



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 6, 2023 – 12:38 PM EDT

PDB ID : 1LOJ  
Title : Crystal structure of a Methanobacterial Sm-like archaeal protein (SmAP1) bound to uridine-5'-monophosphate (UMP)  
Authors : Mura, C.; Kozhukhovskiy, A.; Eisenberg, D.  
Deposited on : 2002-05-06  
Resolution : 1.90 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35

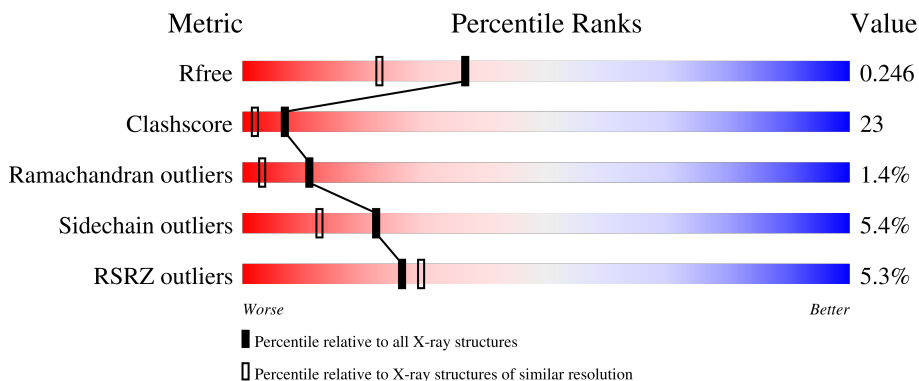
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	87	 6% 55% 24% 8% 13%
1	B	87	 3% 54% 25% 8% 13%
1	C	87	 % 56% 26% 6% 11%
1	D	87	 2% 59% 24% • 15%
1	E	87	 5% 62% 21% • 14%

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Mol	Chain	Length	Quality of chain
1	F	87	
1	G	87	
1	H	87	
1	I	87	
1	J	87	
1	K	87	
1	L	87	
1	M	87	
1	N	87	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	URI	B	9007	-	-	-	X
4	URI	F	9009	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8974 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called small nuclear ribonucleoprotein homolog (Sm-like).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	76	597	374	110	112	1	0	0	0
1	B	76	592	371	109	111	1	0	0	0
1	C	77	598	374	110	113	1	0	0	0
1	D	74	582	363	108	110	1	0	0	0
1	E	75	590	369	109	111	1	0	0	0
1	F	75	590	369	109	111	1	0	0	0
1	G	75	590	369	109	111	1	0	0	0
1	H	76	595	372	110	112	1	0	0	0
1	I	74	582	363	108	110	1	0	0	0
1	J	76	592	371	109	111	1	0	0	0
1	K	72	569	355	105	108	1	0	0	0
1	L	74	582	363	108	110	1	0	0	0
1	M	73	574	359	106	108	1	0	0	0
1	N	74	580	361	108	110	1	0	0	0

There are 98 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	ARG	PRO	cloning artifact	UNP O26745

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Chain	Residue	Modelled	Actual	Comment	Reference
A	82	GLY	-	cloning artifact	UNP O26745
A	83	LYS	-	cloning artifact	UNP O26745
A	84	LEU	-	cloning artifact	UNP O26745
A	85	ALA	-	cloning artifact	UNP O26745
A	86	ALA	-	cloning artifact	UNP O26745
A	87	ALA	-	cloning artifact	UNP O26745
B	81	ARG	PRO	cloning artifact	UNP O26745
B	82	GLY	-	cloning artifact	UNP O26745
B	83	LYS	-	cloning artifact	UNP O26745
B	84	LEU	-	cloning artifact	UNP O26745
B	85	ALA	-	cloning artifact	UNP O26745
B	86	ALA	-	cloning artifact	UNP O26745
B	87	ALA	-	cloning artifact	UNP O26745
C	81	ARG	PRO	cloning artifact	UNP O26745
C	82	GLY	-	cloning artifact	UNP O26745
C	83	LYS	-	cloning artifact	UNP O26745
C	84	LEU	-	cloning artifact	UNP O26745
C	85	ALA	-	cloning artifact	UNP O26745
C	86	ALA	-	cloning artifact	UNP O26745
C	87	ALA	-	cloning artifact	UNP O26745
D	81	ARG	PRO	cloning artifact	UNP O26745
D	82	GLY	-	cloning artifact	UNP O26745
D	83	LYS	-	cloning artifact	UNP O26745
D	84	LEU	-	cloning artifact	UNP O26745
D	85	ALA	-	cloning artifact	UNP O26745
D	86	ALA	-	cloning artifact	UNP O26745
D	87	ALA	-	cloning artifact	UNP O26745
E	81	ARG	PRO	cloning artifact	UNP O26745
E	82	GLY	-	cloning artifact	UNP O26745
E	83	LYS	-	cloning artifact	UNP O26745
E	84	LEU	-	cloning artifact	UNP O26745
E	85	ALA	-	cloning artifact	UNP O26745
E	86	ALA	-	cloning artifact	UNP O26745
E	87	ALA	-	cloning artifact	UNP O26745
F	81	ARG	PRO	cloning artifact	UNP O26745
F	82	GLY	-	cloning artifact	UNP O26745
F	83	LYS	-	cloning artifact	UNP O26745
F	84	LEU	-	cloning artifact	UNP O26745
F	85	ALA	-	cloning artifact	UNP O26745
F	86	ALA	-	cloning artifact	UNP O26745
F	87	ALA	-	cloning artifact	UNP O26745
G	81	ARG	PRO	cloning artifact	UNP O26745

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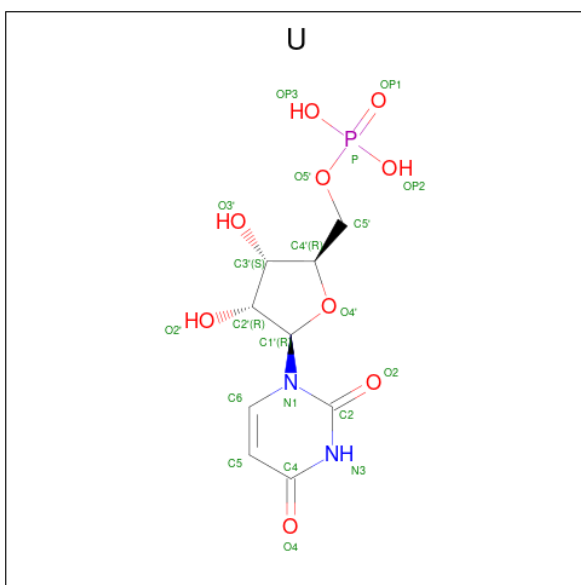
Chain	Residue	Modelled	Actual	Comment	Reference
G	82	GLY	-	cloning artifact	UNP O26745
G	83	LYS	-	cloning artifact	UNP O26745
G	84	LEU	-	cloning artifact	UNP O26745
G	85	ALA	-	cloning artifact	UNP O26745
G	86	ALA	-	cloning artifact	UNP O26745
G	87	ALA	-	cloning artifact	UNP O26745
H	81	ARG	PRO	cloning artifact	UNP O26745
H	82	GLY	-	cloning artifact	UNP O26745
H	83	LYS	-	cloning artifact	UNP O26745
H	84	LEU	-	cloning artifact	UNP O26745
H	85	ALA	-	cloning artifact	UNP O26745
H	86	ALA	-	cloning artifact	UNP O26745
H	87	ALA	-	cloning artifact	UNP O26745
I	81	ARG	PRO	cloning artifact	UNP O26745
I	82	GLY	-	cloning artifact	UNP O26745
I	83	LYS	-	cloning artifact	UNP O26745
I	84	LEU	-	cloning artifact	UNP O26745
I	85	ALA	-	cloning artifact	UNP O26745
I	86	ALA	-	cloning artifact	UNP O26745
I	87	ALA	-	cloning artifact	UNP O26745
J	81	ARG	PRO	cloning artifact	UNP O26745
J	82	GLY	-	cloning artifact	UNP O26745
J	83	LYS	-	cloning artifact	UNP O26745
J	84	LEU	-	cloning artifact	UNP O26745
J	85	ALA	-	cloning artifact	UNP O26745
J	86	ALA	-	cloning artifact	UNP O26745
J	87	ALA	-	cloning artifact	UNP O26745
K	81	ARG	PRO	cloning artifact	UNP O26745
K	82	GLY	-	cloning artifact	UNP O26745
K	83	LYS	-	cloning artifact	UNP O26745
K	84	LEU	-	cloning artifact	UNP O26745
K	85	ALA	-	cloning artifact	UNP O26745
K	86	ALA	-	cloning artifact	UNP O26745
K	87	ALA	-	cloning artifact	UNP O26745
L	81	ARG	PRO	cloning artifact	UNP O26745
L	82	GLY	-	cloning artifact	UNP O26745
L	83	LYS	-	cloning artifact	UNP O26745
L	84	LEU	-	cloning artifact	UNP O26745
L	85	ALA	-	cloning artifact	UNP O26745
L	86	ALA	-	cloning artifact	UNP O26745
L	87	ALA	-	cloning artifact	UNP O26745
M	81	ARG	PRO	cloning artifact	UNP O26745

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Chain	Residue	Modelled	Actual	Comment	Reference
M	82	GLY	-	cloning artifact	UNP O26745
M	83	LYS	-	cloning artifact	UNP O26745
M	84	LEU	-	cloning artifact	UNP O26745
M	85	ALA	-	cloning artifact	UNP O26745
M	86	ALA	-	cloning artifact	UNP O26745
M	87	ALA	-	cloning artifact	UNP O26745
N	81	ARG	PRO	cloning artifact	UNP O26745
N	82	GLY	-	cloning artifact	UNP O26745
N	83	LYS	-	cloning artifact	UNP O26745
N	84	LEU	-	cloning artifact	UNP O26745
N	85	ALA	-	cloning artifact	UNP O26745
N	86	ALA	-	cloning artifact	UNP O26745
N	87	ALA	-	cloning artifact	UNP O26745

- Molecule 2 is URIDINE-5'-MONOPHOSPHATE (three-letter code: U) (formula: C<sub>9</sub>H<sub>13</sub>N<sub>2</sub>O<sub>9</sub>P).



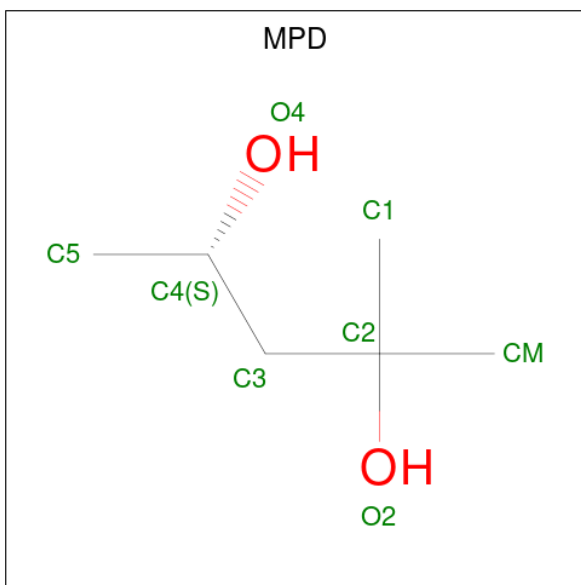
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
2	D	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
2	H	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
2	I	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
2	K	1	Total	C	N	O	P	0	0
			21	9	2	9	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	N	1	21	9	2	9	1	0	0

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	8	6	2	0	0
3	B	1	8	6	2	0	0
3	C	1	8	6	2	0	0
3	D	1	8	6	2	0	0
3	E	1	8	6	2	0	0
3	F	1	8	6	2	0	0
3	G	1	8	6	2	0	0
3	H	1	8	6	2	0	0
3	I	1	8	6	2	0	0
3	J	1	8	6	2	0	0

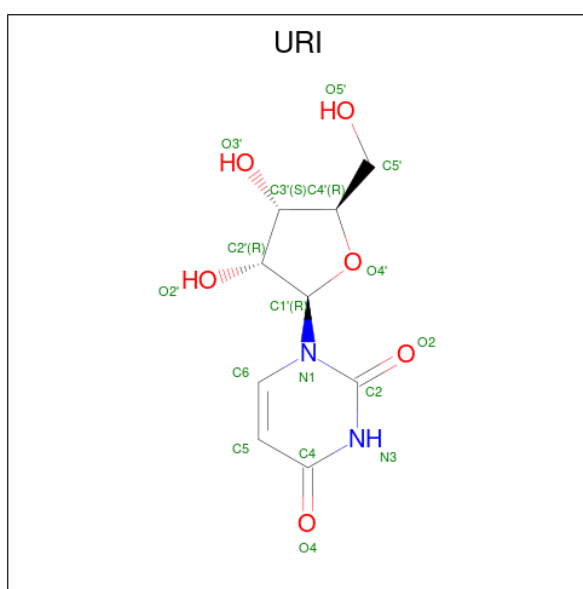
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	K	1	Total	C	O	0	0
			8	6	2		
3	L	1	Total	C	O	0	0
			8	6	2		
3	M	1	Total	C	O	0	0
			8	6	2		
3	N	1	Total	C	O	0	0
			8	6	2		

- Molecule 4 is URIDINE (three-letter code: URI) (formula: C<sub>9</sub>H<sub>12</sub>N<sub>2</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			17	9	2	6		
4	C	1	Total	C	N	O	0	0
			17	9	2	6		
4	E	1	Total	C	N	O	0	0
			17	9	2	6		
4	F	1	Total	C	N	O	0	0
			17	9	2	6		
4	G	1	Total	C	N	O	0	0
			17	9	2	6		
4	J	1	Total	C	N	O	0	0
			17	9	2	6		
4	L	1	Total	C	N	O	0	0
			17	9	2	6		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	M	1	Total	C	N	O	0	0
			17	9	2	6		

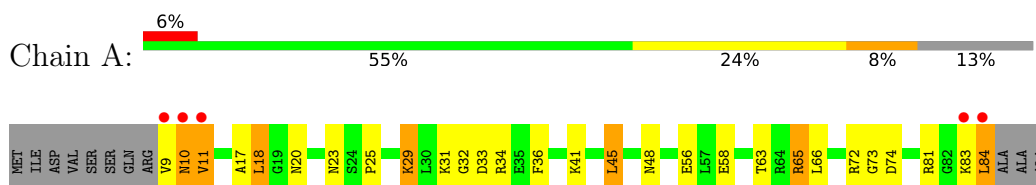
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	32	Total	O	0	0
			32	32		
5	B	31	Total	O	0	0
			31	31		
5	C	38	Total	O	0	0
			38	38		
5	D	32	Total	O	0	0
			32	32		
5	E	24	Total	O	0	0
			24	24		
5	F	32	Total	O	0	0
			32	32		
5	G	37	Total	O	0	0
			37	37		
5	H	20	Total	O	0	0
			20	20		
5	I	20	Total	O	0	0
			20	20		
5	J	33	Total	O	0	0
			33	33		
5	K	19	Total	O	0	0
			19	19		
5	L	16	Total	O	0	0
			16	16		
5	M	23	Total	O	0	0
			23	23		
5	N	30	Total	O	0	0
			30	30		

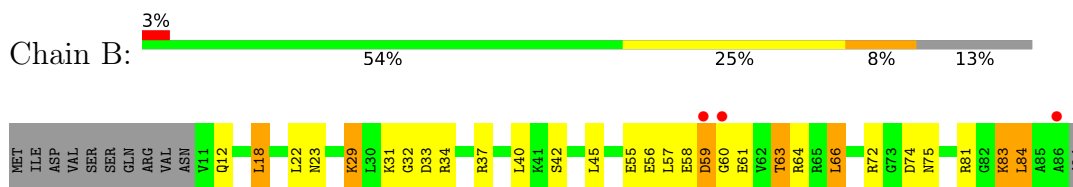
### 3 Residue-property plots [i](#)

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

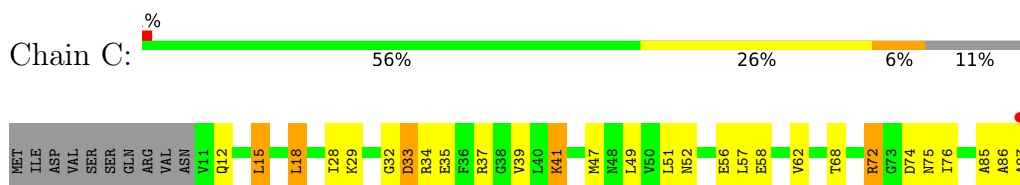
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



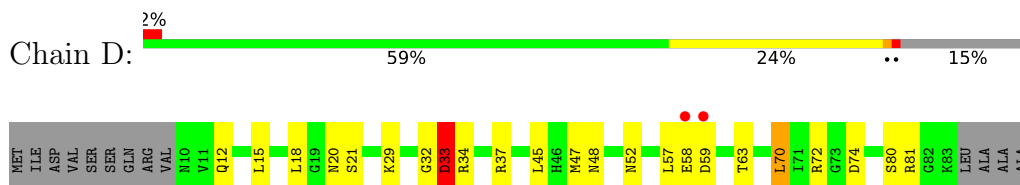
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



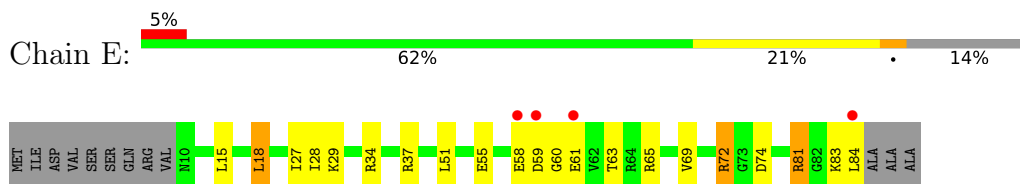
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



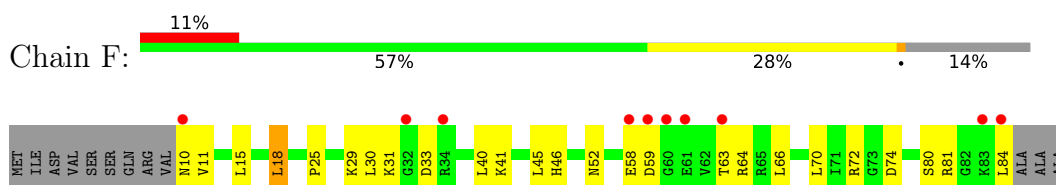
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



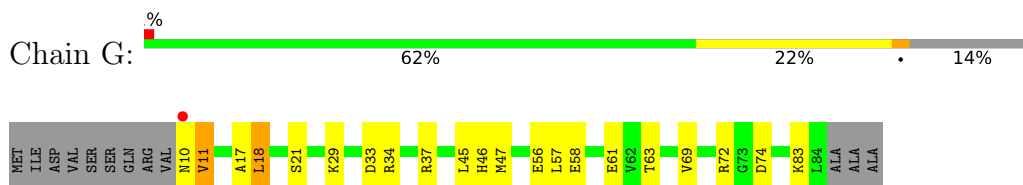
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



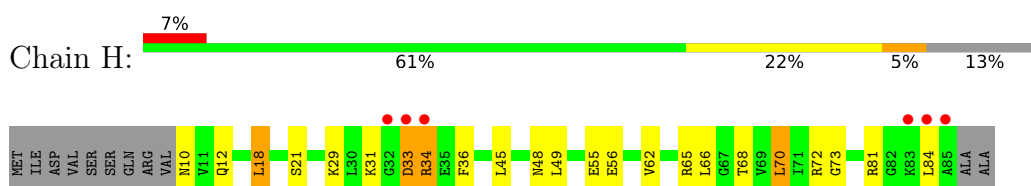
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



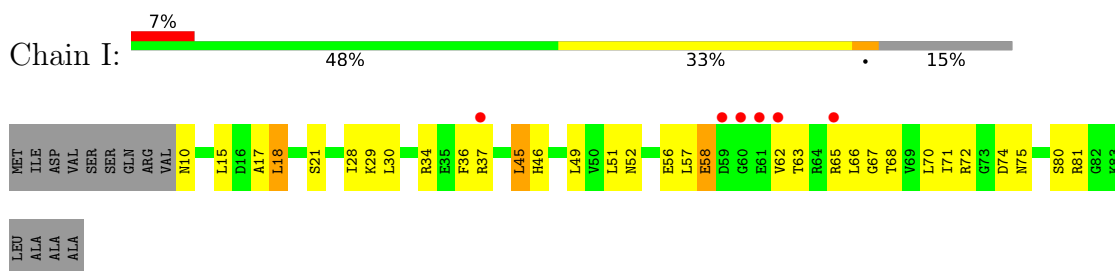
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



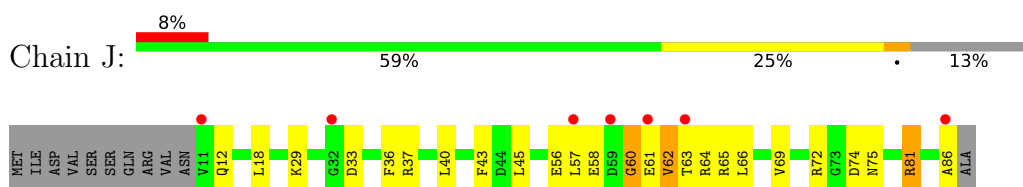
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



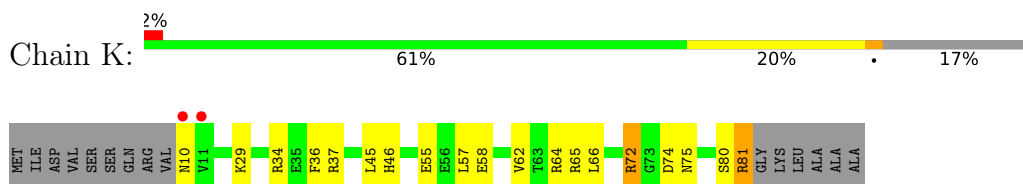
- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



- Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)





• Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



• Molecule 1: small nuclear ribonucleoprotein homolog (Sm-like)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.25Å 109.96Å 83.76Å 90.00° 95.81° 90.00°	Depositor
Resolution (Å)	19.79 – 1.90 41.95 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.3 (19.79-1.90) 93.4 (41.95-1.90)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.48 (at 1.89Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.207 , 0.250 0.202 , 0.246	Depositor DCC
$R_{free}$ test set	4503 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.8	Xtrriage
Anisotropy	0.247	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8974	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, URI

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	0.61	0/602	0.90	0/810
1	B	0.66	0/597	0.90	0/803
1	C	0.72	0/603	0.95	2/810 (0.2%)
1	D	0.61	0/587	0.96	0/789
1	E	0.62	0/595	0.88	1/800 (0.1%)
1	F	0.60	0/595	0.83	0/800
1	G	0.66	0/595	0.90	1/800 (0.1%)
1	H	0.58	0/600	0.89	2/807 (0.2%)
1	I	0.57	0/587	0.84	0/789
1	J	0.66	0/597	1.01	3/803 (0.4%)
1	K	0.58	0/574	0.85	1/773 (0.1%)
1	L	0.57	0/587	0.86	0/789
1	M	0.62	0/579	0.90	0/778
1	N	0.68	0/585	0.99	0/786
All	All	0.63	0/8283	0.91	10/11137 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	81	ARG	NE-CZ-NH2	-7.34	116.63	120.30
1	G	33	ASP	N-CA-C	6.07	127.38	111.00
1	C	72	ARG	NE-CZ-NH1	-6.00	117.30	120.30
1	E	72	ARG	NE-CZ-NH1	-5.96	117.32	120.30
1	H	34	ARG	N-CA-C	-5.94	94.95	111.00

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	597	0	621	37	0
1	B	592	0	616	39	0
1	C	598	0	621	36	0
1	D	582	0	601	35	0
1	E	590	0	612	28	0
1	F	590	0	612	36	0
1	G	590	0	612	31	0
1	H	595	0	617	34	0
1	I	582	0	601	35	0
1	J	592	0	616	34	0
1	K	569	0	585	30	0
1	L	582	0	601	34	0
1	M	574	0	595	37	0
1	N	580	0	594	11	0
2	A	21	0	11	4	0
2	D	21	0	11	1	0
2	H	21	0	11	2	0
2	I	21	0	11	1	0
2	K	21	0	11	2	0
2	N	21	0	11	0	0
3	A	8	0	14	2	0
3	B	8	0	14	4	0
3	C	8	0	14	0	0
3	D	8	0	14	5	0
3	E	8	0	14	0	0
3	F	8	0	14	1	0
3	G	8	0	14	4	0
3	H	8	0	14	1	0
3	I	8	0	14	3	0
3	J	8	0	14	0	0
3	K	8	0	14	0	0
3	L	8	0	14	1	0
3	M	8	0	14	3	0
3	N	8	0	14	1	0
4	B	17	0	12	1	0
4	C	17	0	12	1	0
4	E	17	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	17	0	12	3	0
4	G	17	0	12	4	0
4	J	17	0	12	1	0
4	L	17	0	12	2	0
4	M	17	0	12	4	0
5	A	32	0	0	2	0
5	B	31	0	0	0	0
5	C	38	0	0	6	0
5	D	32	0	0	3	0
5	E	24	0	0	2	0
5	F	32	0	0	4	0
5	G	37	0	0	1	0
5	H	20	0	0	2	0
5	I	20	0	0	1	0
5	J	33	0	0	4	0
5	K	19	0	0	2	0
5	L	16	0	0	2	0
5	M	23	0	0	2	0
5	N	30	0	0	1	0
All	All	8974	0	8862	401	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 23.

The worst 5 of 401 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:F:29:LYS:HZ1	1:F:33:ASP:HA	1.16	1.07
1:B:37:ARG:HH11	1:B:57:LEU:HD22	1.23	1.04
1:M:81:ARG:HG3	1:M:81:ARG:HH11	1.20	1.02
1:G:10:ASN:HD22	1:I:10:ASN:HD22	1.12	0.95
1:L:41:LYS:HD2	1:L:52:ASN:ND2	1.82	0.94

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	74/87 (85%)	71 (96%)	1 (1%)	2 (3%)	5	1
1	B	74/87 (85%)	69 (93%)	3 (4%)	2 (3%)	5	1
1	C	75/87 (86%)	71 (95%)	4 (5%)	0	100	100
1	D	72/87 (83%)	66 (92%)	5 (7%)	1 (1%)	11	3
1	E	73/87 (84%)	70 (96%)	3 (4%)	0	100	100
1	F	73/87 (84%)	70 (96%)	3 (4%)	0	100	100
1	G	73/87 (84%)	68 (93%)	4 (6%)	1 (1%)	11	3
1	H	74/87 (85%)	72 (97%)	1 (1%)	1 (1%)	11	3
1	I	72/87 (83%)	67 (93%)	5 (7%)	0	100	100
1	J	74/87 (85%)	69 (93%)	4 (5%)	1 (1%)	11	3
1	K	70/87 (80%)	70 (100%)	0	0	100	100
1	L	72/87 (83%)	66 (92%)	5 (7%)	1 (1%)	11	3
1	M	71/87 (82%)	64 (90%)	3 (4%)	4 (6%)	2	0
1	N	72/87 (83%)	69 (96%)	2 (3%)	1 (1%)	11	3
All	All	1019/1218 (84%)	962 (94%)	43 (4%)	14 (1%)	11	3

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	D	33	ASP
1	M	33	ASP
1	M	62	VAL
1	A	11	VAL

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	67/75 (89%)	62 (92%)	5 (8%)	13 5
1	B	65/75 (87%)	59 (91%)	6 (9%)	9 3
1	C	65/75 (87%)	62 (95%)	3 (5%)	27 17
1	D	65/75 (87%)	61 (94%)	4 (6%)	18 9
1	E	66/75 (88%)	63 (96%)	3 (4%)	27 18
1	F	66/75 (88%)	61 (92%)	5 (8%)	13 5
1	G	66/75 (88%)	65 (98%)	1 (2%)	65 62
1	H	66/75 (88%)	62 (94%)	4 (6%)	18 9
1	I	65/75 (87%)	62 (95%)	3 (5%)	27 17
1	J	65/75 (87%)	64 (98%)	1 (2%)	65 62
1	K	64/75 (85%)	61 (95%)	3 (5%)	26 16
1	L	65/75 (87%)	63 (97%)	2 (3%)	40 32
1	M	64/75 (85%)	57 (89%)	7 (11%)	6 2
1	N	64/75 (85%)	62 (97%)	2 (3%)	40 32
All	All	913/1050 (87%)	864 (95%)	49 (5%)	22 13

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	33	ASP
1	K	10	ASN
1	H	70	LEU
1	I	45	LEU
1	K	81	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	10	ASN

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Mol	Chain	Res	Type
1	N	46	HIS
1	K	23	ASN
1	M	20	ASN
1	E	12	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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](#)

28 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	MPD	E	7012	-	7,7,7	0.41	0	9,10,10	0.55	0
2	U	K	9014	-	22,22,22	1.15	2 (9%)	33,33,33	1.44	4 (12%)
3	MPD	N	7009	-	7,7,7	0.38	0	9,10,10	0.50	0
3	MPD	G	7007	-	7,7,7	0.69	0	9,10,10	0.63	0
3	MPD	L	7003	-	7,7,7	0.58	0	9,10,10	0.57	0
3	MPD	J	7001	-	7,7,7	0.72	0	9,10,10	0.61	0
3	MPD	B	7011	-	7,7,7	0.55	0	9,10,10	0.46	0
3	MPD	M	7010	-	7,7,7	0.64	0	9,10,10	0.62	0
2	U	D	9008	-	22,22,22	1.21	2 (9%)	33,33,33	1.41	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	MPD	H	7008	-	7,7,7	0.52	0	9,10,10	0.61	0
2	U	N	9013	-	22,22,22	1.24	2 (9%)	33,33,33	1.34	3 (9%)
3	MPD	F	7013	-	7,7,7	0.58	0	9,10,10	0.66	0
4	URI	G	9012	-	18,18,18	1.63	3 (16%)	26,26,26	1.12	1 (3%)
3	MPD	I	7014	-	7,7,7	0.52	0	9,10,10	0.49	0
4	URI	F	9009	-	18,18,18	1.73	3 (16%)	26,26,26	1.15	2 (7%)
3	MPD	A	7005	-	7,7,7	0.56	0	9,10,10	0.41	0
4	URI	L	9005	-	18,18,18	1.61	2 (11%)	26,26,26	1.15	2 (7%)
4	URI	J	9001	-	18,18,18	1.50	2 (11%)	26,26,26	1.04	1 (3%)
2	U	A	9010	-	22,22,22	1.18	1 (4%)	33,33,33	1.53	5 (15%)
4	URI	E	9006	-	18,18,18	1.95	4 (22%)	26,26,26	1.34	5 (19%)
3	MPD	D	7004	-	7,7,7	0.49	0	9,10,10	0.66	0
3	MPD	K	7002	-	7,7,7	0.55	0	9,10,10	0.43	0
2	U	H	9003	-	22,22,22	1.25	2 (9%)	33,33,33	1.32	2 (6%)
2	U	I	9002	-	22,22,22	1.34	3 (13%)	33,33,33	1.54	3 (9%)
4	URI	M	9004	-	18,18,18	1.44	2 (11%)	26,26,26	1.23	3 (11%)
4	URI	B	9007	-	18,18,18	1.70	4 (22%)	26,26,26	1.17	1 (3%)
4	URI	C	9011	-	18,18,18	1.83	3 (16%)	26,26,26	1.35	2 (7%)
3	MPD	C	7006	-	7,7,7	0.69	0	9,10,10	0.48	0

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	MPD	E	7012	-	-	0/5/5/5	-
2	U	K	9014	-	-	2/10/26/26	0/2/2/2
3	MPD	N	7009	-	-	0/5/5/5	-
3	MPD	G	7007	-	-	2/5/5/5	-
3	MPD	L	7003	-	-	0/5/5/5	-
3	MPD	J	7001	-	-	0/5/5/5	-
3	MPD	B	7011	-	-	1/5/5/5	-
3	MPD	M	7010	-	-	0/5/5/5	-
2	U	D	9008	-	-	2/10/26/26	0/2/2/2
3	MPD	H	7008	-	-	1/5/5/5	-
2	U	N	9013	-	-	2/10/26/26	0/2/2/2
3	MPD	F	7013	-	-	3/5/5/5	-
4	URI	G	9012	-	-	4/6/22/22	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MPD	I	7014	-	-	0/5/5/5	-
4	URI	F	9009	-	-	2/6/22/22	0/2/2/2
3	MPD	A	7005	-	-	2/5/5/5	-
4	URI	L	9005	-	-	0/6/22/22	0/2/2/2
4	URI	J	9001	-	-	3/6/22/22	0/2/2/2
2	U	A	9010	-	-	2/10/26/26	0/2/2/2
4	URI	E	9006	-	-	0/6/22/22	0/2/2/2
3	MPD	D	7004	-	-	0/5/5/5	-
3	MPD	K	7002	-	-	2/5/5/5	-
2	U	H	9003	-	-	2/10/26/26	0/2/2/2
2	U	I	9002	-	-	1/10/26/26	0/2/2/2
4	URI	M	9004	-	-	4/6/22/22	0/2/2/2
4	URI	B	9007	-	-	4/6/22/22	0/2/2/2
4	URI	C	9011	-	-	0/6/22/22	0/2/2/2
3	MPD	C	7006	-	-	0/5/5/5	-

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	9006	URI	C2-N1	6.12	1.48	1.38
4	C	9011	URI	C2-N1	5.98	1.48	1.38
4	F	9009	URI	C2-N1	5.47	1.47	1.38
4	B	9007	URI	C2-N1	5.25	1.46	1.38
4	L	9005	URI	C2-N1	4.76	1.46	1.38

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	9008	U	O5'-P-OP1	4.58	119.32	106.47
2	I	9002	U	O5'-P-OP1	4.55	119.23	106.47
2	N	9013	U	O5'-P-OP1	4.25	118.40	106.47
2	K	9014	U	O5'-P-OP1	4.19	118.23	106.47
2	A	9010	U	O5'-P-OP1	4.15	118.13	106.47

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	9010	U	C4'-C5'-O5'-P
2	K	9014	U	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	N	9013	U	O4'-C4'-C5'-O5'
2	N	9013	U	C3'-C4'-C5'-O5'
3	F	7013	MPD	O2-C2-C3-C4

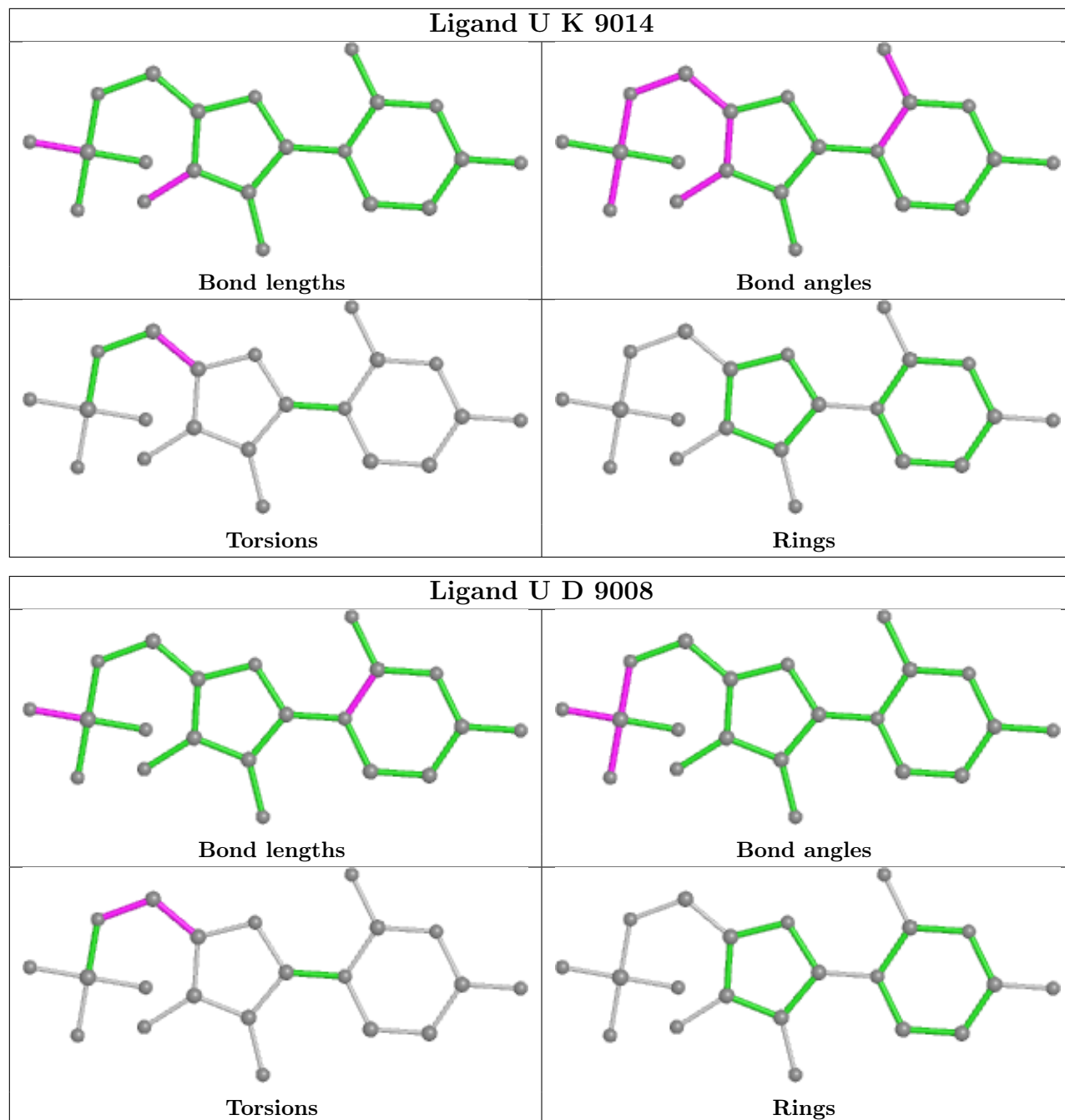
There are no ring outliers.

22 monomers are involved in 48 short contacts:

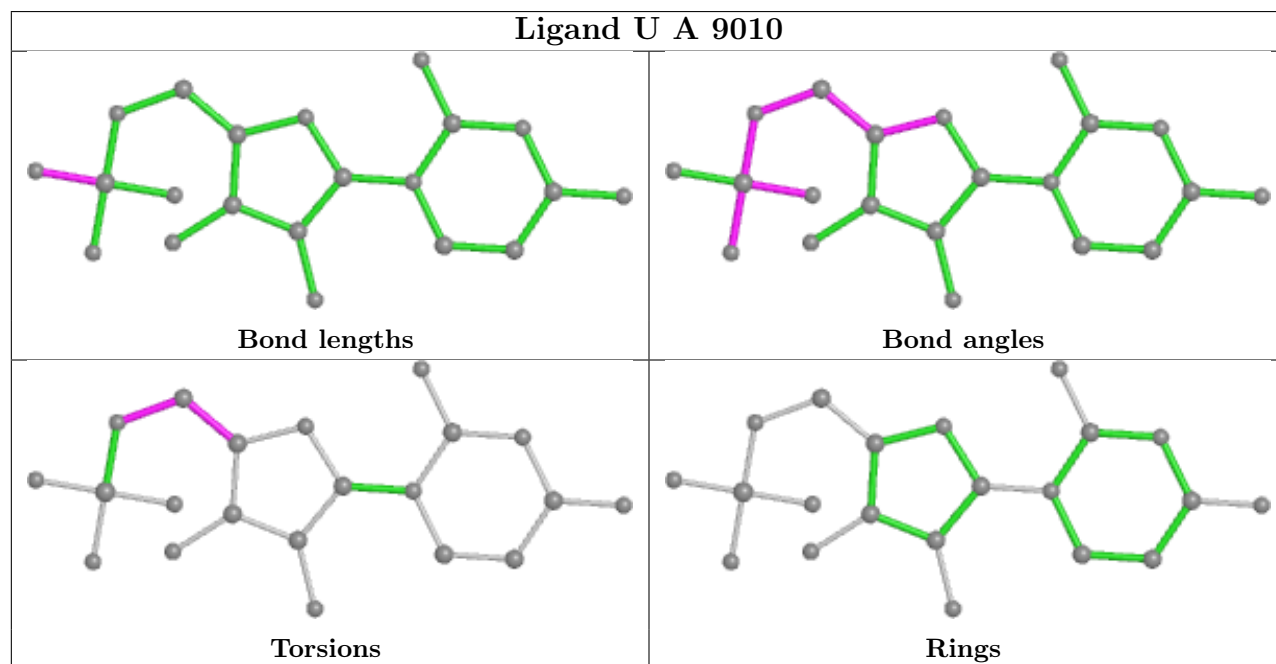
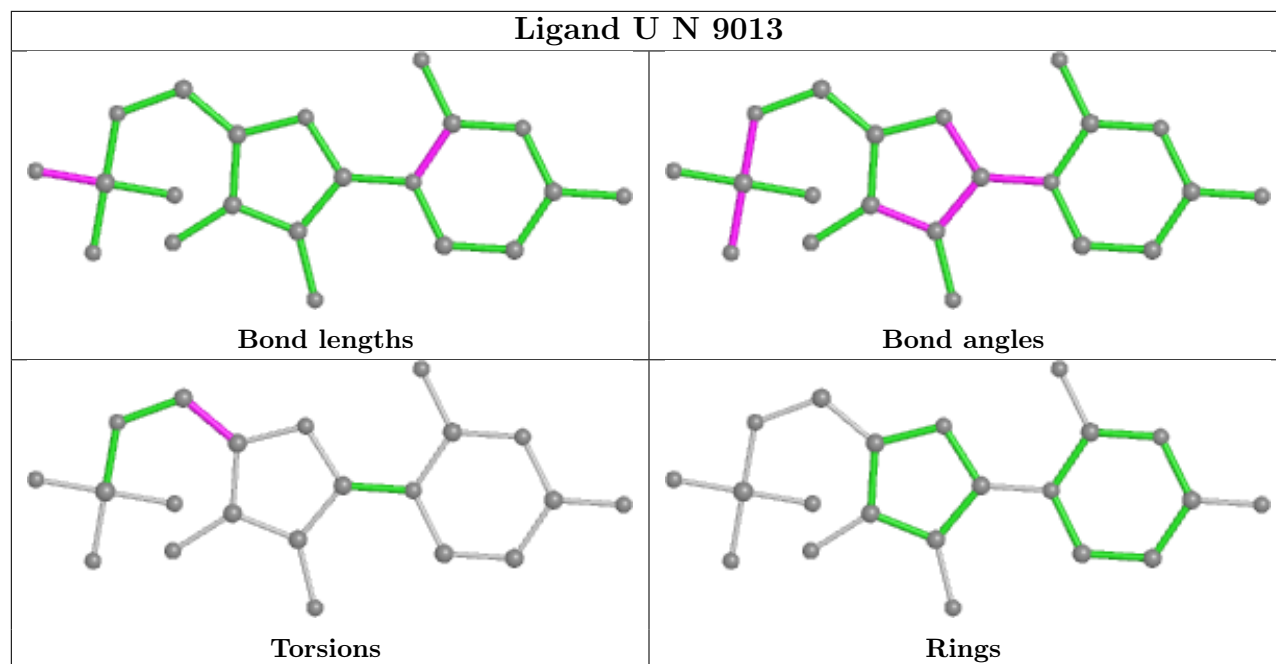
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	9014	U	2	0
3	N	7009	MPD	1	0
3	G	7007	MPD	4	0
3	L	7003	MPD	1	0
3	B	7011	MPD	4	0
3	M	7010	MPD	3	0
2	D	9008	U	1	0
3	H	7008	MPD	1	0
3	F	7013	MPD	1	0
4	G	9012	URI	4	0
3	I	7014	MPD	3	0
4	F	9009	URI	3	0
3	A	7005	MPD	2	0
4	L	9005	URI	2	0
4	J	9001	URI	1	0
2	A	9010	U	4	0
3	D	7004	MPD	5	0
2	H	9003	U	2	0
2	I	9002	U	1	0
4	M	9004	URI	4	0
4	B	9007	URI	1	0
4	C	9011	URI	1	0

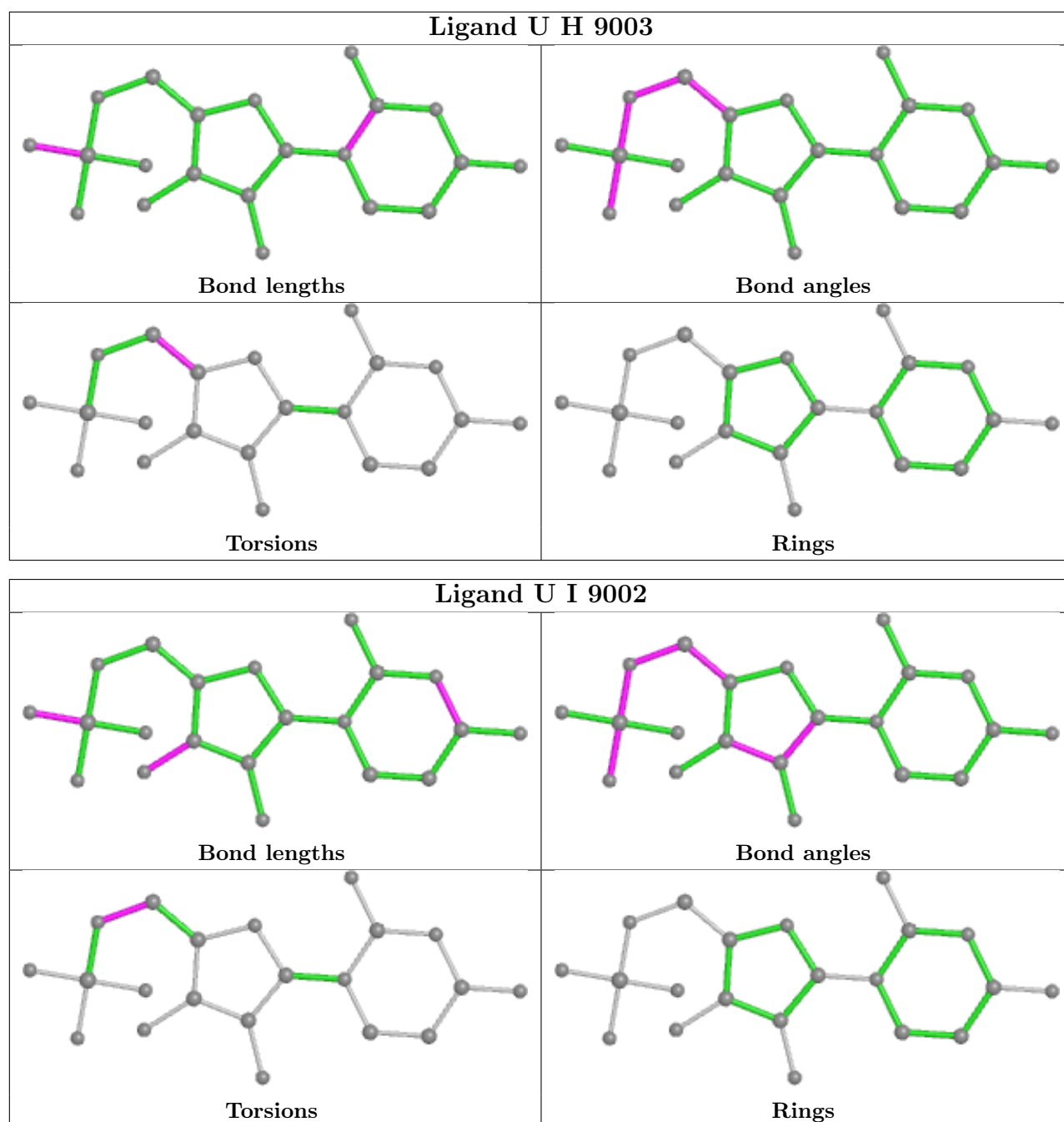
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

equivalents in the CSD to analyse the geometry.









## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	76/87 (87%)	0.25	5 (6%) 18 20	25, 37, 60, 80	0
1	B	76/87 (87%)	0.18	3 (3%) 39 42	26, 37, 63, 75	0
1	C	77/87 (88%)	0.11	1 (1%) 77 79	23, 33, 68, 76	0
1	D	74/87 (85%)	0.07	2 (2%) 54 57	23, 35, 66, 74	0
1	E	75/87 (86%)	0.11	4 (5%) 26 29	22, 36, 67, 72	0
1	F	75/87 (86%)	0.43	10 (13%) 3 3	25, 39, 79, 82	0
1	G	75/87 (86%)	-0.04	1 (1%) 77 79	23, 33, 66, 71	0
1	H	76/87 (87%)	0.33	6 (7%) 12 14	27, 42, 66, 87	0
1	I	74/87 (85%)	0.22	6 (8%) 12 13	28, 41, 78, 85	0
1	J	76/87 (87%)	0.26	7 (9%) 9 10	25, 35, 74, 84	0
1	K	72/87 (82%)	0.13	2 (2%) 53 56	26, 40, 71, 77	0
1	L	74/87 (85%)	0.22	1 (1%) 75 77	26, 41, 68, 79	0
1	M	73/87 (83%)	0.30	5 (6%) 17 19	25, 36, 79, 87	0
1	N	74/87 (85%)	0.06	2 (2%) 54 57	24, 35, 60, 69	0
All	All	1047/1218 (85%)	0.19	55 (5%) 26 29	22, 37, 71, 87	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	9	VAL	10.0
1	H	85	ALA	8.3
1	H	84	LEU	7.9
1	M	59	ASP	7.2
1	A	84	LEU	6.7

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

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

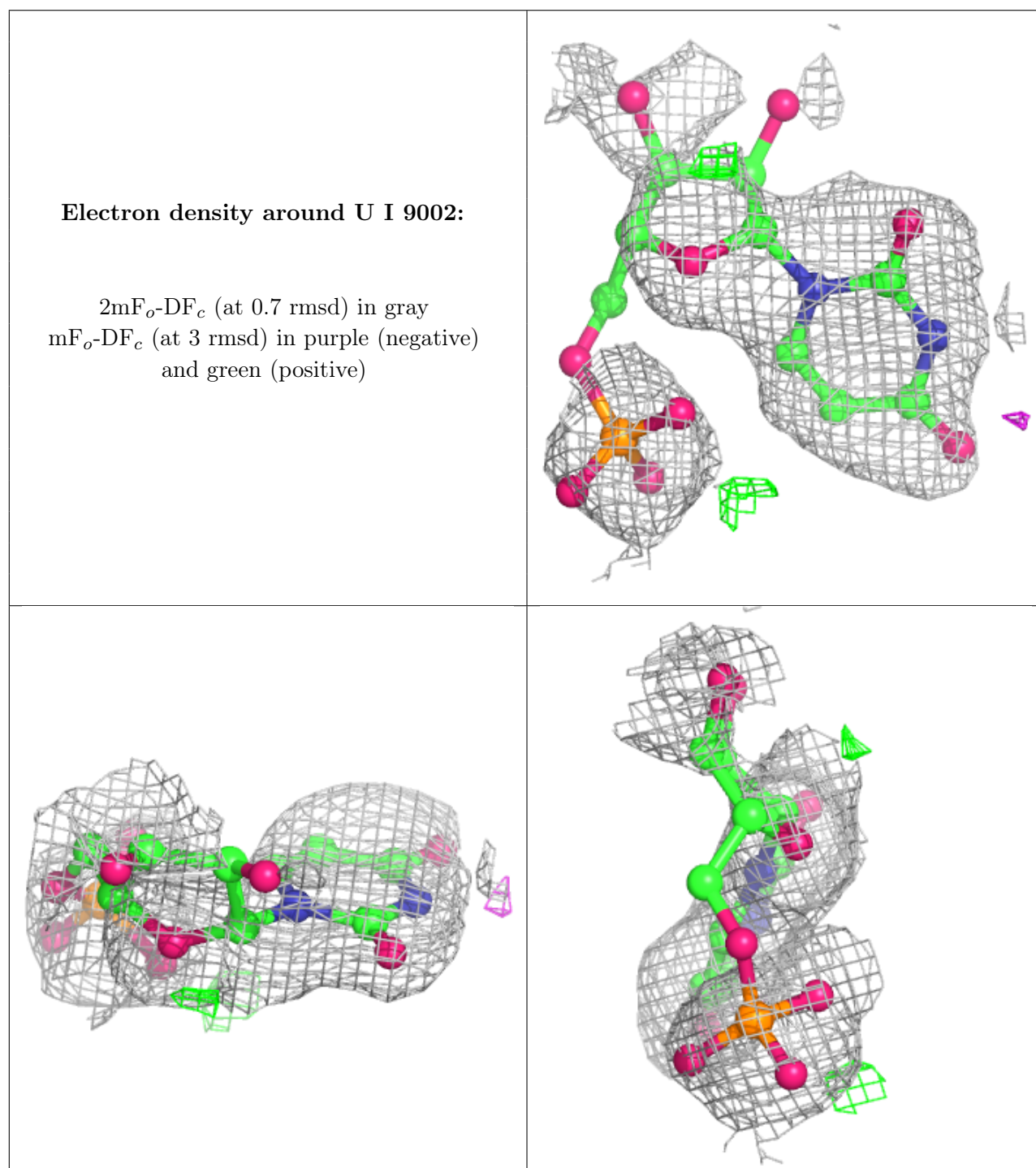
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	URI	B	9007	17/17	0.66	0.57	82,87,93,95	9
4	URI	J	9001	17/17	0.76	0.27	61,69,77,79	10
4	URI	F	9009	17/17	0.78	0.50	64,71,79,81	9
3	MPD	K	7002	8/8	0.81	0.20	51,55,58,59	0
2	U	I	9002	21/21	0.82	0.20	90,98,103,104	9
3	MPD	B	7011	8/8	0.83	0.31	79,81,83,85	0
4	URI	G	9012	17/17	0.84	0.36	65,71,81,81	8
3	MPD	L	7003	8/8	0.86	0.22	59,60,61,61	0
3	MPD	H	7008	8/8	0.86	0.20	60,62,62,66	0
4	URI	C	9011	17/17	0.86	0.26	50,60,72,73	8
2	U	H	9003	21/21	0.87	0.20	92,98,106,107	12
2	U	A	9010	21/21	0.87	0.25	77,87,94,95	12
4	URI	E	9006	17/17	0.87	0.23	57,62,71,72	6
3	MPD	D	7004	8/8	0.89	0.14	53,55,58,60	0
3	MPD	E	7012	8/8	0.89	0.17	47,50,52,54	0
3	MPD	F	7013	8/8	0.89	0.23	63,64,65,67	0
3	MPD	A	7005	8/8	0.89	0.21	61,64,65,65	0
4	URI	L	9005	17/17	0.89	0.27	54,60,71,71	8
2	U	K	9014	21/21	0.90	0.13	75,84,89,89	8
3	MPD	I	7014	8/8	0.91	0.19	52,55,56,57	0
3	MPD	N	7009	8/8	0.91	0.15	46,48,53,53	0
3	MPD	G	7007	8/8	0.91	0.10	32,38,42,43	0
2	U	D	9008	21/21	0.92	0.16	49,64,76,76	12
3	MPD	M	7010	8/8	0.92	0.21	46,50,52,55	0
2	U	N	9013	21/21	0.93	0.12	45,58,70,70	10
3	MPD	C	7006	8/8	0.94	0.10	29,31,33,35	0
4	URI	M	9004	17/17	0.94	0.21	47,54,65,65	9

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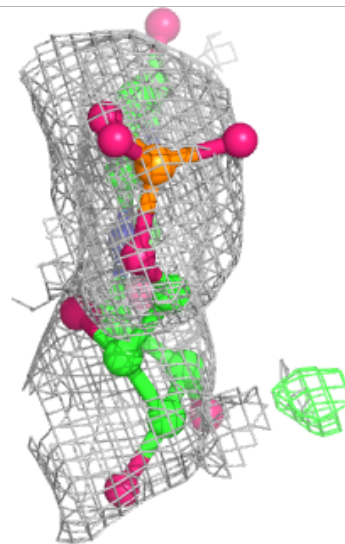
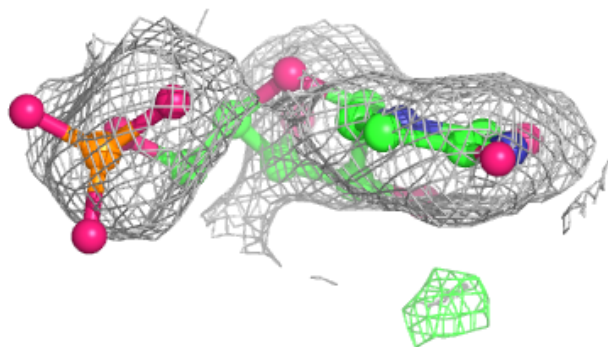
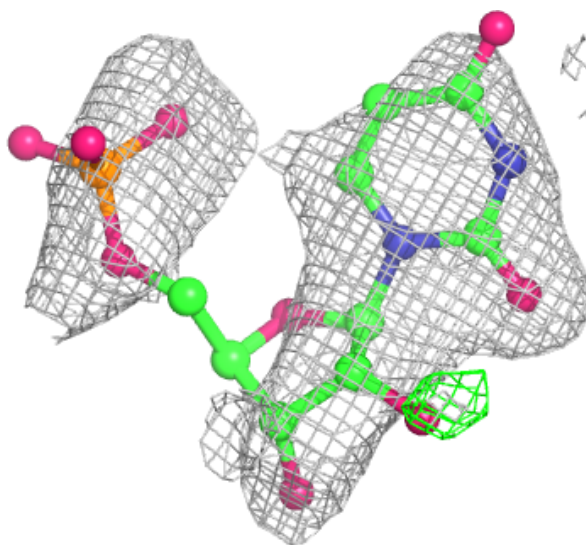
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MPD	J	7001	8/8	0.96	0.11	32,33,35,38	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



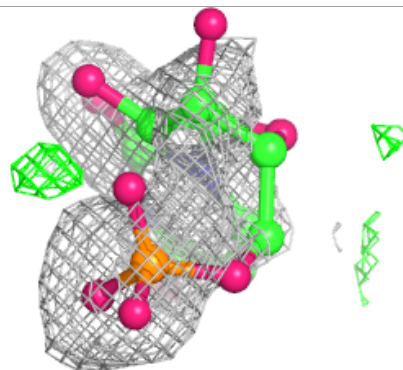
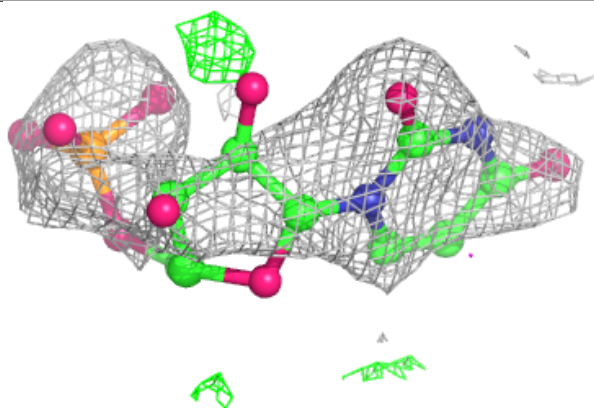
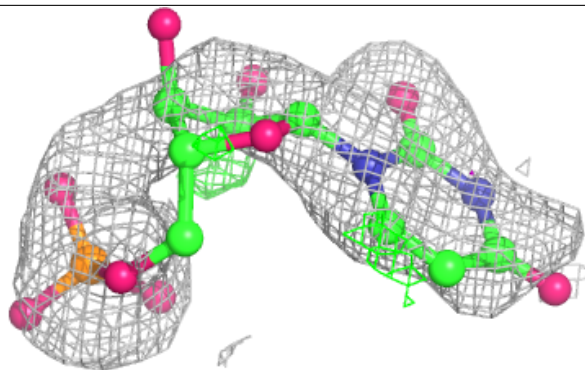
**Electron density around U H 9003:**

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



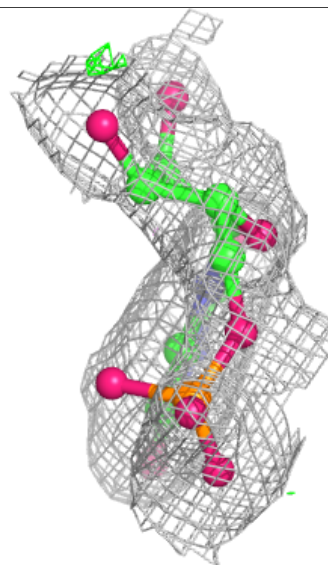
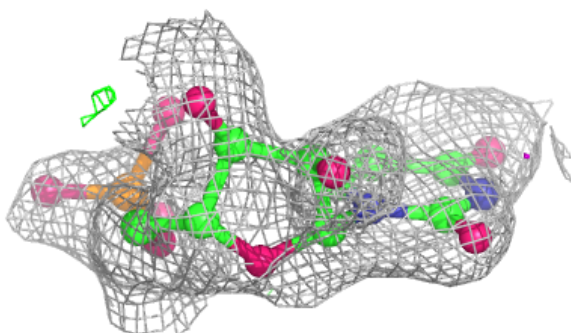
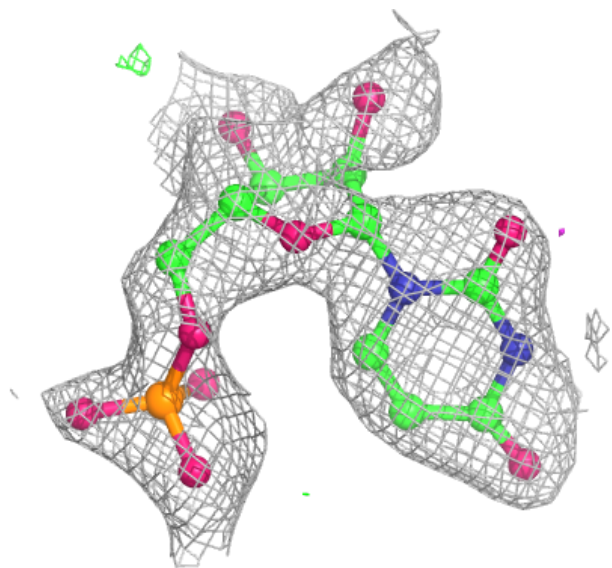
**Electron density around U A 9010:**

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



**Electron density around U K 9014:**

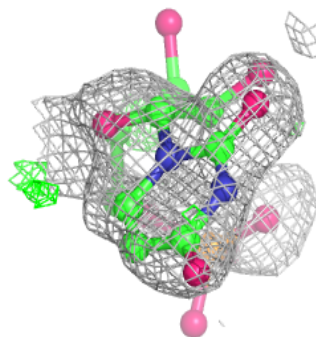
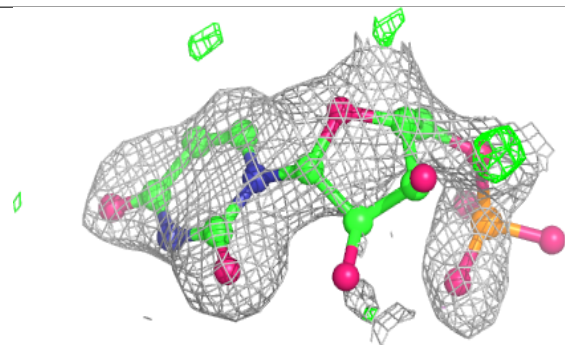
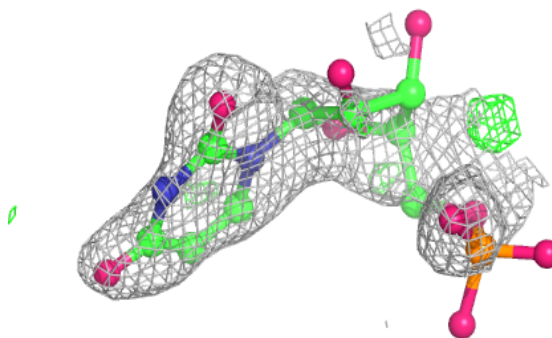
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

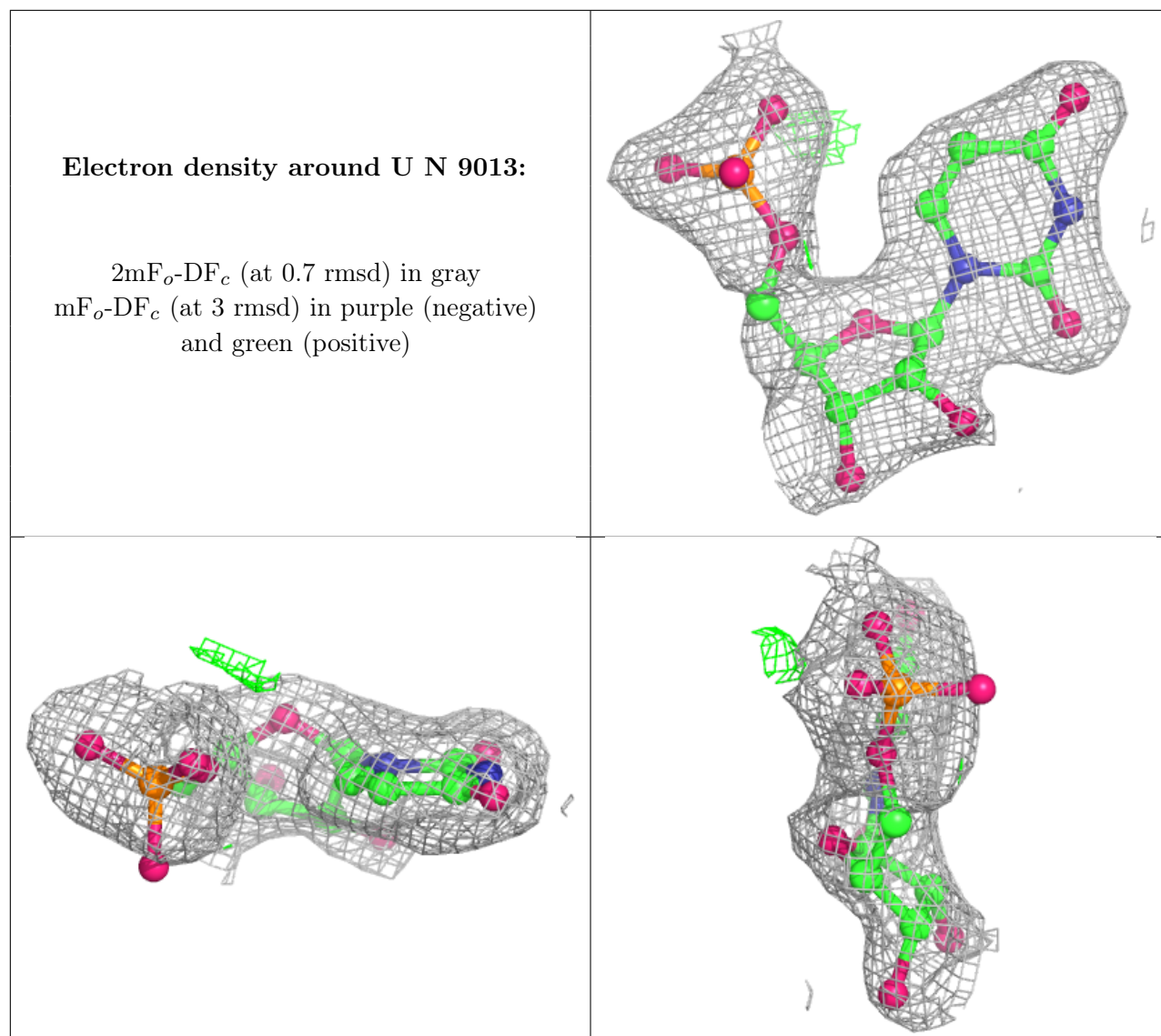




**Electron density around U D 9008:**

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





## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.