



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2025 – 04:20 PM JST

PDB ID : 6K4G
Title : Crystal structure of the PI5P4Kbeta-GMPPNP complex
Authors : Takeuchi, K.; Senda, M.; Senda, T.
Deposited on : 2019-05-23
Resolution : 2.70 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) : 1.21
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.2

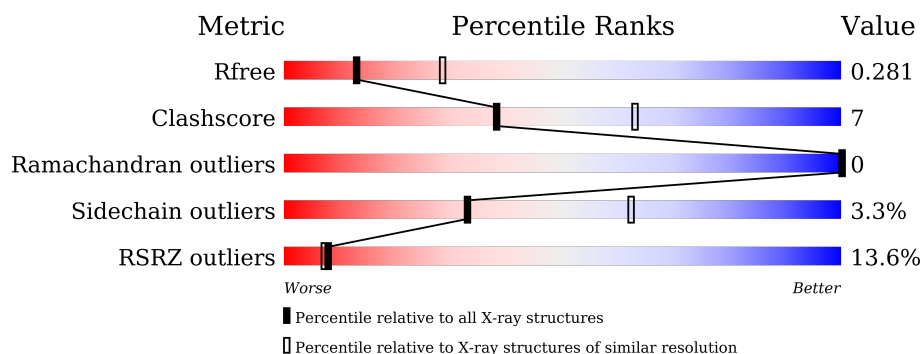
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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 $\leq 5\%$. 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	393	<div> <div>7%</div> <div>64%</div> <div>16%</div> <div>20%</div> </div>
1	B	393	<div> <div>14%</div> <div>66%</div> <div>10%</div> <div>23%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4754 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.

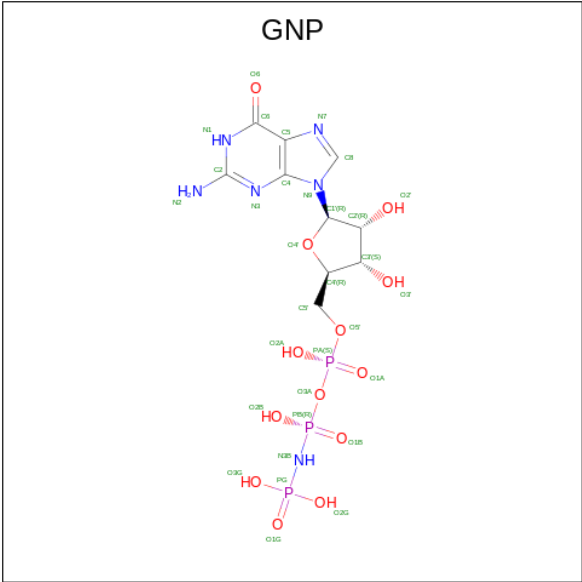
- Molecule 1 is a protein called Phosphatidylinositol 5-phosphate 4-kinase type-2 beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	S	0	1	0
			2441	1561	415	454	11			
1	B	301	Total	C	N	O	S	0	0	0
			2212	1417	375	408	12			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	expression tag	UNP P78356
A	25	PRO	-	expression tag	UNP P78356
A	26	ASN	-	expression tag	UNP P78356
A	27	CYS	-	expression tag	UNP P78356
A	28	ALA	-	expression tag	UNP P78356
A	29	PRO	-	expression tag	UNP P78356
A	30	GLY	-	expression tag	UNP P78356
B	24	GLY	-	expression tag	UNP P78356
B	25	PRO	-	expression tag	UNP P78356
B	26	ASN	-	expression tag	UNP P78356
B	27	CYS	-	expression tag	UNP P78356
B	28	ALA	-	expression tag	UNP P78356
B	29	PRO	-	expression tag	UNP P78356
B	30	GLY	-	expression tag	UNP P78356

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



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

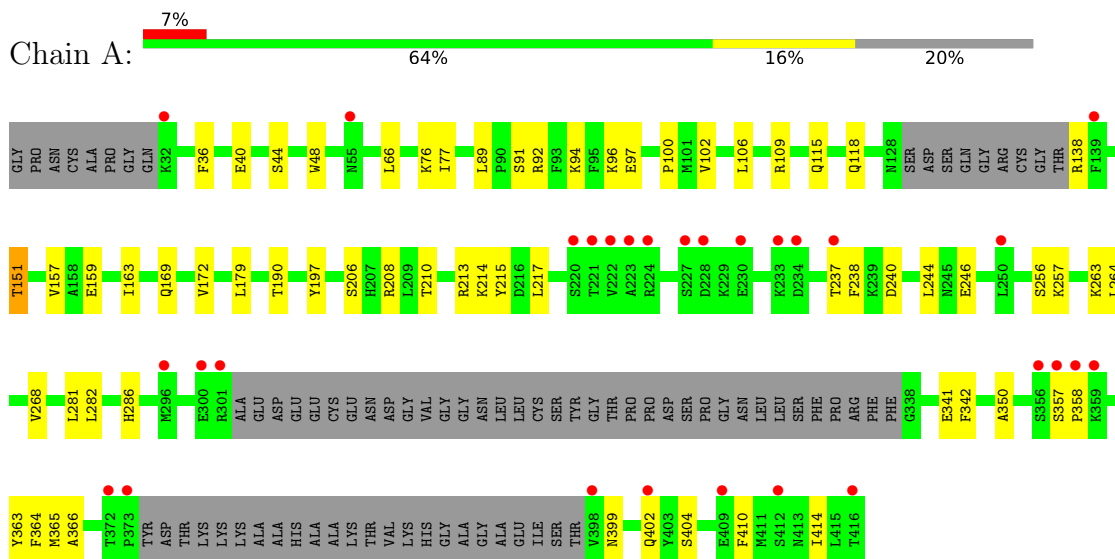
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		
3	B	1	Total	O	0	0
			1	1		

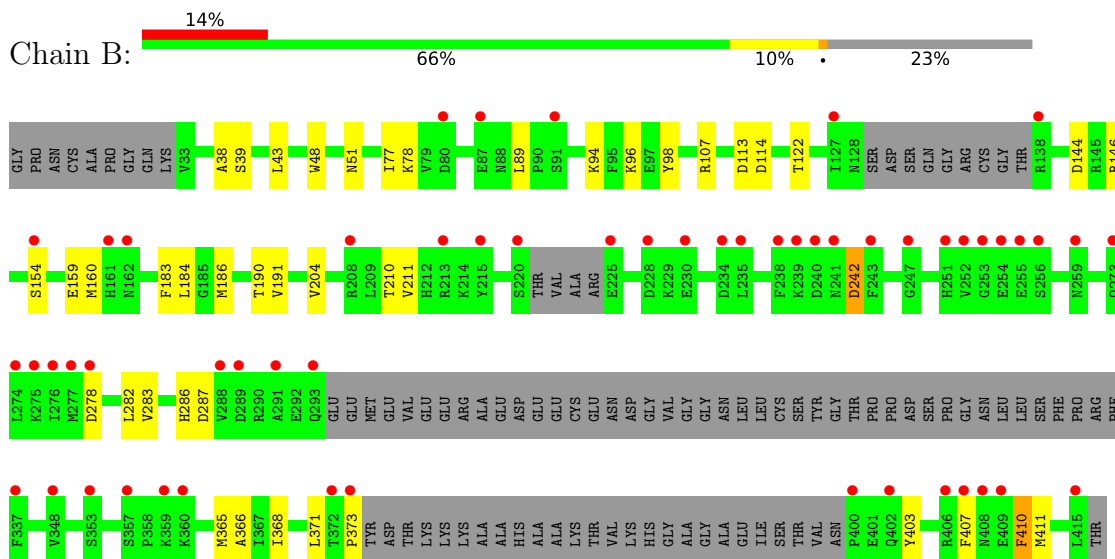
3 Residue-property plots [i](#)

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: Phosphatidylinositol 5-phosphate 4-kinase type-2 beta



- Molecule 1: Phosphatidylinositol 5-phosphate 4-kinase type-2 beta



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	109.78Å 184.62Å 105.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.69 – 2.70 37.69 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (37.69-2.70) 99.3 (37.69-2.70)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.223 , 0.275 0.230 , 0.281	Depositor DCC
R_{free} test set	1486 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	79.7	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 74.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.012 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.020 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4754	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GNP

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	0.49	0/2495	0.65	0/3392
1	B	0.46	0/2261	0.63	0/3082
All	All	0.47	0/4756	0.64	0/6474

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2441	0	2235	37	0
1	B	2212	0	1935	25	0
2	A	64	0	26	2	0
2	B	32	0	13	1	0
3	A	4	0	0	1	0
3	B	1	0	0	0	0
All	All	4754	0	4209	61	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 7.

All (61) 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:B:283:VAL:HG22	1:B:365:MET:HG2	1.58	0.85
1:A:94:LYS:HB2	1:A:190:THR:HB	1.74	0.69
1:A:264:LEU:O	1:A:268:VAL:HG22	1.96	0.66
1:A:208:ARG:NH2	1:A:341:GLU:O	2.30	0.64
1:A:92:ARG:NH2	3:A:601:HOH:O	2.29	0.64
1:A:214:LYS:NZ	2:A:501:GNP:O2'	2.29	0.63
1:B:278:ASP:H	1:B:403:TYR:HE2	1.47	0.63
1:A:399:ASN:OD1	1:A:402:GLN:N	2.24	0.61
1:B:282:LEU:HB2	1:B:368:ILE:HD13	1.84	0.58
1:A:40:GLU:OE1	1:A:138:ARG:NH1	2.34	0.57
1:B:278:ASP:N	1:B:403:TYR:HE2	2.03	0.56
1:A:357:SER:OG	1:A:358:PRO:HD2	2.05	0.55
1:A:48:TRP:HB2	1:A:89:LEU:HD21	1.89	0.54
1:A:109:ARG:CZ	1:A:172:VAL:HG12	2.38	0.54
1:A:169:GLN:HA	1:A:172:VAL:HG22	1.90	0.53
1:B:48:TRP:HB2	1:B:89:LEU:HD21	1.91	0.53
1:A:109:ARG:NH1	1:A:172:VAL:HG12	2.23	0.53
1:B:160:MET:HB3	1:B:186:MET:HE1	1.90	0.52
1:A:138:ARG:HB3	1:A:151:THR:CG2	2.39	0.52
1:B:94:LYS:HB2	1:B:190:THR:HB	1.91	0.52
1:A:206:SER:HB2	1:A:364:PHE:CZ	2.44	0.52
1:B:160:MET:HE1	1:B:183:PHE:CE2	2.46	0.51
1:B:159:GLU:HG2	1:B:373:PRO:HD3	1.92	0.50
1:B:204:VAL:HG23	2:B:501:GNP:O6	2.12	0.50
1:B:407:PHE:O	1:B:411:MET:HG2	2.12	0.50
1:A:77:ILE:HD12	1:B:77:ILE:HD11	1.94	0.49
1:B:204:VAL:HG13	1:B:366:ALA:HB3	1.95	0.49
1:A:217:LEU:HD13	1:A:410:PHE:HE2	1.78	0.49
1:B:38:ALA:HB1	1:B:43:LEU:HB2	1.94	0.49
1:A:138:ARG:HB3	1:A:151:THR:HG21	1.95	0.49
1:B:242:ASP:N	1:B:242:ASP:OD1	2.46	0.48
1:A:213:ARG:NH2	1:A:246:GLU:OE1	2.47	0.48
1:B:51:ASN:HB2	1:B:122:THR:HG21	1.95	0.48
1:A:157:VAL:HG21	1:A:197:TYR:CD2	2.50	0.47
1:A:96:LYS:NZ	2:A:502:GNP:O2A	2.40	0.47
1:A:36:PHE:O	1:A:44:SER:OG	2.26	0.47
1:A:179:LEU:CD2	1:A:263:LYS:HE3	2.45	0.46
1:B:410:PHE:HD1	1:B:410:PHE:O	1.99	0.45
1:A:106:LEU:HD23	1:A:106:LEU:HA	1.74	0.45
1:A:115:GLN:HE22	1:A:118:GLN:HE21	1.65	0.45
1:B:78:LYS:HD2	1:B:94:LYS:HE2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:LEU:HD13	1:A:102:VAL:HG22	1.99	0.45
1:B:210:THR:O	1:B:286:HIS:ND1	2.46	0.45
1:A:179:LEU:HD21	1:A:263:LYS:HE3	1.98	0.44
1:A:97:GLU:OE1	1:A:100:PRO:HB3	2.17	0.44
1:A:410:PHE:O	1:A:414:ILE:HG23	2.17	0.44
1:A:159:GLU:OE1	1:A:163:ILE:HG23	2.18	0.44
1:B:107:ARG:NH1	1:B:184:LEU:O	2.49	0.43
1:B:113:ASP:OD1	1:B:114:ASP:N	2.52	0.43
1:A:282:LEU:O	1:A:365:MET:HA	2.19	0.43
1:B:96:LYS:HE2	1:B:98:TYR:CE2	2.54	0.43
1:B:371:LEU:HD23	1:B:371:LEU:HA	1.60	0.42
1:B:160:MET:HE2	1:B:186:MET:HE3	2.02	0.42
1:A:210:THR:O	1:A:286:HIS:ND1	2.43	0.42
1:A:215:TYR:HA	1:A:238:PHE:O	2.20	0.41
1:A:350:ALA:HA	1:A:363:TYR:O	2.19	0.41
1:A:281:LEU:HD12	1:A:366:ALA:O	2.20	0.41
1:B:144:ASP:OD2	1:B:146:ARG:HD2	2.20	0.41
1:A:115:GLN:NE2	1:A:118:GLN:HE21	2.18	0.41
1:A:208:ARG:HH21	1:A:342:PHE:HA	1.85	0.41
1:A:244:LEU:HD23	1:A:244:LEU:HA	1.86	0.41

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	309/393 (79%)	305 (99%)	4 (1%)	0	100	100
1	B	291/393 (74%)	286 (98%)	5 (2%)	0	100	100
All	All	600/786 (76%)	591 (98%)	9 (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	247/352 (70%)	239 (97%)	8 (3%)	34	63
1	B	206/352 (58%)	199 (97%)	7 (3%)	32	61
All	All	453/704 (64%)	438 (97%)	15 (3%)	33	62

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	LYS
1	A	91	SER
1	A	151	THR
1	A	237	THR
1	A	240	ASP
1	A	256	SER
1	A	257	LYS
1	A	404	SER
1	B	39	SER
1	B	154	SER
1	B	191	VAL
1	B	211	VAL
1	B	242	ASP
1	B	287	ASP
1	B	410	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	118	GLN
1	A	413	ASN

5.3.3 RNA [i](#)

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GNP	B	501	-	29,34,34	1.84	5 (17%)	33,54,54	2.13	5 (15%)
2	GNP	A	502	-	29,34,34	1.81	6 (20%)	33,54,54	2.22	6 (18%)
2	GNP	A	501	-	29,34,34	1.77	6 (20%)	33,54,54	2.11	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	501	-	-	6/14/38/38	0/3/3/3
2	GNP	A	502	-	-	5/14/38/38	0/3/3/3
2	GNP	A	501	-	-	8/14/38/38	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	GNP	PB-O3A	5.98	1.66	1.59
2	A	501	GNP	PB-O3A	5.27	1.65	1.59
2	A	502	GNP	PB-O3A	4.52	1.64	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	502	GNP	PB-O1B	4.03	1.52	1.46
2	A	502	GNP	PG-N3B	3.87	1.73	1.63
2	A	502	GNP	PG-O1G	3.73	1.52	1.46
2	A	501	GNP	PG-N3B	3.66	1.72	1.63
2	B	501	GNP	PG-N3B	3.52	1.72	1.63
2	A	501	GNP	PB-O1B	3.48	1.51	1.46
2	B	501	GNP	PB-O1B	3.45	1.51	1.46
2	B	501	GNP	C6-N1	3.31	1.38	1.33
2	A	502	GNP	C6-N1	3.18	1.38	1.33
2	B	501	GNP	PG-O1G	3.00	1.50	1.46
2	A	501	GNP	C6-N1	2.95	1.38	1.33
2	A	501	GNP	PG-O1G	2.86	1.50	1.46
2	A	501	GNP	C5-C6	2.23	1.45	1.41
2	A	502	GNP	C5-C6	2.13	1.45	1.41

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	GNP	C5-C6-N1	-8.42	111.91	123.43
2	A	501	GNP	C5-C6-N1	-8.33	112.04	123.43
2	A	502	GNP	C5-C6-N1	-8.19	112.23	123.43
2	B	501	GNP	C2-N1-C6	5.87	125.26	115.93
2	A	501	GNP	C2-N1-C6	5.72	125.01	115.93
2	A	502	GNP	C2-N1-C6	5.65	124.91	115.93
2	A	502	GNP	O1B-PB-N3B	-3.75	106.24	111.77
2	A	502	GNP	O3A-PB-N3B	3.22	115.52	106.59
2	B	501	GNP	N3-C2-N1	-2.87	123.40	127.22
2	A	502	GNP	N3-C2-N1	-2.84	123.43	127.22
2	B	501	GNP	C4-C5-C6	-2.79	118.14	120.80
2	A	501	GNP	N3-C2-N1	-2.71	123.61	127.22
2	A	501	GNP	C4-C5-C6	-2.65	118.27	120.80
2	A	502	GNP	C4-C5-C6	-2.50	118.41	120.80
2	A	501	GNP	O2G-PG-O1G	-2.46	107.26	113.45
2	A	501	GNP	C2-N3-C4	-2.09	112.97	115.36
2	B	501	GNP	C2-N3-C4	-2.05	113.02	115.36

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GNP	PB-N3B-PG-O1G
2	A	501	GNP	PG-N3B-PB-O3A

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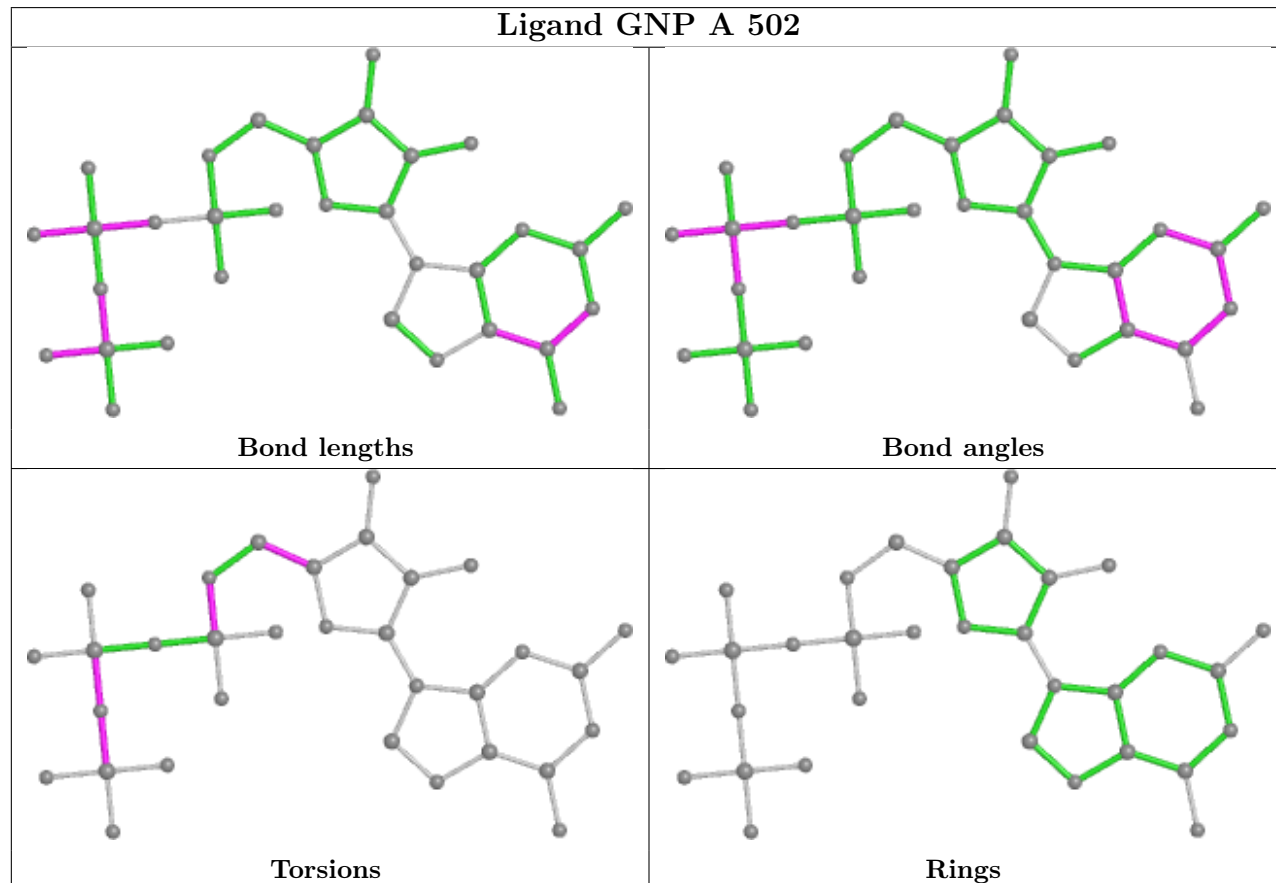
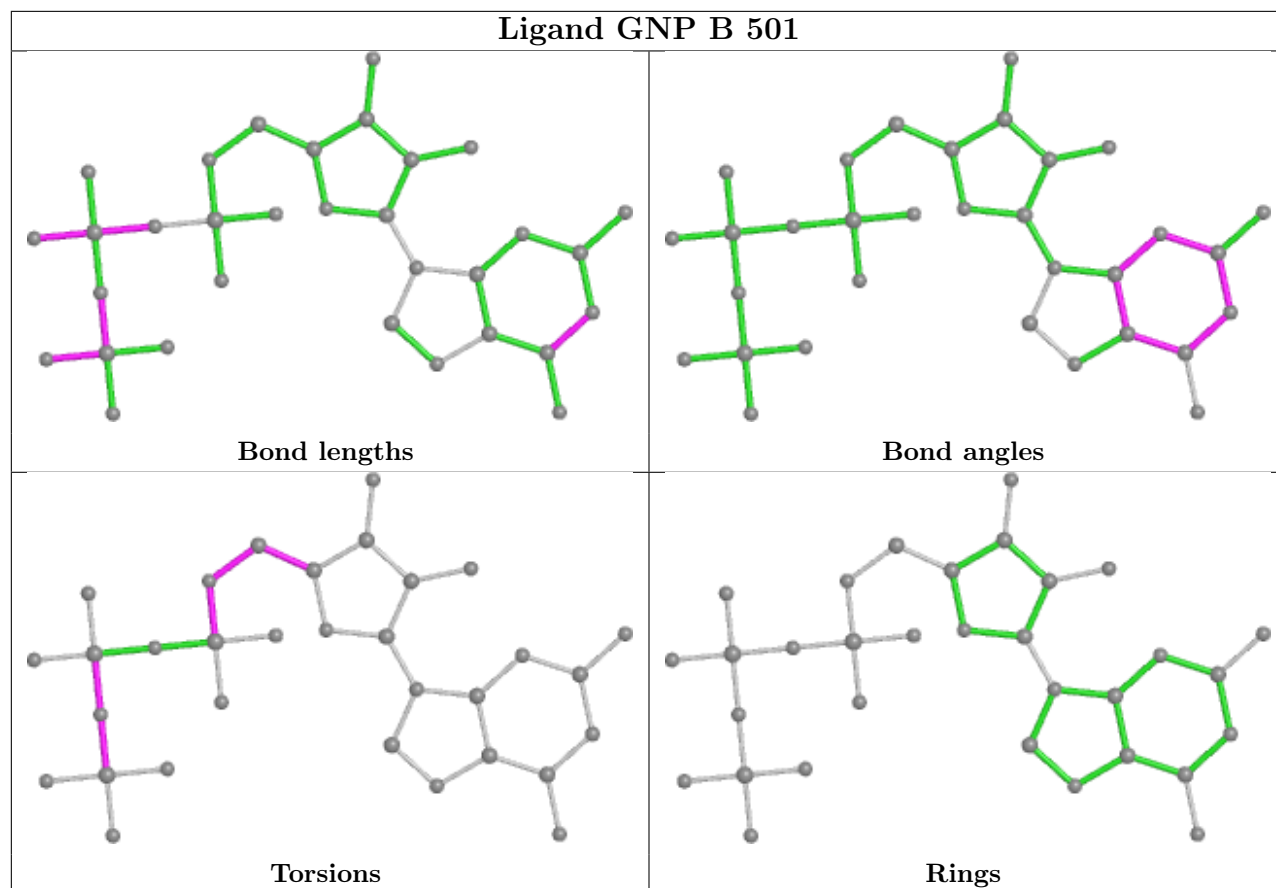
Mol	Chain	Res	Type	Atoms
2	A	501	GNP	PA-O3A-PB-O1B
2	A	501	GNP	C5'-O5'-PA-O3A
2	A	501	GNP	C5'-O5'-PA-O2A
2	A	502	GNP	PB-N3B-PG-O1G
2	A	502	GNP	PG-N3B-PB-O1B
2	B	501	GNP	PB-N3B-PG-O1G
2	B	501	GNP	PG-N3B-PB-O1B
2	B	501	GNP	C5'-O5'-PA-O3A
2	A	501	GNP	C5'-O5'-PA-O1A
2	A	502	GNP	C5'-O5'-PA-O1A
2	B	501	GNP	C5'-O5'-PA-O2A
2	A	501	GNP	PB-O3A-PA-O2A
2	B	501	GNP	C4'-C5'-O5'-PA
2	A	501	GNP	PG-N3B-PB-O1B
2	A	502	GNP	O4'-C4'-C5'-O5'
2	A	502	GNP	C3'-C4'-C5'-O5'
2	B	501	GNP	O4'-C4'-C5'-O5'

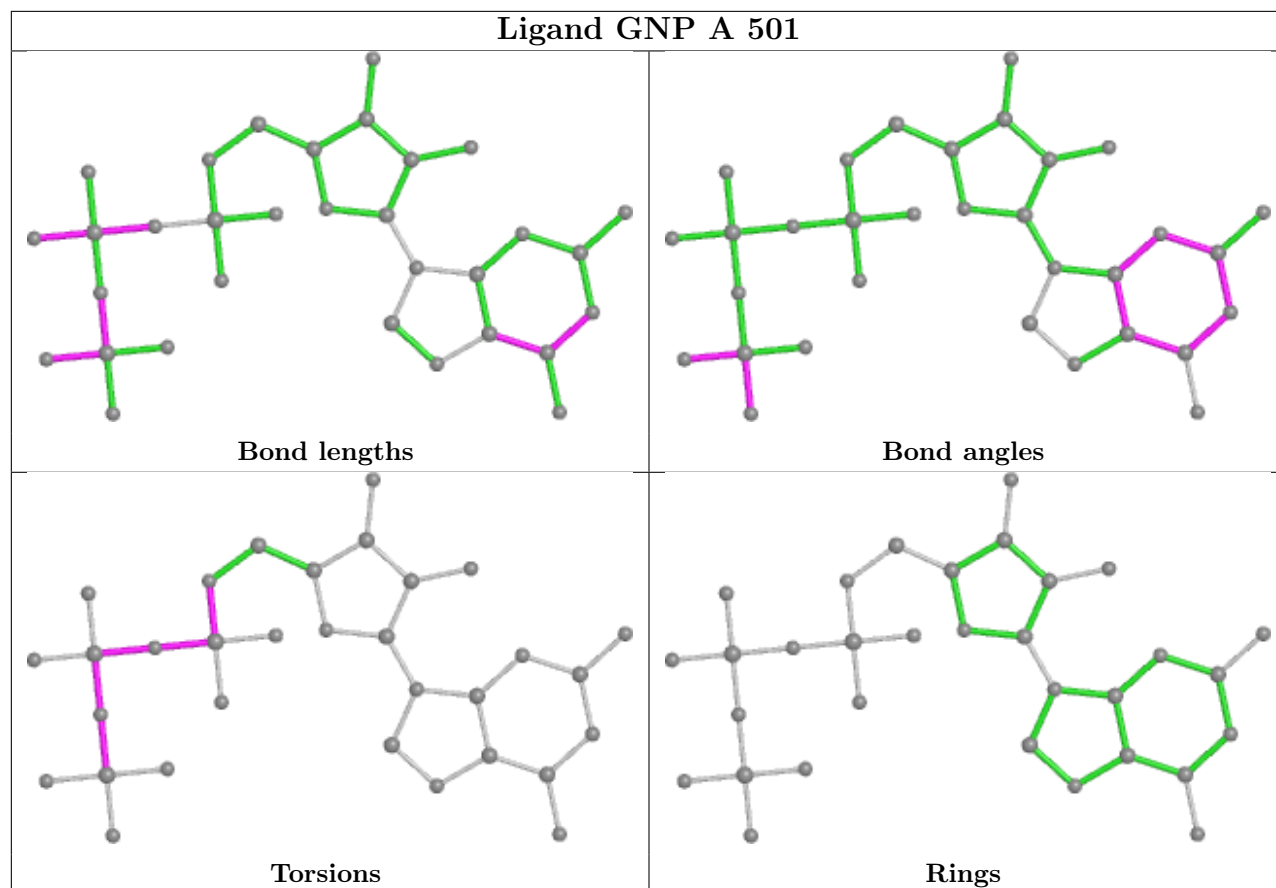
There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	GNP	1	0
2	A	502	GNP	1	0
2	A	501	GNP	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	316/393 (80%)	0.61	29 (9%) 16 15	36, 88, 134, 163	1 (0%)
1	B	301/393 (76%)	0.89	55 (18%) 4 4	57, 94, 156, 189	0
All	All	617/786 (78%)	0.75	84 (13%) 8 7	36, 91, 150, 189	1 (0%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	251	HIS	5.6
1	B	220	SER	5.4
1	B	400	PRO	4.9
1	A	228	ASP	4.9
1	B	402	GLN	4.9
1	A	372	THR	4.8
1	A	301	ARG	4.7
1	B	230	GLU	4.7
1	B	293	GLN	4.6
1	B	240	ASP	4.6
1	A	230	GLU	4.5
1	A	398	VAL	4.1
1	B	235	LEU	4.0
1	B	162	ASN	3.9
1	A	402	GLN	3.9
1	B	276	ILE	3.9
1	B	234	ASP	3.8
1	A	416	THR	3.8
1	B	337	PHE	3.6
1	B	415	LEU	3.5
1	B	254	GLU	3.4
1	B	247	GLY	3.4
1	B	274	LEU	3.4
1	B	252	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	409	GLU	3.1
1	B	273	GLN	3.1
1	B	253	GLY	3.1
1	A	221	THR	3.0
1	B	127	ILE	3.0
1	B	208	ARG	3.0
1	A	296	MET	2.8
1	B	138	ARG	2.8
1	A	227	SER	2.8
1	B	228	ASP	2.7
1	A	32	LYS	2.7
1	A	233	LYS	2.6
1	B	291	ALA	2.6
1	B	215	TYR	2.6
1	B	288	VAL	2.5
1	B	372	THR	2.5
1	A	356	SER	2.5
1	B	408	ASN	2.5
1	B	161	HIS	2.5
1	A	237	THR	2.5
1	B	275	LYS	2.5
1	B	373	PRO	2.5
1	A	250	LEU	2.5
1	B	225	GLU	2.4
1	B	91	SER	2.4
1	B	359	LYS	2.4
1	B	238	PHE	2.4
1	A	300	GLU	2.4
1	B	353	SER	2.4
1	A	223	ALA	2.4
1	B	357	SER	2.3
1	A	55	ASN	2.3
1	B	289	ASP	2.3
1	A	359	LYS	2.3
1	B	360	LYS	2.3
1	A	373	PRO	2.3
1	B	243	PHE	2.3
1	A	220	SER	2.3
1	B	406	ARG	2.3
1	A	222	VAL	2.3
1	B	407	PHE	2.3
1	A	357	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	277	MET	2.3
1	A	409	GLU	2.3
1	B	213	ARG	2.3
1	B	239	LYS	2.2
1	B	87	GLU	2.2
1	B	255	GLU	2.2
1	B	241	ASN	2.2
1	B	278	ASP	2.2
1	A	139	PHE	2.2
1	A	412	SER	2.1
1	A	234	ASP	2.1
1	B	259	ASN	2.1
1	B	348	VAL	2.1
1	A	358	PRO	2.1
1	B	256	SER	2.1
1	A	224	ARG	2.1
1	B	154	SER	2.0
1	B	80	ASP	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.

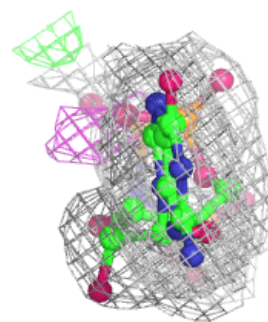
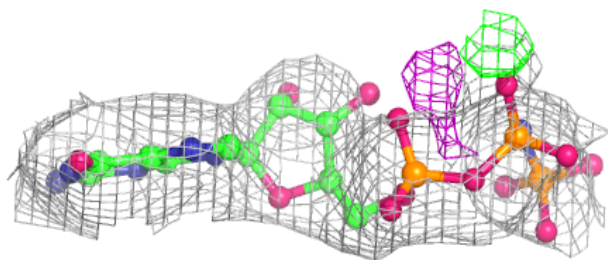
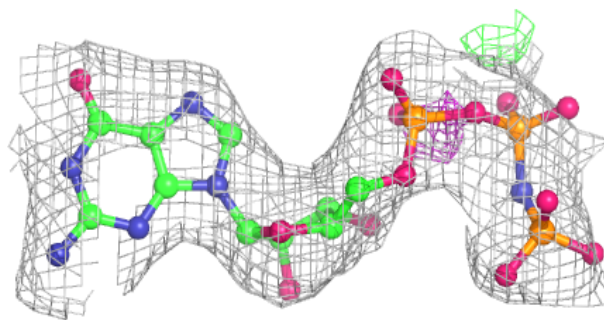
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GNP	B	501	32/32	0.76	0.12	96,129,168,172	0
2	GNP	A	501	32/32	0.84	0.12	72,106,151,158	0
2	GNP	A	502	32/32	0.89	0.11	79,93,109,116	0

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.

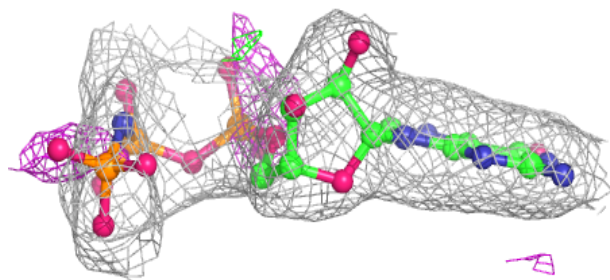
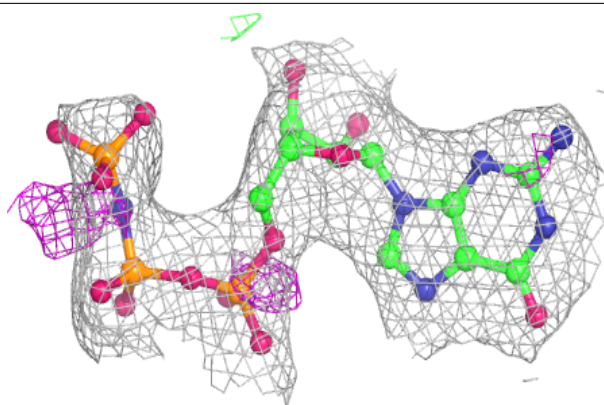
Electron density around GNP B 501:

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

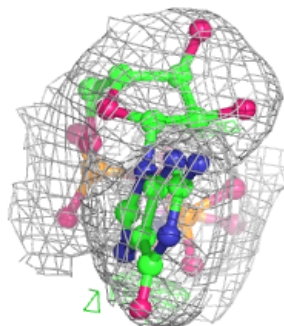
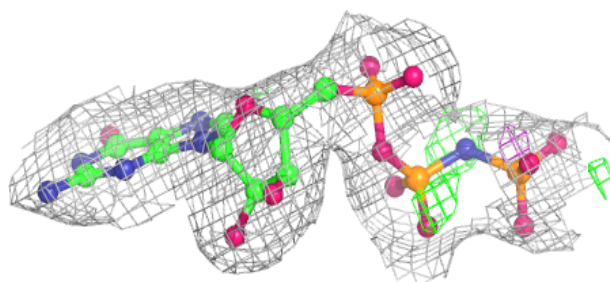
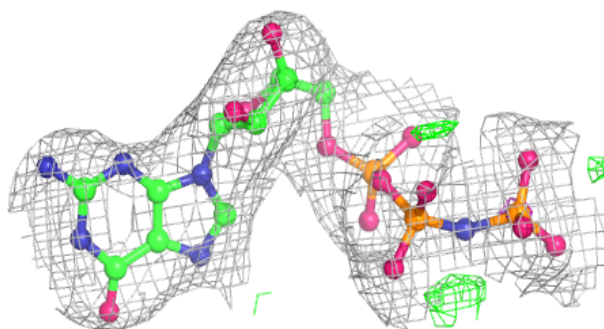


Electron density around GNP A 501:

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

**Electron density around GNP A 502:**

$2mF_o-DF_c$ (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.