



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:14 PM UTC

PDB ID : 7ME2 / pdb_00007me2
Title : YfeA oligomer crystal 2, form 2
Authors : Radka, C.D.; Aller, S.G.
Deposited on : 2021-04-06
Resolution : 1.85 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

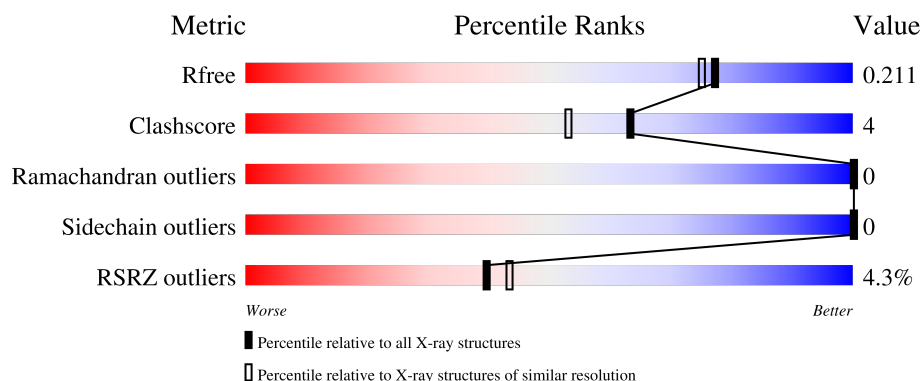
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	323	
1	B	323	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4974 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 Periplasmic chelated iron-binding protein YfeA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2209	1415	379	412	3			
1	B	273	Total	C	N	O	S	0	0	0
			2144	1376	362	403	3			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	312	LEU	-	expression tag	UNP Q56952
A	313	GLU	-	expression tag	UNP Q56952
A	314	HIS	-	expression tag	UNP Q56952
A	315	HIS	-	expression tag	UNP Q56952
A	316	HIS	-	expression tag	UNP Q56952
A	317	HIS	-	expression tag	UNP Q56952
A	318	HIS	-	expression tag	UNP Q56952
A	319	HIS	-	expression tag	UNP Q56952
A	320	HIS	-	expression tag	UNP Q56952
A	321	HIS	-	expression tag	UNP Q56952
A	322	HIS	-	expression tag	UNP Q56952
A	323	HIS	-	expression tag	UNP Q56952
B	312	LEU	-	expression tag	UNP Q56952
B	313	GLU	-	expression tag	UNP Q56952
B	314	HIS	-	expression tag	UNP Q56952
B	315	HIS	-	expression tag	UNP Q56952
B	316	HIS	-	expression tag	UNP Q56952
B	317	HIS	-	expression tag	UNP Q56952
B	318	HIS	-	expression tag	UNP Q56952
B	319	HIS	-	expression tag	UNP Q56952
B	320	HIS	-	expression tag	UNP Q56952
B	321	HIS	-	expression tag	UNP Q56952
B	322	HIS	-	expression tag	UNP Q56952
B	323	HIS	-	expression tag	UNP Q56952

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	1
2	B	1	Total Fe 1 1	0	1

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	1
3	B	2	Total Zn 2 2	0	2

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Mn 2 2	0	1
4	B	5	Total Mn 5 5	0	2

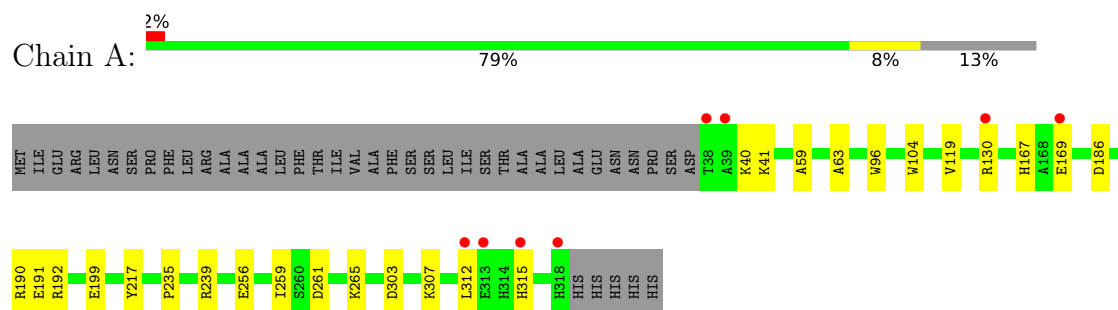
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	337	Total O 337 337	0	0
5	B	272	Total O 272 272	0	0

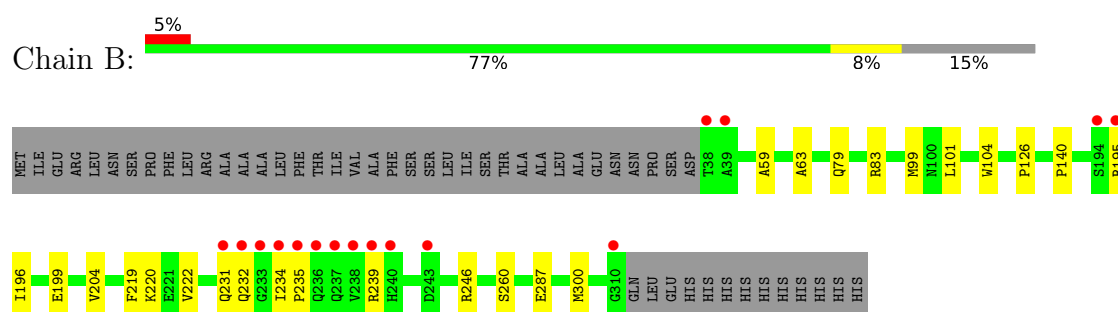
3 Residue-property plots [i](#)

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: Periplasmic chelated iron-binding protein YfeA



- Molecule 1: Periplasmic chelated iron-binding protein YfeA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.31Å 76.43Å 107.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.51 – 1.85 50.51 – 1.85	Depositor EDS
% Data completeness (in resolution range)	93.3 (50.51-1.85) 91.1 (50.51-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.78 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.152 , 0.184 (Not available) , 0.211	Depositor DCC
R_{free} test set	2245 reflections (4.31%)	wwPDB-VP
Wilson B-factor (Å ²)	16.8	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.6	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	0.96	EDS
Total number of atoms	4974	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.24% 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: FE, ZN, MN

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	0.35	0/2265	0.54	0/3083
1	B	0.34	0/2196	0.54	1/2990 (0.0%)
All	All	0.34	0/4461	0.54	1/6073 (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	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	195	ARG	CB-CG-CD	-5.73	98.11	111.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	246	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	2209	0	2195	17	0
1	B	2144	0	2146	20	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
4	A	2	0	0	0	0
4	B	5	0	0	0	0
5	A	337	0	0	4	1
5	B	272	0	0	7	3
All	All	4974	0	4341	35	3

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

All (35) 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:79:GLN:OE1	5:B:501:HOH:O	1.94	0.86
1:B:287:GLU:OE1	5:B:502:HOH:O	1.97	0.82
1:A:186:ASP:OD1	1:B:83:ARG:NH1	2.24	0.70
1:B:231:GLN:NE2	5:B:506:HOH:O	2.27	0.61
1:A:303:ASP:OD2	1:A:307:LYS:HE2	2.01	0.59
1:A:192:ARG:NE	5:A:504:HOH:O	2.38	0.56
1:B:234:ILE:HB	1:B:235:PRO:HD3	1.87	0.55
1:A:239:ARG:NH2	5:A:505:HOH:O	2.41	0.53
1:B:239:ARG:HH11	1:B:239:ARG:HG3	1.75	0.52
1:A:40:LYS:HD2	1:A:41:LYS:N	2.25	0.51
1:A:191:GLU:HG3	5:A:722:HOH:O	2.11	0.51
1:B:196:ILE:HD12	1:B:219:PHE:HZ	1.77	0.50
1:B:59:ALA:HB1	1:B:63:ALA:HB3	1.93	0.49
1:B:220:LYS:NZ	5:B:508:HOH:O	2.40	0.48
1:A:96:TRP:CE2	1:A:119:VAL:HG12	2.48	0.48
1:A:167:HIS:HA	1:A:169:GLU:OE2	2.14	0.47
1:B:232:GLN:HB2	5:B:569:HOH:O	2.15	0.46
1:B:99:MET:HE3	1:B:126:PRO:HB3	1.99	0.45
1:A:261:ASP:OD2	1:A:265:LYS:HE3	2.16	0.45
1:A:104:TRP:CD1	1:A:104:TRP:H	2.35	0.45
1:A:312:LEU:HA	1:A:315:HIS:HE1	1.82	0.45
1:A:59:ALA:HB1	1:A:63:ALA:HB3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300:MET:HE3	1:B:300:MET:HB3	1.70	0.44
1:A:235:PRO:O	1:A:239:ARG:HG3	2.18	0.44
1:B:199:GLU:OE1	5:B:504:HOH:O	2.22	0.43
1:B:239:ARG:HG3	1:B:239:ARG:NH1	2.34	0.42
1:B:79:GLN:HG2	5:B:643:HOH:O	2.19	0.42
1:B:204:VAL:HG22	1:B:222:VAL:HB	2.02	0.41
1:B:104:TRP:CD1	1:B:104:TRP:H	2.38	0.41
1:A:256:GLU:H	1:A:259:ILE:HD11	1.84	0.41
1:A:190:ARG:HG2	1:A:217:TYR:CE1	2.55	0.41
1:B:232:GLN:H	1:B:232:GLN:HG3	1.77	0.41
1:A:199:GLU:HG2	1:B:260:SER:HB2	2.03	0.41
1:A:130:ARG:NH2	5:A:511:HOH:O	2.53	0.40
1:B:101:LEU:HB2	1:B:140:PRO:HB2	2.03	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:616:HOH:O	5:B:672:HOH:O[4_465]	2.11	0.09
5:B:661:HOH:O	5:B:684:HOH:O[4_565]	2.13	0.07
5:A:750:HOH:O	5:B:750:HOH:O[2_465]	2.17	0.03

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	279/323 (86%)	272 (98%)	7 (2%)	0	100	100
1	B	271/323 (84%)	264 (97%)	7 (3%)	0	100	100
All	All	550/646 (85%)	536 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	236/273 (86%)	236 (100%)	0	100	100
1	B	230/273 (84%)	230 (100%)	0	100	100
All	All	466/546 (85%)	466 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	274	GLN
1	A	315	HIS
1	A	317	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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

6.1 Protein, DNA and RNA chains

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	281/323 (86%)	-0.22	8 (2%) 55 58	9, 18, 46, 108	0
1	B	273/323 (84%)	-0.13	16 (5%) 28 31	9, 19, 60, 96	0
All	All	554/646 (85%)	-0.18	24 (4%) 40 43	9, 19, 54, 108	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	39	ALA	7.2
1	A	39	ALA	6.0
1	B	38	THR	5.8
1	B	234	ILE	4.8
1	B	310	GLY	4.3
1	A	38	THR	4.2
1	A	312	LEU	4.2
1	B	237	GLN	4.0
1	B	195	ARG	3.5
1	A	313	GLU	3.4
1	A	318	HIS	3.4
1	B	233	GLY	3.2
1	B	235	PRO	3.0
1	B	232	GLN	3.0
1	B	243	ASP	2.6
1	B	239	ARG	2.4
1	B	194	SER	2.4
1	A	315	HIS	2.4
1	A	169	GLU	2.3
1	B	231	GLN	2.2
1	B	240	HIS	2.2
1	B	236	GLN	2.2
1	B	238	VAL	2.1
1	A	130	ARG	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

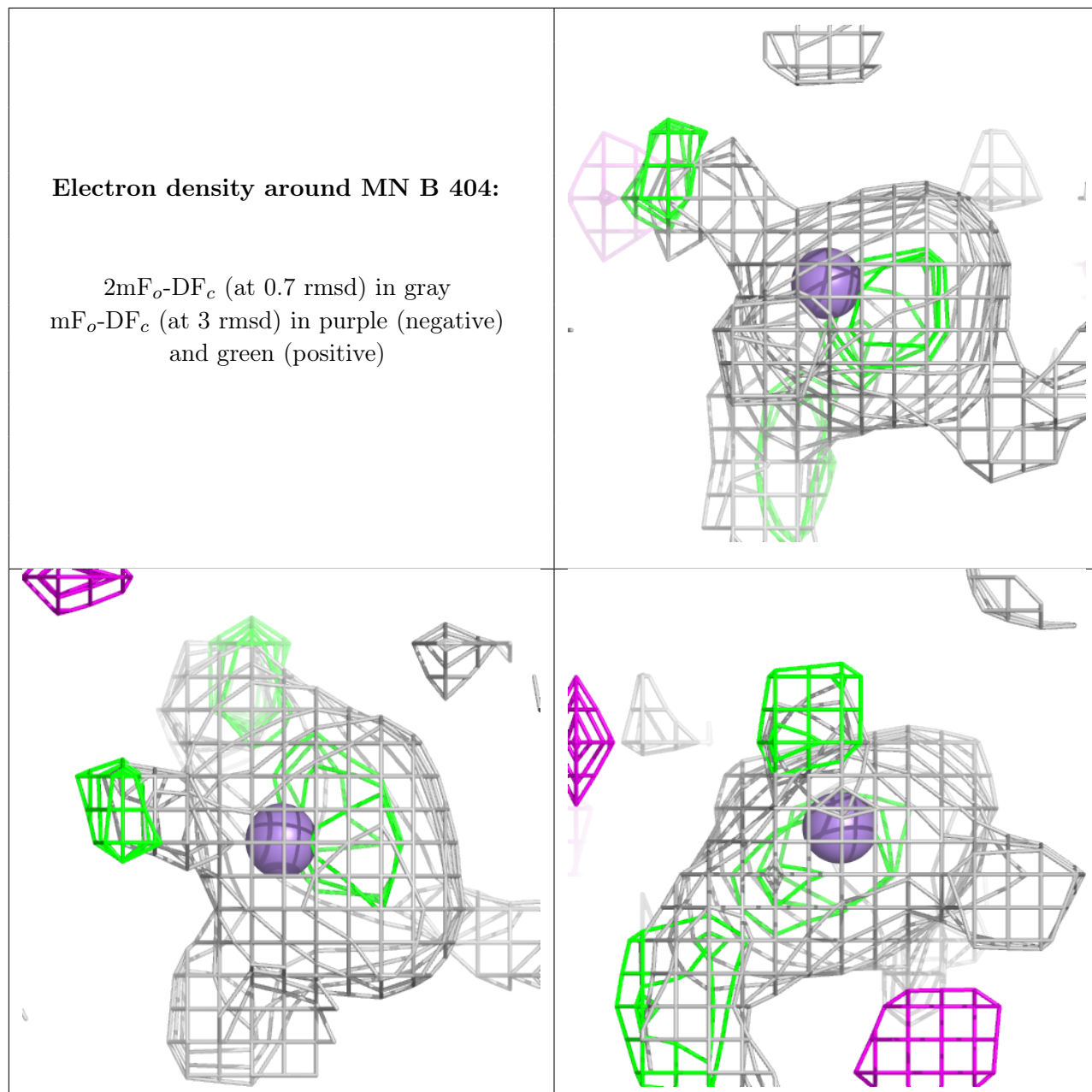
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MN	B	404	1/1	0.69	0.19	98,98,98,98	0
4	MN	B	408	1/1	0.71	0.19	112,112,112,112	0
4	MN	B	407	1/1	0.77	0.16	103,103,103,103	1
4	MN	A	404	1/1	0.90	0.09	36,36,36,36	1
3	ZN	B	406[B]	1/1	0.99	0.04	21,21,21,21	1
4	MN	B	405[A]	1/1	0.99	0.04	21,21,21,21	1
2	FE	B	401[A]	1/1	1.00	0.04	5,5,5,5	1
4	MN	B	403[C]	1/1	1.00	0.03	5,5,5,5	1
3	ZN	A	402[B]	1/1	1.00	0.05	4,4,4,4	1
3	ZN	B	402[B]	1/1	1.00	0.03	6,6,6,6	1
2	FE	A	401[A]	1/1	1.00	0.06	4,4,4,4	1
4	MN	A	403[C]	1/1	1.00	0.06	3,3,3,3	1

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.

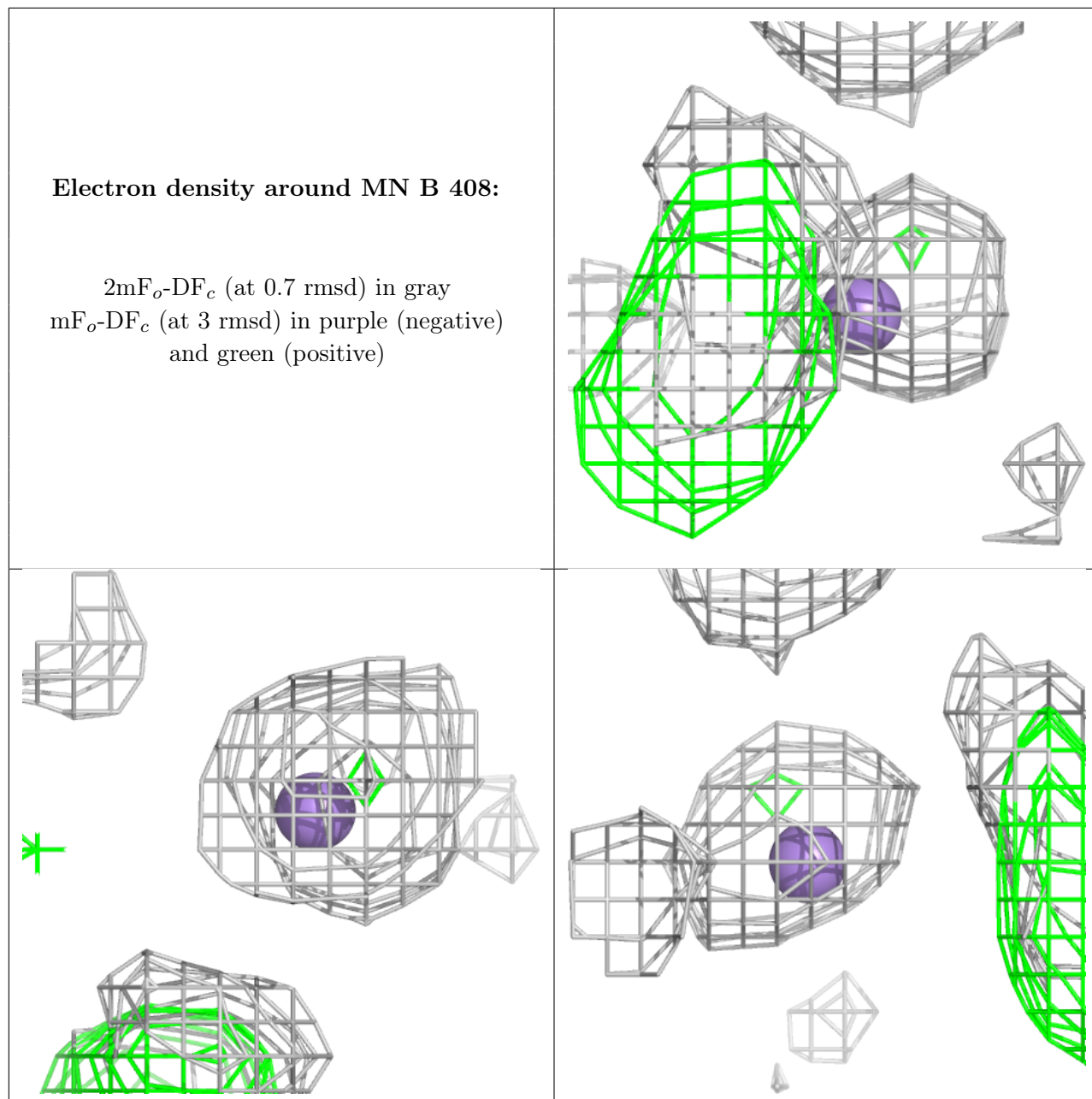
Electron density around MN B 404:

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



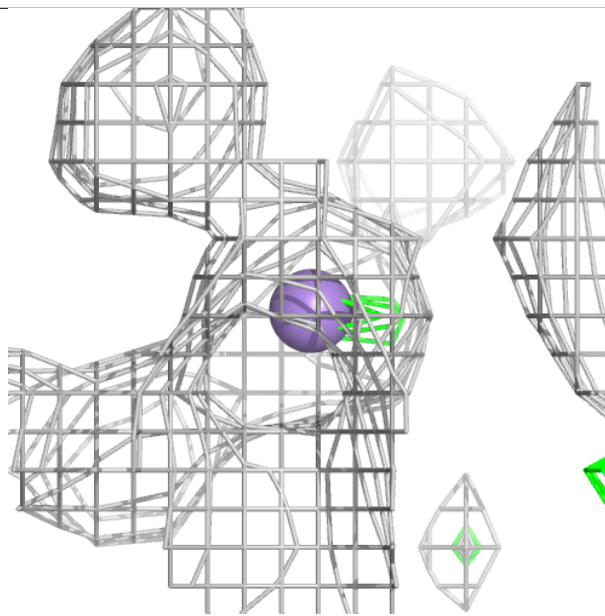
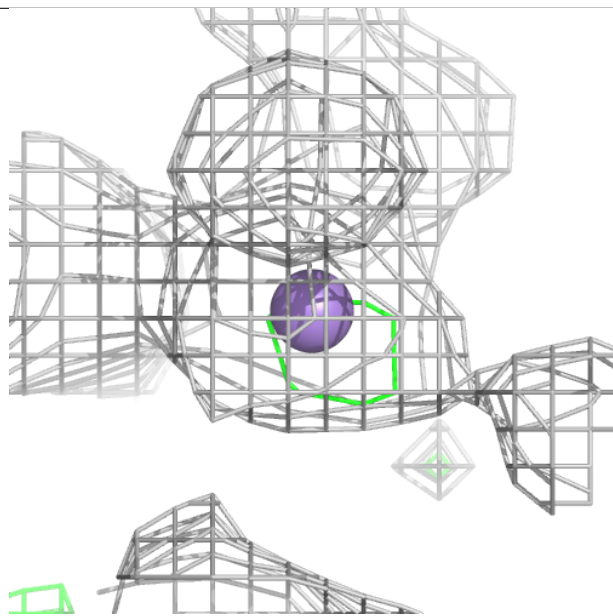
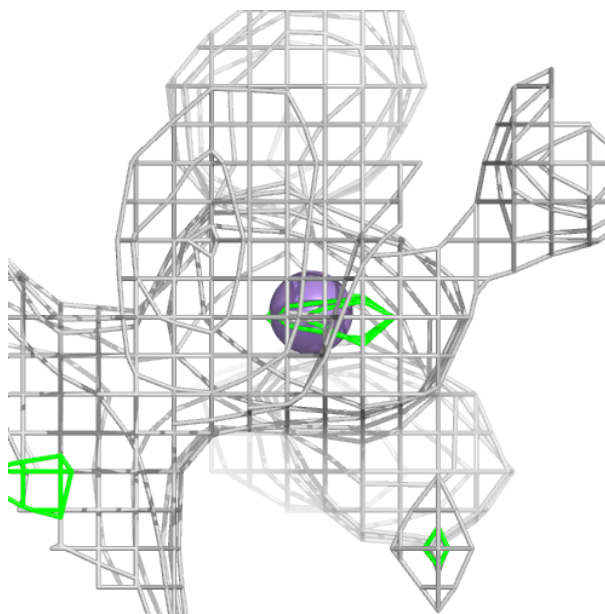
Electron density around MN B 408:

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



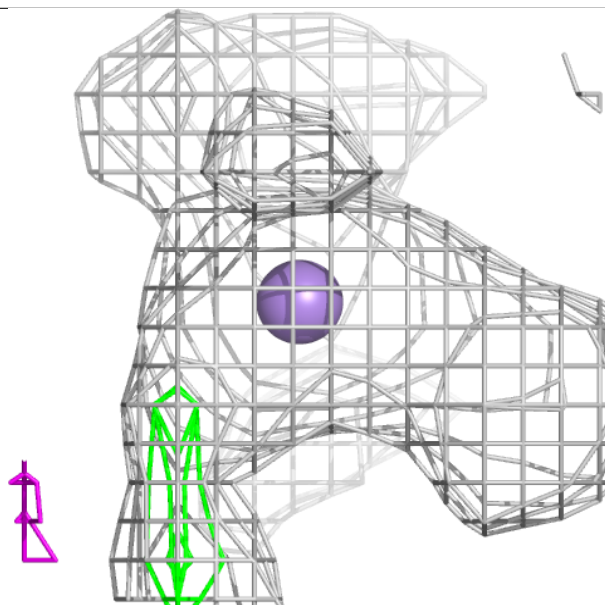
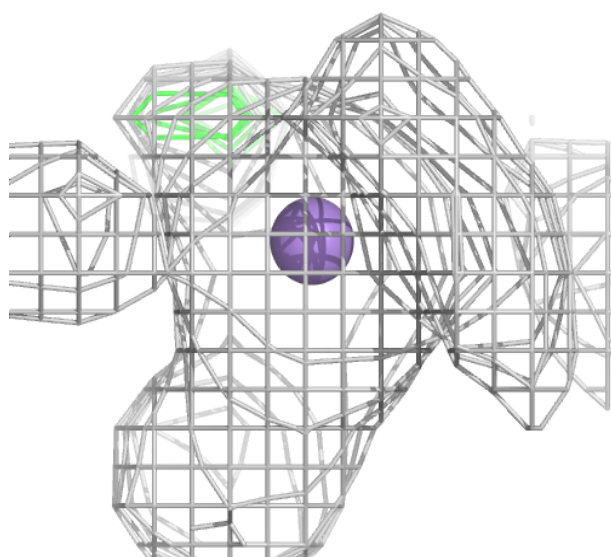
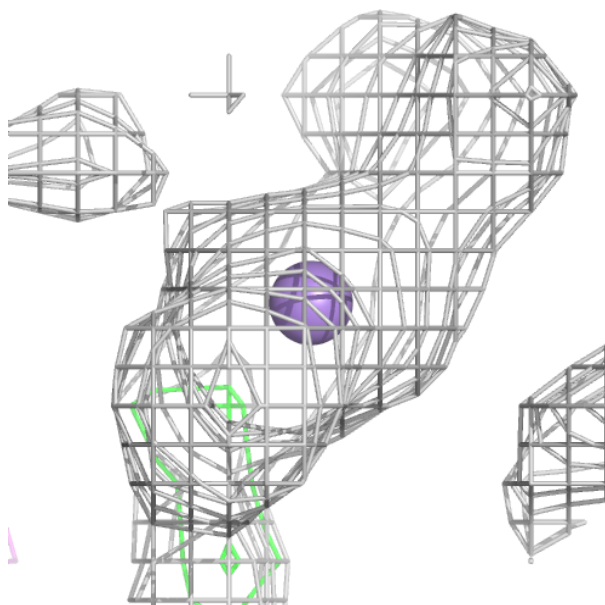
Electron density around MN B 407:

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



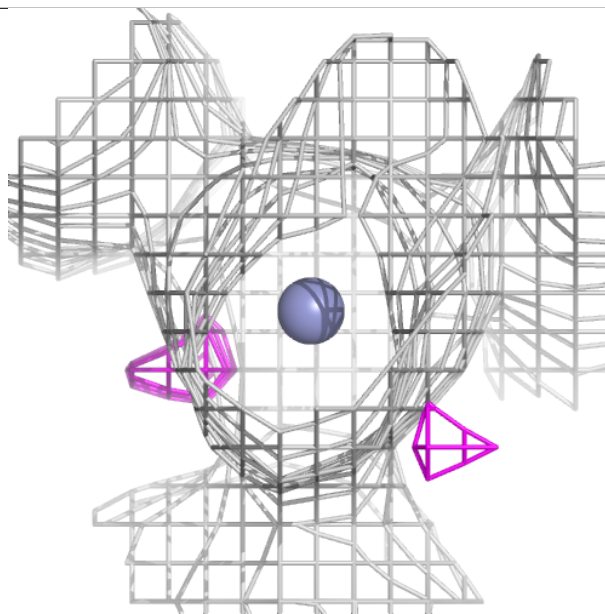
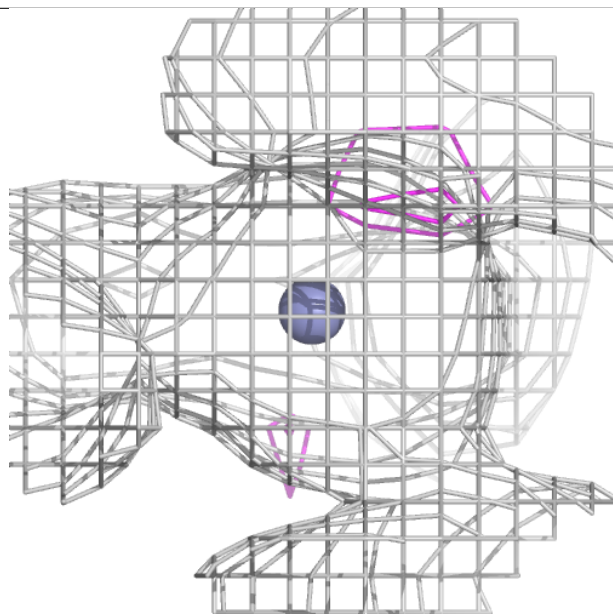
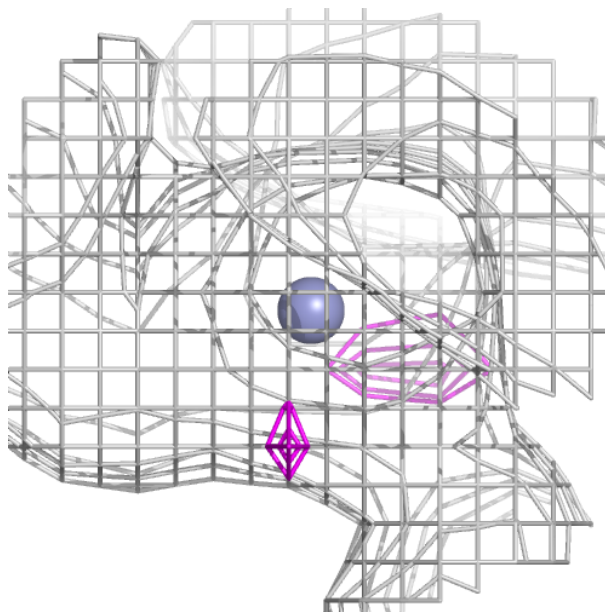
Electron density around MN A 404:

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



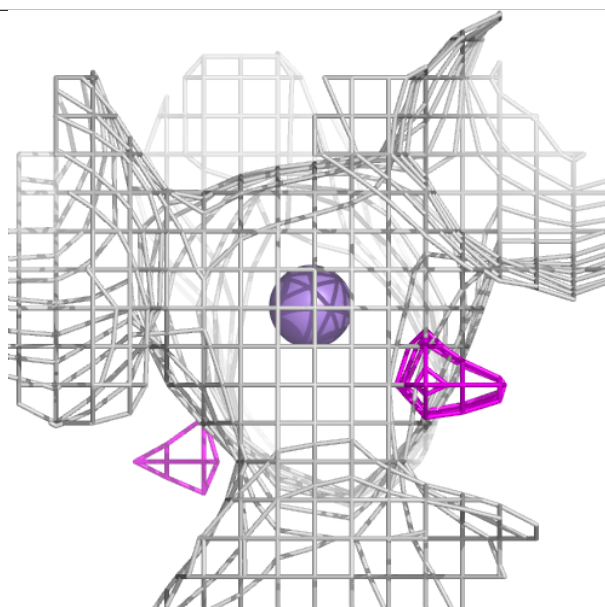
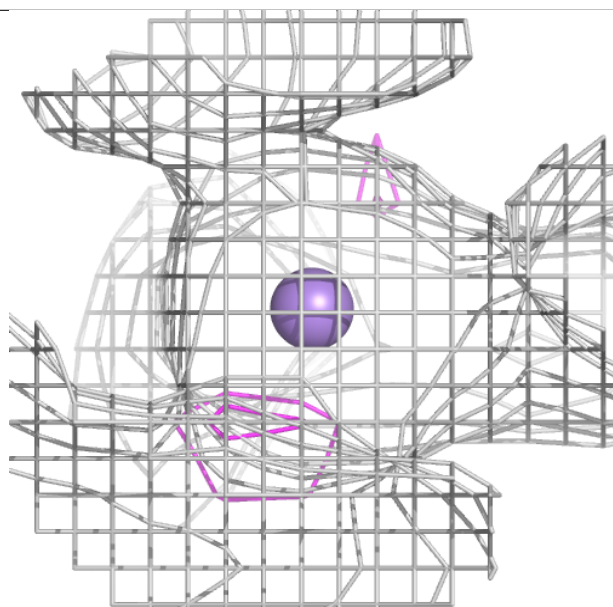
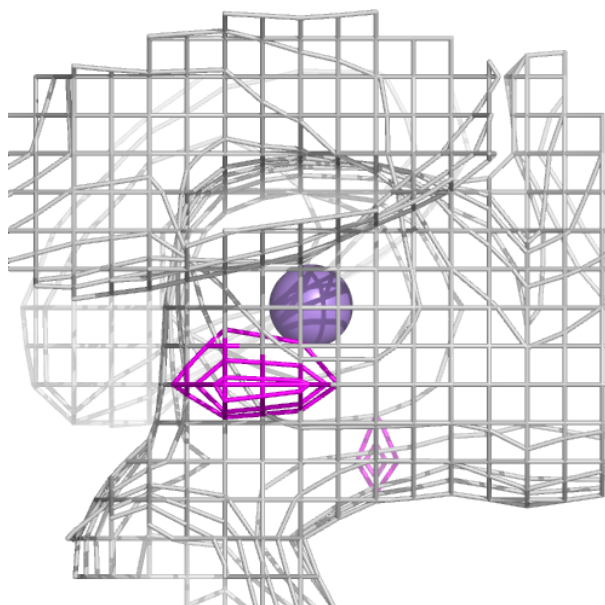
Electron density around ZN B 406 (B):

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



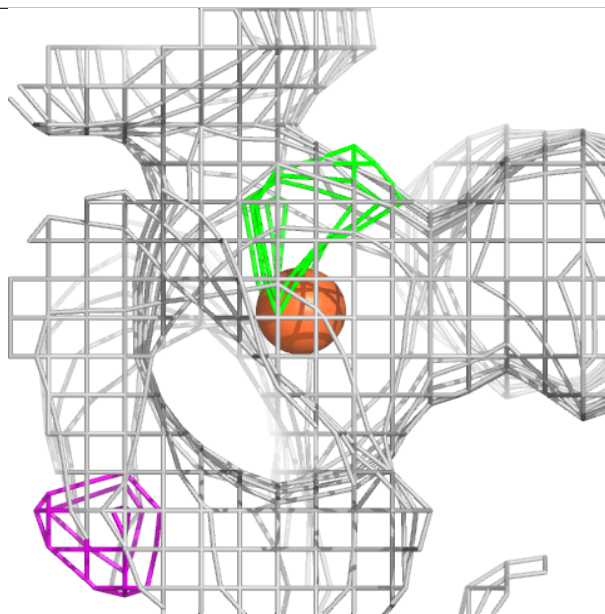
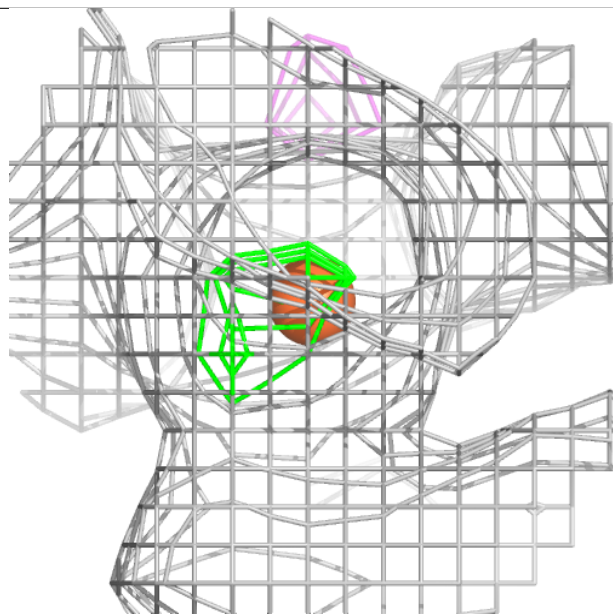
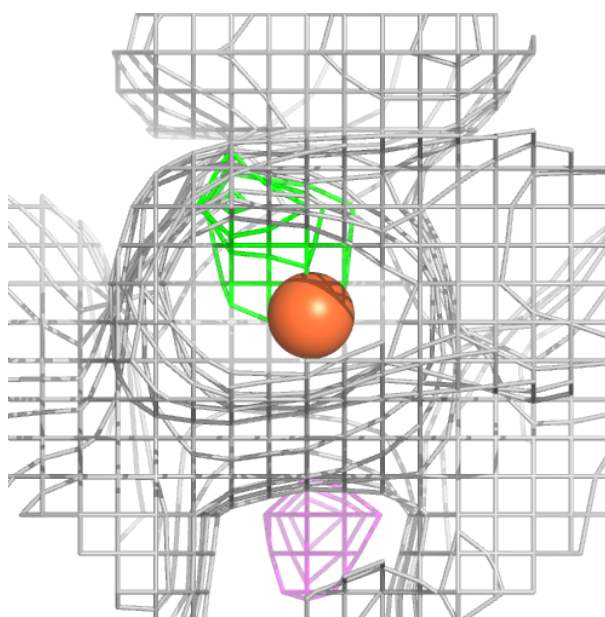
Electron density around MN B 405 (A):

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



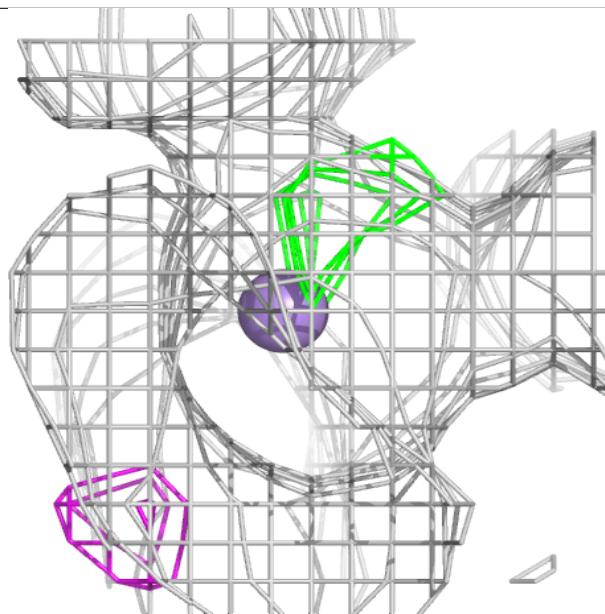
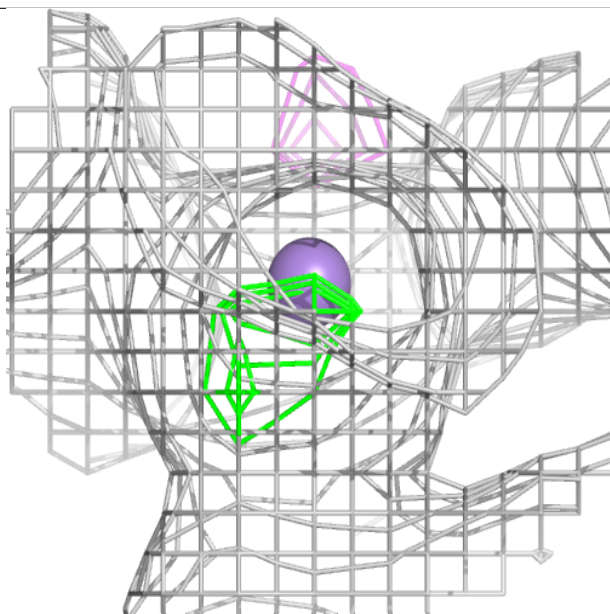
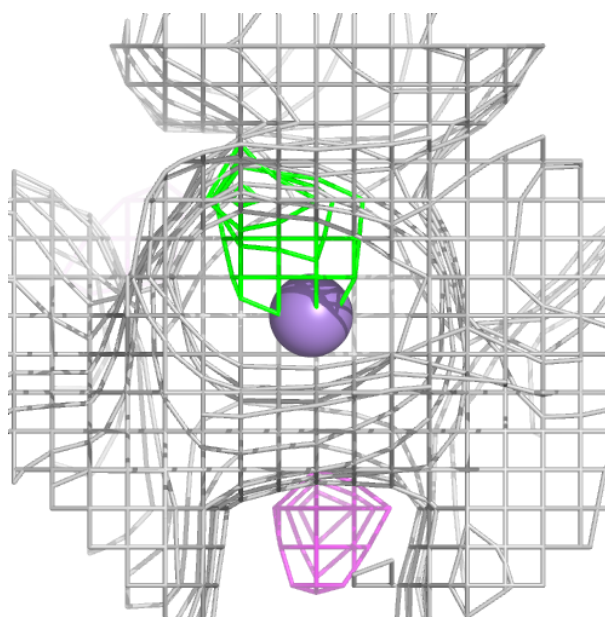
Electron density around FE B 401 (A):

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



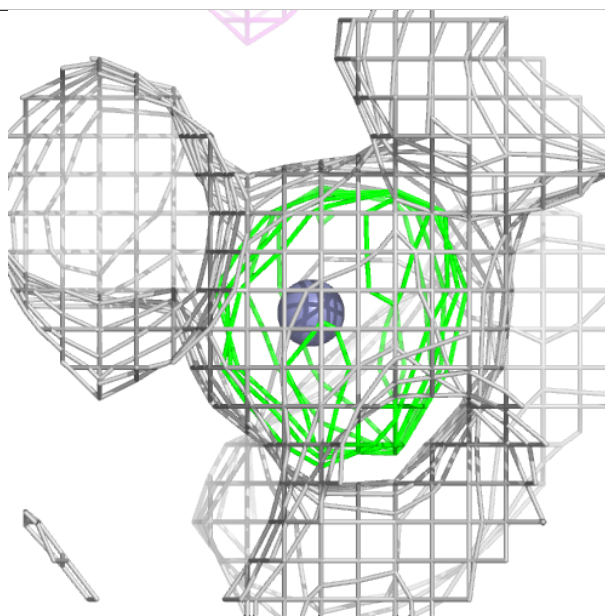
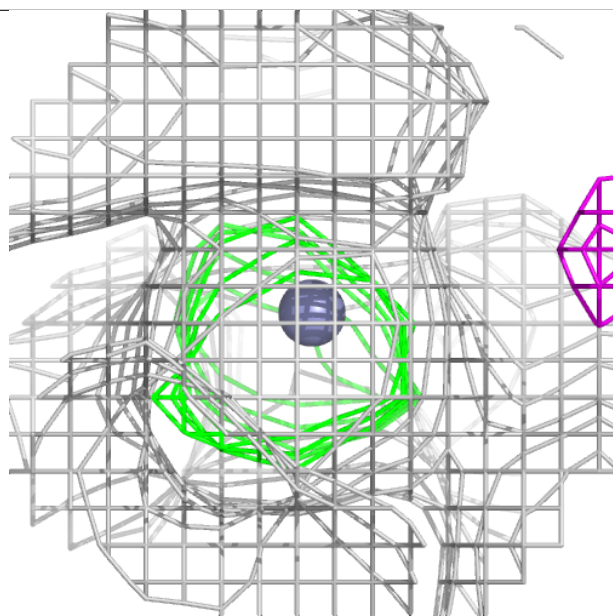
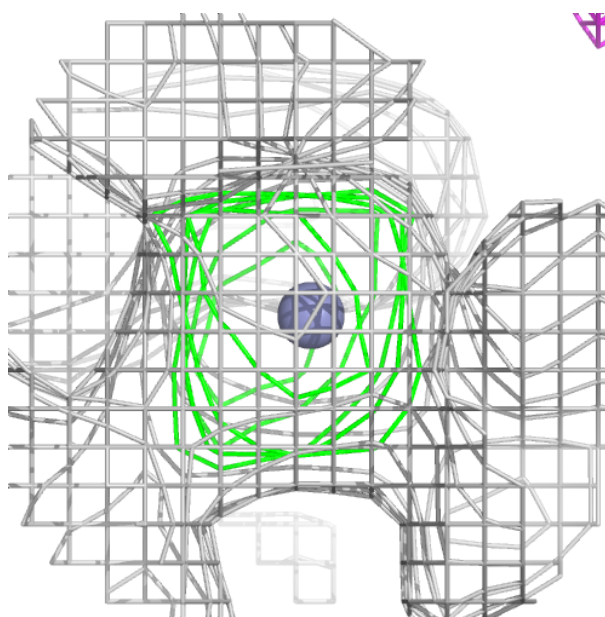
Electron density around MN B 403 (C):

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



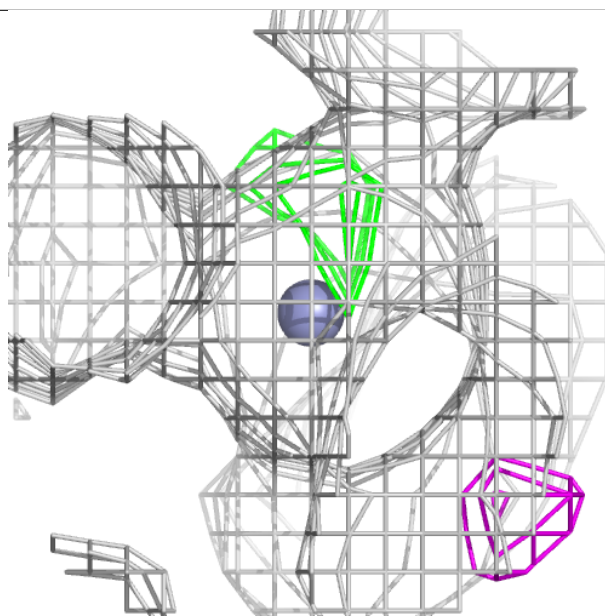
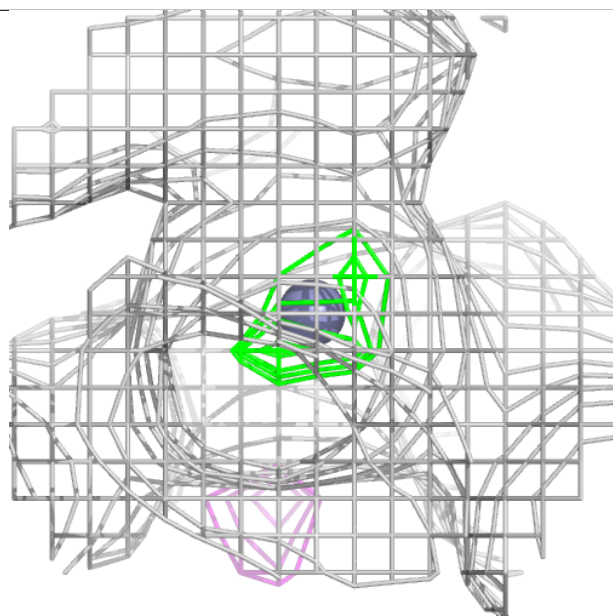
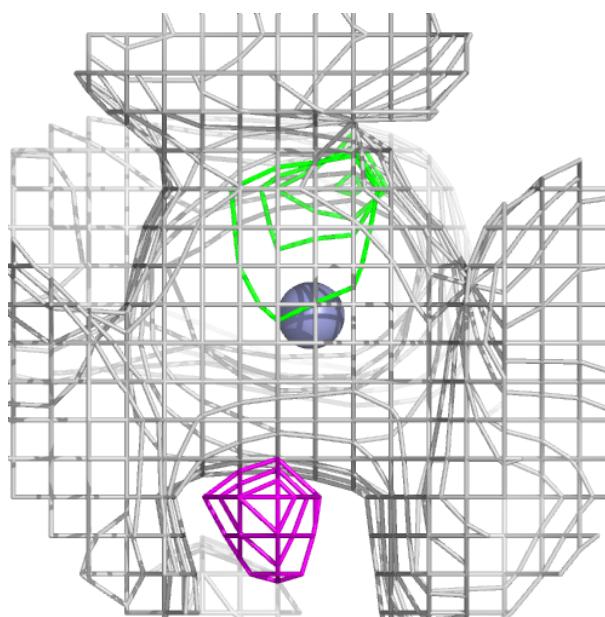
Electron density around ZN A 402 (B):

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



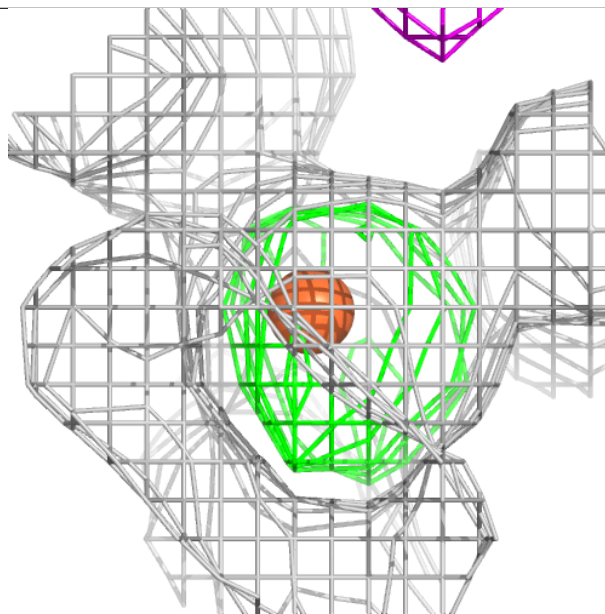
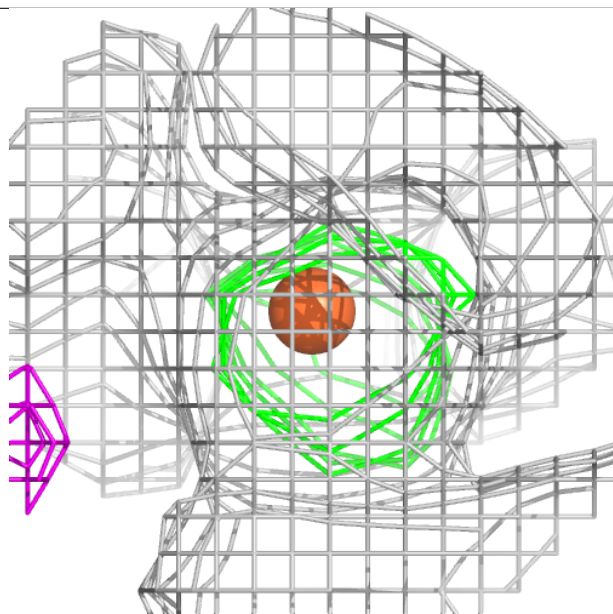
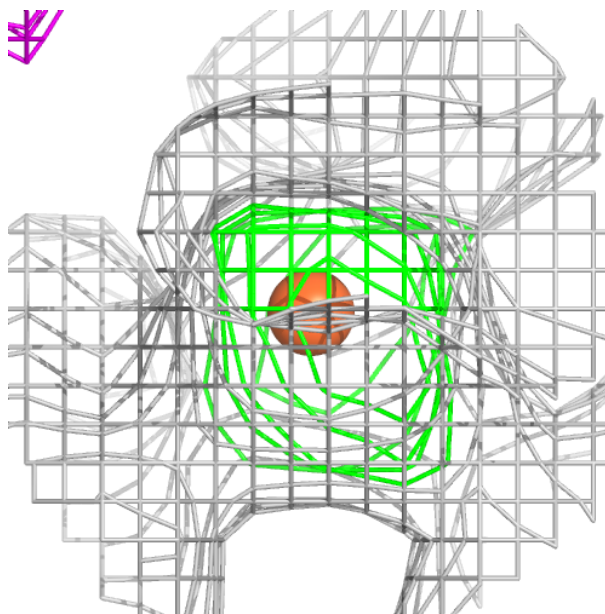
Electron density around ZN B 402 (B):

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



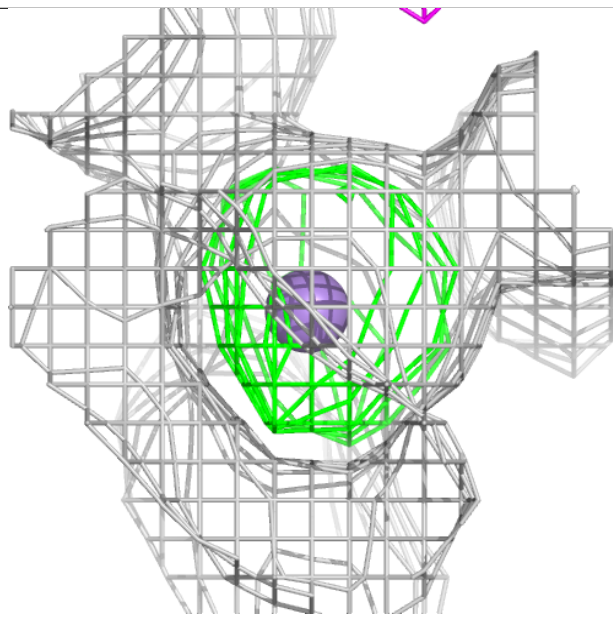
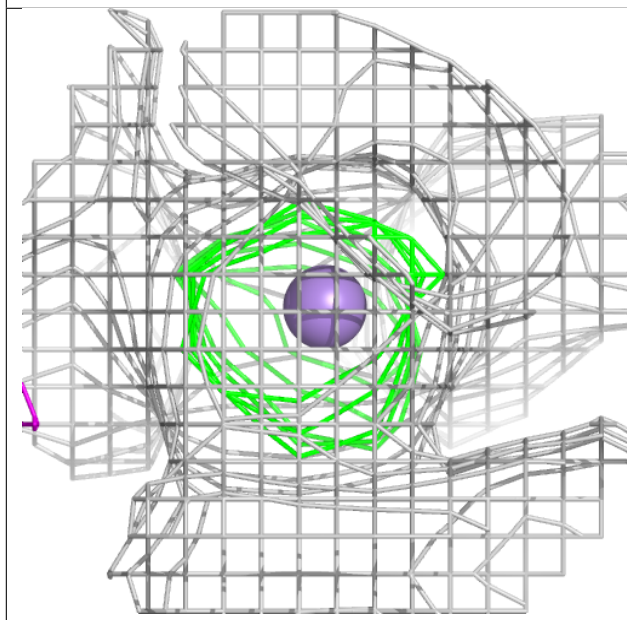
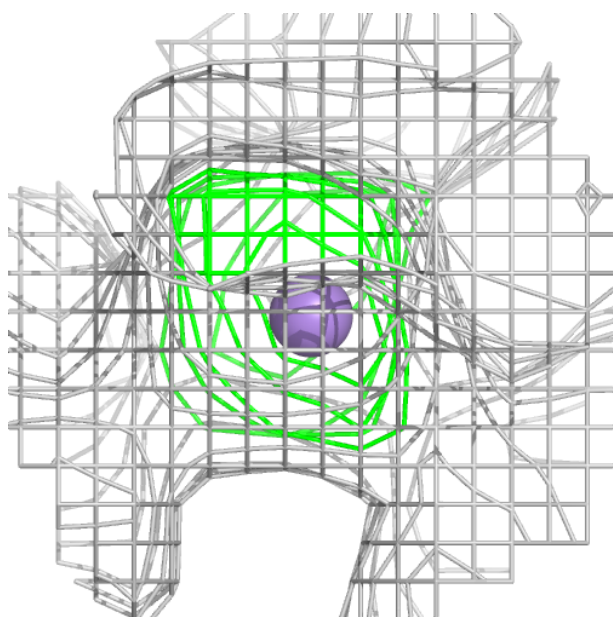
Electron density around FE A 401 (A):

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



Electron density around MN A 403 (C):

$2mF_o-DF_c$ (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.