



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 06:50 AM UTC

PDB ID : 6HUF / pdb_00006huf
Title : Coping with strong translational non-crystallographic symmetry and extreme anisotropy in molecular replacement with Phaser: human Rab27a
Authors : Jamshidiha, M.; Perez-Dorado, I.; Murray, J.W.; Tate, E.W.; Cota, E.; Read, R.J.
Deposited on : 2018-10-08
Resolution : 2.82 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

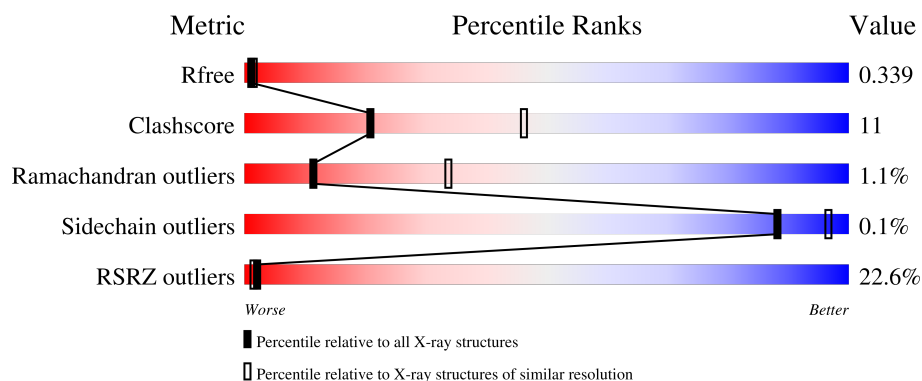
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.82 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	4591 (2.84-2.80)
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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	182	18% 77% 17% 6%
1	B	182	12% 80% 14% 6%
1	C	182	20% 80% 14% 6%
1	D	182	17% 79% 15% 6%

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Mol	Chain	Length	Quality of chain
1	E	182	
1	F	182	
1	G	182	
1	H	182	
1	I	182	
1	J	182	
1	K	182	
1	L	182	
1	M	182	
1	N	182	
1	O	182	
1	P	182	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 18977 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 Ras-related protein Rab-27A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	171	Total	C	N	O	S	0	0	0
			1159	728	199	229	3			
1	O	171	Total	C	N	O	S	0	0	0
			1152	723	198	228	3			
1	N	171	Total	C	N	O	S	0	0	0
			1149	720	198	228	3			
1	B	171	Total	C	N	O	S	0	0	0
			1152	723	198	228	3			
1	E	171	Total	C	N	O	S	0	0	0
			1149	720	198	228	3			
1	C	171	Total	C	N	O	S	0	0	0
			1153	722	198	230	3			
1	K	171	Total	C	N	O	S	0	0	0
			1161	732	198	228	3			
1	M	171	Total	C	N	O	S	0	0	0
			1149	720	198	228	3			
1	D	171	Total	C	N	O	S	0	0	0
			1155	726	198	228	3			
1	P	171	Total	C	N	O	S	0	0	0
			1155	726	198	228	3			
1	F	171	Total	C	N	O	S	0	0	0
			1155	726	198	228	3			
1	J	171	Total	C	N	O	S	0	0	0
			1155	726	198	228	3			
1	G	171	Total	C	N	O	S	0	0	0
			1152	721	199	229	3			
1	I	171	Total	C	N	O	S	0	0	0
			1149	720	198	228	3			
1	H	171	Total	C	N	O	S	0	0	0
			1149	720	198	228	3			
1	L	171	Total	C	N	O	S	0	0	0
			1149	720	198	228	3			

There are 480 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP P51159
A	?	-	ARG	deletion	UNP P51159
A	50	THR	VAL	conflict	UNP P51159
A	51	ILE	VAL	conflict	UNP P51159
A	?	-	ALA	deletion	UNP P51159
A	?	-	SER	deletion	UNP P51159
A	?	-	GLY	deletion	UNP P51159
A	?	-	PRO	deletion	UNP P51159
A	?	-	ASP	deletion	UNP P51159
A	?	-	GLY	deletion	UNP P51159
A	?	-	ALA	deletion	UNP P51159
A	?	-	THR	deletion	UNP P51159
A	?	-	GLY	deletion	UNP P51159
A	54	ASN	ARG	conflict	UNP P51159
A	55	ASP	GLY	conflict	UNP P51159
A	56	LYS	GLN	conflict	UNP P51159
A	59	LYS	HIS	conflict	UNP P51159
A	68	LEU	GLN	conflict	UNP P51159
A	95	GLU	GLN	conflict	UNP P51159
A	108	LYS	GLN	conflict	UNP P51159
A	109	THR	MET	conflict	UNP P51159
A	113	SER	CYS	conflict	UNP P51159
A	130	GLU	GLN	conflict	UNP P51159
A	134	ALA	LYS	conflict	UNP P51159
A	135	ALA	GLU	conflict	UNP P51159
A	136	ALA	GLU	conflict	UNP P51159
A	139	ARG	ILE	conflict	UNP P51159
A	140	GLN	ALA	conflict	UNP P51159
A	144	HIS	LYS	conflict	UNP P51159
A	178	SER	CYS	conflict	UNP P51159
O	1	GLY	-	expression tag	UNP P51159
O	?	-	ARG	deletion	UNP P51159
O	50	THR	VAL	conflict	UNP P51159
O	51	ILE	VAL	conflict	UNP P51159
O	?	-	ALA	deletion	UNP P51159
O	?	-	SER	deletion	UNP P51159
O	?	-	GLY	deletion	UNP P51159
O	?	-	PRO	deletion	UNP P51159
O	?	-	ASP	deletion	UNP P51159
O	?	-	GLY	deletion	UNP P51159
O	?	-	ALA	deletion	UNP P51159
O	?	-	THR	deletion	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
O	?	-	GLY	deletion	UNP P51159
O	54	ASN	ARG	conflict	UNP P51159
O	55	ASP	GLY	conflict	UNP P51159
O	56	LYS	GLN	conflict	UNP P51159
O	59	LYS	HIS	conflict	UNP P51159
O	68	LEU	GLN	conflict	UNP P51159
O	95	GLU	GLN	conflict	UNP P51159
O	108	LYS	GLN	conflict	UNP P51159
O	109	THR	MET	conflict	UNP P51159
O	113	SER	CYS	conflict	UNP P51159
O	130	GLU	GLN	conflict	UNP P51159
O	134	ALA	LYS	conflict	UNP P51159
O	135	ALA	GLU	conflict	UNP P51159
O	136	ALA	GLU	conflict	UNP P51159
O	139	ARG	ILE	conflict	UNP P51159
O	140	GLN	ALA	conflict	UNP P51159
O	144	HIS	LYS	conflict	UNP P51159
O	178	SER	CYS	conflict	UNP P51159
N	1	GLY	-	expression tag	UNP P51159
N	?	-	ARG	deletion	UNP P51159
N	50	THR	VAL	conflict	UNP P51159
N	51	ILE	VAL	conflict	UNP P51159
N	?	-	ALA	deletion	UNP P51159
N	?	-	SER	deletion	UNP P51159
N	?	-	GLY	deletion	UNP P51159
N	?	-	PRO	deletion	UNP P51159
N	?	-	ASP	deletion	UNP P51159
N	?	-	GLY	deletion	UNP P51159
N	?	-	ALA	deletion	UNP P51159
N	?	-	THR	deletion	UNP P51159
N	?	-	GLY	deletion	UNP P51159
N	54	ASN	ARG	conflict	UNP P51159
N	55	ASP	GLY	conflict	UNP P51159
N	56	LYS	GLN	conflict	UNP P51159
N	59	LYS	HIS	conflict	UNP P51159
N	68	LEU	GLN	conflict	UNP P51159
N	95	GLU	GLN	conflict	UNP P51159
N	108	LYS	GLN	conflict	UNP P51159
N	109	THR	MET	conflict	UNP P51159
N	113	SER	CYS	conflict	UNP P51159
N	130	GLU	GLN	conflict	UNP P51159
N	134	ALA	LYS	conflict	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
N	135	ALA	GLU	conflict	UNP P51159
N	136	ALA	GLU	conflict	UNP P51159
N	139	ARG	ILE	conflict	UNP P51159
N	140	GLN	ALA	conflict	UNP P51159
N	144	HIS	LYS	conflict	UNP P51159
N	178	SER	CYS	conflict	UNP P51159
B	1	GLY	-	expression tag	UNP P51159
B	?	-	ARG	deletion	UNP P51159
B	50	THR	VAL	conflict	UNP P51159
B	51	ILE	VAL	conflict	UNP P51159
B	?	-	ALA	deletion	UNP P51159
B	?	-	SER	deletion	UNP P51159
B	?	-	GLY	deletion	UNP P51159
B	?	-	PRO	deletion	UNP P51159
B	?	-	ASP	deletion	UNP P51159
B	?	-	GLY	deletion	UNP P51159
B	?	-	ALA	deletion	UNP P51159
B	?	-	THR	deletion	UNP P51159
B	?	-	GLY	deletion	UNP P51159
B	54	ASN	ARG	conflict	UNP P51159
B	55	ASP	GLY	conflict	UNP P51159
B	56	LYS	GLN	conflict	UNP P51159
B	59	LYS	HIS	conflict	UNP P51159
B	68	LEU	GLN	conflict	UNP P51159
B	95	GLU	GLN	conflict	UNP P51159
B	108	LYS	GLN	conflict	UNP P51159
B	109	THR	MET	conflict	UNP P51159
B	113	SER	CYS	conflict	UNP P51159
B	130	GLU	GLN	conflict	UNP P51159
B	134	ALA	LYS	conflict	UNP P51159
B	135	ALA	GLU	conflict	UNP P51159
B	136	ALA	GLU	conflict	UNP P51159
B	139	ARG	ILE	conflict	UNP P51159
B	140	GLN	ALA	conflict	UNP P51159
B	144	HIS	LYS	conflict	UNP P51159
B	178	SER	CYS	conflict	UNP P51159
E	1	GLY	-	expression tag	UNP P51159
E	?	-	ARG	deletion	UNP P51159
E	50	THR	VAL	conflict	UNP P51159
E	51	ILE	VAL	conflict	UNP P51159
E	?	-	ALA	deletion	UNP P51159
E	?	-	SER	deletion	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	GLY	deletion	UNP P51159
E	?	-	PRO	deletion	UNP P51159
E	?	-	ASP	deletion	UNP P51159
E	?	-	GLY	deletion	UNP P51159
E	?	-	ALA	deletion	UNP P51159
E	?	-	THR	deletion	UNP P51159
E	?	-	GLY	deletion	UNP P51159
E	54	ASN	ARG	conflict	UNP P51159
E	55	ASP	GLY	conflict	UNP P51159
E	56	LYS	GLN	conflict	UNP P51159
E	59	LYS	HIS	conflict	UNP P51159
E	68	LEU	GLN	conflict	UNP P51159
E	95	GLU	GLN	conflict	UNP P51159
E	108	LYS	GLN	conflict	UNP P51159
E	109	THR	MET	conflict	UNP P51159
E	113	SER	CYS	conflict	UNP P51159
E	130	GLU	GLN	conflict	UNP P51159
E	134	ALA	LYS	conflict	UNP P51159
E	135	ALA	GLU	conflict	UNP P51159
E	136	ALA	GLU	conflict	UNP P51159
E	139	ARG	ILE	conflict	UNP P51159
E	140	GLN	ALA	conflict	UNP P51159
E	144	HIS	LYS	conflict	UNP P51159
E	178	SER	CYS	conflict	UNP P51159
C	1	GLY	-	expression tag	UNP P51159
C	?	-	ARG	deletion	UNP P51159
C	50	THR	VAL	conflict	UNP P51159
C	51	ILE	VAL	conflict	UNP P51159
C	?	-	ALA	deletion	UNP P51159
C	?	-	SER	deletion	UNP P51159
C	?	-	GLY	deletion	UNP P51159
C	?	-	PRO	deletion	UNP P51159
C	?	-	ASP	deletion	UNP P51159
C	?	-	GLY	deletion	UNP P51159
C	?	-	ALA	deletion	UNP P51159
C	?	-	THR	deletion	UNP P51159
C	?	-	GLY	deletion	UNP P51159
C	54	ASN	ARG	conflict	UNP P51159
C	55	ASP	GLY	conflict	UNP P51159
C	56	LYS	GLN	conflict	UNP P51159
C	59	LYS	HIS	conflict	UNP P51159
C	68	LEU	GLN	conflict	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
C	95	GLU	GLN	conflict	UNP P51159
C	108	LYS	GLN	conflict	UNP P51159
C	109	THR	MET	conflict	UNP P51159
C	113	SER	CYS	conflict	UNP P51159
C	130	GLU	GLN	conflict	UNP P51159
C	134	ALA	LYS	conflict	UNP P51159
C	135	ALA	GLU	conflict	UNP P51159
C	136	ALA	GLU	conflict	UNP P51159
C	139	ARG	ILE	conflict	UNP P51159
C	140	GLN	ALA	conflict	UNP P51159
C	144	HIS	LYS	conflict	UNP P51159
C	178	SER	CYS	conflict	UNP P51159
K	1	GLY	-	expression tag	UNP P51159
K	?	-	ARG	deletion	UNP P51159
K	50	THR	VAL	conflict	UNP P51159
K	51	ILE	VAL	conflict	UNP P51159
K	?	-	ALA	deletion	UNP P51159
K	?	-	SER	deletion	UNP P51159
K	?	-	GLY	deletion	UNP P51159
K	?	-	PRO	deletion	UNP P51159
K	?	-	ASP	deletion	UNP P51159
K	?	-	GLY	deletion	UNP P51159
K	?	-	ALA	deletion	UNP P51159
K	?	-	THR	deletion	UNP P51159
K	?	-	GLY	deletion	UNP P51159
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K	55	ASP	GLY	conflict	UNP P51159
K	56	LYS	GLN	conflict	UNP P51159
K	59	LYS	HIS	conflict	UNP P51159
K	68	LEU	GLN	conflict	UNP P51159
K	95	GLU	GLN	conflict	UNP P51159
K	108	LYS	GLN	conflict	UNP P51159
K	109	THR	MET	conflict	UNP P51159
K	113	SER	CYS	conflict	UNP P51159
K	130	GLU	GLN	conflict	UNP P51159
K	134	ALA	LYS	conflict	UNP P51159
K	135	ALA	GLU	conflict	UNP P51159
K	136	ALA	GLU	conflict	UNP P51159
K	139	ARG	ILE	conflict	UNP P51159
K	140	GLN	ALA	conflict	UNP P51159
K	144	HIS	LYS	conflict	UNP P51159
K	178	SER	CYS	conflict	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
M	1	GLY	-	expression tag	UNP P51159
M	?	-	ARG	deletion	UNP P51159
M	50	THR	VAL	conflict	UNP P51159
M	51	ILE	VAL	conflict	UNP P51159
M	?	-	ALA	deletion	UNP P51159
M	?	-	SER	deletion	UNP P51159
M	?	-	GLY	deletion	UNP P51159
M	?	-	PRO	deletion	UNP P51159
M	?	-	ASP	deletion	UNP P51159
M	?	-	GLY	deletion	UNP P51159
M	?	-	ALA	deletion	UNP P51159
M	?	-	THR	deletion	UNP P51159
M	?	-	GLY	deletion	UNP P51159
M	54	ASN	ARG	conflict	UNP P51159
M	55	ASP	GLY	conflict	UNP P51159
M	56	LYS	GLN	conflict	UNP P51159
M	59	LYS	HIS	conflict	UNP P51159
M	68	LEU	GLN	conflict	UNP P51159
M	95	GLU	GLN	conflict	UNP P51159
M	108	LYS	GLN	conflict	UNP P51159
M	109	THR	MET	conflict	UNP P51159
M	113	SER	CYS	conflict	UNP P51159
M	130	GLU	GLN	conflict	UNP P51159
M	134	ALA	LYS	conflict	UNP P51159
M	135	ALA	GLU	conflict	UNP P51159
M	136	ALA	GLU	conflict	UNP P51159
M	139	ARG	ILE	conflict	UNP P51159
M	140	GLN	ALA	conflict	UNP P51159
M	144	HIS	LYS	conflict	UNP P51159
M	178	SER	CYS	conflict	UNP P51159
D	1	GLY	-	expression tag	UNP P51159
D	?	-	ARG	deletion	UNP P51159
D	50	THR	VAL	conflict	UNP P51159
D	51	ILE	VAL	conflict	UNP P51159
D	?	-	ALA	deletion	UNP P51159
D	?	-	SER	deletion	UNP P51159
D	?	-	GLY	deletion	UNP P51159
D	?	-	PRO	deletion	UNP P51159
D	?	-	ASP	deletion	UNP P51159
D	?	-	GLY	deletion	UNP P51159
D	?	-	ALA	deletion	UNP P51159
D	?	-	THR	deletion	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	GLY	deletion	UNP P51159
D	54	ASN	ARG	conflict	UNP P51159
D	55	ASP	GLY	conflict	UNP P51159
D	56	LYS	GLN	conflict	UNP P51159
D	59	LYS	HIS	conflict	UNP P51159
D	68	LEU	GLN	conflict	UNP P51159
D	95	GLU	GLN	conflict	UNP P51159
D	108	LYS	GLN	conflict	UNP P51159
D	109	THR	MET	conflict	UNP P51159
D	113	SER	CYS	conflict	UNP P51159
D	130	GLU	GLN	conflict	UNP P51159
D	134	ALA	LYS	conflict	UNP P51159
D	135	ALA	GLU	conflict	UNP P51159
D	136	ALA	GLU	conflict	UNP P51159
D	139	ARG	ILE	conflict	UNP P51159
D	140	GLN	ALA	conflict	UNP P51159
D	144	HIS	LYS	conflict	UNP P51159
D	178	SER	CYS	conflict	UNP P51159
P	1	GLY	-	expression tag	UNP P51159
P	?	-	ARG	deletion	UNP P51159
P	50	THR	VAL	conflict	UNP P51159
P	51	ILE	VAL	conflict	UNP P51159
P	?	-	ALA	deletion	UNP P51159
P	?	-	SER	deletion	UNP P51159
P	?	-	GLY	deletion	UNP P51159
P	?	-	PRO	deletion	UNP P51159
P	?	-	ASP	deletion	UNP P51159
P	?	-	GLY	deletion	UNP P51159
P	?	-	ALA	deletion	UNP P51159
P	?	-	THR	deletion	UNP P51159
P	?	-	GLY	deletion	UNP P51159
P	54	ASN	ARG	conflict	UNP P51159
P	55	ASP	GLY	conflict	UNP P51159
P	56	LYS	GLN	conflict	UNP P51159
P	59	LYS	HIS	conflict	UNP P51159
P	68	LEU	GLN	conflict	UNP P51159
P	95	GLU	GLN	conflict	UNP P51159
P	108	LYS	GLN	conflict	UNP P51159
P	109	THR	MET	conflict	UNP P51159
P	113	SER	CYS	conflict	UNP P51159
P	130	GLU	GLN	conflict	UNP P51159
P	134	ALA	LYS	conflict	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
P	135	ALA	GLU	conflict	UNP P51159
P	136	ALA	GLU	conflict	UNP P51159
P	139	ARG	ILE	conflict	UNP P51159
P	140	GLN	ALA	conflict	UNP P51159
P	144	HIS	LYS	conflict	UNP P51159
P	178	SER	CYS	conflict	UNP P51159
F	1	GLY	-	expression tag	UNP P51159
F	?	-	ARG	deletion	UNP P51159
F	50	THR	VAL	conflict	UNP P51159
F	51	ILE	VAL	conflict	UNP P51159
F	?	-	ALA	deletion	UNP P51159
F	?	-	SER	deletion	UNP P51159
F	?	-	GLY	deletion	UNP P51159
F	?	-	PRO	deletion	UNP P51159
F	?	-	ASP	deletion	UNP P51159
F	?	-	GLY	deletion	UNP P51159
F	?	-	ALA	deletion	UNP P51159
F	?	-	THR	deletion	UNP P51159
F	?	-	GLY	deletion	UNP P51159
F	54	ASN	ARG	conflict	UNP P51159
F	55	ASP	GLY	conflict	UNP P51159
F	56	LYS	GLN	conflict	UNP P51159
F	59	LYS	HIS	conflict	UNP P51159
F	68	LEU	GLN	conflict	UNP P51159
F	95	GLU	GLN	conflict	UNP P51159
F	108	LYS	GLN	conflict	UNP P51159
F	109	THR	MET	conflict	UNP P51159
F	113	SER	CYS	conflict	UNP P51159
F	130	GLU	GLN	conflict	UNP P51159
F	134	ALA	LYS	conflict	UNP P51159
F	135	ALA	GLU	conflict	UNP P51159
F	136	ALA	GLU	conflict	UNP P51159
F	139	ARG	ILE	conflict	UNP P51159
F	140	GLN	ALA	conflict	UNP P51159
F	144	HIS	LYS	conflict	UNP P51159
F	178	SER	CYS	conflict	UNP P51159
J	1	GLY	-	expression tag	UNP P51159
J	?	-	ARG	deletion	UNP P51159
J	50	THR	VAL	conflict	UNP P51159
J	51	ILE	VAL	conflict	UNP P51159
J	?	-	ALA	deletion	UNP P51159
J	?	-	SER	deletion	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
J	?	-	GLY	deletion	UNP P51159
J	?	-	PRO	deletion	UNP P51159
J	?	-	ASP	deletion	UNP P51159
J	?	-	GLY	deletion	UNP P51159
J	?	-	ALA	deletion	UNP P51159
J	?	-	THR	deletion	UNP P51159
J	?	-	GLY	deletion	UNP P51159
J	54	ASN	ARG	conflict	UNP P51159
J	55	ASP	GLY	conflict	UNP P51159
J	56	LYS	GLN	conflict	UNP P51159
J	59	LYS	HIS	conflict	UNP P51159
J	68	LEU	GLN	conflict	UNP P51159
J	95	GLU	GLN	conflict	UNP P51159
J	108	LYS	GLN	conflict	UNP P51159
J	109	THR	MET	conflict	UNP P51159
J	113	SER	CYS	conflict	UNP P51159
J	130	GLU	GLN	conflict	UNP P51159
J	134	ALA	LYS	conflict	UNP P51159
J	135	ALA	GLU	conflict	UNP P51159
J	136	ALA	GLU	conflict	UNP P51159
J	139	ARG	ILE	conflict	UNP P51159
J	140	GLN	ALA	conflict	UNP P51159
J	144	HIS	LYS	conflict	UNP P51159
J	178	SER	CYS	conflict	UNP P51159
G	1	GLY	-	expression tag	UNP P51159
G	?	-	ARG	deletion	UNP P51159
G	50	THR	VAL	conflict	UNP P51159
G	51	ILE	VAL	conflict	UNP P51159
G	?	-	ALA	deletion	UNP P51159
G	?	-	SER	deletion	UNP P51159
G	?	-	GLY	deletion	UNP P51159
G	?	-	PRO	deletion	UNP P51159
G	?	-	ASP	deletion	UNP P51159
G	?	-	GLY	deletion	UNP P51159
G	?	-	ALA	deletion	UNP P51159
G	?	-	THR	deletion	UNP P51159
G	?	-	GLY	deletion	UNP P51159
G	54	ASN	ARG	conflict	UNP P51159
G	55	ASP	GLY	conflict	UNP P51159
G	56	LYS	GLN	conflict	UNP P51159
G	59	LYS	HIS	conflict	UNP P51159
G	68	LEU	GLN	conflict	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
G	95	GLU	GLN	conflict	UNP P51159
G	108	LYS	GLN	conflict	UNP P51159
G	109	THR	MET	conflict	UNP P51159
G	113	SER	CYS	conflict	UNP P51159
G	130	GLU	GLN	conflict	UNP P51159
G	134	ALA	LYS	conflict	UNP P51159
G	135	ALA	GLU	conflict	UNP P51159
G	136	ALA	GLU	conflict	UNP P51159
G	139	ARG	ILE	conflict	UNP P51159
G	140	GLN	ALA	conflict	UNP P51159
G	144	HIS	LYS	conflict	UNP P51159
G	178	SER	CYS	conflict	UNP P51159
I	1	GLY	-	expression tag	UNP P51159
I	?	-	ARG	deletion	UNP P51159
I	50	THR	VAL	conflict	UNP P51159
I	51	ILE	VAL	conflict	UNP P51159
I	?	-	ALA	deletion	UNP P51159
I	?	-	SER	deletion	UNP P51159
I	?	-	GLY	deletion	UNP P51159
I	?	-	PRO	deletion	UNP P51159
I	?	-	ASP	deletion	UNP P51159
I	?	-	GLY	deletion	UNP P51159
I	?	-	ALA	deletion	UNP P51159
I	?	-	THR	deletion	UNP P51159
I	?	-	GLY	deletion	UNP P51159
I	54	ASN	ARG	conflict	UNP P51159
I	55	ASP	GLY	conflict	UNP P51159
I	56	LYS	GLN	conflict	UNP P51159
I	59	LYS	HIS	conflict	UNP P51159
I	68	LEU	GLN	conflict	UNP P51159
I	95	GLU	GLN	conflict	UNP P51159
I	108	LYS	GLN	conflict	UNP P51159
I	109	THR	MET	conflict	UNP P51159
I	113	SER	CYS	conflict	UNP P51159
I	130	GLU	GLN	conflict	UNP P51159
I	134	ALA	LYS	conflict	UNP P51159
I	135	ALA	GLU	conflict	UNP P51159
I	136	ALA	GLU	conflict	UNP P51159
I	139	ARG	ILE	conflict	UNP P51159
I	140	GLN	ALA	conflict	UNP P51159
I	144	HIS	LYS	conflict	UNP P51159
I	178	SER	CYS	conflict	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
H	1	GLY	-	expression tag	UNP P51159
H	?	-	ARG	deletion	UNP P51159
H	50	THR	VAL	conflict	UNP P51159
H	51	ILE	VAL	conflict	UNP P51159
H	?	-	ALA	deletion	UNP P51159
H	?	-	SER	deletion	UNP P51159
H	?	-	GLY	deletion	UNP P51159
H	?	-	PRO	deletion	UNP P51159
H	?	-	ASP	deletion	UNP P51159
H	?	-	GLY	deletion	UNP P51159
H	?	-	ALA	deletion	UNP P51159
H	?	-	THR	deletion	UNP P51159
H	?	-	GLY	deletion	UNP P51159
H	54	ASN	ARG	conflict	UNP P51159
H	55	ASP	GLY	conflict	UNP P51159
H	56	LYS	GLN	conflict	UNP P51159
H	59	LYS	HIS	conflict	UNP P51159
H	68	LEU	GLN	conflict	UNP P51159
H	95	GLU	GLN	conflict	UNP P51159
H	108	LYS	GLN	conflict	UNP P51159
H	109	THR	MET	conflict	UNP P51159
H	113	SER	CYS	conflict	UNP P51159
H	130	GLU	GLN	conflict	UNP P51159
H	134	ALA	LYS	conflict	UNP P51159
H	135	ALA	GLU	conflict	UNP P51159
H	136	ALA	GLU	conflict	UNP P51159
H	139	ARG	ILE	conflict	UNP P51159
H	140	GLN	ALA	conflict	UNP P51159
H	144	HIS	LYS	conflict	UNP P51159
H	178	SER	CYS	conflict	UNP P51159
L	1	GLY	-	expression tag	UNP P51159
L	?	-	ARG	deletion	UNP P51159
L	50	THR	VAL	conflict	UNP P51159
L	51	ILE	VAL	conflict	UNP P51159
L	?	-	ALA	deletion	UNP P51159
L	?	-	SER	deletion	UNP P51159
L	?	-	GLY	deletion	UNP P51159
L	?	-	PRO	deletion	UNP P51159
L	?	-	ASP	deletion	UNP P51159
L	?	-	GLY	deletion	UNP P51159
L	?	-	ALA	deletion	UNP P51159
L	?	-	THR	deletion	UNP P51159

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Chain	Residue	Modelled	Actual	Comment	Reference
L	?	-	GLY	deletion	UNP P51159
L	54	ASN	ARG	conflict	UNP P51159
L	55	ASP	GLY	conflict	UNP P51159
L	56	LYS	GLN	conflict	UNP P51159
L	59	LYS	HIS	conflict	UNP P51159
L	68	LEU	GLN	conflict	UNP P51159
L	95	GLU	GLN	conflict	UNP P51159
L	108	LYS	GLN	conflict	UNP P51159
L	109	THR	MET	conflict	UNP P51159
L	113	SER	CYS	conflict	UNP P51159
L	130	GLU	GLN	conflict	UNP P51159
L	134	ALA	LYS	conflict	UNP P51159
L	135	ALA	GLU	conflict	UNP P51159
L	136	ALA	GLU	conflict	UNP P51159
L	139	ARG	ILE	conflict	UNP P51159
L	140	GLN	ALA	conflict	UNP P51159
L	144	HIS	LYS	conflict	UNP P51159
L	178	SER	CYS	conflict	UNP P51159

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

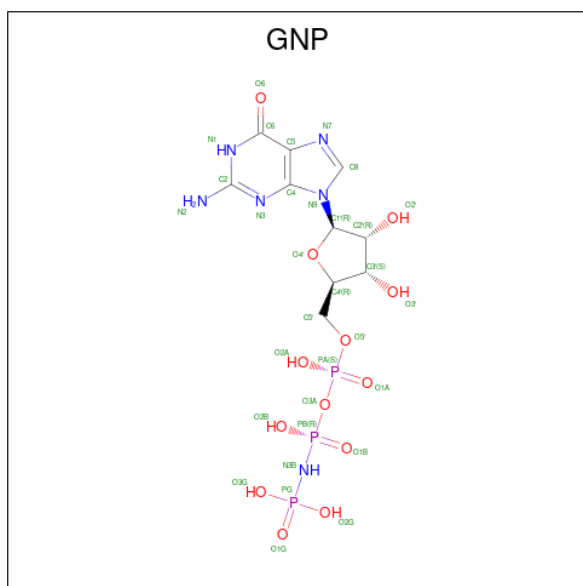
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	O	1	Total Mg 1 1	0	0
2	N	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	K	1	Total Mg 1 1	0	0
2	M	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	P	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	1	Total	Mg	0	0
			1	1		
2	J	1	Total	Mg	0	0
			1	1		
2	G	1	Total	Mg	0	0
			1	1		
2	I	1	Total	Mg	0	0
			1	1		
2	H	1	Total	Mg	0	0
			1	1		
2	L	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	K	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	M	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	D	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	P	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	F	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	J	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	G	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	I	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	H	1	Total 32	C 10	N 6	O 13	P 3	0	0
3	L	1	Total 32	C 10	N 6	O 13	P 3	0	0

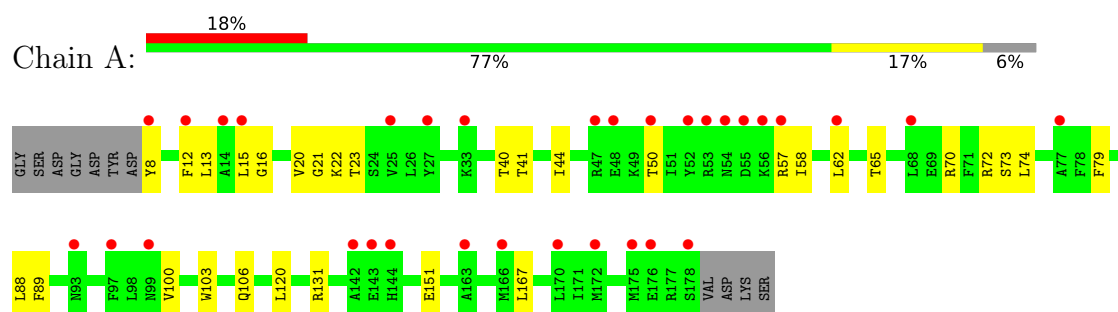
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total 5	O 5	0	0
4	G	1	Total 1	O 1	0	0

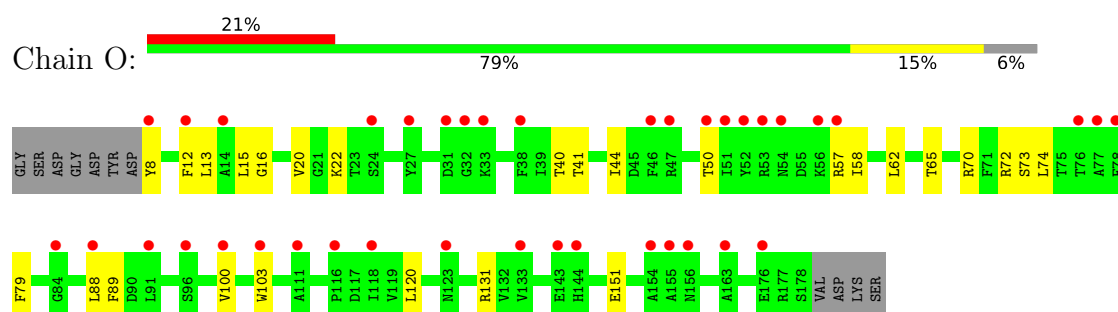
3 Residue-property plots [i](#)

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.

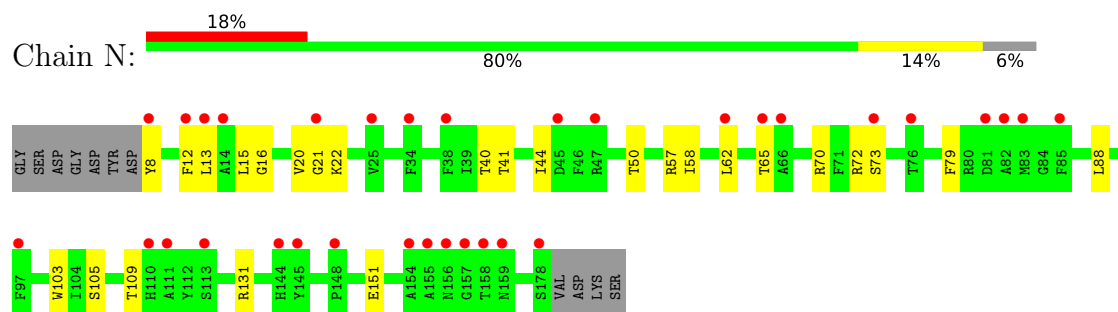
- Molecule 1: Ras-related protein Rab-27A



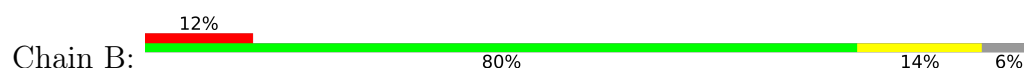
- Molecule 1: Ras-related protein Rab-27A

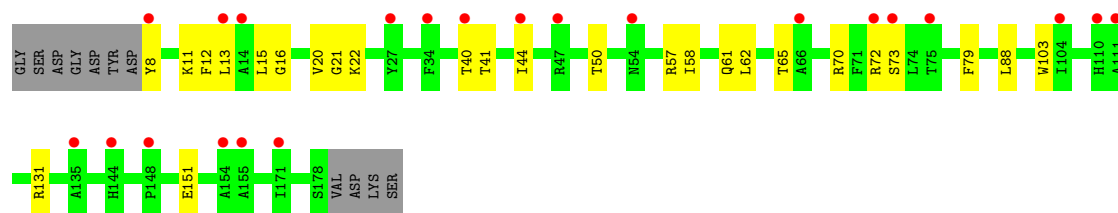


- Molecule 1: Ras-related protein Rab-27A

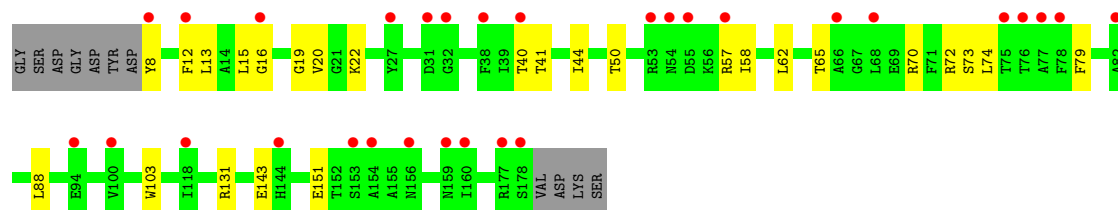
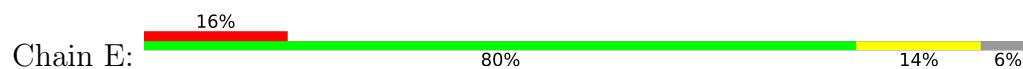


- Molecule 1: Ras-related protein Rab-27A

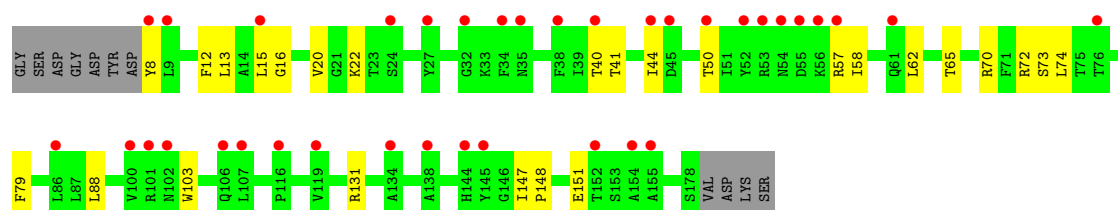
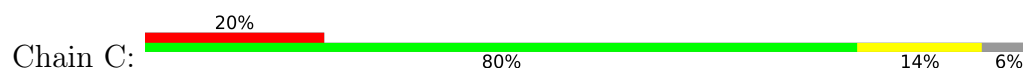




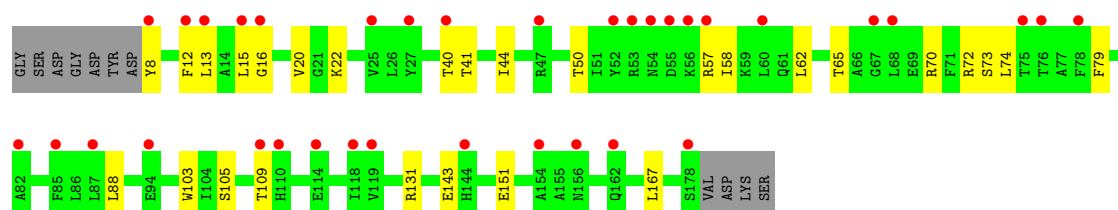
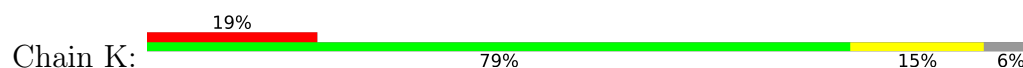
• Molecule 1: Ras-related protein Rab-27A



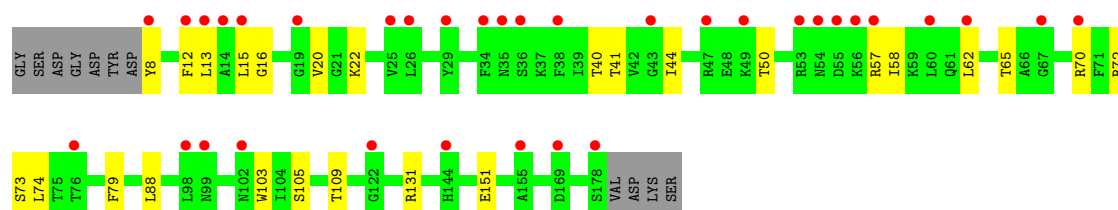
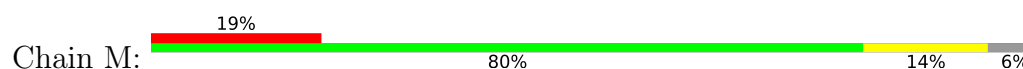
• Molecule 1: Ras-related protein Rab-27A



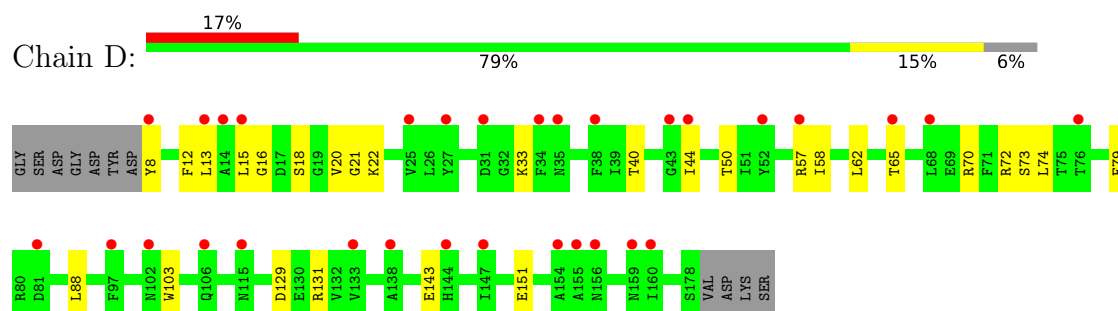
• Molecule 1: Ras-related protein Rab-27A



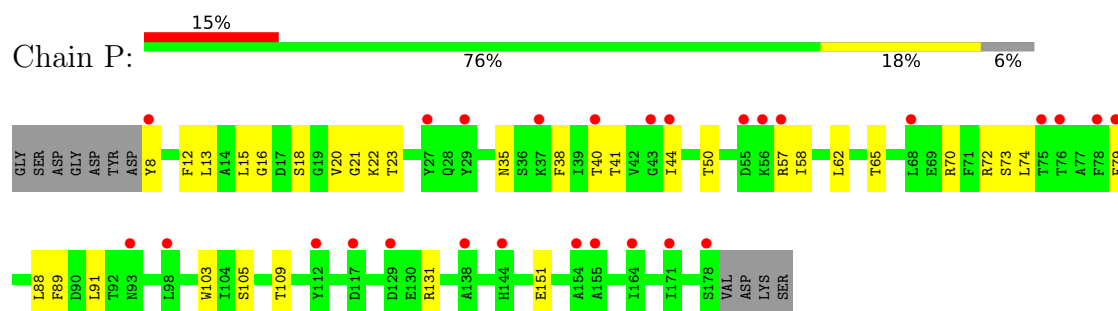
• Molecule 1: Ras-related protein Rab-27A



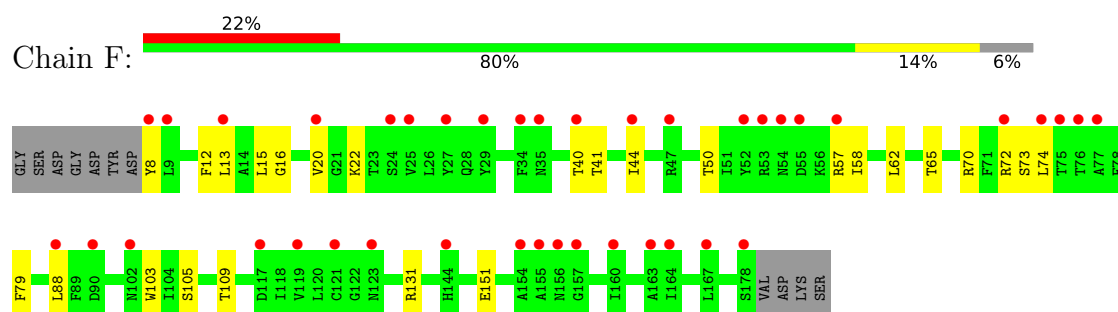
- Molecule 1: Ras-related protein Rab-27A



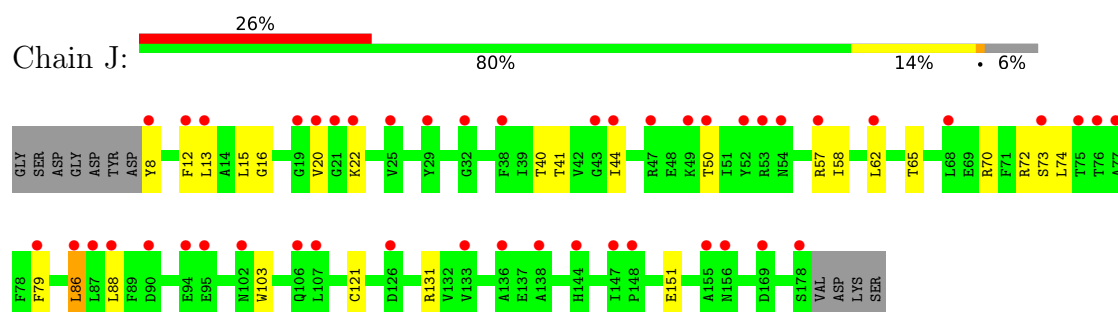
- Molecule 1: Ras-related protein Rab-27A



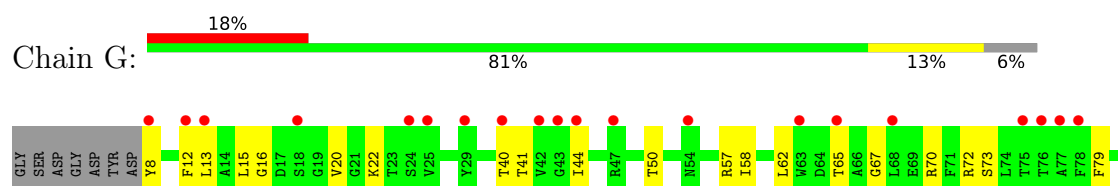
- Molecule 1: Ras-related protein Rab-27A

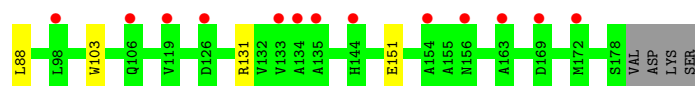


- Molecule 1: Ras-related protein Rab-27A

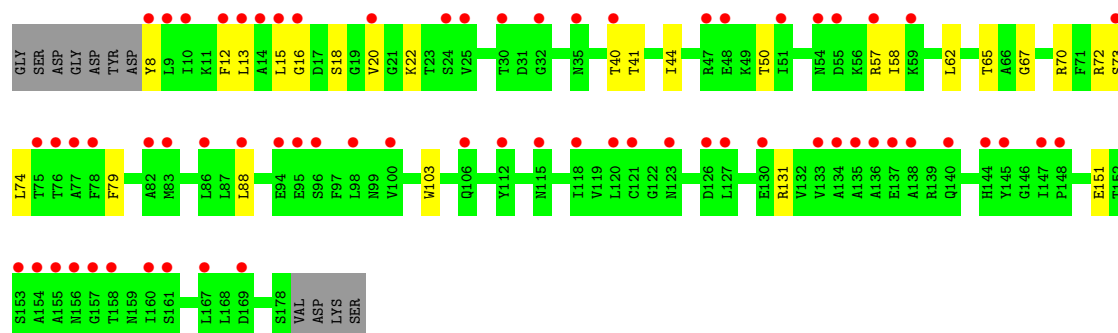
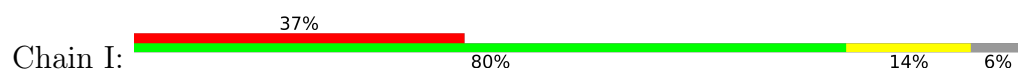


- Molecule 1: Ras-related protein Rab-27A

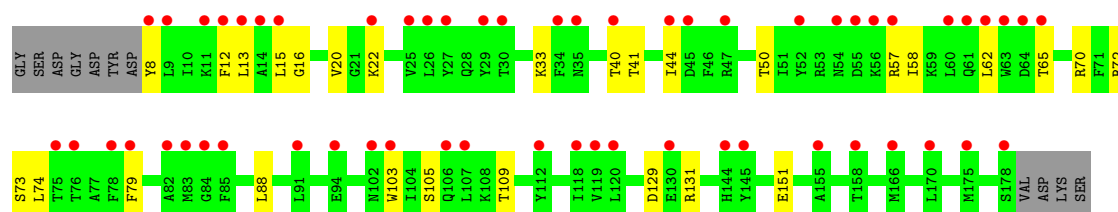
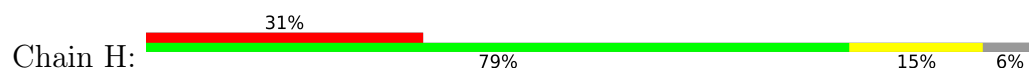




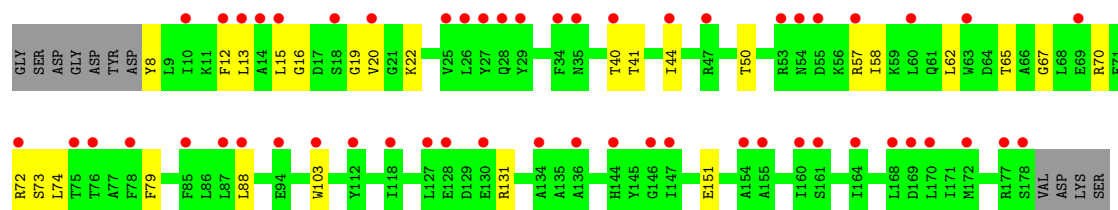
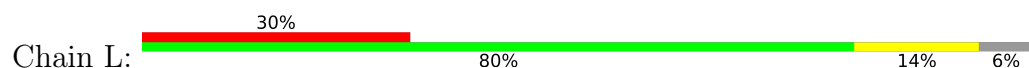
• Molecule 1: Ras-related protein Rab-27A



• Molecule 1: Ras-related protein Rab-27A



• Molecule 1: Ras-related protein Rab-27A



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	130.42Å 132.41Å 230.59Å 90.00° 103.57° 90.00°	Depositor
Resolution (Å)	80.15 – 2.82 80.15 – 2.82	Depositor EDS
% Data completeness (in resolution range)	75.8 (80.15-2.82) 75.8 (80.15-2.82)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.312 , 0.342 0.311 , 0.339	Depositor DCC
R_{free} test set	3513 reflections (3.85%)	wwPDB-VP
Wilson B-factor (Å ²)	55.1	Xtriage
Anisotropy	0.965	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 62.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.000 for k,h,-1/2*h-1/2*k-l 0.000 for -k,-h,-1/2*h+1/2*k-l 0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	18977	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.51 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.2444e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MG, 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	1.07	0/1176	1.54	0/1610
1	B	1.08	0/1169	1.54	0/1601
1	C	1.08	0/1170	1.54	0/1602
1	D	1.08	0/1173	1.54	1/1606 (0.1%)
1	E	1.09	0/1166	1.54	1/1597 (0.1%)
1	F	1.08	0/1173	1.54	0/1606
1	G	1.08	0/1169	1.54	0/1601
1	H	1.08	0/1166	1.54	0/1597
1	I	1.08	0/1166	1.54	0/1597
1	J	1.08	0/1173	1.54	0/1606
1	K	1.09	0/1179	1.54	1/1614 (0.1%)
1	L	1.09	0/1166	1.54	0/1597
1	M	1.08	0/1166	1.54	0/1597
1	N	1.09	0/1166	1.55	0/1597
1	O	1.09	0/1169	1.55	0/1601
1	P	1.08	0/1173	1.55	0/1606
All	All	1.08	0/18720	1.54	3/25635 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	1
All	All	0	16

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	143	GLU	CA-C-O	-5.04	115.71	121.00
1	E	143	GLU	CA-C-O	-5.01	115.74	121.00
1	D	143	GLU	CA-C-O	-5.01	115.74	121.00

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	8	TYR	Peptide
1	B	8	TYR	Peptide
1	E	8	TYR	Peptide
1	N	8	TYR	Peptide
1	O	8	TYR	Peptide

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	1159	0	962	30	0
1	B	1152	0	947	22	0
1	C	1153	0	943	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1155	0	945	26	0
1	E	1149	0	939	22	0
1	F	1155	0	945	23	0
1	G	1152	0	942	22	0
1	H	1149	0	938	25	0
1	I	1149	0	938	24	0
1	J	1155	0	946	23	0
1	K	1161	0	964	24	0
1	L	1149	0	938	24	0
1	M	1149	0	938	22	0
1	N	1149	0	938	23	0
1	O	1152	0	947	25	0
1	P	1155	0	946	27	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	0
3	A	32	0	13	2	0
3	B	32	0	13	1	0
3	C	32	0	13	0	0
3	D	32	0	13	2	0
3	E	32	0	13	1	0
3	F	32	0	13	0	0
3	G	32	0	13	2	0
3	H	32	0	13	0	0
3	I	32	0	13	2	0
3	J	32	0	13	0	0
3	K	32	0	13	0	0
3	L	32	0	13	2	0
3	M	32	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	N	32	0	13	2	0
3	O	32	0	13	0	0
3	P	32	0	13	3	0
4	A	5	0	0	1	0
4	G	1	0	0	0	0
All	All	18977	0	15324	380	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 11.

The worst 5 of 380 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:O:89:PHE:HE1	1:O:120:LEU:HD21	1.30	0.96
1:A:89:PHE:HE1	1:A:120:LEU:HD21	1.32	0.92
1:A:89:PHE:CE1	1:A:120:LEU:HD21	2.13	0.83
1:O:89:PHE:CE1	1:O:120:LEU:HD21	2.13	0.82
1:J:86:LEU:HD11	1:J:121:CYS:SG	2.21	0.81

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	169/182 (93%)	155 (92%)	12 (7%)	2 (1%)	10	31
1	B	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
1	C	169/182 (93%)	153 (90%)	14 (8%)	2 (1%)	10	31
1	D	169/182 (93%)	155 (92%)	13 (8%)	1 (1%)	21	48
1	E	169/182 (93%)	153 (90%)	14 (8%)	2 (1%)	10	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
1	G	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
1	H	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
1	I	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
1	J	169/182 (93%)	153 (90%)	14 (8%)	2 (1%)	10	31
1	K	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
1	L	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
1	M	169/182 (93%)	155 (92%)	12 (7%)	2 (1%)	10	31
1	N	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
1	O	169/182 (93%)	153 (90%)	14 (8%)	2 (1%)	10	31
1	P	169/182 (93%)	154 (91%)	13 (8%)	2 (1%)	10	31
All	All	2704/2912 (93%)	2463 (91%)	210 (8%)	31 (1%)	11	34

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	40	THR
1	P	40	THR
1	A	40	THR
1	O	40	THR
1	N	40	THR

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	92/157 (59%)	92 (100%)	0	100	100
1	B	90/157 (57%)	90 (100%)	0	100	100
1	C	90/157 (57%)	90 (100%)	0	100	100
1	D	90/157 (57%)	90 (100%)	0	100	100
1	E	89/157 (57%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	90/157 (57%)	90 (100%)	0	100	100
1	G	90/157 (57%)	90 (100%)	0	100	100
1	H	89/157 (57%)	89 (100%)	0	100	100
1	I	89/157 (57%)	89 (100%)	0	100	100
1	J	90/157 (57%)	89 (99%)	1 (1%)	65	86
1	K	92/157 (59%)	92 (100%)	0	100	100
1	L	89/157 (57%)	89 (100%)	0	100	100
1	M	89/157 (57%)	89 (100%)	0	100	100
1	N	89/157 (57%)	89 (100%)	0	100	100
1	O	90/157 (57%)	90 (100%)	0	100	100
1	P	90/157 (57%)	90 (100%)	0	100	100
All	All	1438/2512 (57%)	1437 (100%)	1 (0%)	88	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	156	ASN
1	I	156	ASN
1	D	156	ASN
1	G	156	ASN
1	M	156	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 16 are monoatomic - leaving 16 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	GNP	M	202	2	34,34,34	1.09	3 (8%)	47,54,54	1.23	4 (8%)
3	GNP	B	202	2	34,34,34	1.12	5 (14%)	47,54,54	1.26	3 (6%)
3	GNP	I	202	2	34,34,34	1.09	3 (8%)	47,54,54	1.01	2 (4%)
3	GNP	C	202	2	34,34,34	1.11	3 (8%)	47,54,54	1.34	4 (8%)
3	GNP	L	202	2	34,34,34	0.98	3 (8%)	47,54,54	1.51	7 (14%)
3	GNP	O	202	2	34,34,34	1.20	3 (8%)	47,54,54	1.42	5 (10%)
3	GNP	D	202	2	34,34,34	1.17	3 (8%)	47,54,54	1.17	4 (8%)
3	GNP	P	202	2	34,34,34	1.17	3 (8%)	47,54,54	1.35	5 (10%)
3	GNP	F	202	2	34,34,34	1.05	3 (8%)	47,54,54	1.30	6 (12%)
3	GNP	K	202	2	34,34,34	1.27	5 (14%)	47,54,54	1.79	7 (14%)
3	GNP	G	202	2	34,34,34	1.09	4 (11%)	47,54,54	1.47	5 (10%)
3	GNP	H	202	2	34,34,34	1.27	5 (14%)	47,54,54	0.89	2 (4%)
3	GNP	J	202	2	34,34,34	1.35	6 (17%)	47,54,54	1.27	4 (8%)
3	GNP	E	202	2	34,34,34	1.19	5 (14%)	47,54,54	1.18	4 (8%)
3	GNP	N	202	2	34,34,34	1.06	4 (11%)	47,54,54	1.11	3 (6%)
3	GNP	A	202	2	34,34,34	1.43	3 (8%)	47,54,54	1.18	3 (6%)

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	GNP	M	202	2	-	4/18/38/38	0/3/3/3
3	GNP	B	202	2	-	3/18/38/38	0/3/3/3
3	GNP	I	202	2	-	2/18/38/38	0/3/3/3
3	GNP	C	202	2	-	3/18/38/38	0/3/3/3
3	GNP	L	202	2	-	3/18/38/38	0/3/3/3
3	GNP	O	202	2	-	3/18/38/38	0/3/3/3
3	GNP	D	202	2	-	6/18/38/38	0/3/3/3
3	GNP	P	202	2	-	4/18/38/38	0/3/3/3
3	GNP	F	202	2	-	3/18/38/38	0/3/3/3
3	GNP	K	202	2	-	3/18/38/38	0/3/3/3
3	GNP	G	202	2	-	3/18/38/38	0/3/3/3
3	GNP	H	202	2	-	4/18/38/38	0/3/3/3
3	GNP	J	202	2	-	7/18/38/38	0/3/3/3
3	GNP	E	202	2	-	3/18/38/38	0/3/3/3
3	GNP	N	202	2	-	3/18/38/38	0/3/3/3
3	GNP	A	202	2	-	4/18/38/38	0/3/3/3

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	202	GNP	PG-O1G	6.81	1.56	1.46
3	O	202	GNP	PG-O1G	4.79	1.53	1.46
3	J	202	GNP	PG-O1G	4.56	1.53	1.46
3	P	202	GNP	PG-O1G	4.33	1.52	1.46
3	D	202	GNP	PG-O1G	4.33	1.52	1.46

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	202	GNP	O1B-PB-N3B	-7.89	100.15	111.77
3	O	202	GNP	O1G-PG-N3B	-6.24	102.59	111.77
3	C	202	GNP	O3G-PG-O1G	-5.73	99.08	113.45
3	K	202	GNP	O1G-PG-N3B	-5.69	103.39	111.77
3	G	202	GNP	O1B-PB-N3B	-5.41	103.80	111.77

There are no chirality outliers.

5 of 58 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	202	GNP	PG-N3B-PB-O1B
3	A	202	GNP	PG-N3B-PB-O3A
3	A	202	GNP	PA-O3A-PB-O2B
3	O	202	GNP	PB-N3B-PG-O1G
3	O	202	GNP	PG-N3B-PB-O1B

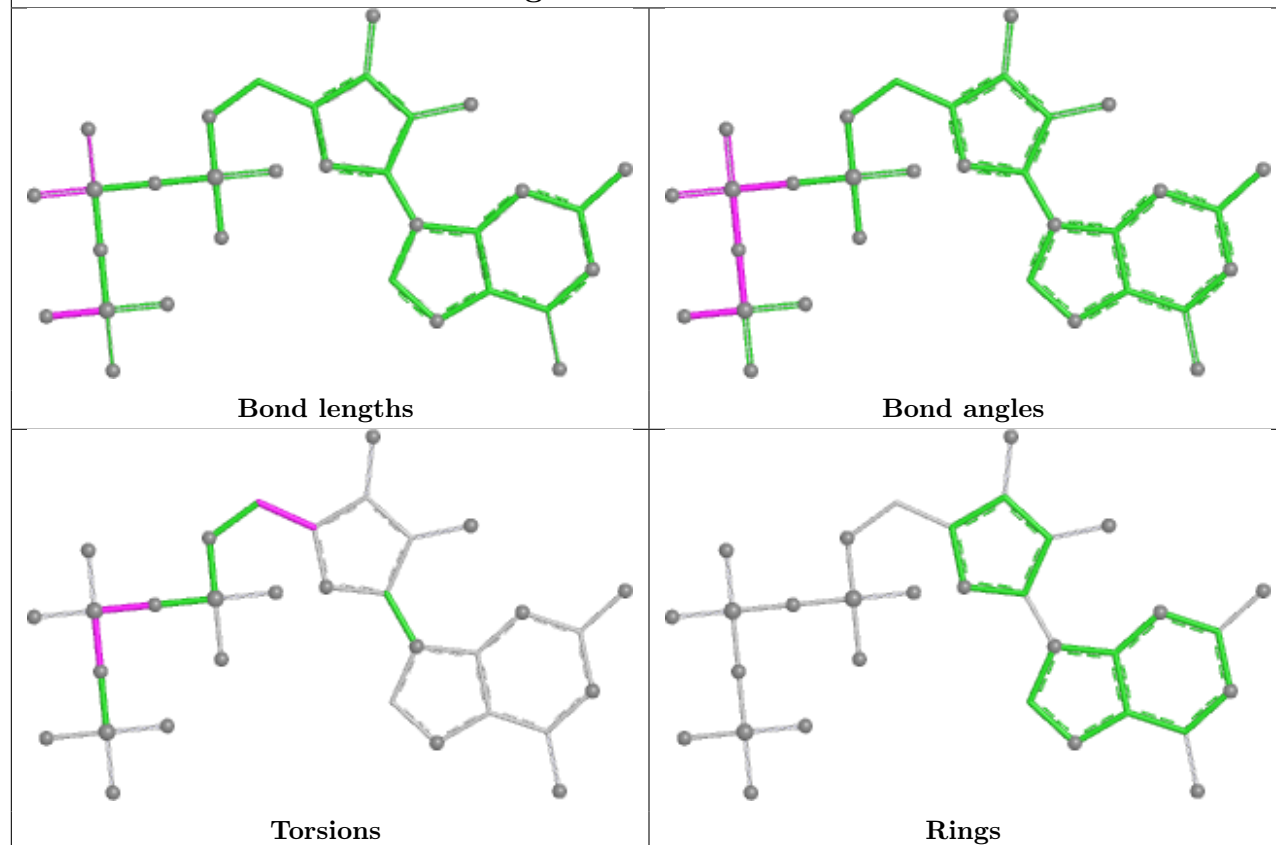
There are no ring outliers.

9 monomers are involved in 17 short contacts:

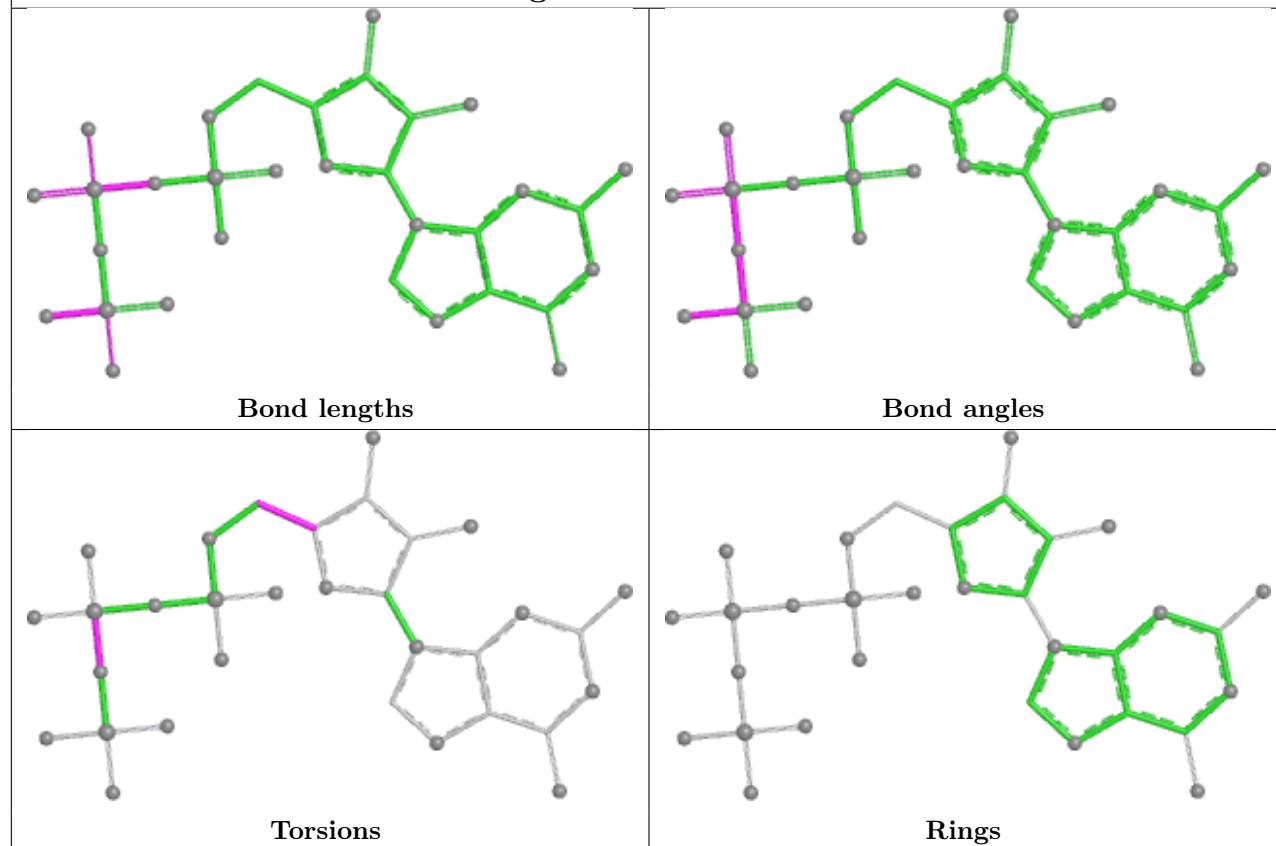
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	202	GNP	1	0
3	I	202	GNP	2	0
3	L	202	GNP	2	0
3	D	202	GNP	2	0
3	P	202	GNP	3	0
3	G	202	GNP	2	0
3	E	202	GNP	1	0
3	N	202	GNP	2	0
3	A	202	GNP	2	0

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

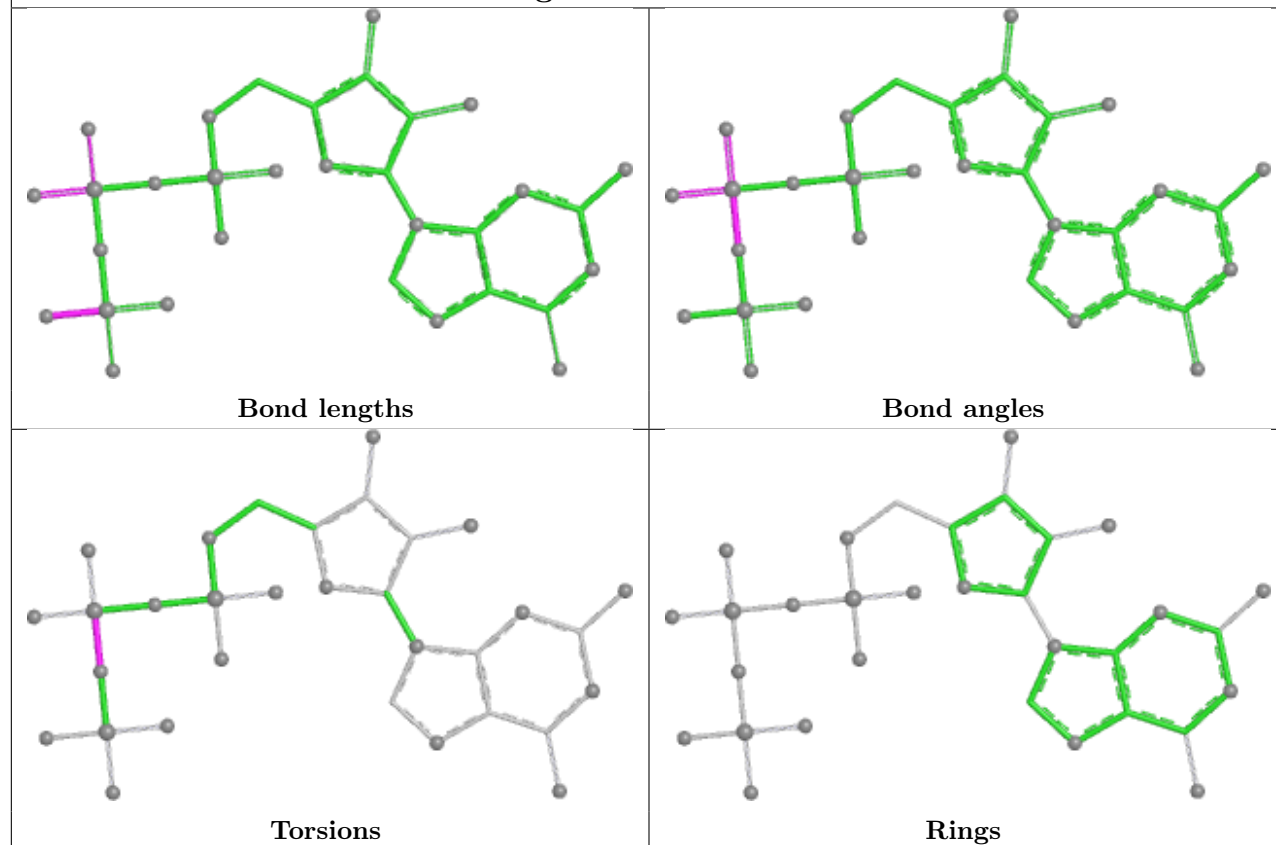
Ligand GNP M 202



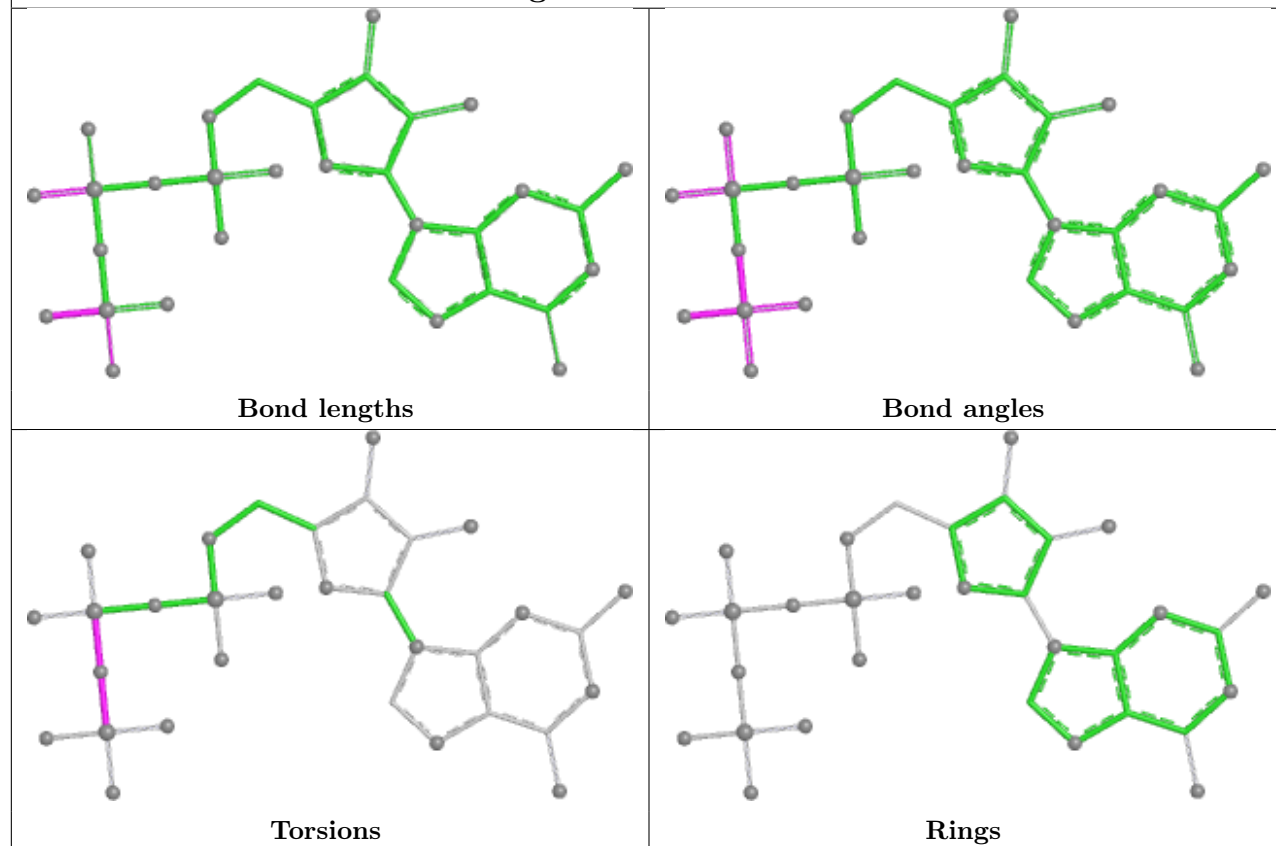
Ligand GNP B 202



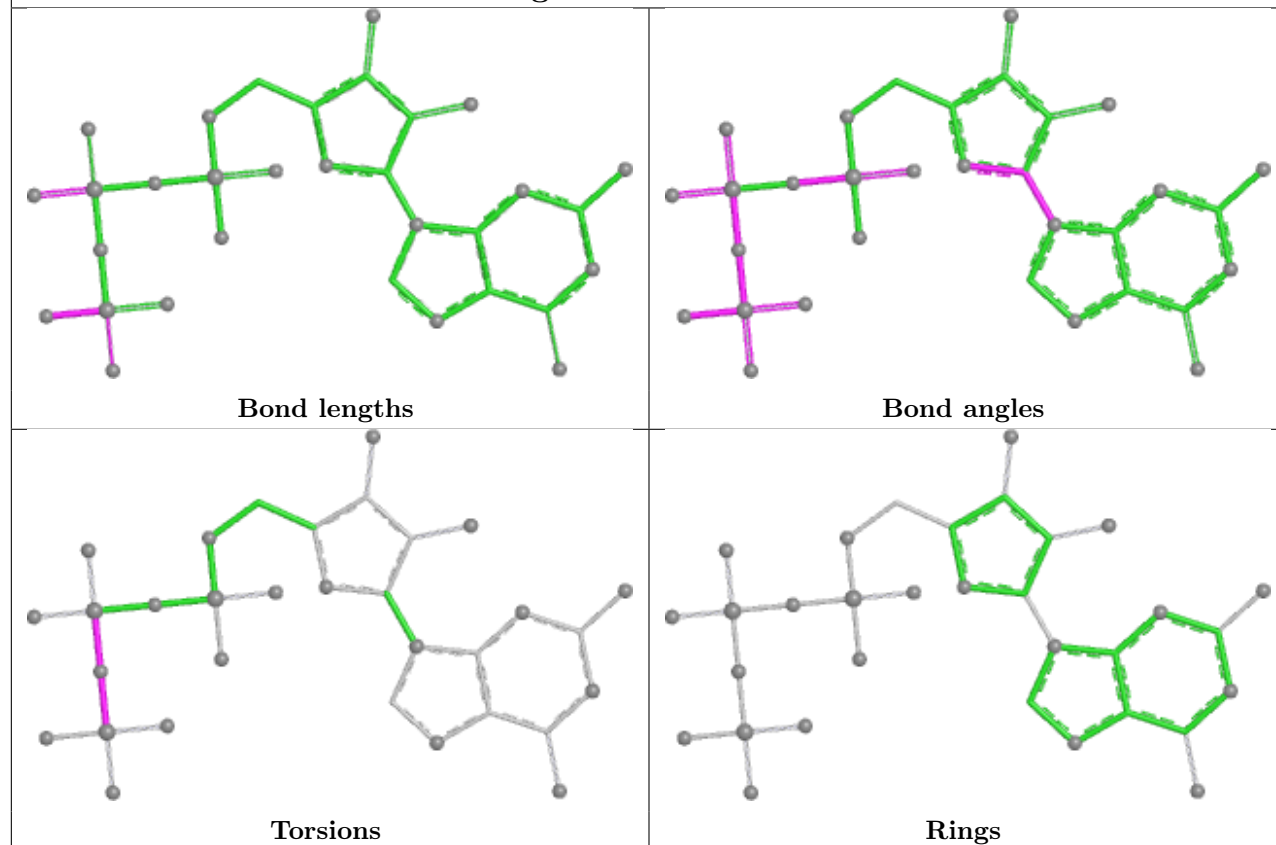
Ligand GNP I 202



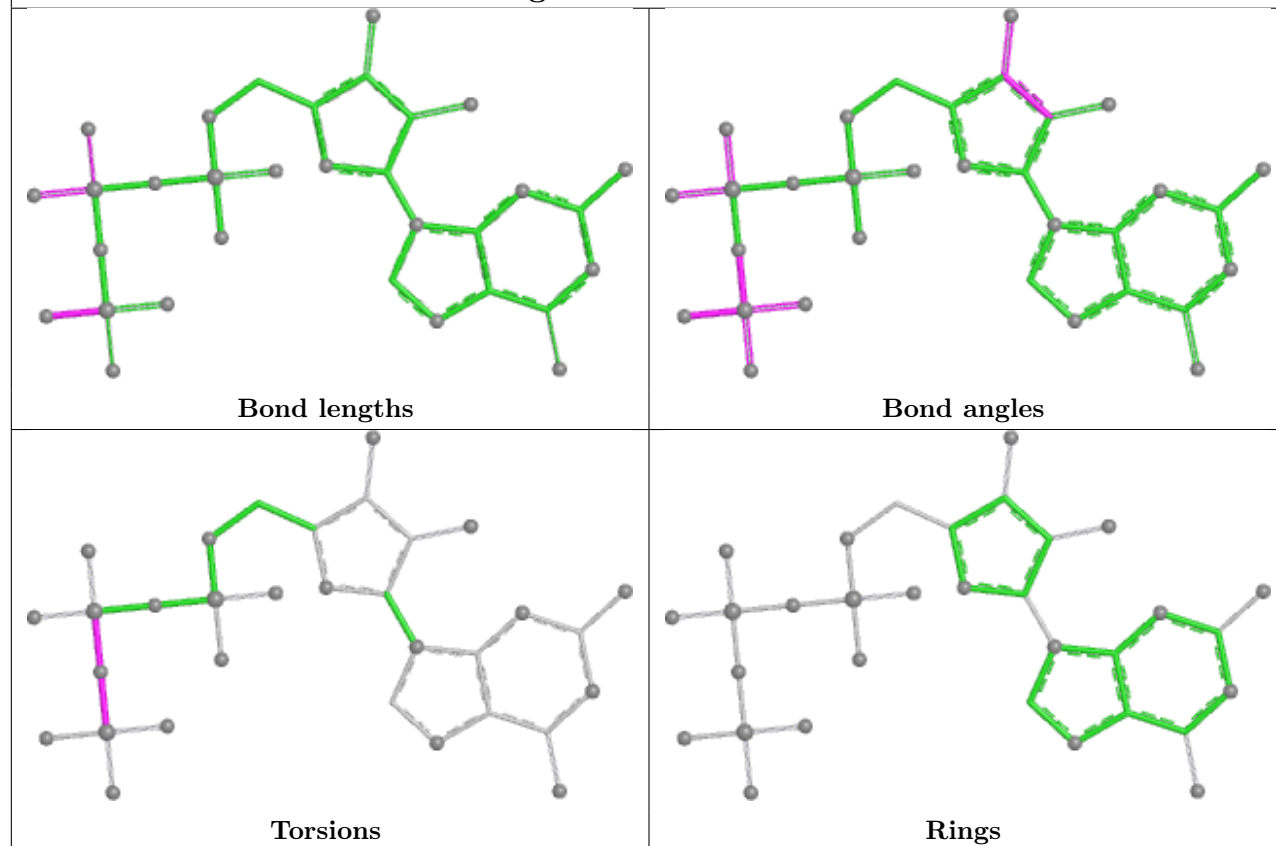
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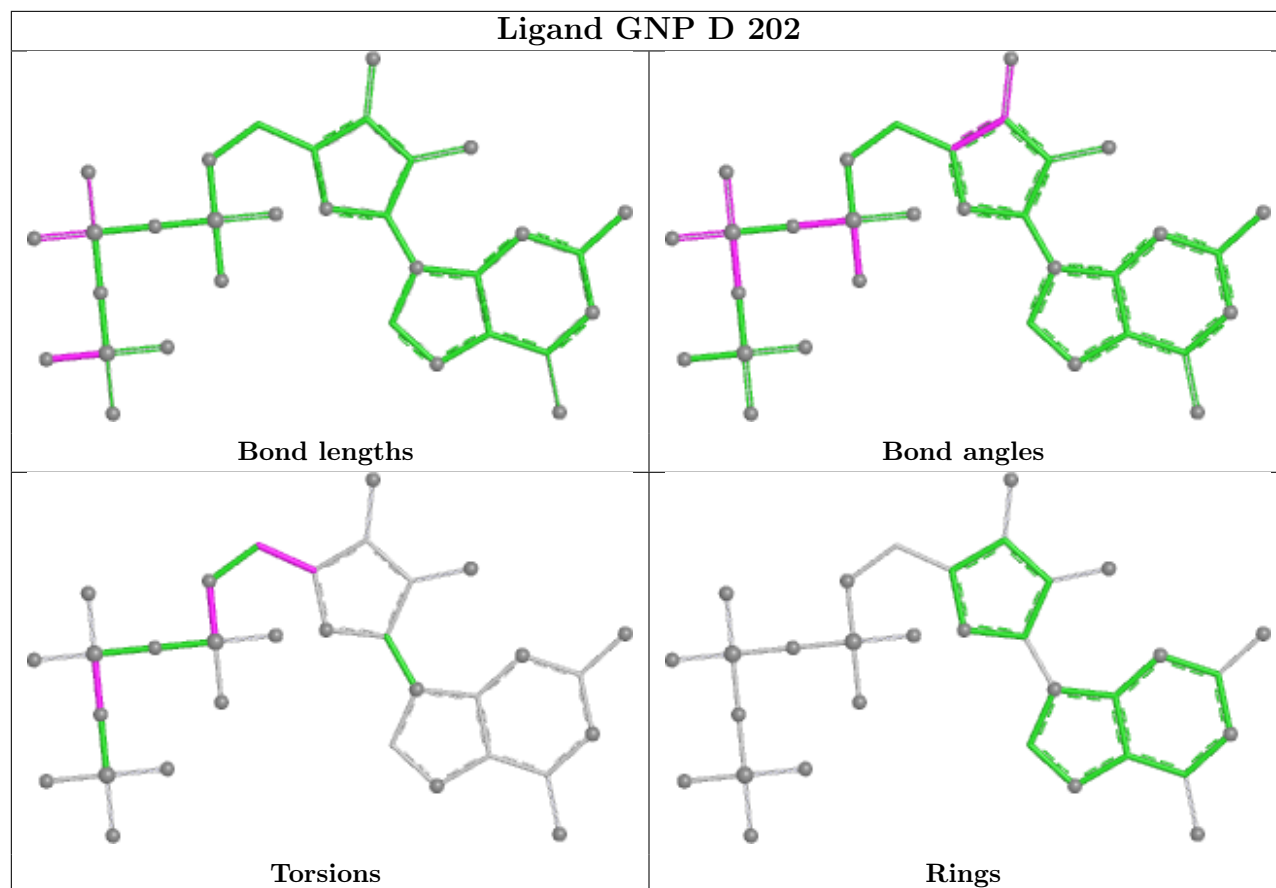
Ligand GNP L 202



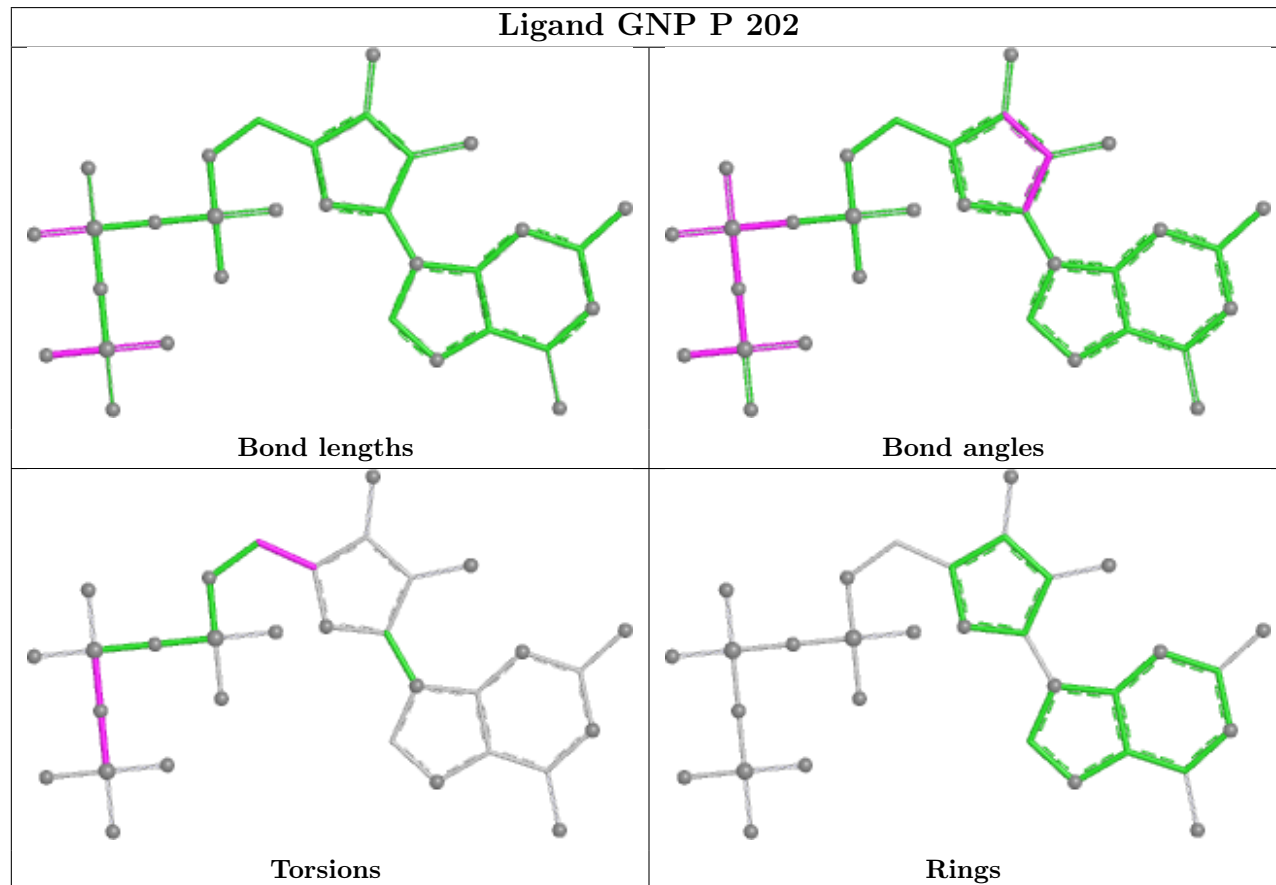
Ligand GNP O 202



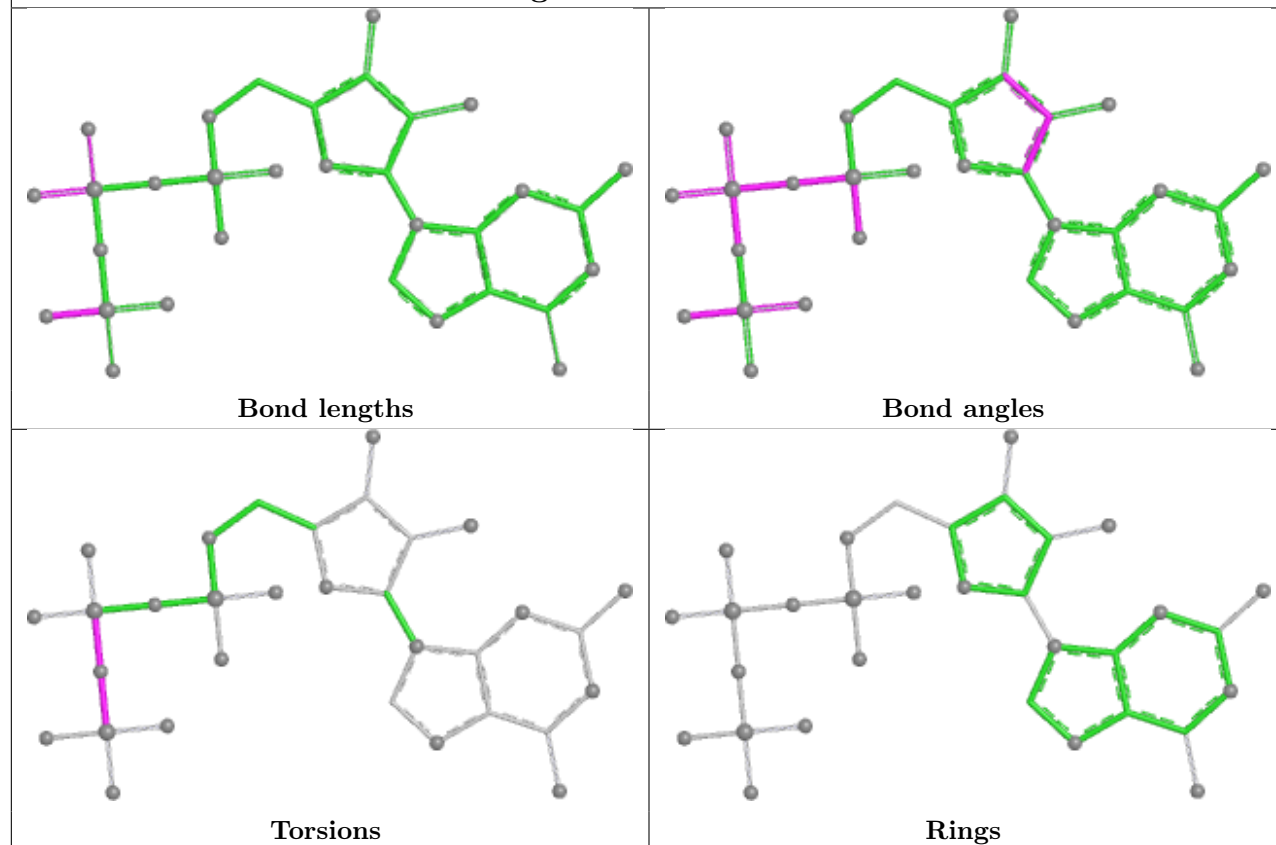
Ligand GNP D 202



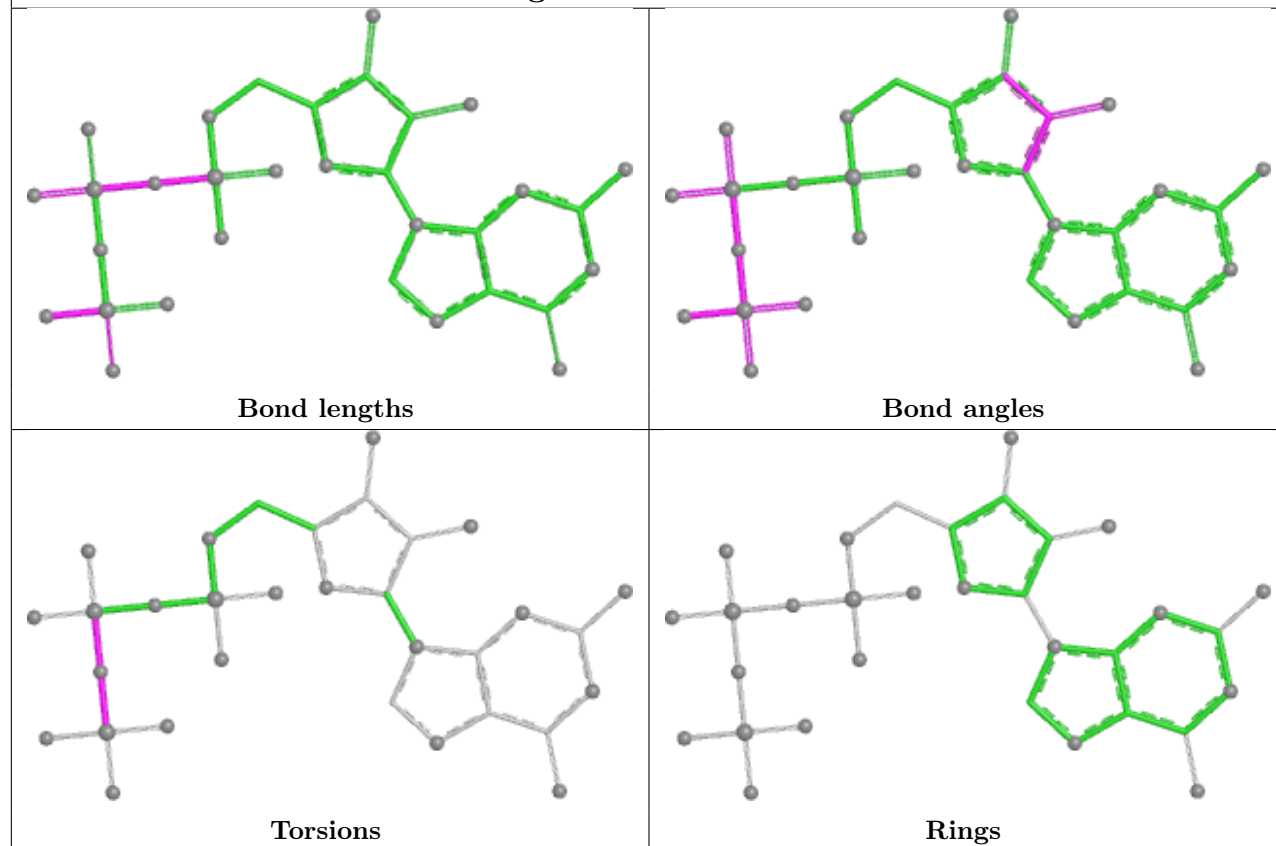
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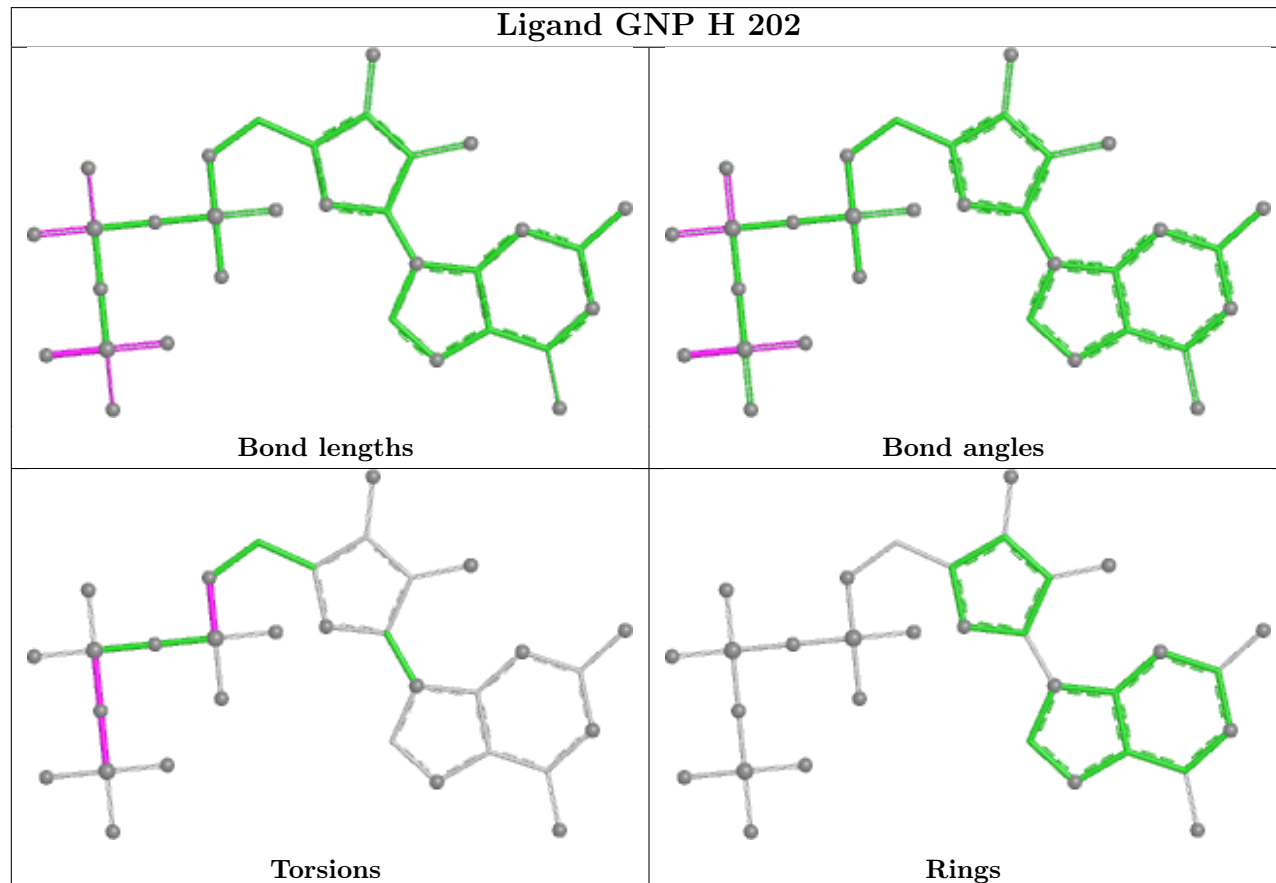
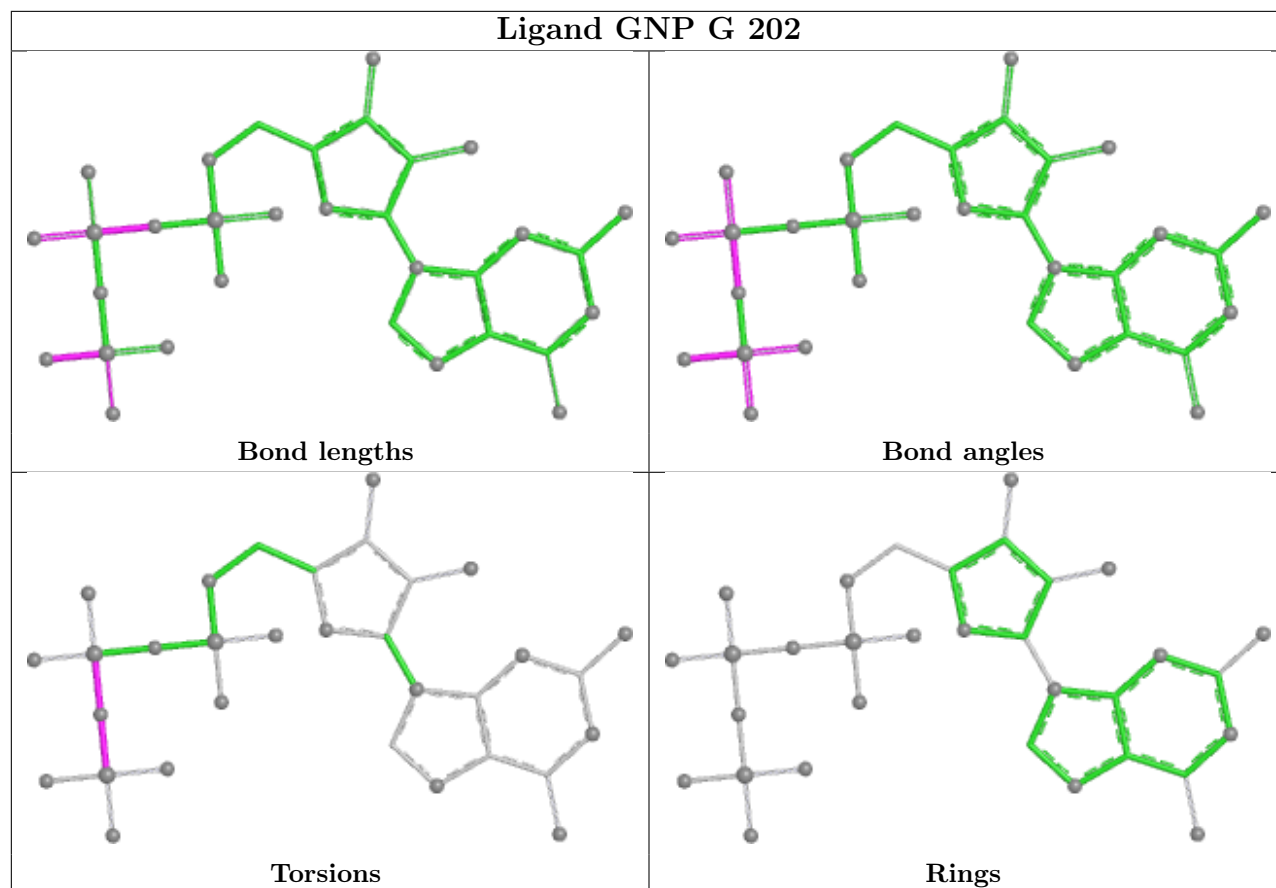


Ligand GNP F 202

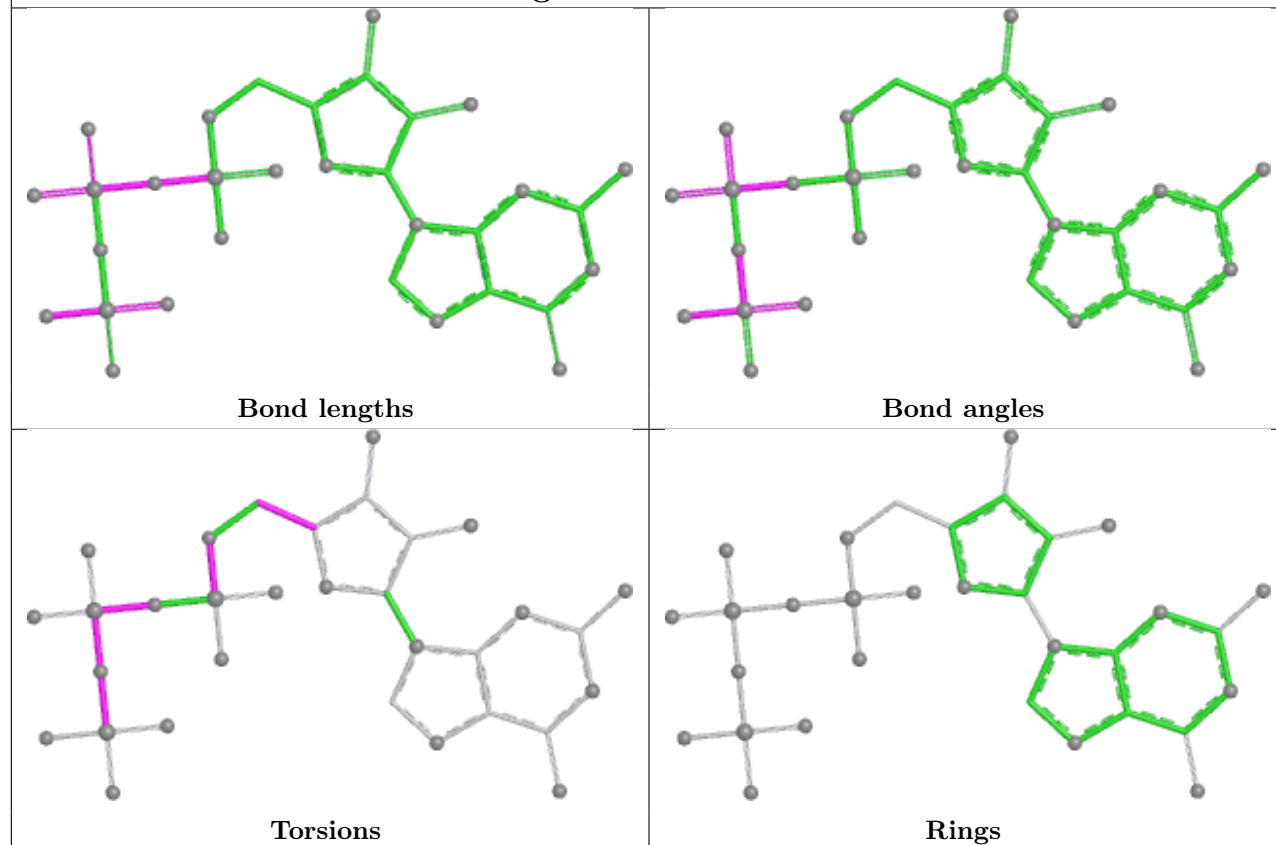


Ligand GNP K 202

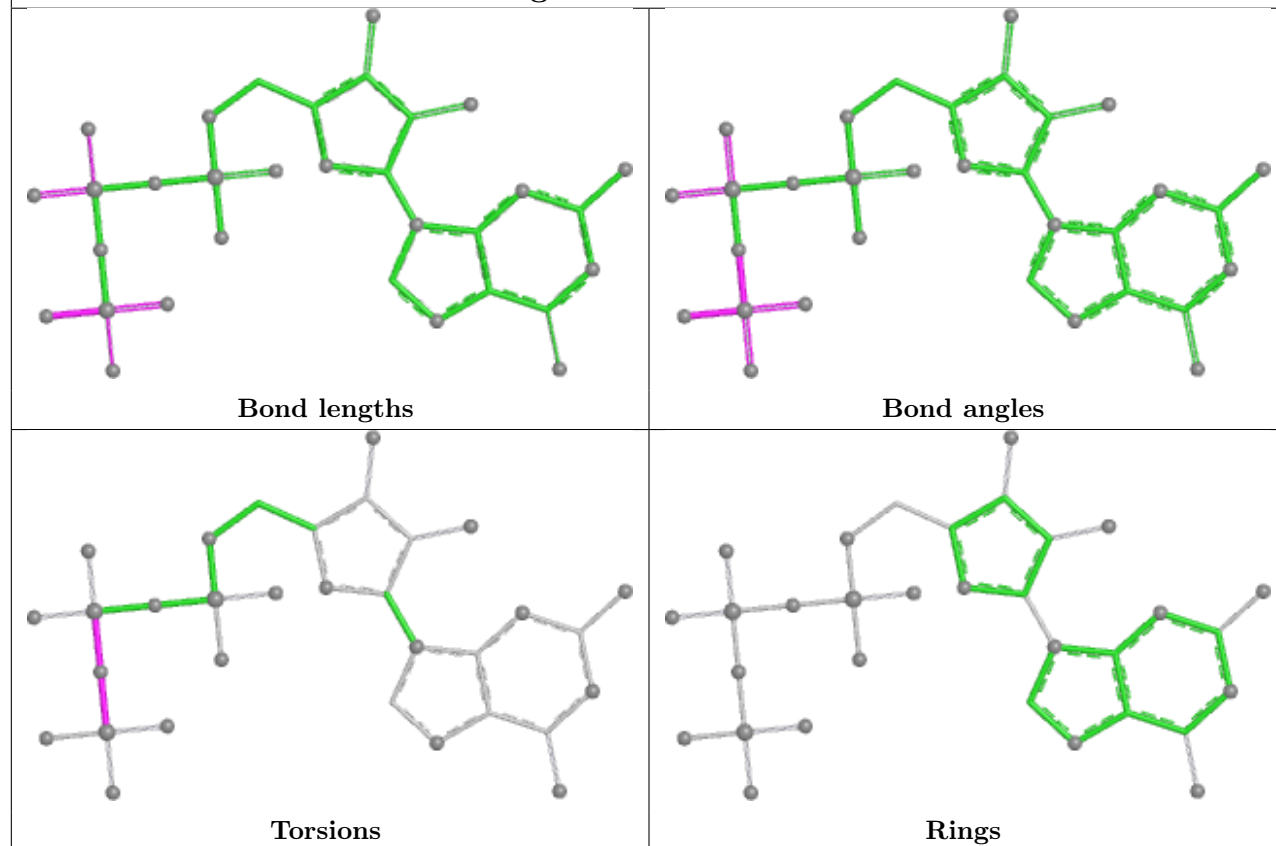


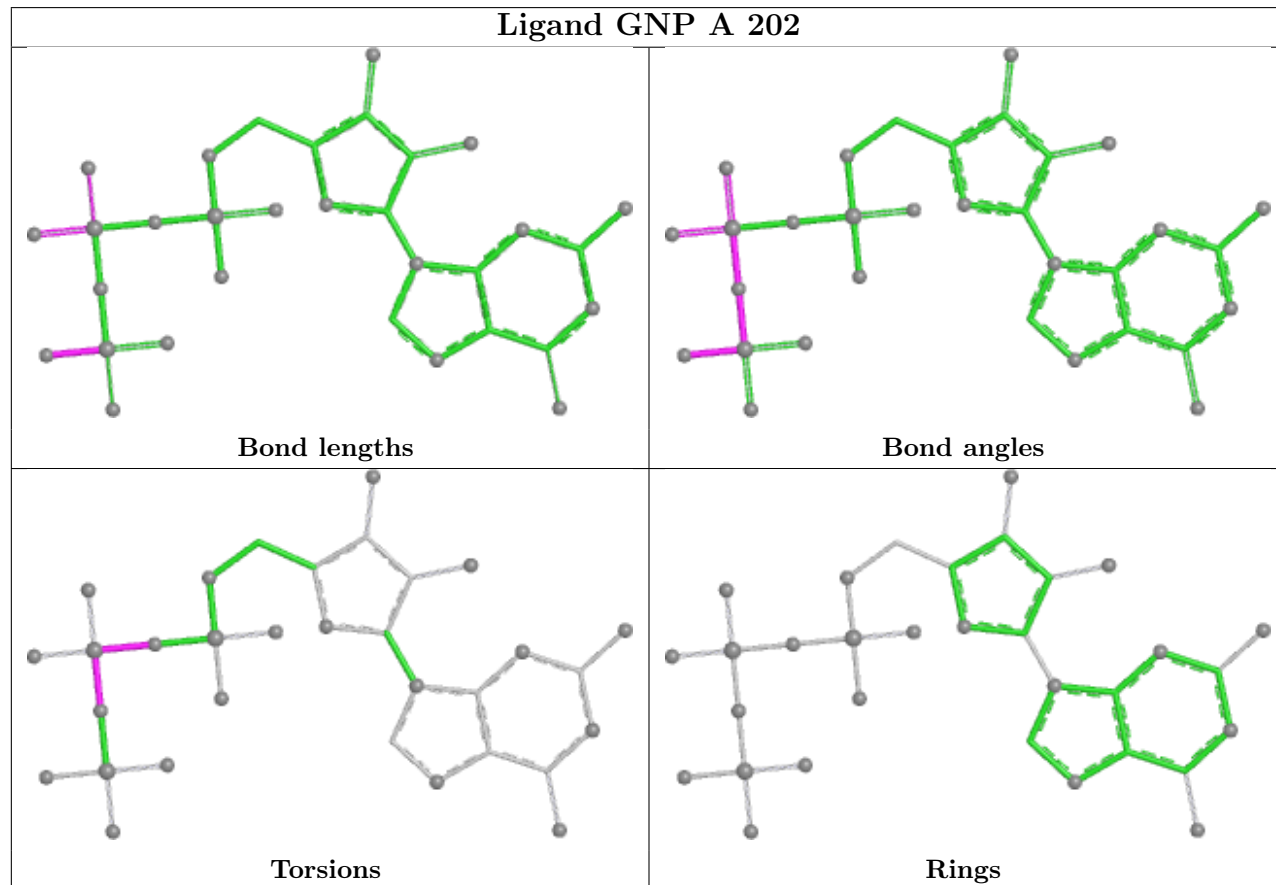
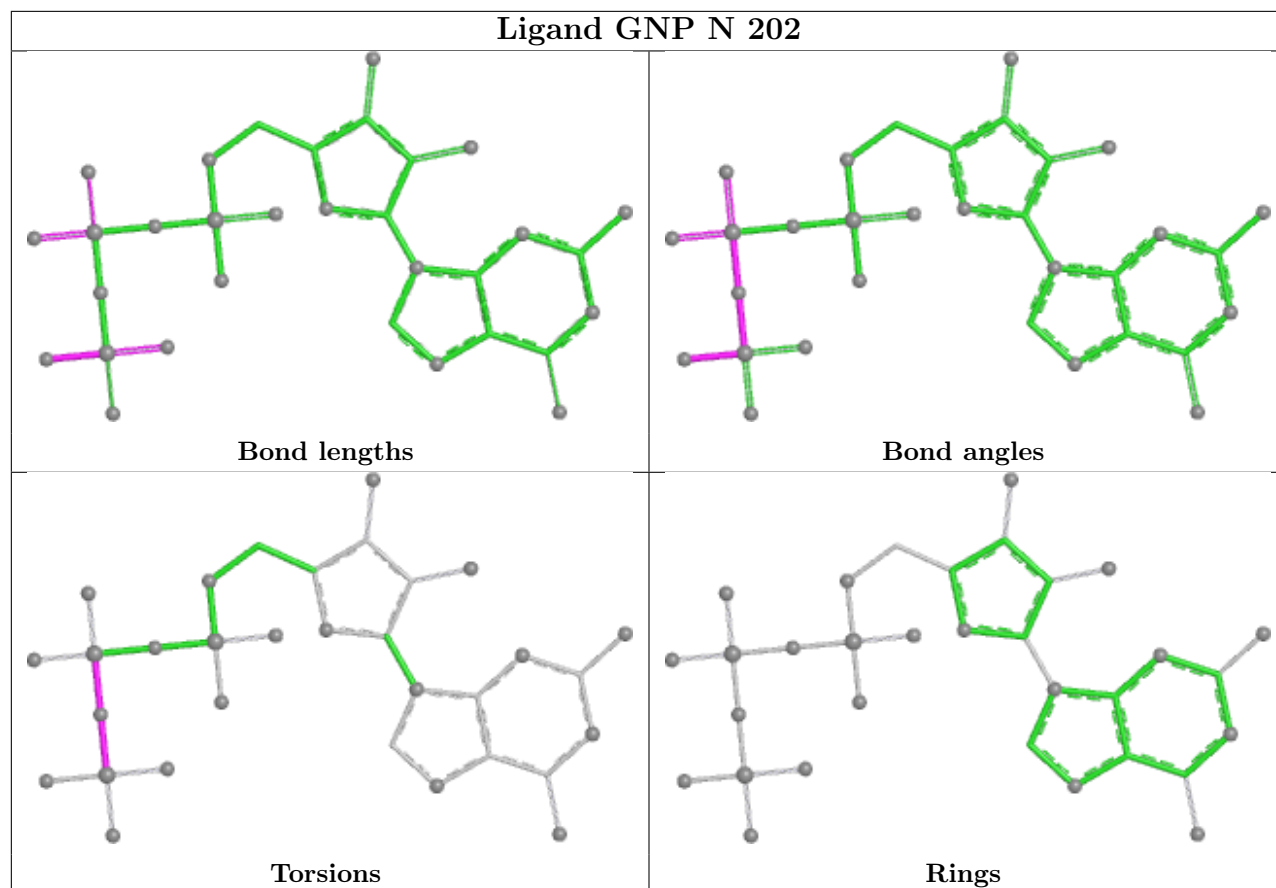


Ligand GNP J 202



Ligand GNP E 202





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, 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	171/182 (93%)	1.10	32 (18%) 3 2	39, 68, 122, 160	0
1	B	171/182 (93%)	0.98	22 (12%) 7 5	49, 74, 108, 137	0
1	C	171/182 (93%)	1.22	36 (21%) 2 2	54, 84, 123, 169	0
1	D	171/182 (93%)	1.10	31 (18%) 3 2	49, 86, 127, 141	0
1	E	171/182 (93%)	1.10	30 (17%) 4 3	45, 68, 124, 153	0
1	F	171/182 (93%)	1.28	40 (23%) 2 1	56, 88, 138, 164	0
1	G	171/182 (93%)	1.26	33 (19%) 3 2	58, 91, 138, 168	0
1	H	171/182 (93%)	1.70	57 (33%) 1 1	60, 94, 166, 211	0
1	I	171/182 (93%)	1.72	67 (39%) 1 0	63, 95, 148, 209	0
1	J	171/182 (93%)	1.51	47 (27%) 1 1	53, 88, 131, 167	0
1	K	171/182 (93%)	1.10	35 (20%) 2 2	41, 68, 121, 171	0
1	L	171/182 (93%)	1.61	54 (31%) 1 1	58, 95, 142, 200	0
1	M	171/182 (93%)	1.10	34 (19%) 3 2	49, 79, 111, 164	0
1	N	171/182 (93%)	0.96	33 (19%) 3 2	45, 68, 113, 134	0
1	O	171/182 (93%)	1.17	39 (22%) 2 1	37, 64, 116, 152	0
1	P	171/182 (93%)	1.05	27 (15%) 5 4	46, 77, 116, 165	0
All	All	2736/2912 (93%)	1.25	617 (22%) 2 1	37, 81, 134, 211	0

The worst 5 of 617 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	12	PHE	9.7
1	H	62	LEU	8.0
1	L	12	PHE	7.5
1	F	160	ILE	7.4
1	L	164	ILE	7.2

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 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.

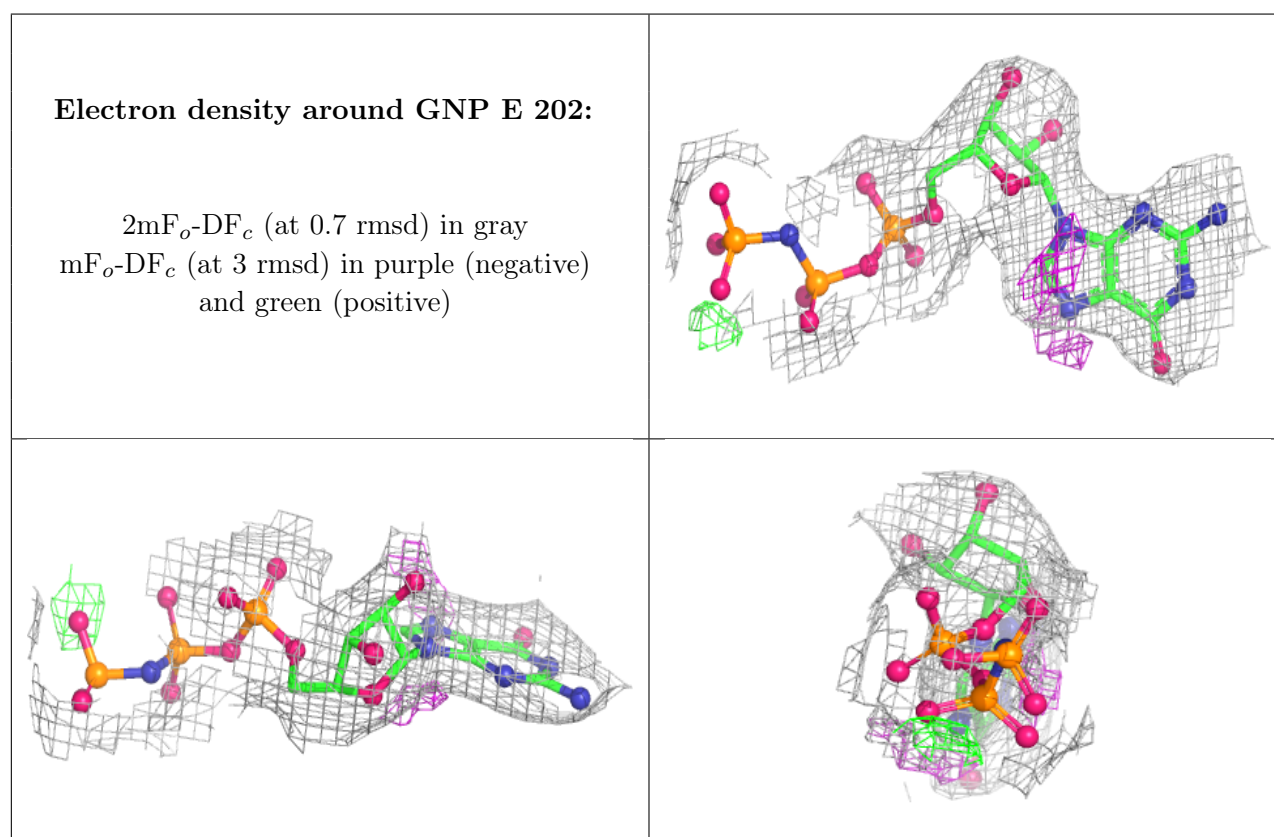
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GNP	E	202	32/32	0.91	0.09	33,44,61,67	0
3	GNP	I	202	32/32	0.92	0.10	54,75,96,98	0
3	GNP	J	202	32/32	0.93	0.09	40,53,82,87	0
3	GNP	K	202	32/32	0.93	0.09	34,44,55,58	0
3	GNP	H	202	32/32	0.93	0.08	46,60,72,78	0
2	MG	I	201	1/1	0.94	0.08	68,68,68,68	0
3	GNP	F	202	32/32	0.94	0.08	42,60,70,71	0
3	GNP	O	202	32/32	0.94	0.08	38,46,55,61	0
3	GNP	G	202	32/32	0.94	0.08	51,67,77,94	0
2	MG	F	201	1/1	0.94	0.08	39,39,39,39	0
3	GNP	C	202	32/32	0.94	0.08	47,57,73,80	0
3	GNP	P	202	32/32	0.95	0.08	40,53,67,83	0
3	GNP	N	202	32/32	0.95	0.08	46,57,65,73	0
3	GNP	A	202	32/32	0.95	0.06	39,47,56,60	0
3	GNP	L	202	32/32	0.95	0.06	46,58,65,69	0
2	MG	P	201	1/1	0.96	0.07	41,41,41,41	0
2	MG	B	201	1/1	0.96	0.10	35,35,35,35	0
2	MG	K	201	1/1	0.96	0.13	34,34,34,34	0
3	GNP	M	202	32/32	0.96	0.07	42,60,68,69	0
3	GNP	D	202	32/32	0.96	0.07	38,52,69,73	0
3	GNP	B	202	32/32	0.96	0.06	44,58,65,75	0
2	MG	E	201	1/1	0.97	0.06	38,38,38,38	0
2	MG	H	201	1/1	0.98	0.12	45,45,45,45	0
2	MG	L	201	1/1	0.98	0.06	45,45,45,45	0
2	MG	O	201	1/1	0.98	0.07	28,28,28,28	0
2	MG	M	201	1/1	0.98	0.08	34,34,34,34	0
2	MG	G	201	1/1	0.98	0.10	36,36,36,36	0

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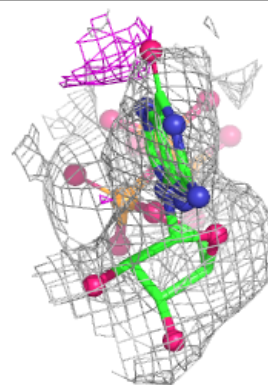
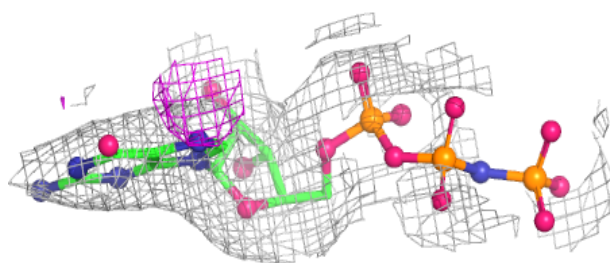
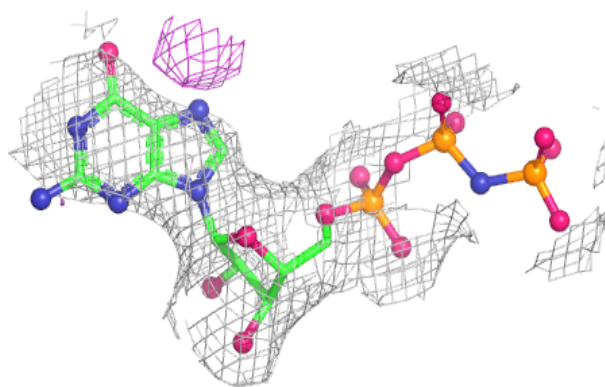
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	D	201	1/1	0.98	0.06	39,39,39,39	0
2	MG	C	201	1/1	0.99	0.02	43,43,43,43	0
2	MG	A	201	1/1	0.99	0.08	29,29,29,29	0
2	MG	N	201	1/1	0.99	0.09	34,34,34,34	0
2	MG	J	201	1/1	0.99	0.06	44,44,44,44	0

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.

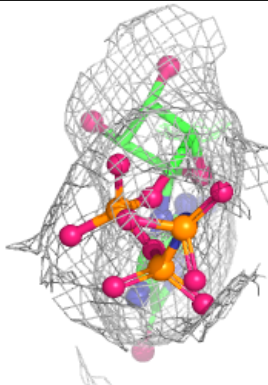
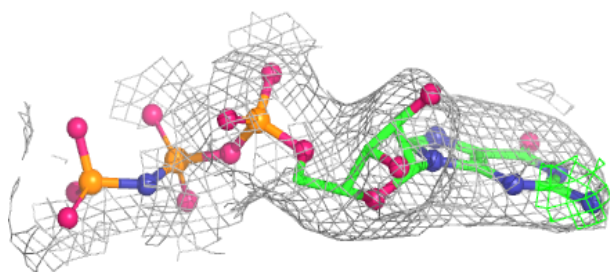
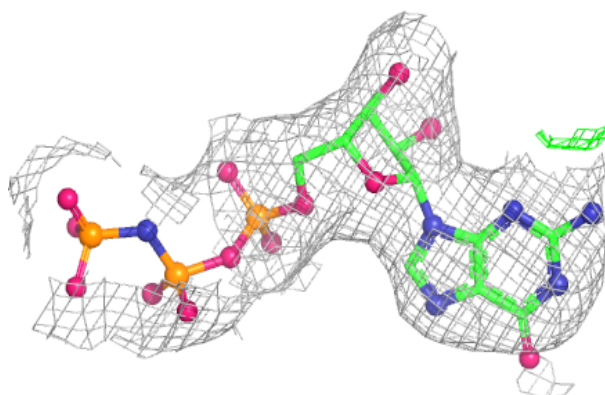


Electron density around GNP I 202:

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

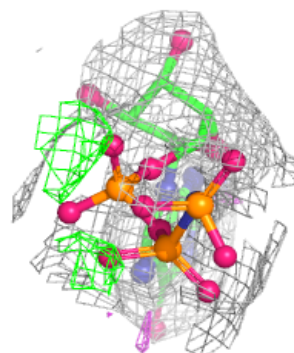
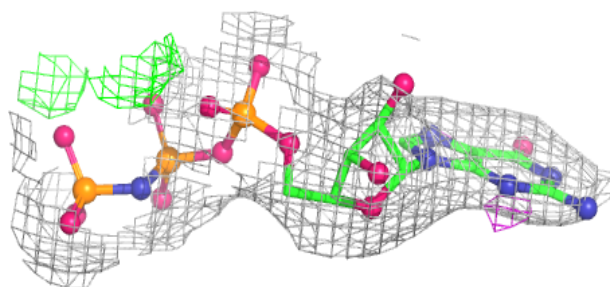
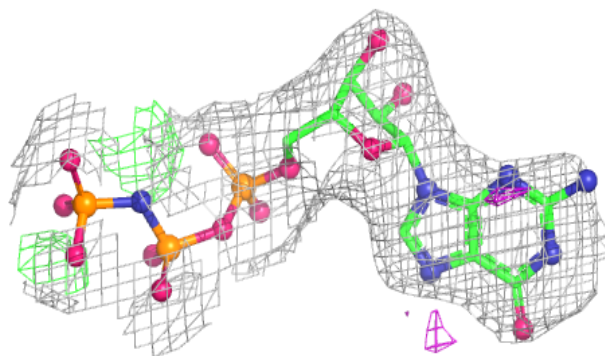
**Electron density around GNP J 202:**

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

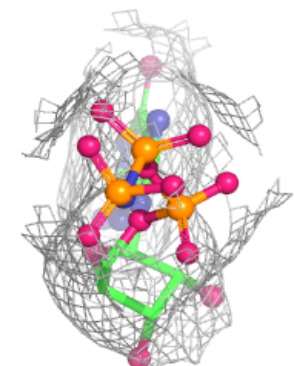
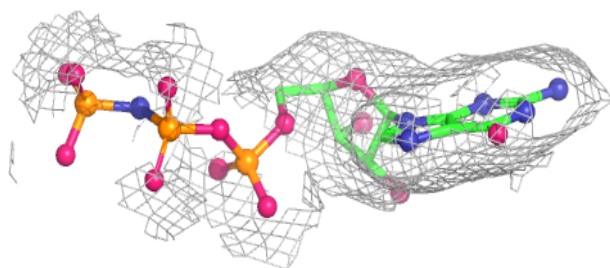
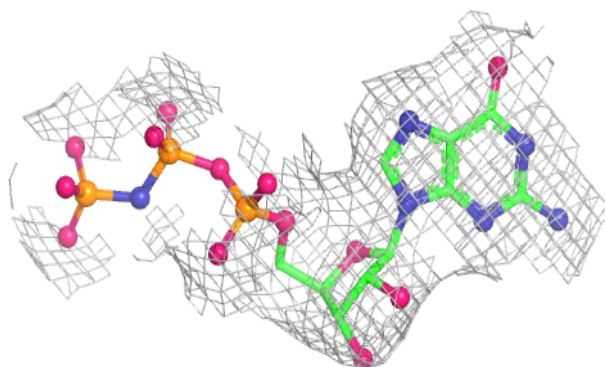


Electron density around GNP K 202:

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

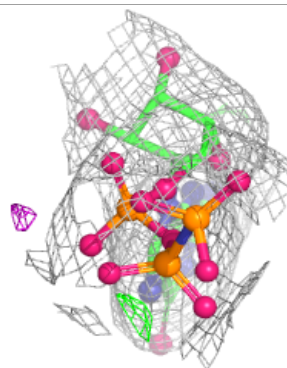
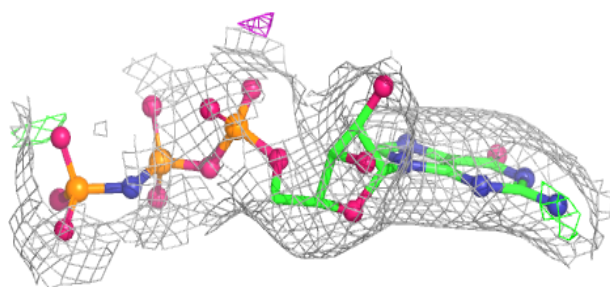
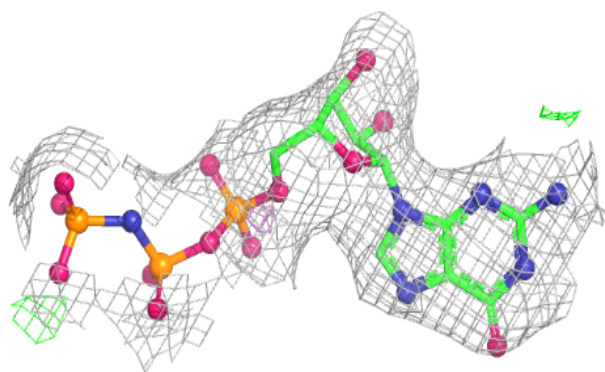
**Electron density around GNP H 202:**

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and green (positive)

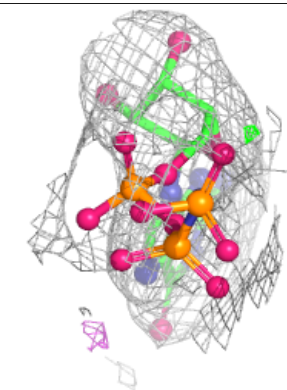
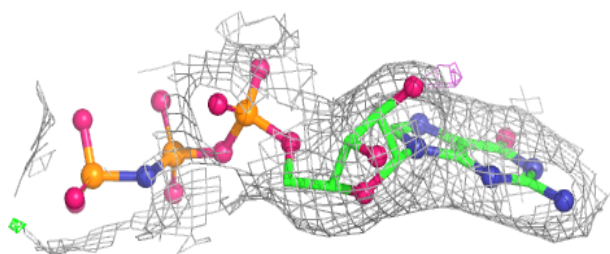
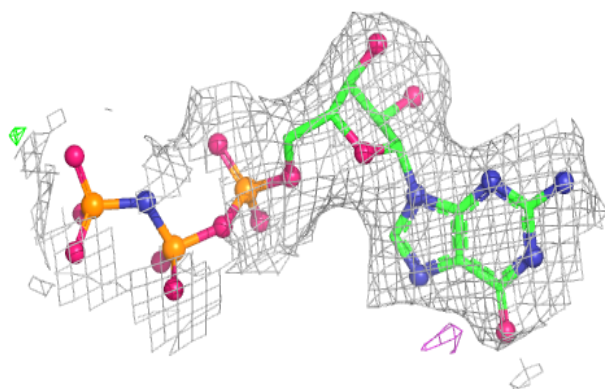


Electron density around GNP F 202:

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

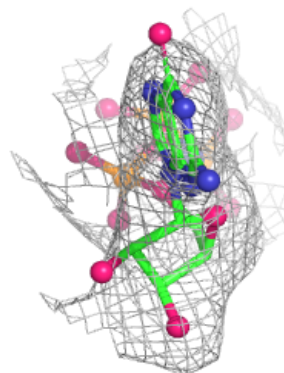
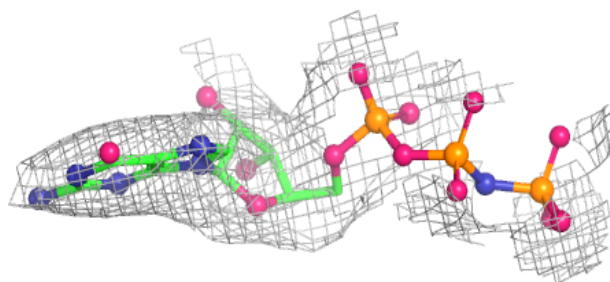
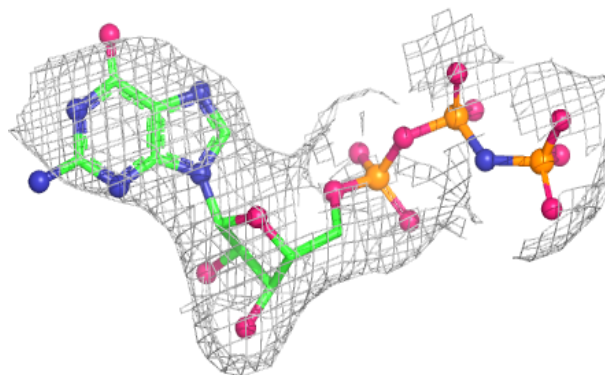
**Electron density around GNP O 202:**

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

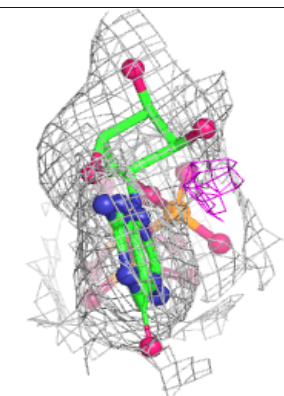
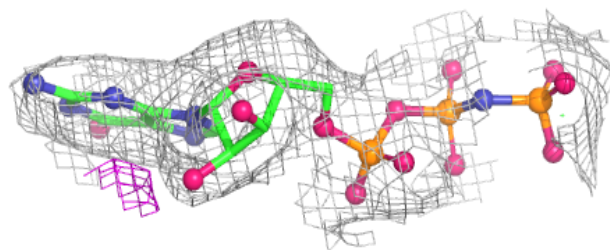
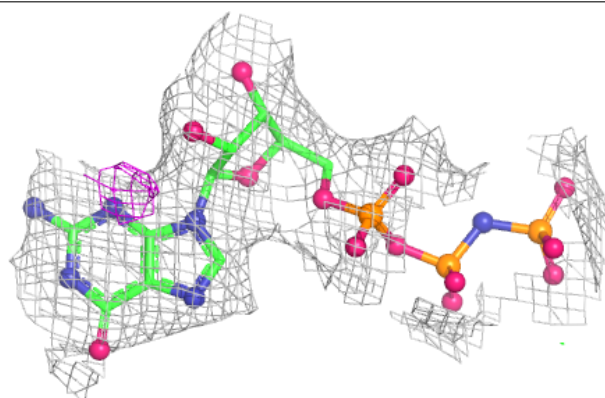


Electron density around GNP G 202:

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

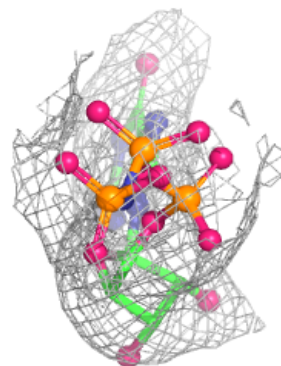
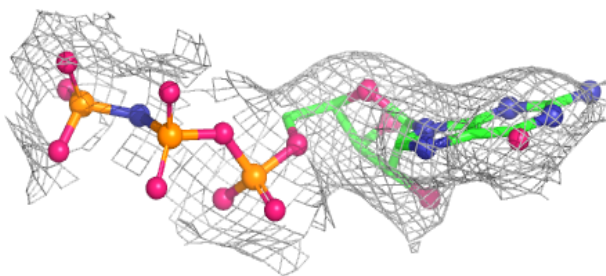
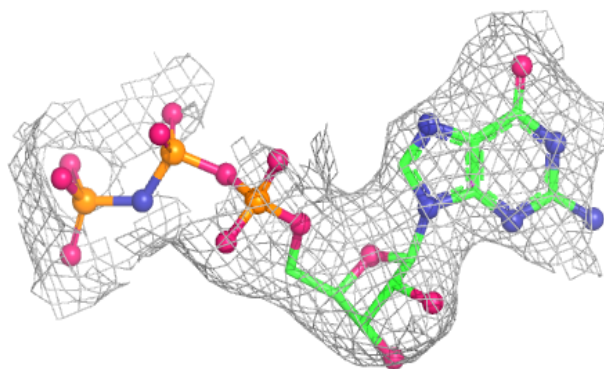
**Electron density around GNP C 202:**

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

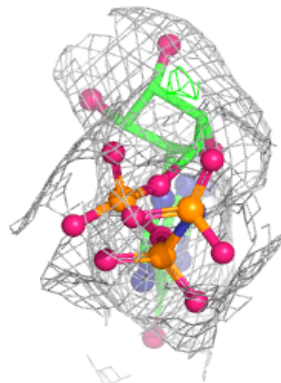
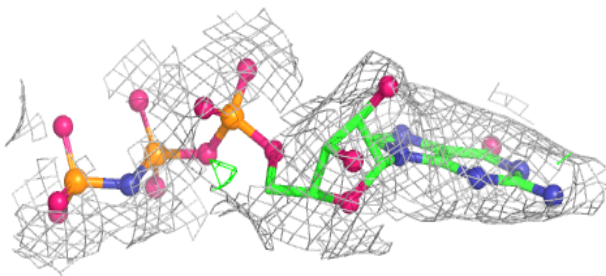
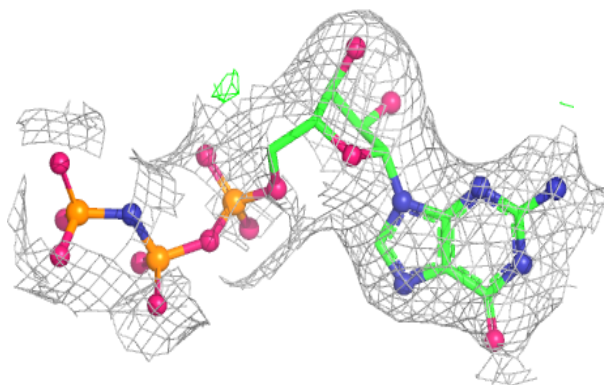


Electron density around GNP P 202:

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

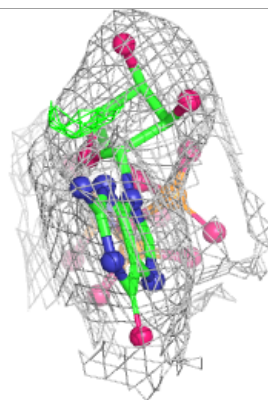
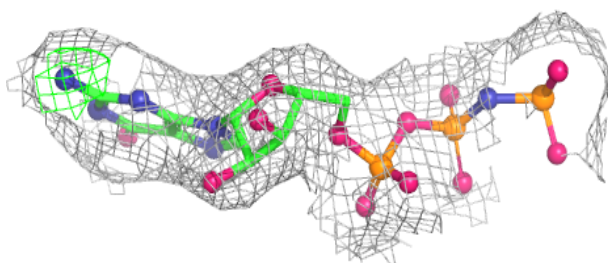
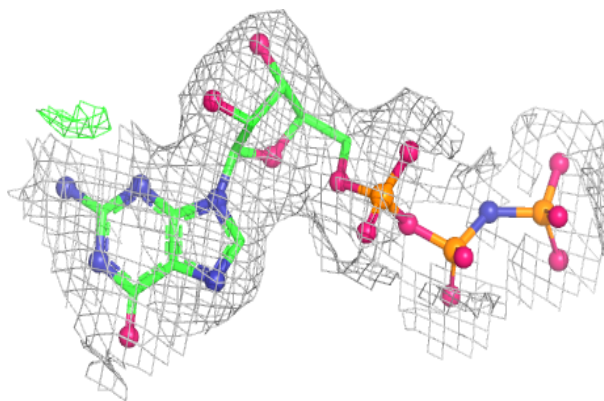
**Electron density around GNP N 202:**

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

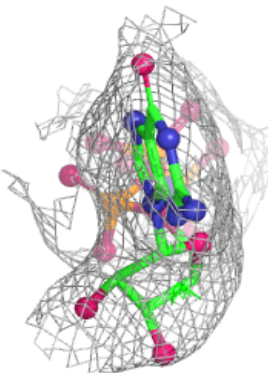
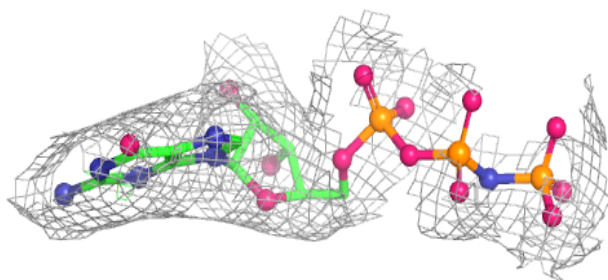
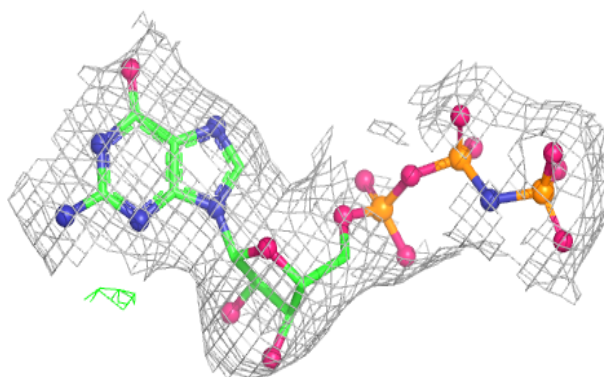


Electron density around GNP A 202:

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

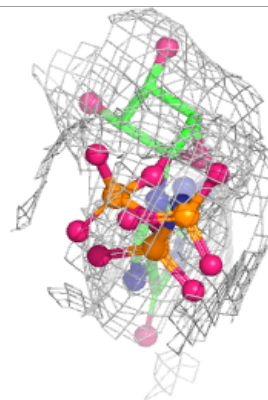
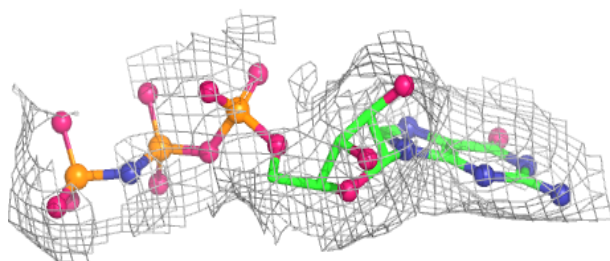
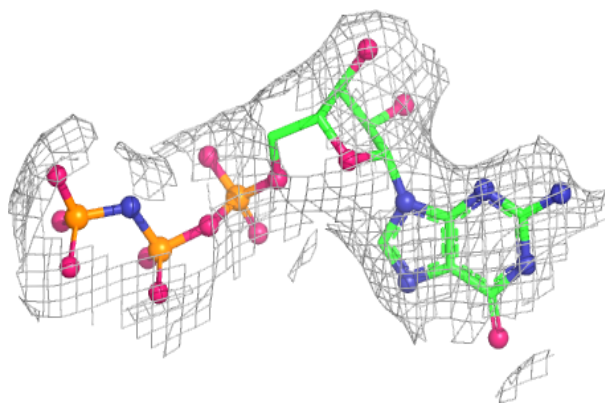
**Electron density around GNP L 202:**

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

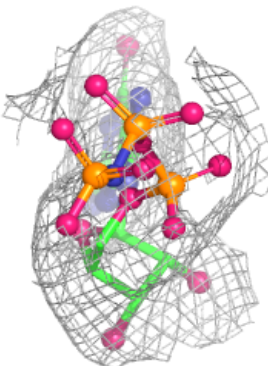
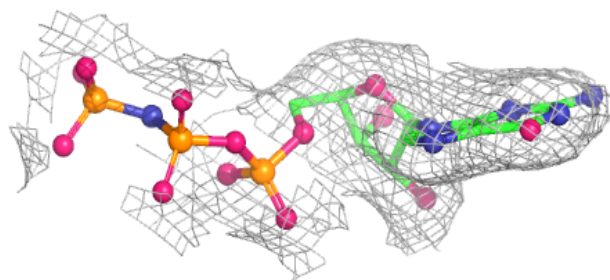
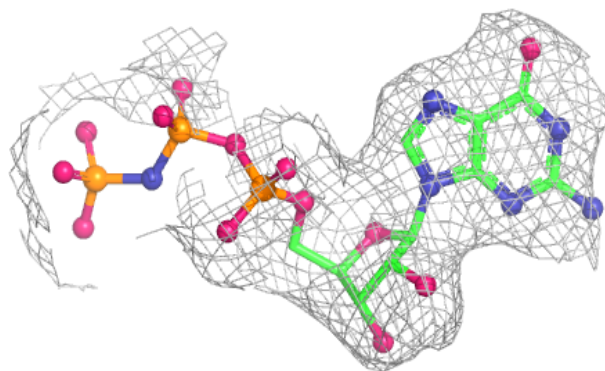


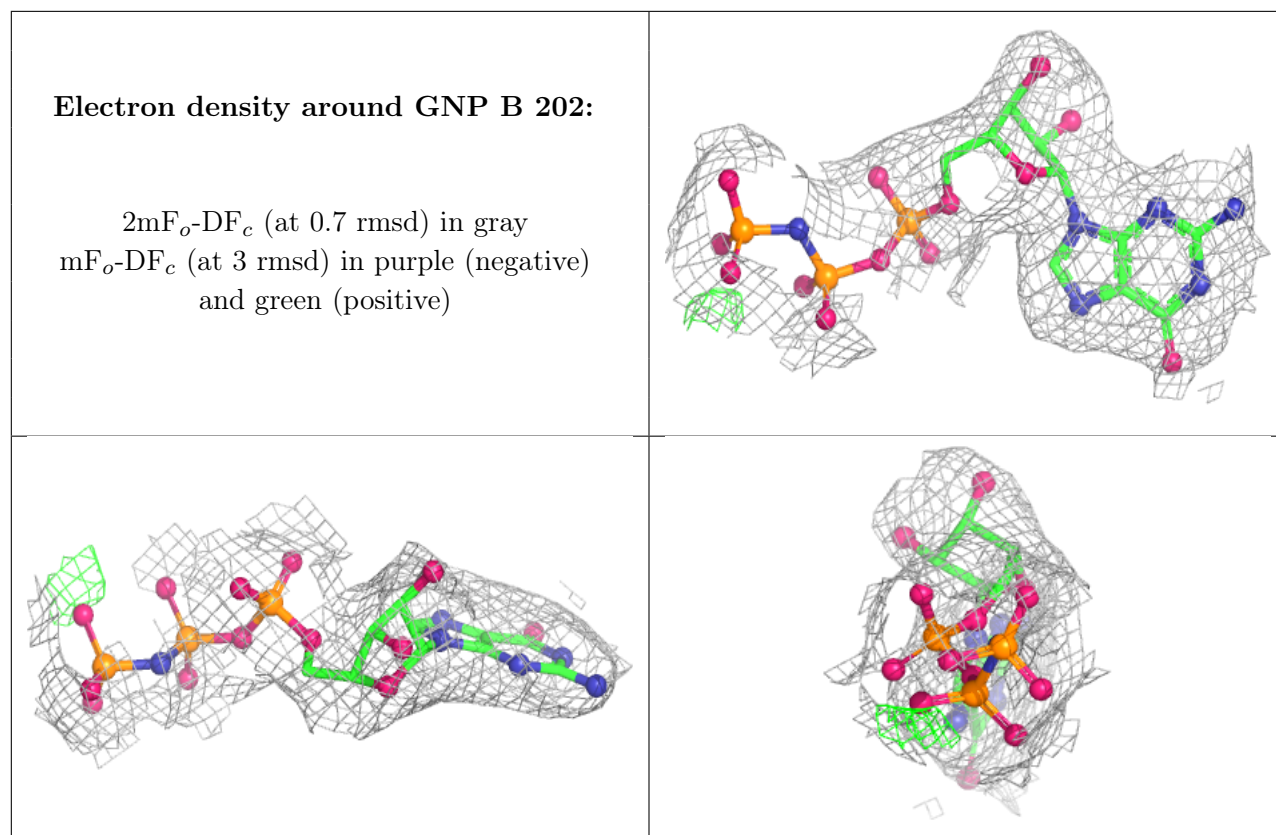
Electron density around GNP M 202:

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

**Electron density around GNP D 202:**

$2mF_o-DF_c$ (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.