



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 4, 2026 – 10:38 PM UTC

PDB ID : 9RG2 / pdb\_00009rg2  
Title : Unspecific peroxygenase from *Psathyrella aberdarensis*, Grogu variant, in complex with alpha-damascone  
Authors : Fernandez-Garcia, A.; Sanz-Aparicio, J.  
Deposited on : 2025-06-05  
Resolution : 1.80 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 Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

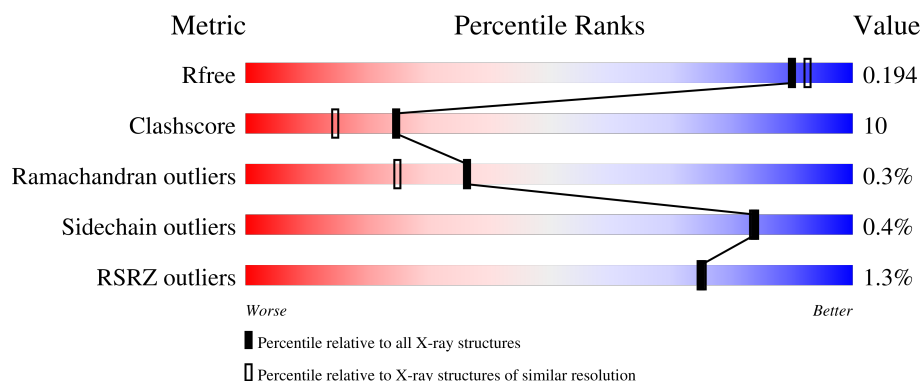
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
$R_{free}$	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	334	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> <span>%</span> <div style="width: 92%; height: 10px; background-color: green;"></div> <span>7%</span> </div> </div>
1	B	334	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> <span>%</span> <div style="width: 90%; height: 10px; background-color: green;"></div> <span>10%</span> </div> </div>
2	C	2	<div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="text-align: center;">100%</div> </div>
2	D	2	<div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="text-align: center;">100%</div> </div>

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
13	PEG	B	413	-	-	X	-
4	GOL	B	410	-	-	X	-
6	NAG	B	401	-	-	X	-
6	NAG	B	408	-	-	X	-

## 2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 6476 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 Heme-thiolate peroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	7	0
			2620	1675	440	498	7			
1	B	334	Total	C	N	O	S	0	5	0
			2607	1667	436	497	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	ALA	SER	engineered mutation	UNP A0A4Q2DF39
A	79	ILE	LEU	engineered mutation	UNP A0A4Q2DF39
A	252	LEU	ALA	engineered mutation	UNP A0A4Q2DF39
B	61	ALA	SER	engineered mutation	UNP A0A4Q2DF39
B	79	ILE	LEU	engineered mutation	UNP A0A4Q2DF39
B	252	LEU	ALA	engineered mutation	UNP A0A4Q2DF39

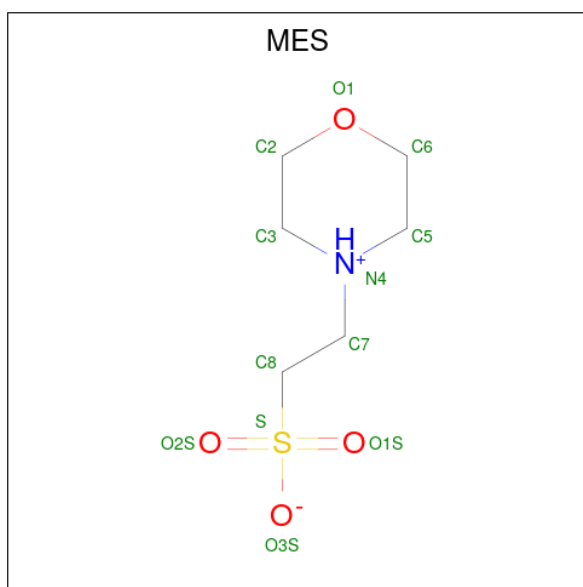
- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

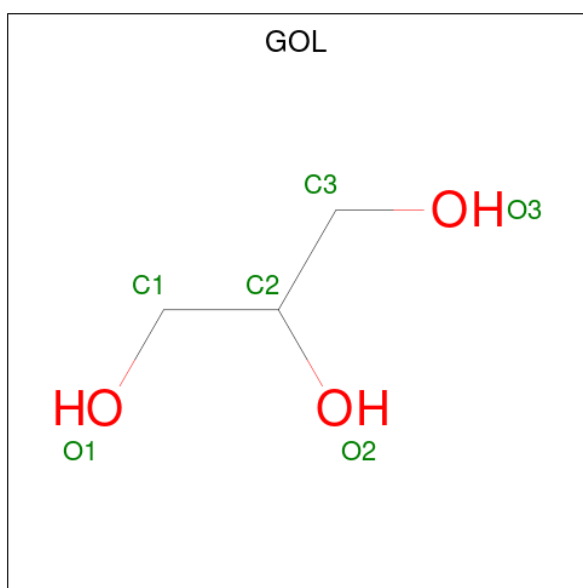
- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula:  $C_3H_8O_3$ ).



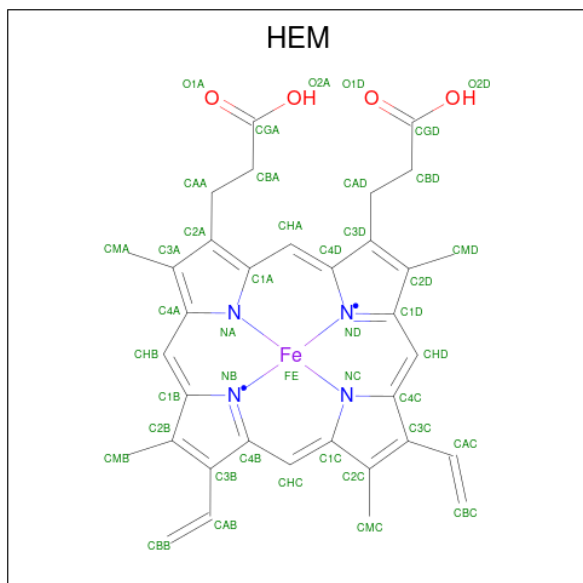
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ) (labeled as "Ligand of Interest" by depositor).



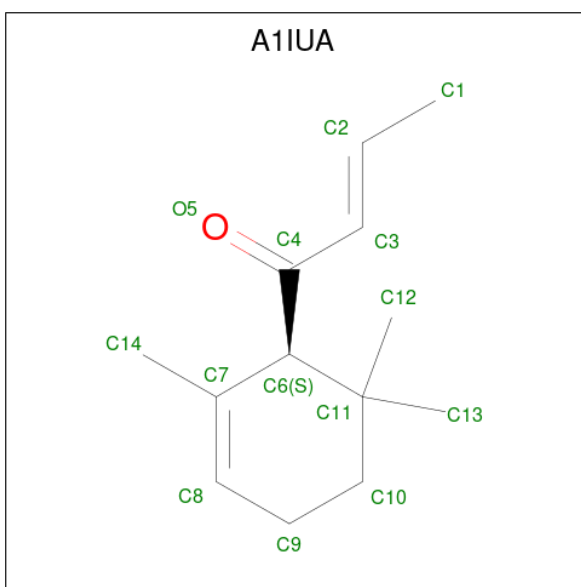
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).



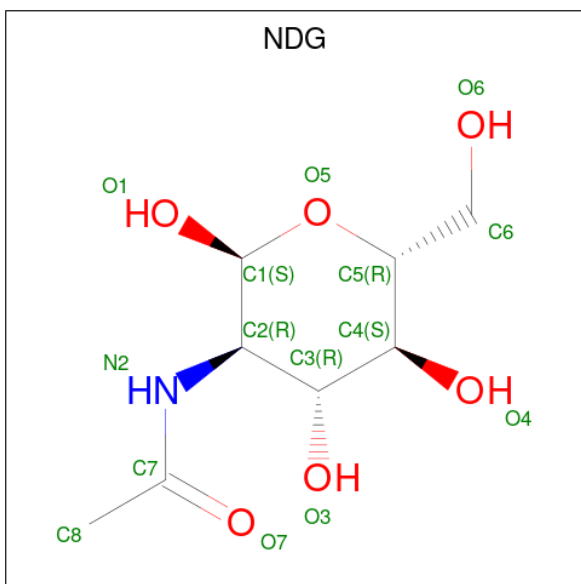
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is alpha-damascone (CCD ID: A1IUUA) (formula: C<sub>13</sub>H<sub>20</sub>O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			14	13	1		
7	B	1	Total	C	O	0	0
			14	13	1		

- Molecule 8 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (CCD ID: NDG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		

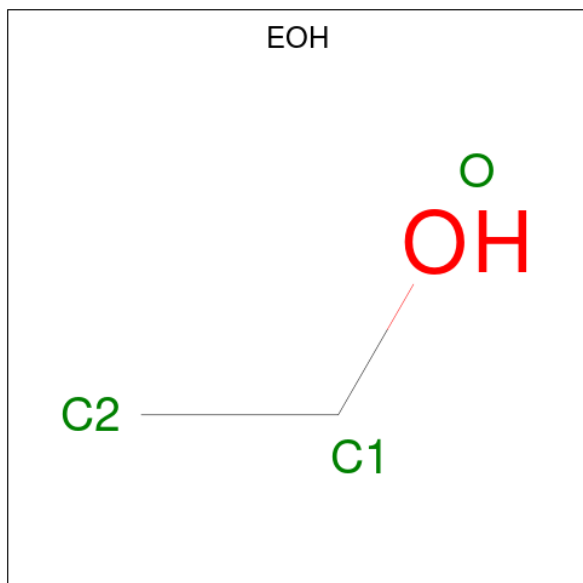
- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	10	Total	Zn	0	0
			10	10		
9	B	5	Total	Zn	0	0
			5	5		

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	Mg	0	0
			1	1		
10	B	1	Total	Mg	0	0
			1	1		

- Molecule 11 is ETHANOL (CCD ID: EOH) (formula: C<sub>2</sub>H<sub>6</sub>O).



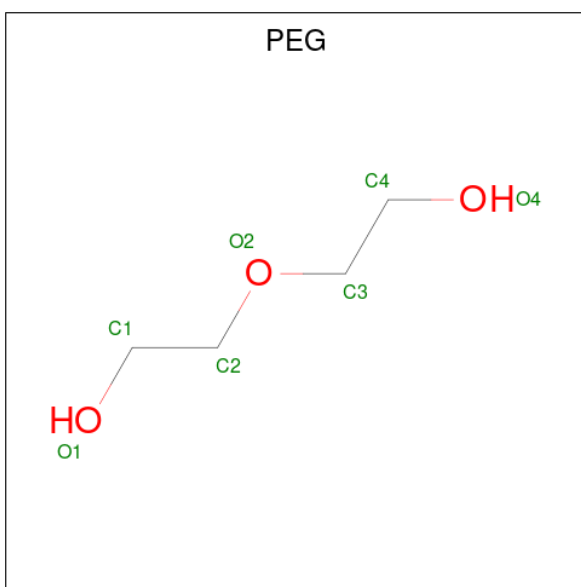
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			3	2	1		
11	B	1	Total	C	O	0	0
			3	2	1		

- Molecule 12 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	O	P	0	0
			5	4	1		
12	B	1	Total	O	P	0	0
			5	4	1		
12	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 13 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	413	Total	O	0	0
			413	413		
14	B	440	Total	O	0	0
			440	440		

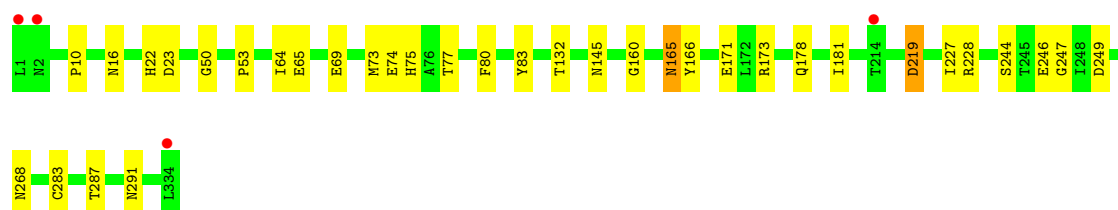
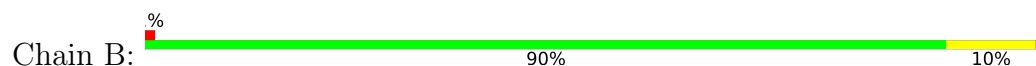
### 3 Residue-property plots [i](#)

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: Heme-thiolate peroxidase



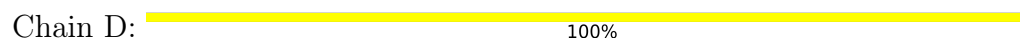
- Molecule 1: Heme-thiolate peroxidase



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.33Å 76.33Å 272.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.46 – 1.80 47.46 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.46-1.80) 99.9 (47.46-1.80)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.92 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, $R_{free}$	0.155 , 0.185 0.164 , 0.194	Depositor DCC
$R_{free}$ test set	4074 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.7	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.053 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6476	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% 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: EOH, PEG, NDG, ZN, MES, HEM, PO4, MG, A1IUA, GOL, NAG

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	0.58	0/2717	0.91	1/3705 (0.0%)
1	B	0.55	0/2698	0.90	2/3680 (0.1%)
All	All	0.56	0/5415	0.90	3/7385 (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

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	219	ASP	CA-CB-CG	5.68	118.28	112.60
1	B	219	ASP	CA-CB-CG	5.61	118.21	112.60
1	B	165	ASN	CB-CG-ND2	-5.09	108.77	116.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	263	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	2620	0	2496	34	0
1	B	2607	0	2477	62	0
2	C	28	0	25	0	0
2	D	28	0	25	0	0
3	A	12	0	13	0	0
3	B	12	0	13	0	0
4	A	6	0	8	1	0
4	B	18	0	24	7	0
5	A	43	0	30	1	0
5	B	43	0	30	2	0
6	A	28	0	26	9	0
6	B	84	0	76	26	0
7	A	14	0	0	0	0
7	B	14	0	0	1	0
8	A	14	0	12	6	0
9	A	10	0	0	0	0
9	B	5	0	0	1	0
10	A	1	0	0	0	0
10	B	1	0	0	0	0
11	A	3	0	6	0	0
11	B	3	0	6	0	0
12	A	5	0	0	0	0
12	B	10	0	0	0	0
13	B	14	0	20	8	0
14	A	413	0	0	16	0
14	B	440	0	0	25	0
All	All	6476	0	5287	107	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 10.

The worst 5 of 107 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:B:145:ASN:ND2	6:B:405:NAG:C1	1.69	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:ASN:HD21	6:A:406:NAG:C1	0.90	1.50
1:B:16:ASN:ND2	6:B:403:NAG:C1	1.68	1.49
1:A:16:ASN:ND2	6:A:404:NAG:C1	1.75	1.49
1:A:291:ASN:ND2	6:A:406:NAG:C1	1.72	1.46

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	339/334 (102%)	325 (96%)	12 (4%)	2 (1%)	21	11
1	B	337/334 (101%)	323 (96%)	12 (4%)	2 (1%)	21	11
All	All	676/668 (101%)	648 (96%)	24 (4%)	4 (1%)	36	11

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	244[A]	SER
1	A	244[B]	SER
1	B	244[A]	SER
1	B	244[B]	SER

### 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	281/274 (103%)	280 (100%)	1 (0%)	84	83
1	B	279/274 (102%)	278 (100%)	1 (0%)	84	83
All	All	560/548 (102%)	558 (100%)	2 (0%)	84	83

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	173	ARG
1	B	173	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	241	GLN
1	B	234	GLN
1	A	291	ASN
1	A	241	GLN
1	B	165	ASN

### 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 ⓘ

4 monosaccharides 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
2	NAG	C	1	2	14,14,15	0.44	0	17,19,21	1.16	2 (11%)
2	NAG	C	2	2	14,14,15	0.31	0	17,19,21	1.12	1 (5%)
2	NAG	D	1	2	14,14,15	0.45	0	17,19,21	1.42	2 (11%)
2	NAG	D	2	2	14,14,15	0.43	0	17,19,21	0.78	1 (5%)

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
2	NAG	C	1	2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	NAG	D	1	2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NAG	O5-C1-C2	-3.99	105.12	111.29
2	C	2	NAG	C1-C2-N2	3.44	115.86	110.43
2	C	1	NAG	O5-C1-C2	3.29	116.38	111.29
2	D	1	NAG	C1-O5-C5	-2.83	108.39	112.19
2	D	2	NAG	C2-N2-C7	2.42	126.15	122.90

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

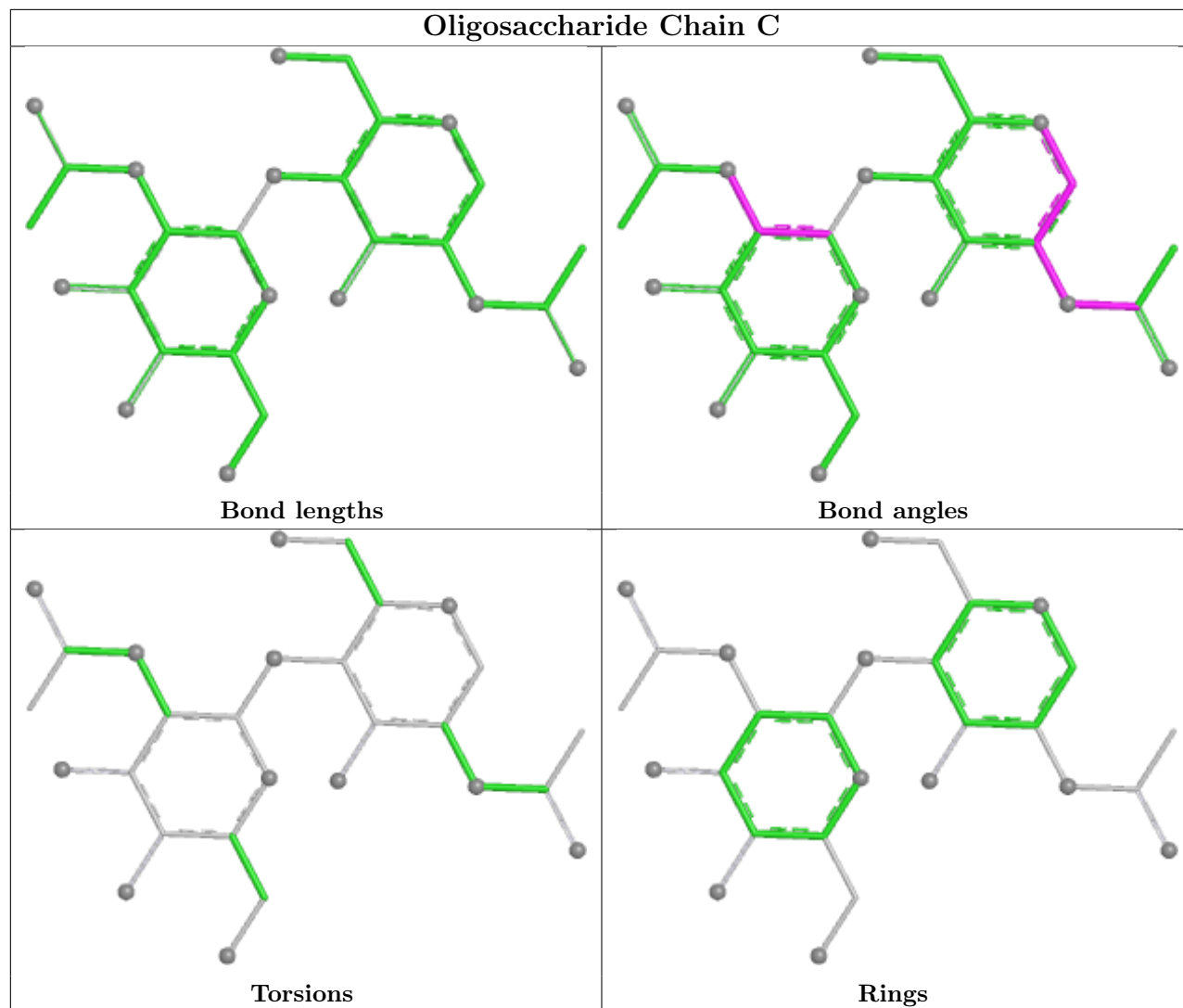
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
2	D	2	NAG	O5-C5-C6-O6

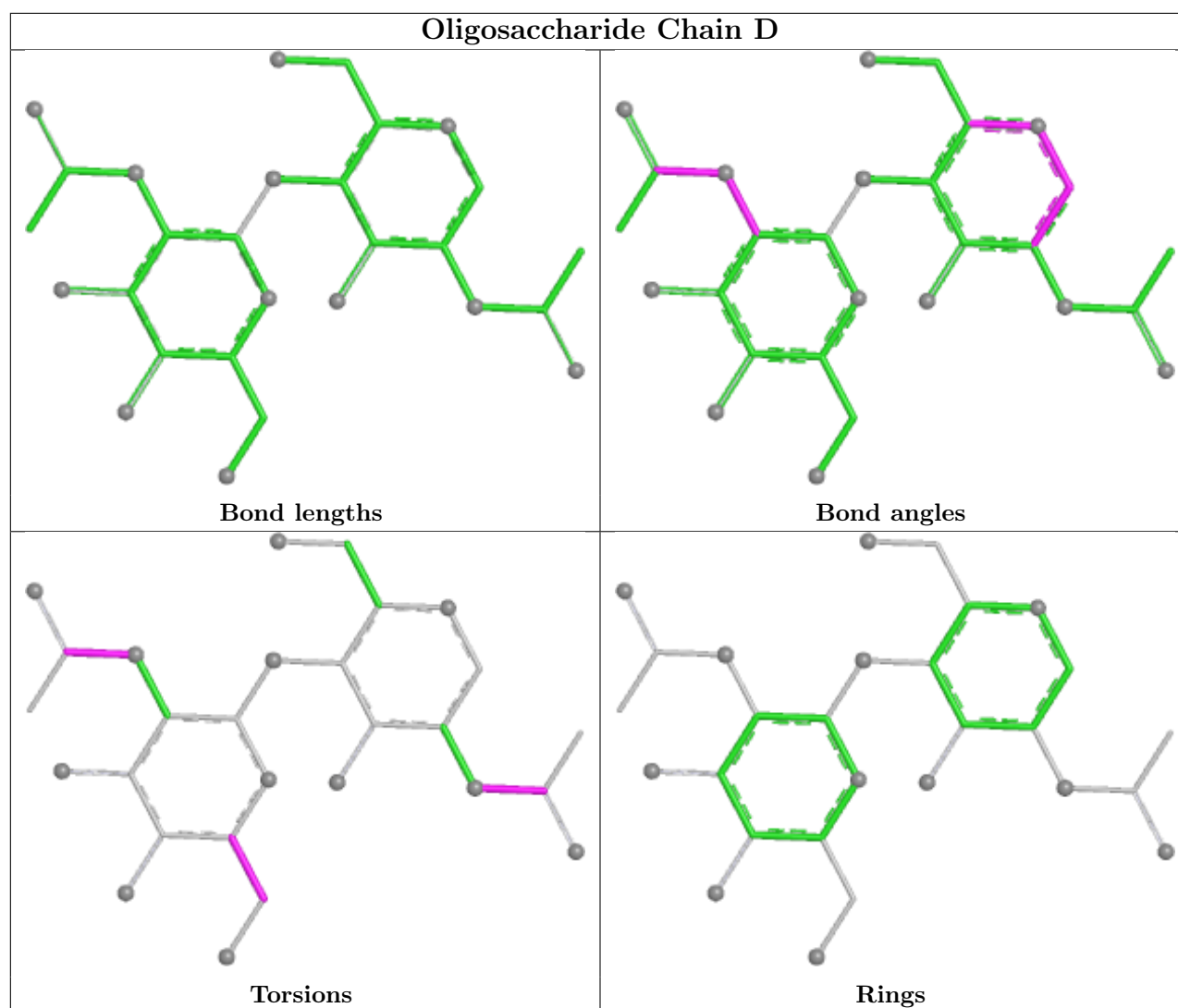
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for oligosaccharide.





## 5.6 Ligand geometry [i](#)

Of 43 ligands modelled in this entry, 17 are monoatomic - leaving 26 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	HEM	B	404	1,14,10	50,50,50	1.43	7 (14%)	67,82,82	1.72	15 (22%)
12	PO4	A	420	-	4,4,4	2.13	1 (25%)	6,6,6	0.51	0
13	PEG	B	411	-	6,6,6	0.36	0	5,5,5	0.09	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	HEM	A	403	1,14,10	50,50,50	1.50	6 (12%)	67,82,82	1.52	14 (20%)
6	NAG	B	405	6	14,14,15	0.39	0	17,19,21	1.31	3 (17%)
4	GOL	B	415	-	5,5,5	0.15	0	5,5,5	0.45	0
6	NAG	A	404	-	14,14,15	0.43	0	17,19,21	1.11	1 (5%)
7	A1IUA	A	405	-	13,14,14	0.68	0	13,20,20	0.72	1 (7%)
6	NAG	B	406	6	14,14,15	0.46	0	17,19,21	1.29	3 (17%)
6	NAG	A	406	-	14,14,15	0.39	0	17,19,21	1.36	2 (11%)
4	GOL	B	410	-	5,5,5	0.30	0	5,5,5	0.52	0
4	GOL	B	414	-	5,5,5	0.17	0	5,5,5	0.46	0
6	NAG	B	403	-	14,14,15	0.39	0	17,19,21	2.43	4 (23%)
12	PO4	B	423	-	4,4,4	1.94	1 (25%)	6,6,6	0.72	0
12	PO4	B	422	-	4,4,4	1.84	1 (25%)	6,6,6	0.77	0
11	EOH	A	419	-	2,2,2	0.32	0	1,1,1	0.03	0
6	NAG	B	401	6	14,14,15	0.84	0	17,19,21	1.63	3 (17%)
11	EOH	B	412	-	2,2,2	0.45	0	1,1,1	0.07	0
7	A1IUA	B	409	-	13,14,14	0.71	1 (7%)	13,20,20	0.77	0
3	MES	A	401	-	12,12,12	0.87	0	15,16,16	0.84	0
3	MES	B	402	-	12,12,12	0.93	0	15,16,16	0.68	0
4	GOL	A	402	-	5,5,5	0.42	0	5,5,5	0.49	0
13	PEG	B	413	-	6,6,6	0.41	0	5,5,5	0.24	0
8	NDG	A	407	-	14,14,15	0.43	0	17,19,21	1.26	2 (11%)
6	NAG	B	407	6	14,14,15	0.41	0	17,19,21	1.37	3 (17%)
6	NAG	B	408	-	14,14,15	0.43	0	17,19,21	1.16	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	HEM	B	404	1,14,10	-	2/14/54/54	-
13	PEG	B	411	-	-	1/4/4/4	-
5	HEM	A	403	1,14,10	-	2/14/54/54	-
6	NAG	B	405	6	-	4/6/23/26	0/1/1/1
4	GOL	B	415	-	-	4/4/4/4	-
6	NAG	A	404	-	-	1/6/23/26	0/1/1/1
7	A1IUA	A	405	-	-	0/6/24/24	0/1/1/1
6	NAG	B	406	6	-	5/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	A	406	-	-	1/6/23/26	0/1/1/1
4	GOL	B	410	-	-	1/4/4/4	-
4	GOL	B	414	-	-	2/4/4/4	-
6	NAG	B	403	-	-	2/6/23/26	0/1/1/1
6	NAG	B	401	6	-	1/6/23/26	0/1/1/1
7	A1IUA	B	409	-	-	0/6/24/24	0/1/1/1
3	MES	A	401	-	-	1/6/14/14	0/1/1/1
3	MES	B	402	-	-	2/6/14/14	0/1/1/1
4	GOL	A	402	-	-	4/4/4/4	-
13	PEG	B	413	-	-	2/4/4/4	-
8	NDG	A	407	-	-	2/6/23/26	0/1/1/1
6	NAG	B	407	6	-	2/6/23/26	0/1/1/1
6	NAG	B	408	-	-	1/6/23/26	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	404	HEM	C1B-NB	-5.13	1.31	1.40
5	A	403	HEM	C1B-NB	-4.76	1.32	1.40
5	A	403	HEM	FE-NB	4.14	2.07	1.94
12	A	420	PO4	P-O1	3.93	1.59	1.50
5	B	404	HEM	FE-NB	3.83	2.06	1.94

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	403	NAG	O5-C1-C2	9.00	125.21	111.29
8	A	407	NDG	O5-C1-C2	-4.01	105.09	111.29
5	B	404	HEM	CHD-C4C-NC	3.95	128.76	124.45
5	B	404	HEM	CHC-C4B-NB	3.94	128.66	124.42
5	A	403	HEM	C1B-NB-C4B	3.89	109.82	105.21

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	MES	C8-C7-N4-C5
3	B	402	MES	C8-C7-N4-C5
4	A	402	GOL	O1-C1-C2-C3
4	A	402	GOL	C1-C2-C3-O3

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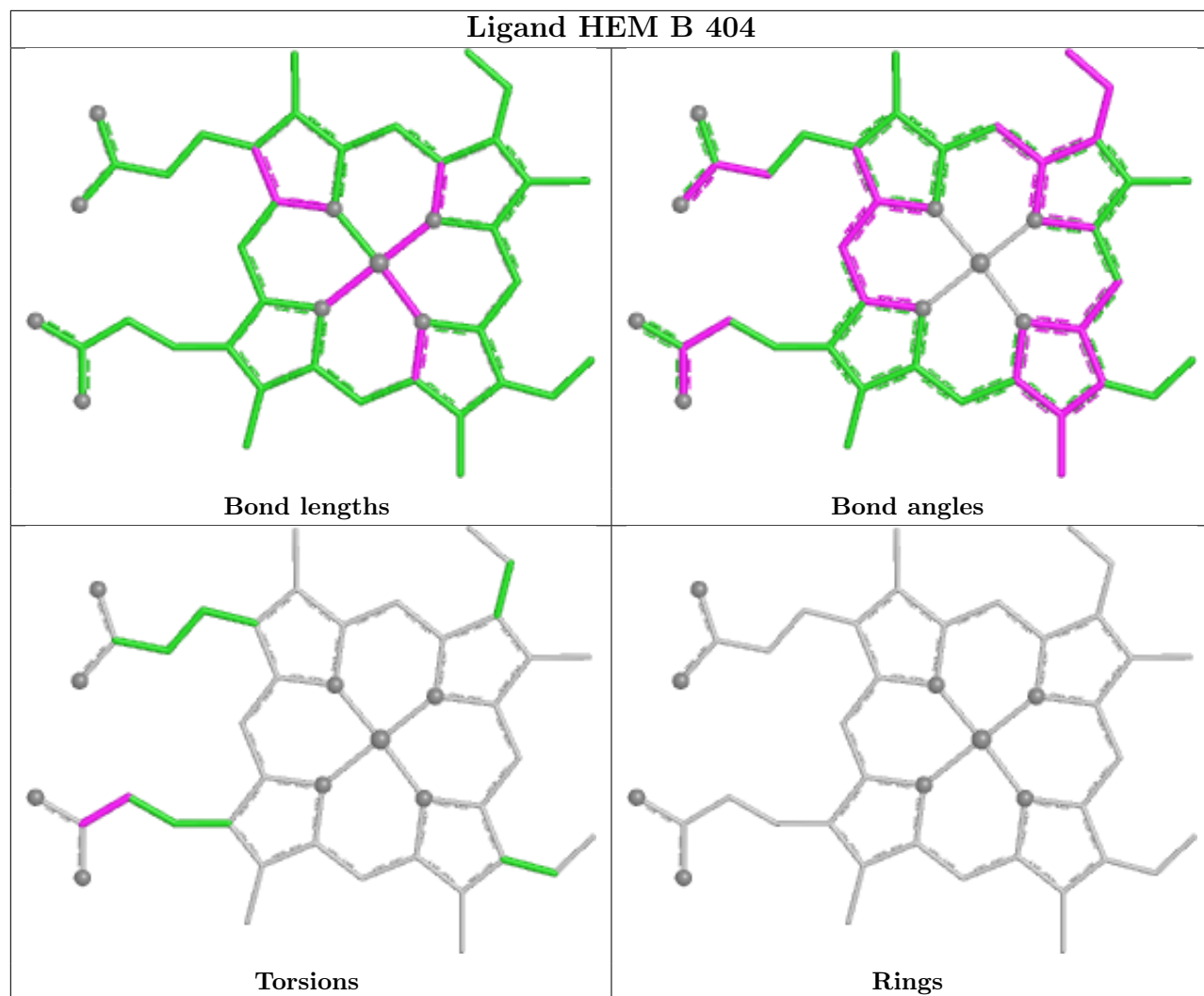
Mol	Chain	Res	Type	Atoms
4	B	415	GOL	C1-C2-C3-O3

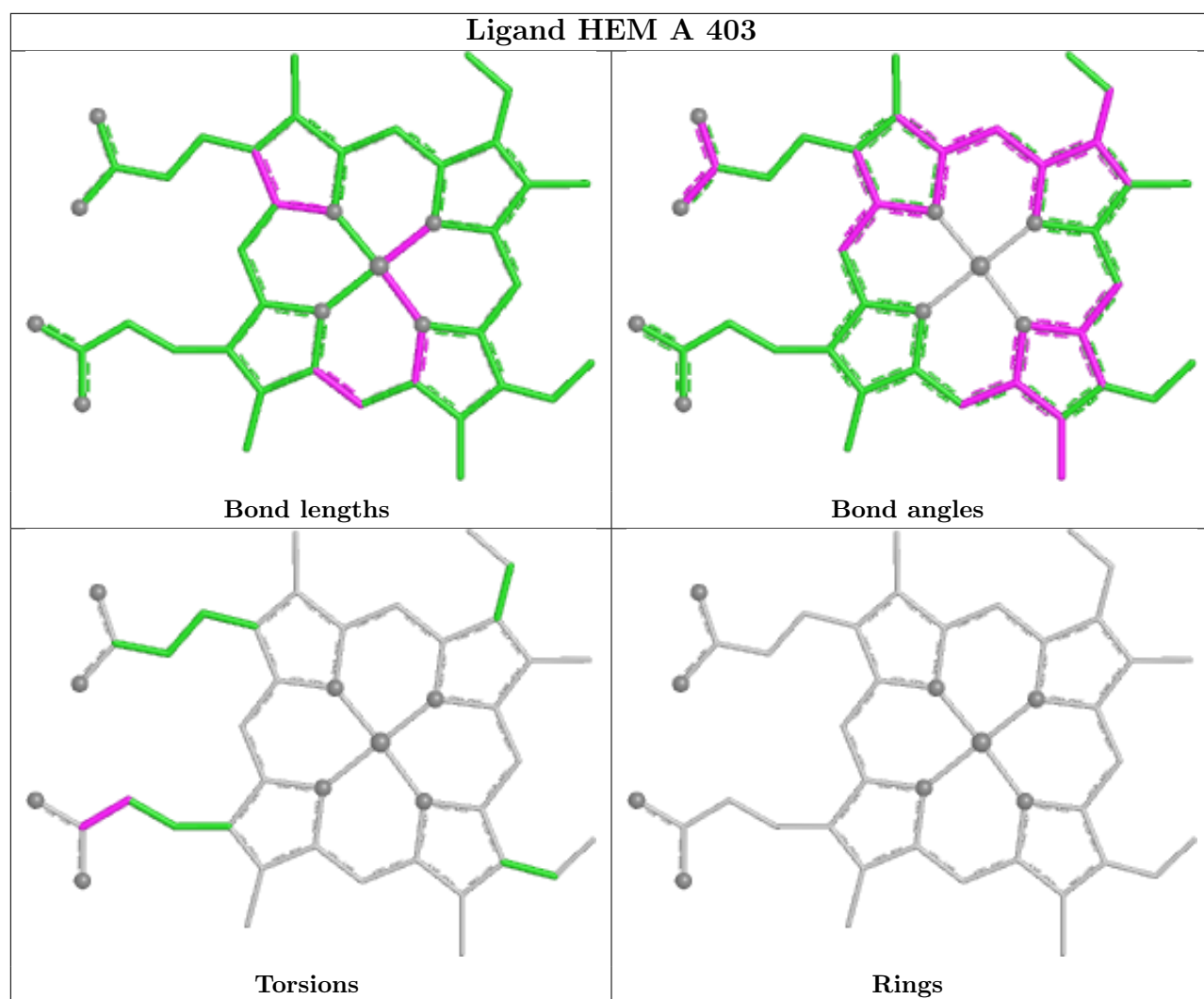
There are no ring outliers.

17 monomers are involved in 61 short contacts:

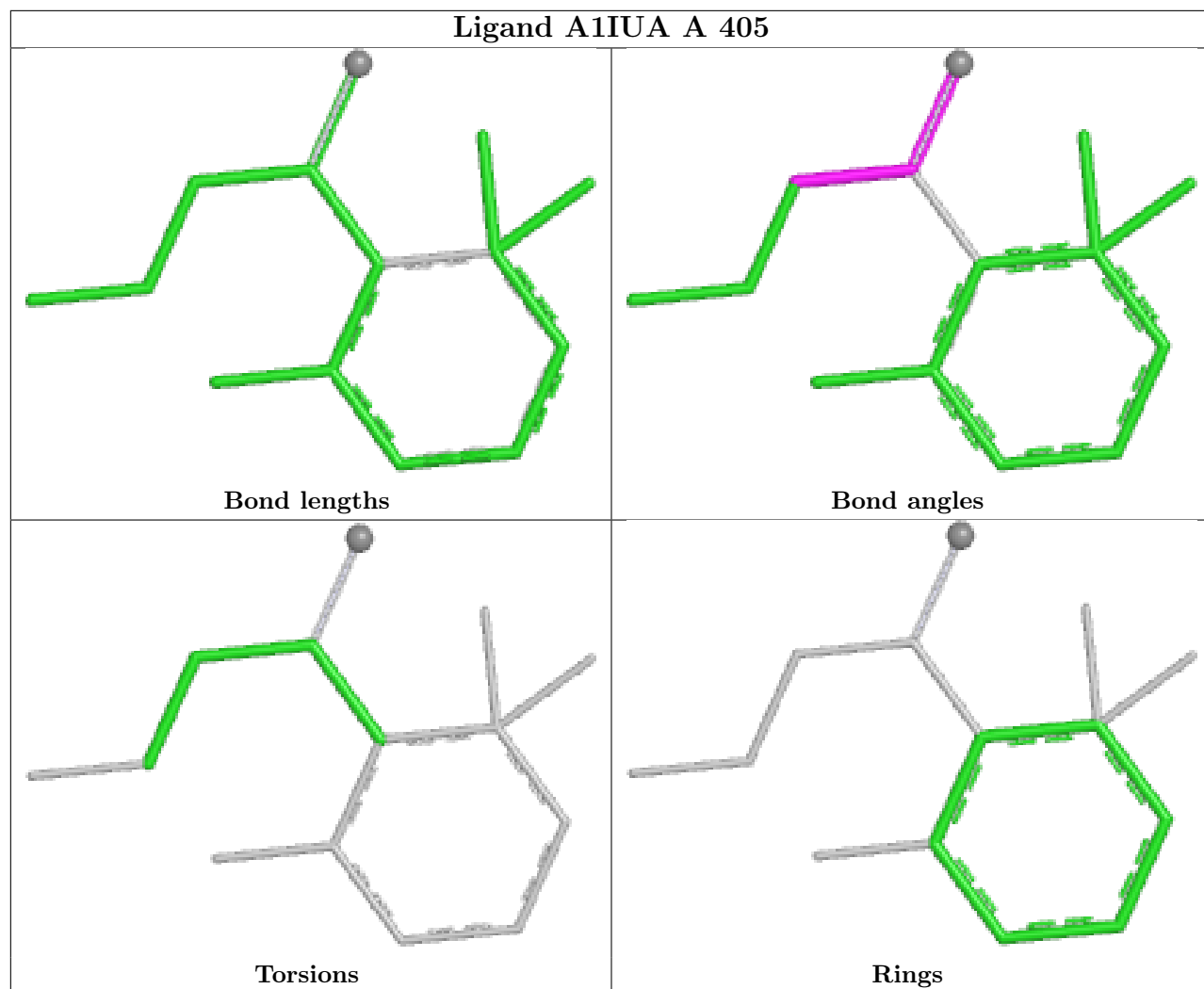
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	404	HEM	2	0
13	B	411	PEG	2	0
5	A	403	HEM	1	0
6	B	405	NAG	4	0
4	B	415	GOL	1	0
6	A	404	NAG	6	0
6	B	406	NAG	1	0
6	A	406	NAG	3	0
4	B	410	GOL	5	0
4	B	414	GOL	1	0
6	B	403	NAG	2	0
6	B	401	NAG	11	0
7	B	409	A1IUA	1	0
4	A	402	GOL	1	0
13	B	413	PEG	6	0
8	A	407	NDG	6	0
6	B	408	NAG	8	0

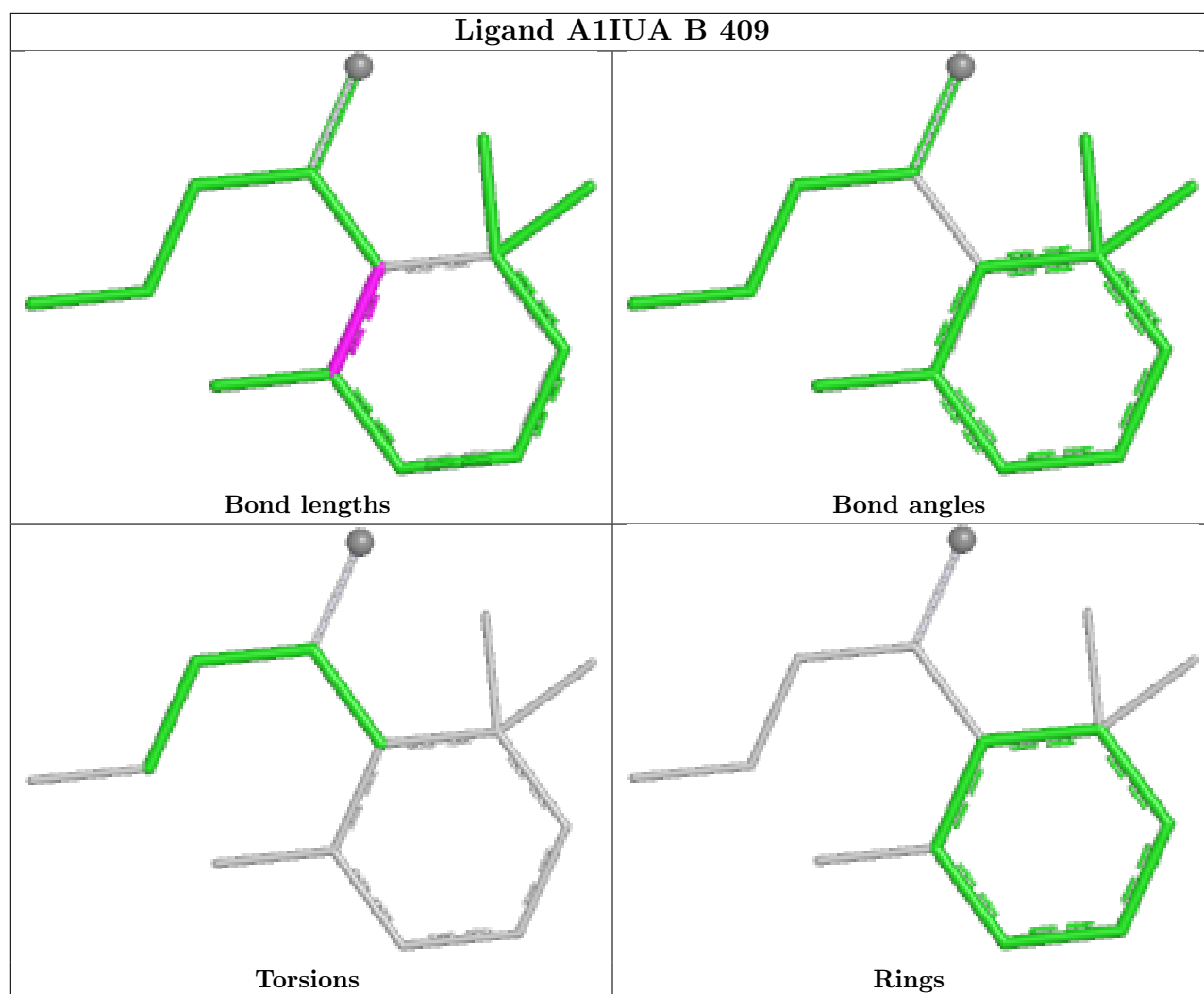
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 A1IUA A 405





## 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	334/334 (100%)	-0.28	5 (1%) 72 72	12, 22, 35, 88	7 (2%)
1	B	334/334 (100%)	-0.18	4 (1%) 76 77	12, 24, 38, 81	5 (1%)
All	All	668/668 (100%)	-0.23	9 (1%) 75 75	12, 23, 36, 88	12 (1%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	LEU	5.9
1	B	1	LEU	5.7
1	B	214	THR	4.4
1	A	2	ASN	3.1
1	B	2	ASN	2.6

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

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

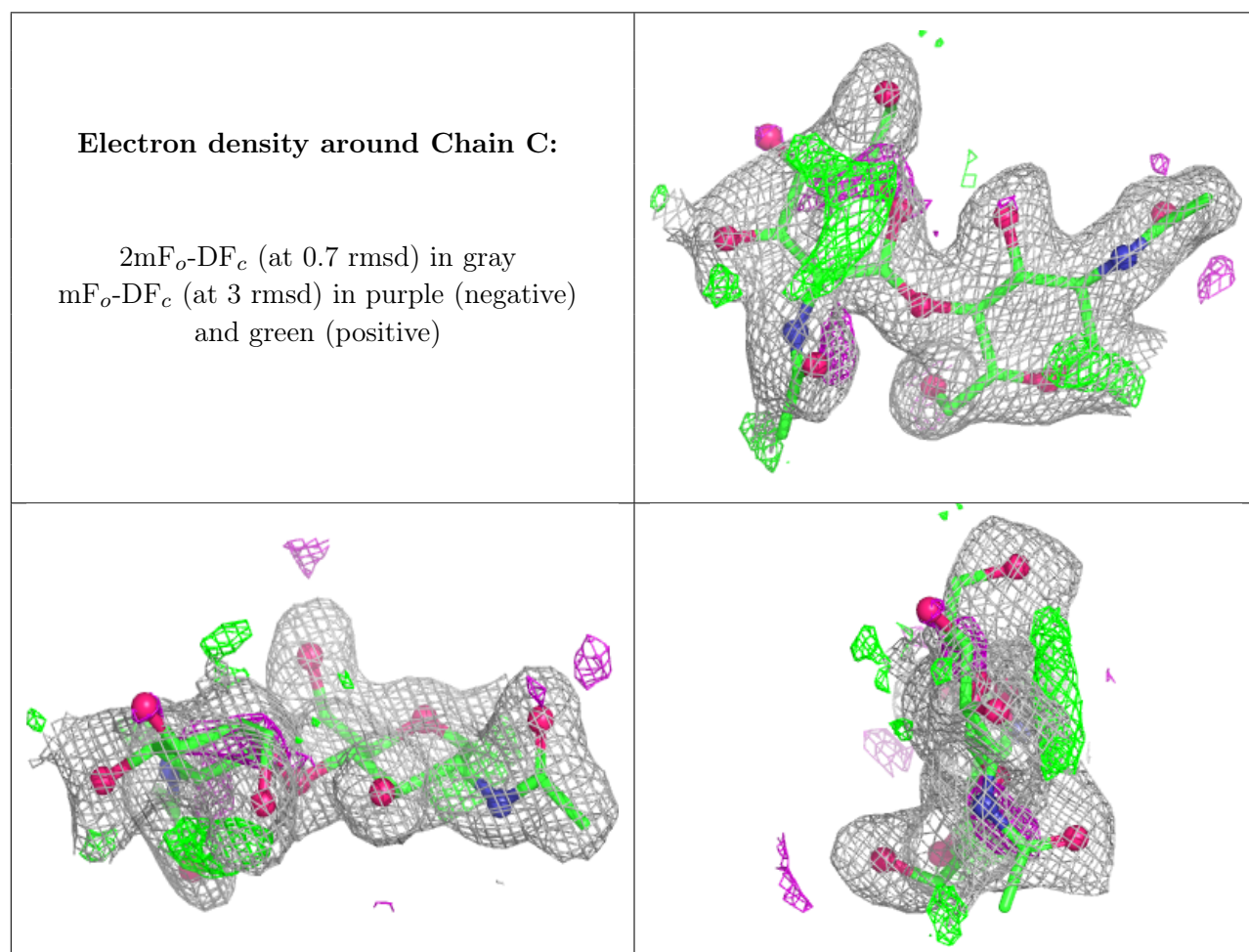
### 6.3 Carbohydrates [i](#)

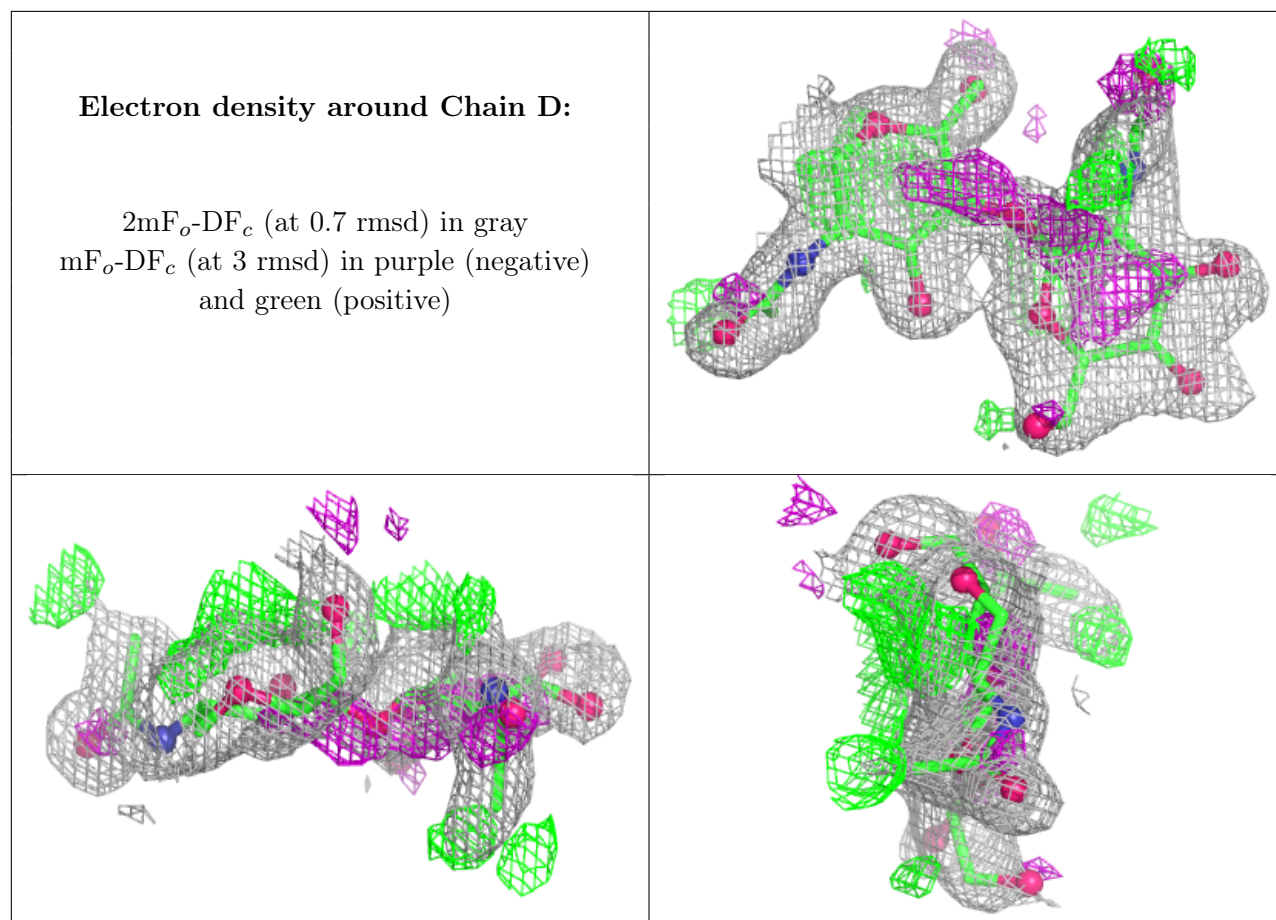
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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
2	NAG	C	2	14/15	0.69	0.16	41,48,53,56	0
2	NAG	D	2	14/15	0.71	0.14	39,45,49,50	0
2	NAG	D	1	14/15	0.81	0.13	33,37,41,42	0
2	NAG	C	1	14/15	0.92	0.09	28,32,34,38	0



The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





## 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(Å <sup>2</sup> )	Q<0.9
6	NAG	B	408	14/15	0.33	0.21	50,55,59,60	0
6	NAG	A	404	14/15	0.51	0.20	51,54,61,62	0
8	NDG	A	407	14/15	0.53	0.18	38,41,44,45	0
6	NAG	B	407	14/15	0.57	0.19	45,53,58,62	0
6	NAG	B	406	14/15	0.58	0.19	47,51,57,60	0
6	NAG	A	406	14/15	0.58	0.17	45,49,53,56	0
12	PO4	B	423	5/5	0.64	0.15	45,45,49,50	0
12	PO4	A	420	5/5	0.65	0.16	41,44,49,50	0
6	NAG	B	405	14/15	0.68	0.17	34,41,46,48	0
7	A1IUA	B	409	14/14	0.69	0.25	35,39,42,49	0
4	GOL	A	402	6/6	0.70	0.21	26,31,33,34	0
11	EOH	A	419	3/3	0.71	0.21	34,34,36,37	0

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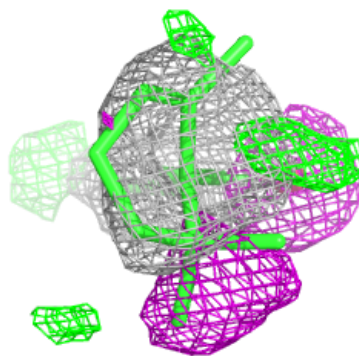
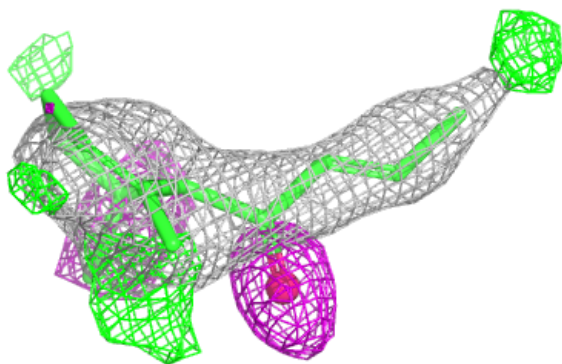
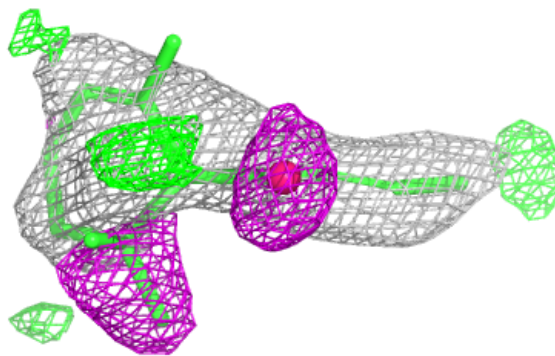
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	B	410	6/6	0.72	0.16	34,37,37,40	0
13	PEG	B	413	7/7	0.73	0.16	33,36,37,38	0
4	GOL	B	415	6/6	0.75	0.15	35,36,39,39	0
12	PO4	B	422	5/5	0.78	0.16	41,45,47,51	0
11	EOH	B	412	3/3	0.78	0.20	36,36,37,37	0
13	PEG	B	411	7/7	0.78	0.15	35,36,38,40	0
7	AI1UA	A	405	14/14	0.78	0.19	32,34,37,38	0
4	GOL	B	414	6/6	0.84	0.12	36,38,39,40	0
9	ZN	B	417	1/1	0.85	0.10	44,44,44,44	0
6	NAG	B	403	14/15	0.85	0.11	35,38,43,43	0
6	NAG	B	401	14/15	0.86	0.13	33,38,43,44	0
9	ZN	A	409	1/1	0.90	0.08	41,41,41,41	0
9	ZN	A	417	1/1	0.93	0.29	51,51,51,51	0
9	ZN	A	414	1/1	0.94	0.07	38,38,38,38	0
9	ZN	B	420	1/1	0.94	0.08	43,43,43,43	0
9	ZN	A	412	1/1	0.94	0.07	33,33,33,33	0
9	ZN	B	416	1/1	0.95	0.22	49,49,49,49	0
3	MES	B	402	12/12	0.95	0.12	22,30,37,39	0
9	ZN	A	415	1/1	0.96	0.06	36,36,36,36	0
3	MES	A	401	12/12	0.96	0.12	21,32,37,38	0
9	ZN	A	416	1/1	0.97	0.05	29,29,29,29	0
9	ZN	A	408	1/1	0.97	0.05	35,35,35,35	0
9	ZN	B	418	1/1	0.97	0.20	43,43,43,43	0
9	ZN	B	419	1/1	0.97	0.05	31,31,31,31	0
9	ZN	A	411	1/1	0.98	0.03	30,30,30,30	0
5	HEM	B	404	43/43	0.98	0.05	17,18,21,26	0
5	HEM	A	403	43/43	0.98	0.06	16,18,19,24	0
9	ZN	A	410	1/1	0.99	0.08	38,38,38,38	0
9	ZN	A	413	1/1	0.99	0.03	27,27,27,27	0
10	MG	B	421	1/1	1.00	0.22	5,5,5,5	0
10	MG	A	418	1/1	1.00	0.24	5,5,5,5	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.

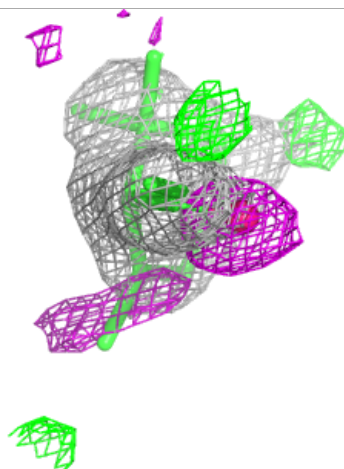
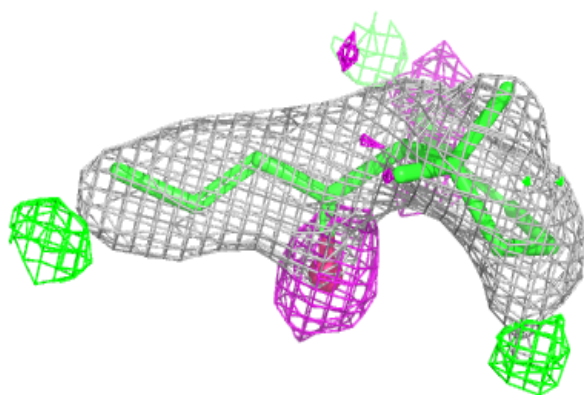
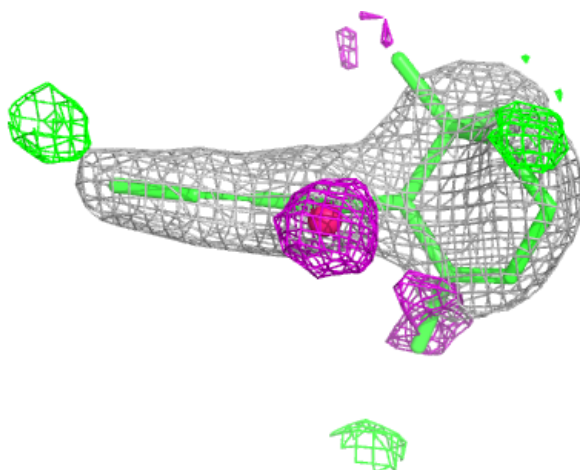
**Electron density around A1IUA B 409:**

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



**Electron density around A1IUUA A 405:**

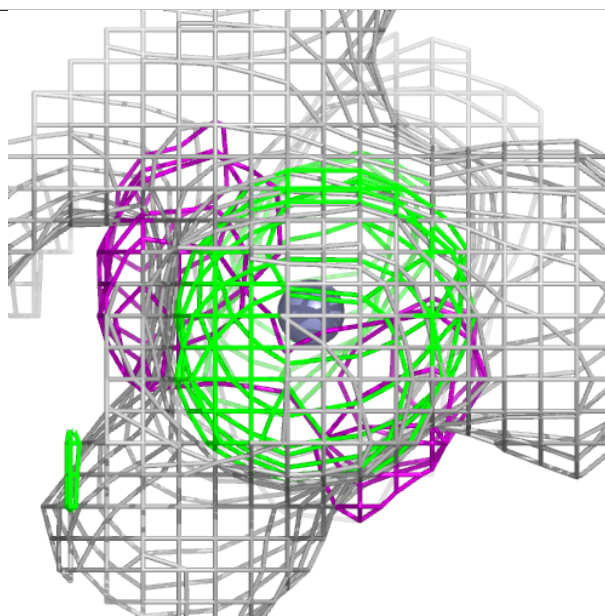
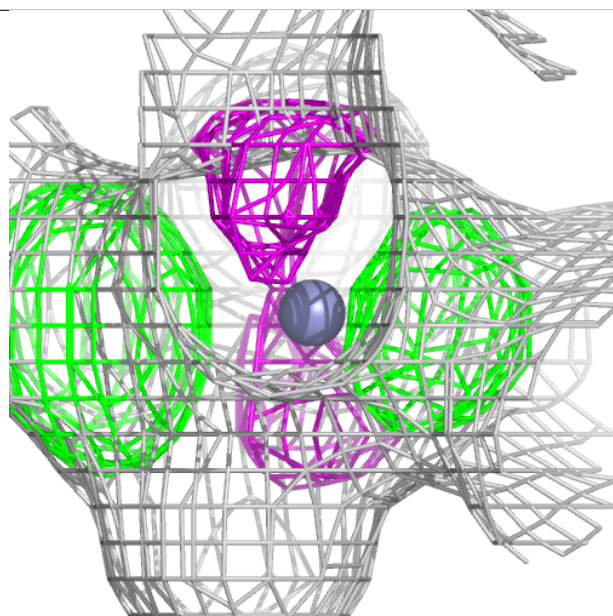
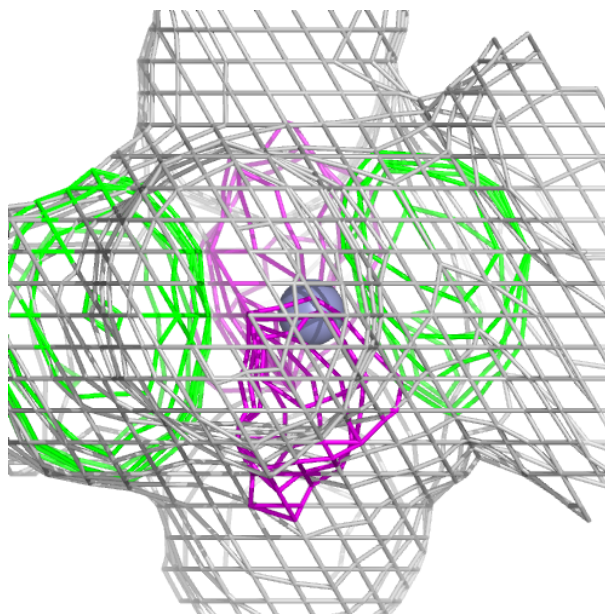
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





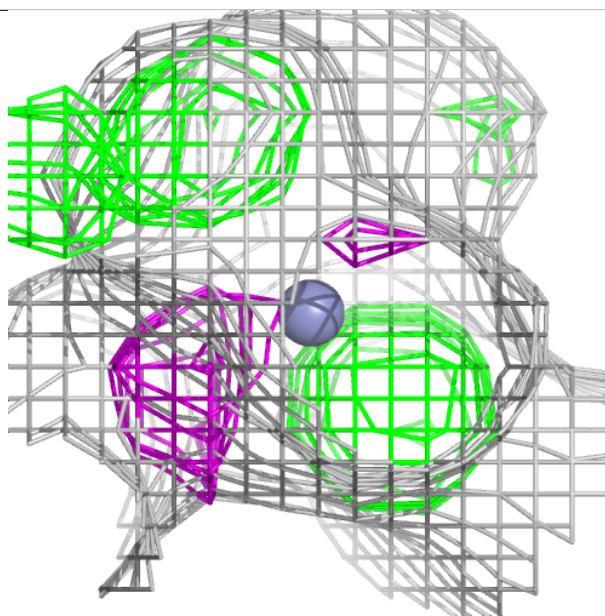
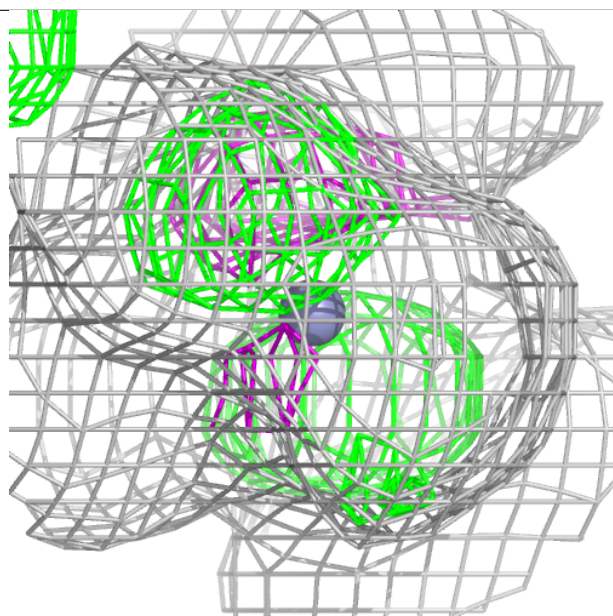
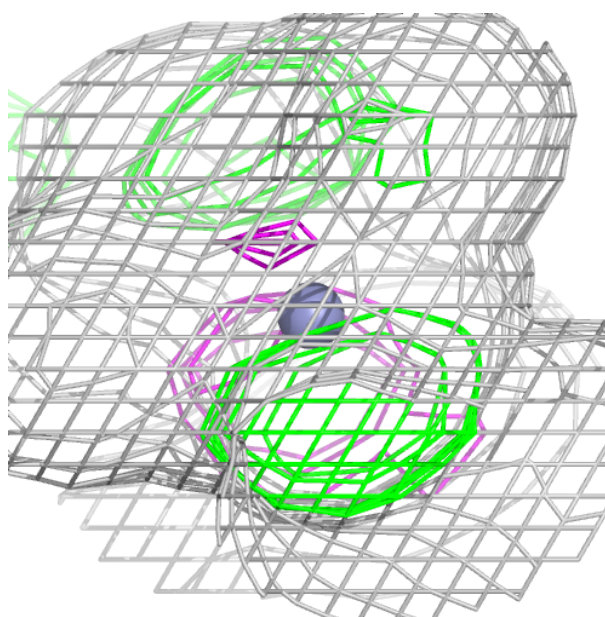
**Electron density around ZN B 417:**

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



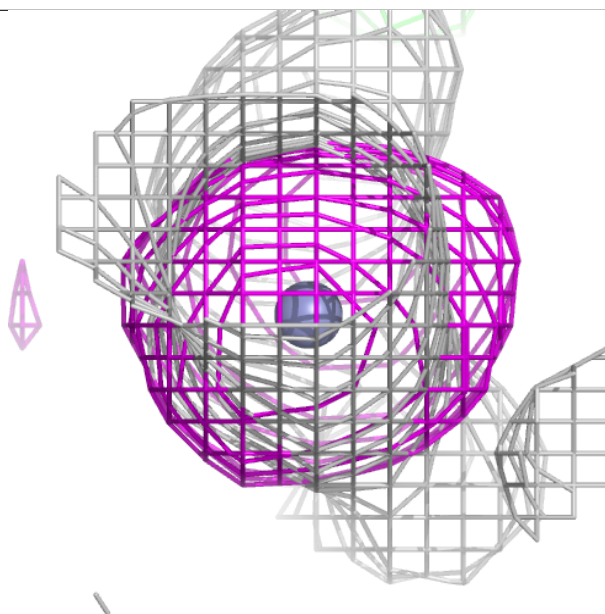
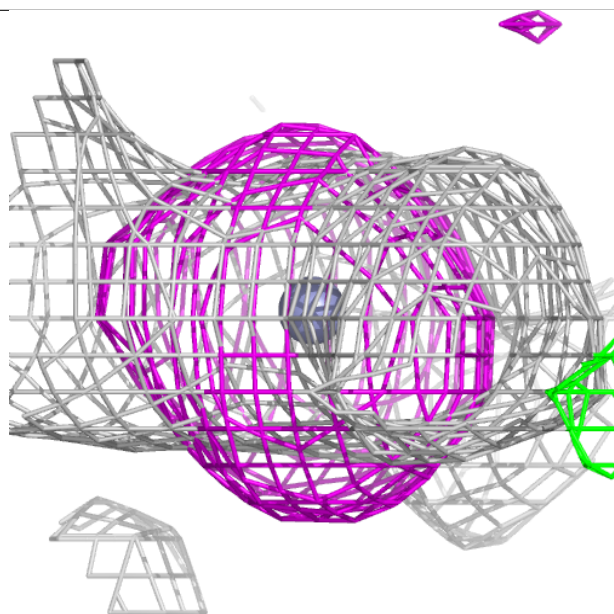
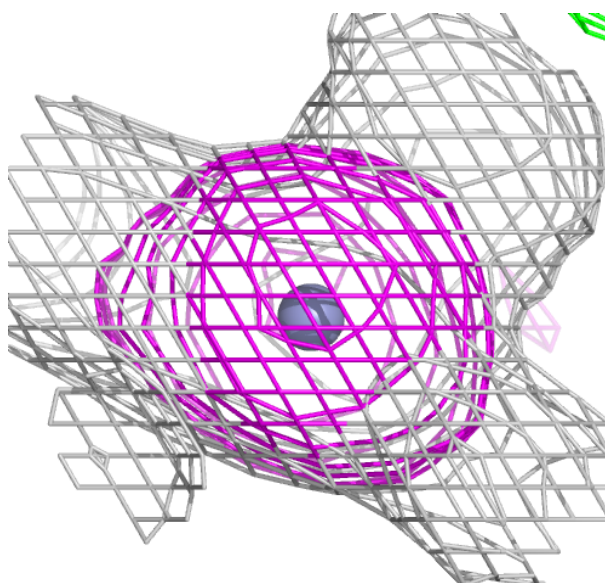
**Electron density around ZN A 409:**

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



**Electron density around ZN A 417:**

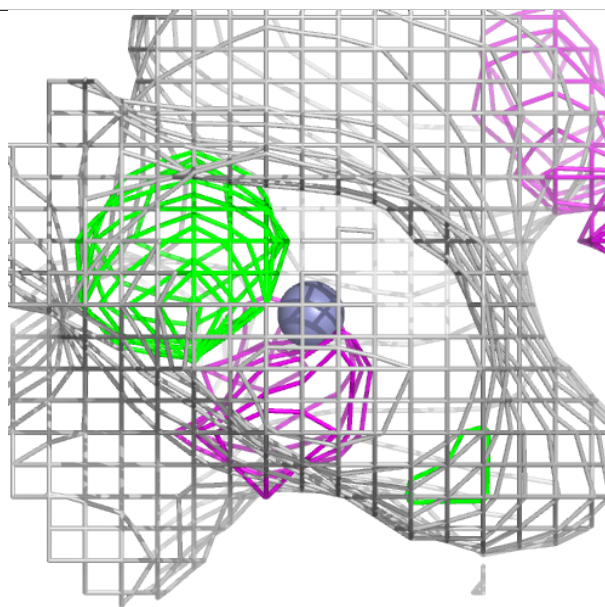
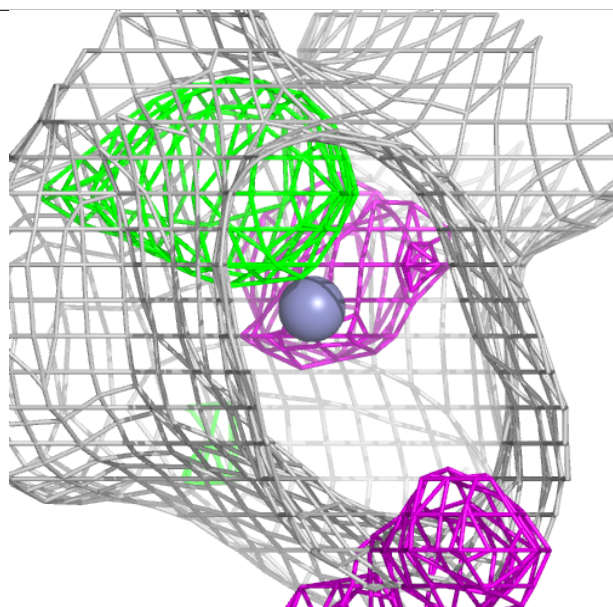
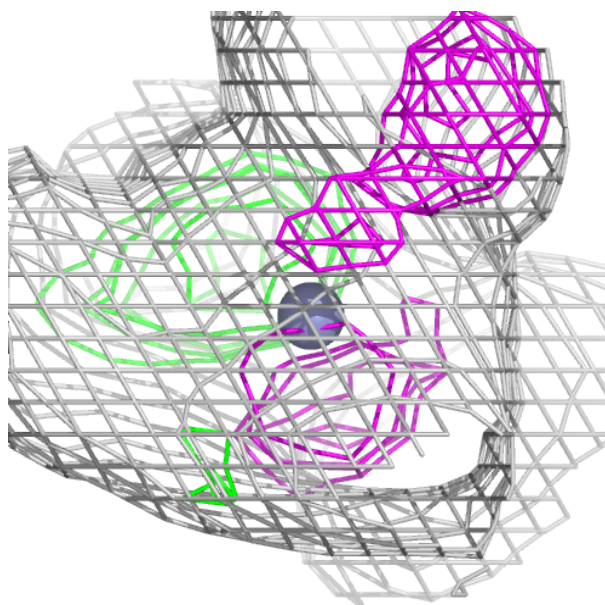
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





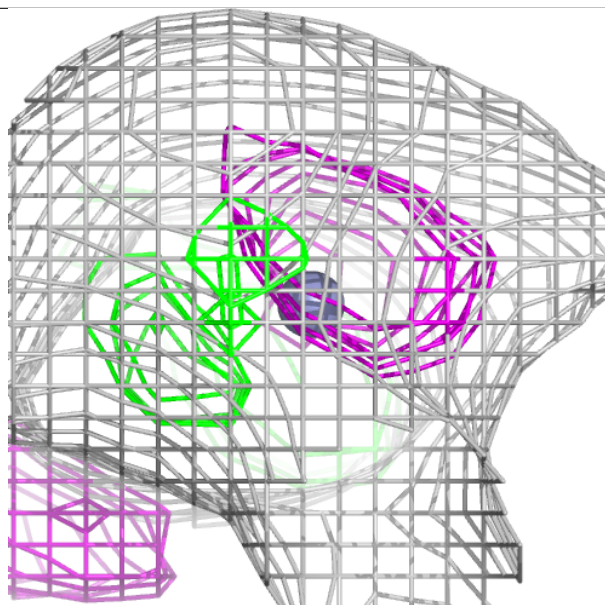
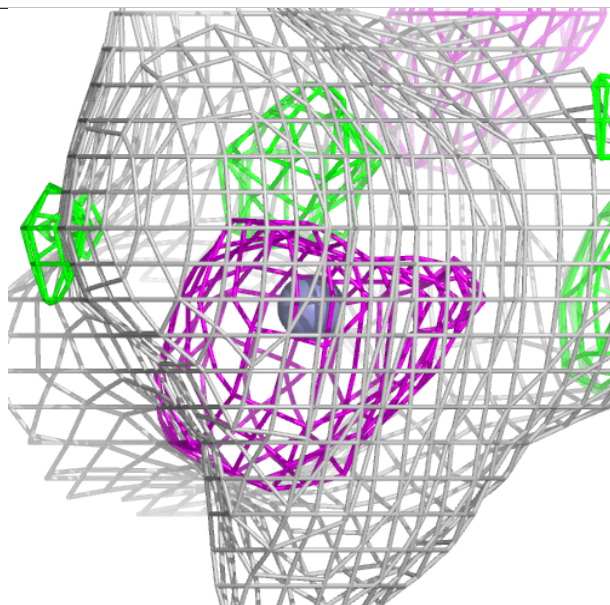
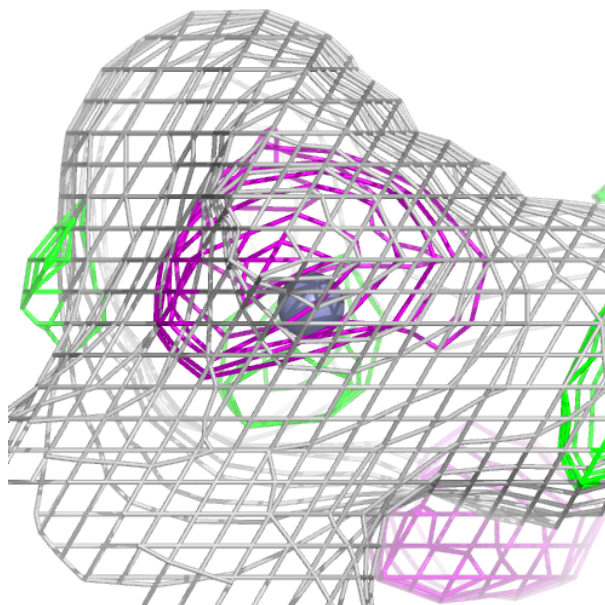
**Electron density around ZN A 414:**

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



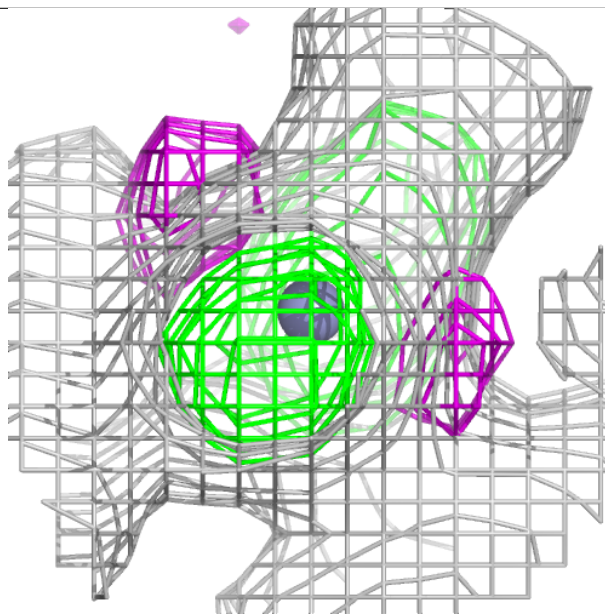
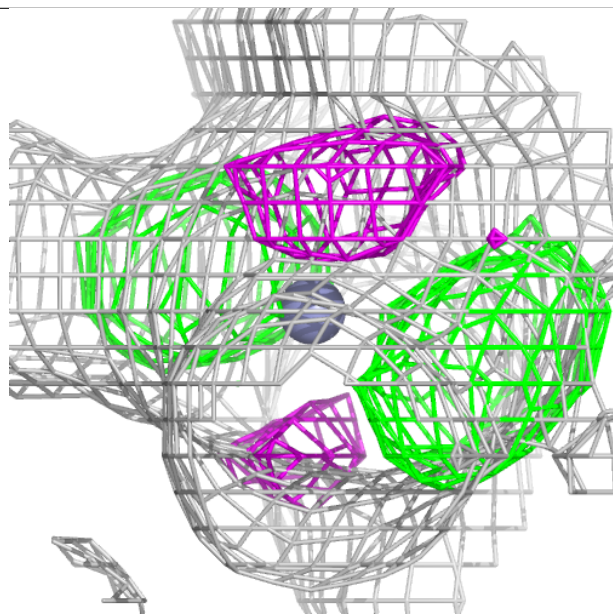
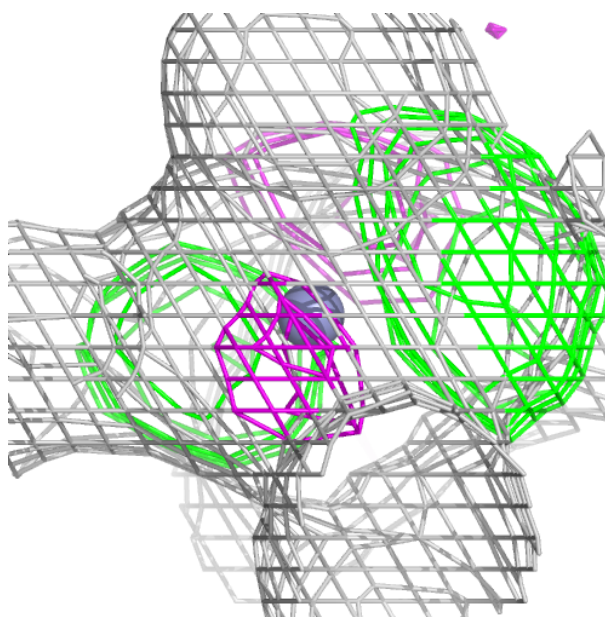
**Electron density around ZN B 420:**

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



**Electron density around ZN A 412:**

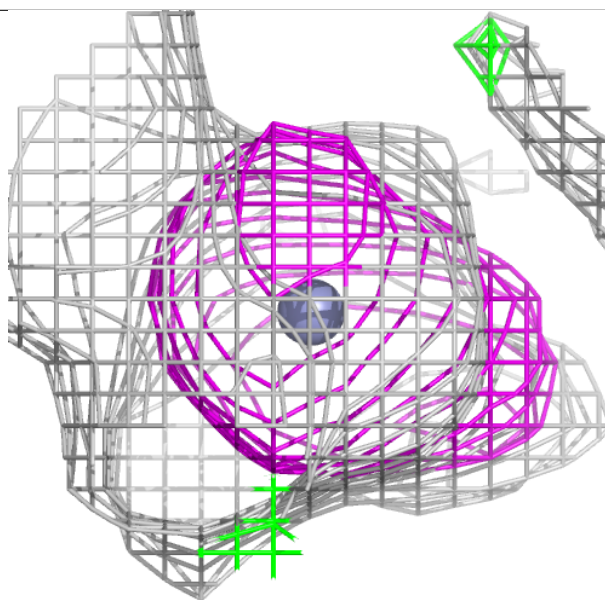
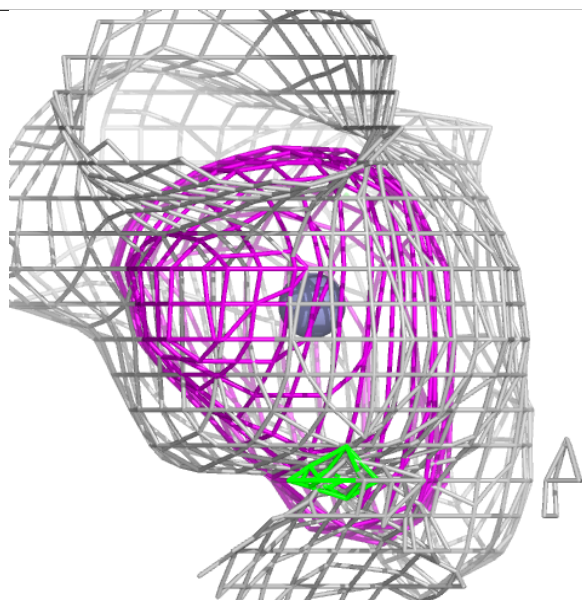
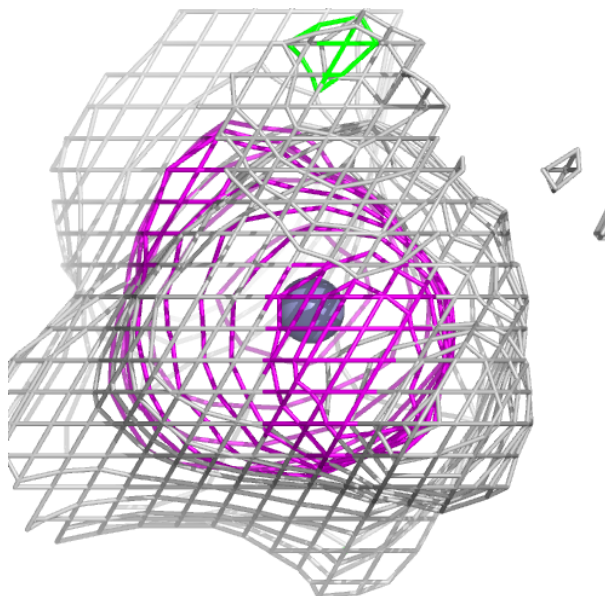
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





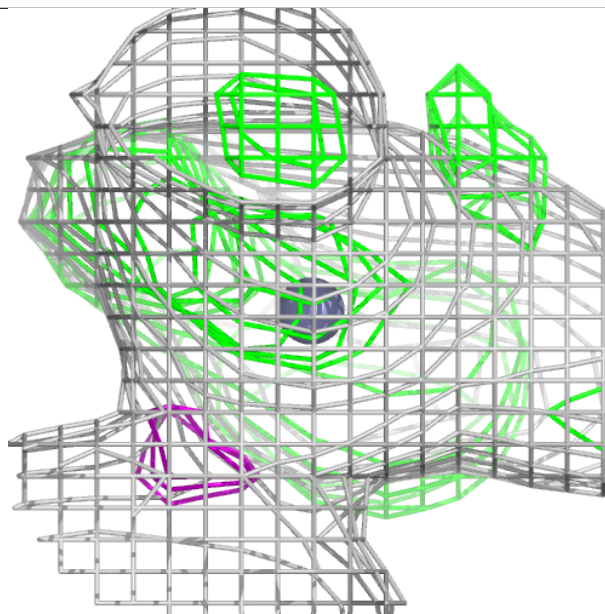
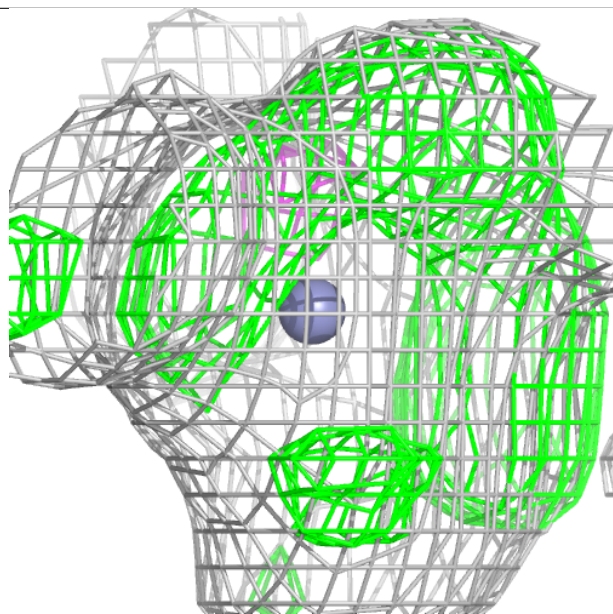
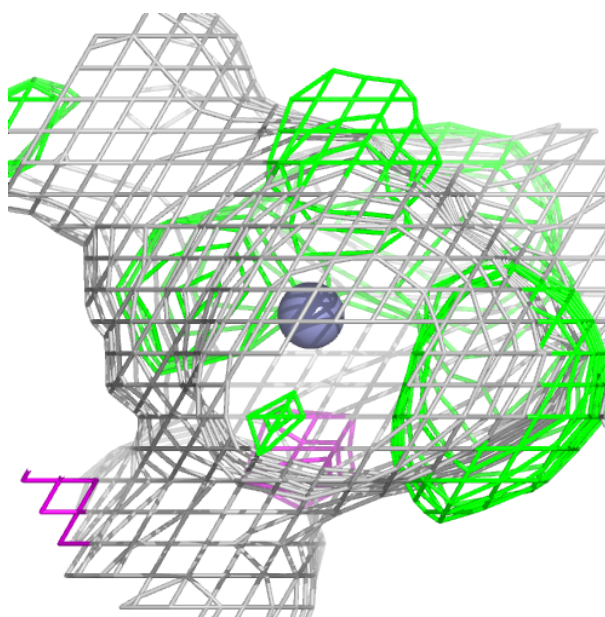
**Electron density around ZN B 416:**

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



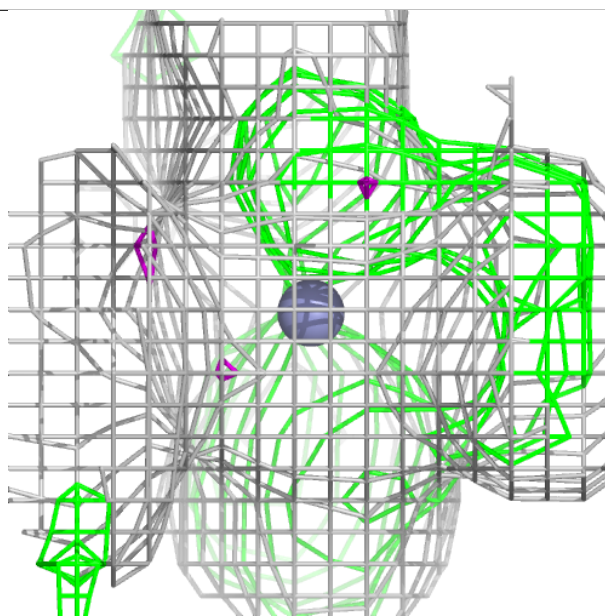
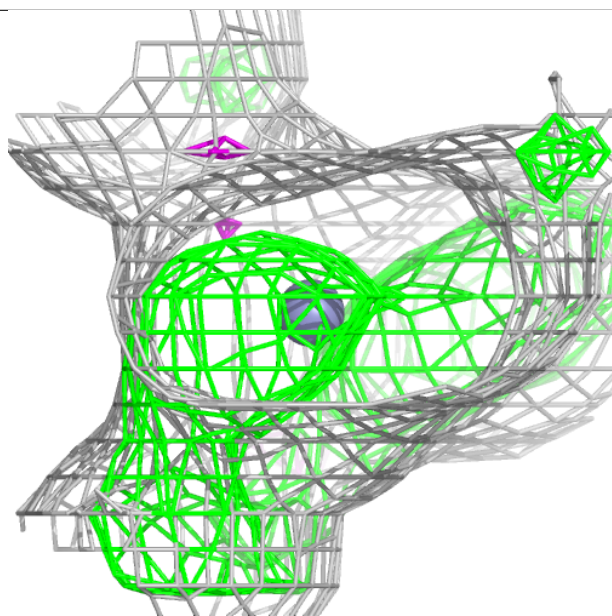
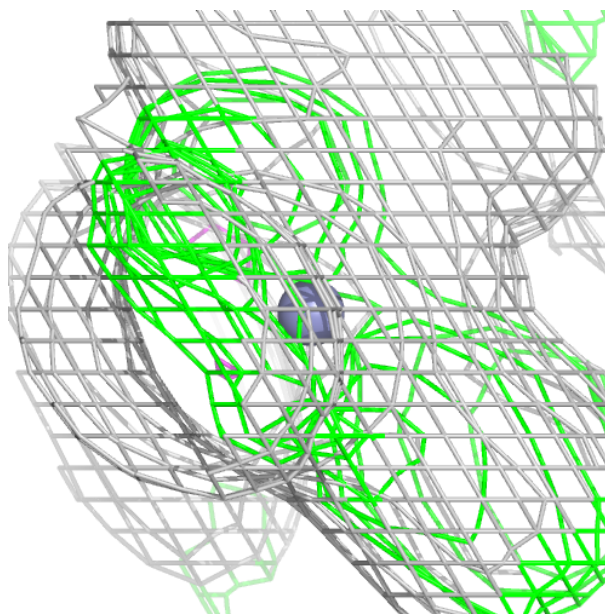
**Electron density around ZN A 415:**

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



**Electron density around ZN A 416:**

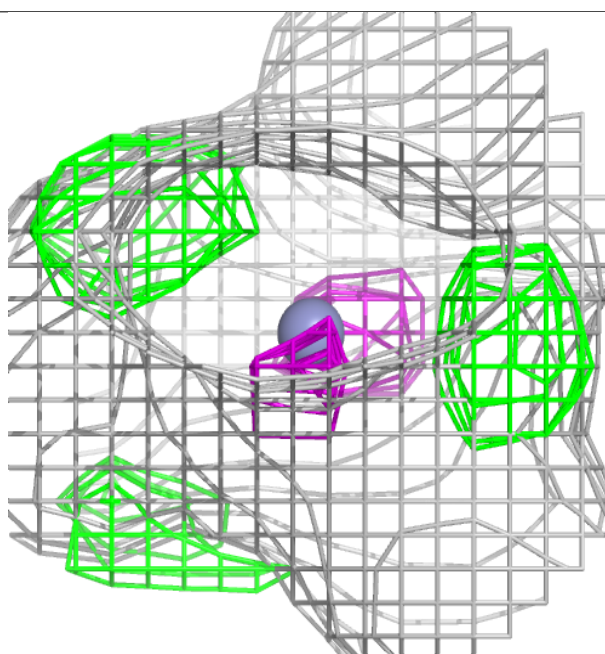
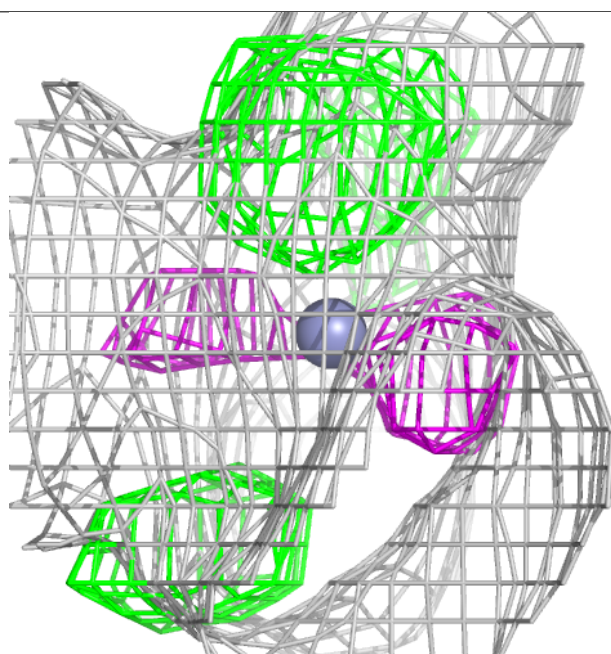
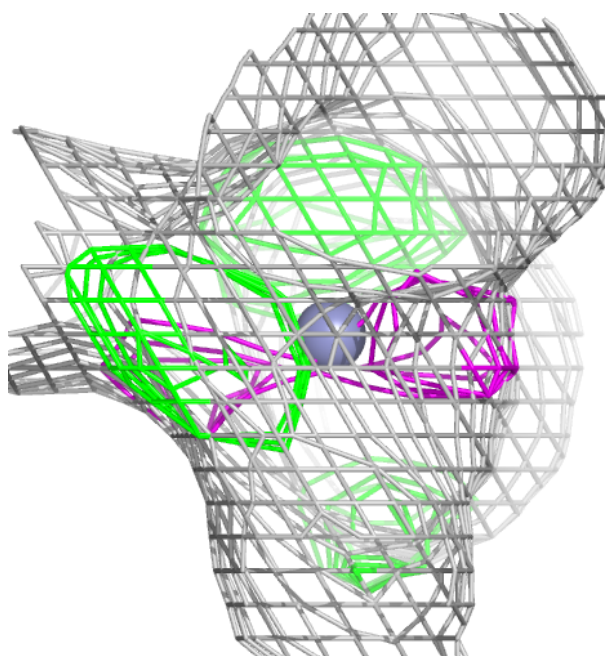
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





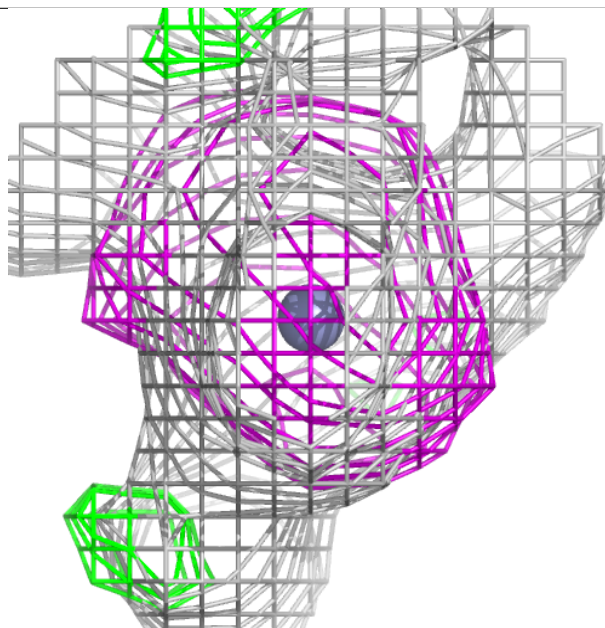
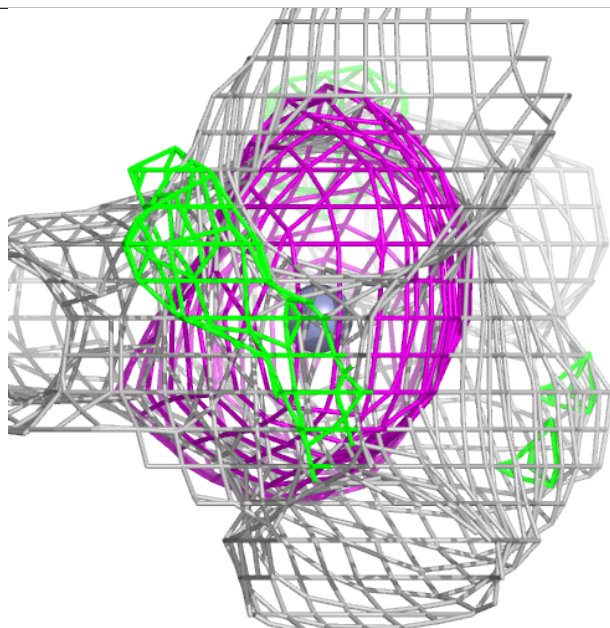
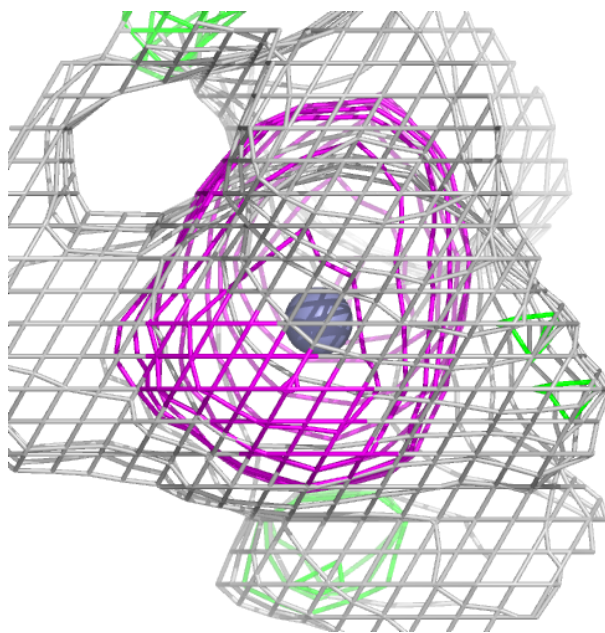
**Electron density around ZN A 408:**

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



**Electron density around ZN B 418:**

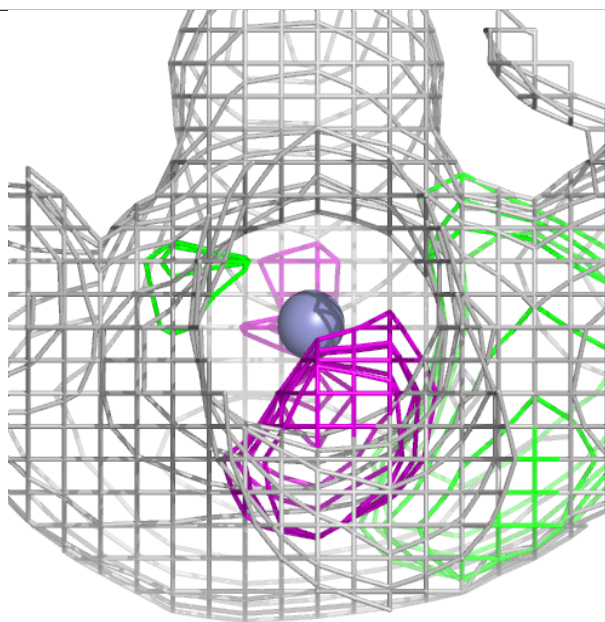
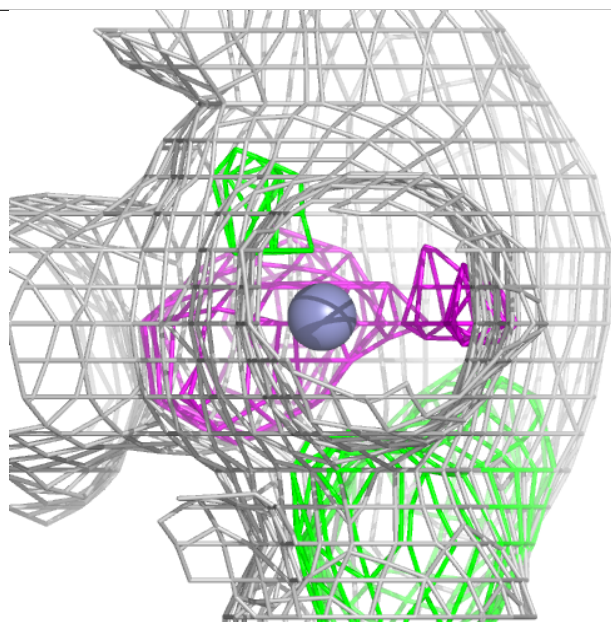
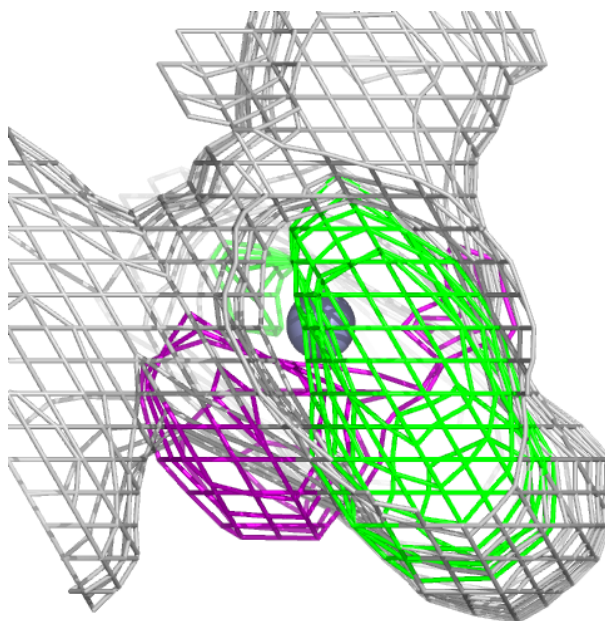
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





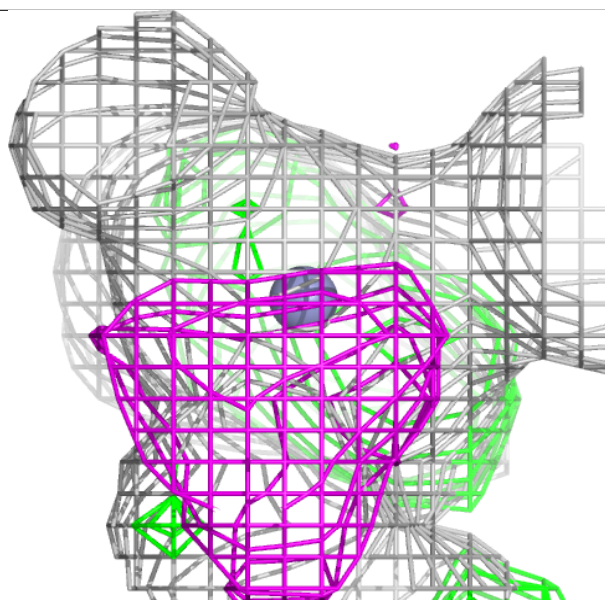
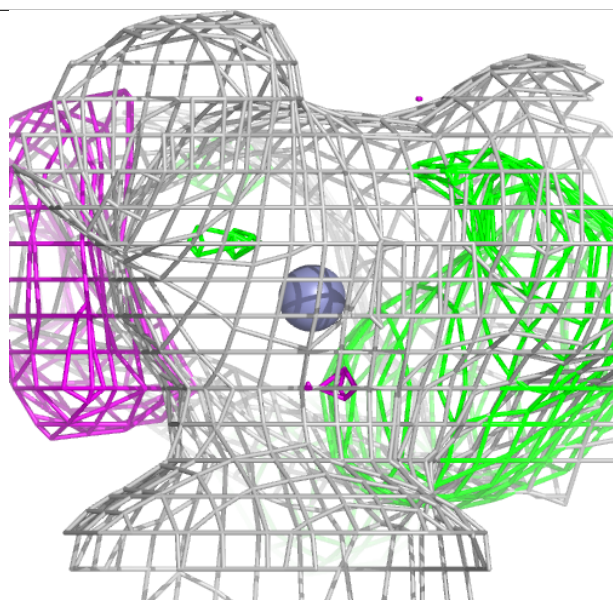
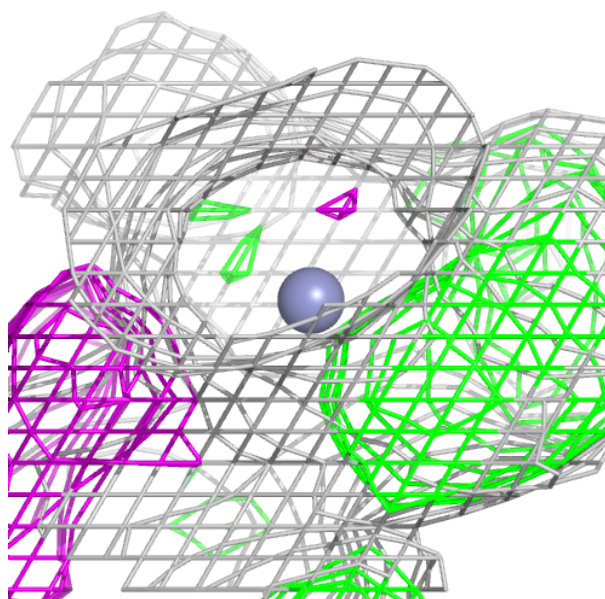
**Electron density around ZN B 419:**

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



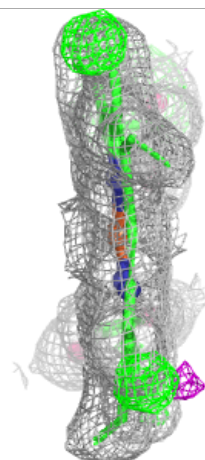
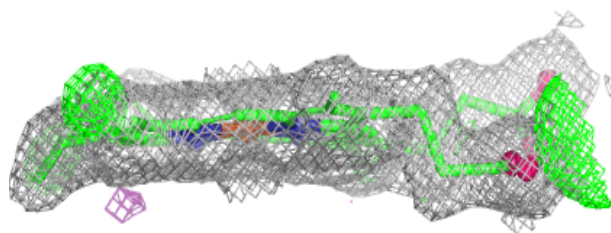
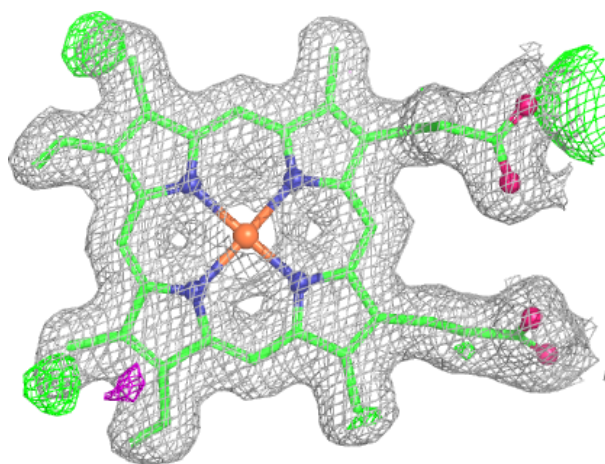
**Electron density around ZN A 411:**

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



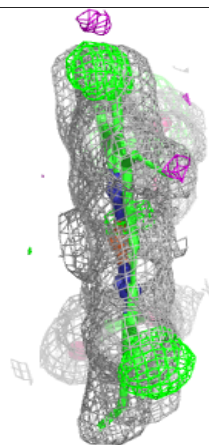
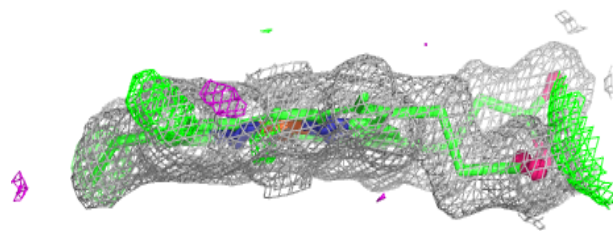
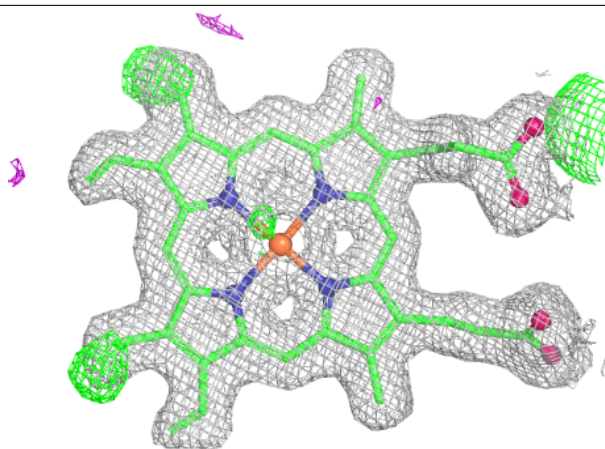
**Electron density around HEM B 404:**

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



**Electron density around HEM A 403:**

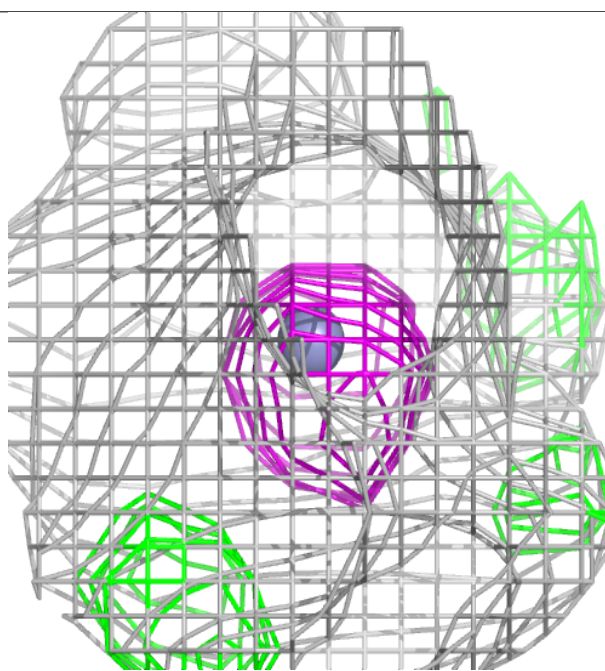
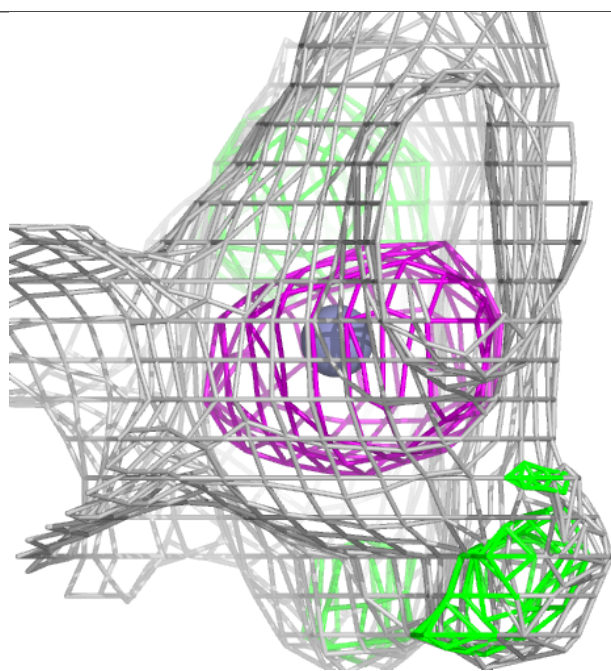
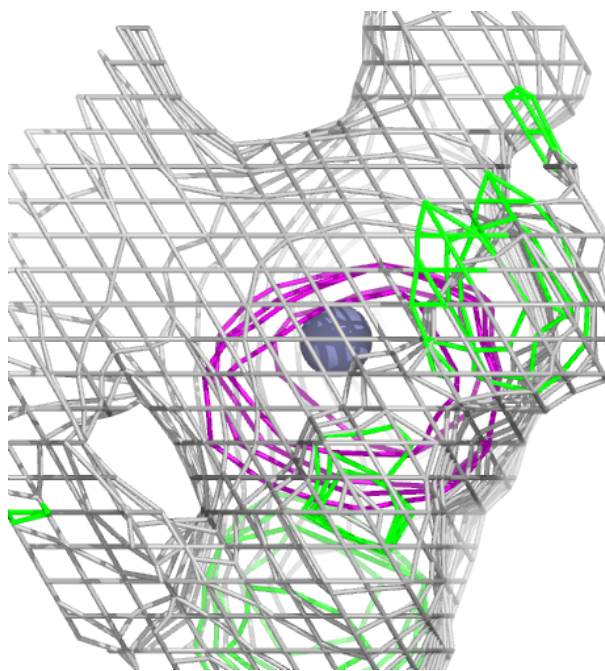
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





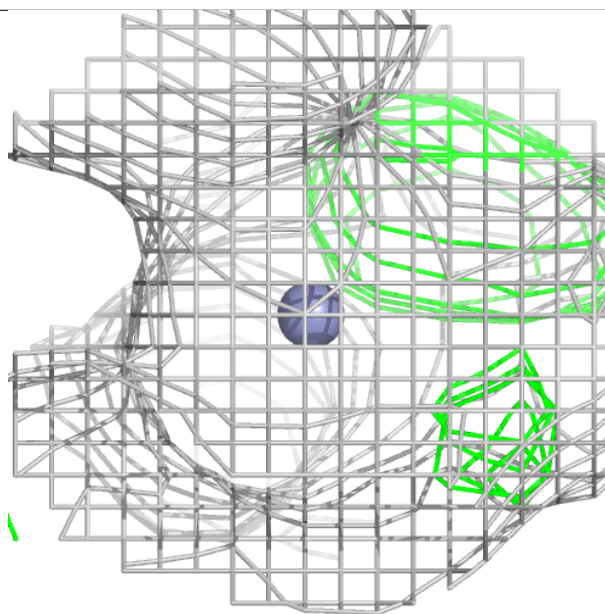
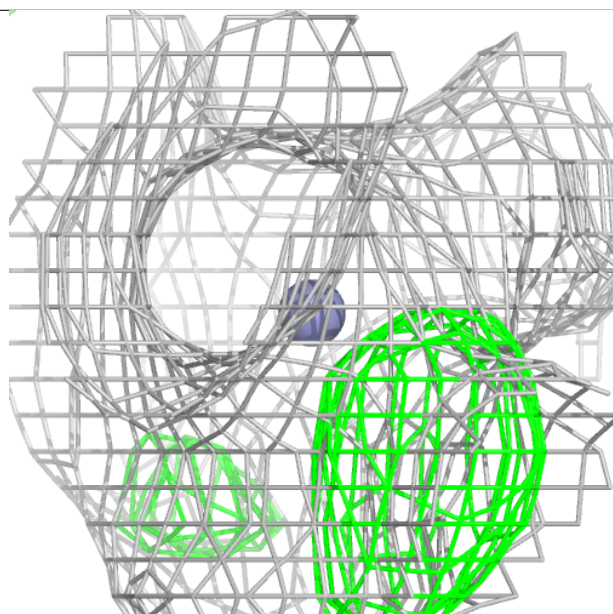
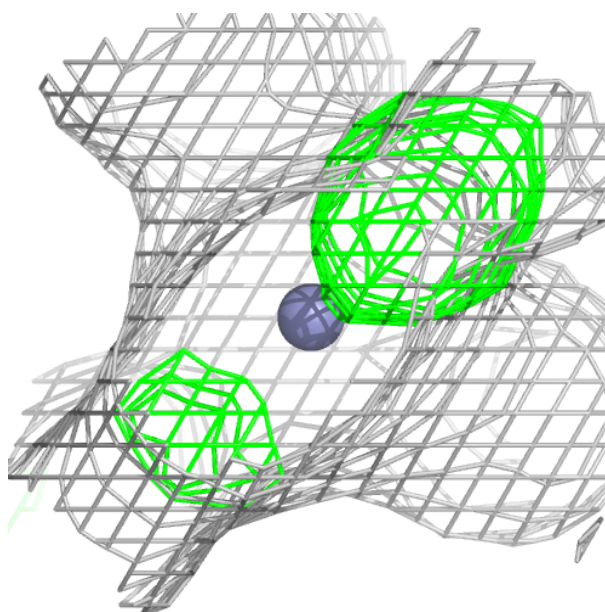
**Electron density around ZN A 410:**

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



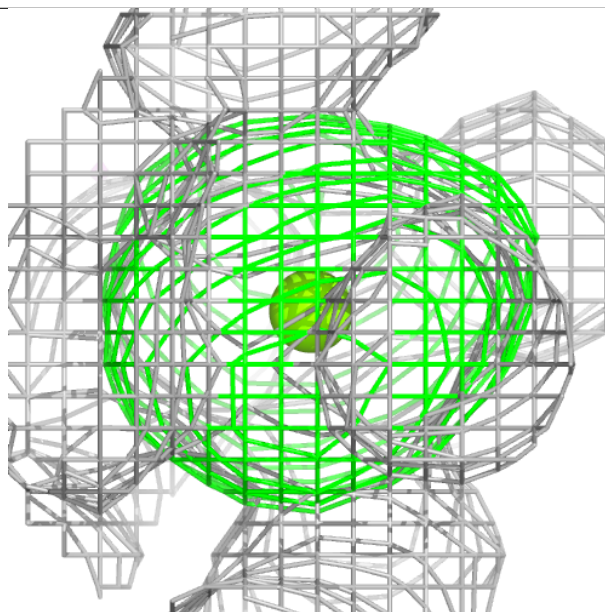
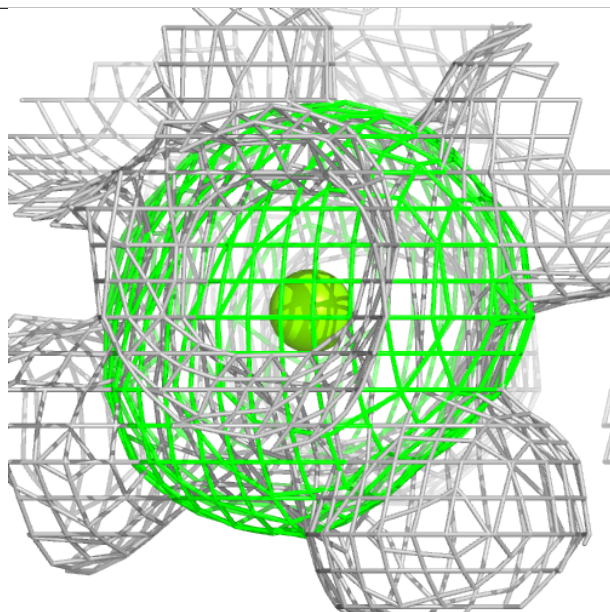
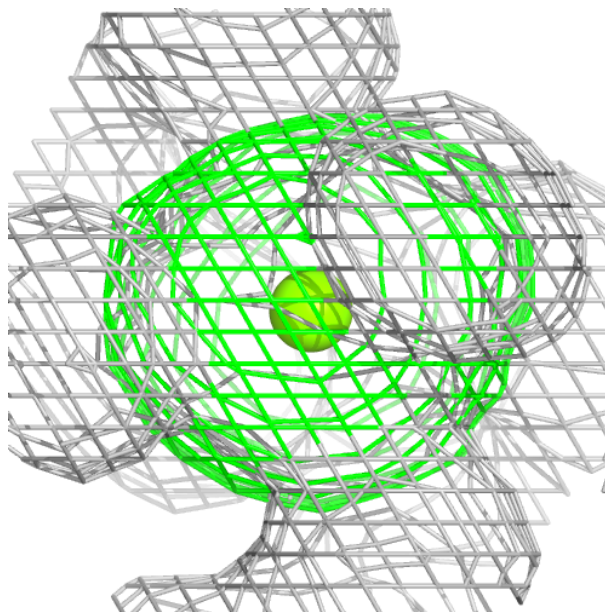
**Electron density around ZN A 413:**

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



**Electron density around MG B 421:**

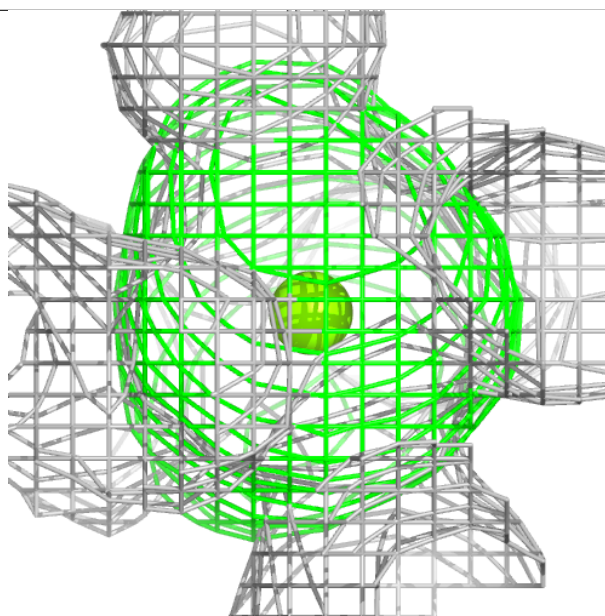
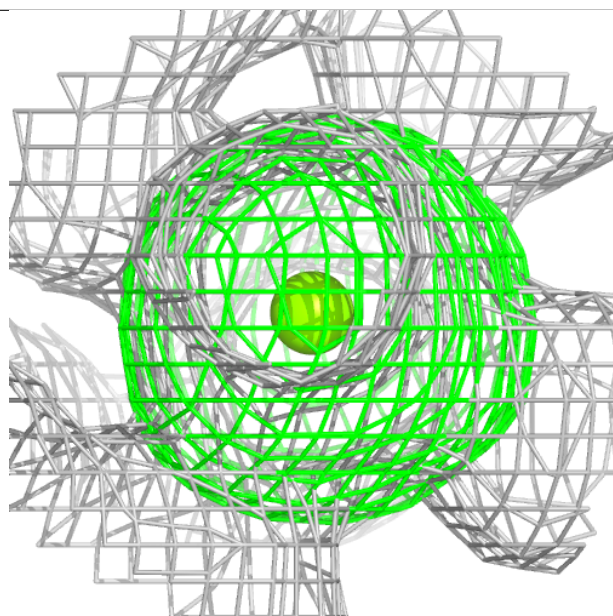
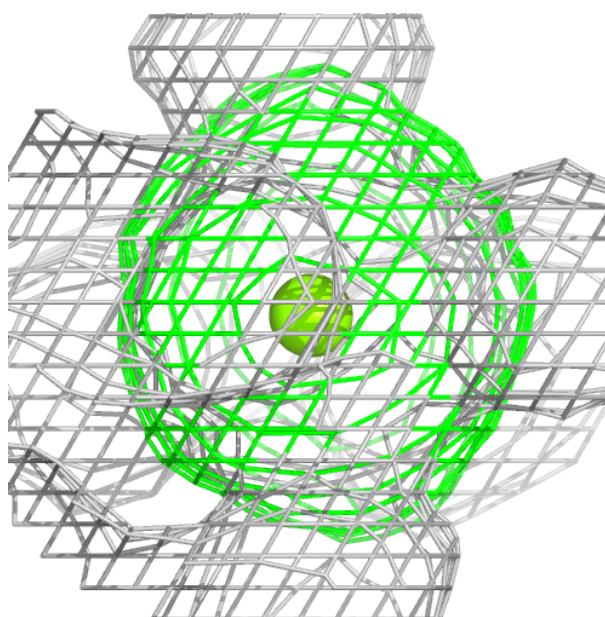
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around MG A 418:**

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



## 6.5 Other polymers ⓘ

There are no such residues in this entry.