



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 3, 2025 – 12:23 PM JST

PDB ID : 8ZRL / pdb_00008zrl
Title : Crystal structure of methanol dehydrogenase2 from *Bacillus methanolicus* complexed with an inhibitor
Authors : Ma, B.D.; Zhang, M.J.; Kong, X.D.
Deposited on : 2024-06-04
Resolution : 2.60 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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:

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

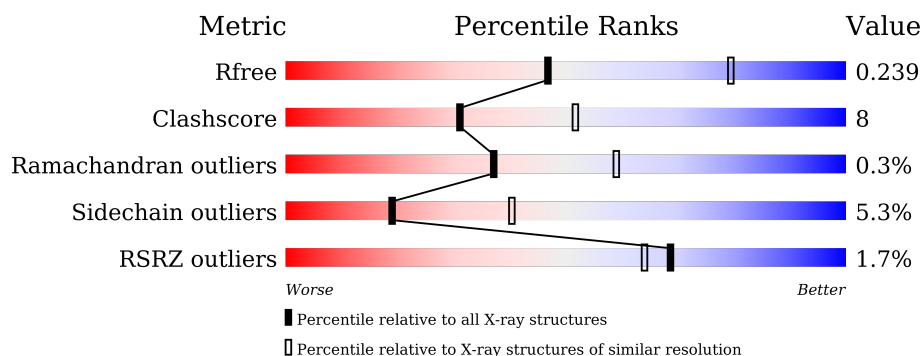
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	393	<div> <div></div> <div>82%</div> <div>15%</div> <div>..</div> </div>
1	B	393	<div> <div></div> <div>83%</div> <div>13%</div> <div>..</div> </div>
1	C	393	<div> <div>%</div> <div>76%</div> <div>20%</div> <div>..</div> </div>
1	D	393	<div> <div>%</div> <div>77%</div> <div>18%</div> <div>..</div> </div>
1	E	393	<div> <div>4%</div> <div>73%</div> <div>21%</div> <div>..</div> </div>
1	F	393	<div> <div>%</div> <div>84%</div> <div>12%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	393	<div><div><div></div><div>4%</div></div><div><div></div><div>75%</div><div>21%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>
1	H	393	<div><div><div></div><div>2%</div></div><div><div></div><div>74%</div><div>22%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>
1	I	393	<div><div><div></div><div>3%</div></div><div><div></div><div>79%</div><div>17%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>
1	J	393	<div><div><div></div><div>%</div></div><div><div></div><div>81%</div><div>15%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 29563 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 NAD-dependent methanol dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			
1	B	384	Total	C	N	O	S	0	1	0
			2858	1808	485	551	14			
1	C	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			
1	D	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			
1	E	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			
1	F	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			
1	G	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			
1	H	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			
1	I	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			
1	J	384	Total	C	N	O	S	0	0	0
			2847	1802	481	550	14			

There are 230 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	THR	LYS	conflict	UNP I3E2P9
A	9	PHE	TYR	conflict	UNP I3E2P9
A	30	ASP	GLY	conflict	UNP I3E2P9
A	46	GLY	SER	conflict	UNP I3E2P9
A	54	SER	ALA	conflict	UNP I3E2P9
A	55	SER	GLY	conflict	UNP I3E2P9
A	59	ALA	GLU	conflict	UNP I3E2P9
A	65	SER	ALA	conflict	UNP I3E2P9
A	118	LYS	THR	conflict	UNP I3E2P9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	130	GLU	LYS	conflict	UNP I3E2P9
A	285	VAL	ILE	conflict	UNP I3E2P9
A	289	TYR	HIS	conflict	UNP I3E2P9
A	320	ASP	GLU	conflict	UNP I3E2P9
A	334	LYS	ARG	conflict	UNP I3E2P9
A	361	LYS	ASN	conflict	UNP I3E2P9
A	386	LEU	-	expression tag	UNP I3E2P9
A	387	GLU	-	expression tag	UNP I3E2P9
A	388	HIS	-	expression tag	UNP I3E2P9
A	389	HIS	-	expression tag	UNP I3E2P9
A	390	HIS	-	expression tag	UNP I3E2P9
A	391	HIS	-	expression tag	UNP I3E2P9
A	392	HIS	-	expression tag	UNP I3E2P9
A	393	HIS	-	expression tag	UNP I3E2P9
B	2	THR	LYS	conflict	UNP I3E2P9
B	9	PHE	TYR	conflict	UNP I3E2P9
B	30	ASP	GLY	conflict	UNP I3E2P9
B	46	GLY	SER	conflict	UNP I3E2P9
B	54	SER	ALA	conflict	UNP I3E2P9
B	55	SER	GLY	conflict	UNP I3E2P9
B	59	ALA	GLU	conflict	UNP I3E2P9
B	65	SER	ALA	conflict	UNP I3E2P9
B	118	LYS	THR	conflict	UNP I3E2P9
B	130	GLU	LYS	conflict	UNP I3E2P9
B	285	VAL	ILE	conflict	UNP I3E2P9
B	289	TYR	HIS	conflict	UNP I3E2P9
B	320	ASP	GLU	conflict	UNP I3E2P9
B	334	LYS	ARG	conflict	UNP I3E2P9
B	361	LYS	ASN	conflict	UNP I3E2P9
B	386	LEU	-	expression tag	UNP I3E2P9
B	387	GLU	-	expression tag	UNP I3E2P9
B	388	HIS	-	expression tag	UNP I3E2P9
B	389	HIS	-	expression tag	UNP I3E2P9
B	390	HIS	-	expression tag	UNP I3E2P9
B	391	HIS	-	expression tag	UNP I3E2P9
B	392	HIS	-	expression tag	UNP I3E2P9
B	393	HIS	-	expression tag	UNP I3E2P9
C	2	THR	LYS	conflict	UNP I3E2P9
C	9	PHE	TYR	conflict	UNP I3E2P9
C	30	ASP	GLY	conflict	UNP I3E2P9
C	46	GLY	SER	conflict	UNP I3E2P9
C	54	SER	ALA	conflict	UNP I3E2P9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	55	SER	GLY	conflict	UNP I3E2P9
C	59	ALA	GLU	conflict	UNP I3E2P9
C	65	SER	ALA	conflict	UNP I3E2P9
C	118	LYS	THR	conflict	UNP I3E2P9
C	130	GLU	LYS	conflict	UNP I3E2P9
C	285	VAL	ILE	conflict	UNP I3E2P9
C	289	TYR	HIS	conflict	UNP I3E2P9
C	320	ASP	GLU	conflict	UNP I3E2P9
C	334	LYS	ARG	conflict	UNP I3E2P9
C	361	LYS	ASN	conflict	UNP I3E2P9
C	386	LEU	-	expression tag	UNP I3E2P9
C	387	GLU	-	expression tag	UNP I3E2P9
C	388	HIS	-	expression tag	UNP I3E2P9
C	389	HIS	-	expression tag	UNP I3E2P9
C	390	HIS	-	expression tag	UNP I3E2P9
C	391	HIS	-	expression tag	UNP I3E2P9
C	392	HIS	-	expression tag	UNP I3E2P9
C	393	HIS	-	expression tag	UNP I3E2P9
D	2	THR	LYS	conflict	UNP I3E2P9
D	9	PHE	TYR	conflict	UNP I3E2P9
D	30	ASP	GLY	conflict	UNP I3E2P9
D	46	GLY	SER	conflict	UNP I3E2P9
D	54	SER	ALA	conflict	UNP I3E2P9
D	55	SER	GLY	conflict	UNP I3E2P9
D	59	ALA	GLU	conflict	UNP I3E2P9
D	65	SER	ALA	conflict	UNP I3E2P9
D	118	LYS	THR	conflict	UNP I3E2P9
D	130	GLU	LYS	conflict	UNP I3E2P9
D	285	VAL	ILE	conflict	UNP I3E2P9
D	289	TYR	HIS	conflict	UNP I3E2P9
D	320	ASP	GLU	conflict	UNP I3E2P9
D	334	LYS	ARG	conflict	UNP I3E2P9
D	361	LYS	ASN	conflict	UNP I3E2P9
D	386	LEU	-	expression tag	UNP I3E2P9
D	387	GLU	-	expression tag	UNP I3E2P9
D	388	HIS	-	expression tag	UNP I3E2P9
D	389	HIS	-	expression tag	UNP I3E2P9
D	390	HIS	-	expression tag	UNP I3E2P9
D	391	HIS	-	expression tag	UNP I3E2P9
D	392	HIS	-	expression tag	UNP I3E2P9
D	393	HIS	-	expression tag	UNP I3E2P9
E	2	THR	LYS	conflict	UNP I3E2P9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	9	PHE	TYR	conflict	UNP I3E2P9
E	30	ASP	GLY	conflict	UNP I3E2P9
E	46	GLY	SER	conflict	UNP I3E2P9
E	54	SER	ALA	conflict	UNP I3E2P9
E	55	SER	GLY	conflict	UNP I3E2P9
E	59	ALA	GLU	conflict	UNP I3E2P9
E	65	SER	ALA	conflict	UNP I3E2P9
E	118	LYS	THR	conflict	UNP I3E2P9
E	130	GLU	LYS	conflict	UNP I3E2P9
E	285	VAL	ILE	conflict	UNP I3E2P9
E	289	TYR	HIS	conflict	UNP I3E2P9
E	320	ASP	GLU	conflict	UNP I3E2P9
E	334	LYS	ARG	conflict	UNP I3E2P9
E	361	LYS	ASN	conflict	UNP I3E2P9
E	386	LEU	-	expression tag	UNP I3E2P9
E	387	GLU	-	expression tag	UNP I3E2P9
E	388	HIS	-	expression tag	UNP I3E2P9
E	389	HIS	-	expression tag	UNP I3E2P9
E	390	HIS	-	expression tag	UNP I3E2P9
E	391	HIS	-	expression tag	UNP I3E2P9
E	392	HIS	-	expression tag	UNP I3E2P9
E	393	HIS	-	expression tag	UNP I3E2P9
F	2	THR	LYS	conflict	UNP I3E2P9
F	9	PHE	TYR	conflict	UNP I3E2P9
F	30	ASP	GLY	conflict	UNP I3E2P9
F	46	GLY	SER	conflict	UNP I3E2P9
F	54	SER	ALA	conflict	UNP I3E2P9
F	55	SER	GLY	conflict	UNP I3E2P9
F	59	ALA	GLU	conflict	UNP I3E2P9
F	65	SER	ALA	conflict	UNP I3E2P9
F	118	LYS	THR	conflict	UNP I3E2P9
F	130	GLU	LYS	conflict	UNP I3E2P9
F	285	VAL	ILE	conflict	UNP I3E2P9
F	289	TYR	HIS	conflict	UNP I3E2P9
F	320	ASP	GLU	conflict	UNP I3E2P9
F	334	LYS	ARG	conflict	UNP I3E2P9
F	361	LYS	ASN	conflict	UNP I3E2P9
F	386	LEU	-	expression tag	UNP I3E2P9
F	387	GLU	-	expression tag	UNP I3E2P9
F	388	HIS	-	expression tag	UNP I3E2P9
F	389	HIS	-	expression tag	UNP I3E2P9
F	390	HIS	-	expression tag	UNP I3E2P9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	391	HIS	-	expression tag	UNP I3E2P9
F	392	HIS	-	expression tag	UNP I3E2P9
F	393	HIS	-	expression tag	UNP I3E2P9
G	2	THR	LYS	conflict	UNP I3E2P9
G	9	PHE	TYR	conflict	UNP I3E2P9
G	30	ASP	GLY	conflict	UNP I3E2P9
G	46	GLY	SER	conflict	UNP I3E2P9
G	54	SER	ALA	conflict	UNP I3E2P9
G	55	SER	GLY	conflict	UNP I3E2P9
G	59	ALA	GLU	conflict	UNP I3E2P9
G	65	SER	ALA	conflict	UNP I3E2P9
G	118	LYS	THR	conflict	UNP I3E2P9
G	130	GLU	LYS	conflict	UNP I3E2P9
G	285	VAL	ILE	conflict	UNP I3E2P9
G	289	TYR	HIS	conflict	UNP I3E2P9
G	320	ASP	GLU	conflict	UNP I3E2P9
G	334	LYS	ARG	conflict	UNP I3E2P9
G	361	LYS	ASN	conflict	UNP I3E2P9
G	386	LEU	-	expression tag	UNP I3E2P9
G	387	GLU	-	expression tag	UNP I3E2P9
G	388	HIS	-	expression tag	UNP I3E2P9
G	389	HIS	-	expression tag	UNP I3E2P9
G	390	HIS	-	expression tag	UNP I3E2P9
G	391	HIS	-	expression tag	UNP I3E2P9
G	392	HIS	-	expression tag	UNP I3E2P9
G	393	HIS	-	expression tag	UNP I3E2P9
H	2	THR	LYS	conflict	UNP I3E2P9
H	9	PHE	TYR	conflict	UNP I3E2P9
H	30	ASP	GLY	conflict	UNP I3E2P9
H	46	GLY	SER	conflict	UNP I3E2P9
H	54	SER	ALA	conflict	UNP I3E2P9
H	55	SER	GLY	conflict	UNP I3E2P9
H	59	ALA	GLU	conflict	UNP I3E2P9
H	65	SER	ALA	conflict	UNP I3E2P9
H	118	LYS	THR	conflict	UNP I3E2P9
H	130	GLU	LYS	conflict	UNP I3E2P9
H	285	VAL	ILE	conflict	UNP I3E2P9
H	289	TYR	HIS	conflict	UNP I3E2P9
H	320	ASP	GLU	conflict	UNP I3E2P9
H	334	LYS	ARG	conflict	UNP I3E2P9
H	361	LYS	ASN	conflict	UNP I3E2P9
H	386	LEU	-	expression tag	UNP I3E2P9

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Chain	Residue	Modelled	Actual	Comment	Reference
H	387	GLU	-	expression tag	UNP I3E2P9
H	388	HIS	-	expression tag	UNP I3E2P9
H	389	HIS	-	expression tag	UNP I3E2P9
H	390	HIS	-	expression tag	UNP I3E2P9
H	391	HIS	-	expression tag	UNP I3E2P9
H	392	HIS	-	expression tag	UNP I3E2P9
H	393	HIS	-	expression tag	UNP I3E2P9
I	2	THR	LYS	conflict	UNP I3E2P9
I	9	PHE	TYR	conflict	UNP I3E2P9
I	30	ASP	GLY	conflict	UNP I3E2P9
I	46	GLY	SER	conflict	UNP I3E2P9
I	54	SER	ALA	conflict	UNP I3E2P9
I	55	SER	GLY	conflict	UNP I3E2P9
I	59	ALA	GLU	conflict	UNP I3E2P9
I	65	SER	ALA	conflict	UNP I3E2P9
I	118	LYS	THR	conflict	UNP I3E2P9
I	130	GLU	LYS	conflict	UNP I3E2P9
I	285	VAL	ILE	conflict	UNP I3E2P9
I	289	TYR	HIS	conflict	UNP I3E2P9
I	320	ASP	GLU	conflict	UNP I3E2P9
I	334	LYS	ARG	conflict	UNP I3E2P9
I	361	LYS	ASN	conflict	UNP I3E2P9
I	386	LEU	-	expression tag	UNP I3E2P9
I	387	GLU	-	expression tag	UNP I3E2P9
I	388	HIS	-	expression tag	UNP I3E2P9
I	389	HIS	-	expression tag	UNP I3E2P9
I	390	HIS	-	expression tag	UNP I3E2P9
I	391	HIS	-	expression tag	UNP I3E2P9
I	392	HIS	-	expression tag	UNP I3E2P9
I	393	HIS	-	expression tag	UNP I3E2P9
J	2	THR	LYS	conflict	UNP I3E2P9
J	9	PHE	TYR	conflict	UNP I3E2P9
J	30	ASP	GLY	conflict	UNP I3E2P9
J	46	GLY	SER	conflict	UNP I3E2P9
J	54	SER	ALA	conflict	UNP I3E2P9
J	55	SER	GLY	conflict	UNP I3E2P9
J	59	ALA	GLU	conflict	UNP I3E2P9
J	65	SER	ALA	conflict	UNP I3E2P9
J	118	LYS	THR	conflict	UNP I3E2P9
J	130	GLU	LYS	conflict	UNP I3E2P9
J	285	VAL	ILE	conflict	UNP I3E2P9
J	289	TYR	HIS	conflict	UNP I3E2P9

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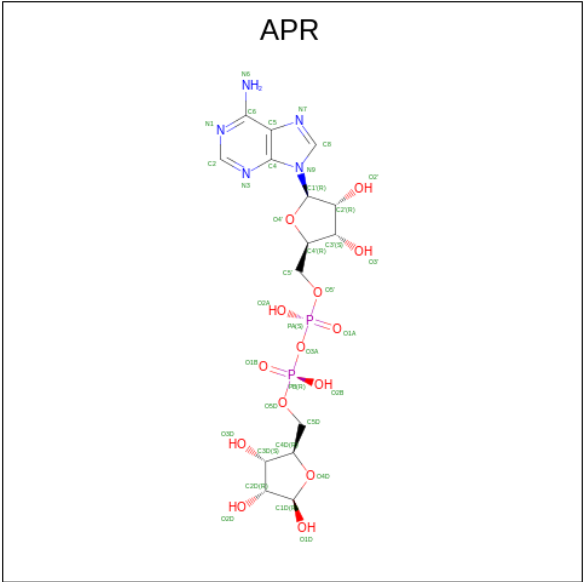
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Chain	Residue	Modelled	Actual	Comment	Reference
J	320	ASP	GLU	conflict	UNP I3E2P9
J	334	LYS	ARG	conflict	UNP I3E2P9
J	361	LYS	ASN	conflict	UNP I3E2P9
J	386	LEU	-	expression tag	UNP I3E2P9
J	387	GLU	-	expression tag	UNP I3E2P9
J	388	HIS	-	expression tag	UNP I3E2P9
J	389	HIS	-	expression tag	UNP I3E2P9
J	390	HIS	-	expression tag	UNP I3E2P9
J	391	HIS	-	expression tag	UNP I3E2P9
J	392	HIS	-	expression tag	UNP I3E2P9
J	393	HIS	-	expression tag	UNP I3E2P9

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 3 is ADENOSINE-5-DIPHOSPHORIBOSE (CCD ID: APR) (formula: C₁₅H₂₃N₅O₁₄P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	B	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	C	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	D	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	E	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	F	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	G	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	H	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	I	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
3	J	1	Total	C	N	O	P	0	0
			36	15	5	14	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	134	Total	O	0	0
			134	134		
4	B	105	Total	O	0	0
			105	105		

Continued on next page...

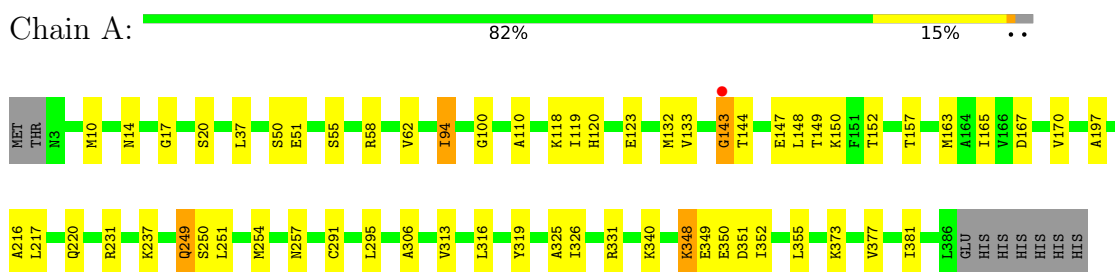
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	58	Total 58	O 58	0	0
4	D	48	Total 48	O 48	0	0
4	E	38	Total 38	O 38	0	0
4	F	105	Total 105	O 105	0	0
4	G	46	Total 46	O 46	0	0
4	H	32	Total 32	O 32	0	0
4	I	65	Total 65	O 65	0	0
4	J	81	Total 81	O 81	0	0

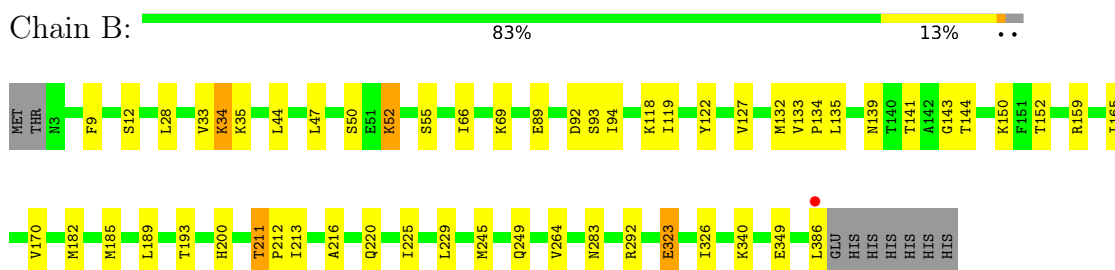
3 Residue-property plots [i](#)

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

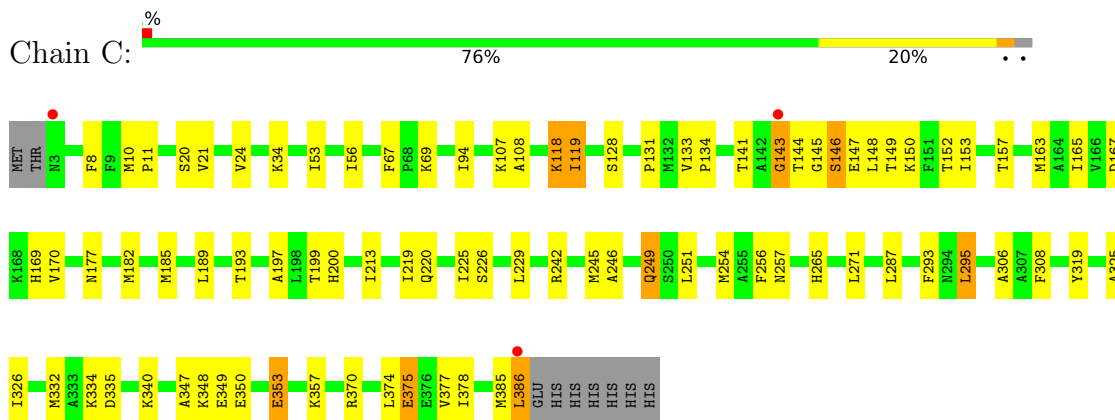
- Molecule 1: NAD-dependent methanol dehydrogenase



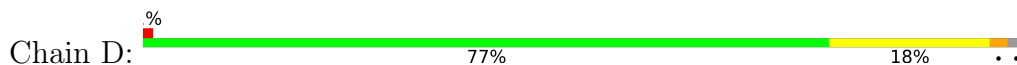
- Molecule 1: NAD-dependent methanol dehydrogenase

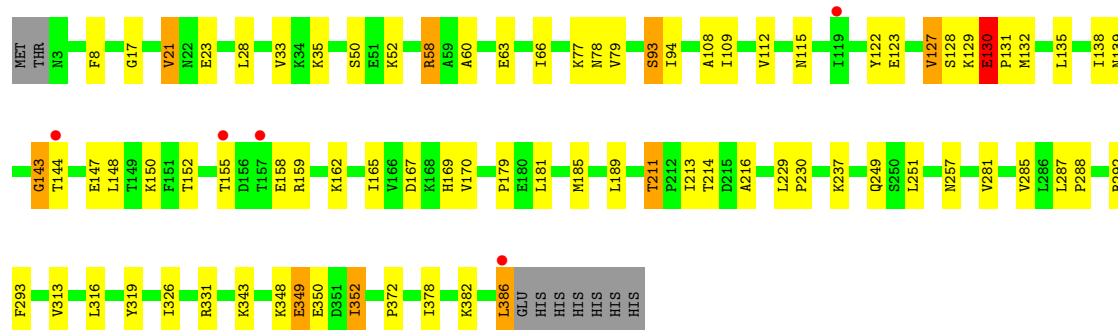


- Molecule 1: NAD-dependent methanol dehydrogenase

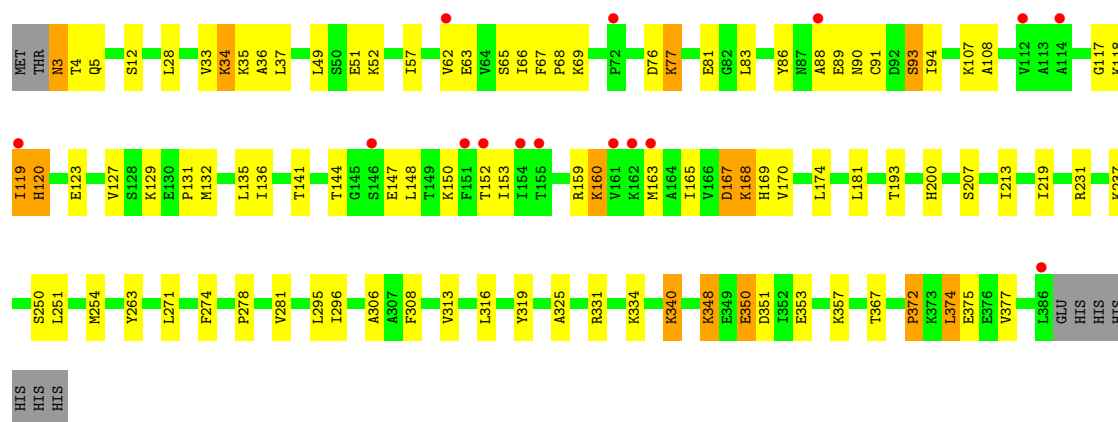
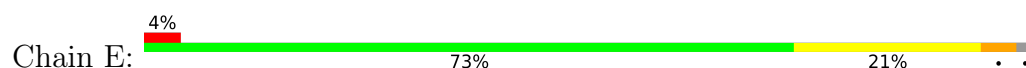


- Molecule 1: NAD-dependent methanol dehydrogenase

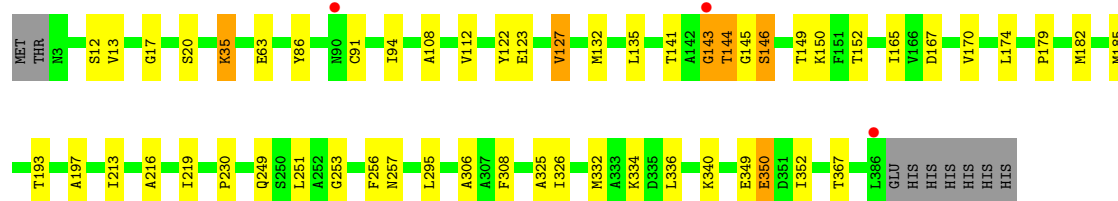
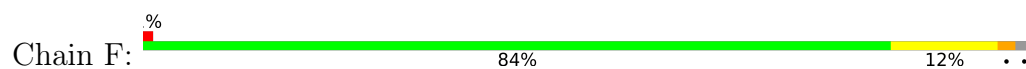




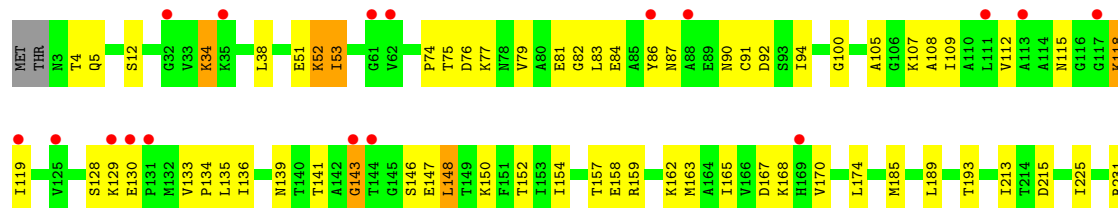
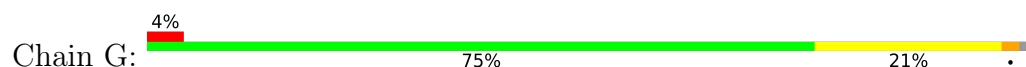
• Molecule 1: NAD-dependent methanol dehydrogenase



• Molecule 1: NAD-dependent methanol dehydrogenase

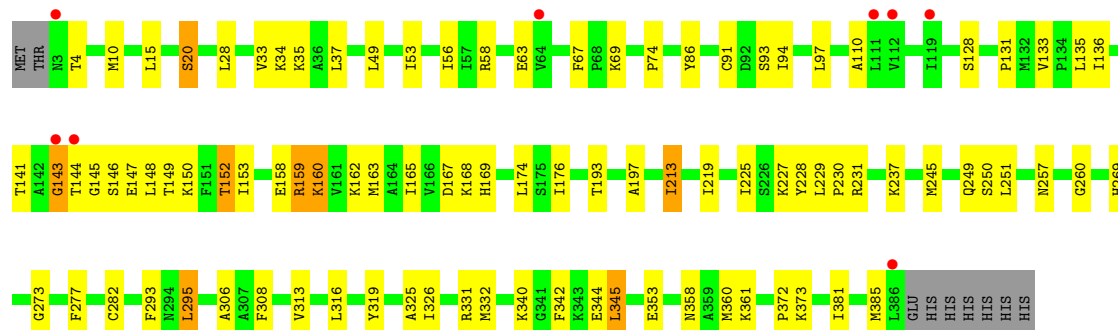
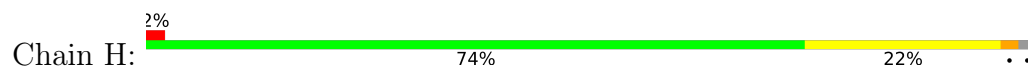


• Molecule 1: NAD-dependent methanol dehydrogenase

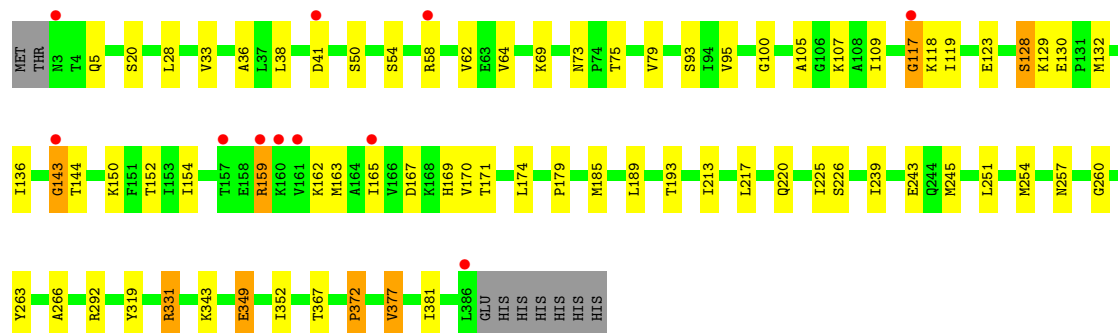
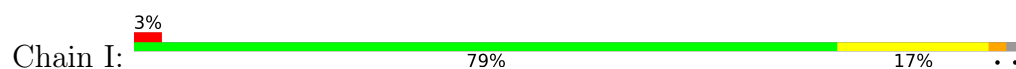




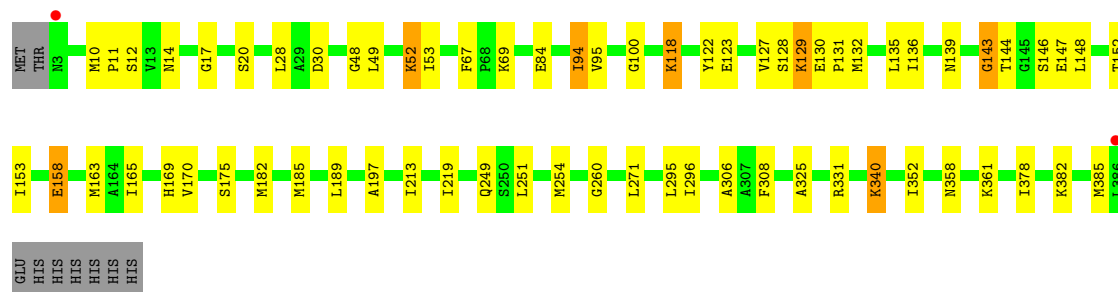
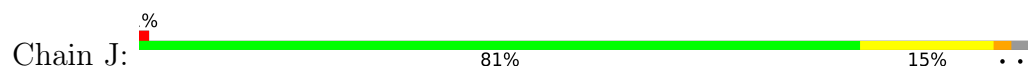
• Molecule 1: NAD-dependent methanol dehydrogenase



• Molecule 1: NAD-dependent methanol dehydrogenase



• Molecule 1: NAD-dependent methanol dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.57Å 204.41Å 258.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.51 – 2.60 79.51 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (79.51-2.60) 99.9 (79.51-2.60)	Depositor EDS
R_{merge}	0.35	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.62Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.193 , 0.240 0.199 , 0.239	Depositor DCC
R_{free} test set	6809 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	42.1	Xtriage
Anisotropy	0.562	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 54.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	29563	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.38	0/2892	0.60	0/3920
1	B	0.37	0/2903	0.62	0/3934
1	C	0.36	0/2892	0.60	0/3920
1	D	0.38	0/2892	0.60	2/3920 (0.1%)
1	E	0.41	0/2892	0.72	1/3920 (0.0%)
1	F	0.33	0/2892	0.55	0/3920
1	G	0.42	0/2892	0.68	0/3920
1	H	0.40	0/2892	0.65	1/3920 (0.0%)
1	I	0.40	0/2892	0.68	3/3920 (0.1%)
1	J	0.34	0/2892	0.59	2/3920 (0.1%)
All	All	0.38	0/28931	0.63	9/39214 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	D	0	2
1	E	0	2
1	G	0	2
1	H	0	2
1	I	0	2
All	All	0	12

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	372	PRO	N-CA-C	5.53	120.87	111.03
1	E	372	PRO	CB-CA-C	-5.27	102.86	111.56
1	I	260	GLY	CA-C-O	-5.25	118.61	122.23
1	I	159	ARG	CD-NE-CZ	5.23	131.72	124.40
1	H	260	GLY	CA-C-O	5.13	126.15	122.45

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	231	ARG	Sidechain
1	B	159	ARG	Sidechain
1	D	159	ARG	Sidechain
1	D	58	ARG	Sidechain
1	E	159	ARG	Sidechain

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	2847	0	2898	36	0
1	B	2858	0	2910	41	0
1	C	2847	0	2898	54	0
1	D	2847	0	2898	54	0
1	E	2847	0	2898	65	0
1	F	2847	0	2898	36	0
1	G	2847	0	2898	55	0
1	H	2847	0	2898	60	0
1	I	2847	0	2898	43	0
1	J	2847	0	2898	41	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	36	0	20	3	0
3	B	36	0	20	1	0
3	C	36	0	20	1	0
3	D	36	0	20	2	0
3	E	36	0	20	1	0
3	F	36	0	20	2	0
3	G	36	0	20	5	0
3	H	36	0	20	1	0
3	I	36	0	20	3	0
3	J	36	0	20	1	0
4	A	134	0	0	2	0
4	B	105	0	0	3	0
4	C	58	0	0	2	0
4	D	48	0	0	1	0
4	E	38	0	0	1	0
4	F	105	0	0	0	0
4	G	46	0	0	1	0
4	H	32	0	0	1	0
4	I	65	0	0	3	0
4	J	81	0	0	1	0
All	All	29563	0	29192	468	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 8.

The worst 5 of 468 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)
3:C:402:APR:C4'	3:C:402:APR:O4'	1.67	1.26
3:D:402:APR:O4'	3:D:402:APR:C4'	1.67	1.23
3:A:402:APR:O4'	3:A:402:APR:C4'	1.67	1.22
3:F:402:APR:O4'	3:F:402:APR:C4'	1.67	1.19
3:B:402:APR:O4'	3:B:402:APR:C4'	1.67	1.18

There are no symmetry-related clashes.

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	382/393 (97%)	374 (98%)	7 (2%)	1 (0%)	37	59
1	B	383/393 (98%)	373 (97%)	10 (3%)	0	100	100
1	C	382/393 (97%)	371 (97%)	10 (3%)	1 (0%)	37	59
1	D	382/393 (97%)	372 (97%)	9 (2%)	1 (0%)	37	59
1	E	382/393 (97%)	367 (96%)	14 (4%)	1 (0%)	37	59
1	F	382/393 (97%)	373 (98%)	8 (2%)	1 (0%)	37	59
1	G	382/393 (97%)	372 (97%)	9 (2%)	1 (0%)	37	59
1	H	382/393 (97%)	370 (97%)	11 (3%)	1 (0%)	37	59
1	I	382/393 (97%)	372 (97%)	8 (2%)	2 (0%)	25	47
1	J	382/393 (97%)	373 (98%)	8 (2%)	1 (0%)	37	59
All	All	3821/3930 (97%)	3717 (97%)	94 (2%)	10 (0%)	37	59

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	117	GLY
1	I	117	GLY
1	A	143	GLY
1	C	143	GLY
1	D	144	THR

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	299/308 (97%)	287 (96%)	12 (4%)	27	52
1	B	300/308 (97%)	288 (96%)	12 (4%)	27	52
1	C	299/308 (97%)	282 (94%)	17 (6%)	17	37
1	D	299/308 (97%)	286 (96%)	13 (4%)	25	49
1	E	299/308 (97%)	272 (91%)	27 (9%)	8	16
1	F	299/308 (97%)	288 (96%)	11 (4%)	29	55
1	G	299/308 (97%)	276 (92%)	23 (8%)	10	22
1	H	299/308 (97%)	282 (94%)	17 (6%)	17	37
1	I	299/308 (97%)	287 (96%)	12 (4%)	27	52
1	J	299/308 (97%)	285 (95%)	14 (5%)	22	45
All	All	2991/3080 (97%)	2833 (95%)	158 (5%)	19	40

5 of 158 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	4	THR
1	I	377	VAL
1	H	128	SER
1	H	353	GLU
1	J	118	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	22	ASN
1	I	45	HIS
1	F	249	GLN
1	I	249	GLN
1	G	169	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 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	APR	C	402	-	34,39,39	5.22	13 (38%)	40,60,60	1.34	6 (15%)
3	APR	E	402	-	34,39,39	5.23	13 (38%)	40,60,60	1.35	4 (10%)
3	APR	F	402	-	34,39,39	5.21	12 (35%)	40,60,60	1.35	3 (7%)
3	APR	I	402	-	34,39,39	5.22	13 (38%)	40,60,60	1.27	3 (7%)
3	APR	D	402	-	34,39,39	5.22	12 (35%)	40,60,60	1.34	4 (10%)
3	APR	J	402	-	34,39,39	5.21	13 (38%)	40,60,60	1.35	5 (12%)
3	APR	G	402	-	34,39,39	5.18	13 (38%)	40,60,60	1.44	5 (12%)
3	APR	H	402	-	34,39,39	5.22	13 (38%)	40,60,60	1.33	4 (10%)
3	APR	A	402	-	34,39,39	5.17	13 (38%)	40,60,60	1.31	3 (7%)
3	APR	B	402	-	34,39,39	5.21	13 (38%)	40,60,60	1.30	3 (7%)

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	APR	C	402	-	-	6/18/54/54	0/4/4/4
3	APR	E	402	-	-	5/18/54/54	0/4/4/4
3	APR	F	402	-	-	5/18/54/54	0/4/4/4
3	APR	I	402	-	-	3/18/54/54	0/4/4/4
3	APR	D	402	-	-	7/18/54/54	0/4/4/4
3	APR	J	402	-	-	2/18/54/54	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	APR	G	402	-	-	6/18/54/54	0/4/4/4
3	APR	H	402	-	-	5/18/54/54	0/4/4/4
3	APR	A	402	-	-	5/18/54/54	0/4/4/4
3	APR	B	402	-	-	2/18/54/54	0/4/4/4

The worst 5 of 128 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	402	APR	C1D-C2D	-18.37	1.31	1.52
3	E	402	APR	C1D-C2D	-18.31	1.31	1.52
3	D	402	APR	C1D-C2D	-18.21	1.31	1.52
3	C	402	APR	C1D-C2D	-18.13	1.31	1.52
3	H	402	APR	C1D-C2D	-18.10	1.31	1.52

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	402	APR	N3-C2-N1	-5.36	120.31	128.68
3	C	402	APR	N3-C2-N1	-5.34	120.33	128.68
3	F	402	APR	N3-C2-N1	-5.31	120.38	128.68
3	I	402	APR	N3-C2-N1	-5.30	120.39	128.68
3	B	402	APR	N3-C2-N1	-5.25	120.47	128.68

There are no chirality outliers.

5 of 46 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	402	APR	C5D-O5D-PB-O1B
3	C	402	APR	C5D-O5D-PB-O2B
3	E	402	APR	C5D-O5D-PB-O2B
3	F	402	APR	PA-O3A-PB-O5D
3	F	402	APR	C5D-O5D-PB-O2B

There are no ring outliers.

10 monomers are involved in 20 short contacts:

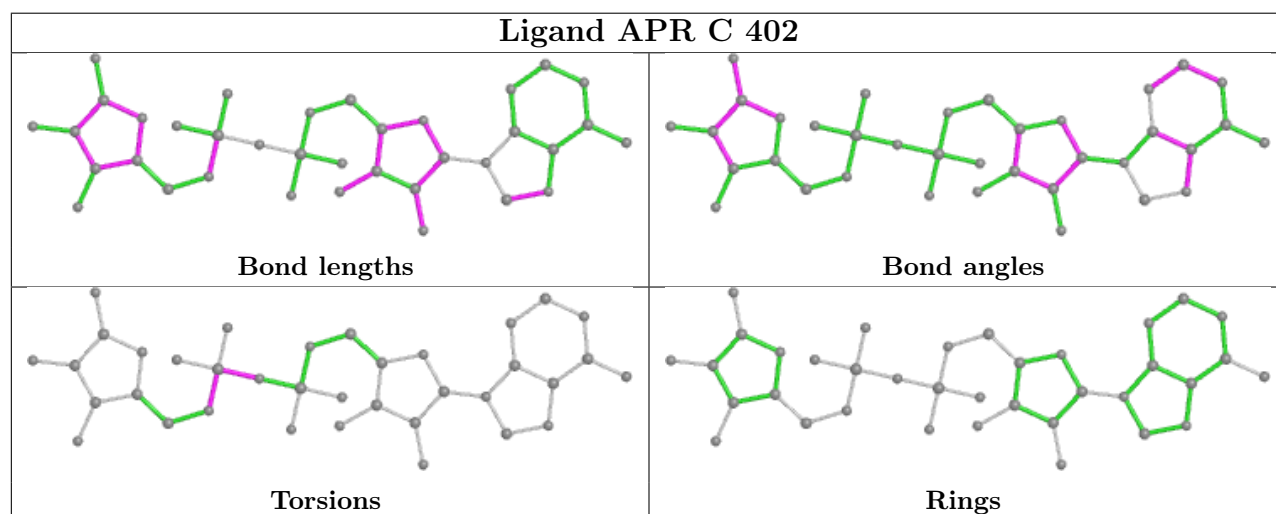
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	402	APR	1	0
3	E	402	APR	1	0
3	F	402	APR	2	0

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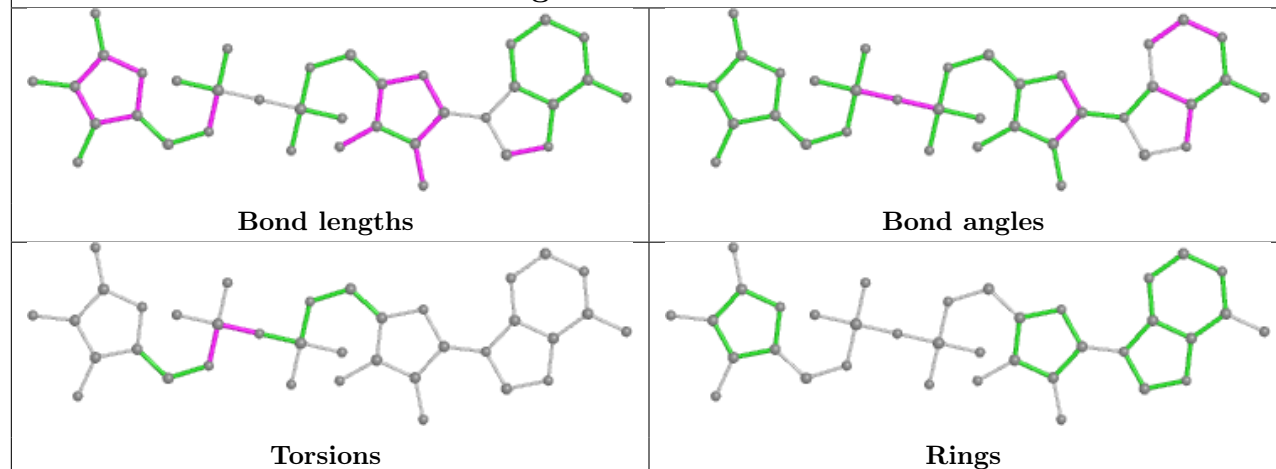
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	402	APR	3	0
3	D	402	APR	2	0
3	J	402	APR	1	0
3	G	402	APR	5	0
3	H	402	APR	1	0
3	A	402	APR	3	0
3	B	402	APR	1	0

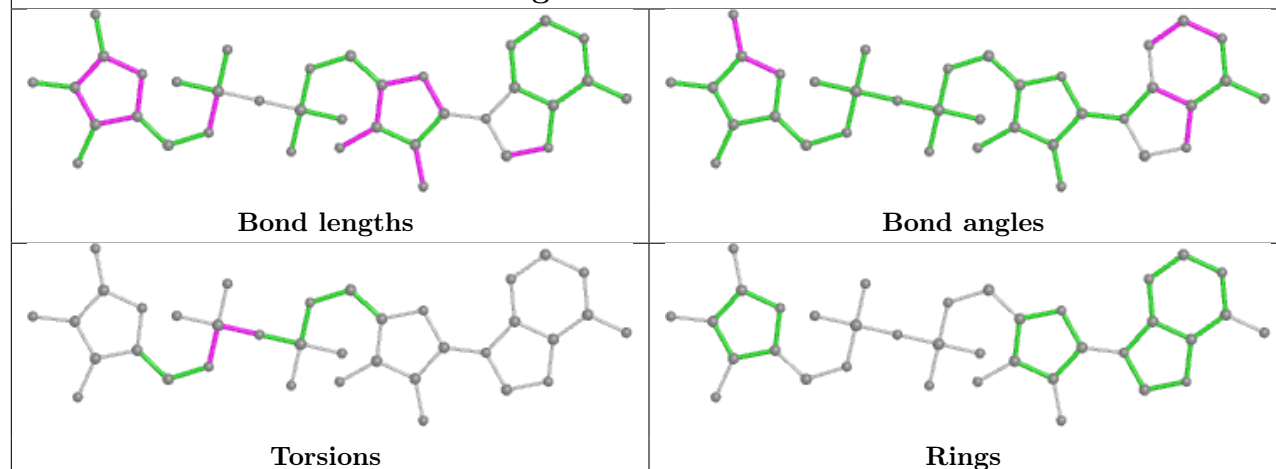
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



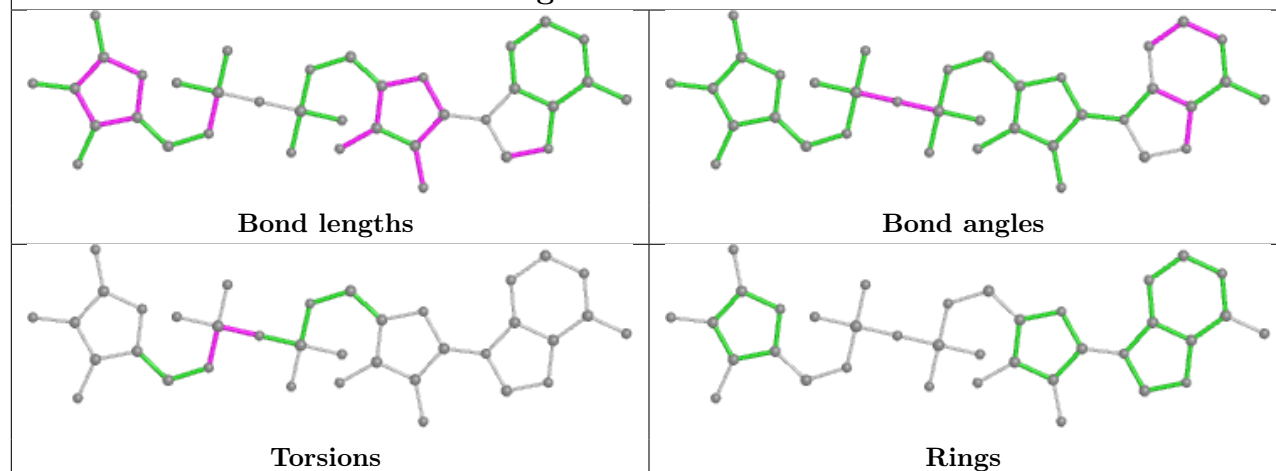
Ligand APR E 402

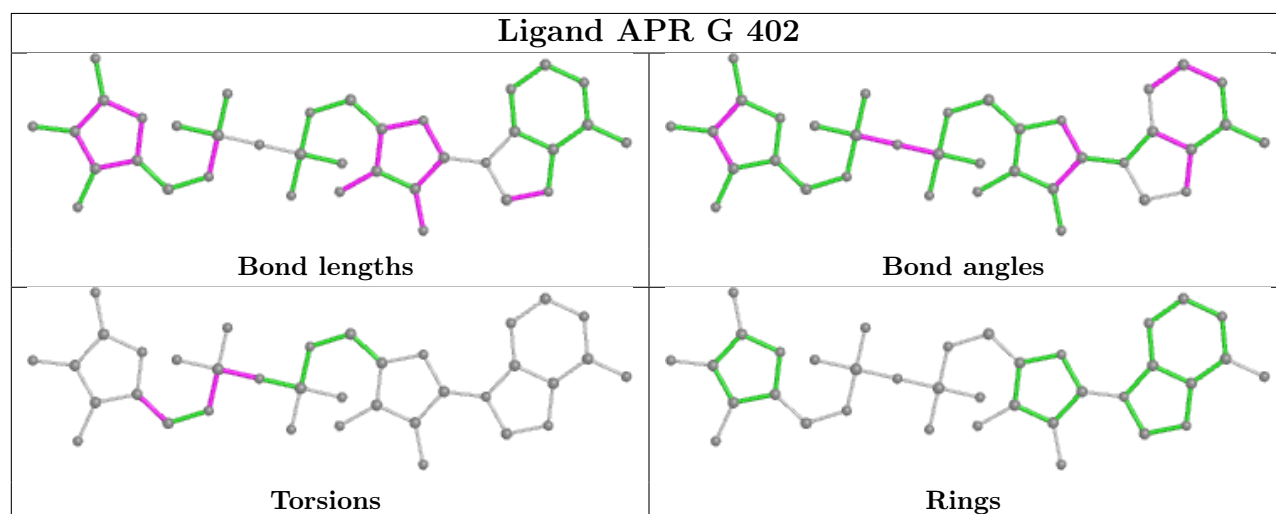
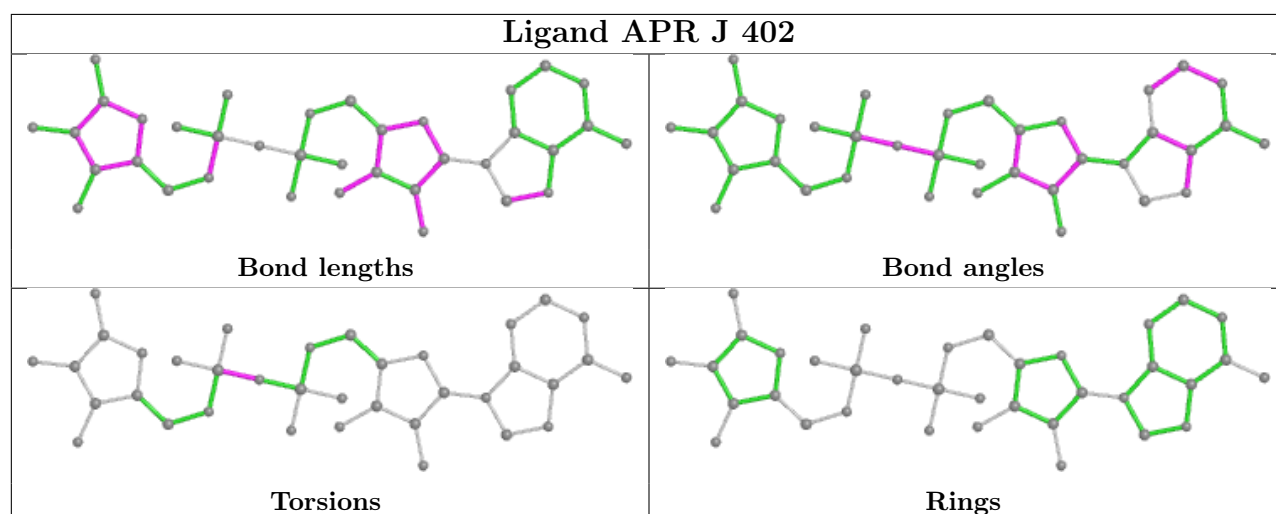
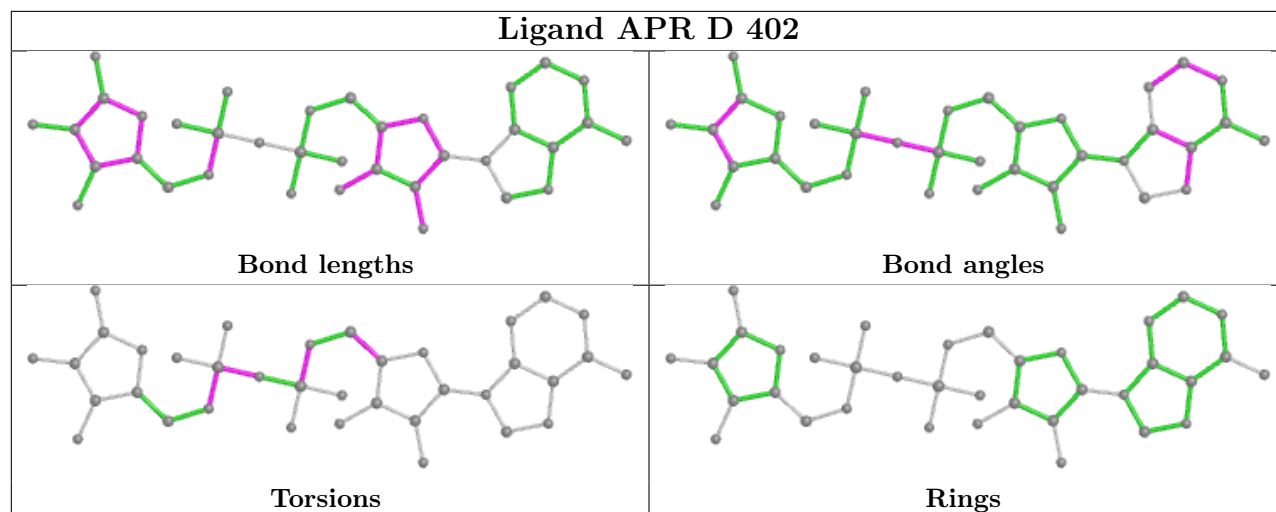


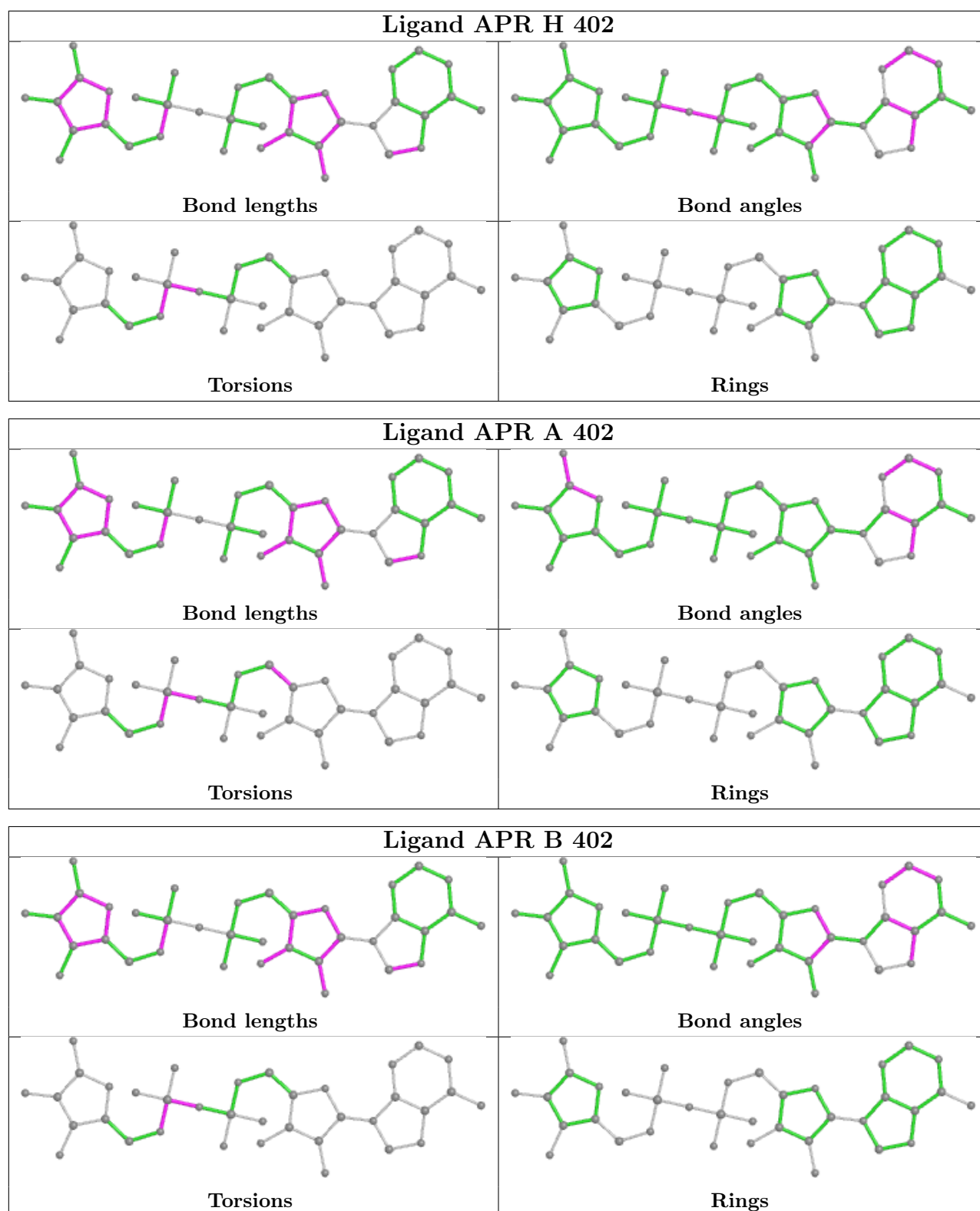
Ligand APR F 402



Ligand APR I 402







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	384/393 (97%)	-0.50	1 (0%) 90 88	18, 28, 42, 66	0
1	B	384/393 (97%)	-0.34	1 (0%) 90 88	17, 31, 54, 66	1 (0%)
1	C	384/393 (97%)	-0.16	3 (0%) 82 79	23, 38, 58, 71	0
1	D	384/393 (97%)	0.08	5 (1%) 74 70	27, 45, 67, 82	0
1	E	384/393 (97%)	0.24	15 (3%) 44 38	27, 47, 81, 100	0
1	F	384/393 (97%)	-0.36	3 (0%) 82 79	19, 31, 50, 69	0
1	G	384/393 (97%)	0.17	17 (4%) 39 33	27, 44, 82, 96	0
1	H	384/393 (97%)	0.24	8 (2%) 63 58	30, 50, 74, 85	0
1	I	384/393 (97%)	-0.05	11 (2%) 54 48	22, 36, 67, 82	0
1	J	384/393 (97%)	-0.22	2 (0%) 87 84	24, 38, 53, 74	0
All	All	3840/3930 (97%)	-0.09	66 (1%) 69 64	17, 38, 70, 100	1 (0%)

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	143	GLY	4.3
1	B	386	LEU	3.8
1	E	161	VAL	3.5
1	H	143	GLY	3.5
1	E	151	PHE	3.3

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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

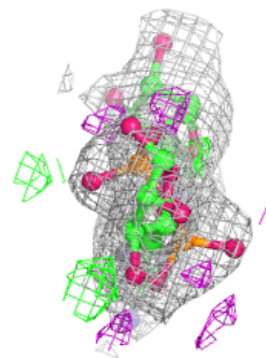
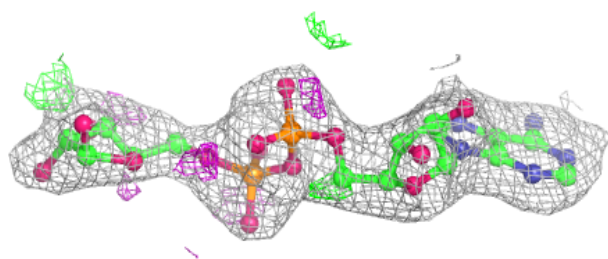
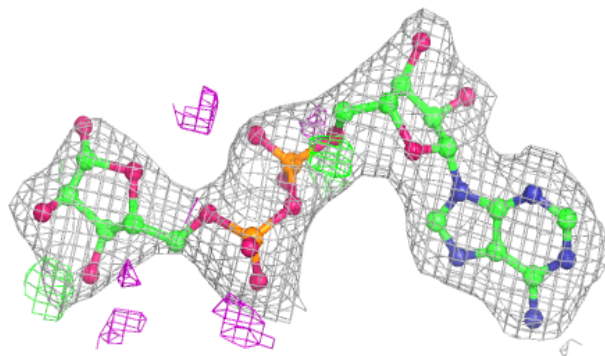
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	APR	G	402	36/36	0.92	0.10	36,45,55,59	0
3	APR	D	402	36/36	0.93	0.09	39,46,62,65	0
3	APR	E	402	36/36	0.94	0.09	34,45,55,57	0
3	APR	H	402	36/36	0.94	0.09	42,49,55,62	0
3	APR	F	402	36/36	0.95	0.08	22,27,32,34	0
3	APR	J	402	36/36	0.95	0.08	26,33,40,42	0
3	APR	A	402	36/36	0.96	0.07	19,25,30,33	0
3	APR	I	402	36/36	0.96	0.08	27,33,40,42	0
3	APR	C	402	36/36	0.96	0.07	28,35,42,44	0
2	MN	I	401	1/1	0.97	0.04	33,33,33,33	0
3	APR	B	402	36/36	0.97	0.07	20,28,37,37	0
2	MN	E	401	1/1	0.98	0.05	42,42,42,42	0
2	MN	D	401	1/1	0.98	0.03	45,45,45,45	0
2	MN	H	401	1/1	0.99	0.03	41,41,41,41	0
2	MN	A	401	1/1	0.99	0.02	23,23,23,23	0
2	MN	B	401	1/1	0.99	0.04	25,25,25,25	0
2	MN	G	401	1/1	0.99	0.03	43,43,43,43	0
2	MN	C	401	1/1	1.00	0.02	33,33,33,33	0
2	MN	J	401	1/1	1.00	0.01	31,31,31,31	0
2	MN	F	401	1/1	1.00	0.03	22,22,22,22	0

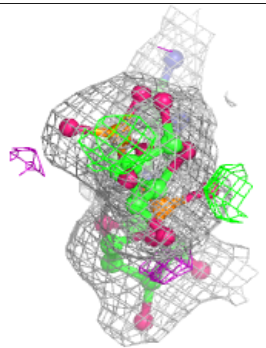
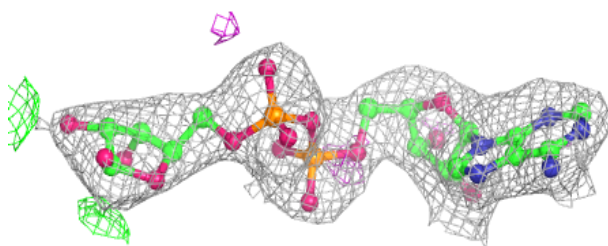
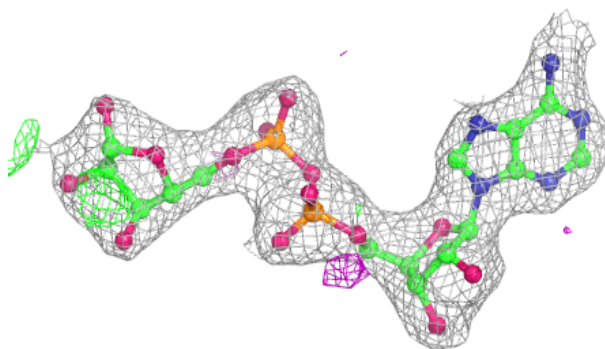
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around APR G 402:

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

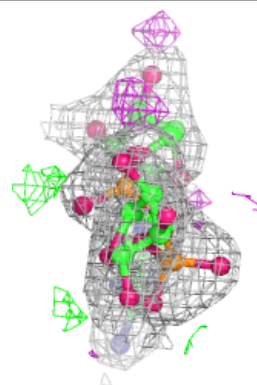
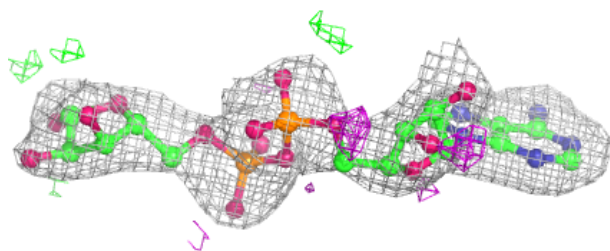
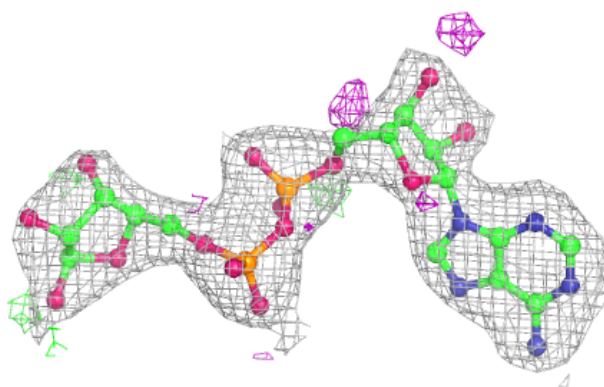
**Electron density around APR D 402:**

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

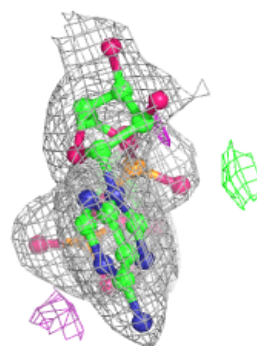
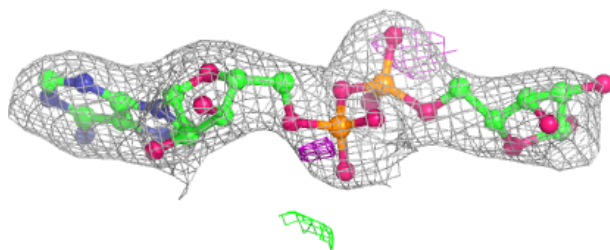
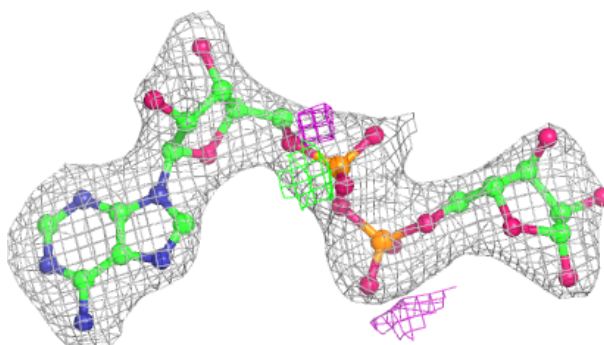


Electron density around APR E 402:

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and green (positive)

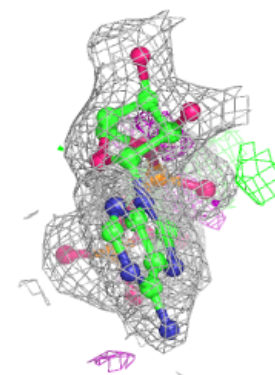
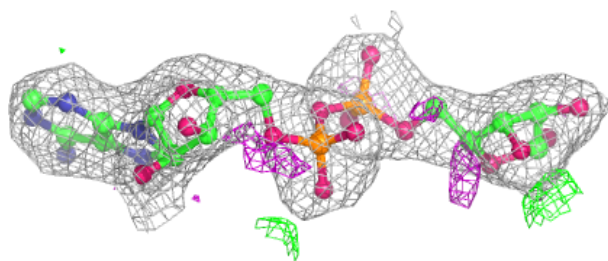
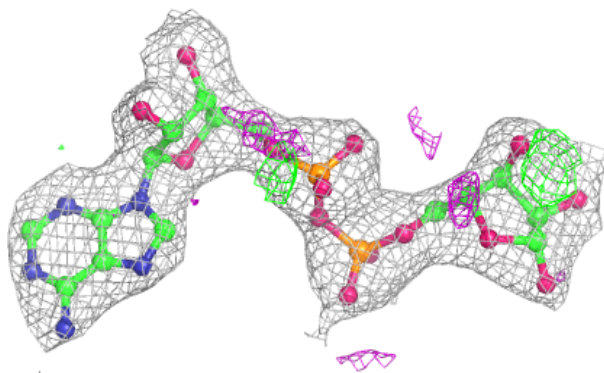
**Electron density around APR H 402:**

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and green (positive)

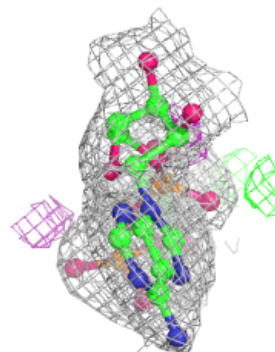
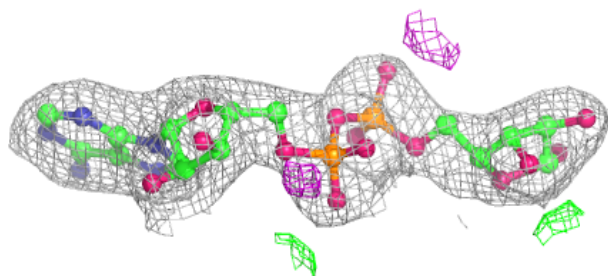
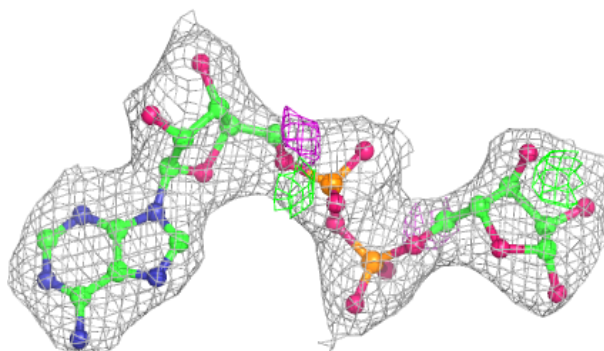


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and green (positive)

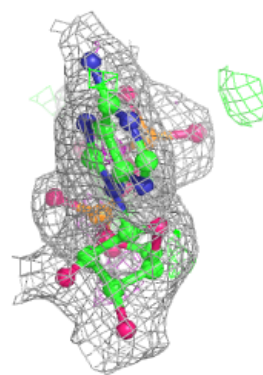
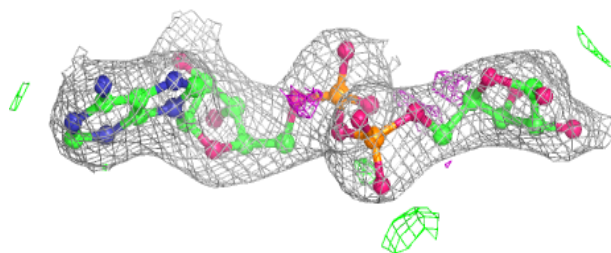
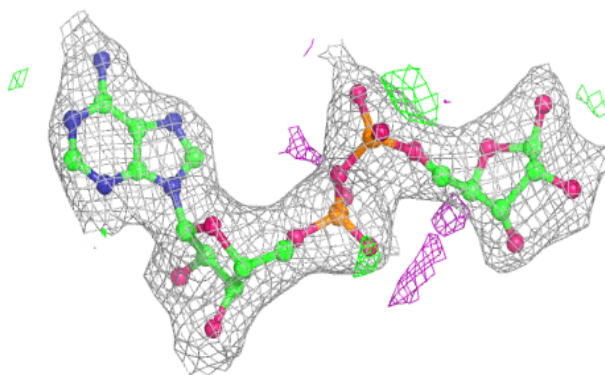
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and green (positive)

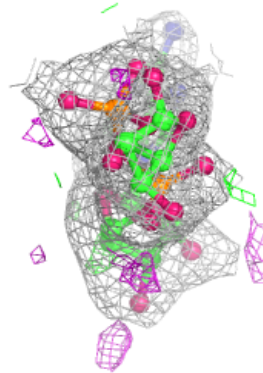
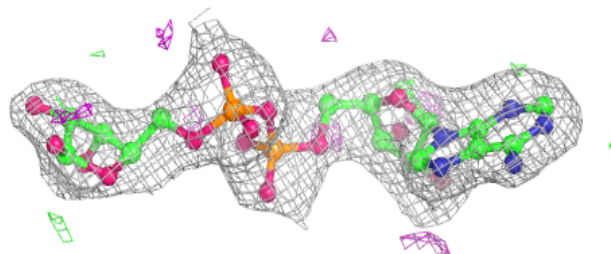
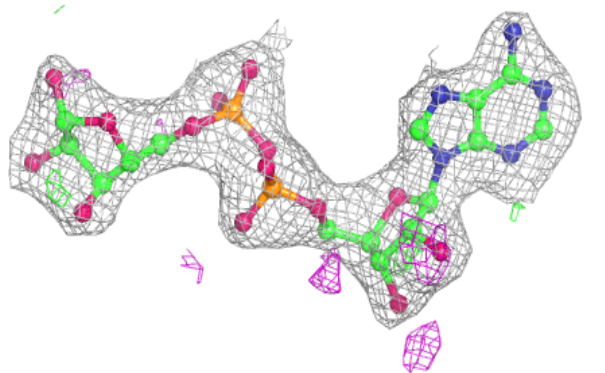


Electron density around APR A 402:

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and green (positive)

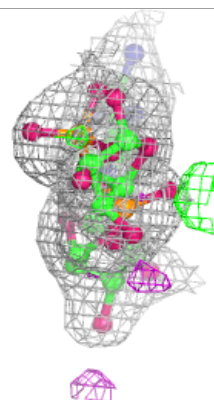
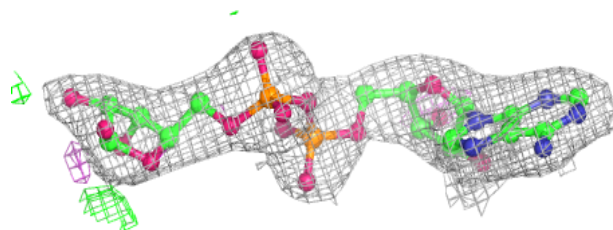
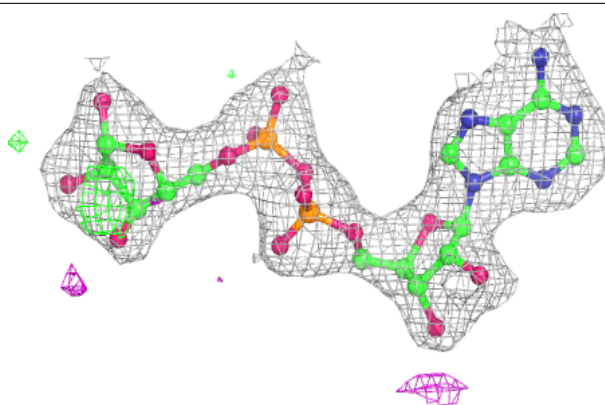
**Electron density around APR I 402:**

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



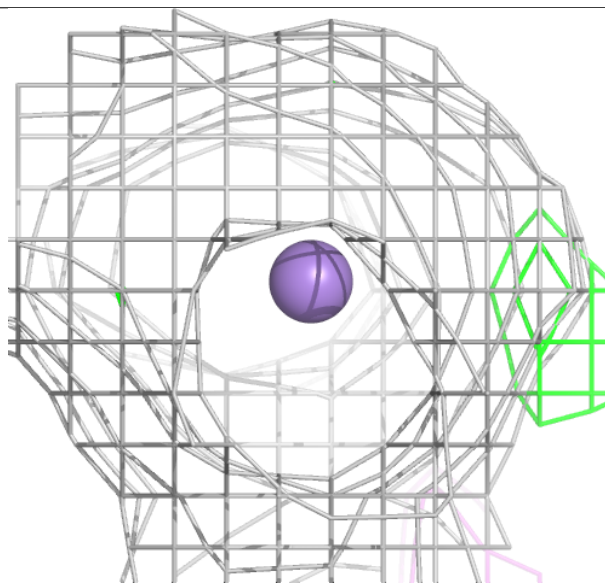
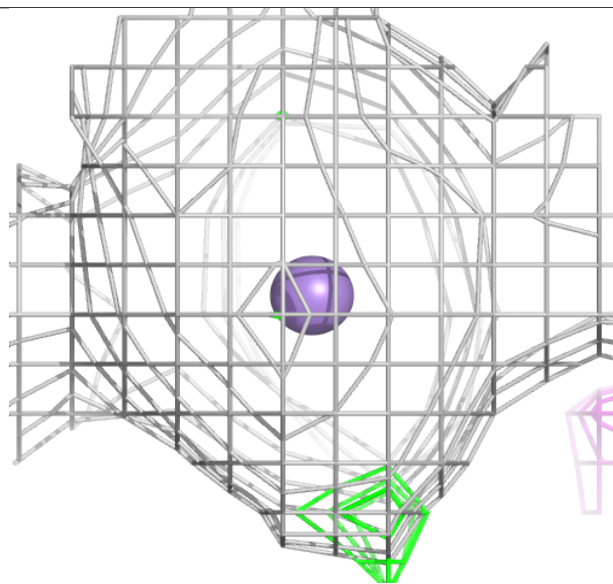
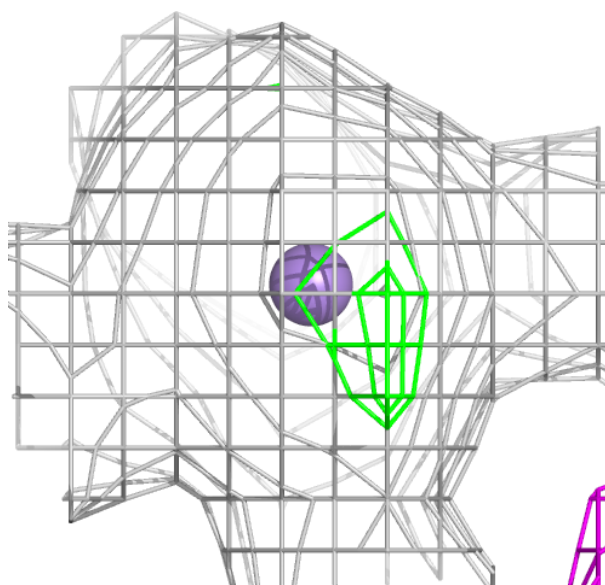
Electron density around APR C 402:

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



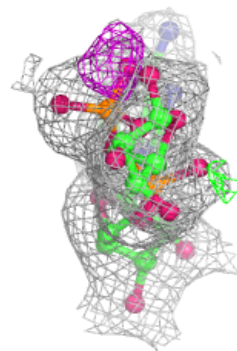
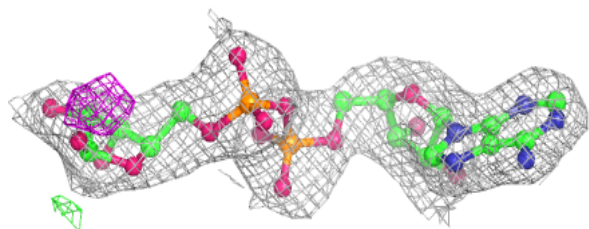
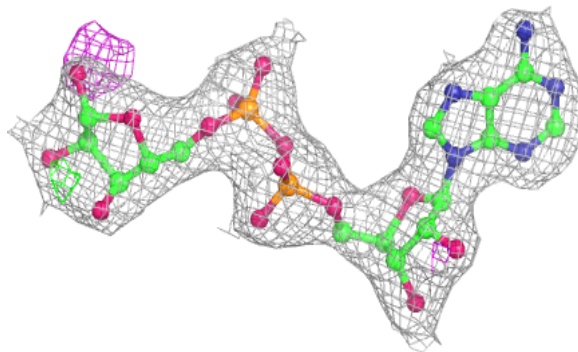
Electron density around MN I 401:

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



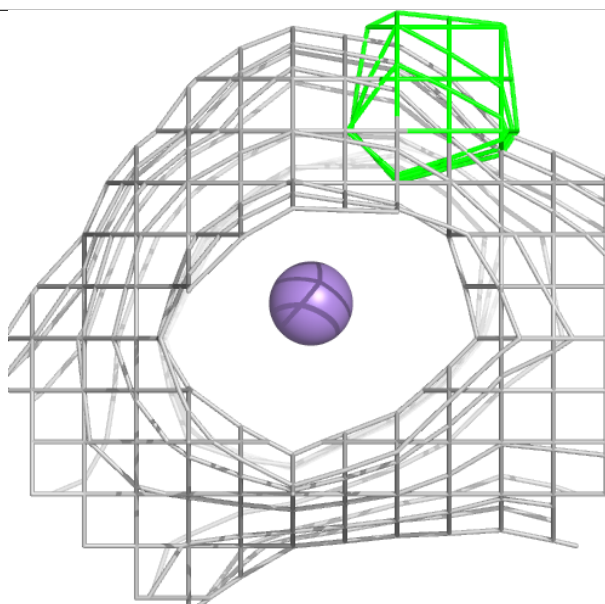
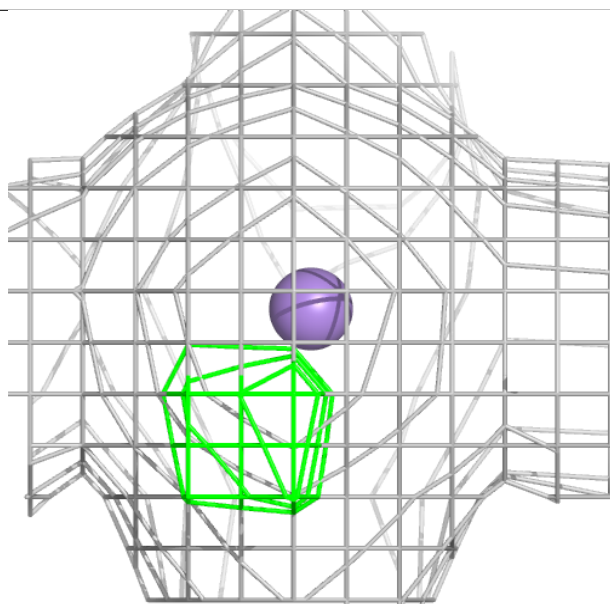
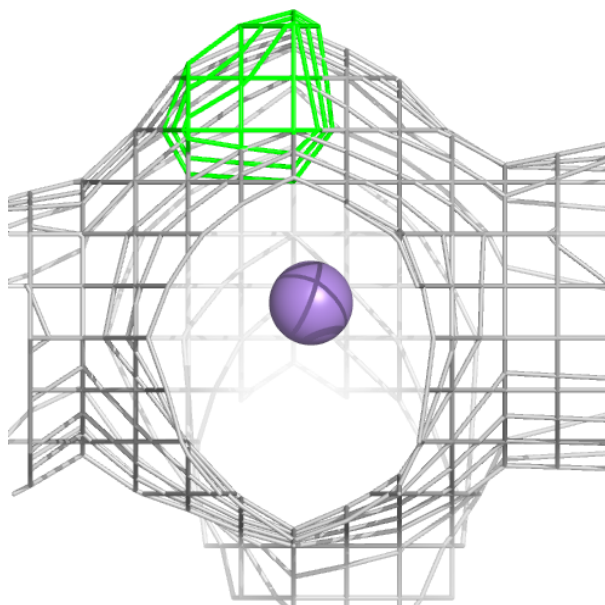
Electron density around APR B 402:

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



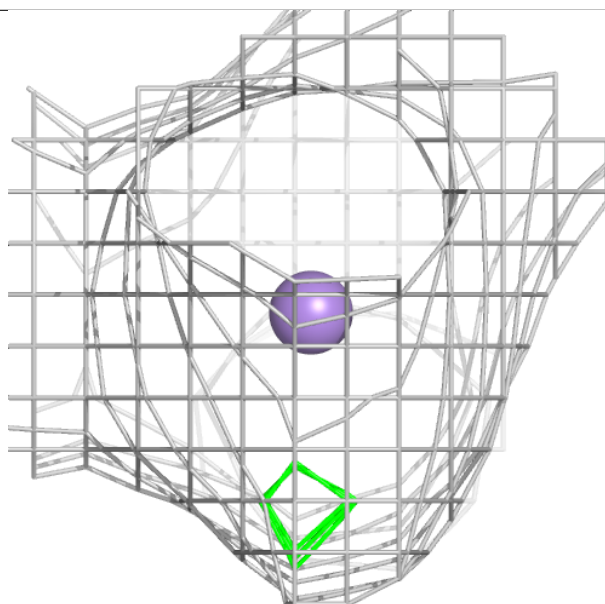
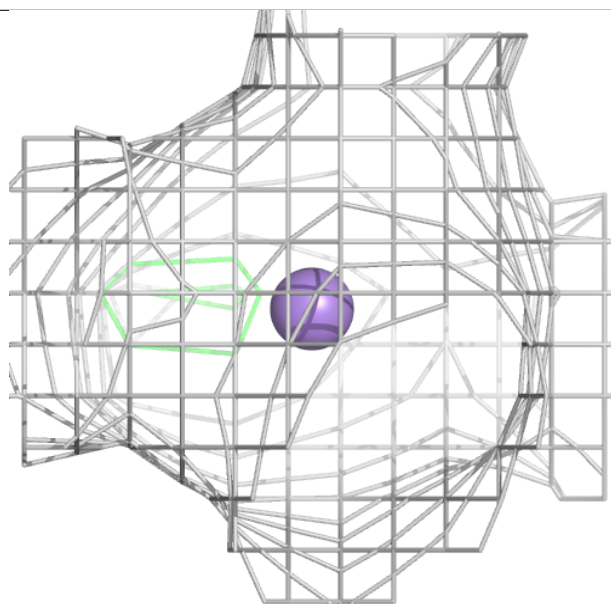
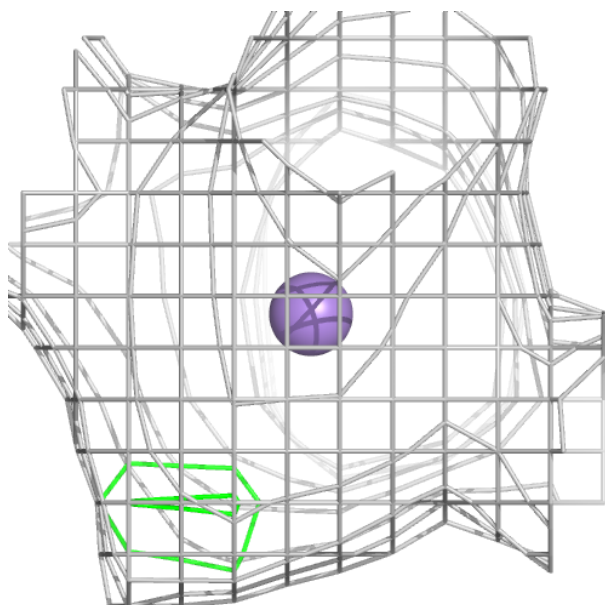
Electron density around MN E 401:

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and green (positive)



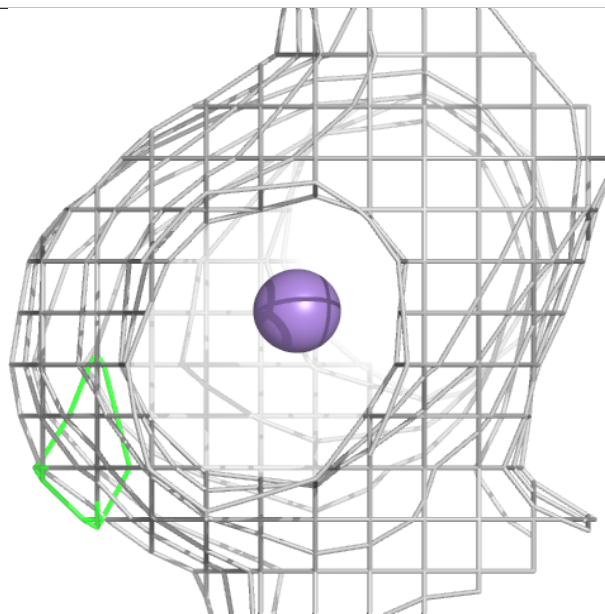
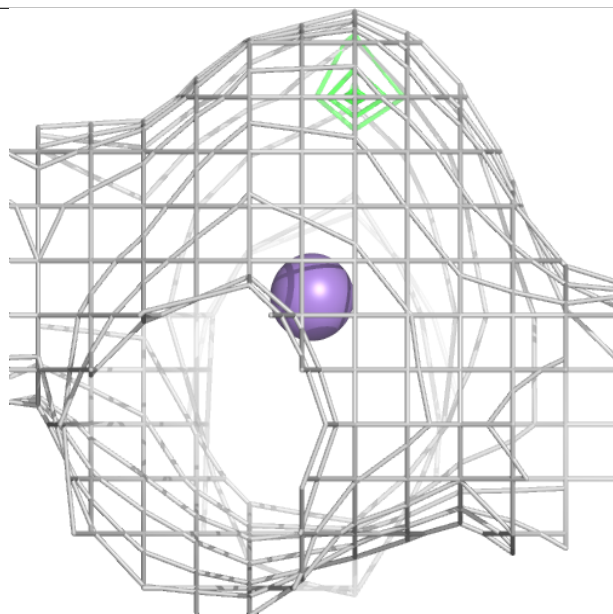
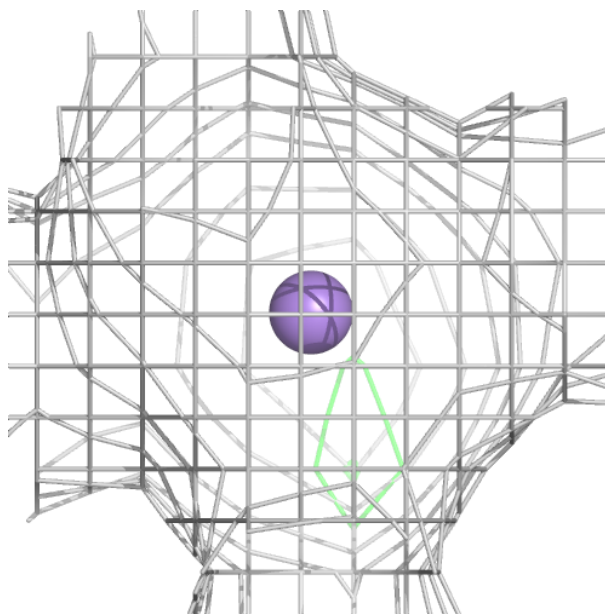
Electron density around MN D 401:

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and green (positive)



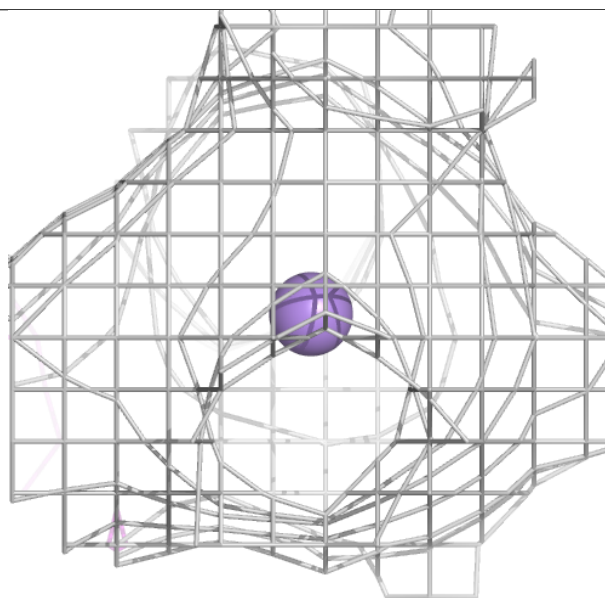
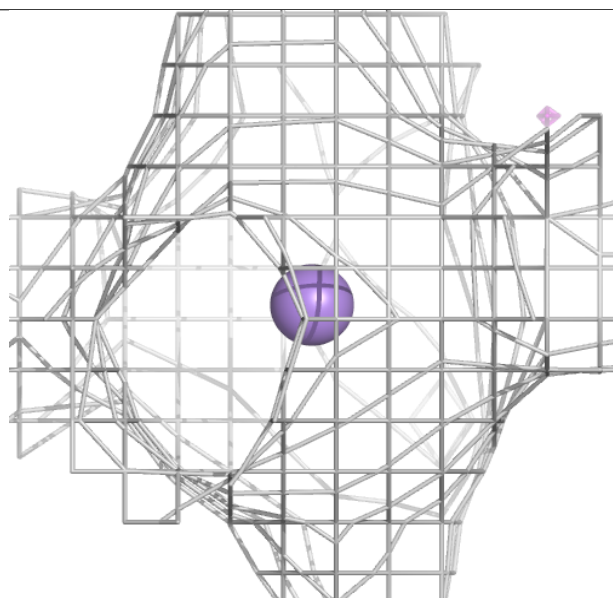
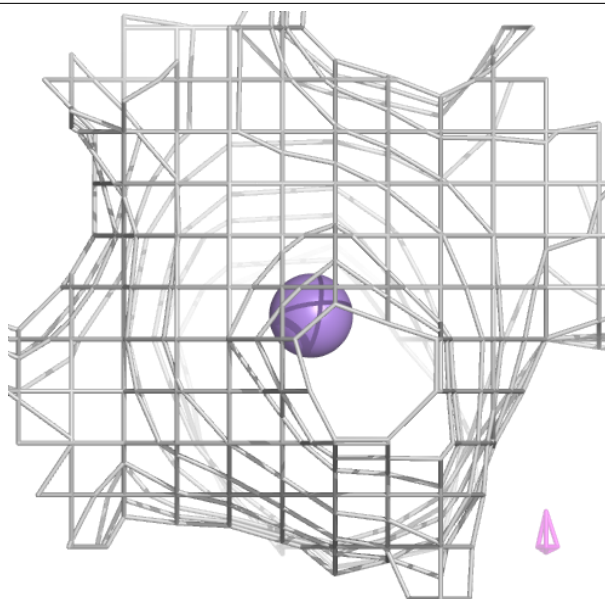
Electron density around MN H 401:

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and green (positive)



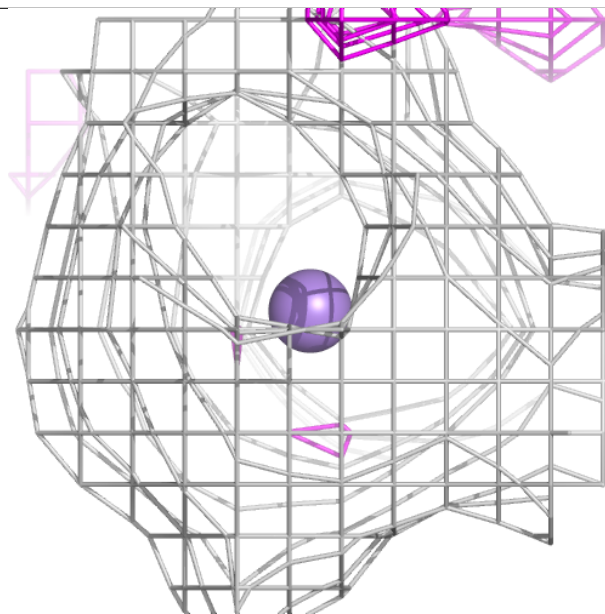
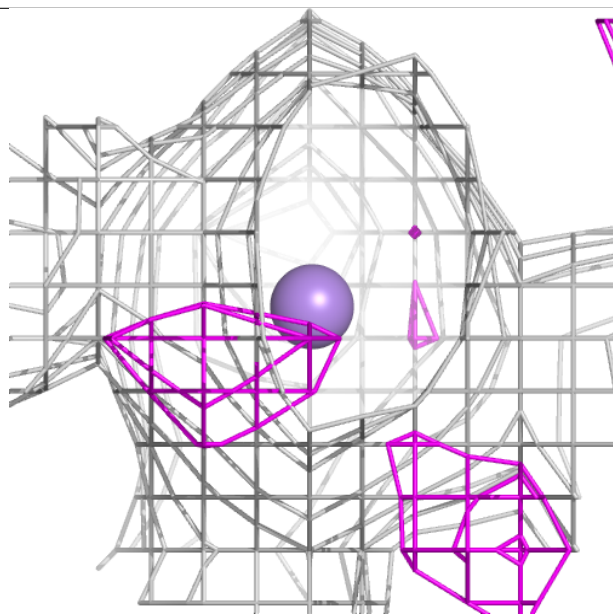
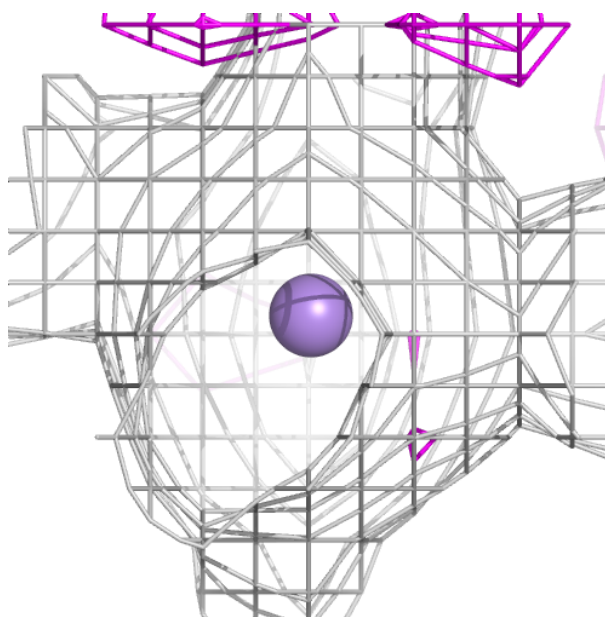
Electron density around MN A 401:

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and green (positive)



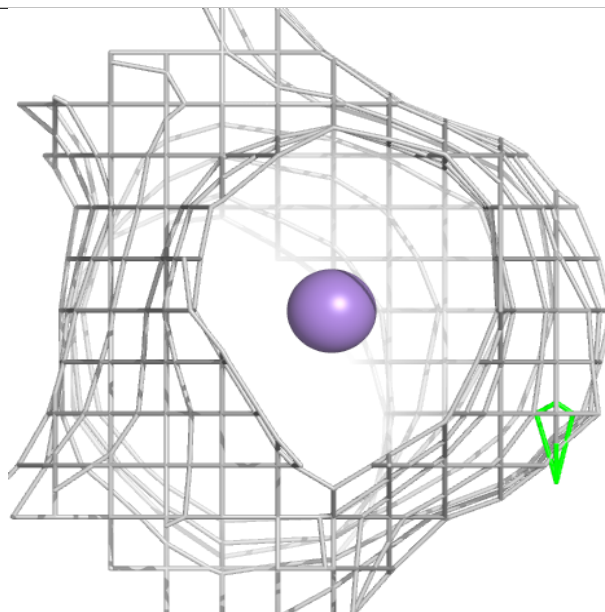
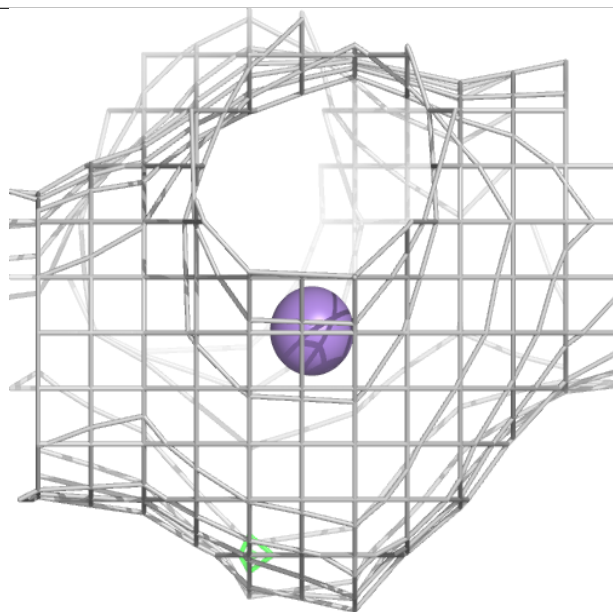
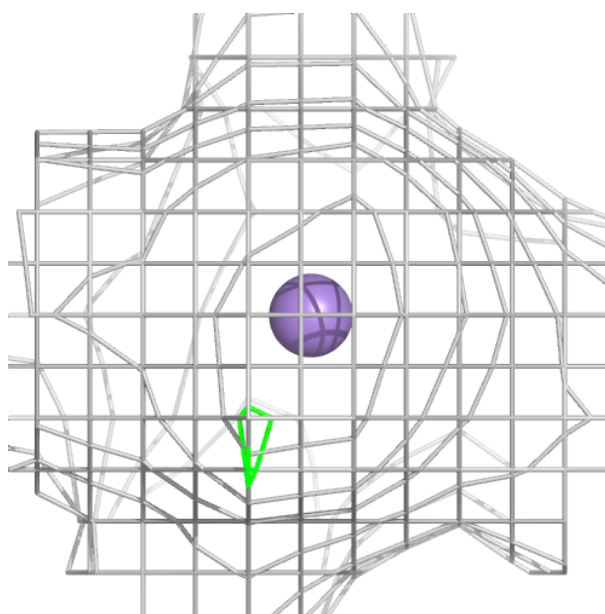
Electron density around MN B 401:

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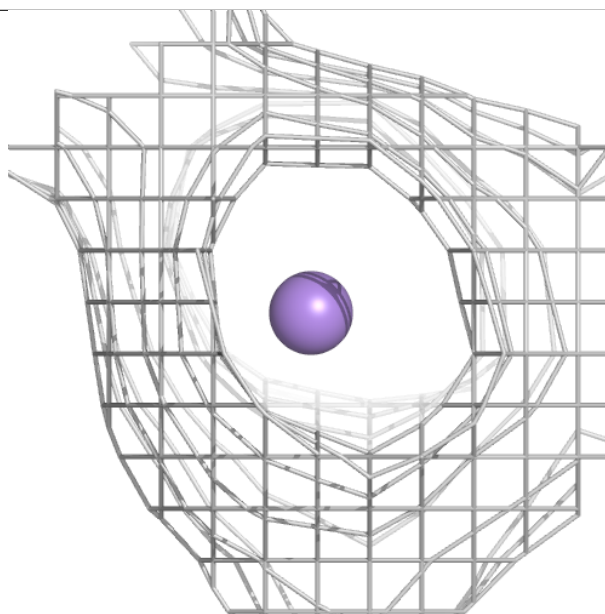
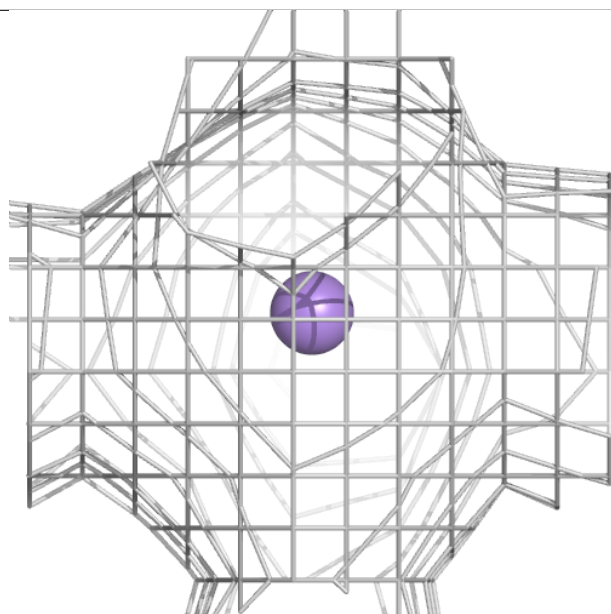
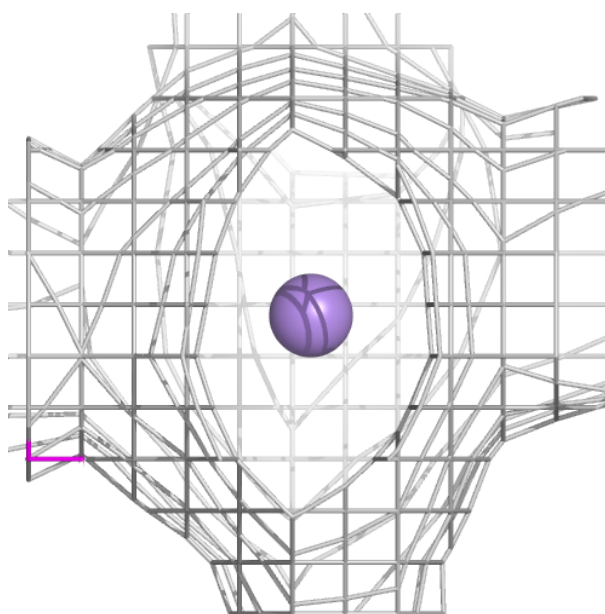
Electron density around MN G 401:

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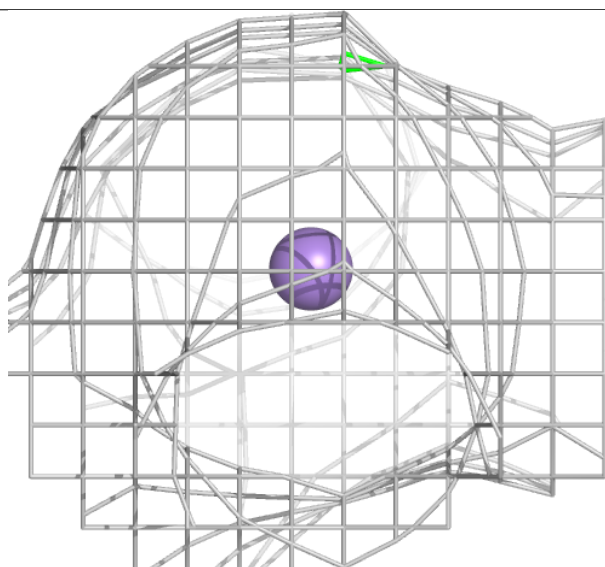
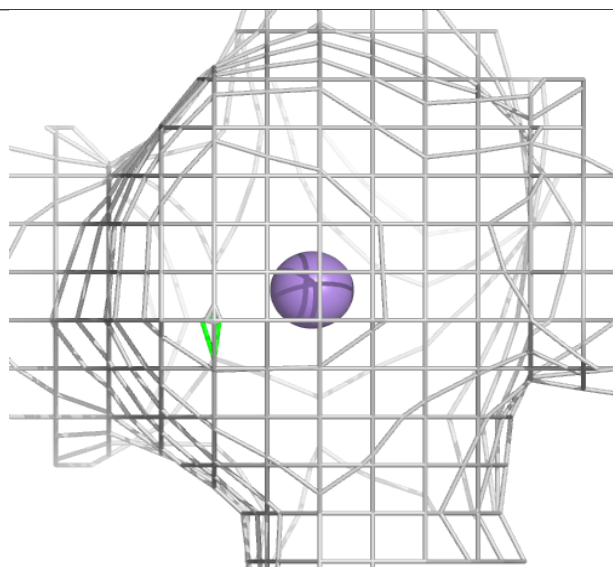
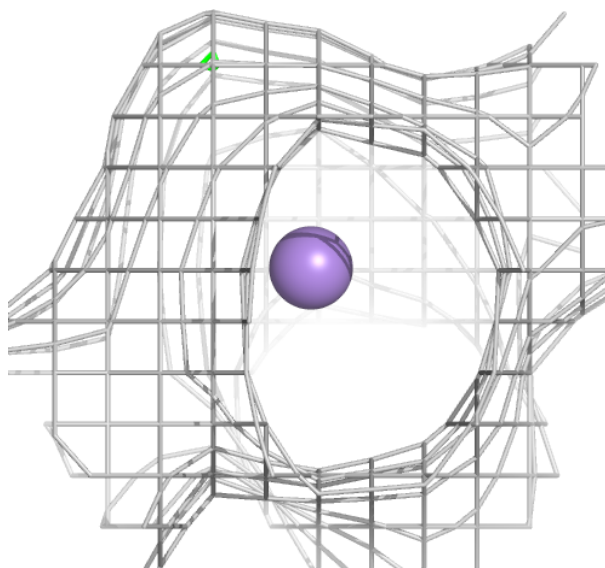
Electron density around MN C 401:

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and green (positive)



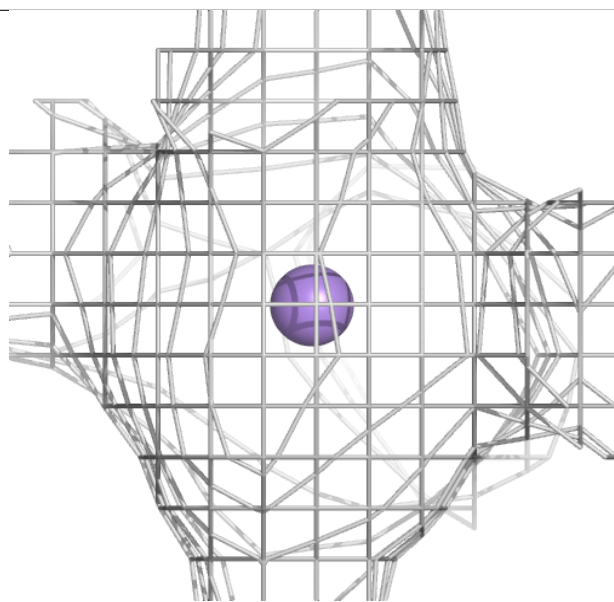
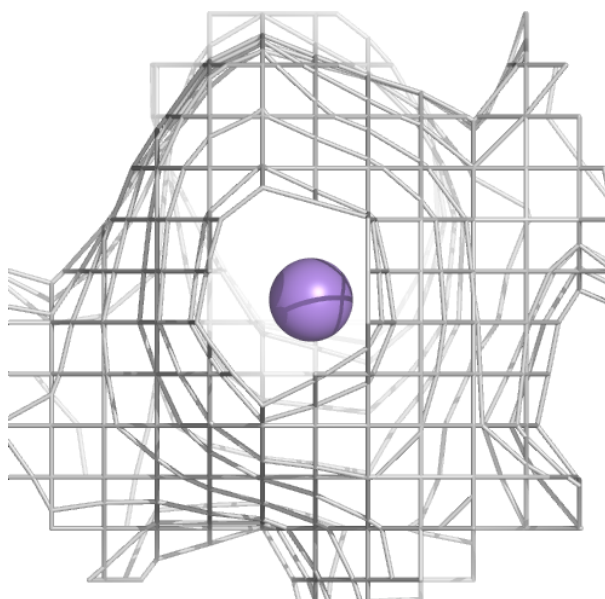
Electron density around MN J 401:

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and green (positive)



Electron density around MN F 401:

$2mF_o-DF_c$ (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.