



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 01:45 AM EDT

PDB ID : 7LI1  
Title : Crystal structure of holo Moraxella catarrhalis ferric binding protein A in an open conformation  
Authors : Chan, C.; Ng, D.; Fraser, M.E.; Schryvers, A.B.  
Deposited on : 2021-01-26  
Resolution : 1.75 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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
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

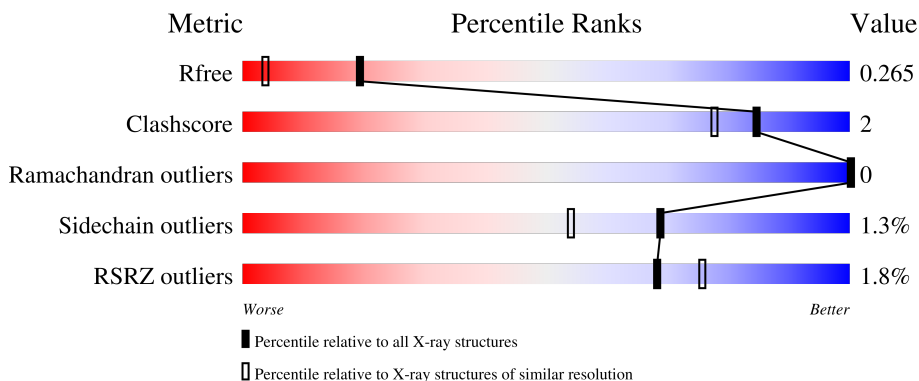
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

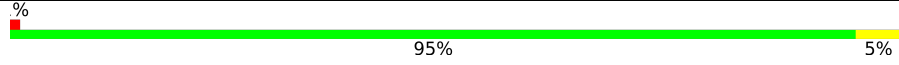
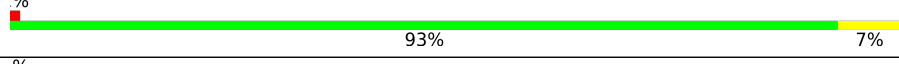
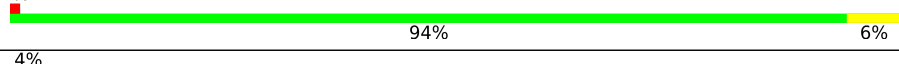

The reported resolution of this entry is 1.75 Å.

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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	312	 95% 5%
1	B	312	 93% 7%
1	C	312	 94% 6%
1	D	312	 90% 10%

## 2 Entry composition [i](#)

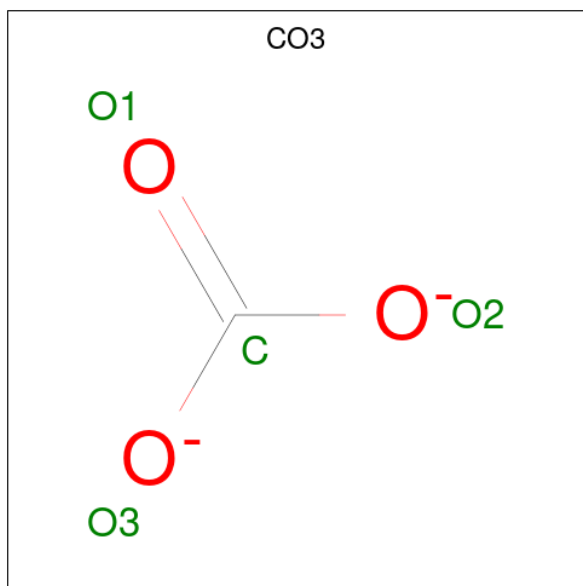
There are 4 unique types of molecules in this entry. The entry contains 9740 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Fe(3+) ABC transporter substrate-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	312	Total 2349	C 1484	N 410	O 449	S 6	5	2	0
1	B	312	Total 2327	C 1467	N 410	O 444	S 6	3	1	0
1	C	311	Total 2330	C 1473	N 413	O 437	S 7	9	3	0
1	D	311	Total 2323	C 1474	N 406	O 437	S 6	14	3	0

- Molecule 2 is CARBONATE ION (three-letter code: CO3) (formula: CO<sub>3</sub>).



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

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

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Fe	0	0
			1	1		
3	B	1	Total	Fe	0	0
			1	1		
3	C	1	Total	Fe	0	0
			1	1		
3	D	3	Total	Fe	0	0
			3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	117	Total	O	0	0
			117	117		
4	B	81	Total	O	0	1
			82	82		
4	C	76	Total	O	0	3
			79	79		
4	D	92	Total	O	0	3
			95	95		

### 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: Fe(3+) ABC transporter substrate-binding protein



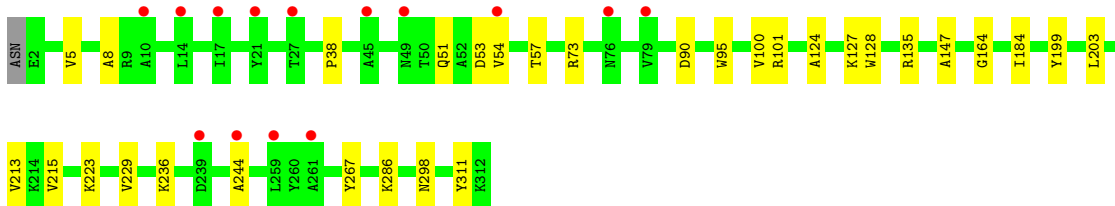
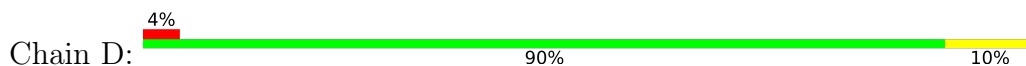
- Molecule 1: Fe(3+) ABC transporter substrate-binding protein



- Molecule 1: Fe(3+) ABC transporter substrate-binding protein



- Molecule 1: Fe(3+) ABC transporter substrate-binding protein



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.13Å 67.56Å 73.77Å 91.02° 92.26° 105.02°	Depositor
Resolution (Å)	29.71 – 1.75 47.57 – 1.75	Depositor EDS
% Data completeness (in resolution range)	94.2 (29.71-1.75) 85.1 (47.57-1.75)	Depositor EDS
$R_{merge}$	0.02	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.61 (at 1.75Å)	Xtrriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.231 , 0.265 0.231 , 0.265	Depositor DCC
$R_{free}$ test set	2005 reflections (1.82%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.6	Xtrriage
Anisotropy	0.348	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 42.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	9740	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	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 62.53 % 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 1.1110e-05. 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE, CO3

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	0.37	0/2399	0.52	0/3279
1	B	0.34	0/2377	0.50	0/3256
1	C	0.34	0/2380	0.51	0/3255
1	D	0.35	0/2376	0.50	0/3252
All	All	0.35	0/9532	0.51	0/13042

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	229	VAL	Peptide
1	D	229	VAL	Peptide

## 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	2349	0	2224	6	0
1	B	2327	0	2185	11	0
1	C	2330	0	2193	10	0
1	D	2323	0	2197	16	0
2	A	8	0	0	0	0
2	B	8	0	0	0	0
2	C	8	0	0	0	0
2	D	8	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	3	0	0	0	0
4	A	117	0	0	0	0
4	B	82	0	0	0	0
4	C	79	0	0	1	0
4	D	95	0	0	3	0
All	All	9740	0	8799	41	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 2.

All (41) 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:D:223:LYS:HG2	4:D:526:HOH:O	2.07	0.55
1:C:160:ARG:NH2	4:C:503[A]:HOH:O	2.32	0.54
1:D:215:VAL:HG12	4:D:565:HOH:O	2.10	0.51
1:A:43:LEU:HD21	1:A:235:VAL:HG22	1.92	0.50
1:B:90:ASP:HB2	1:B:95:TRP:CE2	2.47	0.49
1:A:100:VAL:HB	1:A:267:TYR:HB2	1.94	0.49
1:A:124:ALA:HB1	1:A:164:GLY:HA3	1.94	0.48
1:C:286:LYS:HG3	1:D:38:PRO:HG3	1.95	0.48
1:D:53:ASP:HB3	1:D:244:ALA:HB2	1.95	0.48
1:C:82:SER:OG	1:D:51:GLN:OE1	2.32	0.48
1:C:131:ARG:NH2	1:C:190:ASP:OD2	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:127:LYS:HE3	1:D:128:TRP:CE2	2.49	0.47
1:C:100:VAL:HB	1:C:267:TYR:HB2	1.97	0.46
1:A:147:ALA:HB1	1:A:298:ASN:HB2	1.98	0.46
1:D:5:VAL:HG13	1:D:54:VAL:HG23	1.97	0.46
1:A:182[B]:GLU:OE2	1:A:206:LYS:NZ	2.35	0.45
1:D:8:ALA:HB3	1:D:57:THR:HA	1.97	0.44
1:B:48:LYS:HA	1:B:237:HIS:HB3	2.00	0.44
1:B:8:ALA:HB3	1:B:57:THR:HA	1.99	0.43
1:B:132:LEU:HA	1:B:191:VAL:HG23	1.99	0.43
1:B:108:ASN:HA	1:B:212:ASN:O	2.18	0.43
1:B:258:ARG:NH2	1:B:274:THR:O	2.50	0.43
1:D:124:ALA:HB1	1:D:164:GLY:HA3	2.00	0.43
1:A:90:ASP:HB2	1:A:95:TRP:CE2	2.54	0.43
1:C:34:ASP:HB3	1:C:39:LEU:HD13	2.01	0.43
1:C:197:TYR:HB2	1:C:264:ASN:O	2.20	0.42
1:D:184:ILE:HG22	1:D:213:VAL:HG22	2.01	0.42
1:B:13:LEU:HD21	1:B:264:ASN:HB2	2.01	0.42
1:B:48:LYS:HA	1:B:237:HIS:CG	2.55	0.42
1:D:100:VAL:HB	1:D:267:TYR:HB2	2.02	0.42
1:D:90:ASP:HB2	1:D:95:TRP:CE2	2.54	0.42
1:D:286:LYS:NZ	4:D:514:HOH:O	2.52	0.42
1:B:75:ILE:O	1:B:93:ASN:HB3	2.20	0.41
1:C:56:ILE:HG12	1:C:232:ALA:HB2	2.02	0.41
1:D:199:TYR:CZ	1:D:203:LEU:HD11	2.55	0.41
1:B:77:SER:OG	1:B:249:GLU:OE1	2.33	0.41
1:C:199:TYR:CZ	1:C:203:LEU:HD11	2.55	0.41
1:D:147:ALA:HB1	1:D:298:ASN:HB2	2.02	0.41
1:D:73:ARG:HB3	1:D:236:LYS:HA	2.02	0.40
1:B:55:LEU:O	1:B:232:ALA:HA	2.21	0.40
1:C:157:THR:HG23	1:C:160:ARG:HH21	1.86	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	312/312 (100%)	309 (99%)	3 (1%)	0	100	100
1	B	311/312 (100%)	308 (99%)	3 (1%)	0	100	100
1	C	312/312 (100%)	309 (99%)	3 (1%)	0	100	100
1	D	312/312 (100%)	309 (99%)	3 (1%)	0	100	100
All	All	1247/1248 (100%)	1235 (99%)	12 (1%)	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	231/254 (91%)	228 (99%)	3 (1%)	69	54
1	B	227/254 (89%)	224 (99%)	3 (1%)	69	54
1	C	224/254 (88%)	221 (99%)	3 (1%)	69	54
1	D	225/254 (89%)	222 (99%)	3 (1%)	69	54
All	All	907/1016 (89%)	895 (99%)	12 (1%)	69	54

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	ARG
1	A	135	ARG
1	A	311	TYR
1	B	14	LEU
1	B	101	ARG
1	B	135	ARG
1	C	101	ARG
1	C	135	ARG
1	C	311	TYR
1	D	101	ARG

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Mol	Chain	Res	Type
1	D	135	ARG
1	D	311	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	272	GLN
1	D	300	GLN

### 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 14 ligands modelled in this entry, 6 are monoatomic - leaving 8 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	CO3	C	402	-	2,3,3	0.43	0	2,3,3	0.13	0
2	CO3	B	402	-	2,3,3	0.31	0	2,3,3	0.24	0
2	CO3	C	401	-	2,3,3	0.32	0	2,3,3	0.61	0
2	CO3	A	401	-	2,3,3	0.34	0	2,3,3	0.34	0
2	CO3	A	402	-	2,3,3	0.31	0	2,3,3	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	CO3	D	402	-	2,3,3	0.35	0	2,3,3	0.19	0
2	CO3	B	401	-	2,3,3	0.40	0	2,3,3	0.20	0
2	CO3	D	401	-	2,3,3	0.27	0	2,3,3	0.44	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.

## 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	312/312 (100%)	0.12	3 (0%) 82 87	24, 37, 50, 58	2 (0%)
1	B	312/312 (100%)	0.08	3 (0%) 82 87	27, 40, 50, 55	1 (0%)
1	C	311/312 (99%)	0.21	3 (0%) 82 87	23, 40, 61, 70	5 (1%)
1	D	311/312 (99%)	0.34	14 (4%) 33 39	22, 40, 59, 64	5 (1%)
All	All	1246/1248 (99%)	0.19	23 (1%) 68 76	22, 39, 56, 70	13 (1%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	244	ALA	4.1
1	D	45	ALA	3.9
1	A	10	ALA	3.6
1	D	14	LEU	3.3
1	A	13	LEU	3.2
1	D	21	TYR	3.0
1	C	78	SER	2.6
1	D	76	ASN	2.5
1	D	79	VAL	2.4
1	D	259	LEU	2.4
1	D	10	ALA	2.4
1	B	76	ASN	2.4
1	D	49	ASN	2.4
1	D	239	ASP	2.3
1	D	261	ALA	2.3
1	C	16	PRO	2.3
1	D	54	VAL	2.3
1	C	10	ALA	2.2
1	D	27	THR	2.1
1	A	29	VAL	2.1
1	D	17	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	80	LEU	2.1
1	B	239	ASP	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

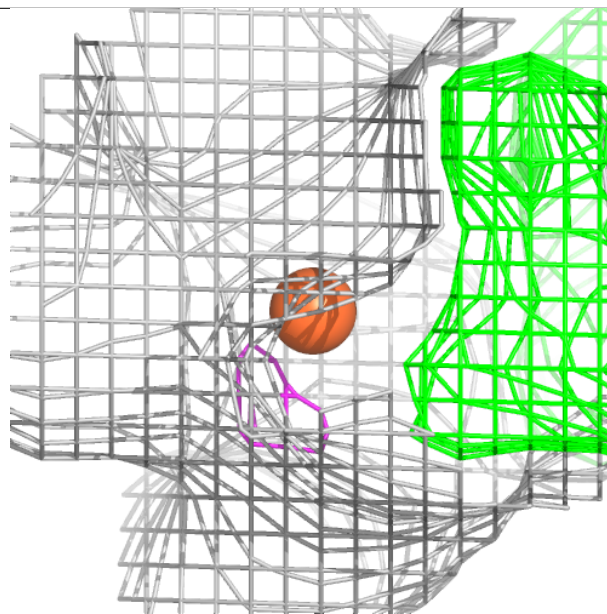
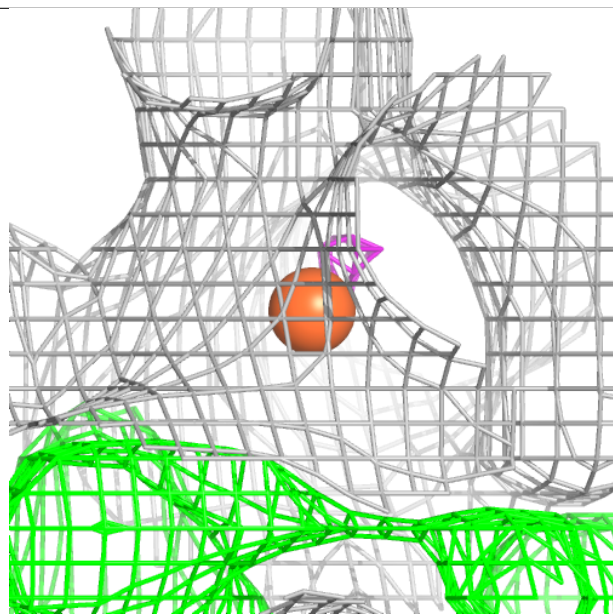
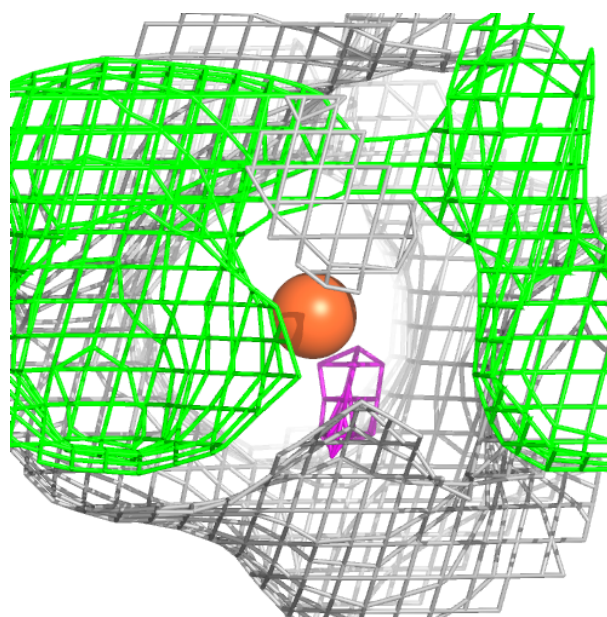
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	CO3	A	402	4/4	0.76	0.17	46,47,51,51	0
2	CO3	D	401	4/4	0.78	0.19	39,43,48,55	0
3	FE	B	403	1/1	0.83	0.05	67,67,67,67	0
2	CO3	B	402	4/4	0.85	0.17	42,43,45,51	0
3	FE	D	404	1/1	0.85	0.07	79,79,79,79	0
3	FE	D	403	1/1	0.89	0.05	71,71,71,71	0
2	CO3	D	402	4/4	0.89	0.11	48,51,52,56	0
2	CO3	C	402	4/4	0.93	0.14	39,47,48,54	0
2	CO3	A	401	4/4	0.94	0.08	37,39,44,47	0
2	CO3	C	401	4/4	0.94	0.08	31,34,36,43	0
3	FE	A	403	1/1	0.96	0.04	56,56,56,56	0
2	CO3	B	401	4/4	0.96	0.07	45,46,48,50	0
3	FE	C	403	1/1	0.98	0.05	50,50,50,50	0
3	FE	D	405	1/1	0.99	0.05	64,64,64,64	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 FE B 403:**

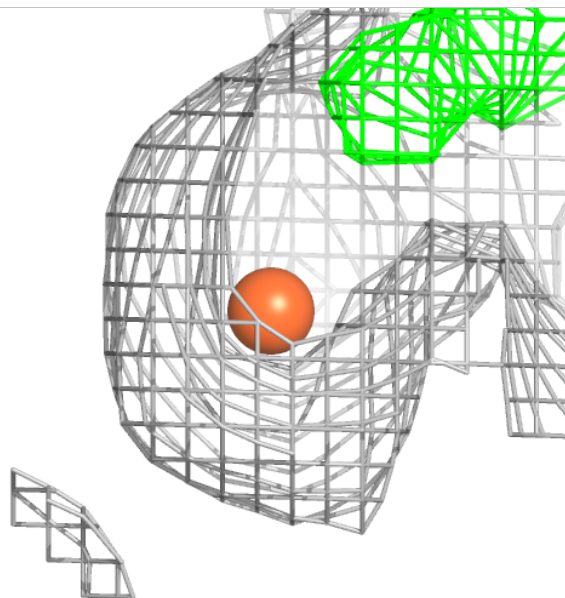
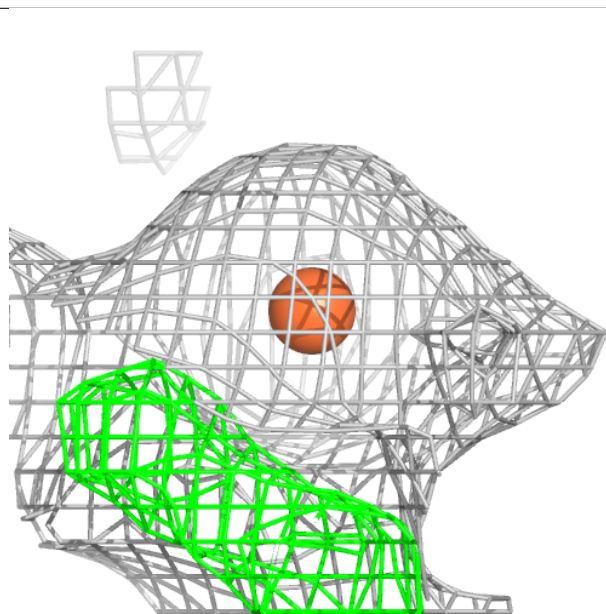
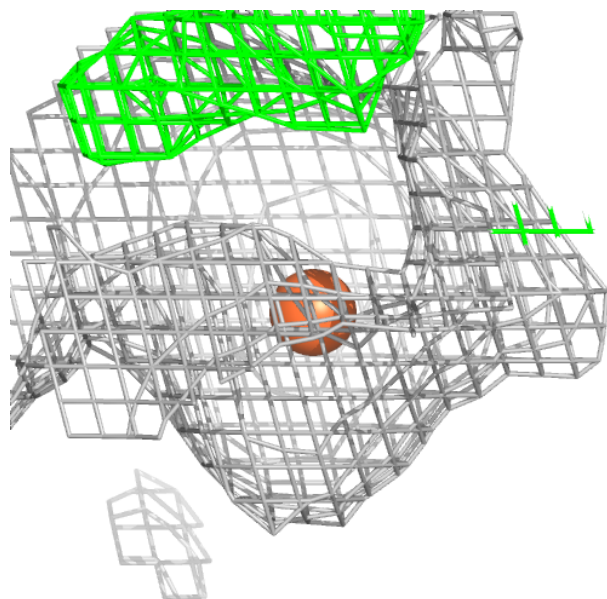
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around FE D 404:**

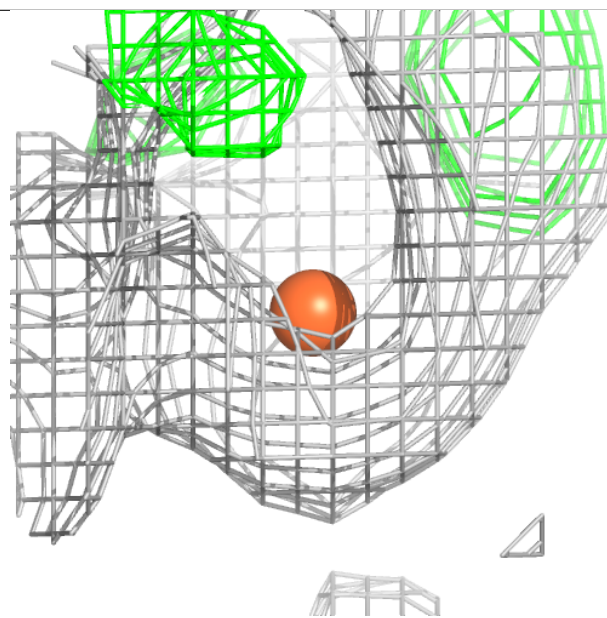
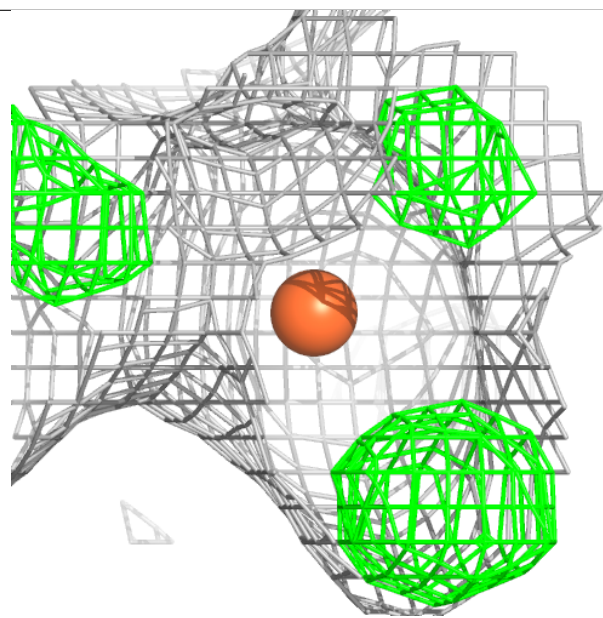
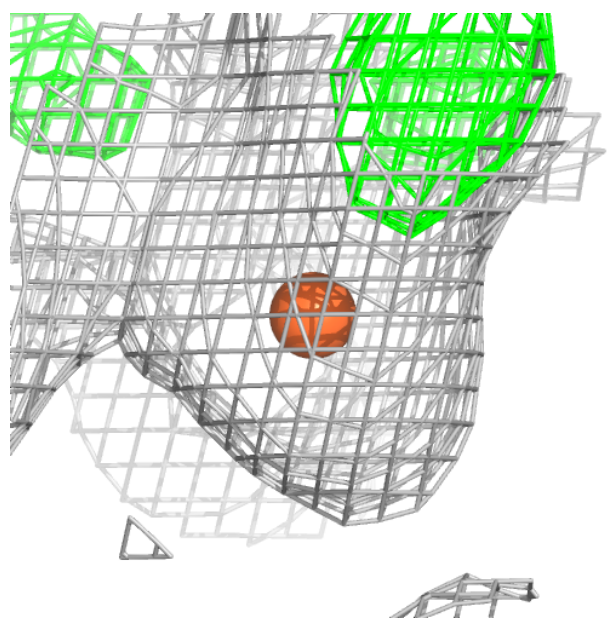
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





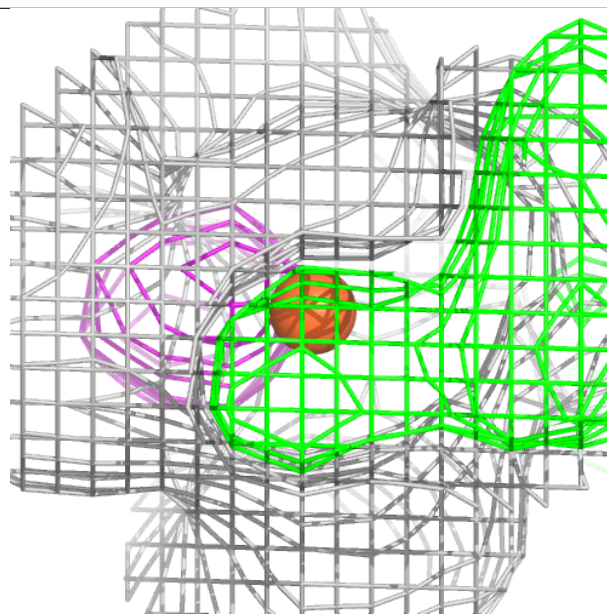
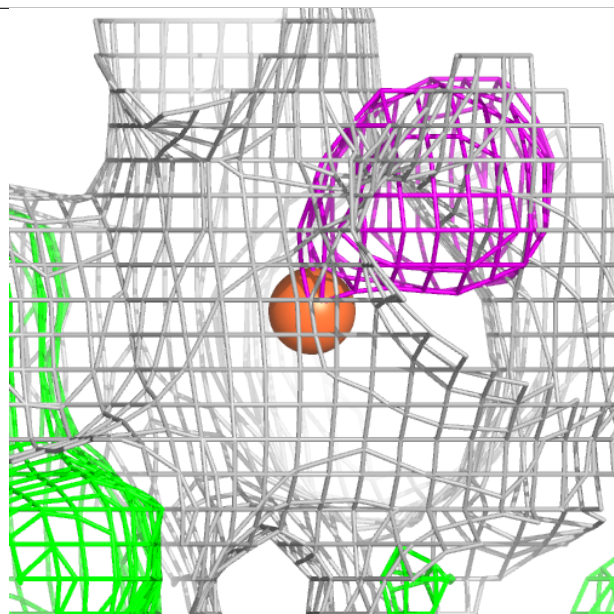
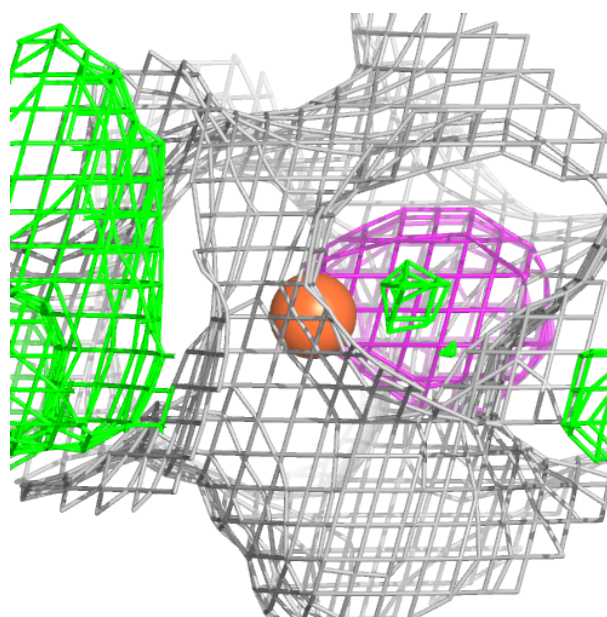
**Electron density around FE D 403:**

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



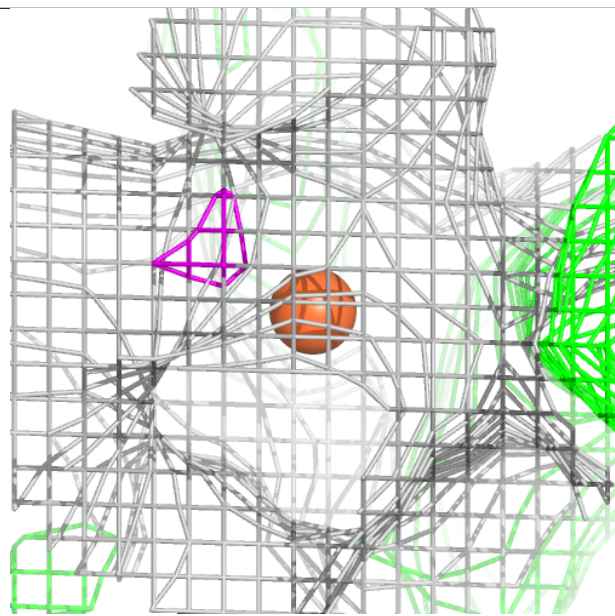
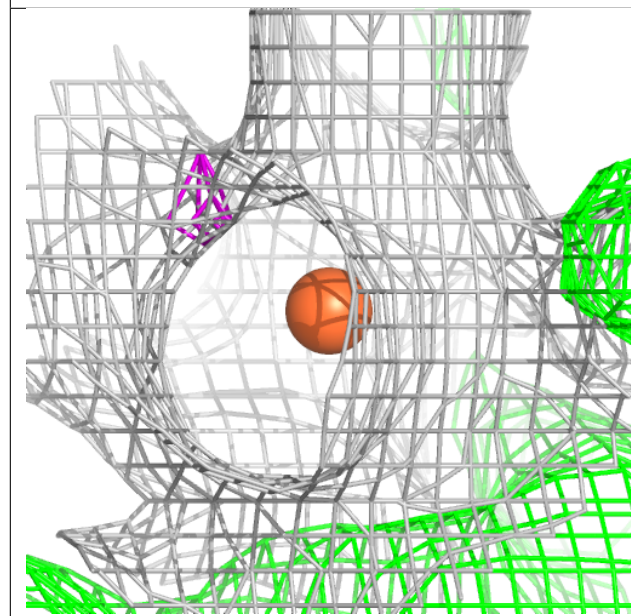
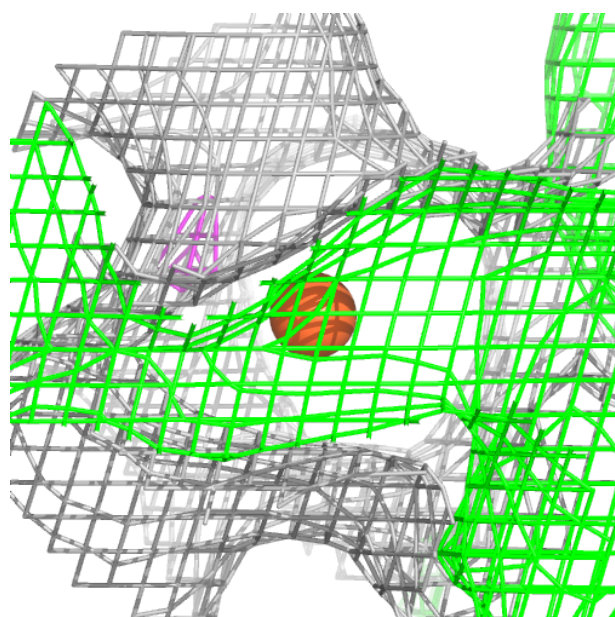
**Electron density around FE A 403:**

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

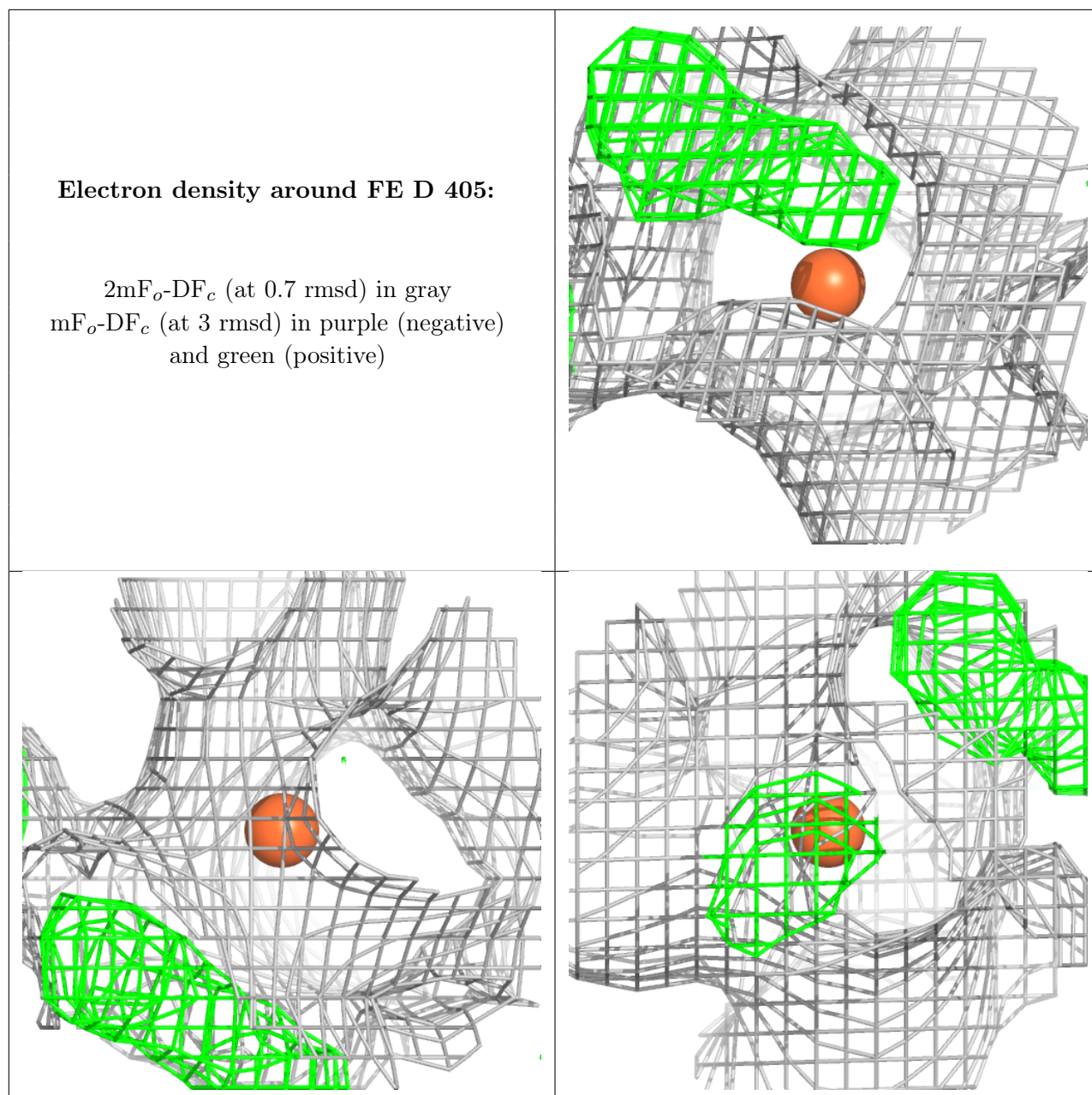


**Electron density around FE C 403:**

$2mF_o-DF_c$  (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.