



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 02:43 PM UTC

PDB ID : 4UJ3 / pdb_00004uj3
Title : Crystal structure of human Rab11-Rabin8-FIP3
Authors : Vetter, M.; Lorentzen, E.
Deposited on : 2015-04-08
Resolution : 3.00 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

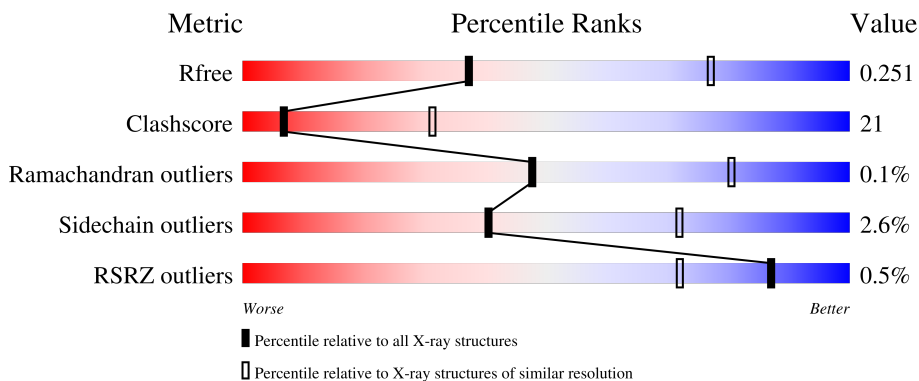
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	187	 68% 25% • 6%
1	D	187	 63% 31% 6%
1	G	187	 61% 29% • 6%
1	J	187	 56% 36% • 7%
1	M	187	 61% 30% • 7%

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Mol	Chain	Length	Quality of chain
1	P	187	% 61% 29% • 9%
1	S	187	2% 57% 34% • 9%
1	V	187	% 66% 24% • 10%
2	B	195	49% 32% • 17%
2	E	195	% 53% 28% • 17%
2	H	195	42% 35% • 21%
2	K	195	44% 35% • 18%
2	N	195	% 53% 29% • 16%
2	Q	195	49% 32% • 17%
2	T	195	54% 28% • 16%
2	W	195	45% 31% • 21%
3	C	66	33% 21% 45%
3	F	66	30% 26% 44%
3	I	66	2% 39% 21% • 38%
3	L	66	44% 14% 42%
3	O	66	41% 14% • 44%
3	R	66	41% 15% 44%
3	U	66	33% 23% 44%
3	X	66	38% 15% • 45%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 23392 atoms, of which 18 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-11A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	176	1365	862	232	270	1	0	0	0
1	D	175	1368	864	233	270	1	0	2	0
1	G	175	1370	865	233	271	1	0	2	0
1	J	174	1336	847	225	263	1	0	0	0
1	M	174	1331	847	223	260	1	0	0	0
1	P	171	1300	825	219	255	1	0	0	0
1	S	171	1318	835	225	257	1	0	0	0
1	V	169	1299	825	222	251	1	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P62491
A	1	ALA	-	expression tag	UNP P62491
A	2	ALA	-	expression tag	UNP P62491
A	3	SER	-	expression tag	UNP P62491
A	70	LEU	GLN	engineered mutation	UNP P62491
D	0	GLY	-	expression tag	UNP P62491
D	1	ALA	-	expression tag	UNP P62491
D	2	ALA	-	expression tag	UNP P62491
D	3	SER	-	expression tag	UNP P62491
D	70	LEU	GLN	engineered mutation	UNP P62491
G	0	GLY	-	expression tag	UNP P62491
G	1	ALA	-	expression tag	UNP P62491
G	2	ALA	-	expression tag	UNP P62491

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Chain	Residue	Modelled	Actual	Comment	Reference
G	3	SER	-	expression tag	UNP P62491
G	70	LEU	GLN	engineered mutation	UNP P62491
J	0	GLY	-	expression tag	UNP P62491
J	1	ALA	-	expression tag	UNP P62491
J	2	ALA	-	expression tag	UNP P62491
J	3	SER	-	expression tag	UNP P62491
J	70	LEU	GLN	engineered mutation	UNP P62491
M	0	GLY	-	expression tag	UNP P62491
M	1	ALA	-	expression tag	UNP P62491
M	2	ALA	-	expression tag	UNP P62491
M	3	SER	-	expression tag	UNP P62491
M	70	LEU	GLN	engineered mutation	UNP P62491
P	0	GLY	-	expression tag	UNP P62491
P	1	ALA	-	expression tag	UNP P62491
P	2	ALA	-	expression tag	UNP P62491
P	3	SER	-	expression tag	UNP P62491
P	70	LEU	GLN	engineered mutation	UNP P62491
S	0	GLY	-	expression tag	UNP P62491
S	1	ALA	-	expression tag	UNP P62491
S	2	ALA	-	expression tag	UNP P62491
S	3	SER	-	expression tag	UNP P62491
S	70	LEU	GLN	engineered mutation	UNP P62491
V	0	GLY	-	expression tag	UNP P62491
V	1	ALA	-	expression tag	UNP P62491
V	2	ALA	-	expression tag	UNP P62491
V	3	SER	-	expression tag	UNP P62491
V	70	LEU	GLN	engineered mutation	UNP P62491

- Molecule 2 is a protein called RAB-3A-INTERACTING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	161	Total	C	N	O	S	0	0	0
			1288	822	211	243	12			
2	E	162	Total	C	N	O	S	0	0	0
			1268	811	207	238	12			
2	H	155	Total	C	N	O	S	0	2	0
			1263	810	208	233	12			
2	K	159	Total	C	N	O	S	0	1	0
			1259	804	204	239	12			
2	N	164	Total	C	N	O	S	0	0	0
			1293	824	211	246	12			
2	Q	161	Total	C	N	O	S	0	1	0
			1281	818	208	243	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	T	164	1291	827	208	245	11	0	1	0
2	W	155	1251	798	203	238	12	0	1	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	266	GLY	-	expression tag	UNP Q96QF0
B	267	ALA	-	expression tag	UNP Q96QF0
B	268	ALA	-	expression tag	UNP Q96QF0
B	269	SER	-	expression tag	UNP Q96QF0
E	266	GLY	-	expression tag	UNP Q96QF0
E	267	ALA	-	expression tag	UNP Q96QF0
E	268	ALA	-	expression tag	UNP Q96QF0
E	269	SER	-	expression tag	UNP Q96QF0
H	266	GLY	-	expression tag	UNP Q96QF0
H	267	ALA	-	expression tag	UNP Q96QF0
H	268	ALA	-	expression tag	UNP Q96QF0
H	269	SER	-	expression tag	UNP Q96QF0
K	266	GLY	-	expression tag	UNP Q96QF0
K	267	ALA	-	expression tag	UNP Q96QF0
K	268	ALA	-	expression tag	UNP Q96QF0
K	269	SER	-	expression tag	UNP Q96QF0
N	266	GLY	-	expression tag	UNP Q96QF0
N	267	ALA	-	expression tag	UNP Q96QF0
N	268	ALA	-	expression tag	UNP Q96QF0
N	269	SER	-	expression tag	UNP Q96QF0
Q	266	GLY	-	expression tag	UNP Q96QF0
Q	267	ALA	-	expression tag	UNP Q96QF0
Q	268	ALA	-	expression tag	UNP Q96QF0
Q	269	SER	-	expression tag	UNP Q96QF0
T	266	GLY	-	expression tag	UNP Q96QF0
T	267	ALA	-	expression tag	UNP Q96QF0
T	268	ALA	-	expression tag	UNP Q96QF0
T	269	SER	-	expression tag	UNP Q96QF0
W	266	GLY	-	expression tag	UNP Q96QF0
W	267	ALA	-	expression tag	UNP Q96QF0
W	268	ALA	-	expression tag	UNP Q96QF0
W	269	SER	-	expression tag	UNP Q96QF0

- Molecule 3 is a protein called RAB11 FAMILY-INTERACTING PROTEIN 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	36	265	169	46	48	2	0	0	0
3	F	37	251	163	40	46	2	0	0	0
3	I	41	287	184	47	54	2	0	0	0
3	L	38	265	172	44	47	2	0	0	0
3	O	37	254	162	43	48	1	0	0	0
3	R	37	255	164	41	49	1	0	0	0
3	U	37	269	175	46	46	2	0	0	0
3	X	36	257	163	43	50	1	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

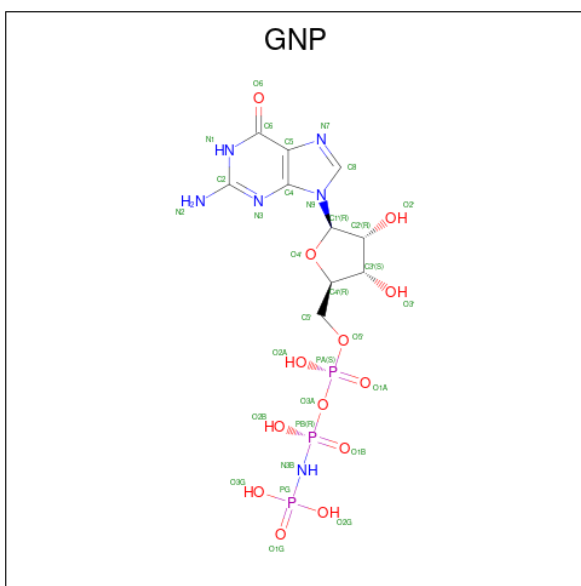
Chain	Residue	Modelled	Actual	Comment	Reference
C	691	GLY	-	expression tag	UNP O75154
C	692	ALA	-	expression tag	UNP O75154
C	693	ALA	-	expression tag	UNP O75154
C	694	SER	-	expression tag	UNP O75154
F	691	GLY	-	expression tag	UNP O75154
F	692	ALA	-	expression tag	UNP O75154
F	693	ALA	-	expression tag	UNP O75154
F	694	SER	-	expression tag	UNP O75154
I	691	GLY	-	expression tag	UNP O75154
I	692	ALA	-	expression tag	UNP O75154
I	693	ALA	-	expression tag	UNP O75154
I	694	SER	-	expression tag	UNP O75154
L	691	GLY	-	expression tag	UNP O75154
L	692	ALA	-	expression tag	UNP O75154
L	693	ALA	-	expression tag	UNP O75154
L	694	SER	-	expression tag	UNP O75154
O	691	GLY	-	expression tag	UNP O75154
O	692	ALA	-	expression tag	UNP O75154
O	693	ALA	-	expression tag	UNP O75154
O	694	SER	-	expression tag	UNP O75154
R	691	GLY	-	expression tag	UNP O75154
R	692	ALA	-	expression tag	UNP O75154
R	693	ALA	-	expression tag	UNP O75154
R	694	SER	-	expression tag	UNP O75154

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Chain	Residue	Modelled	Actual	Comment	Reference
U	691	GLY	-	expression tag	UNP O75154
U	692	ALA	-	expression tag	UNP O75154
U	693	ALA	-	expression tag	UNP O75154
U	694	SER	-	expression tag	UNP O75154
X	691	GLY	-	expression tag	UNP O75154
X	692	ALA	-	expression tag	UNP O75154
X	693	ALA	-	expression tag	UNP O75154
X	694	SER	-	expression tag	UNP O75154

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	D	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	G	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	J	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	M	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	P	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	S	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

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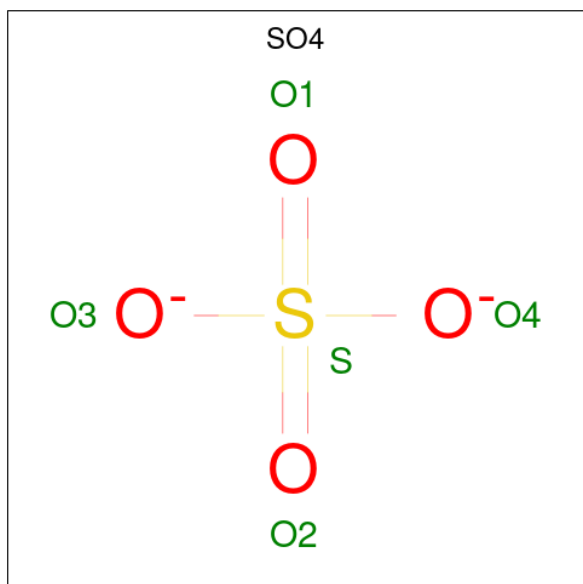
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	V	1	32	10	6	13	3	0	0

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

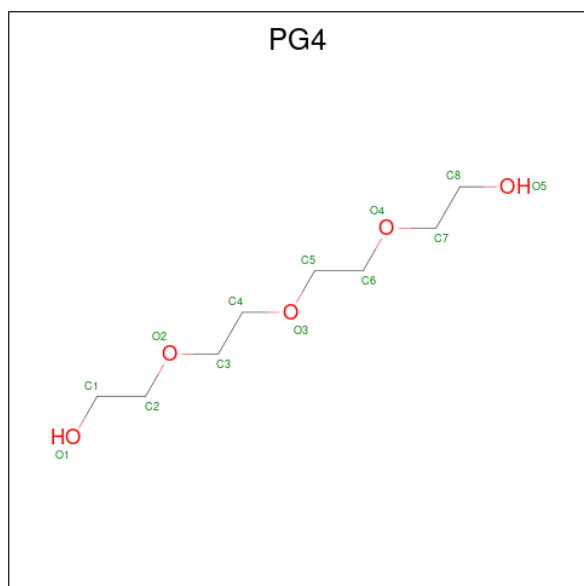
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	D	1	Total	Mg	0	0
			1	1		
5	G	1	Total	Mg	0	0
			1	1		
5	J	1	Total	Mg	0	0
			1	1		
5	M	1	Total	Mg	0	0
			1	1		
5	P	1	Total	Mg	0	0
			1	1		
5	S	1	Total	Mg	0	0
			1	1		
5	V	1	Total	Mg	0	0
			1	1		

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	M	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	V	1	Total	C	H	O	0	0
			31	8	18	5		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	13	Total	O	0	0
			13	13		
8	B	6	Total	O	0	0
			6	6		
8	C	1	Total	O	0	0
			1	1		
8	D	9	Total	O	0	0
			9	9		
8	E	1	Total	O	0	0
			1	1		
8	F	1	Total	O	0	0
			1	1		
8	G	13	Total	O	0	0
			13	13		
8	H	10	Total	O	0	0
			10	10		

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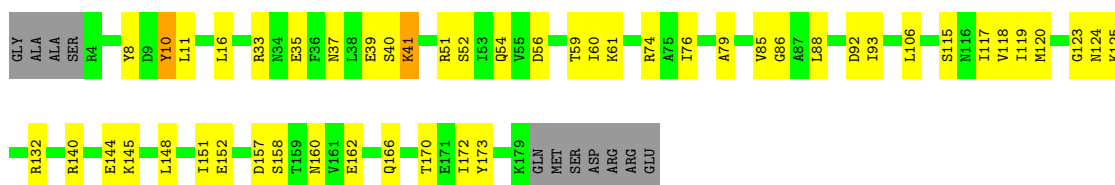
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	J	8	Total O 8 8	0	0
8	K	1	Total O 1 1	0	0
8	N	9	Total O 9 9	0	0
8	P	9	Total O 9 9	0	0
8	Q	5	Total O 5 5	0	0
8	R	1	Total O 1 1	0	0
8	S	4	Total O 4 4	0	0
8	T	3	Total O 3 3	0	0
8	U	1	Total O 1 1	0	0
8	V	6	Total O 6 6	0	0
8	W	7	Total O 7 7	0	0

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.

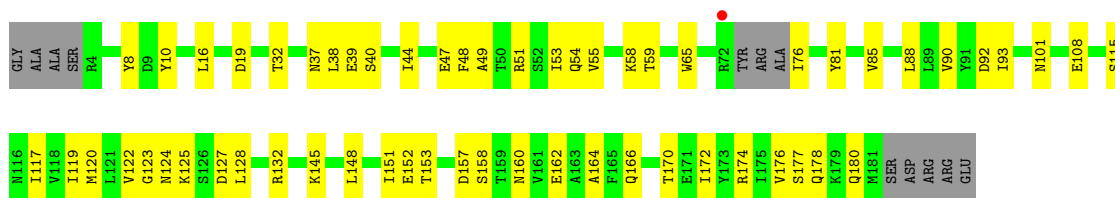
- Molecule 1: RAS-RELATED PROTEIN RAB-11A

Chain A: 



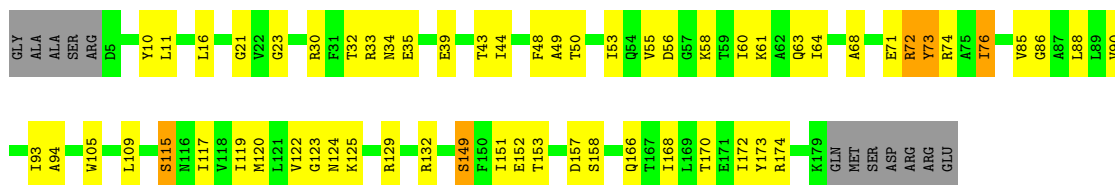
- Molecule 1: RAS-RELATED PROTEIN RAB-11A

Chain D: 



- Molecule 1: RAS-RELATED PROTEIN RAB-11A

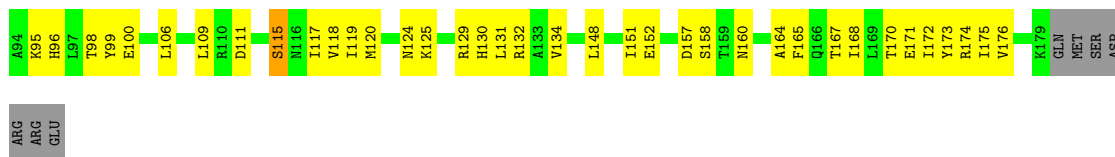
Chain G: 



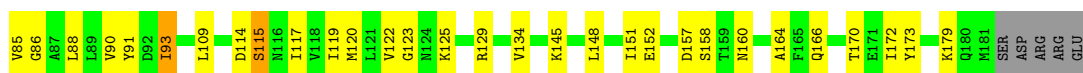
- Molecule 1: RAS-RELATED PROTEIN RAB-11A

Chain J: 





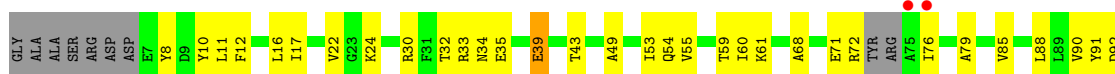
- Molecule 1: RAS-RELATED PROTEIN RAB-11A



- Molecule 1: RAS-RELATED PROTEIN RAB-11A



- Molecule 1: RAS-RELATED PROTEIN RAB-11A



- Molecule 1: RAS-RELATED PROTEIN RAB-11A



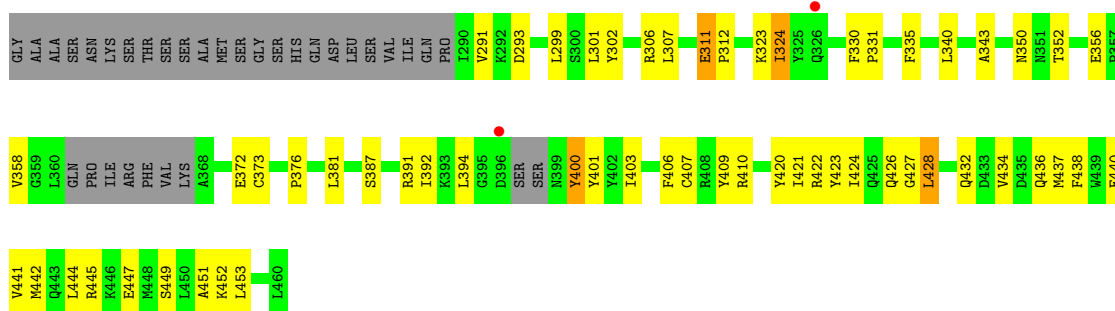
- Molecule 2: RAB-3A-INTERACTING PROTEIN

Chain B:  49% 32% 17%



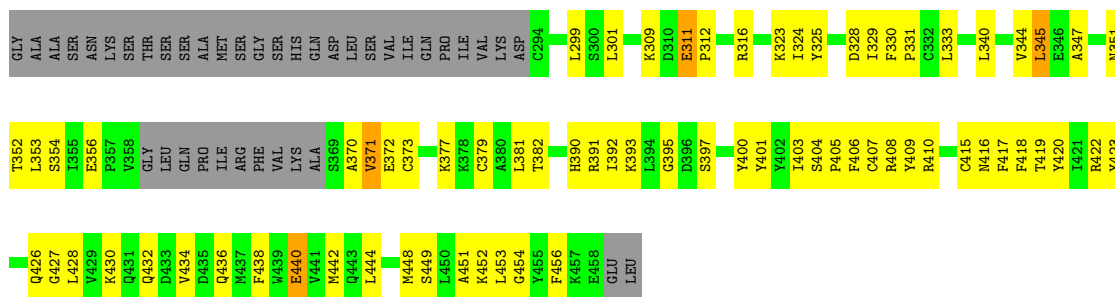
• Molecule 2: RAB-3A-INTERACTING PROTEIN

Chain E:  53% 28% 17%



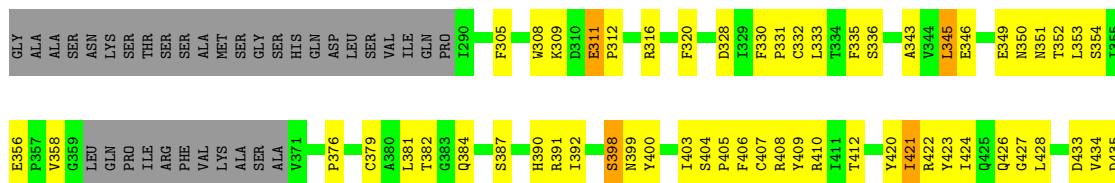
• Molecule 2: RAB-3A-INTERACTING PROTEIN

Chain H:  42% 35% 21%



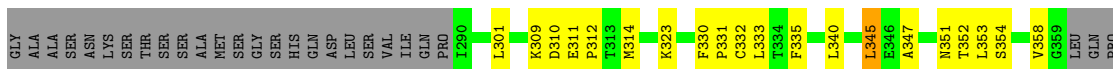
• Molecule 2: RAB-3A-INTERACTING PROTEIN

Chain K:  44% 35% 18%

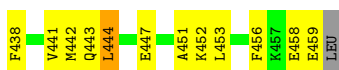
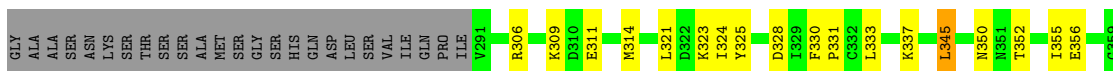




- Molecule 2: RAB-3A-INTERACTING PROTEIN



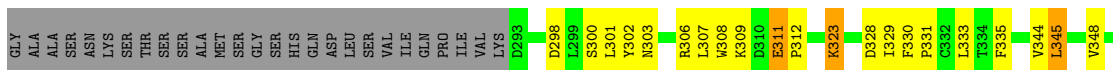
- Molecule 2: RAB-3A-INTERACTING PROTEIN




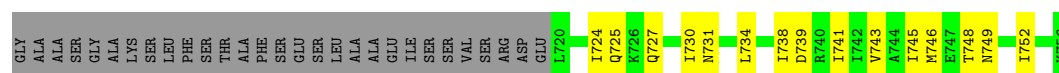
- Molecule 2: RAB-3A-INTERACTING PROTEIN



- Molecule 2: RAB-3A-INTERACTING PROTEIN

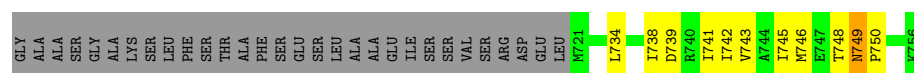


Chain U:  33% 23% 44%



● Molecule 3: RAB11 FAMILY-INTERACTING PROTEIN 3

Chain X:  38% 15% 45%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.50Å 165.37Å 218.69Å 90.00° 95.93° 90.00°	Depositor
Resolution (Å)	48.54 – 3.00 48.54 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.54-3.00) 98.6 (48.54-3.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.93 (at 2.77Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE: DEV_1647)	Depositor
R, R_{free}	0.198 , 0.250 0.202 , 0.251	Depositor DCC
R_{free} test set	5320 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	83.6	Xtrriage
Anisotropy	0.272	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 62.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.043 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	23392	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PG4, GNP, SO4

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	0.40	0/1386	0.77	0/1878
1	D	0.39	0/1394	0.81	1/1889 (0.1%)
1	G	0.44	0/1397	0.86	1/1893 (0.1%)
1	J	0.39	0/1356	0.79	1/1839 (0.1%)
1	M	0.39	0/1351	0.81	2/1833 (0.1%)
1	P	0.35	0/1320	0.78	0/1793
1	S	0.34	0/1338	0.77	0/1814
1	V	0.37	0/1319	0.78	0/1789
2	B	0.39	0/1315	0.86	3/1772 (0.2%)
2	E	0.35	0/1294	0.86	3/1748 (0.2%)
2	H	0.42	0/1296	0.89	3/1746 (0.2%)
2	K	0.34	0/1289	0.87	2/1742 (0.1%)
2	N	0.36	0/1320	0.88	4/1784 (0.2%)
2	Q	0.34	0/1311	0.89	4/1769 (0.2%)
2	T	0.35	0/1323	0.84	1/1790 (0.1%)
2	W	0.40	0/1281	0.90	3/1728 (0.2%)
3	C	0.40	0/266	0.79	0/362
3	F	0.41	0/252	0.86	0/346
3	I	0.39	0/288	0.87	2/394 (0.5%)
3	L	0.39	0/266	0.83	0/364
3	O	0.34	0/255	0.84	0/350
3	R	0.32	0/256	0.79	0/352
3	U	0.35	0/271	0.92	0/369
3	X	0.35	0/258	0.94	2/353 (0.6%)
All	All	0.38	0/23402	0.84	32/31697 (0.1%)

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	G	0	3
2	B	0	1
2	K	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	Q	311	GLU	CA-C-N	7.81	127.87	119.90
2	Q	311	GLU	C-N-CA	7.81	127.87	119.90
2	B	311	GLU	CA-C-N	7.42	127.40	119.76
2	B	311	GLU	C-N-CA	7.42	127.40	119.76
2	H	371	VAL	N-CA-C	7.02	118.65	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	396	ASP	Peptide
1	G	72	ARG	Peptide
1	G	73	TYR	Peptide
1	G	74	ARG	Peptide
2	K	398	SER	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1365	0	1322	44	0
1	D	1368	0	1322	52	0
1	G	1370	0	1328	49	0
1	J	1336	0	1290	62	0
1	M	1331	0	1290	56	0
1	P	1300	0	1242	47	0
1	S	1318	0	1277	68	0
1	V	1299	0	1260	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1288	0	1249	73	0
2	E	1268	0	1197	59	0
2	H	1263	0	1244	75	0
2	K	1259	0	1185	68	0
2	N	1293	0	1229	53	0
2	Q	1281	0	1230	57	0
2	T	1291	0	1216	62	0
2	W	1251	0	1201	59	0
3	C	265	0	255	14	0
3	F	251	0	227	22	0
3	I	287	0	261	16	0
3	L	265	0	249	6	0
3	O	254	0	224	6	0
3	R	255	0	228	10	0
3	U	269	0	256	18	0
3	X	257	0	232	13	0
4	A	32	0	13	0	0
4	D	32	0	13	2	0
4	G	32	0	13	6	0
4	J	32	0	13	2	0
4	M	32	0	13	2	0
4	P	32	0	13	1	0
4	S	32	0	13	1	0
4	V	32	0	13	4	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
5	G	1	0	0	0	0
5	J	1	0	0	0	0
5	M	1	0	0	0	0
5	P	1	0	0	0	0
5	S	1	0	0	0	0
5	V	1	0	0	0	0
6	M	5	0	0	0	0
7	V	13	18	18	1	0
8	A	13	0	0	1	0
8	B	6	0	0	1	0
8	C	1	0	0	0	0
8	D	9	0	0	0	0
8	E	1	0	0	0	0
8	F	1	0	0	0	0
8	G	13	0	0	1	0
8	H	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	J	8	0	0	1	0
8	K	1	0	0	0	0
8	N	9	0	0	3	0
8	P	9	0	0	0	0
8	Q	5	0	0	0	0
8	R	1	0	0	1	0
8	S	4	0	0	0	0
8	T	3	0	0	0	0
8	U	1	0	0	0	0
8	V	6	0	0	0	0
8	W	7	0	0	0	0
All	All	23374	18	22136	970	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 21.

The worst 5 of 970 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:P:132:ARG:HD2	2:Q:356:GLU:HG2	1.36	1.06
2:Q:368:ALA:HB3	2:Q:369:SER:HA	1.34	1.06
2:B:391:ARG:HD3	2:B:400:TYR:HB3	1.35	1.05
1:P:10:TYR:HB2	1:P:60:ILE:HD12	1.40	1.02
2:B:393:LYS:HE2	2:B:397:SER:HB3	1.43	0.99

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	174/187 (93%)	168 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	173/187 (92%)	169 (98%)	4 (2%)	0	100	100
1	G	175/187 (94%)	168 (96%)	5 (3%)	2 (1%)	11	43
1	J	170/187 (91%)	165 (97%)	5 (3%)	0	100	100
1	M	170/187 (91%)	165 (97%)	5 (3%)	0	100	100
1	P	167/187 (89%)	161 (96%)	6 (4%)	0	100	100
1	S	167/187 (89%)	164 (98%)	3 (2%)	0	100	100
1	V	165/187 (88%)	161 (98%)	4 (2%)	0	100	100
2	B	157/195 (80%)	152 (97%)	5 (3%)	0	100	100
2	E	156/195 (80%)	151 (97%)	5 (3%)	0	100	100
2	H	153/195 (78%)	150 (98%)	3 (2%)	0	100	100
2	K	156/195 (80%)	148 (95%)	8 (5%)	0	100	100
2	N	160/195 (82%)	152 (95%)	8 (5%)	0	100	100
2	Q	158/195 (81%)	155 (98%)	3 (2%)	0	100	100
2	T	161/195 (83%)	156 (97%)	5 (3%)	0	100	100
2	W	152/195 (78%)	148 (97%)	4 (3%)	0	100	100
3	C	34/66 (52%)	33 (97%)	1 (3%)	0	100	100
3	F	35/66 (53%)	33 (94%)	2 (6%)	0	100	100
3	I	39/66 (59%)	36 (92%)	3 (8%)	0	100	100
3	L	36/66 (54%)	35 (97%)	1 (3%)	0	100	100
3	O	35/66 (53%)	33 (94%)	2 (6%)	0	100	100
3	R	35/66 (53%)	34 (97%)	1 (3%)	0	100	100
3	U	35/66 (53%)	34 (97%)	1 (3%)	0	100	100
3	X	34/66 (52%)	32 (94%)	2 (6%)	0	100	100
All	All	2897/3584 (81%)	2803 (97%)	92 (3%)	2 (0%)	48	80

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	76	ILE
1	G	73	TYR

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	142/158 (90%)	139 (98%)	3 (2%)	47	75
1	D	143/158 (90%)	141 (99%)	2 (1%)	59	80
1	G	143/158 (90%)	139 (97%)	4 (3%)	38	70
1	J	138/158 (87%)	134 (97%)	4 (3%)	37	70
1	M	137/158 (87%)	134 (98%)	3 (2%)	45	74
1	P	132/158 (84%)	131 (99%)	1 (1%)	73	86
1	S	136/158 (86%)	134 (98%)	2 (2%)	57	80
1	V	133/158 (84%)	131 (98%)	2 (2%)	57	80
2	B	141/175 (81%)	136 (96%)	5 (4%)	32	65
2	E	133/175 (76%)	129 (97%)	4 (3%)	36	69
2	H	140/175 (80%)	137 (98%)	3 (2%)	47	75
2	K	134/175 (77%)	129 (96%)	5 (4%)	30	64
2	N	139/175 (79%)	135 (97%)	4 (3%)	37	70
2	Q	139/175 (79%)	135 (97%)	4 (3%)	37	70
2	T	137/175 (78%)	129 (94%)	8 (6%)	18	51
2	W	138/175 (79%)	132 (96%)	6 (4%)	26	60
3	C	25/56 (45%)	25 (100%)	0	100	100
3	F	21/56 (38%)	21 (100%)	0	100	100
3	I	25/56 (45%)	25 (100%)	0	100	100
3	L	23/56 (41%)	22 (96%)	1 (4%)	26	60
3	O	21/56 (38%)	19 (90%)	2 (10%)	8	31
3	R	22/56 (39%)	22 (100%)	0	100	100
3	U	24/56 (43%)	24 (100%)	0	100	100
3	X	23/56 (41%)	23 (100%)	0	100	100
All	All	2389/3112 (77%)	2326 (97%)	63 (3%)	40	72

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	440	GLU
1	V	39	GLU
2	N	332	CYS
2	T	459	GLU
2	W	352	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	727	GLN
1	M	54	GLN
2	T	390	HIS
2	Q	436	GLN
3	R	749	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 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
4	GNP	P	200	5	34,34,34	1.78	7 (20%)	47,54,54	1.19	5 (10%)
4	GNP	V	200	5	34,34,34	1.62	4 (11%)	47,54,54	1.06	4 (8%)
4	GNP	S	200	5	34,34,34	1.66	4 (11%)	47,54,54	1.17	4 (8%)
7	PG4	V	300	-	12,12,12	0.65	0	11,11,11	0.36	0
4	GNP	J	200	5	34,34,34	1.69	4 (11%)	47,54,54	1.16	3 (6%)
6	SO4	M	1182	-	4,4,4	0.27	0	6,6,6	0.14	0
4	GNP	G	200	5	34,34,34	1.70	5 (14%)	47,54,54	1.20	5 (10%)
4	GNP	A	200	5	34,34,34	1.60	6 (17%)	47,54,54	0.97	3 (6%)
4	GNP	D	200	5	34,34,34	1.72	5 (14%)	47,54,54	1.05	3 (6%)
4	GNP	M	200	5	34,34,34	1.82	4 (11%)	47,54,54	1.12	4 (8%)

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
4	GNP	P	200	5	-	6/18/38/38	0/3/3/3
4	GNP	V	200	5	-	2/18/38/38	0/3/3/3
4	GNP	S	200	5	-	6/18/38/38	0/3/3/3
7	PG4	V	300	-	-	2/10/10/10	-
4	GNP	J	200	5	-	2/18/38/38	0/3/3/3
4	GNP	G	200	5	-	5/18/38/38	0/3/3/3
4	GNP	A	200	5	-	2/18/38/38	0/3/3/3
4	GNP	D	200	5	-	4/18/38/38	0/3/3/3
4	GNP	M	200	5	-	3/18/38/38	0/3/3/3

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	200	GNP	PA-O3A	-6.32	1.52	1.59
4	J	200	GNP	PA-O3A	-6.02	1.53	1.59
4	P	200	GNP	PA-O3A	-5.97	1.53	1.59
4	S	200	GNP	PA-O3A	-5.80	1.53	1.59
4	G	200	GNP	PA-O3A	-5.73	1.53	1.59

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	200	GNP	O2B-PB-O1B	4.42	119.35	109.87
4	G	200	GNP	O2G-PG-O1G	-4.31	102.65	113.45
4	P	200	GNP	O2B-PB-O1B	4.30	119.08	109.87
4	S	200	GNP	O2G-PG-O1G	-4.28	102.72	113.45
4	S	200	GNP	O2B-PB-O1B	4.06	118.58	109.87

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

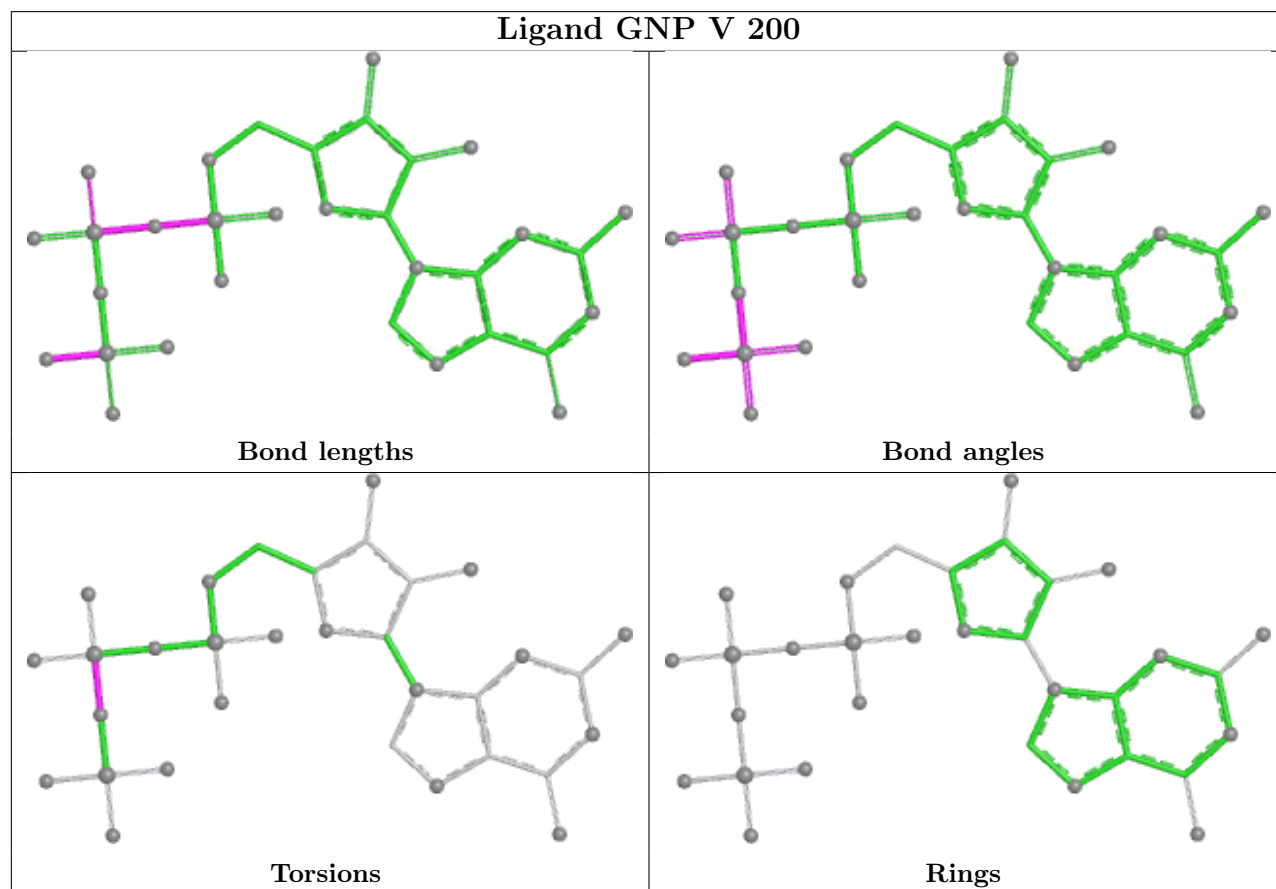
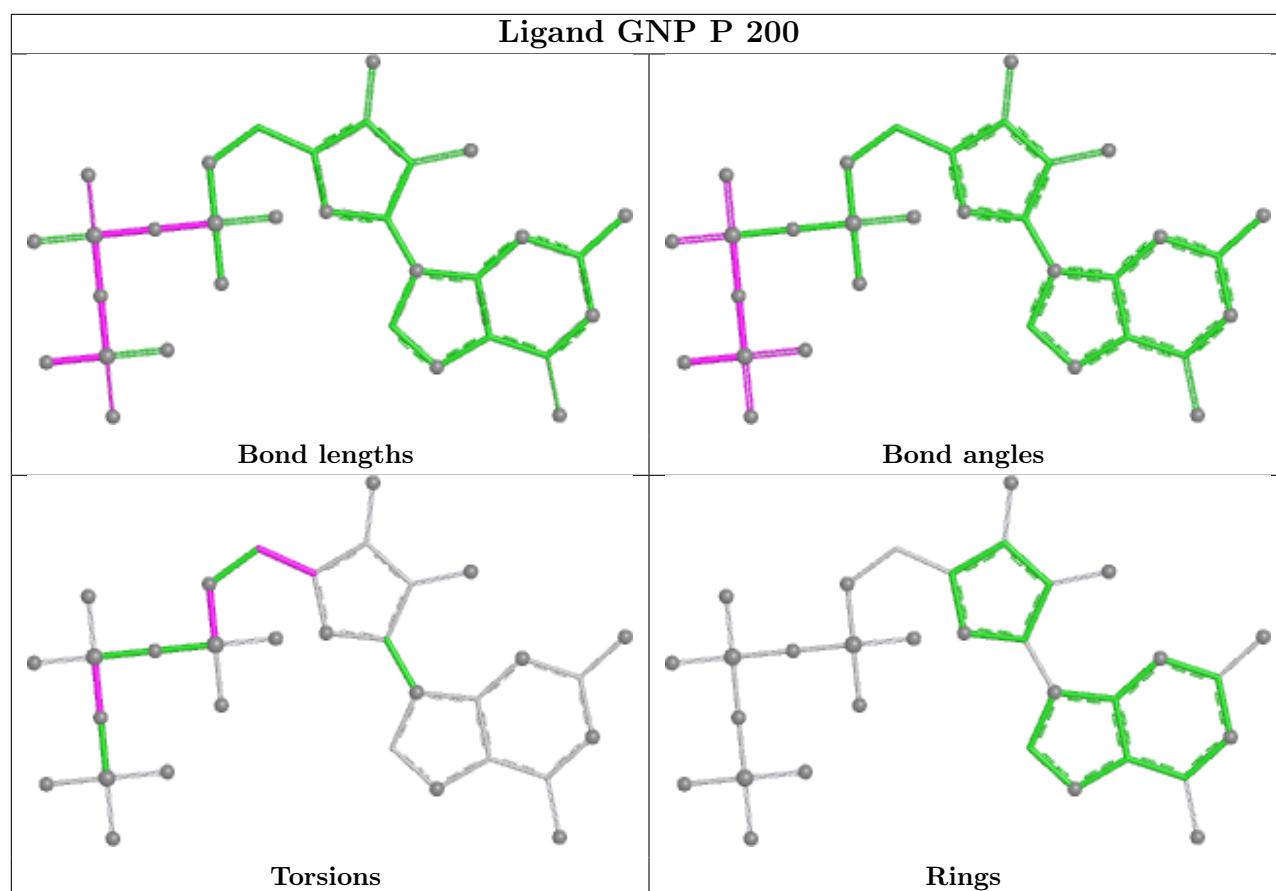
Mol	Chain	Res	Type	Atoms
4	A	200	GNP	PG-N3B-PB-O1B
4	A	200	GNP	PG-N3B-PB-O3A
4	D	200	GNP	PG-N3B-PB-O1B
4	D	200	GNP	PA-O3A-PB-O2B
4	G	200	GNP	PG-N3B-PB-O1B

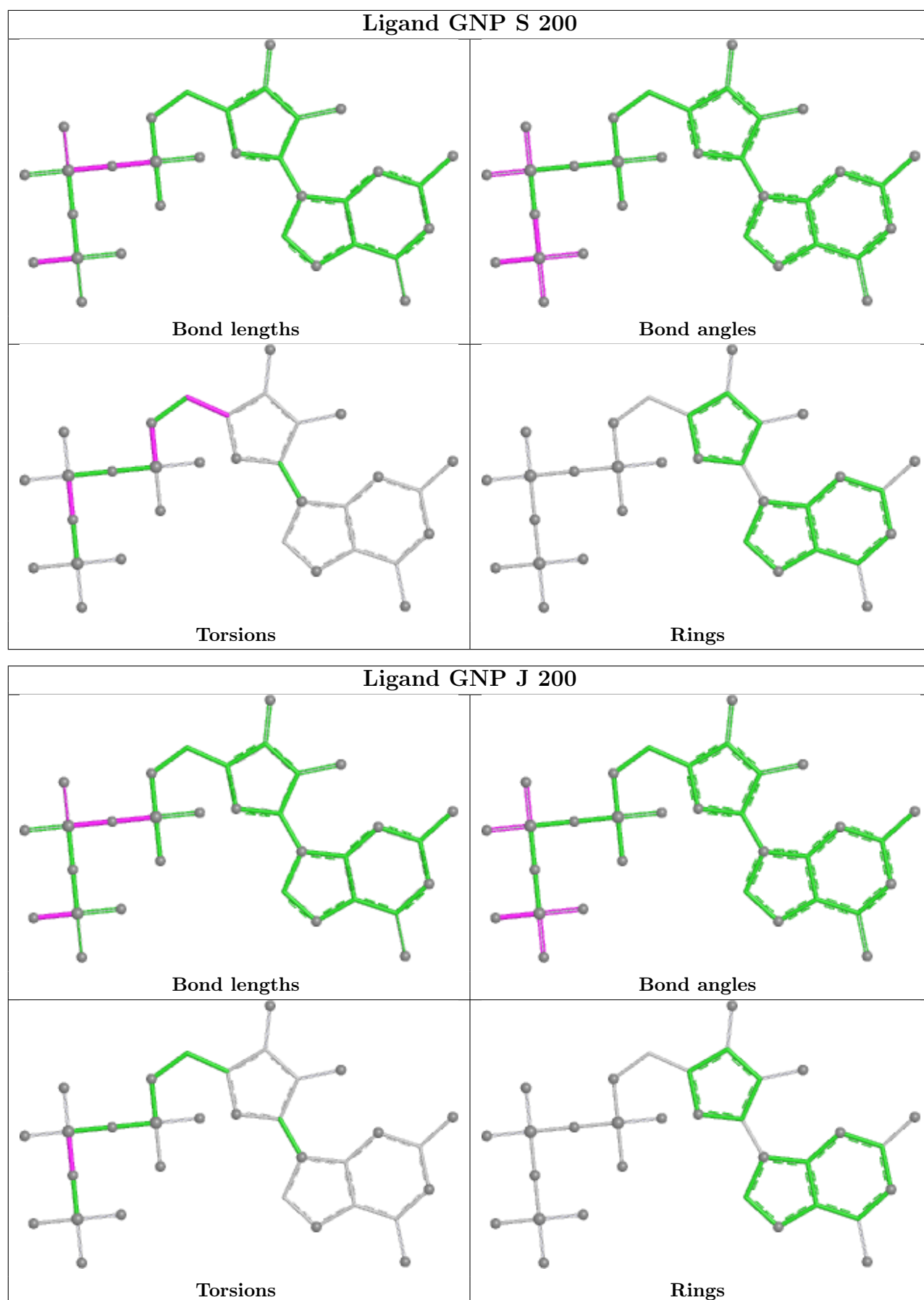
There are no ring outliers.

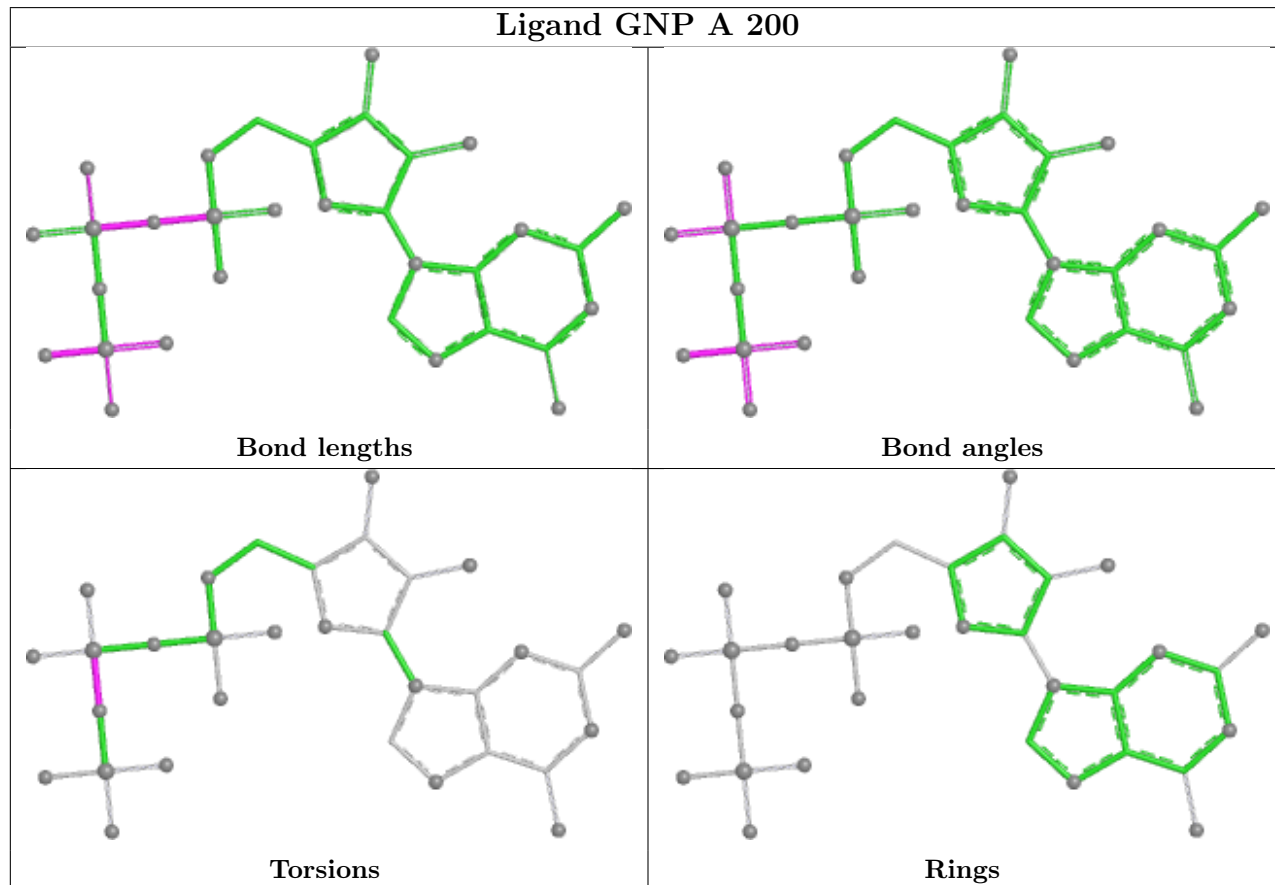
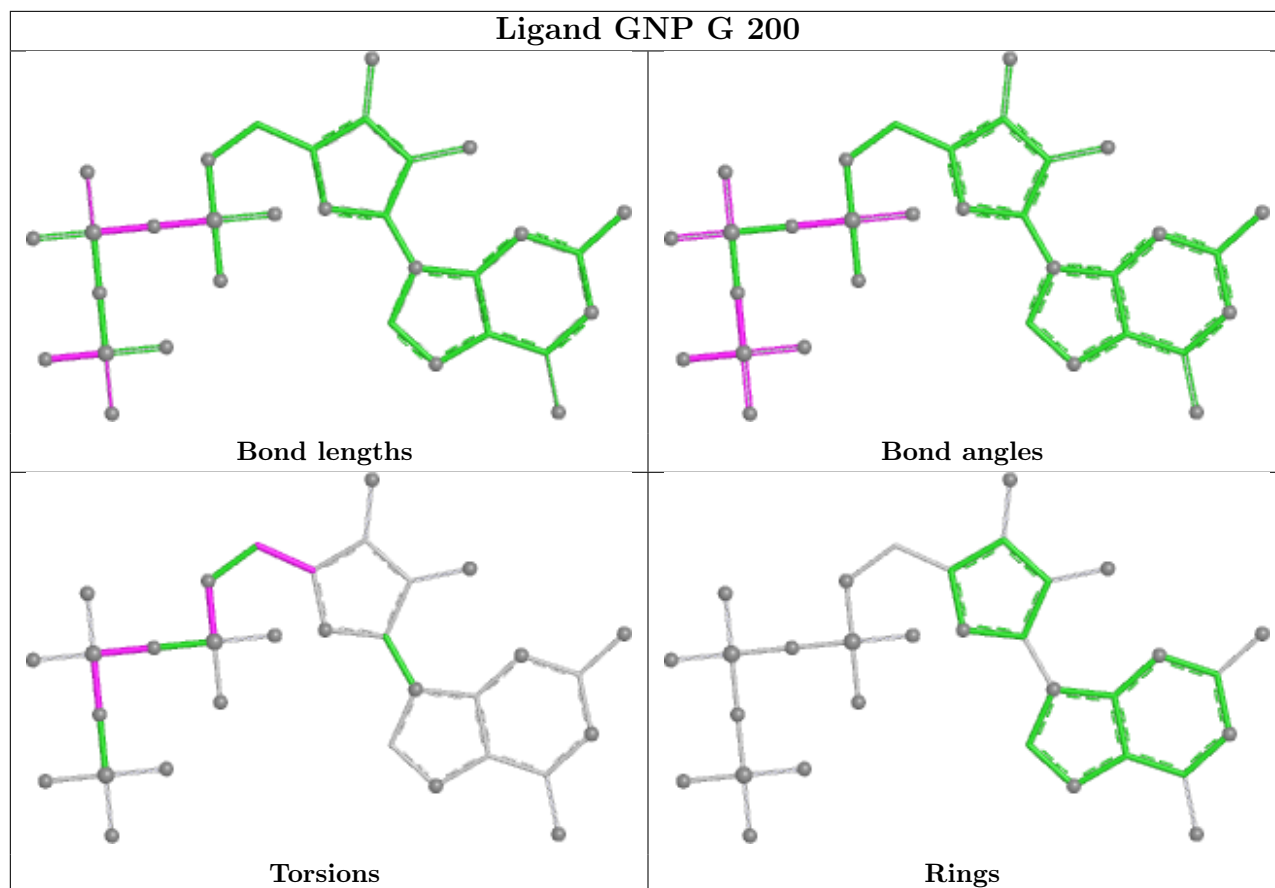
8 monomers are involved in 18 short contacts:

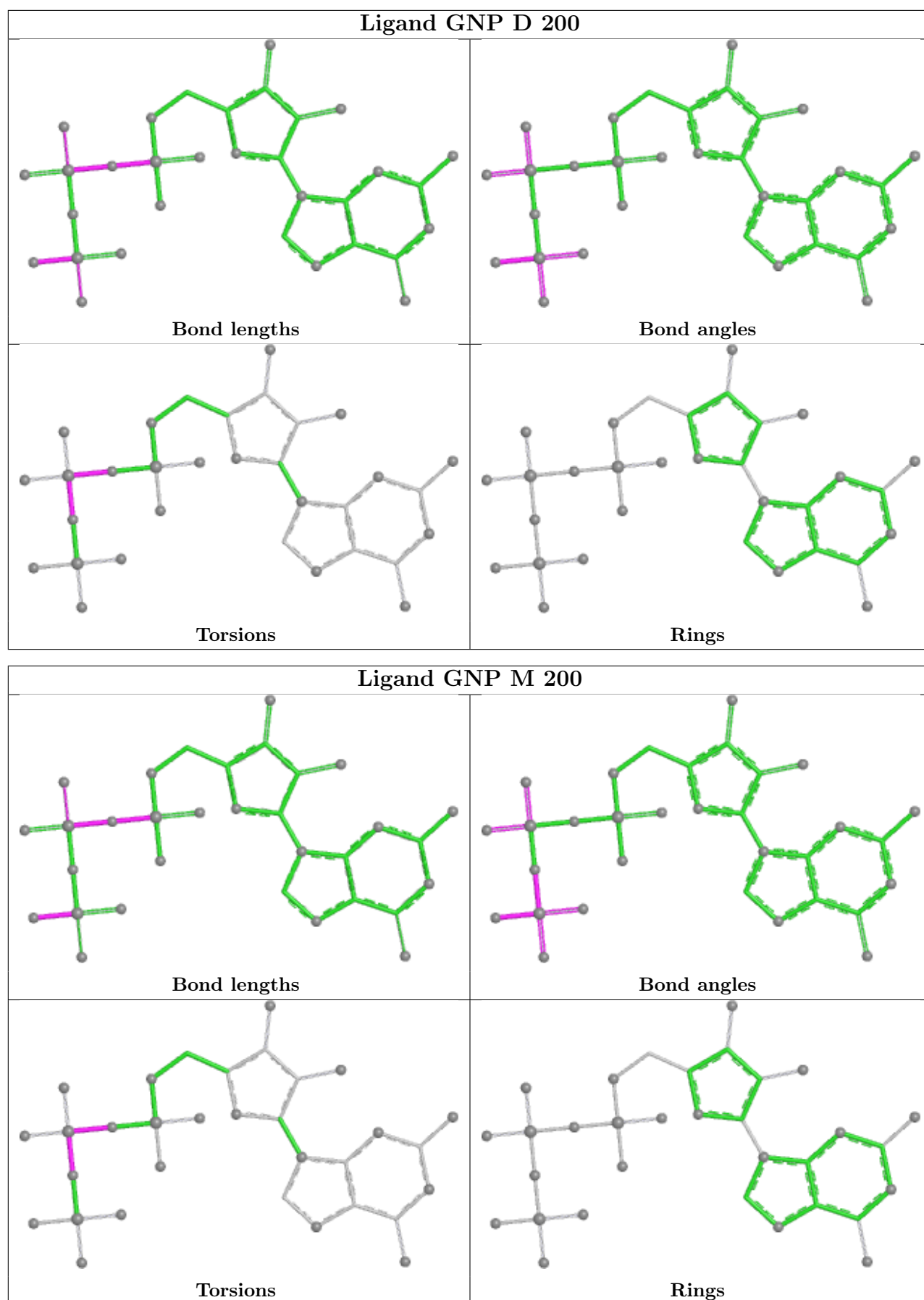
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	P	200	GNP	1	0
4	V	200	GNP	4	0
4	S	200	GNP	1	0
7	V	300	PG4	1	0
4	J	200	GNP	2	0
4	G	200	GNP	6	0
4	D	200	GNP	2	0
4	M	200	GNP	2	0

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.









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	176/187 (94%)	-0.57	0 100 100	51, 69, 109, 153	0
1	D	175/187 (93%)	-0.55	1 (0%) 85 69	41, 68, 102, 125	2 (1%)
1	G	175/187 (93%)	-0.53	0 100 100	37, 63, 101, 150	2 (1%)
1	J	174/187 (93%)	-0.46	1 (0%) 85 69	51, 73, 102, 117	0
1	M	174/187 (93%)	-0.40	2 (1%) 78 57	53, 77, 121, 144	0
1	P	171/187 (91%)	-0.11	2 (1%) 76 55	71, 101, 154, 172	0
1	S	171/187 (91%)	-0.13	3 (1%) 67 44	65, 97, 132, 149	0
1	V	169/187 (90%)	-0.34	1 (0%) 85 69	56, 86, 128, 140	0
2	B	161/195 (82%)	-0.37	0 100 100	48, 79, 141, 187	0
2	E	162/195 (83%)	-0.01	2 (1%) 76 55	65, 99, 137, 169	0
2	H	155/195 (79%)	-0.49	0 100 100	35, 67, 94, 128	2 (1%)
2	K	159/195 (81%)	0.02	0 100 100	60, 100, 130, 147	1 (0%)
2	N	164/195 (84%)	-0.28	2 (1%) 76 55	57, 84, 122, 151	0
2	Q	161/195 (82%)	-0.14	0 100 100	68, 90, 119, 146	1 (0%)
2	T	164/195 (84%)	-0.00	0 100 100	62, 106, 141, 163	1 (0%)
2	W	155/195 (79%)	-0.34	0 100 100	53, 73, 102, 117	1 (0%)
3	C	36/66 (54%)	-0.17	0 100 100	59, 80, 147, 160	0
3	F	37/66 (56%)	-0.28	0 100 100	62, 81, 161, 167	0
3	I	41/66 (62%)	-0.19	1 (2%) 59 36	65, 84, 164, 172	0
3	L	38/66 (57%)	-0.19	0 100 100	60, 84, 167, 168	0
3	O	37/66 (56%)	-0.29	0 100 100	77, 96, 148, 157	0
3	R	37/66 (56%)	-0.10	0 100 100	96, 108, 167, 179	0
3	U	37/66 (56%)	0.05	0 100 100	81, 105, 167, 176	0
3	X	36/66 (54%)	-0.02	0 100 100	87, 115, 159, 167	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	2965/3584 (82%)	-0.28	15 (0%) 87 72	35, 85, 134, 187	10 (0%)

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	396	ASP	3.8
1	M	6	ASP	3.2
1	S	75	ALA	3.2
1	D	72	ARG	2.9
1	M	75	ALA	2.6

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.

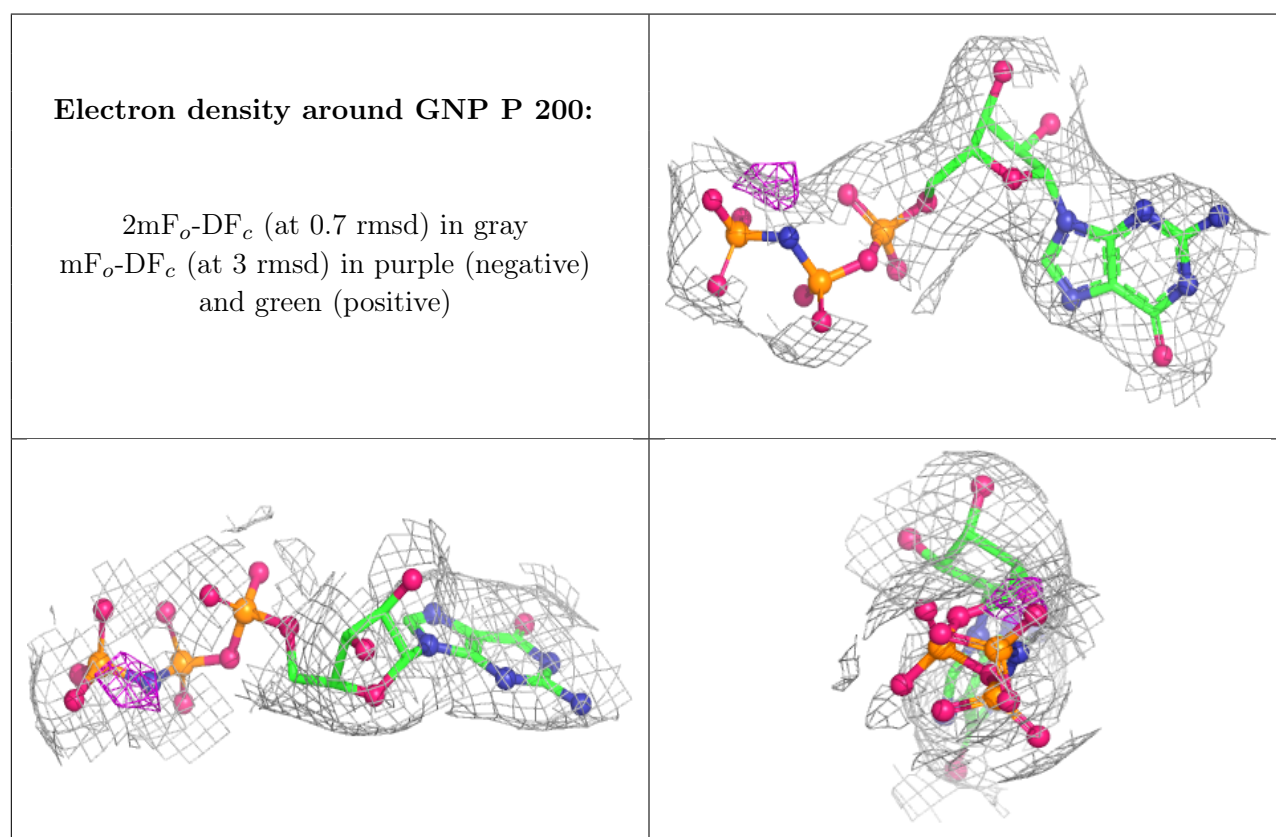
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	SO4	M	1182	5/5	0.71	0.12	127,130,141,167	0
7	PG4	V	300	13/13	0.74	0.17	84,107,125,130	0
4	GNP	P	200	32/32	0.96	0.06	68,82,92,101	0
5	MG	A	201	1/1	0.97	0.07	62,62,62,62	0
4	GNP	J	200	32/32	0.97	0.05	50,64,79,85	0
4	GNP	S	200	32/32	0.97	0.06	61,80,91,93	0
4	GNP	G	200	32/32	0.98	0.05	35,51,65,84	0
4	GNP	V	200	32/32	0.98	0.05	51,63,80,93	0
4	GNP	A	200	32/32	0.98	0.05	46,61,75,77	0
5	MG	J	201	1/1	0.98	0.05	70,70,70,70	0
5	MG	P	201	1/1	0.98	0.04	76,76,76,76	0
5	MG	S	201	1/1	0.98	0.04	61,61,61,61	0
5	MG	V	201	1/1	0.98	0.06	68,68,68,68	0

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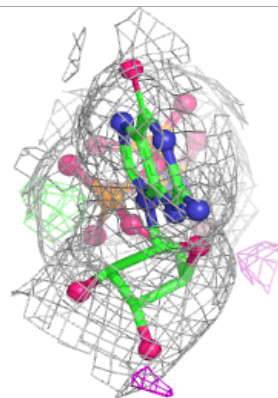
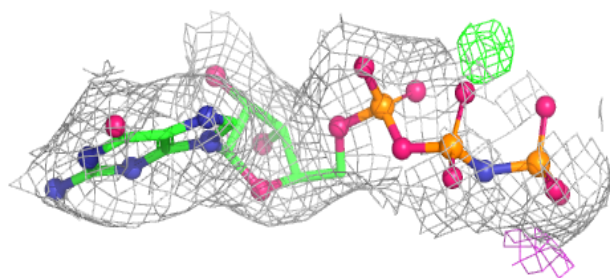
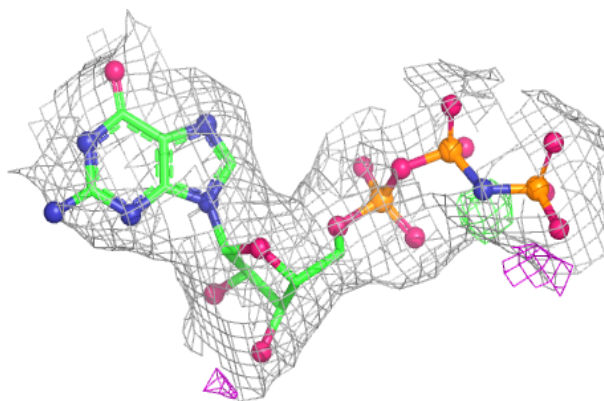
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GNP	M	200	32/32	0.98	0.05	44,61,69,84	0
4	GNP	D	200	32/32	0.98	0.05	49,63,72,79	0
5	MG	M	201	1/1	0.99	0.03	58,58,58,58	0
5	MG	G	201	1/1	0.99	0.05	50,50,50,50	0
5	MG	D	201	1/1	0.99	0.04	63,63,63,63	0

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.

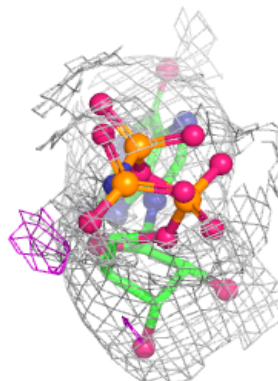
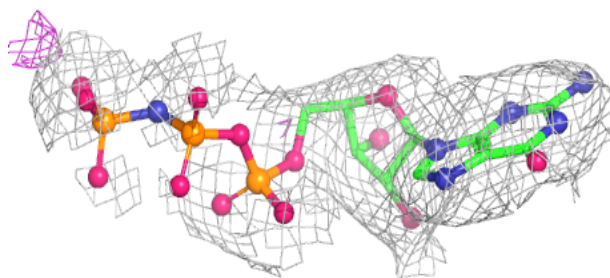
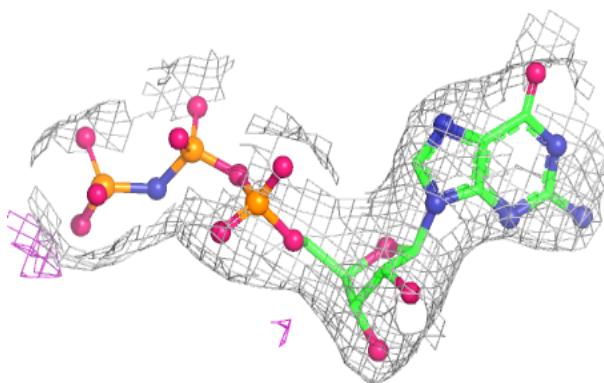


Electron density around GNP J 200:

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

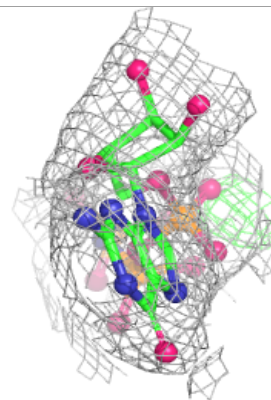
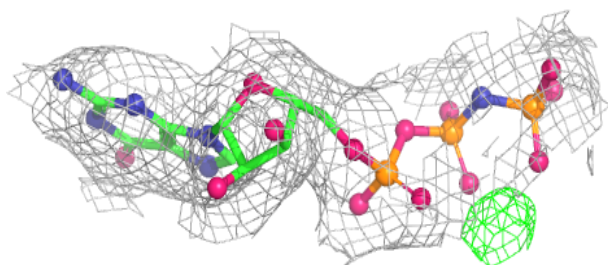
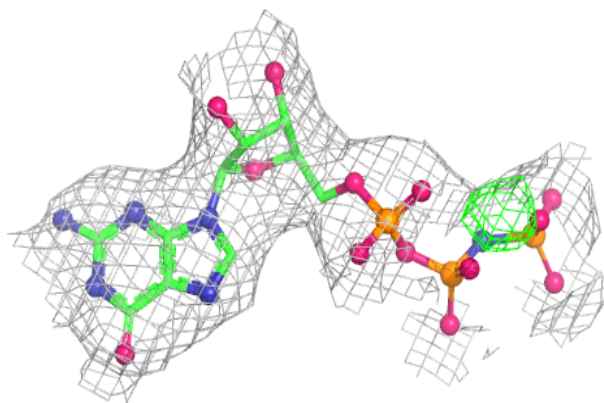
**Electron density around GNP S 200:**

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

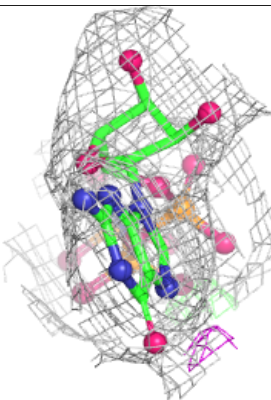
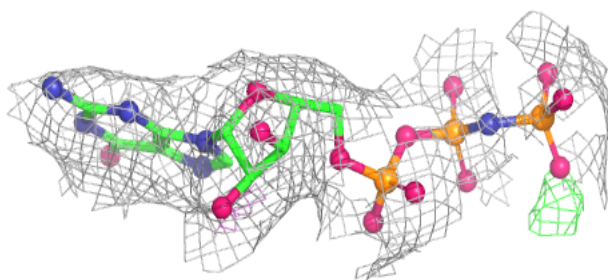
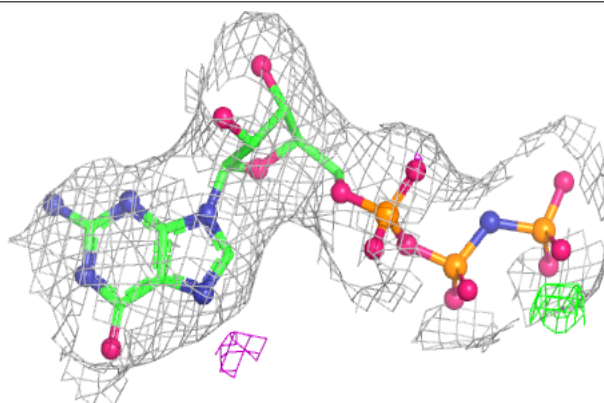


Electron density around GNP G 200:

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

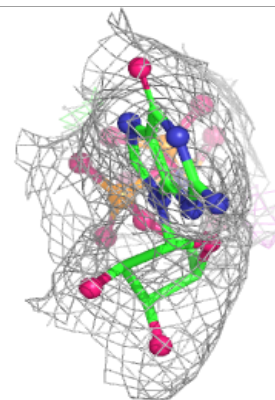
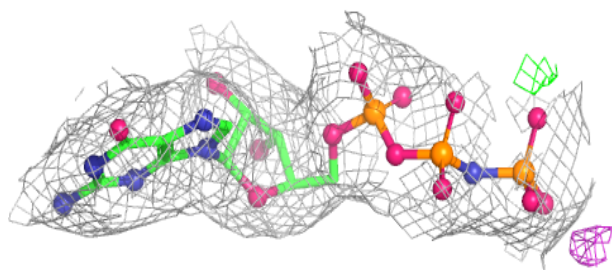
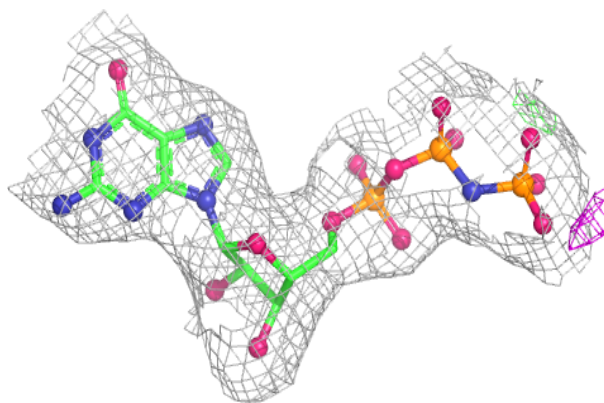
**Electron density around GNP V 200:**

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

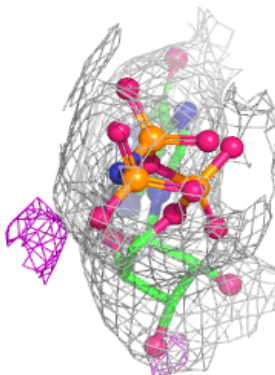
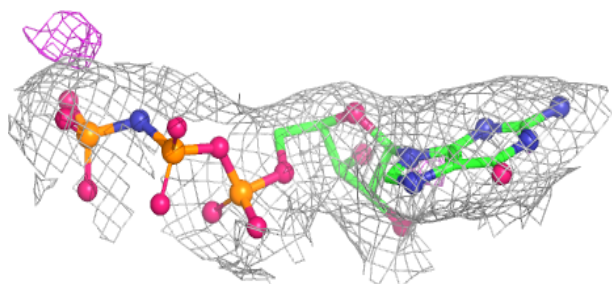
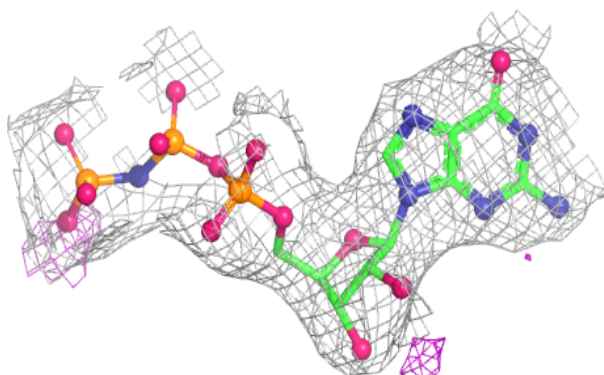


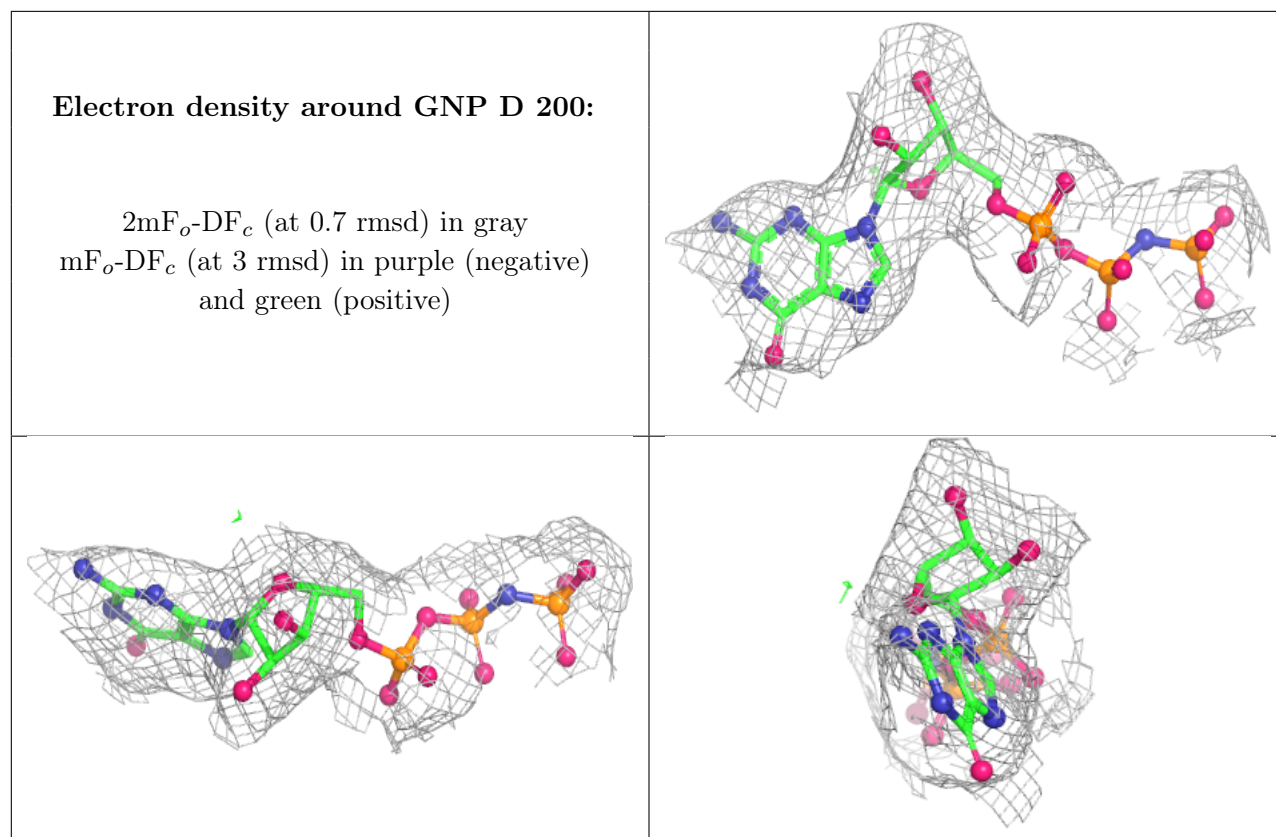
Electron density around GNP A 200:

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

**Electron density around GNP M 200:**

$2mF_o-DF_c$ (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.