Full wwPDB X-ray Structure Validation Report ⓘ

Sep 19, 2023 – 08:13 PM EDT

PDB ID	:	5IQA
Title	:	Aminoglycoside Phosphotransferase (2")-Ia (CTD of AAC(6')-Ie/APH(2'')-Ia) in complex with GMPPNP and Magnesium
Authors	:	Caldwell, S.J.; Berghuis, A.M.
Deposited on	:	2016-03-10
Resolution	:	2.15 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:

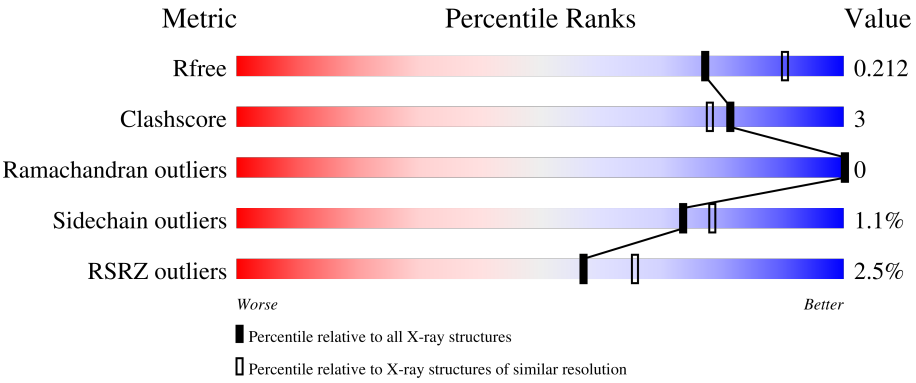
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	305	91% 6%
1	B	305	90% 7%
1	C	305	91% 7%
1	D	305	6% 90% 8%

2 Entry composition

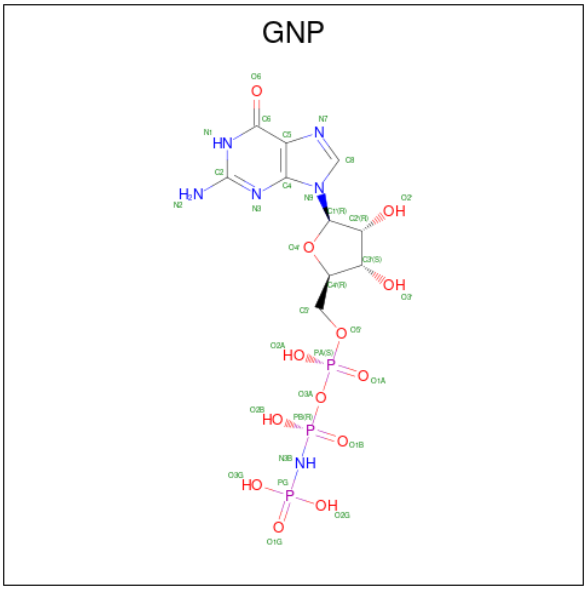
There are 5 unique types of molecules in this entry. The entry contains 10715 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Bifunctional AAC/APH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2446	1560	380	496	10			
1	B	299	Total	C	N	O	S	0	1	0
			2470	1575	384	501	10			
1	C	298	Total	C	N	O	S	0	1	0
			2453	1563	383	497	10			
1	D	299	Total	C	N	O	S	0	1	0
			2468	1573	383	502	10			

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
2	B	1	Total	C	N	O	P	0	1
			41	10	7	19	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
2	D	1	Total	C	N	O	P	0	1
			41	10	7	19	5		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		
3	D	2	Total	Mg	0	0
			2	2		

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

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

- Molecule 5 is water.

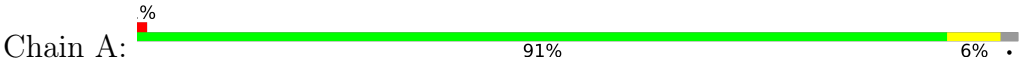
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	187	Total	O	0	0
			187	187		
5	B	229	Total	O	0	0
			229	229		
5	C	180	Total	O	0	0
			180	180		
5	D	125	Total	O	0	0
			125	125		

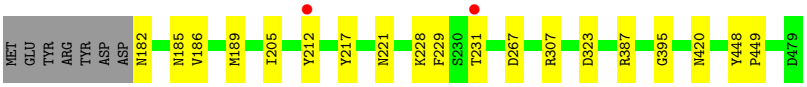
3 Residue-property plots (i)

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: Bifunctional AAC/APH

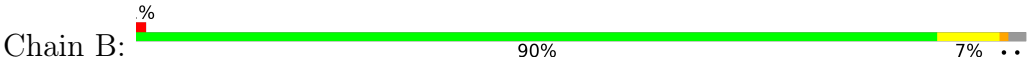
Chain A:

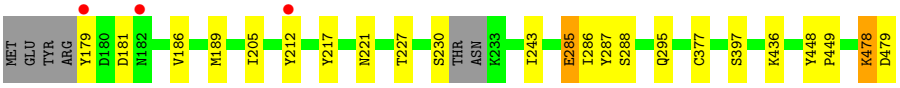




• Molecule 1: Bifunctional AAC/APH

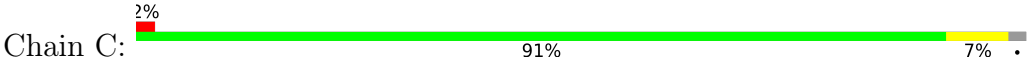
Chain B:

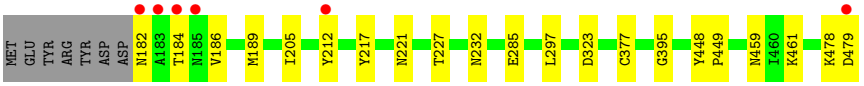




• Molecule 1: Bifunctional AAC/APH

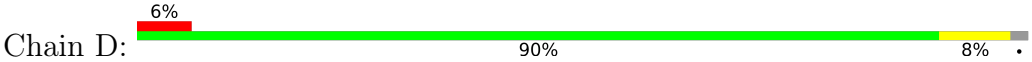
Chain C:

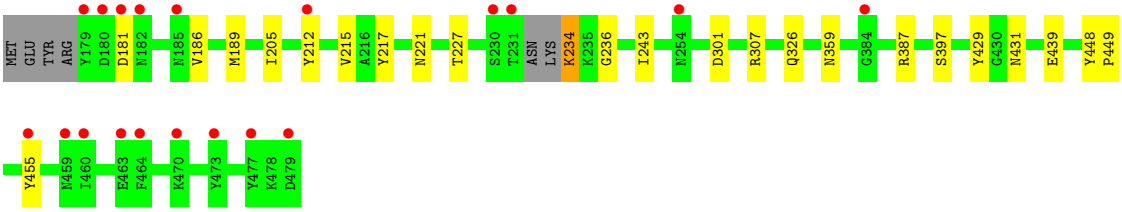




• Molecule 1: Bifunctional AAC/APH

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	90.17Å 100.32Å 94.06Å 90.00° 105.00° 90.00°	Depositor
Resolution (Å)	56.04 – 2.15 56.04 – 2.15	Depositor EDS
% Data completeness (in resolution range)	94.3 (56.04-2.15) 94.3 (56.04-2.15)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.30 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.167 , 0.206 0.174 , 0.212	Depositor DCC
R_{free} test set	4160 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	41.4	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 39.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.017 for l,-k,h	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	10715	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.91% 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: GNP, CL, 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	0.86	0/2490	0.82	2/3359 (0.1%)
1	B	0.86	1/2517 (0.0%)	0.81	0/3393
1	C	0.84	1/2500 (0.0%)	0.82	1/3373 (0.0%)
1	D	0.73	0/2515	0.77	0/3392
All	All	0.83	2/10022 (0.0%)	0.81	3/13517 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	377	CYS	CB-SG	-5.64	1.72	1.81
1	B	377	CYS	CB-SG	-5.03	1.73	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	387	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	C	323	ASP	CB-CG-OD1	5.08	122.87	118.30
1	A	323	ASP	CB-CG-OD1	5.06	122.86	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	234	LYS	Peptide

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	2446	0	2347	10	0
1	B	2470	0	2367	12	1
1	C	2453	0	2353	14	0
1	D	2468	0	2361	18	0
2	A	32	0	13	0	0
2	B	41	0	2	2	0
2	C	32	0	13	0	0
2	D	41	0	2	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	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
5	A	187	0	0	2	0
5	B	229	0	0	3	0
5	C	180	0	0	1	1
5	D	125	0	0	3	0
All	All	10715	0	9458	51	1

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 (51) 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:B:500[A]:GNP:O3G	5:B:924:HOH:O	1.80	0.97
1:D:359:ASN:OD1	5:D:1050:HOH:O	2.12	0.68
1:C:184:THR:HG21	1:D:215:VAL:HG21	1.74	0.67
1:A:228:LYS:HE2	1:A:231:THR:HG21	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:THR:CG2	1:D:215:VAL:HG21	2.31	0.61
1:B:285:GLU:HG3	1:B:286:ILE:N	2.14	0.60
2:B:500[A]:GNP:O1B	5:B:909:HOH:O	2.17	0.59
1:C:478:LYS:O	1:C:479:ASP:HB2	2.04	0.57
1:D:212:TYR:HB3	1:D:455:TYR:OH	2.07	0.54
1:C:186:VAL:HG13	1:C:205:ILE:HG23	1.90	0.53
1:C:212:TYR:HE2	1:C:461:LYS:HZ3	1.57	0.53
1:D:186:VAL:HG13	1:D:205:ILE:HG23	1.91	0.53
1:B:189:MET:HG2	1:B:217:TYR:CE1	2.44	0.52
1:C:189:MET:HG2	1:C:217:TYR:CE1	2.45	0.52
1:D:189:MET:HG2	1:D:217:TYR:CE1	2.45	0.52
1:B:436:LYS:NZ	5:B:1113:HOH:O	2.44	0.51
1:D:326:GLN:NE2	5:D:1013:HOH:O	2.43	0.51
1:A:182:ASN:HA	1:B:181:ASP:OD1	2.13	0.49
1:A:186:VAL:HG13	1:A:205:ILE:HG23	1.94	0.48
1:B:186:VAL:HG13	1:B:205:ILE:HG23	1.96	0.48
1:D:301:ASP:OD1	1:D:387:ARG:NH2	2.38	0.46
1:B:448:TYR:HB3	1:B:449:PRO:HD3	1.98	0.46
1:A:189:MET:HG2	1:A:217:TYR:CE1	2.50	0.46
1:A:395:GLY:HA3	5:A:903:HOH:O	2.15	0.46
1:A:420:ASN:HB2	5:A:1201:HOH:O	2.16	0.46
1:B:243:ILE:HD13	1:B:397:SER:HB2	1.98	0.46
1:C:186:VAL:CG1	1:C:205:ILE:HG23	2.45	0.46
1:D:307[B]:ARG:NH1	1:D:431:ASN:HB2	2.31	0.46
1:A:229:PHE:O	1:A:231:THR:HG23	2.17	0.45
1:B:189:MET:SD	1:B:227:THR:HG21	2.57	0.45
1:C:478:LYS:O	1:C:479:ASP:CB	2.63	0.44
1:C:232:ASN:HB2	1:C:459:ASN:OD1	2.18	0.44
1:D:189:MET:SD	1:D:227:THR:HG21	2.58	0.44
1:C:297:LEU:HA	1:C:297:LEU:HD12	1.86	0.43
1:D:234:LYS:C	1:D:236:GLY:H	2.21	0.43
1:B:287:TYR:CE1	1:B:295:GLN:HG2	2.53	0.43
1:D:448:TYR:HB3	1:D:449:PRO:HD3	1.99	0.43
1:D:307[B]:ARG:HG2	1:D:429:TYR:CD2	2.54	0.43
1:A:186:VAL:CG1	1:A:205:ILE:HG23	2.48	0.42
1:D:307[B]:ARG:HG2	1:D:429:TYR:CE2	2.54	0.42
1:A:185:ASN:ND2	1:B:179:TYR:OH	2.52	0.42
1:D:186:VAL:CG1	1:D:205:ILE:HG23	2.48	0.42
1:D:243:ILE:HD13	1:D:397:SER:HB2	2.02	0.42
1:D:439:GLU:OE1	5:D:1209:HOH:O	2.21	0.42
1:C:448:TYR:HB3	1:C:449:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:TYR:HB3	1:A:449:PRO:HD3	2.02	0.41
1:C:182:ASN:HA	1:D:181:ASP:OD1	2.19	0.41
1:C:395:GLY:HA3	5:C:903:HOH:O	2.19	0.41
1:B:186:VAL:CG1	1:B:205:ILE:HG23	2.50	0.41
1:B:478:LYS:HG3	1:B:479:ASP:N	2.36	0.40
1:C:189:MET:SD	1:C:227:THR:HG21	2.62	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:SER:O	5:C:1219:HOH:O[2_646]	2.05	0.15

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	296/305 (97%)	289 (98%)	7 (2%)	0	100	100
1	B	296/305 (97%)	284 (96%)	12 (4%)	0	100	100
1	C	297/305 (97%)	287 (97%)	10 (3%)	0	100	100
1	D	296/305 (97%)	284 (96%)	12 (4%)	0	100	100
All	All	1185/1220 (97%)	1144 (96%)	41 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	270/281 (96%)	266 (98%)	4 (2%)	65	69
1	B	273/281 (97%)	268 (98%)	5 (2%)	59	63
1	C	271/281 (96%)	269 (99%)	2 (1%)	84	89
1	D	273/281 (97%)	272 (100%)	1 (0%)	91	93
All	All	1087/1124 (97%)	1075 (99%)	12 (1%)	73	78

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	212	TYR
1	A	221	ASN
1	A	267	ASP
1	A	307	ARG
1	B	212	TYR
1	B	221	ASN
1	B	230	SER
1	B	285	GLU
1	B	478	LYS
1	C	221	ASN
1	C	285	GLU
1	D	221	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	ASN
1	A	341	ASN
1	A	385	ASN
1	A	467	ASN
1	B	185	ASN
1	B	467	ASN
1	C	327	ASN
1	C	341	ASN
1	D	295	GLN
1	D	296	ASN
1	D	326	GLN
1	D	420	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 17 ligands modelled in this entry, 11 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	GNP	B	500[A]	3	29,34,34	1.26	3 (10%)	33,54,54	2.06	6 (18%)
2	GNP	B	500[B]	3	29,34,34	1.11	3 (10%)	33,54,54	2.23	8 (24%)
2	GNP	D	500[A]	3	29,34,34	0.92	1 (3%)	33,54,54	2.12	6 (18%)
2	GNP	A	500	3	29,34,34	1.19	3 (10%)	33,54,54	2.13	9 (27%)
2	GNP	D	500[B]	3	29,34,34	0.94	2 (6%)	33,54,54	2.08	5 (15%)
2	GNP	C	500	3	29,34,34	1.43	3 (10%)	33,54,54	2.08	6 (18%)

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	GNP	B	500[A]	3	-	4/14/38/38	0/3/3/3
2	GNP	B	500[B]	3	-	2/14/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GNP	D	500[A]	3	-	2/14/38/38	0/3/3/3
2	GNP	A	500	3	-	2/14/38/38	0/3/3/3
2	GNP	D	500[B]	3	-	2/14/38/38	0/3/3/3
2	GNP	C	500	3	-	3/14/38/38	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	500	GNP	PB-O3A	-4.90	1.52	1.59
2	B	500[A]	GNP	PB-O3A	4.43	1.64	1.59
2	A	500	GNP	C6-N1	3.27	1.38	1.33
2	B	500[B]	GNP	PB-O3A	-3.18	1.55	1.59
2	B	500[A]	GNP	C6-N1	3.09	1.38	1.33
2	B	500[B]	GNP	C6-N1	3.09	1.38	1.33
2	C	500	GNP	C6-N1	3.06	1.38	1.33
2	C	500	GNP	C5-C6	2.80	1.46	1.41
2	D	500[A]	GNP	C6-N1	2.80	1.37	1.33
2	D	500[B]	GNP	C6-N1	2.80	1.37	1.33
2	A	500	GNP	PG-O2G	2.45	1.63	1.56
2	A	500	GNP	PG-O3G	2.32	1.63	1.56
2	D	500[B]	GNP	PB-O3A	-2.24	1.56	1.59
2	B	500[A]	GNP	PA-O2A	-2.08	1.45	1.55
2	B	500[B]	GNP	PA-O2A	-2.08	1.45	1.55

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	500[A]	GNP	C5-C6-N1	-8.51	111.79	123.43
2	D	500[B]	GNP	C5-C6-N1	-8.51	111.79	123.43
2	C	500	GNP	C5-C6-N1	-8.18	112.24	123.43
2	B	500[A]	GNP	C5-C6-N1	-7.78	112.79	123.43
2	B	500[B]	GNP	C5-C6-N1	-7.78	112.79	123.43
2	A	500	GNP	C5-C6-N1	-7.48	113.19	123.43
2	D	500[A]	GNP	C2-N1-C6	5.89	125.28	115.93
2	D	500[B]	GNP	C2-N1-C6	5.89	125.28	115.93
2	B	500[A]	GNP	C2-N1-C6	5.63	124.88	115.93
2	B	500[B]	GNP	C2-N1-C6	5.63	124.88	115.93
2	C	500	GNP	C2-N1-C6	5.51	124.69	115.93
2	A	500	GNP	C2-N1-C6	5.33	124.40	115.93
2	A	500	GNP	O1G-PG-N3B	-3.89	106.04	111.77
2	B	500[B]	GNP	O3G-PG-O1G	-3.27	105.24	113.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	500	GNP	N3-C2-N1	-3.03	123.18	127.22
2	A	500	GNP	O2'-C2'-C1'	-2.87	100.26	110.85
2	B	500[A]	GNP	C4-C5-C6	-2.87	118.06	120.80
2	B	500[B]	GNP	C4-C5-C6	-2.87	118.06	120.80
2	C	500	GNP	C4-C5-C6	-2.83	118.10	120.80
2	B	500[B]	GNP	O1G-PG-N3B	2.80	115.89	111.77
2	A	500	GNP	C4-C5-C6	-2.70	118.22	120.80
2	B	500[B]	GNP	O1B-PB-N3B	2.68	115.72	111.77
2	D	500[A]	GNP	N3-C2-N1	-2.66	123.67	127.22
2	D	500[B]	GNP	N3-C2-N1	-2.66	123.67	127.22
2	D	500[A]	GNP	C2-N3-C4	-2.64	112.34	115.36
2	D	500[B]	GNP	C2-N3-C4	-2.64	112.34	115.36
2	B	500[A]	GNP	C2-N3-C4	-2.61	112.37	115.36
2	B	500[B]	GNP	C2-N3-C4	-2.61	112.37	115.36
2	B	500[A]	GNP	N3-C2-N1	-2.51	123.88	127.22
2	B	500[B]	GNP	N3-C2-N1	-2.51	123.88	127.22
2	C	500	GNP	N3-C2-N1	-2.50	123.88	127.22
2	C	500	GNP	O5'-PA-O1A	2.48	118.74	109.07
2	A	500	GNP	O3'-C3'-C2'	-2.35	104.22	111.82
2	D	500[A]	GNP	C4-C5-C6	-2.25	118.65	120.80
2	D	500[B]	GNP	C4-C5-C6	-2.25	118.65	120.80
2	A	500	GNP	C2-N3-C4	-2.19	112.86	115.36
2	D	500[A]	GNP	O2G-PG-O1G	-2.18	107.98	113.45
2	B	500[A]	GNP	O2G-PG-O1G	-2.15	108.05	113.45
2	C	500	GNP	C2-N3-C4	-2.12	112.94	115.36
2	A	500	GNP	O3G-PG-O1G	2.06	118.64	113.45

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	GNP	PB-N3B-PG-O1G
2	B	500[A]	GNP	PG-N3B-PB-O1B
2	B	500[A]	GNP	PA-O3A-PB-O1B
2	B	500[B]	GNP	PB-N3B-PG-O1G
2	C	500	GNP	PB-N3B-PG-O1G
2	D	500[A]	GNP	PB-N3B-PG-O1G
2	D	500[A]	GNP	PG-N3B-PB-O1B
2	D	500[B]	GNP	PB-N3B-PG-O1G
2	A	500	GNP	PG-N3B-PB-O3A
2	B	500[A]	GNP	C5'-O5'-PA-O1A
2	B	500[B]	GNP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
2	C	500	GNP	C5'-O5'-PA-O1A
2	B	500[A]	GNP	PB-N3B-PG-O1G
2	C	500	GNP	PG-N3B-PB-O3A
2	D	500[B]	GNP	PG-N3B-PB-O3A

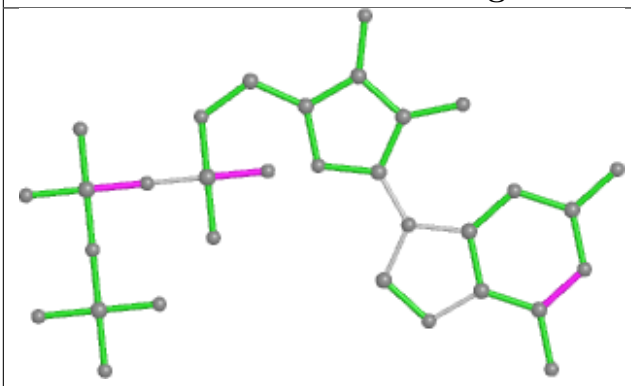
There are no ring outliers.

1 monomer is involved in 2 short contacts:

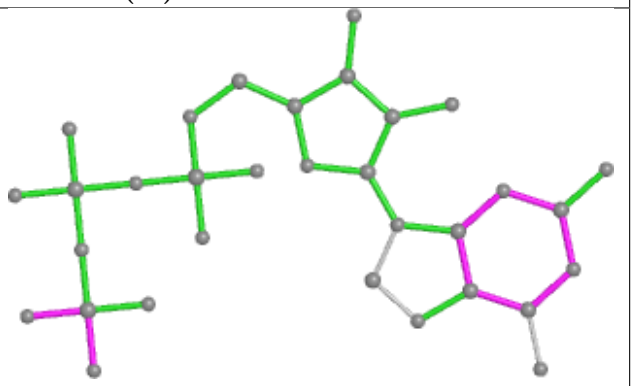
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	500[A]	GNP	2	0

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.

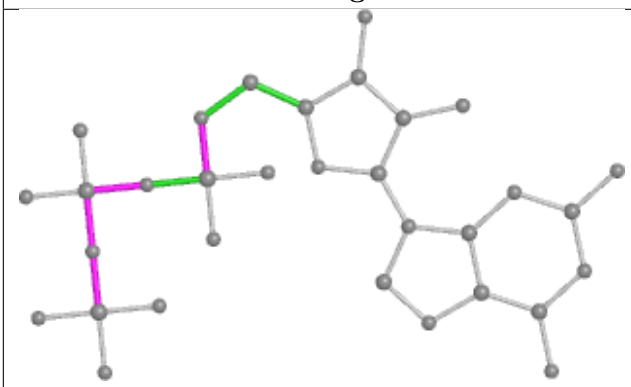
Ligand GNP B 500 (A)



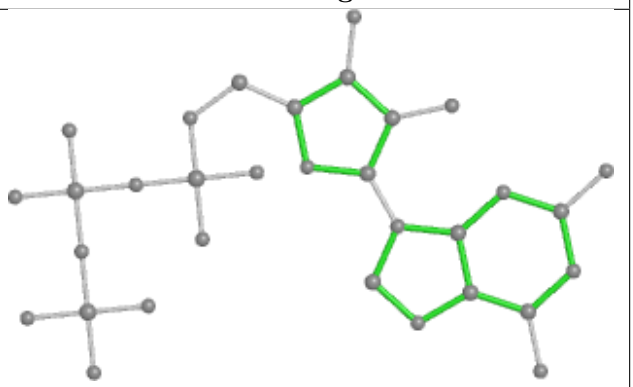
Bond lengths



Bond angles

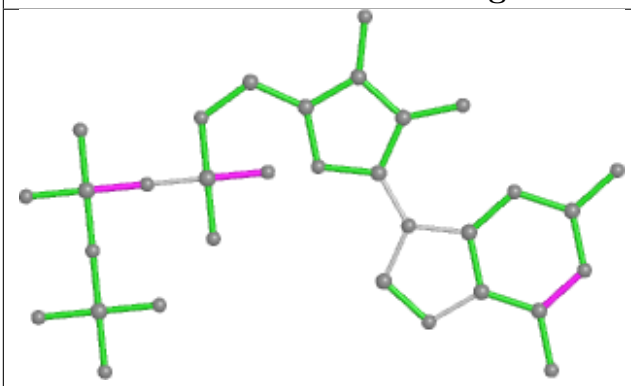


Torsions

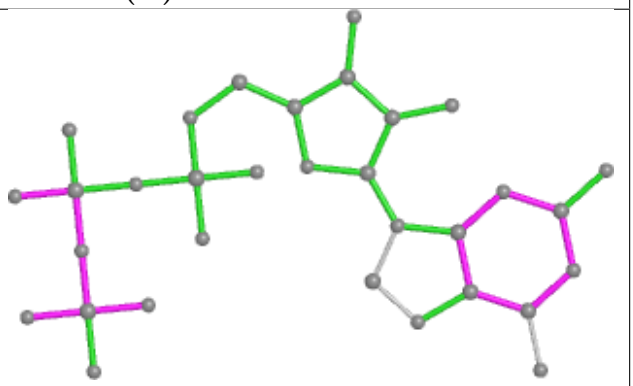


Rings

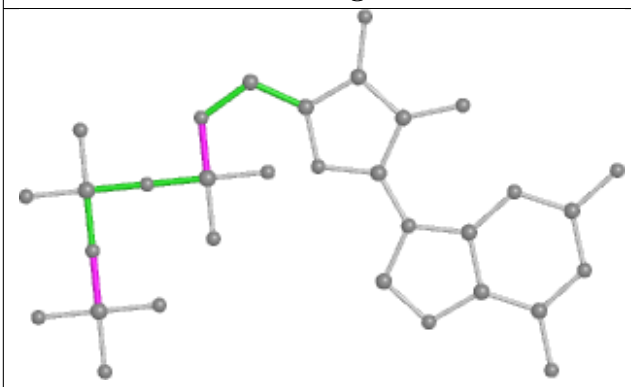
Ligand GNP B 500 (B)



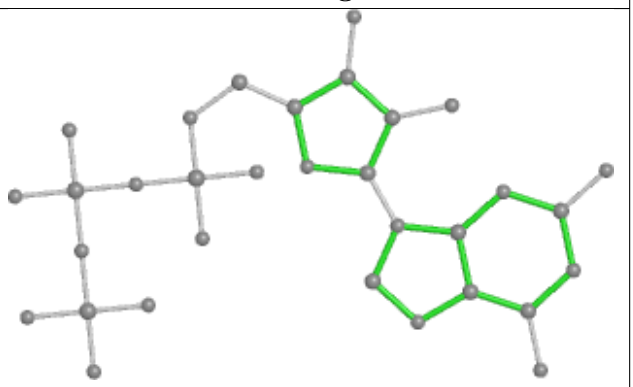
Bond lengths



Bond angles

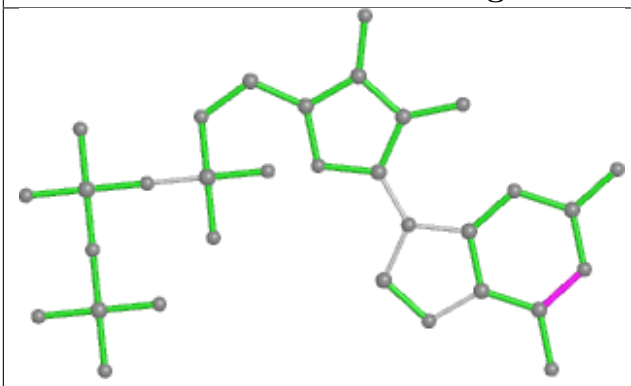


Torsions

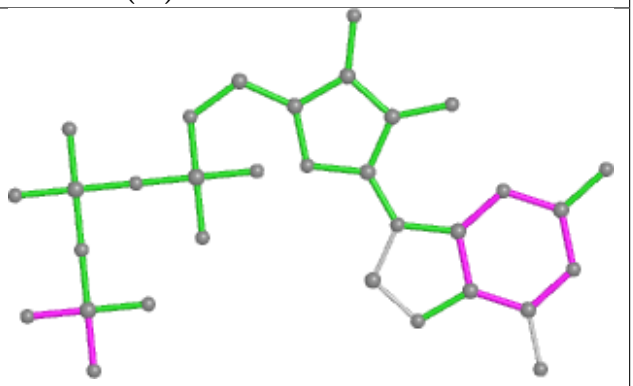


Rings

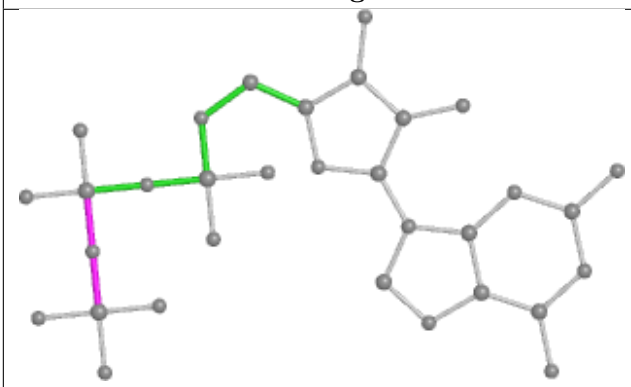
Ligand GNP D 500 (A)



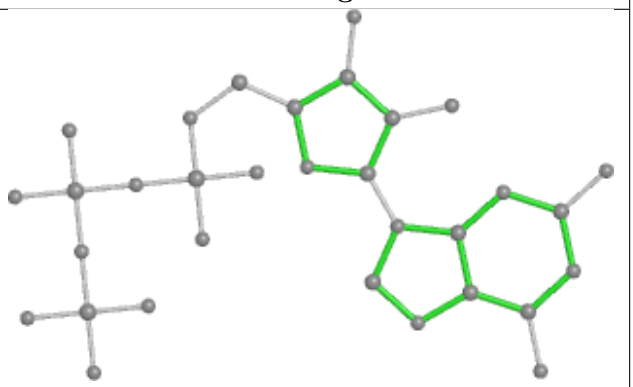
Bond lengths



Bond angles

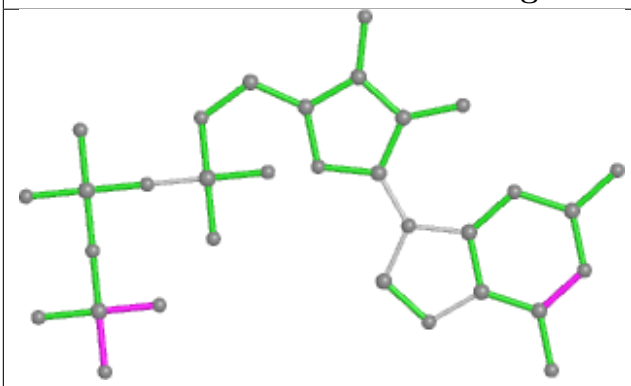


Torsions

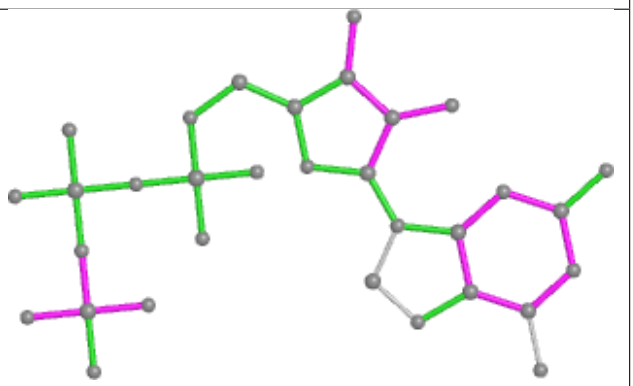


Rings

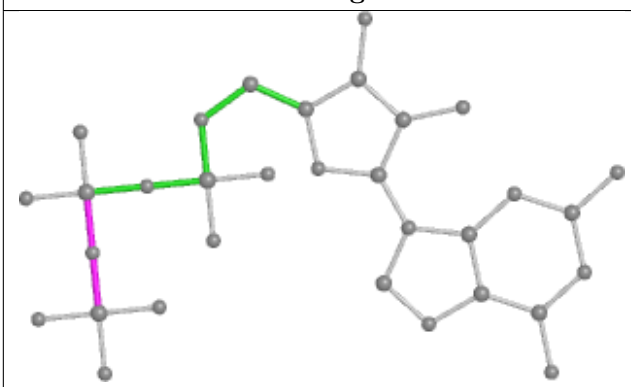
Ligand GNP A 500



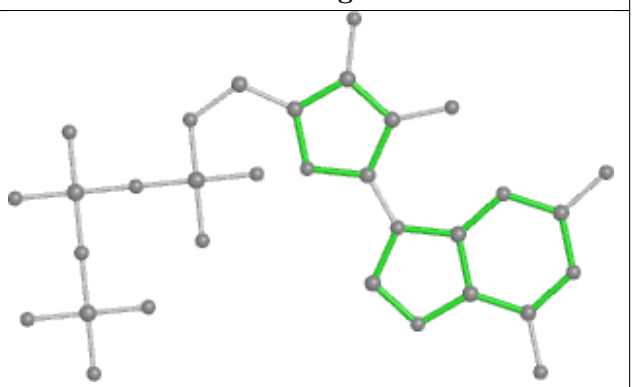
Bond lengths



Bond angles

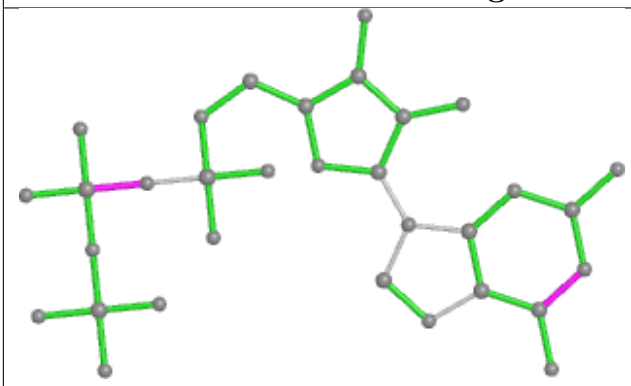


Torsions

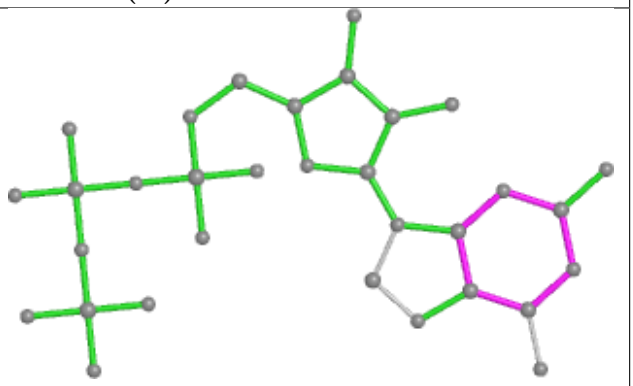


Rings

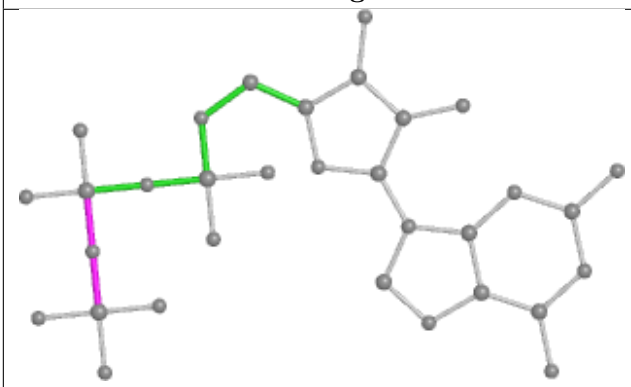
Ligand GNP D 500 (B)



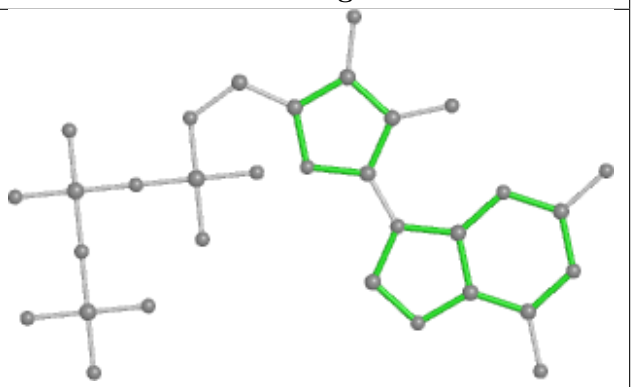
Bond lengths



Bond angles

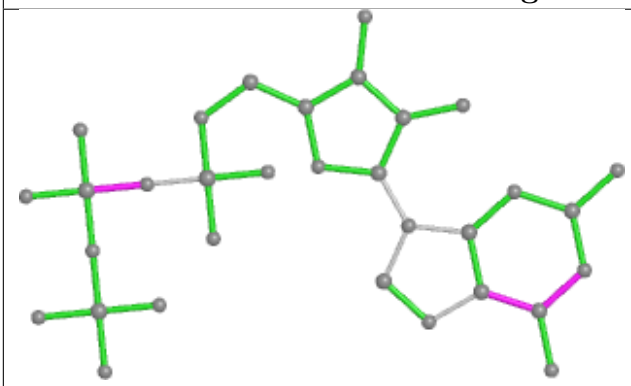


Torsions

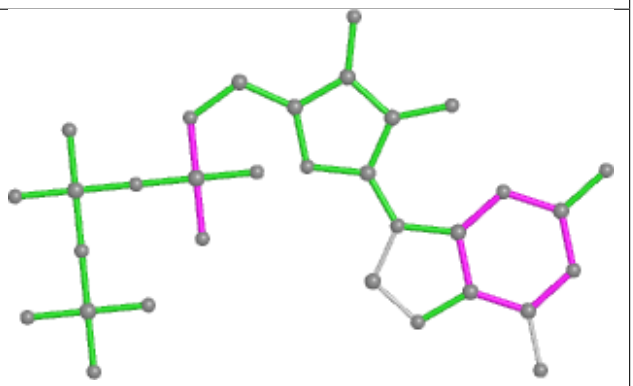


Rings

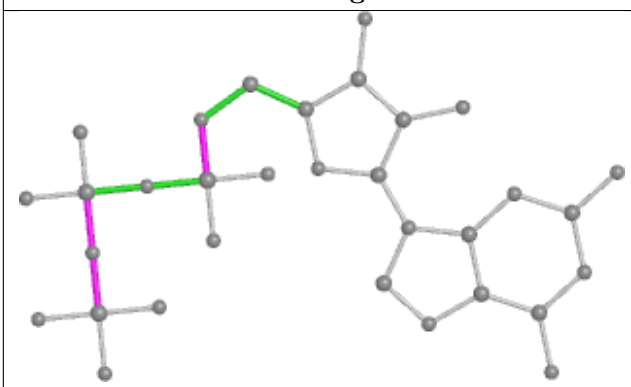
Ligand GNP C 500



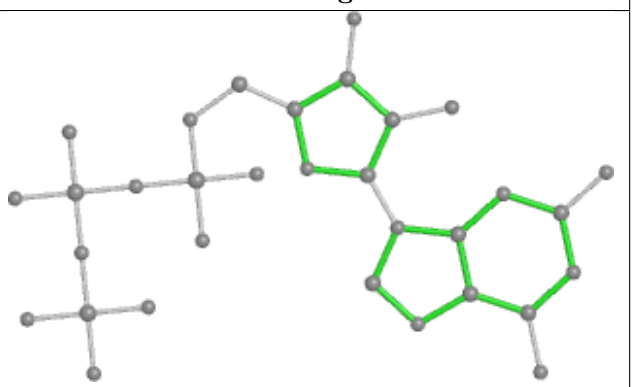
Bond lengths



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

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^{th} 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	298/305 (97%)	-0.14	2 (0%)	87	91	26, 44, 73, 109	0
1	B	299/305 (98%)	-0.16	3 (1%)	82	86	28, 43, 75, 117	0
1	C	298/305 (97%)	-0.09	6 (2%)	65	72	25, 46, 82, 131	0
1	D	299/305 (98%)	0.22	19 (6%)	19	26	38, 56, 109, 142	0
All	All	1194/1220 (97%)	-0.04	30 (2%)	57	65	25, 47, 86, 142	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	179	TYR	9.4
1	D	473	TYR	5.8
1	D	212	TYR	5.5
1	D	479	ASP	4.9
1	D	231	THR	4.9
1	D	180	ASP	4.7
1	D	477	TYR	4.4
1	D	464	PHE	4.2
1	C	184	THR	4.0
1	B	179	TYR	3.9
1	C	182	ASN	3.9
1	A	231	THR	3.8
1	C	183	ALA	3.7
1	B	182	ASN	3.5
1	A	212	TYR	3.5
1	D	181	ASP	3.5
1	D	470	LYS	3.2
1	C	185	ASN	3.0
1	C	479	ASP	2.9
1	D	182	ASN	2.9
1	D	185	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	460	ILE	2.7
1	D	455	TYR	2.6
1	D	254	ASN	2.4
1	D	463	GLU	2.3
1	D	230	SER	2.3
1	D	459	ASN	2.2
1	B	212	TYR	2.1
1	C	212	TYR	2.1
1	D	384	GLY	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, 95^{th} 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	D	702	1/1	0.94	0.09	57,57,57,57	0
3	MG	B	700	1/1	0.95	0.06	39,39,39,39	0
3	MG	D	700	1/1	0.96	0.05	45,45,45,45	0
3	MG	B	702	1/1	0.96	0.04	48,48,48,48	0
4	CL	C	802	1/1	0.96	0.06	60,60,60,60	0
4	CL	A	802	1/1	0.97	0.14	65,65,65,65	0
3	MG	C	700	1/1	0.97	0.08	36,36,36,36	0
2	GNP	A	500	32/32	0.98	0.11	31,34,43,46	0
2	GNP	B	500[A]	32/32	0.98	0.11	36,38,41,44	9
2	GNP	B	500[B]	32/32	0.98	0.11	36,40,44,45	9
2	GNP	D	500[A]	32/32	0.98	0.10	41,47,54,57	9
2	GNP	D	500[B]	32/32	0.98	0.10	41,47,56,59	9
3	MG	A	700	1/1	0.98	0.13	33,33,33,33	0
3	MG	A	702	1/1	0.98	0.06	37,37,37,37	0

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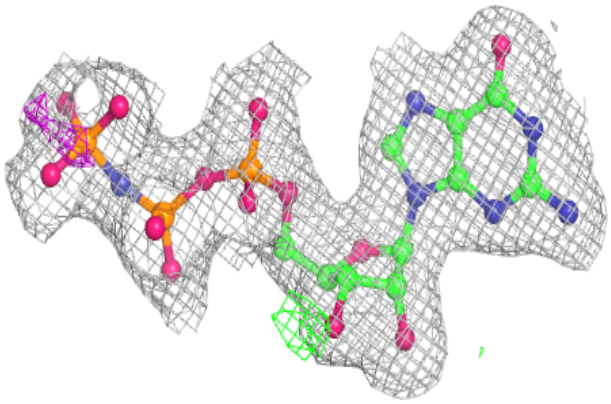
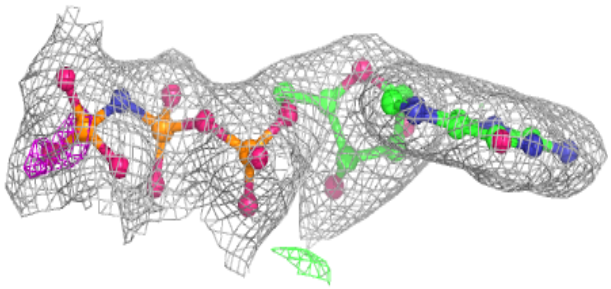
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GNP	C	500	32/32	0.99	0.09	33,41,45,45	0
4	CL	B	802	1/1	0.99	0.08	71,71,71,71	0
3	MG	C	702	1/1	0.99	0.06	38,38,38,38	0

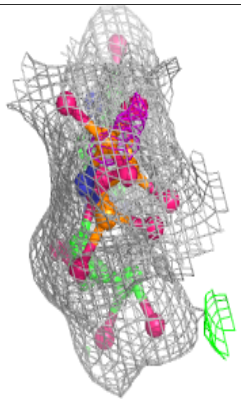
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GNP 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)

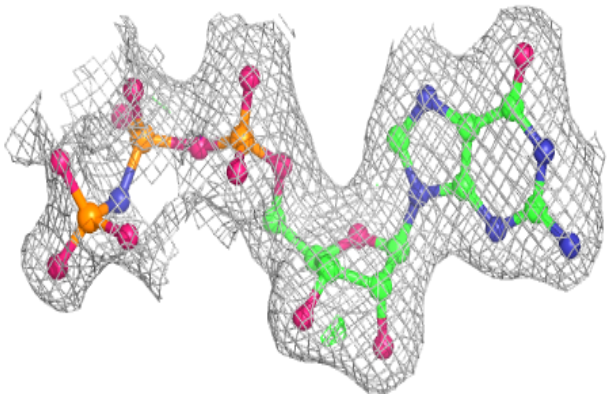


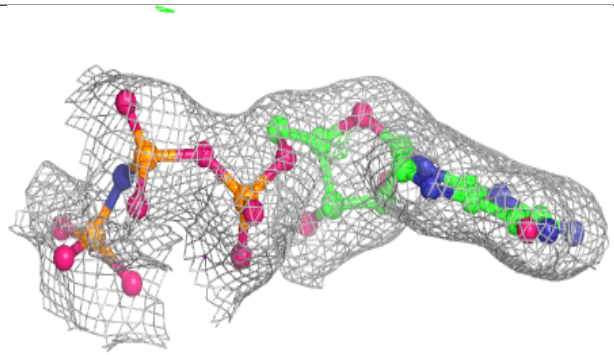


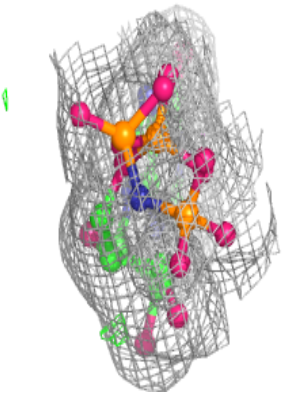


Electron density around GNP B 500 (A):

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

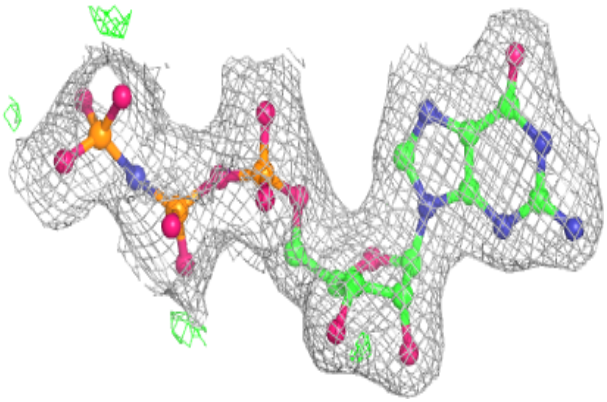


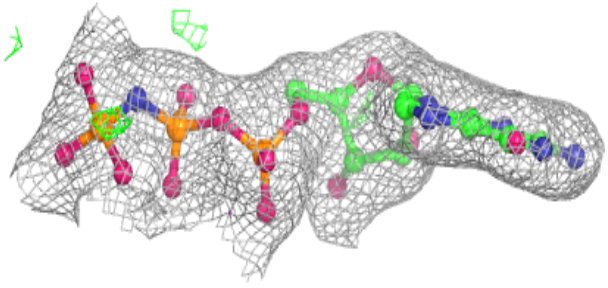


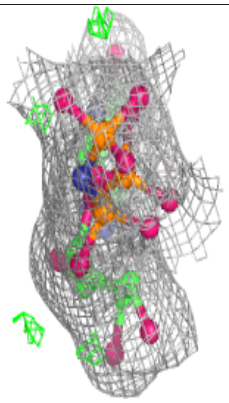


Electron density around GNP B 500 (B):

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

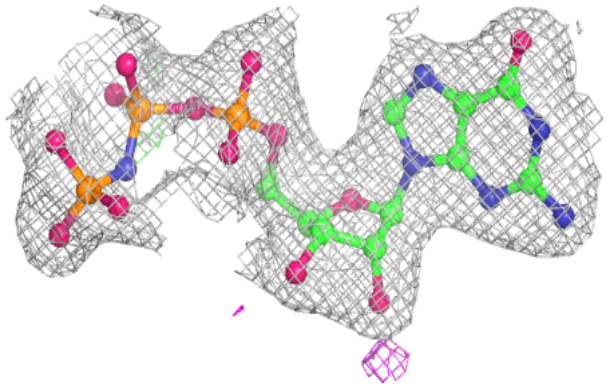


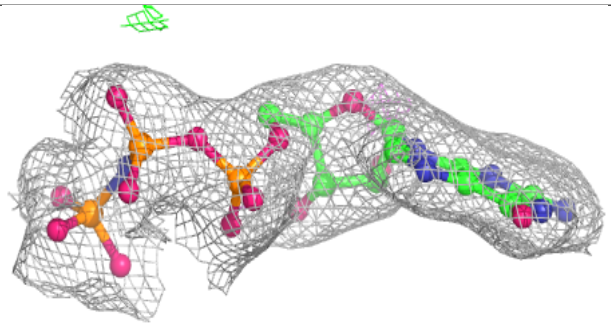


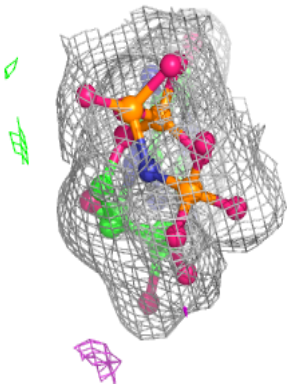


Electron density around GNP D 500 (A):

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

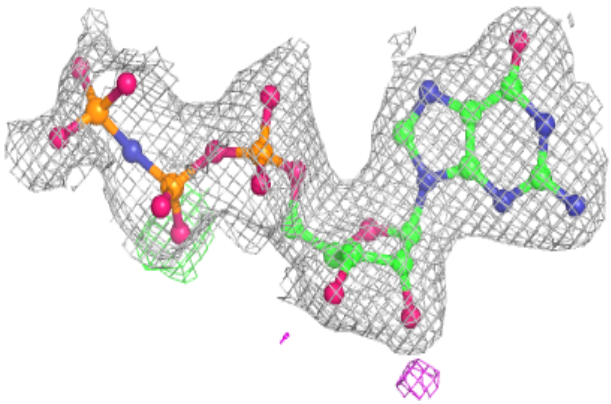


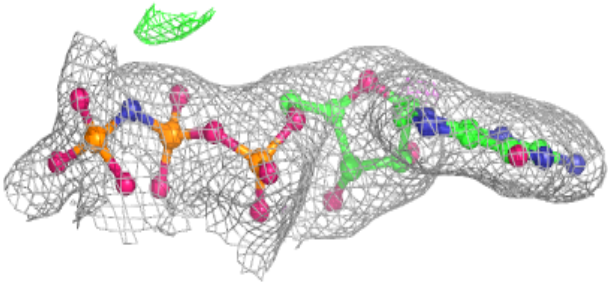


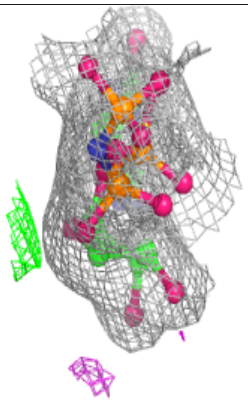


Electron density around GNP D 500 (B):

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

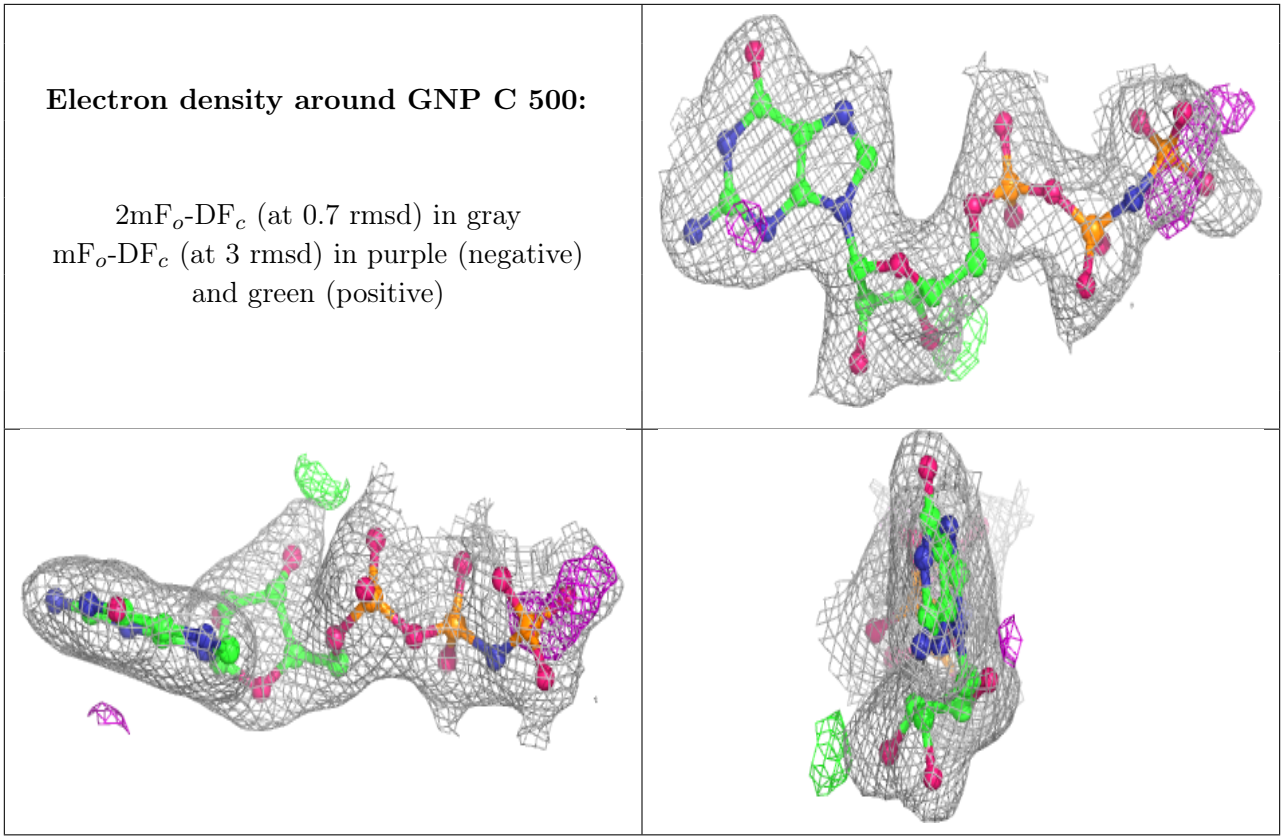






Electron density around GNP C 500:

$2mF_o$-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)

There are no such residues in this entry.