



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 7, 2020 – 02:58 am BST

PDB ID : 6GQT
Title : KRAS-169 Q61H GPPNHP + PPIN-2
Authors : Cruz-Migoni, A.; Canning, P.; Quevedo, C.E.; Carr, S.B.; Phillips, S.E.V.;
Rabbitts, T.H.
Deposited on : 2018-06-08
Resolution : 1.69 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

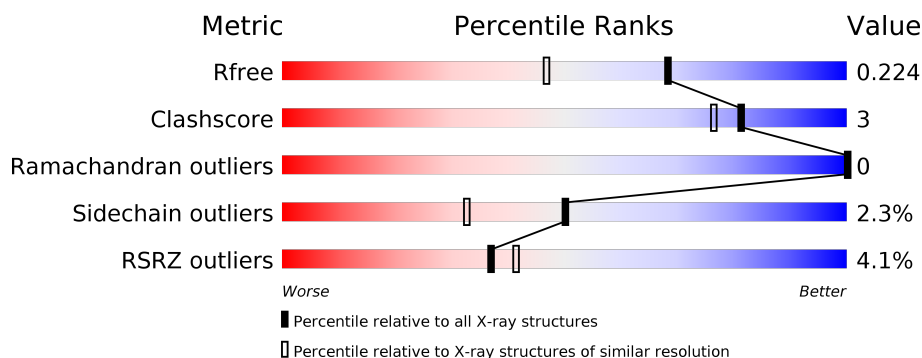
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	171	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>••</div> </div> </div>
1	B	171	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>12%</div> <div>•</div> </div> </div>
1	C	171	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>6%</div> <div>• 7%</div> </div> </div>
1	D	171	<div> <div>5%</div> <div> <div></div> <div>87%</div> <div>6%</div> <div>• 6%</div> </div> </div>
1	E	171	<div> <div>8%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>• •</div> </div> </div>
1	F	171	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>5%</div> <div>• 8%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MG	D	202	-	-	-	X
5	F8N	F	203	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8885 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 GTPase KRas.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	171	Total	C	N	O	S	0	5	0
			1395	876	242	270	7			
1	B	171	Total	C	N	O	S	0	5	0
			1383	863	240	272	8			
1	C	159	Total	C	N	O	S	0	2	0
			1256	791	215	244	6			
1	D	160	Total	C	N	O	S	0	3	0
			1268	797	222	243	6			
1	E	164	Total	C	N	O	S	0	2	0
			1288	809	223	250	6			
1	F	158	Total	C	N	O	S	0	2	0
			1244	783	217	238	6			

There are 24 discrepancies between the modelled and reference sequences:

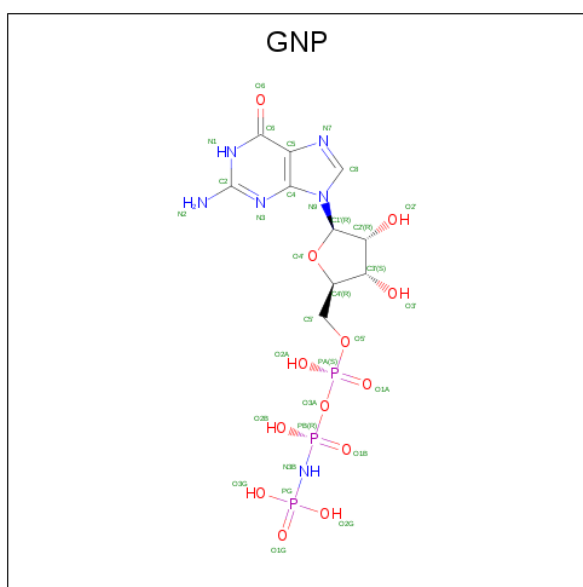
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	PHE	-	expression tag	UNP P01116
A	-1	GLN	-	expression tag	UNP P01116
A	0	GLY	-	expression tag	UNP P01116
A	61	HIS	GLN	engineered mutation	UNP P01116
B	-2	PHE	-	expression tag	UNP P01116
B	-1	GLN	-	expression tag	UNP P01116
B	0	GLY	-	expression tag	UNP P01116
B	61	HIS	GLN	engineered mutation	UNP P01116
C	-2	PHE	-	expression tag	UNP P01116
C	-1	GLN	-	expression tag	UNP P01116
C	0	GLY	-	expression tag	UNP P01116
C	61	HIS	GLN	engineered mutation	UNP P01116
D	-2	PHE	-	expression tag	UNP P01116
D	-1	GLN	-	expression tag	UNP P01116
D	0	GLY	-	expression tag	UNP P01116
D	61	HIS	GLN	engineered mutation	UNP P01116
E	-2	PHE	-	expression tag	UNP P01116

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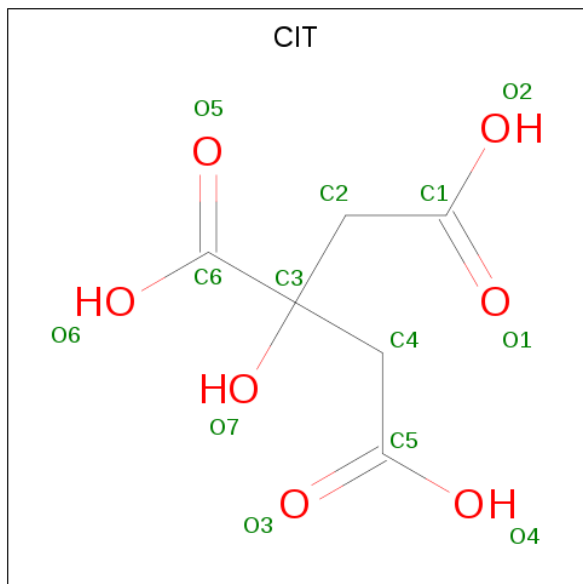
Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	GLN	-	expression tag	UNP P01116
E	0	GLY	-	expression tag	UNP P01116
E	61	HIS	GLN	engineered mutation	UNP P01116
F	-2	PHE	-	expression tag	UNP P01116
F	-1	GLN	-	expression tag	UNP P01116
F	0	GLY	-	expression tag	UNP P01116
F	61	HIS	GLN	engineered mutation	UNP P01116

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



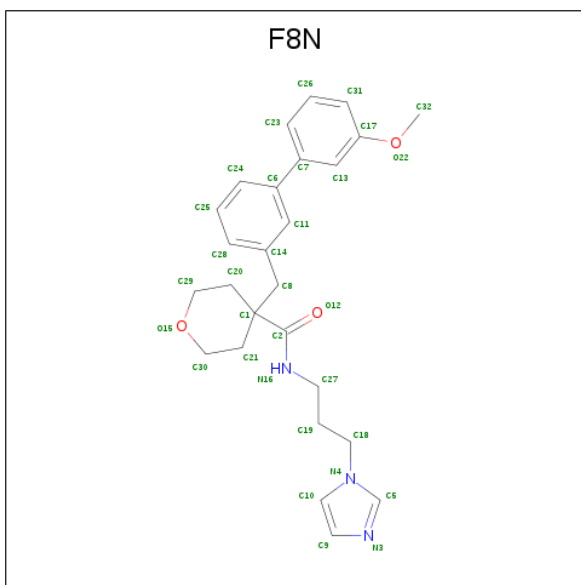
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total Mg 1 1	0	0
3	E	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	F	1	Total Mg 1 1	0	0

- Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 13 6 7	0	0
4	A	1	Total C O 13 6 7	0	0
4	D	1	Total C O 13 6 7	0	0

- Molecule 5 is {N}-(3-imidazol-1-ylpropyl)-4-[[3-(3-methoxyphenyl)phenyl]methyl]oxane-4-carboxamide (three-letter code: F8N) (formula: $C_{26}H_{31}N_3O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			32	26	3	3		
5	C	1	Total	C	N	O	0	0
			32	26	3	3		
5	D	1	Total	C	N	O	0	0
			32	26	3	3		
5	F	1	Total	C	N	O	0	0
			32	26	3	3		

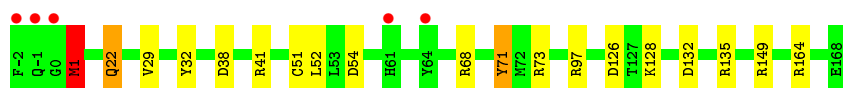
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	178	Total	O	0	0
			178	178		
6	B	153	Total	O	0	0
			153	153		
6	C	74	Total	O	0	0
			74	74		
6	D	79	Total	O	0	0
			79	79		
6	E	85	Total	O	0	0
			85	85		
6	F	117	Total	O	0	0
			117	117		

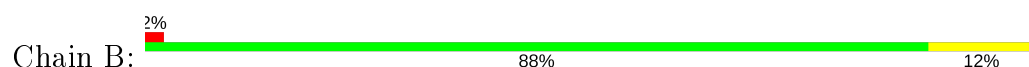
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

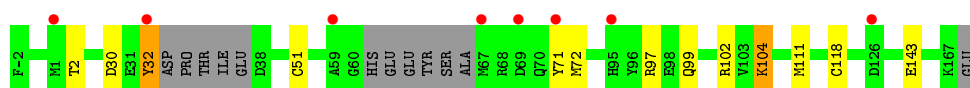
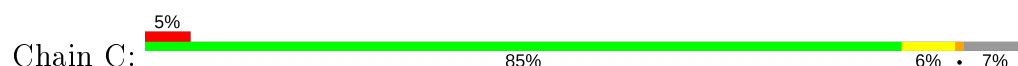
- Molecule 1: GTPase KRas



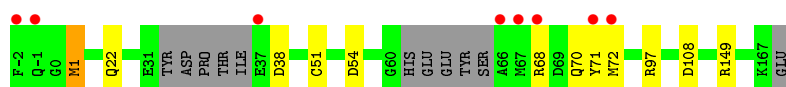
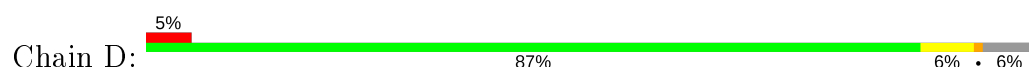
- Molecule 1: GTPase KRas



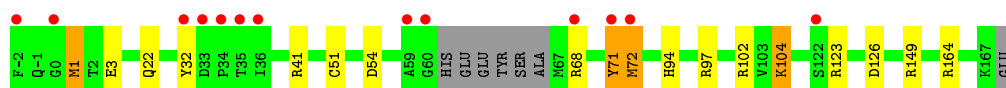
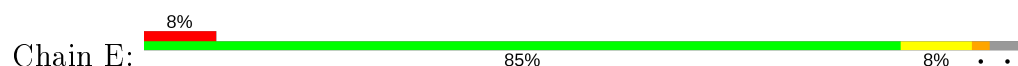
- Molecule 1: GTPase KRas



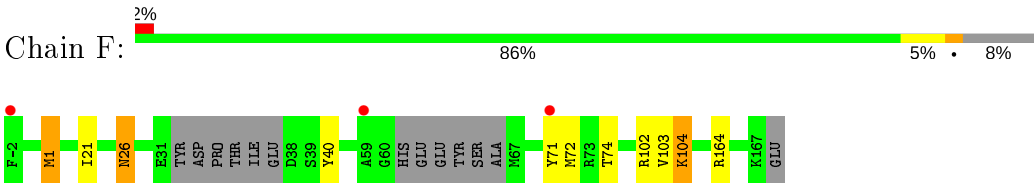
- Molecule 1: GTPase KRas



- Molecule 1: GTPase KRas



- Molecule 1: GTPase KRas



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.27Å 119.55Å 158.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.78 – 1.69 59.77 – 1.69	Depositor EDS
% Data completeness (in resolution range)	100.0 (59.78-1.69) 100.0 (59.77-1.69)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 1.69Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.189 , 0.214 0.202 , 0.224	Depositor DCC
R_{free} test set	6817 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8885	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, F8N, MG, CIT

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	1.17	4/1424 (0.3%)	1.18	19/1922 (1.0%)
1	B	1.06	2/1405 (0.1%)	1.07	9/1896 (0.5%)
1	C	1.01	1/1280 (0.1%)	0.99	6/1725 (0.3%)
1	D	0.97	2/1288 (0.2%)	0.98	5/1736 (0.3%)
1	E	0.92	0/1311	1.00	9/1771 (0.5%)
1	F	1.04	1/1264 (0.1%)	1.02	3/1703 (0.2%)
All	All	1.03	10/7972 (0.1%)	1.05	51/10753 (0.5%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	71	TYR	CE1-CZ	-6.59	1.29	1.38
1	B	106	SER	CB-OG	6.55	1.50	1.42
1	D	108	ASP	C-O	-6.32	1.11	1.23
1	C	51	CYS	CB-SG	-6.27	1.71	1.82
1	F	164	ARG	CZ-NH1	-5.84	1.25	1.33
1	D	51	CYS	CB-SG	-5.43	1.73	1.81
1	B	49	GLU	CD-OE1	5.36	1.31	1.25
1	A	22[A]	GLN	CB-CG	-5.15	1.38	1.52
1	A	22[B]	GLN	CB-CG	-5.15	1.38	1.52
1	A	51	CYS	CB-SG	-5.14	1.73	1.81

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	97[A]	ARG	NE-CZ-NH1	9.31	124.95	120.30
1	B	97[B]	ARG	NE-CZ-NH1	9.31	124.95	120.30
1	C	30	ASP	CB-CG-OD2	-8.33	110.80	118.30
1	A	54	ASP	CB-CG-OD1	-7.66	111.41	118.30
1	B	97[A]	ARG	NE-CZ-NH2	-7.37	116.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	97[B]	ARG	NE-CZ-NH2	-7.37	116.61	120.30
1	E	102	ARG	NE-CZ-NH1	7.37	123.99	120.30
1	B	1	MET	CB-CG-SD	7.30	134.29	112.40
1	A	73	ARG	NE-CZ-NH1	7.26	123.93	120.30
1	A	97[A]	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	A	97[B]	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	B	154	ASP	CB-CG-OD2	-6.76	112.21	118.30
1	A	135	ARG	NE-CZ-NH2	6.68	123.64	120.30
1	A	1	MET	CG-SD-CE	6.67	110.87	100.20
1	D	1	MET	CB-CG-SD	6.63	132.28	112.40
1	A	68	ARG	NE-CZ-NH2	-6.58	117.01	120.30
1	F	102	ARG	NE-CZ-NH1	6.57	123.59	120.30
1	C	97	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	E	1	MET	CB-CG-SD	6.48	131.85	112.40
1	A	126	ASP	CB-CG-OD2	-6.41	112.53	118.30
1	F	104	LYS	CD-CE-NZ	-6.41	96.97	111.70
1	C	104	LYS	CD-CE-NZ	-6.35	97.10	111.70
1	A	41	ARG	NE-CZ-NH1	-6.32	117.14	120.30
1	E	123	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	C	102	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	A	132	ASP	CB-CG-OD1	6.13	123.81	118.30
1	A	164	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	E	104	LYS	CD-CE-NZ	-5.98	97.94	111.70
1	C	30	ASP	CB-CG-OD1	5.98	123.68	118.30
1	E	123	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	D	97	ARG	NE-CZ-NH2	-5.81	117.39	120.30
1	A	22[A]	GLN	CG-CD-NE2	-5.77	102.85	116.70
1	A	22[B]	GLN	CG-CD-NE2	-5.77	102.85	116.70
1	E	126	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	B	126	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	22[A]	GLN	CG-CD-OE1	5.61	132.81	121.60
1	A	22[B]	GLN	CG-CD-OE1	5.61	132.81	121.60
1	A	54	ASP	CB-CG-OD2	5.52	123.27	118.30
1	C	111	MET	CG-SD-CE	-5.51	91.38	100.20
1	E	72	MET	CG-SD-CE	-5.38	91.60	100.20
1	E	97	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	F	1	MET	CB-CG-SD	5.31	128.32	112.40
1	D	51	CYS	CB-CA-C	-5.29	99.83	110.40
1	A	38	ASP	CB-CG-OD1	5.26	123.03	118.30
1	A	97[A]	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	A	97[B]	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	D	70	GLN	C-N-CA	-5.16	108.81	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	111	MET	CG-SD-CE	-5.15	91.96	100.20
1	E	126	ASP	CB-CG-OD1	5.08	122.87	118.30
1	D	97	ARG	NE-CZ-NH1	5.03	122.81	120.30
1	B	132	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1395	0	1373	5	0
1	B	1383	0	1335	9	0
1	C	1256	0	1224	7	0
1	D	1268	0	1245	7	0
1	E	1288	0	1249	7	0
1	F	1244	0	1224	8	0
2	A	32	0	13	0	0
2	B	32	0	13	0	0
2	C	32	0	13	0	0
2	D	32	0	13	0	0
2	E	32	0	13	0	0
2	F	32	0	13	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	26	0	10	0	0
4	D	13	0	5	0	0
5	B	32	0	0	1	0
5	C	32	0	0	0	0
5	D	32	0	0	1	0
5	F	32	0	0	1	0
6	A	178	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	153	0	0	0	0
6	C	74	0	0	1	0
6	D	79	0	0	0	0
6	E	85	0	0	0	0
6	F	117	0	0	1	0
All	All	8885	0	7743	41	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 3.

All (41) 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:A:128:LYS:NZ	6:A:301:HOH:O	1.69	1.19
1:F:72:MET:CB	1:F:103:VAL:HG21	2.17	0.75
1:F:72:MET:O	1:F:104:LYS:HD3	1.86	0.75
1:E:72:MET:O	1:E:104:LYS:HD3	1.90	0.72
1:B:72:MET:CB	1:B:103:VAL:HG11	2.18	0.72
1:F:72:MET:HB3	1:F:103:VAL:HG21	1.75	0.68
1:B:72:MET:HB3	1:B:103:VAL:HG11	1.80	0.64
1:F:74:THR:OG1	5:F:203:F8N:O22	2.15	0.64
1:D:68:ARG:HA	1:D:71:TYR:CE2	2.36	0.59
1:B:72:MET:HB3	1:B:103:VAL:CG1	2.32	0.59
1:F:72:MET:HB3	1:F:103:VAL:CG2	2.35	0.57
1:F:72:MET:HB2	1:F:103:VAL:HG21	1.87	0.56
1:D:71:TYR:CD1	1:D:71:TYR:C	2.83	0.52
1:D:54:ASP:HB3	5:D:203:F8N:C24	2.42	0.49
1:B:72:MET:HB2	1:B:103:VAL:HG11	1.93	0.48
1:E:51:CYS:SG	1:E:164:ARG:NH2	2.86	0.48
1:F:26[A]:ASN:ND2	6:F:301:HOH:O	2.26	0.47
1:D:71:TYR:CD1	1:D:72:MET:N	2.84	0.46
1:E:3:GLU:OE1	1:E:54:ASP:OD2	2.35	0.45
1:B:37:GLU:HG2	1:B:56:LEU:HD11	1.98	0.44
1:C:2:THR:HB	6:C:301:HOH:O	2.17	0.44
1:B:54:ASP:HB3	5:B:203:F8N:C24	2.47	0.44
1:C:72:MET:O	1:C:104:LYS:HD3	2.18	0.44
1:B:41:ARG:NH1	1:E:3:GLU:OE2	2.51	0.43
1:C:118:CYS:CB	1:C:143[B]:GLU:HG3	2.49	0.42
1:E:68:ARG:CZ	1:E:71:TYR:OH	2.67	0.42
1:C:32:TYR:C	1:C:32:TYR:CD1	2.93	0.42
1:B:3:GLU:OE1	1:E:41:ARG:HD2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29[A]:VAL:O	1:A:29[A]:VAL:HG23	2.18	0.42
1:C:118:CYS:HB3	1:C:143[B]:GLU:HG3	2.00	0.42
1:A:22[B]:GLN:HG3	1:A:149:ARG:HG3	2.01	0.41
1:C:72:MET:CE	1:C:99:GLN:HG2	2.50	0.41
1:F:21[A]:ILE:HD11	1:F:40:TYR:OH	2.20	0.41
1:D:22:GLN:HG3	1:D:149:ARG:HG3	2.03	0.41
1:A:1:MET:HG3	1:A:52:LEU:HB2	2.03	0.41
1:A:22[B]:GLN:CG	1:A:149:ARG:HG3	2.51	0.41
1:D:68:ARG:HD2	1:D:72:MET:HE2	2.02	0.41
1:E:22:GLN:HG3	1:E:149:ARG:HG3	2.03	0.40
1:B:22:GLN:HG3	1:B:149:ARG:HG3	2.02	0.40
1:C:32:TYR:C	1:C:32:TYR:HD1	2.24	0.40
1:D:22:GLN:CG	1:D:149:ARG:HG3	2.52	0.40

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	174/171 (102%)	168 (97%)	6 (3%)	0	100	100
1	B	174/171 (102%)	168 (97%)	6 (3%)	0	100	100
1	C	155/171 (91%)	153 (99%)	2 (1%)	0	100	100
1	D	157/171 (92%)	155 (99%)	2 (1%)	0	100	100
1	E	162/171 (95%)	158 (98%)	4 (2%)	0	100	100
1	F	154/171 (90%)	151 (98%)	3 (2%)	0	100	100
All	All	976/1026 (95%)	953 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	153/150 (102%)	150 (98%)	3 (2%)	55	38
1	B	150/150 (100%)	143 (95%)	7 (5%)	26	10
1	C	135/150 (90%)	133 (98%)	2 (2%)	65	51
1	D	136/150 (91%)	134 (98%)	2 (2%)	65	51
1	E	138/150 (92%)	134 (97%)	4 (3%)	42	23
1	F	134/150 (89%)	130 (97%)	4 (3%)	41	22
All	All	846/900 (94%)	824 (97%)	22 (3%)	50	28

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	32	TYR
1	A	71	TYR
1	B	1	MET
1	B	26[A]	ASN
1	B	26[B]	ASN
1	B	32	TYR
1	B	51[A]	CYS
1	B	51[B]	CYS
1	B	71	TYR
1	C	32	TYR
1	C	71	TYR
1	D	1	MET
1	D	38	ASP
1	E	1	MET
1	E	32	TYR
1	E	71	TYR
1	E	94	HIS
1	F	1	MET
1	F	26[A]	ASN
1	F	26[B]	ASN
1	F	71	TYR

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

Mol	Chain	Res	Type
1	A	25	GLN
1	B	99	GLN
1	F	116	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 6 are monoatomic - leaving 13 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	$\# Z > 2$
2	GNP	C	201	3	28,34,34	3.44	11 (39%)	30,54,54	1.94	7 (23%)
4	CIT	D	204	-	3,12,12	1.06	0	3,17,17	4.26	2 (66%)
2	GNP	A	201	3	28,34,34	2.72	8 (28%)	30,54,54	1.81	4 (13%)
5	F8N	B	203	-	34,35,35	1.15	4 (11%)	41,47,47	1.87	8 (19%)
2	GNP	E	201	3	28,34,34	3.46	10 (35%)	30,54,54	1.35	3 (10%)
5	F8N	F	203	-	34,35,35	1.15	2 (5%)	41,47,47	1.36	4 (9%)
4	CIT	A	203	-	3,12,12	1.19	0	3,17,17	1.18	0
5	F8N	D	203	-	34,35,35	1.00	2 (5%)	41,47,47	1.13	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	F8N	C	203	-	34,35,35	1.25	2 (5%)	41,47,47	1.46	8 (19%)
4	CIT	A	204	-	3,12,12	0.54	0	3,17,17	2.26	2 (66%)
2	GNP	B	201	3	28,34,34	3.77	15 (53%)	30,54,54	2.33	12 (40%)
2	GNP	D	201	3	28,34,34	4.04	11 (39%)	30,54,54	1.84	5 (16%)
2	GNP	F	201	3	28,34,34	3.86	8 (28%)	30,54,54	1.81	9 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GNP	C	201	3	-	4/17/38/38	0/3/3/3
4	CIT	D	204	-	-	4/6/16/16	-
2	GNP	A	201	3	-	5/17/38/38	0/3/3/3
5	F8N	B	203	-	-	5/24/34/34	0/4/4/4
2	GNP	E	201	3	-	2/17/38/38	0/3/3/3
5	F8N	F	203	-	-	8/24/34/34	1/4/4/4
4	CIT	A	203	-	-	0/6/16/16	-
5	F8N	D	203	-	-	6/24/34/34	1/4/4/4
5	F8N	C	203	-	-	7/24/34/34	1/4/4/4
4	CIT	A	204	-	-	0/6/16/16	-
2	GNP	B	201	3	-	5/17/38/38	0/3/3/3
2	GNP	D	201	3	-	4/17/38/38	0/3/3/3
2	GNP	F	201	3	-	7/17/38/38	0/3/3/3

All (73) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	201	GNP	C4-N9	-14.24	1.28	1.47
2	B	201	GNP	C4-N9	-13.76	1.29	1.47
2	D	201	GNP	C4-N9	-12.47	1.31	1.47
2	E	201	GNP	C4-N9	-12.11	1.31	1.47
2	D	201	GNP	PG-O1G	11.67	1.64	1.46
2	C	201	GNP	C4-N9	-11.59	1.32	1.47
2	F	201	GNP	PG-O1G	10.57	1.63	1.46
2	A	201	GNP	C4-N9	-10.21	1.34	1.47
2	C	201	GNP	PG-O1G	9.74	1.61	1.46
2	E	201	GNP	PG-O1G	7.41	1.57	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	201	GNP	PB-O1B	6.28	1.56	1.46
2	B	201	GNP	PG-O1G	6.25	1.56	1.46
2	D	201	GNP	PB-O3A	6.24	1.66	1.59
2	D	201	GNP	C5-C6	-5.89	1.42	1.52
2	F	201	GNP	C5-C6	-5.65	1.43	1.52
2	A	201	GNP	PG-O1G	5.52	1.54	1.46
2	B	201	GNP	C5-C6	-5.40	1.43	1.52
2	C	201	GNP	C5-C6	-5.09	1.44	1.52
2	B	201	GNP	PG-N3B	4.72	1.75	1.63
2	D	201	GNP	PB-O2B	-4.55	1.44	1.56
2	E	201	GNP	PB-O1B	-4.47	1.39	1.46
2	E	201	GNP	PG-O2G	-4.46	1.44	1.56
2	E	201	GNP	PG-N3B	4.27	1.74	1.63
2	D	201	GNP	PG-N3B	4.13	1.74	1.63
2	B	201	GNP	PB-O3A	3.98	1.64	1.59
2	F	201	GNP	C8-N9	-3.95	1.31	1.45
2	F	201	GNP	PG-N3B	3.89	1.73	1.63
2	A	201	GNP	PG-N3B	3.84	1.73	1.63
2	E	201	GNP	C8-N9	-3.58	1.33	1.45
2	C	201	GNP	PG-O3G	3.44	1.66	1.56
2	E	201	GNP	PB-N3B	3.38	1.72	1.63
2	E	201	GNP	C5-C6	-3.37	1.47	1.52
2	D	201	GNP	PB-O1B	3.30	1.51	1.46
2	A	201	GNP	PB-O1B	3.28	1.51	1.46
5	C	203	F8N	C2-N16	-3.26	1.27	1.34
2	A	201	GNP	PB-N3B	3.25	1.71	1.63
2	C	201	GNP	PG-N3B	3.11	1.71	1.63
2	C	201	GNP	PB-O3A	3.06	1.62	1.59
2	A	201	GNP	C5-C6	-3.04	1.47	1.52
2	F	201	GNP	PB-O1B	3.00	1.50	1.46
2	B	201	GNP	C6-N1	2.93	1.38	1.33
2	C	201	GNP	C8-N9	-2.86	1.35	1.45
2	E	201	GNP	PA-O2A	-2.85	1.41	1.55
5	C	203	F8N	C13-C7	2.79	1.44	1.39
5	D	203	F8N	C2-N16	-2.77	1.28	1.34
2	E	201	GNP	C2-N1	-2.76	1.32	1.44
2	D	201	GNP	C2'-C1'	-2.72	1.44	1.53
2	B	201	GNP	O2'-C2'	2.65	1.49	1.43
2	B	201	GNP	PG-O3G	-2.57	1.49	1.56
2	B	201	GNP	O6-C6	2.55	1.28	1.23
2	A	201	GNP	C2-N1	-2.54	1.33	1.44
5	F	203	F8N	C13-C17	2.50	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	GNP	C8-N9	-2.48	1.37	1.45
2	B	201	GNP	O3'-C3'	2.45	1.48	1.43
2	C	201	GNP	PB-N3B	2.43	1.69	1.63
5	B	203	F8N	C11-C6	2.42	1.44	1.39
5	D	203	F8N	C13-C17	2.35	1.43	1.38
5	F	203	F8N	C2-N16	-2.34	1.29	1.34
5	B	203	F8N	C2-N16	-2.31	1.29	1.34
5	B	203	F8N	C13-C17	2.30	1.43	1.38
2	D	201	GNP	PG-O3G	-2.26	1.50	1.56
2	B	201	GNP	O4'-C1'	2.26	1.47	1.42
2	F	201	GNP	C6-N1	2.24	1.37	1.33
2	C	201	GNP	C6-N1	2.18	1.37	1.33
2	C	201	GNP	PA-O1A	2.16	1.58	1.50
2	B	201	GNP	C8-N9	-2.12	1.38	1.45
2	A	201	GNP	PG-O3G	-2.12	1.51	1.56
2	B	201	GNP	PB-N3B	2.12	1.68	1.63
5	B	203	F8N	C11-C14	2.12	1.42	1.39
2	B	201	GNP	PB-O2B	-2.11	1.51	1.56
2	C	201	GNP	PA-O2A	-2.08	1.45	1.55
2	F	201	GNP	C2-N1	-2.07	1.35	1.44
2	D	201	GNP	PB-N3B	2.03	1.68	1.63

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	204	CIT	C4-C3-C2	6.92	127.85	109.33
5	B	203	F8N	C27-N16-C2	6.58	134.12	122.12
2	D	201	GNP	O1G-PG-N3B	-5.76	103.29	111.77
2	A	201	GNP	C4-C5-N7	5.61	109.90	102.46
2	A	201	GNP	O1G-PG-N3B	-5.46	103.74	111.77
5	D	203	F8N	C27-N16-C2	5.00	131.25	122.12
2	C	201	GNP	C4-C5-N7	4.96	109.03	102.46
2	B	201	GNP	O6-C6-N1	-4.77	116.29	122.69
2	D	201	GNP	O6-C6-N1	-4.56	116.56	122.69
2	B	201	GNP	O6-C6-C5	4.40	128.84	119.86
2	B	201	GNP	O1G-PG-N3B	-4.35	105.36	111.77
2	B	201	GNP	O2G-PG-O1G	-4.31	102.61	113.45
2	B	201	GNP	C4-C5-N7	4.31	108.17	102.46
5	F	203	F8N	C1-C2-N16	4.25	121.51	117.46
2	E	201	GNP	O3G-PG-O1G	-4.23	102.81	113.45
5	C	203	F8N	C1-C8-C14	-4.22	110.42	116.29
2	C	201	GNP	O1B-PB-N3B	4.21	117.98	111.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	203	F8N	C8-C14-C28	-4.10	115.59	121.07
5	C	203	F8N	C27-N16-C2	3.88	129.20	122.12
2	F	201	GNP	C4-C5-N7	3.84	107.55	102.46
2	C	201	GNP	O3G-PG-O2G	3.72	117.54	107.64
5	F	203	F8N	C27-N16-C2	3.65	128.78	122.12
2	F	201	GNP	O3G-PG-O1G	-3.22	105.36	113.45
2	F	201	GNP	C3'-C2'-C1'	3.21	107.53	101.43
2	B	201	GNP	O3'-C3'-C4'	-3.19	101.83	111.05
2	C	201	GNP	O1G-PG-N3B	-3.18	107.09	111.77
5	F	203	F8N	C32-O22-C17	3.13	124.30	117.51
2	B	201	GNP	O2B-PB-O1B	3.06	116.33	109.92
2	A	201	GNP	C5-C6-N1	-3.02	114.46	118.19
5	B	203	F8N	C8-C14-C11	3.00	124.00	120.34
2	D	201	GNP	C4-C5-N7	2.97	106.39	102.46
2	C	201	GNP	O2G-PG-O1G	-2.96	106.02	113.45
4	A	204	CIT	C3-C2-C1	2.91	119.64	114.98
5	B	203	F8N	C20-C1-C2	-2.90	105.43	111.08
2	C	201	GNP	O4'-C1'-N9	-2.88	104.76	109.04
5	B	203	F8N	C24-C6-C7	-2.81	116.49	121.36
2	E	201	GNP	O1B-PB-N3B	-2.75	107.72	111.77
2	D	201	GNP	O4'-C1'-N9	-2.74	104.96	109.04
2	F	201	GNP	O6-C6-N1	-2.73	119.03	122.69
2	B	201	GNP	O3A-PB-N3B	-2.71	99.06	106.59
2	B	201	GNP	C5-C6-N1	-2.69	114.88	118.19
2	C	201	GNP	O3G-PG-O1G	-2.67	106.73	113.45
5	B	203	F8N	C11-C6-C7	2.63	125.22	120.86
2	E	201	GNP	C4-C5-N7	2.61	105.91	102.46
5	C	203	F8N	O15-C29-C20	2.59	114.31	111.56
2	B	201	GNP	O3G-PG-O2G	2.57	114.48	107.64
2	F	201	GNP	O4'-C1'-C2'	-2.56	101.07	106.64
5	C	203	F8N	C20-C1-C8	2.52	115.00	109.84
2	F	201	GNP	O2G-PG-O1G	-2.48	107.23	113.45
4	D	204	CIT	C3-C2-C1	-2.47	111.04	114.98
2	F	201	GNP	C4'-O4'-C1'	2.43	114.84	109.47
2	F	201	GNP	O3'-C3'-C4'	-2.42	104.04	111.05
5	C	203	F8N	C29-O15-C30	2.32	117.65	109.89
2	A	201	GNP	O2B-PB-O1B	2.28	114.69	109.92
2	D	201	GNP	O6-C6-C5	2.27	124.49	119.86
5	D	203	F8N	C29-O15-C30	2.24	117.38	109.89
4	A	204	CIT	C3-C4-C5	2.23	118.56	114.98
2	F	201	GNP	O4'-C4'-C5'	2.22	116.68	109.37
5	C	203	F8N	C21-C1-C2	-2.20	106.78	111.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	203	F8N	C24-C6-C7	2.17	125.12	121.36
5	B	203	F8N	C13-C7-C6	2.13	124.38	120.86
5	B	203	F8N	C23-C7-C6	-2.12	117.69	121.36
5	C	203	F8N	C8-C14-C28	-2.09	118.28	121.07
2	B	201	GNP	PA-O3A-PB	-2.08	125.29	132.62
5	C	203	F8N	O15-C30-C21	2.06	113.74	111.56
2	B	201	GNP	O2B-PB-O3A	2.01	111.37	104.64

There are no chirality outliers.

All (57) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	201	GNP	PB-N3B-PG-O1G
2	C	201	GNP	PG-N3B-PB-O1B
2	C	201	GNP	PA-O3A-PB-O2B
2	C	201	GNP	C2'-C1'-N9-C4
4	D	204	CIT	C1-C2-C3-C4
4	D	204	CIT	C2-C3-C4-C5
4	D	204	CIT	C6-C3-C4-C5
2	A	201	GNP	PG-N3B-PB-O1B
2	A	201	GNP	PA-O3A-PB-O1B
2	A	201	GNP	PA-O3A-PB-O2B
2	A	201	GNP	C2'-C1'-N9-C4
5	B	203	F8N	C2-C1-C8-C14
5	B	203	F8N	C21-C1-C8-C14
5	B	203	F8N	C20-C1-C8-C14
5	B	203	F8N	C19-C18-N4-C5
5	B	203	F8N	C19-C18-N4-C10
2	E	201	GNP	PB-N3B-PG-O1G
2	E	201	GNP	C2'-C1'-N9-C4
5	F	203	F8N	C2-C1-C8-C14
5	C	203	F8N	C2-C1-C8-C14
5	C	203	F8N	C21-C1-C8-C14
5	C	203	F8N	C20-C1-C8-C14
2	B	201	GNP	PG-N3B-PB-O1B
2	B	201	GNP	PG-N3B-PB-O3A
2	B	201	GNP	PA-O3A-PB-O1B
2	B	201	GNP	PA-O3A-PB-O2B
2	B	201	GNP	C2'-C1'-N9-C4
2	D	201	GNP	PG-N3B-PB-O1B
2	D	201	GNP	PA-O3A-PB-O1B
2	D	201	GNP	PA-O3A-PB-O2B

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Mol	Chain	Res	Type	Atoms
2	D	201	GNP	C2'-C1'-N9-C4
2	F	201	GNP	PB-N3B-PG-O1G
2	F	201	GNP	PG-N3B-PB-O1B
2	F	201	GNP	PA-O3A-PB-O1B
2	F	201	GNP	PA-O3A-PB-O2B
2	F	201	GNP	O4'-C1'-N9-C4
2	F	201	GNP	C2'-C1'-N9-C4
5	C	203	F8N	C31-C17-O22-C32
5	C	203	F8N	C13-C17-O22-C32
5	F	203	F8N	C13-C17-O22-C32
5	F	203	F8N	C31-C17-O22-C32
5	C	203	F8N	C18-C19-C27-N16
5	F	203	F8N	N4-C18-C19-C27
5	D	203	F8N	N4-C18-C19-C27
5	C	203	F8N	N4-C18-C19-C27
4	D	204	CIT	O7-C3-C4-C5
5	D	203	F8N	C19-C18-N4-C5
5	D	203	F8N	C19-C18-N4-C10
5	D	203	F8N	C31-C17-O22-C32
5	D	203	F8N	C13-C17-O22-C32
5	D	203	F8N	C18-C19-C27-N16
2	A	201	GNP	PG-N3B-PB-O3A
2	F	201	GNP	PG-N3B-PB-O3A
5	F	203	F8N	C11-C6-C7-C23
5	F	203	F8N	C21-C1-C8-C14
5	F	203	F8N	C20-C1-C8-C14
5	F	203	F8N	C24-C6-C7-C23

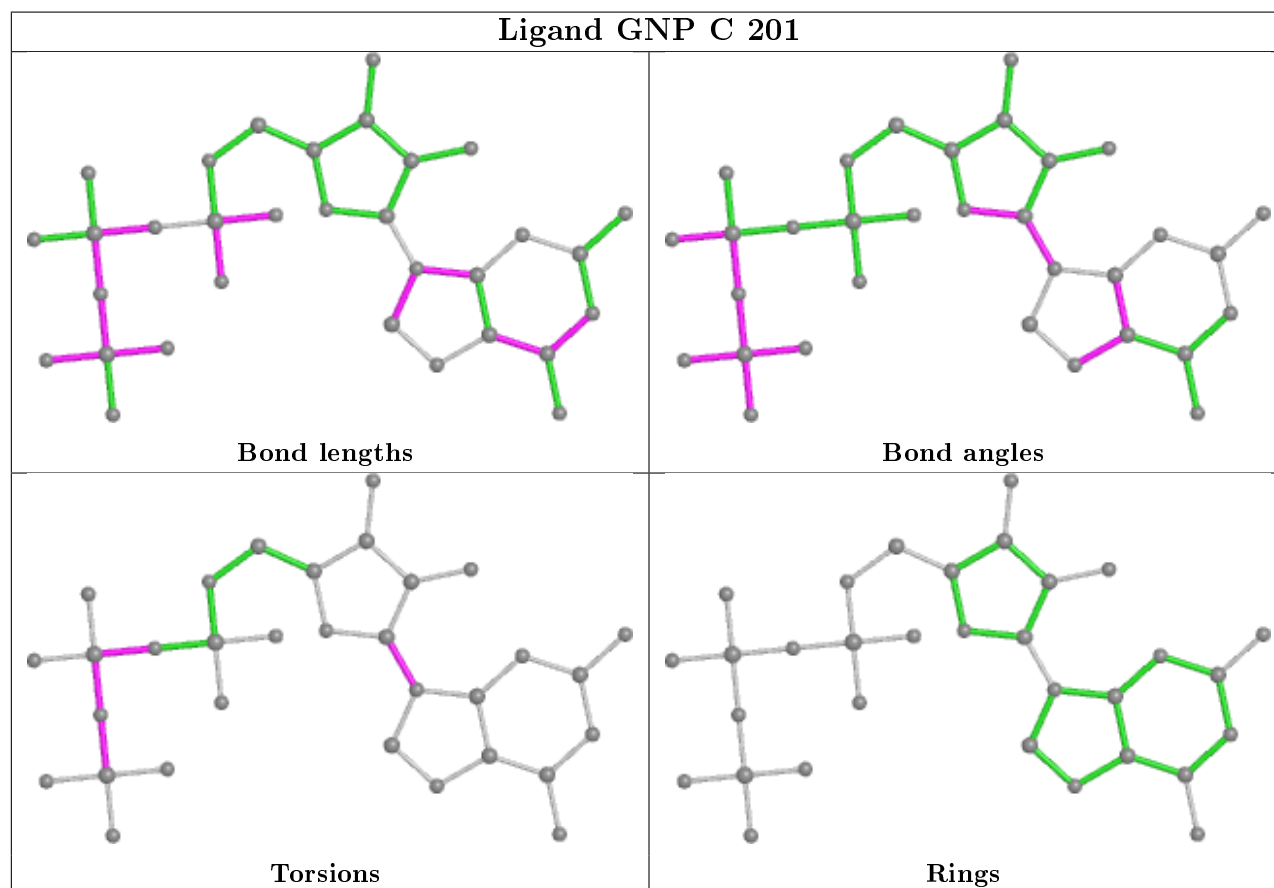
All (3) ring outliers are listed below:

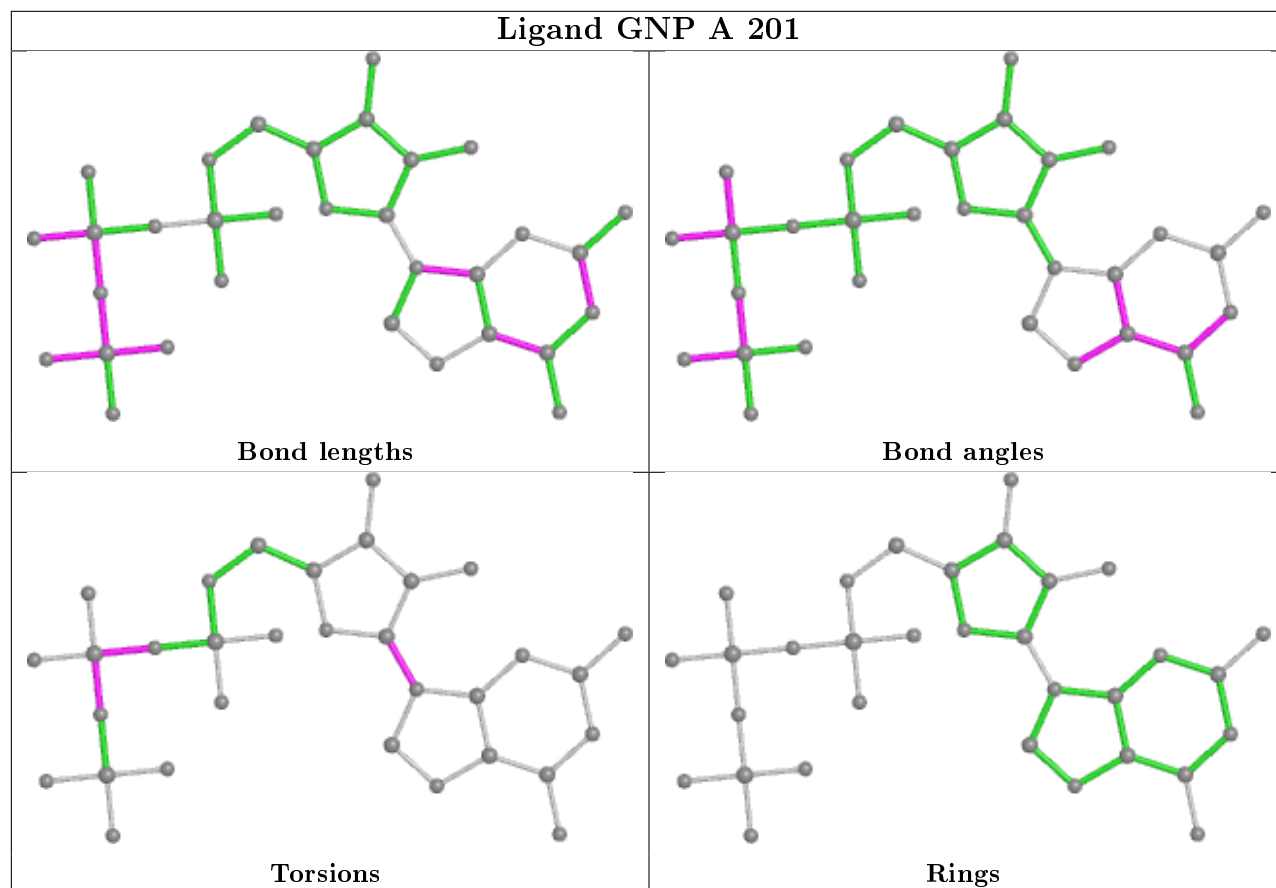
Mol	Chain	Res	Type	Atoms
5	C	203	F8N	C1-C20-C21-C29-C30-O15
5	D	203	F8N	C1-C20-C21-C29-C30-O15
5	F	203	F8N	C1-C20-C21-C29-C30-O15

3 monomers are involved in 3 short contacts:

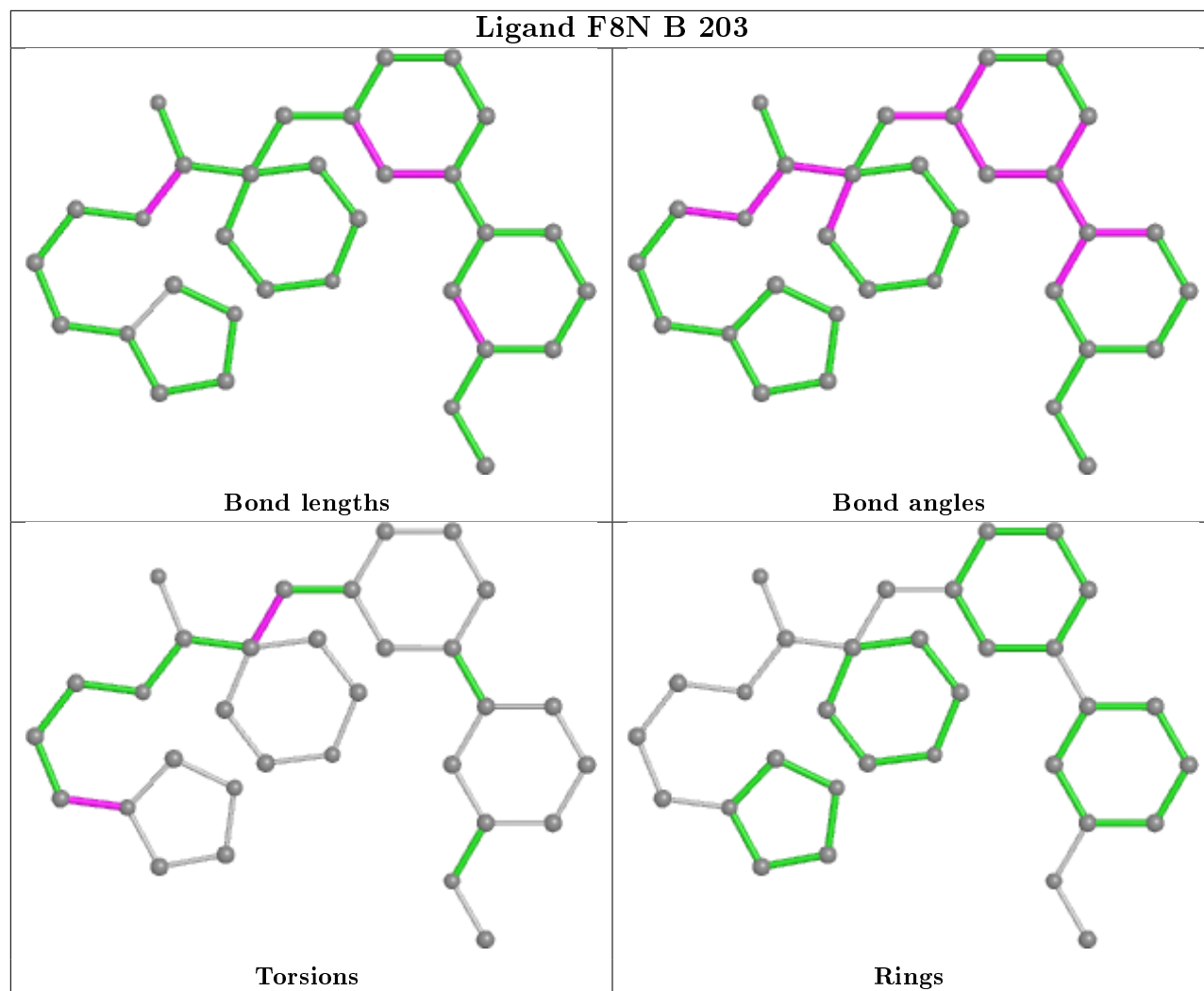
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	203	F8N	1	0
5	F	203	F8N	1	0
5	D	203	F8N	1	0

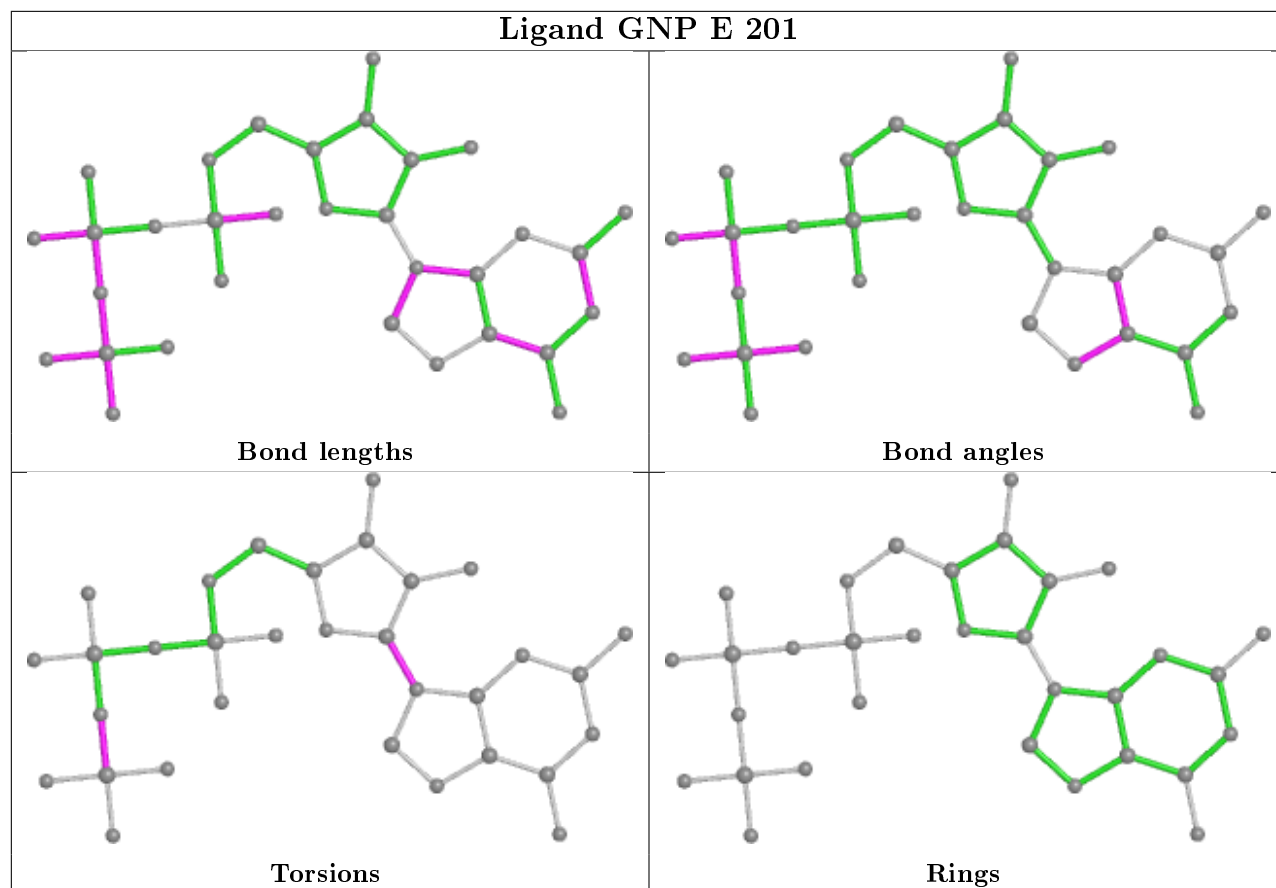
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



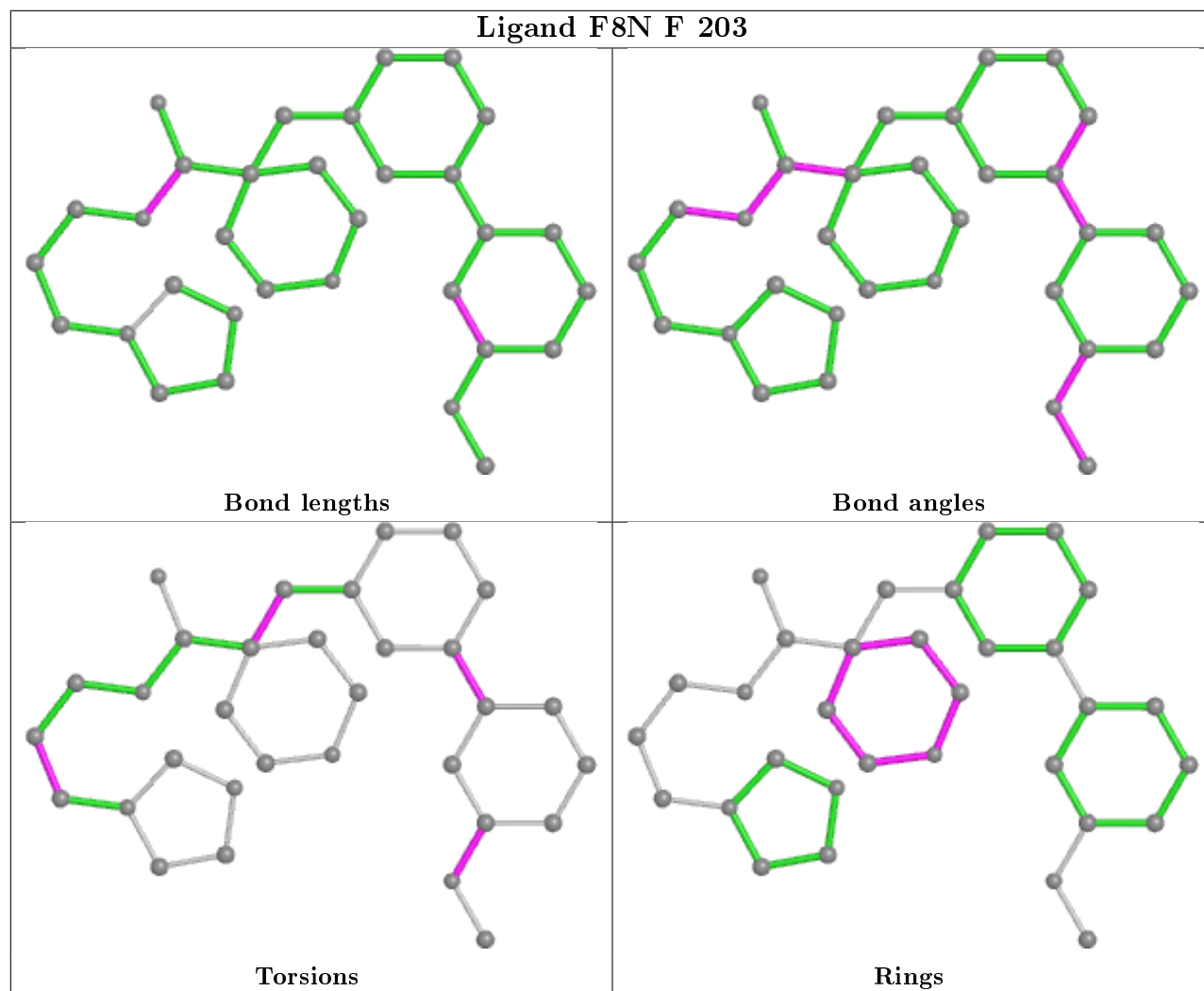


Ligand F8N B 203

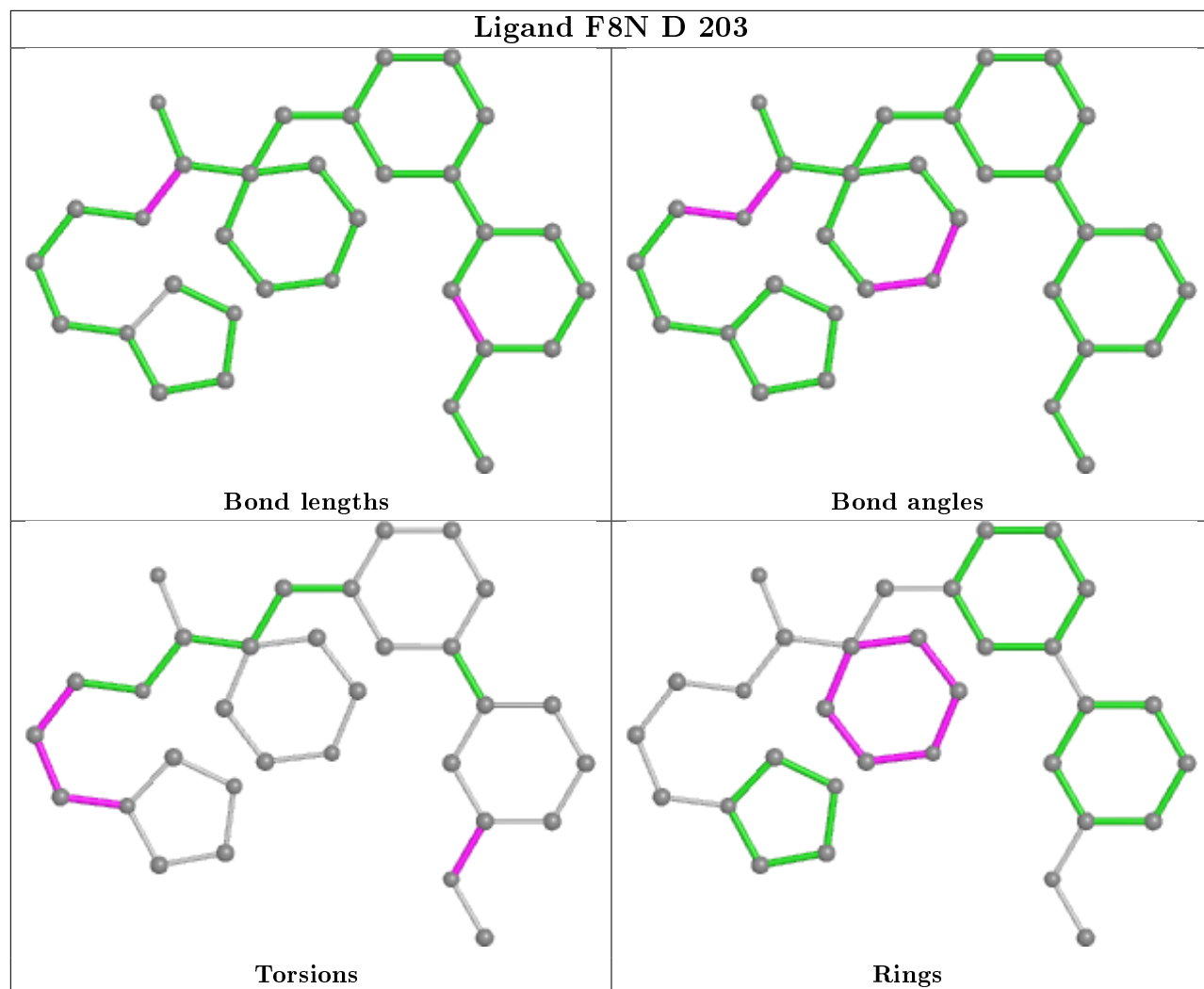




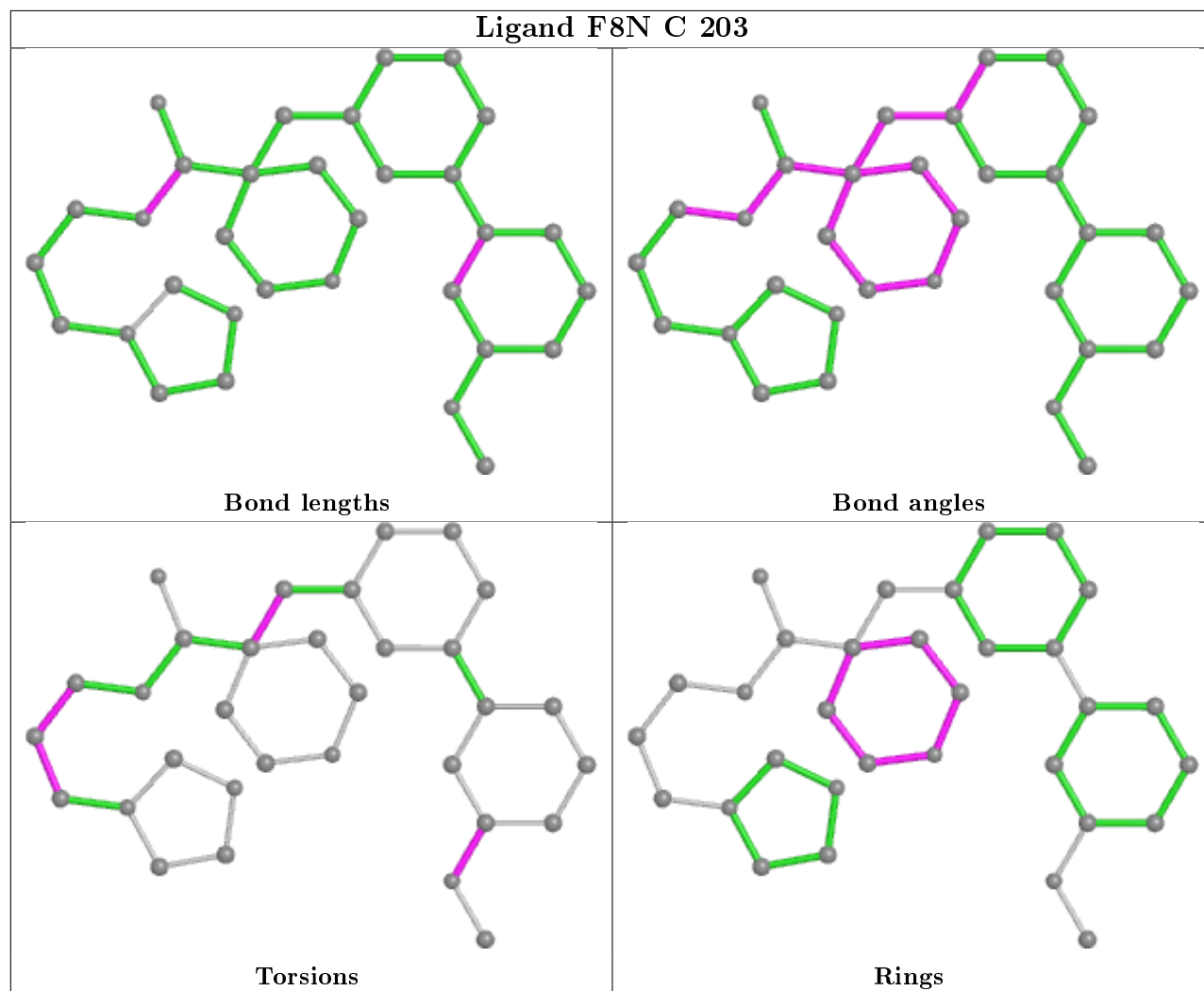
Ligand F8N F 203

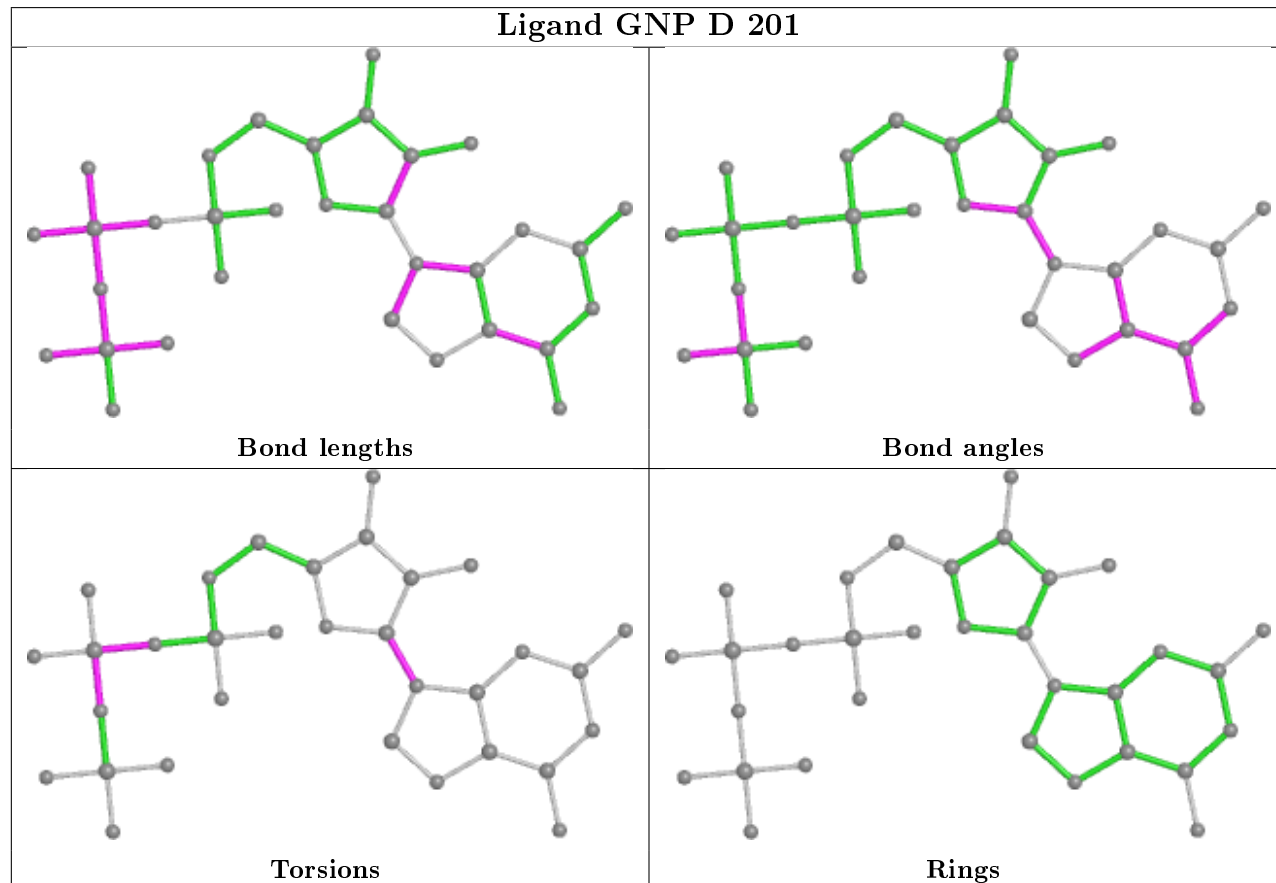
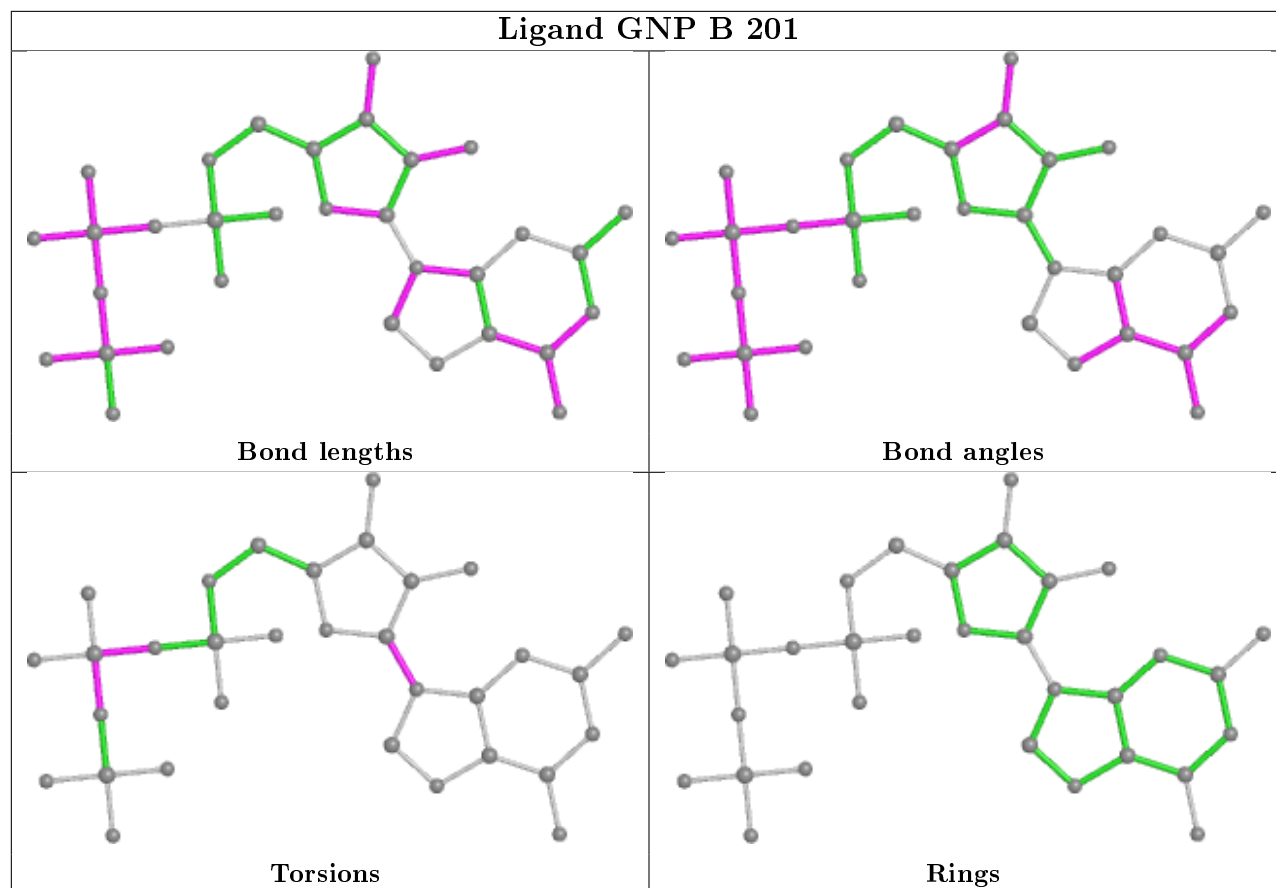


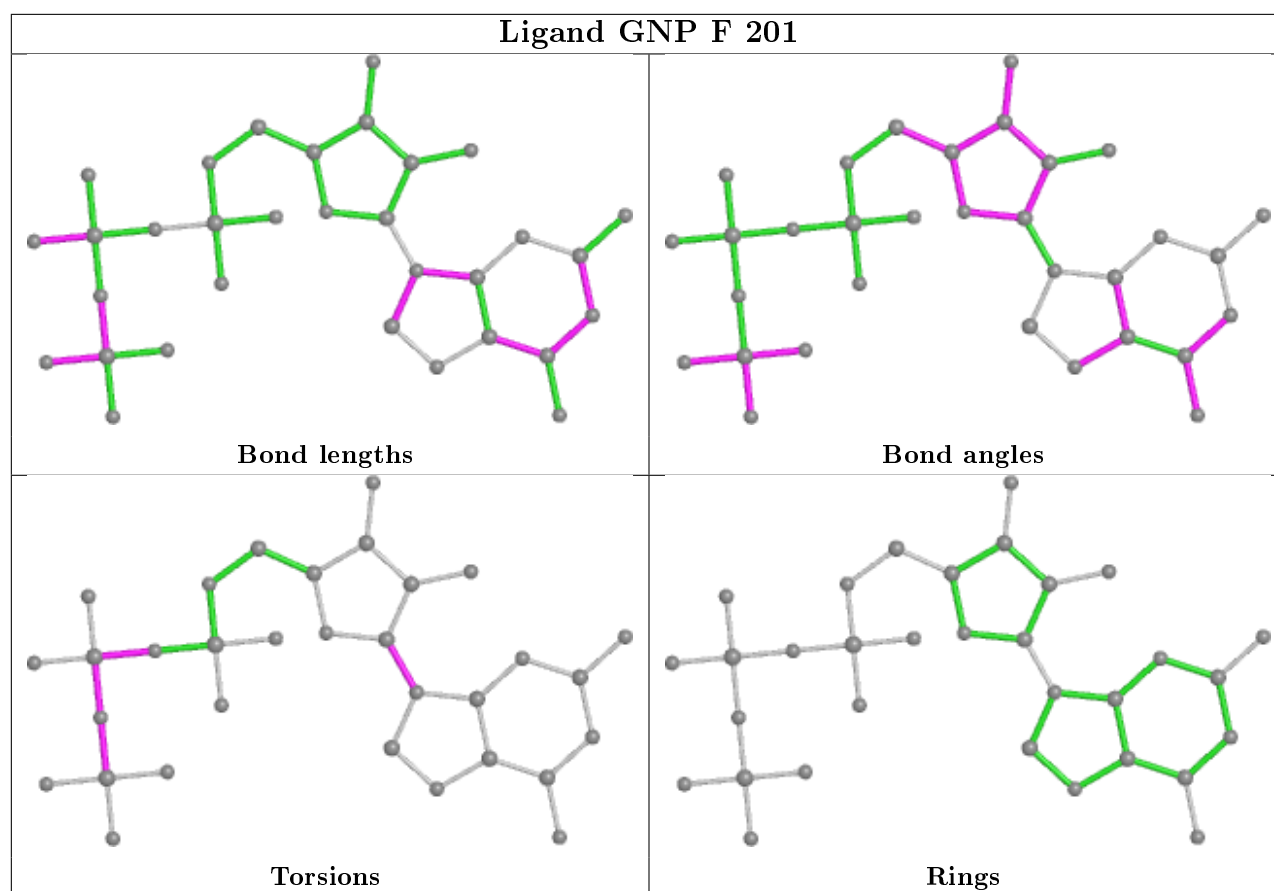
Ligand F8N D 203



Ligand F8N C 203







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	171/171 (100%)	0.13	5 (2%)	51	56	15, 23, 52, 86	0
1	B	171/171 (100%)	0.13	3 (1%)	68	72	17, 27, 61, 103	0
1	C	159/171 (92%)	0.18	8 (5%)	28	32	22, 35, 64, 76	0
1	D	160/171 (93%)	0.28	8 (5%)	28	32	19, 36, 75, 133	0
1	E	164/171 (95%)	0.16	13 (7%)	12	14	24, 37, 76, 92	0
1	F	158/171 (92%)	-0.09	3 (1%)	66	70	18, 28, 64, 83	0
All	All	983/1026 (95%)	0.13	40 (4%)	37	41	15, 31, 68, 133	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	71	TYR	11.5
1	C	32	TYR	10.6
1	E	32	TYR	6.5
1	D	66	ALA	5.3
1	E	36	ILE	5.3
1	A	-1	GLN	5.1
1	E	71	TYR	4.8
1	A	61	HIS	4.5
1	E	33	ASP	4.5
1	D	-2	PHE	4.2
1	C	71	TYR	3.9
1	D	68	ARG	3.9
1	E	34	PRO	3.9
1	E	35	THR	3.8
1	D	72	MET	3.8
1	A	-2	PHE	3.7
1	B	103	VAL	3.6
1	F	59	ALA	3.5
1	E	-2	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
1	E	59	ALA	3.1
1	A	64	TYR	3.0
1	D	37	GLU	3.0
1	D	-1	GLN	2.9
1	C	1	MET	2.8
1	E	72	MET	2.6
1	C	59	ALA	2.6
1	B	0	GLY	2.6
1	E	0	GLY	2.5
1	F	-2	PHE	2.5
1	C	69	ASP	2.4
1	A	0	GLY	2.4
1	E	60	GLY	2.4
1	E	122	SER	2.3
1	C	67	MET	2.3
1	C	95	HIS	2.3
1	C	126	ASP	2.3
1	D	67	MET	2.2
1	F	71	TYR	2.1
1	E	68	ARG	2.1
1	B	-1	GLN	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [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(\AA^2)	Q<0.9
5	F8N	D	203	32/32	0.69	0.40	53,124,171,175	0
3	MG	F	202	1/1	0.71	0.21	61,61,61,61	0

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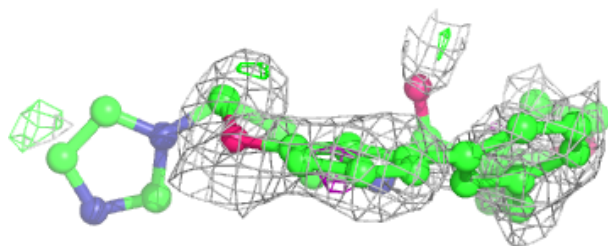
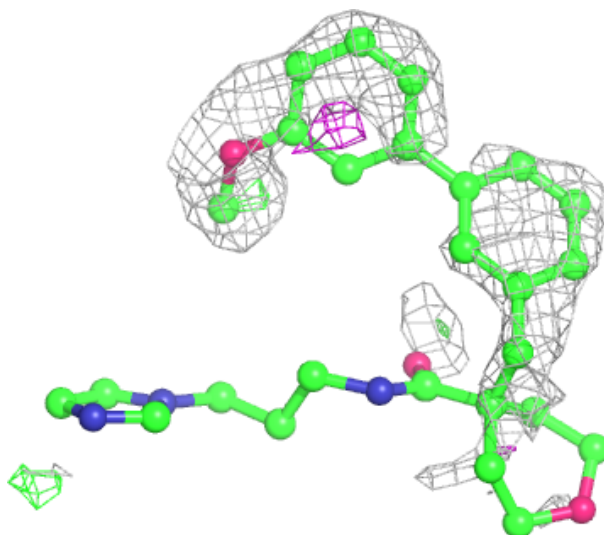
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	D	202	1/1	0.75	0.52	73,73,73,73	0
5	F8N	F	203	32/32	0.78	0.42	44,110,152,153	0
5	F8N	B	203	32/32	0.78	0.33	42,105,146,151	0
4	CIT	A	203	13/13	0.79	0.16	40,49,64,71	0
3	MG	C	202	1/1	0.81	0.23	57,57,57,57	0
5	F8N	C	203	32/32	0.82	0.28	37,85,134,137	0
4	CIT	D	204	13/13	0.84	0.20	62,83,113,114	0
3	MG	E	202	1/1	0.91	0.30	54,54,54,54	0
2	GNP	C	201	32/32	0.94	0.09	26,32,54,61	0
2	GNP	D	201	32/32	0.95	0.09	26,34,62,69	0
2	GNP	E	201	32/32	0.96	0.08	27,32,49,54	0
4	CIT	A	204	13/13	0.96	0.09	23,29,33,35	0
2	GNP	F	201	32/32	0.97	0.08	20,26,44,54	0
3	MG	B	202	1/1	0.98	0.04	25,25,25,25	0
2	GNP	B	201	32/32	0.99	0.09	16,19,25,25	0
2	GNP	A	201	32/32	0.99	0.08	16,17,20,20	0
3	MG	A	202	1/1	1.00	0.10	17,17,17,17	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.

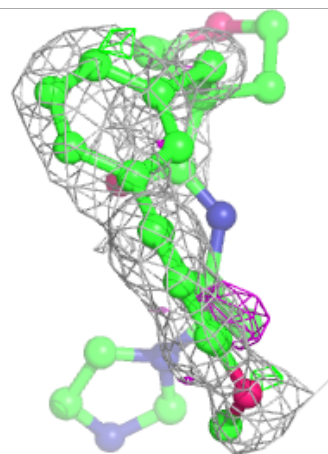
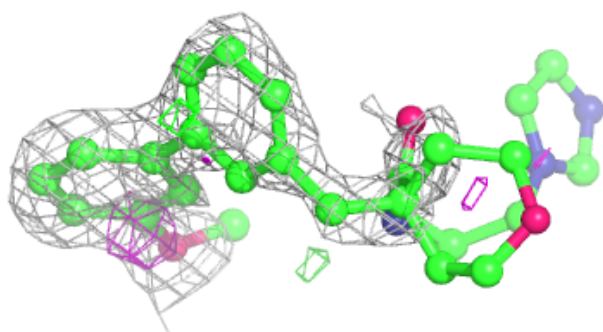
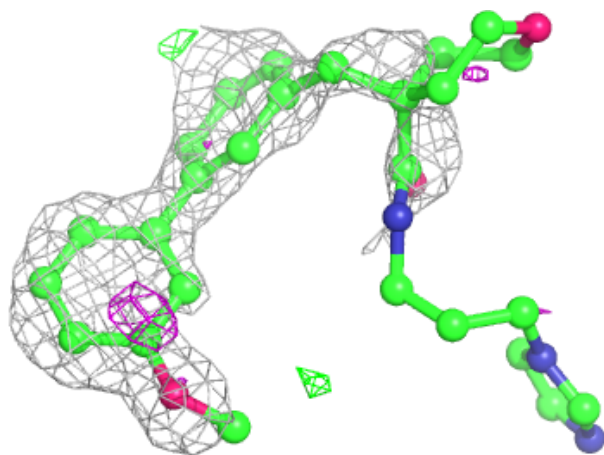
Electron density around F8N D 203:

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



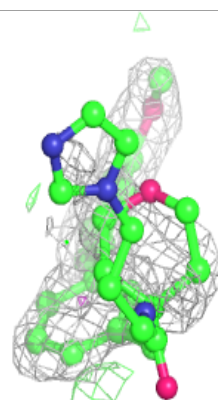
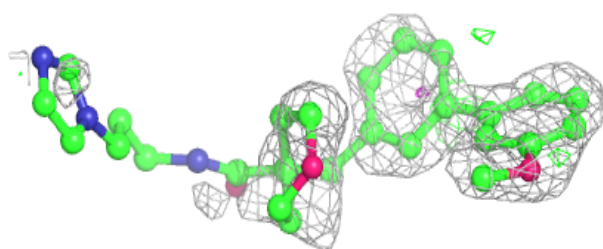
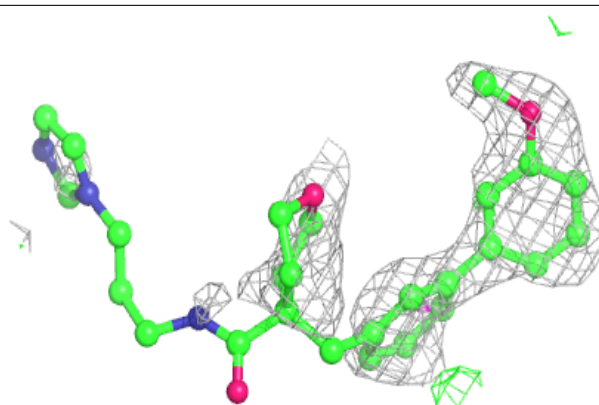
Electron density around F8N F 203:

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

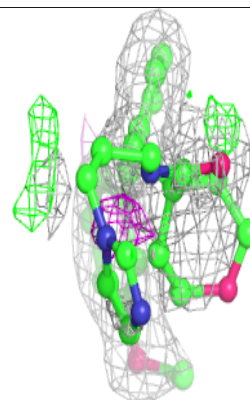
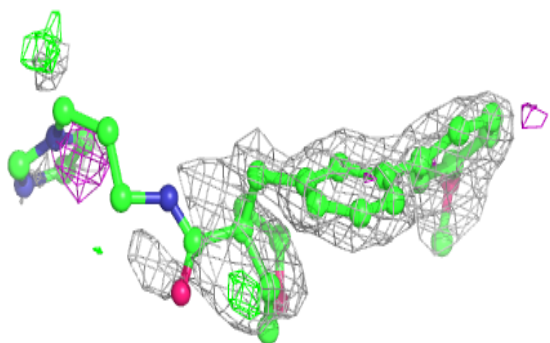
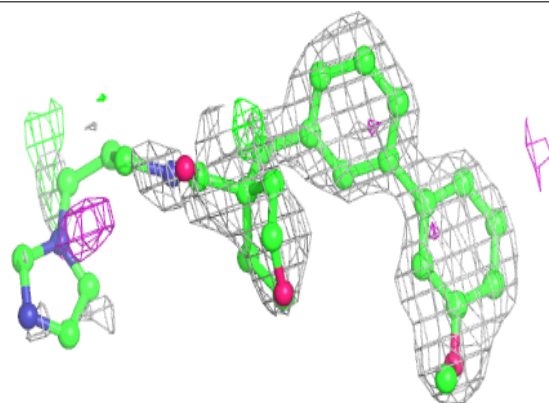


Electron density around F8N B 203:

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

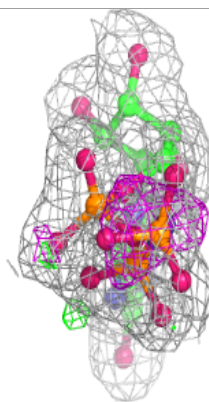
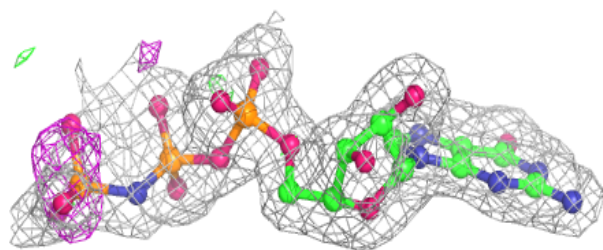
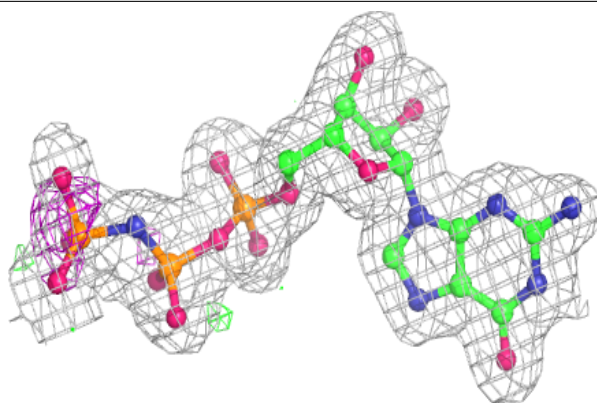
**Electron density around F8N C 203:**

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

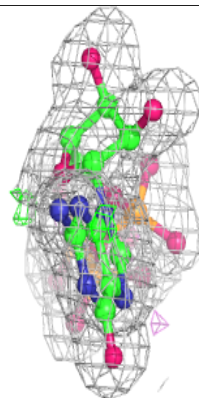
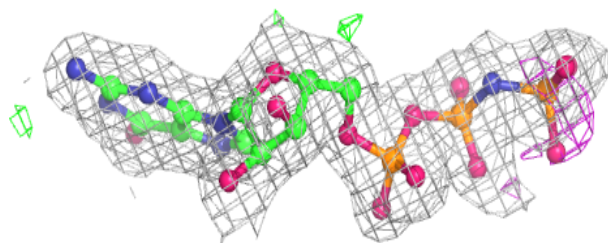
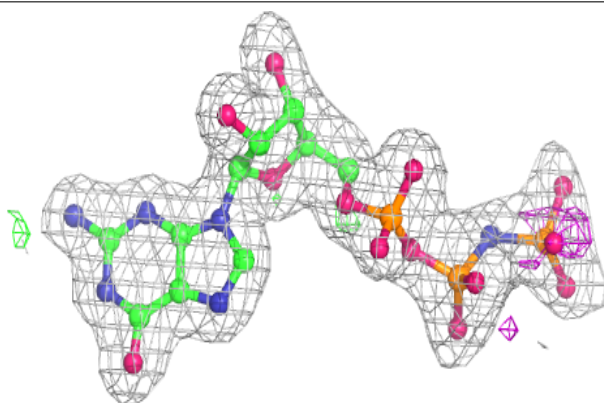


Electron density around GNP C 201:

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

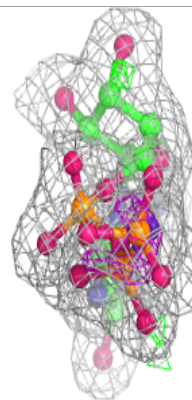
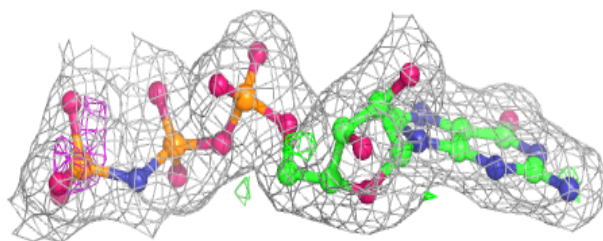
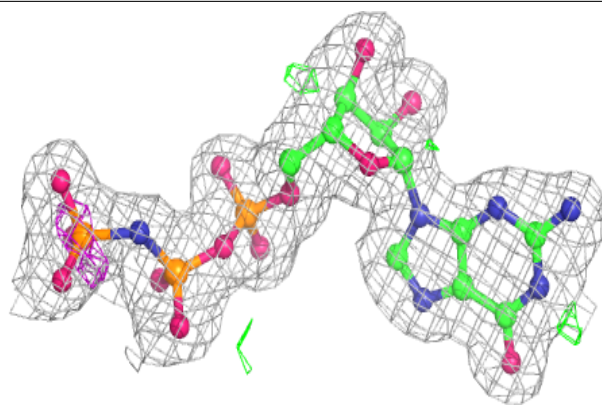
**Electron density around GNP D 201:**

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

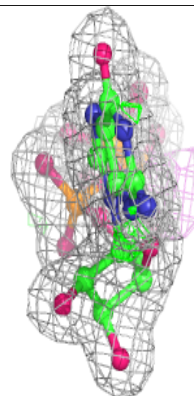
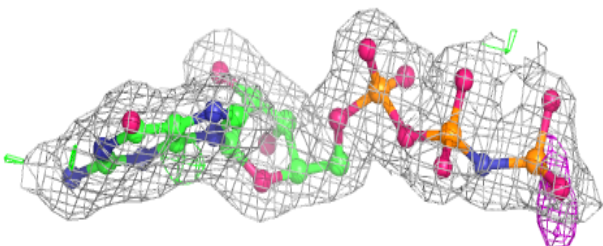
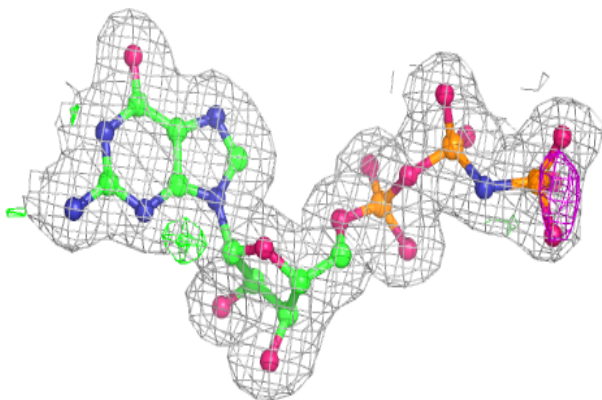


Electron density around GNP E 201:

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

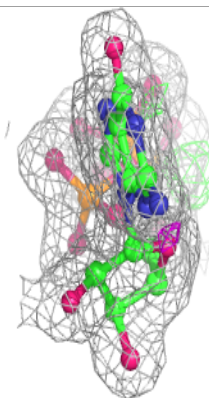
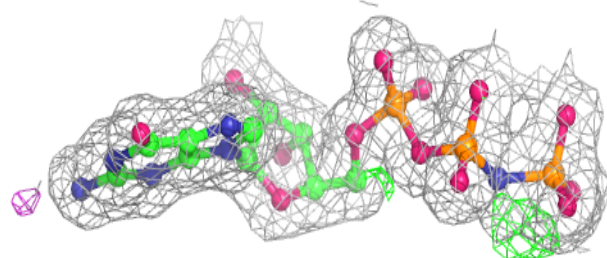
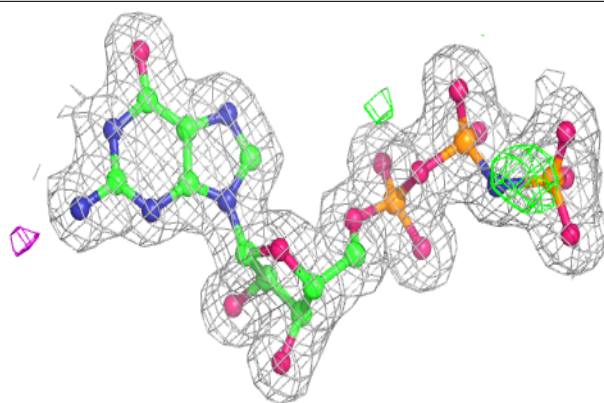
**Electron density around GNP F 201:**

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

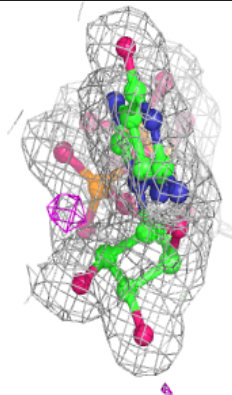
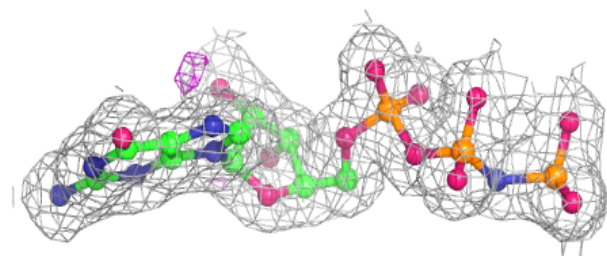
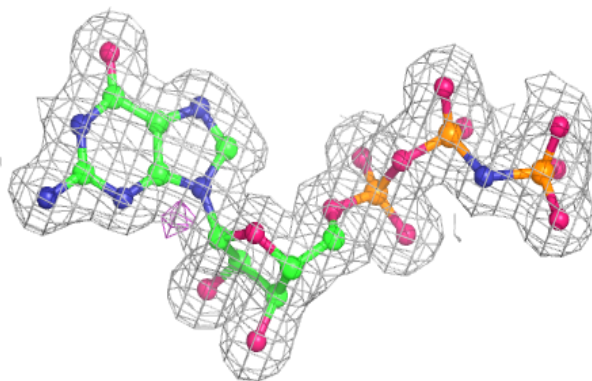


Electron density around GNP B 201:

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

**Electron density around GNP A 201:**

$2mF_o-DF_c$ (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.