



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 04:52 am BST

PDB ID : 6C5U  
Title : Aminoglycoside Phosphotransferase (2'')-Ia in complex with GMPPNP, Magnesium, and Ribostamycin, Alternate form  
Authors : Caldwell, S.J.; Berghuis, A.M.  
Deposited on : 2018-01-16  
Resolution : 2.41 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](mailto: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.

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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

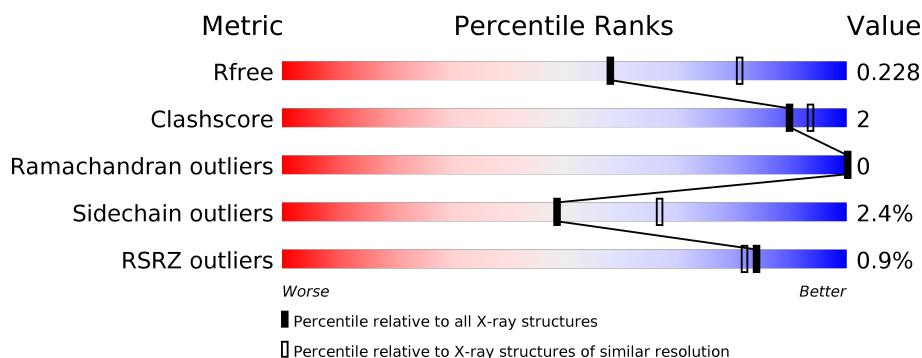
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.41 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	4647 (2.44-2.40)
Clashscore	141614	5161 (2.44-2.40)
Ramachandran outliers	138981	5073 (2.44-2.40)
Sidechain outliers	138945	5074 (2.44-2.40)
RSRZ outliers	127900	4543 (2.44-2.40)

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  $\geq 3$ , 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	305	<div> <div>86%</div> <div>10%</div> <div>.</div> </div>
1	B	305	<div> <div>%</div> <div>87%</div> <div>8%</div> <div>.</div> <div>.</div> </div>
1	C	305	<div> <div>87%</div> <div>7%</div> <div>6%</div> </div>
1	D	305	<div> <div>2%</div> <div>90%</div> <div>5%</div> <div>5%</div> </div>

## 2 Entry composition [i](#)

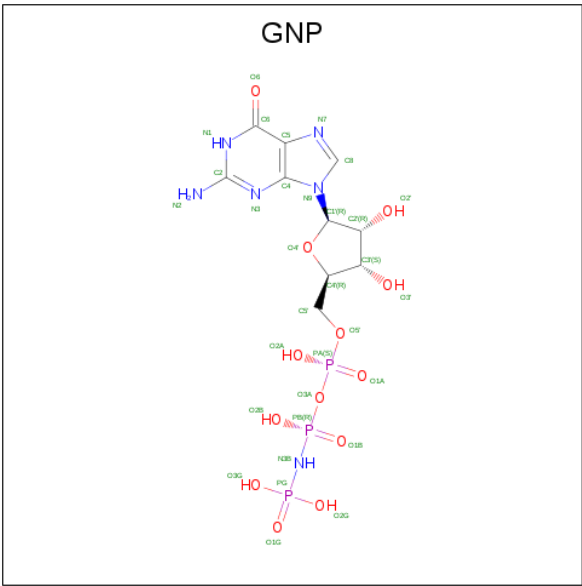
There are 6 unique types of molecules in this entry. The entry contains 10345 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	293	Total	C	N	O	S	0	3	0
			2424	1547	377	490	10			
1	B	292	Total	C	N	O	S	0	2	0
			2418	1546	373	489	10			
1	C	287	Total	C	N	O	S	0	2	0
			2382	1524	369	479	10			
1	D	291	Total	C	N	O	S	0	1	0
			2376	1512	372	482	10			

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>13</sub>P<sub>3</sub>).



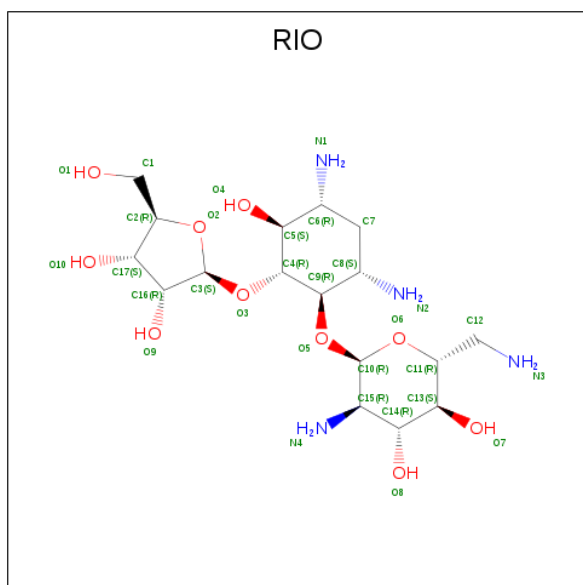
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
2	B	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

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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	0
			32	10	6	13	3		

- Molecule 3 is RIBOSTAMYCIN (three-letter code: RIO) (formula:  $C_{17}H_{34}N_4O_{10}$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			31	17	4	10		
3	B	1	Total	C	N	O	0	0
			31	17	4	10		
3	D	1	Total	C	N	O	0	0
			31	17	4	10		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

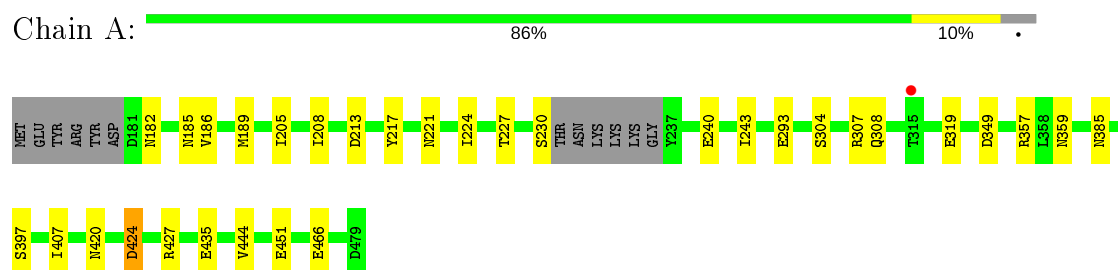
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	144	Total 144	O 144	0	0
6	B	167	Total 167	O 167	0	0
6	C	124	Total 124	O 124	0	0
6	D	78	Total 78	O 78	0	0

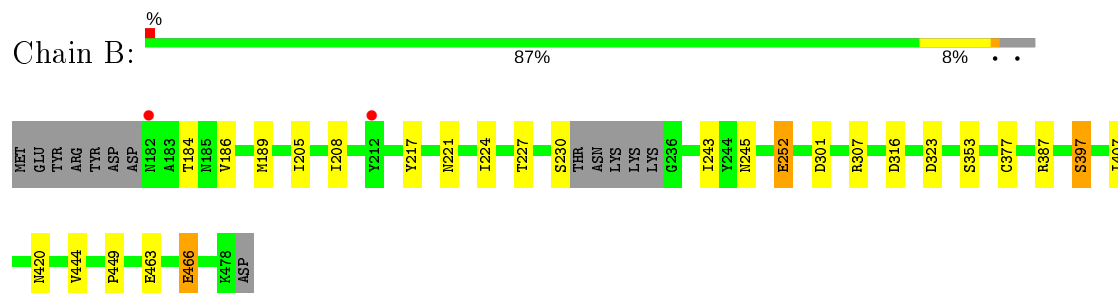
### 3 Residue-property plots [i](#)

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.

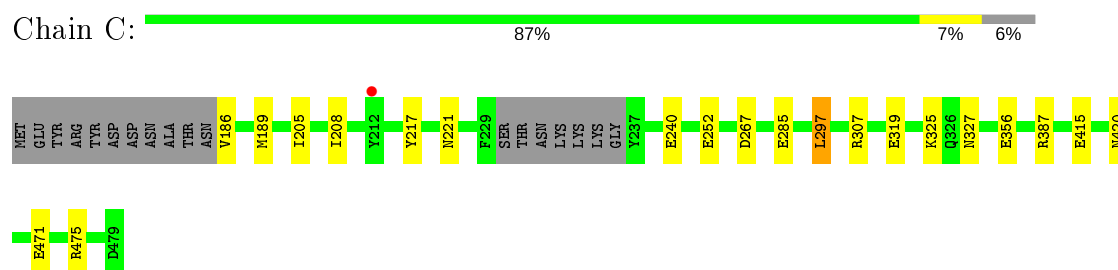
- Molecule 1: Bifunctional AAC/APH



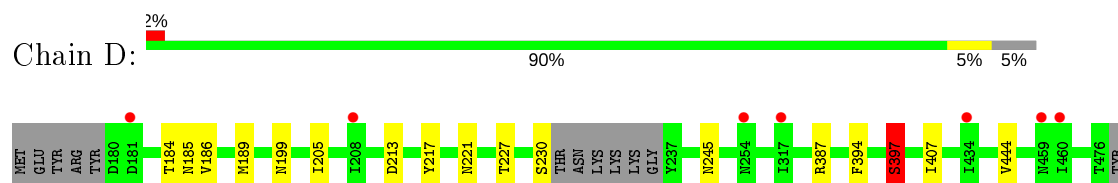
- Molecule 1: Bifunctional AAC/APH



- Molecule 1: Bifunctional AAC/APH



- Molecule 1: Bifunctional AAC/APH



LYS  
ASP

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.25Å 100.28Å 94.04Å 90.00° 105.29° 90.00°	Depositor
Resolution (Å)	90.71 – 2.41 87.05 – 2.42	Depositor EDS
% Data completeness (in resolution range)	99.9 (90.71-2.41) 99.9 (87.05-2.42)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.31 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.180 , 0.227 0.185 , 0.228	Depositor DCC
$R_{free}$ test set	3119 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.9	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 45.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.020 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10345	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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

### 5.1 Standard geometry

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

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	0.96	5/2475 (0.2%)	0.94	7/3338 (0.2%)
1	B	0.95	6/2467 (0.2%)	0.91	6/3326 (0.2%)
1	C	0.96	4/2431 (0.2%)	0.95	7/3278 (0.2%)
1	D	0.84	1/2419 (0.0%)	0.89	1/3264 (0.0%)
All	All	0.93	16/9792 (0.2%)	0.92	21/13206 (0.2%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	377	CYS	CB-SG	-7.00	1.70	1.82
1	B	353	SER	CB-OG	-6.70	1.33	1.42
1	C	471	GLU	CD-OE2	6.03	1.32	1.25
1	C	356	GLU	CD-OE1	5.96	1.32	1.25
1	A	385	ASN	CB-CG	-5.92	1.37	1.51
1	D	397	SER	CB-OG	-5.90	1.34	1.42
1	A	435	GLU	CD-OE2	5.77	1.31	1.25
1	A	319	GLU	CD-OE2	5.74	1.31	1.25
1	B	397	SER	CB-OG	-5.73	1.34	1.42
1	B	252	GLU	CD-OE1	5.41	1.31	1.25
1	A	240	GLU	CD-OE1	5.36	1.31	1.25
1	C	356	GLU	CD-OE2	5.33	1.31	1.25
1	B	463	GLU	CD-OE1	5.28	1.31	1.25
1	B	466	GLU	CD-OE1	5.26	1.31	1.25
1	A	435	GLU	CG-CD	5.14	1.59	1.51
1	C	240	GLU	CD-OE1	5.02	1.31	1.25

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	387	ARG	NE-CZ-NH1	7.11	123.86	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	424	ASP	CB-CG-OD1	6.63	124.26	118.30
1	C	319	GLU	OE1-CD-OE2	-6.61	115.37	123.30
1	C	307[A]	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	C	307[B]	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	B	301	ASP	CB-CG-OD1	6.37	124.03	118.30
1	C	475	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	B	323	ASP	CB-CG-OD2	-6.20	112.72	118.30
1	C	297	LEU	CB-CG-CD1	6.20	121.54	111.00
1	A	307[A]	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	A	307[B]	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	A	357	ARG	NE-CZ-NH2	-6.04	117.28	120.30
1	C	387	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	B	307	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	A	349	ASP	CB-CG-OD2	-5.43	113.42	118.30
1	D	387	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	451	GLU	OE1-CD-OE2	-5.29	116.95	123.30
1	B	301	ASP	CB-CG-OD2	-5.22	113.60	118.30
1	A	308	GLN	CA-CB-CG	5.05	124.51	113.40
1	B	316	ASP	CB-CG-OD1	5.03	122.83	118.30
1	C	267	ASP	CB-CG-OD1	5.02	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2424	0	2333	10	1
1	B	2418	0	2333	8	0
1	C	2382	0	2292	6	0
1	D	2376	0	2267	9	0
2	A	32	0	13	1	0
2	B	32	0	13	0	0
2	C	32	0	13	0	0
2	D	32	0	13	0	0
3	A	31	0	34	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	31	0	34	0	0
3	D	31	0	34	0	0
4	A	2	0	0	1	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	1	0
5	C	1	0	0	0	0
6	A	144	0	0	4	0
6	B	167	0	0	0	0
6	C	124	0	0	4	1
6	D	78	0	0	0	0
All	All	10345	0	9379	35	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 2.

All (35) 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:A:500:GNP:O2B	6:A:901:HOH:O	1.75	1.01
4:A:700:MG:MG	6:A:901:HOH:O	1.25	0.79
1:A:243:ILE:HD13	1:A:397:SER:HB2	1.81	0.62
1:D:185:ASN:ND2	1:D:217:TYR:OH	2.37	0.58
1:D:394:PHE:O	1:D:397:SER:OG	2.23	0.56
1:A:185:ASN:ND2	1:A:217:TYR:OH	2.39	0.54
1:D:186:VAL:HG13	1:D:205:ILE:HG23	1.91	0.52
1:D:186:VAL:CG1	1:D:205:ILE:HG23	2.40	0.51
1:B:189:MET:HG2	1:B:217:TYR:CE1	2.45	0.51
1:C:189:MET:HG2	1:C:217:TYR:CE1	2.46	0.51
1:B:208:ILE:CD1	1:B:224:ILE:HD12	2.41	0.51
1:B:243:ILE:HD13	1:B:397:SER:HB2	1.94	0.50
1:A:208:ILE:CD1	1:A:224:ILE:HD12	2.42	0.49
1:D:407:ILE:HD12	1:D:444:VAL:HG11	1.94	0.49
1:A:189:MET:HG2	1:A:217:TYR:CE1	2.48	0.48
1:C:415:GLU:HG3	6:C:1560:HOH:O	2.13	0.48
1:C:415:GLU:N	6:C:1560:HOH:O	2.47	0.48
1:A:359:ASN:ND2	6:A:1050:HOH:O	2.47	0.47
1:A:424:ASP:OD1	1:A:427:ARG:NH1	2.42	0.47
1:B:186:VAL:CG1	1:B:205:ILE:HG23	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:189:MET:HG2	1:D:217:TYR:CE1	2.49	0.46
1:A:186:VAL:CG1	1:A:205:ILE:HG23	2.46	0.45
6:A:1587:HOH:O	1:D:199:ASN:ND2	2.49	0.45
1:C:186:VAL:CG1	1:C:205:ILE:HG23	2.46	0.45
1:D:189:MET:SD	1:D:227:THR:HG21	2.56	0.45
1:B:466:GLU:HG3	5:B:802:CL:CL	2.56	0.43
1:A:189:MET:SD	1:A:227:THR:HG21	2.59	0.43
1:B:189:MET:SD	1:B:227:THR:HG21	2.58	0.43
1:D:394:PHE:HB3	1:D:397:SER:OG	2.19	0.42
1:C:325:LYS:NZ	6:C:1258:HOH:O	2.44	0.42
1:B:407:ILE:HD12	1:B:444:VAL:HG11	2.01	0.41
1:A:420:ASN:HA	1:A:420:ASN:HD22	1.72	0.41
1:A:407:ILE:HD12	1:A:444:VAL:HG11	2.03	0.41
1:C:327:ASN:ND2	6:C:1181:HOH:O	2.54	0.40
1:B:208:ILE:HD11	1:B:224:ILE:HD12	2.03	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:A:293:GLU:OE1	6:C:1080:HOH:O 2_747	2.14	0.06

## 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	292/305 (96%)	280 (96%)	12 (4%)	0	100	100
1	B	290/305 (95%)	281 (97%)	9 (3%)	0	100	100
1	C	285/305 (93%)	275 (96%)	10 (4%)	0	100	100
1	D	288/305 (94%)	277 (96%)	11 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1155/1220 (95%)	1113 (96%)	42 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	269/281 (96%)	262 (97%)	7 (3%)	46	64
1	B	269/281 (96%)	262 (97%)	7 (3%)	46	64
1	C	264/281 (94%)	258 (98%)	6 (2%)	50	68
1	D	261/281 (93%)	255 (98%)	6 (2%)	50	68
All	All	1063/1124 (95%)	1037 (98%)	26 (2%)	49	67

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	182	ASN
1	A	213	ASP
1	A	221[A]	ASN
1	A	221[B]	ASN
1	A	230	SER
1	A	304	SER
1	A	466	GLU
1	B	184	THR
1	B	221	ASN
1	B	230	SER
1	B	245	ASN
1	B	252	GLU
1	B	420	ASN
1	B	449	PRO
1	C	208	ILE
1	C	221	ASN
1	C	252	GLU

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Mol	Chain	Res	Type
1	C	285	GLU
1	C	297	LEU
1	C	420	ASN
1	D	184	THR
1	D	213	ASP
1	D	221	ASN
1	D	230	SER
1	D	245	ASN
1	D	397	SER

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

Mol	Chain	Res	Type
1	A	182	ASN
1	A	185	ASN
1	A	341	ASN
1	A	420	ASN
1	A	467	ASN
1	B	467	ASN
1	C	327	ASN
1	C	341	ASN
1	D	185	ASN
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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 18 ligands modelled in this entry, 11 are monoatomic - leaving 7 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
3	RIO	A	600	-	33,33,33	0.50	0	47,49,49	1.14	5 (10%)
3	RIO	B	600	-	33,33,33	0.63	0	47,49,49	1.79	13 (27%)
3	RIO	D	600	-	33,33,33	0.49	0	47,49,49	2.25	10 (21%)
2	GNP	C	500	4	28,34,34	2.45	6 (21%)	30,54,54	2.05	7 (23%)
2	GNP	A	500	4	28,34,34	3.63	9 (32%)	30,54,54	1.95	8 (26%)
2	GNP	D	500	4	28,34,34	2.51	8 (28%)	30,54,54	2.07	10 (33%)
2	GNP	B	500	4	28,34,34	2.64	7 (25%)	30,54,54	2.42	8 (26%)

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
3	RIO	A	600	-	-	5/12/68/68	0/3/3/3
3	RIO	B	600	-	-	7/12/68/68	0/3/3/3
3	RIO	D	600	-	-	5/12/68/68	0/3/3/3
2	GNP	C	500	4	-	5/17/38/38	0/3/3/3
2	GNP	A	500	4	-	5/17/38/38	0/3/3/3
2	GNP	D	500	4	-	9/17/38/38	0/3/3/3
2	GNP	B	500	4	-	4/17/38/38	0/3/3/3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	GNP	C5-C6	-12.28	1.31	1.52
2	A	500	GNP	C4-N9	-8.83	1.36	1.47
2	D	500	GNP	C4-N9	-8.04	1.37	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	GNP	C4-N9	-7.78	1.37	1.47
2	B	500	GNP	PG-O2G	7.57	1.77	1.56
2	C	500	GNP	C4-N9	-7.19	1.38	1.47
2	C	500	GNP	C5-C6	-6.89	1.41	1.52
2	A	500	GNP	PG-O2G	5.99	1.72	1.56
2	C	500	GNP	PG-O2G	5.78	1.72	1.56
2	B	500	GNP	PG-O3G	5.73	1.72	1.56
2	A	500	GNP	PB-O3A	-5.59	1.52	1.59
2	D	500	GNP	PG-O2G	5.06	1.70	1.56
2	D	500	GNP	PB-O2B	4.86	1.69	1.56
2	D	500	GNP	PG-O3G	4.71	1.69	1.56
2	A	500	GNP	PB-O2B	4.44	1.68	1.56
2	A	500	GNP	PG-O3G	4.05	1.67	1.56
2	D	500	GNP	C5-C6	-3.34	1.47	1.52
2	C	500	GNP	C6-N1	3.29	1.38	1.33
2	B	500	GNP	C6-N1	3.28	1.38	1.33
2	D	500	GNP	C6-N1	3.19	1.38	1.33
2	A	500	GNP	C6-N1	3.11	1.38	1.33
2	B	500	GNP	C5-C6	-3.10	1.47	1.52
2	C	500	GNP	C5-C4	-2.84	1.35	1.53
2	A	500	GNP	C5-C4	-2.81	1.35	1.53
2	A	500	GNP	C8-N9	-2.52	1.37	1.45
2	C	500	GNP	C8-N9	-2.48	1.37	1.45
2	B	500	GNP	C5-C4	-2.44	1.38	1.53
2	D	500	GNP	C8-N9	-2.38	1.37	1.45
2	B	500	GNP	C8-N9	-2.33	1.37	1.45
2	D	500	GNP	C5-C4	-2.27	1.39	1.53

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	600	RIO	O3-C3-O2	-7.99	102.78	111.43
3	D	600	RIO	O5-C10-C15	7.17	120.56	108.22
2	A	500	GNP	C4-C5-N7	6.45	111.00	102.46
2	C	500	GNP	C4-C5-N7	6.19	110.67	102.46
2	D	500	GNP	C4-C5-N7	6.05	110.47	102.46
2	B	500	GNP	C4-C5-N7	6.04	110.46	102.46
2	B	500	GNP	O1G-PG-N3B	-5.99	102.94	111.77
3	D	600	RIO	O3-C4-C5	-5.35	93.05	107.28
2	D	500	GNP	C5-C6-N1	-5.04	111.98	118.19
2	C	500	GNP	C5-C6-N1	-4.89	112.16	118.19
2	B	500	GNP	O2B-PB-O3A	4.84	120.79	104.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	GNP	C5-C6-N1	-4.78	112.30	118.19
3	B	600	RIO	O3-C4-C5	-4.56	95.16	107.28
3	B	600	RIO	O3-C3-O2	-4.44	106.62	111.43
3	B	600	RIO	C3-O3-C4	4.35	128.72	117.96
2	D	500	GNP	O6-C6-C5	4.25	128.54	119.86
2	C	500	GNP	O6-C6-C5	4.12	128.27	119.86
2	B	500	GNP	O2B-PB-O1B	-4.02	101.48	109.92
2	B	500	GNP	O6-C6-C5	3.97	127.96	119.86
2	A	500	GNP	O1B-PB-N3B	-3.46	106.68	111.77
3	D	600	RIO	O3-C4-C9	-3.43	98.76	107.48
2	A	500	GNP	C5-C6-N1	-3.41	113.99	118.19
2	C	500	GNP	O2B-PB-O1B	3.39	117.03	109.92
2	A	500	GNP	O6-C6-C5	3.21	126.42	119.86
3	D	600	RIO	C10-C15-N4	3.21	115.99	110.20
3	A	600	RIO	O5-C9-C8	-3.08	101.83	109.18
3	B	600	RIO	C4-C5-C6	3.01	116.97	109.63
3	D	600	RIO	C5-C4-C9	3.01	118.53	111.66
2	C	500	GNP	O5'-PA-O1A	2.96	120.63	109.07
2	A	500	GNP	O3A-PB-N3B	-2.95	98.41	106.59
3	B	600	RIO	O10-C17-C2	-2.94	102.54	111.05
3	A	600	RIO	C14-C15-N4	2.90	117.00	111.05
2	B	500	GNP	O3G-PG-O1G	2.90	120.75	113.45
3	D	600	RIO	O5-C9-C4	2.88	114.80	107.48
2	D	500	GNP	O3A-PB-N3B	2.60	113.81	106.59
3	B	600	RIO	C4-C9-C8	2.59	116.00	111.16
3	A	600	RIO	O3-C4-C9	2.57	114.02	107.48
3	D	600	RIO	C3-O3-C4	2.53	124.21	117.96
2	D	500	GNP	O2G-PG-O1G	-2.52	107.11	113.45
3	B	600	RIO	C8-C7-C6	-2.47	106.12	111.18
2	A	500	GNP	O5'-PA-O1A	2.46	118.68	109.07
2	D	500	GNP	O6-C6-N1	-2.39	119.48	122.69
2	D	500	GNP	PA-O3A-PB	2.38	140.99	132.62
2	A	500	GNP	O6-C6-N1	-2.37	119.50	122.69
3	A	600	RIO	O5-C10-C15	2.37	112.30	108.22
2	C	500	GNP	O6-C6-N1	-2.34	119.54	122.69
2	D	500	GNP	O3G-PG-O2G	2.34	113.86	107.64
3	B	600	RIO	O10-C17-C16	2.32	119.33	111.82
3	D	600	RIO	C4-C9-C8	2.31	115.48	111.16
3	B	600	RIO	O5-C9-C4	2.30	113.32	107.48
2	D	500	GNP	O1G-PG-N3B	-2.30	108.39	111.77
2	B	500	GNP	O6-C6-N1	-2.29	119.61	122.69
3	B	600	RIO	C10-O6-C11	2.27	118.14	113.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	500	GNP	O2G-PG-O1G	-2.19	107.95	113.45
2	A	500	GNP	O5'-C5'-C4'	-2.17	101.53	108.99
3	A	600	RIO	C8-C7-C6	-2.14	106.79	111.18
3	D	600	RIO	C10-O6-C11	2.13	117.87	113.69
3	B	600	RIO	C5-C4-C9	2.09	116.43	111.66
3	B	600	RIO	C3-O2-C2	2.08	113.84	106.13
2	D	500	GNP	O2B-PB-O3A	2.06	111.52	104.64
3	B	600	RIO	O5-C10-C15	2.01	111.69	108.22

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	600	RIO	O2-C3-O3-C4
3	A	600	RIO	C16-C3-O3-C4
3	B	600	RIO	O2-C3-O3-C4
3	B	600	RIO	C16-C3-O3-C4
3	B	600	RIO	O6-C11-C12-N3
3	D	600	RIO	O2-C3-O3-C4
3	D	600	RIO	C16-C3-O3-C4
3	D	600	RIO	O6-C11-C12-N3
2	C	500	GNP	PB-N3B-PG-O1G
2	C	500	GNP	PG-N3B-PB-O3A
2	C	500	GNP	C2'-C1'-N9-C8
2	C	500	GNP	C2'-C1'-N9-C4
2	A	500	GNP	PG-N3B-PB-O1B
2	A	500	GNP	C2'-C1'-N9-C8
2	A	500	GNP	C2'-C1'-N9-C4
2	D	500	GNP	PB-N3B-PG-O1G
2	D	500	GNP	PG-N3B-PB-O1B
2	D	500	GNP	PA-O3A-PB-O1B
2	D	500	GNP	PA-O3A-PB-O2B
2	D	500	GNP	O4'-C1'-N9-C4
2	D	500	GNP	C2'-C1'-N9-C8
2	D	500	GNP	C2'-C1'-N9-C4
2	B	500	GNP	PG-N3B-PB-O1B
2	B	500	GNP	C2'-C1'-N9-C8
2	B	500	GNP	C2'-C1'-N9-C4
3	B	600	RIO	O1-C1-C2-O2
3	B	600	RIO	O6-C10-O5-C9
3	A	600	RIO	C5-C4-O3-C3
3	B	600	RIO	O1-C1-C2-C17

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Mol	Chain	Res	Type	Atoms
3	D	600	RIO	O6-C10-O5-C9
2	B	500	GNP	PB-O3A-PA-O1A
3	A	600	RIO	C4-C9-O5-C10
3	D	600	RIO	C4-C9-O5-C10
3	A	600	RIO	C8-C9-O5-C10
3	B	600	RIO	C4-C9-O5-C10
2	A	500	GNP	PG-N3B-PB-O3A
2	A	500	GNP	PB-O3A-PA-O1A
2	D	500	GNP	PB-O3A-PA-O1A
2	C	500	GNP	PB-O3A-PA-O2A
2	D	500	GNP	PB-O3A-PA-O2A

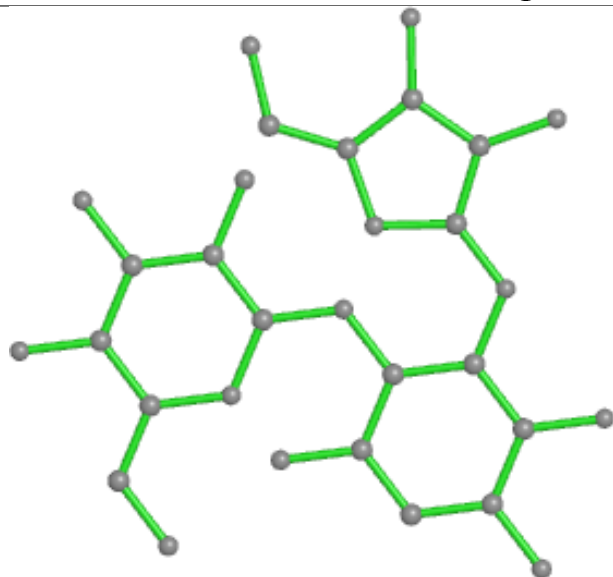
There are no ring outliers.

1 monomer is involved in 1 short contact:

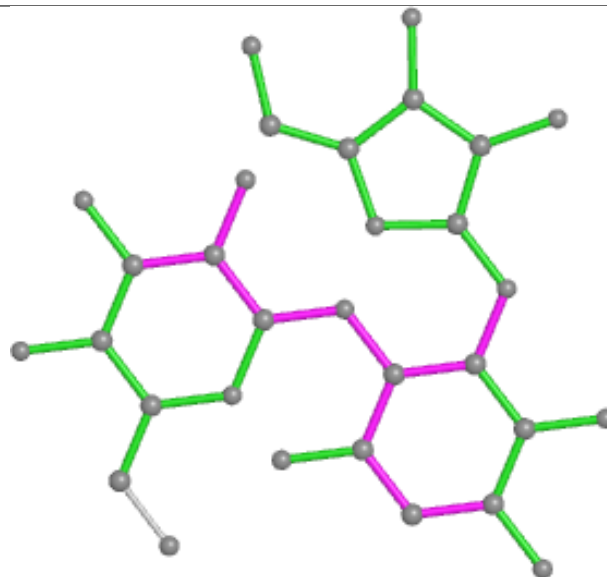
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	GNP	1	0

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.

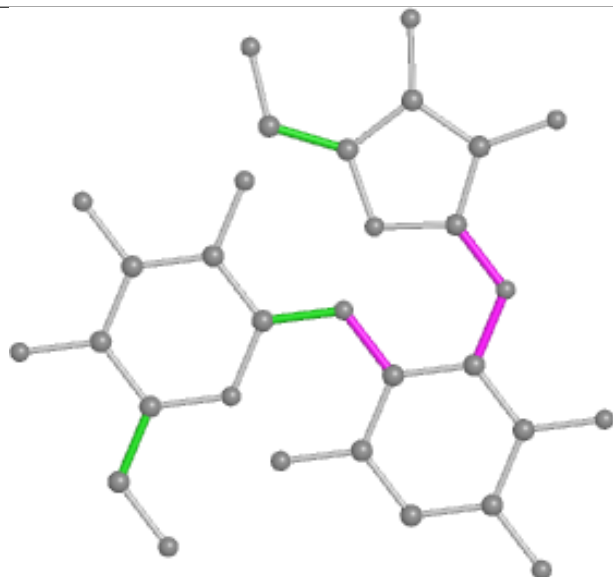
## Ligand RIO A 600



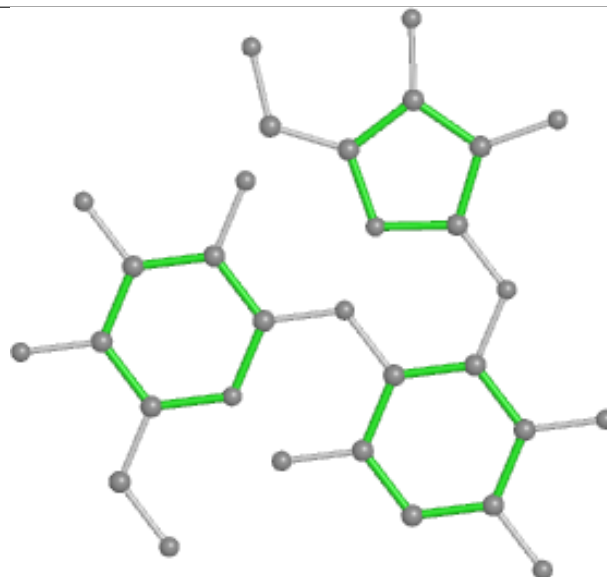
Bond lengths



Bond angles

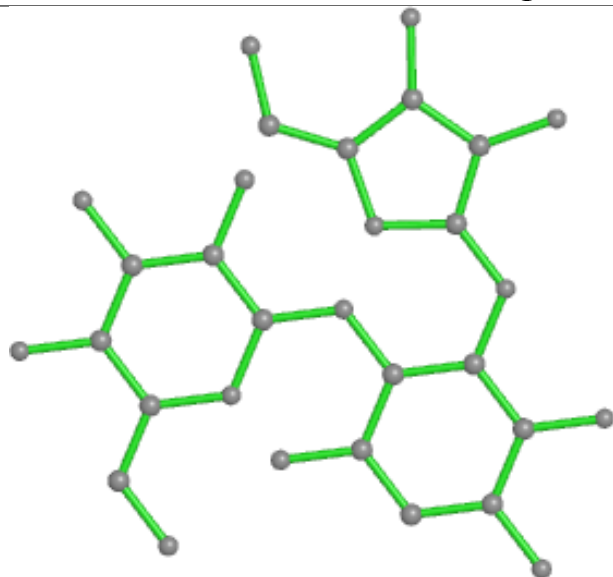


Torsions

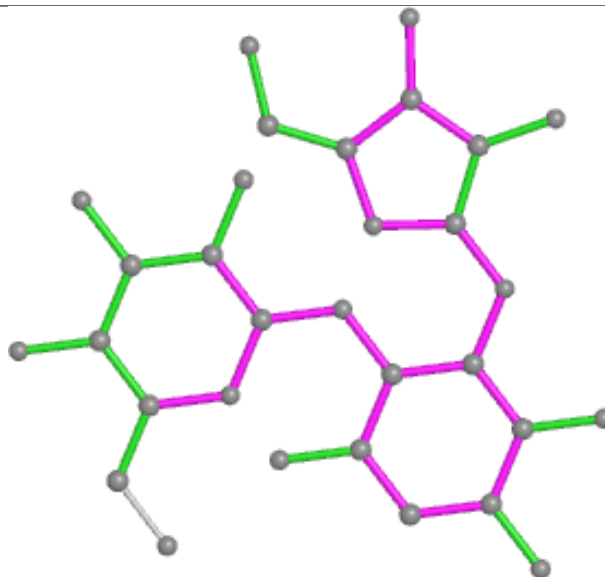


Rings

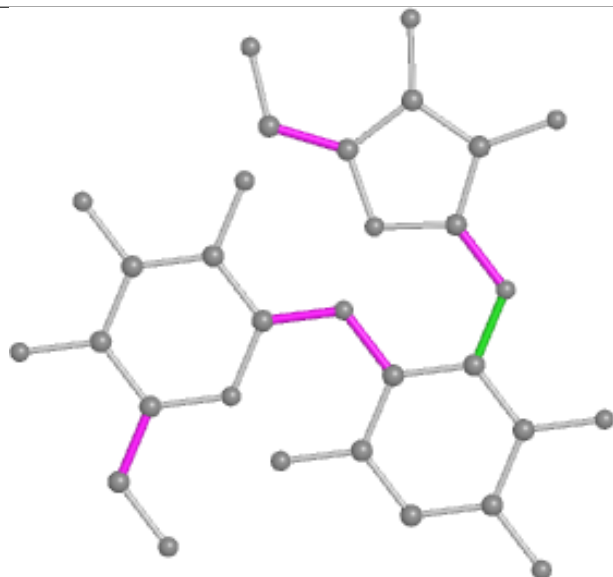
## Ligand RIO B 600



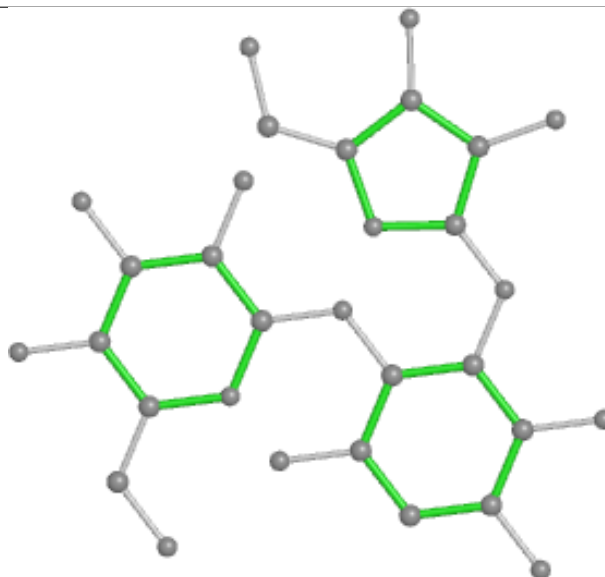
Bond lengths



Bond angles

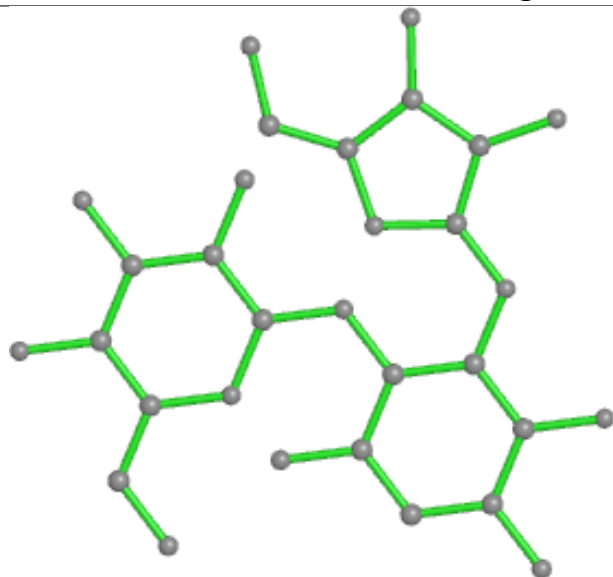


Torsions

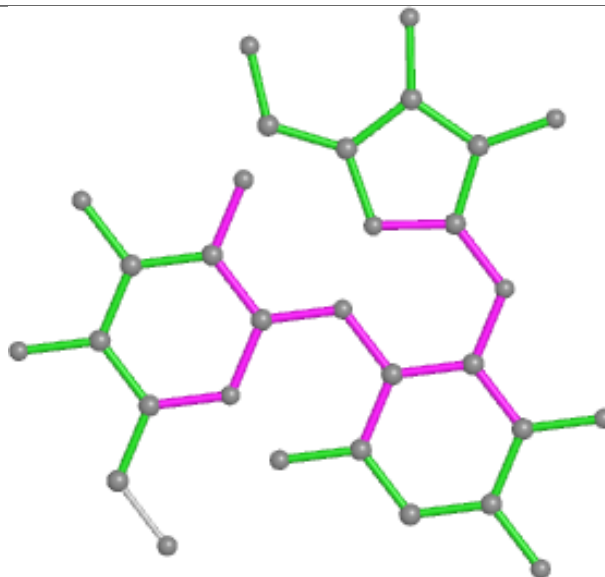


Rings

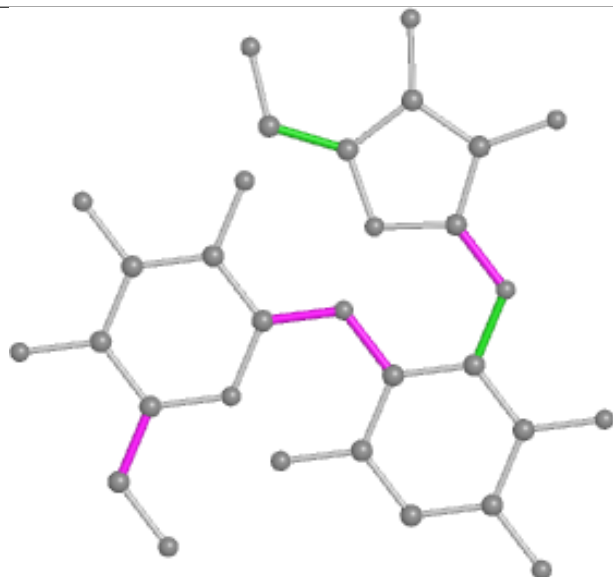
## Ligand RIO D 600



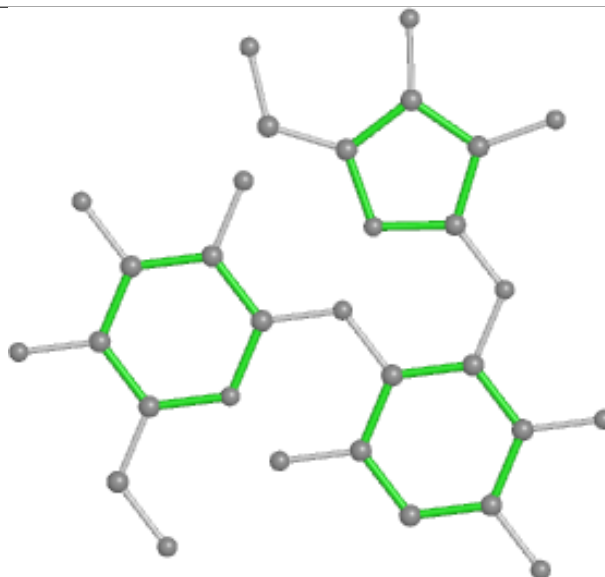
Bond lengths



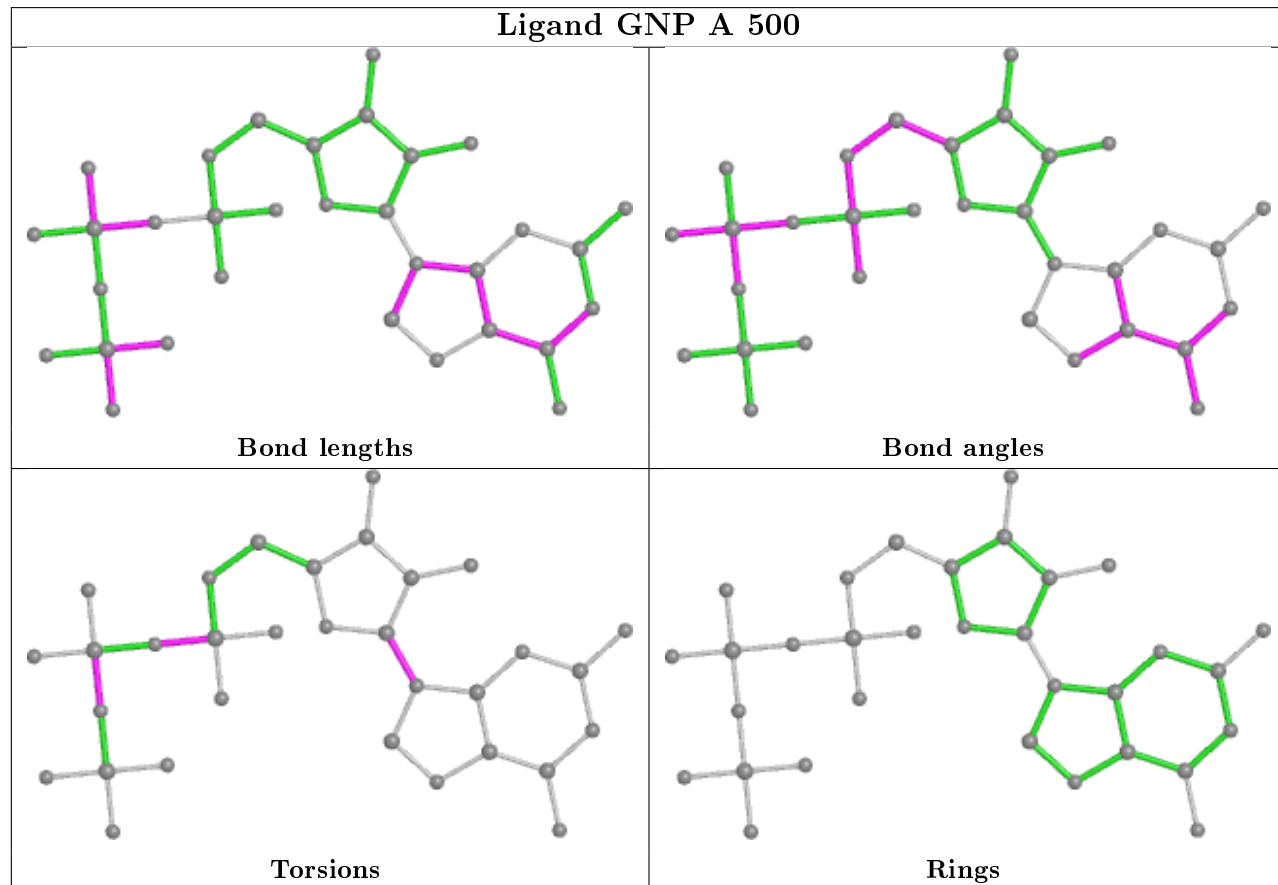
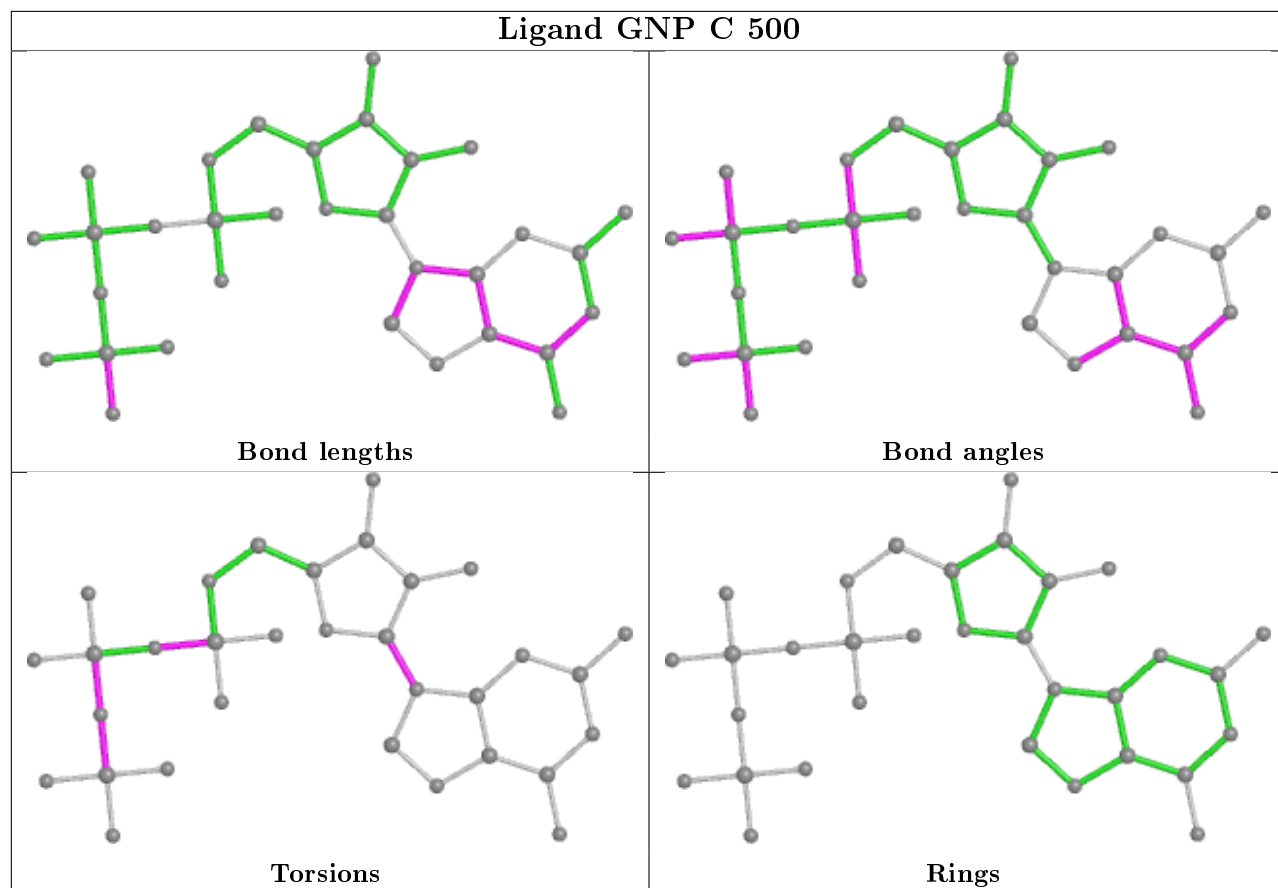
Bond angles

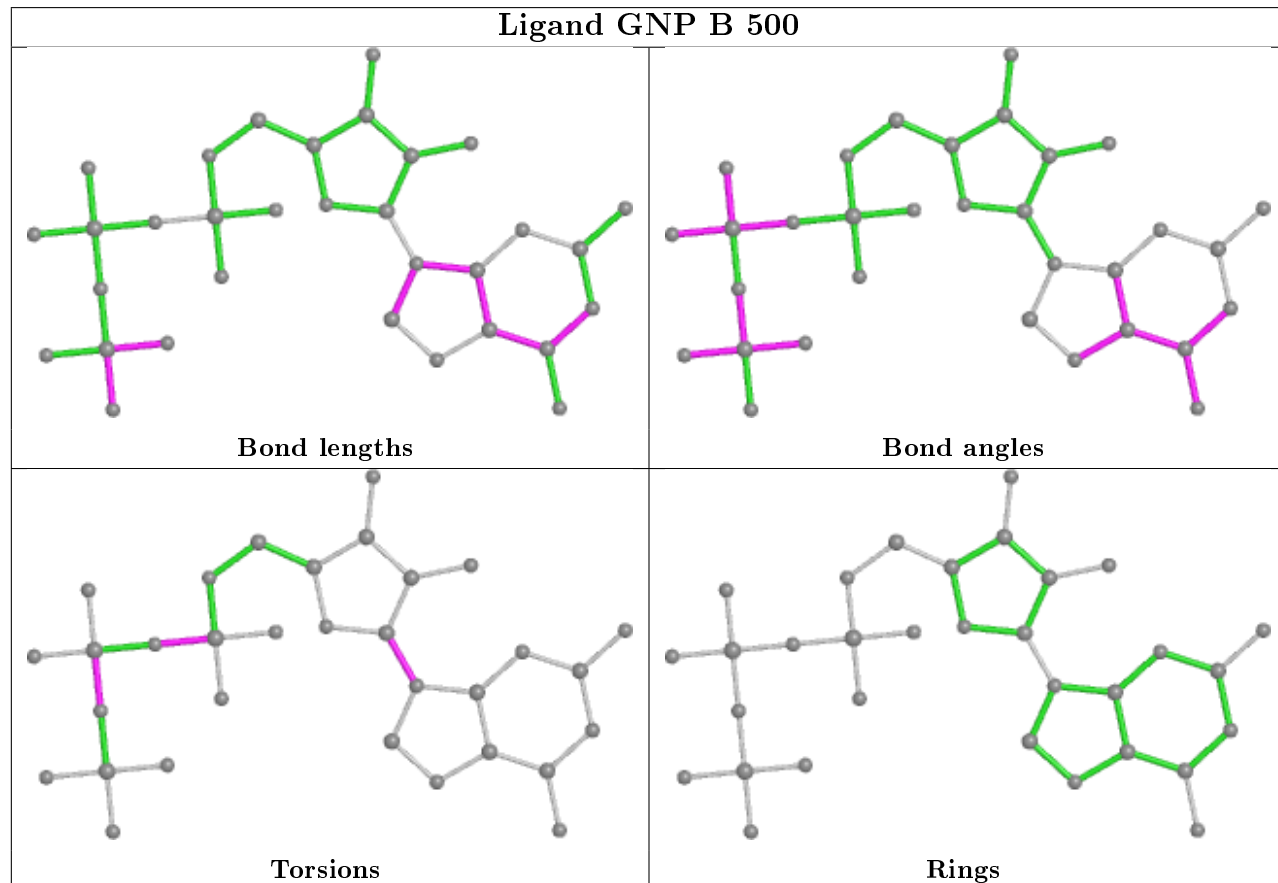
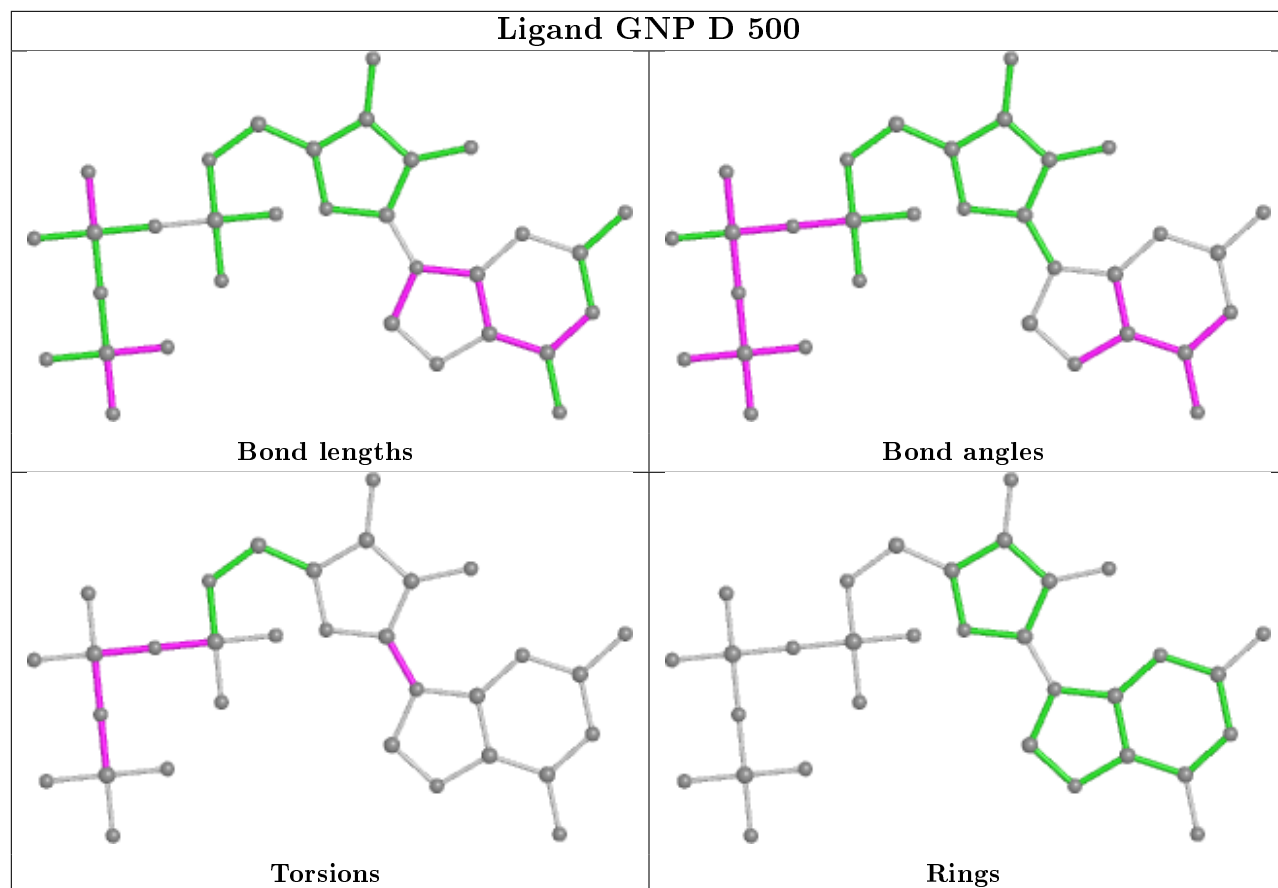


Torsions



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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	293/305 (96%)	-0.17	1 (0%) 94 93	46, 67, 91, 143	0
1	B	292/305 (95%)	-0.07	2 (0%) 87 86	43, 63, 95, 128	0
1	C	287/305 (94%)	0.01	1 (0%) 94 93	44, 71, 106, 138	0
1	D	291/305 (95%)	-0.10	7 (2%) 59 56	62, 84, 118, 134	0
All	All	1163/1220 (95%)	-0.08	11 (0%) 84 82	43, 72, 109, 143	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	212	TYR	4.2
1	A	315	THR	3.6
1	D	208	ILE	3.0
1	D	434	ILE	2.6
1	D	460	ILE	2.6
1	D	459	ASN	2.3
1	D	317	ILE	2.3
1	D	181	ASP	2.3
1	D	254	ASN	2.1
1	C	212	TYR	2.1
1	B	182	ASN	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 carbohydrates in this entry.

## 6.4 Ligands ⓘ

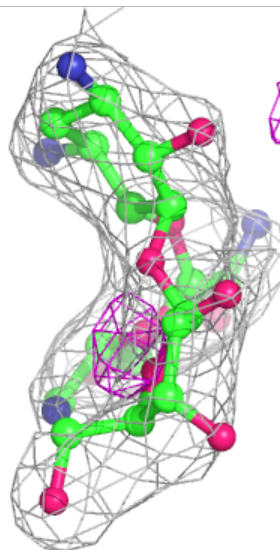
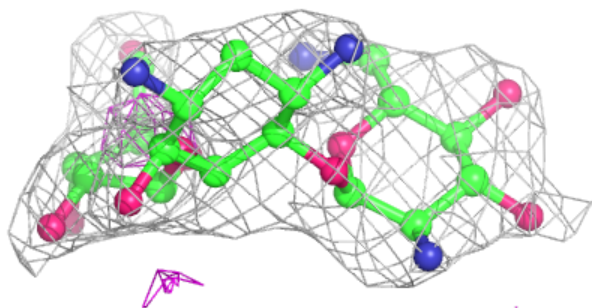
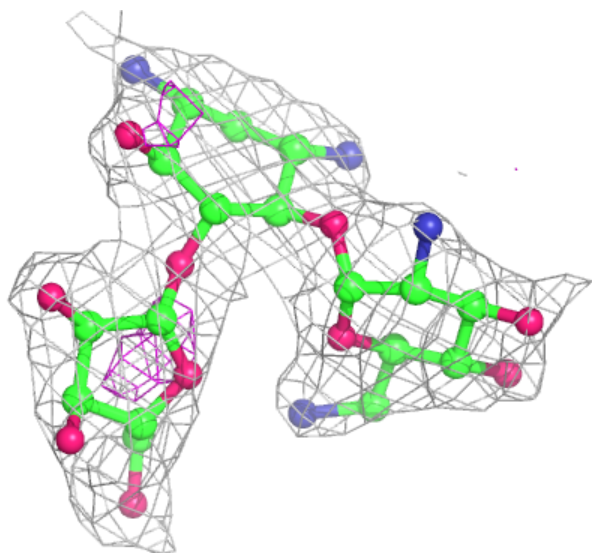
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	RIO	B	600	31/31	0.88	0.18	82,96,104,109	0
3	RIO	D	600	31/31	0.89	0.14	83,94,107,114	0
4	MG	A	700	1/1	0.90	0.13	87,87,87,87	0
5	CL	A	802	1/1	0.91	0.11	98,98,98,98	0
3	RIO	A	600	31/31	0.92	0.12	77,99,123,139	0
5	CL	B	802	1/1	0.93	0.12	89,89,89,89	0
5	CL	C	802	1/1	0.94	0.13	76,76,76,76	0
4	MG	C	700	1/1	0.96	0.09	76,76,76,76	0
4	MG	D	700	1/1	0.96	0.05	62,62,62,62	0
2	GNP	A	500	32/32	0.96	0.15	60,68,78,83	0
2	GNP	D	500	32/32	0.96	0.10	65,71,109,118	0
2	GNP	C	500	32/32	0.97	0.12	56,68,87,93	0
4	MG	D	702	1/1	0.97	0.07	90,90,90,90	0
4	MG	C	702	1/1	0.97	0.07	85,85,85,85	0
4	MG	B	702	1/1	0.98	0.07	73,73,73,73	0
4	MG	A	702	1/1	0.98	0.08	75,75,75,75	0
2	GNP	B	500	32/32	0.98	0.12	53,57,79,87	0
4	MG	B	700	1/1	0.99	0.12	57,57,57,57	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.

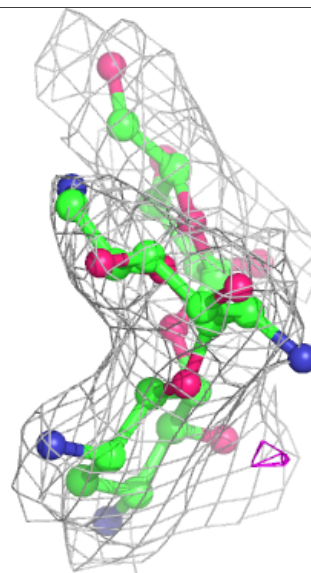
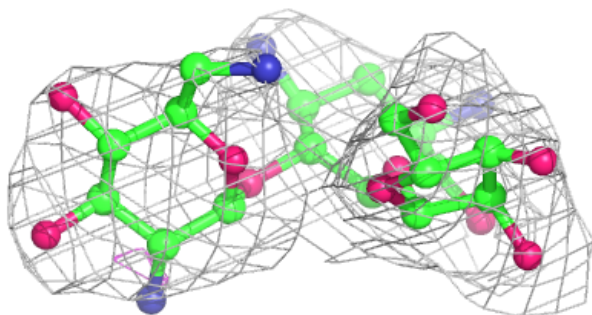
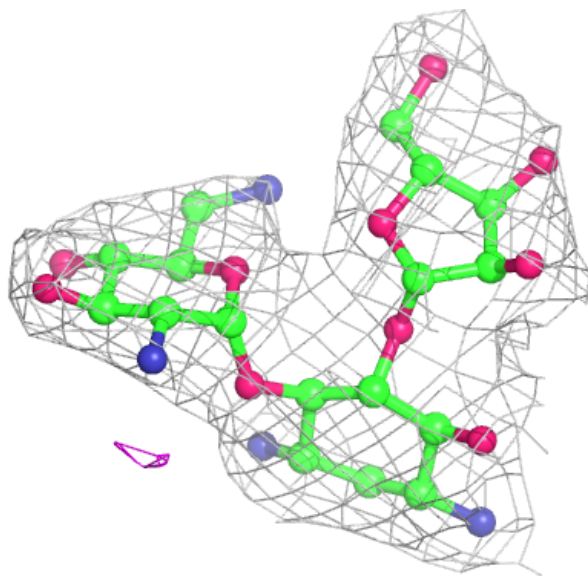
**Electron density around RIO B 600:**

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



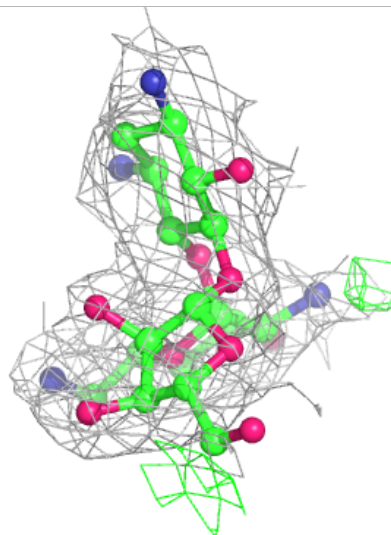
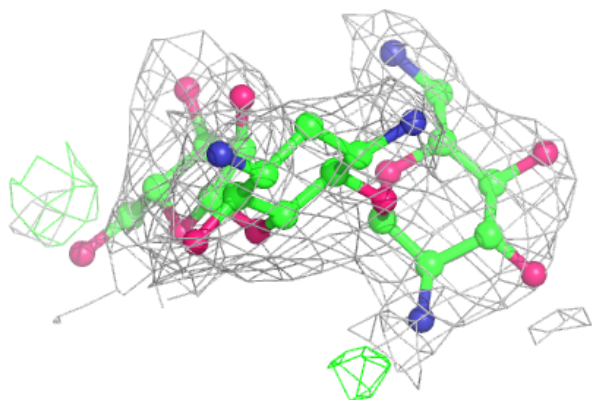
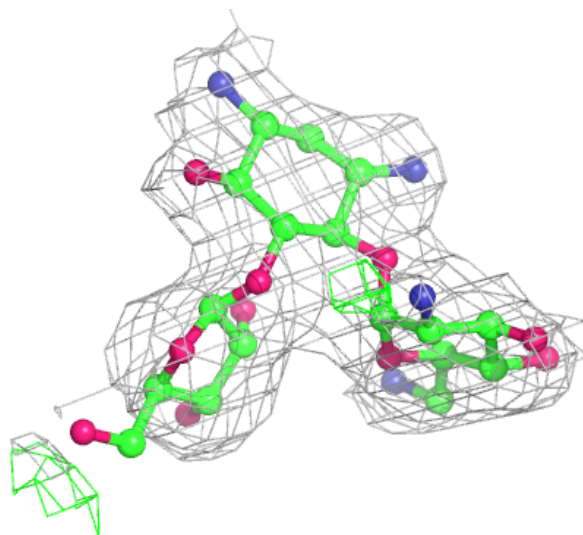
**Electron density around RIO D 600:**

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



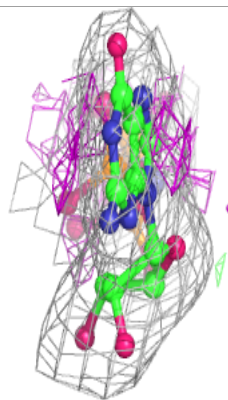
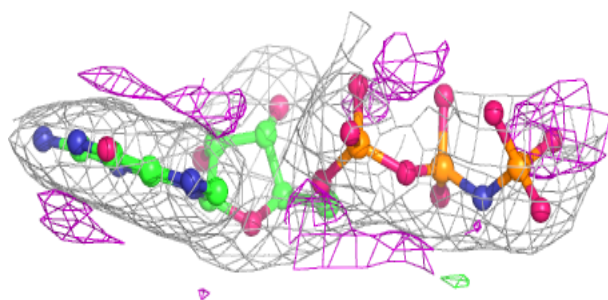
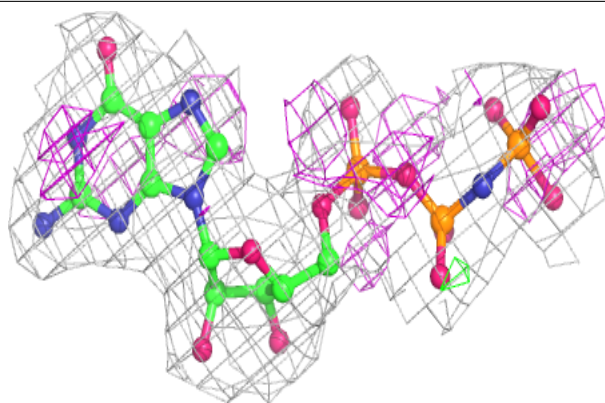
**Electron density around RIO A 600:**

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

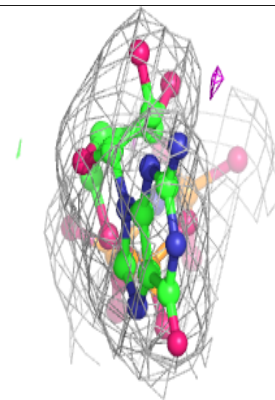
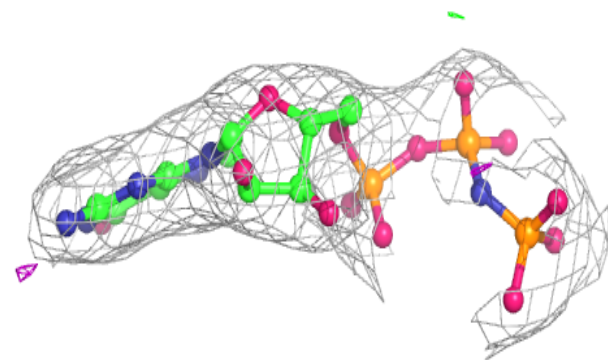
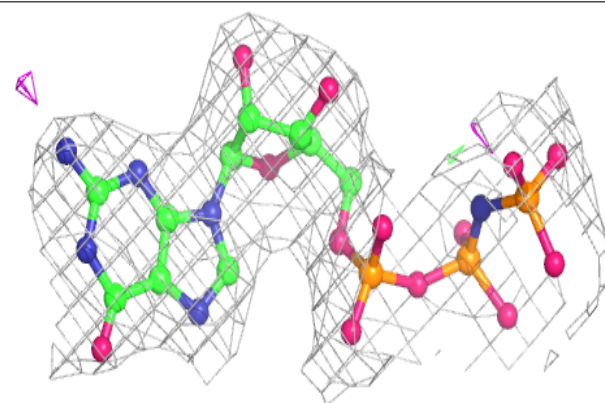


**Electron density around GNP A 500:**

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

**Electron density around GNP D 500:**

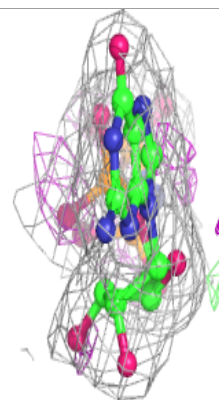
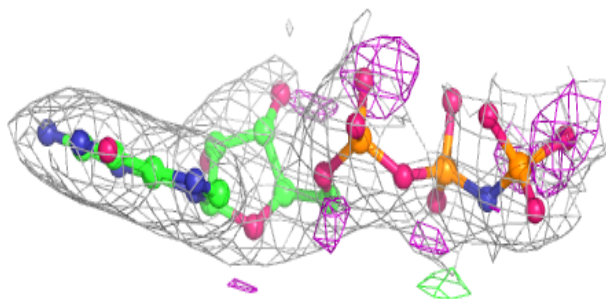
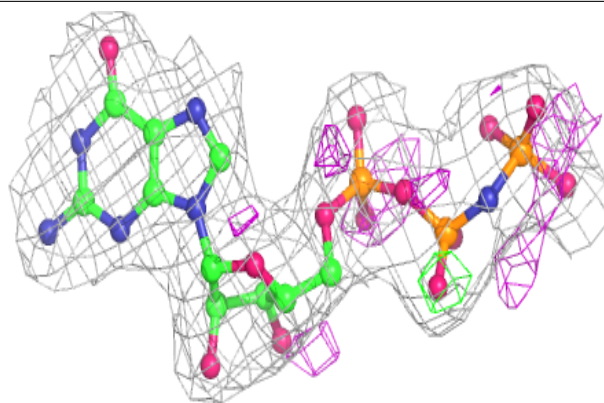
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



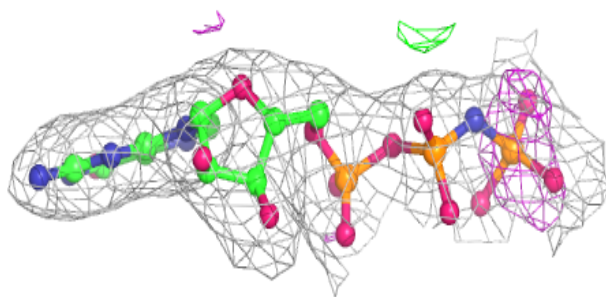
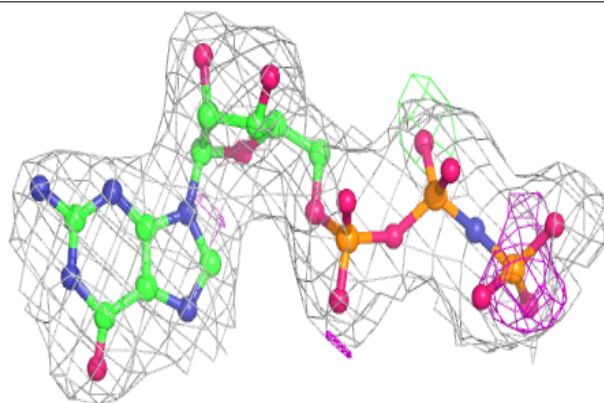


**Electron density around GNP C 500:**

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

**Electron density around GNP B 500:**

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





## 6.5 Other polymers

There are no such residues in this entry.