



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:24 PM UTC

PDB ID : 6XB3 / pdb_00006xb3
Title : Structure of AcNPV poxin in post-reactive state with Gp[2'-5']Ap[3']
Authors : Eaglesham, J.B.; McCarty, K.L.; Kranzusch, P.J.
Deposited on : 2020-06-05
Resolution : 1.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

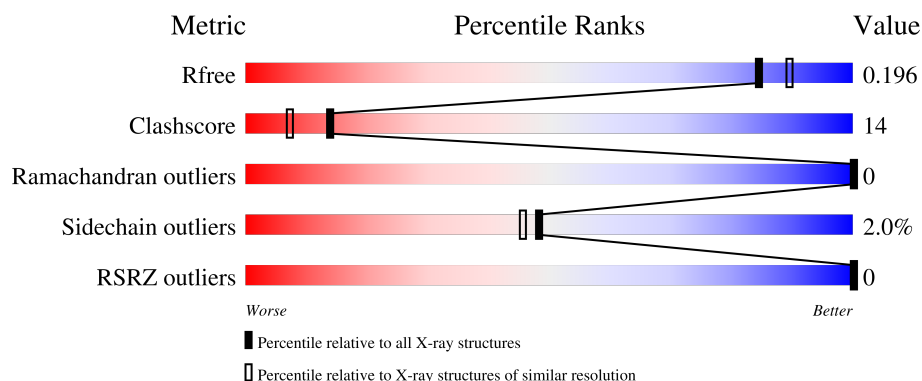
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	241	
1	B	241	
1	C	241	
1	D	241	
1	E	241	

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Mol	Chain	Length	Quality of chain
1	F	241	 68%22%9%
1	G	241	 72%21%6%
1	H	241	 71%25%.
1	I	241	 67%28%5%
1	J	241	 70%25%. .
1	K	241	 70%21%. 7%
1	L	241	 67%26%. 7%
1	M	241	 67%27%6%
1	N	241	 68%24%7%
1	O	241	 68%25%. 6%
1	P	241	 70%24%5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 33148 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.

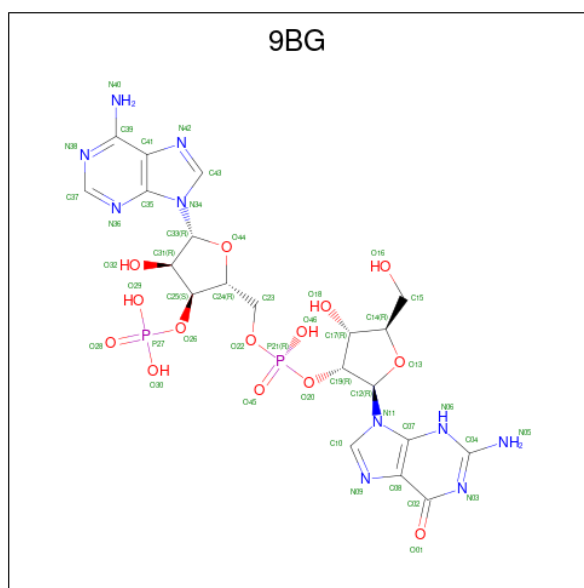
- Molecule 1 is a protein called Poxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	234	Total	C	N	O	S	0	0	0
			1869	1202	316	343	8			
1	B	229	Total	C	N	O	S	0	0	0
			1831	1179	309	335	8			
1	C	226	Total	C	N	O	S	0	0	0
			1810	1168	305	329	8			
1	D	225	Total	C	N	O	S	0	0	0
			1802	1162	304	328	8			
1	E	231	Total	C	N	O	S	0	0	0
			1847	1189	312	338	8			
1	F	220	Total	C	N	O	S	0	0	0
			1762	1141	297	316	8			
1	G	226	Total	C	N	O	S	0	0	0
			1807	1166	304	329	8			
1	H	232	Total	C	N	O	S	0	0	0
			1854	1194	313	339	8			
1	I	229	Total	C	N	O	S	0	0	0
			1831	1179	309	335	8			
1	J	231	Total	C	N	O	S	0	0	0
			1847	1190	312	337	8			
1	K	223	Total	C	N	O	S	0	0	0
			1785	1155	301	321	8			
1	L	225	Total	C	N	O	S	0	0	0
			1797	1162	302	325	8			
1	M	226	Total	C	N	O	S	0	0	0
			1808	1165	304	331	8			
1	N	224	Total	C	N	O	S	0	0	0
			1792	1157	302	325	8			
1	O	227	Total	C	N	O	S	0	0	0
			1815	1170	306	331	8			
1	P	228	Total	C	N	O	S	0	0	0
			1821	1174	307	332	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P08358
B	0	SER	-	expression tag	UNP P08358
C	0	SER	-	expression tag	UNP P08358
D	0	SER	-	expression tag	UNP P08358
E	0	SER	-	expression tag	UNP P08358
F	0	SER	-	expression tag	UNP P08358
G	0	SER	-	expression tag	UNP P08358
H	0	SER	-	expression tag	UNP P08358
I	0	SER	-	expression tag	UNP P08358
J	0	SER	-	expression tag	UNP P08358
K	0	SER	-	expression tag	UNP P08358
L	0	SER	-	expression tag	UNP P08358
M	0	SER	-	expression tag	UNP P08358
N	0	SER	-	expression tag	UNP P08358
O	0	SER	-	expression tag	UNP P08358
P	0	SER	-	expression tag	UNP P08358

- Molecule 2 is 2',5'-GpAp (CCD ID: 9BG) (formula: $C_{20}H_{26}N_{10}O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
2	B	1	Total	C	N	O	P	0	0
			46	20	10	14	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	C	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	E	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	F	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	G	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	G	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	I	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	J	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	K	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	K	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	M	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	M	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	P	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	P	1	Total 46	C 20	N 10	O 14	P 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	234	Total 234	O 234	0	0
3	B	226	Total 226	O 226	0	0
3	C	211	Total 211	O 211	0	0
3	D	170	Total 170	O 170	0	0
3	E	211	Total 211	O 211	0	0

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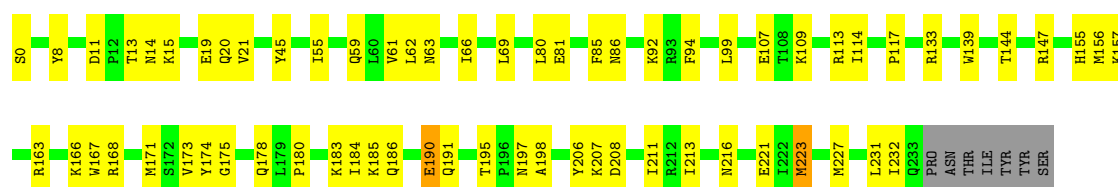
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	208	Total 208	O 208	0	0
3	G	220	Total 220	O 220	0	0
3	H	198	Total 198	O 198	0	0
3	I	254	Total 254	O 254	0	0
3	J	228	Total 228	O 228	0	0
3	K	201	Total 201	O 201	0	0
3	L	178	Total 178	O 178	0	0
3	M	239	Total 239	O 239	0	0
3	N	205	Total 205	O 205	0	0
3	O	176	Total 176	O 176	0	0
3	P	175	Total 175	O 175	0	0

3 Residue-property plots

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.

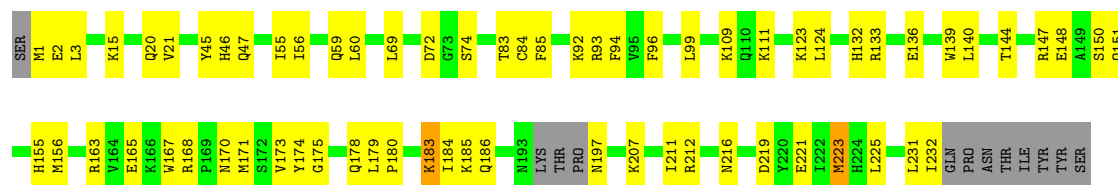
• Molecule 1: Poxin

Chain A: 



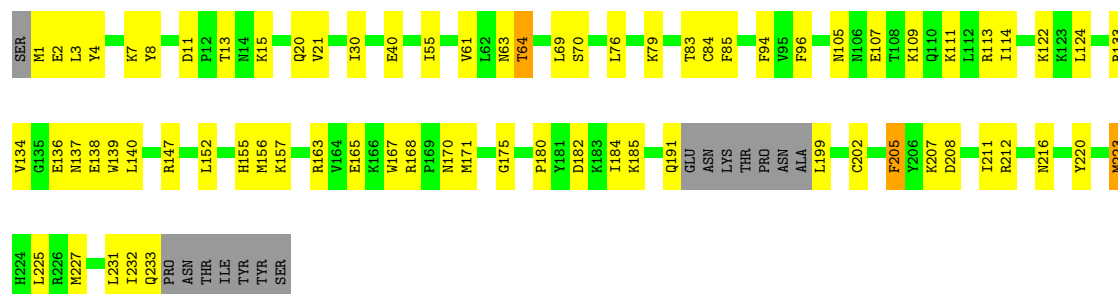
• Molecule 1: Poxin

Chain B: 



• Molecule 1: Poxin

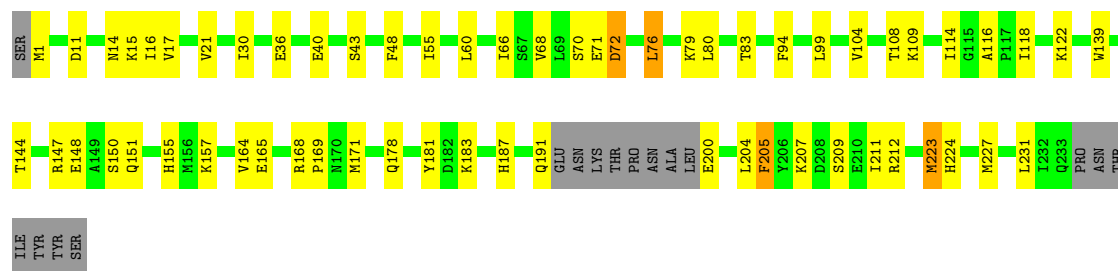
Chain C: 



• Molecule 1: Poxin

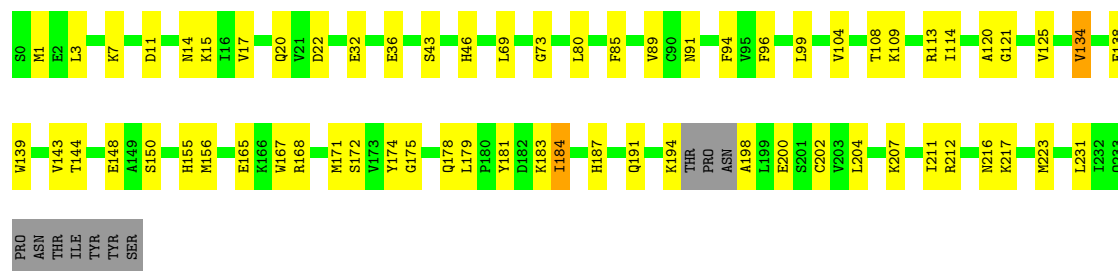
Chain D: 





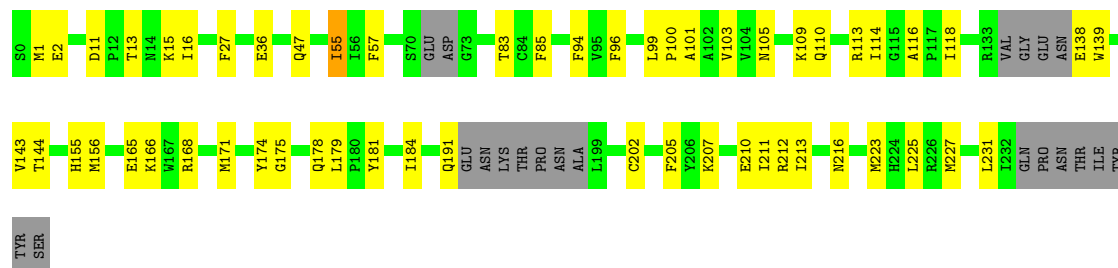
• Molecule 1: Poxin

Chain E: 69% 26%



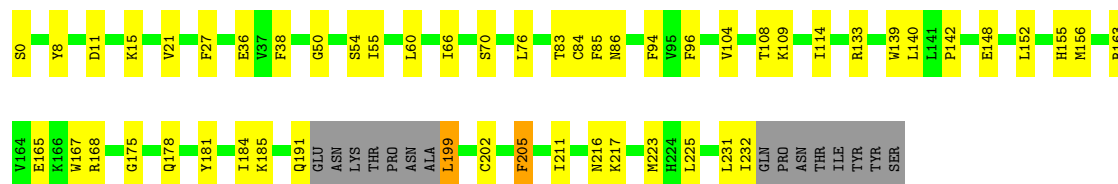
• Molecule 1: Poxin

Chain F: 68% 22% 9%



• Molecule 1: Poxin

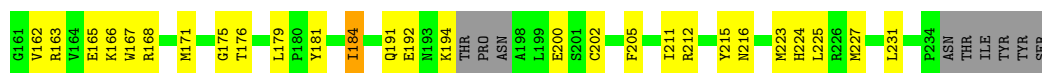
Chain G: 72% 21% 6%



• Molecule 1: Poxin

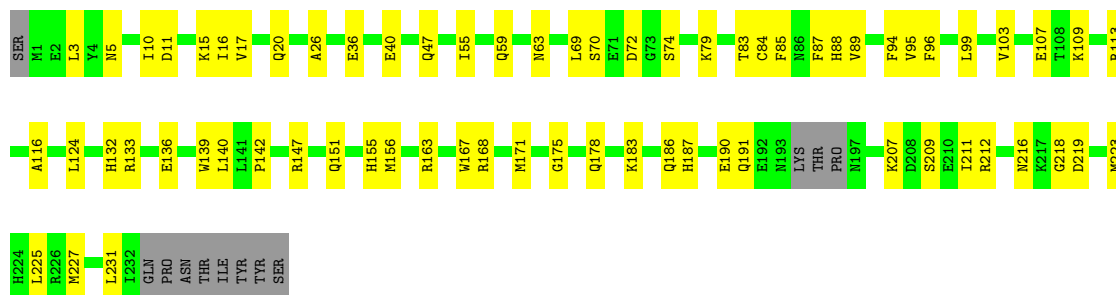
Chain H: 71% 25%





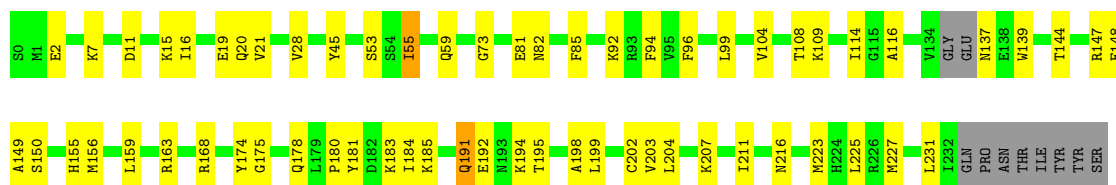
- Molecule 1: Poxin

Chain I: 67% 28% 5%



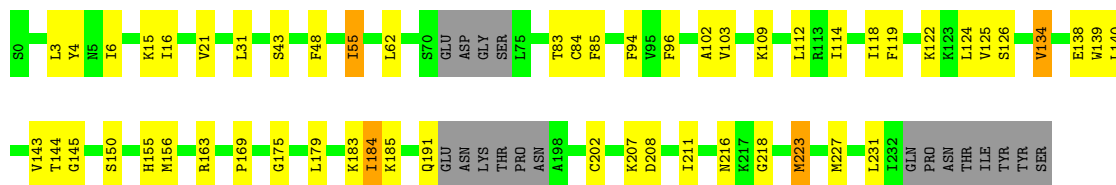
- Molecule 1: Poxin

Chain J: 70% 25% 5%



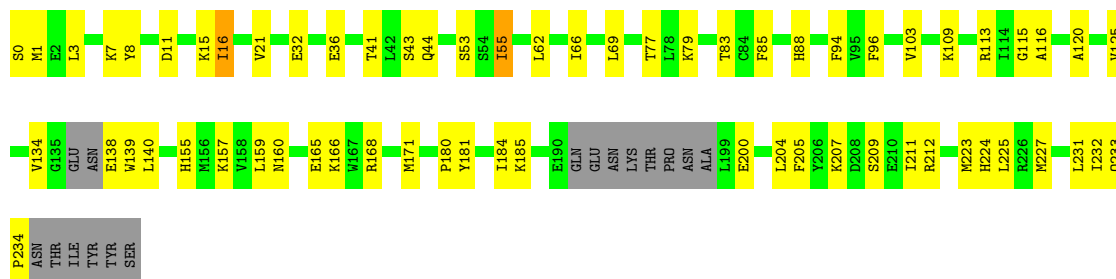
- Molecule 1: Poxin

Chain K: 70% 21% 7%



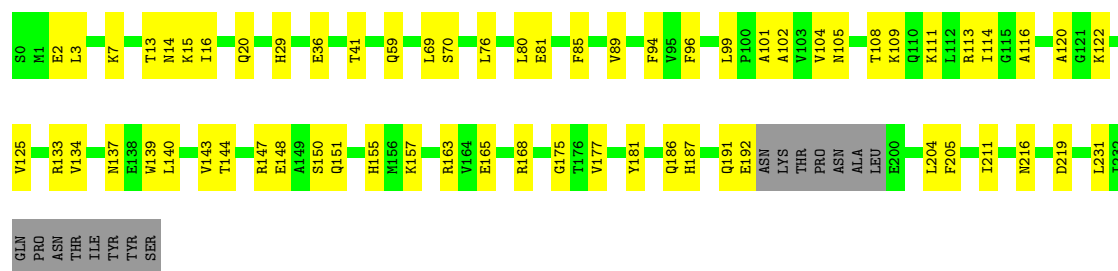
- Molecule 1: Poxin

Chain L: 67% 26% 7%



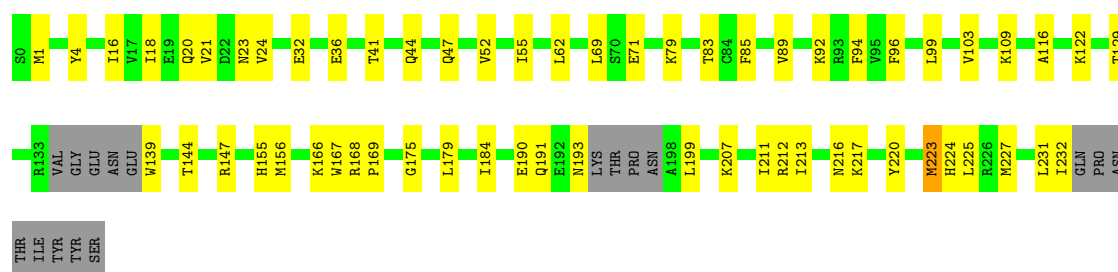
- Molecule 1: Poxin

Chain M:  67% 27% 6%



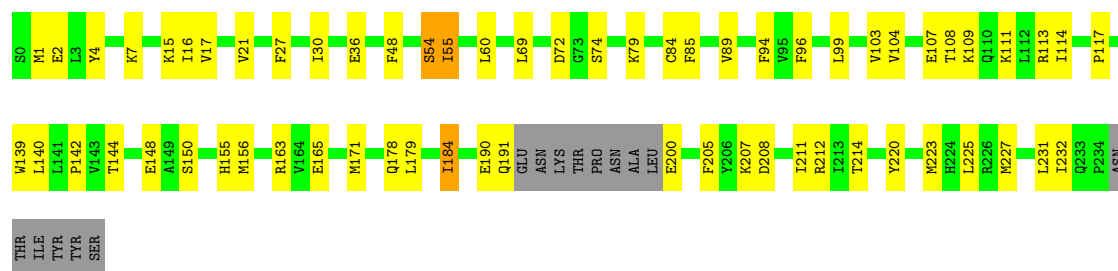
• Molecule 1: Poxin

Chain N:  68% 24% 7%



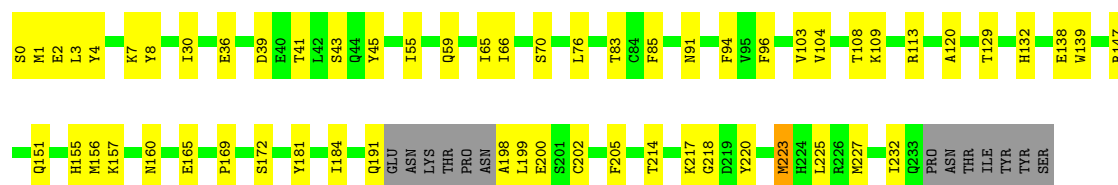
• Molecule 1: Poxin

Chain O:  68% 25% 6%



• Molecule 1: Poxin

Chain P:  70% 24% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	127.23Å 127.19Å 127.15Å 124.81° 102.39° 102.39°	Depositor
Resolution (Å)	38.31 – 1.90 38.31 – 1.90	Depositor EDS
% Data completeness (in resolution range)	92.3 (38.31-1.90) 92.2 (38.31-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.10 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.175 , 0.208 0.163 , 0.196	Depositor DCC
R_{free} test set	2037 reflections (0.48%)	wwPDB-VP
Wilson B-factor (Å ²)	28.3	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.458 for -l,-h,h+k+l 0.458 for -k,h+k+l,-h 0.468 for -h-k-l,l,k 0.084 for -h,-l,-k 0.084 for h+k+l,-k,-l 0.080 for k,h,-h-k-l 0.080 for l,-h-k-l,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	33148	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.81% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 9BG

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	0.33	0/1910	0.57	0/2592
1	B	0.32	0/1870	0.55	0/2536
1	C	0.30	0/1849	0.54	0/2507
1	D	0.29	0/1841	0.52	0/2496
1	E	0.31	0/1886	0.56	0/2556
1	F	0.32	0/1799	0.56	0/2436
1	G	0.29	0/1846	0.54	0/2503
1	H	0.29	0/1894	0.55	0/2568
1	I	0.33	0/1870	0.57	0/2536
1	J	0.32	0/1887	0.56	0/2560
1	K	0.30	0/1823	0.55	0/2471
1	L	0.29	0/1836	0.56	0/2489
1	M	0.30	0/1847	0.58	0/2504
1	N	0.29	0/1830	0.54	0/2480
1	O	0.29	0/1855	0.52	0/2516
1	P	0.29	0/1860	0.55	0/2522
All	All	0.31	0/29703	0.55	0/40272

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

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	1869	0	1890	66	0
1	B	1831	0	1849	57	0
1	C	1810	0	1832	58	1
1	D	1802	0	1823	49	0
1	E	1847	0	1869	53	0
1	F	1762	0	1795	53	0
1	G	1807	0	1830	38	0
1	H	1854	0	1876	51	0
1	I	1831	0	1849	57	0
1	J	1847	0	1872	52	0
1	K	1785	0	1815	43	0
1	L	1797	0	1825	55	1
1	M	1808	0	1826	57	1
1	N	1792	0	1817	50	0
1	O	1815	0	1835	48	0
1	P	1821	0	1844	46	0
2	A	46	0	0	5	0
2	B	46	0	0	2	0
2	C	92	0	0	9	0
2	E	46	0	0	3	0
2	F	46	0	0	2	0
2	G	92	0	0	6	0
2	I	46	0	0	2	0
2	J	46	0	0	4	0
2	K	92	0	0	3	0
2	M	92	0	0	4	0
2	P	92	0	0	8	0
3	A	234	0	0	31	1
3	B	226	0	0	26	7
3	C	211	0	0	28	1
3	D	170	0	0	21	1
3	E	211	0	0	23	1
3	F	208	0	0	29	1
3	G	220	0	0	17	3
3	H	198	0	0	26	1
3	I	254	0	0	31	5
3	J	228	0	0	19	0
3	K	201	0	0	22	4
3	L	178	0	0	27	0
3	M	239	0	0	28	0
3	N	205	0	0	25	2
3	O	176	0	0	17	0
3	P	175	0	0	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	33148	0	29447	851	15

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 14.

The worst 5 of 851 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:F:301:9BG:C33	2:F:301:9BG:O44	1.66	1.23
2:J:301:9BG:C33	2:J:301:9BG:O44	1.66	1.22
2:K:302:9BG:O44	2:K:302:9BG:C33	1.67	1.20
2:C:301:9BG:C33	2:C:301:9BG:O44	1.67	1.19
2:C:302:9BG:O44	2:C:302:9BG:C33	1.67	1.19

The worst 5 of 15 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)
3:B:429:HOH:O	3:C:434:HOH:O[1_655]	1.75	0.45
3:G:498:HOH:O	3:I:631:HOH:O[1_566]	1.81	0.39
3:B:442:HOH:O	3:F:409:HOH:O[1_655]	2.00	0.20
3:A:459:HOH:O	3:H:452:HOH:O[1_554]	2.02	0.18
3:B:445:HOH:O	3:K:458:HOH:O[1_544]	2.03	0.17

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	232/241 (96%)	226 (97%)	6 (3%)	0	100	100
1	B	225/241 (93%)	220 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	222/241 (92%)	216 (97%)	6 (3%)	0	100	100
1	D	221/241 (92%)	215 (97%)	6 (3%)	0	100	100
1	E	227/241 (94%)	221 (97%)	6 (3%)	0	100	100
1	F	212/241 (88%)	209 (99%)	3 (1%)	0	100	100
1	G	222/241 (92%)	217 (98%)	5 (2%)	0	100	100
1	H	228/241 (95%)	221 (97%)	7 (3%)	0	100	100
1	I	225/241 (93%)	221 (98%)	4 (2%)	0	100	100
1	J	227/241 (94%)	219 (96%)	8 (4%)	0	100	100
1	K	217/241 (90%)	213 (98%)	4 (2%)	0	100	100
1	L	219/241 (91%)	212 (97%)	7 (3%)	0	100	100
1	M	222/241 (92%)	218 (98%)	4 (2%)	0	100	100
1	N	218/241 (90%)	214 (98%)	4 (2%)	0	100	100
1	O	223/241 (92%)	218 (98%)	5 (2%)	0	100	100
1	P	224/241 (93%)	219 (98%)	5 (2%)	0	100	100
All	All	3564/3856 (92%)	3479 (98%)	85 (2%)	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	211/218 (97%)	209 (99%)	2 (1%)	70	73
1	B	206/218 (94%)	203 (98%)	3 (2%)	57	56
1	C	204/218 (94%)	200 (98%)	4 (2%)	48	46
1	D	203/218 (93%)	197 (97%)	6 (3%)	36	30
1	E	208/218 (95%)	204 (98%)	4 (2%)	50	47
1	F	199/218 (91%)	196 (98%)	3 (2%)	57	56
1	G	204/218 (94%)	199 (98%)	5 (2%)	42	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	209/218 (96%)	206 (99%)	3 (1%)	59	59
1	I	206/218 (94%)	203 (98%)	3 (2%)	57	56
1	J	209/218 (96%)	207 (99%)	2 (1%)	68	70
1	K	201/218 (92%)	193 (96%)	8 (4%)	28	20
1	L	203/218 (93%)	197 (97%)	6 (3%)	36	30
1	M	204/218 (94%)	203 (100%)	1 (0%)	81	84
1	N	202/218 (93%)	198 (98%)	4 (2%)	48	46
1	O	205/218 (94%)	200 (98%)	5 (2%)	43	38
1	P	205/218 (94%)	200 (98%)	5 (2%)	43	38
All	All	3279/3488 (94%)	3215 (98%)	64 (2%)	48	46

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	103	VAL
1	P	3	LEU
1	G	184	ILE
1	G	83	THR
1	P	55	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	63	ASN
1	O	23	ASN
1	L	132	HIS
1	N	44	GLN
1	F	187	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

16 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	9BG	B	301	-	51,51,51	3.67	25 (49%)	71,79,79	1.85	16 (22%)
2	9BG	I	301	-	51,51,51	3.67	24 (47%)	71,79,79	1.90	18 (25%)
2	9BG	P	301	-	51,51,51	3.71	25 (49%)	71,79,79	1.81	15 (21%)
2	9BG	G	301	-	51,51,51	3.68	25 (49%)	71,79,79	1.91	19 (26%)
2	9BG	M	302	-	51,51,51	3.73	24 (47%)	71,79,79	1.85	17 (23%)
2	9BG	P	302	-	51,51,51	3.71	24 (47%)	71,79,79	1.90	18 (25%)
2	9BG	C	302	-	51,51,51	3.76	25 (49%)	71,79,79	1.86	17 (23%)
2	9BG	G	302	-	51,51,51	3.71	24 (47%)	71,79,79	1.94	20 (28%)
2	9BG	A	301	-	51,51,51	3.70	24 (47%)	71,79,79	1.85	18 (25%)
2	9BG	C	301	-	51,51,51	3.70	24 (47%)	71,79,79	1.86	19 (26%)
2	9BG	F	301	-	51,51,51	3.67	24 (47%)	71,79,79	1.85	18 (25%)
2	9BG	J	301	-	51,51,51	3.70	25 (49%)	71,79,79	1.82	17 (23%)
2	9BG	M	301	-	51,51,51	3.69	23 (45%)	71,79,79	1.92	18 (25%)
2	9BG	E	301	-	51,51,51	3.69	24 (47%)	71,79,79	1.88	18 (25%)
2	9BG	K	302	-	51,51,51	3.71	23 (45%)	71,79,79	1.88	15 (21%)
2	9BG	K	301	-	51,51,51	3.71	25 (49%)	71,79,79	1.94	16 (22%)

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	9BG	B	301	-	-	6/26/58/58	0/6/6/6
2	9BG	I	301	-	-	9/26/58/58	0/6/6/6
2	9BG	P	301	-	-	4/26/58/58	0/6/6/6
2	9BG	G	301	-	-	7/26/58/58	0/6/6/6
2	9BG	M	302	-	-	6/26/58/58	0/6/6/6
2	9BG	P	302	-	-	6/26/58/58	0/6/6/6
2	9BG	C	302	-	-	6/26/58/58	0/6/6/6
2	9BG	G	302	-	-	7/26/58/58	0/6/6/6
2	9BG	A	301	-	-	5/26/58/58	0/6/6/6
2	9BG	C	301	-	-	9/26/58/58	0/6/6/6
2	9BG	F	301	-	-	5/26/58/58	0/6/6/6
2	9BG	J	301	-	-	6/26/58/58	0/6/6/6
2	9BG	M	301	-	-	7/26/58/58	0/6/6/6
2	9BG	E	301	-	-	5/26/58/58	0/6/6/6
2	9BG	K	302	-	-	6/26/58/58	0/6/6/6
2	9BG	K	301	-	-	3/26/58/58	0/6/6/6

The worst 5 of 388 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	301	9BG	O44-C33	11.06	1.67	1.42
2	C	302	9BG	O44-C33	10.95	1.67	1.42
2	K	302	9BG	O44-C33	10.94	1.67	1.42
2	C	301	9BG	O44-C33	10.92	1.67	1.42
2	P	302	9BG	O44-C33	10.84	1.67	1.42

The worst 5 of 279 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	9BG	N38-C37-N36	-6.39	118.90	128.58
2	M	301	9BG	N38-C37-N36	-6.32	119.01	128.58
2	I	301	9BG	N38-C37-N36	-6.11	119.33	128.58
2	E	301	9BG	N38-C37-N36	-6.08	119.37	128.58
2	G	301	9BG	N38-C37-N36	-6.06	119.41	128.58

There are no chirality outliers.

5 of 97 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	9BG	C23-O22-P21-O20
2	A	301	9BG	C23-O22-P21-O46
2	B	301	9BG	C23-O22-P21-O20
2	B	301	9BG	C23-O22-P21-O46
2	C	301	9BG	C31-C25-O26-P27

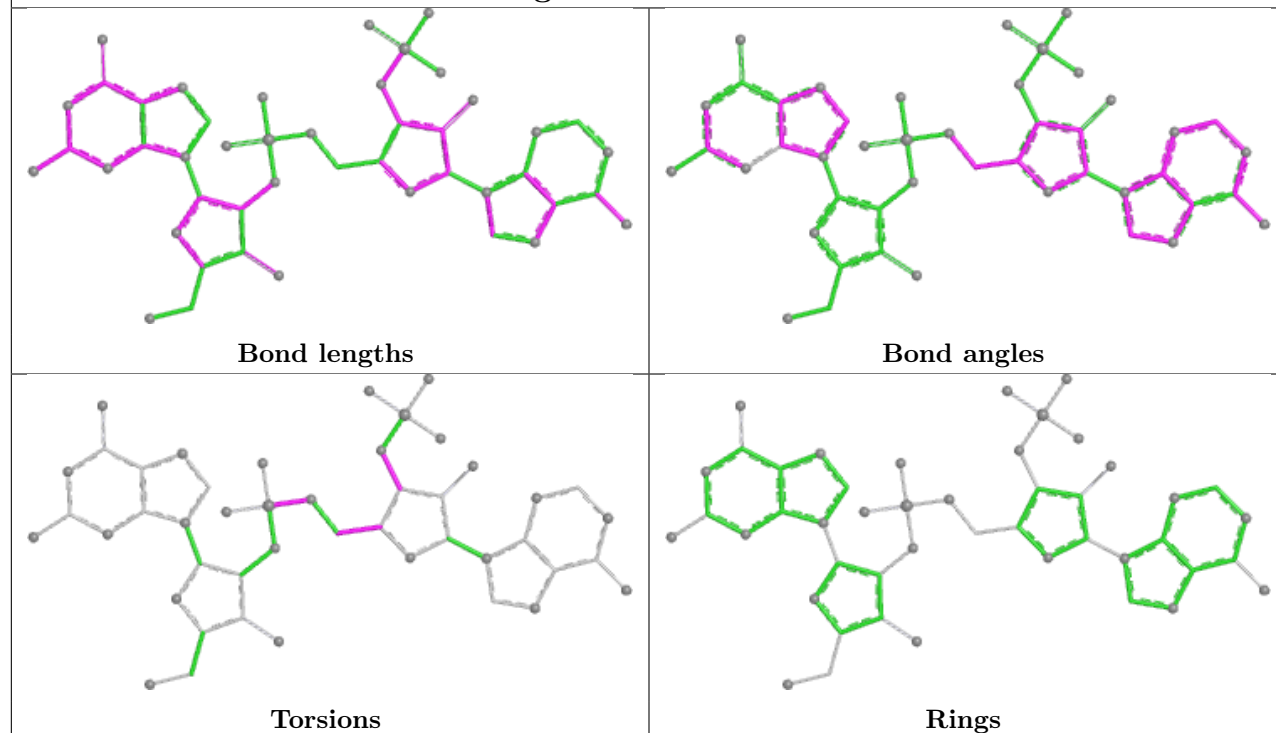
There are no ring outliers.

16 monomers are involved in 48 short contacts:

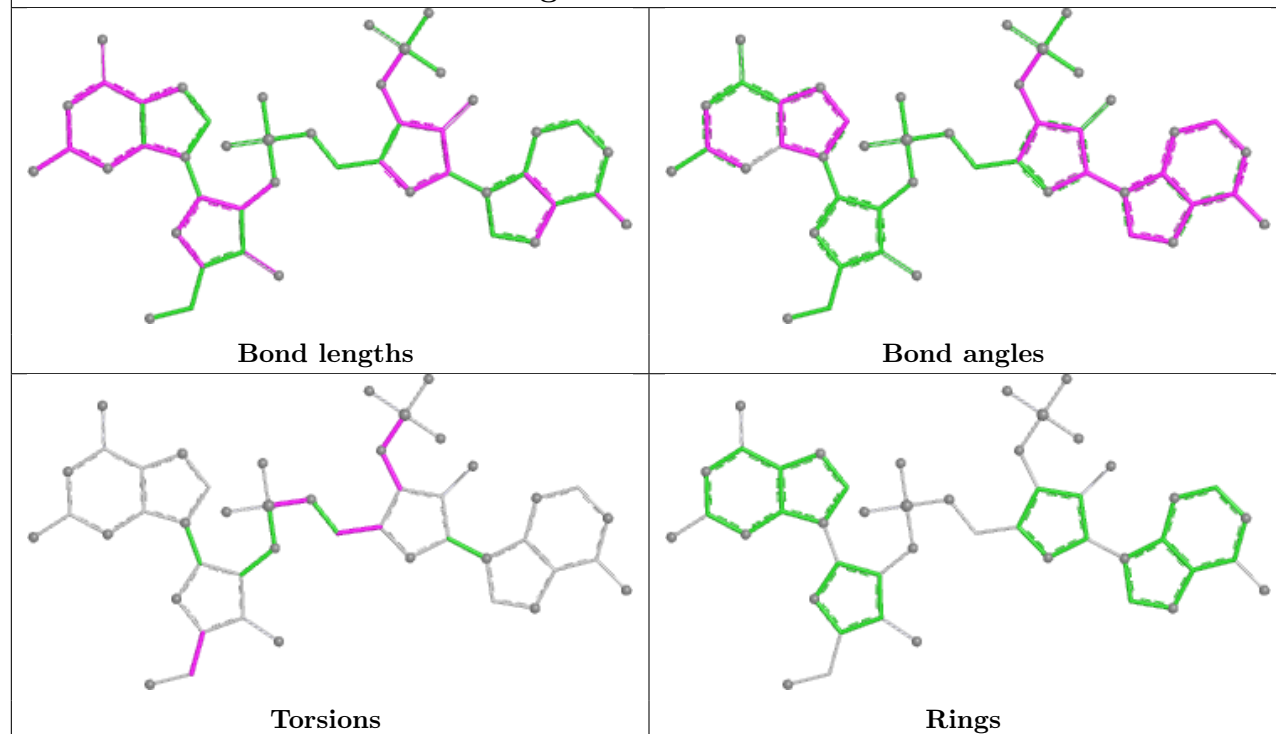
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	9BG	2	0
2	I	301	9BG	2	0
2	P	301	9BG	3	0
2	G	301	9BG	3	0
2	M	302	9BG	2	0
2	P	302	9BG	5	0
2	C	302	9BG	3	0
2	G	302	9BG	3	0
2	A	301	9BG	5	0
2	C	301	9BG	6	0
2	F	301	9BG	2	0
2	J	301	9BG	4	0
2	M	301	9BG	2	0
2	E	301	9BG	3	0
2	K	302	9BG	2	0
2	K	301	9BG	1	0

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.

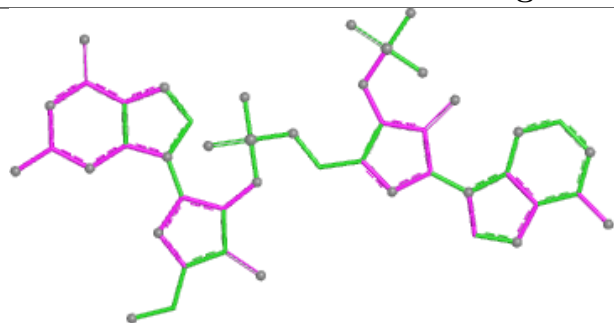
Ligand 9BG B 301



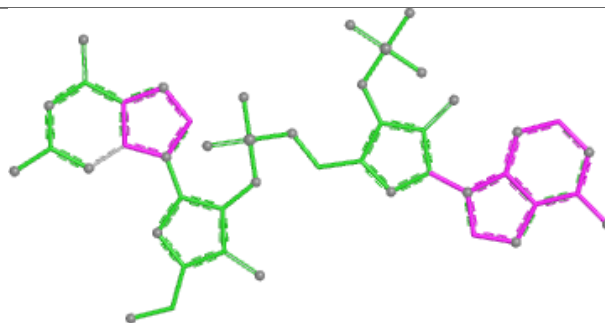
Ligand 9BG I 301



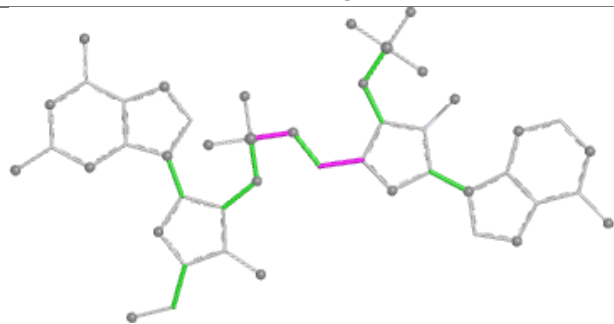
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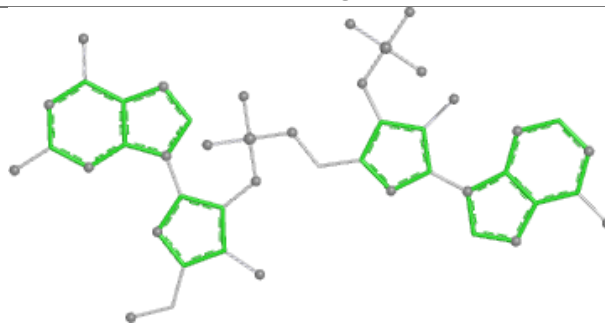
Bond lengths



Bond angles

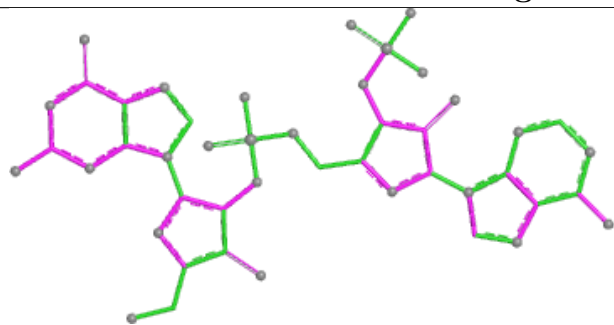


Torsions

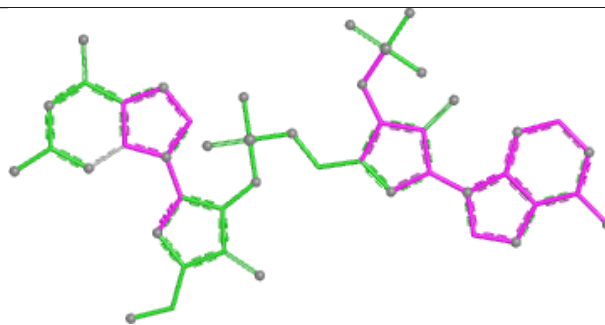


Rings

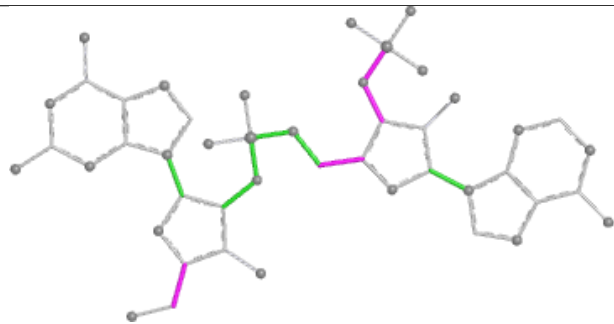
Ligand 9BG G 301



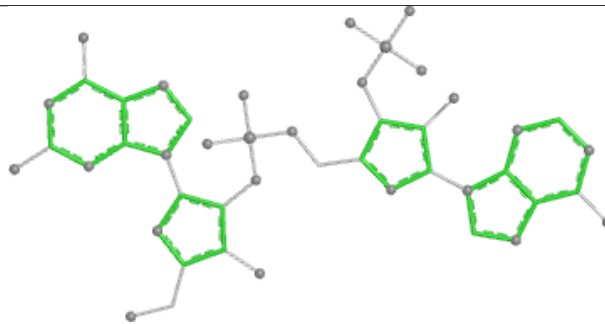
Bond lengths



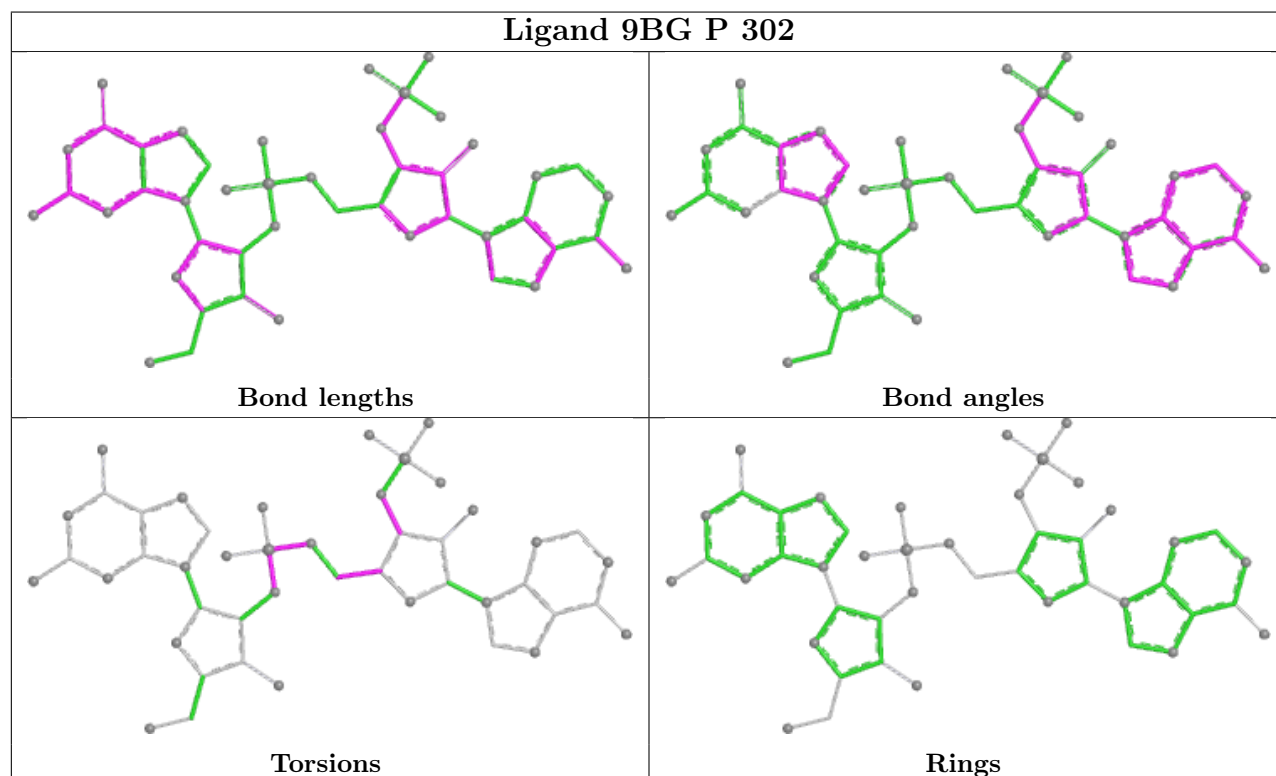
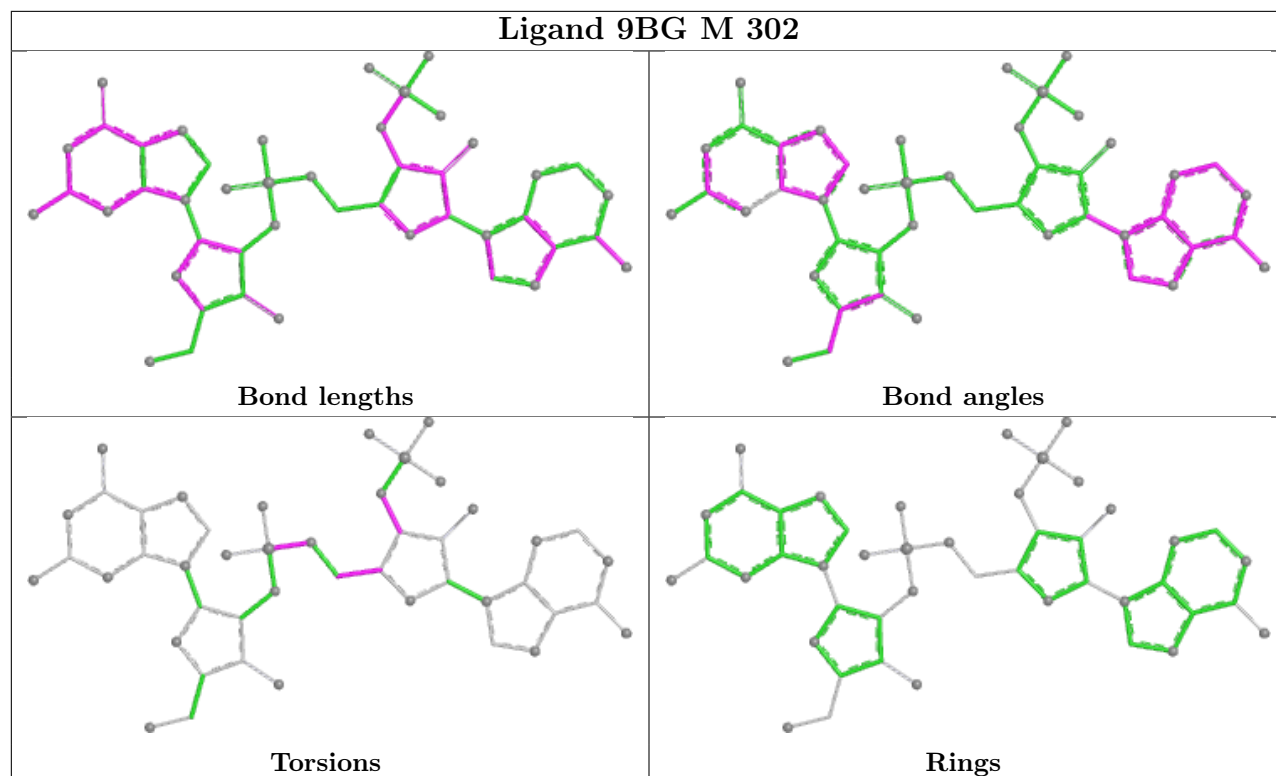
Bond angles



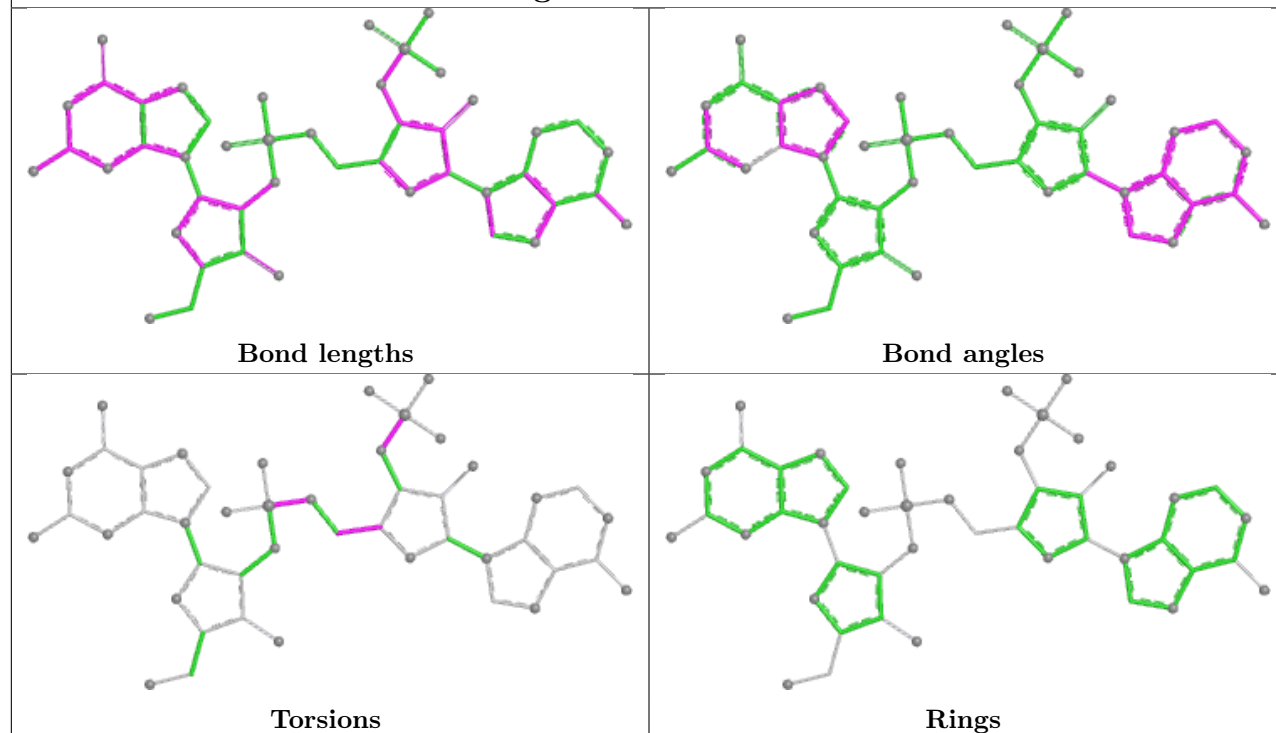
Torsions



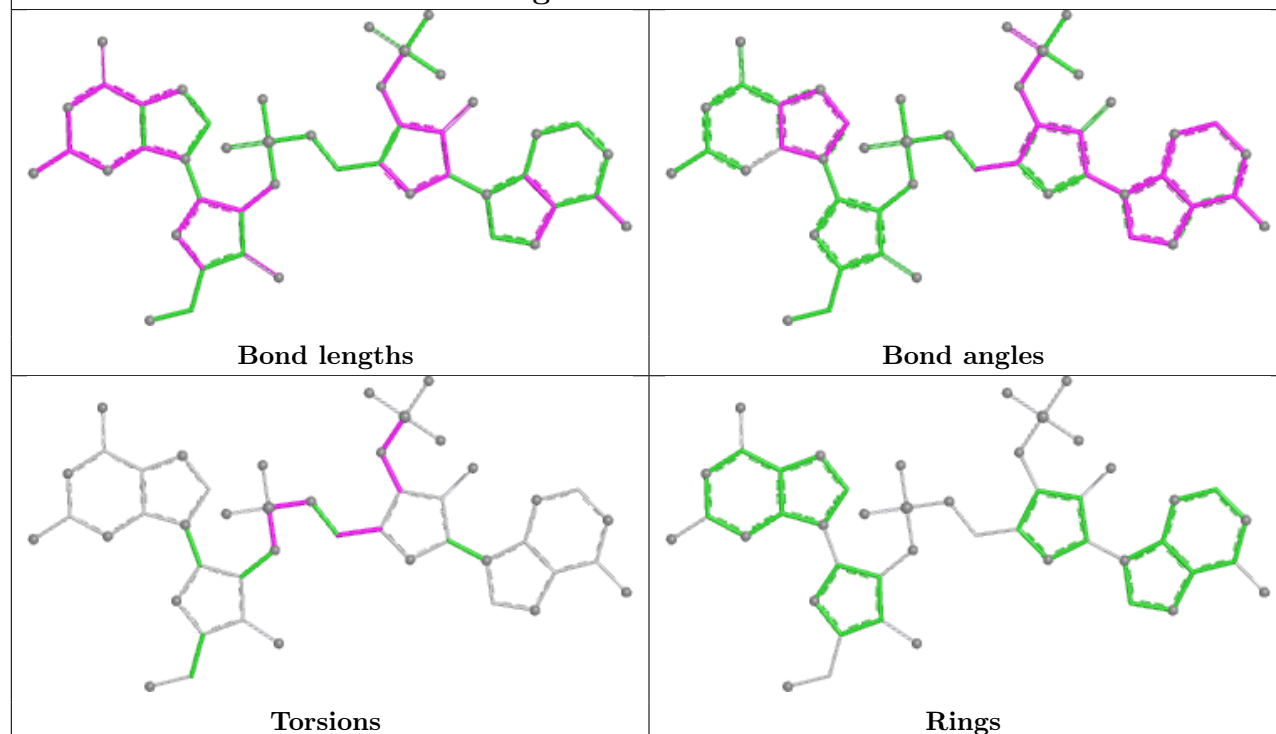
Rings



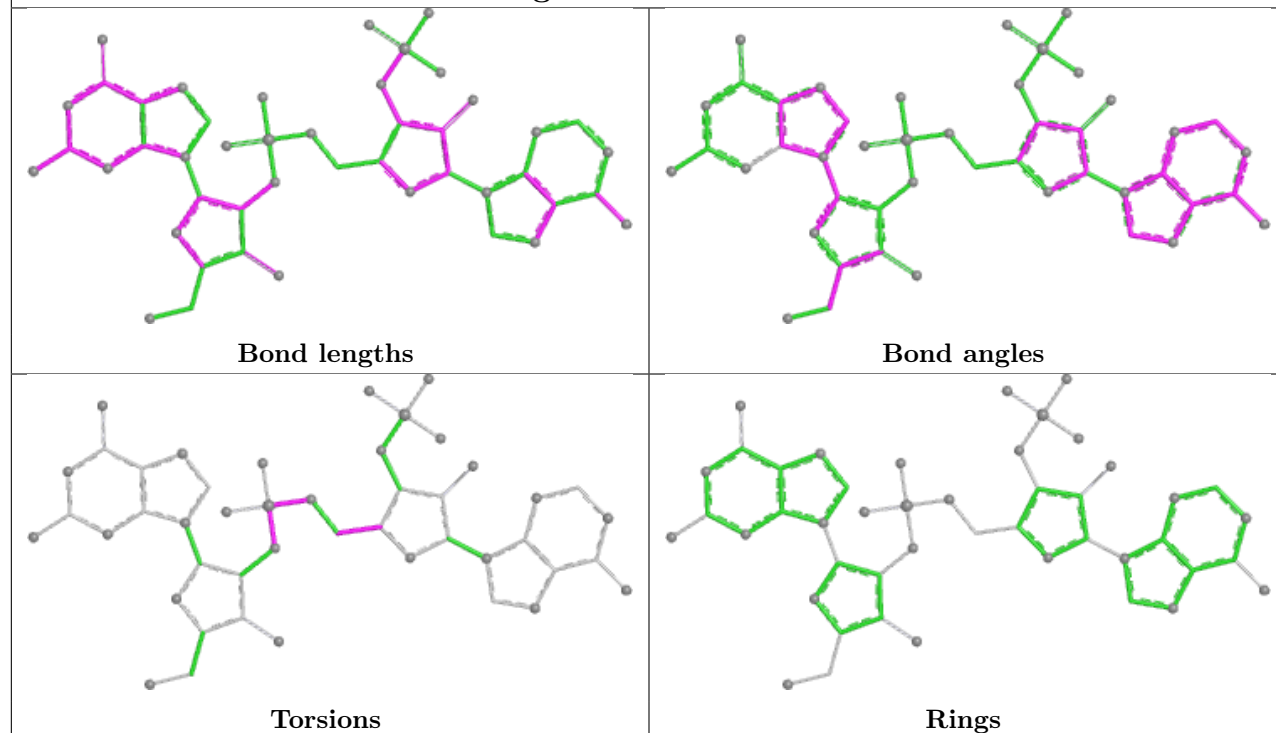
Ligand 9BG C 302



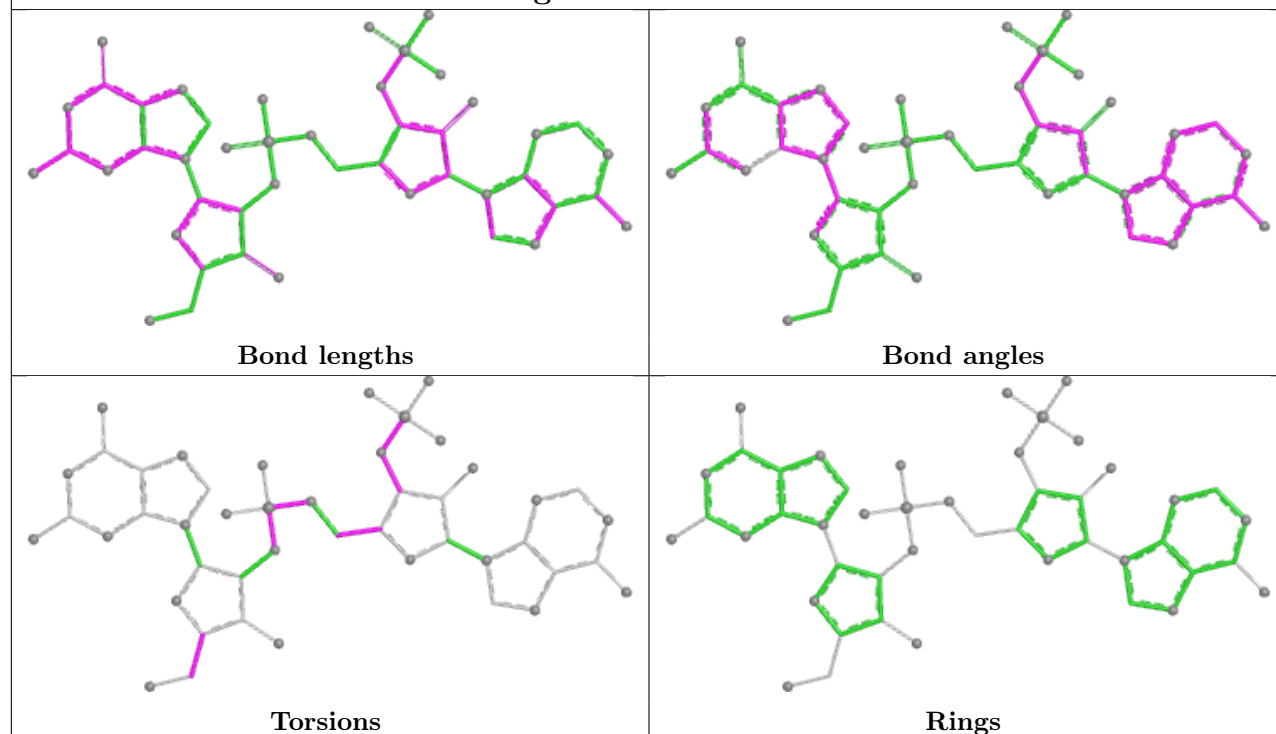
Ligand 9BG G 302



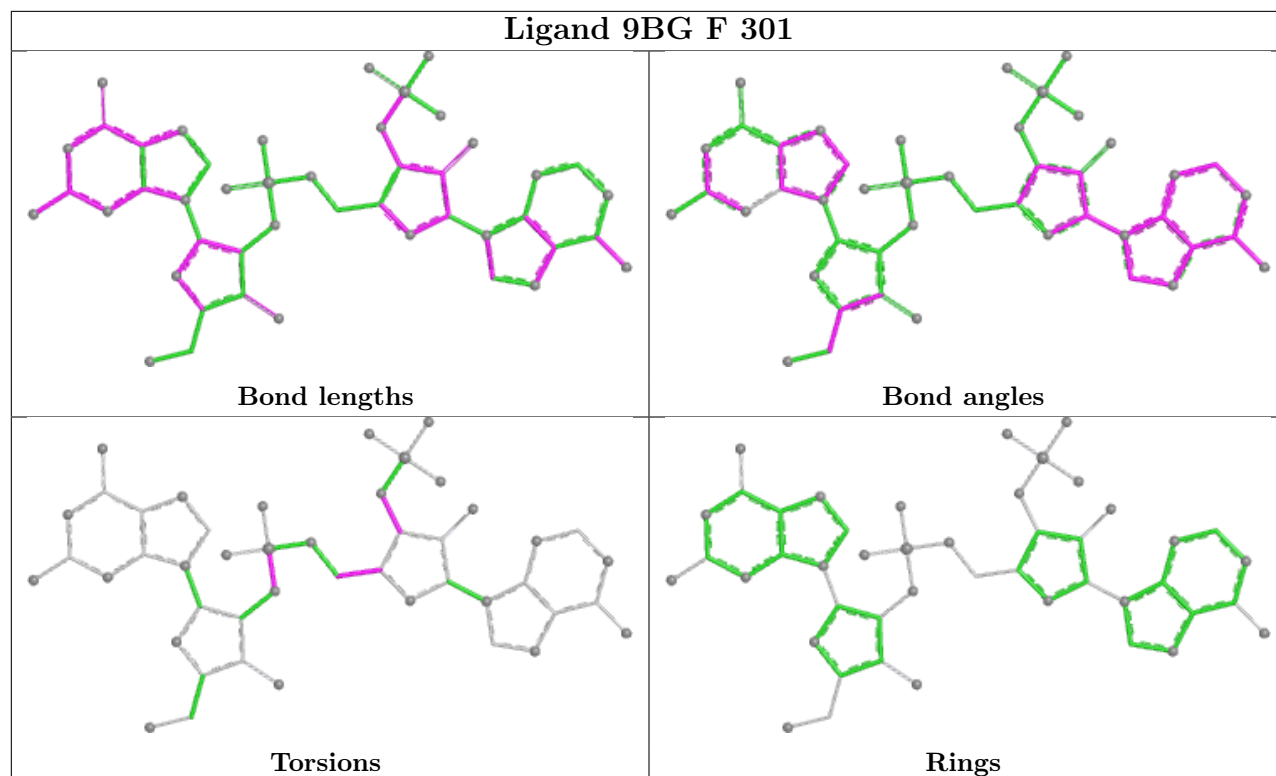
Ligand 9BG A 301



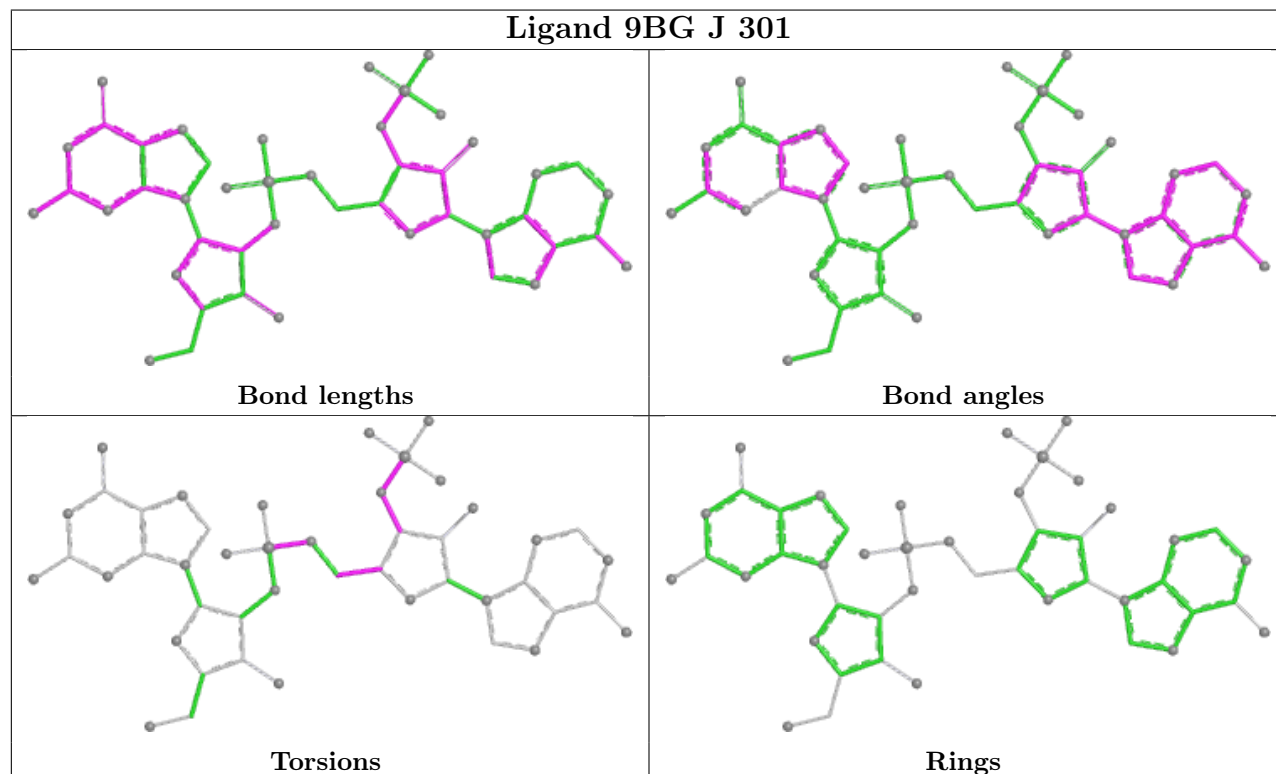
Ligand 9BG C 301

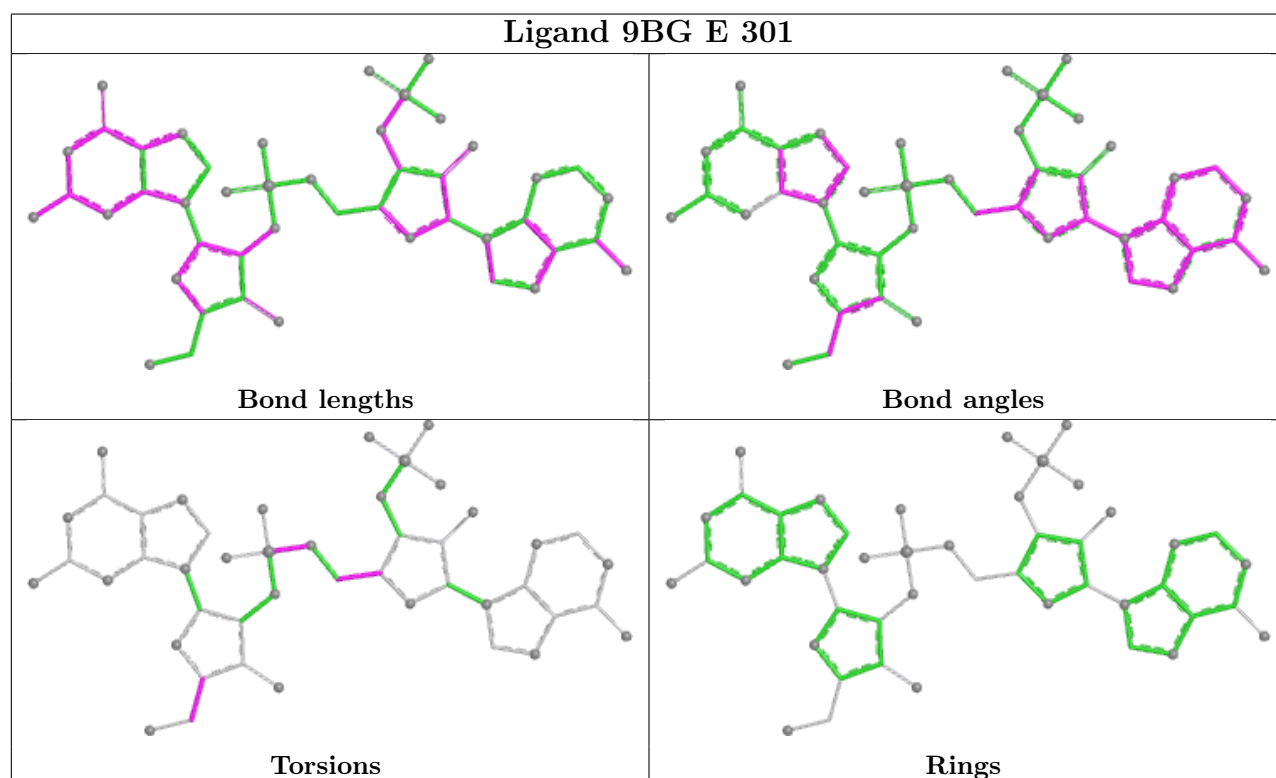
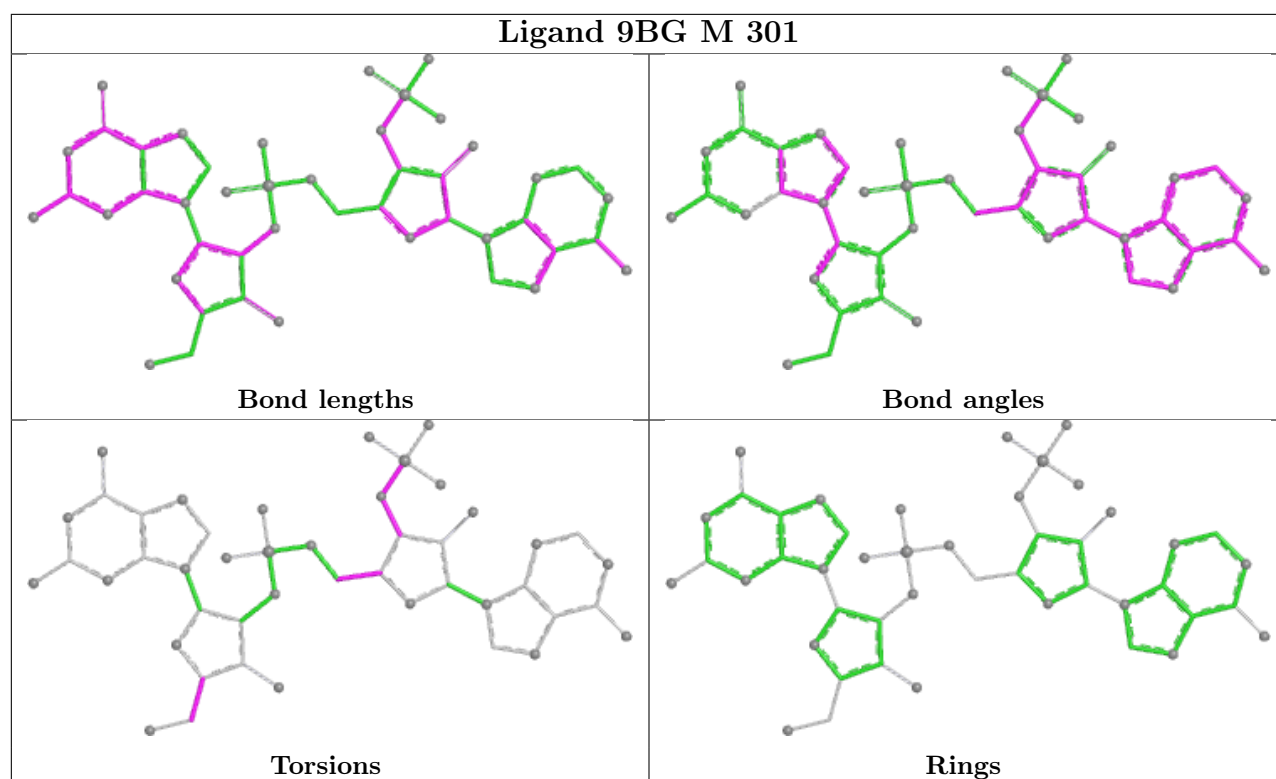


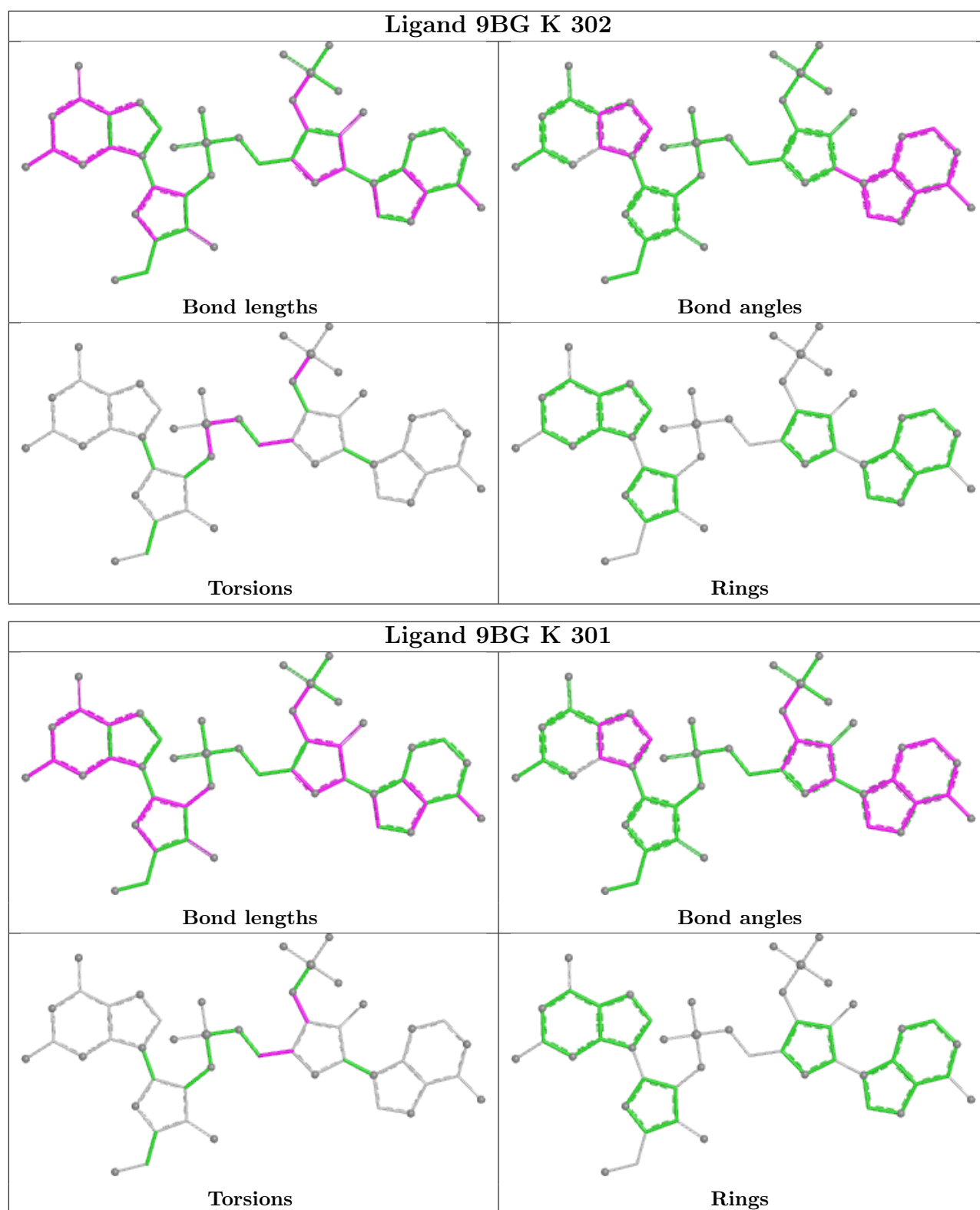
Ligand 9BG F 301



Ligand 9BG J 301







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	234/241 (97%)	-1.27	0 100 100	15, 24, 38, 48	0
1	B	229/241 (95%)	-1.28	0 100 100	16, 24, 35, 54	0
1	C	226/241 (93%)	-1.23	0 100 100	18, 28, 39, 47	0
1	D	225/241 (93%)	-1.22	0 100 100	19, 28, 44, 57	0
1	E	231/241 (95%)	-1.24	0 100 100	18, 26, 37, 54	0
1	F	220/241 (91%)	-1.22	0 100 100	18, 27, 38, 48	0
1	G	226/241 (93%)	-1.22	0 100 100	18, 26, 41, 52	0
1	H	232/241 (96%)	-1.21	0 100 100	17, 26, 43, 61	0
1	I	229/241 (95%)	-1.26	0 100 100	15, 24, 36, 53	0
1	J	231/241 (95%)	-1.26	0 100 100	15, 23, 39, 46	0
1	K	223/241 (92%)	-1.24	0 100 100	18, 26, 37, 49	0
1	L	225/241 (93%)	-1.24	0 100 100	17, 26, 39, 55	0
1	M	226/241 (93%)	-1.25	0 100 100	18, 25, 37, 53	0
1	N	224/241 (92%)	-1.19	0 100 100	19, 27, 42, 55	0
1	O	227/241 (94%)	-1.18	0 100 100	19, 28, 43, 55	0
1	P	228/241 (94%)	-1.21	0 100 100	19, 28, 40, 58	0
All	All	3636/3856 (94%)	-1.23	0 100 100	15, 26, 40, 61	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

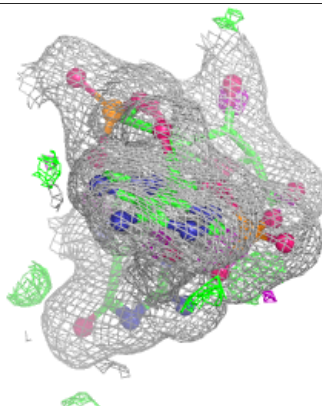
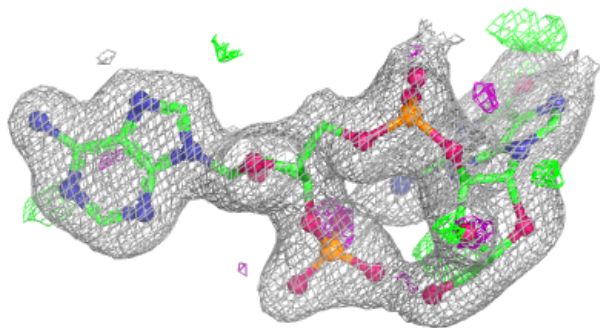
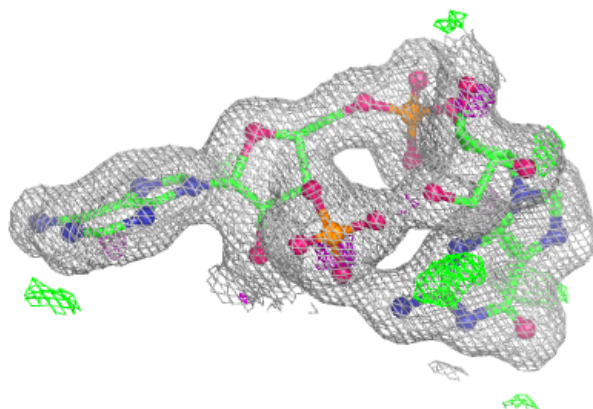
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	9BG	A	301	46/46	0.99	0.03	14,21,26,29	0
2	9BG	B	301	46/46	0.99	0.03	12,20,24,25	0
2	9BG	C	301	46/46	0.99	0.03	16,26,30,30	0
2	9BG	C	302	46/46	0.99	0.03	18,26,34,37	0
2	9BG	E	301	46/46	0.99	0.03	16,22,27,33	0
2	9BG	F	301	46/46	0.99	0.03	15,27,32,34	0
2	9BG	G	301	46/46	0.99	0.03	15,21,26,31	0
2	9BG	G	302	46/46	0.99	0.03	17,27,33,39	0
2	9BG	I	301	46/46	0.99	0.03	13,19,24,27	0
2	9BG	J	301	46/46	0.99	0.03	13,20,26,27	0
2	9BG	K	301	46/46	0.99	0.03	16,20,25,29	0
2	9BG	K	302	46/46	0.99	0.03	17,27,32,36	0
2	9BG	M	301	46/46	0.99	0.03	16,22,26,30	0
2	9BG	M	302	46/46	0.99	0.03	17,25,32,34	0
2	9BG	P	301	46/46	0.99	0.03	17,28,33,34	0
2	9BG	P	302	46/46	0.99	0.03	17,26,30,31	0

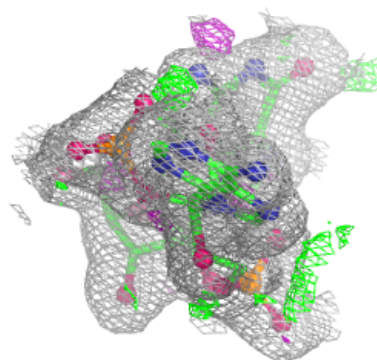
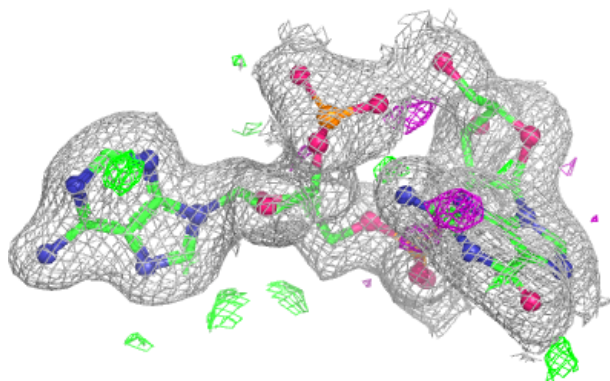
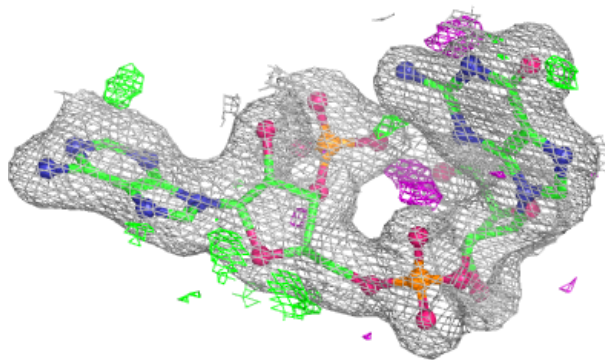
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 9BG A 301:

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

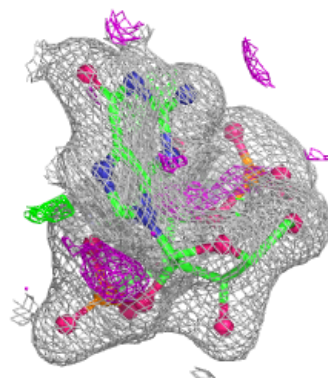
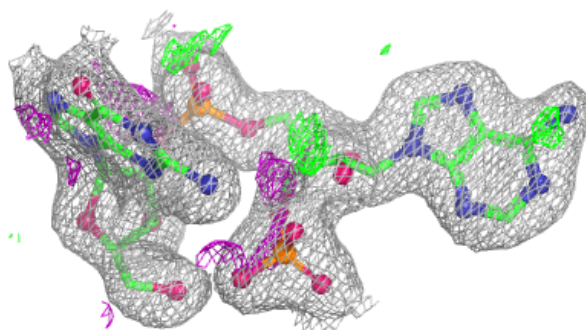
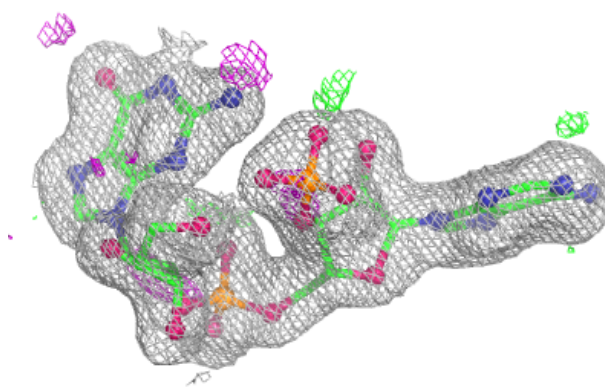
**Electron density around 9BG B 301:**

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

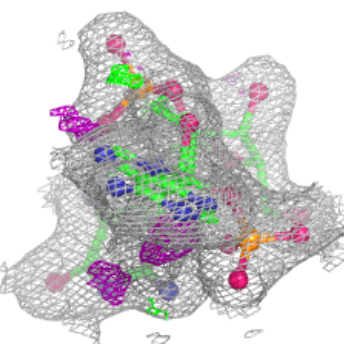
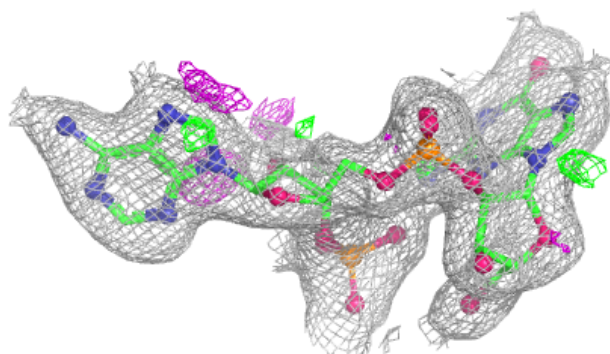
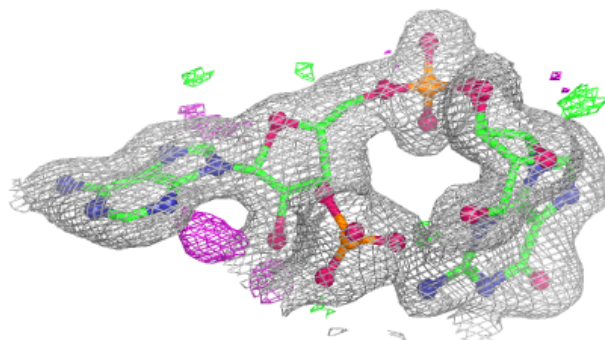


Electron density around 9BG C 301:

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

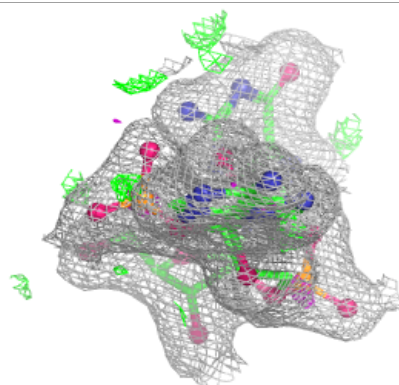
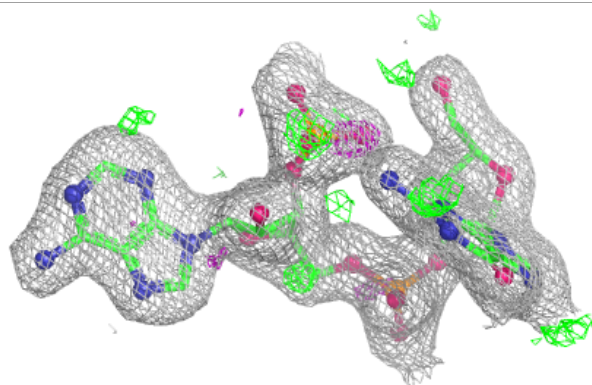
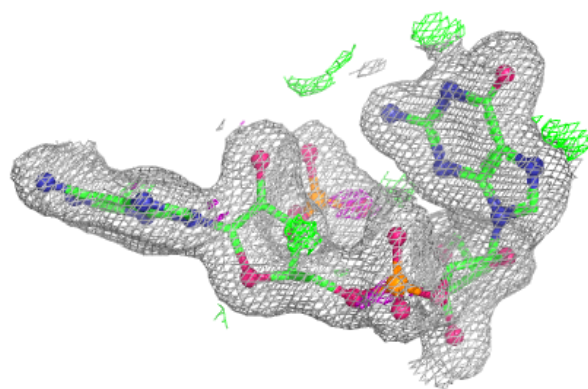
**Electron density around 9BG C 302:**

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

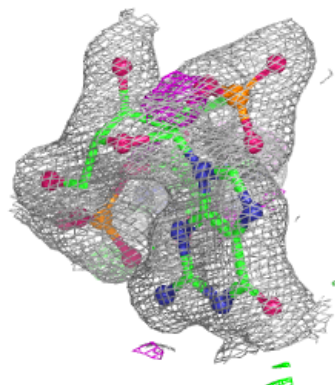
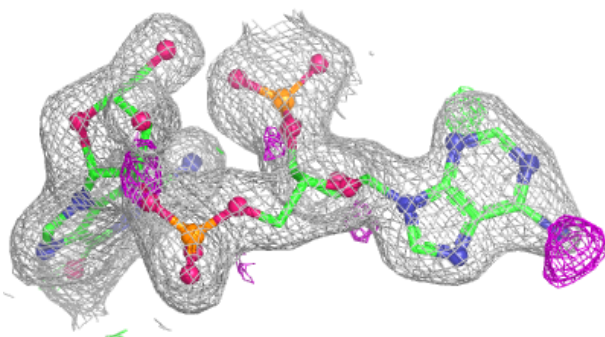
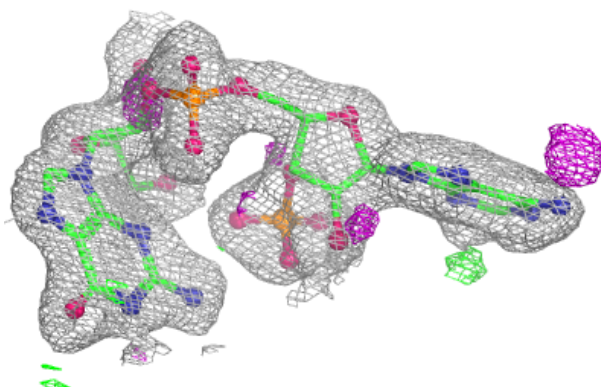


Electron density around 9BG E 301:

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

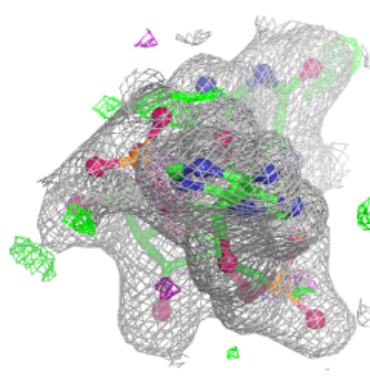
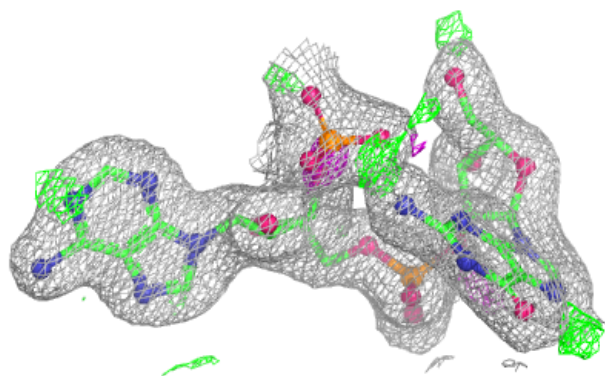
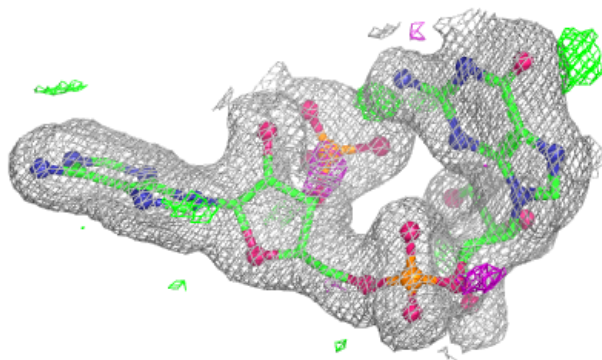
**Electron density around 9BG F 301:**

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

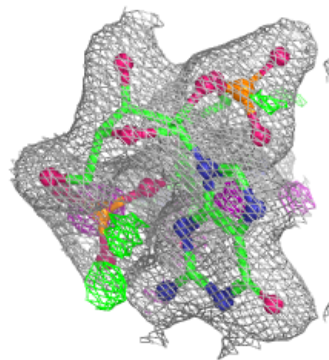
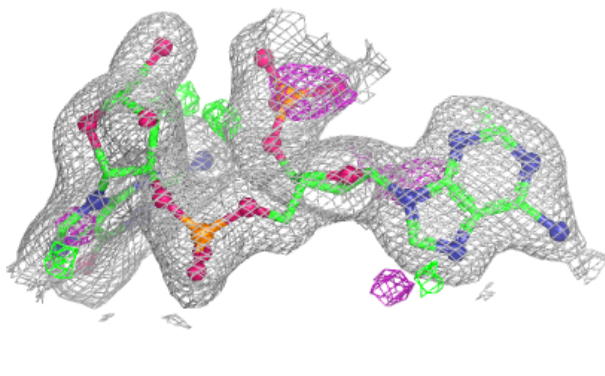
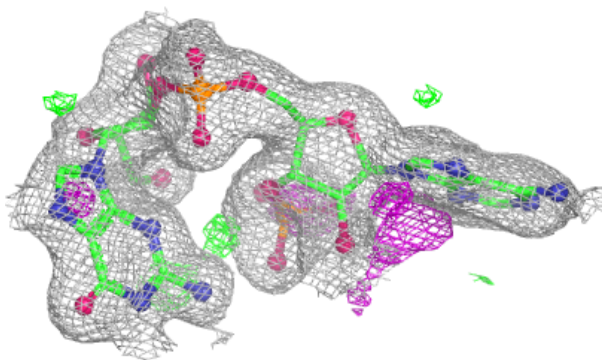


Electron density around 9BG G 301:

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

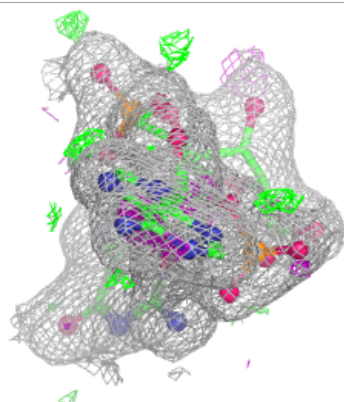
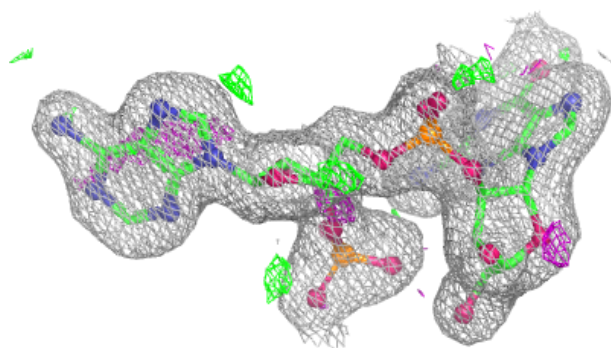
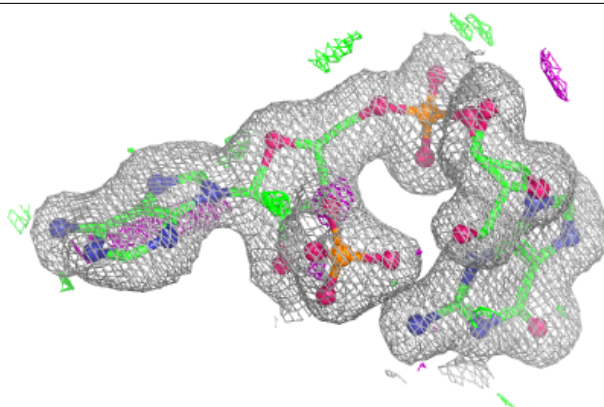
**Electron density around 9BG G 302:**

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

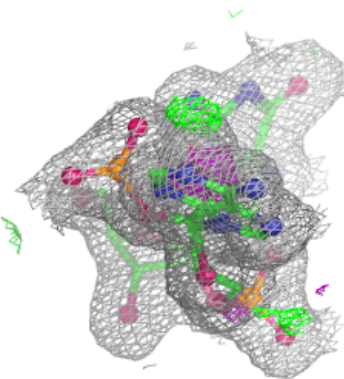
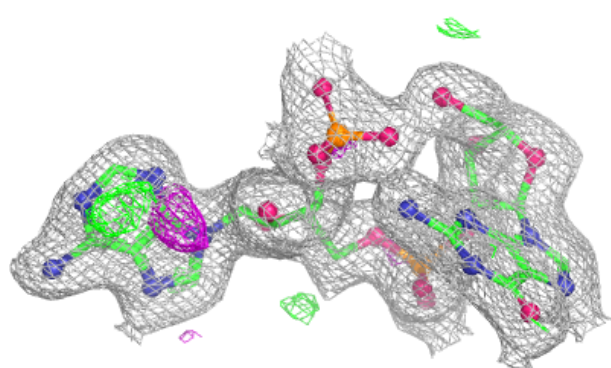
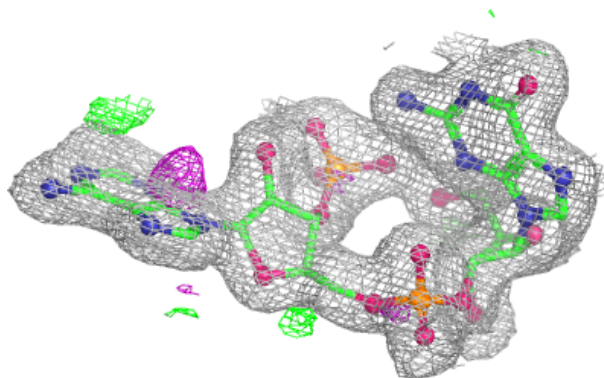


Electron density around 9BG I 301:

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

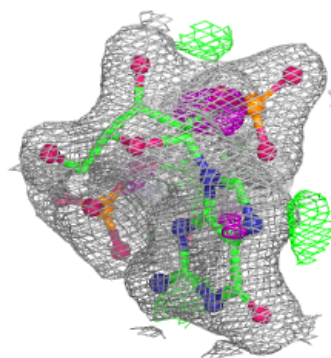
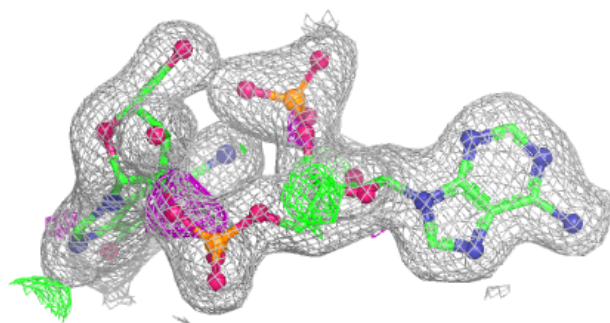
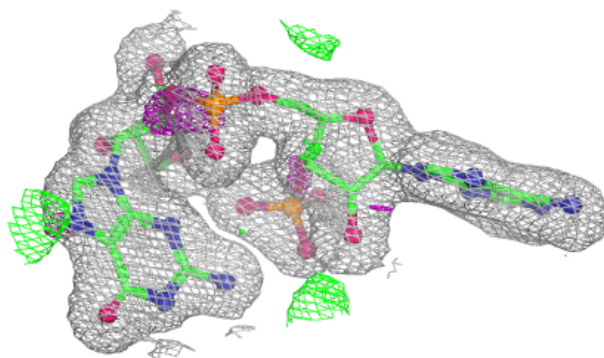
**Electron density around 9BG J 301:**

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

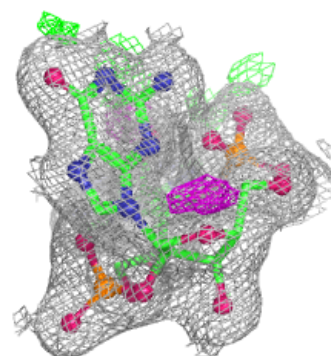
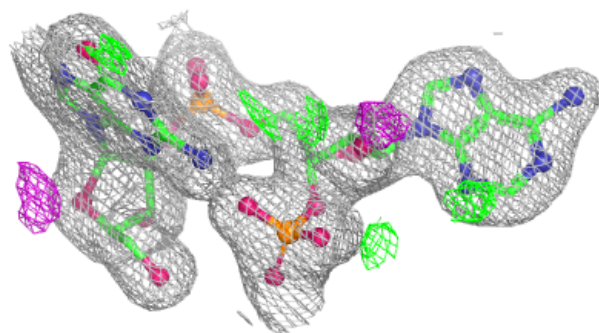
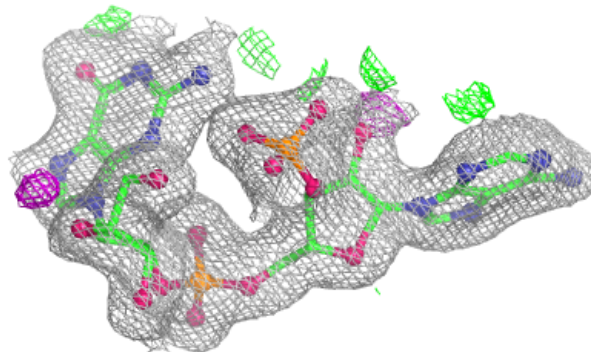


Electron density around 9BG K 301:

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

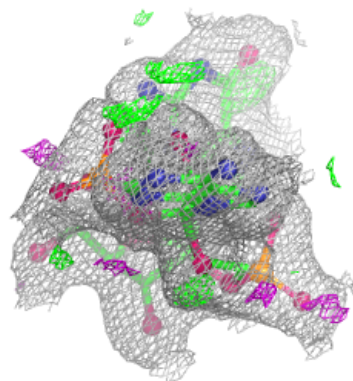
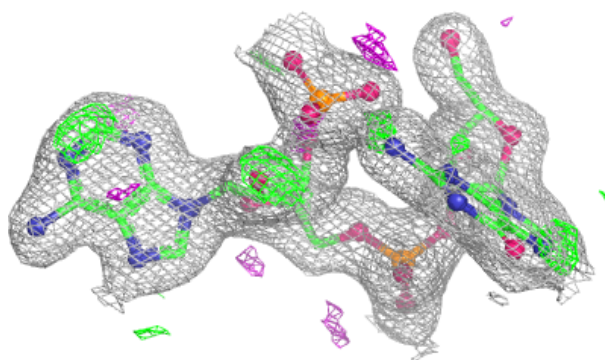
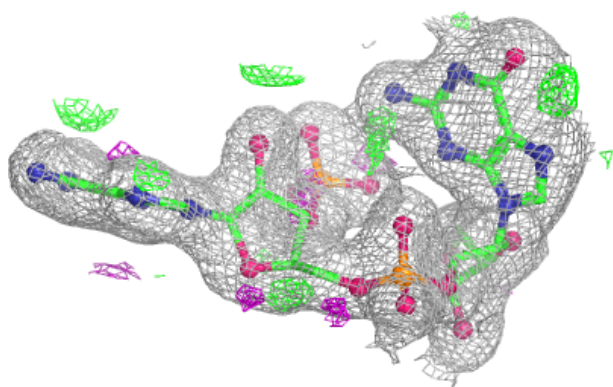
**Electron density around 9BG K 302:**

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

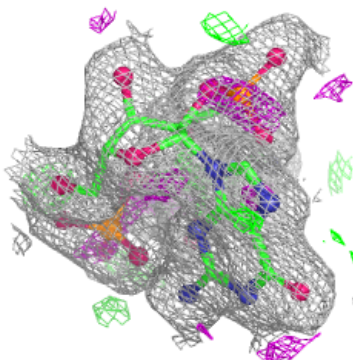
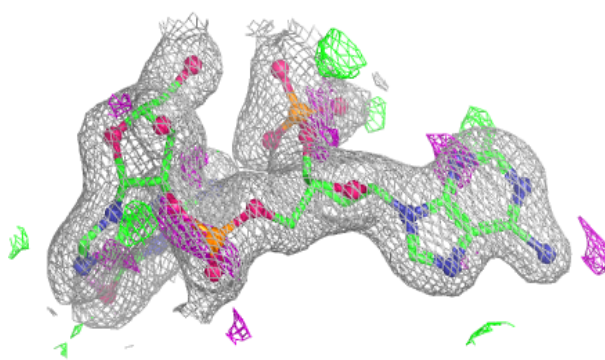
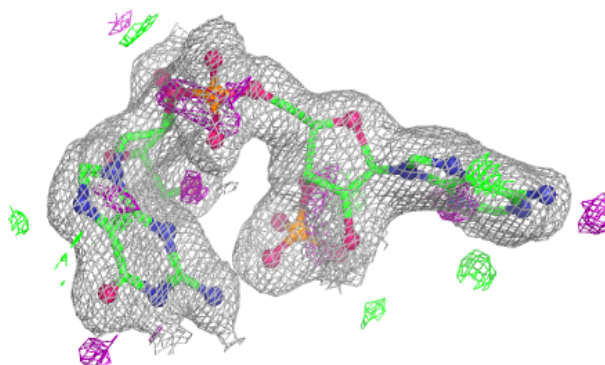


Electron density around 9BG M 301:

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

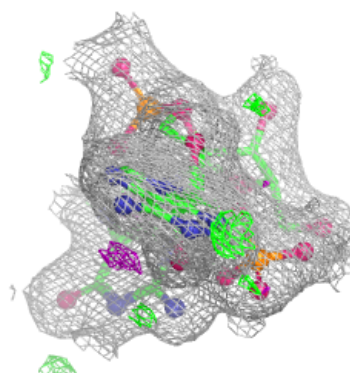
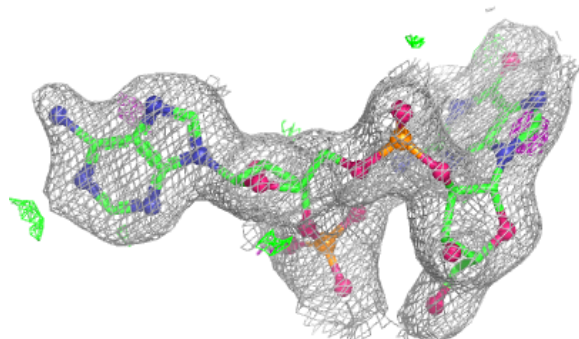
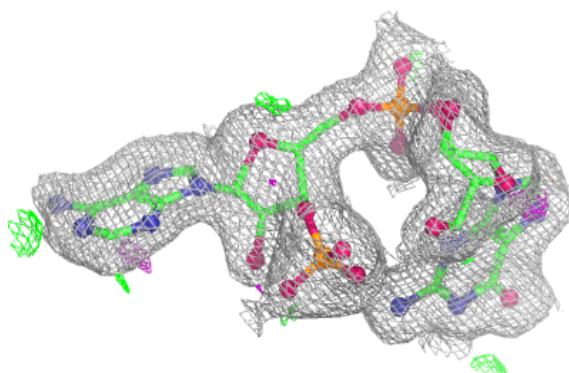
**Electron density around 9BG M 302:**

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

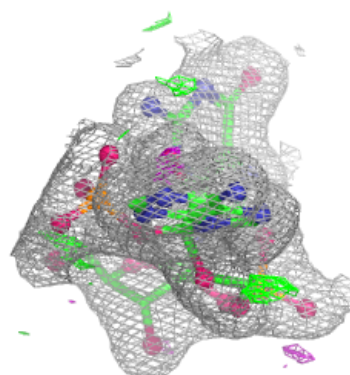
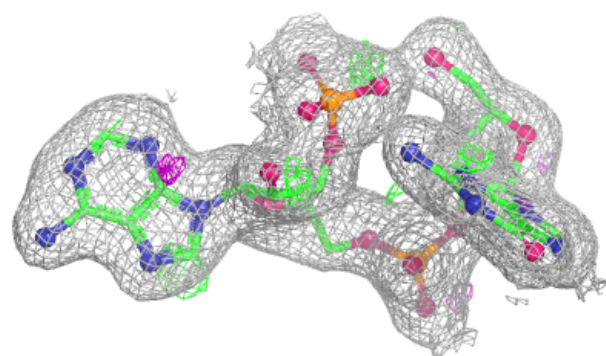
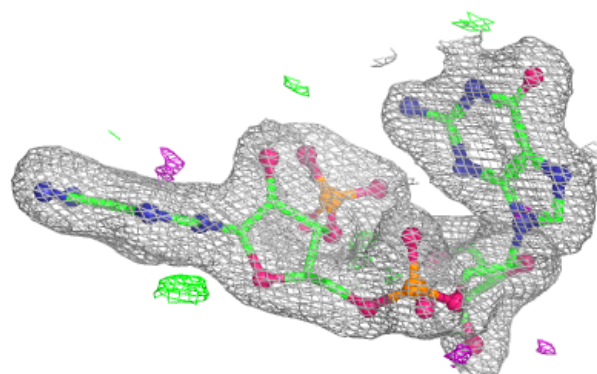


Electron density around 9BG P 301:

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

**Electron density around 9BG P 302:**

$2mF_o-DF_c$ (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.