Full wwPDB X-ray Structure Validation Report (i)

Mar 13, 2024 – 02:08 PM JST

PDB ID	:	4TLA
Title	:	Crystal structure of N-terminal C1 domain of KaiC
Authors	:	Abe, J.; Hiyama, T.B.; Mukaiyama, A.; Son, S.; Akiyama, S.
Deposited on	:	2014-05-29
Resolution	:	1.80 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 (i) 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 (i)) were used in the production of this report:

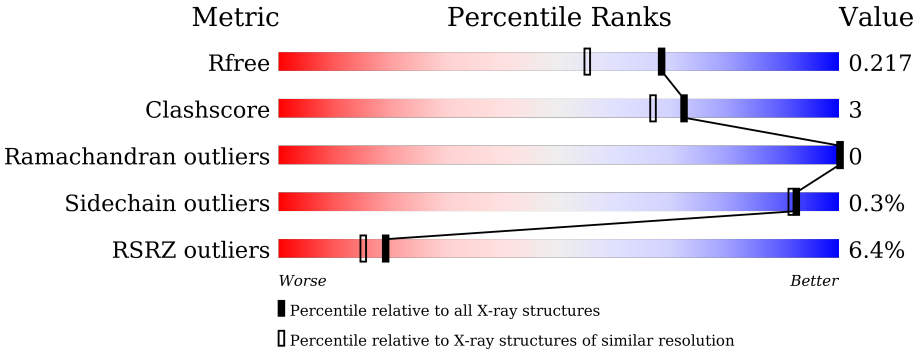
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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% 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	253	10% 77% 9% 15%
1	B	253	5% 78% 7% 15%
1	C	253	7% 81% 9% 10%
1	D	253	4% 84% 6% 9%
1	E	253	6% 89% • 7%
1	F	253	3% 80% 8% 11%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 11899 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.

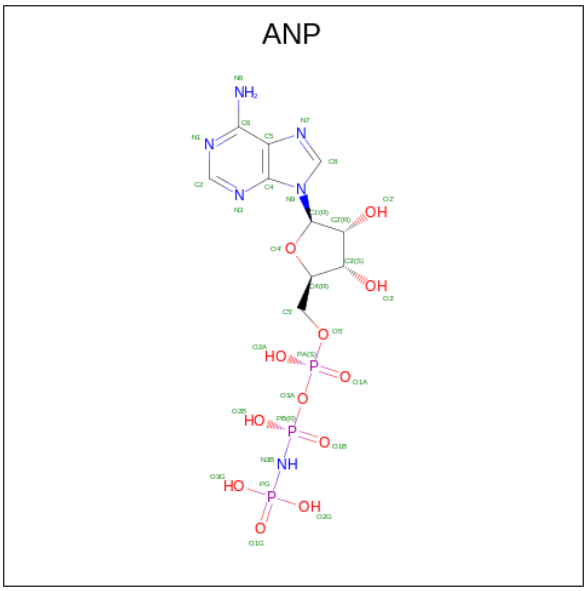
- Molecule 1 is a protein called Circadian clock protein kinase KaiC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	216	1750	1111	306	329	4	0	5	0
1	B	216	1771	1122	307	337	5	0	9	0
1	C	227	1866	1186	326	349	5	0	8	0
1	D	229	1845	1174	318	349	4	0	5	0
1	E	236	1887	1200	327	356	4	0	3	0
1	F	224	1807	1154	311	338	4	0	4	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	THR	SER	engineered mutation	UNP Q79PF4
B	48	THR	SER	engineered mutation	UNP Q79PF4
C	48	THR	SER	engineered mutation	UNP Q79PF4
D	48	THR	SER	engineered mutation	UNP Q79PF4
E	48	THR	SER	engineered mutation	UNP Q79PF4
F	48	THR	SER	engineered mutation	UNP Q79PF4

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	31	10	6	12	3	0	0
2	F	1	31	10	6	12	3	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	1	1	1	0	0
3	B	1	1	1	0	0
3	C	1	1	1	0	0
3	D	1	1	1	0	0
3	E	1	1	1	0	0
3	F	1	1	1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	A	1	1	1	0	0

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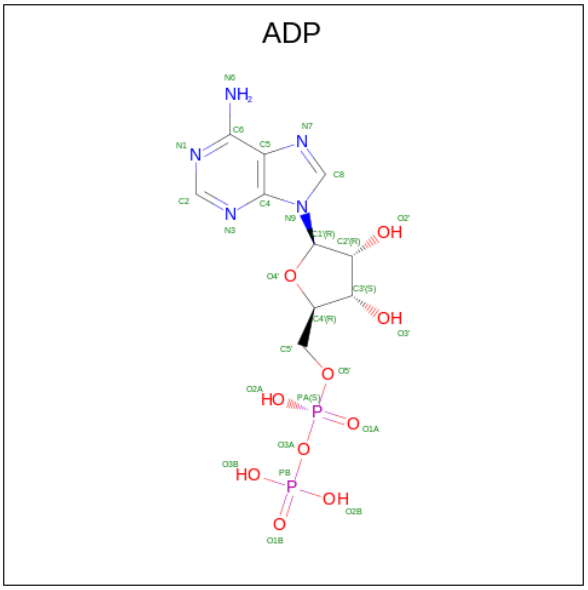
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0
4	C	1	Total Cl 1 1	0	0
4	D	1	Total Cl 1 1	0	0
4	E	1	Total Cl 1 1	0	0
4	F	1	Total Cl 1 1	0	0

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



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

- Molecule 6 is water.

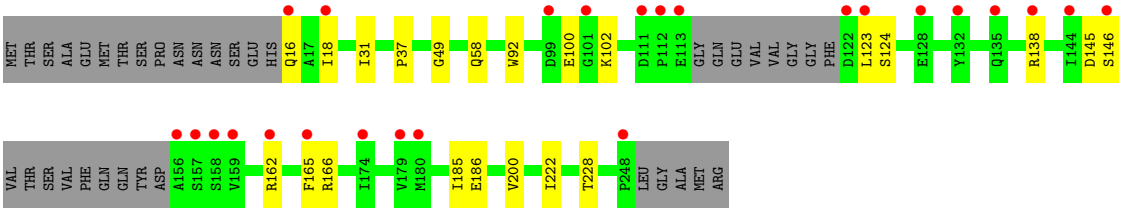
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	96	96	96	0	0
			Total	O		
6	B	119	119	119	0	0
			Total	O		
6	C	121	121	121	0	0
			Total	O		
6	D	160	160	160	0	0
			Total	O		
6	E	140	140	140	0	0
			Total	O		
6	F	155	155	155	0	0

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 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.

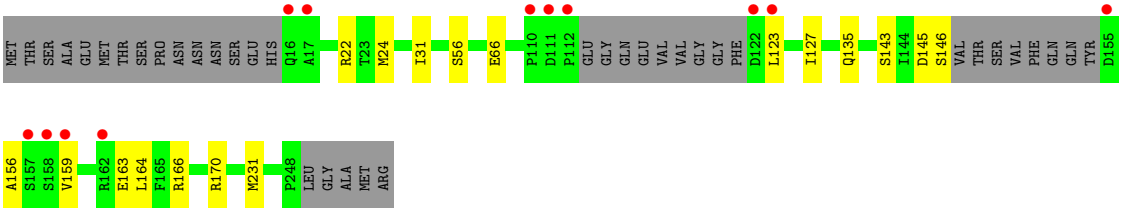
• Molecule 1: Circadian clock protein kinase KaiC

Chain A:



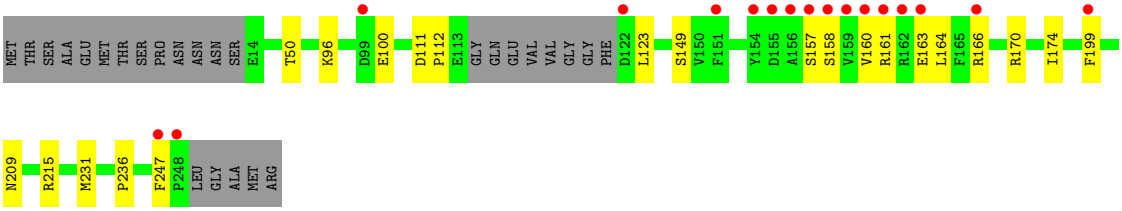
• Molecule 1: Circadian clock protein kinase KaiC

Chain B:



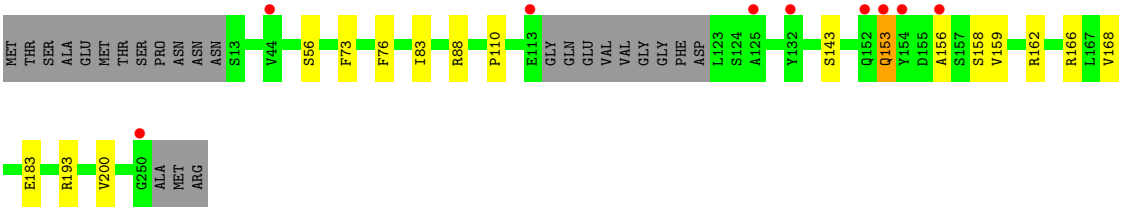
• Molecule 1: Circadian clock protein kinase KaiC

Chain C:



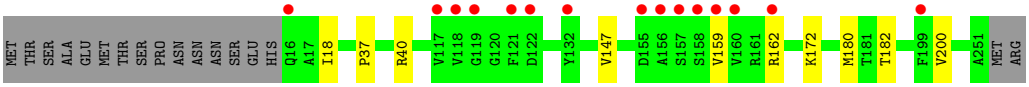
• Molecule 1: Circadian clock protein kinase KaiC

Chain D:



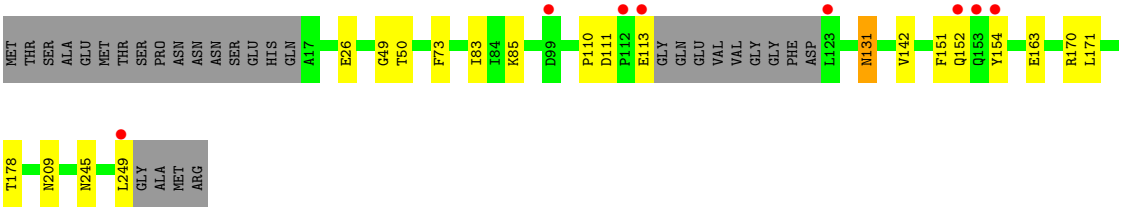
- Molecule 1: Circadian clock protein kinase KaiC

Chain E:



- Molecule 1: Circadian clock protein kinase KaiC

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	79.78Å 133.59Å 153.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.88 – 1.80 39.89 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.3 (38.88-1.80) 99.3 (39.89-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.81 (at 1.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.177 , 0.217 0.179 , 0.217	Depositor DCC
R_{free} test set	7606 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	29.6	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 50.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	11899	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ANP, MG, CL, ADP

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	0.50	0/1783	0.60	0/2401
1	B	0.55	0/1811	0.63	0/2439
1	C	0.52	0/1910	0.63	2/2575 (0.1%)
1	D	0.59	0/1889	0.67	0/2549
1	E	0.62	0/1920	0.66	0/2592
1	F	0.63	0/1844	0.66	0/2490
All	All	0.57	0/11157	0.64	2/15046 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	215	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	C	215	ARG	NE-CZ-NH2	-5.14	117.73	120.30

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	1750	0	1771	16	0
1	B	1771	0	1779	14	0
1	C	1866	0	1888	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1845	0	1862	12	0
1	E	1887	0	1897	8	0
1	F	1807	0	1834	14	0
2	A	31	0	13	1	0
2	F	31	0	13	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	B	27	0	12	0	0
5	C	27	0	12	0	0
5	D	27	0	12	1	0
5	E	27	0	12	0	0
6	A	96	0	0	0	0
6	B	119	0	0	3	0
6	C	121	0	0	1	0
6	D	160	0	0	4	0
6	E	140	0	0	0	0
6	F	155	0	0	0	0
All	All	11899	0	11105	76	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 (76) 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:C:123:LEU:HB3	1:C:163:GLU:HG2	1.46	0.94
1:F:142:VAL:HB	1:F:178[B]:THR:HG22	1.53	0.89
1:E:147:VAL:HG21	1:E:180:MET:HE3	1.58	0.84
1:B:22:ARG:NH1	6:B:509:HOH:O	2.12	0.82
1:D:183:GLU:OE2	6:D:483:HOH:O	2.03	0.76
1:C:231[B]:MET:SD	6:C:491:HOH:O	2.48	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:ARG:O	1:A:138:ARG:HG3	1.89	0.71
1:D:153:GLN:CG	1:D:193:ARG:HH22	2.06	0.68
1:F:49:GLY:H	2:F:301:ANP:HNB1	1.40	0.67
1:A:162:ARG:HH11	1:A:162:ARG:HG2	1.58	0.67
1:F:171:LEU:HD13	1:F:178[B]:THR:HG21	1.77	0.66
1:A:18:ILE:HG22	1:F:85:LYS:HE3	1.80	0.62
1:B:135:GLN:NE2	6:B:401:HOH:O	2.33	0.61
1:A:18:ILE:HD13	1:A:37:PRO:HB3	1.82	0.60
1:B:145[A]:ASP:OD1	6:B:506:HOH:O	2.14	0.60
1:A:124:SER:OG	1:A:166:ARG:NH2	2.31	0.60
1:C:157:SER:O	1:C:160:VAL:HG12	2.03	0.58
1:D:153:GLN:HG2	1:D:193:ARG:HH22	1.70	0.57
1:C:170:ARG:O	1:C:174:ILE:HG13	2.05	0.56
1:A:58:GLN:HG2	1:A:92:TRP:CH2	2.42	0.55
1:C:158:SER:HA	1:C:161:ARG:HG3	1.90	0.54
1:E:147:VAL:CG2	1:E:180:MET:HE3	2.34	0.53
1:D:158:SER:O	1:D:162:ARG:HG3	2.08	0.53
1:B:24:MET:HG3	1:B:66:GLU:HG3	1.92	0.52
1:B:156:ALA:HB3	1:B:159:VAL:HG23	1.92	0.52
1:B:31:ILE:HG22	1:B:231[B]:MET:SD	2.50	0.51
1:F:49:GLY:N	2:F:301:ANP:HNB1	2.09	0.51
1:A:165:PHE:CE1	1:F:110:PRO:HG2	2.47	0.50
1:F:73:PHE:CE1	1:F:83[B]:ILE:HD13	2.47	0.49
1:B:56[A]:SER:HB2	1:B:143:SER:HB3	1.94	0.49
1:E:18:ILE:HD12	1:E:37:PRO:HB3	1.93	0.49
1:E:40:ARG:HG2	1:E:172[B]:LYS:HE2	1.95	0.49
1:B:123:LEU:HD22	1:B:163:GLU:HB3	1.95	0.48
1:D:88:ARG:NH1	6:D:514:HOH:O	2.45	0.48
1:A:100:GLU:OE1	1:A:102:LYS:NZ	2.46	0.48
1:A:31:ILE:HG22	1:A:222:ILE:HD12	1.95	0.48
1:A:49:GLY:H	2:A:301:ANP:HNB1	1.60	0.47
1:F:111:ASP:OD1	1:F:113:GLU:HG2	2.14	0.47
1:B:56[B]:SER:HB3	1:B:143:SER:HB3	1.95	0.47
1:C:161:ARG:HB3	1:C:199:PHE:CZ	2.49	0.46
1:F:152:GLN:HB3	1:F:154:TYR:CE2	2.51	0.46
1:E:159:VAL:HA	1:E:162:ARG:HH21	1.82	0.45
1:F:249:LEU:HD23	1:F:249:LEU:HA	1.79	0.45
1:D:76:PHE:O	1:D:110:PRO:HD3	2.17	0.44
1:C:149:SER:HB3	6:D:560:HOH:O	2.17	0.44
1:A:18:ILE:HD11	1:A:228:THR:HG21	1.99	0.44
1:C:161:ARG:O	1:C:164:LEU:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:180:MET:CE	1:E:200:VAL:HG21	2.47	0.44
1:B:159:VAL:O	1:B:163:GLU:HG2	2.18	0.43
1:A:165:PHE:HB2	1:A:200:VAL:HG21	2.00	0.43
1:E:180:MET:HE2	1:E:200:VAL:HG21	2.01	0.43
1:B:145[A]:ASP:HA	1:B:146[A]:SER:HA	1.64	0.43
1:C:163:GLU:OE1	1:C:166:ARG:NH1	2.30	0.43
1:D:168:VAL:HG11	1:D:200:VAL:O	2.19	0.43
1:F:50:THR:HG22	1:F:209:ASN:HB2	2.00	0.43
1:D:153:GLN:HG2	1:D:193:ARG:NH2	2.33	0.43
1:A:123:LEU:HD12	1:A:123:LEU:HA	1.71	0.42
1:C:236:PRO:HG2	1:C:247:PHE:CE1	2.55	0.42
1:F:151:PHE:HE1	1:F:163:GLU:OE1	2.01	0.42
1:C:111:ASP:OD1	1:C:112:PRO:HD2	2.20	0.42
1:C:96:LYS:HE2	1:C:100:GLU:OE1	2.20	0.41
1:F:131:ASN:OD1	1:F:170:ARG:HD2	2.20	0.41
1:A:185:ILE:HD12	1:A:186:GLU:HG2	2.02	0.41
1:C:50:THR:HG22	1:C:209:ASN:HB2	2.03	0.41
1:D:56[A]:SER:HB2	1:D:143:SER:HB3	2.03	0.41
1:A:145[B]:ASP:HA	1:A:146[B]:SER:HA	1.65	0.41
1:D:156:ALA:HB3	1:D:159:VAL:HG23	2.01	0.41
1:B:127:ILE:CG2	1:B:170:ARG:HG2	2.51	0.41
1:C:112:PRO:O	1:D:166:ARG:HG3	2.21	0.41
1:B:123:LEU:HD23	1:B:166:ARG:HH11	1.86	0.41
1:E:159:VAL:HG22	1:E:162:ARG:HH21	1.87	0.41
1:F:26:GLU:OE1	1:F:245:ASN:ND2	2.55	0.41
1:D:73:PHE:CE2	1:D:83[B]:ILE:HD13	2.56	0.40
1:A:16:GLN:HG2	1:A:16:GLN:O	2.20	0.40
1:B:164:LEU:HA	1:B:164:LEU:HD23	1.75	0.40
5:D:301:ADP:H5'1	6:D:546:HOH:O	2.22	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	214/253 (85%)	208 (97%)	6 (3%)	0	100	100
1	B	218/253 (86%)	214 (98%)	4 (2%)	0	100	100
1	C	231/253 (91%)	225 (97%)	6 (3%)	0	100	100
1	D	230/253 (91%)	226 (98%)	4 (2%)	0	100	100
1	E	237/253 (94%)	233 (98%)	4 (2%)	0	100	100
1	F	224/253 (88%)	222 (99%)	2 (1%)	0	100	100
All	All	1354/1518 (89%)	1328 (98%)	26 (2%)	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	191/217 (88%)	191 (100%)	0	100	100
1	B	195/217 (90%)	195 (100%)	0	100	100
1	C	205/217 (94%)	205 (100%)	0	100	100
1	D	203/217 (94%)	202 (100%)	1 (0%)	88	87
1	E	204/217 (94%)	203 (100%)	1 (0%)	88	87
1	F	198/217 (91%)	197 (100%)	1 (0%)	88	87
All	All	1196/1302 (92%)	1193 (100%)	3 (0%)	92	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	153	GLN
1	E	182	THR
1	F	131	ASN

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 18 ligands modelled in this entry, 12 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	$\#\|Z\| > 2$
2	ANP	F	301	3	29,33,33	1.59	2 (6%)	31,52,52	2.11	5 (16%)
5	ADP	C	301	3	24,29,29	1.27	2 (8%)	29,45,45	1.58	5 (17%)
5	ADP	D	301	3	24,29,29	1.09	0	29,45,45	1.47	4 (13%)
5	ADP	E	301	3	24,29,29	1.04	1 (4%)	29,45,45	1.51	6 (20%)
2	ANP	A	301	3	29,33,33	1.84	5 (17%)	31,52,52	1.22	4 (12%)
5	ADP	B	301	3	24,29,29	0.98	0	29,45,45	1.67	4 (13%)

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	ANP	F	301	3	-	7/14/38/38	0/3/3/3
5	ADP	C	301	3	-	3/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ADP	D	301	3	-	6/12/32/32	0/3/3/3
5	ADP	E	301	3	-	2/12/32/32	0/3/3/3
2	ANP	A	301	3	-	5/14/38/38	0/3/3/3
5	ADP	B	301	3	-	7/12/32/32	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	ANP	PG-O1G	7.67	1.58	1.46
2	F	301	ANP	PG-O1G	6.39	1.56	1.46
5	C	301	ADP	O4'-C1'	3.74	1.46	1.41
2	A	301	ANP	PB-O1B	3.43	1.51	1.46
2	F	301	ANP	PB-O3A	3.17	1.63	1.59
5	E	301	ADP	O4'-C1'	2.92	1.45	1.41
2	A	301	ANP	PG-N3B	2.40	1.69	1.63
2	A	301	ANP	PG-O2G	-2.32	1.50	1.56
5	C	301	ADP	C2-N3	2.30	1.35	1.32
2	A	301	ANP	PB-O2B	-2.26	1.50	1.56

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	301	ANP	O1G-PG-N3B	-9.57	97.67	111.77
5	B	301	ADP	N3-C2-N1	-4.69	121.35	128.68
5	E	301	ADP	N3-C2-N1	-4.39	121.82	128.68
5	C	301	ADP	N3-C2-N1	-4.38	121.83	128.68
5	D	301	ADP	N3-C2-N1	-4.38	121.84	128.68
5	B	301	ADP	C5'-C4'-C3'	-3.68	101.39	115.18
2	A	301	ANP	O1B-PB-N3B	3.55	117.00	111.77
5	C	301	ADP	C1'-N9-C4	-3.55	120.40	126.64
2	A	301	ANP	O1G-PG-N3B	-3.49	106.63	111.77
2	F	301	ANP	O2B-PB-O1B	3.21	116.66	109.92
5	D	301	ADP	C1'-N9-C4	-3.12	121.15	126.64
5	E	301	ADP	C1'-N9-C4	-2.90	121.55	126.64
5	B	301	ADP	C1'-N9-C4	-2.86	121.61	126.64
5	C	301	ADP	N6-C6-N1	2.64	124.06	118.57
5	C	301	ADP	C2-N1-C6	2.63	123.25	118.75
5	B	301	ADP	C2-N1-C6	2.54	123.10	118.75
5	E	301	ADP	C4-C5-N7	-2.51	106.78	109.40
5	D	301	ADP	C5'-C4'-C3'	-2.45	105.99	115.18
5	E	301	ADP	C2-N1-C6	2.39	122.85	118.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	301	ADP	C5'-C4'-C3'	-2.38	106.25	115.18
2	A	301	ANP	C5-C6-N6	2.31	123.86	120.35
2	A	301	ANP	O3G-PG-O1G	-2.23	107.86	113.45
5	D	301	ADP	C4-C5-N7	-2.18	107.13	109.40
5	E	301	ADP	O3B-PB-O2B	2.15	115.85	107.64
2	F	301	ANP	O2A-PA-O1A	2.07	122.46	112.24
2	F	301	ANP	C5-C6-N6	2.02	123.43	120.35
2	F	301	ANP	O2G-PG-O3G	2.01	113.00	107.64
5	E	301	ADP	O3'-C3'-C4'	-2.00	105.26	111.05

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	ANP	PB-N3B-PG-O1G
2	A	301	ANP	PA-O3A-PB-O2B
2	A	301	ANP	C5'-O5'-PA-O1A
2	F	301	ANP	PB-N3B-PG-O1G
2	F	301	ANP	PG-N3B-PB-O1B
2	F	301	ANP	PA-O3A-PB-O1B
2	F	301	ANP	PA-O3A-PB-O2B
2	F	301	ANP	C5'-O5'-PA-O1A
5	B	301	ADP	PA-O3A-PB-O2B
5	B	301	ADP	C5'-O5'-PA-O1A
5	D	301	ADP	PA-O3A-PB-O2B
5	D	301	ADP	C5'-O5'-PA-O3A
5	D	301	ADP	C3'-C4'-C5'-O5'
5	D	301	ADP	O4'-C4'-C5'-O5'
5	B	301	ADP	O4'-C4'-C5'-O5'
2	A	301	ANP	C5'-O5'-PA-O3A
2	F	301	ANP	C5'-O5'-PA-O3A
5	B	301	ADP	C3'-C4'-C5'-O5'
2	A	301	ANP	C5'-O5'-PA-O2A
2	F	301	ANP	C5'-O5'-PA-O2A
5	B	301	ADP	C5'-O5'-PA-O2A
5	D	301	ADP	C5'-O5'-PA-O1A
5	D	301	ADP	C5'-O5'-PA-O2A
5	C	301	ADP	PA-O3A-PB-O1B
5	E	301	ADP	PA-O3A-PB-O1B
5	B	301	ADP	PA-O3A-PB-O3B
5	C	301	ADP	PA-O3A-PB-O2B
5	C	301	ADP	PA-O3A-PB-O3B

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Mol	Chain	Res	Type	Atoms
5	E	301	ADP	PA-O3A-PB-O2B
5	B	301	ADP	C5'-O5'-PA-O3A

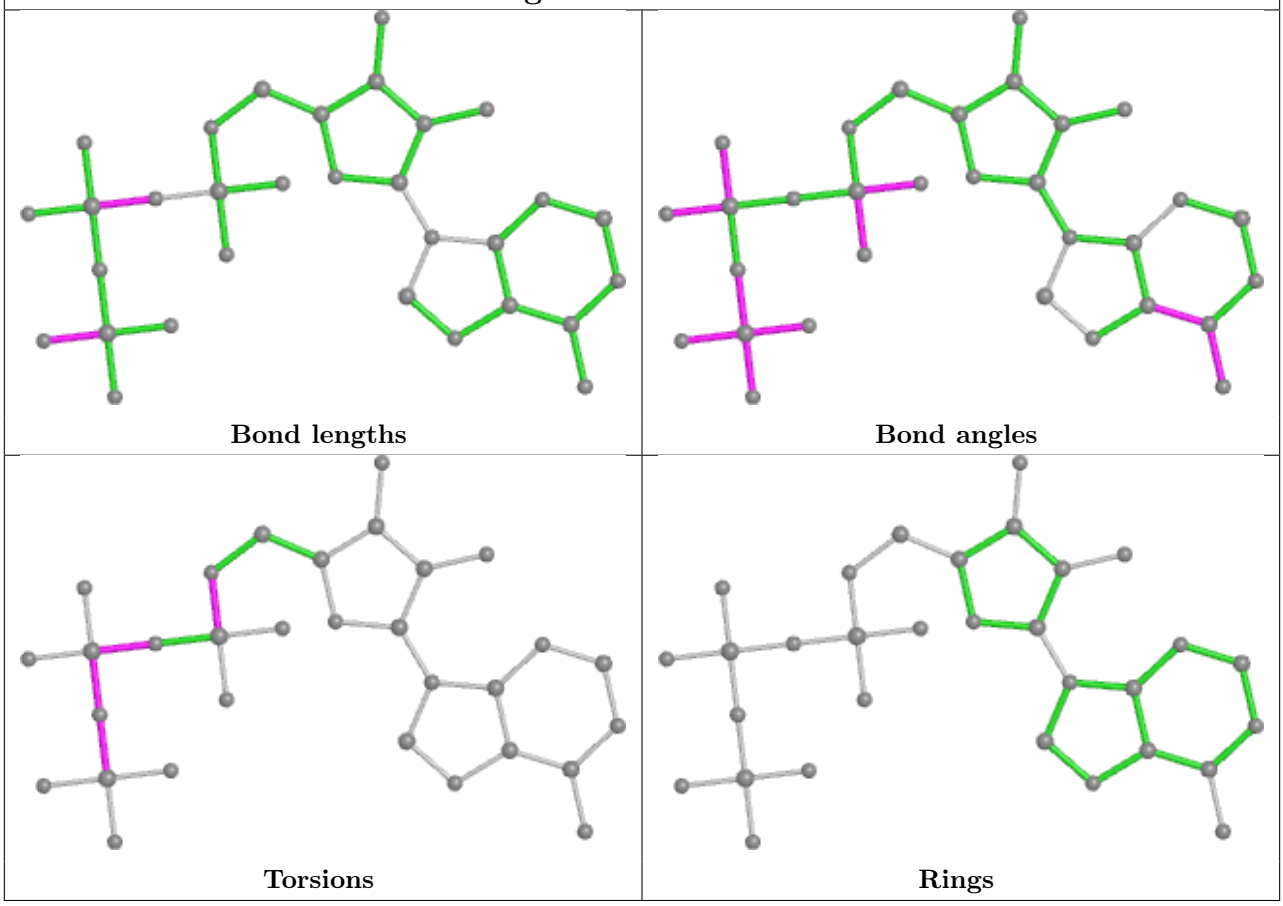
There are no ring outliers.

3 monomers are involved in 4 short contacts:

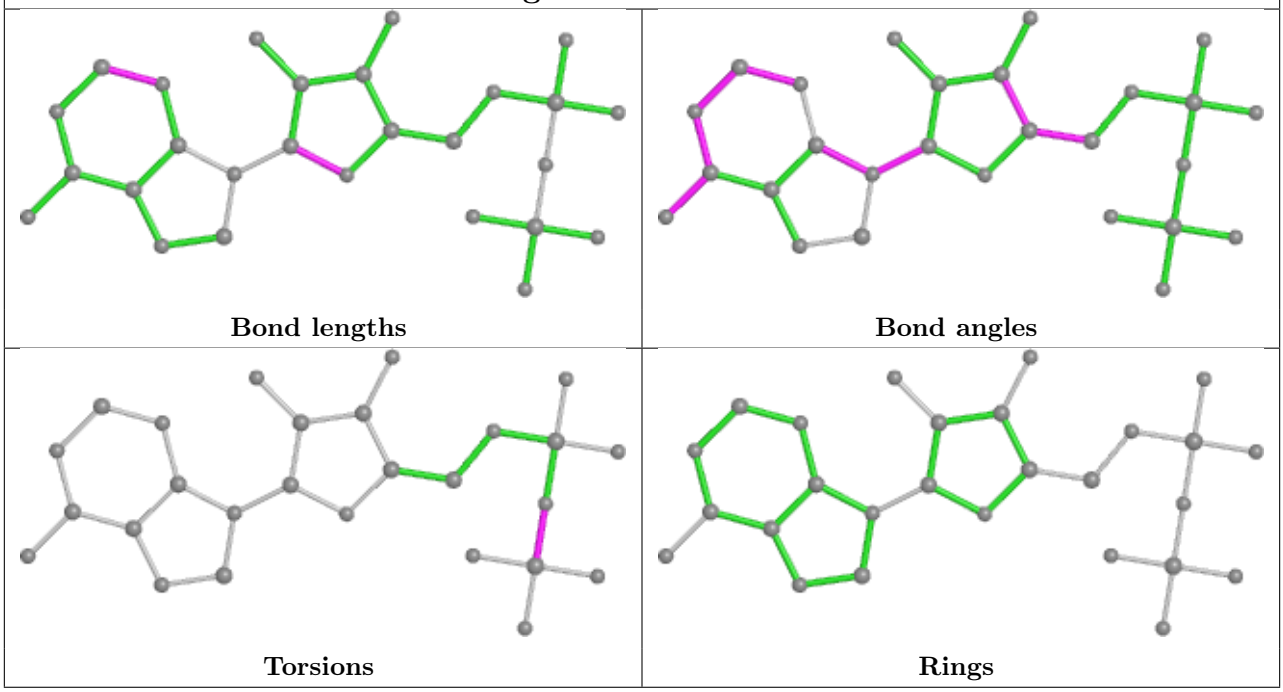
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	ANP	2	0
5	D	301	ADP	1	0
2	A	301	ANP	1	0

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.

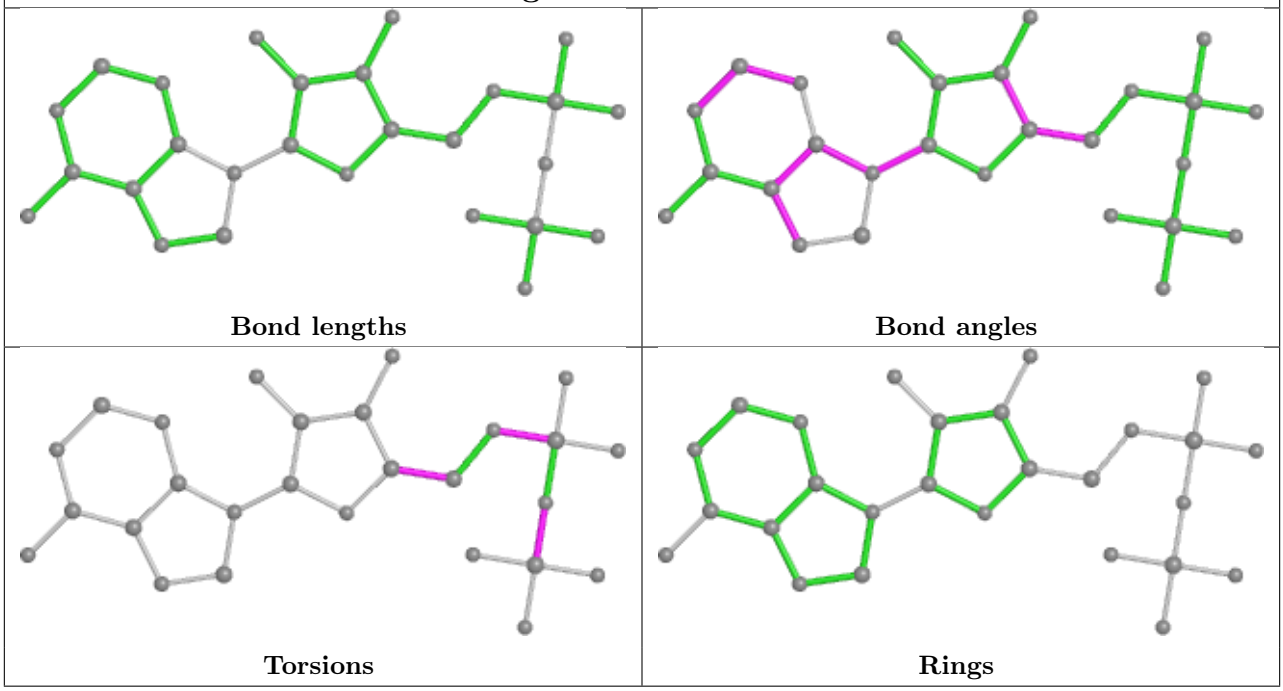
Ligand ANP F 301



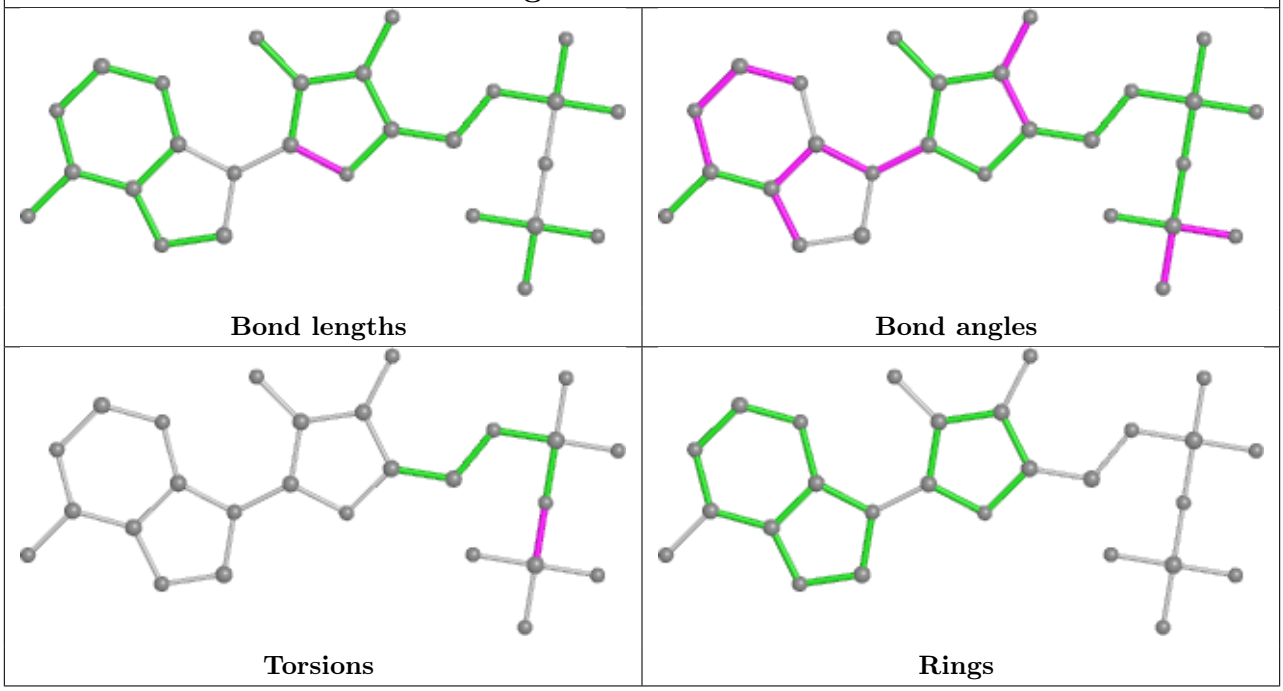
Ligand ADP C 301



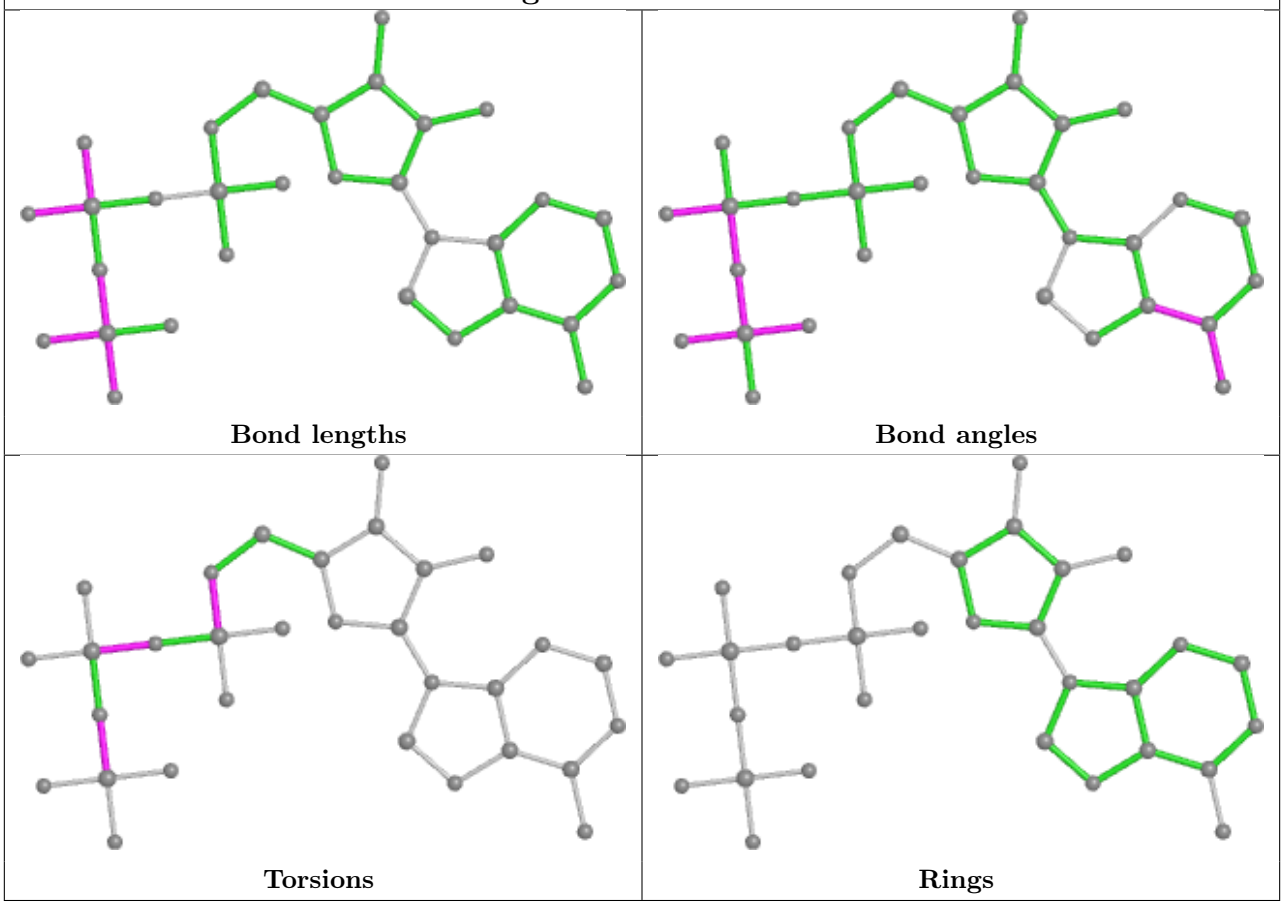
Ligand ADP D 301



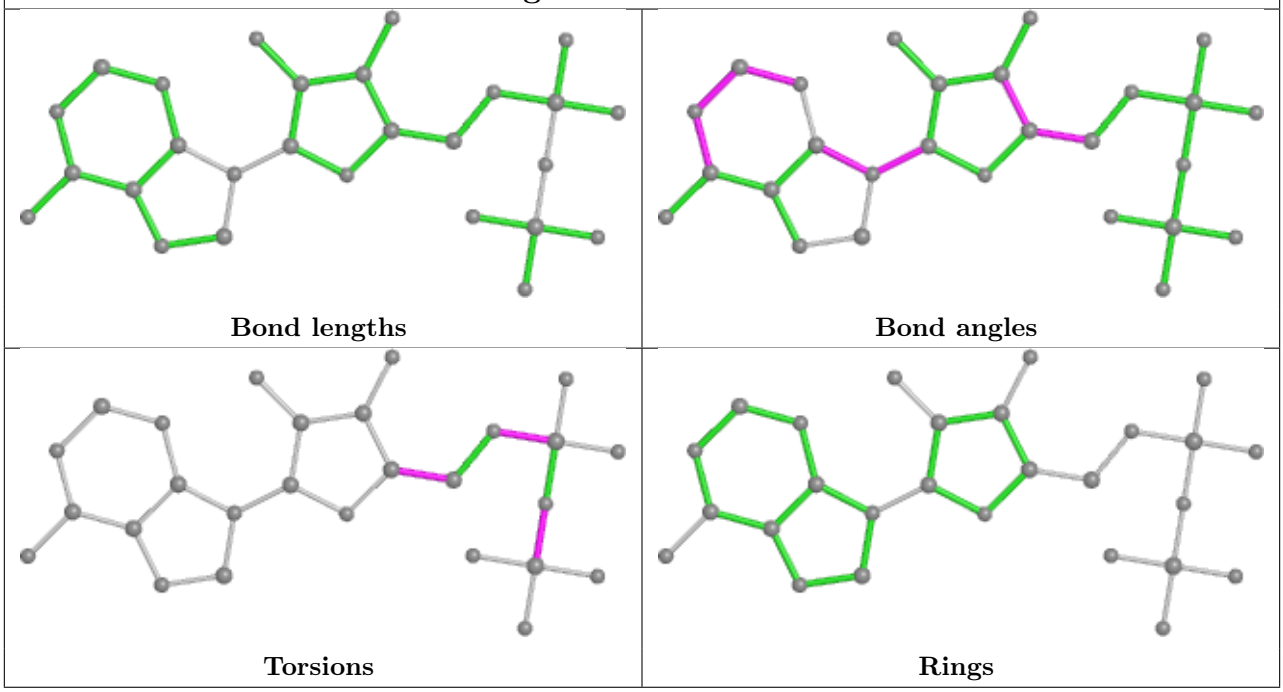
Ligand ADP E 301



Ligand ANP A 301



Ligand ADP B 301



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 (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(Å^2)	Q<0.9
1	A	216/253 (85%)	0.43	25 (11%)	4	3	25, 43, 81, 128	0
1	B	216/253 (85%)	-0.05	12 (5%)	24	19	25, 36, 66, 106	0
1	C	227/253 (89%)	0.14	17 (7%)	14	11	24, 38, 83, 115	0
1	D	229/253 (90%)	-0.03	9 (3%)	39	33	21, 33, 66, 101	0
1	E	236/253 (93%)	0.06	15 (6%)	19	15	20, 33, 74, 122	0
1	F	224/253 (88%)	-0.22	8 (3%)	42	37	21, 33, 60, 100	0
All	All	1348/1518 (88%)	0.06	86 (6%)	19	15	20, 36, 72, 128	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	118	VAL	11.6
1	F	154	TYR	9.1
1	E	121	PHE	8.5
1	A	132	TYR	7.1
1	A	156	ALA	7.1
1	C	159	VAL	5.8
1	C	154	TYR	5.6
1	C	156	ALA	5.5
1	D	154	TYR	5.4
1	A	112	PRO	5.3
1	A	113	GLU	5.2
1	C	157	SER	5.1
1	E	132	TYR	4.8
1	E	156	ALA	4.6
1	C	160	VAL	4.5
1	B	112	PRO	4.5
1	C	247	PHE	4.4
1	C	122	ASP	4.2
1	E	162	ARG	4.1

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Mol	Chain	Res	Type	RSRZ
1	F	113	GLU	4.0
1	A	146[A]	SER	3.9
1	B	122	ASP	3.8
1	B	123	LEU	3.8
1	E	159	VAL	3.7
1	A	157	SER	3.7
1	B	111	ASP	3.7
1	E	117	VAL	3.6
1	D	250	GLY	3.6
1	B	110	PRO	3.6
1	F	153	GLN	3.5
1	A	159	VAL	3.4
1	E	160	VAL	3.3
1	D	153	GLN	3.3
1	C	248	PRO	3.3
1	F	249	LEU	3.3
1	F	112	PRO	3.3
1	A	16	GLN	3.2
1	E	119	GLY	3.2
1	C	199	PHE	3.2
1	E	158	SER	3.2
1	A	158	SER	3.1
1	C	162	ARG	3.1
1	A	138	ARG	3.1
1	C	158	SER	3.0
1	A	174	ILE	3.0
1	C	166	ARG	3.0
1	A	165	PHE	3.0
1	D	152	GLN	2.9
1	E	199	PHE	2.9
1	B	16	GLN	2.8
1	A	99	ASP	2.8
1	A	123	LEU	2.7
1	A	135	GLN	2.6
1	F	99	ASP	2.6
1	D	156	ALA	2.6
1	A	111	ASP	2.6
1	A	144	ILE	2.6
1	C	151	PHE	2.5
1	D	113	GLU	2.5
1	A	18	ILE	2.4
1	D	44	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	128	GLU	2.4
1	B	157	SER	2.3
1	D	125	ALA	2.3
1	E	155	ASP	2.3
1	A	248	PRO	2.3
1	A	162	ARG	2.3
1	E	122	ASP	2.3
1	C	161	ARG	2.3
1	F	152	GLN	2.2
1	B	17	ALA	2.2
1	A	122	ASP	2.2
1	C	155	ASP	2.2
1	E	16	GLN	2.2
1	D	132	TYR	2.2
1	B	159	VAL	2.2
1	E	157	SER	2.1
1	B	158	SER	2.1
1	B	162	ARG	2.1
1	F	123	LEU	2.1
1	A	101	GLY	2.1
1	A	179	VAL	2.1
1	C	163	GLU	2.0
1	B	155	ASP	2.0
1	C	99	ASP	2.0
1	A	180	MET	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 monosaccharides in this entry.

6.4 Ligands (i)

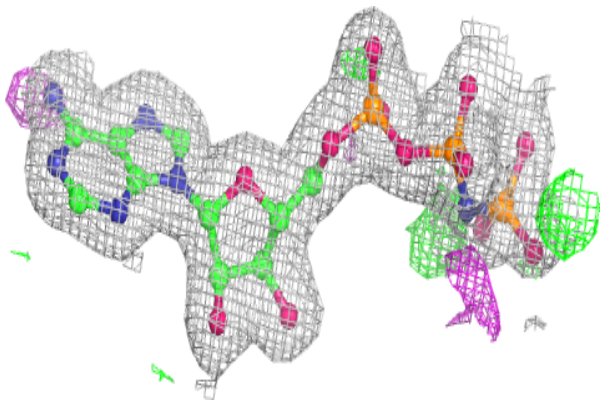
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

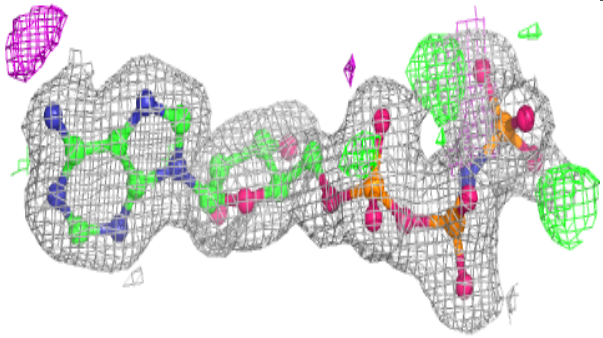
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	A	302	1/1	0.93	0.03	48,48,48,48	0
2	ANP	F	301	31/31	0.97	0.09	22,30,35,38	3
2	ANP	A	301	31/31	0.97	0.09	28,34,45,60	3
3	MG	F	302	1/1	0.97	0.04	31,31,31,31	0
5	ADP	E	301	27/27	0.97	0.08	20,25,30,36	0
3	MG	B	302	1/1	0.98	0.06	35,35,35,35	0
5	ADP	B	301	27/27	0.98	0.09	26,29,33,38	0
3	MG	C	302	1/1	0.98	0.06	31,31,31,31	0
4	CL	A	303	1/1	0.99	0.06	34,34,34,34	0
4	CL	B	303	1/1	0.99	0.04	33,33,33,33	0
4	CL	F	303	1/1	0.99	0.05	29,29,29,29	0
3	MG	E	302	1/1	0.99	0.09	27,27,27,27	0
5	ADP	C	301	27/27	0.99	0.07	22,27,31,33	0
5	ADP	D	301	27/27	0.99	0.10	22,26,30,38	0
3	MG	D	302	1/1	0.99	0.09	29,29,29,29	0
4	CL	E	303	1/1	1.00	0.04	30,30,30,30	0
4	CL	C	303	1/1	1.00	0.07	30,30,30,30	0
4	CL	D	303	1/1	1.00	0.07	27,27,27,27	0

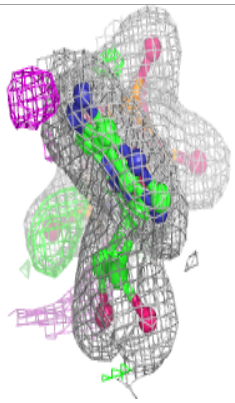
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ANP F 301:

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

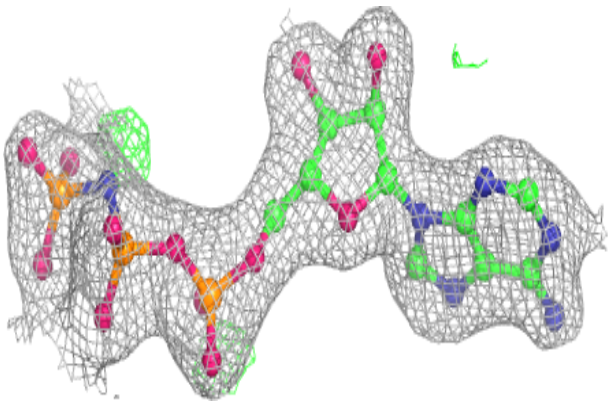


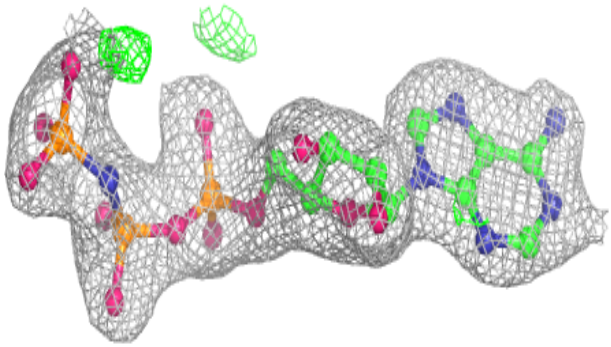


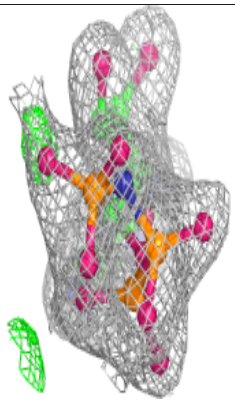


Electron density around ANP A 301:

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

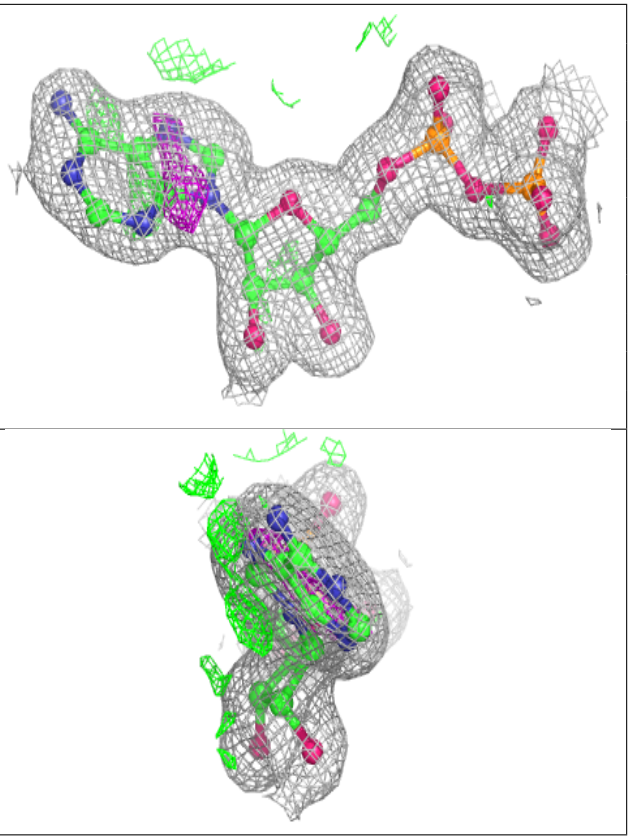


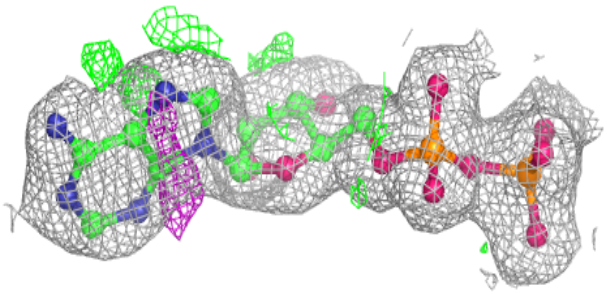




Electron density around ADP E 301:

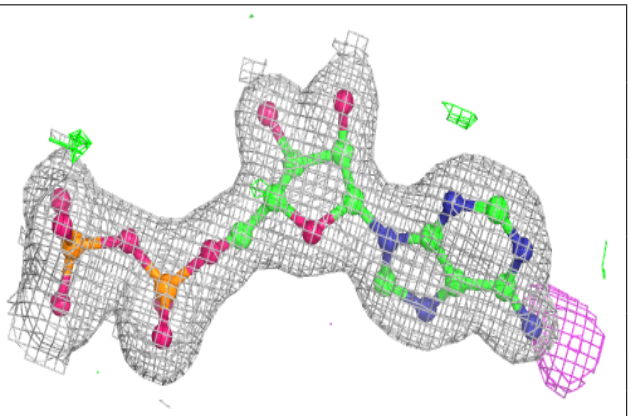
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

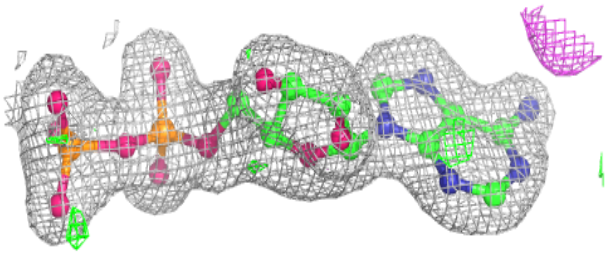


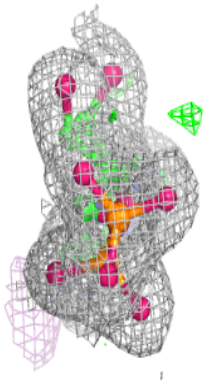


Electron density around ADP B 301:

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

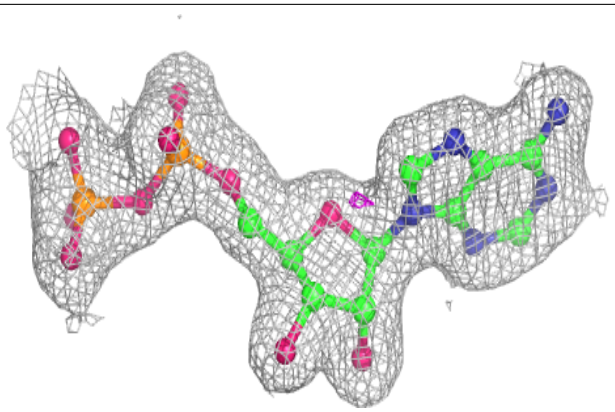


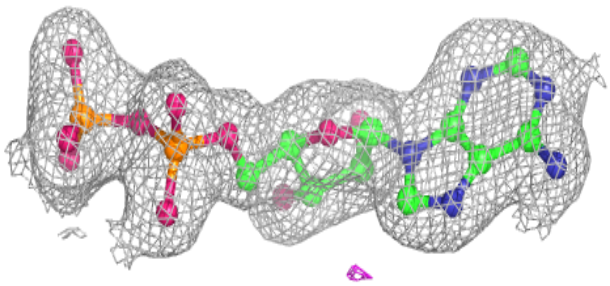




Electron density around ADP C 301:

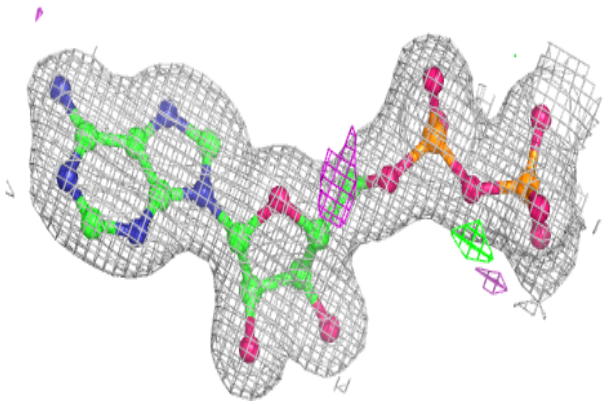
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

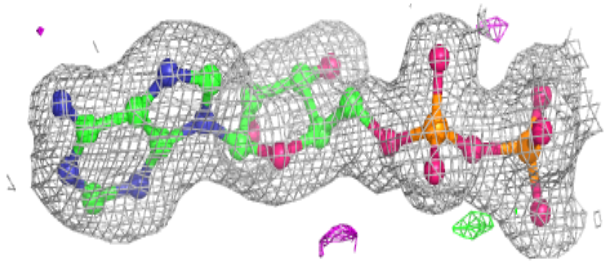


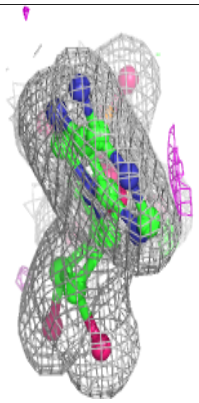


Electron density around ADP D 301:

$2mF_o$-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.