Full wwPDB X-ray Structure Validation Report ⓘ

Nov 11, 2024 – 07:32 PM JST

PDB ID	:	9IXC
Title	:	Crystal structure of Manganese-rebound N(omega)-hydroxy-L-arginine hydrolase with oxidized Cys86
Authors	:	Oda, K.; Matoba, Y.
Deposited on	:	2024-07-27
Resolution	:	1.26 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

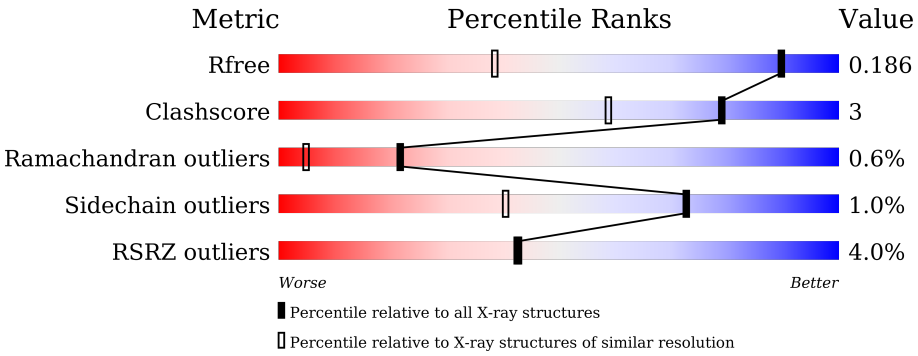
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.26 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}	164625	1447 (1.28-1.24)
Clashscore	180529	1571 (1.28-1.24)
Ramachandran outliers	177936	1538 (1.28-1.24)
Sidechain outliers	177891	1537 (1.28-1.24)
RSRZ outliers	164620	1447 (1.28-1.24)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	282	5% 90% 6%
1	B	282	2% 92% 5%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4683 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 N(omega)-hydroxy-L-arginine amidinohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	3	0
			2039	1278	358	396	7			
1	B	273	Total	C	N	O	S	0	3	0
			2057	1287	361	400	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	274	LEU	-	expression tag	UNP D2Z025
A	275	GLU	-	expression tag	UNP D2Z025
A	276	HIS	-	expression tag	UNP D2Z025
A	277	HIS	-	expression tag	UNP D2Z025
A	278	HIS	-	expression tag	UNP D2Z025
A	279	HIS	-	expression tag	UNP D2Z025
A	280	HIS	-	expression tag	UNP D2Z025
A	281	HIS	-	expression tag	UNP D2Z025
B	274	LEU	-	expression tag	UNP D2Z025
B	275	GLU	-	expression tag	UNP D2Z025
B	276	HIS	-	expression tag	UNP D2Z025
B	277	HIS	-	expression tag	UNP D2Z025
B	278	HIS	-	expression tag	UNP D2Z025
B	279	HIS	-	expression tag	UNP D2Z025
B	280	HIS	-	expression tag	UNP D2Z025
B	281	HIS	-	expression tag	UNP D2Z025

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mn 2 2	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0

- Molecule 4 is water.

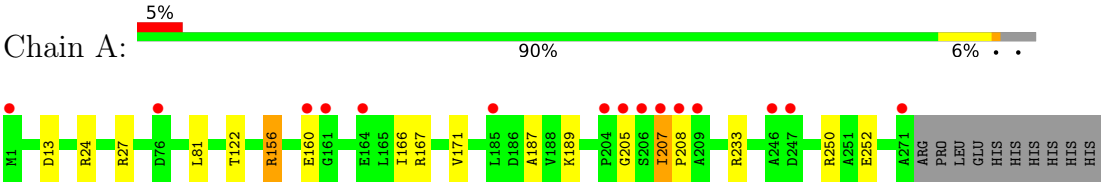
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	300	Total O 300 300	0	0
4	B	282	Total O 282 282	0	0

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.

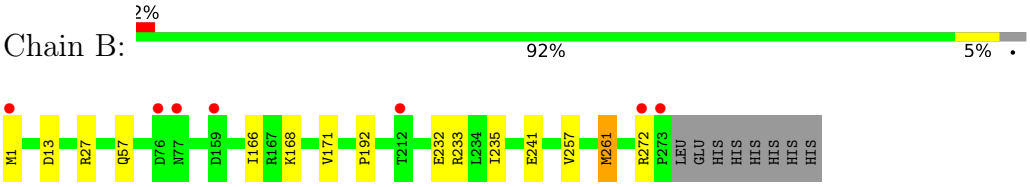
• Molecule 1: N(omega)-hydroxy-L-arginine amidinohydrolase

Chain A:



• Molecule 1: N(omega)-hydroxy-L-arginine amidinohydrolase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	45.94Å 46.74Å 58.34Å 85.33° 86.91° 70.59°	Depositor
Resolution (Å)	35.22 – 1.26 35.22 – 1.26	Depositor EDS
% Data completeness (in resolution range)	89.9 (35.22-1.26) 89.9 (35.22-1.26)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.86 (at 1.26Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.165 , 0.186 0.165 , 0.186	Depositor DCC
R_{free} test set	6094 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	11.5	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 37.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.015 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	4683	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, CSO, MN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.31	0/2085	0.57	0/2851
1	B	0.31	0/2093	0.61	1/2860 (0.0%)
All	All	0.31	0/4178	0.59	1/5711 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	261	MET	CG-SD-CE	-12.60	80.04	100.20

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	2039	0	2013	12	0
1	B	2057	0	2023	11	1
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
4	A	300	0	0	3	0
4	B	282	0	0	2	0
All	All	4683	0	4036	20	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 3.

All (20) 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:207:ILE:HB	1:A:208:PRO:HD2	1.67	0.77
1:B:1:MET:HE2	1:B:272:ARG:HH11	1.58	0.68
1:A:233:ARG:NH2	4:A:501:HOH:O	2.29	0.66
1:A:24:ARG:NE	1:A:252:GLU:OE1	2.34	0.58
1:B:257:VAL:O	1:B:261:MET:HG2	2.05	0.56
1:A:167:ARG:NH1	4:A:504:HOH:O	2.39	0.54
1:B:192:PRO:HB2	1:B:235:ILE:HD11	1.90	0.54
1:B:232:GLU:CD	1:B:232:GLU:H	2.12	0.53
1:A:24:ARG:NH1	1:A:27[B]:ARG:HG2	2.25	0.51
1:A:156[B]:ARG:NH2	4:A:510:HOH:O	2.45	0.50
1:A:187:ALA:O	1:A:189:LYS:HD3	2.13	0.48
1:A:160:GLU:H	1:A:160:GLU:CD	2.18	0.47
1:B:27[B]:ARG:NH2	4:B:504:HOH:O	2.39	0.47
1:A:250:ARG:HH12	1:B:1:MET:H1	1.62	0.47
1:A:250:ARG:HH12	1:B:1:MET:N	2.15	0.45
1:B:166:ILE:HG23	1:B:171:VAL:HB	2.00	0.44
1:B:233:ARG:HD2	4:B:564:HOH:O	2.17	0.44
1:A:166:ILE:HG23	1:A:171:VAL:HB	1.99	0.43
1:A:122:THR:HG21	1:B:27[B]:ARG:HG2	2.02	0.41
1:B:168:LYS:HE2	1:B:168:LYS:HB2	1.91	0.40

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)
1:B:57:GLN:NE2	1:B:232:GLU:OE2[1_655]	2.19	0.01

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	272/282 (96%)	262 (96%)	8 (3%)	2 (1%)	19 3
1	B	272/282 (96%)	266 (98%)	5 (2%)	1 (0%)	30 9
All	All	544/564 (96%)	528 (97%)	13 (2%)	3 (1%)	22 5

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	GLY
1	A	207	ILE
1	B	241	GLU

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	208/215 (97%)	204 (98%)	4 (2%)	52 17
1	B	209/215 (97%)	208 (100%)	1 (0%)	86 66
All	All	417/430 (97%)	412 (99%)	5 (1%)	73 33

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASP
1	A	81	LEU
1	A	156[A]	ARG
1	A	156[B]	ARG
1	B	13	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	253	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	CSO	B	86[B]	1,2	3,6,7	0.82	0	0,6,8	-	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSO	B	86[B]	1,2	-	0/1/5/7	-

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.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 5 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

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^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	272/282 (96%)	0.42	15 (5%)	32	31	6, 14, 29, 67	3 (1%)
1	B	272/282 (96%)	0.27	7 (2%)	57	57	6, 14, 26, 37	2 (0%)
All	All	544/564 (96%)	0.35	22 (4%)	43	42	6, 14, 28, 67	5 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	207	ILE	8.4
1	A	208	PRO	5.7
1	A	206	SER	4.7
1	A	209	ALA	4.5
1	A	205	GLY	4.3
1	A	246	ALA	4.3
1	A	204	PRO	3.3
1	A	161	GLY	3.1
1	B	273	PRO	3.0
1	A	1	MET	3.0
1	A	76	ASP	2.9
1	B	77	ASN	2.9
1	A	160	GLU	2.9
1	B	76	ASP	2.9
1	A	271	ALA	2.8
1	B	1	MET	2.8
1	B	272	ARG	2.6
1	A	247	ASP	2.6
1	B	159	ASP	2.5
1	A	164	GLU	2.4
1	A	185	LEU	2.3
1	B	212	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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^{th} 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^2)	Q<0.9
1	CSO	B	86[B]	7/8	-	-	8,8,9,12	7

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

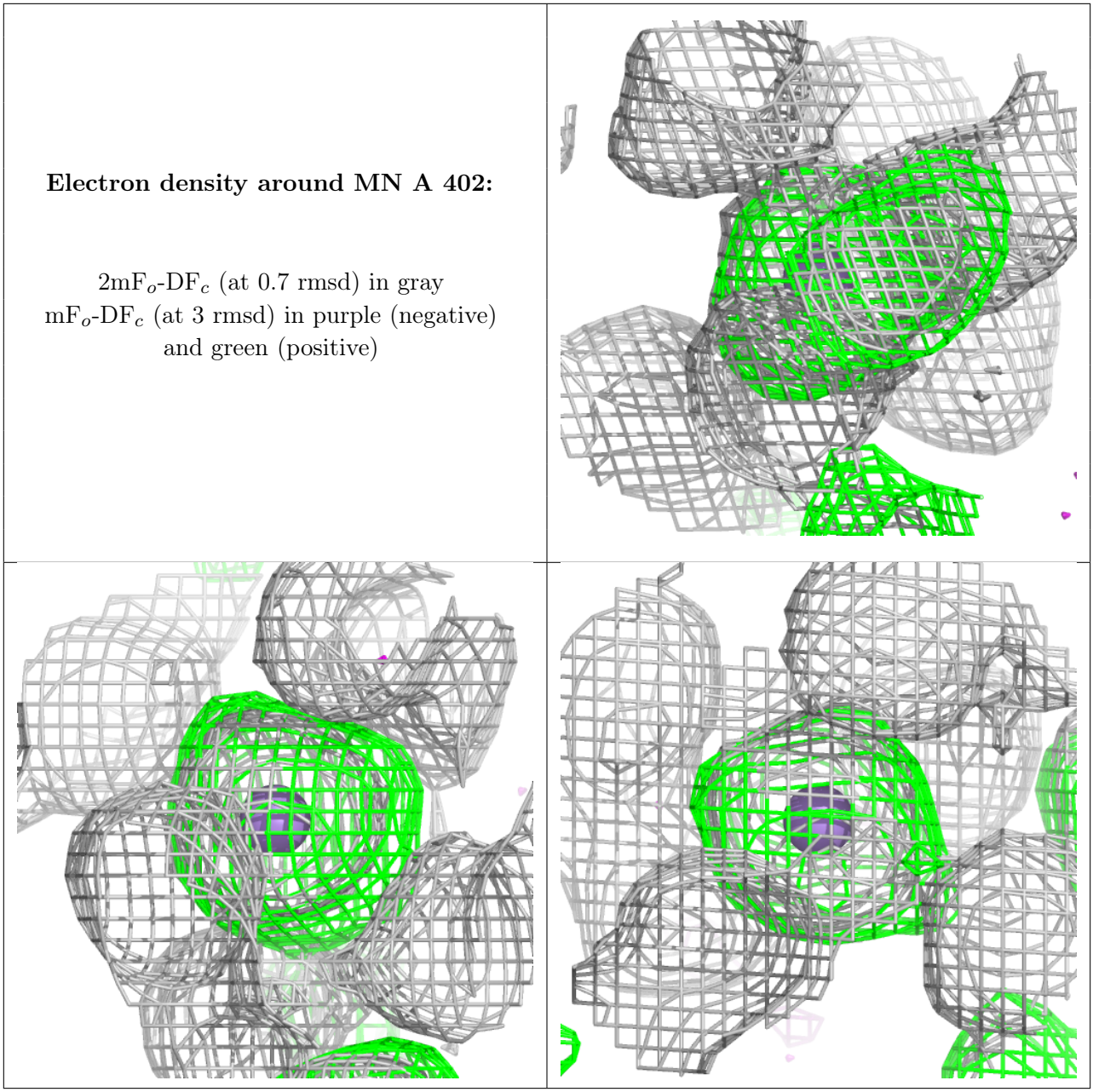
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	A	403	1/1	0.96	0.07	20,20,20,20	1
2	MN	A	402	1/1	1.00	0.07	2,2,2,2	1
2	MN	B	401	1/1	1.00	0.06	6,6,6,6	1
2	MN	B	402	1/1	1.00	0.06	6,6,6,6	1
2	MN	A	401	1/1	1.00	0.06	3,3,3,3	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

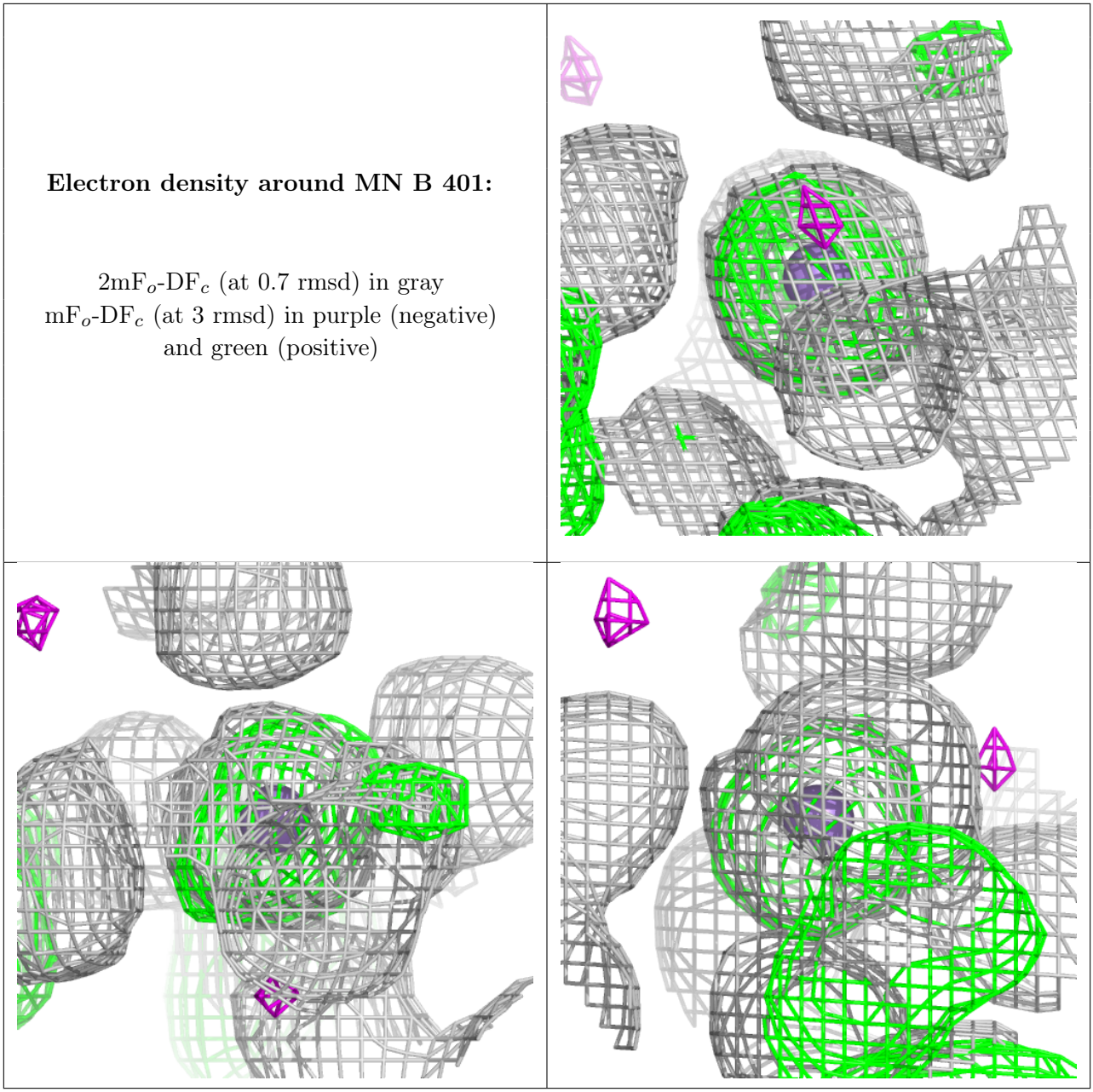
Electron density around MN A 402:

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



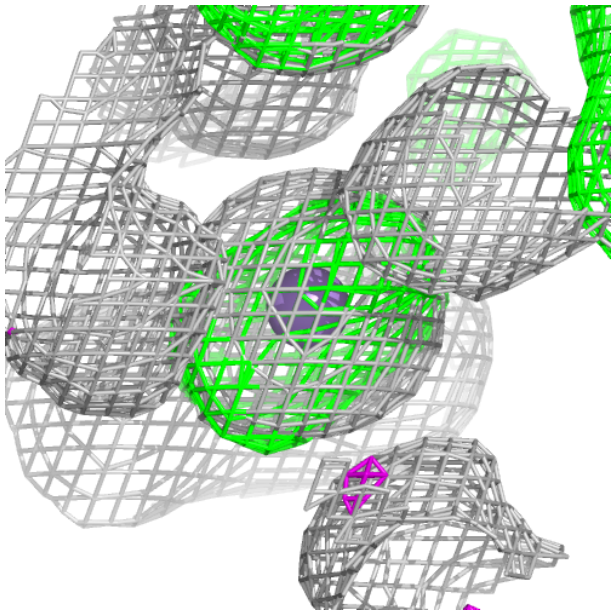
Electron density around MN B 401:

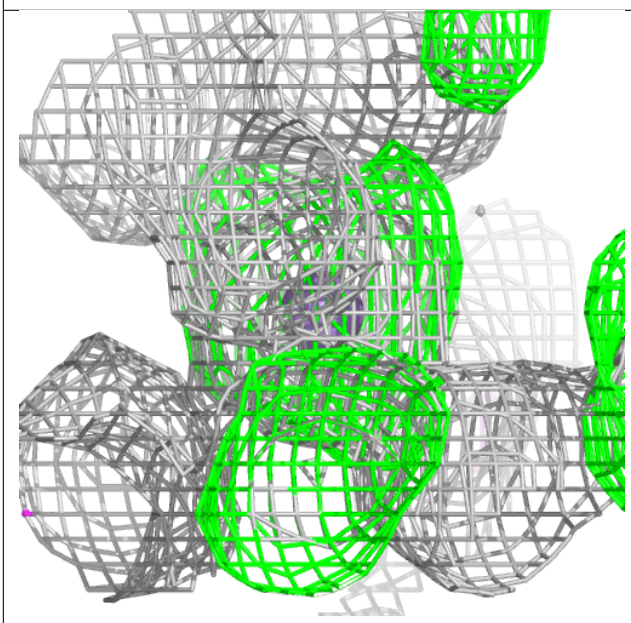
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

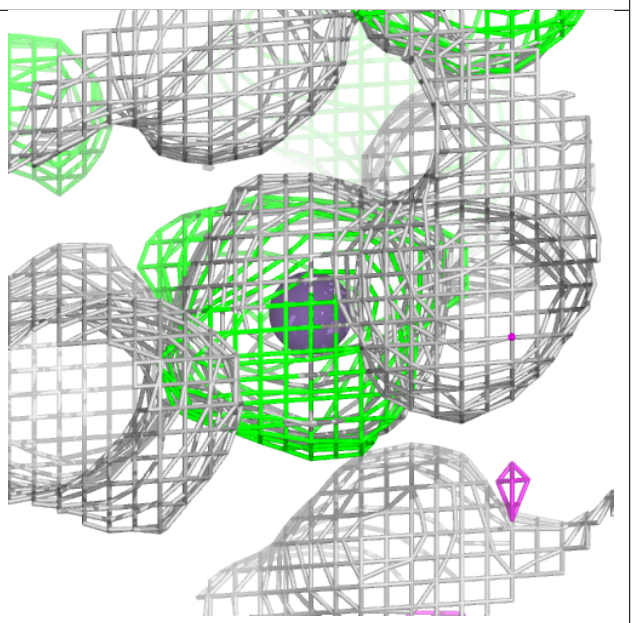


Electron density around MN B 402:

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

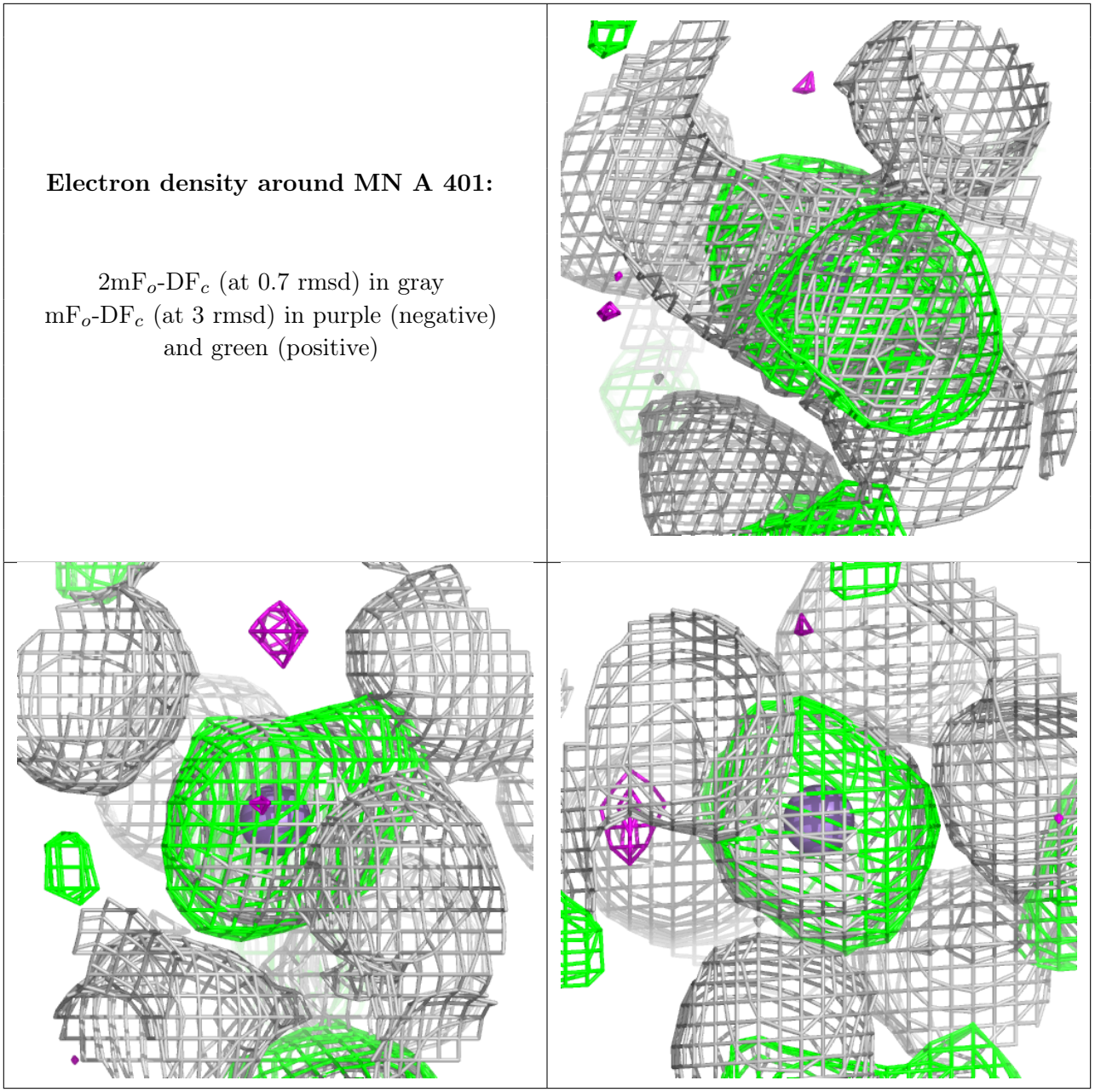






Electron density around MN A 401:

$2mF_o$-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.