wwPDB X-ray Structure Validation Summary Report (i)

Jan 8, 2024 – 06:34 am GMT

PDB ID	:	5OCO
Title	:	Discovery of small molecules binding to KRAS via high affinity antibody fragment competition method.
Authors	:	Cruz-Migoni, A.; Ehebauer, M.T.; Phillips, S.E.V.; Quevedo, C.E.; Rabbitts, T.H.
Deposited on	:	2017-07-03
Resolution	:	1.66 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 (i) 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 (i)) were used in the production of this report:

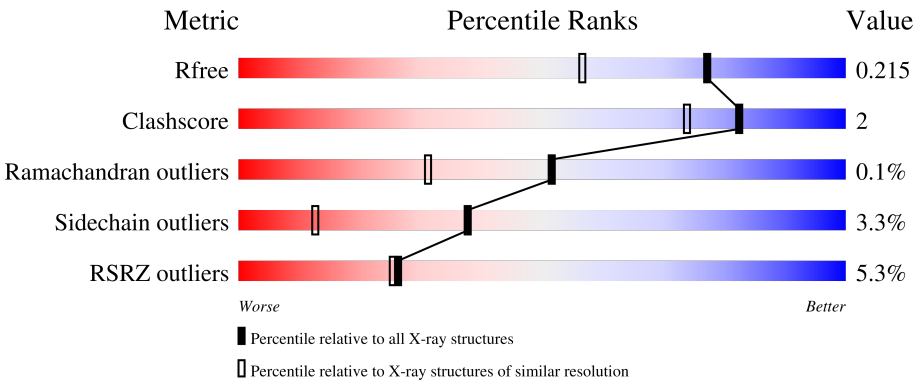
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.66 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	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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 <=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	2%, 80%, 8%, •, 8%
1	B	187	%, 80%, 10%, • •, 7%
1	C	187	3%, 82%, 7%, •, 8%
1	D	187	9%, 82%, 9%, •, 8%

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Mol	Chain	Length	Quality of chain
1	E	187	6% 80% 10% • 7%
1	F	187	8% 79% 10% •• 8%

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	9RK	D	202	-	-	-	X
3	9RK	E	202	-	-	-	X
6	CIT	A	203	-	X	-	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 9234 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
			Total	C	N	O	S			
1	B	173	1382	868	238	269	7	0	1	0
1	A	172	1385	868	237	273	7	0	2	0
1	C	172	1374	860	237	270	7	0	2	0
1	D	172	1402	877	240	278	7	0	4	0
1	E	173	1395	872	241	275	7	0	3	0
1	F	172	1403	876	241	278	8	0	5	0

There are 114 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	MET	-	initiating methionine	UNP P01116
B	-16	HIS	-	expression tag	UNP P01116
B	-15	HIS	-	expression tag	UNP P01116
B	-14	HIS	-	expression tag	UNP P01116
B	-13	HIS	-	expression tag	UNP P01116
B	-12	HIS	-	expression tag	UNP P01116
B	-11	HIS	-	expression tag	UNP P01116
B	-10	SER	-	expression tag	UNP P01116
B	-9	SER	-	expression tag	UNP P01116
B	-8	GLY	-	expression tag	UNP P01116
B	-7	ARG	-	expression tag	UNP P01116
B	-6	GLU	-	expression tag	UNP P01116
B	-5	ASN	-	expression tag	UNP P01116
B	-4	LEU	-	expression tag	UNP P01116
B	-3	TYR	-	expression tag	UNP P01116
B	-2	PHE	-	expression tag	UNP P01116
B	-1	GLN	-	expression tag	UNP P01116

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP P01116
B	61	HIS	GLN	engineered mutation	UNP P01116
A	-17	MET	-	initiating methionine	UNP P01116
A	-16	HIS	-	expression tag	UNP P01116
A	-15	HIS	-	expression tag	UNP P01116
A	-14	HIS	-	expression tag	UNP P01116
A	-13	HIS	-	expression tag	UNP P01116
A	-12	HIS	-	expression tag	UNP P01116
A	-11	HIS	-	expression tag	UNP P01116
A	-10	SER	-	expression tag	UNP P01116
A	-9	SER	-	expression tag	UNP P01116
A	-8	GLY	-	expression tag	UNP P01116
A	-7	ARG	-	expression tag	UNP P01116
A	-6	GLU	-	expression tag	UNP P01116
A	-5	ASN	-	expression tag	UNP P01116
A	-4	LEU	-	expression tag	UNP P01116
A	-3	TYR	-	expression tag	UNP P01116
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
C	-17	MET	-	initiating methionine	UNP P01116
C	-16	HIS	-	expression tag	UNP P01116
C	-15	HIS	-	expression tag	UNP P01116
C	-14	HIS	-	expression tag	UNP P01116
C	-13	HIS	-	expression tag	UNP P01116
C	-12	HIS	-	expression tag	UNP P01116
C	-11	HIS	-	expression tag	UNP P01116
C	-10	SER	-	expression tag	UNP P01116
C	-9	SER	-	expression tag	UNP P01116
C	-8	GLY	-	expression tag	UNP P01116
C	-7	ARG	-	expression tag	UNP P01116
C	-6	GLU	-	expression tag	UNP P01116
C	-5	ASN	-	expression tag	UNP P01116
C	-4	LEU	-	expression tag	UNP P01116
C	-3	TYR	-	expression tag	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	-17	MET	-	initiating methionine	UNP P01116
D	-16	HIS	-	expression tag	UNP P01116

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-15	HIS	-	expression tag	UNP P01116
D	-14	HIS	-	expression tag	UNP P01116
D	-13	HIS	-	expression tag	UNP P01116
D	-12	HIS	-	expression tag	UNP P01116
D	-11	HIS	-	expression tag	UNP P01116
D	-10	SER	-	expression tag	UNP P01116
D	-9	SER	-	expression tag	UNP P01116
D	-8	GLY	-	expression tag	UNP P01116
D	-7	ARG	-	expression tag	UNP P01116
D	-6	GLU	-	expression tag	UNP P01116
D	-5	ASN	-	expression tag	UNP P01116
D	-4	LEU	-	expression tag	UNP P01116
D	-3	TYR	-	expression tag	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	-17	MET	-	initiating methionine	UNP P01116
E	-16	HIS	-	expression tag	UNP P01116
E	-15	HIS	-	expression tag	UNP P01116
E	-14	HIS	-	expression tag	UNP P01116
E	-13	HIS	-	expression tag	UNP P01116
E	-12	HIS	-	expression tag	UNP P01116
E	-11	HIS	-	expression tag	UNP P01116
E	-10	SER	-	expression tag	UNP P01116
E	-9	SER	-	expression tag	UNP P01116
E	-8	GLY	-	expression tag	UNP P01116
E	-7	ARG	-	expression tag	UNP P01116
E	-6	GLU	-	expression tag	UNP P01116
E	-5	ASN	-	expression tag	UNP P01116
E	-4	LEU	-	expression tag	UNP P01116
E	-3	TYR	-	expression tag	UNP P01116
E	-2	PHE	-	expression tag	UNP P01116
E	-1	GLN	-	expression tag	UNP P01116
E	0	GLY	-	expression tag	UNP P01116
E	61	HIS	GLN	engineered mutation	UNP P01116
F	-17	MET	-	initiating methionine	UNP P01116
F	-16	HIS	-	expression tag	UNP P01116
F	-15	HIS	-	expression tag	UNP P01116
F	-14	HIS	-	expression tag	UNP P01116
F	-13	HIS	-	expression tag	UNP P01116
F	-12	HIS	-	expression tag	UNP P01116

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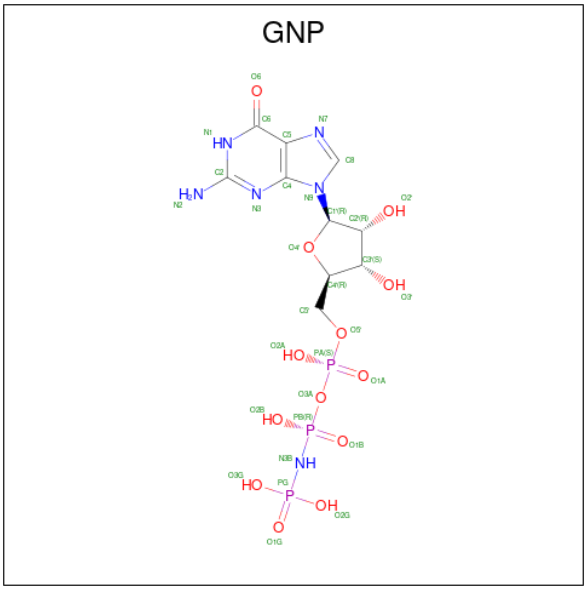
Chain	Residue	Modelled	Actual	Comment	Reference
F	-11	HIS	-	expression tag	UNP P01116
F	-10	SER	-	expression tag	UNP P01116
F	-9	SER	-	expression tag	UNP P01116
F	-8	GLY	-	expression tag	UNP P01116
F	-7	ARG	-	expression tag	UNP P01116
F	-6	GLU	-	expression tag	UNP P01116
F	-5	ASN	-	expression tag	UNP P01116
F	-4	LEU	-	expression tag	UNP P01116
F	-3	TYR	-	expression tag	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
			Total	C	N	O	P		
2	B	1	32	10	6	13	3	0	0
			Total	C	N	O	P		
2	A	1	32	10	6	13	3	0	0
			Total	C	N	O	P		
2	C	1	32	10	6	13	3	0	0
			Total	C	N	O	P		
2	D	1	32	10	6	13	3	0	0

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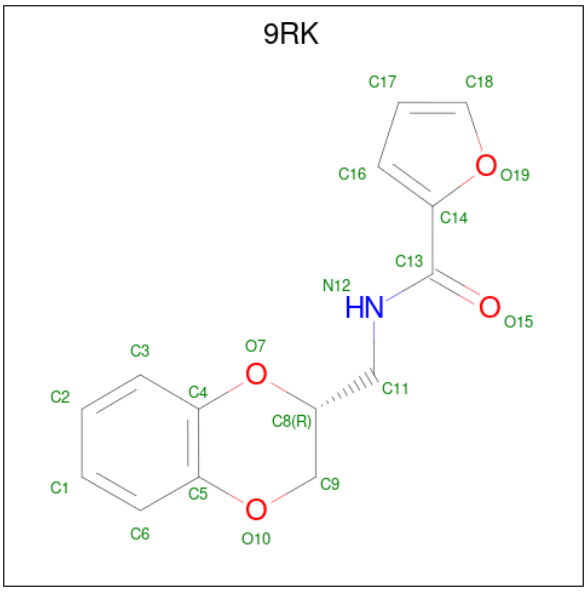
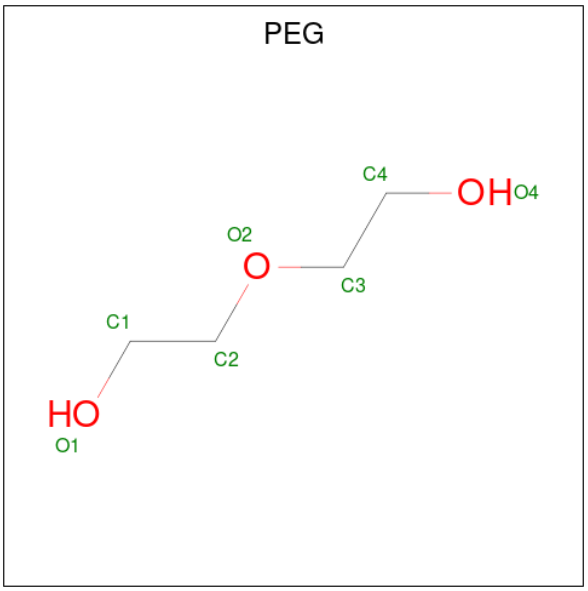
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	E	1	32	10	6	13	3	0	0
			Total	C	N	O	P		
2	F	1	32	10	6	13	3	0	0

- Molecule 3 is {N}-[[(3 {R})-2,3-dihydro-1,4-benzodioxin-3-yl]methyl]furan-2-carboxamide (three-letter code: 9RK) (formula: $C_{14}H_{13}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	B	1	19	14	1	4	0	0
			Total	C	N	O		
3	C	1	19	14	1	4	0	0
			Total	C	N	O		
3	D	1	19	14	1	4	0	0
			Total	C	N	O		
3	E	1	19	14	1	4	0	0
			Total	C	N	O		
3	F	1	19	14	1	4	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).

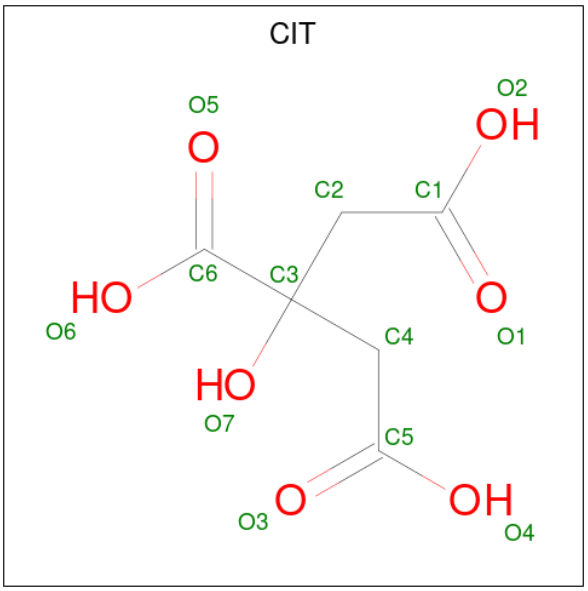


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 7 4 3	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 6 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



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

- Molecule 7 is water.

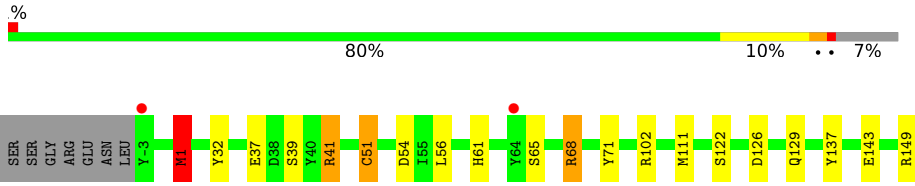
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	134	Total O 134 134	0	0
7	A	138	Total O 138 138	0	0
7	C	66	Total O 66 66	0	0
7	D	66	Total O 66 66	0	0
7	E	57	Total O 57 57	0	0
7	F	93	Total O 93 93	0	0

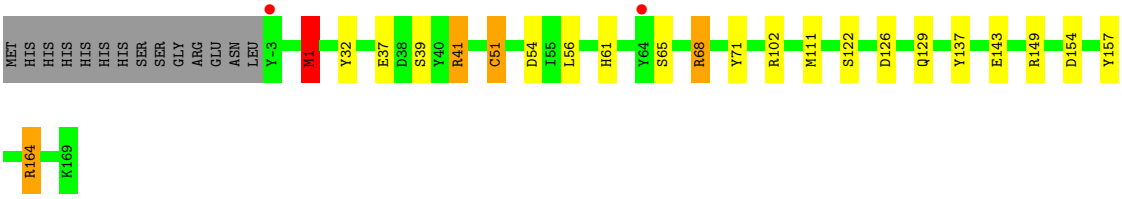
3 Residue-property plots (i)

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: GTPase KRas

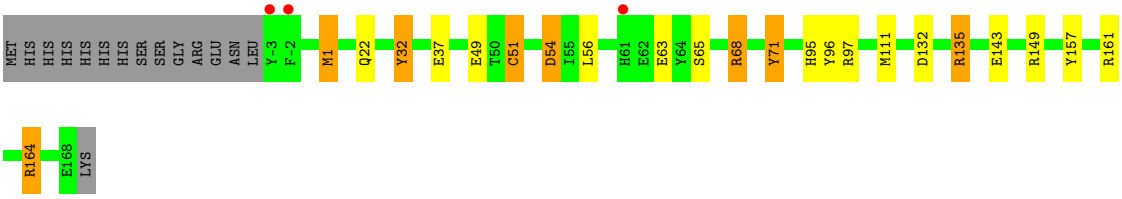
Chain B:





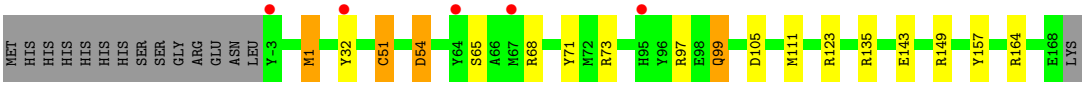
• Molecule 1: GTPase KRas

Chain A:



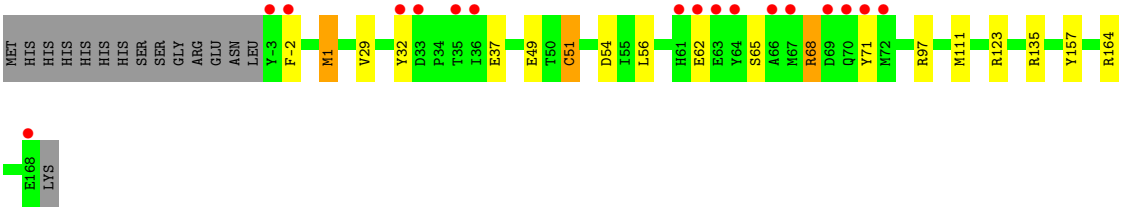
• Molecule 1: GTPase KRas

Chain C:



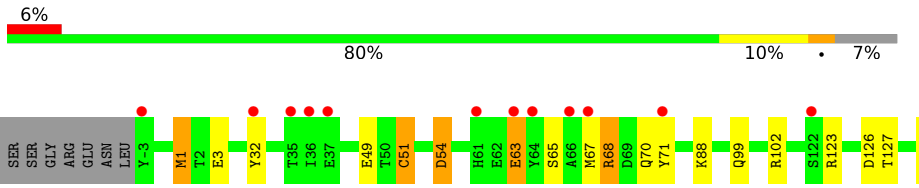
• Molecule 1: GTPase KRas

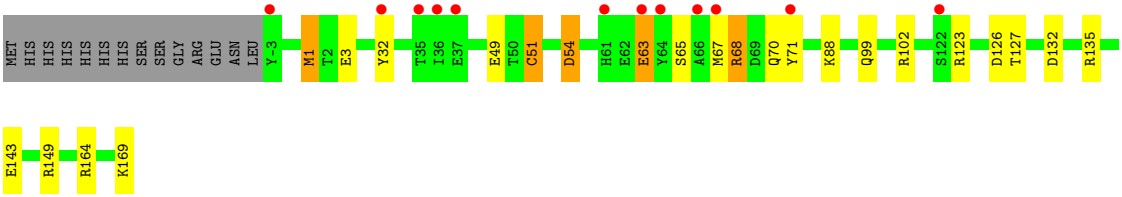
Chain D:



- Molecule 1: GTPase KRas

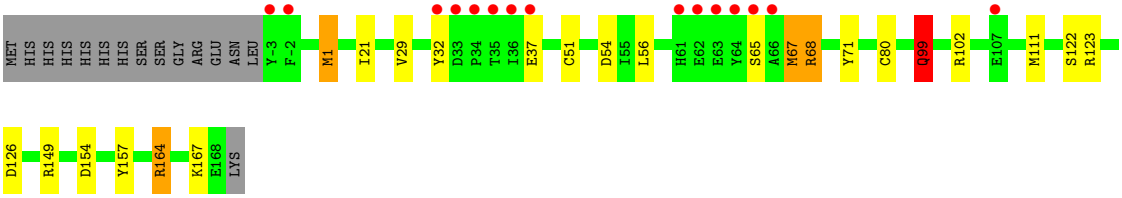
Chain E:





- Molecule 1: GTPase KRas

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	63.60Å 118.76Å 156.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.38 – 1.66 59.38 – 1.66	Depositor EDS
% Data completeness (in resolution range)	100.0 (59.38-1.66) 100.0 (59.38-1.66)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.58 (at 1.66Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.179 , 0.205 0.189 , 0.215	Depositor DCC
R_{free} test set	7000 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	24.8	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 39.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	9234	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 3.77% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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, PEG, GNP, CSO, CIT, 9RK

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	1.21	8/1403 (0.6%)	1.24	11/1891 (0.6%)
1	B	1.09	5/1400 (0.4%)	1.21	12/1886 (0.6%)
1	C	0.96	3/1391 (0.2%)	1.14	12/1875 (0.6%)
1	D	0.97	1/1420 (0.1%)	1.07	10/1914 (0.5%)
1	E	0.91	1/1412 (0.1%)	1.15	13/1902 (0.7%)
1	F	1.07	1/1420 (0.1%)	1.16	12/1913 (0.6%)
All	All	1.04	19/8446 (0.2%)	1.16	70/11381 (0.6%)

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	71	TYR	CE1-CZ	-6.95	1.29	1.38
1	F	164	ARG	CZ-NH1	-6.42	1.24	1.33
1	B	143	GLU	CD-OE2	6.02	1.32	1.25
1	A	157	TYR	CE2-CZ	-5.89	1.30	1.38
1	C	54	ASP	CB-CG	-5.78	1.39	1.51

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	149	ARG	NE-CZ-NH1	19.01	129.81	120.30
1	B	149	ARG	NE-CZ-NH1	16.50	128.55	120.30
1	F	149	ARG	NE-CZ-NH1	16.40	128.50	120.30
1	E	149	ARG	NE-CZ-NH1	15.83	128.21	120.30
1	A	149	ARG	NE-CZ-NH1	15.17	127.89	120.30

There are no chirality outliers.

There are no planarity outliers.

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	1385	0	1353	6	0
1	B	1382	0	1359	9	0
1	C	1374	0	1342	4	0
1	D	1402	0	1363	7	0
1	E	1395	0	1364	6	0
1	F	1403	0	1364	11	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	B	19	0	0	0	0
3	C	19	0	0	0	0
3	D	19	0	0	0	0
3	E	19	0	0	0	0
3	F	19	0	0	0	0
4	B	7	0	10	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
6	A	26	0	10	2	0
6	D	13	0	5	0	0
7	A	138	0	0	1	0
7	B	134	0	0	3	1
7	C	66	0	0	2	1
7	D	66	0	0	0	0
7	E	57	0	0	0	0
7	F	93	0	0	5	0
All	All	9234	0	8248	42	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 42 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)
6:A:203:CIT:O2	6:A:203:CIT:O7	1.97	0.82
1:E:127:THR:HG22	1:E:143:GLU:OE2	1.83	0.78
1:F:99:GLN:OE1	7:F:301:HOH:O	2.09	0.68
1:F:80:CYS:SG	1:F:111[A]:MET:HE3	2.42	0.60
1:C:105:ASP:HB2	7:C:360:HOH:O	2.04	0.56

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:351:HOH:O	7:C:306:HOH:O[1_455]	1.99	0.21

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	171/187 (91%)	166 (97%)	5 (3%)	0	100	100
1	B	171/187 (91%)	165 (96%)	6 (4%)	0	100	100
1	C	171/187 (91%)	165 (96%)	6 (4%)	0	100	100
1	D	173/187 (92%)	168 (97%)	5 (3%)	0	100	100
1	E	173/187 (92%)	168 (97%)	4 (2%)	1 (1%)	25	8
1	F	174/187 (93%)	169 (97%)	5 (3%)	0	100	100
All	All	1033/1122 (92%)	1001 (97%)	31 (3%)	1 (0%)	51	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	63	GLU

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	151/164 (92%)	147 (97%)	4 (3%)	46	21
1	B	150/164 (92%)	147 (98%)	3 (2%)	55	32
1	C	149/164 (91%)	144 (97%)	5 (3%)	37	12
1	D	153/164 (93%)	150 (98%)	3 (2%)	55	32
1	E	152/164 (93%)	143 (94%)	9 (6%)	19	3
1	F	153/164 (93%)	148 (97%)	5 (3%)	38	12
All	All	908/984 (92%)	879 (97%)	29 (3%)	38	13

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	65	SER
1	F	67	MET
1	E	54	ASP
1	F	1	MET
1	E	32	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	95	HIS
1	E	99	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	CSO	D	51	1	3,6,7	2.25	1 (33%)	0,6,8	-	-
1	CSO	E	51	1	3,6,7	1.75	1 (33%)	0,6,8	-	-
1	CSO	A	51	1	3,6,7	1.67	1 (33%)	0,6,8	-	-
1	CSO	C	51	1	3,6,7	1.83	1 (33%)	0,6,8	-	-
1	CSO	F	51	1	3,6,7	1.28	0	0,6,8	-	-
1	CSO	B	51	1	3,6,7	1.39	1 (33%)	0,6,8	-	-

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
1	CSO	D	51	1	-	0/1/5/7	-
1	CSO	E	51	1	-	0/1/5/7	-
1	CSO	A	51	1	-	0/1/5/7	-
1	CSO	C	51	1	-	0/1/5/7	-
1	CSO	F	51	1	-	0/1/5/7	-
1	CSO	B	51	1	-	0/1/5/7	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	51	CSO	CB-CA	-3.75	1.44	1.53
1	A	51	CSO	CB-CA	-2.83	1.46	1.53
1	E	51	CSO	CB-CA	-2.72	1.46	1.53
1	C	51	CSO	CB-CA	-2.53	1.47	1.53
1	B	51	CSO	CB-CA	-2.07	1.48	1.53

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	51	CSO	1	0
1	E	51	CSO	1	0
1	A	51	CSO	1	0
1	C	51	CSO	1	0
1	F	51	CSO	1	0
1	B	51	CSO	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 21 ligands modelled in this entry, 6 are monoatomic - leaving 15 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	9RK	E	202	-	17,21,21	0.44	0	19,28,28	0.70	0
3	9RK	D	202	-	17,21,21	0.53	0	19,28,28	0.72	1 (5%)
4	PEG	B	203	-	6,6,6	0.70	0	5,5,5	0.39	0
6	CIT	A	203	-	12,12,12	2.79	6 (50%)	17,17,17	3.14	10 (58%)
3	9RK	F	202	-	17,21,21	0.50	0	19,28,28	0.69	0
2	GNP	F	201	5	29,34,34	1.94	9 (31%)	33,54,54	2.30	10 (30%)
2	GNP	E	201	5	29,34,34	2.16	7 (24%)	33,54,54	2.16	13 (39%)
3	9RK	B	202	-	17,21,21	0.58	0	19,28,28	0.84	1 (5%)
2	GNP	B	201	5	29,34,34	2.57	11 (37%)	33,54,54	2.23	9 (27%)
2	GNP	C	201	5	29,34,34	2.22	12 (41%)	33,54,54	1.99	9 (27%)
3	9RK	C	202	-	17,21,21	0.30	0	19,28,28	0.50	0
2	GNP	A	201	5	29,34,34	2.47	10 (34%)	33,54,54	2.51	8 (24%)
6	CIT	D	203	-	12,12,12	1.21	0	17,17,17	1.99	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	CIT	A	202	-	12,12,12	1.29	2 (16%)	17,17,17	1.75	4 (23%)
2	GNP	D	201	5	29,34,34	2.80	9 (31%)	33,54,54	2.30	12 (36%)

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	9RK	E	202	-	-	1/6/18/18	0/3/3/3
3	9RK	D	202	-	-	2/6/18/18	0/3/3/3
4	PEG	B	203	-	-	1/4/4/4	-
6	CIT	A	203	-	-	10/16/16/16	-
3	9RK	F	202	-	-	2/6/18/18	0/3/3/3
2	GNP	F	201	5	-	3/14/38/38	0/3/3/3
2	GNP	E	201	5	-	4/14/38/38	0/3/3/3
3	9RK	B	202	-	-	0/6/18/18	0/3/3/3
2	GNP	B	201	5	-	4/14/38/38	0/3/3/3
2	GNP	C	201	5	-	5/14/38/38	0/3/3/3
3	9RK	C	202	-	-	0/6/18/18	0/3/3/3
2	GNP	A	201	5	-	4/14/38/38	0/3/3/3
6	CIT	D	203	-	-	8/16/16/16	-
6	CIT	A	202	-	-	0/16/16/16	-
2	GNP	D	201	5	-	3/14/38/38	0/3/3/3

The worst 5 of 66 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	GNP	PB-O3A	9.90	1.71	1.59
2	B	201	GNP	PG-O1G	8.37	1.59	1.46
2	A	201	GNP	PG-O1G	7.29	1.57	1.46
6	A	203	CIT	O7-C3	6.43	1.55	1.43
2	D	201	GNP	C2'-C1'	-6.31	1.44	1.53

The worst 5 of 82 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	201	GNP	C5-C6-N1	-8.11	112.34	123.43
2	A	201	GNP	C5-C6-N1	-7.71	112.89	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	203	CIT	O6-C6-C3	6.55	124.42	113.05
2	A	201	GNP	C2-N1-C6	6.40	126.11	115.93
2	A	201	GNP	O1G-PG-N3B	-6.20	102.64	111.77

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	201	GNP	PG-N3B-PB-O1B
2	B	201	GNP	PA-O3A-PB-O1B
2	B	201	GNP	PA-O3A-PB-O2B
2	A	201	GNP	PG-N3B-PB-O1B
2	A	201	GNP	PA-O3A-PB-O1B

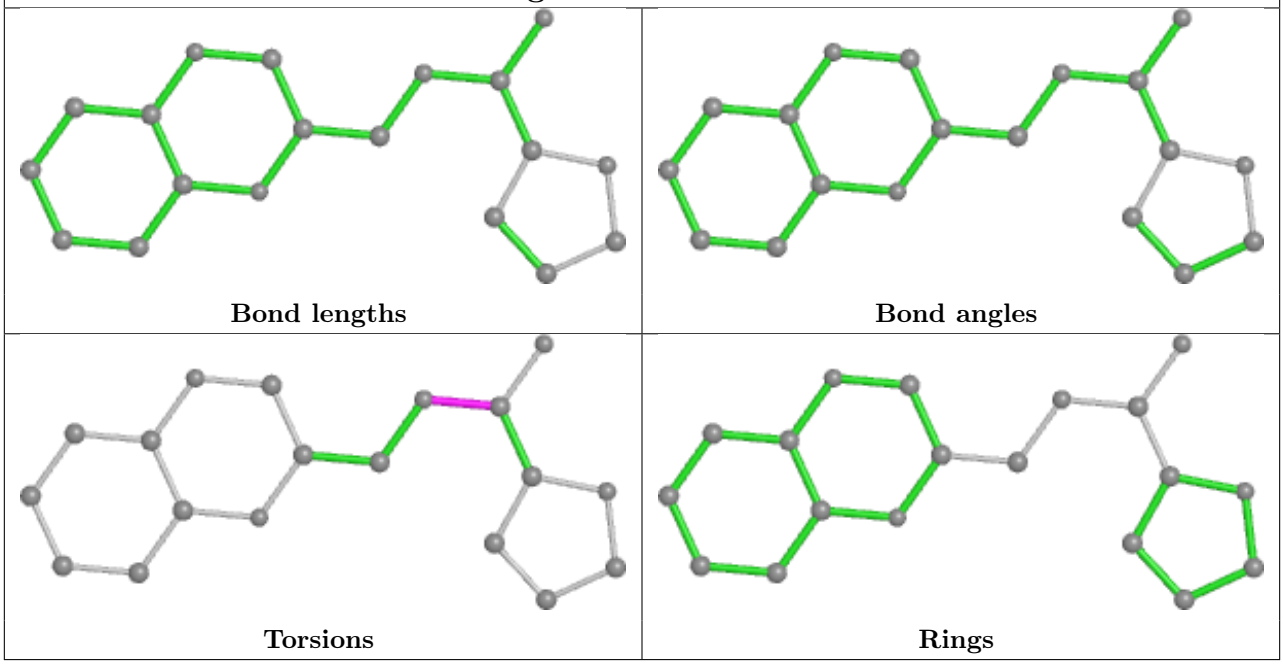
There are no ring outliers.

1 monomer is involved in 2 short contacts:

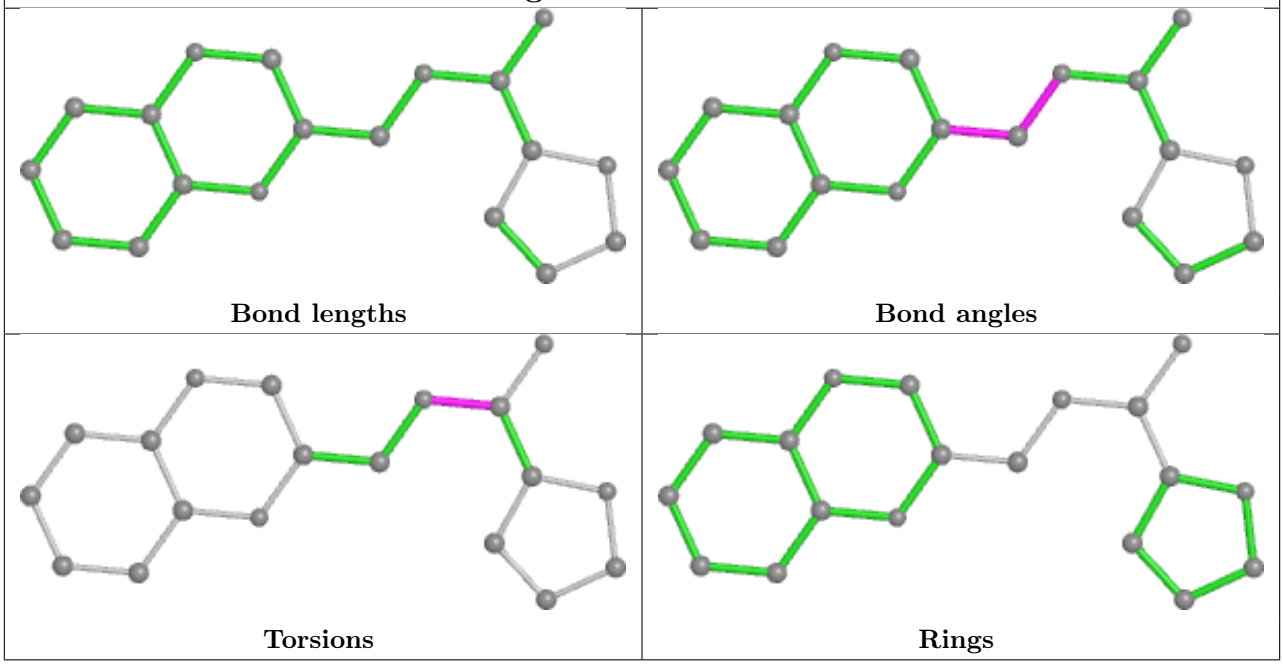
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	203	CIT	2	0

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 then 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.

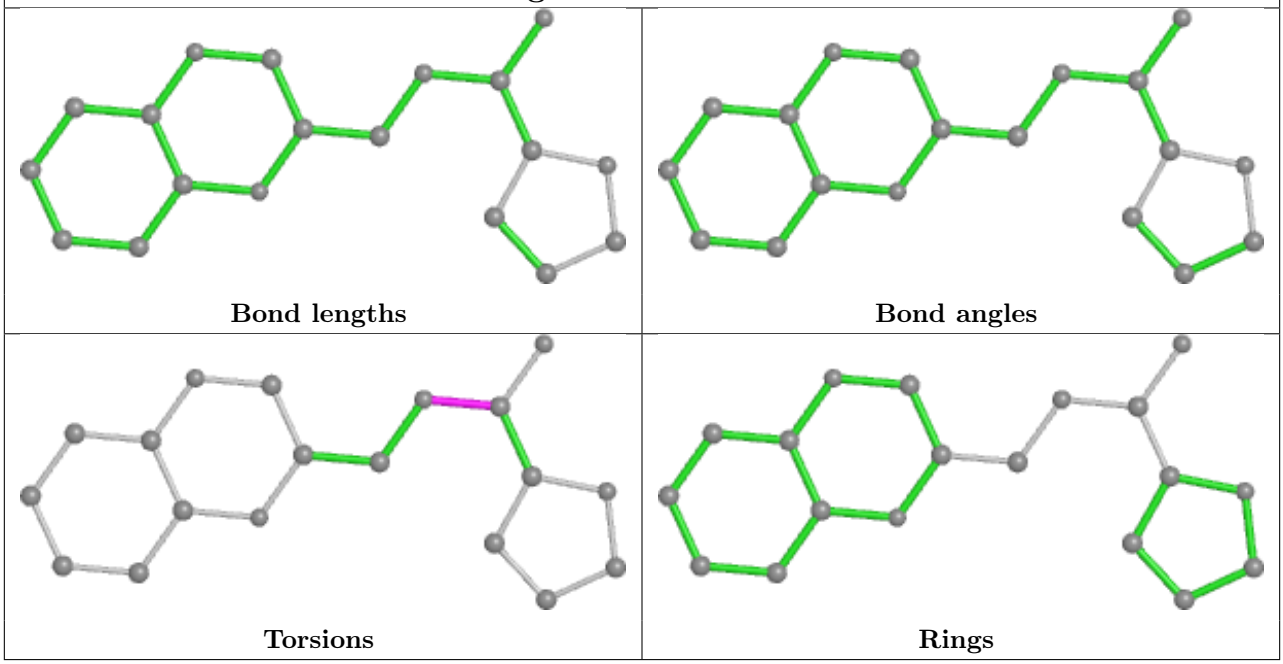
Ligand 9RK E 202



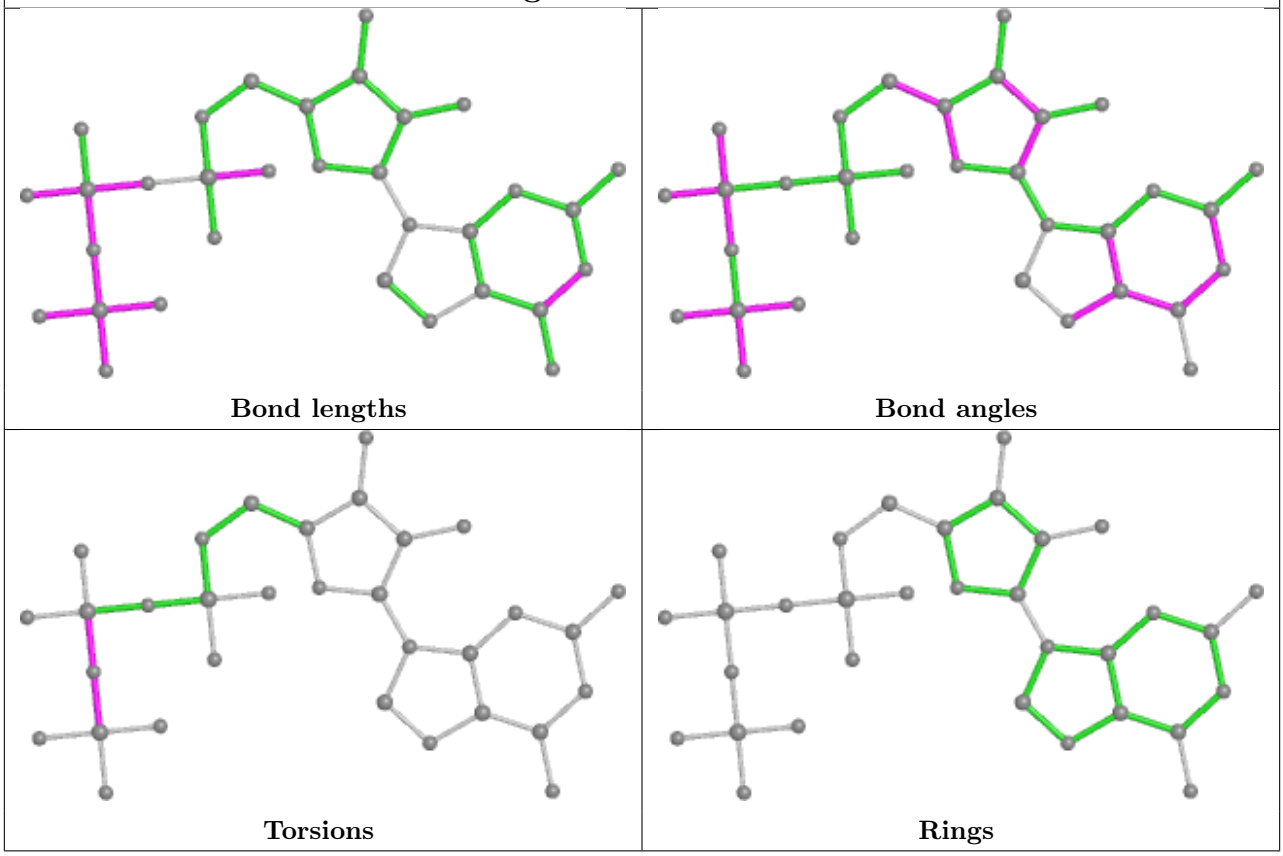
Ligand 9RK D 202



Ligand 9RK F 202



Ligand GNP F 201



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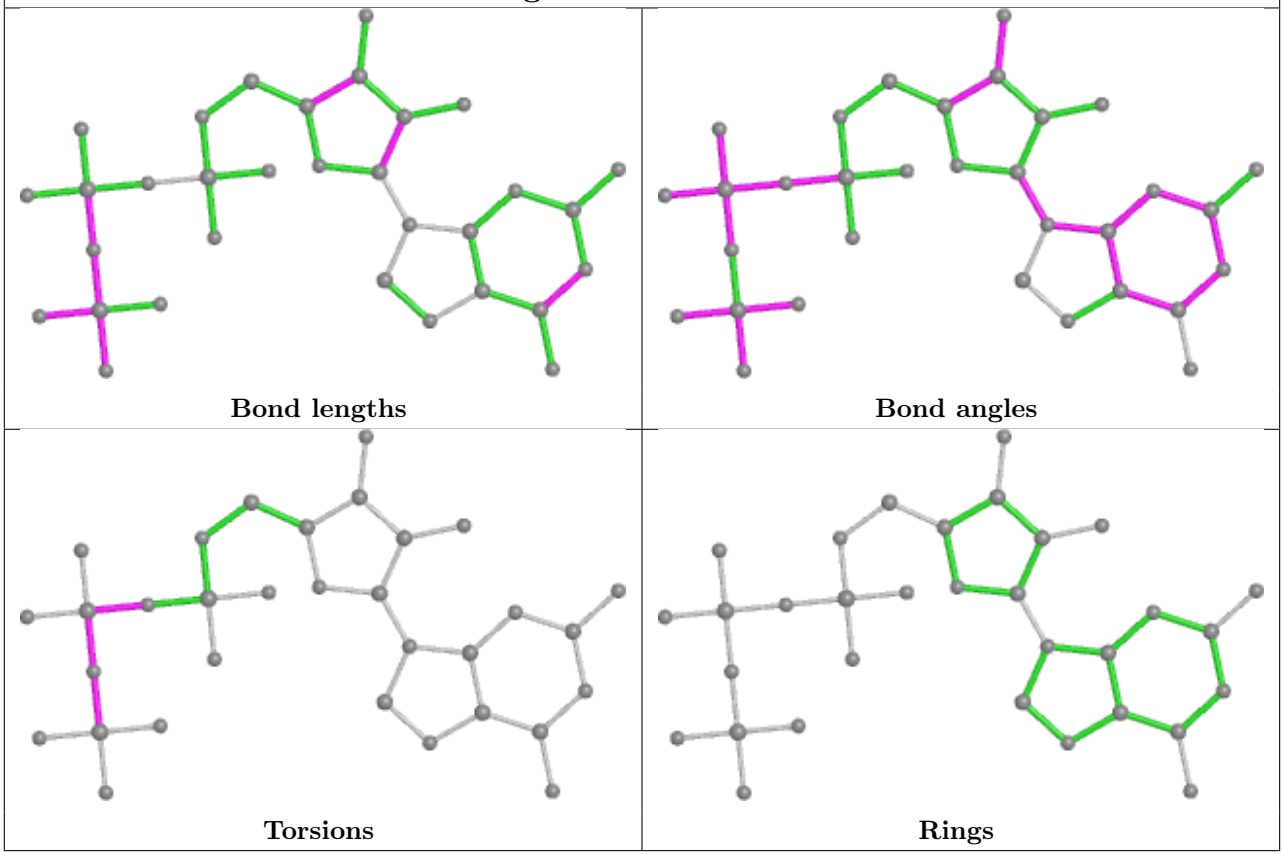
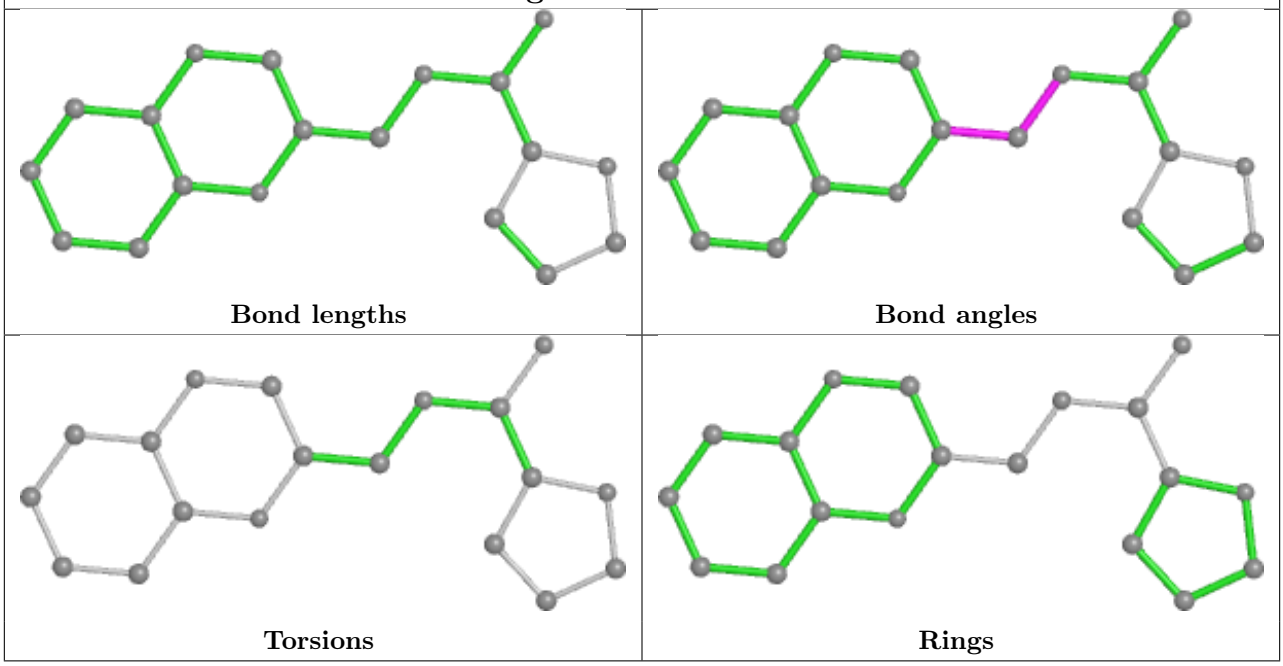


Ligand 9RK B 202



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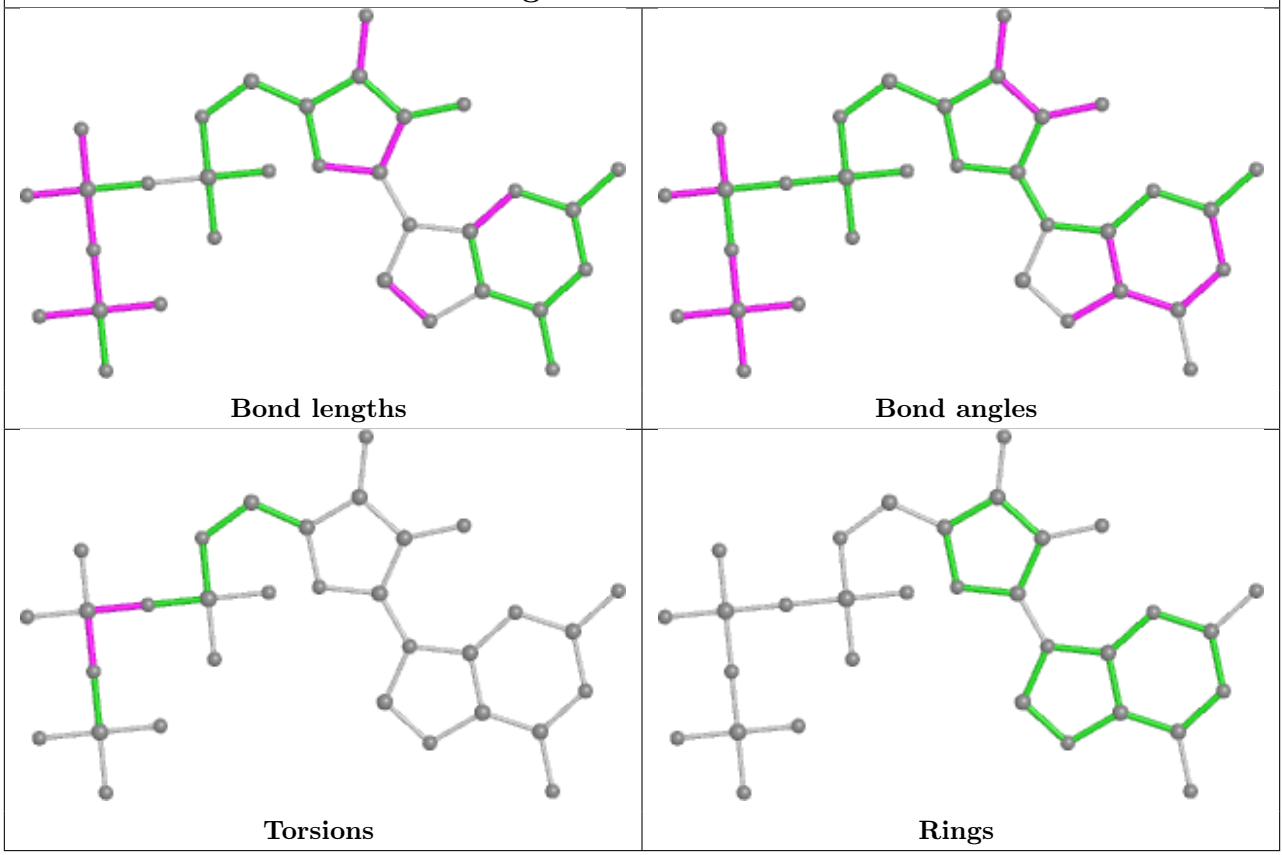

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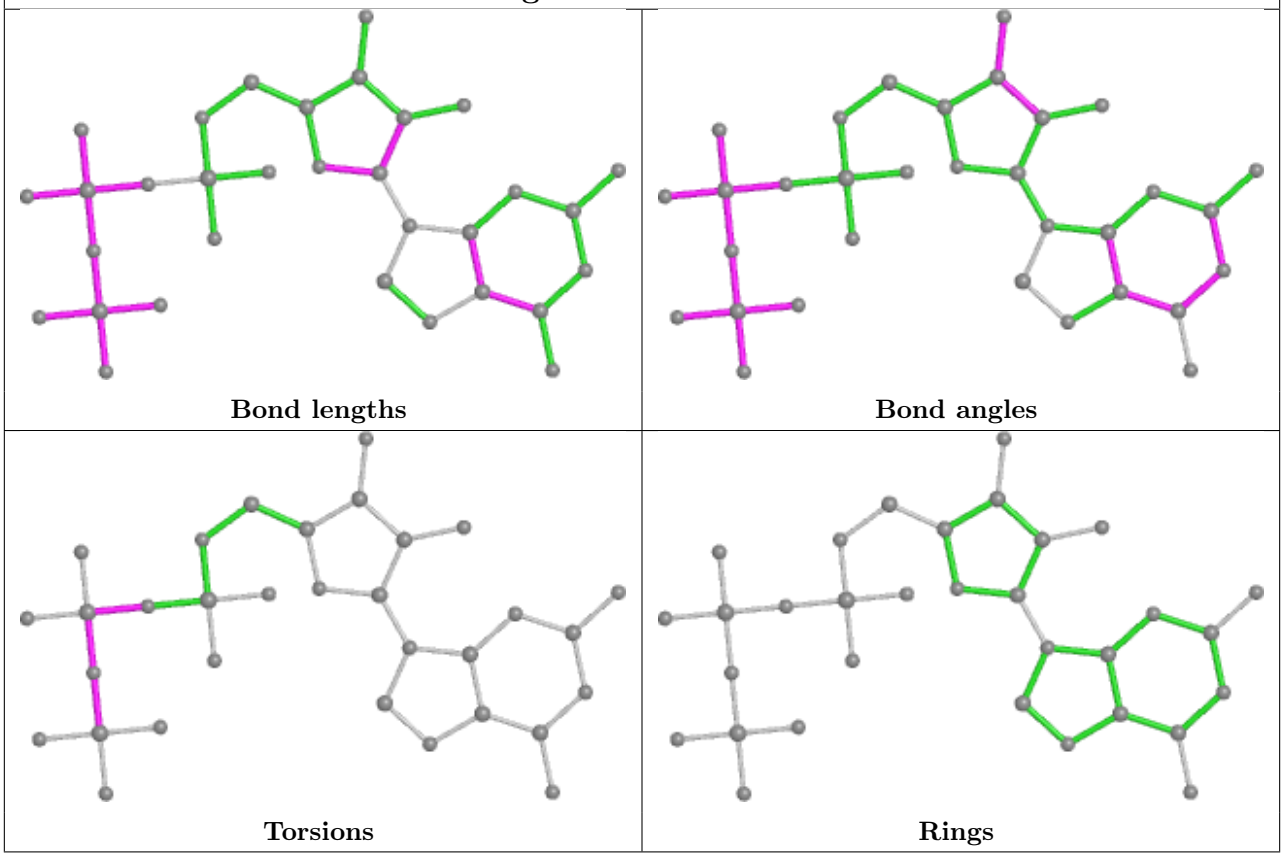

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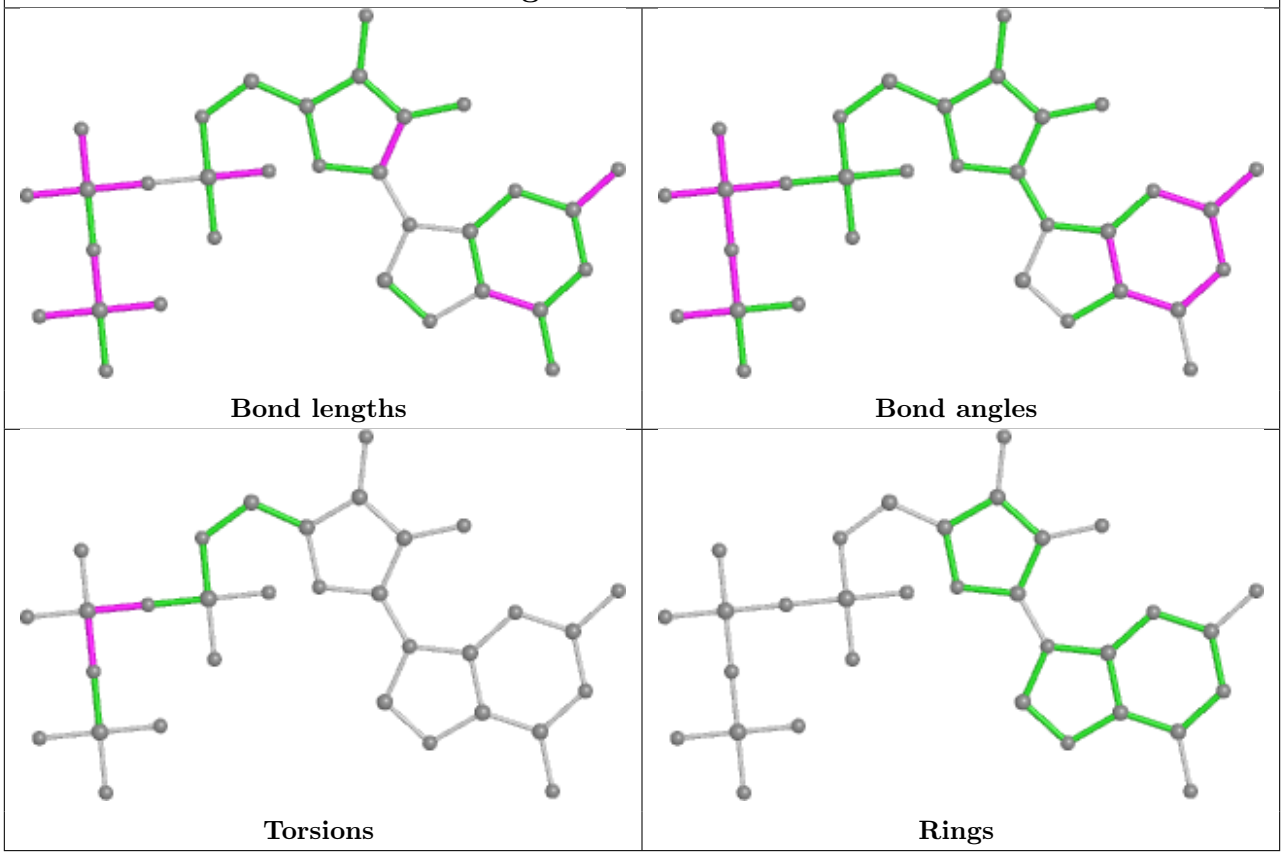

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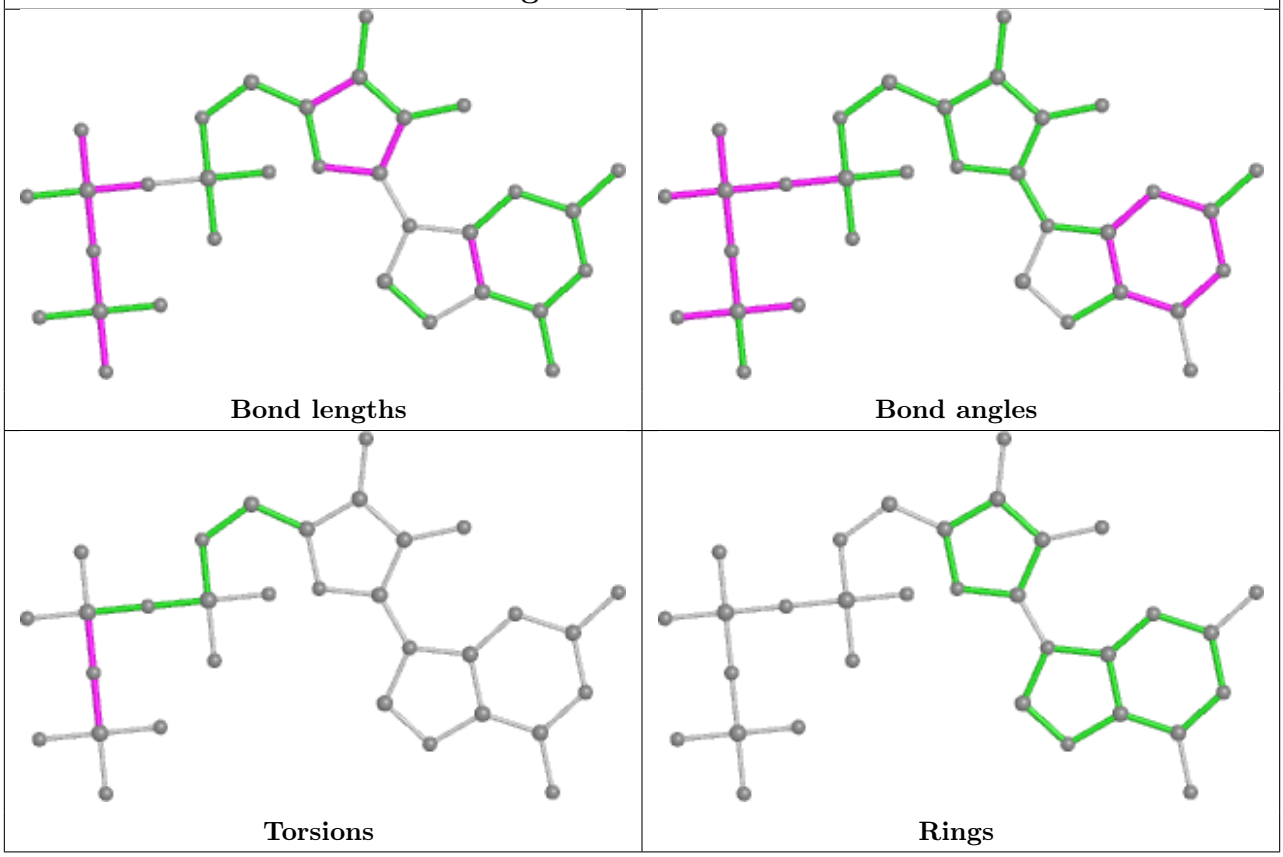

5.7 Other polymers (i)

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	171/187 (91%)	-0.03	3 (1%)	68	71	14, 22, 49, 89	0
1	B	172/187 (91%)	-0.04	2 (1%)	79	81	16, 25, 59, 98	0
1	C	171/187 (91%)	-0.09	5 (2%)	51	52	21, 33, 66, 98	0
1	D	171/187 (91%)	0.31	17 (9%)	7	6	20, 35, 94, 148	0
1	E	172/187 (91%)	0.04	12 (6%)	16	15	24, 37, 83, 118	0
1	F	171/187 (91%)	0.14	15 (8%)	10	9	18, 28, 88, 108	0
All	All	1028/1122 (91%)	0.05	54 (5%)	26	25	14, 30, 74, 148	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	64	TYR	14.0
1	D	-3	TYR	9.3
1	F	64	TYR	7.5
1	A	-3	TYR	7.2
1	F	32	TYR	6.5

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	CSO	D	51	7/8	0.94	0.08	23,24,32,37	0
1	CSO	E	51	7/8	0.95	0.08	23,26,36,40	0
1	CSO	A	51	7/8	0.96	0.10	21,23,28,32	0
1	CSO	C	51	7/8	0.96	0.09	23,27,38,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CSO	F	51	7/8	0.96	0.07	24,26,34,39	0
1	CSO	B	51	7/8	0.97	0.09	23,26,34,38	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

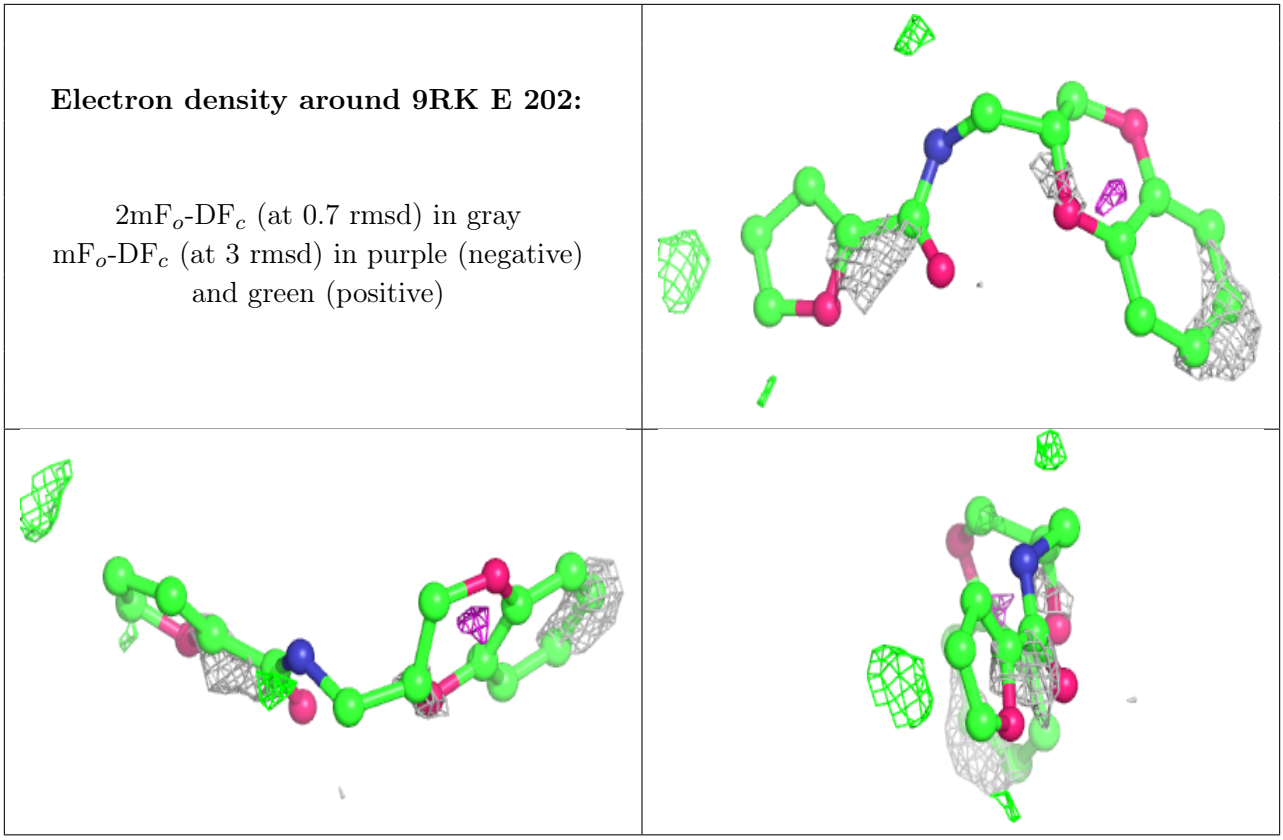
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	9RK	E	202	19/19	0.40	0.53	58,71,78,78	19
3	9RK	D	202	19/19	0.47	0.55	40,67,76,77	19
6	CIT	D	203	13/13	0.49	0.33	72,102,117,118	0
3	9RK	F	202	19/19	0.65	0.38	37,60,102,103	19
6	CIT	A	203	13/13	0.69	0.21	44,57,71,92	0
4	PEG	B	203	7/7	0.73	0.13	56,67,75,80	0
3	9RK	C	202	19/19	0.75	0.30	41,56,77,77	19
3	9RK	B	202	19/19	0.87	0.16	31,47,69,69	19
5	MG	D	204	1/1	0.94	0.15	46,46,46,46	0
6	CIT	A	202	13/13	0.95	0.12	23,30,35,35	0
5	MG	E	203	1/1	0.96	0.12	33,33,33,33	0
5	MG	F	203	1/1	0.97	0.13	34,34,34,34	0
2	GNP	C	201	32/32	0.98	0.06	25,28,33,33	0
2	GNP	D	201	32/32	0.98	0.06	25,29,38,40	0
2	GNP	E	201	32/32	0.98	0.06	23,29,38,42	0
2	GNP	B	201	32/32	0.99	0.09	15,18,20,22	0
2	GNP	F	201	32/32	0.99	0.06	19,23,32,34	0
5	MG	A	204	1/1	0.99	0.09	16,16,16,16	0
5	MG	C	203	1/1	0.99	0.03	30,30,30,30	0
2	GNP	A	201	32/32	0.99	0.08	14,16,19,20	0
5	MG	B	204	1/1	1.00	0.06	19,19,19,19	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.

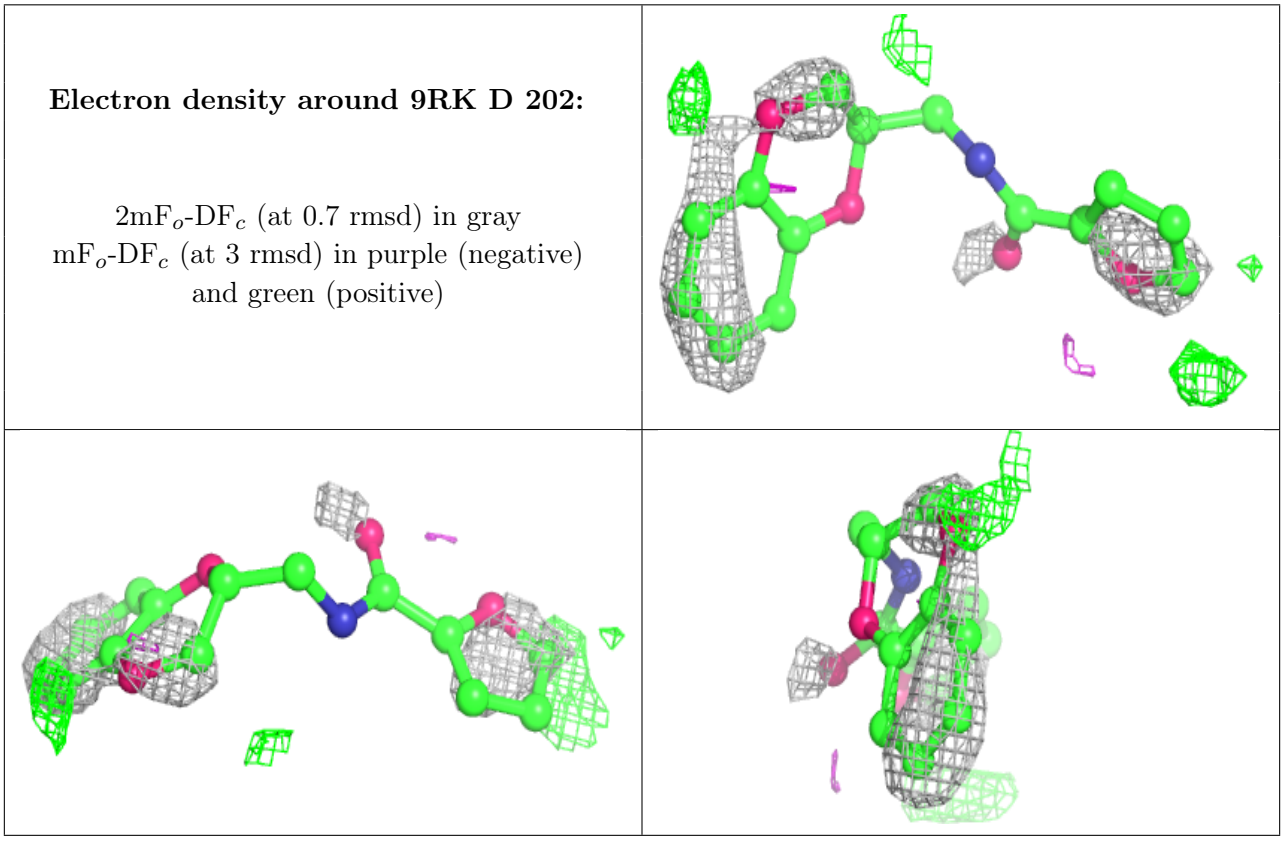
Electron density around 9RK E 202:

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



Electron density around 9RK 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)



Electron density around 9RK F 202:

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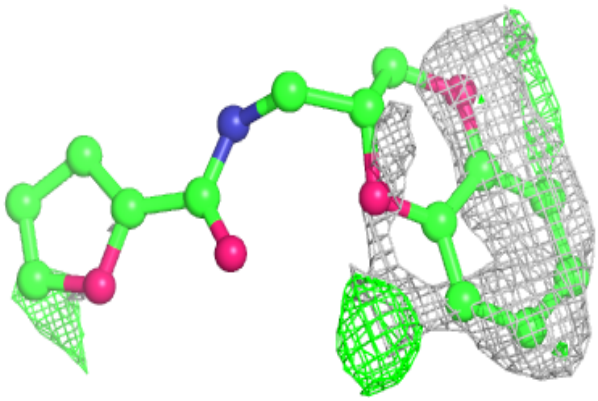
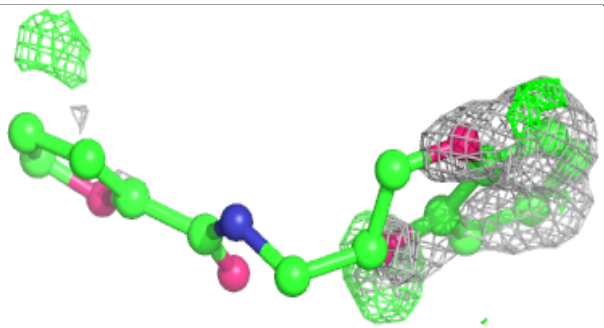
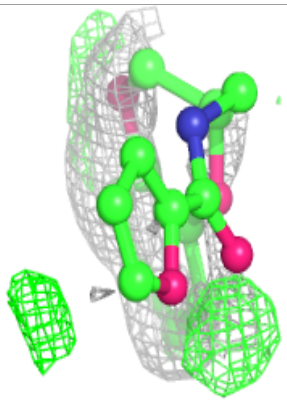
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around 9RK B 202:

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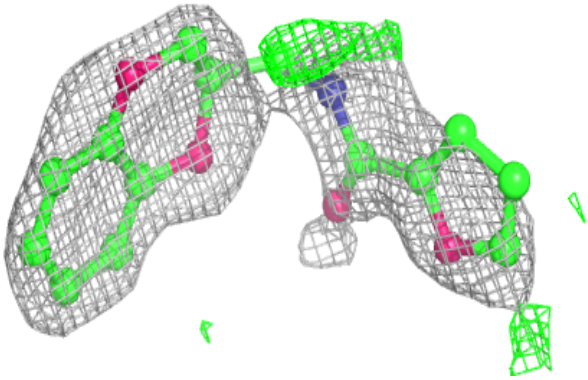
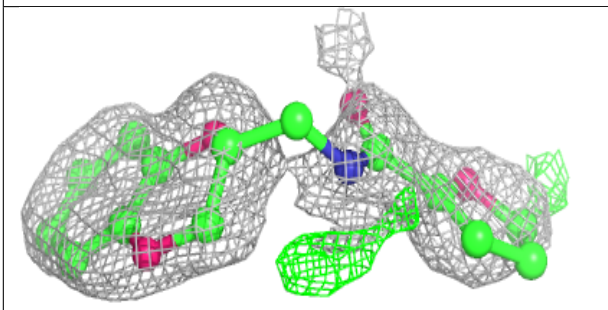
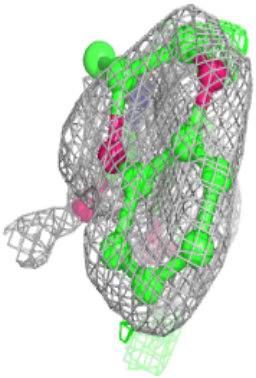
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

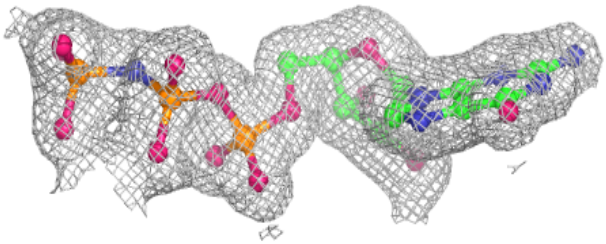


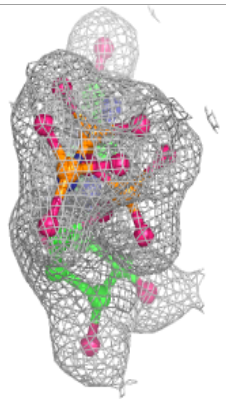




Electron density around GNP C 201:

$2mF_o$-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 D 201:

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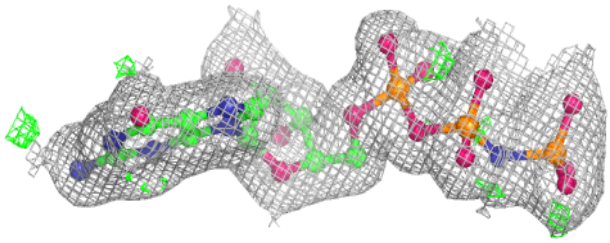
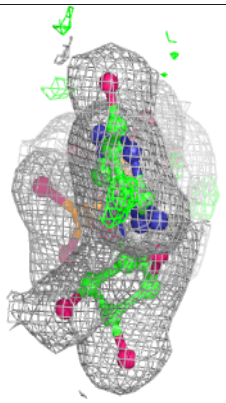
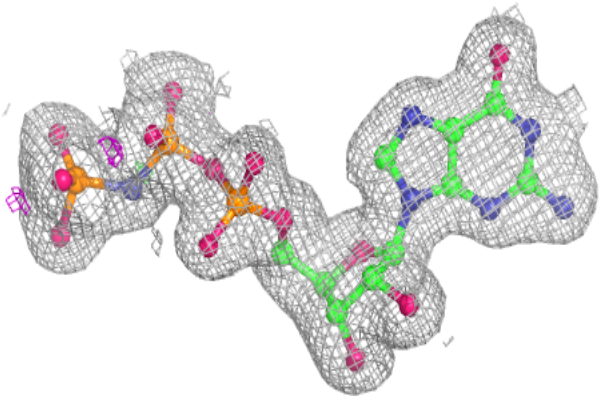
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

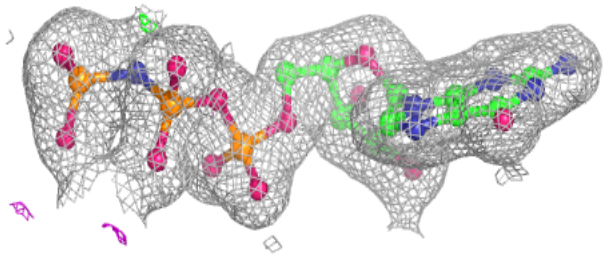


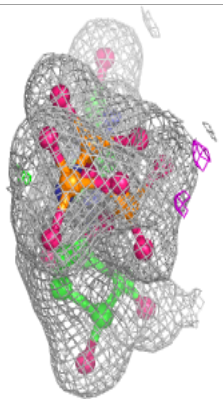


Electron density around GNP E 201:

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

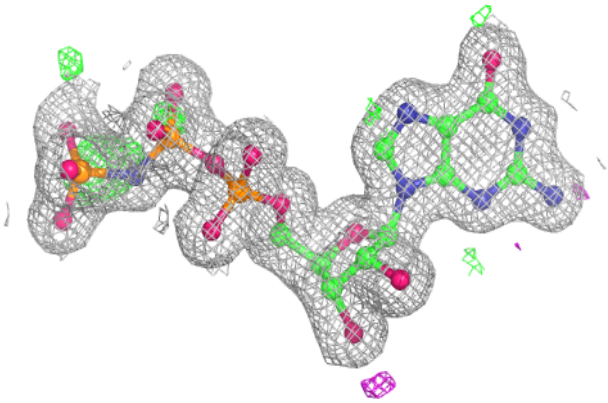


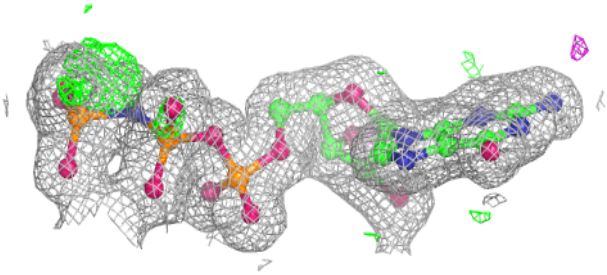


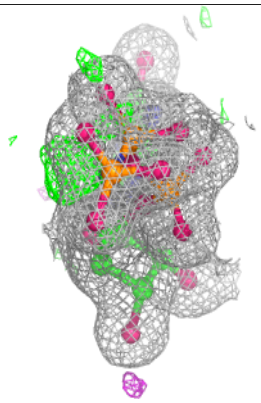


Electron density around GNP B 201:

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

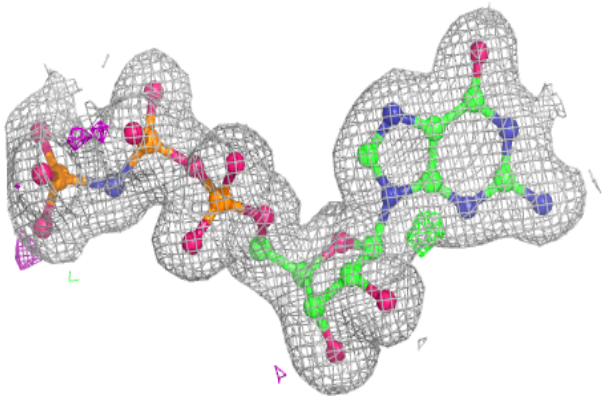


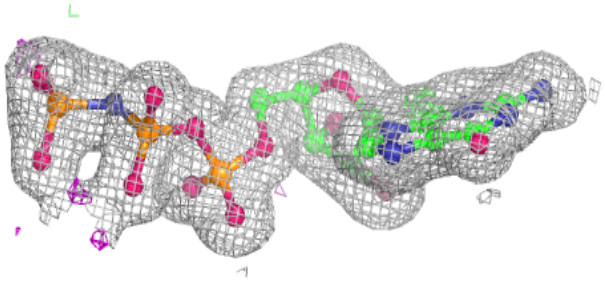


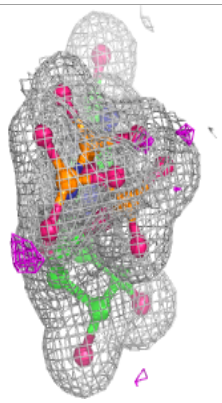


Electron density around GNP F 201:

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

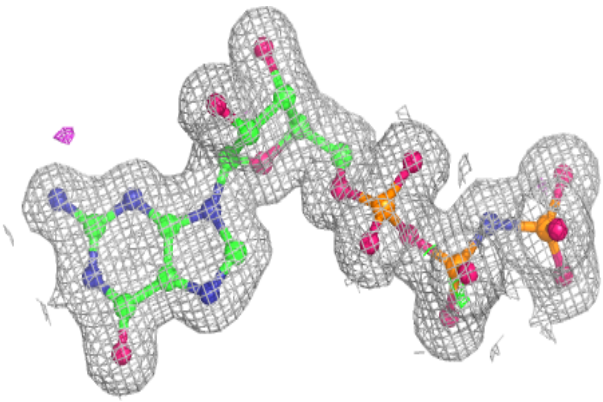


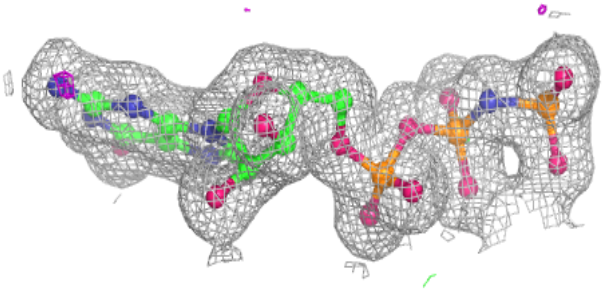


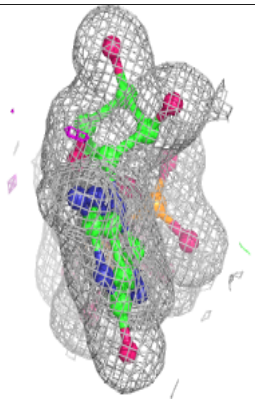


Electron density around GNP A 201:

$2mF_o$-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.