Full wwPDB X-ray Structure Validation Report ⓘ

Feb 12, 2024 – 12:37 AM EST

PDB ID	:	3D36
Title	:	How to Switch Off a Histidine Kinase: Crystal Structure of Geobacillus stearothermophilus KinB with the Inhibitor Sda
Authors	:	Bick, M.J.; Lamour, V.; Rajashankar, K.R.; Gordiyenko, Y.; Robinson, C.V.; Darst, S.A.
Deposited on	:	2008-05-09
Resolution	:	2.03 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:

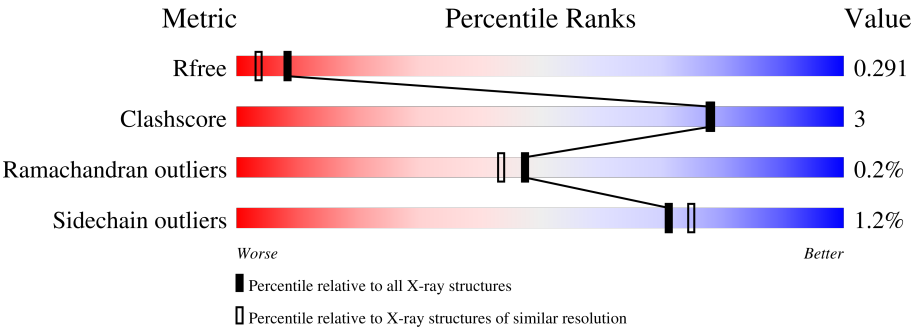
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	244	84% 5% 11%
1	B	244	82% 8% 9%
2	C	46	76% 15% 9%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4224 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 Sporulation kinase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1687	1068	296	313	10			
1	B	221	Total	C	N	O	S	0	0	0
			1720	1088	303	319	10			

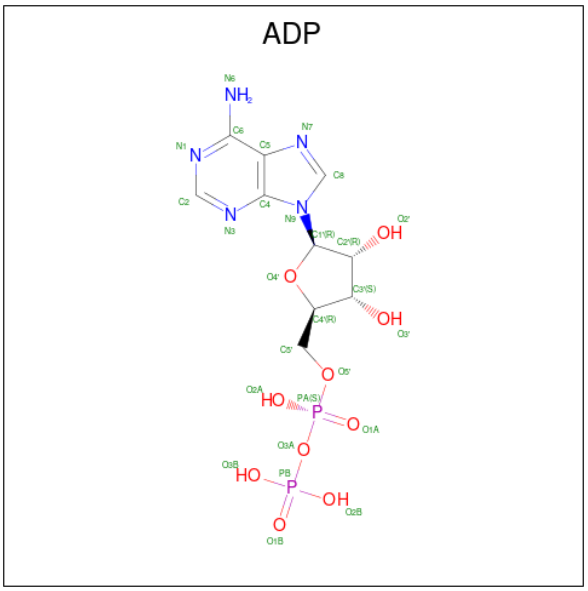
- Molecule 2 is a protein called Sporulation kinase inhibitor Sda.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	42	Total	C	N	O	S	0	0	0
			356	230	59	66	1			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

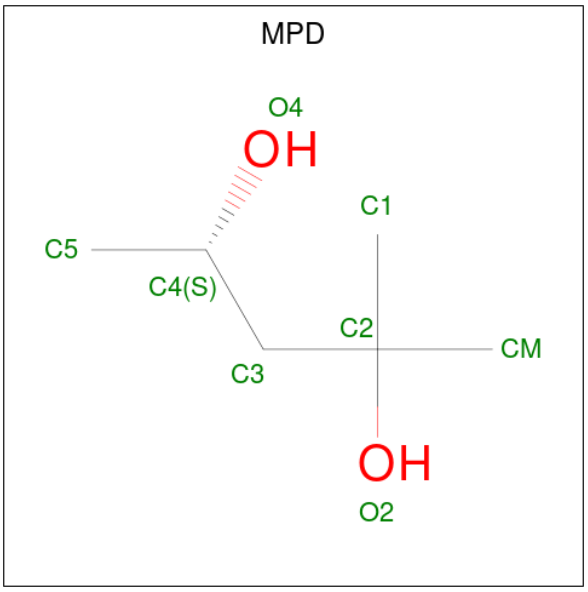
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O		0	0
			8	6	2			

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C O 8 6 2	0	0
5	B	1	Total C O 8 6 2	0	0
5	C	1	Total C O 8 6 2	0	0

- Molecule 6 is water.

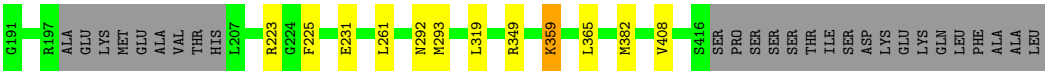
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	123	Total O 123 123	0	0
6	B	209	Total O 209 209	0	0
6	C	41	Total O 41 41	0	0

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. 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. 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.

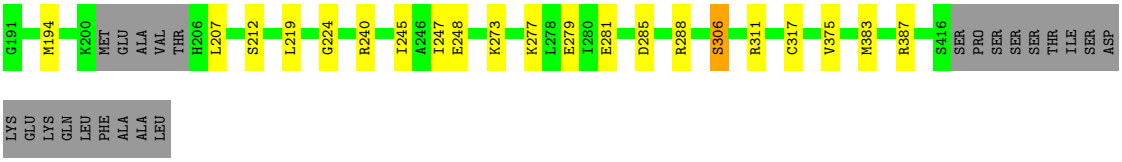
• Molecule 1: Sporulation kinase B

Chain A:



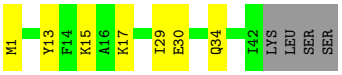
• Molecule 1: Sporulation kinase B

Chain B:



• Molecule 2: Sporulation kinase inhibitor Sda

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	66.11Å 66.11Å 315.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.41 – 2.03 42.41 – 2.03	Depositor EDS
% Data completeness (in resolution range)	98.9 (42.41-2.03) 98.9 (42.41-2.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.21 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.200 , 0.215 0.282 , 0.291	Depositor DCC
R_{free} test set	2649 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	33.7	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 43.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	4224	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ADP, MG, MPD

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	0.41	1/1710 (0.1%)	0.50	0/2310
1	B	0.42	1/1744 (0.1%)	0.53	0/2355
2	C	0.41	0/361	0.51	0/481
All	All	0.41	2/3815 (0.1%)	0.51	0/5146

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	359	LYS	CE-NZ	8.69	1.70	1.49
1	B	317	CYS	CB-SG	-5.35	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

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	1687	0	1754	10	0
1	B	1720	0	1785	11	0
2	C	356	0	374	5	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	27	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	27	0	12	0	0
5	B	24	0	42	2	0
5	C	8	0	14	0	0
6	A	123	0	0	1	0
6	B	209	0	0	3	0
6	C	41	0	0	0	0
All	All	4224	0	3993	23	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 (23) 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:359:LYS:CE	1:A:359:LYS:NZ	1.70	1.49
5:B:702:MPD:H51	5:B:703:MPD:H51	1.70	0.73
1:A:231:GLU:HG2	2:C:15:LYS:HB3	1.82	0.61
1:A:225:PHE:HZ	2:C:1:MET:HE3	1.67	0.60
1:A:365:LEU:HD11	1:A:382:MET:HG3	1.86	0.57
1:B:245:ILE:HG23	6:B:847:HOH:O	2.07	0.55
1:A:292:ASN:O	1:A:293:MET:HB3	2.07	0.54
1:B:383:MET:O	1:B:387:ARG:HG3	2.09	0.52
1:B:224:GLY:HA3	5:B:700:MPD:H11	1.97	0.46
1:B:248:GLU:OE2	6:B:847:HOH:O	2.21	0.46
1:A:223:ARG:HG3	1:B:247:ILE:HD12	1.97	0.46
1:B:273:LYS:HG2	1:B:306:SER:OG	2.16	0.45
1:A:292:ASN:O	1:A:293:MET:CB	2.65	0.45
1:A:261:LEU:O	1:B:212:SER:HB3	2.17	0.44
2:C:30:GLU:O	2:C:34:GLN:HG3	2.17	0.44
2:C:13:TYR:HB2	2:C:29:ILE:HG21	2.00	0.43
1:A:349:ARG:HA	1:A:408:VAL:O	2.18	0.43
1:B:285:ASP:OD1	1:B:288:ARG:NH1	2.52	0.41
2:C:13:TYR:CZ	2:C:17:LYS:HD2	2.55	0.41
1:B:277:LYS:HE2	1:B:281:GLU:OE2	2.20	0.41
1:A:359:LYS:NZ	6:A:616:HOH:O	2.47	0.41
1:B:240:ARG:NH2	6:B:842:HOH:O	2.53	0.41
1:B:279:GLU:OE2	1:B:311:ARG:NH1	2.54	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	213/244 (87%)	209 (98%)	4 (2%)	0	100 100
1	B	217/244 (89%)	214 (99%)	2 (1%)	1 (0%)	29 22
2	C	40/46 (87%)	40 (100%)	0	0	100 100
All	All	470/534 (88%)	463 (98%)	6 (1%)	1 (0%)	47 43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	207	LEU

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	183/206 (89%)	182 (100%)	1 (0%)	88 91
1	B	186/206 (90%)	182 (98%)	4 (2%)	52 53
2	C	41/45 (91%)	41 (100%)	0	100 100
All	All	410/457 (90%)	405 (99%)	5 (1%)	71 75

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	319	LEU
1	B	194	MET

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Mol	Chain	Res	Type
1	B	219	LEU
1	B	306	SER
1	B	375	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	ADP	A	500	3	24,29,29	1.01	1 (4%)	29,45,45	1.23	2 (6%)
4	ADP	B	500	3	24,29,29	0.98	1 (4%)	29,45,45	1.26	3 (10%)
5	MPD	B	700	-	7,7,7	0.27	0	9,10,10	0.26	0
5	MPD	B	702	-	7,7,7	0.29	0	9,10,10	0.31	0
5	MPD	C	701	-	7,7,7	0.28	0	9,10,10	0.50	0
5	MPD	B	703	-	7,7,7	0.25	0	9,10,10	0.28	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
4	ADP	A	500	3	-	2/12/32/32	0/3/3/3
4	ADP	B	500	3	-	2/12/32/32	0/3/3/3
5	MPD	B	700	-	-	1/5/5/5	-
5	MPD	B	702	-	-	1/5/5/5	-
5	MPD	C	701	-	-	0/5/5/5	-
5	MPD	B	703	-	-	1/5/5/5	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	500	ADP	C5-C4	2.53	1.47	1.40
4	B	500	ADP	C5-C4	2.46	1.47	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	500	ADP	N3-C2-N1	-3.94	122.52	128.68
4	A	500	ADP	N3-C2-N1	-3.57	123.10	128.68
4	A	500	ADP	C4-C5-N7	-2.54	106.75	109.40
4	B	500	ADP	C2-N1-C6	2.22	122.56	118.75
4	B	500	ADP	C4-C5-N7	-2.09	107.22	109.40

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	500	ADP	PA-O3A-PB-O2B
4	A	500	ADP	PA-O3A-PB-O3B
4	B	500	ADP	PA-O3A-PB-O2B
4	B	500	ADP	PA-O3A-PB-O3B
5	B	700	MPD	O2-C2-C3-C4
5	B	702	MPD	O2-C2-C3-C4
5	B	703	MPD	C2-C3-C4-C5

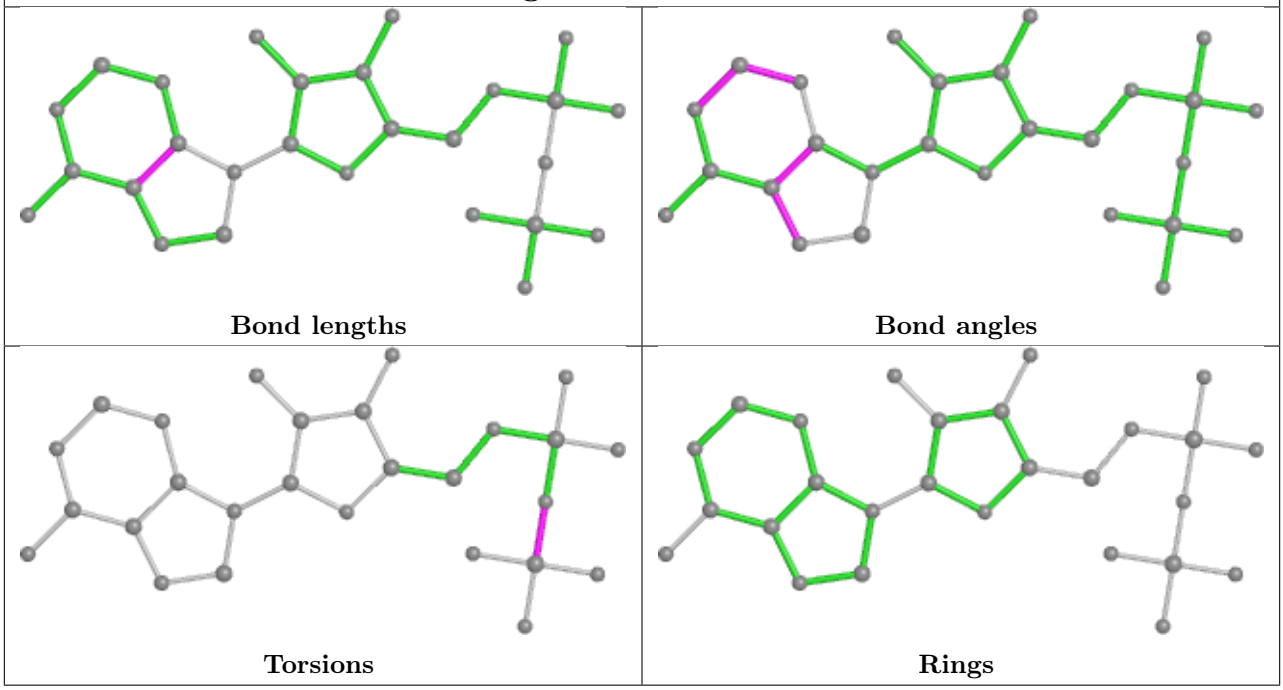
There are no ring outliers.

3 monomers are involved in 2 short contacts:

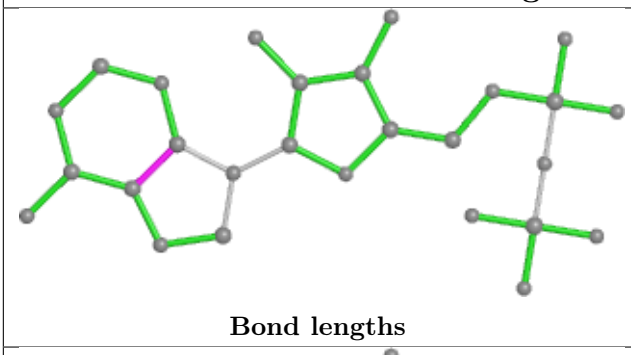
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	700	MPD	1	0
5	B	702	MPD	1	0
5	B	703	MPD	1	0

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 then 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.

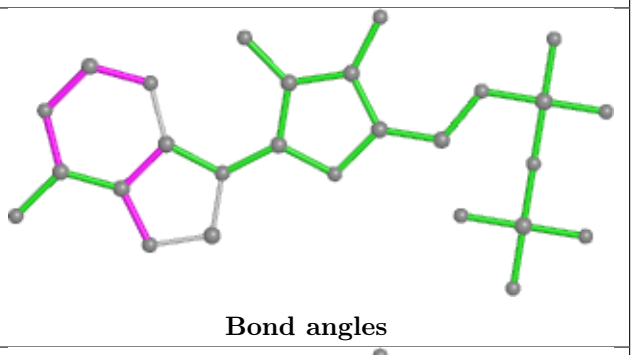
Ligand ADP A 500



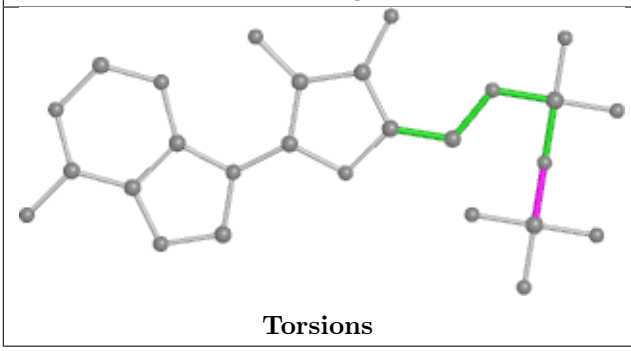
Ligand ADP B 500



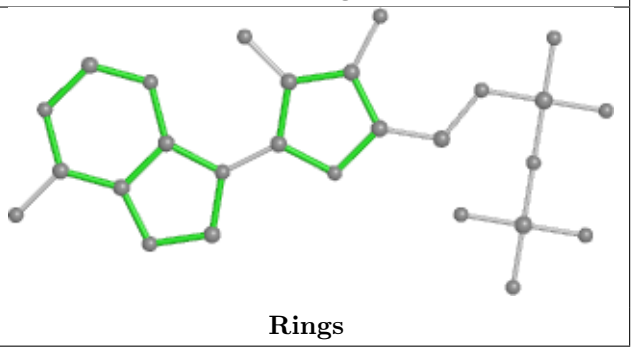
Bond lengths



Bond angles



Torsions



Rings

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

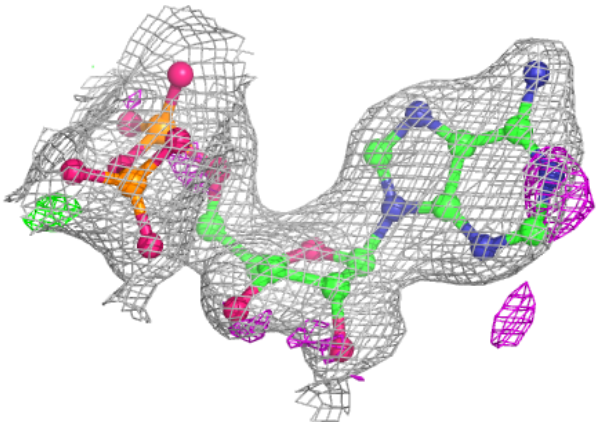
6.4 Ligands

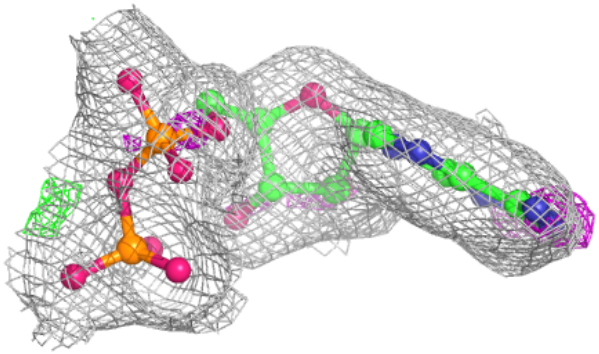
Unable to reproduce the depositors R factor - this section is therefore empty.

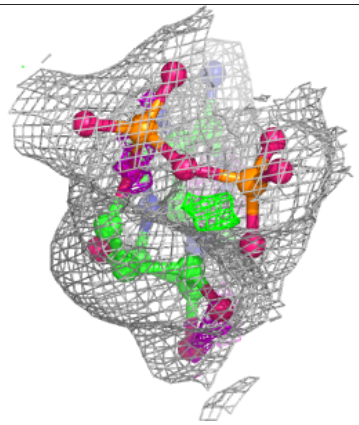
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP A 500:

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

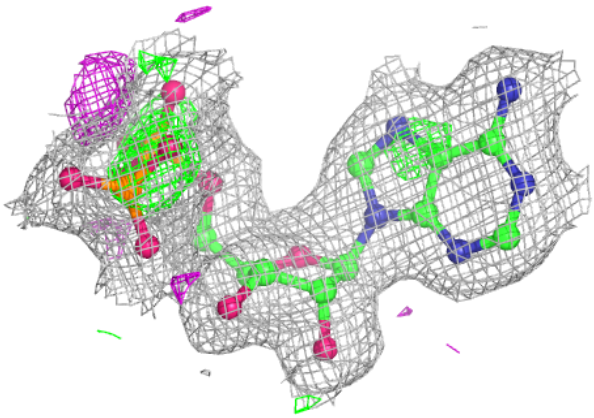


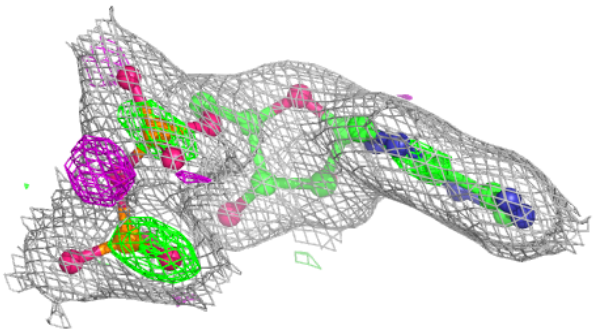


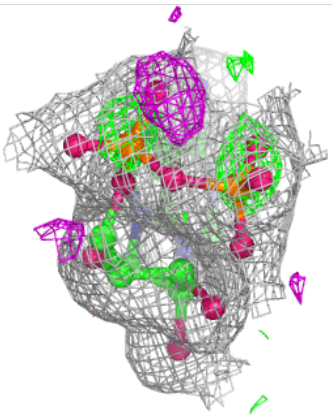


Electron density around ADP B 500:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.