



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 29, 2026 – 08:10 AM JST

PDB ID : 9X2G / pdb_00009x2g
Title : Crystal Structure of Extradiol Dioxygenase (Edo4) from Rhizorhabdus wittichii RW1
Authors : Kayastha, A.; Kumar, P.
Deposited on : 2025-10-05
Resolution : 2.05 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

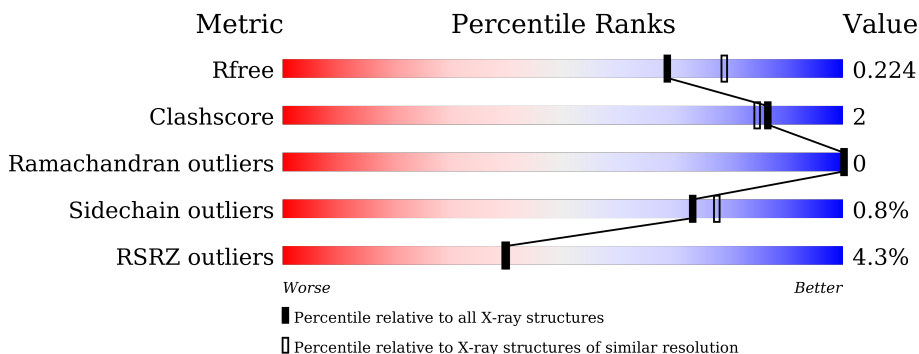
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	298	
1	B	298	
1	C	298	
1	D	298	

2 Entry composition [i](#)

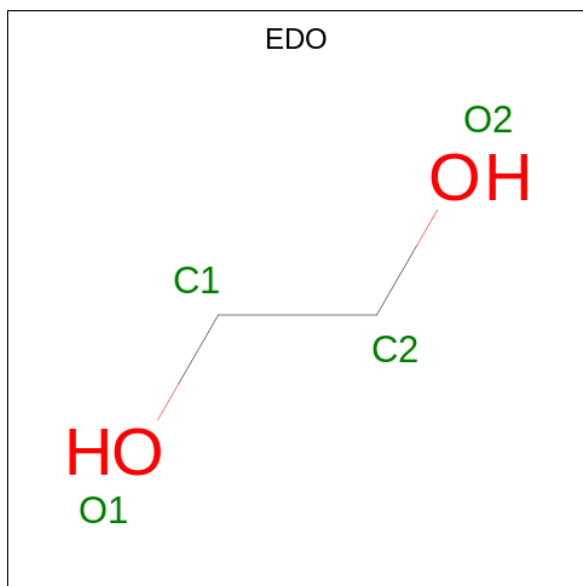
There are 5 unique types of molecules in this entry. The entry contains 10260 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glyoxalase/bleomycin resistance protein/dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	297	Total 2330	C 1477	N 417	O 428	S 8	0	0	0
1	C	297	Total 2330	C 1478	N 416	O 427	S 9	0	0	0
1	A	298	Total 2338	C 1482	N 418	O 429	S 9	0	0	0
1	D	296	Total 2310	C 1465	N 410	O 427	S 8	0	0	0

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 3 is FLUORIDE ION (CCD ID: F) (formula: F).

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

- Molecule 4 is FE (II) ION (CCD ID: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	279	Total	O	0	0
			279	279		
5	C	234	Total	O	0	0
			234	234		
5	A	308	Total	O	0	0
			308	308		
5	D	107	Total	O	0	0
			107	107		

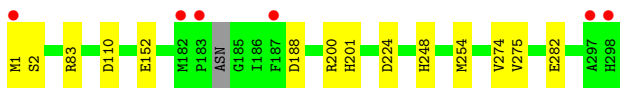
3 Residue-property plots [i](#)

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: Glyoxalase/bleomycin resistance protein/dioxygenase



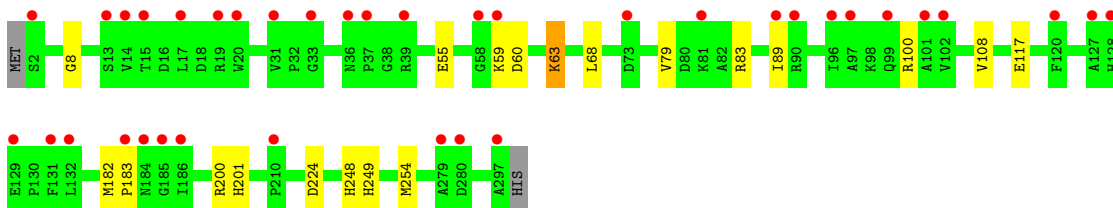
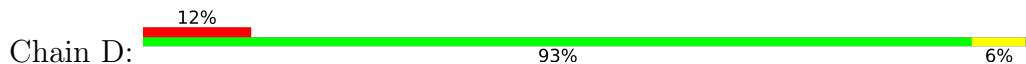
- Molecule 1: Glyoxalase/bleomycin resistance protein/dioxygenase



- Molecule 1: Glyoxalase/bleomycin resistance protein/dioxygenase



- Molecule 1: Glyoxalase/bleomycin resistance protein/dioxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	133.00Å 133.00Å 181.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.47 – 2.05 25.47 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (25.47-2.05) 99.8 (25.47-2.05)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.04Å)	Xtrriage
Refinement program	REFMAC 5.8.0403	Depositor
R, R_{free}	0.193 , 0.224 0.193 , 0.224	Depositor DCC
R_{free} test set	5014 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	12.8	Xtrriage
Anisotropy	0.074	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10260	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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 30.41 % 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 1.3136e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, FE2, F

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	0.73	0/2400	1.02	3/3251 (0.1%)
1	B	0.68	0/2392	1.03	2/3241 (0.1%)
1	C	0.64	0/2391	0.98	1/3237 (0.0%)
1	D	0.56	0/2371	0.99	2/3215 (0.1%)
All	All	0.66	0/9554	1.01	8/12944 (0.1%)

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	2
1	B	0	2
1	C	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	56	ARG	CB-CG-CD	8.28	130.35	111.30
1	B	260	ARG	CG-CD-NE	-8.02	94.35	112.00
1	B	155	ARG	CG-CD-NE	-6.71	97.25	112.00
1	D	63	LYS	CB-CG-CD	6.36	125.92	111.30
1	A	36	ASN	CB-CA-C	5.46	115.90	110.33

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	260	ARG	Sidechain
1	A	83	ARG	Sidechain
1	B	137	ARG	Sidechain
1	B	83	ARG	Sidechain
1	C	83	ARG	Sidechain

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	2338	0	2252	13	0
1	B	2330	0	2240	10	0
1	C	2330	0	2245	5	0
1	D	2310	0	2211	14	0
2	A	4	0	6	0	0
2	B	4	0	5	0	0
2	C	4	0	6	0	0
3	A	4	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
3	D	1	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
5	A	308	0	0	1	2
5	B	279	0	0	0	0
5	C	234	0	0	0	1
5	D	107	0	0	1	1
All	All	10260	0	8965	39	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 39 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:8:GLY:HA3	1:D:68:LEU:HD13	1.78	0.66
1:D:59:LYS:HG3	1:D:60:ASP:H	1.64	0.63
1:D:100:ARG:NH1	1:D:117:GLU:OE2	2.33	0.61
1:A:112:ASN:ND2	1:A:155:ARG:H	1.99	0.59
1:A:188:ASP:HB3	5:A:642:HOH:O	2.04	0.57

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:569:HOH:O	5:A:569:HOH:O[8_555]	1.01	1.19
5:A:674:HOH:O	5:A:674:HOH:O[8_555]	1.62	0.58
5:C:908:HOH:O	5:D:466:HOH:O[8_554]	1.86	0.34

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	296/298 (99%)	288 (97%)	8 (3%)	0	100	100
1	B	295/298 (99%)	288 (98%)	7 (2%)	0	100	100
1	C	293/298 (98%)	286 (98%)	7 (2%)	0	100	100
1	D	294/298 (99%)	288 (98%)	6 (2%)	0	100	100
All	All	1178/1192 (99%)	1150 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	242/242 (100%)	239 (99%)	3 (1%)	63	65
1	B	241/242 (100%)	238 (99%)	3 (1%)	63	65
1	C	241/242 (100%)	239 (99%)	2 (1%)	73	77
1	D	238/242 (98%)	238 (100%)	0	100	100
All	All	962/968 (99%)	954 (99%)	8 (1%)	73	77

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	284	LYS
1	A	274	VAL
1	C	282	GLU
1	C	188	ASP
1	A	81	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	ASN
1	D	92	GLN
1	C	288	GLN
1	C	296	HIS
1	C	298	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 12 are monoatomic - leaving 3 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	EDO	A	301	-	3,3,3	0.06	0	2,2,2	0.44	0
2	EDO	B	301	-	3,3,3	0.84	0	2,2,2	1.68	1 (50%)
2	EDO	C	301	-	3,3,3	0.21	0	2,2,2	0.38	0

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
2	EDO	A	301	-	-	0/1/1/1	-
2	EDO	B	301	-	-	0/1/1/1	-
2	EDO	C	301	-	-	0/1/1/1	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	EDO	O2-C2-C1	-2.36	94.96	111.91

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

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	298/298 (100%)	-0.52	2 (0%) 84 85	3, 8, 23, 74	0
1	B	297/298 (99%)	-0.48	6 (2%) 65 67	4, 10, 29, 87	0
1	C	297/298 (99%)	-0.36	6 (2%) 65 67	7, 14, 31, 89	0
1	D	296/298 (99%)	0.79	37 (12%) 8 7	13, 33, 53, 75	0
All	All	1188/1192 (99%)	-0.14	51 (4%) 40 40	3, 13, 44, 89	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	298	HIS	6.7
1	B	298	HIS	6.4
1	C	1	MET	6.2
1	D	17	LEU	4.2
1	D	37	PRO	4.1

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 [i](#)

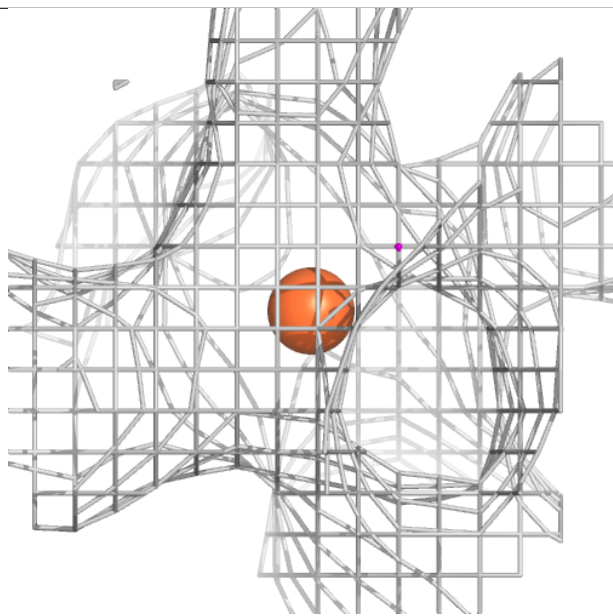
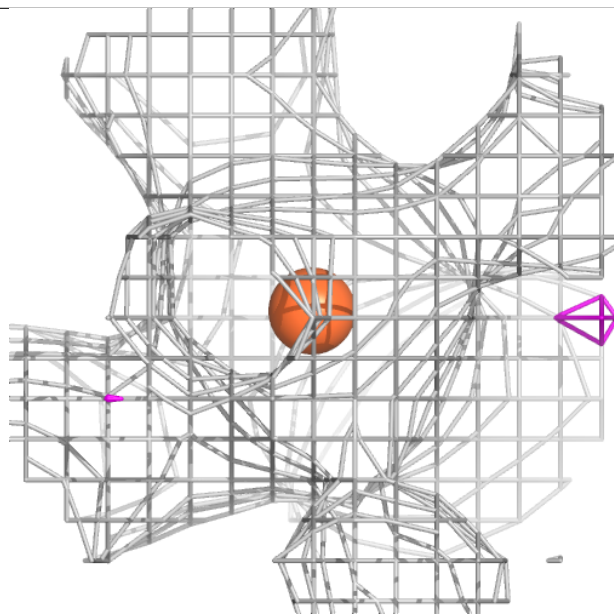
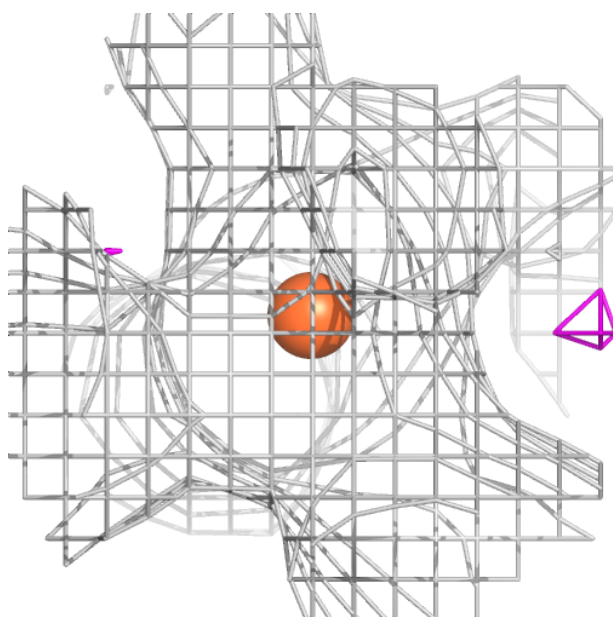
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	EDO	B	301	4/4	0.95	0.07	16,16,17,17	0
3	F	A	302	1/1	0.95	0.12	25,25,25,25	0
4	FE2	D	302	1/1	0.96	0.09	47,47,47,47	0
3	F	D	301	1/1	0.97	0.06	17,17,17,17	0
4	FE2	C	304	1/1	0.97	0.09	37,37,37,37	0
2	EDO	A	301	4/4	0.97	0.06	16,16,16,17	0
3	F	A	305	1/1	0.98	0.09	15,15,15,15	0
3	F	C	303	1/1	0.98	0.04	15,15,15,15	0
4	FE2	B	303	1/1	0.98	0.08	31,31,31,31	0
2	EDO	C	301	4/4	0.98	0.04	16,16,17,17	0
4	FE2	A	306	1/1	0.98	0.09	27,27,27,27	0
3	F	A	304	1/1	0.98	0.03	15,15,15,15	0
3	F	C	302	1/1	0.99	0.05	14,14,14,14	0
3	F	A	303	1/1	0.99	0.03	9,9,9,9	0
3	F	B	302	1/1	0.99	0.05	10,10,10,10	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.

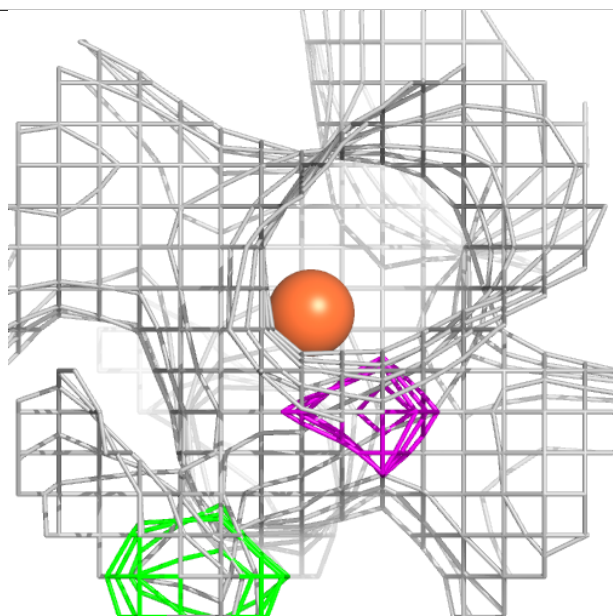
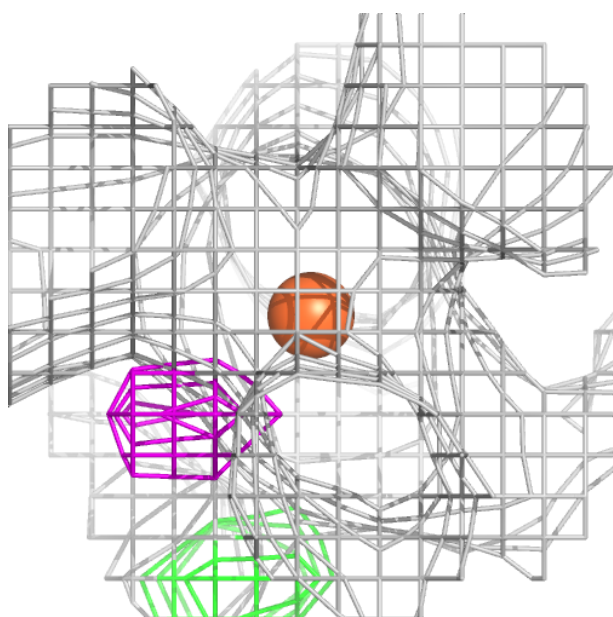
Electron density around FE2 D 302:

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



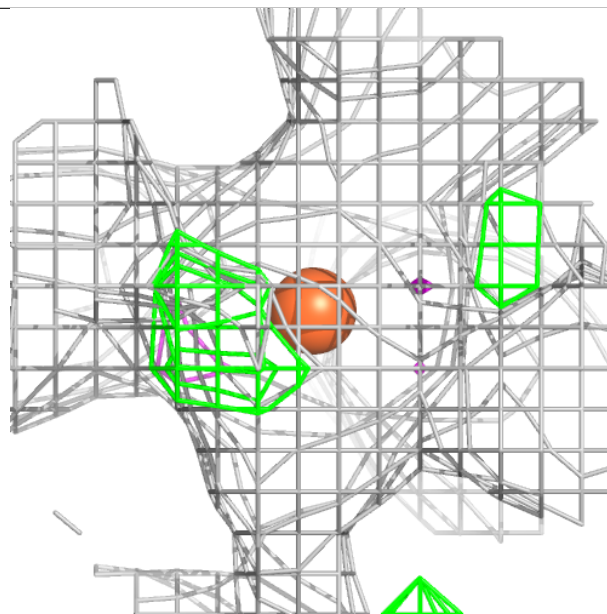
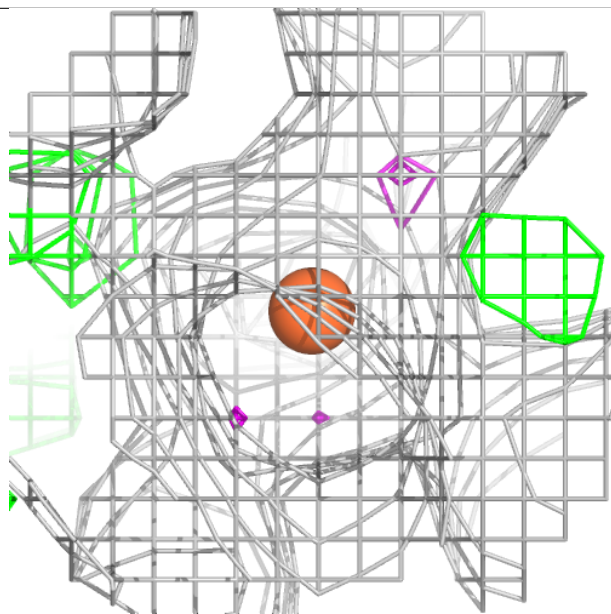
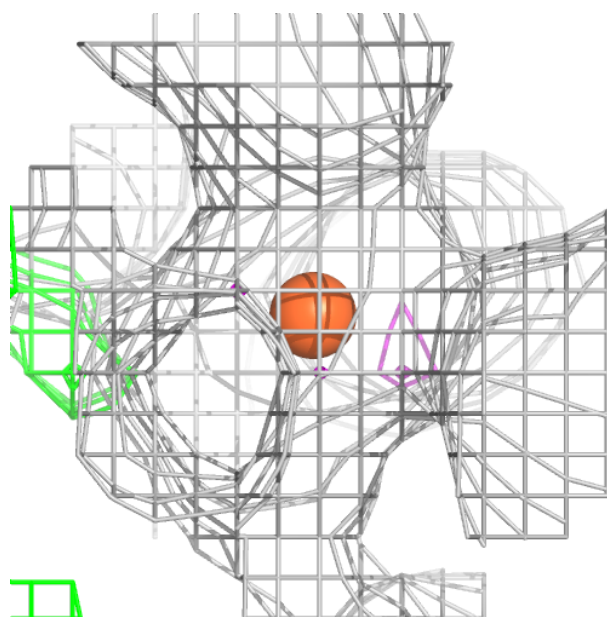
Electron density around FE2 C 304:

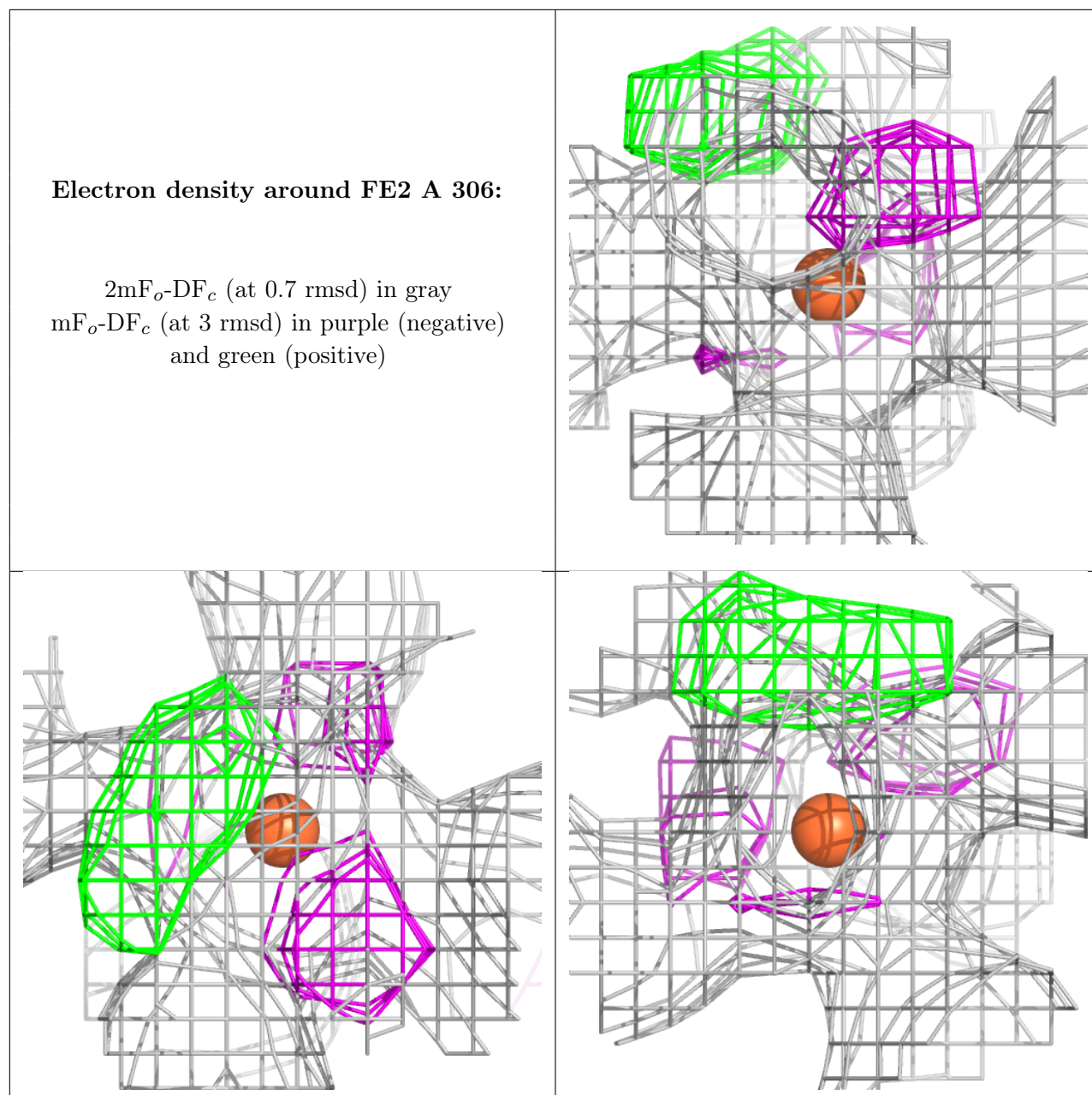
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FE2 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)





6.5 Other polymers ⓘ

There are no such residues in this entry.