



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 19, 2023 – 10:42 PM JST

PDB ID : 7BZI  
Title : The mutant variant of PNGM-1. H91 was substituted for alanine to study metal coordination.  
Authors : Park, Y.S.; Kang, L.W.; Lee, J.H.  
Deposited on : 2020-04-28  
Resolution : 1.94 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 : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

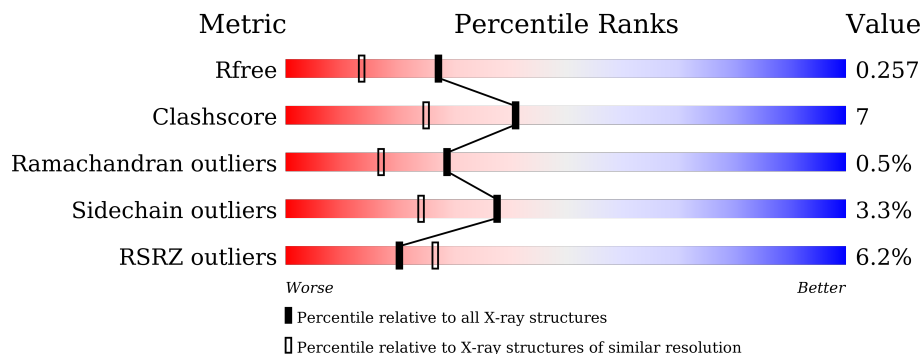
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

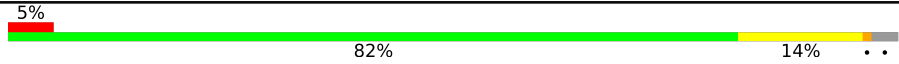


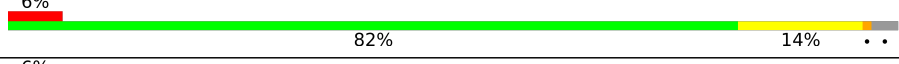
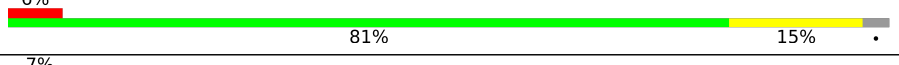

The reported resolution of this entry is 1.94 Å.

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.



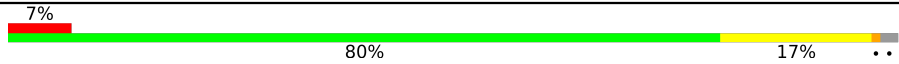

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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	372	
1	B	372	
1	C	372	
1	D	372	
1	E	372	
1	F	372	

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Mol	Chain	Length	Quality of chain
1	G	372	
1	H	372	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24617 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 Metallo-beta-lactamase PNGM-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	G	366	2874	1818	497	539	20	0	0	0
1	B	365	2869	1815	496	538	20	0	0	0
1	C	357	2818	1787	484	527	20	0	0	0
1	F	363	2848	1805	490	533	20	0	0	0
1	E	359	2831	1794	487	530	20	0	0	0
1	D	360	2836	1797	488	531	20	0	0	0
1	A	360	2836	1797	488	531	20	0	0	0
1	H	357	2818	1787	484	527	20	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	91	ALA	HIS	engineered mutation	UNP A0A2U8UYM6
B	91	ALA	HIS	engineered mutation	UNP A0A2U8UYM6
C	91	ALA	HIS	engineered mutation	UNP A0A2U8UYM6
F	91	ALA	HIS	engineered mutation	UNP A0A2U8UYM6
E	91	ALA	HIS	engineered mutation	UNP A0A2U8UYM6
D	91	ALA	HIS	engineered mutation	UNP A0A2U8UYM6
A	91	ALA	HIS	engineered mutation	UNP A0A2U8UYM6
H	91	ALA	HIS	engineered mutation	UNP A0A2U8UYM6

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

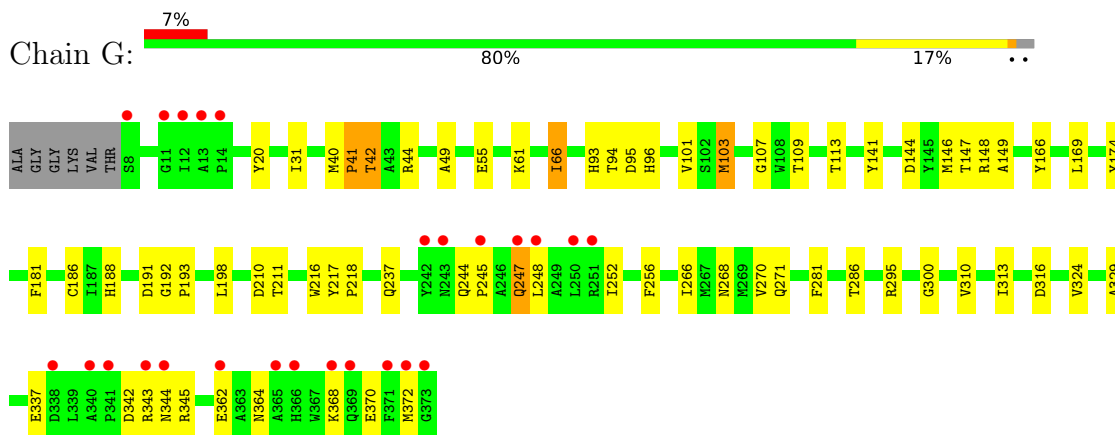
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	213	Total 213	O 213	0	0
3	B	209	Total 209	O 209	0	0
3	C	257	Total 257	O 257	0	0
3	F	268	Total 268	O 268	0	0
3	E	229	Total 229	O 229	0	0
3	D	218	Total 218	O 218	0	0
3	A	251	Total 251	O 251	0	0
3	H	234	Total 234	O 234	0	0

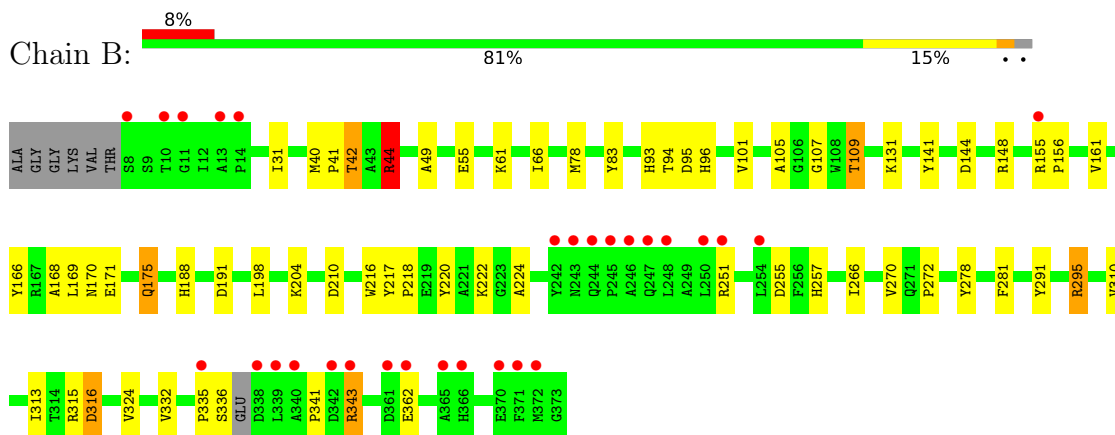
### 3 Residue-property plots [i](#)

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.

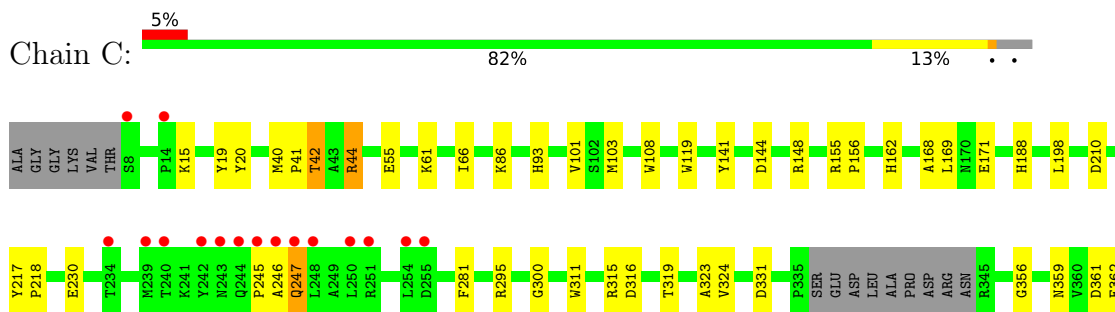
- Molecule 1: Metallo-beta-lactamase PNGM-1

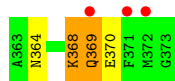


- Molecule 1: Metallo-beta-lactamase PNGM-1

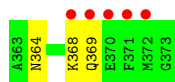
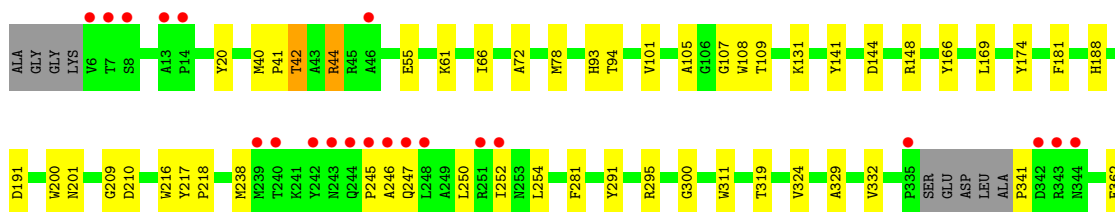
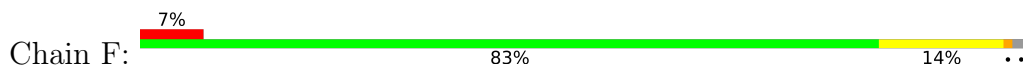


- Molecule 1: Metallo-beta-lactamase PNGM-1

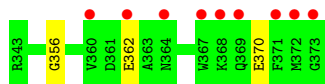
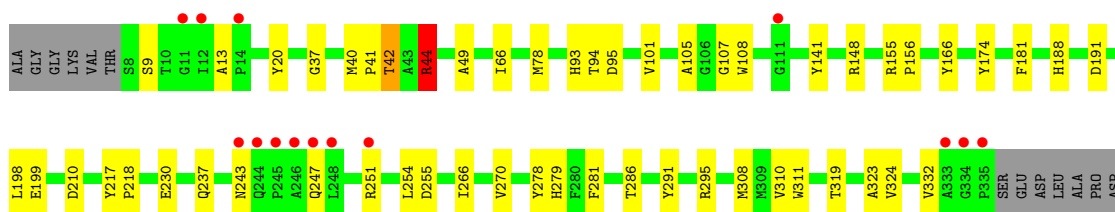
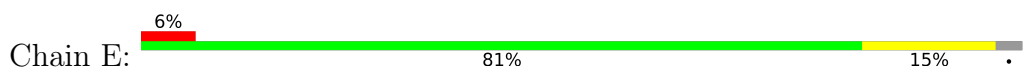




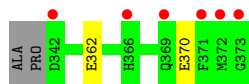
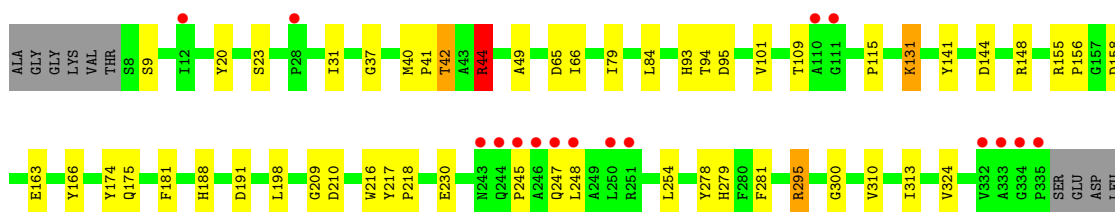
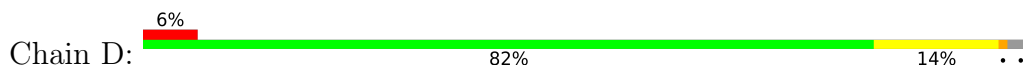
- Molecule 1: Metallo-beta-lactamase PNGM-1



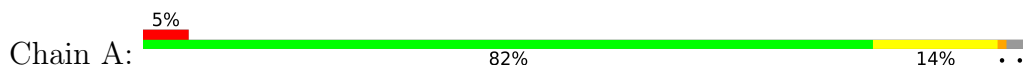
- Molecule 1: Metallo-beta-lactamase PNGM-1

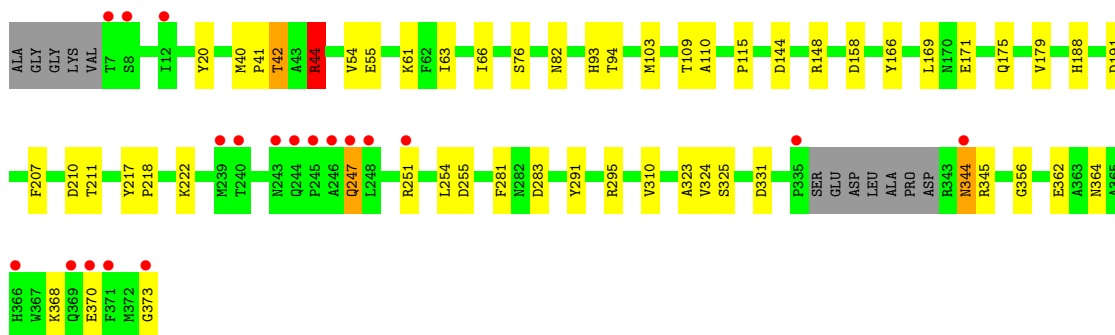


- Molecule 1: Metallo-beta-lactamase PNGM-1

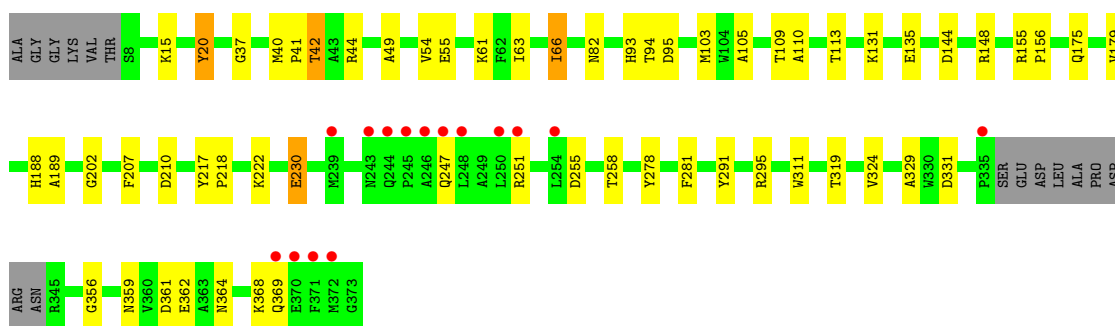
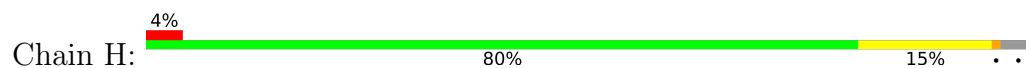


- Molecule 1: Metallo-beta-lactamase PNGM-1





● Molecule 1: Metallo-beta-lactamase PNGM-1





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.38Å 83.06Å 163.58Å 90.00° 110.69° 90.00°	Depositor
Resolution (Å)	49.04 – 1.94 49.00 – 1.94	Depositor EDS
% Data completeness (in resolution range)	95.1 (49.04-1.94) 95.2 (49.00-1.94)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.77 (at 1.94Å)	Xtrriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.210 , 0.255 0.216 , 0.257	Depositor DCC
$R_{free}$ test set	10778 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.6	Xtrriage
Anisotropy	0.040	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 39.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.024 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	24617	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 83.68 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0365e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.67	0/2919	0.85	1/3979 (0.0%)
1	B	0.68	0/2953	0.84	3/4026 (0.1%)
1	C	0.68	0/2901	0.82	0/3954
1	D	0.68	0/2919	0.86	3/3979 (0.1%)
1	E	0.69	0/2914	0.85	2/3972 (0.1%)
1	F	0.68	0/2931	0.84	1/3996 (0.0%)
1	G	0.69	0/2959	0.85	0/4036
1	H	0.67	0/2901	0.84	1/3954 (0.0%)
All	All	0.68	0/23397	0.84	11/31896 (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.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	44	ARG	NE-CZ-NH2	-9.40	115.60	120.30
1	D	44	ARG	NE-CZ-NH2	-7.86	116.37	120.30
1	E	44	ARG	NE-CZ-NH1	7.21	123.90	120.30
1	B	44	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	D	44	ARG	NE-CZ-NH1	6.04	123.32	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	211	THR	Peptide

## 5.2 Too-close contacts [i](#)

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	2836	0	2649	39	0
1	B	2869	0	2671	48	0
1	C	2818	0	2639	36	0
1	D	2836	0	2649	42	0
1	E	2831	0	2647	41	0
1	F	2848	0	2651	38	0
1	G	2874	0	2674	57	0
1	H	2818	0	2639	51	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	251	0	0	13	1
3	B	209	0	0	4	1
3	C	257	0	0	6	0
3	D	218	0	0	15	0
3	E	229	0	0	11	0
3	F	268	0	0	4	0
3	G	213	0	0	4	0
3	H	234	0	0	11	0
All	All	24617	0	21219	314	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 314 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:A:93:HIS:HE1	1:A:188:HIS:NE2	1.60	1.00
1:E:93:HIS:HE1	1:E:188:HIS:NE2	1.63	0.95
1:E:42:THR:CG2	3:E:577:HOH:O	2.14	0.95
1:H:93:HIS:HE1	1:H:188:HIS:NE2	1.68	0.92
1:C:315:ARG:HD2	3:C:548:HOH:O	1.69	0.92

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:570:HOH:O	3:A:729:HOH:O[2_655]	2.13	0.07

## 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	356/372 (96%)	342 (96%)	13 (4%)	1 (0%)	41	32
1	B	361/372 (97%)	342 (95%)	18 (5%)	1 (0%)	41	32
1	C	353/372 (95%)	336 (95%)	15 (4%)	2 (1%)	25	13
1	D	356/372 (96%)	343 (96%)	10 (3%)	3 (1%)	19	9
1	E	355/372 (95%)	344 (97%)	9 (2%)	2 (1%)	25	13
1	F	359/372 (96%)	342 (95%)	15 (4%)	2 (1%)	25	13
1	G	364/372 (98%)	342 (94%)	21 (6%)	1 (0%)	41	32
1	H	353/372 (95%)	339 (96%)	13 (4%)	1 (0%)	41	32
All	All	2857/2976 (96%)	2730 (96%)	114 (4%)	13 (0%)	29	17

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	246	ALA

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Mol	Chain	Res	Type
1	B	66	ILE
1	F	246	ALA
1	G	66	ILE
1	E	279	HIS

### 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	288/301 (96%)	278 (96%)	10 (4%)	36	21
1	B	290/301 (96%)	280 (97%)	10 (3%)	37	22
1	C	287/301 (95%)	275 (96%)	12 (4%)	30	14
1	D	288/301 (96%)	278 (96%)	10 (4%)	36	21
1	E	288/301 (96%)	278 (96%)	10 (4%)	36	21
1	F	287/301 (95%)	281 (98%)	6 (2%)	53	41
1	G	290/301 (96%)	280 (97%)	10 (3%)	37	22
1	H	287/301 (95%)	278 (97%)	9 (3%)	40	26
All	All	2305/2408 (96%)	2228 (97%)	77 (3%)	38	24

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	370	GLU
1	H	222	LYS
1	A	44	ARG
1	A	344	ASN
1	H	362	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	93	HIS

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Mol	Chain	Res	Type
1	A	369	GLN
1	H	93	HIS
1	A	93	HIS
1	C	93	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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 [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	360/372 (96%)	0.03	19 (5%) 26 33	12, 21, 59, 80	0
1	B	365/372 (98%)	0.23	29 (7%) 12 18	15, 28, 58, 83	0
1	C	357/372 (95%)	0.02	19 (5%) 26 33	11, 21, 57, 95	0
1	D	360/372 (96%)	0.17	22 (6%) 21 27	14, 27, 56, 73	0
1	E	359/372 (96%)	0.13	23 (6%) 19 26	14, 25, 53, 75	0
1	F	363/372 (97%)	0.07	26 (7%) 15 21	11, 20, 59, 90	0
1	G	366/372 (98%)	0.34	25 (6%) 17 23	17, 30, 59, 80	0
1	H	357/372 (95%)	-0.01	15 (4%) 36 43	12, 22, 58, 84	0
All	All	2887/2976 (97%)	0.12	178 (6%) 20 27	11, 24, 58, 95	0

The worst 5 of 178 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	243	ASN	6.2
1	G	343	ARG	6.2
1	F	245	PRO	5.9
1	E	372	MET	5.9
1	F	248	LEU	5.7

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands

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

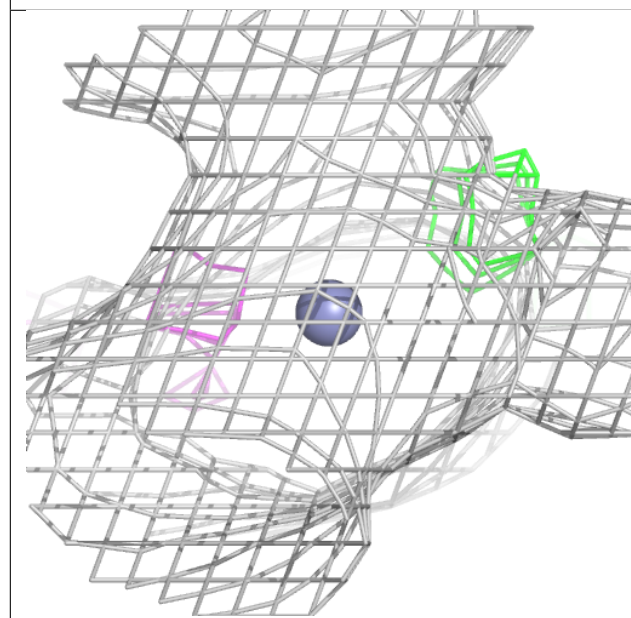
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	G	401	1/1	0.99	0.07	25,25,25,25	0
2	ZN	B	401	1/1	1.00	0.06	23,23,23,23	0
2	ZN	C	401	1/1	1.00	0.04	20,20,20,20	0
2	ZN	F	401	1/1	1.00	0.05	18,18,18,18	0
2	ZN	E	401	1/1	1.00	0.06	20,20,20,20	0
2	ZN	D	401	1/1	1.00	0.07	22,22,22,22	0
2	ZN	A	401	1/1	1.00	0.05	19,19,19,19	0
2	ZN	H	401	1/1	1.00	0.05	21,21,21,21	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.



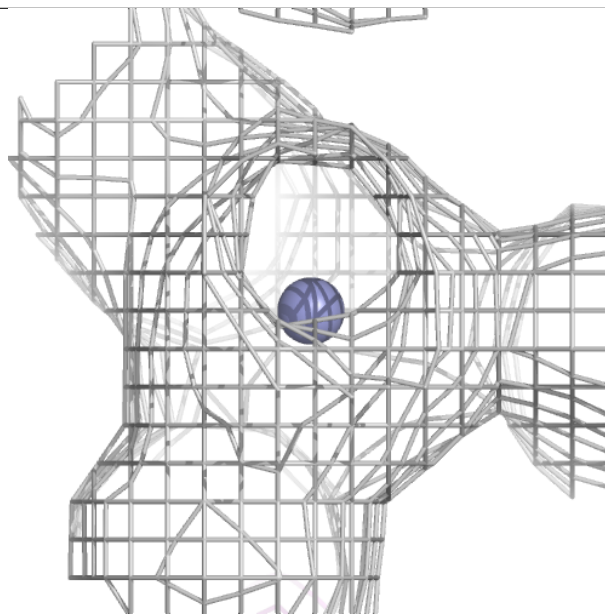
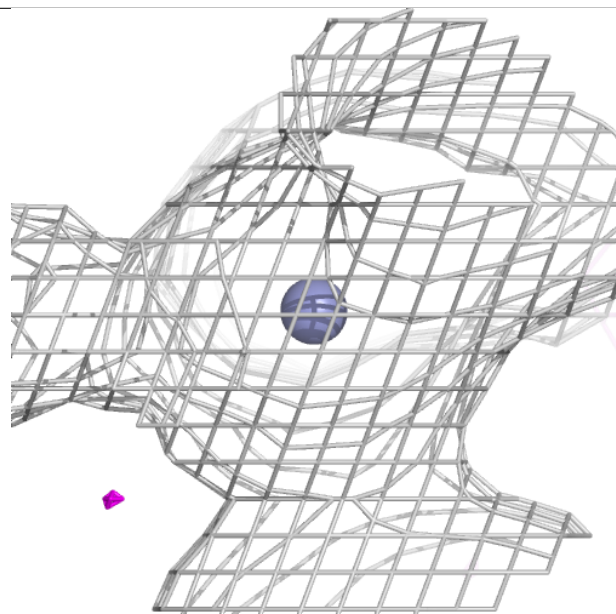
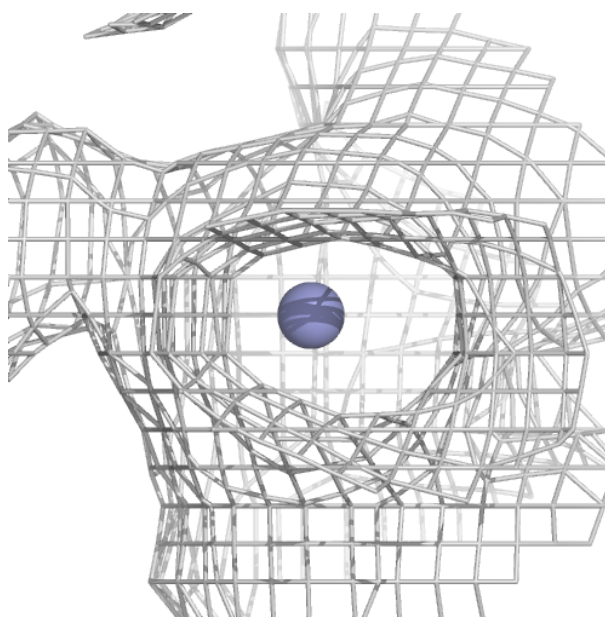
**Electron density around ZN G 401:**

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



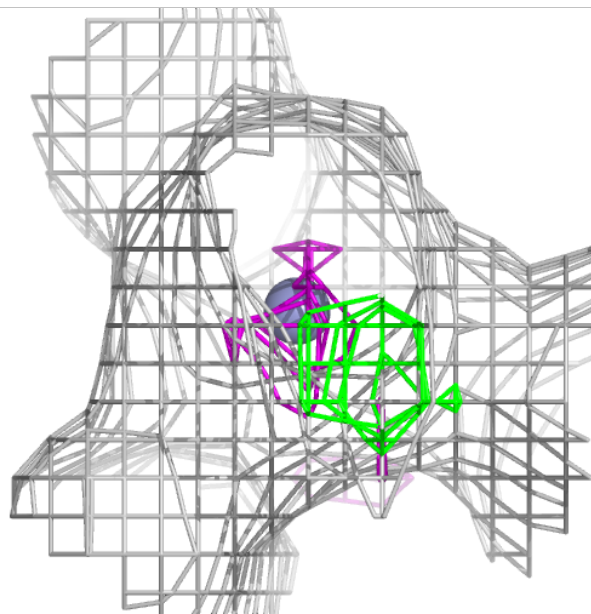
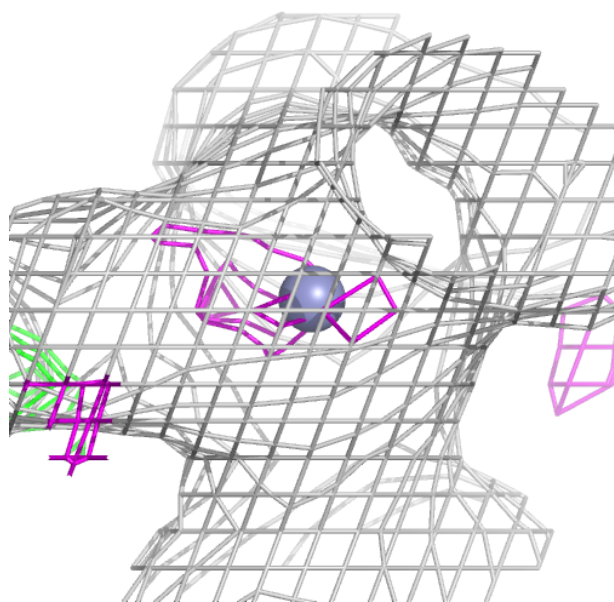
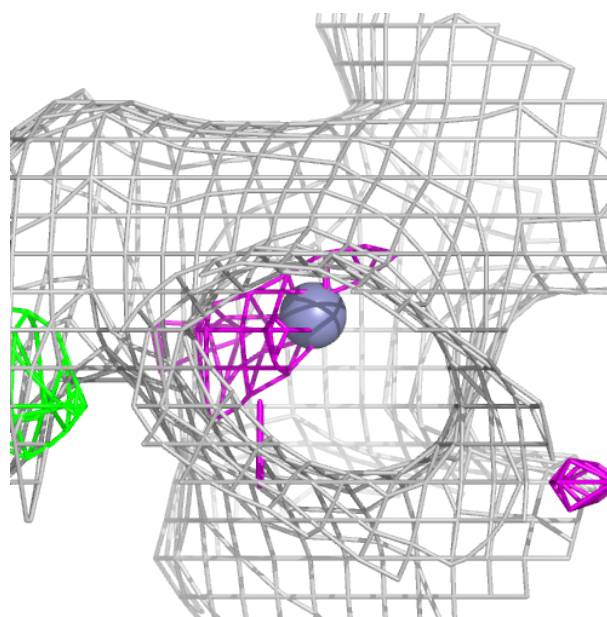
**Electron density around ZN B 401:**

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



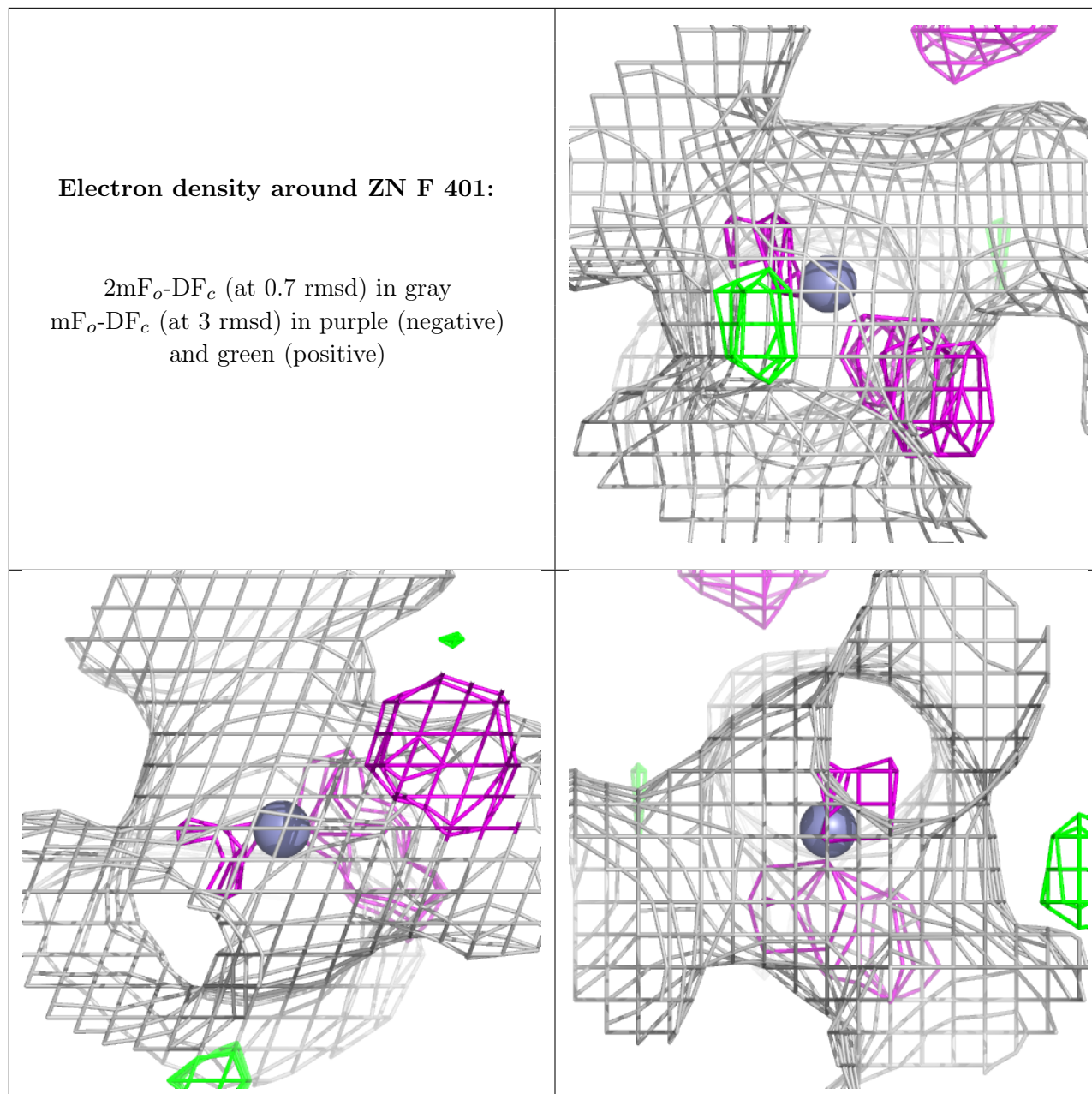
**Electron density around ZN C 401:**

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



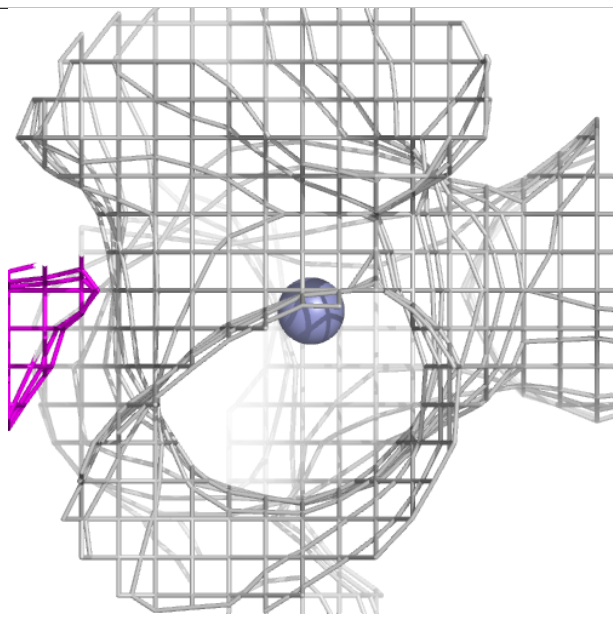
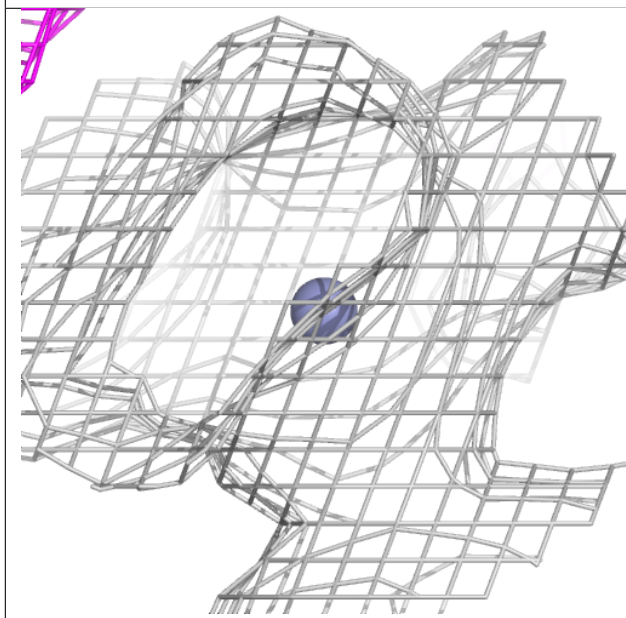
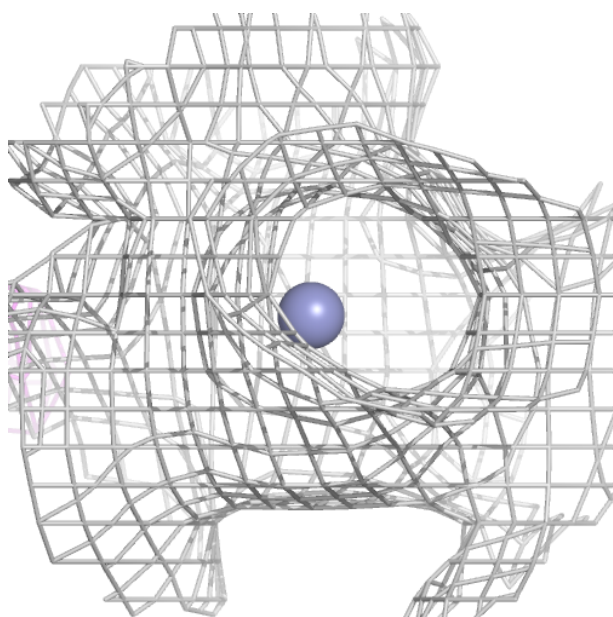
**Electron density around ZN F 401:**

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



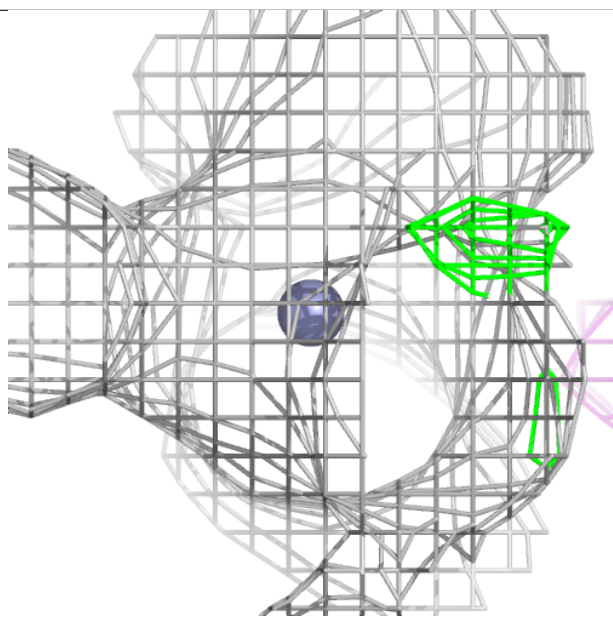
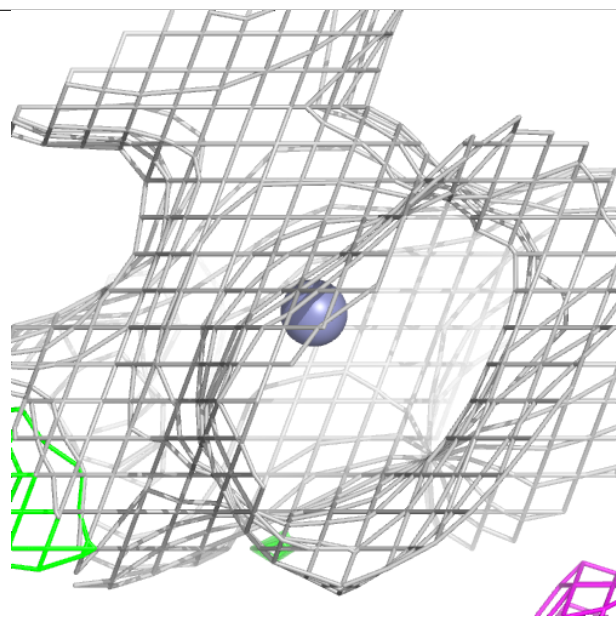
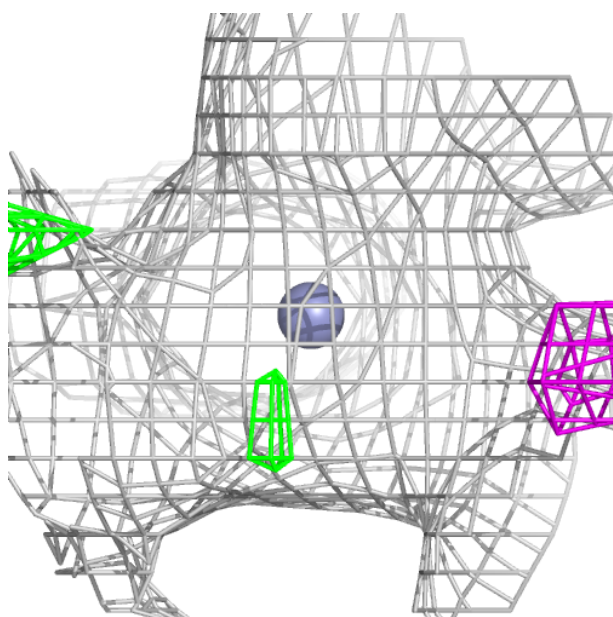
**Electron density around ZN E 401:**

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



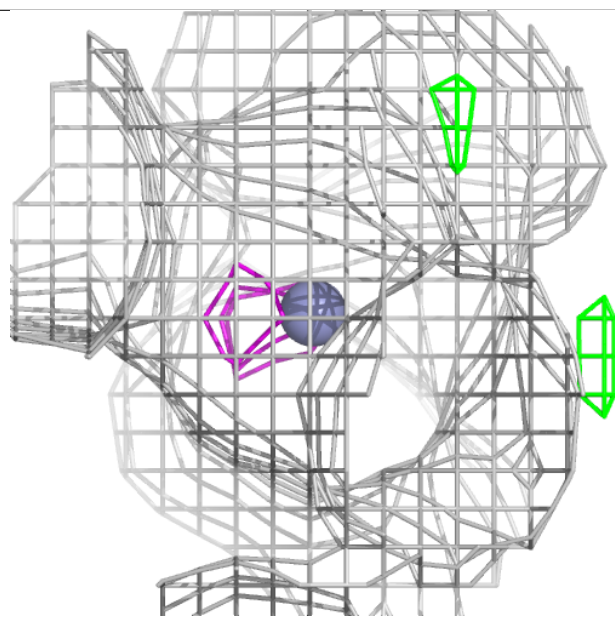
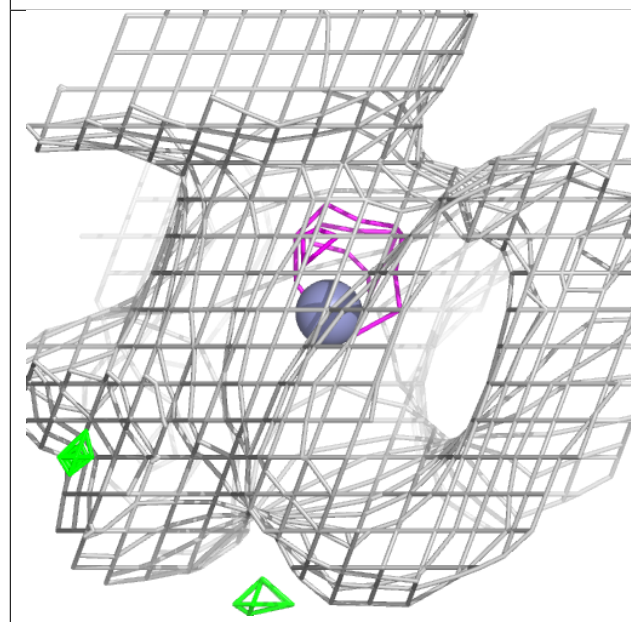
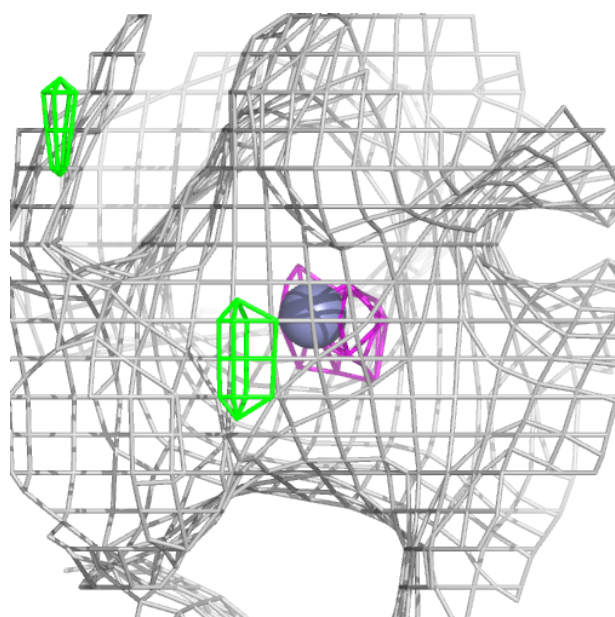
**Electron density around ZN D 401:**

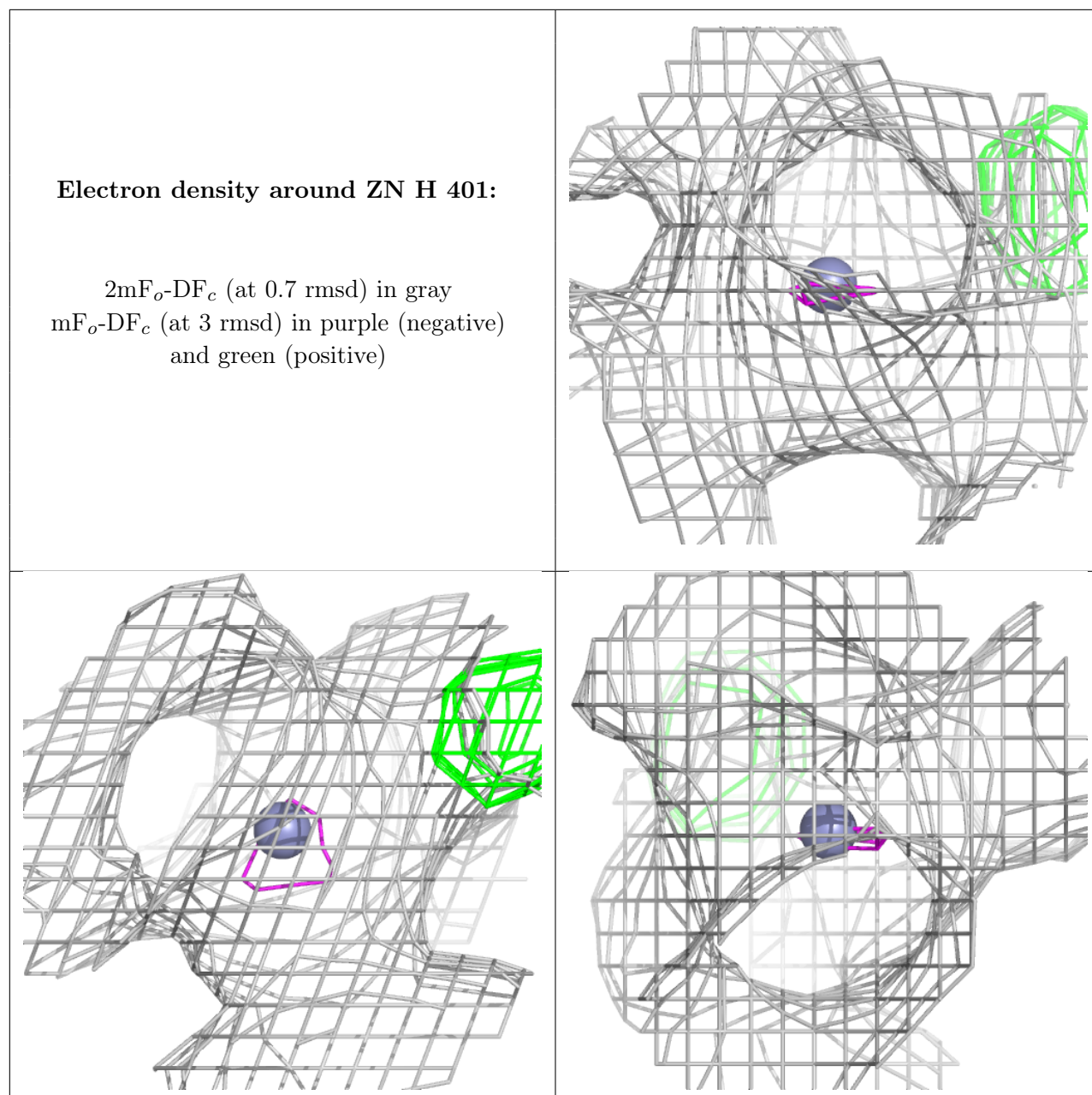
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around ZN A 401:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.