Full wwPDB EM Validation Report ⓘ

Nov 23, 2022 – 03:46 AM JST

PDB ID	:	7FGH
EMDB ID	:	EMD-31581
Title	:	Cryo-EM Structure of Chikungunya Virus Nonstructural Protein 1 with m7GMP
Authors	:	Zhang, K.; Law, M.C.Y.; Nguyen, T.M.; Tan, Y.B.; Wirawan, M.; Law, Y.S.; Luo, D.H.
Deposited on	:	2021-07-27
Resolution	:	2.18 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

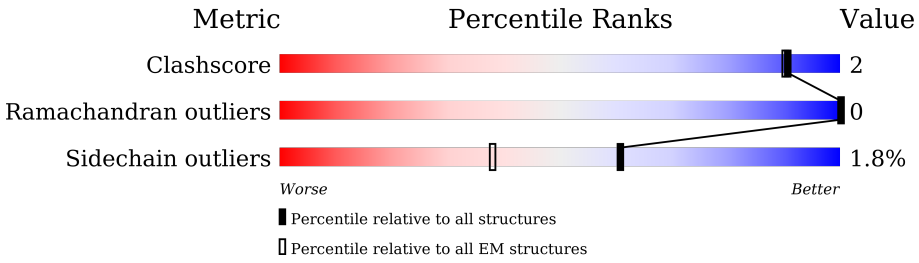
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.18 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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	552	77% 5% 18%
1	B	552	77% 5% 18%
1	C	552	78% 5% 18%
1	D	552	77% 5% 18%
1	E	552	78% 18%
1	F	552	77% 5% 18%
1	G	552	77% 5% 18%
1	H	552	77% 5% 18%

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Mol	Chain	Length	Quality of chain
1	I	552	
1	J	552	
1	K	552	
1	L	552	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 44532 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 mRNA-capping enzyme nsP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	B	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	C	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	D	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	E	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	F	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	G	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	H	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	I	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	J	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	K	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		
1	L	453	Total	C	N	O	S	0	0
			3542	2240	615	660	27		

There are 432 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	517	GLY	-	expression tag	UNP Q8JUX6
A	518	GLY	-	expression tag	UNP Q8JUX6
A	519	GLY	-	expression tag	UNP Q8JUX6
A	520	GLY	-	expression tag	UNP Q8JUX6
A	521	SER	-	expression tag	UNP Q8JUX6
A	522	TRP	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	523	SER	-	expression tag	UNP Q8JUX6
A	524	HIS	-	expression tag	UNP Q8JUX6
A	525	PRO	-	expression tag	UNP Q8JUX6
A	526	GLN	-	expression tag	UNP Q8JUX6
A	527	PHE	-	expression tag	UNP Q8JUX6
A	528	GLU	-	expression tag	UNP Q8JUX6
A	529	LYS	-	expression tag	UNP Q8JUX6
A	530	MET	-	expression tag	UNP Q8JUX6
A	531	ASP	-	expression tag	UNP Q8JUX6
A	532	TYR	-	expression tag	UNP Q8JUX6
A	533	LYS	-	expression tag	UNP Q8JUX6
A	534	ASP	-	expression tag	UNP Q8JUX6
A	535	HIS	-	expression tag	UNP Q8JUX6
A	536	ASP	-	expression tag	UNP Q8JUX6
A	537	GLY	-	expression tag	UNP Q8JUX6
A	538	ASP	-	expression tag	UNP Q8JUX6
A	539	TYR	-	expression tag	UNP Q8JUX6
A	540	LYS	-	expression tag	UNP Q8JUX6
A	541	ASP	-	expression tag	UNP Q8JUX6
A	542	HIS	-	expression tag	UNP Q8JUX6
A	543	ASP	-	expression tag	UNP Q8JUX6
A	544	ILE	-	expression tag	UNP Q8JUX6
A	545	ASP	-	expression tag	UNP Q8JUX6
A	546	TYR	-	expression tag	UNP Q8JUX6
A	547	LYS	-	expression tag	UNP Q8JUX6
A	548	ASP	-	expression tag	UNP Q8JUX6
A	549	ASP	-	expression tag	UNP Q8JUX6
A	550	ASP	-	expression tag	UNP Q8JUX6
A	551	ASP	-	expression tag	UNP Q8JUX6
A	552	LYS	-	expression tag	UNP Q8JUX6
B	517	GLY	-	expression tag	UNP Q8JUX6
B	518	GLY	-	expression tag	UNP Q8JUX6
B	519	GLY	-	expression tag	UNP Q8JUX6
B	520	GLY	-	expression tag	UNP Q8JUX6
B	521	SER	-	expression tag	UNP Q8JUX6
B	522	TRP	-	expression tag	UNP Q8JUX6
B	523	SER	-	expression tag	UNP Q8JUX6
B	524	HIS	-	expression tag	UNP Q8JUX6
B	525	PRO	-	expression tag	UNP Q8JUX6
B	526	GLN	-	expression tag	UNP Q8JUX6
B	527	PHE	-	expression tag	UNP Q8JUX6
B	528	GLU	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	529	LYS	-	expression tag	UNP Q8JUX6
B	530	MET	-	expression tag	UNP Q8JUX6
B	531	ASP	-	expression tag	UNP Q8JUX6
B	532	TYR	-	expression tag	UNP Q8JUX6
B	533	LYS	-	expression tag	UNP Q8JUX6
B	534	ASP	-	expression tag	UNP Q8JUX6
B	535	HIS	-	expression tag	UNP Q8JUX6
B	536	ASP	-	expression tag	UNP Q8JUX6
B	537	GLY	-	expression tag	UNP Q8JUX6
B	538	ASP	-	expression tag	UNP Q8JUX6
B	539	TYR	-	expression tag	UNP Q8JUX6
B	540	LYS	-	expression tag	UNP Q8JUX6
B	541	ASP	-	expression tag	UNP Q8JUX6
B	542	HIS	-	expression tag	UNP Q8JUX6
B	543	ASP	-	expression tag	UNP Q8JUX6
B	544	ILE	-	expression tag	UNP Q8JUX6
B	545	ASP	-	expression tag	UNP Q8JUX6
B	546	TYR	-	expression tag	UNP Q8JUX6
B	547	LYS	-	expression tag	UNP Q8JUX6
B	548	ASP	-	expression tag	UNP Q8JUX6
B	549	ASP	-	expression tag	UNP Q8JUX6
B	550	ASP	-	expression tag	UNP Q8JUX6
B	551	ASP	-	expression tag	UNP Q8JUX6
B	552	LYS	-	expression tag	UNP Q8JUX6
C	517	GLY	-	expression tag	UNP Q8JUX6
C	518	GLY	-	expression tag	UNP Q8JUX6
C	519	GLY	-	expression tag	UNP Q8JUX6
C	520	GLY	-	expression tag	UNP Q8JUX6
C	521	SER	-	expression tag	UNP Q8JUX6
C	522	TRP	-	expression tag	UNP Q8JUX6
C	523	SER	-	expression tag	UNP Q8JUX6
C	524	HIS	-	expression tag	UNP Q8JUX6
C	525	PRO	-	expression tag	UNP Q8JUX6
C	526	GLN	-	expression tag	UNP Q8JUX6
C	527	PHE	-	expression tag	UNP Q8JUX6
C	528	GLU	-	expression tag	UNP Q8JUX6
C	529	LYS	-	expression tag	UNP Q8JUX6
C	530	MET	-	expression tag	UNP Q8JUX6
C	531	ASP	-	expression tag	UNP Q8JUX6
C	532	TYR	-	expression tag	UNP Q8JUX6
C	533	LYS	-	expression tag	UNP Q8JUX6
C	534	ASP	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	535	HIS	-	expression tag	UNP Q8JUX6
C	536	ASP	-	expression tag	UNP Q8JUX6
C	537	GLY	-	expression tag	UNP Q8JUX6
C	538	ASP	-	expression tag	UNP Q8JUX6
C	539	TYR	-	expression tag	UNP Q8JUX6
C	540	LYS	-	expression tag	UNP Q8JUX6
C	541	ASP	-	expression tag	UNP Q8JUX6
C	542	HIS	-	expression tag	UNP Q8JUX6
C	543	ASP	-	expression tag	UNP Q8JUX6
C	544	ILE	-	expression tag	UNP Q8JUX6
C	545	ASP	-	expression tag	UNP Q8JUX6
C	546	TYR	-	expression tag	UNP Q8JUX6
C	547	LYS	-	expression tag	UNP Q8JUX6
C	548	ASP	-	expression tag	UNP Q8JUX6
C	549	ASP	-	expression tag	UNP Q8JUX6
C	550	ASP	-	expression tag	UNP Q8JUX6
C	551	ASP	-	expression tag	UNP Q8JUX6
C	552	LYS	-	expression tag	UNP Q8JUX6
D	517	GLY	-	expression tag	UNP Q8JUX6
D	518	GLY	-	expression tag	UNP Q8JUX6
D	519	GLY	-	expression tag	UNP Q8JUX6
D	520	GLY	-	expression tag	UNP Q8JUX6
D	521	SER	-	expression tag	UNP Q8JUX6
D	522	TRP	-	expression tag	UNP Q8JUX6
D	523	SER	-	expression tag	UNP Q8JUX6
D	524	HIS	-	expression tag	UNP Q8JUX6
D	525	PRO	-	expression tag	UNP Q8JUX6
D	526	GLN	-	expression tag	UNP Q8JUX6
D	527	PHE	-	expression tag	UNP Q8JUX6
D	528	GLU	-	expression tag	UNP Q8JUX6
D	529	LYS	-	expression tag	UNP Q8JUX6
D	530	MET	-	expression tag	UNP Q8JUX6
D	531	ASP	-	expression tag	UNP Q8JUX6
D	532	TYR	-	expression tag	UNP Q8JUX6
D	533	LYS	-	expression tag	UNP Q8JUX6
D	534	ASP	-	expression tag	UNP Q8JUX6
D	535	HIS	-	expression tag	UNP Q8JUX6
D	536	ASP	-	expression tag	UNP Q8JUX6
D	537	GLY	-	expression tag	UNP Q8JUX6
D	538	ASP	-	expression tag	UNP Q8JUX6
D	539	TYR	-	expression tag	UNP Q8JUX6
D	540	LYS	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	541	ASP	-	expression tag	UNP Q8JUX6
D	542	HIS	-	expression tag	UNP Q8JUX6
D	543	ASP	-	expression tag	UNP Q8JUX6
D	544	ILE	-	expression tag	UNP Q8JUX6
D	545	ASP	-	expression tag	UNP Q8JUX6
D	546	TYR	-	expression tag	UNP Q8JUX6
D	547	LYS	-	expression tag	UNP Q8JUX6
D	548	ASP	-	expression tag	UNP Q8JUX6
D	549	ASP	-	expression tag	UNP Q8JUX6
D	550	ASP	-	expression tag	UNP Q8JUX6
D	551	ASP	-	expression tag	UNP Q8JUX6
D	552	LYS	-	expression tag	UNP Q8JUX6
E	517	GLY	-	expression tag	UNP Q8JUX6
E	518	GLY	-	expression tag	UNP Q8JUX6
E	519	GLY	-	expression tag	UNP Q8JUX6
E	520	GLY	-	expression tag	UNP Q8JUX6
E	521	SER	-	expression tag	UNP Q8JUX6
E	522	TRP	-	expression tag	UNP Q8JUX6
E	523	SER	-	expression tag	UNP Q8JUX6
E	524	HIS	-	expression tag	UNP Q8JUX6
E	525	PRO	-	expression tag	UNP Q8JUX6
E	526	GLN	-	expression tag	UNP Q8JUX6
E	527	PHE	-	expression tag	UNP Q8JUX6
E	528	GLU	-	expression tag	UNP Q8JUX6
E	529	LYS	-	expression tag	UNP Q8JUX6
E	530	MET	-	expression tag	UNP Q8JUX6
E	531	ASP	-	expression tag	UNP Q8JUX6
E	532	TYR	-	expression tag	UNP Q8JUX6
E	533	LYS	-	expression tag	UNP Q8JUX6
E	534	ASP	-	expression tag	UNP Q8JUX6
E	535	HIS	-	expression tag	UNP Q8JUX6
E	536	ASP	-	expression tag	UNP Q8JUX6
E	537	GLY	-	expression tag	UNP Q8JUX6
E	538	ASP	-	expression tag	UNP Q8JUX6
E	539	TYR	-	expression tag	UNP Q8JUX6
E	540	LYS	-	expression tag	UNP Q8JUX6
E	541	ASP	-	expression tag	UNP Q8JUX6
E	542	HIS	-	expression tag	UNP Q8JUX6
E	543	ASP	-	expression tag	UNP Q8JUX6
E	544	ILE	-	expression tag	UNP Q8JUX6
E	545	ASP	-	expression tag	UNP Q8JUX6
E	546	TYR	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	547	LYS	-	expression tag	UNP Q8JUX6
E	548	ASP	-	expression tag	UNP Q8JUX6
E	549	ASP	-	expression tag	UNP Q8JUX6
E	550	ASP	-	expression tag	UNP Q8JUX6
E	551	ASP	-	expression tag	UNP Q8JUX6
E	552	LYS	-	expression tag	UNP Q8JUX6
F	517	GLY	-	expression tag	UNP Q8JUX6
F	518	GLY	-	expression tag	UNP Q8JUX6
F	519	GLY	-	expression tag	UNP Q8JUX6
F	520	GLY	-	expression tag	UNP Q8JUX6
F	521	SER	-	expression tag	UNP Q8JUX6
F	522	TRP	-	expression tag	UNP Q8JUX6
F	523	SER	-	expression tag	UNP Q8JUX6
F	524	HIS	-	expression tag	UNP Q8JUX6
F	525	PRO	-	expression tag	UNP Q8JUX6
F	526	GLN	-	expression tag	UNP Q8JUX6
F	527	PHE	-	expression tag	UNP Q8JUX6
F	528	GLU	-	expression tag	UNP Q8JUX6
F	529	LYS	-	expression tag	UNP Q8JUX6
F	530	MET	-	expression tag	UNP Q8JUX6
F	531	ASP	-	expression tag	UNP Q8JUX6
F	532	TYR	-	expression tag	UNP Q8JUX6
F	533	LYS	-	expression tag	UNP Q8JUX6
F	534	ASP	-	expression tag	UNP Q8JUX6
F	535	HIS	-	expression tag	UNP Q8JUX6
F	536	ASP	-	expression tag	UNP Q8JUX6
F	537	GLY	-	expression tag	UNP Q8JUX6
F	538	ASP	-	expression tag	UNP Q8JUX6
F	539	TYR	-	expression tag	UNP Q8JUX6
F	540	LYS	-	expression tag	UNP Q8JUX6
F	541	ASP	-	expression tag	UNP Q8JUX6
F	542	HIS	-	expression tag	UNP Q8JUX6
F	543	ASP	-	expression tag	UNP Q8JUX6
F	544	ILE	-	expression tag	UNP Q8JUX6
F	545	ASP	-	expression tag	UNP Q8JUX6
F	546	TYR	-	expression tag	UNP Q8JUX6
F	547	LYS	-	expression tag	UNP Q8JUX6
F	548	ASP	-	expression tag	UNP Q8JUX6
F	549	ASP	-	expression tag	UNP Q8JUX6
F	550	ASP	-	expression tag	UNP Q8JUX6
F	551	ASP	-	expression tag	UNP Q8JUX6
F	552	LYS	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
G	517	GLY	-	expression tag	UNP Q8JUX6
G	518	GLY	-	expression tag	UNP Q8JUX6
G	519	GLY	-	expression tag	UNP Q8JUX6
G	520	GLY	-	expression tag	UNP Q8JUX6
G	521	SER	-	expression tag	UNP Q8JUX6
G	522	TRP	-	expression tag	UNP Q8JUX6
G	523	SER	-	expression tag	UNP Q8JUX6
G	524	HIS	-	expression tag	UNP Q8JUX6
G	525	PRO	-	expression tag	UNP Q8JUX6
G	526	GLN	-	expression tag	UNP Q8JUX6
G	527	PHE	-	expression tag	UNP Q8JUX6
G	528	GLU	-	expression tag	UNP Q8JUX6
G	529	LYS	-	expression tag	UNP Q8JUX6
G	530	MET	-	expression tag	UNP Q8JUX6
G	531	ASP	-	expression tag	UNP Q8JUX6
G	532	TYR	-	expression tag	UNP Q8JUX6
G	533	LYS	-	expression tag	UNP Q8JUX6
G	534	ASP	-	expression tag	UNP Q8JUX6
G	535	HIS	-	expression tag	UNP Q8JUX6
G	536	ASP	-	expression tag	UNP Q8JUX6
G	537	GLY	-	expression tag	UNP Q8JUX6
G	538	ASP	-	expression tag	UNP Q8JUX6
G	539	TYR	-	expression tag	UNP Q8JUX6
G	540	LYS	-	expression tag	UNP Q8JUX6
G	541	ASP	-	expression tag	UNP Q8JUX6
G	542	HIS	-	expression tag	UNP Q8JUX6
G	543	ASP	-	expression tag	UNP Q8JUX6
G	544	ILE	-	expression tag	UNP Q8JUX6
G	545	ASP	-	expression tag	UNP Q8JUX6
G	546	TYR	-	expression tag	UNP Q8JUX6
G	547	LYS	-	expression tag	UNP Q8JUX6
G	548	ASP	-	expression tag	UNP Q8JUX6
G	549	ASP	-	expression tag	UNP Q8JUX6
G	550	ASP	-	expression tag	UNP Q8JUX6
G	551	ASP	-	expression tag	UNP Q8JUX6
G	552	LYS	-	expression tag	UNP Q8JUX6
H	517	GLY	-	expression tag	UNP Q8JUX6
H	518	GLY	-	expression tag	UNP Q8JUX6
H	519	GLY	-	expression tag	UNP Q8JUX6
H	520	GLY	-	expression tag	UNP Q8JUX6
H	521	SER	-	expression tag	UNP Q8JUX6
H	522	TRP	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
H	523	SER	-	expression tag	UNP Q8JUX6
H	524	HIS	-	expression tag	UNP Q8JUX6
H	525	PRO	-	expression tag	UNP Q8JUX6
H	526	GLN	-	expression tag	UNP Q8JUX6
H	527	PHE	-	expression tag	UNP Q8JUX6
H	528	GLU	-	expression tag	UNP Q8JUX6
H	529	LYS	-	expression tag	UNP Q8JUX6
H	530	MET	-	expression tag	UNP Q8JUX6
H	531	ASP	-	expression tag	UNP Q8JUX6
H	532	TYR	-	expression tag	UNP Q8JUX6
H	533	LYS	-	expression tag	UNP Q8JUX6
H	534	ASP	-	expression tag	UNP Q8JUX6
H	535	HIS	-	expression tag	UNP Q8JUX6
H	536	ASP	-	expression tag	UNP Q8JUX6
H	537	GLY	-	expression tag	UNP Q8JUX6
H	538	ASP	-	expression tag	UNP Q8JUX6
H	539	TYR	-	expression tag	UNP Q8JUX6
H	540	LYS	-	expression tag	UNP Q8JUX6
H	541	ASP	-	expression tag	UNP Q8JUX6
H	542	HIS	-	expression tag	UNP Q8JUX6
H	543	ASP	-	expression tag	UNP Q8JUX6
H	544	ILE	-	expression tag	UNP Q8JUX6
H	545	ASP	-	expression tag	UNP Q8JUX6
H	546	TYR	-	expression tag	UNP Q8JUX6
H	547	LYS	-	expression tag	UNP Q8JUX6
H	548	ASP	-	expression tag	UNP Q8JUX6
H	549	ASP	-	expression tag	UNP Q8JUX6
H	550	ASP	-	expression tag	UNP Q8JUX6
H	551	ASP	-	expression tag	UNP Q8JUX6
H	552	LYS	-	expression tag	UNP Q8JUX6
I	517	GLY	-	expression tag	UNP Q8JUX6
I	518	GLY	-	expression tag	UNP Q8JUX6
I	519	GLY	-	expression tag	UNP Q8JUX6
I	520	GLY	-	expression tag	UNP Q8JUX6
I	521	SER	-	expression tag	UNP Q8JUX6
I	522	TRP	-	expression tag	UNP Q8JUX6
I	523	SER	-	expression tag	UNP Q8JUX6
I	524	HIS	-	expression tag	UNP Q8JUX6
I	525	PRO	-	expression tag	UNP Q8JUX6
I	526	GLN	-	expression tag	UNP Q8JUX6
I	527	PHE	-	expression tag	UNP Q8JUX6
I	528	GLU	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
I	529	LYS	-	expression tag	UNP Q8JUX6
I	530	MET	-	expression tag	UNP Q8JUX6
I	531	ASP	-	expression tag	UNP Q8JUX6
I	532	TYR	-	expression tag	UNP Q8JUX6
I	533	LYS	-	expression tag	UNP Q8JUX6
I	534	ASP	-	expression tag	UNP Q8JUX6
I	535	HIS	-	expression tag	UNP Q8JUX6
I	536	ASP	-	expression tag	UNP Q8JUX6
I	537	GLY	-	expression tag	UNP Q8JUX6
I	538	ASP	-	expression tag	UNP Q8JUX6
I	539	TYR	-	expression tag	UNP Q8JUX6
I	540	LYS	-	expression tag	UNP Q8JUX6
I	541	ASP	-	expression tag	UNP Q8JUX6
I	542	HIS	-	expression tag	UNP Q8JUX6
I	543	ASP	-	expression tag	UNP Q8JUX6
I	544	ILE	-	expression tag	UNP Q8JUX6
I	545	ASP	-	expression tag	UNP Q8JUX6
I	546	TYR	-	expression tag	UNP Q8JUX6
I	547	LYS	-	expression tag	UNP Q8JUX6
I	548	ASP	-	expression tag	UNP Q8JUX6
I	549	ASP	-	expression tag	UNP Q8JUX6
I	550	ASP	-	expression tag	UNP Q8JUX6
I	551	ASP	-	expression tag	UNP Q8JUX6
I	552	LYS	-	expression tag	UNP Q8JUX6
J	517	GLY	-	expression tag	UNP Q8JUX6
J	518	GLY	-	expression tag	UNP Q8JUX6
J	519	GLY	-	expression tag	UNP Q8JUX6
J	520	GLY	-	expression tag	UNP Q8JUX6
J	521	SER	-	expression tag	UNP Q8JUX6
J	522	TRP	-	expression tag	UNP Q8JUX6
J	523	SER	-	expression tag	UNP Q8JUX6
J	524	HIS	-	expression tag	UNP Q8JUX6
J	525	PRO	-	expression tag	UNP Q8JUX6
J	526	GLN	-	expression tag	UNP Q8JUX6
J	527	PHE	-	expression tag	UNP Q8JUX6
J	528	GLU	-	expression tag	UNP Q8JUX6
J	529	LYS	-	expression tag	UNP Q8JUX6
J	530	MET	-	expression tag	UNP Q8JUX6
J	531	ASP	-	expression tag	UNP Q8JUX6
J	532	TYR	-	expression tag	UNP Q8JUX6
J	533	LYS	-	expression tag	UNP Q8JUX6
J	534	ASP	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
J	535	HIS	-	expression tag	UNP Q8JUX6
J	536	ASP	-	expression tag	UNP Q8JUX6
J	537	GLY	-	expression tag	UNP Q8JUX6
J	538	ASP	-	expression tag	UNP Q8JUX6
J	539	TYR	-	expression tag	UNP Q8JUX6
J	540	LYS	-	expression tag	UNP Q8JUX6
J	541	ASP	-	expression tag	UNP Q8JUX6
J	542	HIS	-	expression tag	UNP Q8JUX6
J	543	ASP	-	expression tag	UNP Q8JUX6
J	544	ILE	-	expression tag	UNP Q8JUX6
J	545	ASP	-	expression tag	UNP Q8JUX6
J	546	TYR	-	expression tag	UNP Q8JUX6
J	547	LYS	-	expression tag	UNP Q8JUX6
J	548	ASP	-	expression tag	UNP Q8JUX6
J	549	ASP	-	expression tag	UNP Q8JUX6
J	550	ASP	-	expression tag	UNP Q8JUX6
J	551	ASP	-	expression tag	UNP Q8JUX6
J	552	LYS	-	expression tag	UNP Q8JUX6
K	517	GLY	-	expression tag	UNP Q8JUX6
K	518	GLY	-	expression tag	UNP Q8JUX6
K	519	GLY	-	expression tag	UNP Q8JUX6
K	520	GLY	-	expression tag	UNP Q8JUX6
K	521	SER	-	expression tag	UNP Q8JUX6
K	522	TRP	-	expression tag	UNP Q8JUX6
K	523	SER	-	expression tag	UNP Q8JUX6
K	524	HIS	-	expression tag	UNP Q8JUX6
K	525	PRO	-	expression tag	UNP Q8JUX6
K	526	GLN	-	expression tag	UNP Q8JUX6
K	527	PHE	-	expression tag	UNP Q8JUX6
K	528	GLU	-	expression tag	UNP Q8JUX6
K	529	LYS	-	expression tag	UNP Q8JUX6
K	530	MET	-	expression tag	UNP Q8JUX6
K	531	ASP	-	expression tag	UNP Q8JUX6
K	532	TYR	-	expression tag	UNP Q8JUX6
K	533	LYS	-	expression tag	UNP Q8JUX6
K	534	ASP	-	expression tag	UNP Q8JUX6
K	535	HIS	-	expression tag	UNP Q8JUX6
K	536	ASP	-	expression tag	UNP Q8JUX6
K	537	GLY	-	expression tag	UNP Q8JUX6
K	538	ASP	-	expression tag	UNP Q8JUX6
K	539	TYR	-	expression tag	UNP Q8JUX6
K	540	LYS	-	expression tag	UNP Q8JUX6

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Chain	Residue	Modelled	Actual	Comment	Reference
K	541	ASP	-	expression tag	UNP Q8JUX6
K	542	HIS	-	expression tag	UNP Q8JUX6
K	543	ASP	-	expression tag	UNP Q8JUX6
K	544	ILE	-	expression tag	UNP Q8JUX6
K	545	ASP	-	expression tag	UNP Q8JUX6
K	546	TYR	-	expression tag	UNP Q8JUX6
K	547	LYS	-	expression tag	UNP Q8JUX6
K	548	ASP	-	expression tag	UNP Q8JUX6
K	549	ASP	-	expression tag	UNP Q8JUX6
K	550	ASP	-	expression tag	UNP Q8JUX6
K	551	ASP	-	expression tag	UNP Q8JUX6
K	552	LYS	-	expression tag	UNP Q8JUX6
L	517	GLY	-	expression tag	UNP Q8JUX6
L	518	GLY	-	expression tag	UNP Q8JUX6
L	519	GLY	-	expression tag	UNP Q8JUX6
L	520	GLY	-	expression tag	UNP Q8JUX6
L	521	SER	-	expression tag	UNP Q8JUX6
L	522	TRP	-	expression tag	UNP Q8JUX6
L	523	SER	-	expression tag	UNP Q8JUX6
L	524	HIS	-	expression tag	UNP Q8JUX6
L	525	PRO	-	expression tag	UNP Q8JUX6
L	526	GLN	-	expression tag	UNP Q8JUX6
L	527	PHE	-	expression tag	UNP Q8JUX6
L	528	GLU	-	expression tag	UNP Q8JUX6
L	529	LYS	-	expression tag	UNP Q8JUX6
L	530	MET	-	expression tag	UNP Q8JUX6
L	531	ASP	-	expression tag	UNP Q8JUX6
L	532	TYR	-	expression tag	UNP Q8JUX6
L	533	LYS	-	expression tag	UNP Q8JUX6
L	534	ASP	-	expression tag	UNP Q8JUX6
L	535	HIS	-	expression tag	UNP Q8JUX6
L	536	ASP	-	expression tag	UNP Q8JUX6
L	537	GLY	-	expression tag	UNP Q8JUX6
L	538	ASP	-	expression tag	UNP Q8JUX6
L	539	TYR	-	expression tag	UNP Q8JUX6
L	540	LYS	-	expression tag	UNP Q8JUX6
L	541	ASP	-	expression tag	UNP Q8JUX6
L	542	HIS	-	expression tag	UNP Q8JUX6
L	543	ASP	-	expression tag	UNP Q8JUX6
L	544	ILE	-	expression tag	UNP Q8JUX6
L	545	ASP	-	expression tag	UNP Q8JUX6
L	546	TYR	-	expression tag	UNP Q8JUX6

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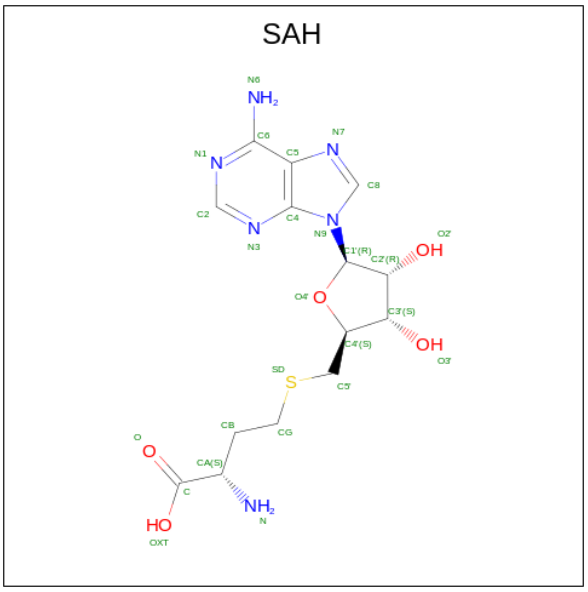
Chain	Residue	Modelled	Actual	Comment	Reference
L	547	LYS	-	expression tag	UNP Q8JUX6
L	548	ASP	-	expression tag	UNP Q8JUX6
L	549	ASP	-	expression tag	UNP Q8JUX6
L	550	ASP	-	expression tag	UNP Q8JUX6
L	551	ASP	-	expression tag	UNP Q8JUX6
L	552	LYS	-	expression tag	UNP Q8JUX6

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

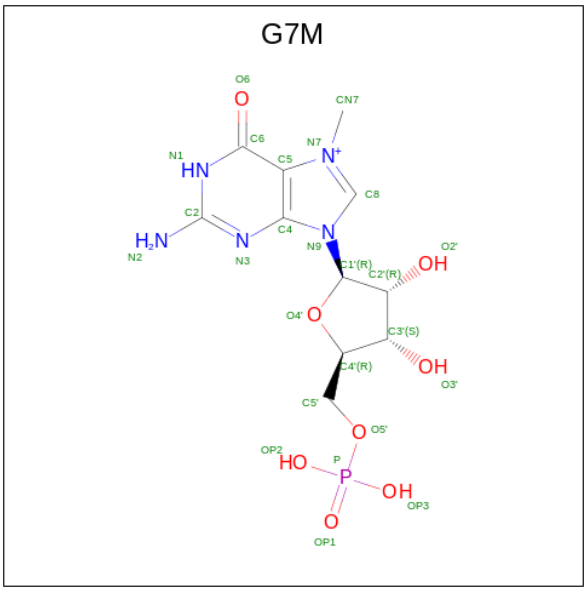
Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total Zn 1 1	0
2	B	1	Total Zn 1 1	0
2	C	1	Total Zn 1 1	0
2	D	1	Total Zn 1 1	0
2	E	1	Total Zn 1 1	0
2	F	1	Total Zn 1 1	0
2	G	1	Total Zn 1 1	0
2	H	1	Total Zn 1 1	0
2	I	1	Total Zn 1 1	0
2	J	1	Total Zn 1 1	0
2	K	1	Total Zn 1 1	0
2	L	1	Total Zn 1 1	0

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	B	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	C	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	D	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	E	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	F	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	G	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	H	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	I	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	J	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	K	1	Total	C	N	O	S	0
			26	14	6	5	1	
3	L	1	Total	C	N	O	S	0
			26	14	6	5	1	

- Molecule 4 is N7-METHYL-GUANOSINE-5'-MONOPHOSPHATE (three-letter code: G7M) (formula: $C_{11}H_{17}N_5O_8P$).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	B	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	C	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	D	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	E	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	F	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	G	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	H	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	I	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	J	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	K	1	Total	C	N	O	P	0
			24	11	5	7	1	
4	L	1	Total	C	N	O	P	0
			24	11	5	7	1	

- Molecule 5 is water.

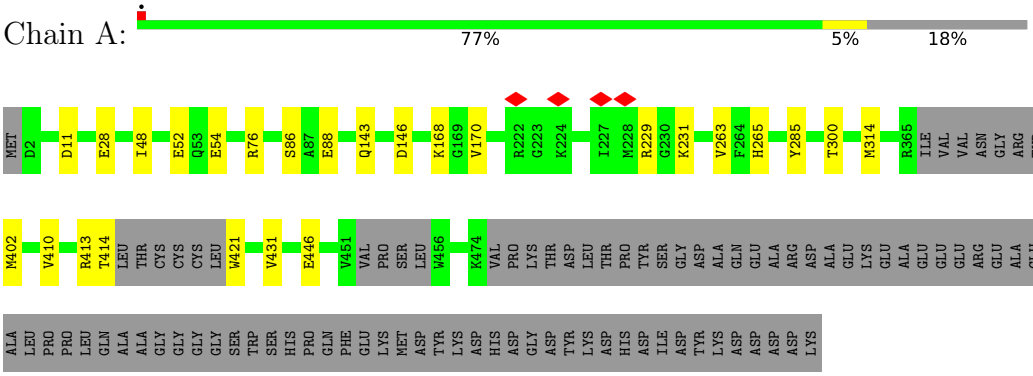
Mol	Chain	Residues	Atoms	AltConf
5	A	118	Total O 118 118	0
5	B	118	Total O 118 118	0
5	C	118	Total O 118 118	0
5	D	118	Total O 118 118	0
5	E	118	Total O 118 118	0
5	F	118	Total O 118 118	0
5	G	118	Total O 118 118	0
5	H	118	Total O 118 118	0
5	I	118	Total O 118 118	0
5	J	118	Total O 118 118	0
5	K	118	Total O 118 118	0
5	L	118	Total O 118 118	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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

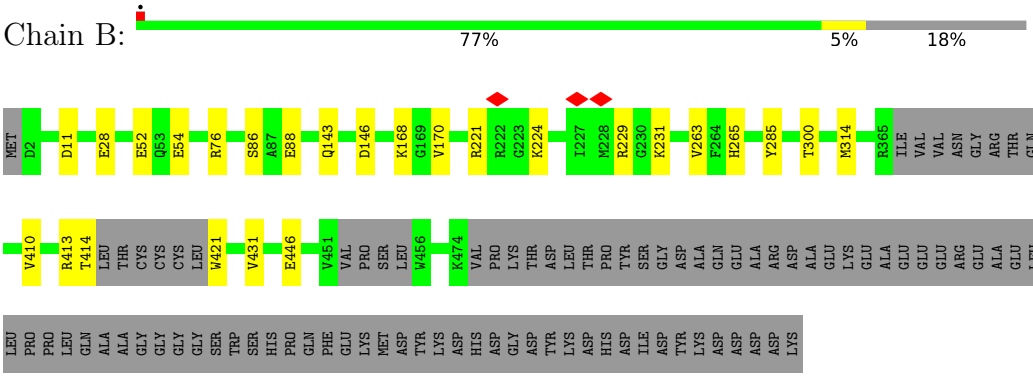
• Molecule 1: mRNA-capping enzyme nsP1

Chain A:



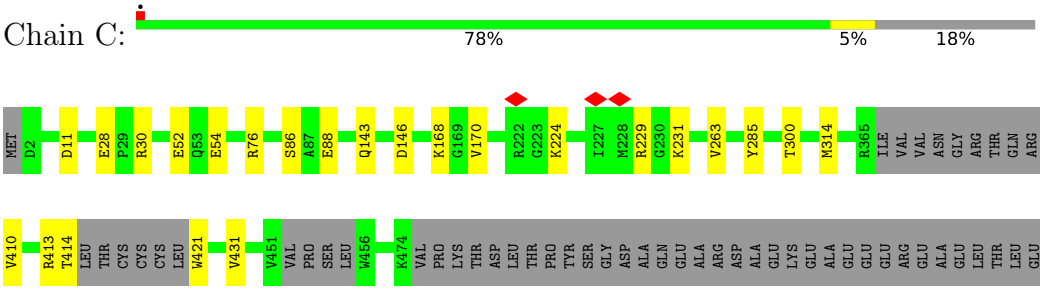
• Molecule 1: mRNA-capping enzyme nsP1

Chain B:



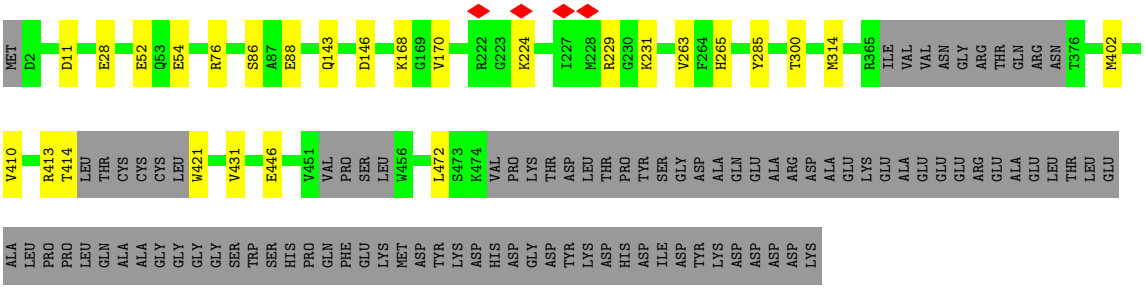
• Molecule 1: mRNA-capping enzyme nsP1

Chain C:



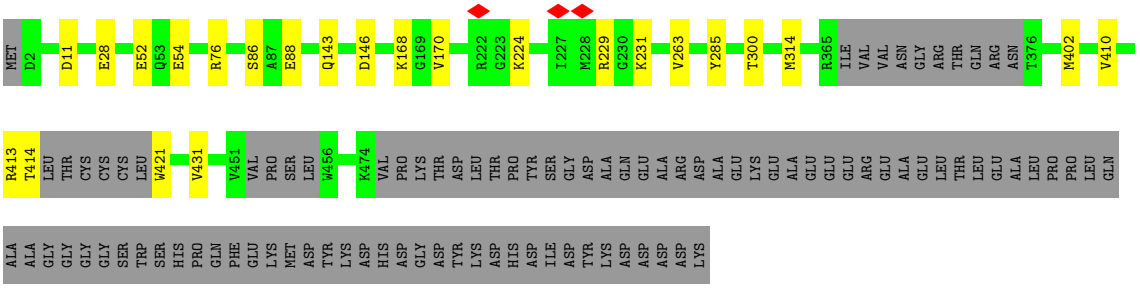
• Molecule 1: mRNA-capping enzyme nsP1

Chain D:



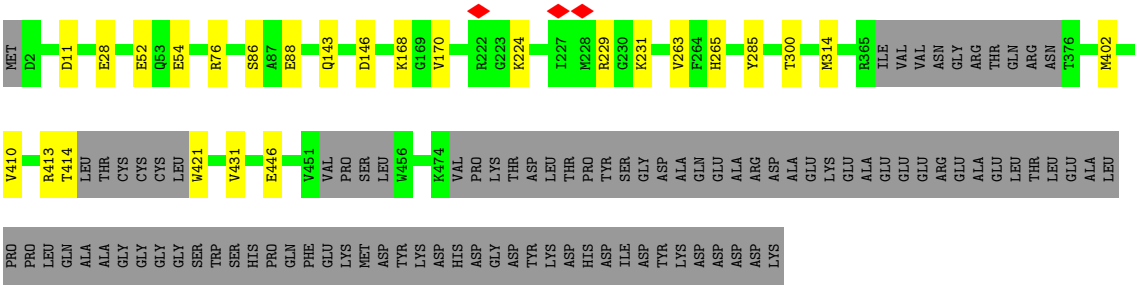
• Molecule 1: mRNA-capping enzyme nsP1

Chain E:



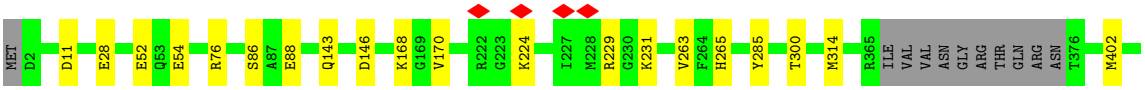
• Molecule 1: mRNA-capping enzyme nsP1

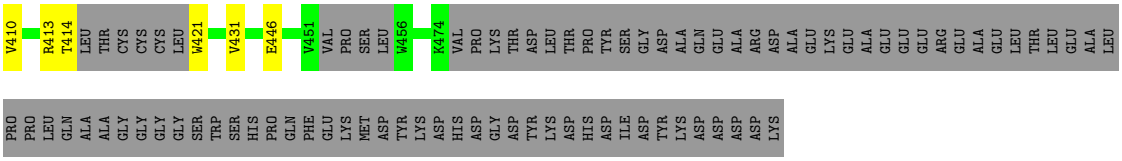
Chain F:



• Molecule 1: mRNA-capping enzyme nsP1

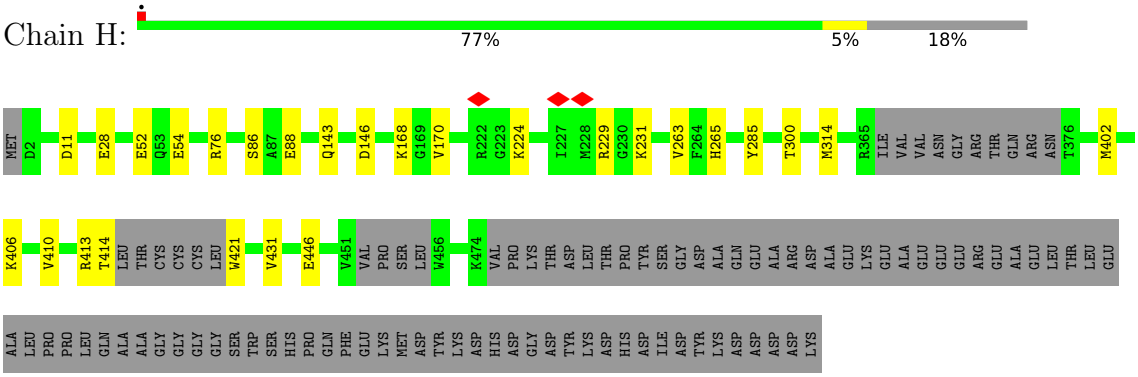
Chain G:





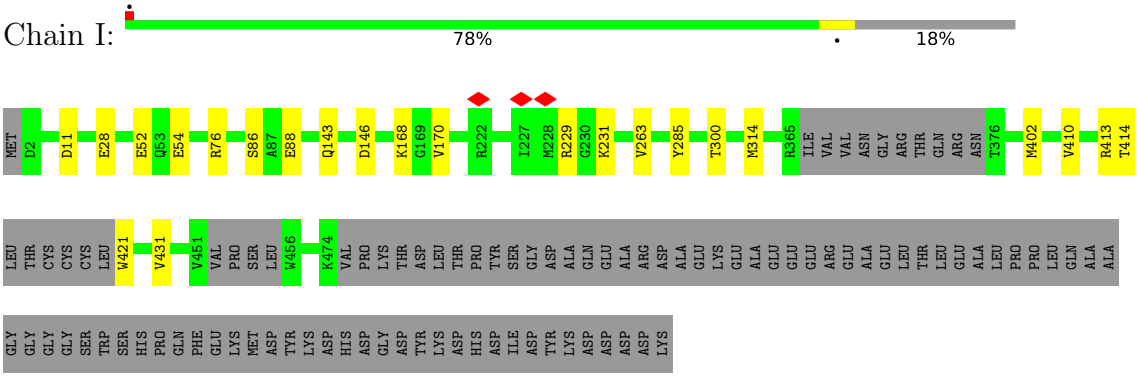
• Molecule 1: mRNA-capping enzyme nsP1

Chain H:



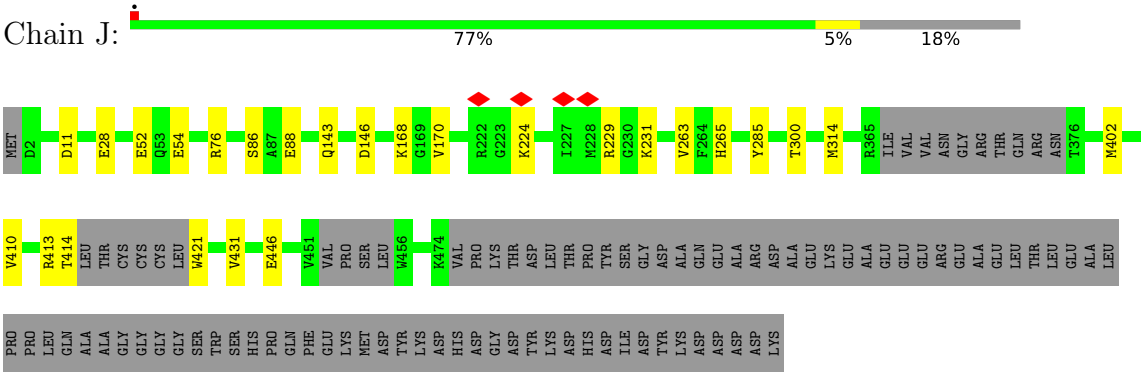
• Molecule 1: mRNA-capping enzyme nsP1

Chain I:



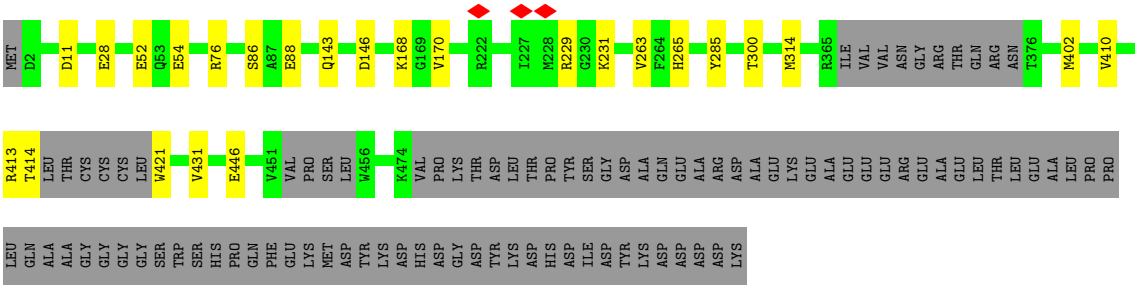
• Molecule 1: mRNA-capping enzyme nsP1

Chain J:



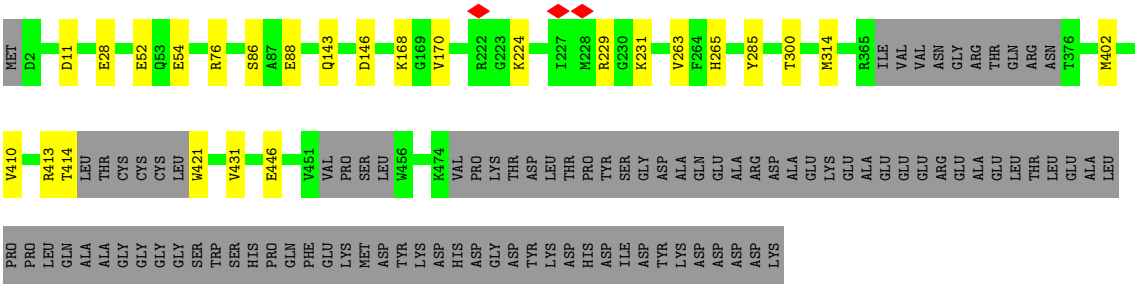
• Molecule 1: mRNA-capping enzyme nsP1

Chain K:



• Molecule 1: mRNA-capping enzyme nsP1

Chain L:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	225575	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.496	Depositor
Minimum map value	-1.194	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	408.0, 408.0, 408.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, G7M, SAH

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	0.36	0/3618	0.54	0/4902
1	B	0.36	0/3618	0.54	0/4902
1	C	0.36	0/3618	0.54	0/4902
1	D	0.36	0/3618	0.54	0/4902
1	E	0.36	0/3618	0.54	0/4902
1	F	0.36	0/3618	0.54	0/4902
1	G	0.36	0/3618	0.54	0/4902
1	H	0.36	0/3618	0.54	0/4902
1	I	0.36	0/3618	0.54	0/4902
1	J	0.36	0/3618	0.54	0/4902
1	K	0.36	0/3618	0.54	0/4902
1	L	0.36	0/3618	0.54	0/4902
All	All	0.36	0/43416	0.54	0/58824

There are no bond length outliers.

There are no bond angle outliers.

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	3542	0	3505	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3542	0	3505	14	0
1	C	3542	0	3505	12	0
1	D	3542	0	3505	14	0
1	E	3542	0	3505	12	0
1	F	3542	0	3505	13	0
1	G	3542	0	3505	12	0
1	H	3542	0	3505	12	0
1	I	3542	0	3505	9	0
1	J	3542	0	3505	13	0
1	K	3542	0	3505	11	0
1	L	3542	0	3505	12	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	26	0	19	1	0
3	B	26	0	19	1	0
3	C	26	0	19	1	0
3	D	26	0	19	1	0
3	E	26	0	19	1	0
3	F	26	0	19	1	0
3	G	26	0	19	1	0
3	H	26	0	19	1	0
3	I	26	0	19	1	0
3	J	26	0	19	1	0
3	K	26	0	19	1	0
3	L	26	0	19	1	0
4	A	24	0	14	0	0
4	B	24	0	14	0	0
4	C	24	0	14	0	0
4	D	24	0	14	0	0
4	E	24	0	14	0	0
4	F	24	0	14	0	0
4	G	24	0	14	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	24	0	14	0	0
4	I	24	0	14	0	0
4	J	24	0	14	0	0
4	K	24	0	14	0	0
4	L	24	0	14	0	0
5	A	118	0	0	0	0
5	B	118	0	0	0	0
5	C	118	0	0	0	0
5	D	118	0	0	0	0
5	E	118	0	0	0	0
5	F	118	0	0	0	0
5	G	118	0	0	0	0
5	H	118	0	0	0	0
5	I	118	0	0	0	0
5	J	118	0	0	0	0
5	K	118	0	0	0	0
5	L	118	0	0	0	0
All	All	44532	0	42456	139	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 2.

All (139) 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:414:THR:O	1:A:421:TRP:N	2.33	0.62
1:B:414:THR:O	1:B:421:TRP:N	2.33	0.62
1:C:414:THR:O	1:C:421:TRP:N	2.33	0.62
1:H:414:THR:O	1:H:421:TRP:N	2.33	0.62
1:L:414:THR:O	1:L:421:TRP:N	2.33	0.62
1:I:414:THR:O	1:I:421:TRP:N	2.33	0.62
1:D:414:THR:O	1:D:421:TRP:N	2.33	0.61
1:G:414:THR:O	1:G:421:TRP:N	2.33	0.61
1:J:414:THR:O	1:J:421:TRP:N	2.33	0.61
1:K:414:THR:O	1:K:421:TRP:N	2.33	0.61
1:E:414:THR:O	1:E:421:TRP:N	2.33	0.61
1:F:414:THR:O	1:F:421:TRP:N	2.33	0.61
1:D:314:MET:HB3	1:D:431:VAL:HG22	1.86	0.58
1:B:314:MET:HB3	1:B:431:VAL:HG22	1.86	0.58
1:A:314:MET:HB3	1:A:431:VAL:HG22	1.86	0.58
1:E:314:MET:HB3	1:E:431:VAL:HG22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:314:MET:HB3	1:G:431:VAL:HG22	1.86	0.57
1:C:314:MET:HB3	1:C:431:VAL:HG22	1.86	0.57
1:F:314:MET:HB3	1:F:431:VAL:HG22	1.86	0.56
1:I:314:MET:HB3	1:I:431:VAL:HG22	1.86	0.56
1:K:314:MET:HB3	1:K:431:VAL:HG22	1.86	0.56
1:H:314:MET:HB3	1:H:431:VAL:HG22	1.86	0.56
1:J:314:MET:HB3	1:J:431:VAL:HG22	1.86	0.56
1:L:314:MET:HB3	1:L:431:VAL:HG22	1.86	0.56
1:C:86:SER:OG	1:C:88:GLU:OE1	2.26	0.54
1:B:86:SER:OG	1:B:88:GLU:OE1	2.26	0.54
1:J:86:SER:OG	1:J:88:GLU:OE1	2.26	0.54
1:D:86:SER:OG	1:D:88:GLU:OE1	2.26	0.54
1:I:86:SER:OG	1:I:88:GLU:OE1	2.26	0.54
1:A:86:SER:OG	1:A:88:GLU:OE1	2.26	0.54
1:H:86:SER:OG	1:H:88:GLU:OE1	2.26	0.53
1:K:86:SER:OG	1:K:88:GLU:OE1	2.26	0.53
1:E:86:SER:OG	1:E:88:GLU:OE1	2.26	0.53
1:G:86:SER:OG	1:G:88:GLU:OE1	2.26	0.53
1:L:86:SER:OG	1:L:88:GLU:OE1	2.26	0.53
1:F:86:SER:OG	1:F:88:GLU:OE1	2.26	0.53
1:I:231:LYS:HZ1	1:J:413:ARG:H	1.58	0.52
1:G:263:VAL:HG12	1:G:300:THR:HG22	1.93	0.51
1:E:263:VAL:HG12	1:E:300:THR:HG22	1.93	0.51
1:D:263:VAL:HG12	1:D:300:THR:HG22	1.93	0.51
1:F:263:VAL:HG12	1:F:300:THR:HG22	1.93	0.51
1:L:263:VAL:HG12	1:L:300:THR:HG22	1.93	0.51
1:H:263:VAL:HG12	1:H:300:THR:HG22	1.93	0.51
1:A:146:ASP:HA	1:A:170:VAL:HA	1.93	0.50
1:A:263:VAL:HG12	1:A:300:THR:HG22	1.93	0.50
1:K:263:VAL:HG12	1:K:300:THR:HG22	1.93	0.50
1:K:146:ASP:HA	1:K:170:VAL:HA	1.93	0.50
1:D:146:ASP:HA	1:D:170:VAL:HA	1.93	0.50
1:B:146:ASP:HA	1:B:170:VAL:HA	1.93	0.50
1:B:263:VAL:HG12	1:B:300:THR:HG22	1.93	0.50
1:J:263:VAL:HG12	1:J:300:THR:HG22	1.93	0.50
1:C:263:VAL:HG12	1:C:300:THR:HG22	1.93	0.50
1:A:52:GLU:O	1:A:76:ARG:NH1	2.45	0.50
1:C:146:ASP:HA	1:C:170:VAL:HA	1.93	0.50
1:E:52:GLU:O	1:E:76:ARG:NH1	2.45	0.50
1:I:263:VAL:HG12	1:I:300:THR:HG22	1.93	0.50
1:K:52:GLU:O	1:K:76:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:52:GLU:O	1:G:76:ARG:NH1	2.45	0.49
1:I:52:GLU:O	1:I:76:ARG:NH1	2.45	0.49
1:I:146:ASP:HA	1:I:170:VAL:HA	1.93	0.49
1:C:52:GLU:O	1:C:76:ARG:NH1	2.45	0.49
1:F:146:ASP:HA	1:F:170:VAL:HA	1.93	0.49
1:H:52:GLU:O	1:H:76:ARG:NH1	2.45	0.49
1:B:52:GLU:O	1:B:76:ARG:NH1	2.45	0.49
1:L:146:ASP:HA	1:L:170:VAL:HA	1.93	0.49
1:D:52:GLU:O	1:D:76:ARG:NH1	2.45	0.49
1:J:52:GLU:O	1:J:76:ARG:NH1	2.45	0.49
1:E:146:ASP:HA	1:E:170:VAL:HA	1.93	0.49
1:G:146:ASP:HA	1:G:170:VAL:HA	1.93	0.49
1:F:52:GLU:O	1:F:76:ARG:NH1	2.45	0.49
1:L:52:GLU:O	1:L:76:ARG:NH1	2.45	0.48
1:H:146:ASP:HA	1:H:170:VAL:HA	1.93	0.48
1:J:146:ASP:HA	1:J:170:VAL:HA	1.93	0.48
3:K:1002:SAH:H4'	3:K:1002:SAH:HG1	1.61	0.47
3:F:1002:SAH:HG1	3:F:1002:SAH:H4'	1.61	0.47
1:J:231:LYS:HZ1	1:K:413:ARG:H	1.61	0.47
3:H:1002:SAH:HG1	3:H:1002:SAH:H4'	1.61	0.47
1:K:143:GLN:O	1:K:168:LYS:HE3	2.15	0.47
1:L:143:GLN:O	1:L:168:LYS:HE3	2.15	0.47
1:J:143:GLN:O	1:J:168:LYS:HE3	2.15	0.47
1:A:143:GLN:O	1:A:168:LYS:HE3	2.15	0.47
1:I:143:GLN:O	1:I:168:LYS:HE3	2.15	0.46
3:I:1002:SAH:HG1	3:I:1002:SAH:H4'	1.61	0.46
1:B:143:GLN:O	1:B:168:LYS:HE3	2.15	0.46
1:H:143:GLN:O	1:H:168:LYS:HE3	2.15	0.46
1:C:143:GLN:O	1:C:168:LYS:HE3	2.15	0.46
3:D:1002:SAH:HG1	3:D:1002:SAH:H4'	1.61	0.46
3:C:1002:SAH:HG1	3:C:1002:SAH:H4'	1.61	0.46
1:G:143:GLN:O	1:G:168:LYS:HE3	2.15	0.46
1:D:143:GLN:O	1:D:168:LYS:HE3	2.15	0.45
1:F:143:GLN:O	1:F:168:LYS:HE3	2.15	0.45
1:E:143:GLN:O	1:E:168:LYS:HE3	2.15	0.45
3:L:1002:SAH:HG1	3:L:1002:SAH:H4'	1.61	0.45
1:B:224:LYS:HD2	1:B:224:LYS:HA	1.83	0.45
1:A:231:LYS:HZ1	1:B:413:ARG:H	1.64	0.45
1:C:231:LYS:HZ1	1:D:413:ARG:H	1.64	0.45
1:E:224:LYS:HD2	1:E:224:LYS:HA	1.83	0.44
1:D:224:LYS:HD2	1:D:224:LYS:HA	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:1002:SAH:HG1	3:B:1002:SAH:H4'	1.61	0.44
1:B:231:LYS:HZ1	1:C:413:ARG:H	1.65	0.43
1:D:231:LYS:HZ1	1:E:413:ARG:H	1.65	0.43
1:F:224:LYS:HD2	1:F:224:LYS:HA	1.83	0.43
3:J:1002:SAH:HG1	3:J:1002:SAH:H4'	1.61	0.43
1:H:231:LYS:NZ	1:I:413:ARG:H	2.17	0.42
1:C:224:LYS:HD2	1:C:224:LYS:HA	1.83	0.42
1:A:231:LYS:NZ	1:B:413:ARG:H	2.17	0.42
3:G:1002:SAH:HG1	3:G:1002:SAH:H4'	1.61	0.42
3:A:1002:SAH:H4'	3:A:1002:SAH:HG1	1.61	0.42
1:E:231:LYS:HZ1	1:F:413:ARG:H	1.67	0.42
1:J:224:LYS:HA	1:J:224:LYS:HD2	1.83	0.42
1:G:224:LYS:HA	1:G:224:LYS:HD2	1.83	0.41
1:F:231:LYS:NZ	1:G:413:ARG:H	2.18	0.41
1:C:231:LYS:NZ	1:D:413:ARG:H	2.18	0.41
1:L:224:LYS:HD2	1:L:224:LYS:HA	1.83	0.41
1:B:265:HIS:HB2	1:B:446:GLU:OE1	2.21	0.41
1:K:231:LYS:NZ	1:L:413:ARG:H	2.18	0.41
3:E:1002:SAH:H4'	3:E:1002:SAH:HG1	1.61	0.41
1:D:472:LEU:HD23	1:D:472:LEU:HA	1.96	0.41
1:L:265:HIS:HB2	1:L:446:GLU:OE1	2.21	0.41
1:B:221:ARG:H	1:B:221:ARG:HG2	1.74	0.41
1:B:231:LYS:NZ	1:C:413:ARG:H	2.18	0.41
1:D:265:HIS:HB2	1:D:446:GLU:OE1	2.21	0.41
1:A:48:ILE:HD13	1:A:48:ILE:HA	1.92	0.41
1:A:413:ARG:H	1:L:231:LYS:NZ	2.19	0.41
1:G:231:LYS:NZ	1:H:413:ARG:H	2.19	0.41
1:H:406:LYS:HA	1:H:406:LYS:HD3	1.92	0.41
1:J:231:LYS:HD3	1:J:231:LYS:HA	1.93	0.41
1:K:265:HIS:HB2	1:K:446:GLU:OE1	2.21	0.41
1:F:265:HIS:HB2	1:F:446:GLU:OE1	2.21	0.40
1:G:265:HIS:HB2	1:G:446:GLU:OE1	2.21	0.40
1:J:231:LYS:NZ	1:K:413:ARG:H	2.18	0.40
1:E:231:LYS:NZ	1:F:413:ARG:H	2.18	0.40
1:A:265:HIS:HB2	1:A:446:GLU:OE1	2.21	0.40
1:J:265:HIS:HB2	1:J:446:GLU:OE1	2.21	0.40
1:A:413:ARG:H	1:L:231:LYS:HZ3	1.69	0.40
1:D:231:LYS:NZ	1:E:413:ARG:H	2.18	0.40
1:F:231:LYS:HZ1	1:G:413:ARG:H	1.69	0.40
1:H:224:LYS:HA	1:H:224:LYS:HD2	1.83	0.40
1:H:265:HIS:HB2	1:H:446:GLU:OE1	2.21	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 PDB entries followed by that with respect to all EM entries.

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	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	B	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	C	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	D	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	E	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	F	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	G	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	H	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	I	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	J	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	K	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
1	L	445/552 (81%)	428 (96%)	17 (4%)	0	100	100
All	All	5340/6624 (81%)	5136 (96%)	204 (4%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	B	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	C	383/475 (81%)	375 (98%)	8 (2%)	53	64
1	D	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	E	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	F	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	G	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	H	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	I	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	J	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	K	383/475 (81%)	376 (98%)	7 (2%)	59	70
1	L	383/475 (81%)	376 (98%)	7 (2%)	59	70
All	All	4596/5700 (81%)	4511 (98%)	85 (2%)	61	70

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ASP
1	A	28	GLU
1	A	54	GLU
1	A	229	ARG
1	A	285	TYR
1	A	402	MET
1	A	410	VAL
1	B	11	ASP
1	B	28	GLU
1	B	54	GLU
1	B	229	ARG
1	B	285	TYR
1	B	402	MET
1	B	410	VAL
1	C	11	ASP
1	C	28	GLU
1	C	30	ARG
1	C	54	GLU
1	C	229	ARG
1	C	285	TYR
1	C	402	MET
1	C	410	VAL

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Mol	Chain	Res	Type
1	D	11	ASP
1	D	28	GLU
1	D	54	GLU
1	D	229	ARG
1	D	285	TYR
1	D	402	MET
1	D	410	VAL
1	E	11	ASP
1	E	28	GLU
1	E	54	GLU
1	E	229	ARG
1	E	285	TYR
1	E	402	MET
1	E	410	VAL
1	F	11	ASP
1	F	28	GLU
1	F	54	GLU
1	F	229	ARG
1	F	285	TYR
1	F	402	MET
1	F	410	VAL
1	G	11	ASP
1	G	28	GLU
1	G	54	GLU
1	G	229	ARG
1	G	285	TYR
1	G	402	MET
1	G	410	VAL
1	H	11	ASP
1	H	28	GLU
1	H	54	GLU
1	H	229	ARG
1	H	285	TYR
1	H	402	MET
1	H	410	VAL
1	I	11	ASP
1	I	28	GLU
1	I	54	GLU
1	I	229	ARG
1	I	285	TYR
1	I	402	MET
1	I	410	VAL

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Mol	Chain	Res	Type
1	J	11	ASP
1	J	28	GLU
1	J	54	GLU
1	J	229	ARG
1	J	285	TYR
1	J	402	MET
1	J	410	VAL
1	K	11	ASP
1	K	28	GLU
1	K	54	GLU
1	K	229	ARG
1	K	285	TYR
1	K	402	MET
1	K	410	VAL
1	L	11	ASP
1	L	28	GLU
1	L	54	GLU
1	L	229	ARG
1	L	285	TYR
1	L	402	MET
1	L	410	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 36 ligands modelled in this entry, 12 are monoatomic - leaving 24 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	SAH	K	1002	-	24,28,28	1.14	2 (8%)	25,40,40	1.68	4 (16%)
4	G7M	J	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)
4	G7M	H	1003	1	20,26,27	3.99	12 (60%)	17,39,42	1.61	4 (23%)
4	G7M	G	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)
3	SAH	C	1002	-	24,28,28	1.16	2 (8%)	25,40,40	1.68	4 (16%)
3	SAH	A	1002	-	24,28,28	1.16	2 (8%)	25,40,40	1.68	4 (16%)
3	SAH	D	1002	-	24,28,28	1.16	2 (8%)	25,40,40	1.68	4 (16%)
3	SAH	L	1002	-	24,28,28	1.16	2 (8%)	25,40,40	1.68	4 (16%)
3	SAH	G	1002	-	24,28,28	1.16	2 (8%)	25,40,40	1.68	4 (16%)
3	SAH	H	1002	-	24,28,28	1.16	2 (8%)	25,40,40	1.68	4 (16%)
3	SAH	I	1002	-	24,28,28	1.15	2 (8%)	25,40,40	1.68	4 (16%)
3	SAH	F	1002	-	24,28,28	1.15	2 (8%)	25,40,40	1.68	4 (16%)
4	G7M	C	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)
4	G7M	F	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)
4	G7M	D	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)
3	SAH	B	1002	-	24,28,28	1.15	2 (8%)	25,40,40	1.68	4 (16%)
4	G7M	B	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)
3	SAH	E	1002	-	24,28,28	1.16	2 (8%)	25,40,40	1.68	4 (16%)
4	G7M	E	1003	1	20,26,27	3.99	12 (60%)	17,39,42	1.61	4 (23%)
4	G7M	K	1003	1	20,26,27	3.97	12 (60%)	17,39,42	1.61	4 (23%)
4	G7M	I	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)
4	G7M	L	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)
3	SAH	J	1002	-	24,28,28	1.16	2 (8%)	25,40,40	1.68	4 (16%)
4	G7M	A	1003	1	20,26,27	3.98	12 (60%)	17,39,42	1.61	4 (23%)

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	SAH	K	1002	-	-	2/11/31/31	0/3/3/3
4	G7M	J	1003	1	-	1/3/25/26	0/3/3/3
4	G7M	H	1003	1	-	1/3/25/26	0/3/3/3
4	G7M	G	1003	1	-	1/3/25/26	0/3/3/3
3	SAH	C	1002	-	-	2/11/31/31	0/3/3/3
3	SAH	A	1002	-	-	2/11/31/31	0/3/3/3
3	SAH	D	1002	-	-	2/11/31/31	0/3/3/3
3	SAH	L	1002	-	-	2/11/31/31	0/3/3/3
3	SAH	G	1002	-	-	2/11/31/31	0/3/3/3
3	SAH	H	1002	-	-	2/11/31/31	0/3/3/3
3	SAH	I	1002	-	-	2/11/31/31	0/3/3/3
3	SAH	F	1002	-	-	2/11/31/31	0/3/3/3
4	G7M	C	1003	1	-	1/3/25/26	0/3/3/3
4	G7M	F	1003	1	-	1/3/25/26	0/3/3/3
4	G7M	D	1003	1	-	1/3/25/26	0/3/3/3
3	SAH	B	1002	-	-	2/11/31/31	0/3/3/3
4	G7M	B	1003	1	-	1/3/25/26	0/3/3/3
3	SAH	E	1002	-	-	2/11/31/31	0/3/3/3
4	G7M	E	1003	1	-	1/3/25/26	0/3/3/3
4	G7M	K	1003	1	-	1/3/25/26	0/3/3/3
4	G7M	I	1003	1	-	1/3/25/26	0/3/3/3
4	G7M	L	1003	1	-	1/3/25/26	0/3/3/3
3	SAH	J	1002	-	-	2/11/31/31	0/3/3/3
4	G7M	A	1003	1	-	1/3/25/26	0/3/3/3

All (168) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1003	G7M	C3'-C4'	-9.24	1.29	1.53
4	I	1003	G7M	C3'-C4'	-9.24	1.29	1.53
4	A	1003	G7M	C3'-C4'	-9.23	1.29	1.53
4	D	1003	G7M	C3'-C4'	-9.23	1.29	1.53
4	G	1003	G7M	C3'-C4'	-9.23	1.29	1.53
4	J	1003	G7M	C3'-C4'	-9.23	1.29	1.53
4	C	1003	G7M	C3'-C4'	-9.22	1.29	1.53
4	L	1003	G7M	C3'-C4'	-9.22	1.29	1.53
4	B	1003	G7M	C3'-C4'	-9.22	1.29	1.53
4	H	1003	G7M	C3'-C4'	-9.22	1.29	1.53
4	K	1003	G7M	C3'-C4'	-9.22	1.29	1.53
4	F	1003	G7M	C3'-C4'	-9.20	1.29	1.53
4	E	1003	G7M	O4'-C1'	-7.54	1.30	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1003	G7M	O4'-C1'	-7.54	1.30	1.41
4	A	1003	G7M	O4'-C1'	-7.49	1.30	1.41
4	D	1003	G7M	O4'-C1'	-7.49	1.30	1.41
4	G	1003	G7M	O4'-C1'	-7.49	1.30	1.41
4	J	1003	G7M	O4'-C1'	-7.49	1.30	1.41
4	C	1003	G7M	O4'-C1'	-7.49	1.30	1.41
4	F	1003	G7M	O4'-C1'	-7.49	1.30	1.41
4	L	1003	G7M	O4'-C1'	-7.49	1.30	1.41
4	I	1003	G7M	O4'-C1'	-7.47	1.30	1.41
4	B	1003	G7M	O4'-C1'	-7.46	1.30	1.41
4	K	1003	G7M	O4'-C1'	-7.46	1.30	1.41
4	H	1003	G7M	O4'-C4'	7.39	1.61	1.45
4	E	1003	G7M	O4'-C4'	7.37	1.61	1.45
4	C	1003	G7M	O4'-C4'	7.37	1.61	1.45
4	F	1003	G7M	O4'-C4'	7.37	1.61	1.45
4	L	1003	G7M	O4'-C4'	7.37	1.61	1.45
4	A	1003	G7M	O4'-C4'	7.37	1.61	1.45
4	D	1003	G7M	O4'-C4'	7.37	1.61	1.45
4	G	1003	G7M	O4'-C4'	7.37	1.61	1.45
4	J	1003	G7M	O4'-C4'	7.37	1.61	1.45
4	B	1003	G7M	O4'-C4'	7.36	1.61	1.45
4	K	1003	G7M	O4'-C4'	7.36	1.61	1.45
4	I	1003	G7M	O4'-C4'	7.36	1.61	1.45
4	C	1003	G7M	C2-N3	4.83	1.44	1.33
4	F	1003	G7M	C2-N3	4.83	1.44	1.33
4	L	1003	G7M	C2-N3	4.83	1.44	1.33
4	A	1003	G7M	C2-N3	4.82	1.44	1.33
4	B	1003	G7M	C2-N3	4.82	1.44	1.33
4	D	1003	G7M	C2-N3	4.82	1.44	1.33
4	G	1003	G7M	C2-N3	4.82	1.44	1.33
4	H	1003	G7M	C2-N3	4.82	1.44	1.33
4	J	1003	G7M	C2-N3	4.82	1.44	1.33
4	K	1003	G7M	C2-N3	4.82	1.44	1.33
4	E	1003	G7M	C2-N3	4.81	1.44	1.33
4	I	1003	G7M	C2-N3	4.80	1.44	1.33
4	E	1003	G7M	C4-N3	4.78	1.49	1.37
4	K	1003	G7M	C4-N3	4.78	1.49	1.37
4	C	1003	G7M	C4-N3	4.78	1.49	1.37
4	F	1003	G7M	C4-N3	4.78	1.49	1.37
4	I	1003	G7M	C4-N3	4.78	1.49	1.37
4	L	1003	G7M	C4-N3	4.78	1.49	1.37
4	A	1003	G7M	C4-N3	4.78	1.49	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1003	G7M	C4-N3	4.78	1.49	1.37
4	G	1003	G7M	C4-N3	4.78	1.49	1.37
4	J	1003	G7M	C4-N3	4.78	1.49	1.37
4	H	1003	G7M	C4-N3	4.78	1.49	1.37
4	B	1003	G7M	C4-N3	4.77	1.48	1.37
4	F	1003	G7M	C2-N2	4.27	1.44	1.34
4	B	1003	G7M	C2-N2	4.27	1.44	1.34
4	H	1003	G7M	C2-N2	4.27	1.44	1.34
4	I	1003	G7M	C2-N2	4.26	1.44	1.34
4	L	1003	G7M	C2-N2	4.25	1.44	1.34
4	A	1003	G7M	C2-N2	4.25	1.44	1.34
4	D	1003	G7M	C2-N2	4.25	1.44	1.34
4	J	1003	G7M	C2-N2	4.25	1.44	1.34
4	G	1003	G7M	C2-N2	4.25	1.44	1.34
4	E	1003	G7M	C2-N2	4.25	1.44	1.34
4	K	1003	G7M	C2-N2	4.24	1.44	1.34
4	C	1003	G7M	C2-N2	4.24	1.44	1.34
3	G	1002	SAH	C2-N3	3.55	1.37	1.32
3	C	1002	SAH	C2-N3	3.53	1.37	1.32
3	L	1002	SAH	C2-N3	3.53	1.37	1.32
3	E	1002	SAH	C2-N3	3.51	1.37	1.32
3	H	1002	SAH	C2-N3	3.51	1.37	1.32
3	A	1002	SAH	C2-N3	3.49	1.37	1.32
3	D	1002	SAH	C2-N3	3.49	1.37	1.32
3	J	1002	SAH	C2-N3	3.49	1.37	1.32
3	F	1002	SAH	C2-N3	3.49	1.37	1.32
3	I	1002	SAH	C2-N3	3.49	1.37	1.32
3	B	1002	SAH	C2-N3	3.49	1.37	1.32
3	K	1002	SAH	C2-N3	3.43	1.37	1.32
4	C	1003	G7M	O2'-C2'	-3.35	1.35	1.43
4	I	1003	G7M	O2'-C2'	-3.35	1.35	1.43
4	K	1003	G7M	O2'-C2'	-3.35	1.35	1.43
4	A	1003	G7M	O2'-C2'	-3.33	1.35	1.43
4	D	1003	G7M	O2'-C2'	-3.33	1.35	1.43
4	G	1003	G7M	O2'-C2'	-3.33	1.35	1.43
4	J	1003	G7M	O2'-C2'	-3.33	1.35	1.43
4	F	1003	G7M	O2'-C2'	-3.33	1.35	1.43
4	L	1003	G7M	O2'-C2'	-3.33	1.35	1.43
4	B	1003	G7M	O2'-C2'	-3.33	1.35	1.43
4	E	1003	G7M	O2'-C2'	-3.33	1.35	1.43
4	H	1003	G7M	O2'-C2'	-3.29	1.35	1.43
4	E	1003	G7M	C6-N1	3.15	1.42	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1003	G7M	C6-N1	3.15	1.42	1.37
4	K	1003	G7M	C6-N1	3.15	1.42	1.37
4	A	1003	G7M	C6-N1	3.15	1.42	1.37
4	D	1003	G7M	C6-N1	3.15	1.42	1.37
4	G	1003	G7M	C6-N1	3.15	1.42	1.37
4	J	1003	G7M	C6-N1	3.15	1.42	1.37
4	C	1003	G7M	C6-N1	3.14	1.42	1.37
4	F	1003	G7M	C6-N1	3.14	1.42	1.37
4	I	1003	G7M	C6-N1	3.14	1.42	1.37
4	L	1003	G7M	C6-N1	3.14	1.42	1.37
4	B	1003	G7M	C6-N1	3.14	1.42	1.37
4	B	1003	G7M	C5-C6	2.95	1.53	1.45
4	H	1003	G7M	C5-C6	2.95	1.53	1.45
4	I	1003	G7M	C5-C6	2.93	1.53	1.45
4	C	1003	G7M	C5-C6	2.93	1.53	1.45
4	A	1003	G7M	C5-C6	2.93	1.53	1.45
4	D	1003	G7M	C5-C6	2.93	1.53	1.45
4	G	1003	G7M	C5-C6	2.93	1.53	1.45
4	J	1003	G7M	C5-C6	2.93	1.53	1.45
4	E	1003	G7M	C5-C6	2.92	1.53	1.45
4	K	1003	G7M	C5-C6	2.91	1.53	1.45
4	F	1003	G7M	C5-C6	2.91	1.52	1.45
4	L	1003	G7M	C5-C6	2.91	1.52	1.45
4	B	1003	G7M	O6-C6	-2.71	1.17	1.23
4	E	1003	G7M	O6-C6	-2.70	1.17	1.23
4	H	1003	G7M	O6-C6	-2.70	1.17	1.23
4	C	1003	G7M	O6-C6	-2.69	1.17	1.23
4	F	1003	G7M	O6-C6	-2.69	1.17	1.23
4	I	1003	G7M	O6-C6	-2.69	1.17	1.23
4	L	1003	G7M	O6-C6	-2.69	1.17	1.23
4	A	1003	G7M	O6-C6	-2.69	1.17	1.23
4	D	1003	G7M	O6-C6	-2.69	1.17	1.23
4	G	1003	G7M	O6-C6	-2.69	1.17	1.23
4	J	1003	G7M	O6-C6	-2.69	1.17	1.23
4	K	1003	G7M	O6-C6	-2.65	1.17	1.23
4	C	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	F	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	I	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	L	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	B	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	E	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	H	1003	G7M	O3'-C3'	2.55	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	A	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	D	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	G	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	J	1003	G7M	O3'-C3'	2.55	1.49	1.43
4	C	1003	G7M	O5'-C5'	-2.38	1.38	1.44
4	E	1003	G7M	O5'-C5'	-2.38	1.38	1.44
4	F	1003	G7M	O5'-C5'	-2.37	1.39	1.44
4	L	1003	G7M	O5'-C5'	-2.37	1.39	1.44
4	A	1003	G7M	O5'-C5'	-2.37	1.39	1.44
4	D	1003	G7M	O5'-C5'	-2.37	1.39	1.44
4	G	1003	G7M	O5'-C5'	-2.37	1.39	1.44
4	J	1003	G7M	O5'-C5'	-2.37	1.39	1.44
4	B	1003	G7M	O5'-C5'	-2.36	1.39	1.44
4	H	1003	G7M	O5'-C5'	-2.36	1.39	1.44
4	K	1003	G7M	O5'-C5'	-2.36	1.39	1.44
4	I	1003	G7M	O5'-C5'	-2.36	1.39	1.44
3	G	1002	SAH	OXT-C	-2.30	1.23	1.30
3	C	1002	SAH	OXT-C	-2.28	1.23	1.30
3	L	1002	SAH	OXT-C	-2.28	1.23	1.30
3	B	1002	SAH	OXT-C	-2.28	1.23	1.30
3	H	1002	SAH	OXT-C	-2.28	1.23	1.30
3	E	1002	SAH	OXT-C	-2.27	1.23	1.30
3	A	1002	SAH	OXT-C	-2.27	1.23	1.30
3	D	1002	SAH	OXT-C	-2.27	1.23	1.30
3	J	1002	SAH	OXT-C	-2.27	1.23	1.30
3	I	1002	SAH	OXT-C	-2.26	1.23	1.30
3	K	1002	SAH	OXT-C	-2.24	1.23	1.30
3	F	1002	SAH	OXT-C	-2.24	1.23	1.30

All (96) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1002	SAH	N3-C2-N1	-5.65	119.84	128.68
3	H	1002	SAH	N3-C2-N1	-5.65	119.85	128.68
3	L	1002	SAH	N3-C2-N1	-5.65	119.85	128.68
3	F	1002	SAH	N3-C2-N1	-5.64	119.86	128.68
3	G	1002	SAH	N3-C2-N1	-5.64	119.86	128.68
3	A	1002	SAH	N3-C2-N1	-5.63	119.87	128.68
3	C	1002	SAH	N3-C2-N1	-5.63	119.87	128.68
3	D	1002	SAH	N3-C2-N1	-5.63	119.87	128.68
3	J	1002	SAH	N3-C2-N1	-5.63	119.87	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	K	1002	SAH	N3-C2-N1	-5.63	119.88	128.68
3	I	1002	SAH	N3-C2-N1	-5.63	119.88	128.68
3	E	1002	SAH	N3-C2-N1	-5.62	119.89	128.68
4	I	1003	G7M	C3'-C2'-C1'	3.72	106.57	100.98
4	E	1003	G7M	C3'-C2'-C1'	3.70	106.55	100.98
4	H	1003	G7M	C3'-C2'-C1'	3.70	106.55	100.98
4	F	1003	G7M	C3'-C2'-C1'	3.69	106.54	100.98
4	B	1003	G7M	C3'-C2'-C1'	3.69	106.54	100.98
4	K	1003	G7M	C3'-C2'-C1'	3.69	106.54	100.98
4	A	1003	G7M	C3'-C2'-C1'	3.69	106.53	100.98
4	D	1003	G7M	C3'-C2'-C1'	3.69	106.53	100.98
4	G	1003	G7M	C3'-C2'-C1'	3.69	106.53	100.98
4	J	1003	G7M	C3'-C2'-C1'	3.69	106.53	100.98
4	C	1003	G7M	C3'-C2'-C1'	3.68	106.52	100.98
4	L	1003	G7M	C3'-C2'-C1'	3.68	106.52	100.98
3	I	1002	SAH	C5'-SD-CG	-3.61	91.42	102.27
3	B	1002	SAH	C5'-SD-CG	-3.61	91.42	102.27
3	H	1002	SAH	C5'-SD-CG	-3.61	91.42	102.27
3	E	1002	SAH	C5'-SD-CG	-3.61	91.43	102.27
3	A	1002	SAH	C5'-SD-CG	-3.61	91.43	102.27
3	D	1002	SAH	C5'-SD-CG	-3.61	91.43	102.27
3	J	1002	SAH	C5'-SD-CG	-3.61	91.43	102.27
3	K	1002	SAH	C5'-SD-CG	-3.61	91.44	102.27
3	F	1002	SAH	C5'-SD-CG	-3.61	91.44	102.27
3	L	1002	SAH	C5'-SD-CG	-3.61	91.44	102.27
3	C	1002	SAH	C5'-SD-CG	-3.61	91.45	102.27
3	G	1002	SAH	C5'-SD-CG	-3.60	91.46	102.27
3	F	1002	SAH	OXT-C-O	-2.58	118.23	124.09
3	E	1002	SAH	OXT-C-O	-2.58	118.23	124.09
3	K	1002	SAH	OXT-C-O	-2.57	118.25	124.09
3	A	1002	SAH	OXT-C-O	-2.57	118.26	124.09
3	D	1002	SAH	OXT-C-O	-2.57	118.26	124.09
3	J	1002	SAH	OXT-C-O	-2.57	118.26	124.09
3	I	1002	SAH	OXT-C-O	-2.57	118.26	124.09
3	C	1002	SAH	OXT-C-O	-2.57	118.26	124.09
3	L	1002	SAH	OXT-C-O	-2.57	118.26	124.09
3	B	1002	SAH	OXT-C-O	-2.55	118.29	124.09
3	H	1002	SAH	OXT-C-O	-2.55	118.29	124.09
3	G	1002	SAH	OXT-C-O	-2.54	118.32	124.09
3	E	1002	SAH	OXT-C-CA	2.23	120.98	113.38
3	F	1002	SAH	OXT-C-CA	2.22	120.96	113.38
3	A	1002	SAH	OXT-C-CA	2.22	120.95	113.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	1002	SAH	OXT-C-CA	2.22	120.95	113.38
3	J	1002	SAH	OXT-C-CA	2.22	120.95	113.38
3	C	1002	SAH	OXT-C-CA	2.22	120.95	113.38
3	K	1002	SAH	OXT-C-CA	2.22	120.95	113.38
3	L	1002	SAH	OXT-C-CA	2.22	120.95	113.38
3	G	1002	SAH	OXT-C-CA	2.22	120.93	113.38
3	I	1002	SAH	OXT-C-CA	2.22	120.93	113.38
3	B	1002	SAH	OXT-C-CA	2.21	120.91	113.38
3	H	1002	SAH	OXT-C-CA	2.21	120.91	113.38
4	F	1003	G7M	C2'-C3'-C4'	2.19	106.89	102.64
4	H	1003	G7M	C2'-C3'-C4'	2.18	106.89	102.64
4	C	1003	G7M	C2'-C3'-C4'	2.18	106.89	102.64
4	L	1003	G7M	C2'-C3'-C4'	2.18	106.89	102.64
4	B	1003	G7M	C2'-C3'-C4'	2.18	106.88	102.64
4	K	1003	G7M	C2'-C3'-C4'	2.18	106.88	102.64
4	A	1003	G7M	C2'-C3'-C4'	2.18	106.88	102.64
4	D	1003	G7M	C2'-C3'-C4'	2.18	106.88	102.64
4	G	1003	G7M	C2'-C3'-C4'	2.18	106.88	102.64
4	J	1003	G7M	C2'-C3'-C4'	2.18	106.88	102.64
4	E	1003	G7M	C2'-C3'-C4'	2.17	106.86	102.64
4	I	1003	G7M	C2'-C3'-C4'	2.17	106.85	102.64
4	G	1003	G7M	C2-N1-C6	-2.10	121.22	125.10
4	C	1003	G7M	C2-N1-C6	-2.10	121.22	125.10
4	I	1003	G7M	C2-N1-C6	-2.10	121.22	125.10
4	E	1003	G7M	C2-N1-C6	-2.10	121.23	125.10
4	H	1003	G7M	C2-N1-C6	-2.10	121.23	125.10
4	F	1003	G7M	C2-N1-C6	-2.10	121.23	125.10
4	L	1003	G7M	C2-N1-C6	-2.10	121.23	125.10
4	A	1003	G7M	C2-N1-C6	-2.10	121.23	125.10
4	D	1003	G7M	C2-N1-C6	-2.10	121.23	125.10
4	J	1003	G7M	C2-N1-C6	-2.10	121.23	125.10
4	K	1003	G7M	C2-N1-C6	-2.10	121.24	125.10
4	B	1003	G7M	C2-N1-C6	-2.09	121.25	125.10
4	I	1003	G7M	N1-C2-N3	-2.04	119.50	123.32
4	B	1003	G7M	N1-C2-N3	-2.04	119.51	123.32
4	K	1003	G7M	N1-C2-N3	-2.04	119.51	123.32
4	A	1003	G7M	N1-C2-N3	-2.03	119.52	123.32
4	D	1003	G7M	N1-C2-N3	-2.03	119.52	123.32
4	J	1003	G7M	N1-C2-N3	-2.03	119.52	123.32
4	E	1003	G7M	N1-C2-N3	-2.03	119.52	123.32
4	F	1003	G7M	N1-C2-N3	-2.03	119.52	123.32
4	H	1003	G7M	N1-C2-N3	-2.03	119.52	123.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	L	1003	G7M	N1-C2-N3	-2.03	119.52	123.32
4	C	1003	G7M	N1-C2-N3	-2.03	119.53	123.32
4	G	1003	G7M	N1-C2-N3	-2.03	119.53	123.32

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1002	SAH	N-CA-CB-CG
3	A	1002	SAH	C-CA-CB-CG
3	B	1002	SAH	N-CA-CB-CG
3	B	1002	SAH	C-CA-CB-CG
3	C	1002	SAH	N-CA-CB-CG
3	C	1002	SAH	C-CA-CB-CG
3	D	1002	SAH	N-CA-CB-CG
3	D	1002	SAH	C-CA-CB-CG
3	E	1002	SAH	N-CA-CB-CG
3	E	1002	SAH	C-CA-CB-CG
3	F	1002	SAH	N-CA-CB-CG
3	F	1002	SAH	C-CA-CB-CG
3	G	1002	SAH	N-CA-CB-CG
3	G	1002	SAH	C-CA-CB-CG
3	H	1002	SAH	N-CA-CB-CG
3	H	1002	SAH	C-CA-CB-CG
3	I	1002	SAH	N-CA-CB-CG
3	I	1002	SAH	C-CA-CB-CG
3	J	1002	SAH	N-CA-CB-CG
3	J	1002	SAH	C-CA-CB-CG
3	K	1002	SAH	N-CA-CB-CG
3	K	1002	SAH	C-CA-CB-CG
3	L	1002	SAH	N-CA-CB-CG
3	L	1002	SAH	C-CA-CB-CG
4	A	1003	G7M	O4'-C4'-C5'-O5'
4	B	1003	G7M	O4'-C4'-C5'-O5'
4	C	1003	G7M	O4'-C4'-C5'-O5'
4	D	1003	G7M	O4'-C4'-C5'-O5'
4	E	1003	G7M	O4'-C4'-C5'-O5'
4	F	1003	G7M	O4'-C4'-C5'-O5'
4	G	1003	G7M	O4'-C4'-C5'-O5'
4	H	1003	G7M	O4'-C4'-C5'-O5'
4	I	1003	G7M	O4'-C4'-C5'-O5'
4	J	1003	G7M	O4'-C4'-C5'-O5'

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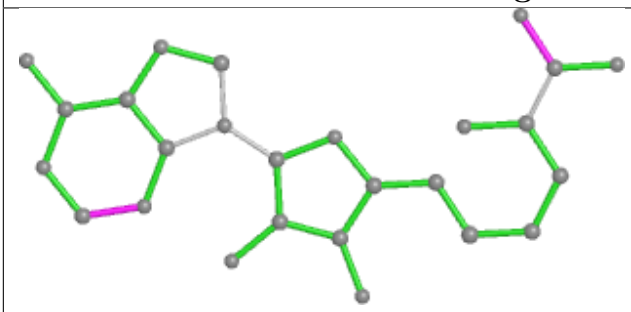
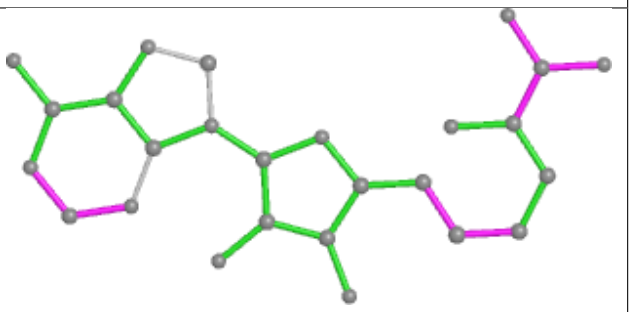
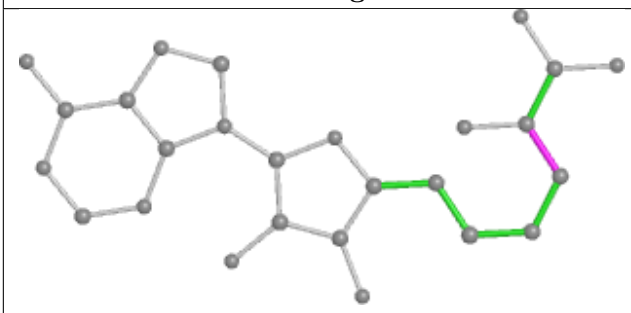
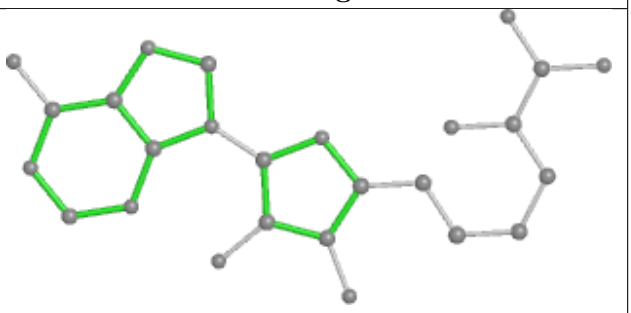
Mol	Chain	Res	Type	Atoms
4	K	1003	G7M	O4'-C4'-C5'-O5'
4	L	1003	G7M	O4'-C4'-C5'-O5'

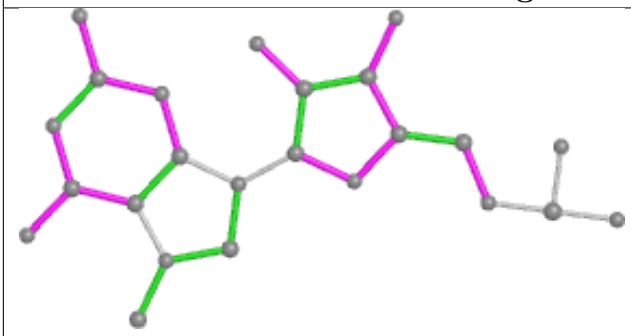
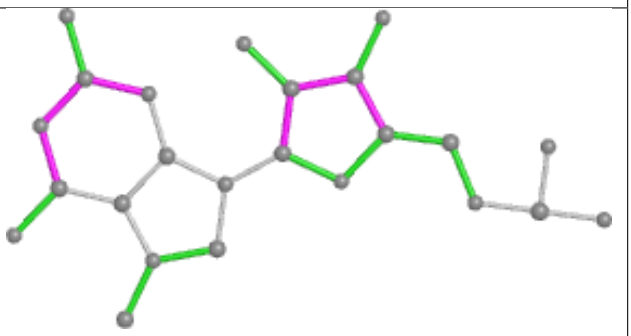
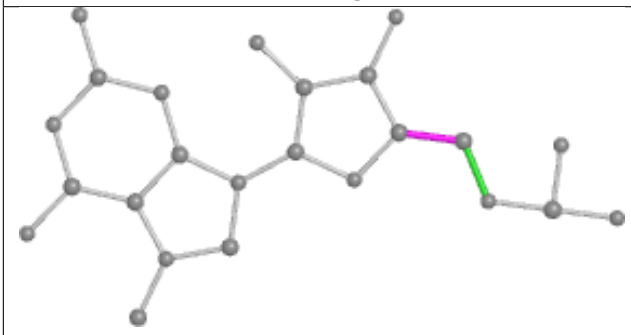
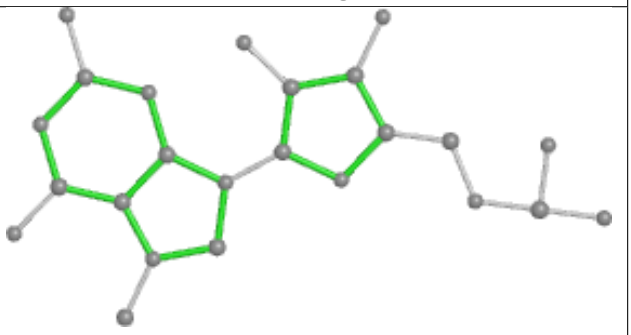
There are no ring outliers.

12 monomers are involved in 12 short contacts:

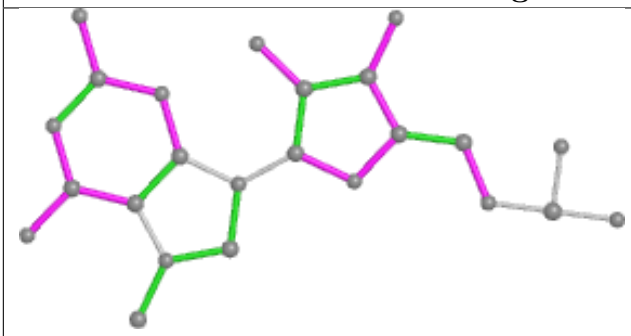
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	K	1002	SAH	1	0
3	C	1002	SAH	1	0
3	A	1002	SAH	1	0
3	D	1002	SAH	1	0
3	L	1002	SAH	1	0
3	G	1002	SAH	1	0
3	H	1002	SAH	1	0
3	I	1002	SAH	1	0
3	F	1002	SAH	1	0
3	B	1002	SAH	1	0
3	E	1002	SAH	1	0
3	J	1002	SAH	1	0

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 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.

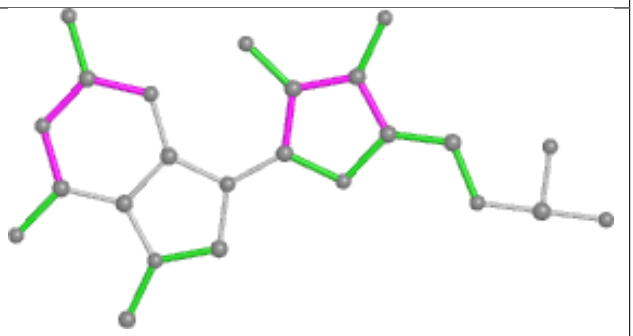
Ligand SAH K 1002	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand G7M J 1003	
 Bond lengths	 Bond angles
 Torsions	 Rings

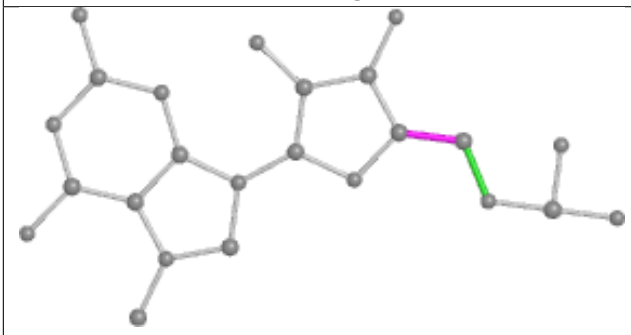
Ligand G7M H 1003



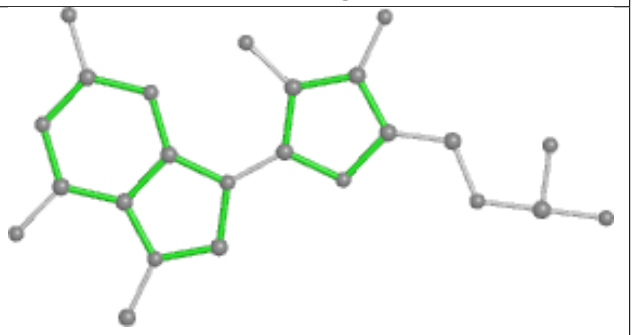
Bond lengths



Bond angles

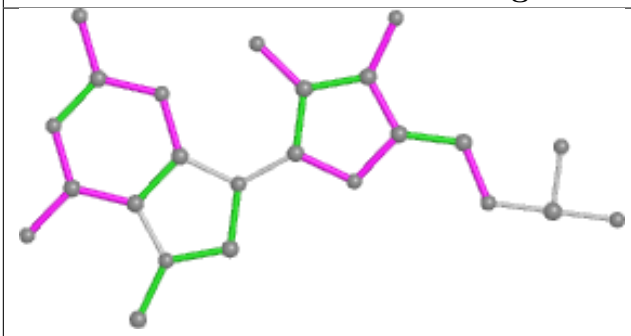


Torsions



Rings

Ligand G7M G 1003



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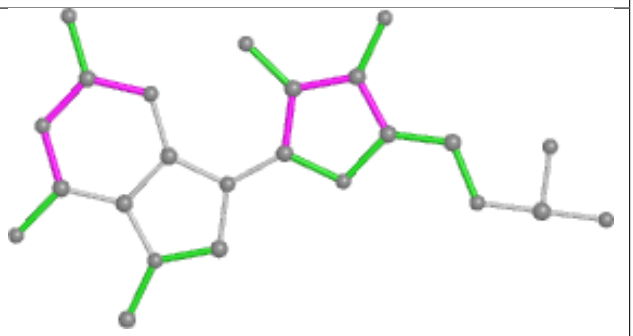

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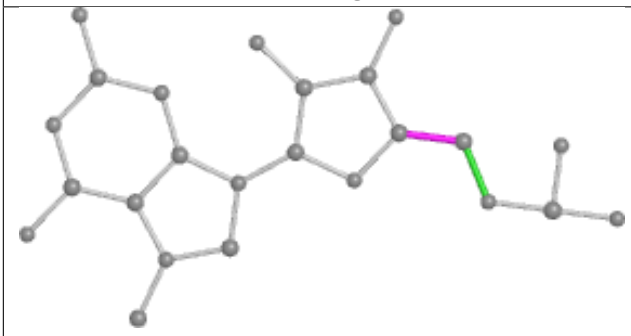

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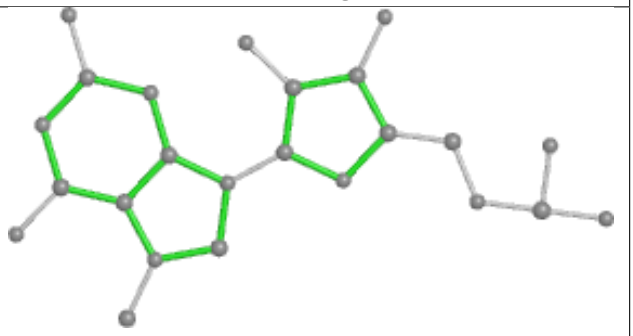
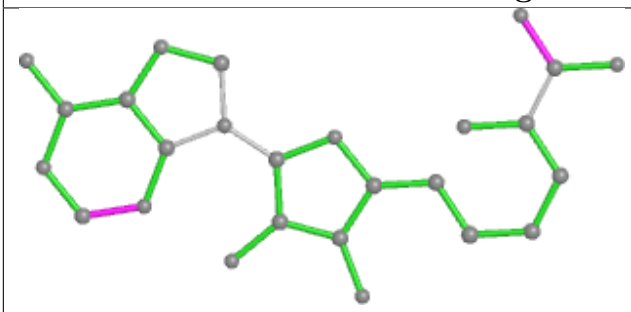
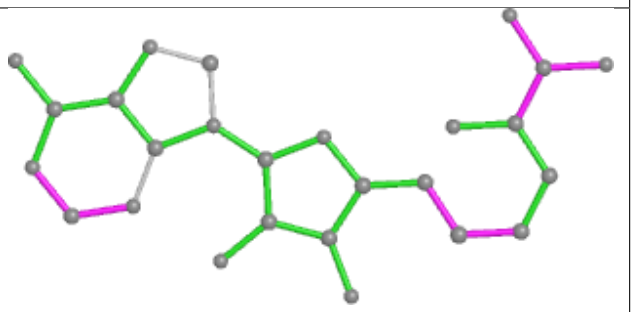


Rings

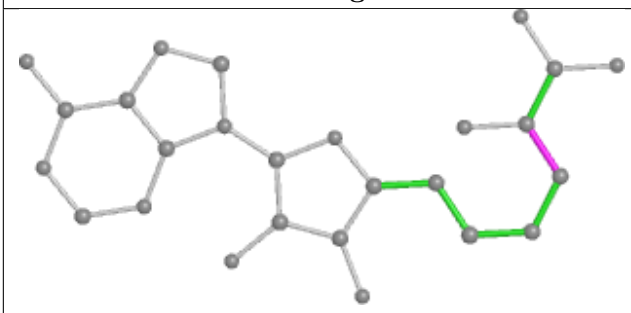
Ligand SAH C 1002



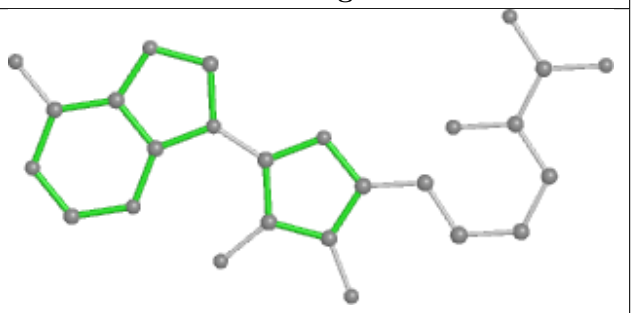
Bond lengths



Bond angles



Torsions



Rings

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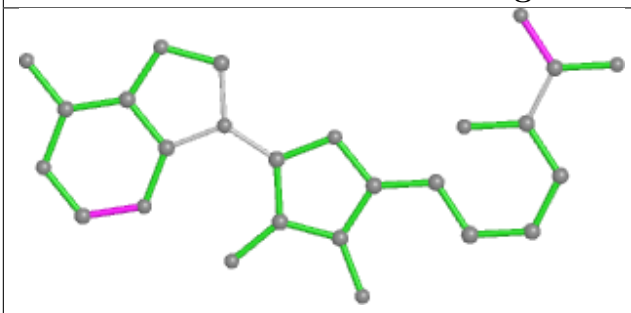
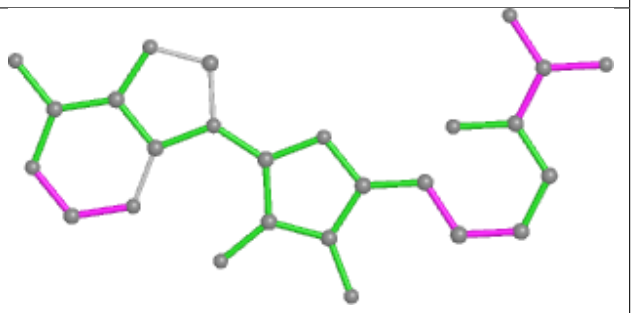
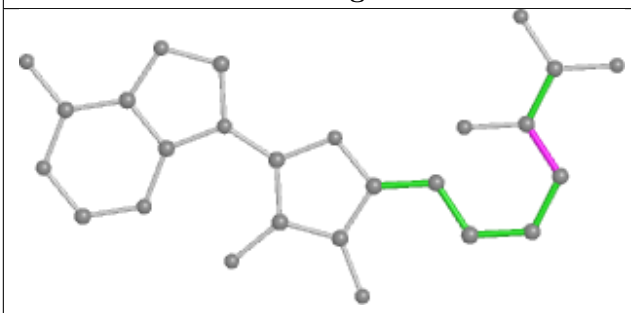


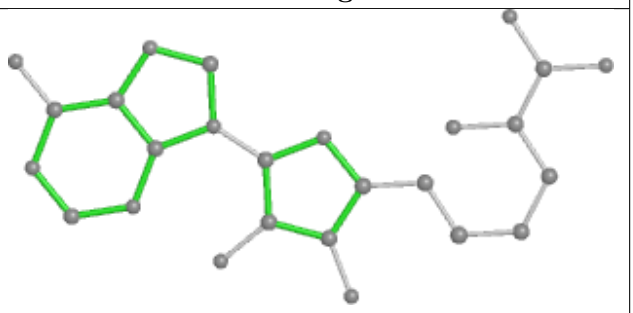
Bond lengths



Bond angles



Torsions



Rings

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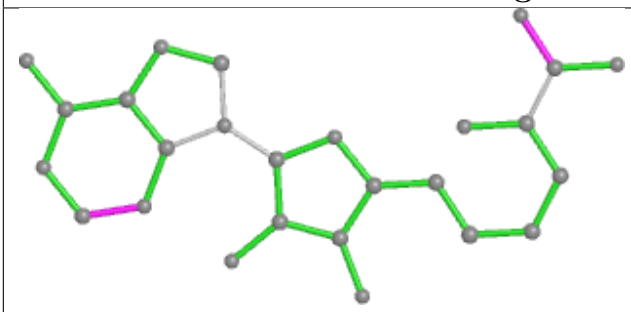
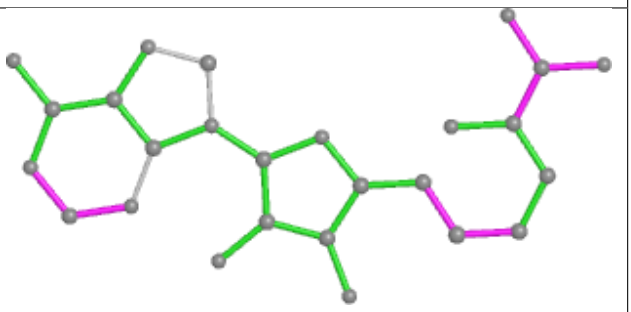
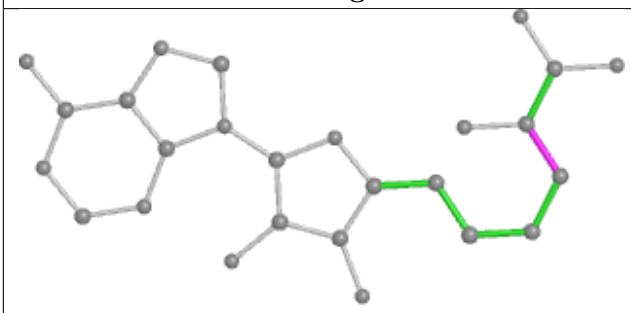
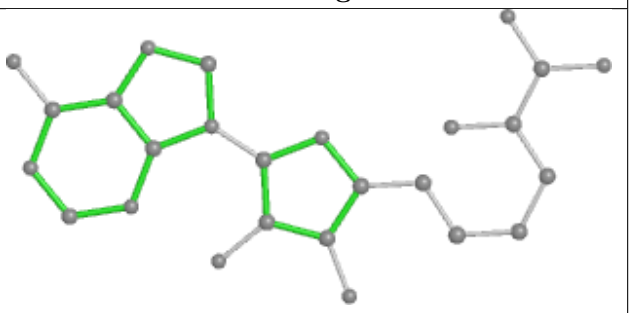
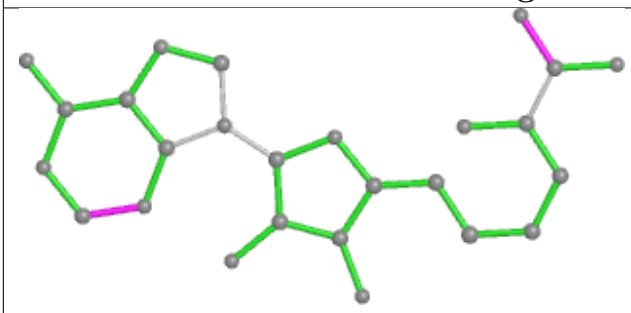
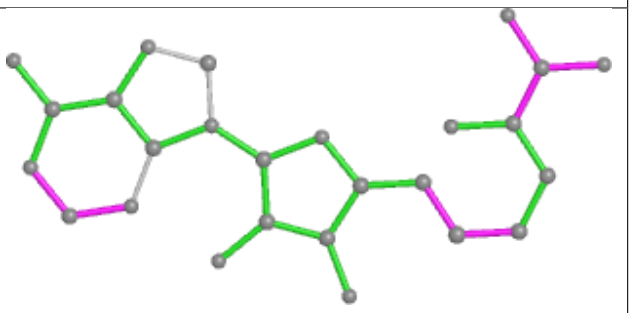
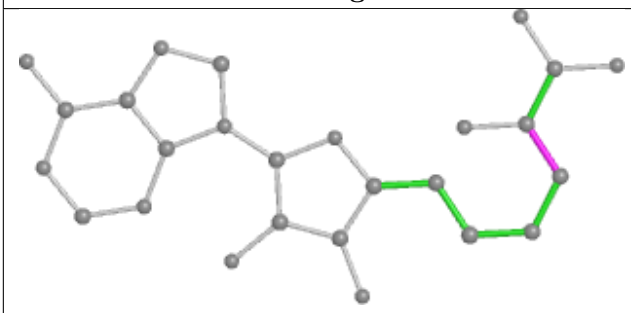
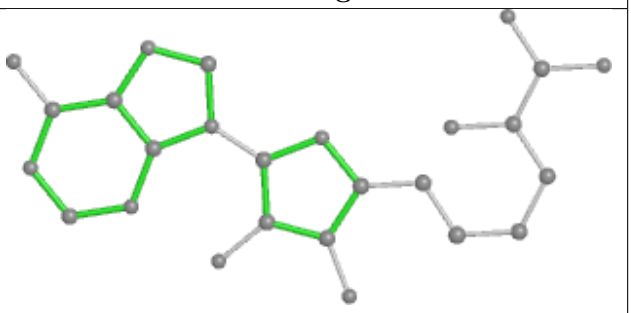
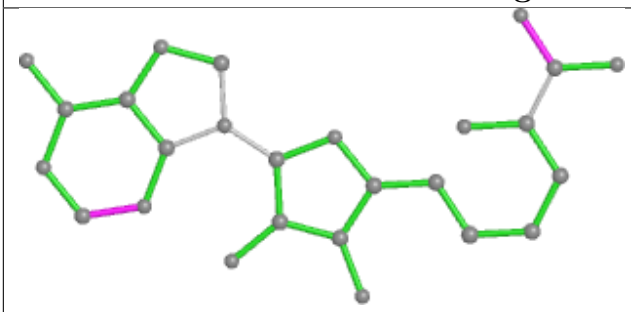
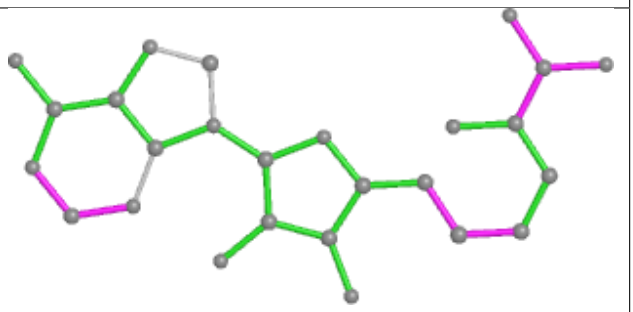
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand SAH L 1002	
 Bond lengths	 Bond angles
 Torsions	 Rings

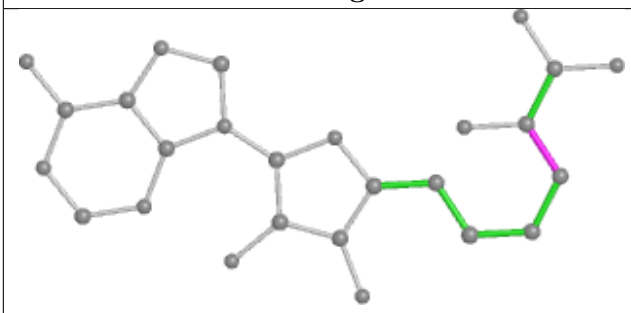
Ligand SAH G 1002



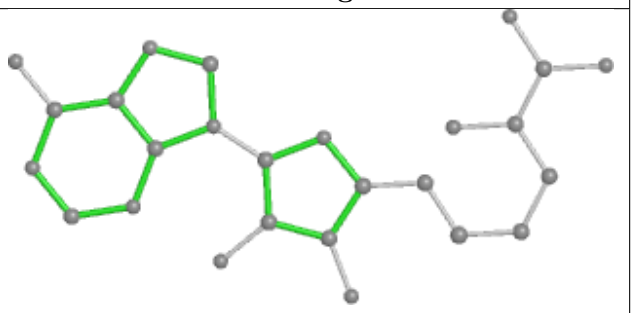
Bond lengths



Bond angles

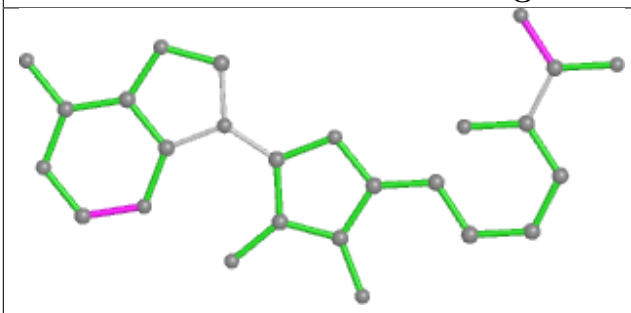


Torsions



Rings

Ligand SAH H 1002



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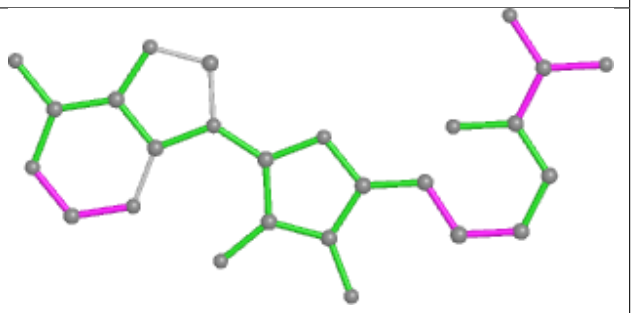
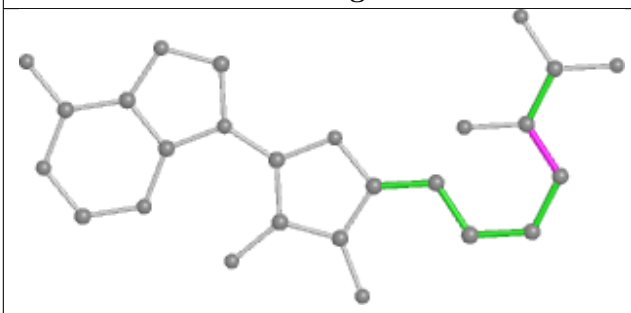
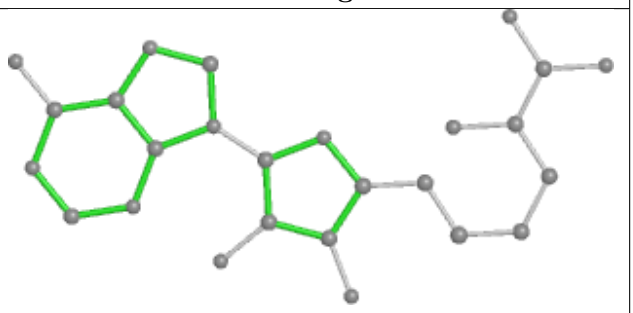


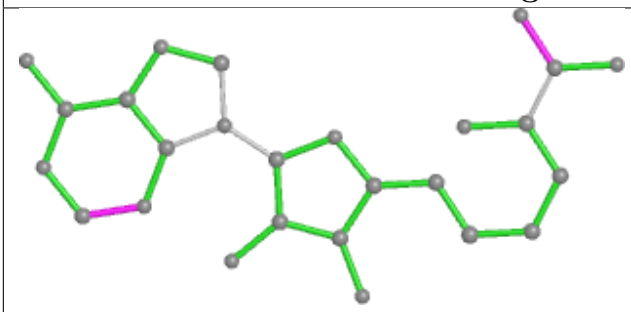
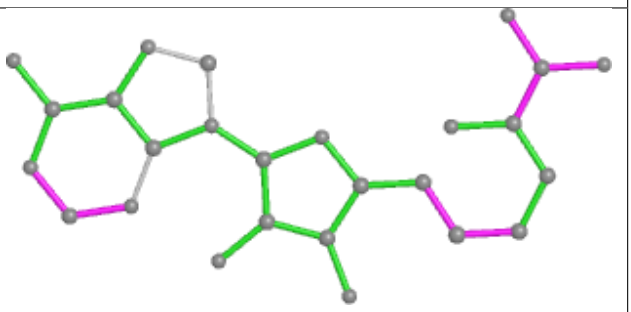
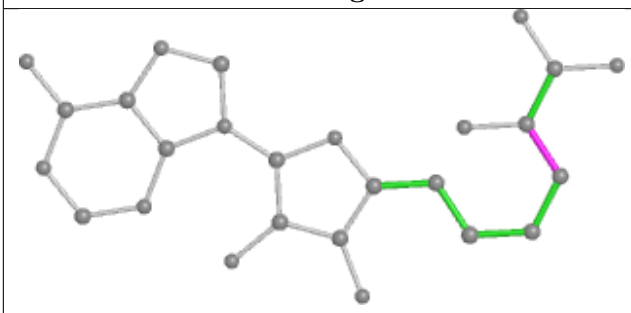
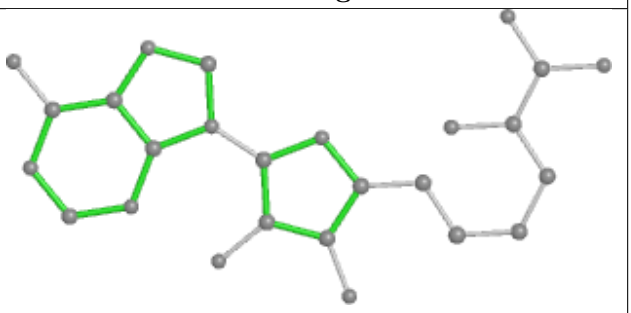
Bond angles

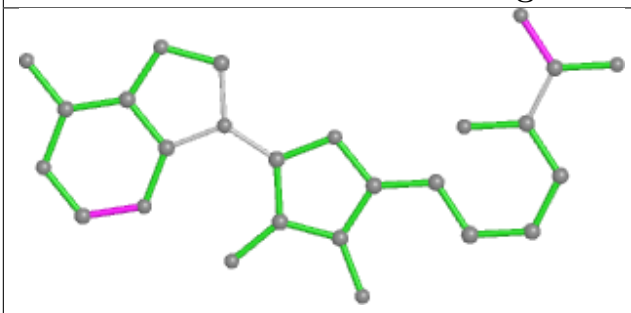
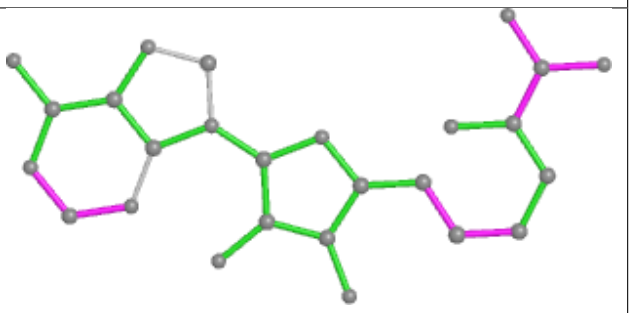
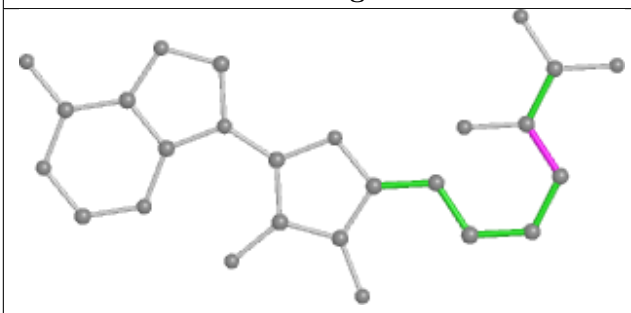
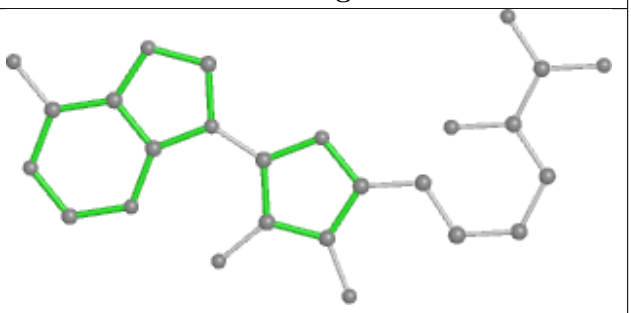


Torsions

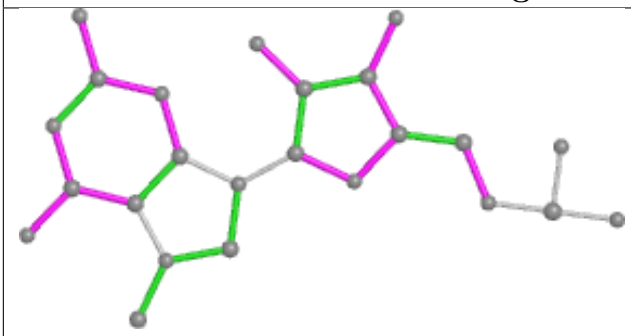


Rings

Ligand SAH I 1002	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand SAH F 1002	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand G7M C 1003



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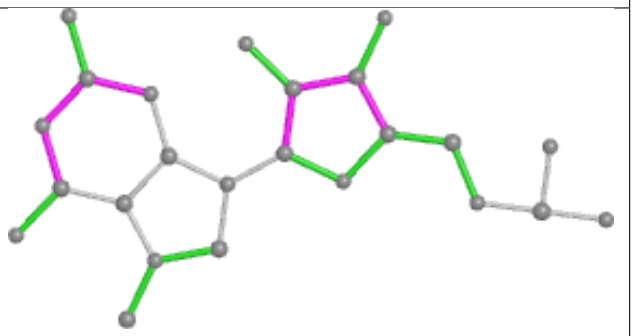
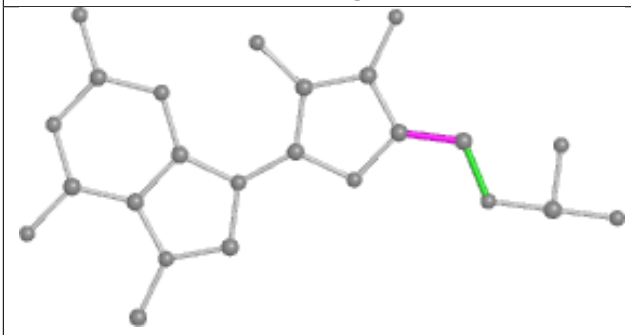
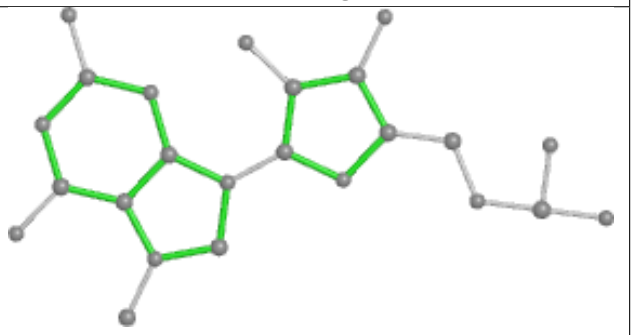


Bond angles

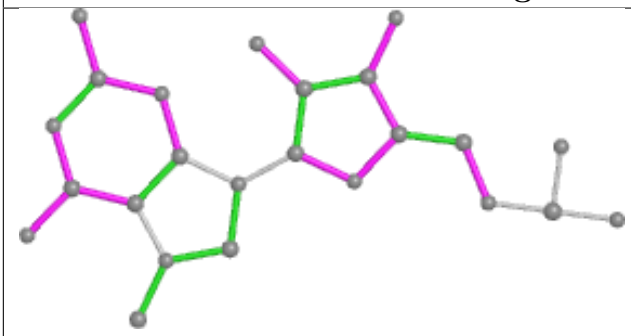


Torsions

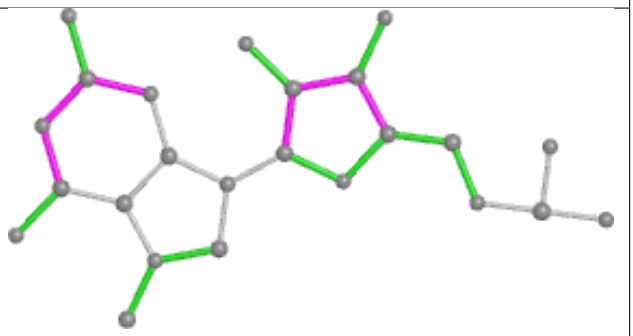


Rings

Ligand G7M F 1003



Bond lengths



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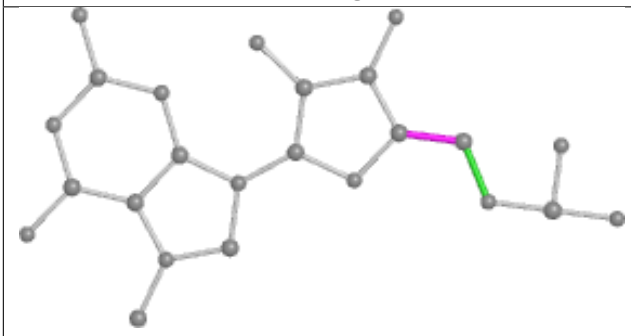
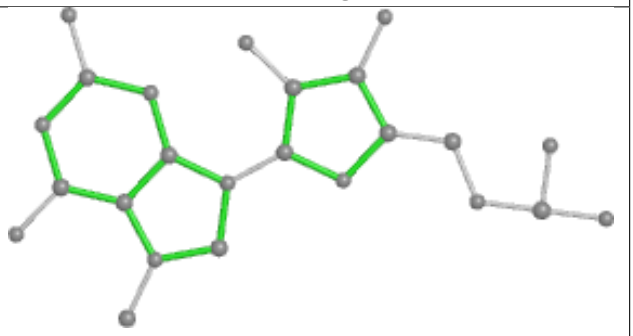
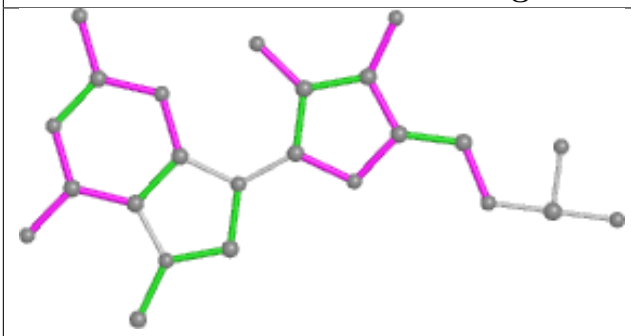


Torsions

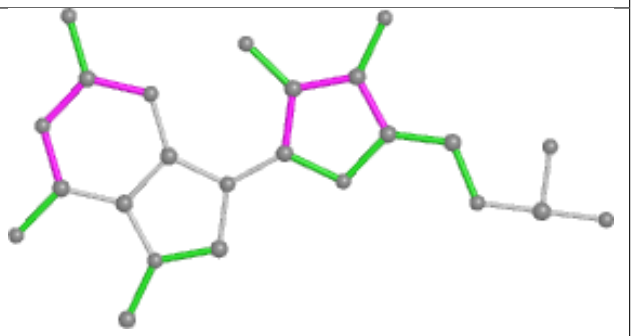


Rings

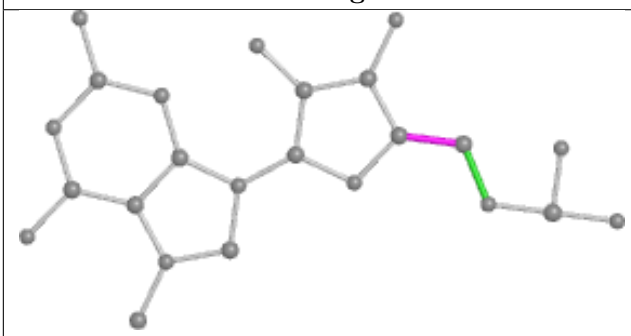
Ligand G7M D 1003



Bond lengths



Bond angles



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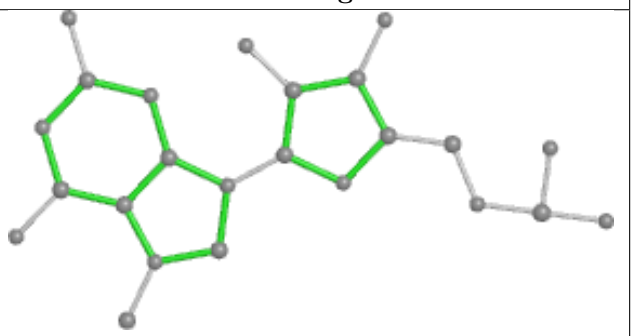
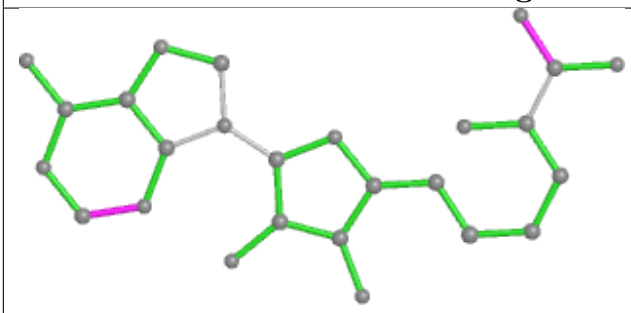


Rings

Ligand SAH B 1002



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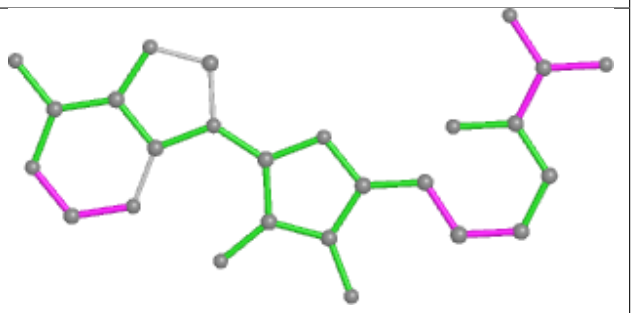
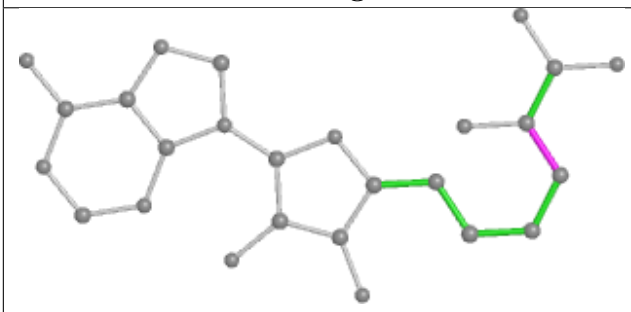


Bond angles



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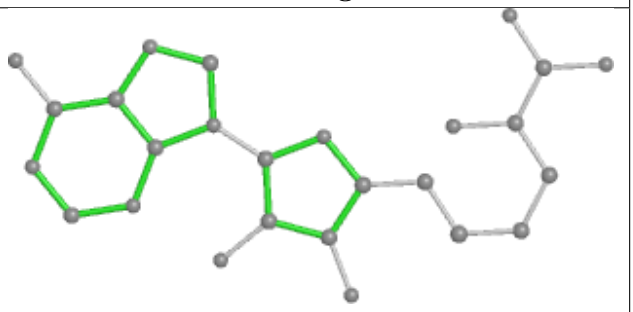
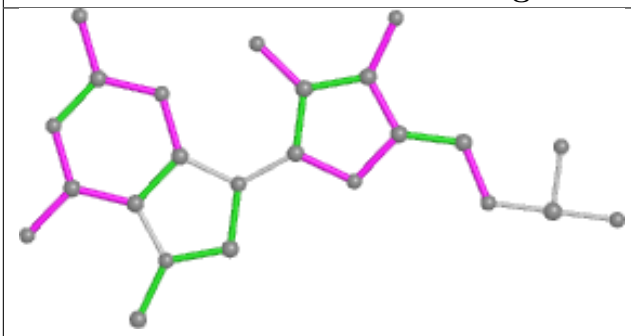
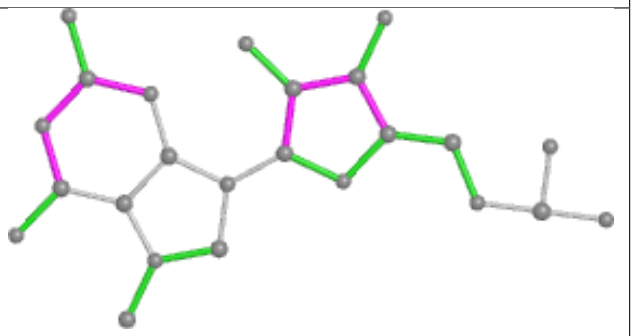


Rings

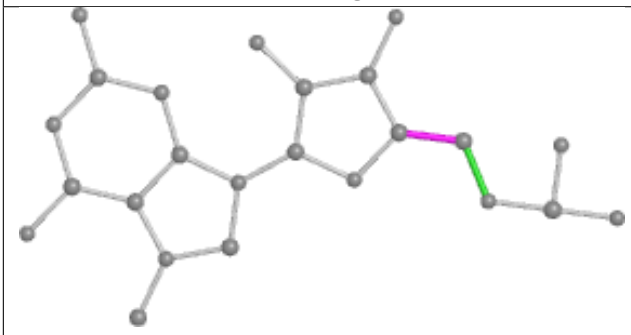
Ligand G7M B 1003



Bond lengths



Bond angles



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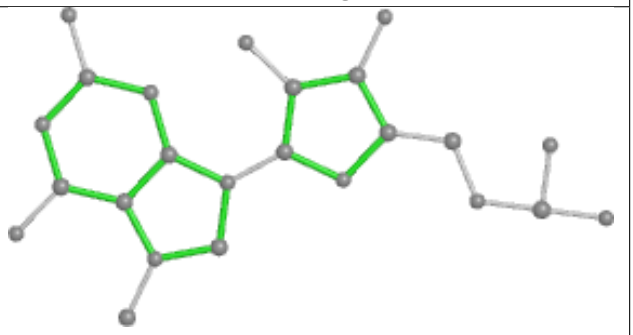
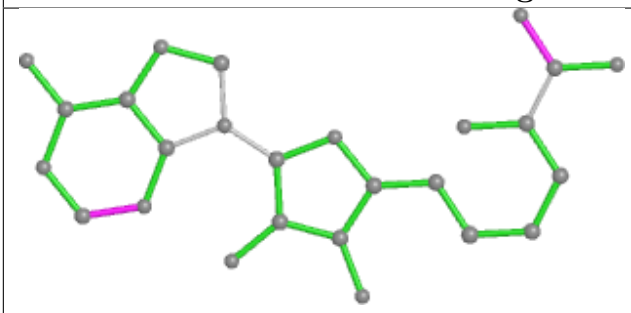


Rings

Ligand SAH E 1002



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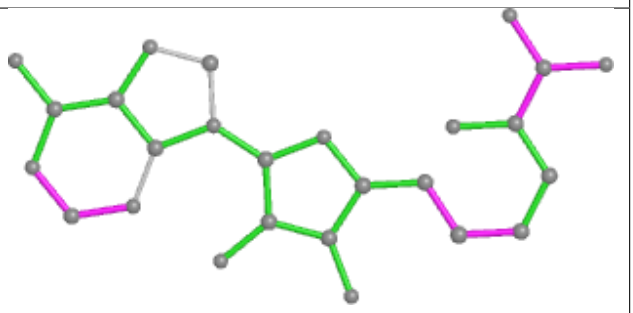
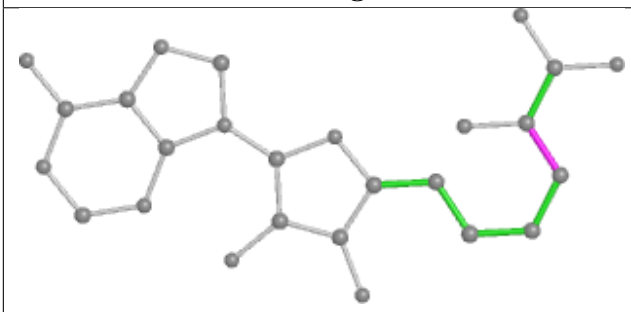


Bond angles



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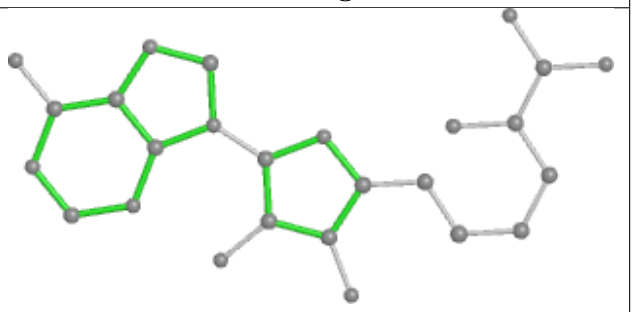
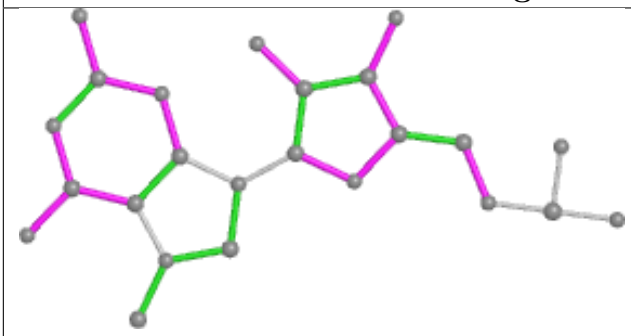


Rings

Ligand G7M E 1003



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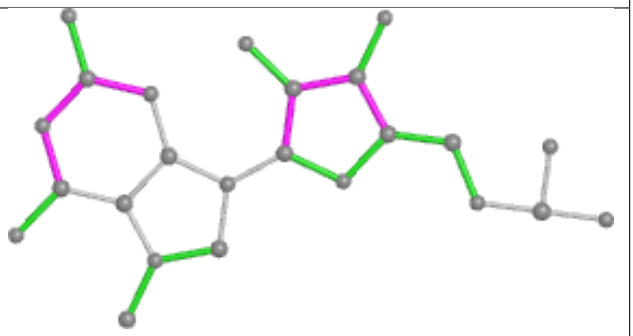
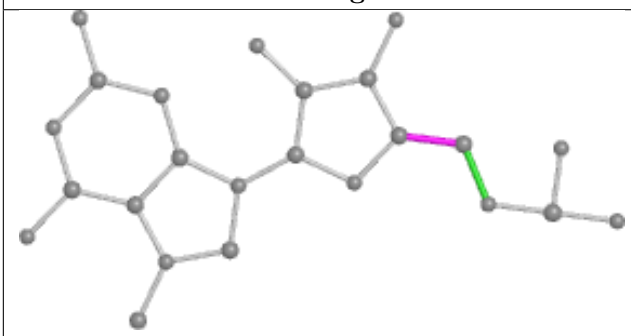


Bond angles



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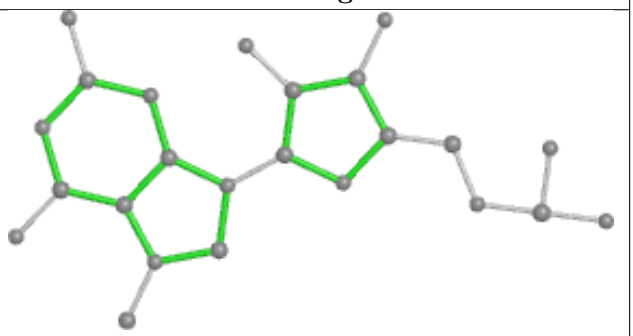
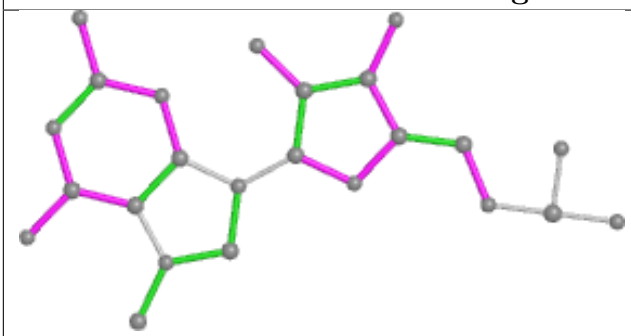


Rings

Ligand G7M K 1003



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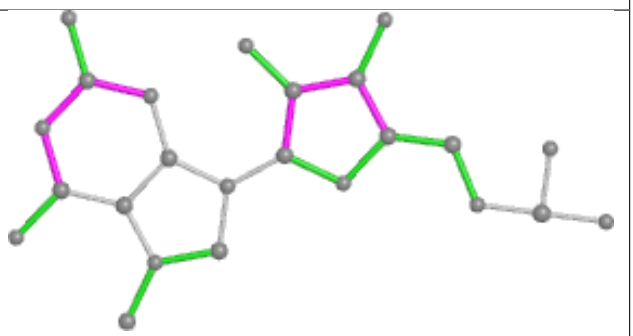
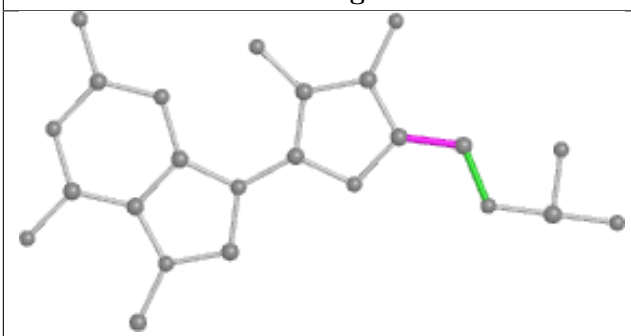


Bond angles



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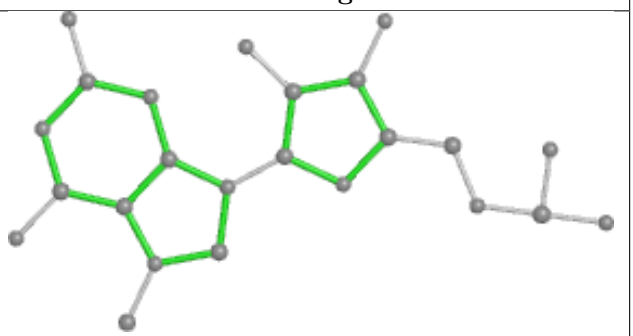
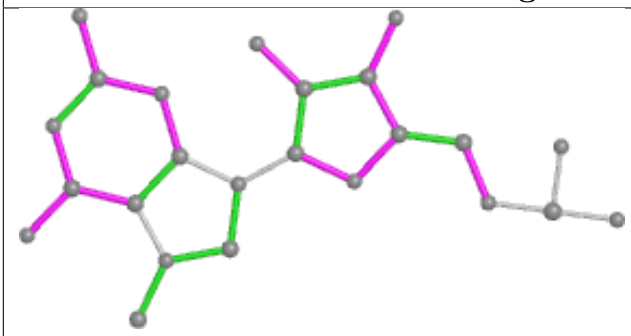
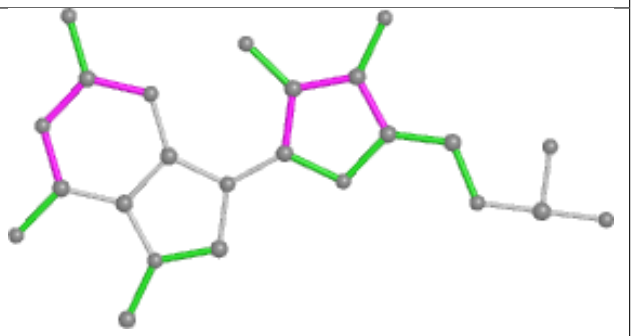


Rings

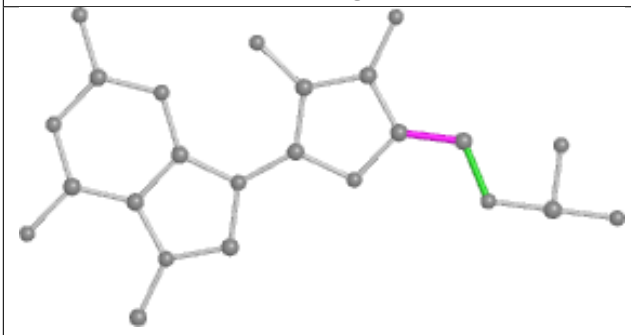
Ligand G7M I 1003



Bond lengths



Bond angles



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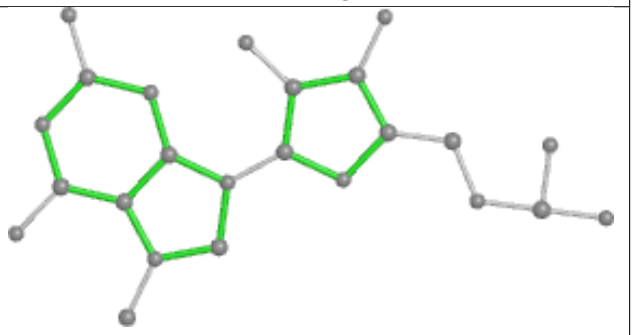
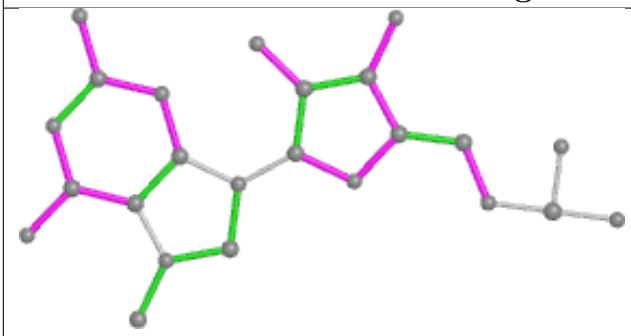


Rings

Ligand G7M L 1003



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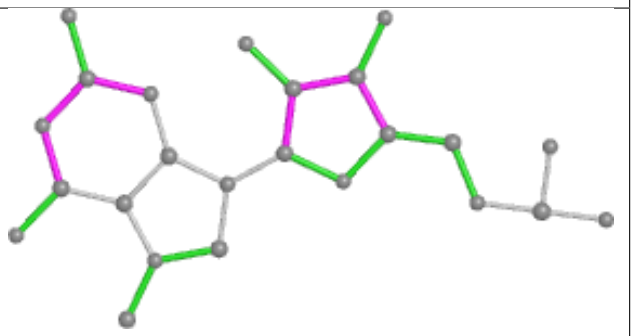
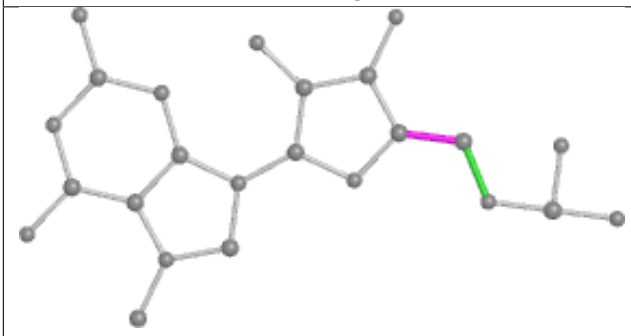
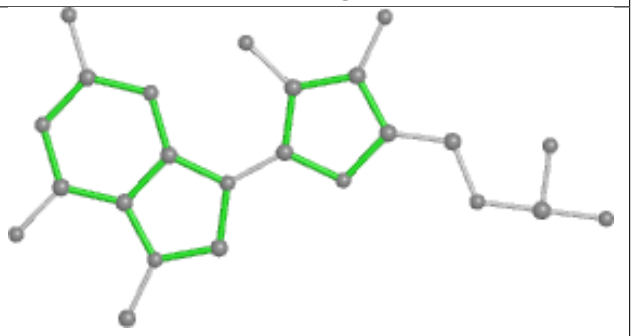


Bond angles

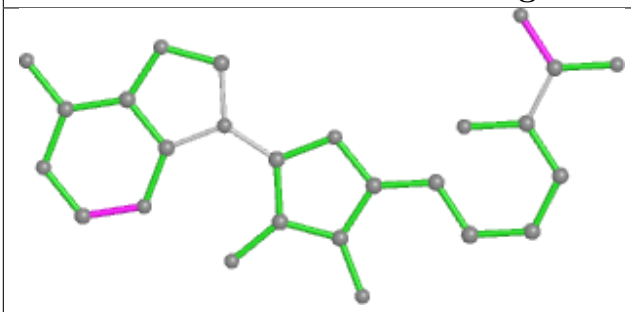


Torsions



Rings

Ligand SAH J 1002



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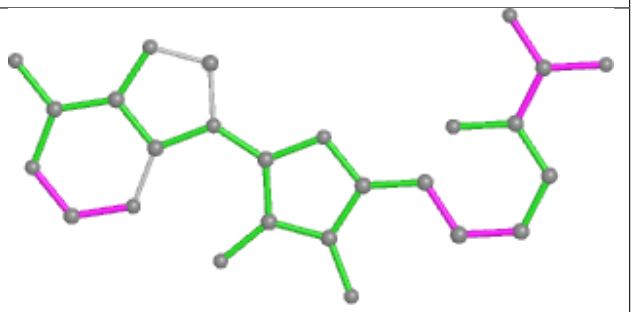
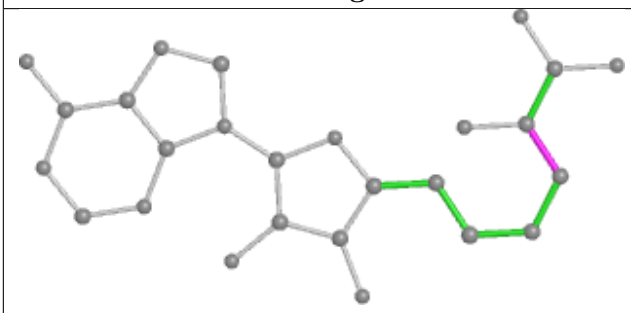
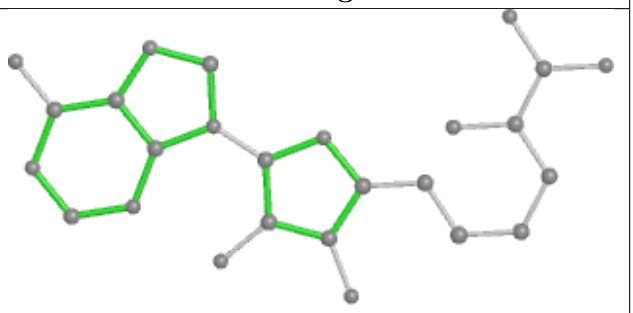


Bond angles

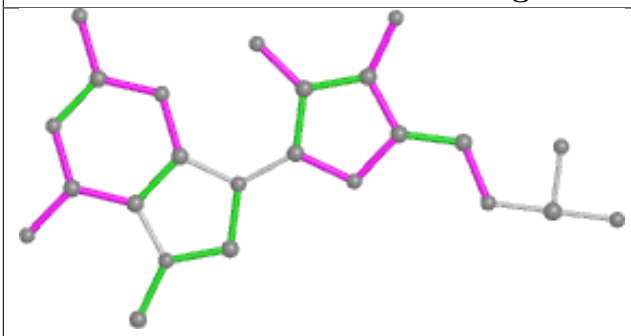


Torsions

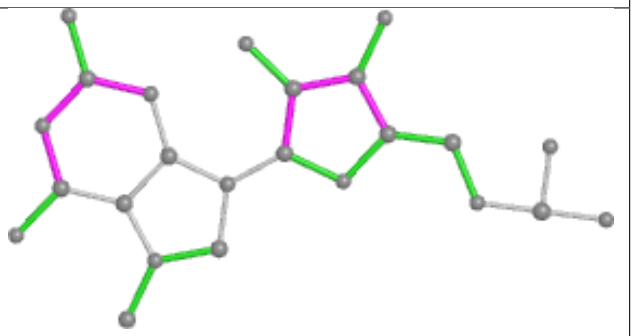


Rings

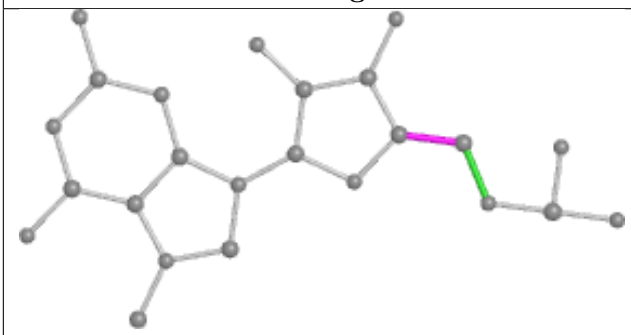
Ligand G7M A 1003



Bond lengths



Bond angles



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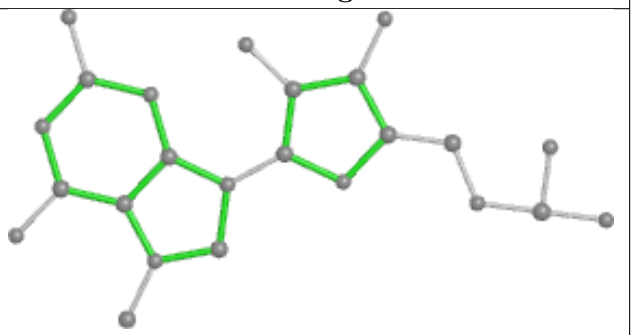


Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

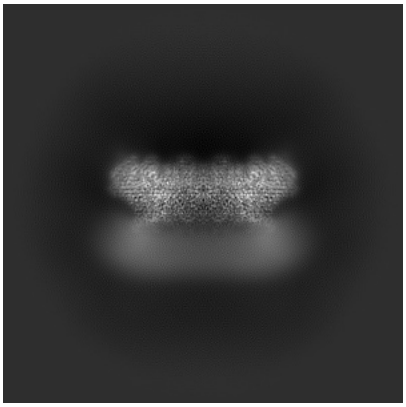
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-31581. These allow visual inspection of the internal detail of the map and identification of artifacts.

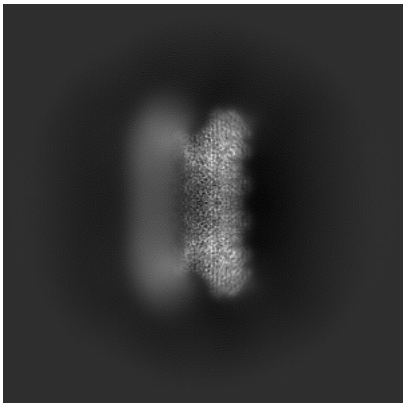
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

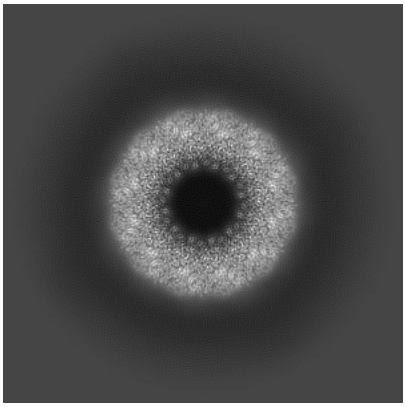
6.1.1 Primary map



X



Y

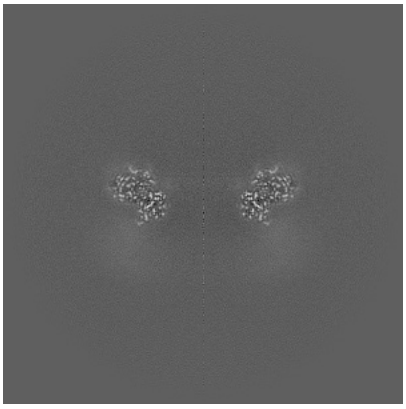


Z

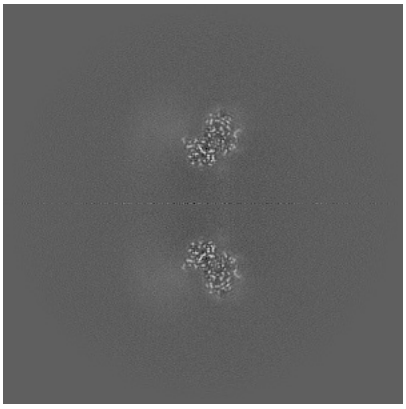
The images above show the map projected in three orthogonal directions.

6.2 Central slices

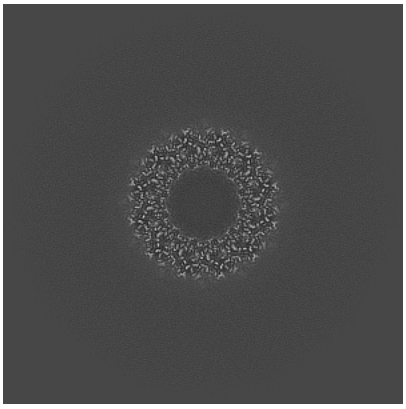
6.2.1 Primary map



X Index: 240



Y Index: 240

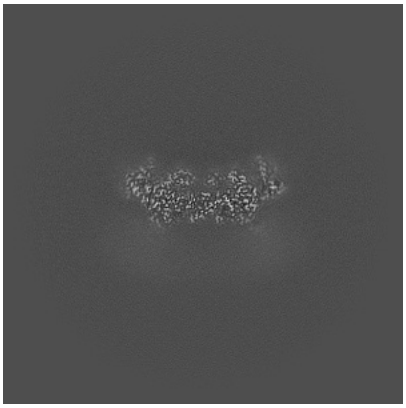


Z Index: 240

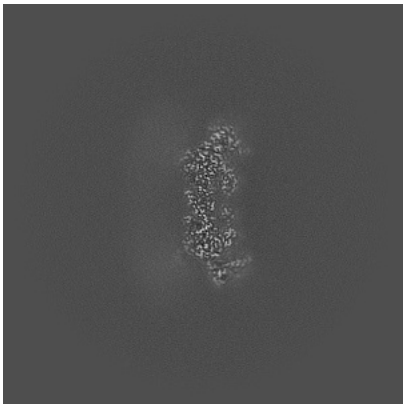
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

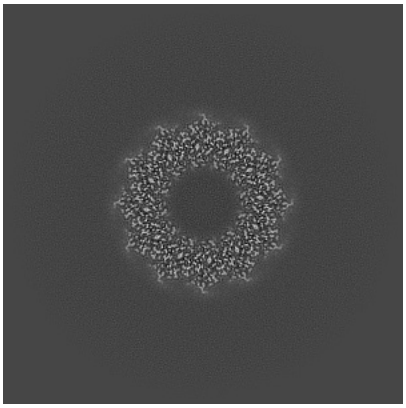
6.3.1 Primary map



X Index: 297



Y Index: 297

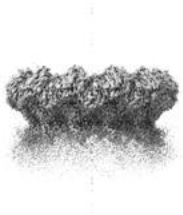


Z Index: 249

The images above show the largest variance slices of the map in three orthogonal directions.

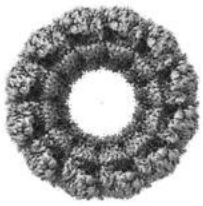
6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

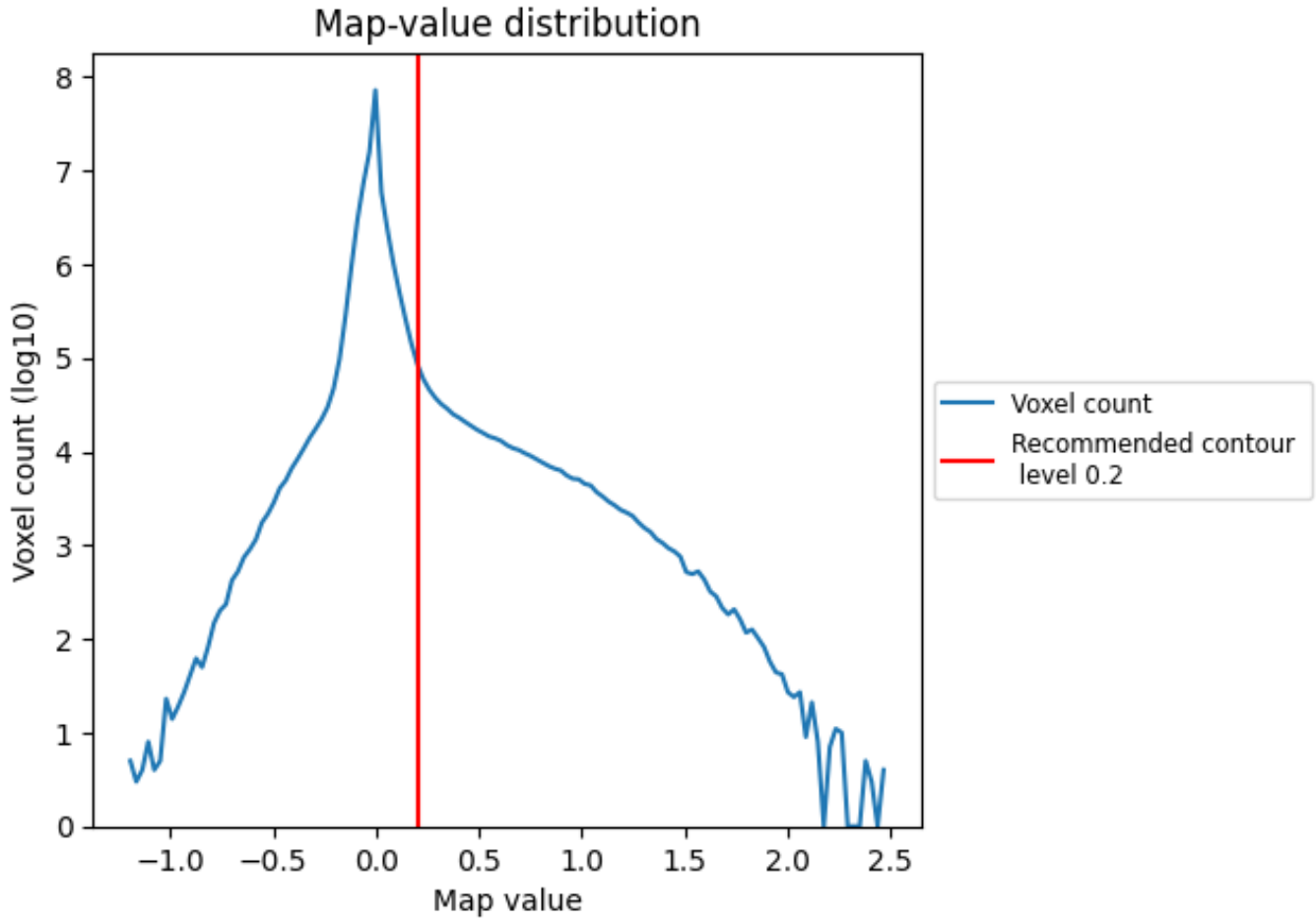
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

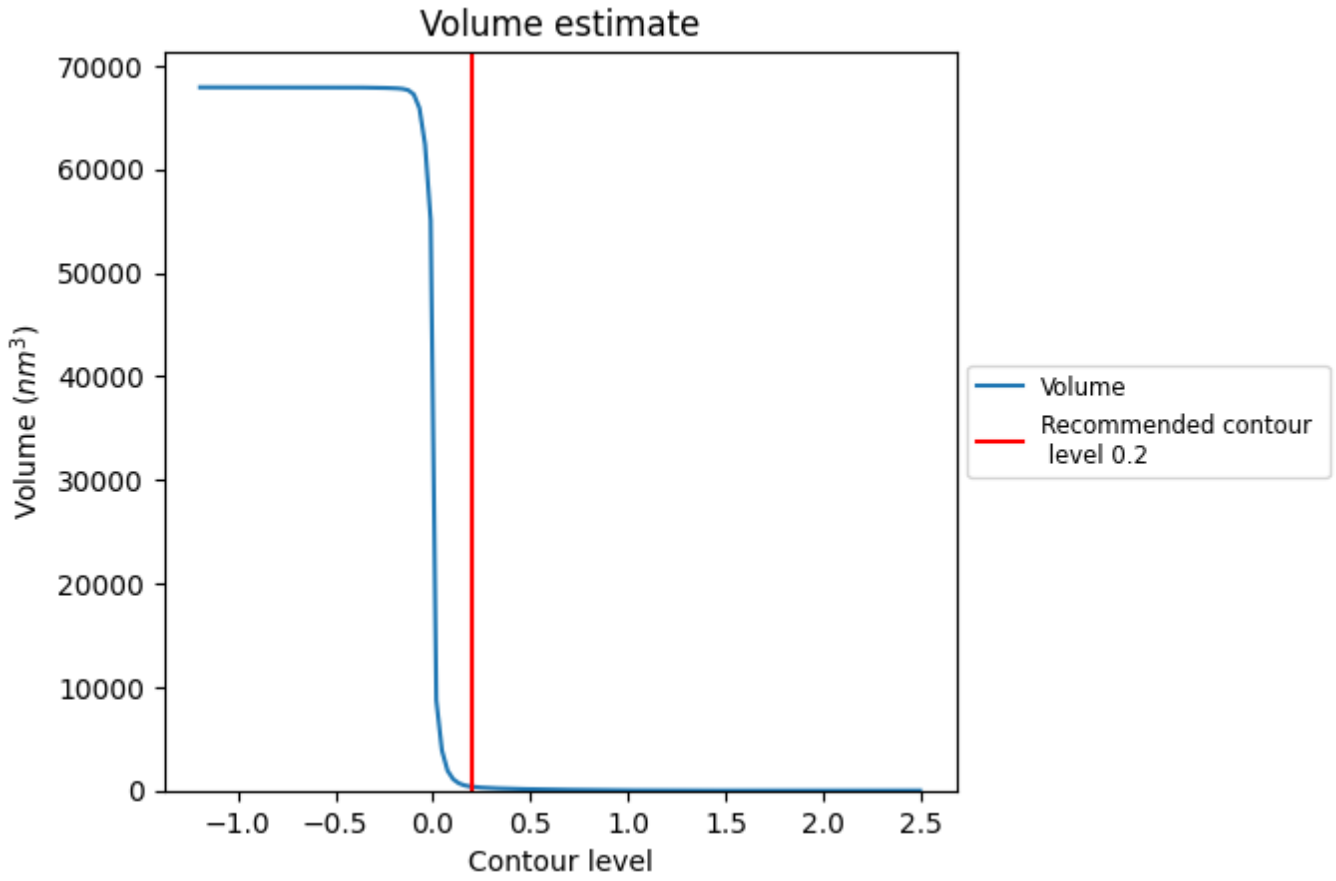
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

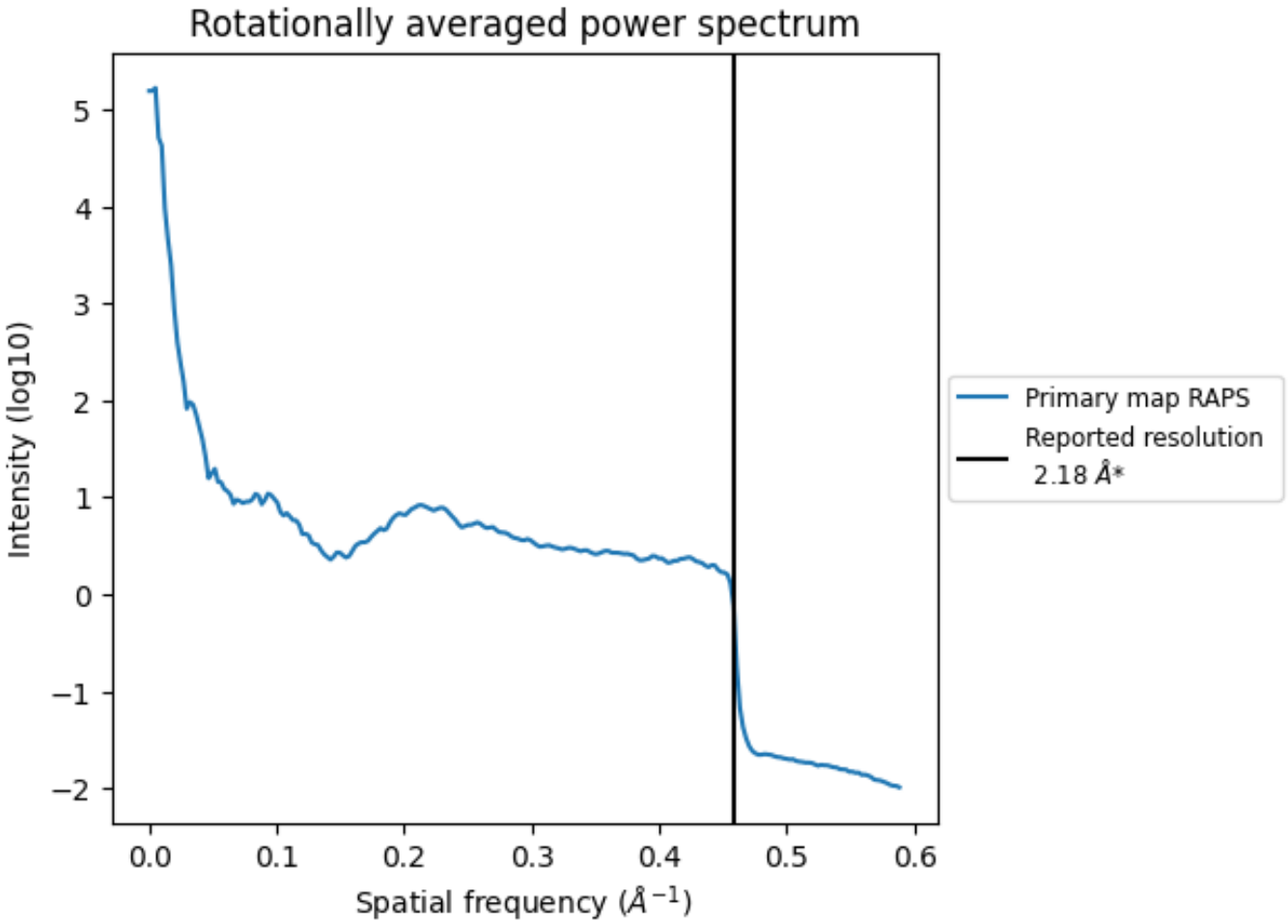
7.2 Volume estimate



The volume at the recommended contour level is 372 nm^3; this corresponds to an approximate mass of 336 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.459 Å^{-1}

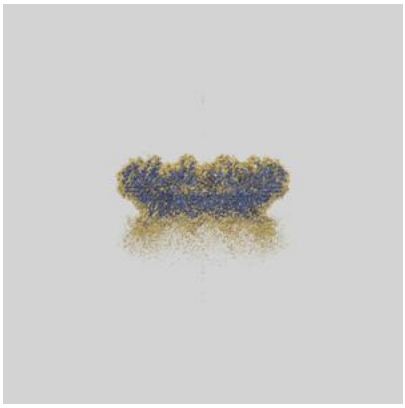
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

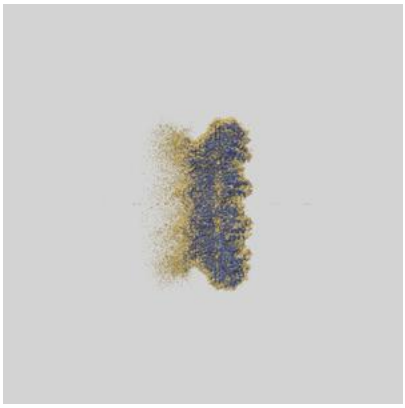
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-31581 and PDB model 7FGH. Per-residue inclusion information can be found in section 3 on page 19.

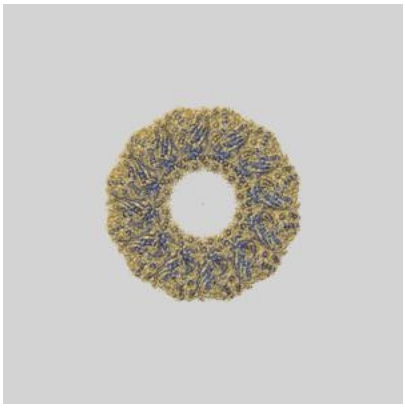
9.1 Map-model overlay



X



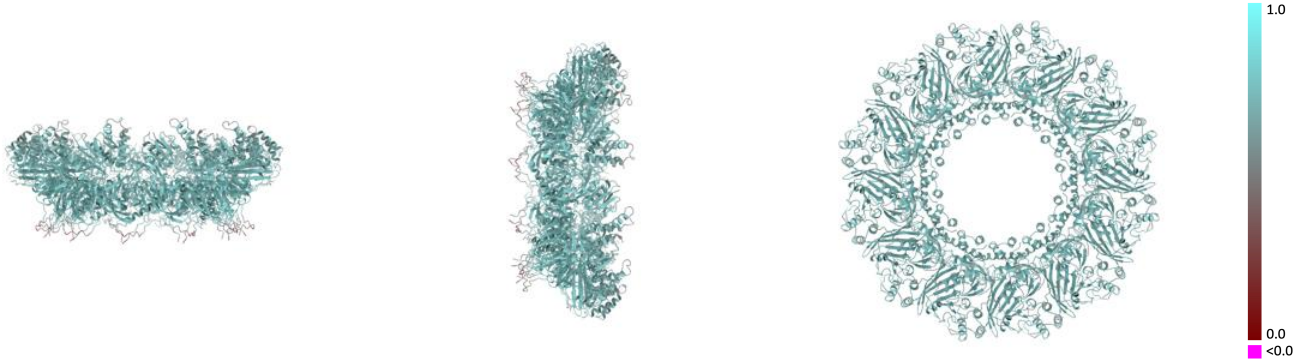
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

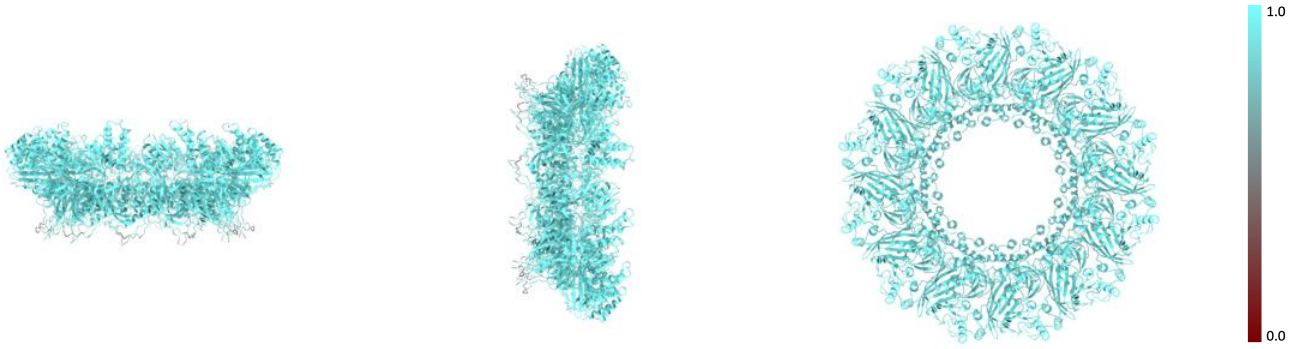
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

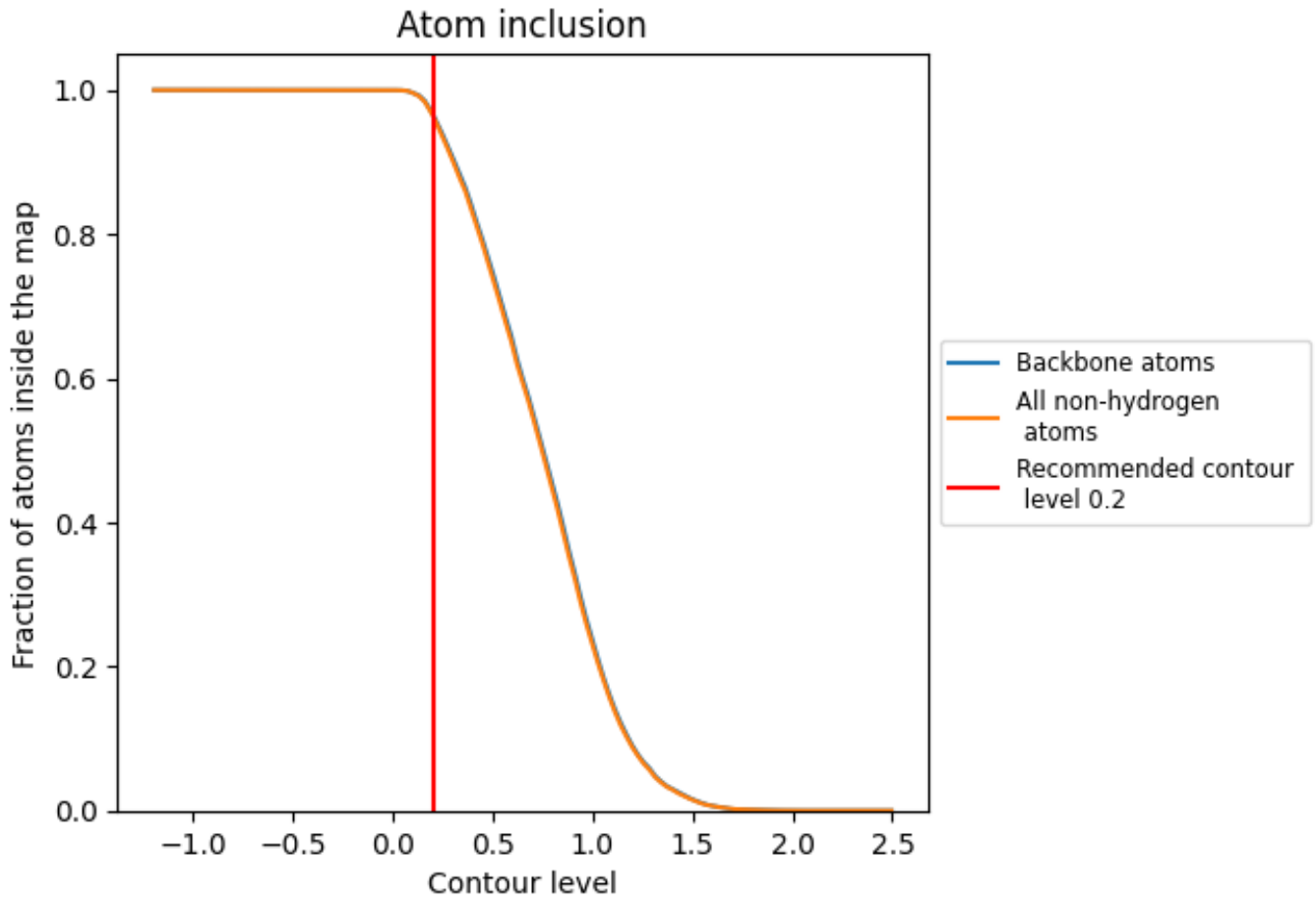
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9647	0.6880
A	0.9662	0.6880
B	0.9662	0.6890
C	0.9664	0.6880
D	0.9662	0.6880
E	0.9667	0.6880
F	0.9670	0.6880
G	0.9664	0.6870
H	0.9664	0.6890
I	0.9662	0.6890
J	0.9662	0.6880
K	0.9670	0.6900
L	0.9664	0.6890