



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 08:09 am BST

PDB ID : 3IS5
Title : Crystal structure of CDPK kinase domain from toxoplasma Gondii, TGME49_018720
Authors : Wernimont, A.K.; Artz, J.D.; Senisterra, G.; MacKenzie, F.; Hutchinson, A.; Kozieradzki, I.; Cossar, D.; Bochkarev, A.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Weigelt, J.; Hui, R.; Lin, Y.H.; Structural Genomics Consortium (SGC)
Deposited on : 2009-08-25
Resolution : 2.55 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

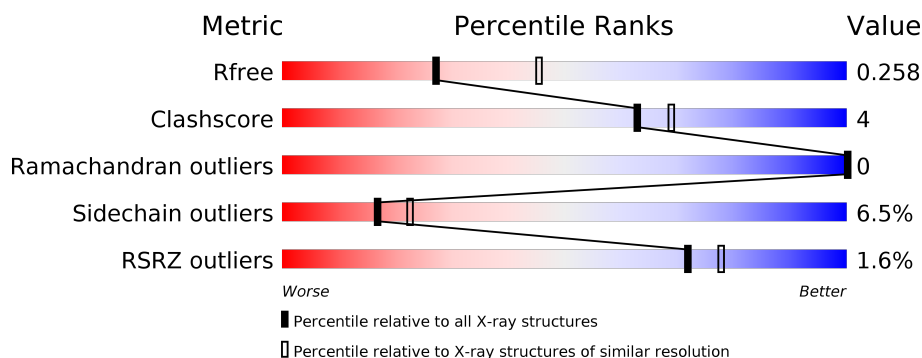
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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 ≥ 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	285	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>12%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	285	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>12%</div> <div>•</div> <div>9%</div> </div> </div>
1	C	285	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>11%</div> <div>•</div> <div>9%</div> </div> </div>
1	D	285	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>11%</div> <div>•</div> <div>17%</div> </div> </div>
1	E	285	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>11%</div> <div>•</div> <div>12%</div> </div> </div>
1	F	285	<div> <div></div> <div> <div></div> <div>82%</div> <div>10%</div> <div>•</div> <div>7%</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	ANP	A	1	X	-	-	-
2	ANP	B	1	X	-	-	-
2	ANP	C	1	X	-	-	-
2	ANP	D	1	X	-	-	-
2	ANP	E	1	X	-	-	-
2	ANP	F	398	X	-	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12282 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 Calcium-dependent protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	2	0
			2028	1304	340	373	11			
1	B	260	Total	C	N	O	S	0	0	0
			2050	1322	338	378	12			
1	C	259	Total	C	N	O	S	0	0	0
			1983	1278	326	368	11			
1	D	236	Total	C	N	O	S	0	1	0
			1797	1160	297	328	12			
1	E	252	Total	C	N	O	S	0	0	0
			1926	1239	319	356	12			
1	F	266	Total	C	N	O	S	0	1	0
			2107	1357	345	392	13			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	112	MET	-	EXPRESSION TAG	UNP B6KS23
A	113	HIS	-	EXPRESSION TAG	UNP B6KS23
A	114	HIS	-	EXPRESSION TAG	UNP B6KS23
A	115	HIS	-	EXPRESSION TAG	UNP B6KS23
A	116	HIS	-	EXPRESSION TAG	UNP B6KS23
A	117	HIS	-	EXPRESSION TAG	UNP B6KS23
A	118	HIS	-	EXPRESSION TAG	UNP B6KS23
A	119	SER	-	EXPRESSION TAG	UNP B6KS23
A	120	SER	-	EXPRESSION TAG	UNP B6KS23
A	121	GLY	-	EXPRESSION TAG	UNP B6KS23
A	122	ARG	-	EXPRESSION TAG	UNP B6KS23
A	123	GLU	-	EXPRESSION TAG	UNP B6KS23
A	124	ASN	-	EXPRESSION TAG	UNP B6KS23
A	125	LEU	-	EXPRESSION TAG	UNP B6KS23
A	126	TYR	-	EXPRESSION TAG	UNP B6KS23
A	127	PHE	-	EXPRESSION TAG	UNP B6KS23
A	128	GLN	-	EXPRESSION TAG	UNP B6KS23

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Chain	Residue	Modelled	Actual	Comment	Reference
A	129	GLY	-	EXPRESSION TAG	UNP B6KS23
B	112	MET	-	EXPRESSION TAG	UNP B6KS23
B	113	HIS	-	EXPRESSION TAG	UNP B6KS23
B	114	HIS	-	EXPRESSION TAG	UNP B6KS23
B	115	HIS	-	EXPRESSION TAG	UNP B6KS23
B	116	HIS	-	EXPRESSION TAG	UNP B6KS23
B	117	HIS	-	EXPRESSION TAG	UNP B6KS23
B	118	HIS	-	EXPRESSION TAG	UNP B6KS23
B	119	SER	-	EXPRESSION TAG	UNP B6KS23
B	120	SER	-	EXPRESSION TAG	UNP B6KS23
B	121	GLY	-	EXPRESSION TAG	UNP B6KS23
B	122	ARG	-	EXPRESSION TAG	UNP B6KS23
B	123	GLU	-	EXPRESSION TAG	UNP B6KS23
B	124	ASN	-	EXPRESSION TAG	UNP B6KS23
B	125	LEU	-	EXPRESSION TAG	UNP B6KS23
B	126	TYR	-	EXPRESSION TAG	UNP B6KS23
B	127	PHE	-	EXPRESSION TAG	UNP B6KS23
B	128	GLN	-	EXPRESSION TAG	UNP B6KS23
B	129	GLY	-	EXPRESSION TAG	UNP B6KS23
C	112	MET	-	EXPRESSION TAG	UNP B6KS23
C	113	HIS	-	EXPRESSION TAG	UNP B6KS23
C	114	HIS	-	EXPRESSION TAG	UNP B6KS23
C	115	HIS	-	EXPRESSION TAG	UNP B6KS23
C	116	HIS	-	EXPRESSION TAG	UNP B6KS23
C	117	HIS	-	EXPRESSION TAG	UNP B6KS23
C	118	HIS	-	EXPRESSION TAG	UNP B6KS23
C	119	SER	-	EXPRESSION TAG	UNP B6KS23
C	120	SER	-	EXPRESSION TAG	UNP B6KS23
C	121	GLY	-	EXPRESSION TAG	UNP B6KS23
C	122	ARG	-	EXPRESSION TAG	UNP B6KS23
C	123	GLU	-	EXPRESSION TAG	UNP B6KS23
C	124	ASN	-	EXPRESSION TAG	UNP B6KS23
C	125	LEU	-	EXPRESSION TAG	UNP B6KS23
C	126	TYR	-	EXPRESSION TAG	UNP B6KS23
C	127	PHE	-	EXPRESSION TAG	UNP B6KS23
C	128	GLN	-	EXPRESSION TAG	UNP B6KS23
C	129	GLY	-	EXPRESSION TAG	UNP B6KS23
D	112	MET	-	EXPRESSION TAG	UNP B6KS23
D	113	HIS	-	EXPRESSION TAG	UNP B6KS23
D	114	HIS	-	EXPRESSION TAG	UNP B6KS23
D	115	HIS	-	EXPRESSION TAG	UNP B6KS23
D	116	HIS	-	EXPRESSION TAG	UNP B6KS23

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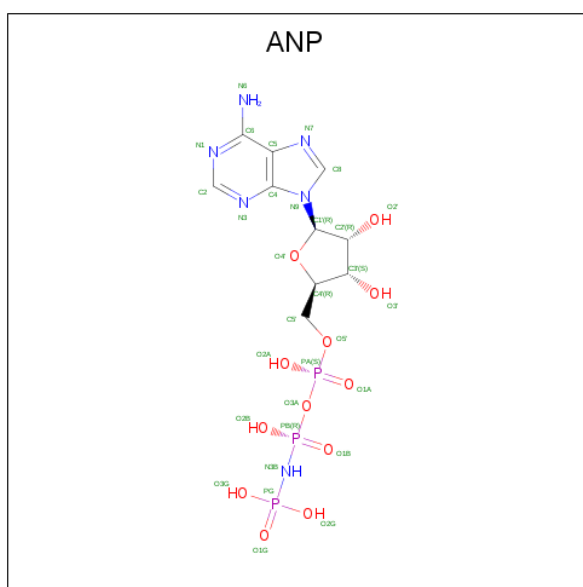
Chain	Residue	Modelled	Actual	Comment	Reference
D	117	HIS	-	EXPRESSION TAG	UNP B6KS23
D	118	HIS	-	EXPRESSION TAG	UNP B6KS23
D	119	SER	-	EXPRESSION TAG	UNP B6KS23
D	120	SER	-	EXPRESSION TAG	UNP B6KS23
D	121	GLY	-	EXPRESSION TAG	UNP B6KS23
D	122	ARG	-	EXPRESSION TAG	UNP B6KS23
D	123	GLU	-	EXPRESSION TAG	UNP B6KS23
D	124	ASN	-	EXPRESSION TAG	UNP B6KS23
D	125	LEU	-	EXPRESSION TAG	UNP B6KS23
D	126	TYR	-	EXPRESSION TAG	UNP B6KS23
D	127	PHE	-	EXPRESSION TAG	UNP B6KS23
D	128	GLN	-	EXPRESSION TAG	UNP B6KS23
D	129	GLY	-	EXPRESSION TAG	UNP B6KS23
E	112	MET	-	EXPRESSION TAG	UNP B6KS23
E	113	HIS	-	EXPRESSION TAG	UNP B6KS23
E	114	HIS	-	EXPRESSION TAG	UNP B6KS23
E	115	HIS	-	EXPRESSION TAG	UNP B6KS23
E	116	HIS	-	EXPRESSION TAG	UNP B6KS23
E	117	HIS	-	EXPRESSION TAG	UNP B6KS23
E	118	HIS	-	EXPRESSION TAG	UNP B6KS23
E	119	SER	-	EXPRESSION TAG	UNP B6KS23
E	120	SER	-	EXPRESSION TAG	UNP B6KS23
E	121	GLY	-	EXPRESSION TAG	UNP B6KS23
E	122	ARG	-	EXPRESSION TAG	UNP B6KS23
E	123	GLU	-	EXPRESSION TAG	UNP B6KS23
E	124	ASN	-	EXPRESSION TAG	UNP B6KS23
E	125	LEU	-	EXPRESSION TAG	UNP B6KS23
E	126	TYR	-	EXPRESSION TAG	UNP B6KS23
E	127	PHE	-	EXPRESSION TAG	UNP B6KS23
E	128	GLN	-	EXPRESSION TAG	UNP B6KS23
E	129	GLY	-	EXPRESSION TAG	UNP B6KS23
F	112	MET	-	EXPRESSION TAG	UNP B6KS23
F	113	HIS	-	EXPRESSION TAG	UNP B6KS23
F	114	HIS	-	EXPRESSION TAG	UNP B6KS23
F	115	HIS	-	EXPRESSION TAG	UNP B6KS23
F	116	HIS	-	EXPRESSION TAG	UNP B6KS23
F	117	HIS	-	EXPRESSION TAG	UNP B6KS23
F	118	HIS	-	EXPRESSION TAG	UNP B6KS23
F	119	SER	-	EXPRESSION TAG	UNP B6KS23
F	120	SER	-	EXPRESSION TAG	UNP B6KS23
F	121	GLY	-	EXPRESSION TAG	UNP B6KS23
F	122	ARG	-	EXPRESSION TAG	UNP B6KS23

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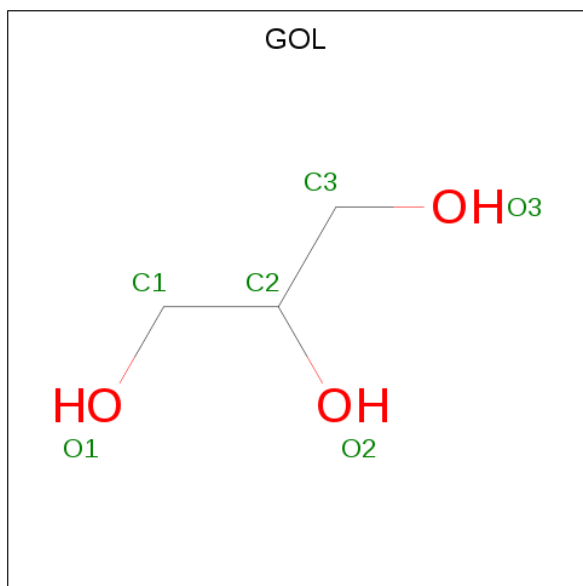
Chain	Residue	Modelled	Actual	Comment	Reference
F	123	GLU	-	EXPRESSION TAG	UNP B6KS23
F	124	ASN	-	EXPRESSION TAG	UNP B6KS23
F	125	LEU	-	EXPRESSION TAG	UNP B6KS23
F	126	TYR	-	EXPRESSION TAG	UNP B6KS23
F	127	PHE	-	EXPRESSION TAG	UNP B6KS23
F	128	GLN	-	EXPRESSION TAG	UNP B6KS23
F	129	GLY	-	EXPRESSION TAG	UNP B6KS23

- 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
3	A	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0
3	F	1	Total Ca 1 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	F	1	Total C O 6 3 3	0	0

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

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

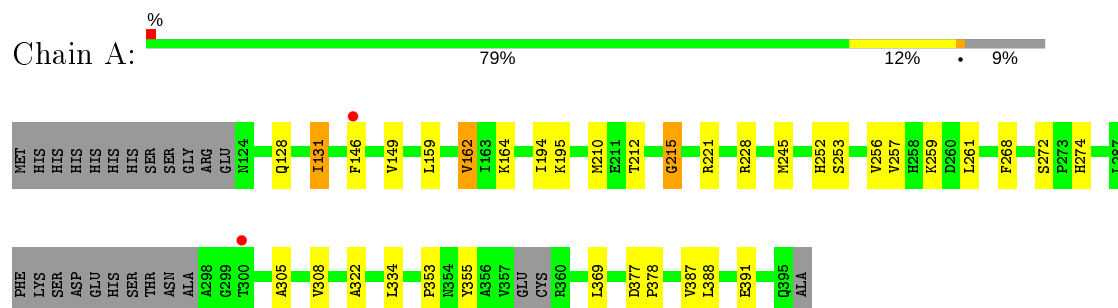
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	38	Total O 38 38	0	0
6	B	32	Total O 32 32	0	0
6	C	17	Total O 17 17	0	0
6	D	12	Total O 12 12	0	0
6	E	28	Total O 28 28	0	0
6	F	27	Total O 27 27	0	0

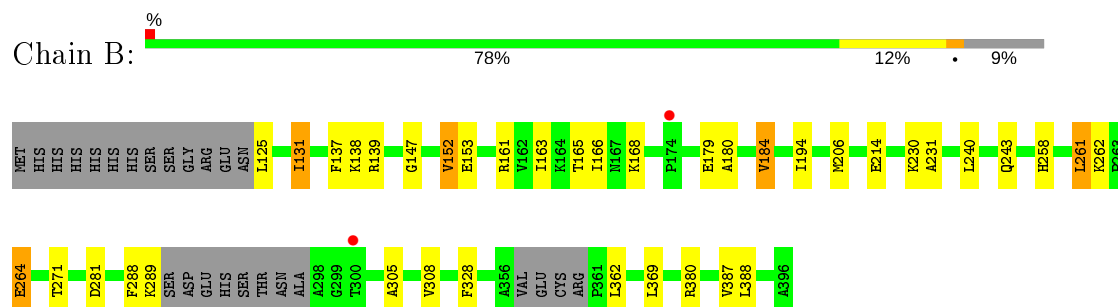
3 Residue-property plots [i](#)

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.

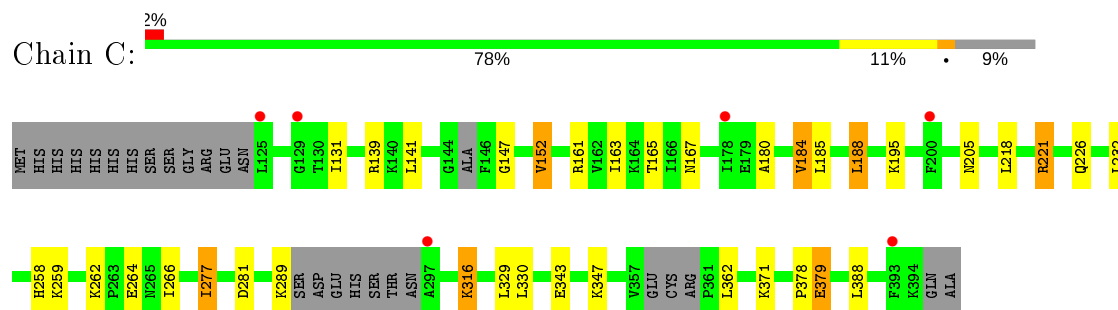
- Molecule 1: Calcium-dependent protein kinase



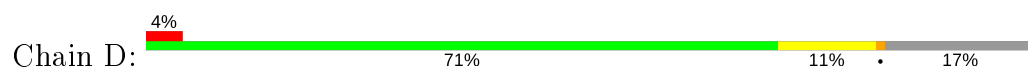
- Molecule 1: Calcium-dependent protein kinase

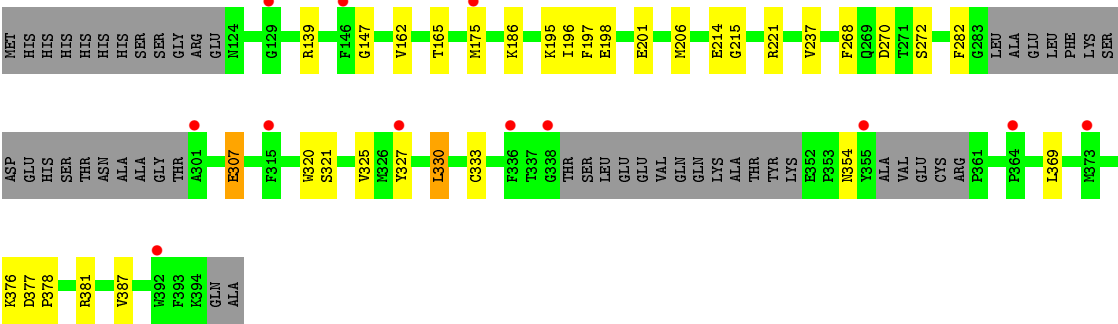


- Molecule 1: Calcium-dependent protein kinase

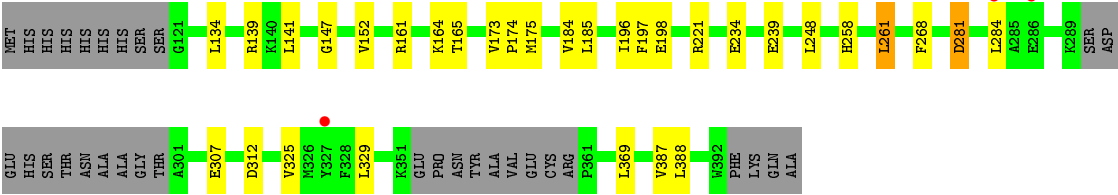


- Molecule 1: Calcium-dependent protein kinase

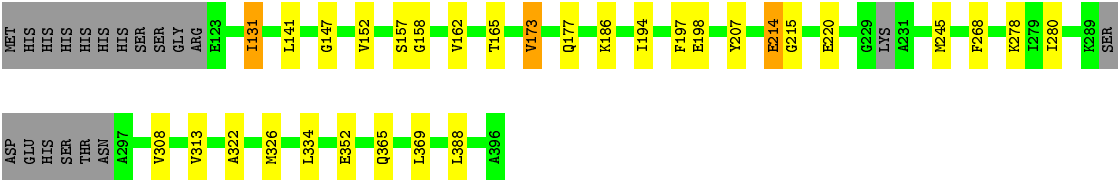
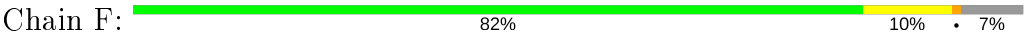




• Molecule 1: Calcium-dependent protein kinase



• Molecule 1: Calcium-dependent protein kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	113.97Å 113.97Å 153.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.55 45.75 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.1 (50.00-2.55) 99.1 (45.75-2.55)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.54Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.218 , 0.259 0.220 , 0.258	Depositor DCC
R_{free} test set	3620 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	49.7	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l 0.058 for h,-h-k,-l 0.024 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12282	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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: GOL, CA, ANP, MG

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	0.36	0/2078	0.53	1/2817 (0.0%)
1	B	0.37	0/2095	0.52	0/2830
1	C	0.35	0/2024	0.50	0/2741
1	D	0.35	0/1842	0.47	0/2498
1	E	0.35	0/1966	0.50	0/2663
1	F	0.39	0/2156	0.54	0/2917
All	All	0.36	0/12161	0.51	1/16466 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	215	GLY	N-CA-C	5.37	126.52	113.10

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	2028	0	1963	21	0
1	B	2050	0	2020	16	0
1	C	1983	0	1906	19	0
1	D	1797	0	1690	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1926	0	1833	14	0
1	F	2107	0	2060	15	0
2	A	31	0	13	5	0
2	B	31	0	13	1	0
2	C	31	0	13	1	0
2	D	31	0	13	2	0
2	E	31	0	13	0	0
2	F	31	0	13	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	F	1	0	0	0	0
4	A	12	0	16	0	0
4	B	6	0	8	1	0
4	D	12	0	16	1	0
4	E	6	0	8	2	0
4	F	6	0	8	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
6	A	38	0	0	0	0
6	B	32	0	0	0	0
6	C	17	0	0	0	0
6	D	12	0	0	0	0
6	E	28	0	0	0	0
6	F	27	0	0	2	0
All	All	12282	0	11606	102	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 4.

The worst 5 of 102 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:221:ARG:HH21	1:C:221:ARG:HG2	1.29	0.94
1:D:270:ASP:OD2	1:D:272:SER:HB3	1.83	0.79
2:C:1:ANP:O2A	2:C:1:ANP:H4'	1.88	0.72
1:C:266:ILE:HG22	1:C:277:ILE:HD12	1.73	0.71
2:A:1:ANP:O2B	2:A:1:ANP:O2A	2.10	0.70

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	256/285 (90%)	249 (97%)	7 (3%)	0	100	100
1	B	254/285 (89%)	248 (98%)	6 (2%)	0	100	100
1	C	251/285 (88%)	242 (96%)	9 (4%)	0	100	100
1	D	229/285 (80%)	219 (96%)	10 (4%)	0	100	100
1	E	246/285 (86%)	238 (97%)	8 (3%)	0	100	100
1	F	261/285 (92%)	252 (97%)	9 (3%)	0	100	100
All	All	1497/1710 (88%)	1448 (97%)	49 (3%)	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	211/250 (84%)	199 (94%)	12 (6%)	20	27
1	B	218/250 (87%)	200 (92%)	18 (8%)	11	14
1	C	203/250 (81%)	186 (92%)	17 (8%)	11	13
1	D	182/250 (73%)	172 (94%)	10 (6%)	21	29
1	E	195/250 (78%)	185 (95%)	10 (5%)	24	32
1	F	224/250 (90%)	211 (94%)	13 (6%)	20	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1233/1500 (82%)	1153 (94%)	80 (6%)	17	23

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	195	LYS
1	C	371	LYS
1	F	278	LYS
1	C	221	ARG
1	C	277	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	124	ASN
1	F	167	ASN
1	D	167	ASN
1	B	345	GLN
1	E	226	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 9 are monoatomic - leaving 13 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	E	1	-	29,33,33	1.86	6 (20%)	31,52,52	1.89	8 (25%)
4	GOL	F	399	-	5,5,5	0.35	0	5,5,5	0.20	0
2	ANP	A	1	-	29,33,33	1.95	8 (27%)	31,52,52	1.81	7 (22%)
4	GOL	A	398	-	5,5,5	0.36	0	5,5,5	0.30	0
4	GOL	B	398	-	5,5,5	0.37	0	5,5,5	0.34	0
2	ANP	D	1	-	29,33,33	1.88	7 (24%)	31,52,52	1.81	7 (22%)
2	ANP	F	398	-	29,33,33	1.97	7 (24%)	31,52,52	1.77	8 (25%)
2	ANP	B	1	5	29,33,33	1.90	6 (20%)	31,52,52	1.80	7 (22%)
4	GOL	D	397	-	5,5,5	0.37	0	5,5,5	0.27	0
4	GOL	E	397	-	5,5,5	0.35	0	5,5,5	0.32	0
4	GOL	D	398	-	5,5,5	0.35	0	5,5,5	0.18	0
4	GOL	A	400	-	5,5,5	0.28	0	5,5,5	0.29	0
2	ANP	C	1	-	29,33,33	1.90	6 (20%)	31,52,52	1.82	6 (19%)

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	E	1	-	1/1/7/8	7/14/38/38	0/3/3/3
4	GOL	F	399	-	-	0/4/4/4	-
2	ANP	A	1	-	1/1/7/8	10/14/38/38	0/3/3/3
4	GOL	A	398	-	-	4/4/4/4	-
4	GOL	B	398	-	-	0/4/4/4	-
2	ANP	D	1	-	1/1/7/8	8/14/38/38	0/3/3/3
2	ANP	F	398	-	1/1/7/8	4/14/38/38	0/3/3/3
2	ANP	B	1	5	1/1/7/8	8/14/38/38	0/3/3/3
4	GOL	D	397	-	-	2/4/4/4	-
4	GOL	E	397	-	-	4/4/4/4	-
4	GOL	D	398	-	-	2/4/4/4	-
4	GOL	A	400	-	-	2/4/4/4	-
2	ANP	C	1	-	1/1/7/8	9/14/38/38	0/3/3/3

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	ANP	PG-N3B	4.84	1.76	1.63
2	F	398	ANP	PG-N3B	4.82	1.76	1.63
2	C	1	ANP	PB-N3B	4.82	1.76	1.63
2	F	398	ANP	PB-N3B	4.80	1.75	1.63
2	D	1	ANP	PB-N3B	4.66	1.75	1.63

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	ANP	O1G-PG-N3B	-5.24	104.06	111.77
2	F	398	ANP	O1G-PG-N3B	-4.95	104.48	111.77
2	E	1	ANP	O2B-PB-O1B	4.77	119.93	109.92
2	E	1	ANP	O1G-PG-N3B	-4.74	104.79	111.77
2	C	1	ANP	O1G-PG-N3B	-4.63	104.95	111.77

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1	ANP	C4'
2	D	1	ANP	C4'
2	C	1	ANP	C4'
2	E	1	ANP	C4'
2	F	398	ANP	C4'

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	ANP	PB-N3B-PG-O1G
2	A	1	ANP	PA-O3A-PB-O1B
2	A	1	ANP	PA-O3A-PB-O2B
2	A	1	ANP	C5'-O5'-PA-O2A
2	A	1	ANP	C5'-O5'-PA-O3A

There are no ring outliers.

7 monomers are involved in 13 short contacts:

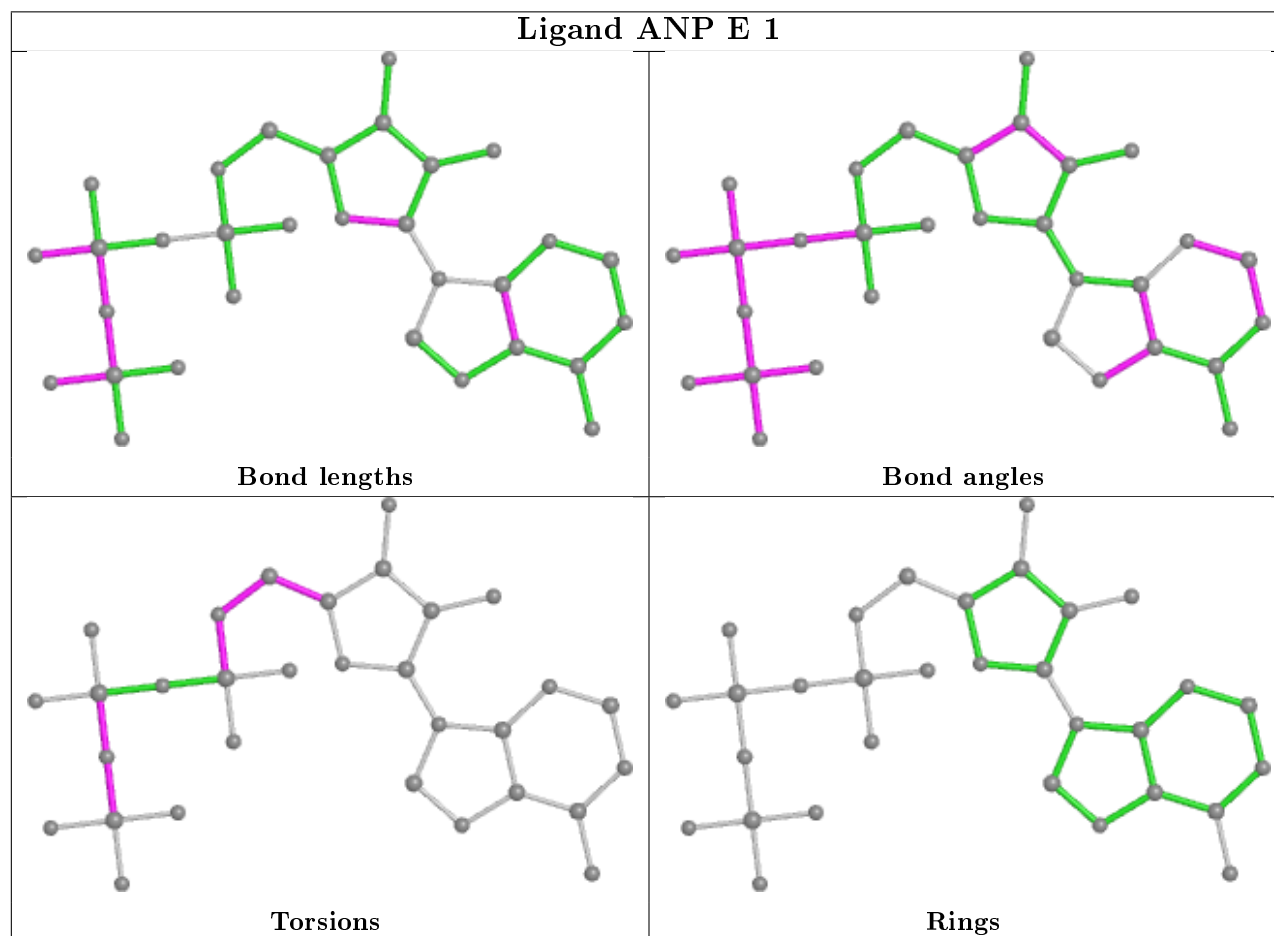
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	ANP	5	0
4	B	398	GOL	1	0
2	D	1	ANP	2	0
2	B	1	ANP	1	0

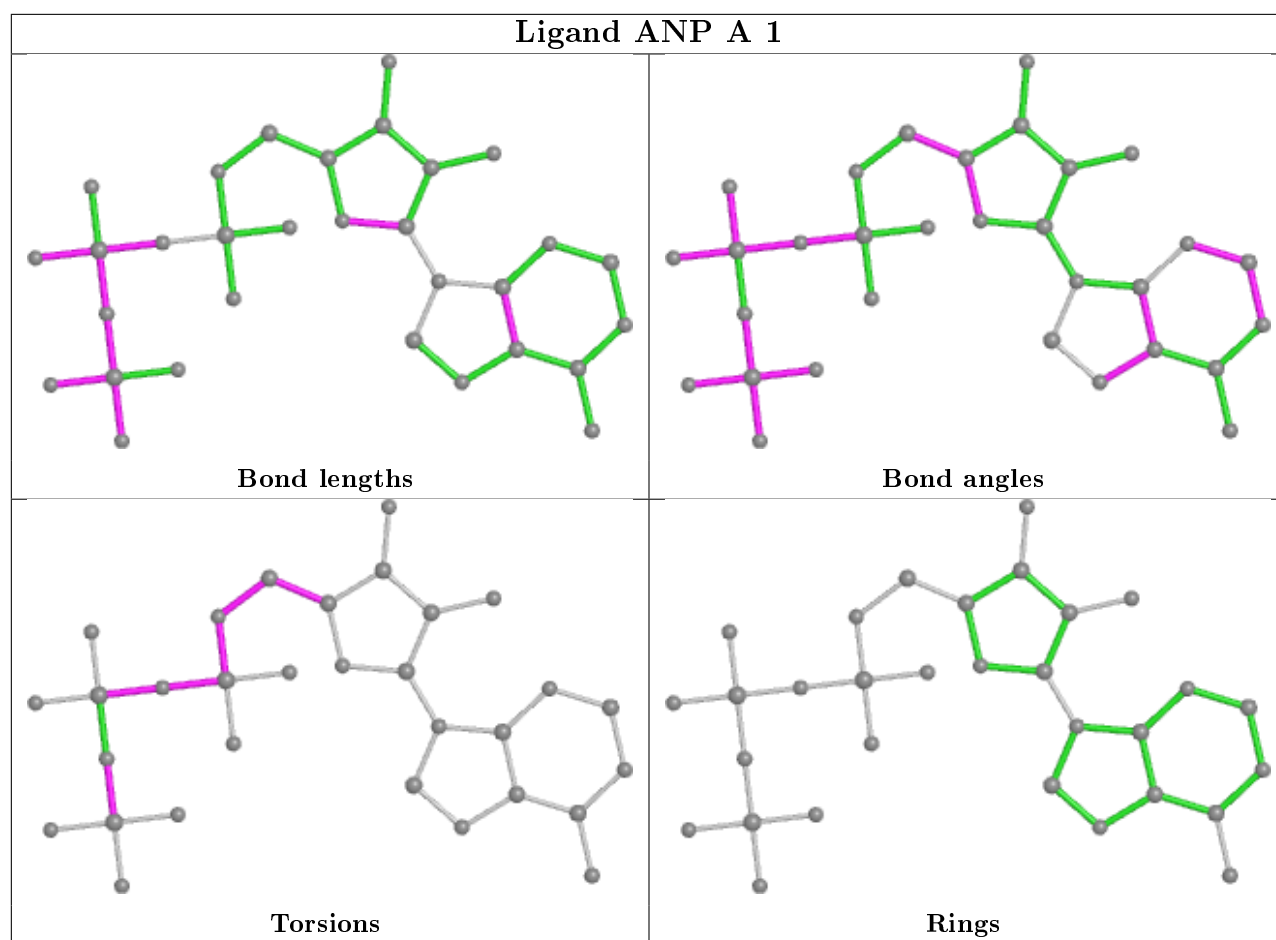
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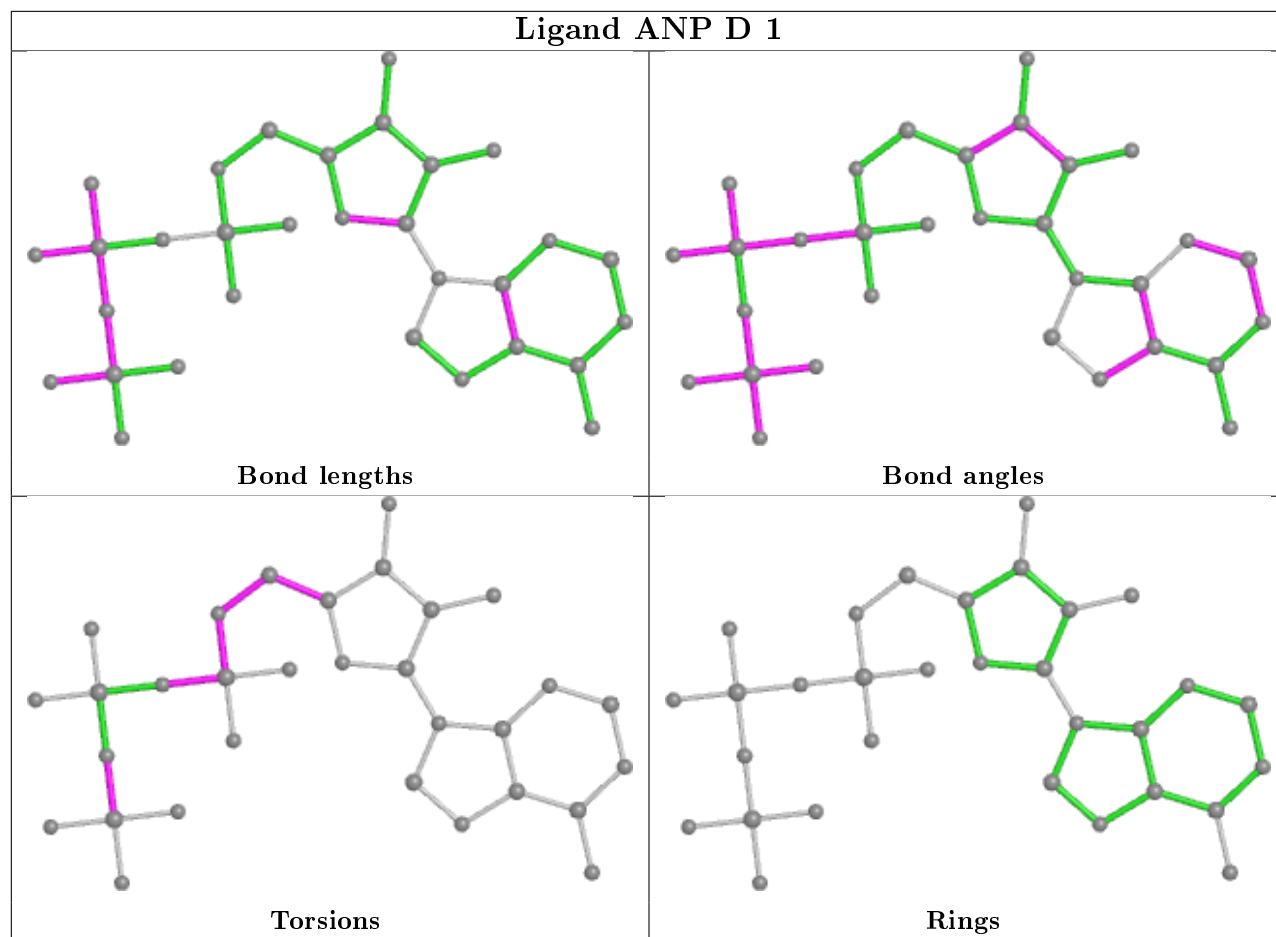
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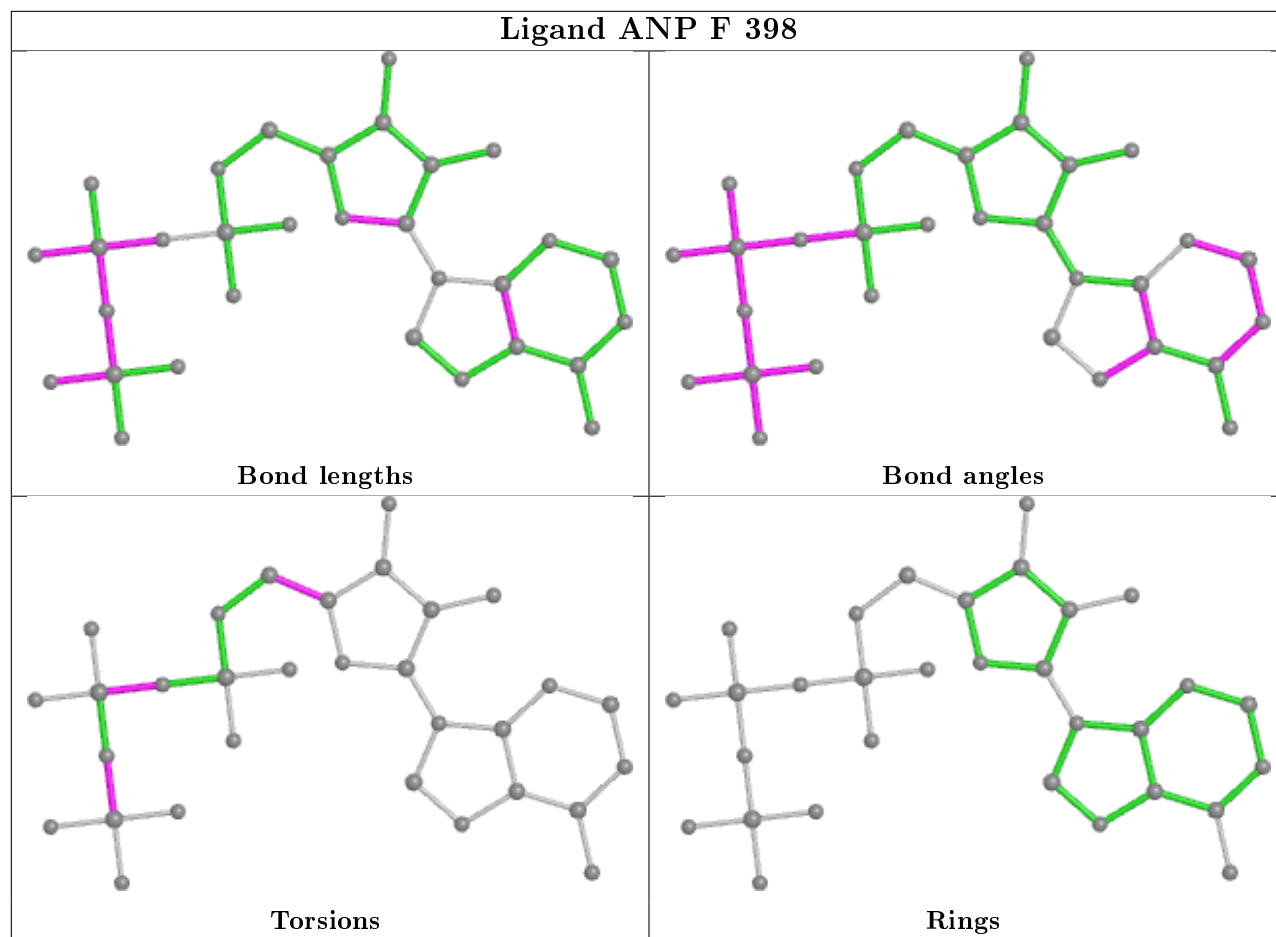
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	397	GOL	2	0
4	D	398	GOL	1	0
2	C	1	ANP	1	0

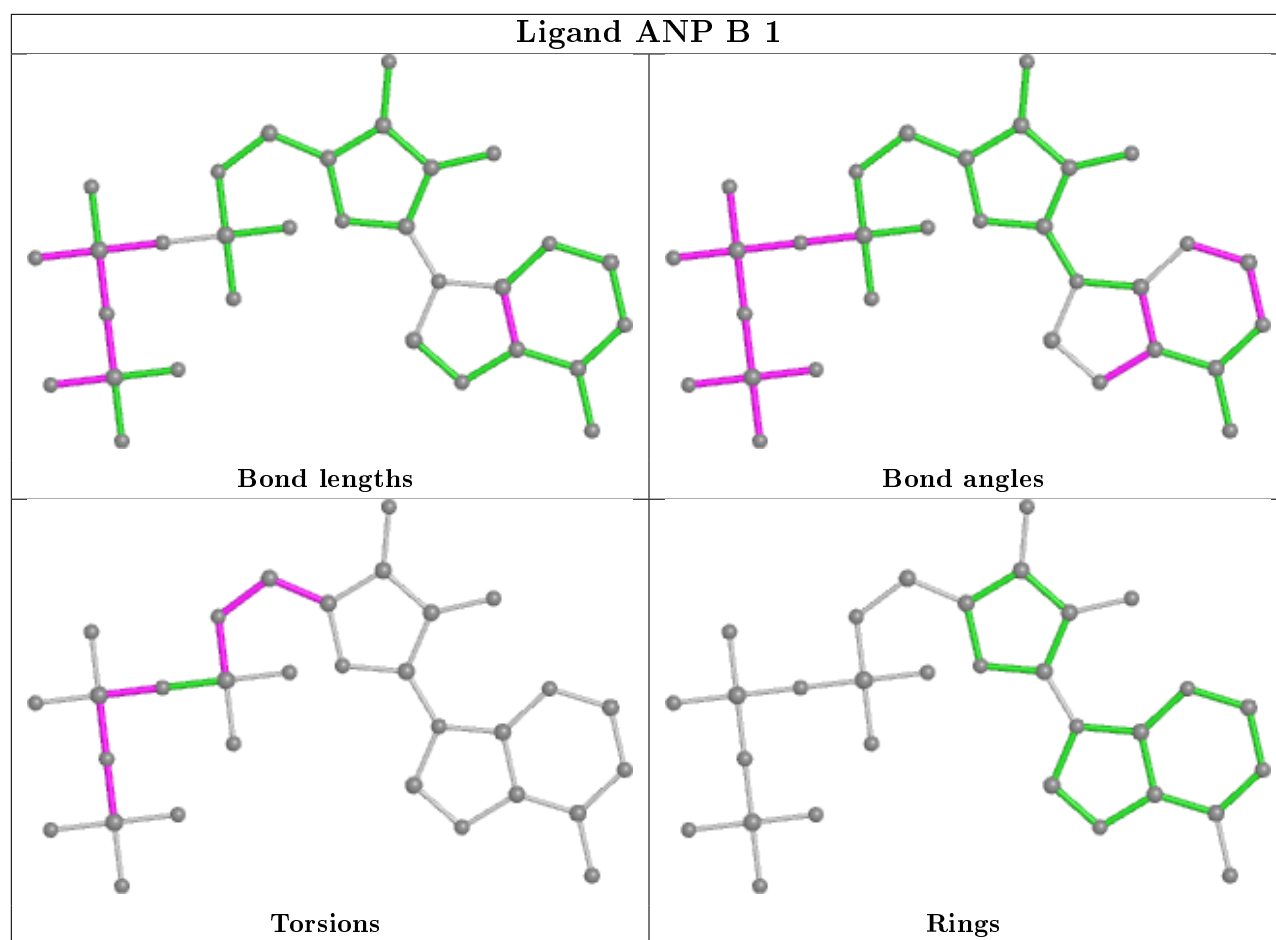
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

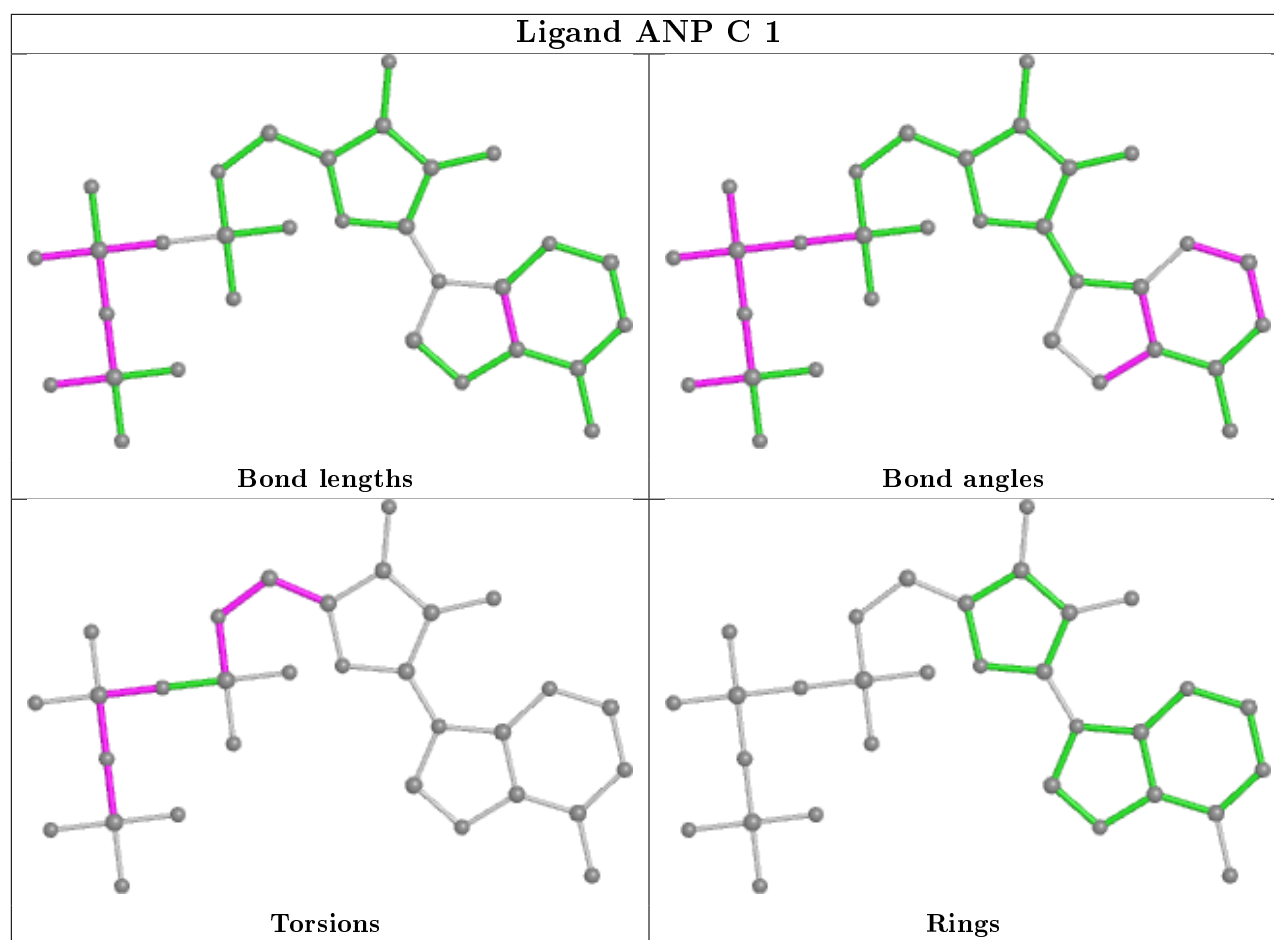












5.7 Other polymers [i](#)

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, 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	260/285 (91%)	-0.06	2 (0%) 86 89	12, 25, 38, 42	1 (0%)
1	B	260/285 (91%)	-0.06	2 (0%) 86 89	12, 25, 33, 37	1 (0%)
1	C	259/285 (90%)	0.11	6 (2%) 60 67	13, 26, 43, 45	1 (0%)
1	D	236/285 (82%)	0.24	12 (5%) 28 33	18, 34, 42, 51	2 (0%)
1	E	252/285 (88%)	-0.01	3 (1%) 79 84	4, 25, 39, 50	2 (0%)
1	F	266/285 (93%)	-0.07	0 100 100	13, 20, 26, 33	0
All	All	1533/1710 (89%)	0.02	25 (1%) 72 78	4, 25, 40, 51	7 (0%)

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	THR	3.5
1	A	146	PHE	3.4
1	C	129	GLY	3.2
1	D	392	TRP	3.2
1	D	338	GLY	3.1

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 ⓘ

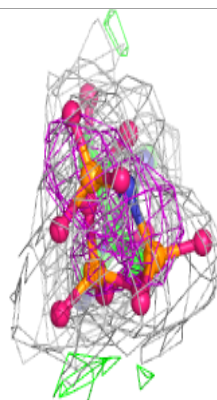
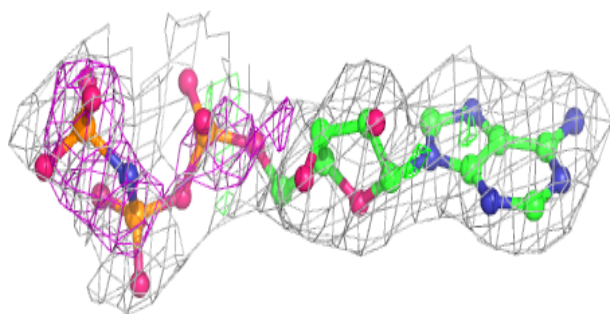
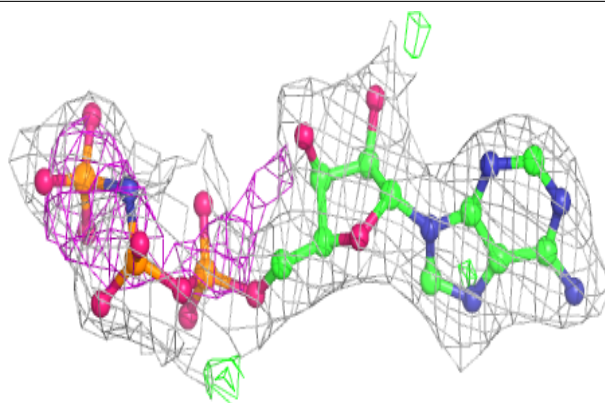
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	A	400	6/6	0.81	0.28	61,62,62,62	0
2	ANP	F	398	31/31	0.84	0.20	28,45,75,75	0
3	CA	C	397	1/1	0.87	0.19	94,94,94,94	0
5	MG	F	397	1/1	0.87	0.16	33,33,33,33	0
2	ANP	C	1	31/31	0.88	0.17	43,54,74,74	0
4	GOL	D	397	6/6	0.88	0.13	76,77,77,77	0
3	CA	F	1	1/1	0.88	0.20	68,68,68,68	0
5	MG	B	397	1/1	0.88	0.24	54,54,54,54	0
2	ANP	A	1	31/31	0.89	0.18	34,41,50,51	13
2	ANP	D	1	31/31	0.89	0.18	45,50,56,57	12
2	ANP	B	1	31/31	0.89	0.14	39,49,74,75	0
4	GOL	E	397	6/6	0.90	0.19	54,54,55,55	0
5	MG	C	398	1/1	0.90	0.41	61,61,61,61	0
5	MG	A	399	1/1	0.90	0.25	49,49,49,49	0
3	CA	A	397	1/1	0.92	0.14	93,93,93,93	0
4	GOL	A	398	6/6	0.92	0.17	51,51,51,51	0
4	GOL	B	398	6/6	0.93	0.18	52,53,54,55	0
2	ANP	E	1	31/31	0.93	0.17	32,38,45,45	13
5	MG	E	398	1/1	0.95	0.25	52,52,52,52	0
4	GOL	D	398	6/6	0.95	0.16	59,59,60,60	0
5	MG	D	399	1/1	0.96	0.20	40,40,40,40	0
4	GOL	F	399	6/6	0.96	0.16	53,54,55,55	0

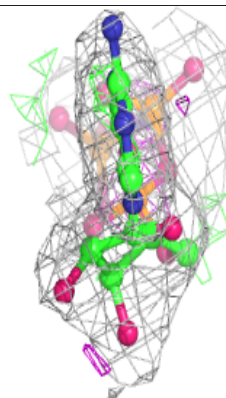
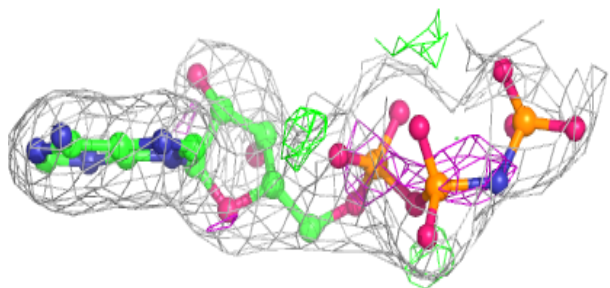
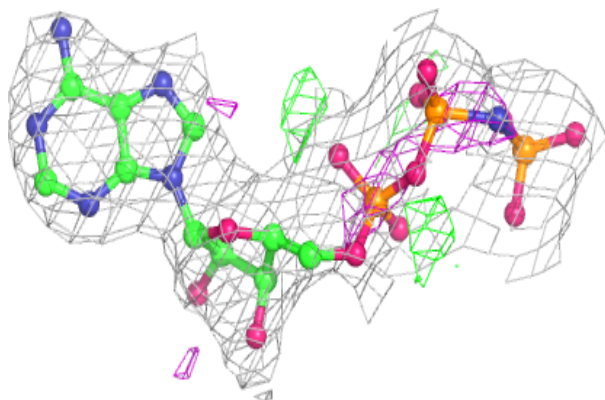
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ANP F 398:

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

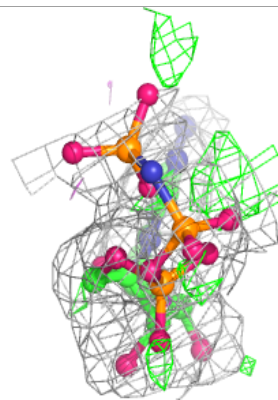
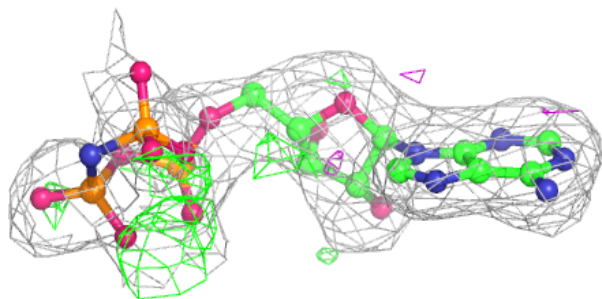
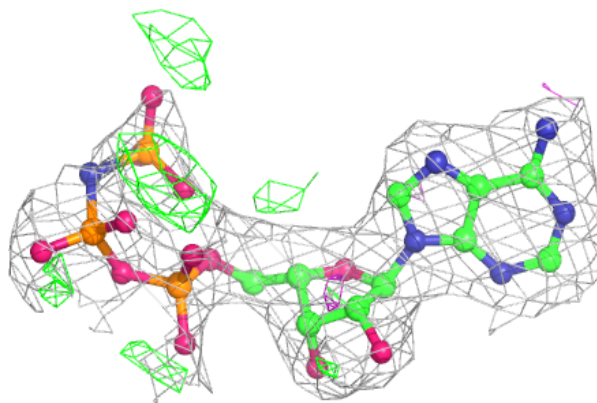
**Electron density around ANP C 1:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

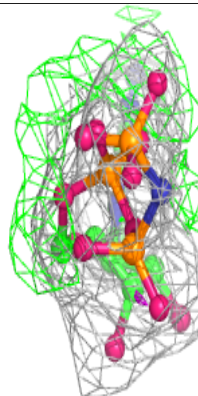
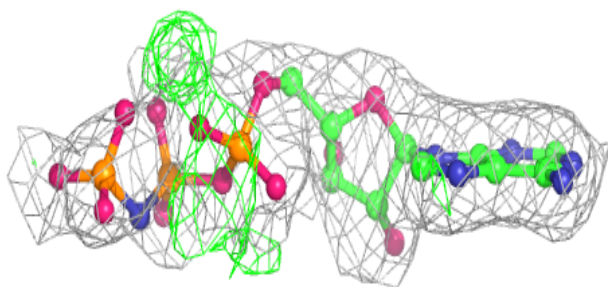
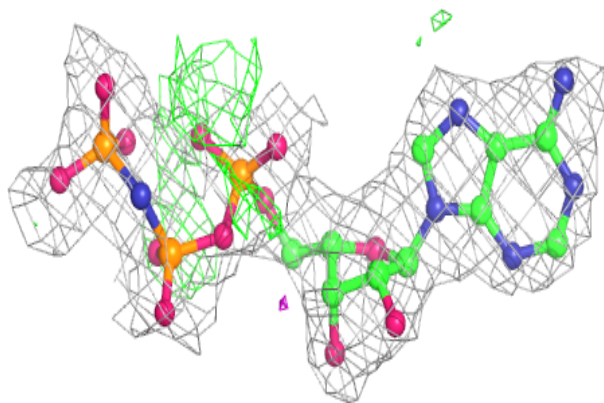


Electron density around ANP A 1:

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

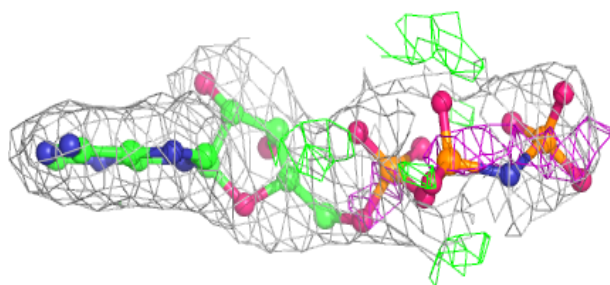
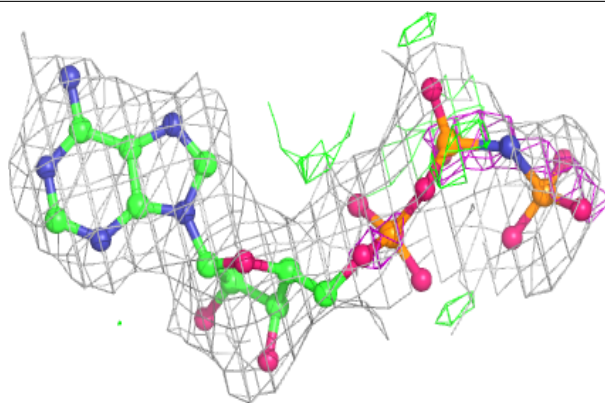
**Electron density around ANP D 1:**

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

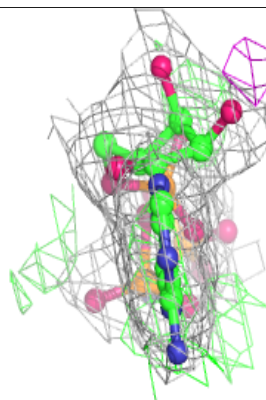
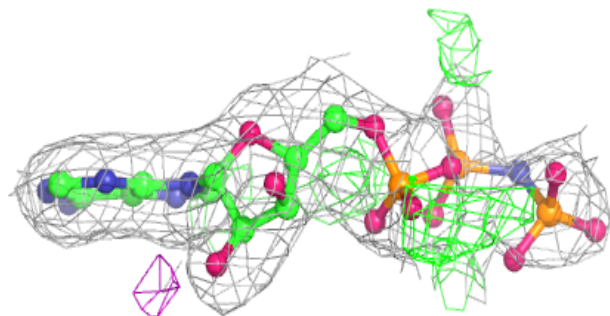
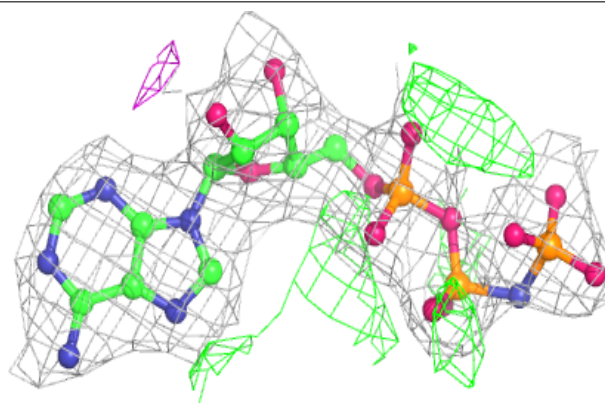


Electron density around ANP B 1:

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

**Electron density around ANP E 1:**

$2mF_o-DF_c$ (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.