



wwPDB X-ray Structure Validation Summary Report ⓘ

May 17, 2020 – 10:28 pm BST

PDB ID : 5F98
Title : Crystal structure of RIG-I in complex with Cap-0 RNA
Authors : Wang, C.; Marcotrigiano, J.; Miller, M.; Jiang, F.
Deposited on : 2015-12-09
Resolution : 3.28 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 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

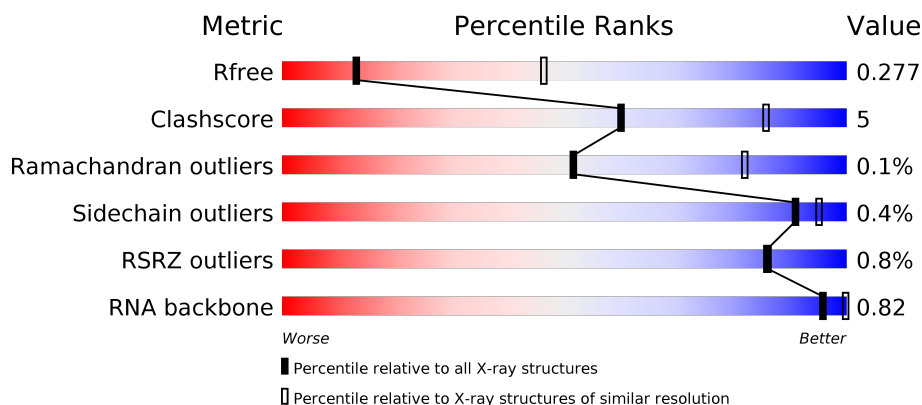
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.28 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	1177 (3.32-3.24)
Clashscore	141614	1044 (3.30-3.26)
Ramachandran outliers	138981	1026 (3.30-3.26)
Sidechain outliers	138945	1025 (3.30-3.26)
RSRZ outliers	127900	1141 (3.32-3.24)
RNA backbone	3102	1091 (3.66-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	695	
1	C	695	
1	E	695	
1	G	695	

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Mol	Chain	Length	Quality of chain
1	I	695	
1	K	695	% 
2	B	24	
2	D	24	
2	F	24	
2	H	24	
2	J	24	
2	L	24	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 32719 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 Probable ATP-dependent RNA helicase DDX58.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	650	Total	C	N	O	S	0	0	0
			5060	3237	855	938	30			
1	C	648	Total	C	N	O	S	0	0	0
			4949	3169	832	917	31			
1	E	641	Total	C	N	O	S	0	0	0
			4832	3087	822	894	29			
1	G	647	Total	C	N	O	S	0	1	0
			4965	3182	836	916	31			
1	I	647	Total	C	N	O	S	0	0	0
			4838	3093	810	906	29			
1	K	644	Total	C	N	O	S	0	0	0
			4859	3115	812	901	31			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	231	SER	-	expression tag	UNP O95786
C	231	SER	-	expression tag	UNP O95786
E	231	SER	-	expression tag	UNP O95786
G	231	SER	-	expression tag	UNP O95786
I	231	SER	-	expression tag	UNP O95786
K	231	SER	-	expression tag	UNP O95786

- Molecule 2 is a RNA chain called RNA (5'-R(P*GP*AP*AP*UP*AP*UP*AP*AP*UP*AP*GP*UP*GP*AP*UP*AP*UP*UP*AP*UP*AP*UP*UP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	24	Total	C	N	O	P	0	0	0
			509	229	88	168	24			
2	D	24	Total	C	N	O	P	0	0	0
			509	229	88	168	24			
2	F	24	Total	C	N	O	P	0	0	0
			509	229	88	168	24			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	24	Total	C	N	O	P	0	0	0
			509	229	88	168	24			
2	J	24	Total	C	N	O	P	0	0	0
			509	229	88	168	24			
2	L	24	Total	C	N	O	P	0	0	0
			509	229	88	168	24			

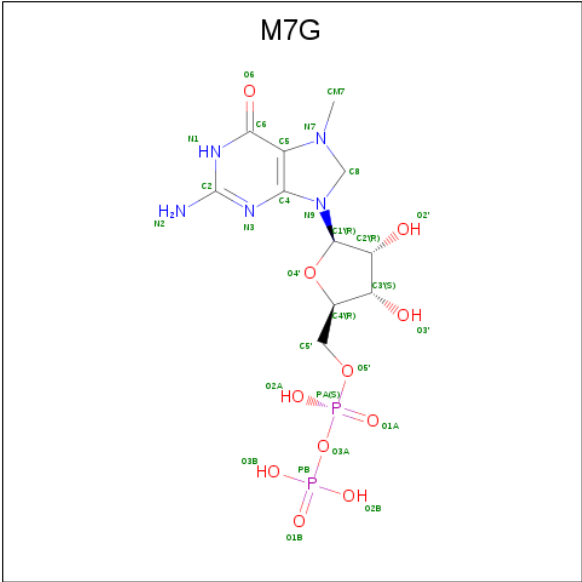
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Zn	0	0
			1	1		
3	K	1	Total	Zn	0	0
			1	1		
3	E	1	Total	Zn	0	0
			1	1		
3	I	1	Total	Zn	0	0
			1	1		
3	C	1	Total	Zn	0	0
			1	1		
3	A	1	Total	Zn	0	0
			1	1		

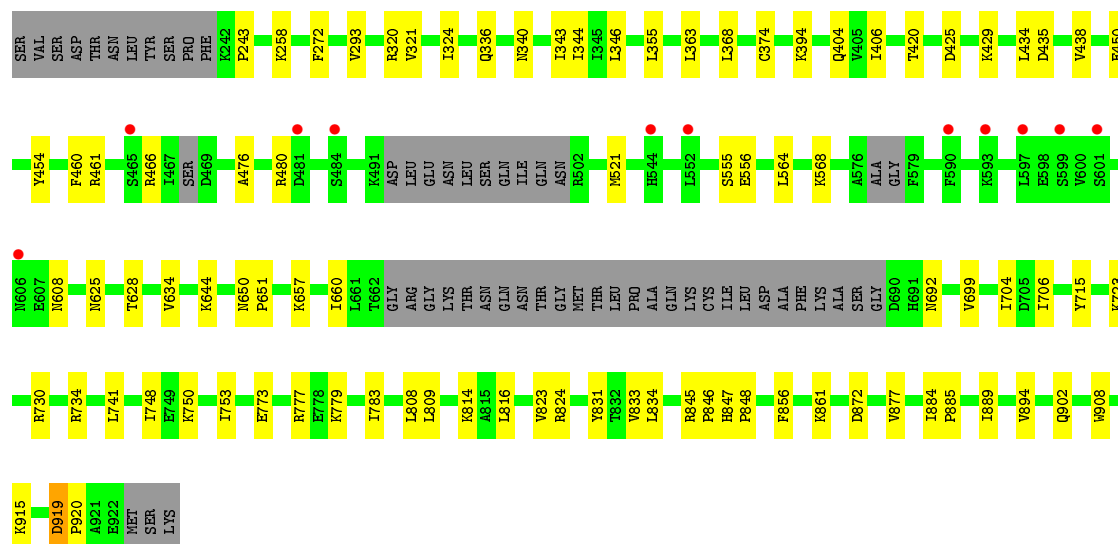
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	Mg	0	0
			1	1		
4	K	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		
4	I	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is 7N-METHYL-8-HYDROGUANOSINE-5'-DIPHOSPHATE (three-letter code: M7G) (formula: C₁₁H₁₉N₅O₁₁P₂).

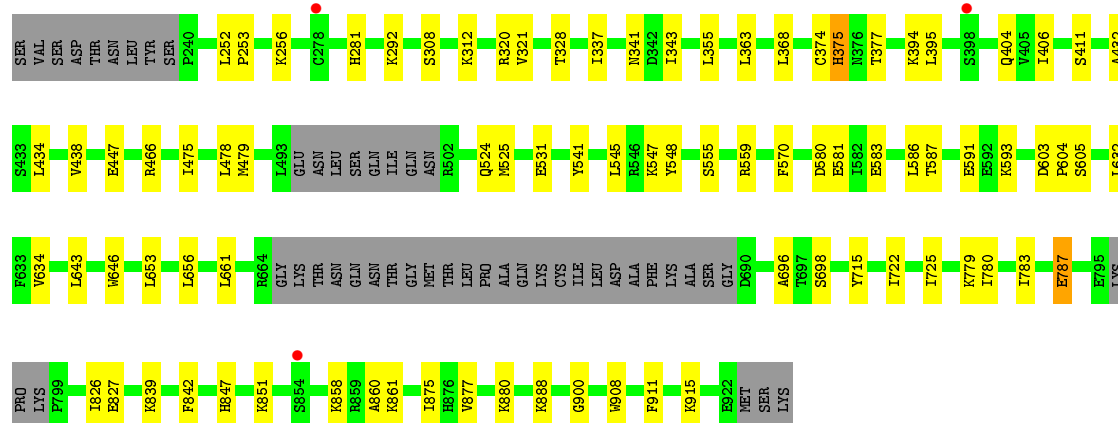


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
5	D	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
5	F	1	Total	C	O	P		0	0
			17	5	10	2			
5	H	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
5	J	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
5	L	1	Total	C	O	P		0	0
			17	5	10	2			



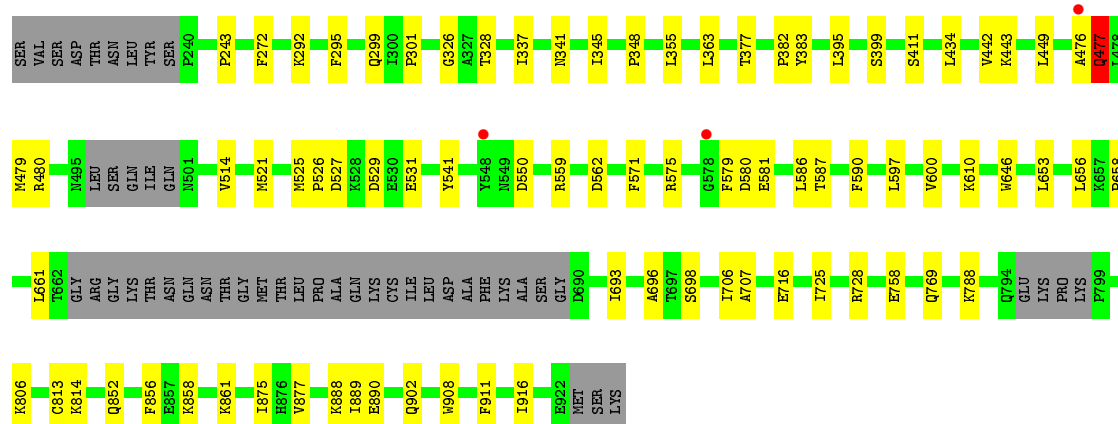
- Molecule 1: Probable ATP-dependent RNA helicase DDX58

Chain G: 81% 12% 7%

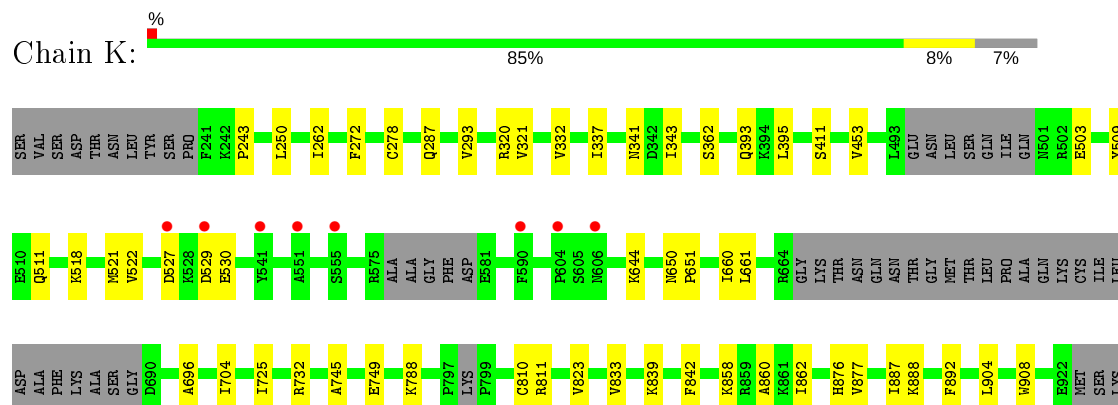


- Molecule 1: Probable ATP-dependent RNA helicase DDX58

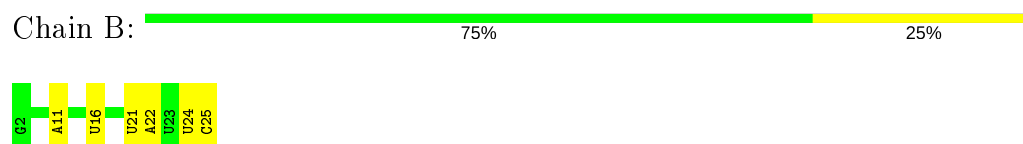
Chain I: 81% 12% 7%



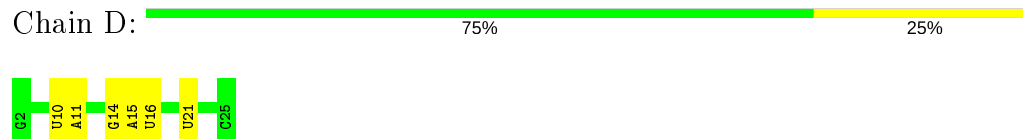
- Molecule 1: Probable ATP-dependent RNA helicase DDX58



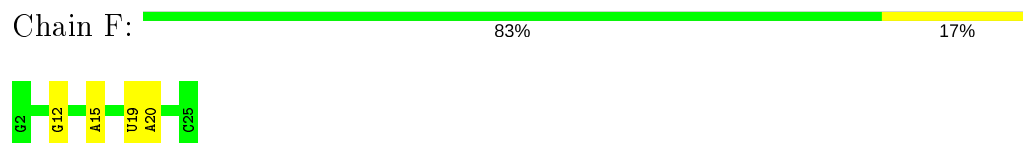
- Molecule 2: RNA (5'-R(P*GP*AP*AP*UP*AP*UP*AP*AP*UP*AP*GP*UP*GP*AP*UP*A P*UP*UP*AP*UP*AP*UP*UP*C)-3')



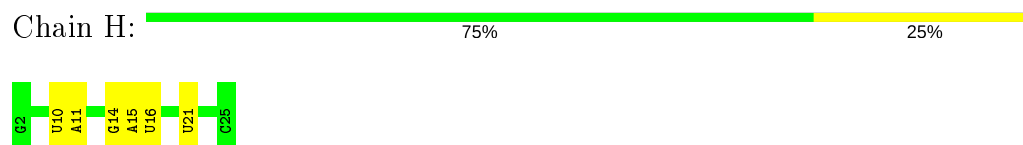
- Molecule 2: RNA (5'-R(P*GP*AP*AP*UP*AP*UP*AP*AP*UP*AP*GP*UP*GP*AP*UP*A P*UP*UP*AP*UP*AP*UP*UP*C)-3')




- Molecule 2: RNA (5'-R(P*GP*AP*AP*UP*AP*UP*AP*AP*UP*AP*GP*UP*GP*AP*UP*A P*UP*UP*AP*UP*AP*UP*UP*C)-3')



- Molecule 2: RNA (5'-R(P*GP*AP*AP*UP*AP*UP*AP*AP*UP*AP*GP*UP*GP*AP*UP*A P*UP*UP*AP*UP*AP*UP*UP*C)-3')



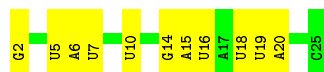
- Molecule 2: RNA (5'-R(P*GP*AP*AP*UP*AP*UP*AP*AP*UP*AP*GP*UP*GP*AP*UP*A P*UP*UP*AP*UP*AP*UP*UP*C)-3')

Chain J:  88% 13%



● Molecule 2: RNA (5'-R(P*GP*AP*AP*UP*AP*UP*AP*AP*UP*AP*GP*UP*GP*AP*UP*A
P*UP*UP*AP*UP*AP*UP*UP*C)-3')

Chain L:  54% 46%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	111.18Å 174.57Å 309.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.00 – 3.28 84.00 – 3.28	Depositor EDS
% Data completeness (in resolution range)	99.3 (84.00-3.28) 92.1 (84.00-3.28)	Depositor EDS
R_{merge}	0.56	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 3.26Å)	Xtriage
Refinement program	PHENIX 1.9_1690	Depositor
R, R_{free}	0.221 , 0.277 0.224 , 0.277	Depositor DCC
R_{free} test set	2000 reflections (2.17%)	wwPDB-VP
Wilson B-factor (Å ²)	51.9	Xtriage
Anisotropy	0.499	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 53.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	32719	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.75% 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: ZN, M7G, MG

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	0.22	0/5167	0.38	0/7005
1	C	0.22	0/5052	0.41	1/6858 (0.0%)
1	E	0.22	0/4933	0.38	0/6708
1	G	0.22	0/5069	0.37	0/6881
1	I	0.21	0/4942	0.38	0/6730
1	K	0.22	0/4960	0.37	0/6745
2	B	0.13	0/569	0.67	0/883
2	D	0.13	0/569	0.65	0/883
2	F	0.13	0/569	0.66	0/883
2	H	0.13	0/569	0.66	0/883
2	J	0.13	0/569	0.67	0/883
2	L	0.46	1/569 (0.2%)	0.65	0/881
All	All	0.22	1/33537 (0.0%)	0.42	1/46223 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	I	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	2	G	OP3-P	-10.66	1.48	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	485	LEU	CA-CB-CG	8.52	134.89	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	I	477	GLN	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	5060	0	4907	53	0
1	C	4949	0	4755	49	0
1	E	4832	0	4529	50	0
1	G	4965	0	4768	51	0
1	I	4838	0	4460	51	0
1	K	4859	0	4582	32	0
2	B	509	0	255	3	0
2	D	509	0	255	3	0
2	F	509	0	255	2	0
2	H	509	0	255	3	0
2	J	509	0	255	3	0
2	L	509	0	255	7	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
3	K	1	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
4	K	1	0	0	0	0
5	B	29	0	15	0	0
5	D	29	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	17	0	7	0	0
5	H	29	0	16	0	0
5	J	29	0	15	1	0
5	L	17	0	7	0	0
All	All	32719	0	29607	289	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 5.

The worst 5 of 289 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:I:477:GLN:HA	1:I:480:ARG:H	1.54	0.72
1:E:644:LYS:HD2	1:E:660:ILE:HD11	1.73	0.71
1:E:258:LYS:HE3	1:E:438:VAL:HG21	1.72	0.71
1:I:443:LYS:NZ	1:I:769:GLN:OE1	2.21	0.69
1:E:831:TYR:OH	1:E:915:LYS:NZ	2.21	0.69

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	644/695 (93%)	602 (94%)	42 (6%)	0	100	100
1	C	640/695 (92%)	595 (93%)	44 (7%)	1 (0%)	47	77
1	E	631/695 (91%)	588 (93%)	42 (7%)	1 (0%)	47	77
1	G	640/695 (92%)	596 (93%)	43 (7%)	1 (0%)	47	77
1	I	639/695 (92%)	588 (92%)	51 (8%)	0	100	100
1	K	634/695 (91%)	596 (94%)	38 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	3828/4170 (92%)	3565 (93%)	260 (7%)	3 (0%)	51 82

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	799	PRO
1	G	375	HIS
1	E	704	ILE

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	537/623 (86%)	536 (100%)	1 (0%)	93 97
1	C	516/623 (83%)	510 (99%)	6 (1%)	71 83
1	E	487/623 (78%)	486 (100%)	1 (0%)	93 97
1	G	517/623 (83%)	516 (100%)	1 (0%)	93 97
1	I	480/623 (77%)	477 (99%)	3 (1%)	86 91
1	K	495/623 (80%)	494 (100%)	1 (0%)	93 97
All	All	3032/3738 (81%)	3019 (100%)	13 (0%)	91 95

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	597	LEU
1	C	656	LEU
1	I	477	GLN
1	C	546	ARG
1	I	399	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	305	GLN
1	E	340	ASN
1	I	340	ASN
1	E	289	GLN
1	G	708	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	23/24 (95%)	2 (8%)	0
2	D	23/24 (95%)	1 (4%)	0
2	F	23/24 (95%)	0	0
2	H	23/24 (95%)	1 (4%)	0
2	J	23/24 (95%)	0	0
2	L	23/24 (95%)	1 (4%)	0
All	All	138/144 (95%)	5 (3%)	0

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	11	A
2	B	16	U
2	D	16	U
2	H	16	U
2	L	16	U

There are no RNA pucker outliers to report.

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 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 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	$\# Z > 2$
5	M7G	L	101	2	15,17,31	3.89	5 (33%)	21,26,49	1.20	3 (14%)
5	M7G	F	101	2	15,17,31	3.89	5 (33%)	21,26,49	1.10	2 (9%)
5	M7G	H	101	2	28,31,31	3.92	13 (46%)	39,49,49	1.84	11 (28%)
5	M7G	B	101	2	28,31,31	3.90	11 (39%)	39,49,49	1.63	8 (20%)
5	M7G	D	101	2	28,31,31	3.91	11 (39%)	39,49,49	1.72	10 (25%)
5	M7G	J	101	2	28,31,31	3.90	11 (39%)	39,49,49	1.65	8 (20%)

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
5	M7G	L	101	2	-	3/12/25/44	0/1/1/3
5	M7G	F	101	2	-	4/12/25/44	0/1/1/3
5	M7G	H	101	2	-	6/16/44/44	0/3/3/3
5	M7G	B	101	2	-	9/16/44/44	0/3/3/3
5	M7G	D	101	2	-	4/16/44/44	0/3/3/3
5	M7G	J	101	2	-	4/16/44/44	0/3/3/3

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	101	M7G	O4'-C4'	9.54	1.60	1.44
5	F	101	M7G	O4'-C4'	9.46	1.59	1.44
5	H	101	M7G	C4-N3	8.97	1.45	1.34
5	F	101	M7G	C3'-C4'	-8.71	1.30	1.53
5	D	101	M7G	C4-N3	8.71	1.45	1.34

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	H	101	M7G	C5-C4-N3	-4.41	119.28	126.49
5	H	101	M7G	C6-C5-C4	4.15	119.65	115.20
5	D	101	M7G	C6-C5-C4	3.94	119.43	115.20
5	D	101	M7G	C5-C4-N3	-3.82	120.26	126.49
5	J	101	M7G	C6-C5-C4	3.77	119.25	115.20

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

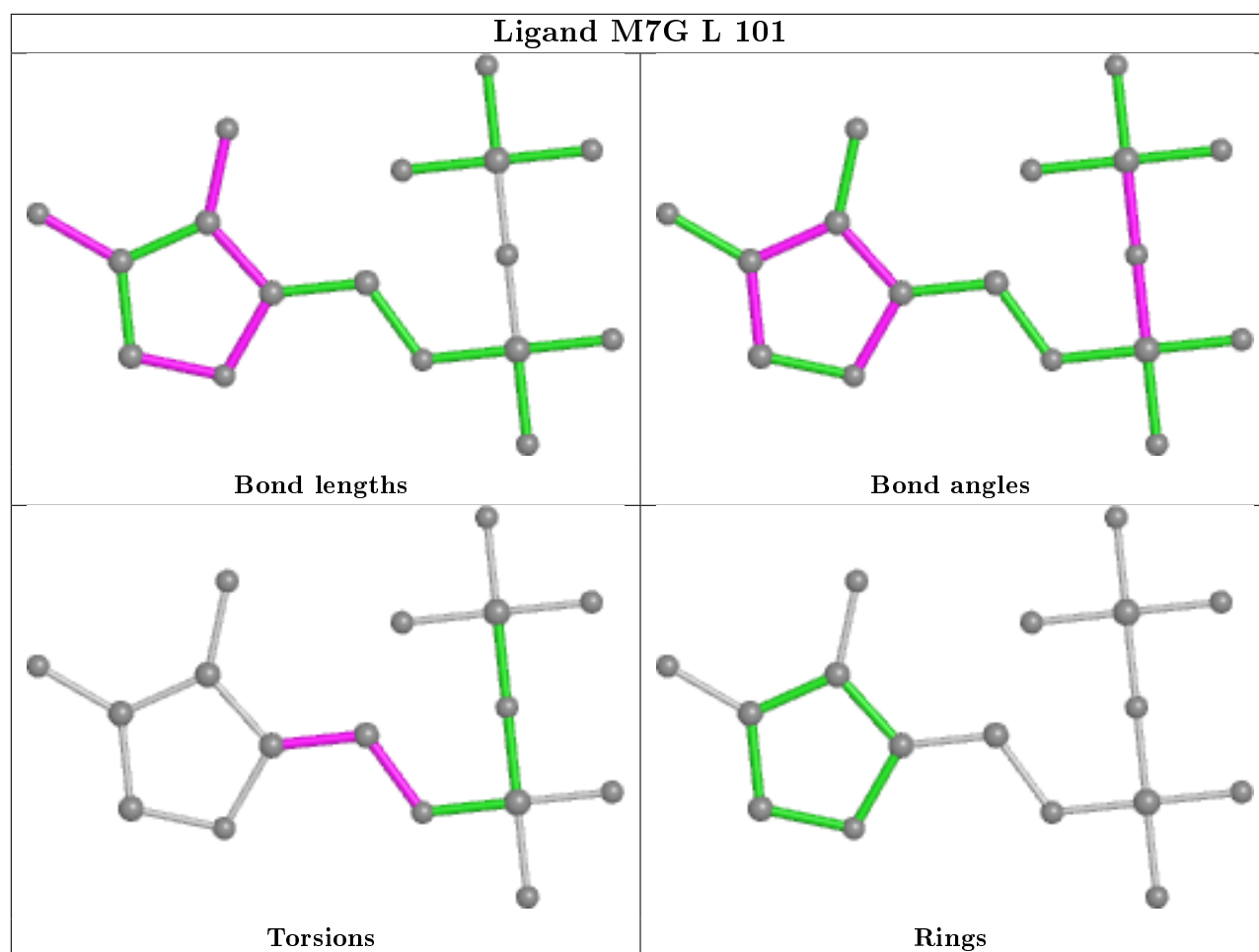
Mol	Chain	Res	Type	Atoms
5	H	101	M7G	O4'-C4'-C5'-O5'
5	H	101	M7G	C3'-C4'-C5'-O5'
5	J	101	M7G	C5'-O5'-PA-O3A
5	B	101	M7G	C5'-O5'-PA-O1A
5	D	101	M7G	C5'-O5'-PA-O1A

There are no ring outliers.

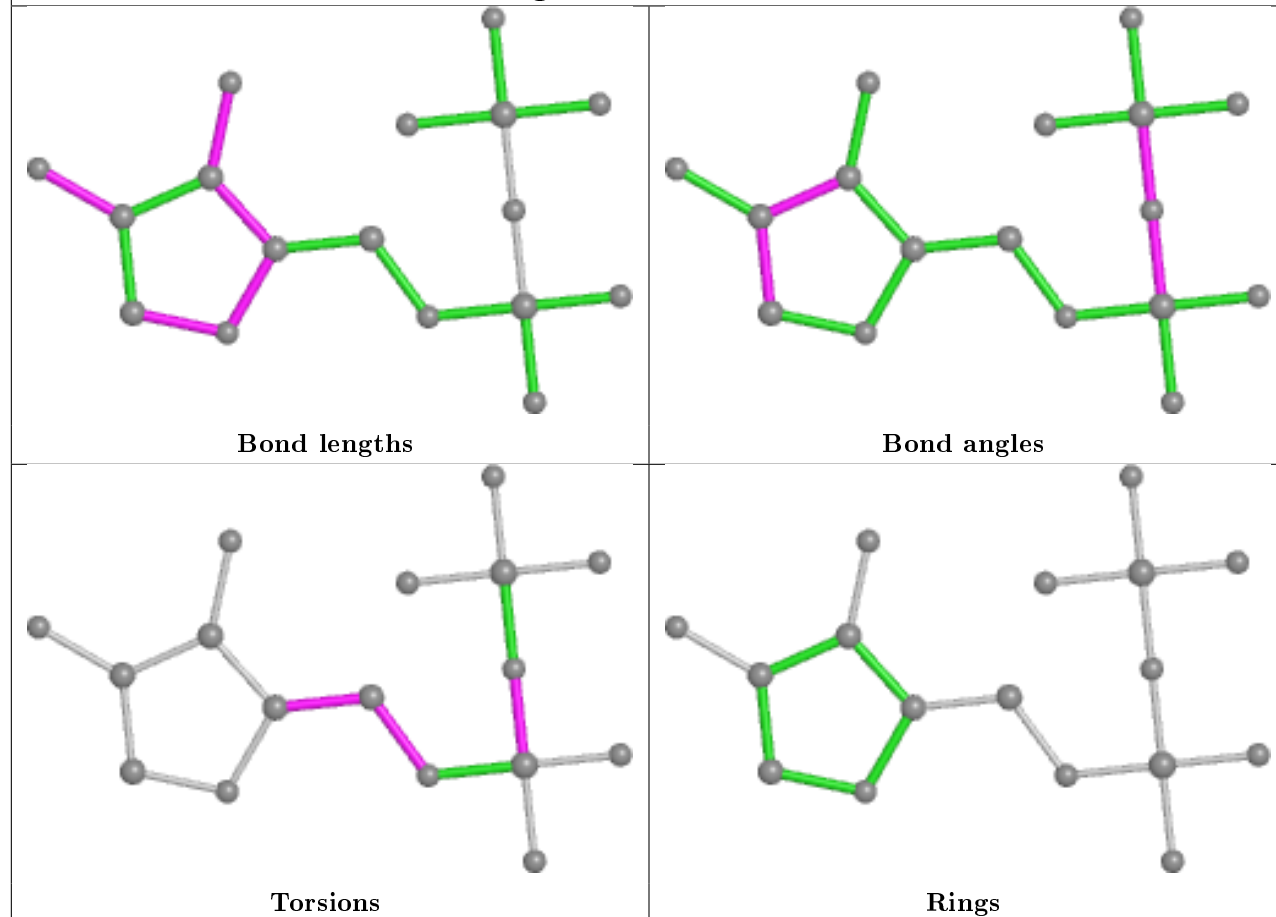
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	J	101	M7G	1	0

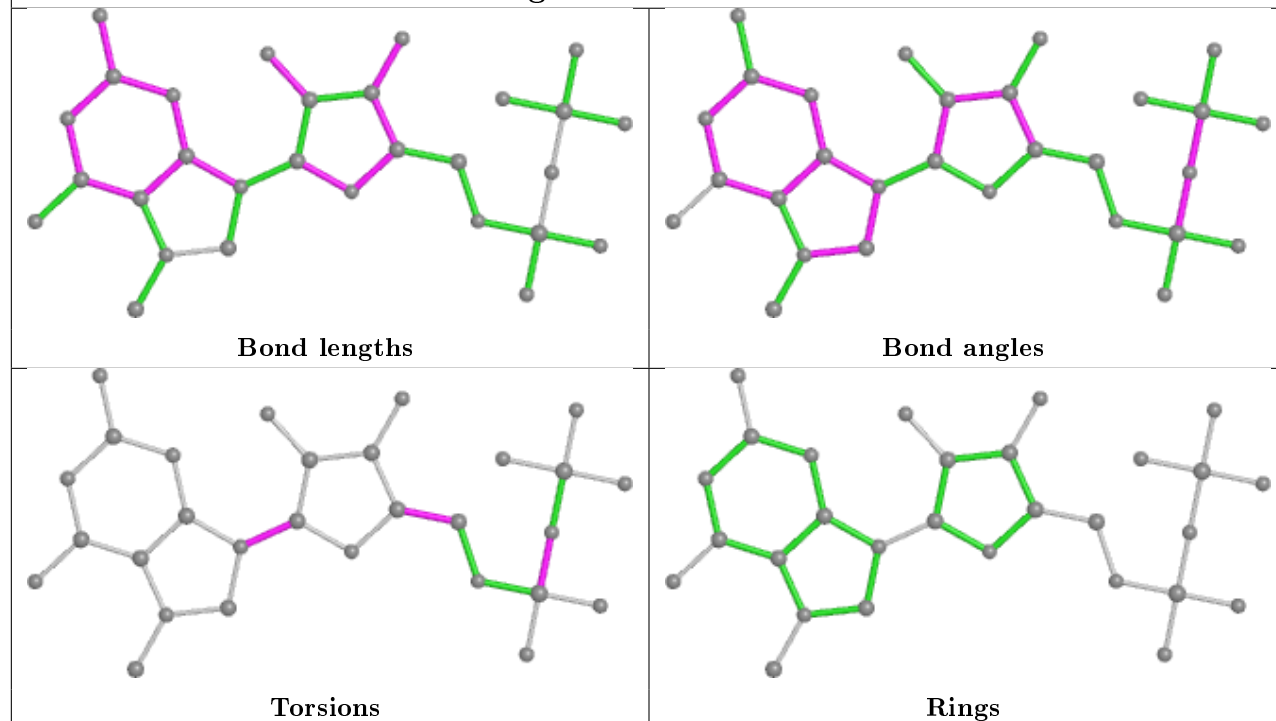
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

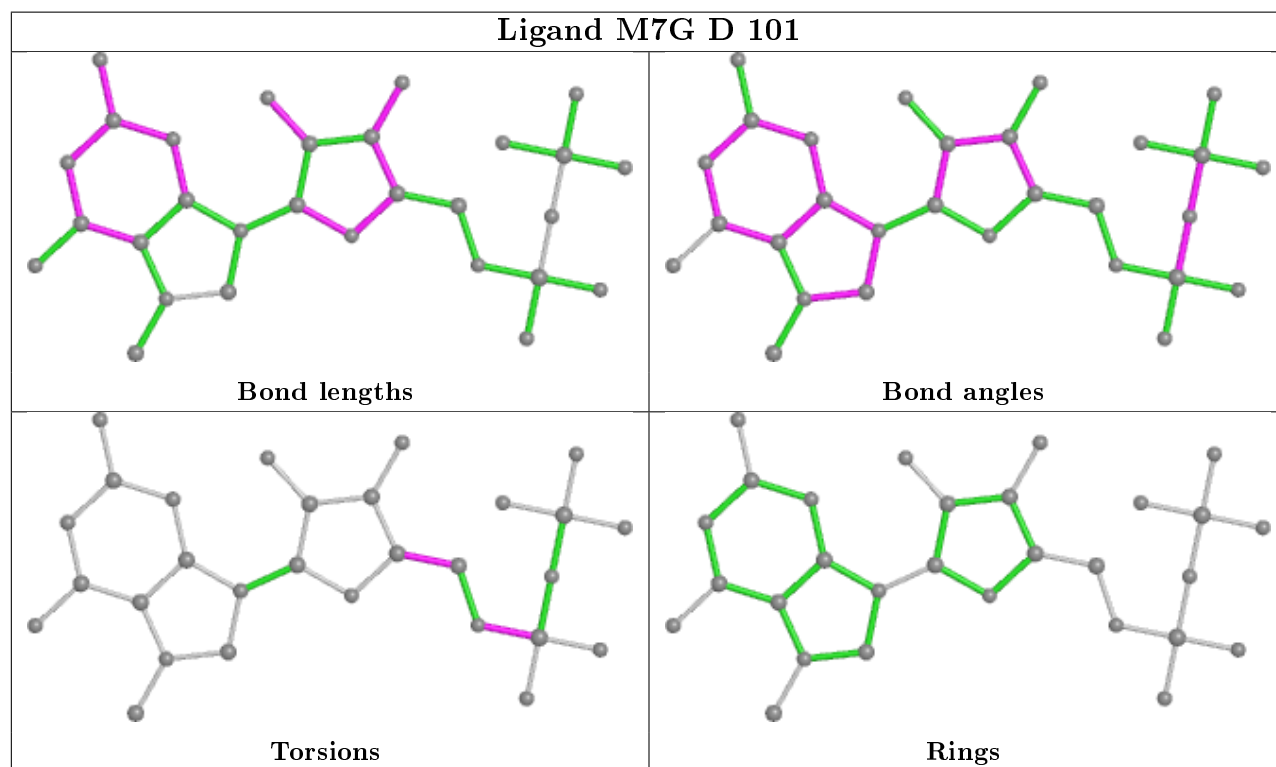
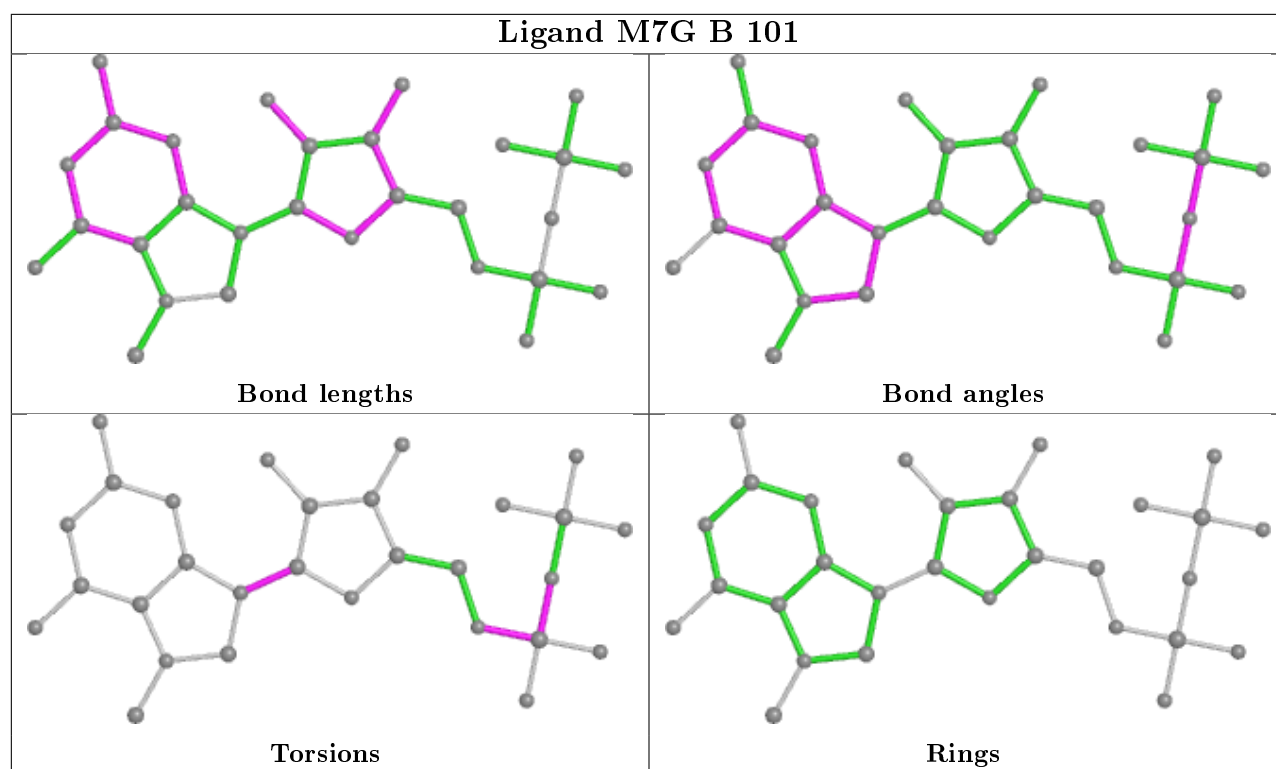


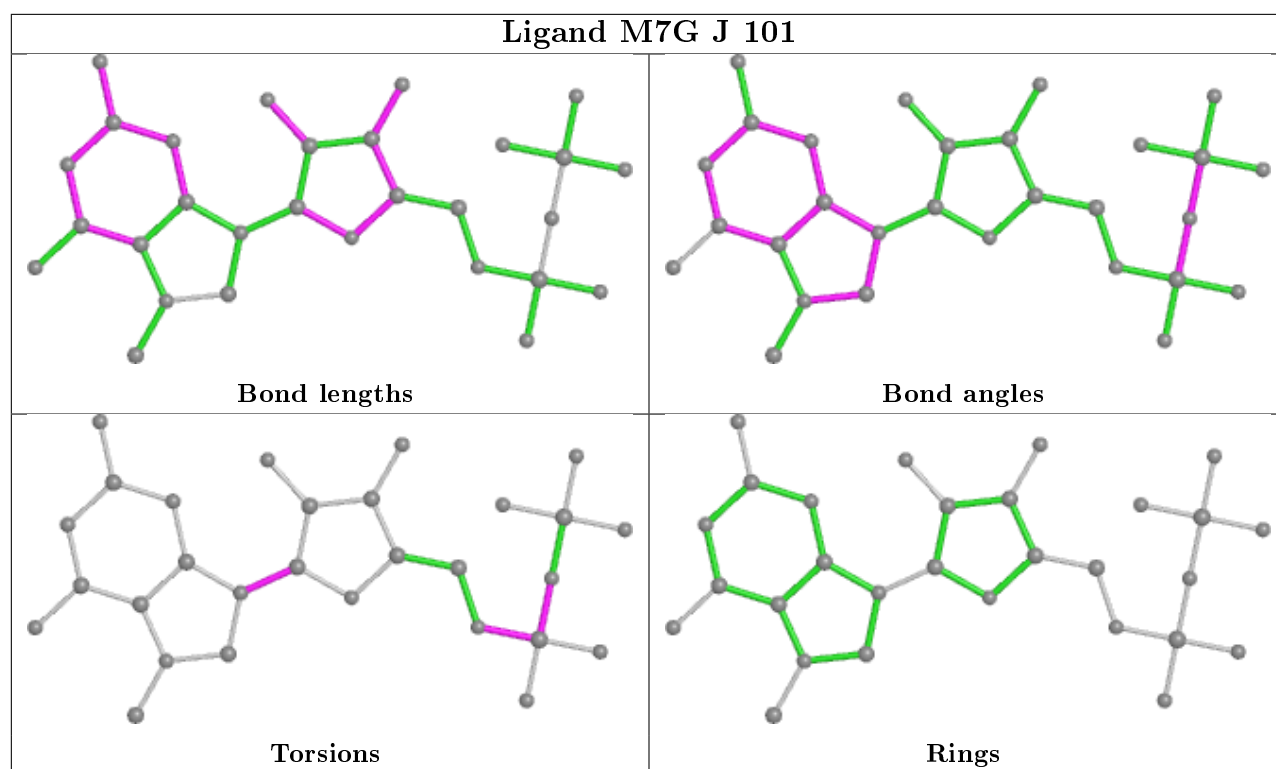
Ligand M7G F 101



Ligand M7G H 101







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	650/695 (93%)	-0.12	1 (0%) 95 96	16, 52, 88, 122	0
1	C	648/695 (93%)	-0.03	6 (0%) 84 84	16, 53, 97, 135	0
1	E	641/695 (92%)	0.09	11 (1%) 70 67	20, 60, 97, 108	0
1	G	647/695 (93%)	-0.00	3 (0%) 91 91	22, 53, 87, 106	0
1	I	647/695 (93%)	-0.07	3 (0%) 91 91	19, 57, 96, 121	0
1	K	644/695 (92%)	0.03	8 (1%) 79 78	21, 57, 97, 123	0
2	B	24/24 (100%)	-0.17	0 100 100	32, 43, 122, 140	0
2	D	24/24 (100%)	-0.30	0 100 100	20, 39, 117, 133	0
2	F	24/24 (100%)	-0.24	0 100 100	34, 51, 111, 118	0
2	H	24/24 (100%)	-0.22	0 100 100	30, 43, 121, 124	0
2	J	24/24 (100%)	-0.28	0 100 100	29, 42, 118, 131	0
2	L	24/24 (100%)	-0.20	0 100 100	33, 45, 114, 132	0
All	All	4021/4314 (93%)	-0.02	32 (0%) 86 86	16, 55, 96, 140	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	473	TYR	4.9
1	E	606	ASN	4.4
1	E	590	PHE	4.0
1	E	599	SER	3.6
1	I	476	ALA	3.4

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

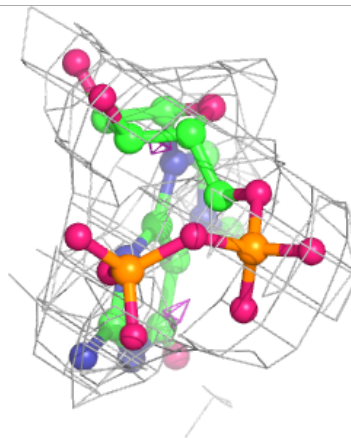
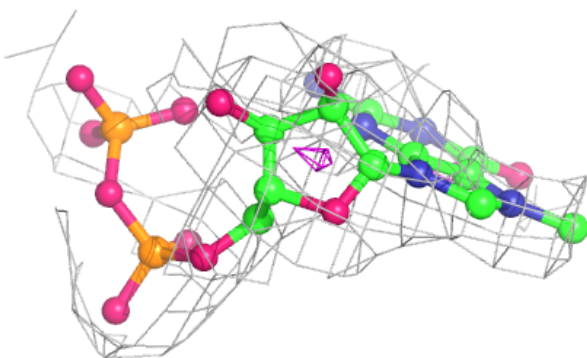
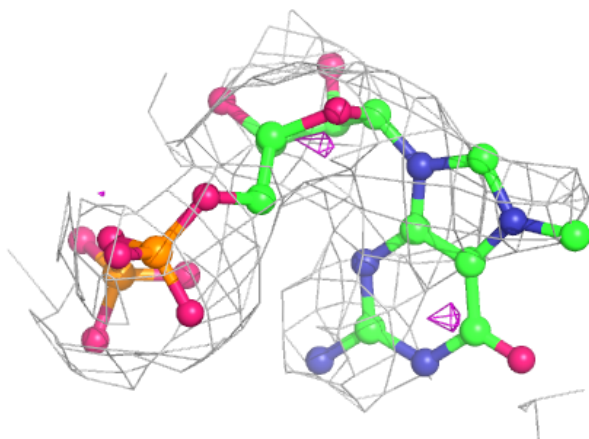
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MG	I	1002	1/1	0.70	0.36	47,47,47,47	0
4	MG	E	1002	1/1	0.83	0.19	46,46,46,46	0
5	M7G	H	101	29/29	0.90	0.21	46,93,124,131	0
4	MG	G	1002	1/1	0.90	0.20	27,27,27,27	0
4	MG	K	1002	1/1	0.91	0.19	18,18,18,18	0
3	ZN	C	1001	1/1	0.92	0.11	50,50,50,50	0
5	M7G	J	101	29/29	0.92	0.24	43,107,137,143	0
4	MG	A	1002	1/1	0.92	0.10	28,28,28,28	0
5	M7G	D	101	29/29	0.93	0.20	42,99,123,127	0
5	M7G	L	101	17/29	0.94	0.16	39,67,94,100	0
5	M7G	B	101	29/29	0.94	0.23	48,112,135,137	0
5	M7G	F	101	17/29	0.95	0.13	64,88,103,109	0
4	MG	C	1002	1/1	0.95	0.13	21,21,21,21	0
3	ZN	K	1001	1/1	0.96	0.11	69,69,69,69	0
3	ZN	E	1001	1/1	0.97	0.10	73,73,73,73	0
3	ZN	I	1001	1/1	0.98	0.13	44,44,44,44	0
3	ZN	A	1001	1/1	0.98	0.13	46,46,46,46	0
3	ZN	G	1001	1/1	0.99	0.23	96,96,96,96	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.

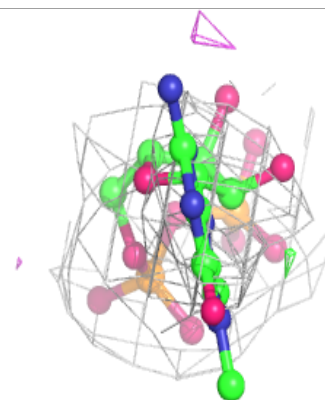
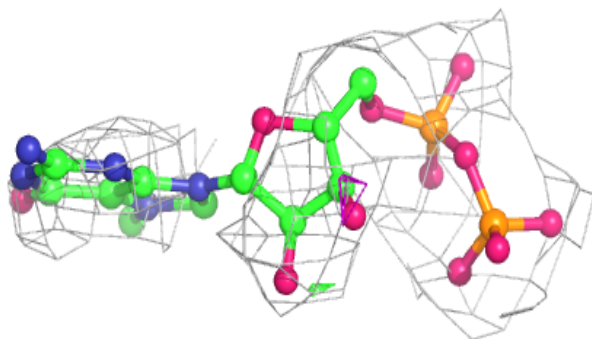
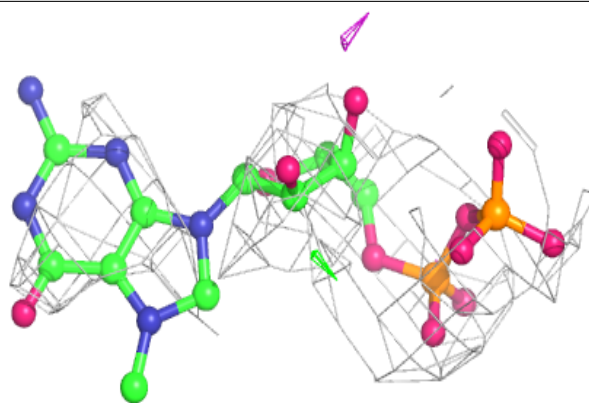
Electron density around M7G H 101:

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

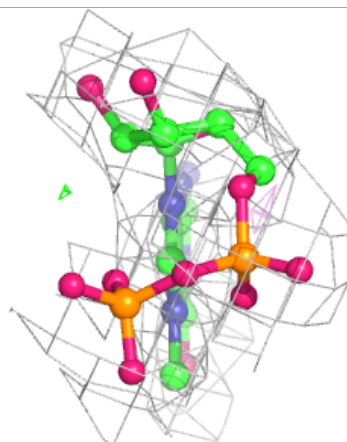
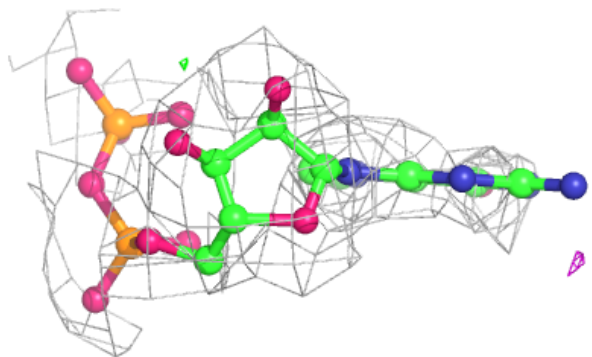
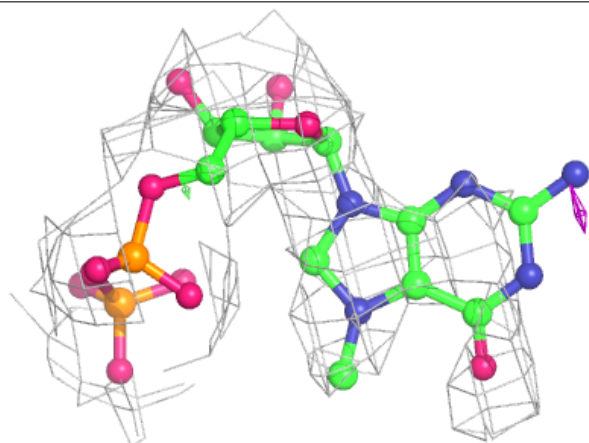


Electron density around M7G J 101:

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

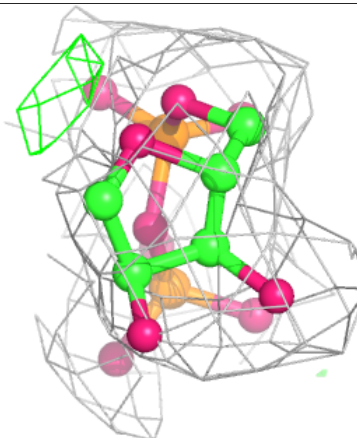
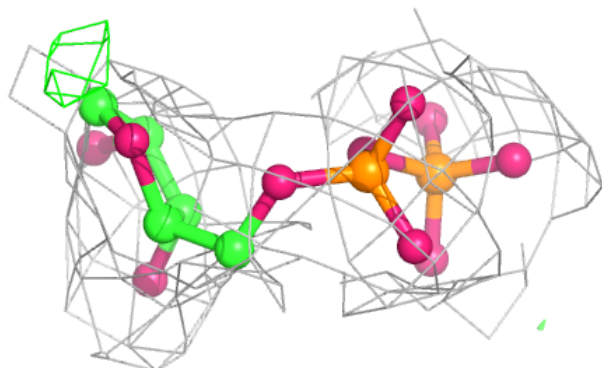
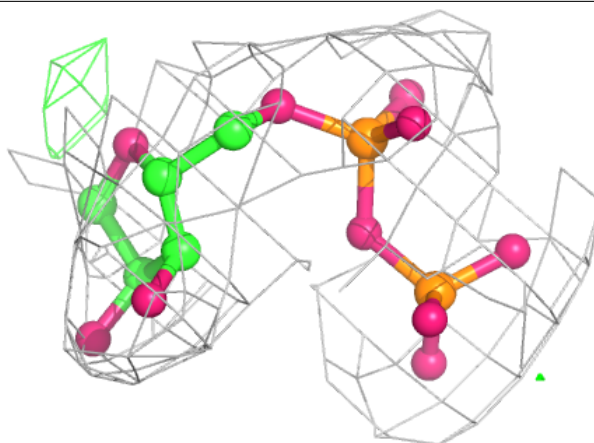
**Electron density around M7G D 101:**

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

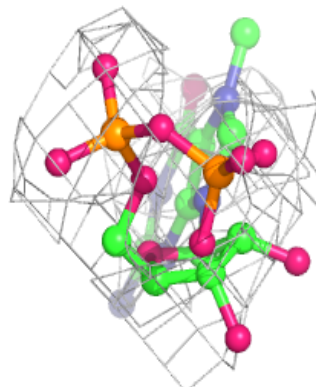
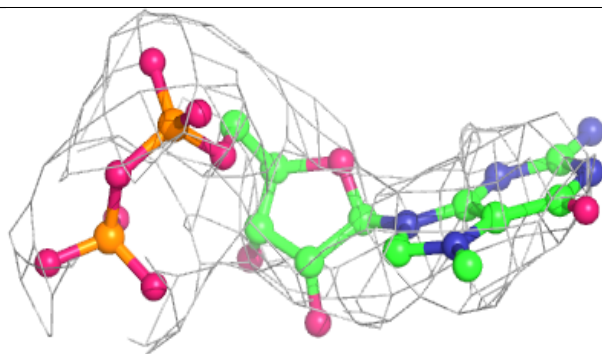
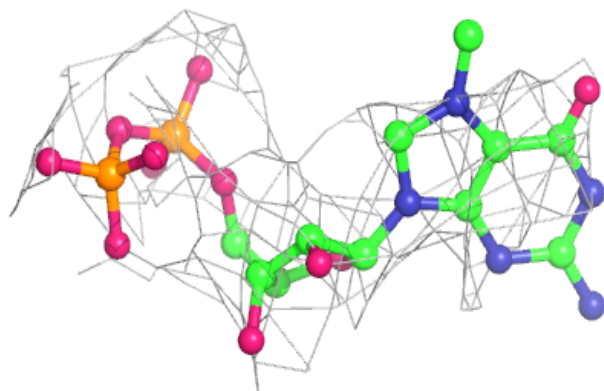


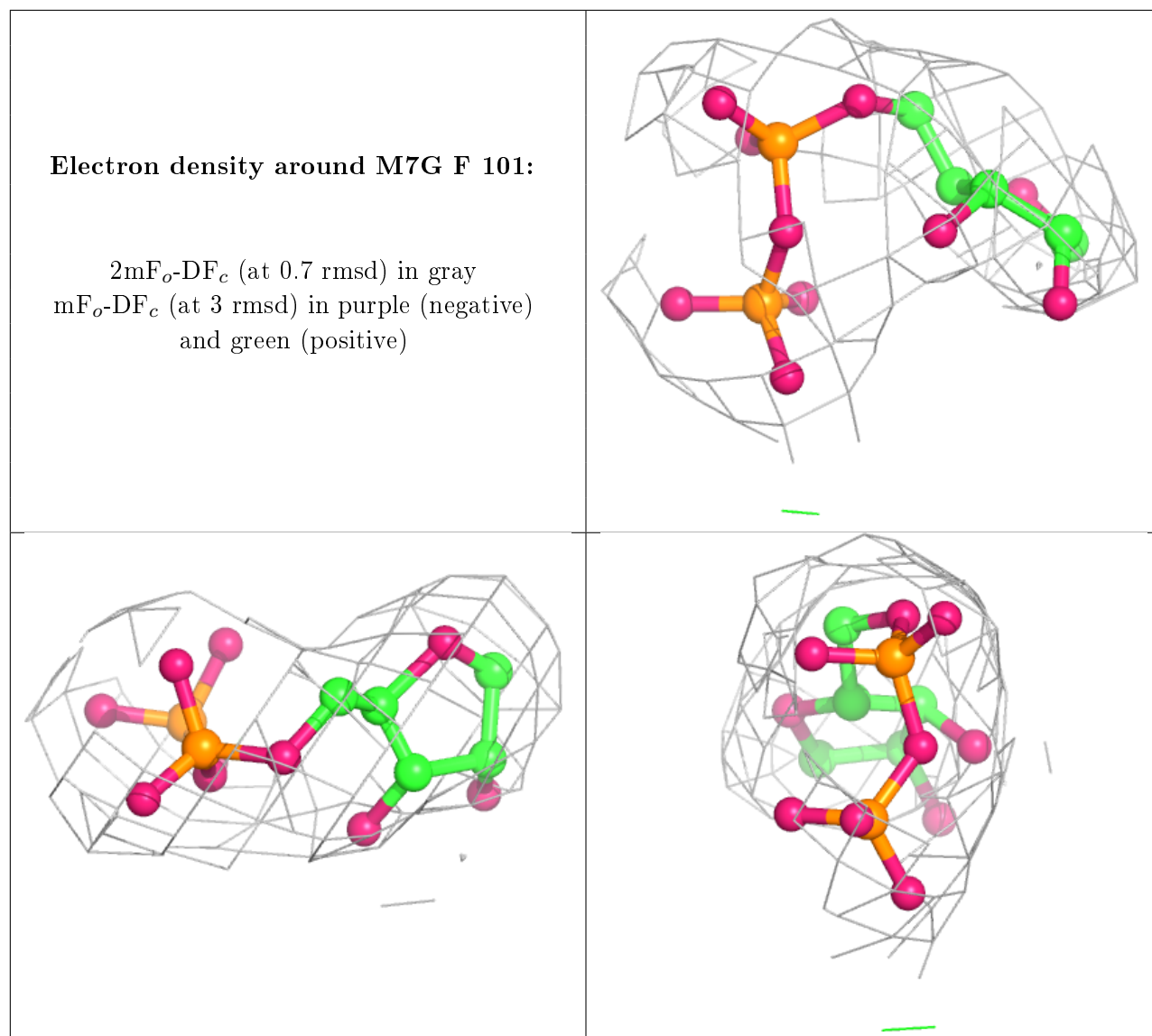
Electron density around M7G L 101:

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

**Electron density around M7G B 101:**

$2mF_o-DF_c$ (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.