53	12/13	0.95	0.17	35,39,41,46	0
2	BFD	C	53	12/13	0.95	0.15	33,39,43,46	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

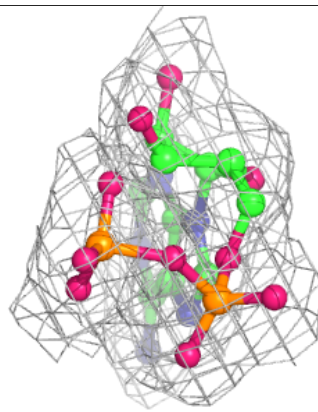
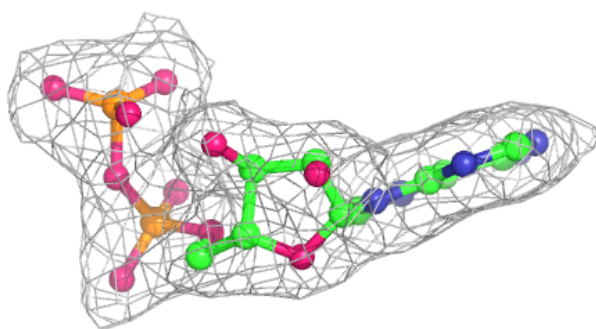
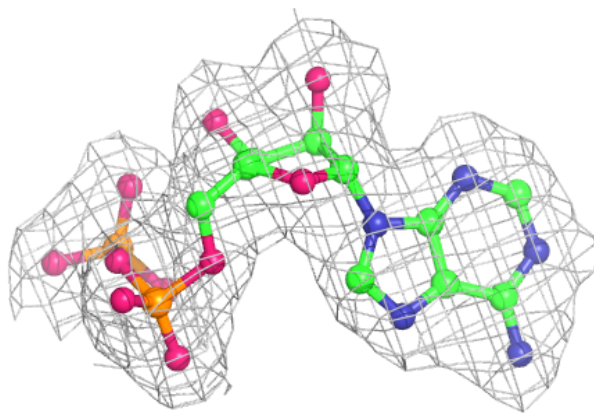
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	CIT	D	206	13/13	0.89	0.16	83,100,108,108	0
4	SO4	C	203	5/5	0.89	0.15	103,109,110,122	0
4	SO4	D	205	5/5	0.91	0.25	81,83,96,100	0
4	SO4	B	504	5/5	0.92	0.18	82,93,98,99	0
4	SO4	D	202	5/5	0.94	0.19	80,91,97,102	0
4	SO4	A	502	5/5	0.94	0.12	85,100,101,105	0
4	SO4	A	503	5/5	0.94	0.14	73,75,84,88	0
4	SO4	D	203	5/5	0.94	0.12	61,74,76,81	0
4	SO4	A	504	5/5	0.95	0.21	77,83,95,100	0
4	SO4	B	502	5/5	0.96	0.12	75,76,82,84	0
4	SO4	B	503	5/5	0.96	0.12	78,80,92,94	0
4	SO4	C	204	5/5	0.97	0.16	73,74,78,79	0
4	SO4	D	204	5/5	0.98	0.13	67,69,75,81	0
5	MG	C	201	1/1	0.98	0.08	42,42,42,42	0
4	SO4	C	202	5/5	0.98	0.16	66,67,72,74	0
3	ADP	A	501	27/27	0.98	0.12	35,39,45,45	0
3	ADP	B	501	27/27	0.98	0.13	35,39,45,46	0
5	MG	D	201	1/1	0.99	0.09	41,41,41,41	0

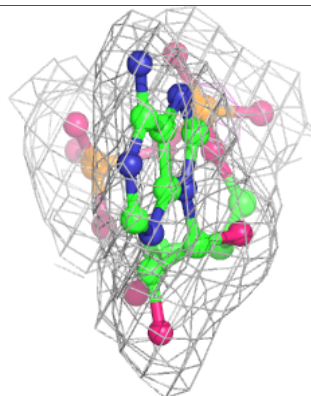
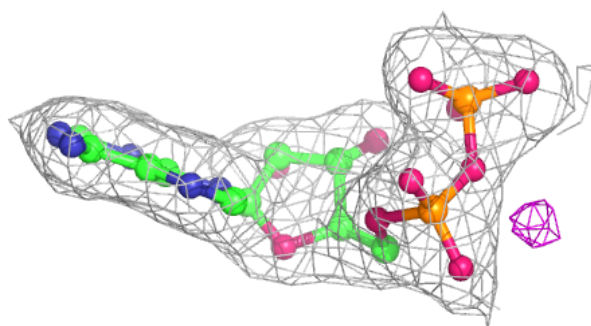
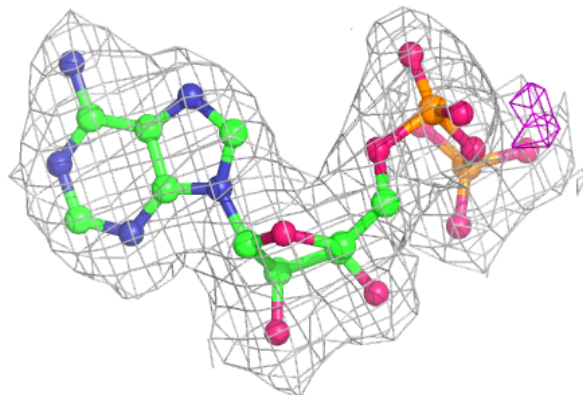
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around ADP A 501:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around ADP B 501:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.