



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 03:20 AM UTC

PDB ID : 9UG7 / pdb\_00009ug7  
Title : Structure of sulfonamide synthase SbzM from Actinokineospora mزابensis  
Authors : Zhu, Y.; Mori, T.; Abe, I.  
Deposited on : 2025-04-11  
Resolution : 1.94 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](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

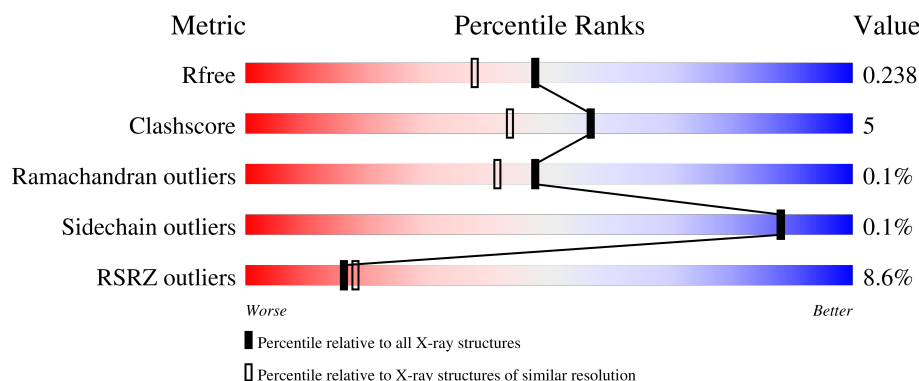
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.94 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	215	<div> <div>4%</div> <div>70%</div> <div>11%</div> <div>19%</div> </div>
1	B	215	<div> <div>8%</div> <div>69%</div> <div>12%</div> <div>19%</div> </div>
1	C	215	<div> <div>7%</div> <div>72%</div> <div>9%</div> <div>20%</div> </div>
1	D	215	<div> <div>5%</div> <div>79%</div> <div>.</div> <div>19%</div> </div>
1	E	215	<div> <div>12%</div> <div>68%</div> <div>12%</div> <div>20%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	215	<div> <div></div> <div>7%</div> <div>75%</div> <div>7%</div> <div>19%</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8017 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 Cupin type-2 domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	174	Total	C	N	O	S	0	2	0
			1270	796	230	234	10			
1	F	175	Total	C	N	O	S	0	0	0
			1242	781	222	230	9			
1	D	175	Total	C	N	O	S	0	1	0
			1260	793	223	235	9			
1	B	174	Total	C	N	O	S	0	0	0
			1249	784	221	235	9			
1	C	173	Total	C	N	O	S	0	0	0
			1245	782	220	234	9			
1	E	173	Total	C	N	O	S	0	0	0
			1245	782	220	234	9			

There are 156 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A8E2X4A6
A	2	LYS	-	expression tag	UNP A0A8E2X4A6
A	3	HIS	-	expression tag	UNP A0A8E2X4A6
A	4	HIS	-	expression tag	UNP A0A8E2X4A6
A	5	HIS	-	expression tag	UNP A0A8E2X4A6
A	6	HIS	-	expression tag	UNP A0A8E2X4A6
A	7	HIS	-	expression tag	UNP A0A8E2X4A6
A	8	HIS	-	expression tag	UNP A0A8E2X4A6
A	9	HIS	-	expression tag	UNP A0A8E2X4A6
A	10	SER	-	expression tag	UNP A0A8E2X4A6
A	11	ASP	-	expression tag	UNP A0A8E2X4A6
A	12	TYR	-	expression tag	UNP A0A8E2X4A6
A	13	ASP	-	expression tag	UNP A0A8E2X4A6
A	14	ILE	-	expression tag	UNP A0A8E2X4A6
A	15	PRO	-	expression tag	UNP A0A8E2X4A6
A	16	THR	-	expression tag	UNP A0A8E2X4A6
A	17	THR	-	expression tag	UNP A0A8E2X4A6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	18	GLU	-	expression tag	UNP A0A8E2X4A6
A	19	ASN	-	expression tag	UNP A0A8E2X4A6
A	20	LEU	-	expression tag	UNP A0A8E2X4A6
A	21	TYR	-	expression tag	UNP A0A8E2X4A6
A	22	PHE	-	expression tag	UNP A0A8E2X4A6
A	23	GLN	-	expression tag	UNP A0A8E2X4A6
A	24	GLY	-	expression tag	UNP A0A8E2X4A6
A	25	SER	-	expression tag	UNP A0A8E2X4A6
A	26	VAL	-	expression tag	UNP A0A8E2X4A6
F	1	MET	-	initiating methionine	UNP A0A8E2X4A6
F	2	LYS	-	expression tag	UNP A0A8E2X4A6
F	3	HIS	-	expression tag	UNP A0A8E2X4A6
F	4	HIS	-	expression tag	UNP A0A8E2X4A6
F	5	HIS	-	expression tag	UNP A0A8E2X4A6
F	6	HIS	-	expression tag	UNP A0A8E2X4A6
F	7	HIS	-	expression tag	UNP A0A8E2X4A6
F	8	HIS	-	expression tag	UNP A0A8E2X4A6
F	9	HIS	-	expression tag	UNP A0A8E2X4A6
F	10	SER	-	expression tag	UNP A0A8E2X4A6
F	11	ASP	-	expression tag	UNP A0A8E2X4A6
F	12	TYR	-	expression tag	UNP A0A8E2X4A6
F	13	ASP	-	expression tag	UNP A0A8E2X4A6
F	14	ILE	-	expression tag	UNP A0A8E2X4A6
F	15	PRO	-	expression tag	UNP A0A8E2X4A6
F	16	THR	-	expression tag	UNP A0A8E2X4A6
F	17	THR	-	expression tag	UNP A0A8E2X4A6
F	18	GLU	-	expression tag	UNP A0A8E2X4A6
F	19	ASN	-	expression tag	UNP A0A8E2X4A6
F	20	LEU	-	expression tag	UNP A0A8E2X4A6
F	21	TYR	-	expression tag	UNP A0A8E2X4A6
F	22	PHE	-	expression tag	UNP A0A8E2X4A6
F	23	GLN	-	expression tag	UNP A0A8E2X4A6
F	24	GLY	-	expression tag	UNP A0A8E2X4A6
F	25	SER	-	expression tag	UNP A0A8E2X4A6
F	26	VAL	-	expression tag	UNP A0A8E2X4A6
D	1	MET	-	initiating methionine	UNP A0A8E2X4A6
D	2	LYS	-	expression tag	UNP A0A8E2X4A6
D	3	HIS	-	expression tag	UNP A0A8E2X4A6
D	4	HIS	-	expression tag	UNP A0A8E2X4A6
D	5	HIS	-	expression tag	UNP A0A8E2X4A6
D	6	HIS	-	expression tag	UNP A0A8E2X4A6
D	7	HIS	-	expression tag	UNP A0A8E2X4A6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	8	HIS	-	expression tag	UNP A0A8E2X4A6
D	9	HIS	-	expression tag	UNP A0A8E2X4A6
D	10	SER	-	expression tag	UNP A0A8E2X4A6
D	11	ASP	-	expression tag	UNP A0A8E2X4A6
D	12	TYR	-	expression tag	UNP A0A8E2X4A6
D	13	ASP	-	expression tag	UNP A0A8E2X4A6
D	14	ILE	-	expression tag	UNP A0A8E2X4A6
D	15	PRO	-	expression tag	UNP A0A8E2X4A6
D	16	THR	-	expression tag	UNP A0A8E2X4A6
D	17	THR	-	expression tag	UNP A0A8E2X4A6
D	18	GLU	-	expression tag	UNP A0A8E2X4A6
D	19	ASN	-	expression tag	UNP A0A8E2X4A6
D	20	LEU	-	expression tag	UNP A0A8E2X4A6
D	21	TYR	-	expression tag	UNP A0A8E2X4A6
D	22	PHE	-	expression tag	UNP A0A8E2X4A6
D	23	GLN	-	expression tag	UNP A0A8E2X4A6
D	24	GLY	-	expression tag	UNP A0A8E2X4A6
D	25	SER	-	expression tag	UNP A0A8E2X4A6
D	26	VAL	-	expression tag	UNP A0A8E2X4A6
B	1	MET	-	initiating methionine	UNP A0A8E2X4A6
B	2	LYS	-	expression tag	UNP A0A8E2X4A6
B	3	HIS	-	expression tag	UNP A0A8E2X4A6
B	4	HIS	-	expression tag	UNP A0A8E2X4A6
B	5	HIS	-	expression tag	UNP A0A8E2X4A6
B	6	HIS	-	expression tag	UNP A0A8E2X4A6
B	7	HIS	-	expression tag	UNP A0A8E2X4A6
B	8	HIS	-	expression tag	UNP A0A8E2X4A6
B	9	HIS	-	expression tag	UNP A0A8E2X4A6
B	10	SER	-	expression tag	UNP A0A8E2X4A6
B	11	ASP	-	expression tag	UNP A0A8E2X4A6
B	12	TYR	-	expression tag	UNP A0A8E2X4A6
B	13	ASP	-	expression tag	UNP A0A8E2X4A6
B	14	ILE	-	expression tag	UNP A0A8E2X4A6
B	15	PRO	-	expression tag	UNP A0A8E2X4A6
B	16	THR	-	expression tag	UNP A0A8E2X4A6
B	17	THR	-	expression tag	UNP A0A8E2X4A6
B	18	GLU	-	expression tag	UNP A0A8E2X4A6
B	19	ASN	-	expression tag	UNP A0A8E2X4A6
B	20	LEU	-	expression tag	UNP A0A8E2X4A6
B	21	TYR	-	expression tag	UNP A0A8E2X4A6
B	22	PHE	-	expression tag	UNP A0A8E2X4A6
B	23	GLN	-	expression tag	UNP A0A8E2X4A6

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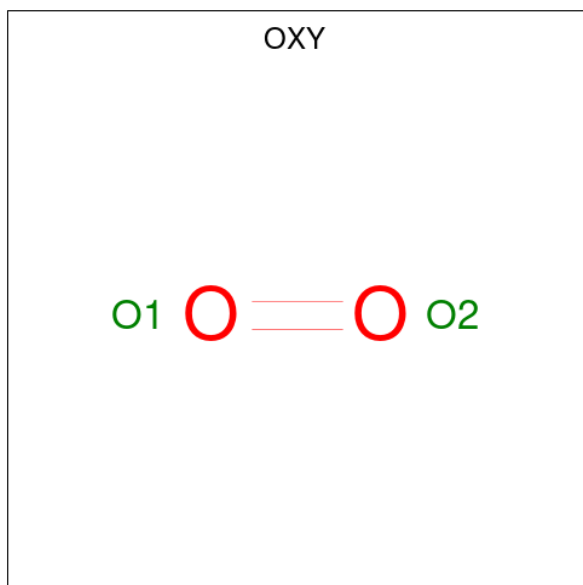
Chain	Residue	Modelled	Actual	Comment	Reference
B	24	GLY	-	expression tag	UNP A0A8E2X4A6
B	25	SER	-	expression tag	UNP A0A8E2X4A6
B	26	VAL	-	expression tag	UNP A0A8E2X4A6
C	1	MET	-	initiating methionine	UNP A0A8E2X4A6
C	2	LYS	-	expression tag	UNP A0A8E2X4A6
C	3	HIS	-	expression tag	UNP A0A8E2X4A6
C	4	HIS	-	expression tag	UNP A0A8E2X4A6
C	5	HIS	-	expression tag	UNP A0A8E2X4A6
C	6	HIS	-	expression tag	UNP A0A8E2X4A6
C	7	HIS	-	expression tag	UNP A0A8E2X4A6
C	8	HIS	-	expression tag	UNP A0A8E2X4A6
C	9	HIS	-	expression tag	UNP A0A8E2X4A6
C	10	SER	-	expression tag	UNP A0A8E2X4A6
C	11	ASP	-	expression tag	UNP A0A8E2X4A6
C	12	TYR	-	expression tag	UNP A0A8E2X4A6
C	13	ASP	-	expression tag	UNP A0A8E2X4A6
C	14	ILE	-	expression tag	UNP A0A8E2X4A6
C	15	PRO	-	expression tag	UNP A0A8E2X4A6
C	16	THR	-	expression tag	UNP A0A8E2X4A6
C	17	THR	-	expression tag	UNP A0A8E2X4A6
C	18	GLU	-	expression tag	UNP A0A8E2X4A6
C	19	ASN	-	expression tag	UNP A0A8E2X4A6
C	20	LEU	-	expression tag	UNP A0A8E2X4A6
C	21	TYR	-	expression tag	UNP A0A8E2X4A6
C	22	PHE	-	expression tag	UNP A0A8E2X4A6
C	23	GLN	-	expression tag	UNP A0A8E2X4A6
C	24	GLY	-	expression tag	UNP A0A8E2X4A6
C	25	SER	-	expression tag	UNP A0A8E2X4A6
C	26	VAL	-	expression tag	UNP A0A8E2X4A6
E	1	MET	-	initiating methionine	UNP A0A8E2X4A6
E	2	LYS	-	expression tag	UNP A0A8E2X4A6
E	3	HIS	-	expression tag	UNP A0A8E2X4A6
E	4	HIS	-	expression tag	UNP A0A8E2X4A6
E	5	HIS	-	expression tag	UNP A0A8E2X4A6
E	6	HIS	-	expression tag	UNP A0A8E2X4A6
E	7	HIS	-	expression tag	UNP A0A8E2X4A6
E	8	HIS	-	expression tag	UNP A0A8E2X4A6
E	9	HIS	-	expression tag	UNP A0A8E2X4A6
E	10	SER	-	expression tag	UNP A0A8E2X4A6
E	11	ASP	-	expression tag	UNP A0A8E2X4A6
E	12	TYR	-	expression tag	UNP A0A8E2X4A6
E	13	ASP	-	expression tag	UNP A0A8E2X4A6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	14	ILE	-	expression tag	UNP A0A8E2X4A6
E	15	PRO	-	expression tag	UNP A0A8E2X4A6
E	16	THR	-	expression tag	UNP A0A8E2X4A6
E	17	THR	-	expression tag	UNP A0A8E2X4A6
E	18	GLU	-	expression tag	UNP A0A8E2X4A6
E	19	ASN	-	expression tag	UNP A0A8E2X4A6
E	20	LEU	-	expression tag	UNP A0A8E2X4A6
E	21	TYR	-	expression tag	UNP A0A8E2X4A6
E	22	PHE	-	expression tag	UNP A0A8E2X4A6
E	23	GLN	-	expression tag	UNP A0A8E2X4A6
E	24	GLY	-	expression tag	UNP A0A8E2X4A6
E	25	SER	-	expression tag	UNP A0A8E2X4A6
E	26	VAL	-	expression tag	UNP A0A8E2X4A6

- Molecule 2 is OXYGEN MOLECULE (CCD ID: OXY) (formula: O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O 2 2	0	0
2	F	1	Total O 2 2	0	0
2	D	1	Total O 2 2	0	0
2	B	1	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total	O	0	0
			2	2		
2	E	1	Total	O	0	0
			2	2		

- 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	2	Total	Zn	0	0
			2	2		
3	F	2	Total	Zn	0	0
			2	2		
3	D	2	Total	Zn	0	0
			2	2		
3	B	2	Total	Zn	0	0
			2	2		
3	C	2	Total	Zn	0	0
			2	2		
3	E	2	Total	Zn	0	0
			2	2		

- Molecule 4 is NICKEL (II) ION (CCD ID: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ni	0	0
			1	1		
4	F	1	Total	Ni	0	0
			1	1		
4	D	1	Total	Ni	0	0
			1	1		
4	B	1	Total	Ni	0	0
			1	1		
4	C	1	Total	Ni	0	0
			1	1		
4	E	1	Total	Ni	0	0
			1	1		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	F	1	Total Cl 1 1	0	0

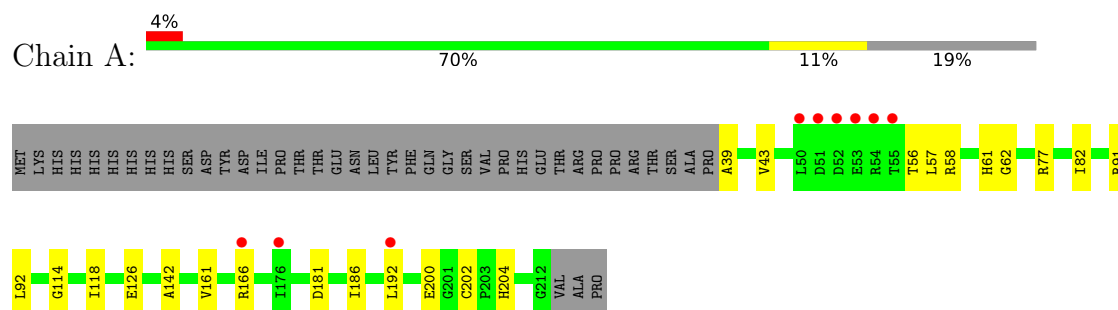
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	91	Total O 91 91	0	0
6	F	93	Total O 93 93	0	0
6	D	91	Total O 91 91	0	0
6	B	64	Total O 64 64	0	0
6	C	75	Total O 75 75	0	0
6	E	61	Total O 61 61	0	0

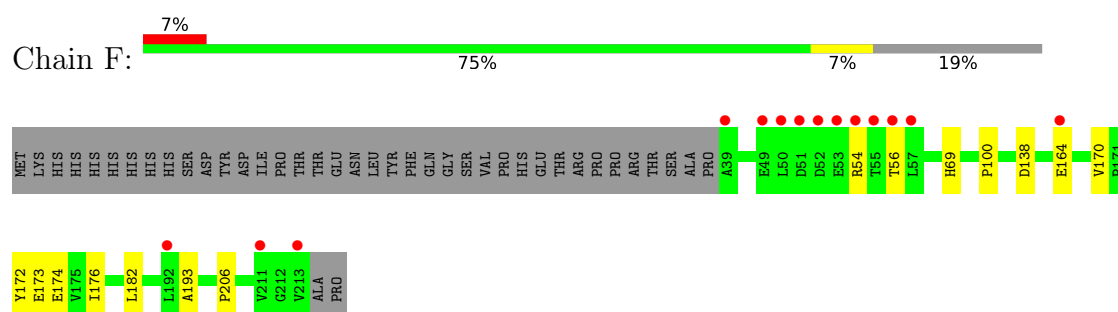
### 3 Residue-property plots [i](#)

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.

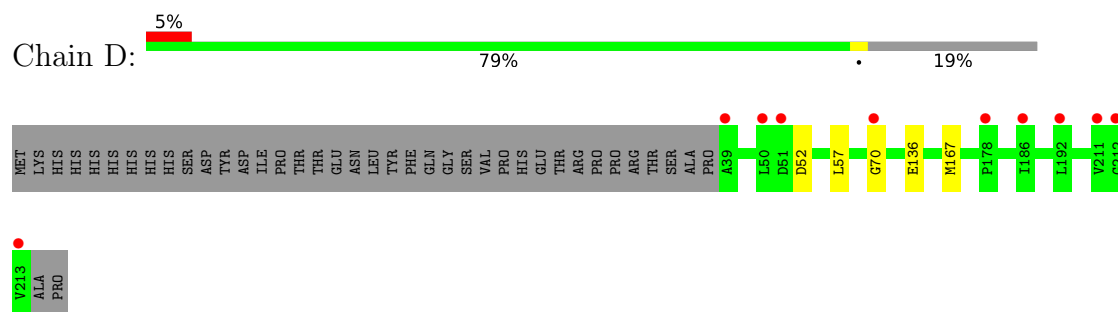
- Molecule 1: Cupin type-2 domain-containing protein



- Molecule 1: Cupin type-2 domain-containing protein

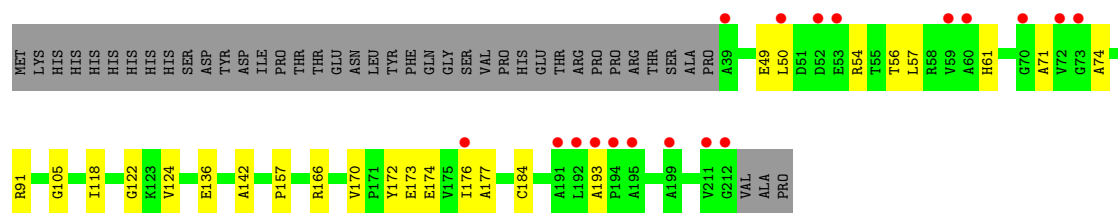


- Molecule 1: Cupin type-2 domain-containing protein

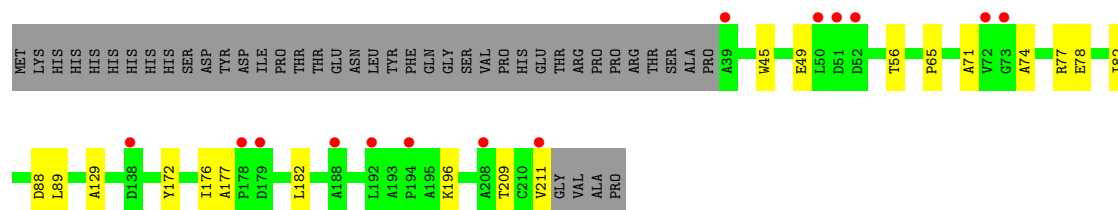


- Molecule 1: Cupin type-2 domain-containing protein

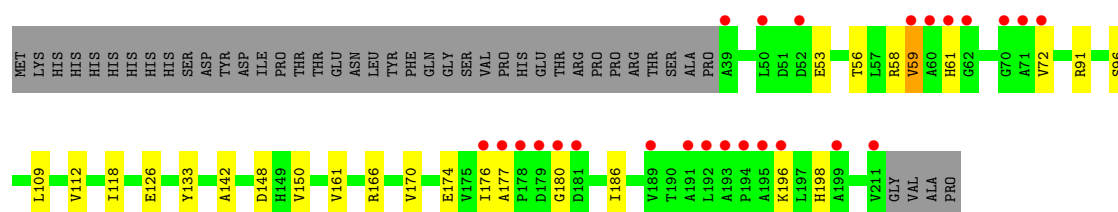




● Molecule 1: Cupin type-2 domain-containing protein



● Molecule 1: Cupin type-2 domain-containing protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.62Å 75.97Å 105.03Å 90.00° 103.19° 90.00°	Depositor
Resolution (Å)	47.36 – 1.94 47.36 – 1.94	Depositor EDS
% Data completeness (in resolution range)	95.4 (47.36-1.94) 95.4 (47.36-1.94)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.64 (at 1.94Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.203 , 0.238 0.203 , 0.238	Depositor DCC
$R_{free}$ test set	1916 reflections (2.23%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.3	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 33.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8017	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.95% 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: CL, OXY, ZN, NI

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	0.32	0/1302	0.53	0/1786
1	B	0.27	0/1281	0.49	0/1760
1	C	0.30	0/1277	0.51	0/1755
1	D	0.30	0/1292	0.50	0/1776
1	E	0.28	0/1277	0.50	0/1755
1	F	0.35	0/1274	0.53	0/1752
All	All	0.30	0/7703	0.51	0/10584

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1270	0	1236	17	0
1	B	1249	0	1215	17	0
1	C	1245	0	1212	12	0
1	D	1260	0	1230	3	0
1	E	1245	0	1212	18	0
1	F	1242	0	1205	10	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	F	1	0	0	1	0
6	A	91	0	0	2	0
6	B	64	0	0	1	0
6	C	75	0	0	0	0
6	D	91	0	0	0	0
6	E	61	0	0	2	0
6	F	93	0	0	1	0
All	All	8017	0	7310	68	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 5.

All (68) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:56:THR:HG23	1:E:56:THR:HG23	1.72	0.72
1:C:176:ILE:HD13	1:C:182:LEU:HB2	1.72	0.71
1:C:49:GLU:HG3	1:C:56:THR:HB	1.74	0.69
1:E:61:HIS:O	1:E:91:ARG:NH1	2.26	0.66
1:E:61:HIS:O	1:E:91:ARG:HD2	1.97	0.64
1:F:170:VAL:HB	1:F:174:GLU:HG3	1.82	0.62
1:B:173:GLU:HA	1:B:176:ILE:HD12	1.84	0.60
1:A:62:GLY:O	1:A:91:ARG:HD3	2.01	0.60
1:A:57:LEU:HB2	1:B:57:LEU:HB2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:ALA:N	6:A:405:HOH:O	2.38	0.55
1:D:70:GLY:HA3	1:D:167:MET:HE2	1.88	0.55
1:E:53:GLU:N	1:E:53:GLU:OE1	2.40	0.54
1:E:126:GLU:HB2	1:E:186:ILE:HD11	1.91	0.53
1:C:172:TYR:CE2	1:C:176:ILE:HD11	2.44	0.52
1:A:82:ILE:HD13	1:B:136:GLU:HG2	1.90	0.52
1:B:71:ALA:HB3	1:B:74:ALA:HB2	1.91	0.52
1:D:136:GLU:HG2	1:C:82:ILE:HD13	1.91	0.52
1:E:176:ILE:HD12	1:E:180:GLY:HA2	1.91	0.51
1:B:176:ILE:HD13	1:B:193:ALA:HB2	1.93	0.51
1:A:56:THR:HG23	1:B:56:THR:HG23	1.91	0.51
1:E:170:VAL:HB	1:E:174:GLU:HG3	1.93	0.50
1:E:91:ARG:HG3	1:E:150:VAL:HG22	1.94	0.50
1:A:161:VAL:HA	1:A:166[B]:ARG:NE	2.26	0.50
1:A:200:GLU:OE1	6:A:401:HOH:O	2.20	0.50
1:E:161:VAL:HA	1:E:166:ARG:HD2	1.94	0.50
1:A:43:VAL:HG13	1:A:77:ARG:NH2	2.27	0.49
1:B:166:ARG:NH2	6:B:407:HOH:O	2.46	0.49
1:B:61:HIS:O	1:B:91:ARG:NE	2.41	0.49
1:E:96:SER:OG	6:E:401:HOH:O	2.20	0.48
1:F:69:HIS:O	5:F:305:CL:CL	2.68	0.48
1:B:49:GLU:HG2	1:B:56:THR:HB	1.96	0.48
1:C:209:THR:O	1:C:211:VAL:HG23	2.13	0.48
1:E:176:ILE:HG13	1:E:177:ALA:O	2.14	0.48
1:A:58:ARG:HD3	1:B:54:ARG:HD2	1.96	0.47
1:B:118:ILE:HD12	1:B:142:ALA:O	2.15	0.47
1:E:109:LEU:HD12	1:E:133:TYR:CE2	2.50	0.47
1:F:54:ARG:HD3	1:E:58:ARG:HD3	1.96	0.46
1:C:45:TRP:HB2	1:C:89:LEU:HD11	1.95	0.46
1:E:59:VAL:HG11	1:E:112:VAL:HG23	1.97	0.46
1:E:148:ASP:OD2	6:E:402:HOH:O	2.20	0.46
1:A:61:HIS:O	1:A:91:ARG:HD2	2.15	0.46
1:F:172:TYR:OH	1:F:182:LEU:HD23	2.15	0.46
1:F:176:ILE:HD13	1:F:193:ALA:HB2	1.98	0.45
1:A:161:VAL:HA	1:A:166[B]:ARG:HE	1.81	0.45
1:C:172:TYR:CZ	1:C:196:LYS:HG3	2.52	0.45
1:B:105:GLY:HA2	1:B:157:PRO:HD2	1.99	0.45
1:F:100:PRO:HD3	1:F:206:PRO:O	2.17	0.45
1:A:114:GLY:HA2	1:B:50:LEU:HD22	1.99	0.44
1:B:172:TYR:CE1	1:B:176:ILE:HD11	2.53	0.44
1:E:196:LYS:HB2	1:E:198:HIS:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:GLU:HB2	1:A:186:ILE:HG12	2.00	0.43
1:A:91:ARG:HG2	1:A:92:LEU:N	2.33	0.43
1:D:57:LEU:HD21	1:C:129:ALA:HB1	2.00	0.43
1:B:122:GLY:HA3	1:B:177:ALA:HB2	2.02	0.42
1:A:202:CYS:SG	1:A:204:HIS:HB2	2.58	0.42
1:F:173:GLU:HA	1:F:176:ILE:HD12	2.00	0.42
1:F:164:GLU:H	1:F:164:GLU:CD	2.28	0.42
1:C:176:ILE:HG22	1:C:177:ALA:O	2.20	0.41
1:E:72:VAL:O	1:E:96:SER:OG	2.29	0.41
1:B:170:VAL:HB	1:B:174:GLU:HG3	2.02	0.41
1:A:118:ILE:HD12	1:A:142:ALA:O	2.20	0.41
1:C:78:GLU:HA	1:C:88:ASP:OD1	2.21	0.41
1:B:124:VAL:HB	1:B:184:CYS:HA	2.03	0.41
1:C:71:ALA:HB3	1:C:74:ALA:HB2	2.01	0.41
1:F:138:ASP:OD1	6:F:401:HOH:O	2.21	0.41
1:E:118:ILE:HD12	1:E:142:ALA:O	2.21	0.40
1:A:181:ASP:OD1	1:A:192:LEU:HD12	2.21	0.40
1:C:65:PRO:HD2	1:C:77:ARG:HB2	2.03	0.40

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	175/215 (81%)	173 (99%)	2 (1%)	0	100	100
1	B	172/215 (80%)	168 (98%)	4 (2%)	0	100	100
1	C	171/215 (80%)	169 (99%)	2 (1%)	0	100	100
1	D	174/215 (81%)	170 (98%)	3 (2%)	1 (1%)	21	11
1	E	171/215 (80%)	164 (96%)	7 (4%)	0	100	100
1	F	173/215 (80%)	172 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1036/1290 (80%)	1016 (98%)	19 (2%)	1 (0%)	48	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	52	ASP

### 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	129/168 (77%)	129 (100%)	0	100	100
1	B	129/168 (77%)	129 (100%)	0	100	100
1	C	129/168 (77%)	129 (100%)	0	100	100
1	D	130/168 (77%)	130 (100%)	0	100	100
1	E	129/168 (77%)	128 (99%)	1 (1%)	73	71
1	F	126/168 (75%)	126 (100%)	0	100	100
All	All	772/1008 (77%)	771 (100%)	1 (0%)	88	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	59	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	HIS
1	A	107	HIS
1	D	165	ASN
1	B	128	ASN
1	C	99	GLN

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Mol	Chain	Res	Type
1	C	128	ASN
1	E	41	ASN
1	E	128	ASN

### 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 25 ligands modelled in this entry, 19 are monoatomic - leaving 6 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	$\# Z  > 2$
2	OXY	E	301	4	1,1,1	0.17	0	-		
2	OXY	D	301	4	1,1,1	0.21	0	-		
2	OXY	C	301	4	1,1,1	0.21	0	-		
2	OXY	B	301	4	1,1,1	0.21	0	-		
2	OXY	F	301	4	1,1,1	0.15	0	-		
2	OXY	A	301	4	1,1,1	0.23	0	-		

There are no bond length outliers.

There are no bond angle outliers.

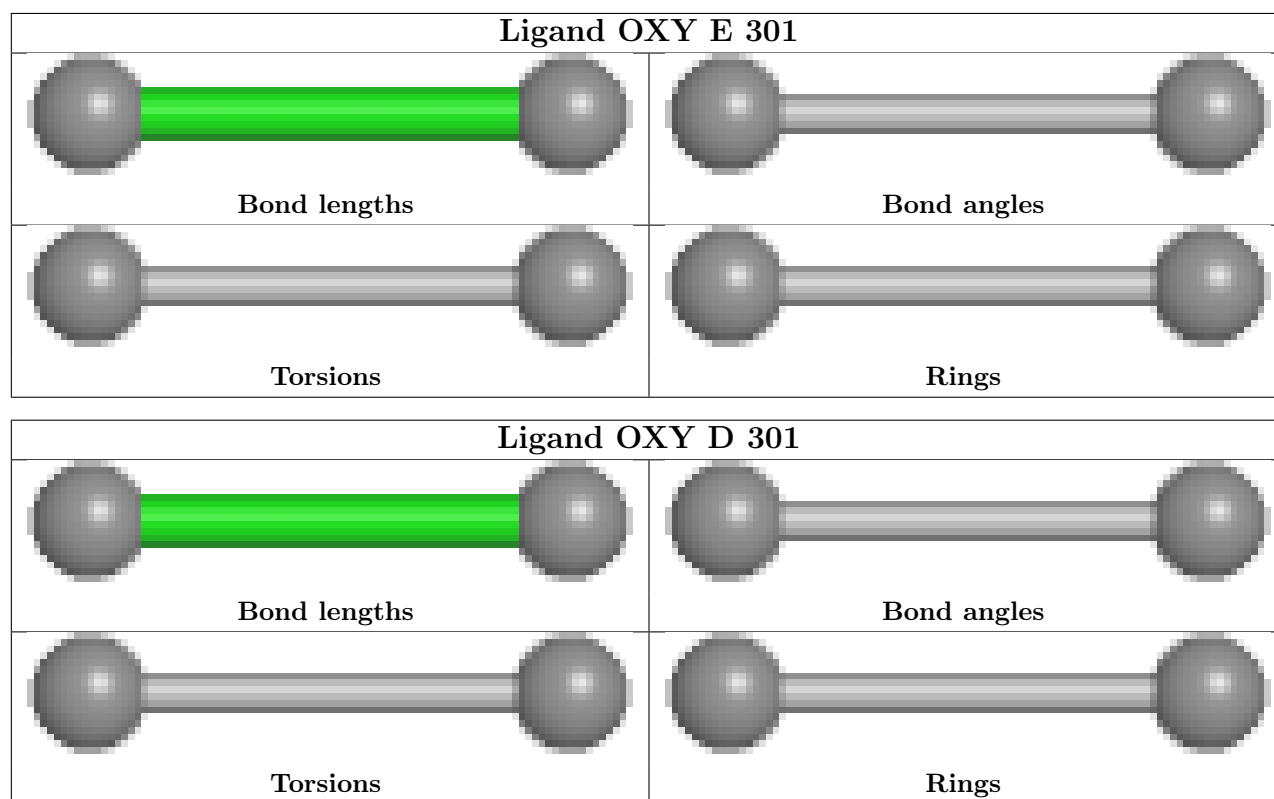
There are no chirality outliers.

There are no torsion outliers.

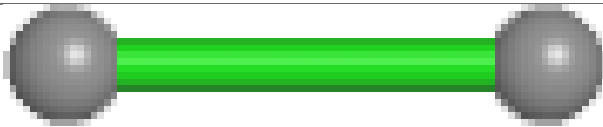



There are no ring outliers.

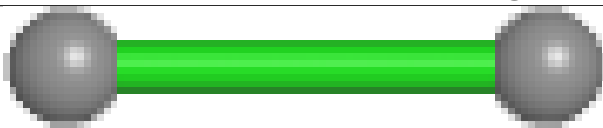
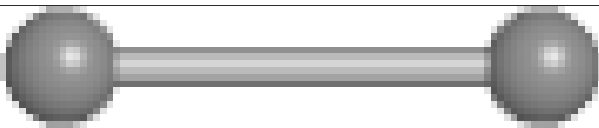


No monomer is involved in short contacts.

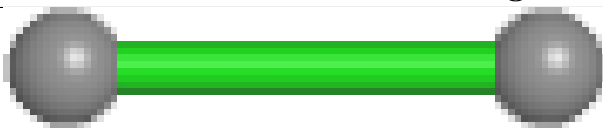
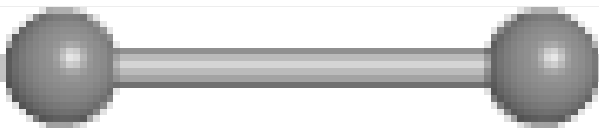
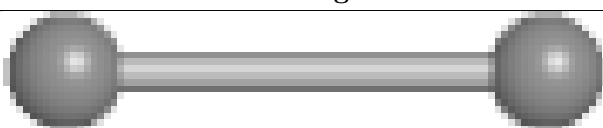
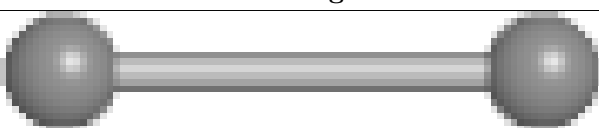
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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


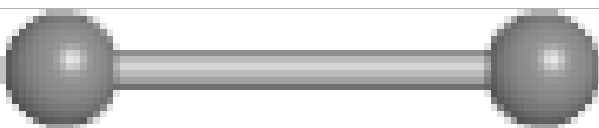






Ligand OXY C 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand OXY B 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand OXY F 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand OXY A 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

## 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, 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	174/215 (80%)	0.34	9 (5%) 33 37	8, 26, 44, 79	2 (1%)
1	B	174/215 (80%)	0.73	18 (10%) 12 13	21, 32, 49, 68	0
1	C	173/215 (80%)	0.43	14 (8%) 18 20	19, 28, 46, 63	0
1	D	175/215 (81%)	0.25	10 (5%) 29 32	14, 27, 42, 60	1 (0%)
1	E	173/215 (80%)	0.95	25 (14%) 6 6	20, 34, 58, 70	0
1	F	175/215 (81%)	0.42	14 (8%) 18 20	19, 25, 48, 80	0
All	All	1044/1290 (80%)	0.52	90 (8%) 16 18	8, 28, 50, 80	3 (0%)

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	50	LEU	8.0
1	F	55	THR	6.4
1	B	193	ALA	6.4
1	F	52	ASP	6.4
1	E	193	ALA	6.0
1	D	186[A]	ILE	5.6
1	A	50	LEU	5.5
1	E	192	LEU	5.2
1	E	60	ALA	5.1
1	E	194	PRO	5.1
1	E	59	VAL	5.1
1	B	194	PRO	5.0
1	F	56	THR	4.8
1	F	213	VAL	4.4
1	E	195	ALA	4.2
1	A	53	GLU	4.0
1	C	211	VAL	4.0
1	E	211	VAL	4.0
1	E	191	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
1	F	54	ARG	3.9
1	E	62	GLY	3.9
1	B	72	VAL	3.9
1	E	61	HIS	3.7
1	F	49	GLU	3.7
1	D	213	VAL	3.7
1	C	50	LEU	3.7
1	F	51	ASP	3.7
1	B	39	ALA	3.5
1	E	70	GLY	3.5
1	B	192	LEU	3.5
1	E	181	ASP	3.4
1	D	212	GLY	3.4
1	E	52	ASP	3.3
1	B	50	LEU	3.3
1	A	52	ASP	3.2
1	D	39	ALA	3.2
1	B	195	ALA	3.2
1	B	52	ASP	3.2
1	B	176	ILE	3.1
1	E	199	ALA	3.1
1	F	57	LEU	3.1
1	E	180	GLY	2.9
1	A	166[A]	ARG	2.9
1	B	212	GLY	2.9
1	A	51	ASP	2.9
1	C	72	VAL	2.8
1	C	39	ALA	2.8
1	B	60	ALA	2.8
1	E	179	ASP	2.8
1	B	73	GLY	2.8
1	D	50	LEU	2.8
1	C	73	GLY	2.7
1	C	192	LEU	2.7
1	E	189	VAL	2.7
1	E	39	ALA	2.7
1	E	176	ILE	2.7
1	F	39	ALA	2.7
1	F	53	GLU	2.7
1	C	194	PRO	2.6
1	C	179	ASP	2.6
1	C	51	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	192	LEU	2.5
1	E	178	PRO	2.5
1	F	192	LEU	2.5
1	D	192	LEU	2.4
1	F	164	GLU	2.4
1	D	178	PRO	2.4
1	E	50	LEU	2.4
1	C	178	PRO	2.4
1	B	211	VAL	2.4
1	C	138	ASP	2.4
1	B	53	GLU	2.4
1	B	70	GLY	2.3
1	E	177	ALA	2.3
1	A	55	THR	2.3
1	B	199	ALA	2.2
1	E	72	VAL	2.2
1	E	196	LYS	2.2
1	C	52	ASP	2.2
1	B	191	ALA	2.2
1	F	211	VAL	2.2
1	B	59	VAL	2.2
1	A	54	ARG	2.2
1	C	188	ALA	2.1
1	E	71	ALA	2.1
1	A	176	ILE	2.1
1	D	51	ASP	2.1
1	C	208	ALA	2.0
1	D	70	GLY	2.0
1	D	211	VAL	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands ⓘ

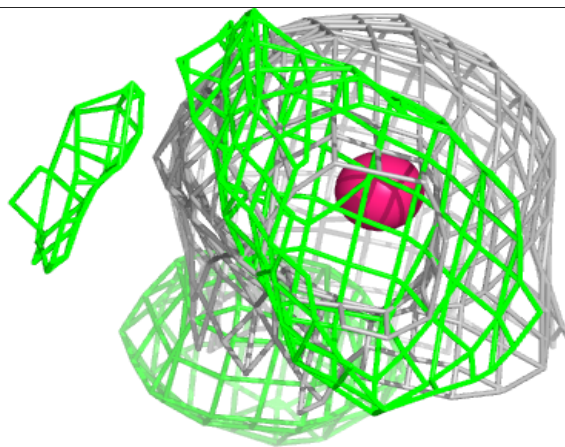
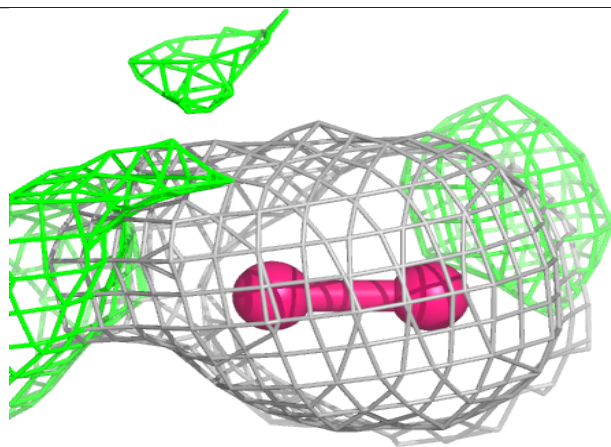
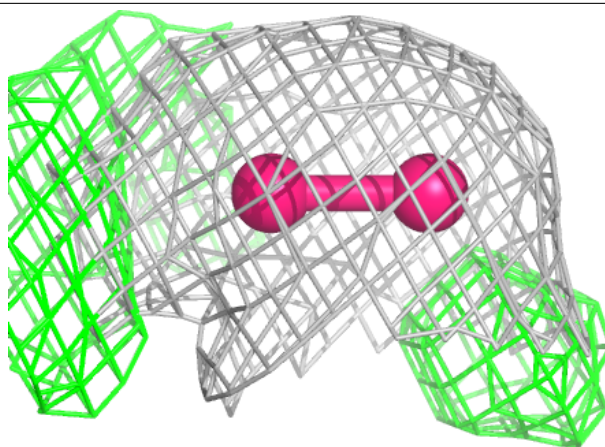
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<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	OXY	D	301	2/2	0.95	0.09	19,19,19,33	0
5	CL	F	305	1/1	0.96	0.08	34,34,34,34	0
2	OXY	B	301	2/2	0.97	0.10	23,23,23,28	0
2	OXY	C	301	2/2	0.97	0.07	23,23,23,24	0
2	OXY	E	301	2/2	0.97	0.13	18,18,18,42	0
2	OXY	A	301	2/2	0.97	0.08	18,18,18,30	0
3	ZN	E	303	1/1	0.98	0.04	44,44,44,44	0
2	OXY	F	301	2/2	0.98	0.07	17,17,17,33	0
3	ZN	F	302	1/1	0.99	0.03	23,23,23,23	0
3	ZN	F	303	1/1	0.99	0.02	25,25,25,25	0
3	ZN	D	303	1/1	0.99	0.03	26,26,26,26	0
3	ZN	B	302	1/1	0.99	0.03	31,31,31,31	0
3	ZN	B	303	1/1	0.99	0.04	38,38,38,38	0
3	ZN	C	303	1/1	0.99	0.03	38,38,38,38	0
3	ZN	E	302	1/1	0.99	0.03	35,35,35,35	0
3	ZN	A	302	1/1	0.99	0.02	25,25,25,25	0
4	NI	A	304	1/1	0.99	0.03	22,22,22,22	0
4	NI	E	304	1/1	0.99	0.02	29,29,29,29	0
3	ZN	A	303	1/1	0.99	0.03	27,27,27,27	0
4	NI	F	304	1/1	1.00	0.02	19,19,19,19	0
4	NI	D	304	1/1	1.00	0.02	20,20,20,20	0
4	NI	B	304	1/1	1.00	0.01	24,24,24,24	0
4	NI	C	304	1/1	1.00	0.01	24,24,24,24	0
3	ZN	D	302	1/1	1.00	0.02	30,30,30,30	0
3	ZN	C	302	1/1	1.00	0.02	35,35,35,35	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.

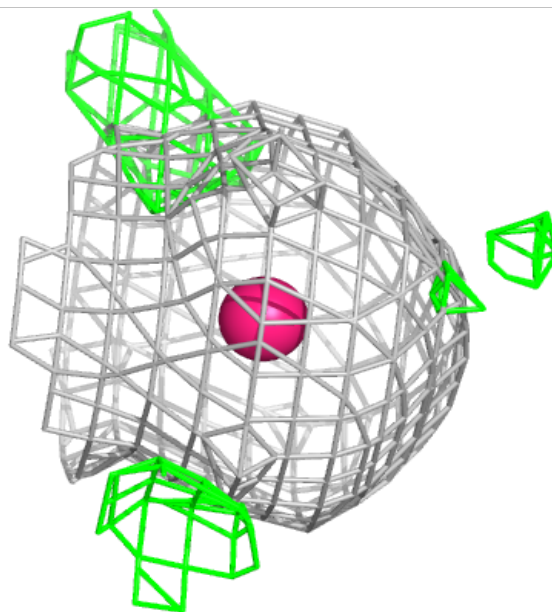
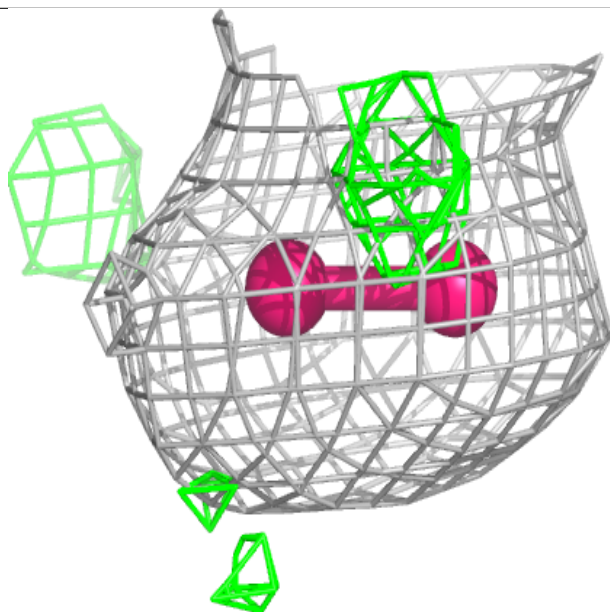
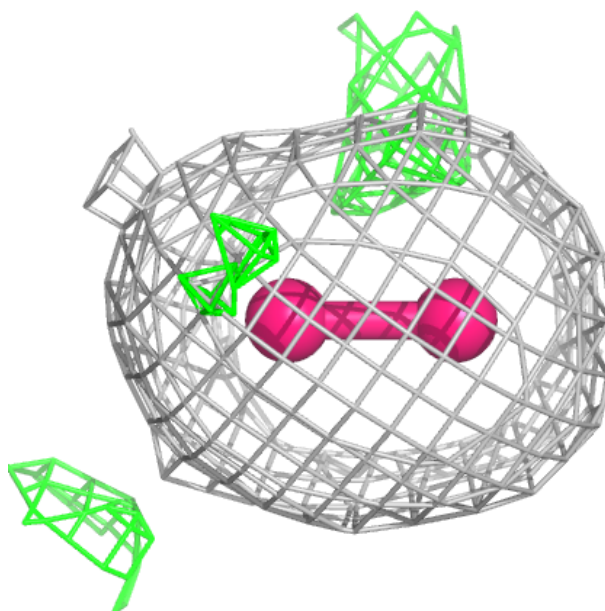
**Electron density around OXY D 301:**

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



**Electron density around OXY B 301:**

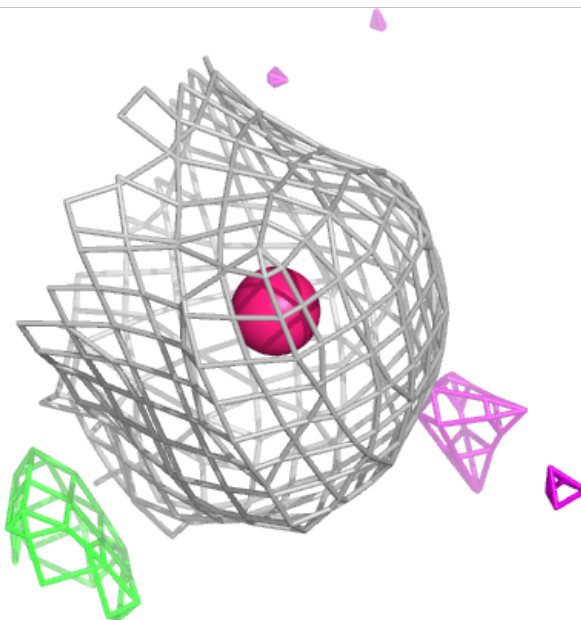
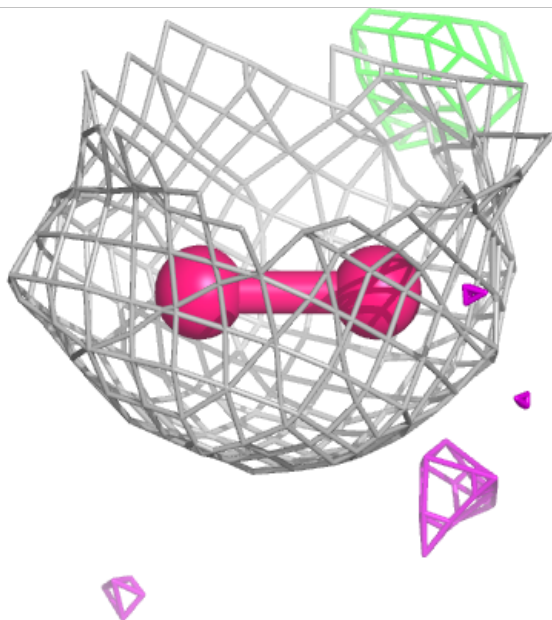
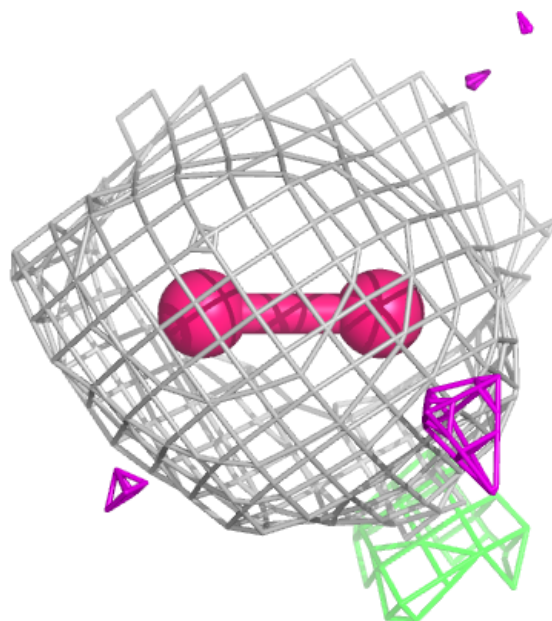
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





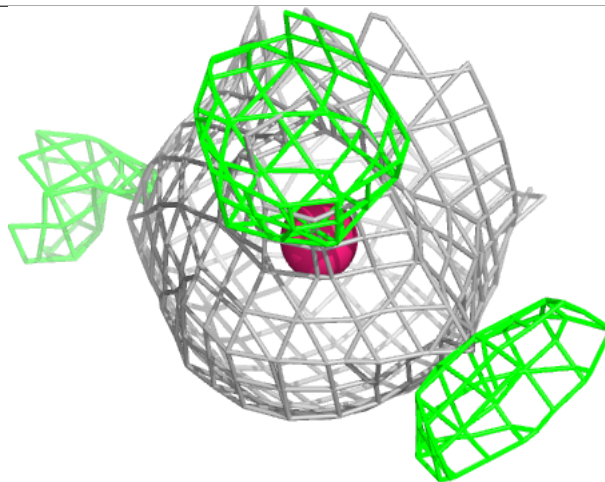
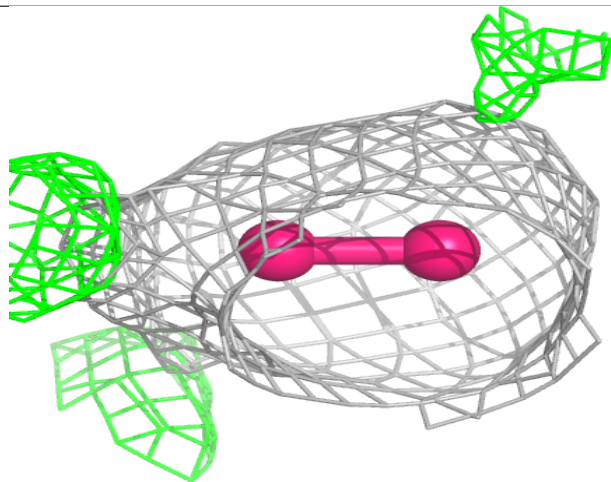
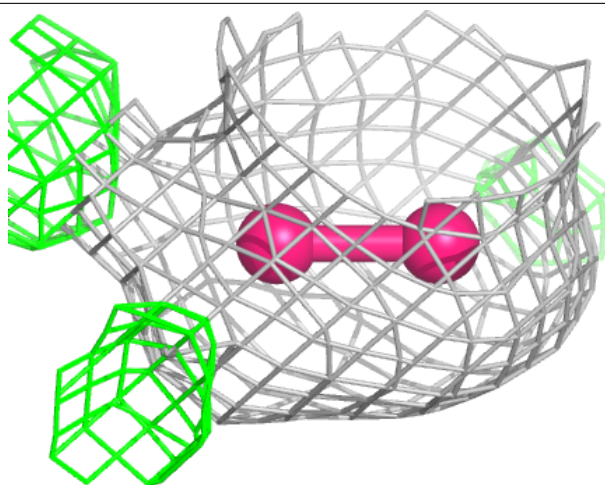
**Electron density around OXY C 301:**

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



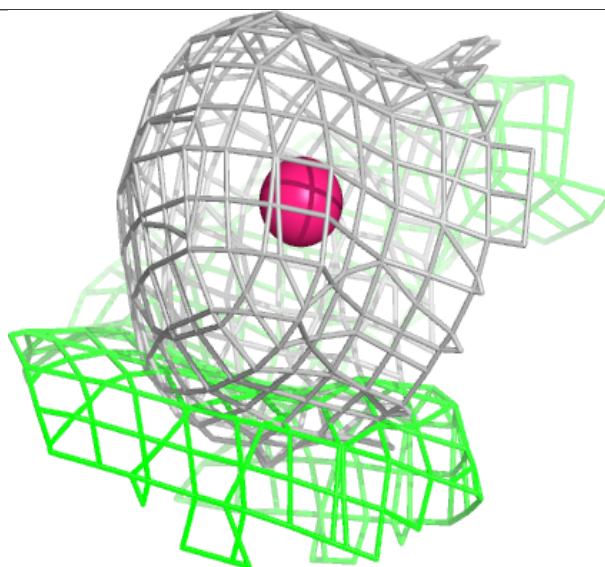
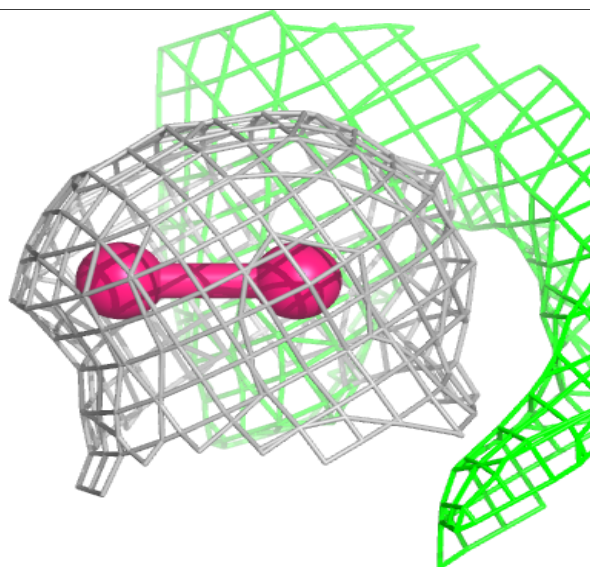
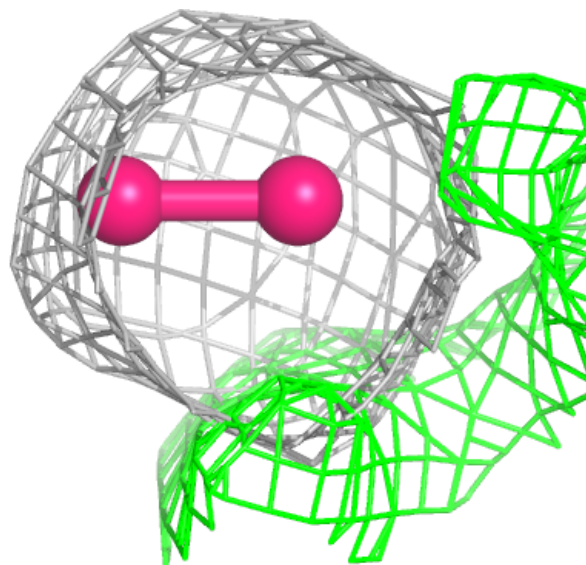
**Electron density around OXY E 301:**

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



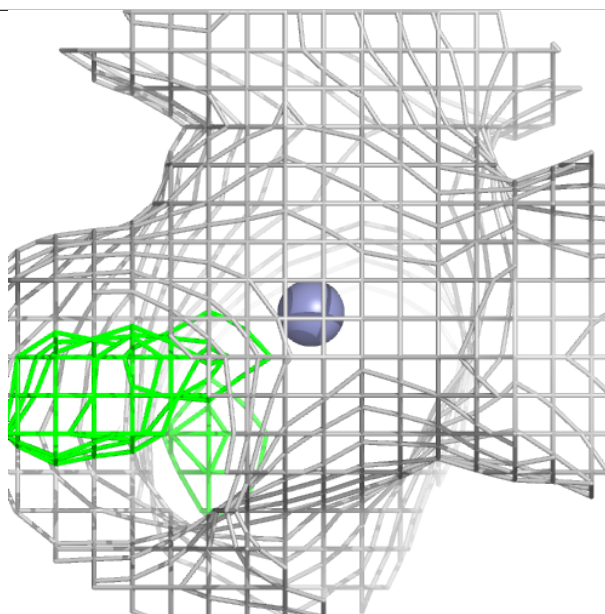
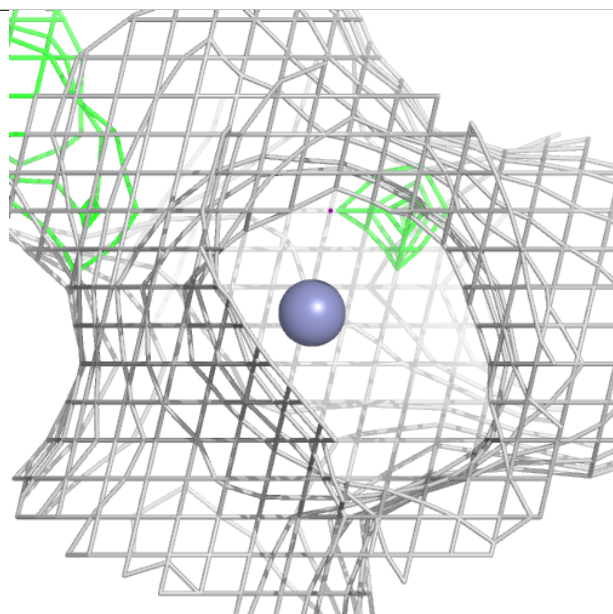
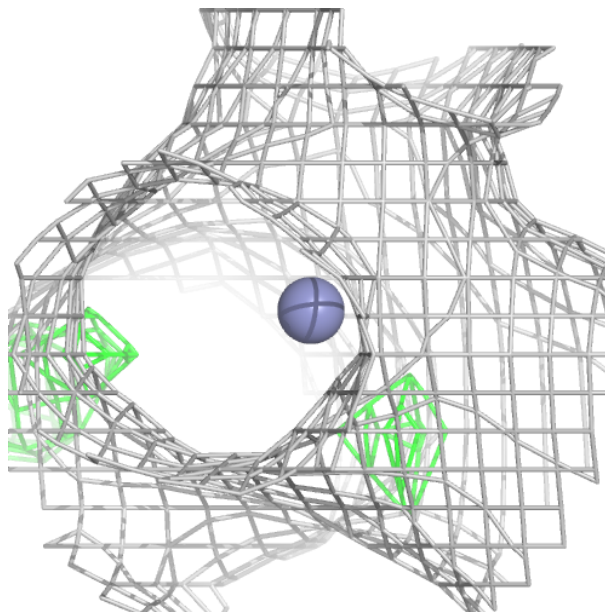
**Electron density around OXY A 301:**

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



**Electron density around ZN E 303:**

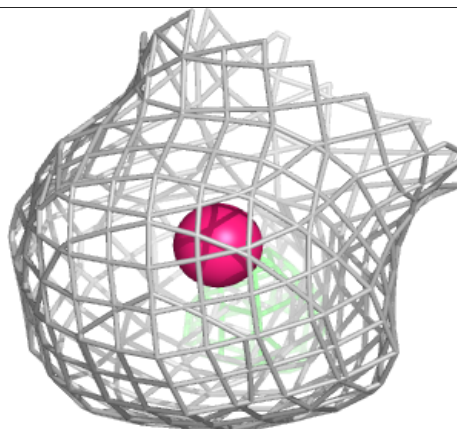
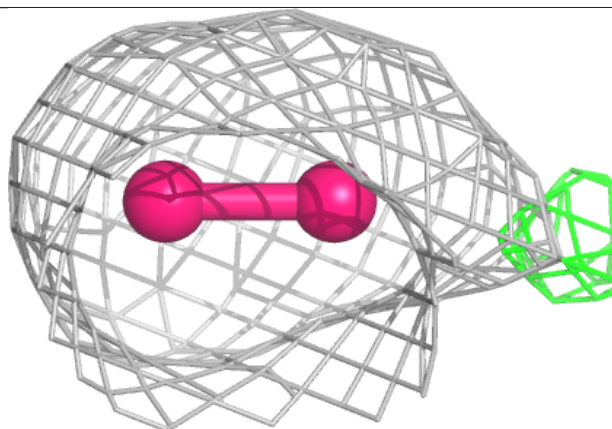
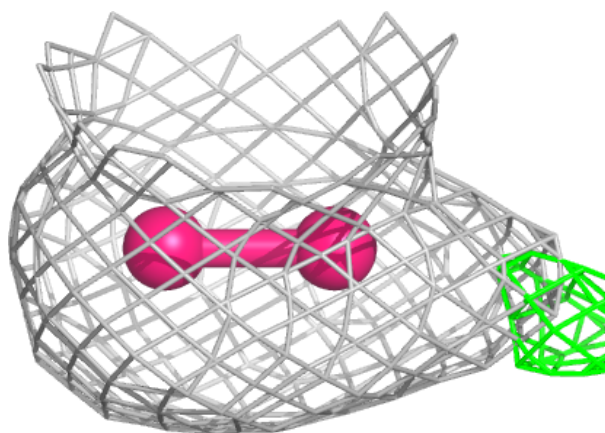
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





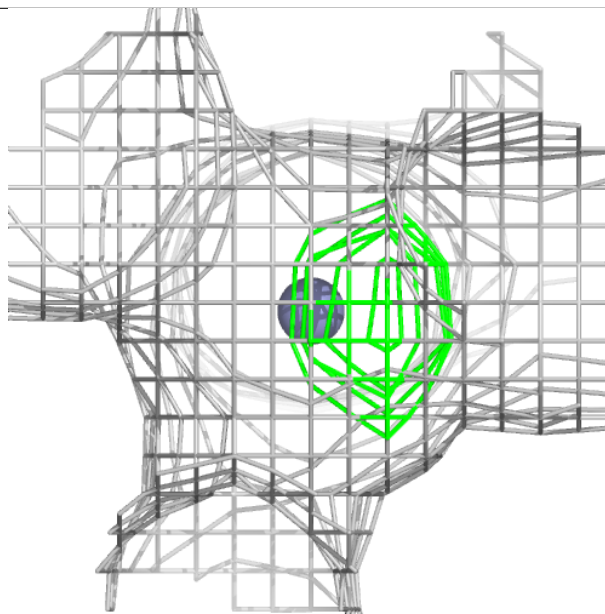
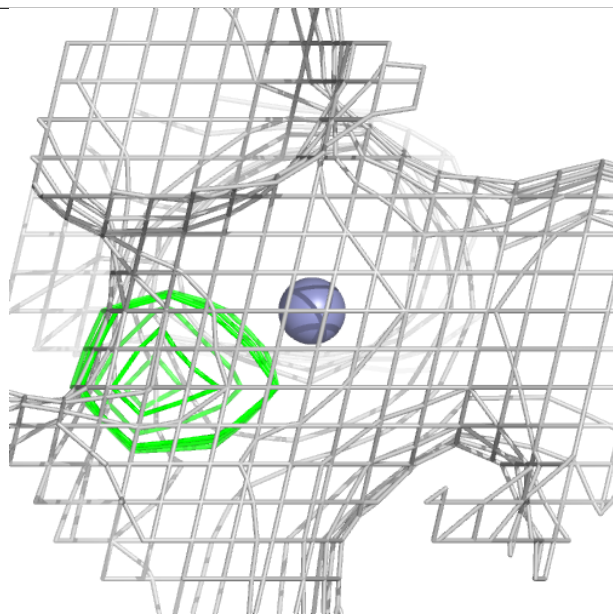
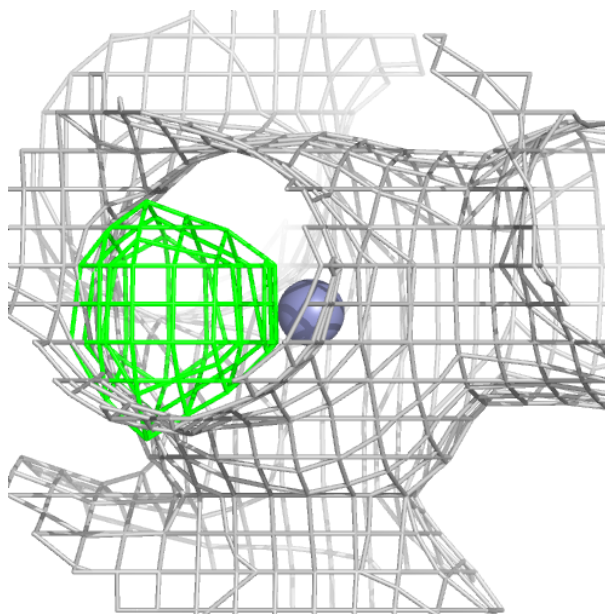
**Electron density around OXY F 301:**

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



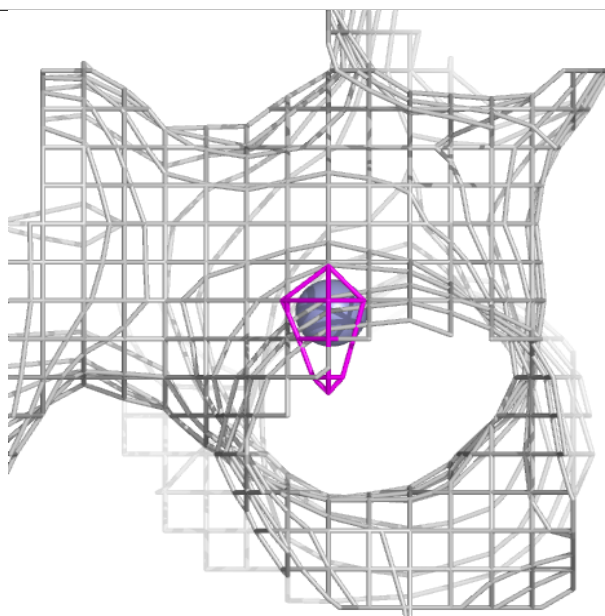
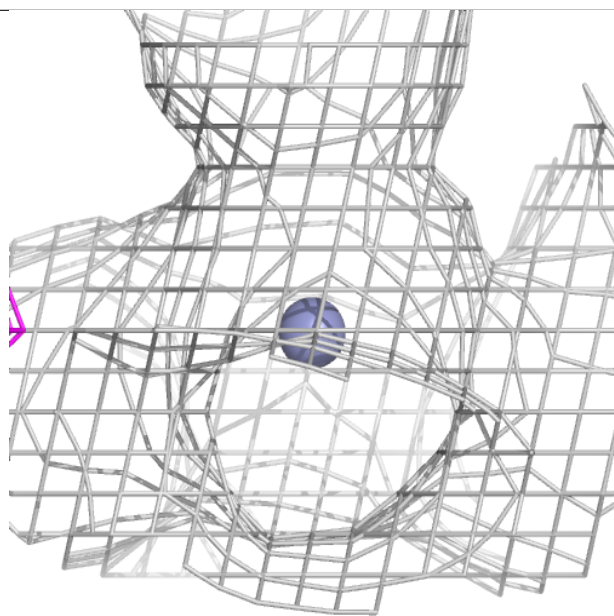
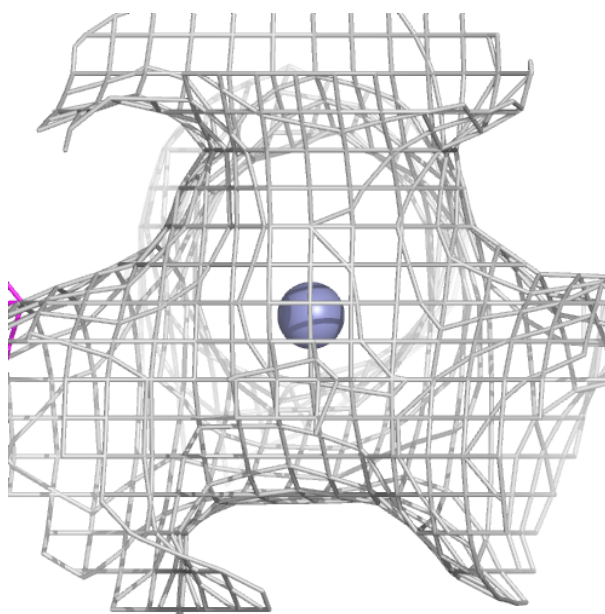
**Electron density around ZN F 302:**

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



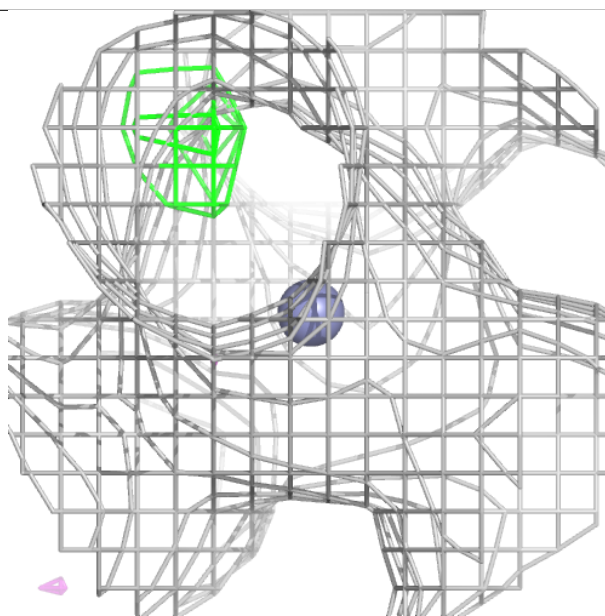
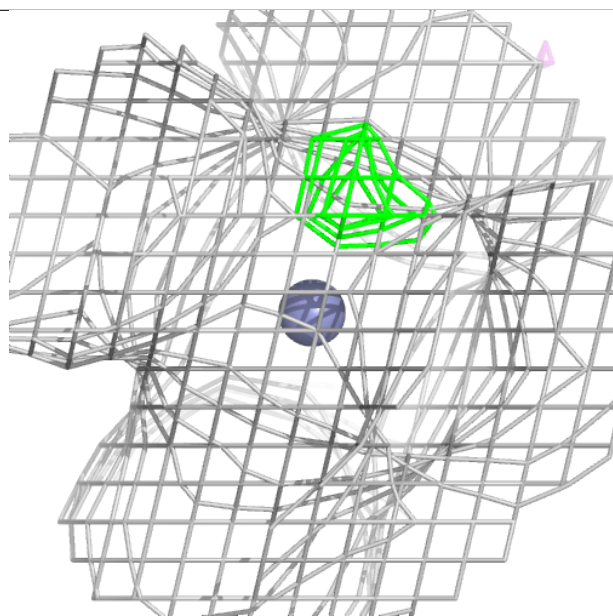
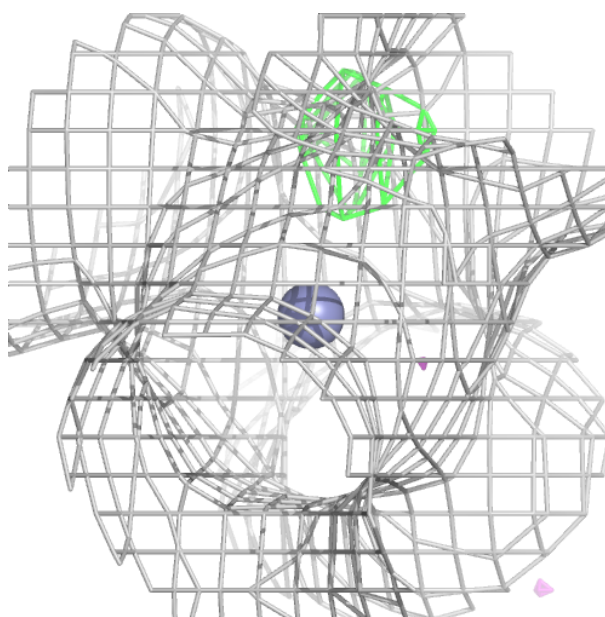
**Electron density around ZN F 303:**

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



**Electron density around ZN D 303:**

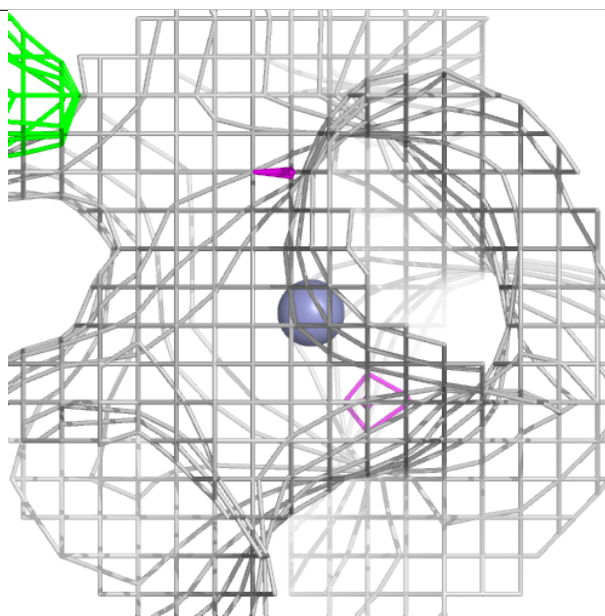
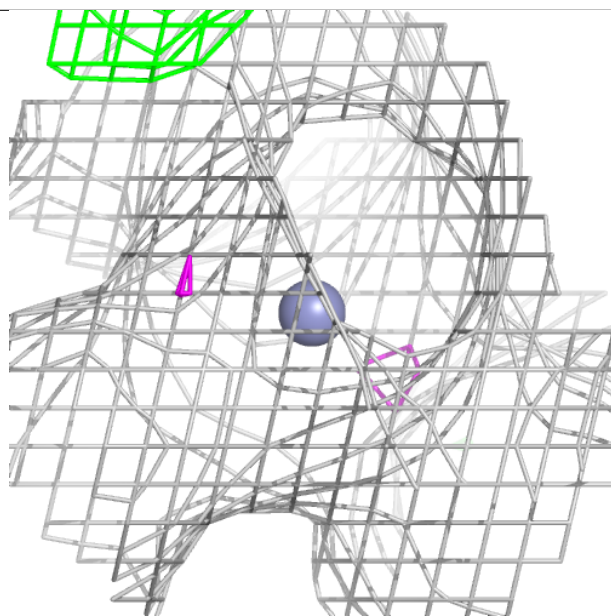
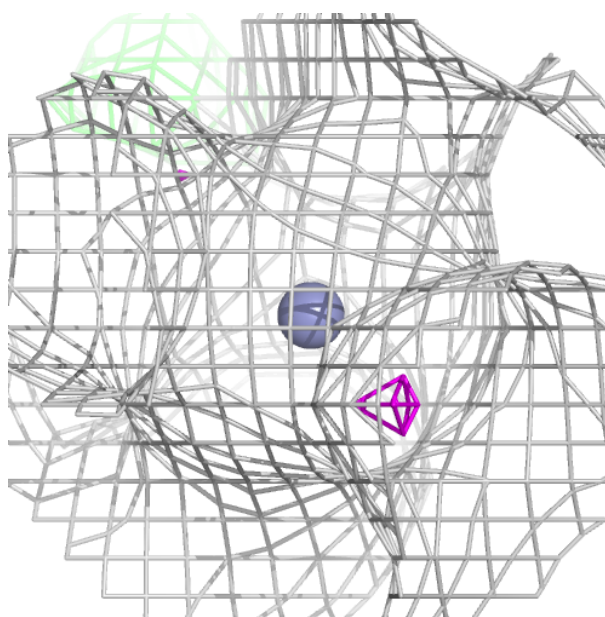
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





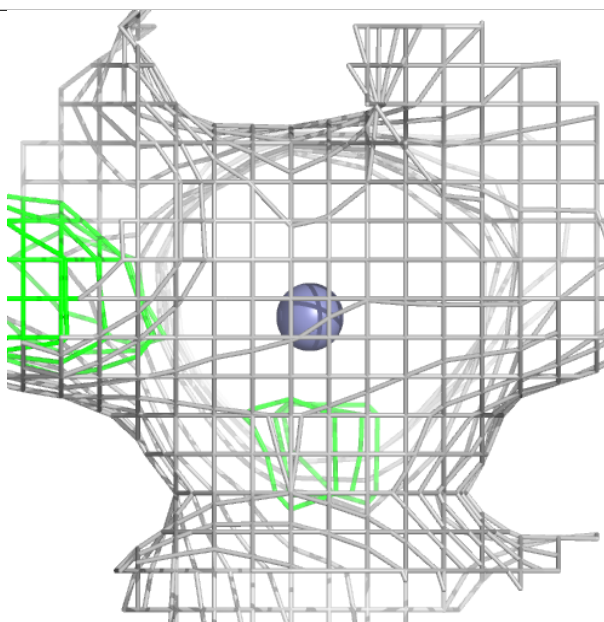
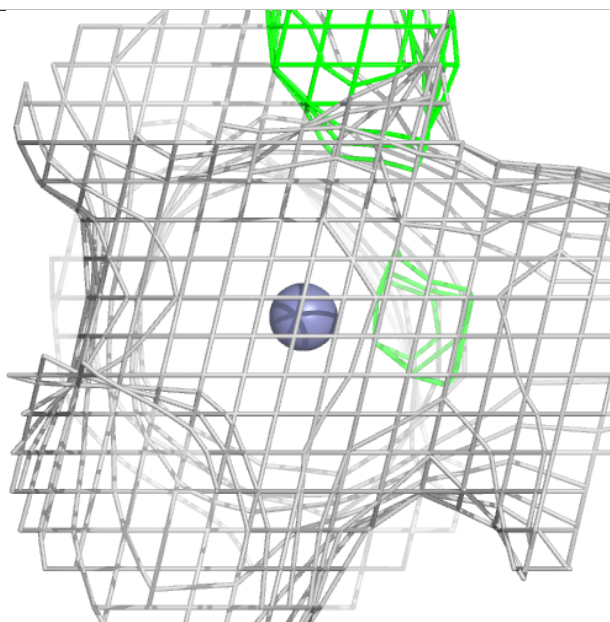
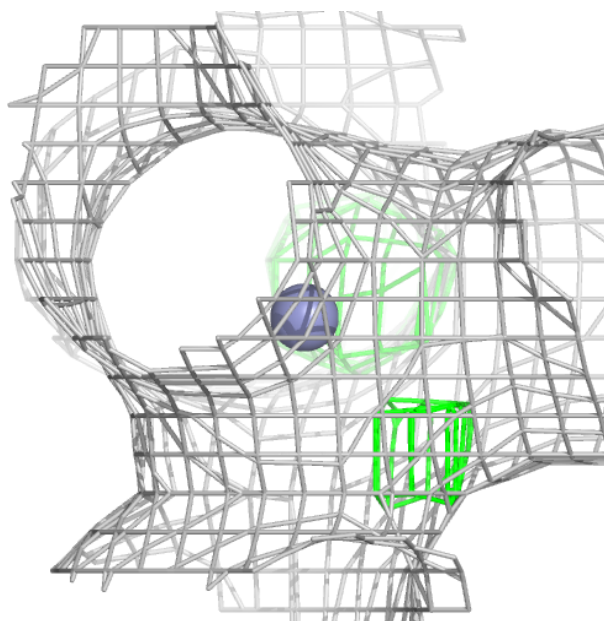
**Electron density around ZN B 302:**

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



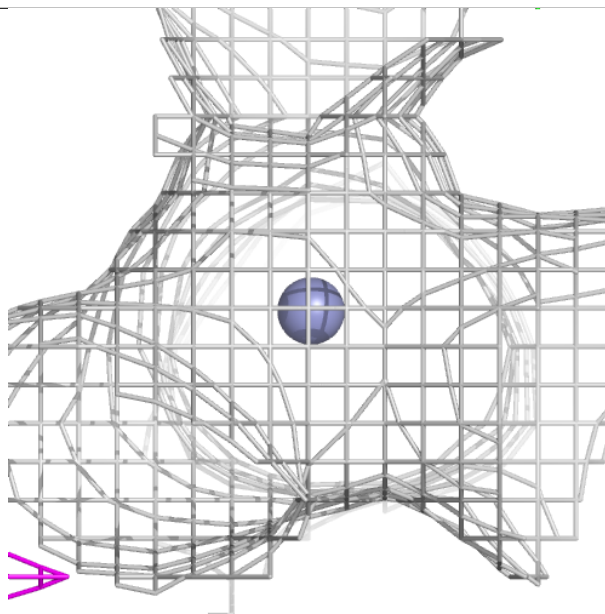
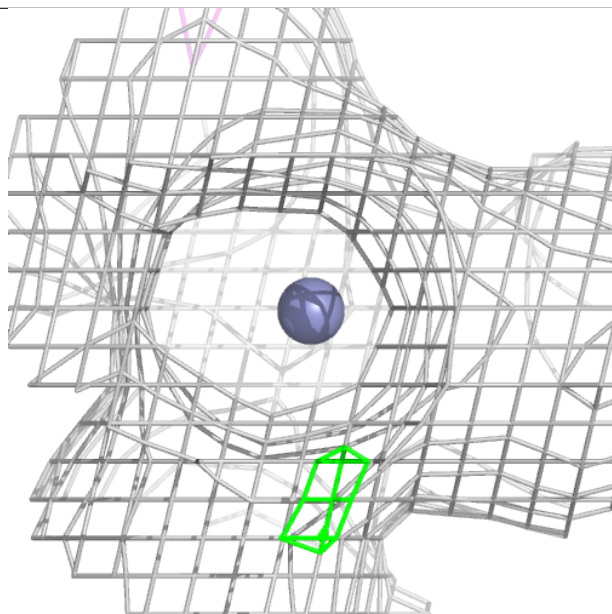
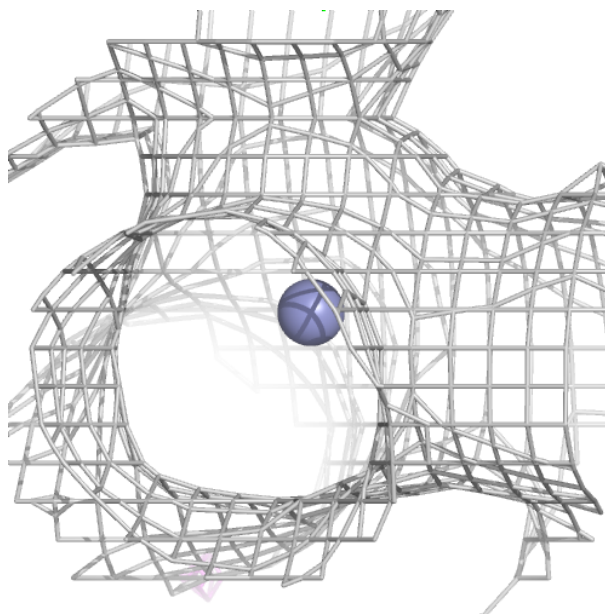
**Electron density around ZN B 303:**

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



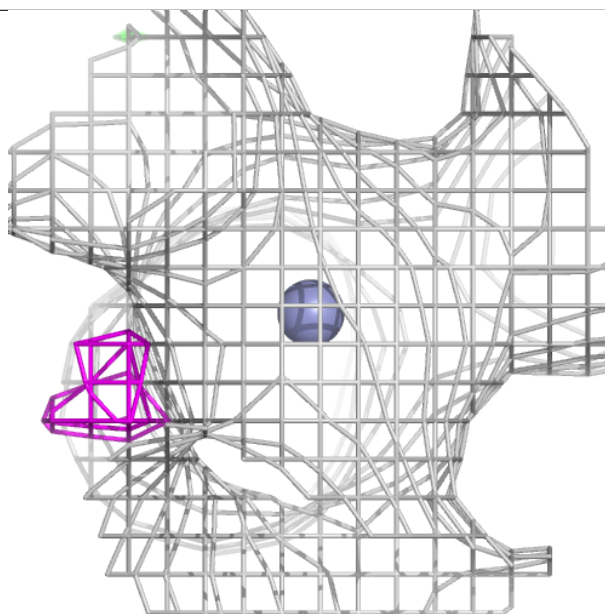
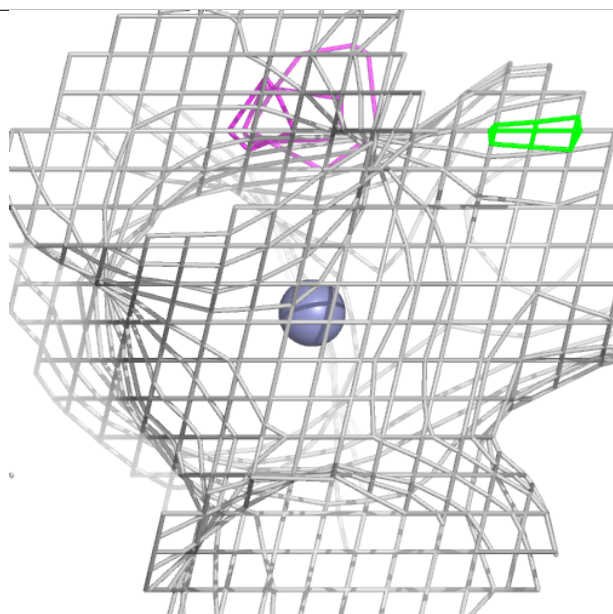
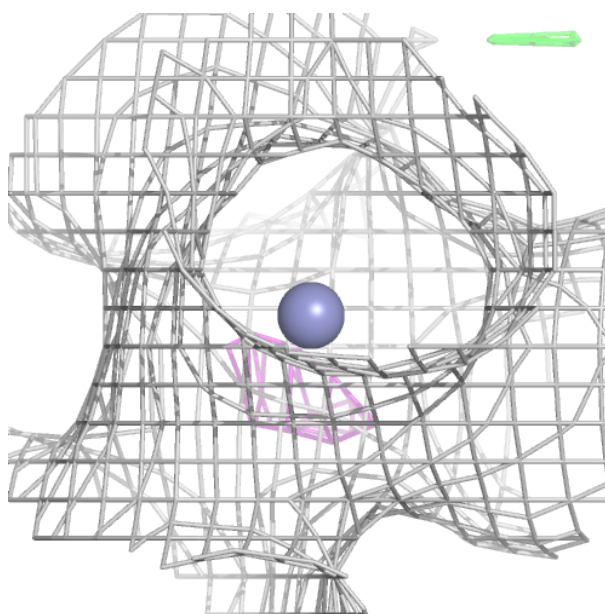
**Electron density around ZN C 303:**

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



**Electron density around ZN E 302:**

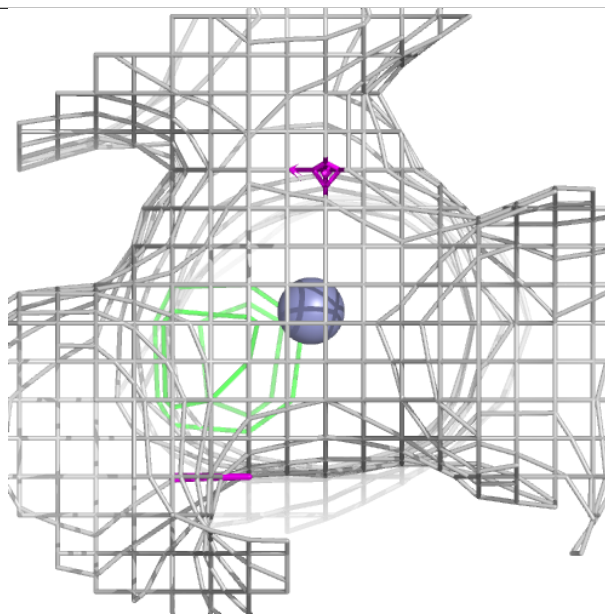
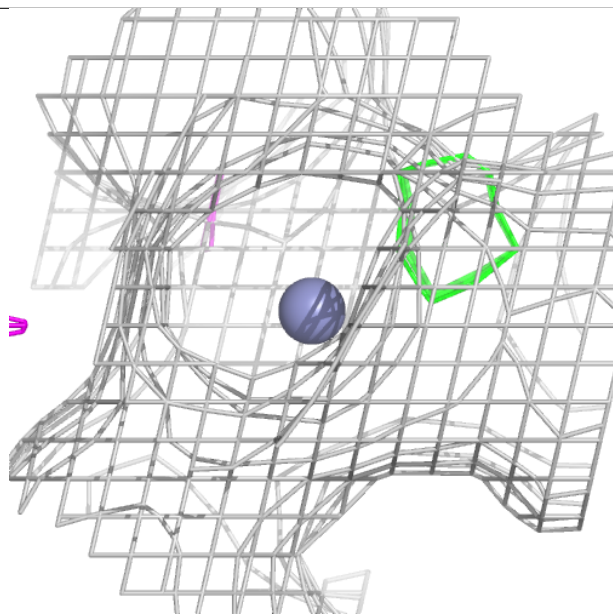
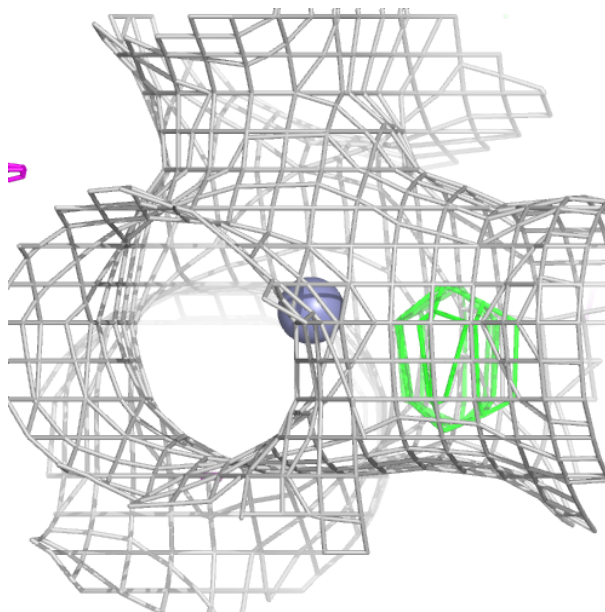
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





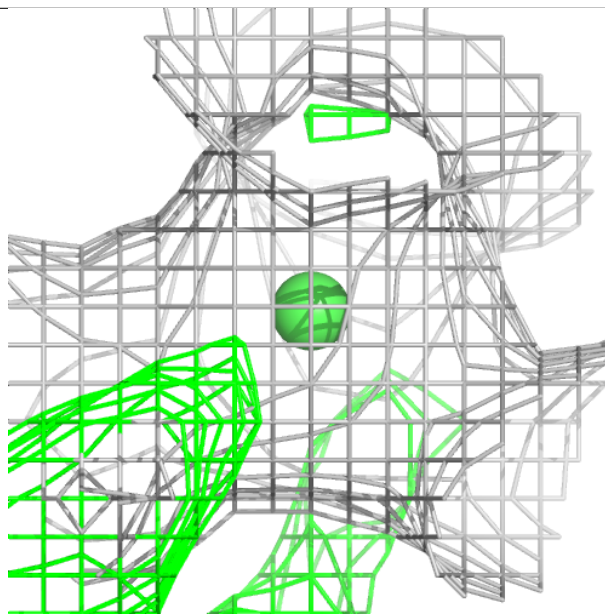
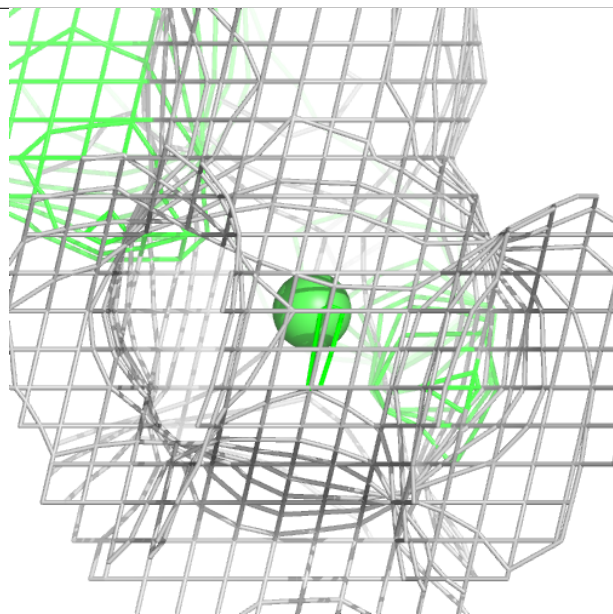
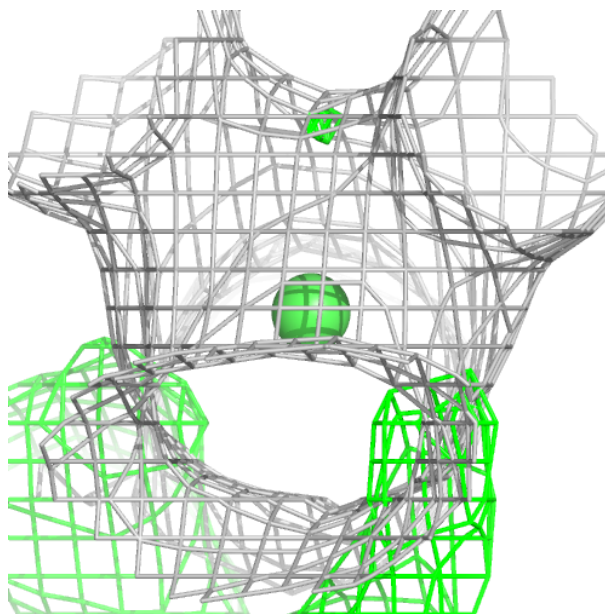
**Electron density around ZN A 302:**

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



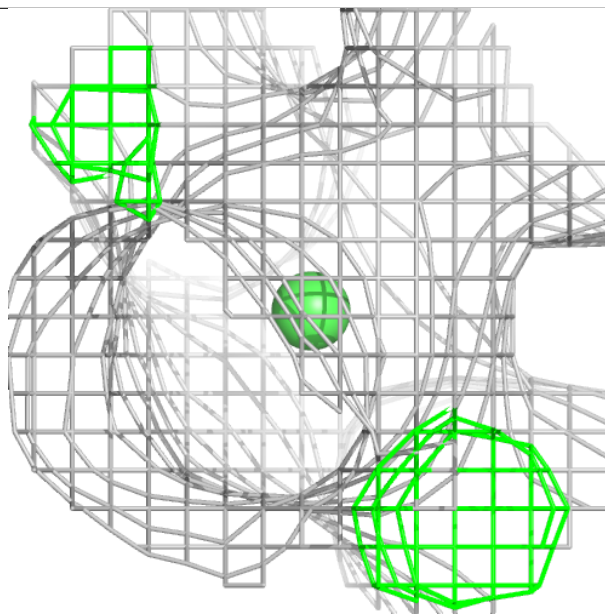
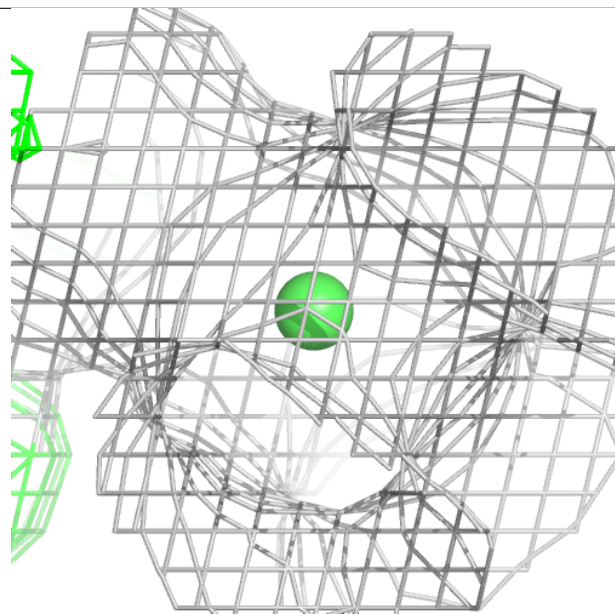
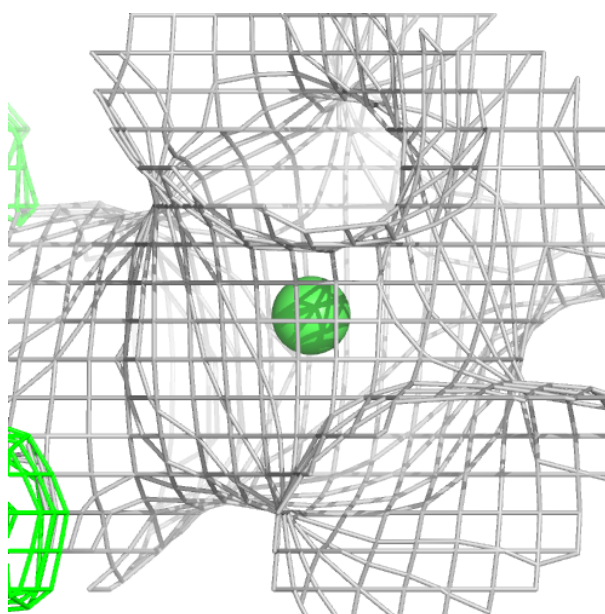
**Electron density around NI A 304:**

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



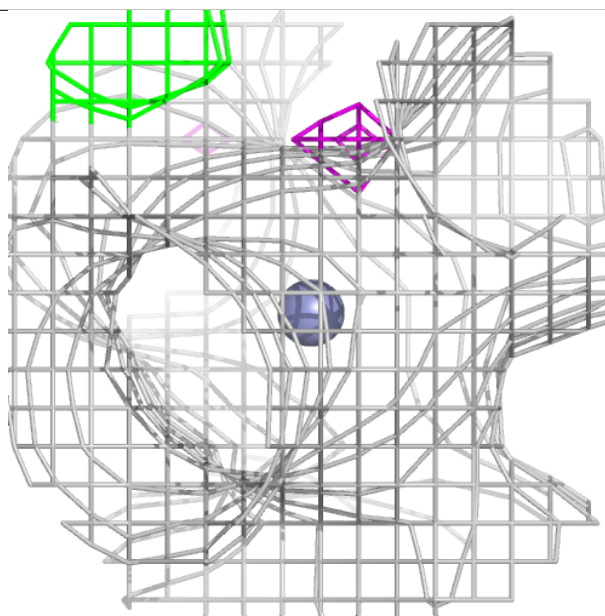
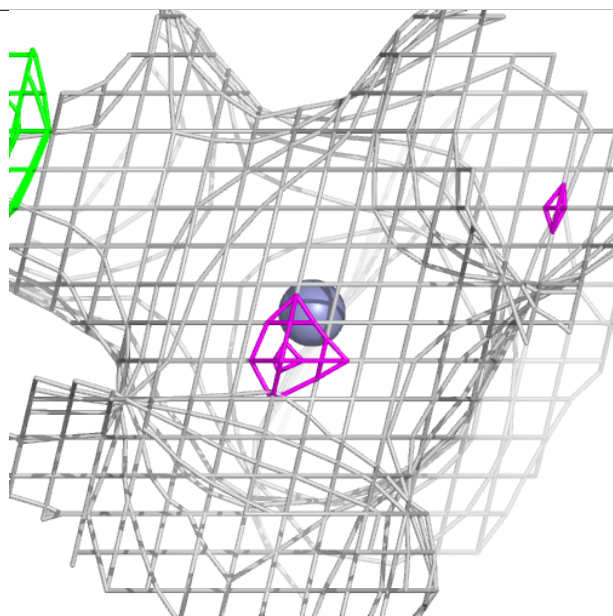
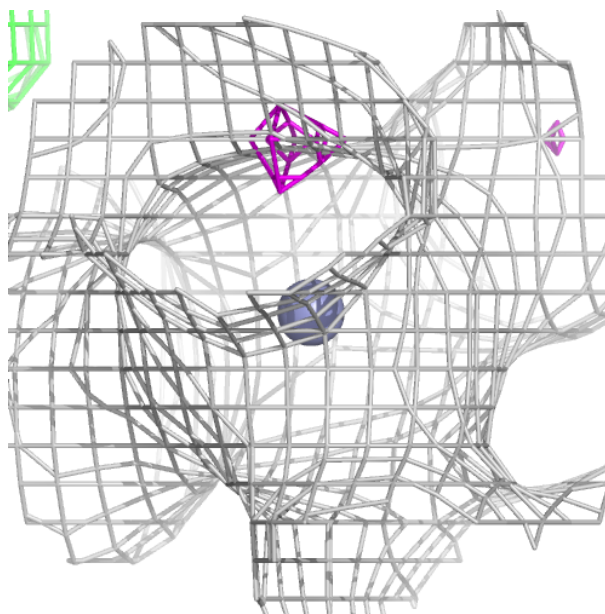
**Electron density around NI E 304:**

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



**Electron density around ZN A 303:**

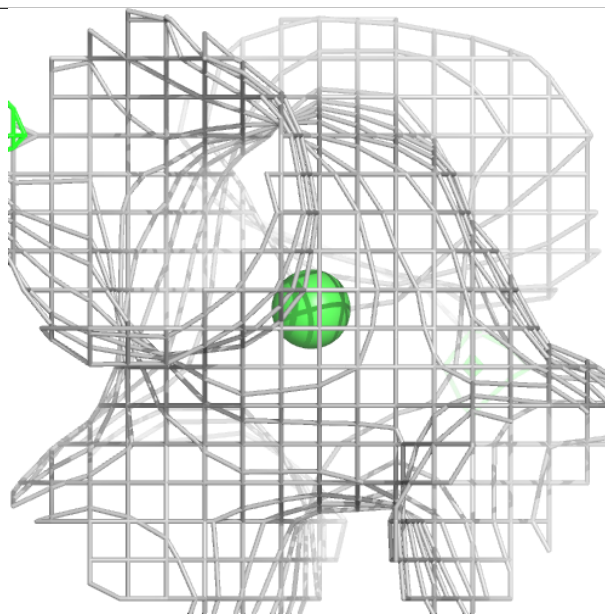
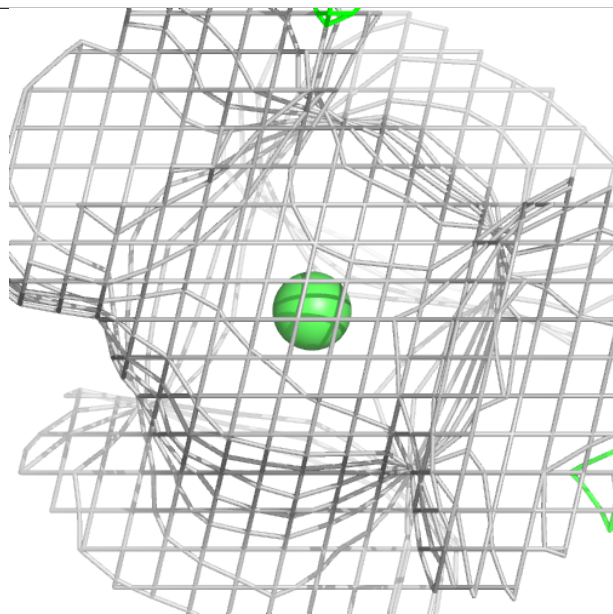
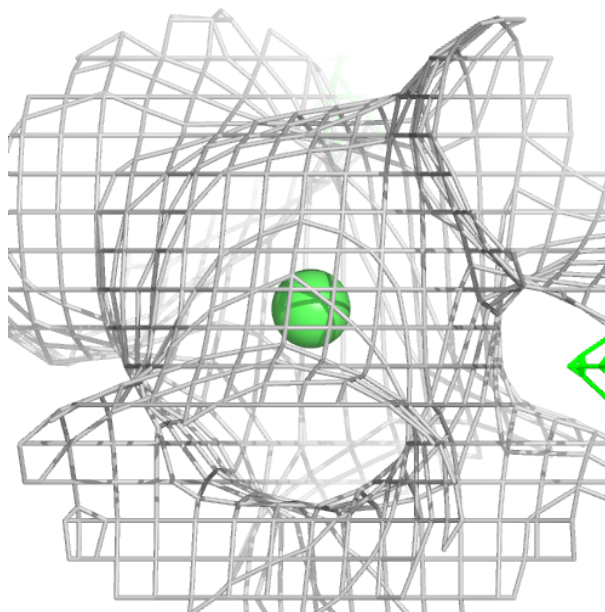
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





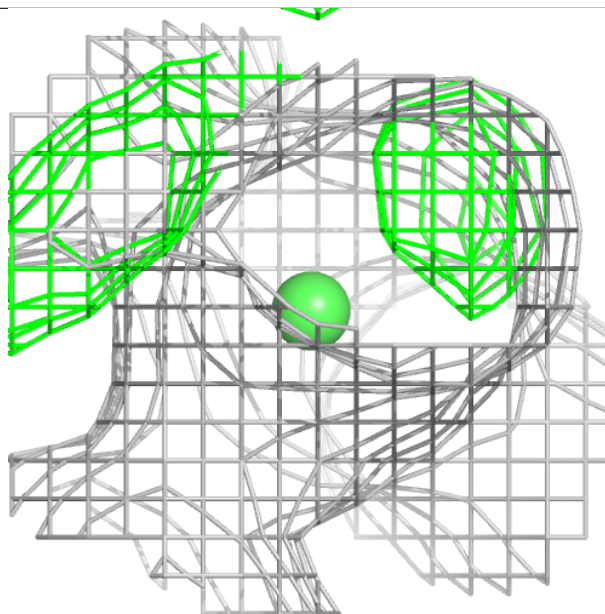
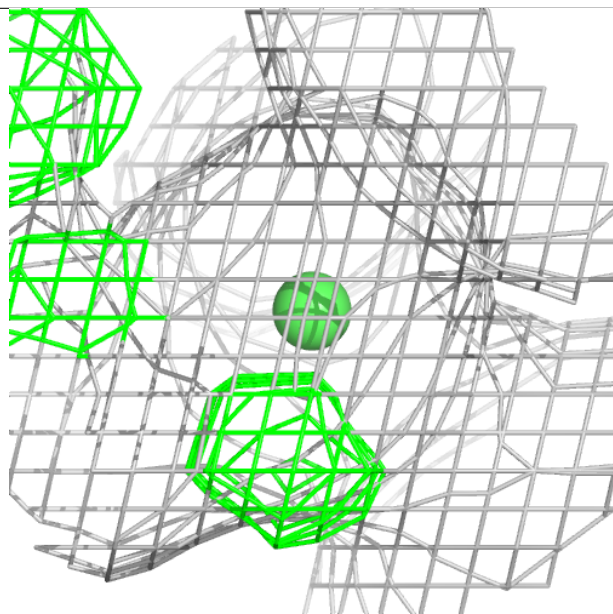
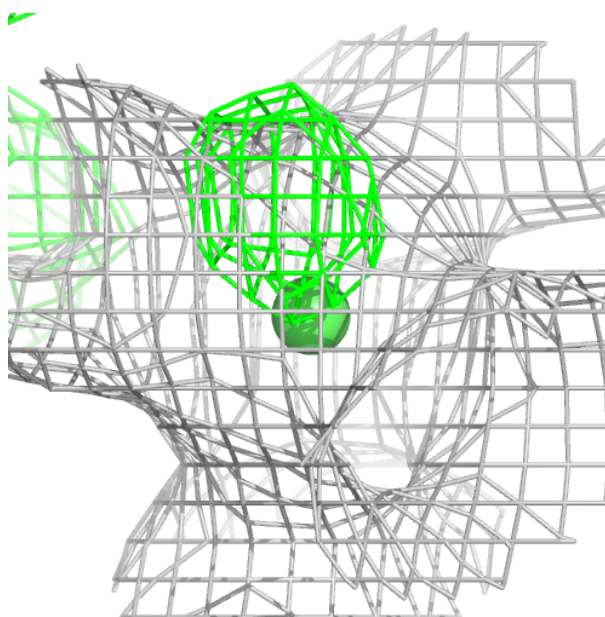
**Electron density around NI F 304:**

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



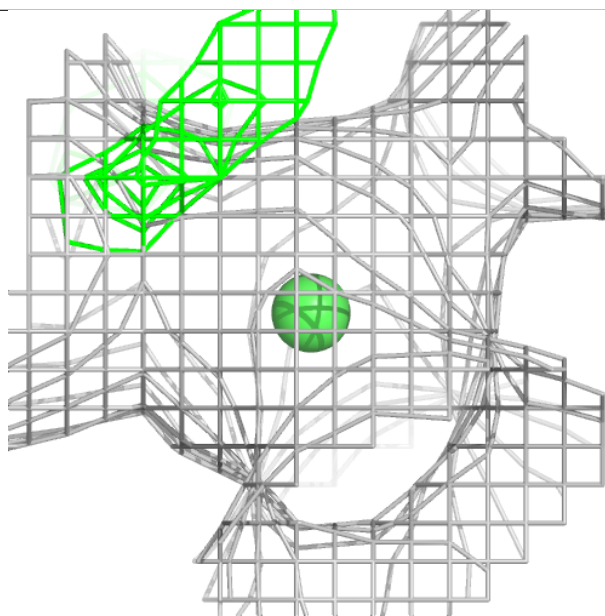
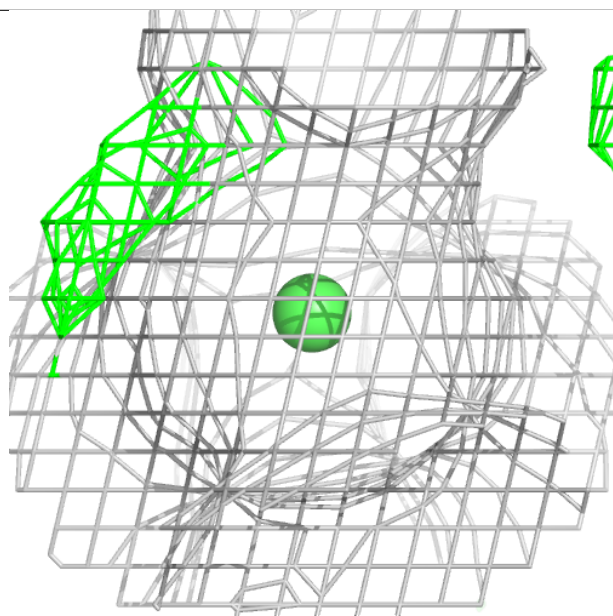
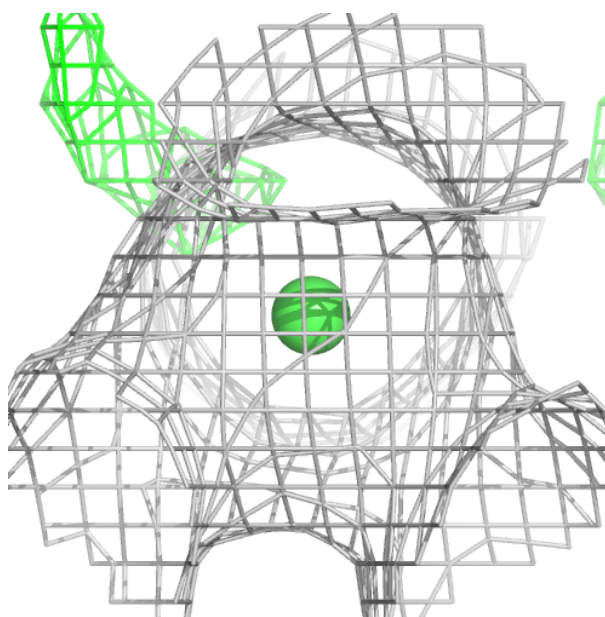
**Electron density around NI D 304:**

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



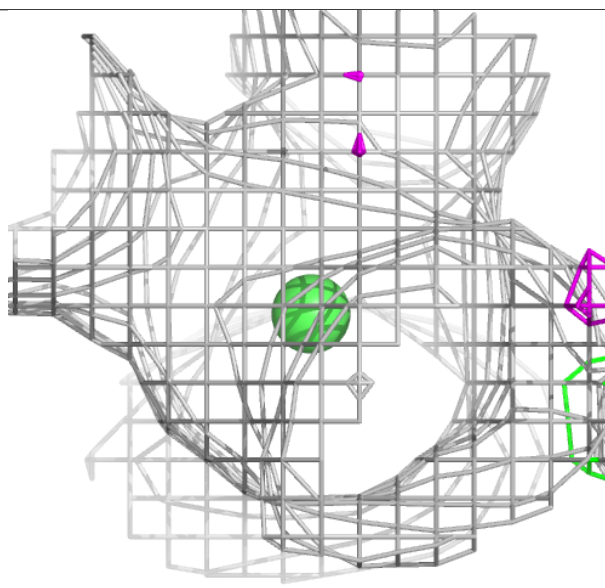
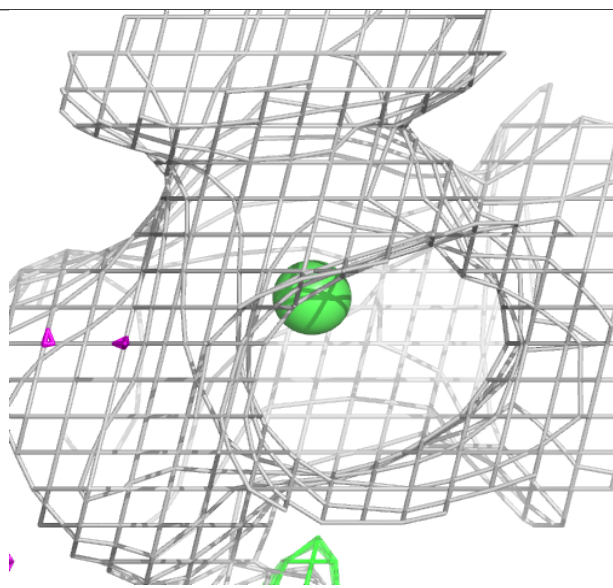
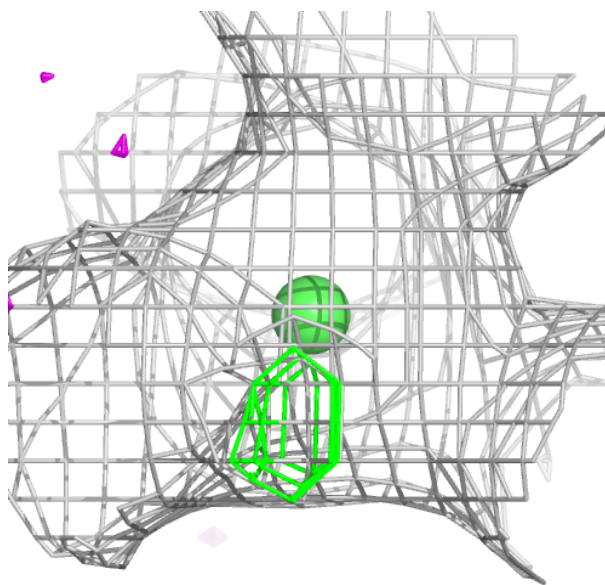
**Electron density around NI B 304:**

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



**Electron density around NI C 304:**

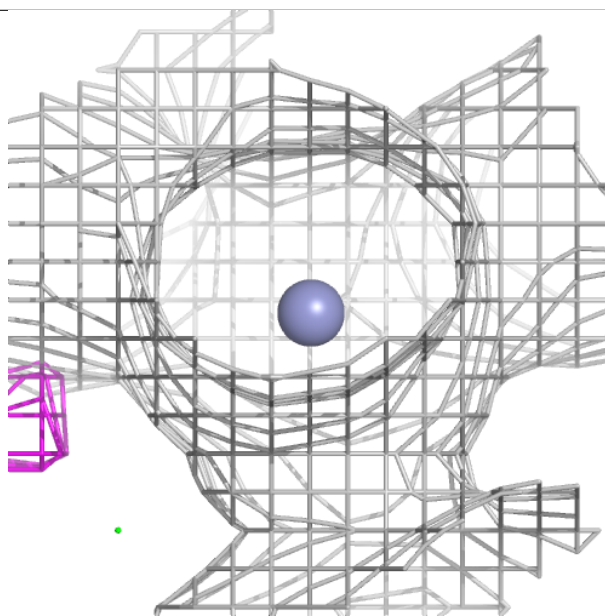
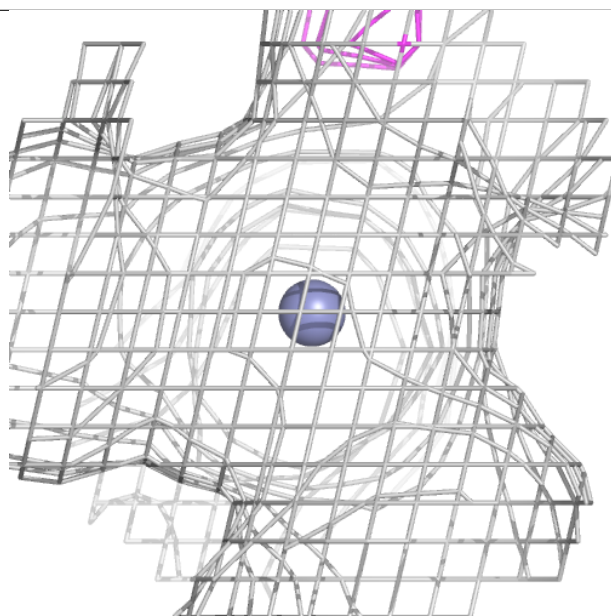
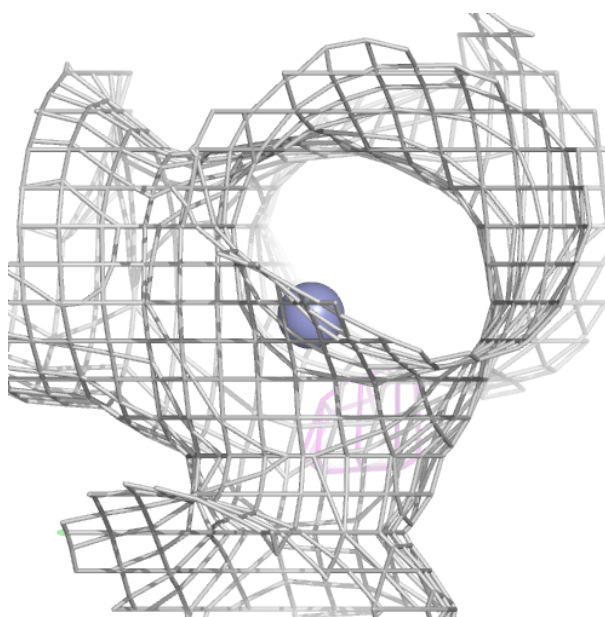
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





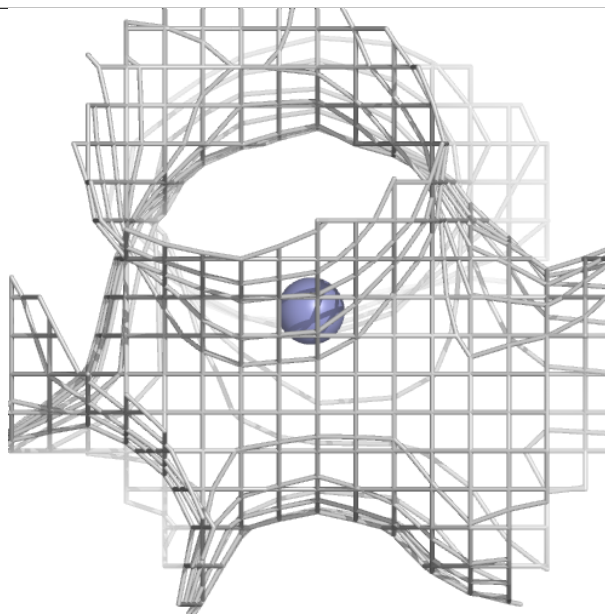
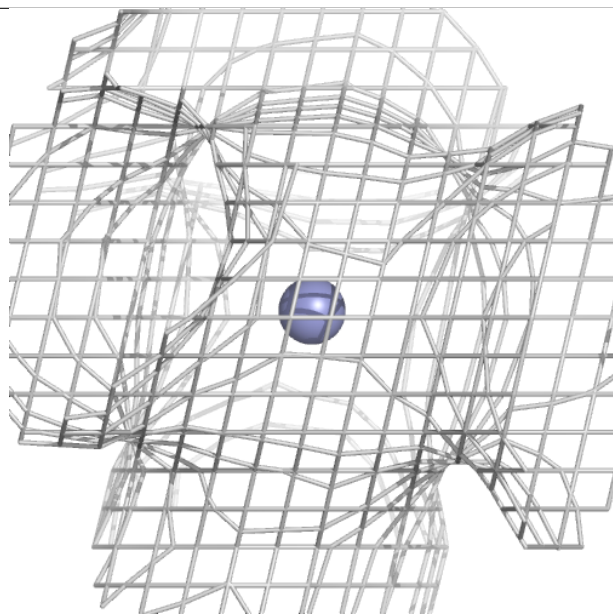
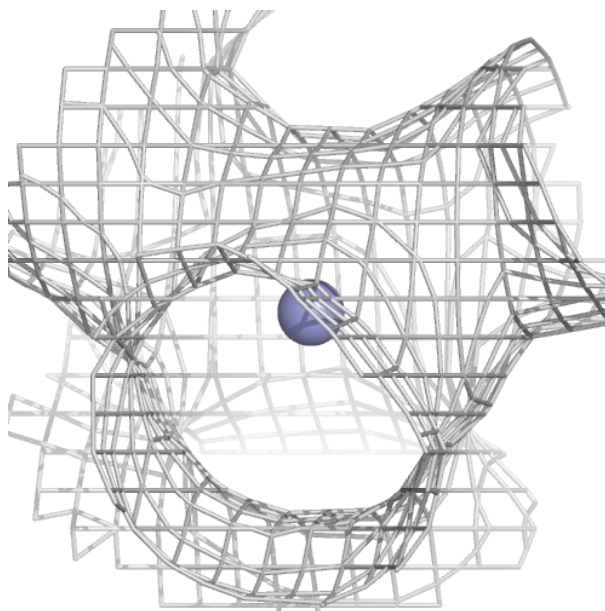
**Electron density around ZN D 302:**

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



**Electron density around ZN C 302:**

$2mF_o-DF_c$  (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.