



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 28, 2025 – 06:09 PM EDT

PDB ID : 9DBJ / pdb\_00009dbj  
Title : Structure of Hailong HalB R164A mutant with non-hydrolyzable dATP  
Authors : Tan, J.M.J.; Melamed, S.; Cofsky, J.C.; Hobbs, S.J.; Kruse, A.C.; Sorek, R.;  
Kranzusch, P.J.  
Deposited on : 2024-08-23  
Resolution : 2.41 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 : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

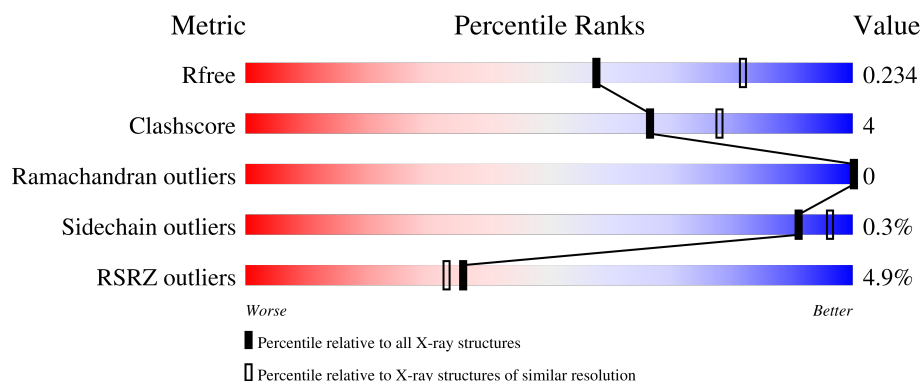
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.41 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))
$R_{free}$	164625	5670 (2.44-2.40)
Clashscore	180529	6299 (2.44-2.40)
Ramachandran outliers	177936	6232 (2.44-2.40)
Sidechain outliers	177891	6233 (2.44-2.40)
RSRZ outliers	164620	5670 (2.44-2.40)

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	229	<div> <div>2%</div> <div>86%</div> <div>8%</div> <div>5%</div> </div>
1	B	229	<div> <div>9%</div> <div>78%</div> <div>14%</div> <div>8%</div> </div>
1	C	229	<div> <div>3%</div> <div>89%</div> <div>6%</div> <div>5%</div> </div>
1	D	229	<div> <div>4%</div> <div>90%</div> <div>5%</div> <div>5%</div> </div>
1	E	229	<div> <div>4%</div> <div>90%</div> <div>7%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	229	<div><div></div><div>4%</div><div>87%</div><div>7%</div><div>6%</div></div>

## 2 Entry composition [i](#)

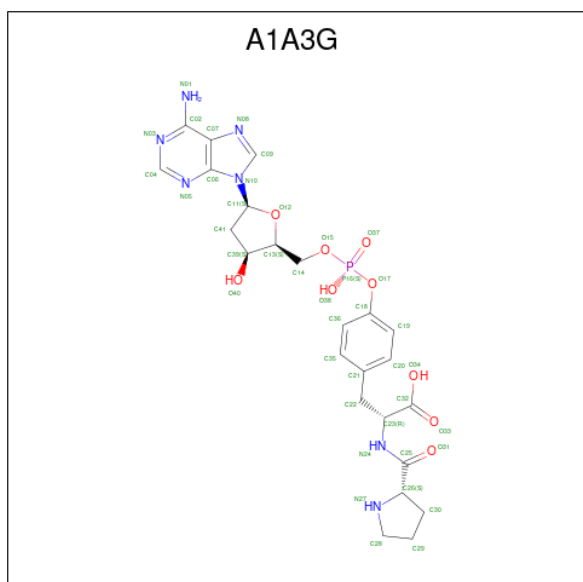
There are 7 unique types of molecules in this entry. The entry contains 11025 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HalB.

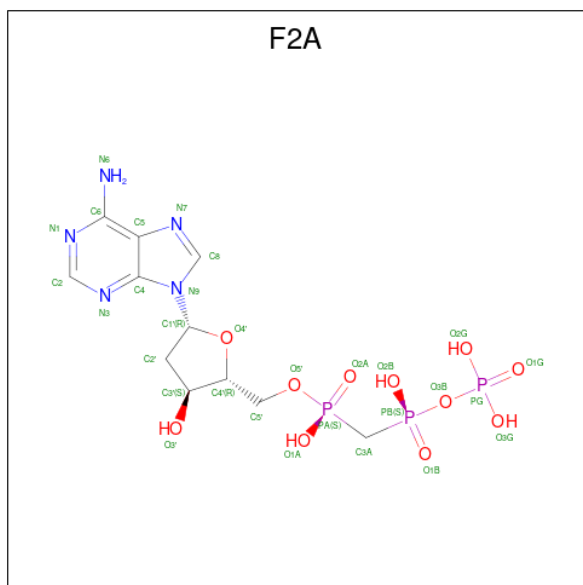
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1739	1097	312	327	3			
1	B	210	Total	C	N	O	S	0	0	0
			1680	1066	299	312	3			
1	C	217	Total	C	N	O	S	0	0	0
			1731	1093	311	324	3			
1	D	217	Total	C	N	O	S	0	0	0
			1730	1091	310	326	3			
1	E	220	Total	C	N	O	S	0	0	0
			1761	1112	315	331	3			
1	F	216	Total	C	N	O	S	0	0	0
			1721	1085	308	325	3			

- Molecule 2 is (2R)-3-(4-{[(S)-{(2R,3R,5R)-5-(6-amino-9H-purin-9-yl)-3-hydroxyoxolan-2-yl]methoxy}(hydroxy)phosphoryl]oxy}phenyl)-2-{[(2R)-pyrrolidine-2-carbonyl]amino}propanoic acid (non-preferred name) (CCD ID: A1A3G) (formula: C<sub>24</sub>H<sub>30</sub>N<sub>7</sub>O<sub>9</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			41	24	7	9	1		

- Molecule 3 is 2'-deoxy-5'-O-[(S)-hydroxy{[(S)-hydroxy(phosphonooxy)phosphoryl]methyl}phosphoryl]adenosine (CCD ID: F2A) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>11</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 30	C 11	N 5	O 11	P 3	0	0
3	B	1	Total 30	C 11	N 5	O 11	P 3	0	0
3	C	1	Total 30	C 11	N 5	O 11	P 3	0	0
3	D	1	Total 30	C 11	N 5	O 11	P 3	0	0
3	E	1	Total 30	C 11	N 5	O 11	P 3	0	0
3	F	1	Total 30	C 11	N 5	O 11	P 3	0	0

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

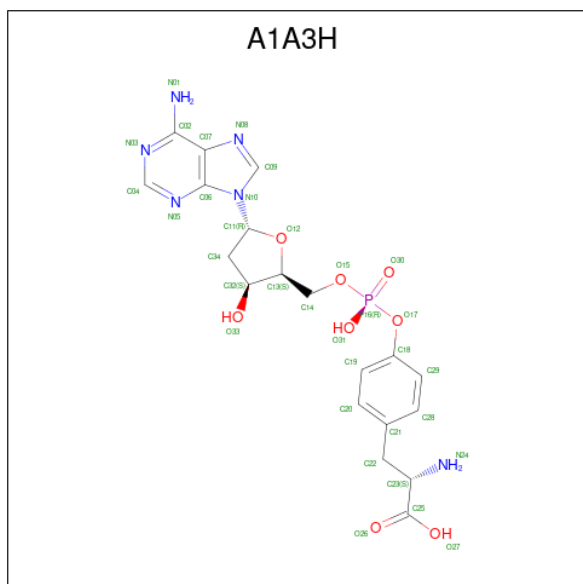
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Mn 2 2	0	0

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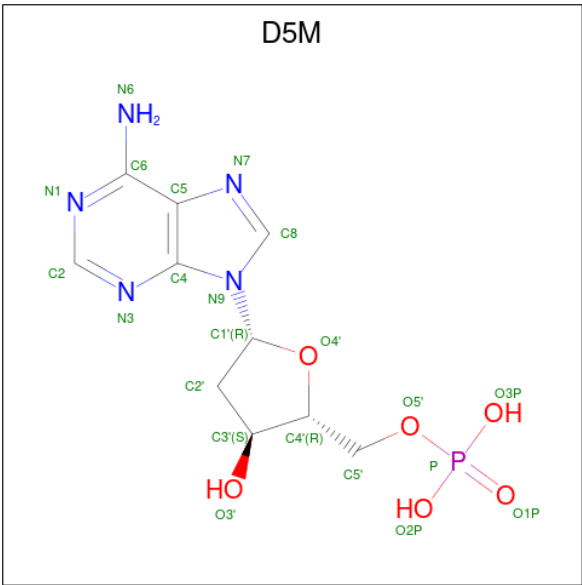
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Mn	0	0
			2	2		
4	C	2	Total	Mn	0	0
			2	2		
4	D	2	Total	Mn	0	0
			2	2		
4	E	2	Total	Mn	0	0
			2	2		
4	F	2	Total	Mn	0	0
			2	2		

- Molecule 5 is (2R)-2-amino-3-(4-[[[(R)-{[(2R,3R,5R)-5-(6-amino-9H-purin-9-yl)-3-hydroxyoxolan-2-yl]methoxy}(hydroxy)phosphoryl]oxy}phenyl]propanoic acid (non-preferred name) (CCD ID: A1A3H) (formula: C<sub>19</sub>H<sub>23</sub>N<sub>6</sub>O<sub>8</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total	C	N	O	P	0	0
			34	19	6	8	1		

- Molecule 6 is 2'-DEOXYADENOSINE-5'-MONOPHOSPHATE (CCD ID: D5M) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>6</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	D	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

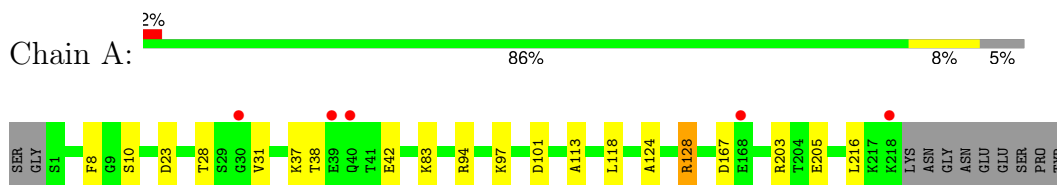
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	79	Total	O	0	0
			79	79		
7	B	51	Total	O	0	0
			51	51		
7	C	33	Total	O	0	0
			33	33		
7	D	46	Total	O	0	0
			46	46		
7	E	110	Total	O	0	0
			110	110		
7	F	55	Total	O	0	0
			55	55		

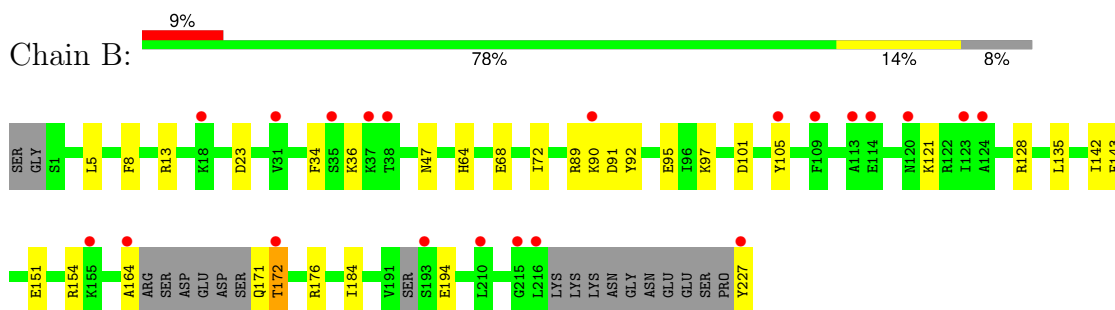
### 3 Residue-property plots [i](#)

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.

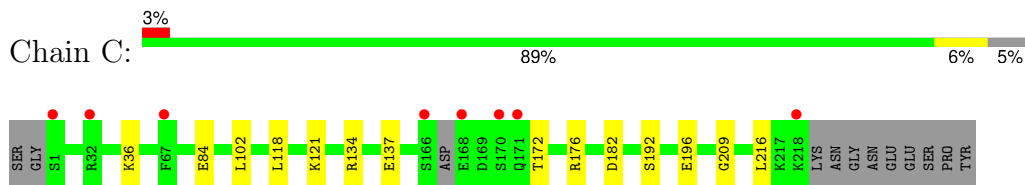
- Molecule 1: HalB



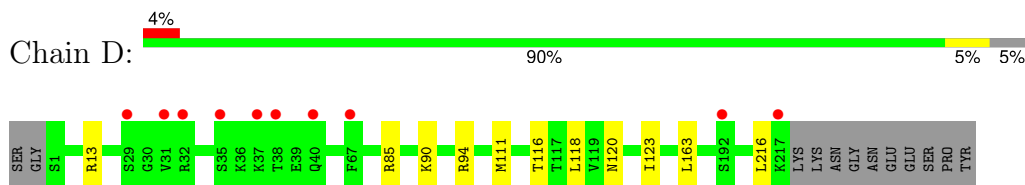
- Molecule 1: HalB



- Molecule 1: HalB



- Molecule 1: HalB



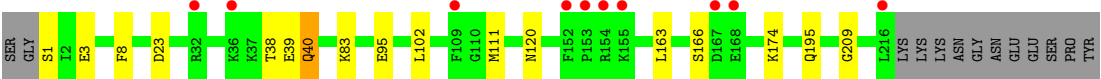
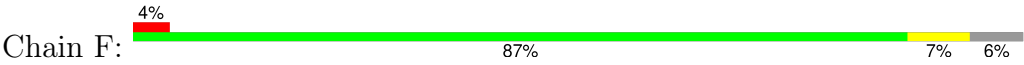
- Molecule 1: HalB







● Molecule 1: HalB



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.05Å 169.05Å 139.38Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.06 – 2.41 46.06 – 2.41	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.06-2.41) 99.9 (46.06-2.41)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.207 , 0.239 0.205 , 0.234	Depositor DCC
$R_{free}$ test set	86772 reflections (2.25%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.3	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 43.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11025	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A1A3G, F2A, D5M, MN, A1A3H

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	0.09	0/1769	0.25	0/2380
1	B	0.09	0/1708	0.24	0/2295
1	C	0.11	0/1760	0.25	0/2366
1	D	0.08	0/1760	0.23	0/2369
1	E	0.10	0/1791	0.27	0/2406
1	F	0.09	0/1751	0.25	0/2358
All	All	0.09	0/10539	0.25	0/14174

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	1739	0	1752	16	0
1	B	1680	0	1690	20	0
1	C	1731	0	1747	11	0
1	D	1730	0	1739	8	0
1	E	1761	0	1773	11	0
1	F	1721	0	1726	12	0
2	A	41	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	30	0	14	0	0
3	B	30	0	14	4	0
3	C	30	0	14	1	0
3	D	30	0	14	1	0
3	E	30	0	14	1	0
3	F	30	0	14	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
5	C	34	0	0	0	0
6	D	22	0	12	0	0
7	A	79	0	0	6	1
7	B	51	0	0	2	0
7	C	33	0	0	5	0
7	D	46	0	0	4	0
7	E	110	0	0	4	1
7	F	55	0	0	3	0
All	All	11025	0	10523	77	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 77 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:D:111:MET:HE1	1:D:123:ILE:HD11	1.63	0.80
1:E:59:ASP:OD1	7:E:401:HOH:O	2.01	0.79
1:D:85:ARG:NH1	7:D:401:HOH:O	2.15	0.78
1:F:3:GLU:OE2	7:F:401:HOH:O	2.07	0.71
1:A:113:ALA:O	7:A:401:HOH:O	2.09	0.70

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:446:HOH:O	7:E:497:HOH:O[2_445]	2.05	0.15

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	216/229 (94%)	212 (98%)	4 (2%)	0	100	100
1	B	203/229 (89%)	199 (98%)	4 (2%)	0	100	100
1	C	213/229 (93%)	202 (95%)	11 (5%)	0	100	100
1	D	215/229 (94%)	208 (97%)	7 (3%)	0	100	100
1	E	217/229 (95%)	210 (97%)	7 (3%)	0	100	100
1	F	214/229 (93%)	207 (97%)	7 (3%)	0	100	100
All	All	1278/1374 (93%)	1238 (97%)	40 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	188/197 (95%)	187 (100%)	1 (0%)	86	94
1	B	180/197 (91%)	179 (99%)	1 (1%)	84	92
1	C	187/197 (95%)	187 (100%)	0	100	100
1	D	187/197 (95%)	187 (100%)	0	100	100
1	E	190/197 (96%)	190 (100%)	0	100	100
1	F	186/197 (94%)	185 (100%)	1 (0%)	86	94
All	All	1118/1182 (95%)	1115 (100%)	3 (0%)	91	96

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	ARG
1	B	172	THR
1	F	40	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	100	ASN
1	D	156	HIS
1	F	40	GLN
1	F	156	HIS

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 12 are monoatomic - leaving 9 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	F2A	B	301	4	25,32,32	3.46	9 (36%)	31,50,50	1.63	4 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	F2A	E	301	4	25,32,32	3.47	9 (36%)	31,50,50	1.41	2 (6%)
3	F2A	F	301	4	25,32,32	3.48	9 (36%)	31,50,50	1.43	3 (9%)
2	A1A3G	A	301	4	42,45,45	2.91	12 (28%)	54,65,65	1.60	9 (16%)
3	F2A	D	302	4	25,32,32	3.48	9 (36%)	31,50,50	1.40	2 (6%)
3	F2A	C	302	4	25,32,32	3.49	9 (36%)	31,50,50	1.39	2 (6%)
3	F2A	A	302	4	25,32,32	3.46	9 (36%)	31,50,50	1.40	2 (6%)
6	D5M	D	301	4	21,24,24	3.63	11 (52%)	24,36,36	1.83	5 (20%)
5	A1A3H	C	301	-	33,37,37	2.43	7 (21%)	39,54,54	2.16	6 (15%)

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	F2A	B	301	4	-	6/15/34/34	0/3/3/3
3	F2A	E	301	4	-	6/15/34/34	0/3/3/3
3	F2A	F	301	4	-	4/15/34/34	0/3/3/3
2	A1A3G	A	301	4	-	6/27/50/50	0/5/5/5
3	F2A	D	302	4	-	5/15/34/34	0/3/3/3
3	F2A	C	302	4	-	4/15/34/34	0/3/3/3
3	F2A	A	302	4	-	5/15/34/34	0/3/3/3
6	D5M	D	301	4	-	2/6/22/22	0/3/3/3
5	A1A3H	C	301	-	-	3/19/35/35	0/4/4/4

The worst 5 of 84 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	302	F2A	C3'-C4'	-10.14	1.26	1.53
3	F	301	F2A	C3'-C4'	-10.14	1.26	1.53
3	E	301	F2A	C3'-C4'	-10.10	1.26	1.53
3	C	302	F2A	C3'-C4'	-10.10	1.26	1.53
3	A	302	F2A	C3'-C4'	-10.02	1.26	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	301	A1A3H	O12-C11-N10	-9.35	96.34	108.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	A1A3G	N05-C04-N03	-6.60	119.71	128.67
6	D	301	D5M	N3-C2-N1	-6.37	120.02	128.67
3	A	302	F2A	N3-C2-N1	-5.77	120.84	128.67
3	E	301	F2A	N3-C2-N1	-5.75	120.87	128.67

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	A1A3G	N24-C25-C26-N27
2	A	301	A1A3G	O31-C25-C26-N27
3	A	302	F2A	PA-C3A-PB-O1B
3	A	302	F2A	PA-C3A-PB-O2B
3	A	302	F2A	PA-C3A-PB-O3B

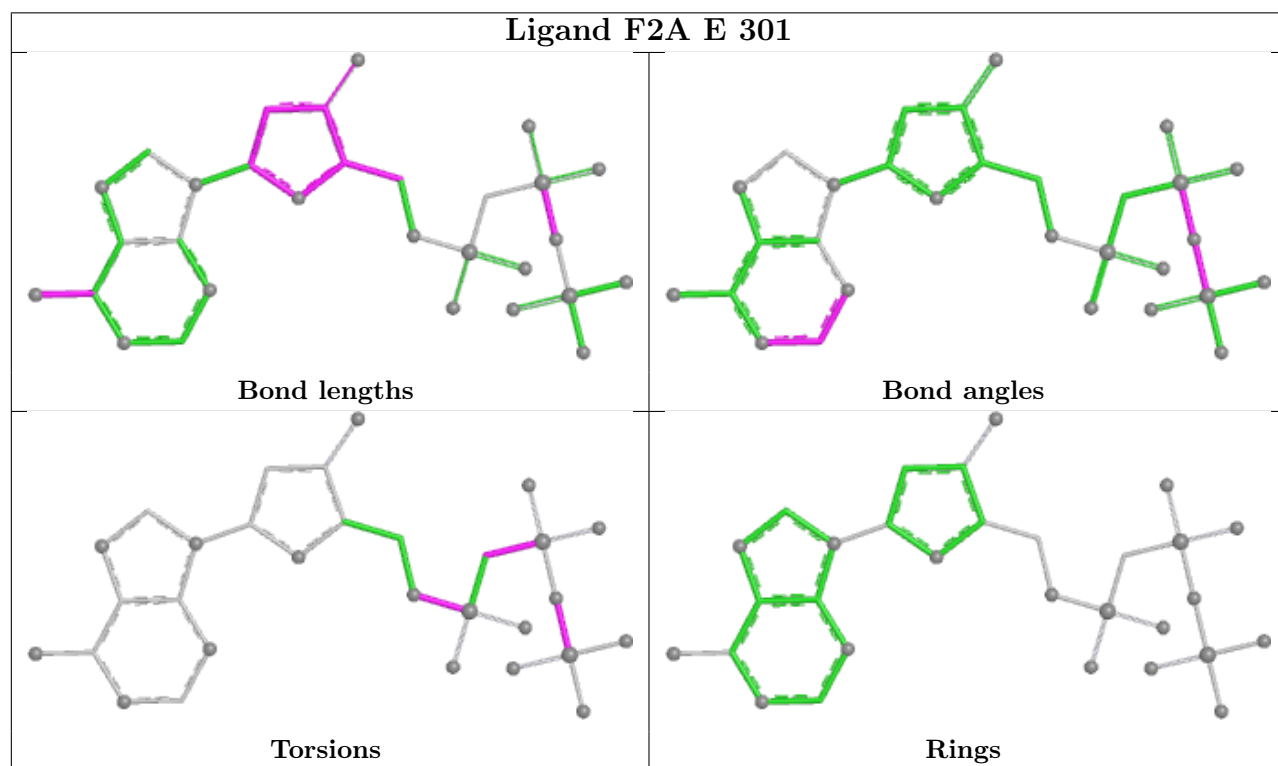
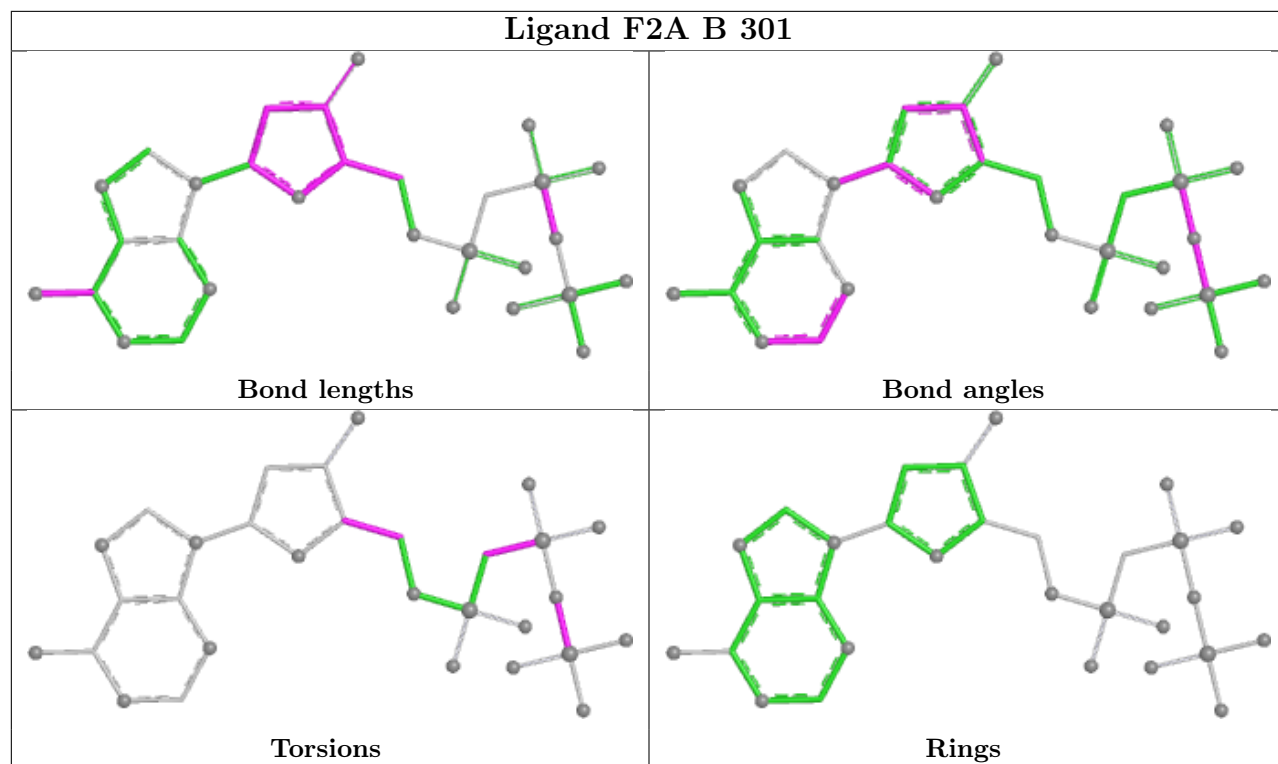
There are no ring outliers.

5 monomers are involved in 8 short contacts:

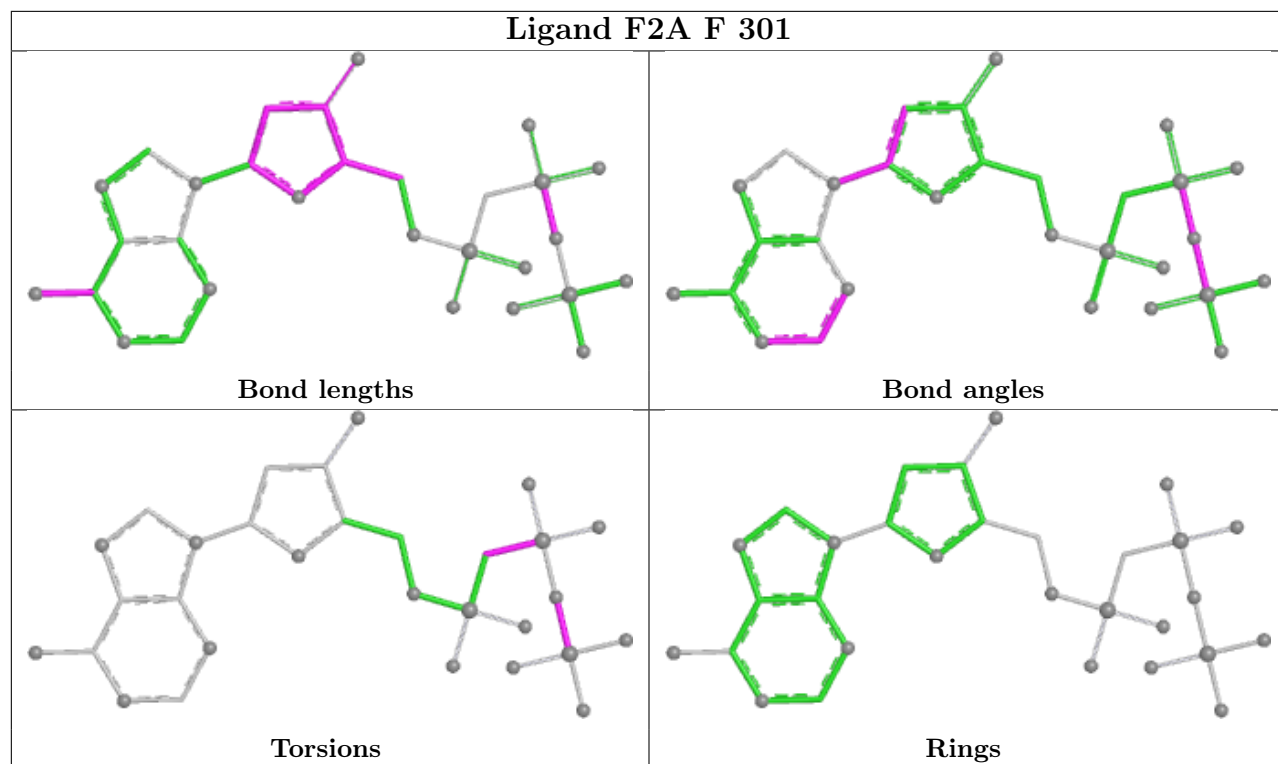
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	F2A	4	0
3	E	301	F2A	1	0
2	A	301	A1A3G	1	0
3	D	302	F2A	1	0
3	C	302	F2A	1	0

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

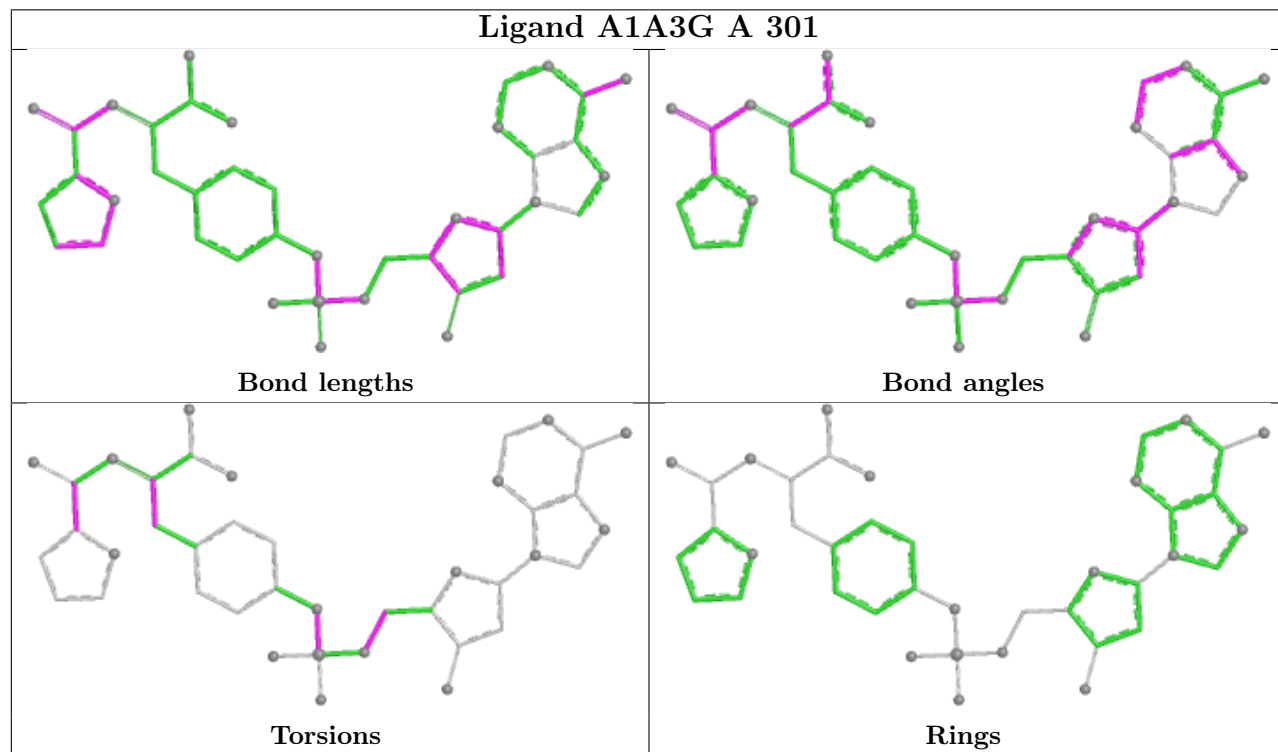




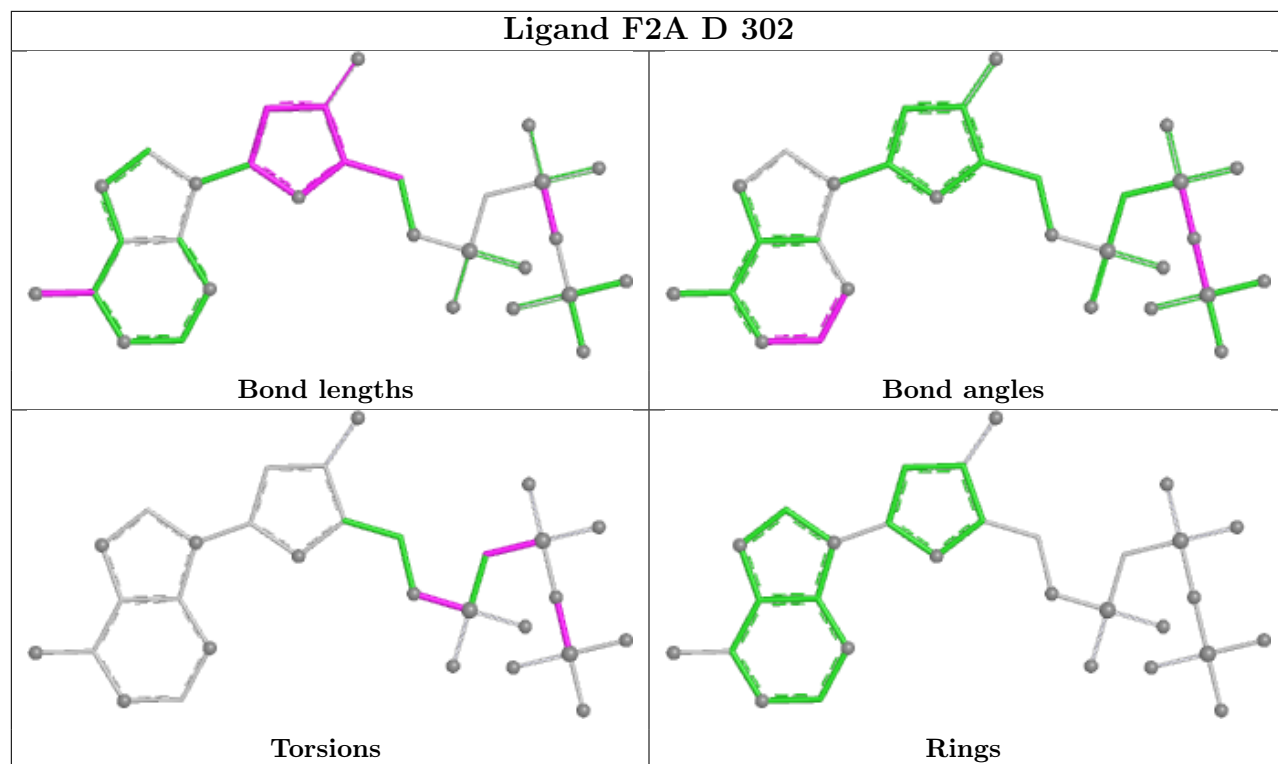
## Ligand F2A F 301



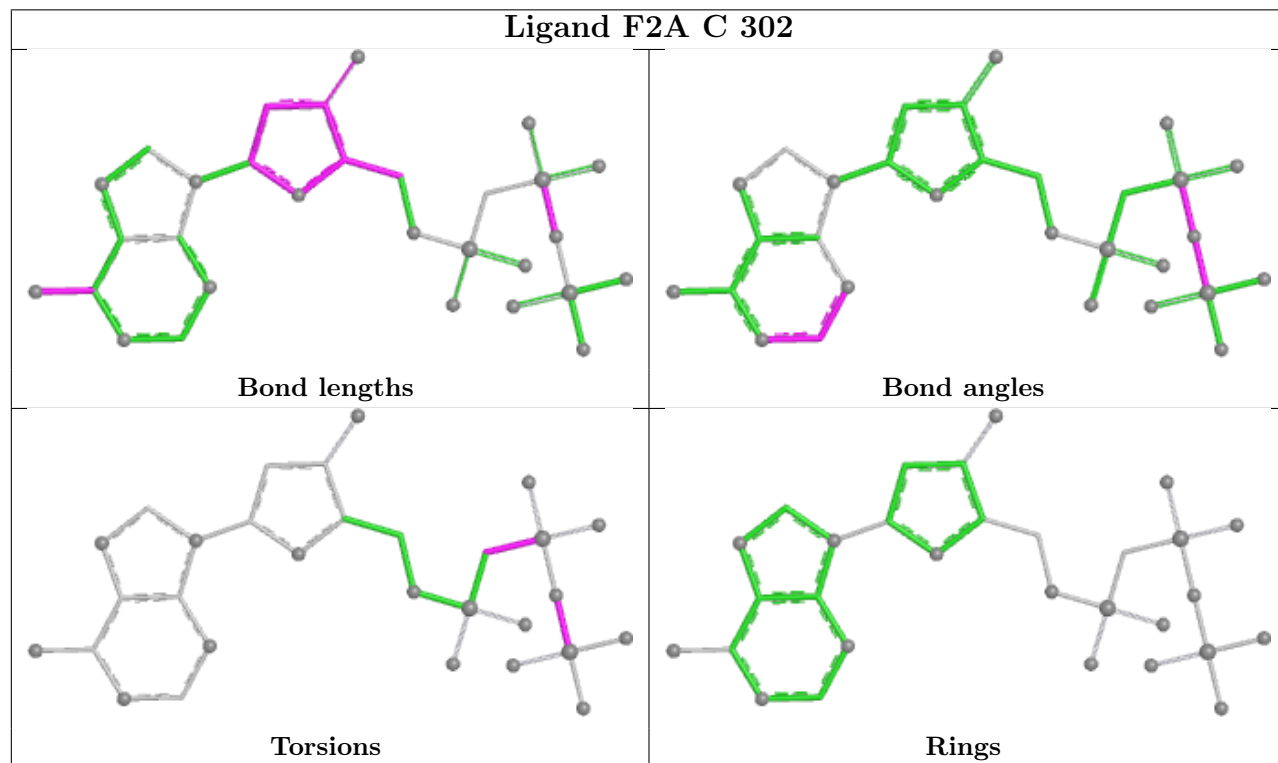
## Ligand A1A3G A 301



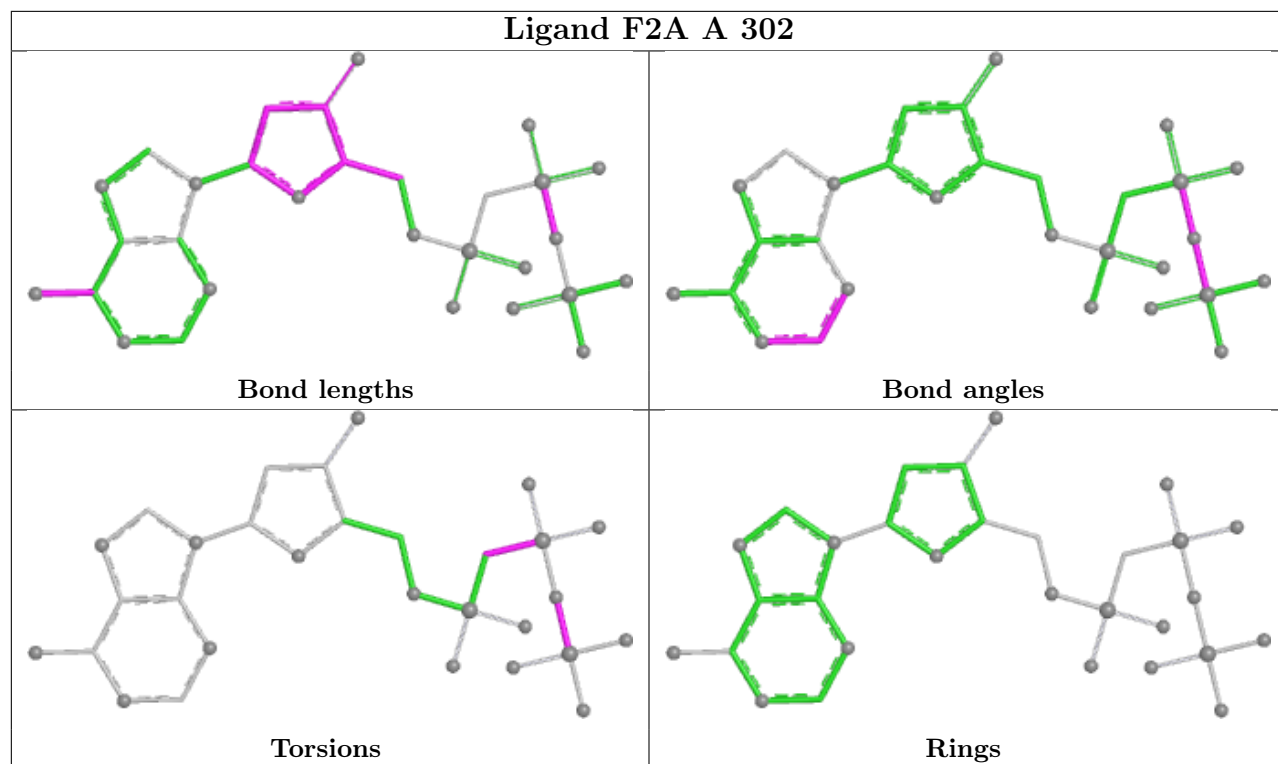
## Ligand F2A D 302



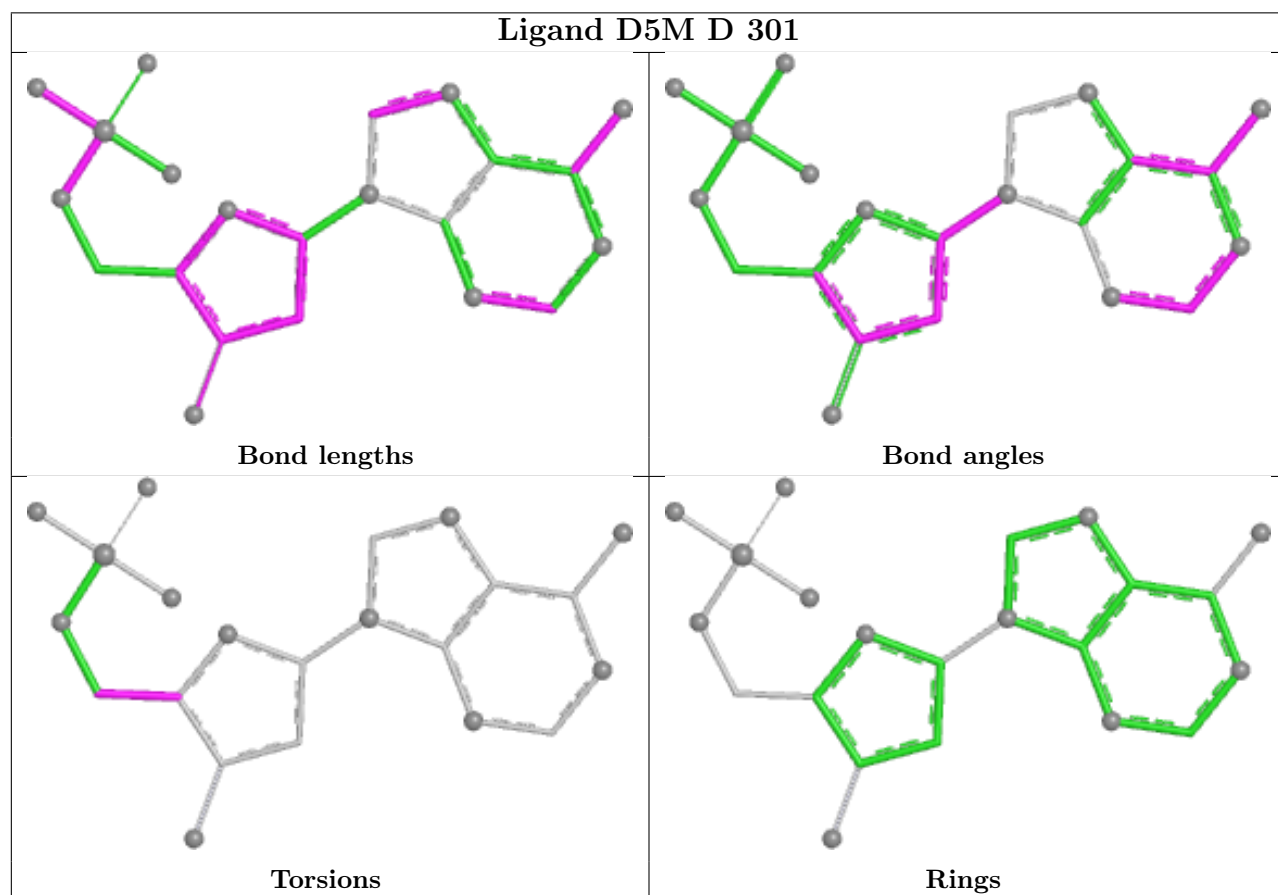
## Ligand F2A C 302

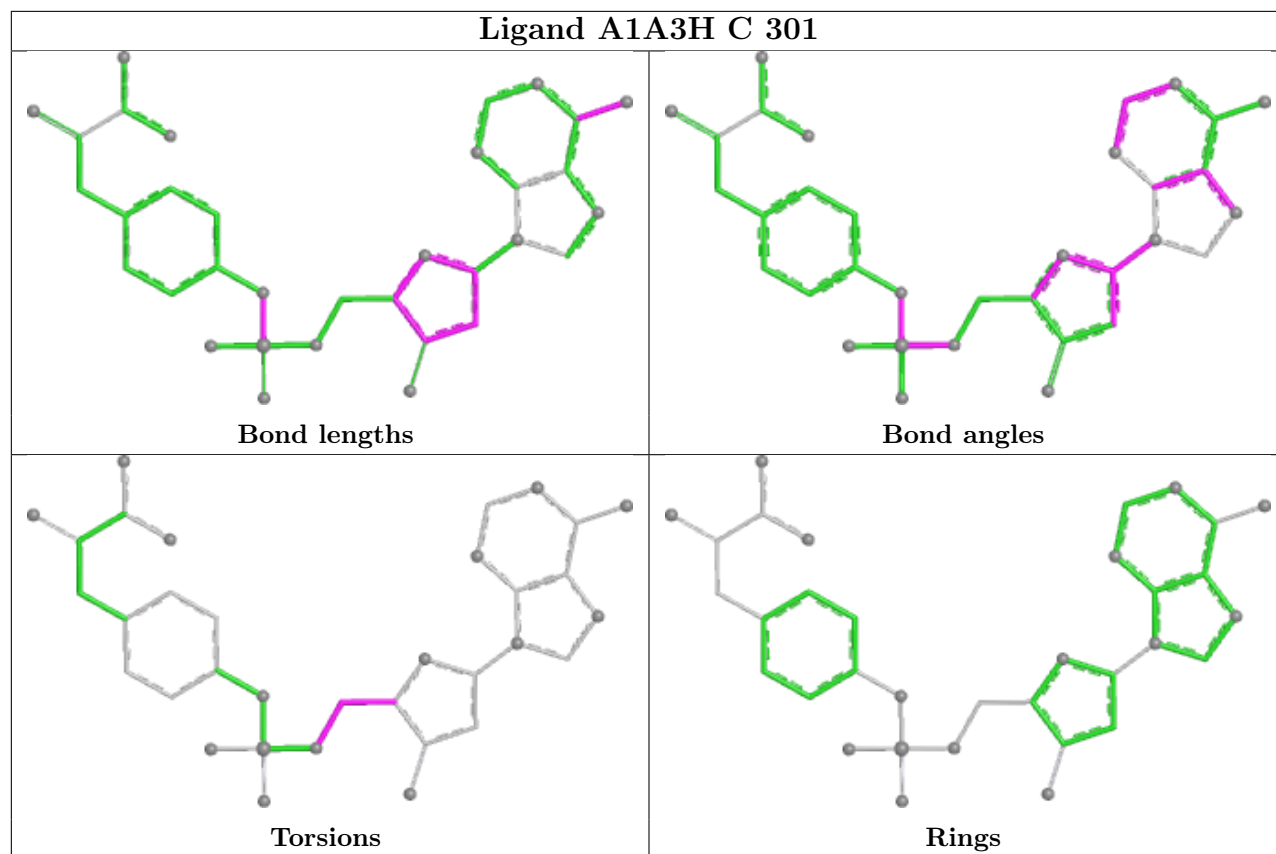


## Ligand F2A A 302



## Ligand D5M D 301





## 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	218/229 (95%)	-0.23	5 (2%) 61 58	32, 46, 81, 101	0
1	B	210/229 (91%)	0.57	21 (10%) 14 12	36, 65, 106, 134	0
1	C	217/229 (94%)	0.10	8 (3%) 45 43	35, 58, 90, 114	0
1	D	217/229 (94%)	0.13	10 (4%) 38 35	38, 57, 95, 112	0
1	E	220/229 (96%)	-0.22	9 (4%) 42 40	31, 42, 77, 100	0
1	F	216/229 (94%)	0.18	10 (4%) 38 35	32, 59, 103, 121	0
All	All	1298/1374 (94%)	0.09	63 (4%) 36 33	31, 52, 96, 134	0

The worst 5 of 63 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	216	LEU	6.7
1	E	227	TYR	5.9
1	E	219	LYS	4.1
1	B	227	TYR	4.0
1	C	166	SER	3.9

### 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

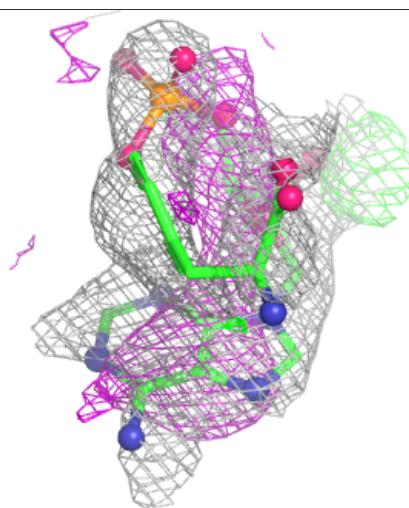
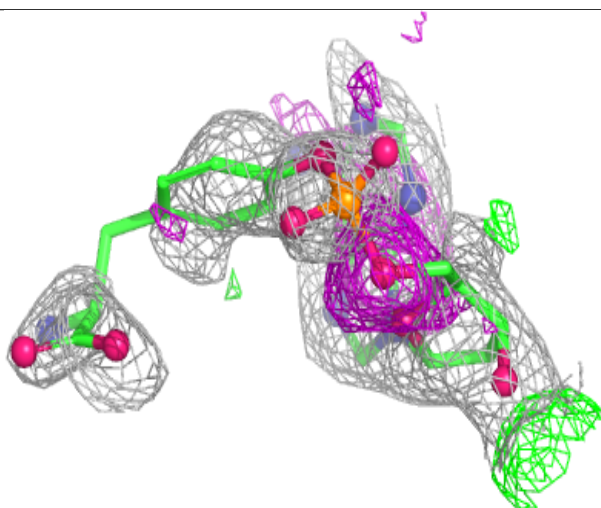
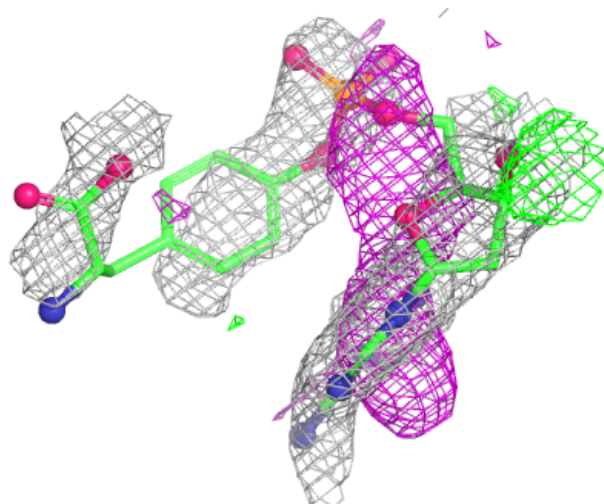
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	A1A3H	C	301	34/34	0.60	0.22	75,101,114,136	0
2	A1A3G	A	301	41/41	0.67	0.23	61,89,108,116	0
6	D5M	D	301	22/22	0.72	0.19	65,89,107,159	0
3	F2A	B	301	30/30	0.97	0.07	38,48,55,58	0
4	MN	E	302	1/1	0.97	0.05	40,40,40,40	0
3	F2A	E	301	30/30	0.98	0.06	34,39,44,46	0
3	F2A	F	301	30/30	0.98	0.05	32,39,47,50	0
4	MN	C	303	1/1	0.98	0.05	43,43,43,43	0
3	F2A	A	302	30/30	0.98	0.06	33,38,40,40	0
3	F2A	C	302	30/30	0.98	0.05	36,44,49,54	0
3	F2A	D	302	30/30	0.98	0.06	42,45,52,53	0
4	MN	F	302	1/1	0.99	0.04	41,41,41,41	0
4	MN	A	303	1/1	0.99	0.04	39,39,39,39	0
4	MN	B	302	1/1	0.99	0.03	43,43,43,43	0
4	MN	D	304	1/1	1.00	0.02	47,47,47,47	0
4	MN	B	303	1/1	1.00	0.03	43,43,43,43	0
4	MN	E	303	1/1	1.00	0.01	40,40,40,40	0
4	MN	A	304	1/1	1.00	0.03	39,39,39,39	0
4	MN	F	303	1/1	1.00	0.01	40,40,40,40	0
4	MN	C	304	1/1	1.00	0.01	44,44,44,44	0
4	MN	D	303	1/1	1.00	0.02	46,46,46,46	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 A1A3H C 301:**

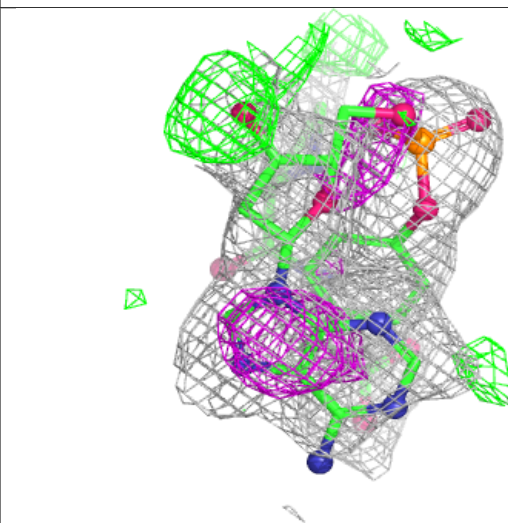
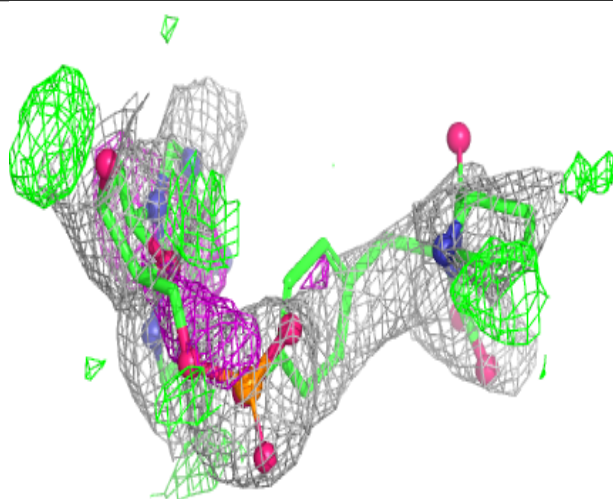
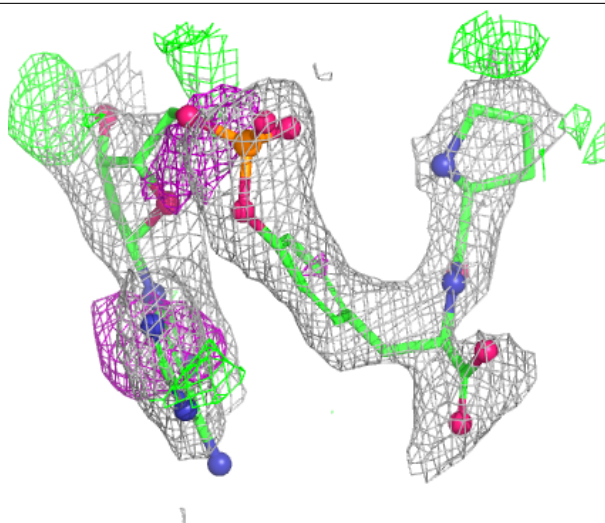
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





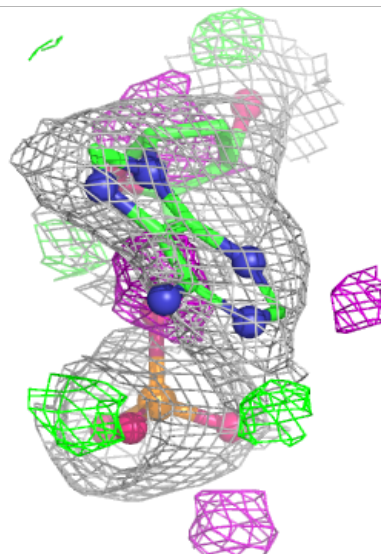
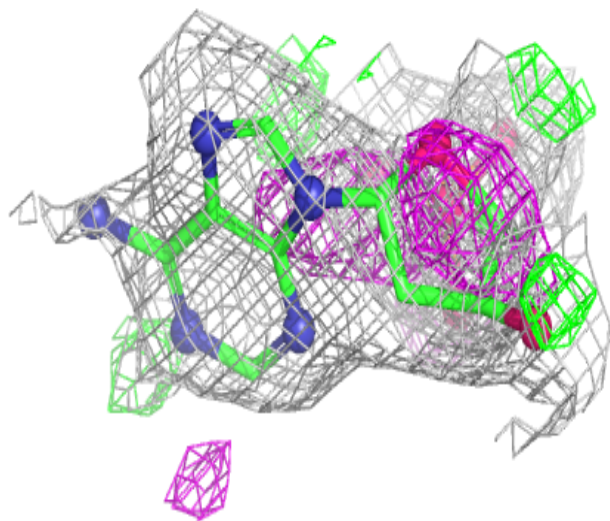
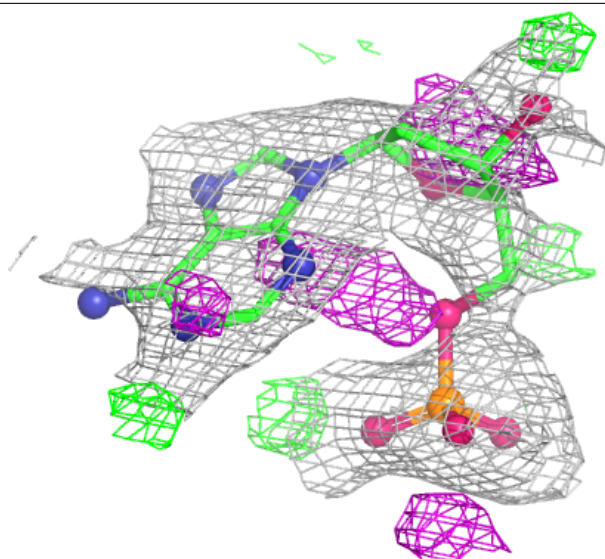
**Electron density around A1A3G A 301:**

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



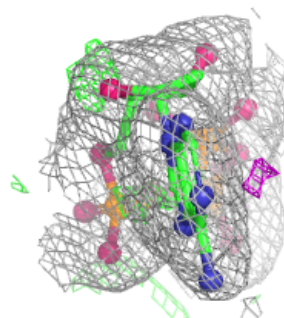
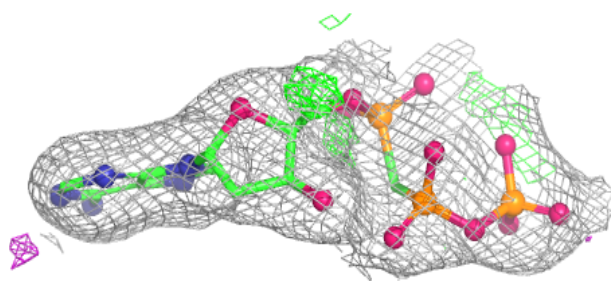
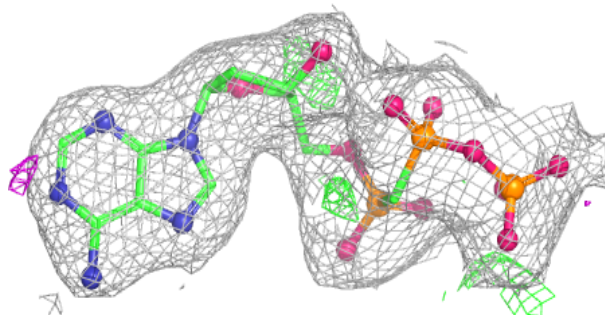
**Electron density around D5M D 301:**

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and green (positive)



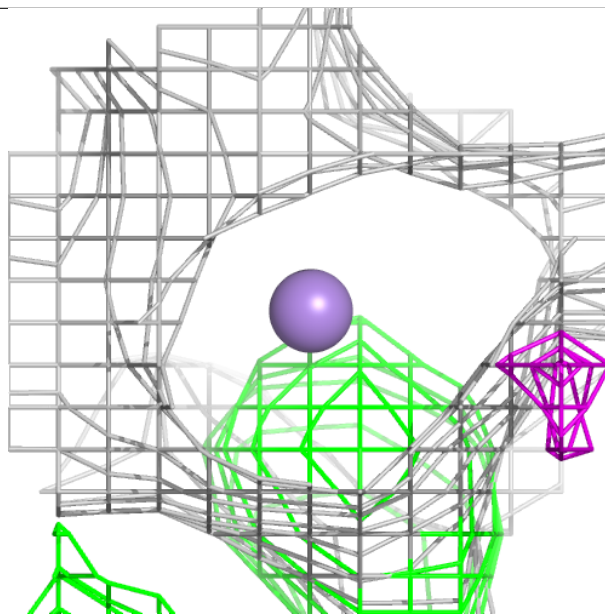
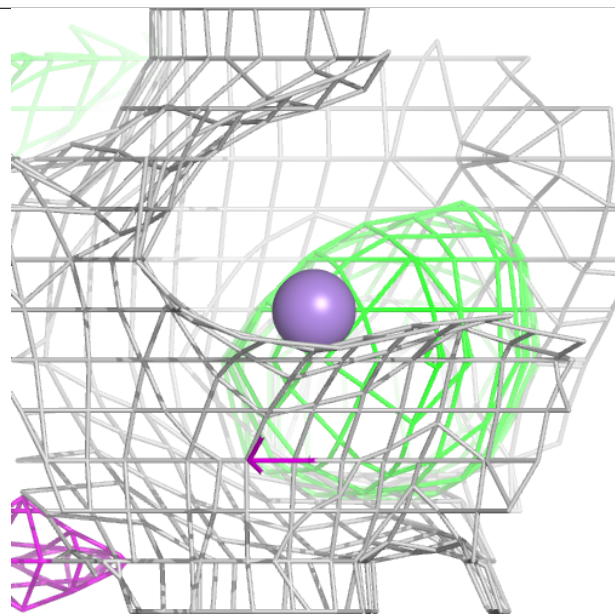
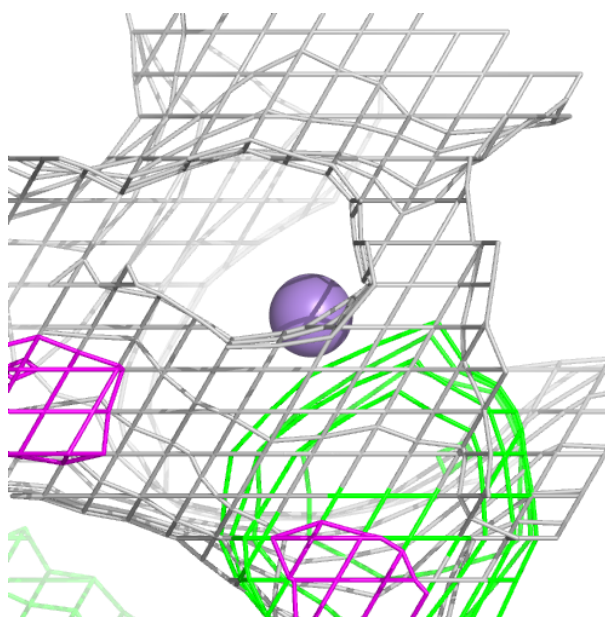
**Electron density around F2A B 301:**

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and green (positive)



**Electron density around MN E 302:**

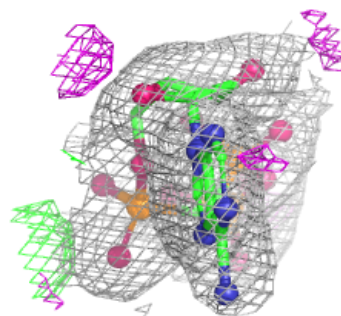
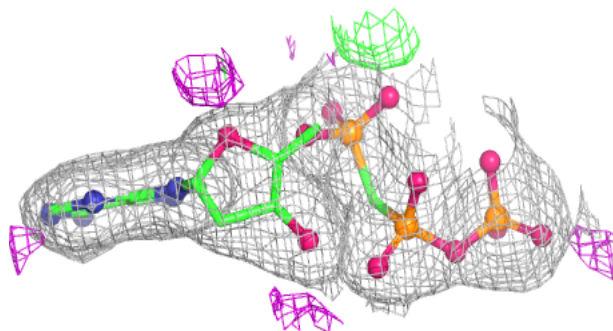
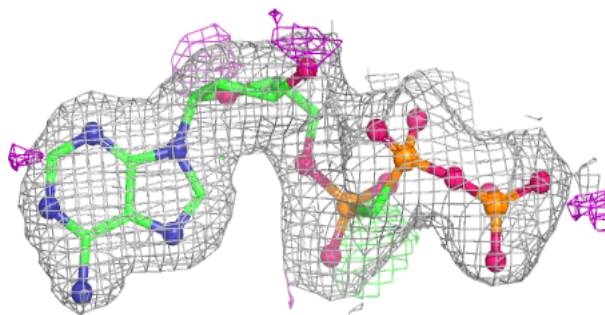
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
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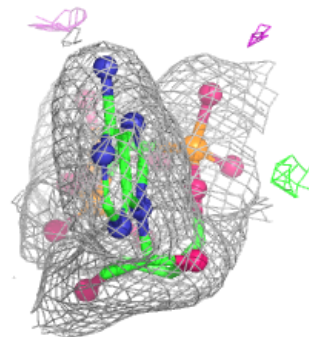
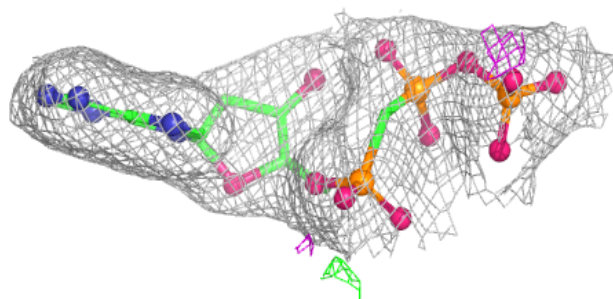
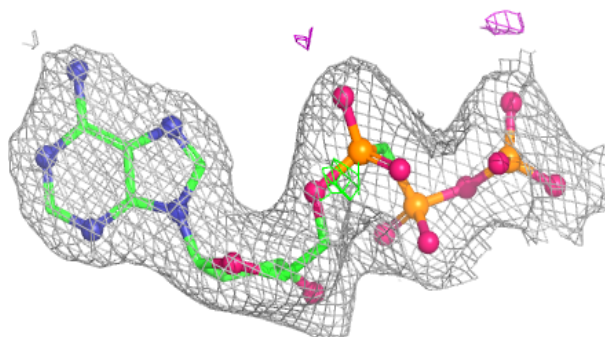


**Electron density around F2A E 301:**

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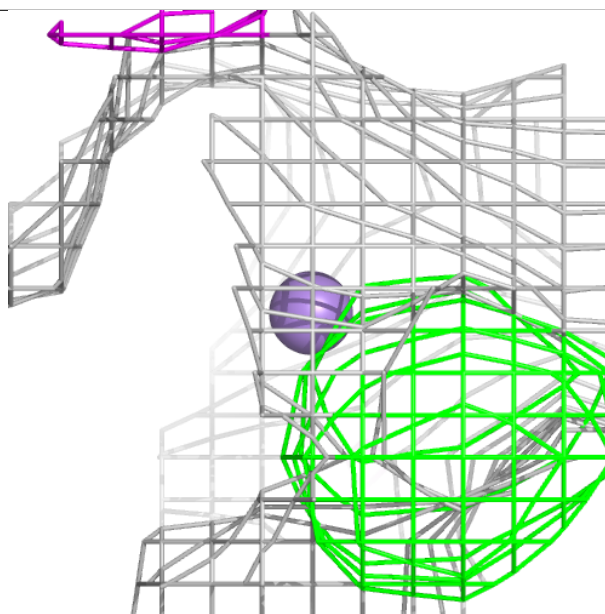
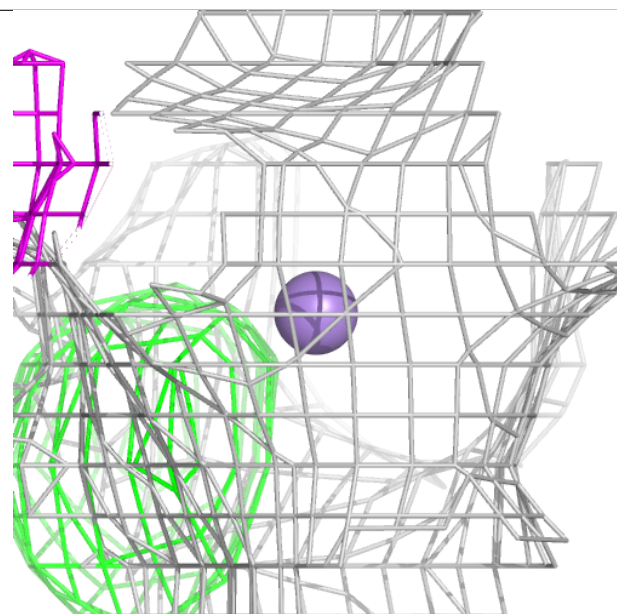
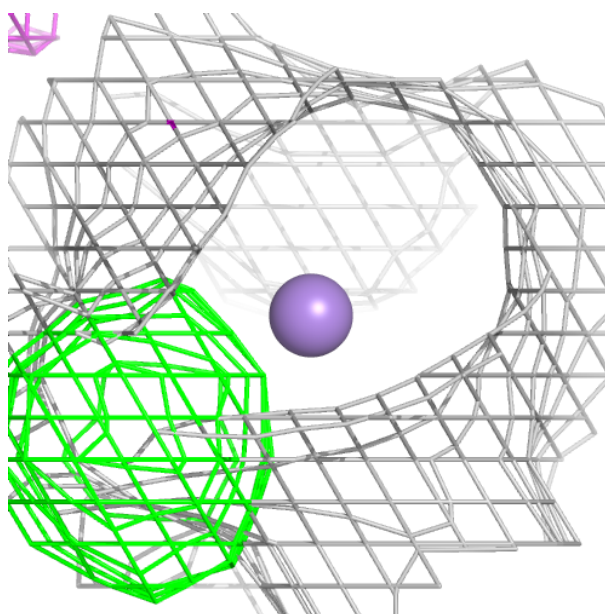
**Electron density around F2A F 301:**

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and green (positive)



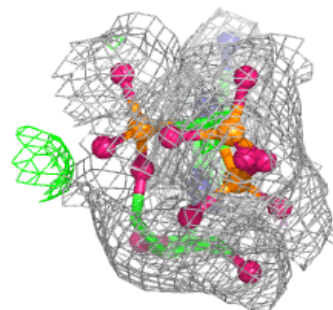
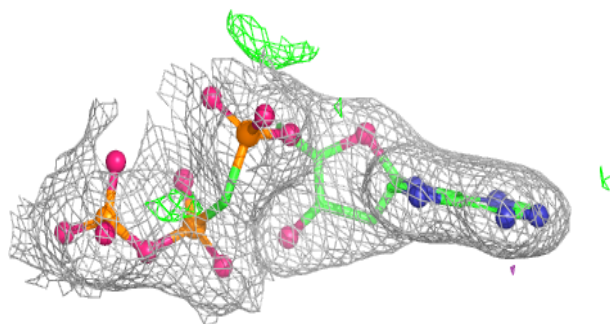
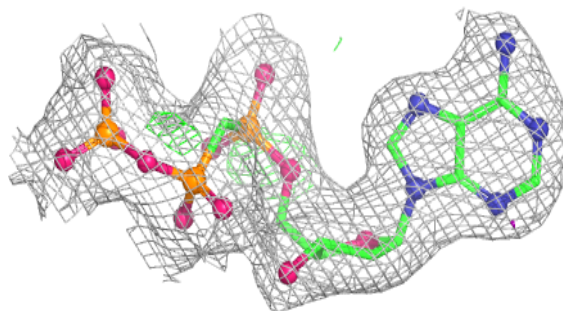
**Electron density around MN C 303:**

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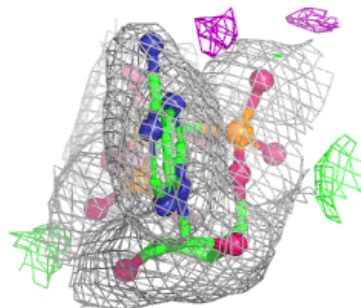
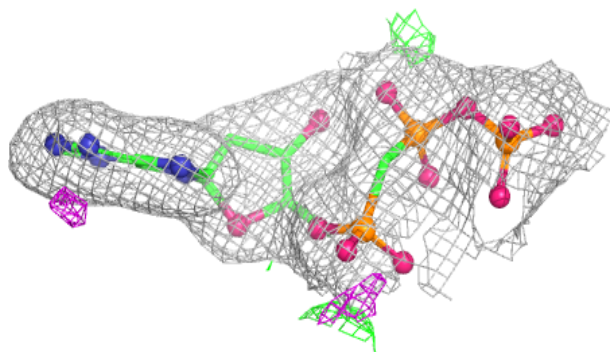
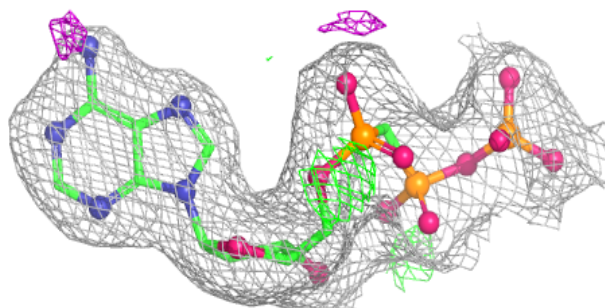


**Electron density around F2A A 302:**

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and green (positive)

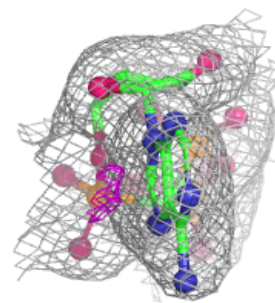
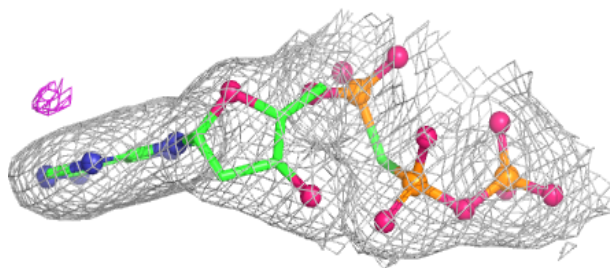
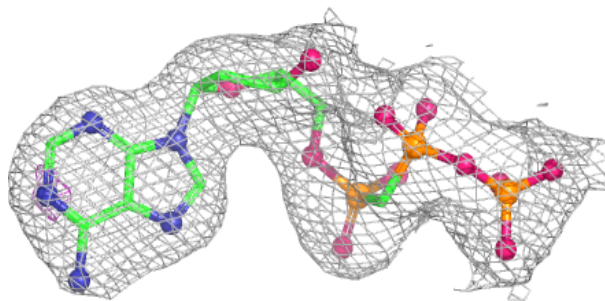
**Electron density around F2A C 302:**

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and green (positive)



**Electron density around F2A D 302:**

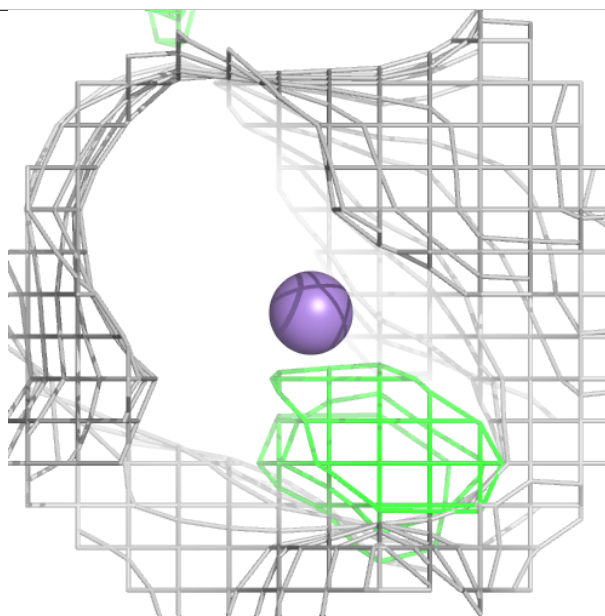
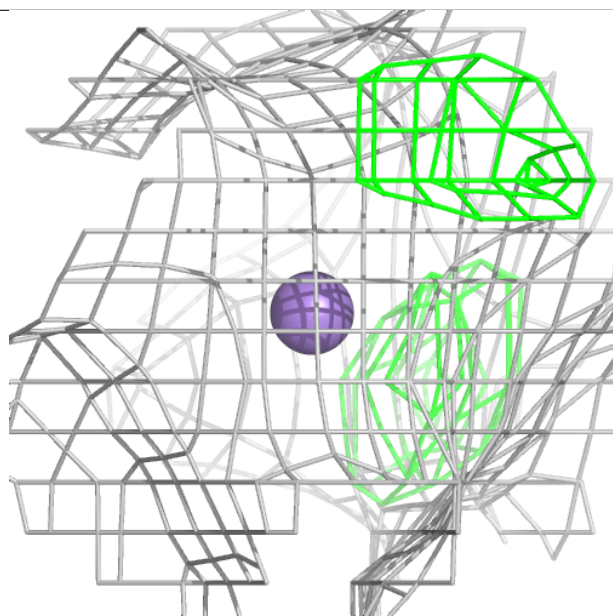
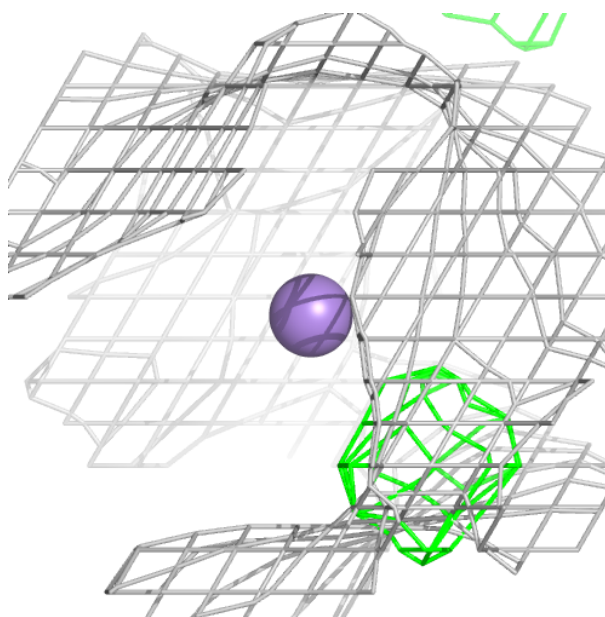
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
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and green (positive)





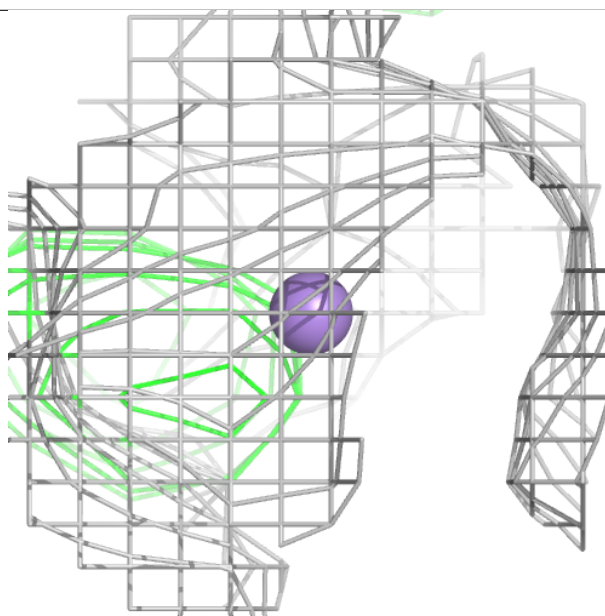
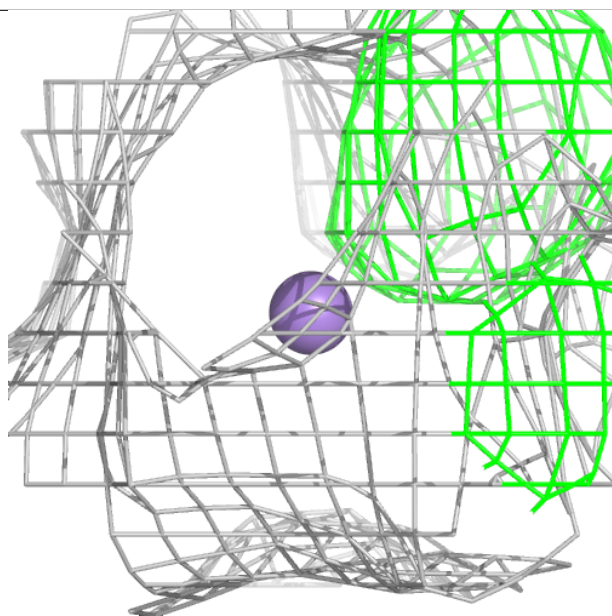
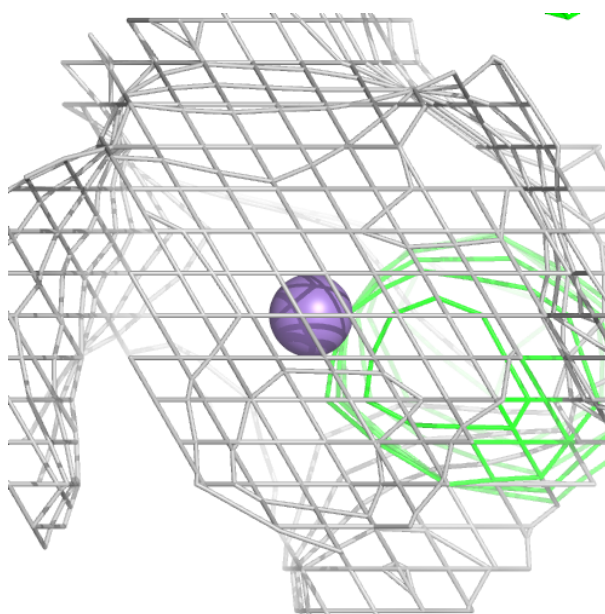
**Electron density around MN F 302:**

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



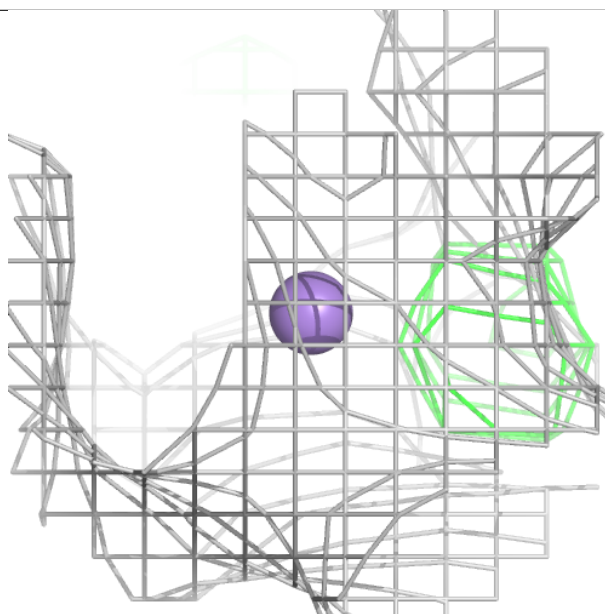
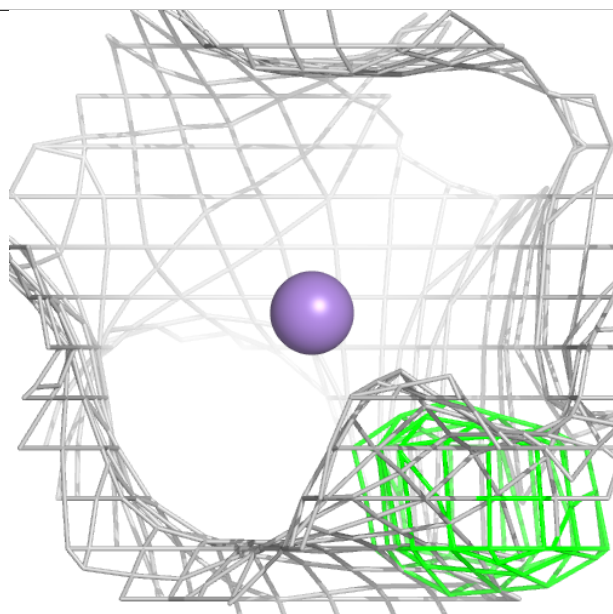
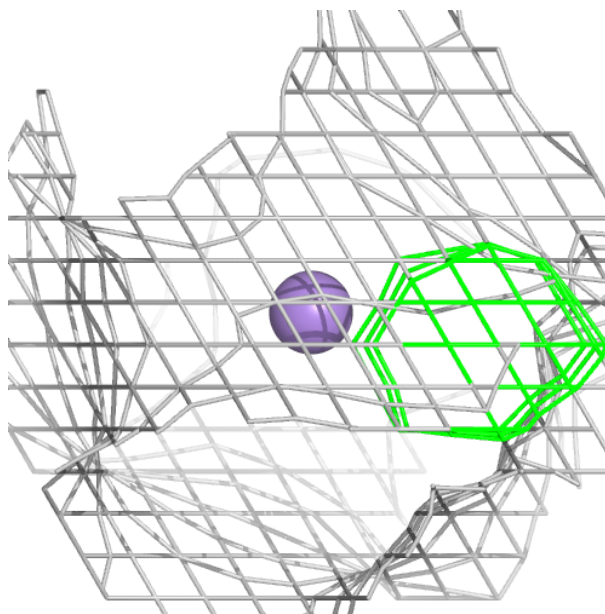
**Electron density around MN A 303:**

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and green (positive)



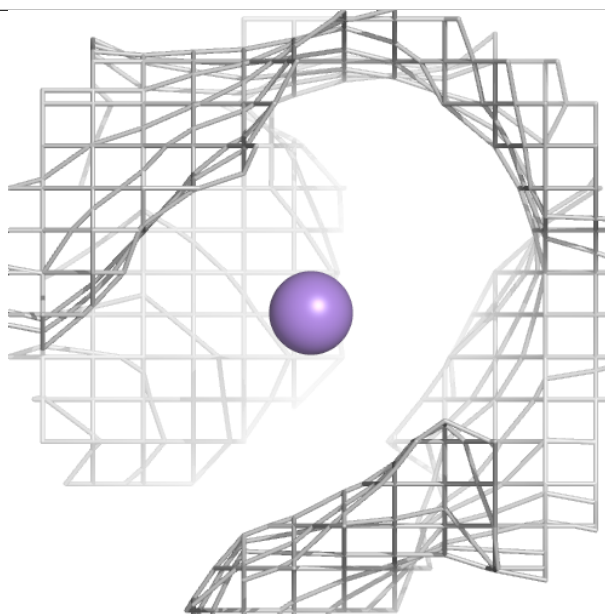
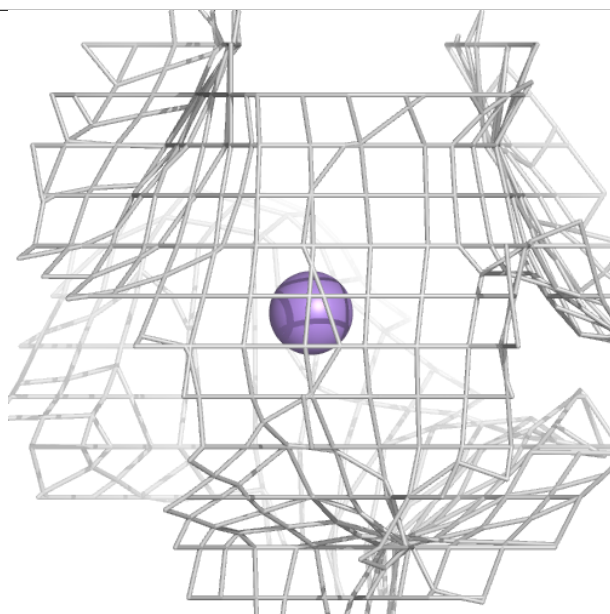
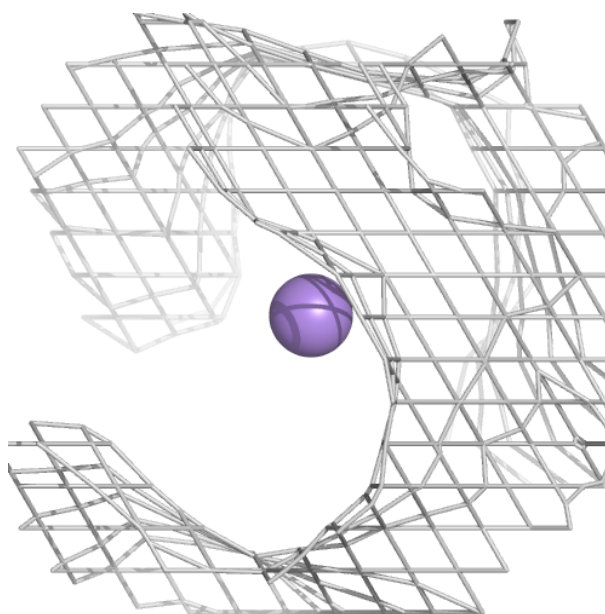
**Electron density around MN B 302:**

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



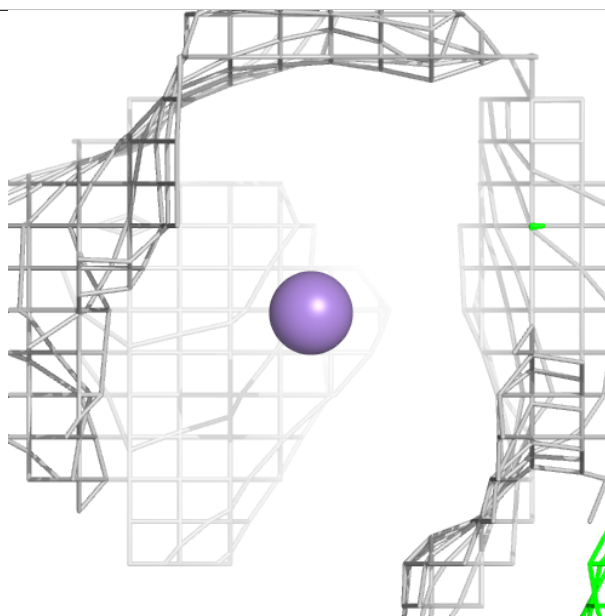
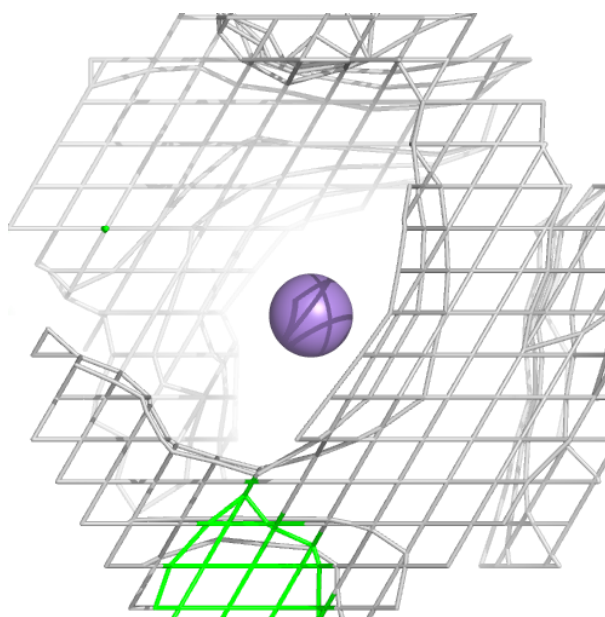
**Electron density around MN D 304:**

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



**Electron density around MN B 303:**

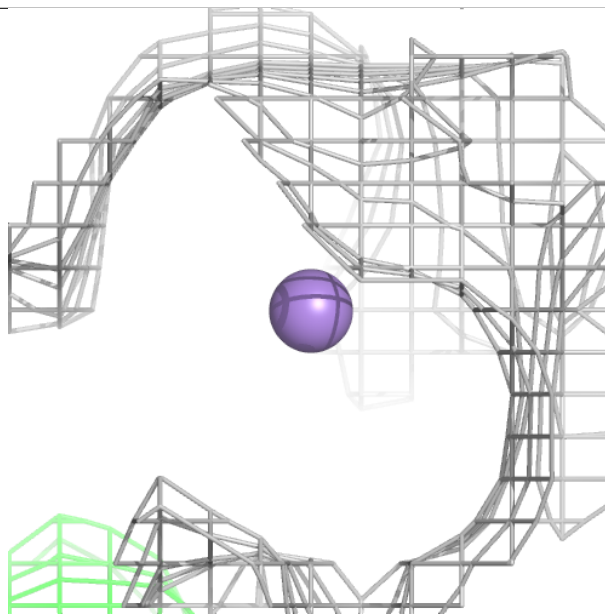
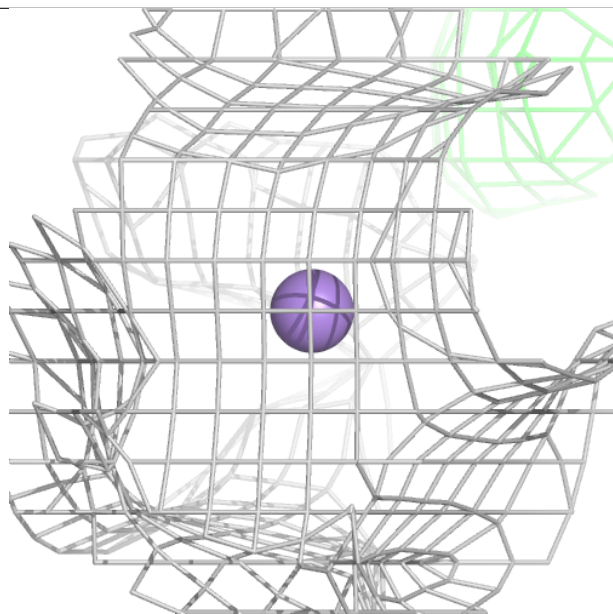
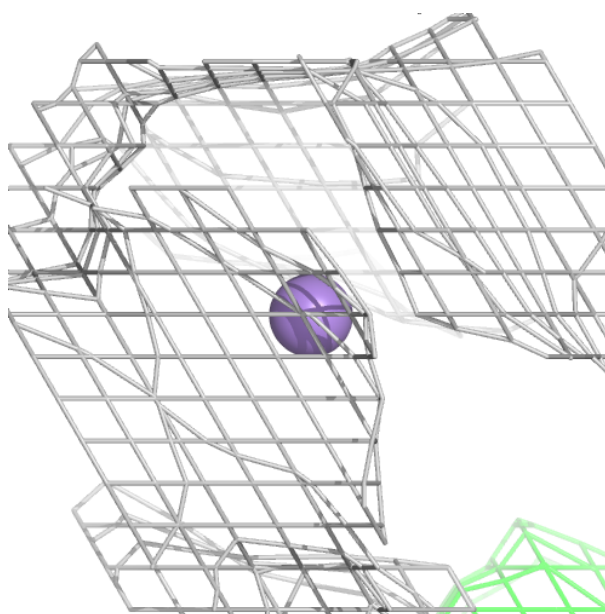
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





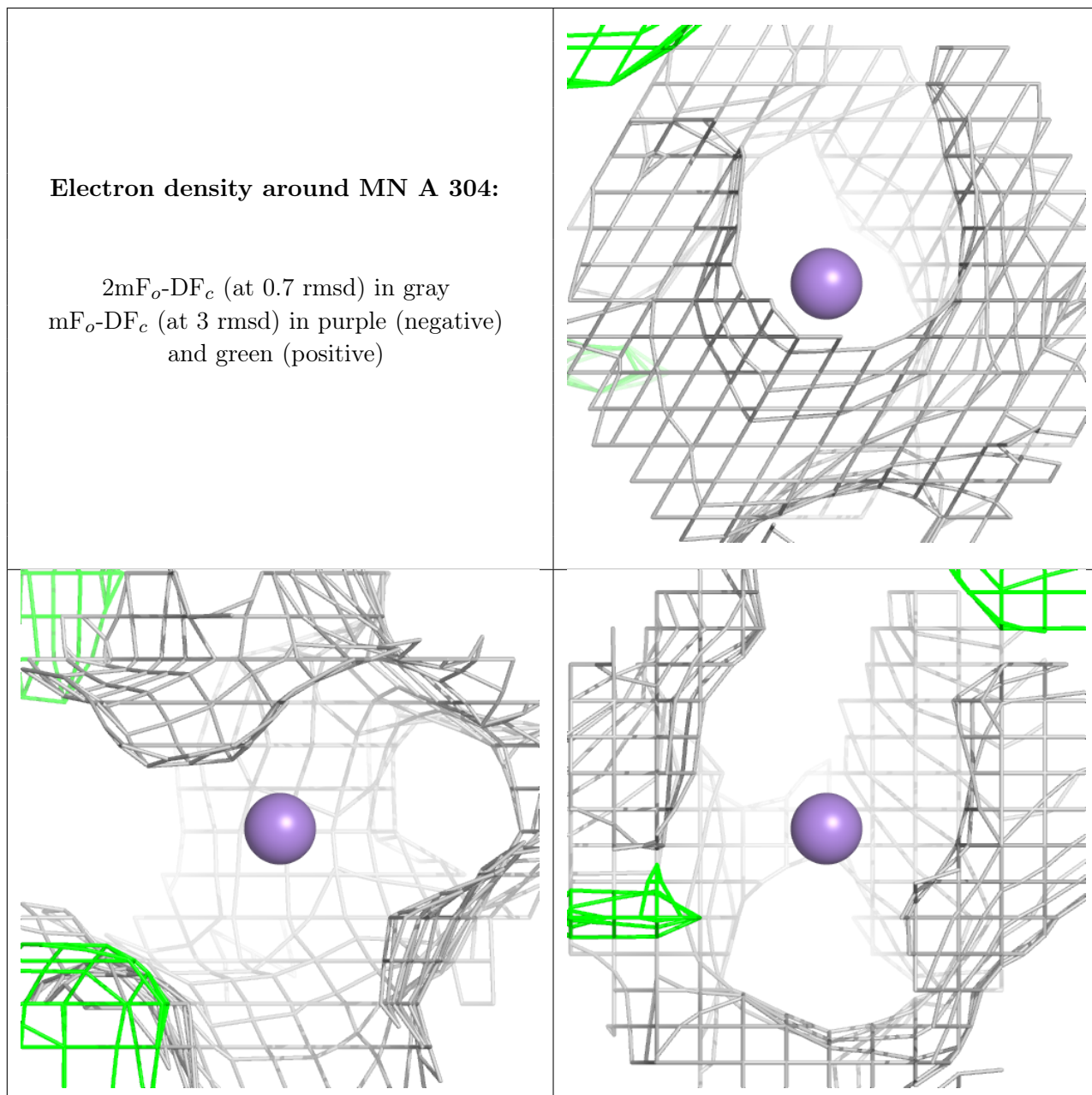
**Electron density around MN E 303:**

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



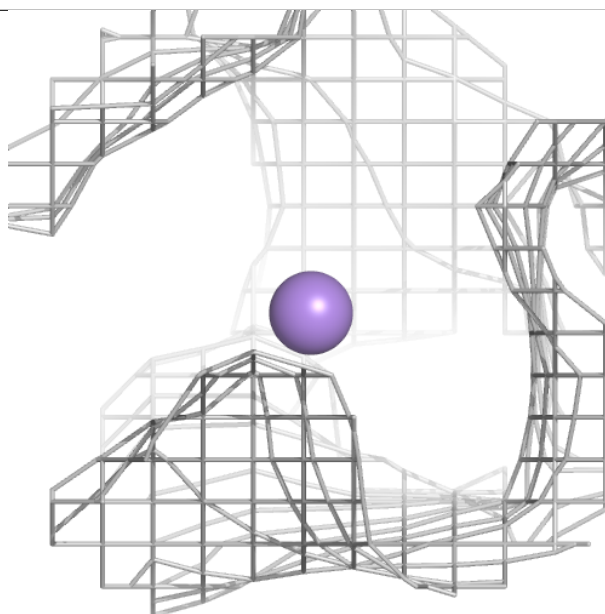
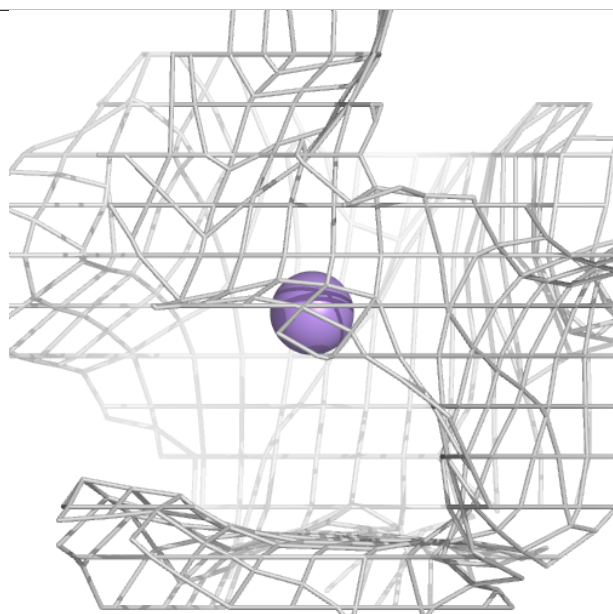
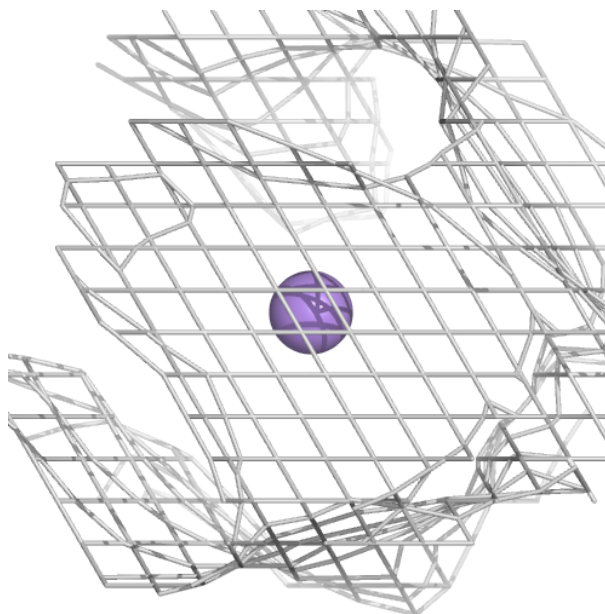
**Electron density around MN A 304:**

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



**Electron density around MN F 303:**

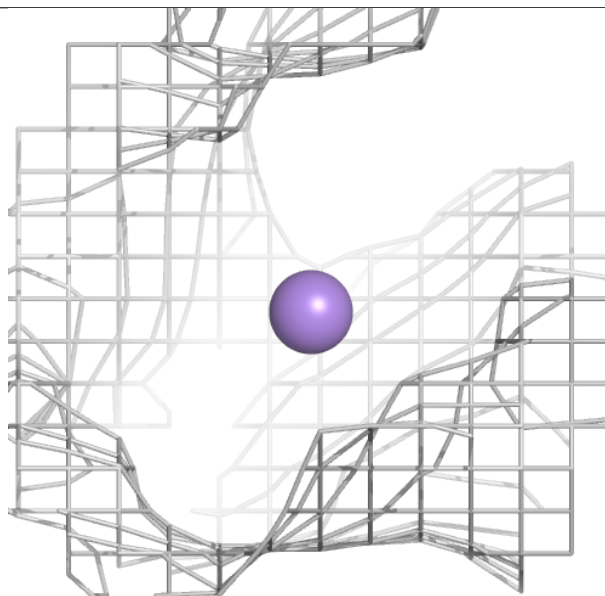
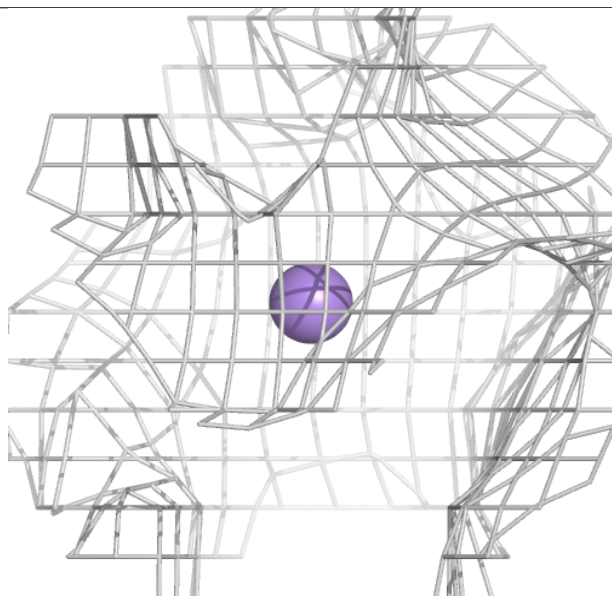
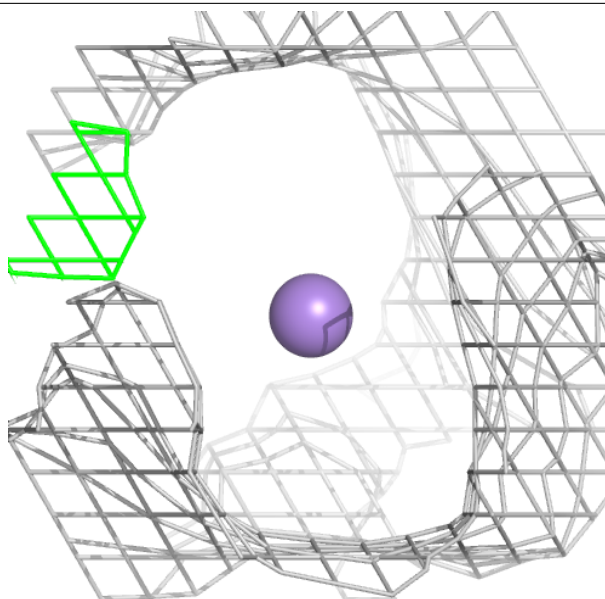
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





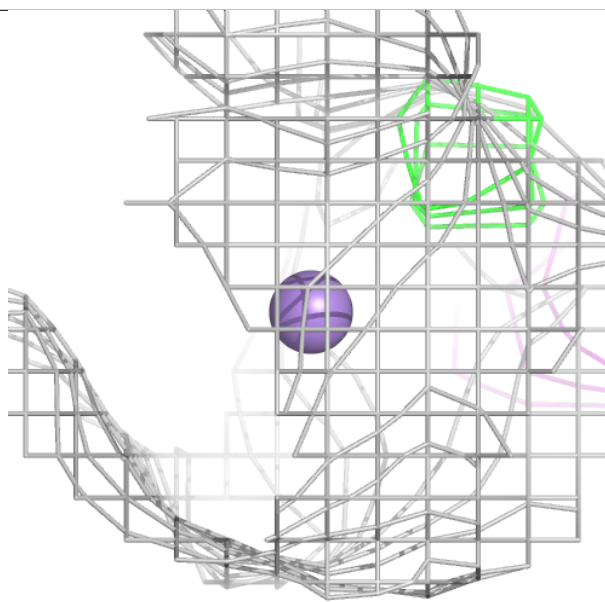
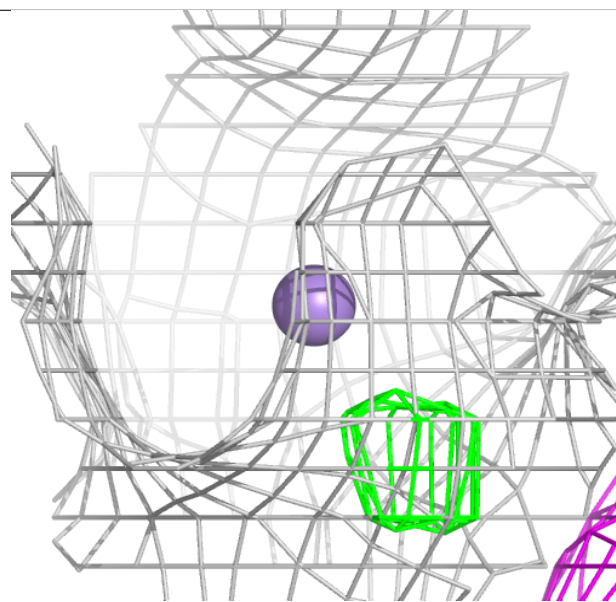
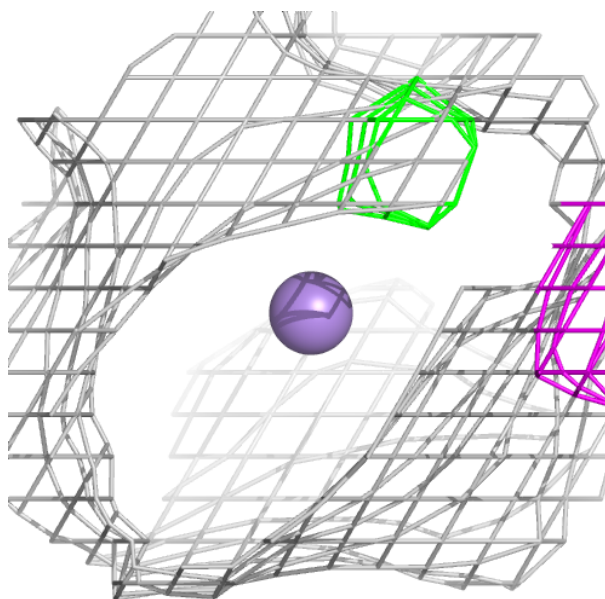
**Electron density around MN C 304:**

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



**Electron density around MN D 303:**

$2mF_o-DF_c$  (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.