



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 9, 2026 – 04:14 pm BST

PDB ID : 7R1H / pdb_00007r1h
Title : Crystal structure of a flavodiiron protein D52K mutant in the reduced state from Escherichia coli
Authors : Borges, P.T.; Teixeira, M.; Romao, C.V.; Frazao, C.
Deposited on : 2022-02-03
Resolution : 1.95 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	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
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

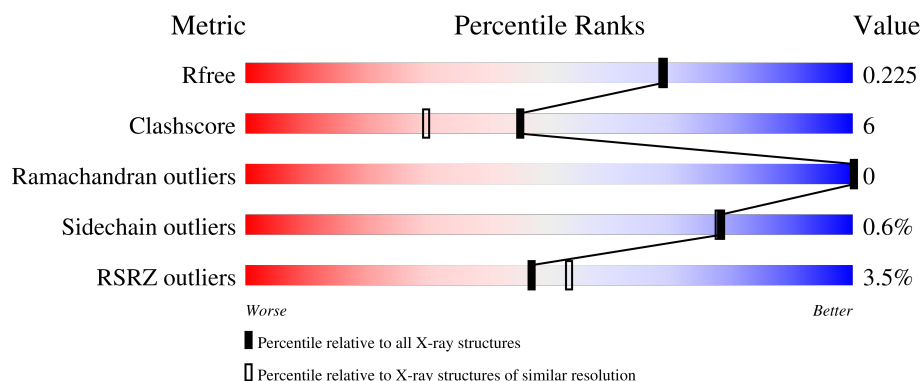
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

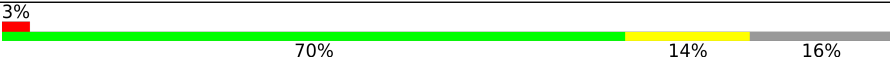
The reported resolution of this entry is 1.95 Å.

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 ≥ 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	479	
1	B	479	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7251 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.

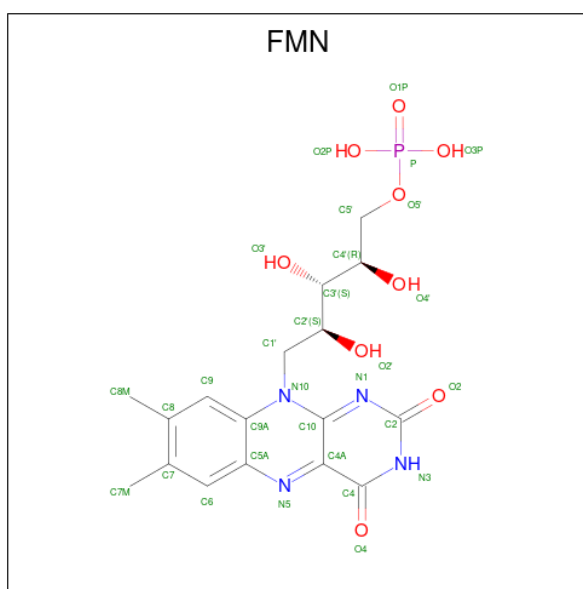
- Molecule 1 is a protein called Anaerobic nitric oxide reductase flavorubredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	0	1	0
			3226	2035	568	606	17			
1	B	400	Total	C	N	O	S	0	2	0
			3229	2037	568	607	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	52	LYS	ASP	engineered mutation	UNP Q46877
B	52	LYS	ASP	engineered mutation	UNP Q46877

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

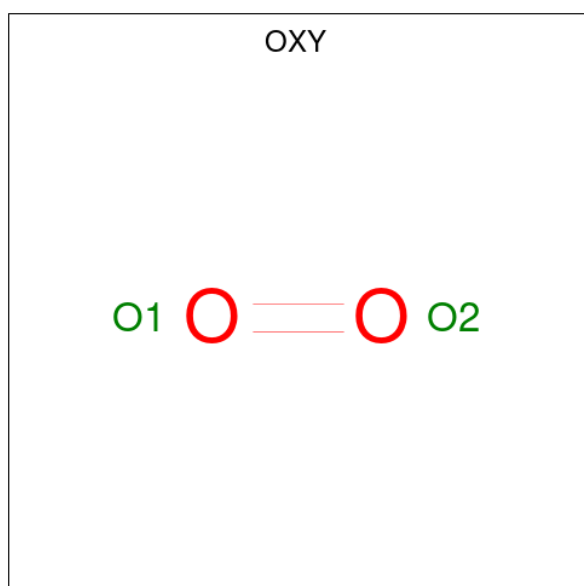
- Molecule 3 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Fe	0	0
			2	2		
3	B	2	Total	Fe	0	0
			2	2		

- Molecule 4 is OXYGEN ATOM (CCD ID: O) (formula: O) (labeled as "Ligand of Interest" by depositor).

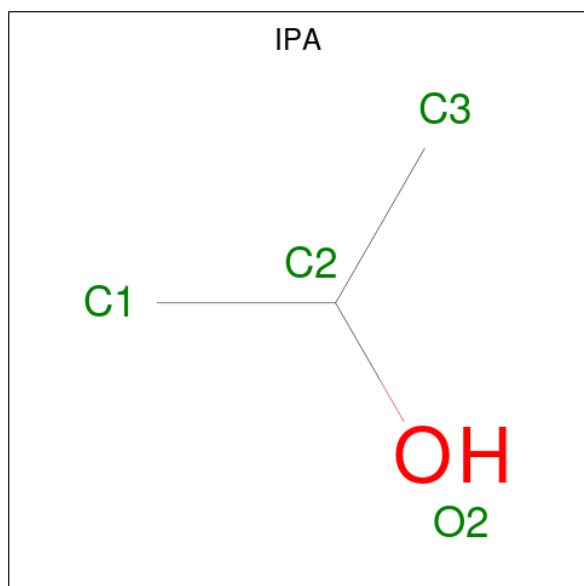
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O	0	0
			1	1		
4	B	1	Total	O	0	0
			1	1		

- Molecule 5 is OXYGEN MOLECULE (CCD ID: OXY) (formula: O₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 6 is ISOPROPYL ALCOHOL (CCD ID: IPA) (formula: C_3H_8O) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	370	Total	O	0	0
			370	370		
7	B	352	Total	O	0	0
			352	352		

4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	88.95Å 64.86Å 146.75Å 90.00° 91.53° 90.00°	Depositor
Resolution (Å)	75.16 – 1.95 75.16 – 1.96	Depositor EDS
% Data completeness (in resolution range)	98.2 (75.16-1.95) 85.0 (75.16-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.38 (at 1.95Å)	Xtriage
Refinement program	PHENIX dev_1436	Depositor
R, R_{free}	0.187 , 0.187 0.211 , 0.225	Depositor DCC
R_{free} test set	881 reflections (1.48%)	wwPDB-VP
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.243	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.004 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7251	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.43% of the height of the origin peak. No significant pseudotranslation is detected.*

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: FE, O, OXY, FMN, IPA

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	0.29	0/3300	0.69	1/4478 (0.0%)
1	B	0.28	0/3307	0.69	0/4488
All	All	0.28	0/6607	0.69	1/8966 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	165	ASN	CB-CA-C	-5.11	110.67	116.54

There are no chirality outliers.

There are no planarity outliers.

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	3226	0	3132	36	0
1	B	3229	0	3135	41	0
2	A	31	0	19	1	0
2	B	31	0	19	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	2	0	0	0	0
6	B	4	0	8	2	0
7	A	370	0	0	3	0
7	B	352	0	0	4	0
All	All	7251	0	6313	76	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 6.

All (76) 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:185:THR:HG21	1:B:185[A]:THR:HG21	1.46	0.97
1:A:207:THR:HB	1:A:208:PRO:HD3	1.72	0.72
1:B:207:THR:HB	1:B:208:PRO:HD3	1.72	0.72
1:A:60:VAL:HG21	1:A:90:GLU:HG3	1.77	0.65
1:B:60:VAL:HG21	1:B:90:GLU:HG3	1.77	0.65
1:B:3:ILE:HD11	1:B:15:ARG:HH22	1.66	0.60
1:A:3:ILE:HD11	1:A:15:ARG:HH22	1.68	0.59
1:B:394:ARG:NH1	7:B:609:HOH:O	2.38	0.56
1:B:311:GLY:HA2	1:B:343:PHE:O	2.06	0.55
1:A:311:GLY:HA2	1:A:343:PHE:O	2.06	0.55
1:A:9:ILE:HD11	1:A:156:LEU:HD23	1.88	0.54
1:B:9:ILE:HD11	1:B:156:LEU:HD23	1.89	0.54
1:A:60:VAL:HG21	1:A:90:GLU:CG	2.38	0.52
1:A:257:PHE:CE2	1:A:326:LEU:HD23	2.44	0.52
1:B:60:VAL:HG21	1:B:90:GLU:CG	2.38	0.52
1:A:200:THR:N	1:A:201:PRO:HD2	2.24	0.52
1:B:22:PHE:HZ	1:B:35:TYR:HE1	1.58	0.52
1:B:193:ARG:NH2	1:B:296:ASN:HB2	2.26	0.51
1:A:22:PHE:HZ	1:A:35:TYR:HE1	1.59	0.50
1:B:348:TRP:CD1	1:B:349:SER:H	2.30	0.49
1:A:312:THR:O	1:A:344:GLY:HA3	2.11	0.49
1:B:200:THR:N	1:B:201:PRO:HD2	2.27	0.49
1:B:295:LYS:HD2	7:B:603:HOH:O	2.14	0.48
1:B:23:HIS:CE1	6:B:505:IPA:H33	2.49	0.47
1:B:298:ILE:O	1:B:302:VAL:HG23	2.14	0.47
1:A:347:GLY:HA3	2:A:501:FMN:H1'1	1.95	0.47
1:A:348:TRP:CD1	1:A:349:SER:H	2.32	0.47
1:B:3:ILE:HD11	1:B:15:ARG:NH2	2.29	0.46
1:A:38:TYR:CZ	1:A:224:ALA:HB1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:PHE:CE2	1:B:326:LEU:HD23	2.51	0.46
1:A:336:ARG:NH1	7:A:622:HOH:O	2.48	0.46
1:A:298:ILE:O	1:A:302:VAL:HG23	2.15	0.46
1:B:347:GLY:HA3	2:B:501:FMN:H1'1	1.98	0.46
1:B:262:SER:O	1:B:263:ASN:HB2	2.16	0.46
1:A:388:HIS:O	1:A:392:ILE:HG12	2.16	0.45
1:B:400:PRO:O	1:B:401:LEU:HB3	2.16	0.45
1:B:401:LEU:N	7:B:611:HOH:O	2.40	0.45
1:B:88:LEU:O	1:B:92:MET:HG2	2.16	0.44
1:B:308:VAL:O	1:B:340:ALA:HA	2.18	0.44
1:B:312:THR:O	1:B:344:GLY:HA3	2.17	0.44
1:A:193:ARG:NH2	1:A:296:ASN:HB2	2.31	0.44
1:A:262:SER:O	1:A:263:ASN:HB2	2.17	0.44
1:B:388:HIS:O	1:B:392:ILE:HG12	2.17	0.44
1:B:146:LEU:HA	1:B:147:HIS:HA	1.81	0.44
1:A:376[B]:ARG:HA	1:A:377:PRO:HD3	1.91	0.44
1:A:60:VAL:O	1:A:64:ARG:HG3	2.18	0.43
1:A:400:PRO:O	1:A:401:LEU:HB3	2.17	0.43
1:A:308:VAL:O	1:A:340:ALA:HA	2.19	0.43
1:A:386:ARG:O	1:A:390:ARG:HG3	2.18	0.43
1:A:43:GLU:HB2	1:A:133:GLY:HA3	2.01	0.43
1:B:21:ASP:OD1	1:B:28:LYS:HD3	2.19	0.43
1:B:178:PHE:CD1	1:B:232:ARG:HD3	2.54	0.42
1:A:268:MET:O	1:A:272:ILE:HG13	2.19	0.42
1:B:153:MET:HE2	1:B:167:ALA:HB3	2.02	0.42
1:B:218:LEU:HA	1:B:219:PRO:HD3	1.93	0.42
1:B:98:THR:HA	1:B:99:PRO:HD3	1.82	0.42
1:A:21:ASP:HB3	1:A:24:GLY:O	2.19	0.42
1:A:36:ASN:HB2	1:A:226:SER:HA	2.01	0.42
1:A:88:LEU:O	1:A:92:MET:HG2	2.19	0.42
1:A:253:ARG:NH2	7:A:633:HOH:O	2.51	0.41
1:A:335:PHE:HB3	1:A:338:LYS:HD2	2.01	0.41
1:B:20:ARG:HD3	1:B:29:THR:O	2.20	0.41
1:A:257:PHE:HA	1:A:288:PHE:O	2.21	0.41
1:B:268:MET:O	1:B:272:ILE:HG13	2.21	0.41
1:B:23:HIS:NE2	1:B:81:GLU:OE2	2.53	0.41
1:B:272:ILE:HG21	1:B:309:LEU:HD22	2.03	0.41
1:B:319:MET:HE1	1:B:356:LEU:HA	2.02	0.41
1:B:336:ARG:NH1	7:B:619:HOH:O	2.44	0.41
1:A:98:THR:HA	1:A:99:PRO:HD3	1.87	0.40
1:B:38:TYR:CZ	1:B:224:ALA:HB1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:PHE:HB2	7:A:873:HOH:O	2.20	0.40
1:A:5:VAL:HG22	1:A:177:LEU:HD21	2.03	0.40
1:A:178:PHE:CD1	1:A:232:ARG:HD3	2.57	0.40
1:B:23:HIS:HE1	6:B:505:IPA:H33	1.86	0.40
1:B:60:VAL:O	1:B:64:ARG:HG3	2.21	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	399/479 (83%)	387 (97%)	12 (3%)	0	100	100
1	B	400/479 (84%)	389 (97%)	11 (3%)	0	100	100
All	All	799/958 (83%)	776 (97%)	23 (3%)	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	349/417 (84%)	347 (99%)	2 (1%)	78	78
1	B	350/417 (84%)	348 (99%)	2 (1%)	78	78
All	All	699/834 (84%)	695 (99%)	4 (1%)	78	78

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	GLU
1	A	170	GLN
1	B	82	GLU
1	B	170	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	137	GLN
1	A	176	HIS
1	A	250	GLN
1	A	263	ASN
1	B	79	HIS
1	B	361	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 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	FMN	A	501	-	33,33,33	1.05	2 (6%)	48,50,50	1.21	8 (16%)
5	OXY	A	505	3	1,1,1	0.13	0	-		
2	FMN	B	501	-	33,33,33	1.07	2 (6%)	48,50,50	1.19	6 (12%)
6	IPA	B	505	3	3,3,3	0.55	0	3,3,3	0.23	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	FMN	A	501	-	-	0/18/18/18	0/3/3/3
2	FMN	B	501	-	-	0/18/18/18	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	FMN	C4A-N5	4.14	1.38	1.30
2	A	501	FMN	C4A-N5	4.00	1.38	1.30
2	B	501	FMN	C10-N1	2.41	1.38	1.33
2	A	501	FMN	C10-N1	2.37	1.38	1.33

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	FMN	C4-N3-C2	-3.00	120.11	125.64
2	A	501	FMN	C4-N3-C2	-2.92	120.24	125.64
2	B	501	FMN	C4A-C10-N10	2.70	120.42	116.48
2	A	501	FMN	C4A-C10-N10	2.63	120.32	116.48
2	B	501	FMN	C4A-C4-N3	2.61	119.81	113.19
2	A	501	FMN	C4A-C4-N3	2.60	119.80	113.19
2	B	501	FMN	C10-C4A-N5	-2.53	119.50	124.86
2	A	501	FMN	O4-C4-C4A	-2.36	120.34	126.60
2	A	501	FMN	C10-C4A-N5	-2.33	119.91	124.86
2	A	501	FMN	C9A-C5A-N5	-2.23	120.00	122.43
2	B	501	FMN	O4-C4-C4A	-2.16	120.88	126.60
2	A	501	FMN	C5A-C9A-N10	2.07	120.09	117.95
2	B	501	FMN	C9A-C5A-N5	-2.05	120.21	122.43
2	A	501	FMN	C4A-C10-N1	-2.01	120.06	124.73

There are no chirality outliers.

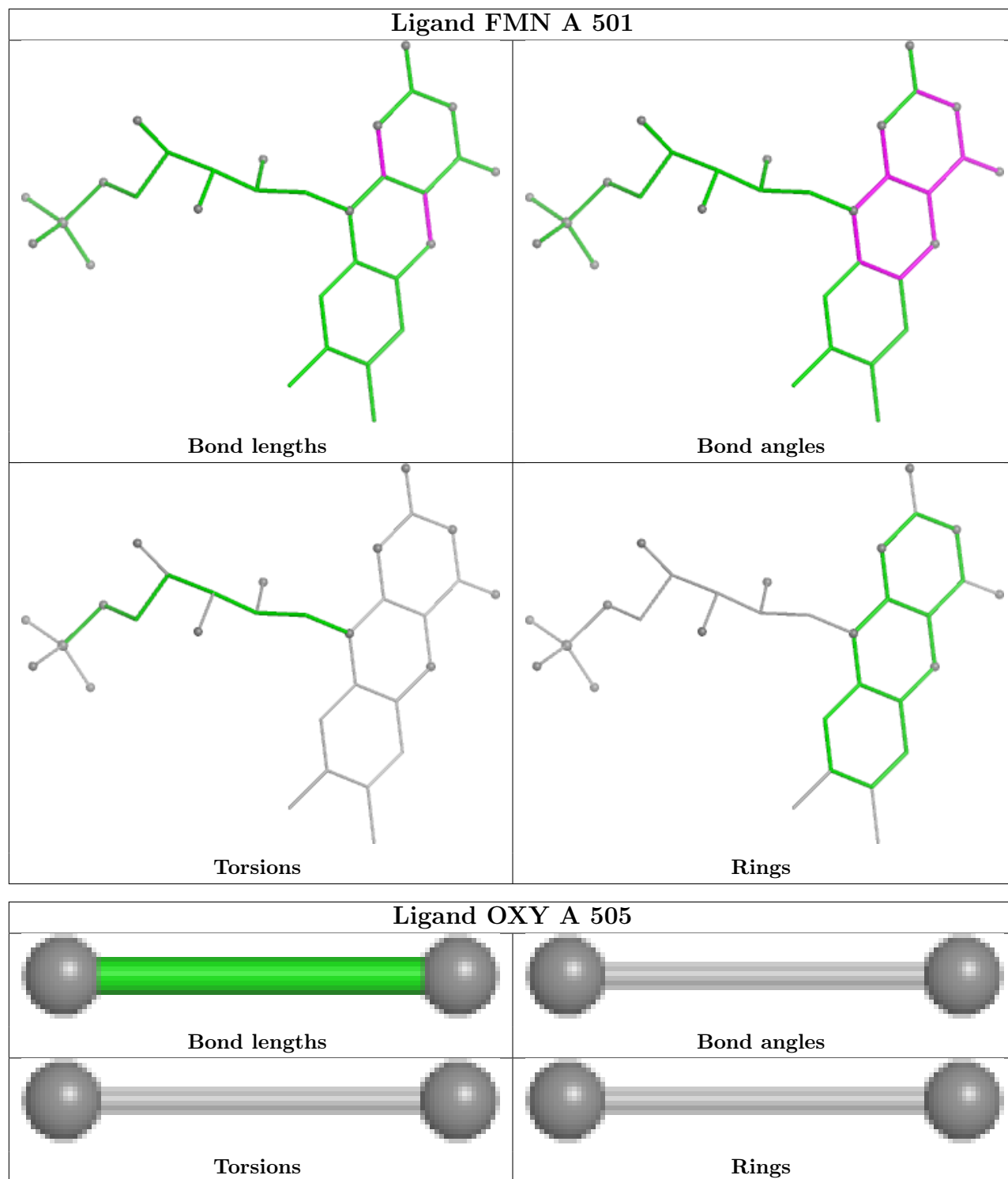
There are no torsion outliers.

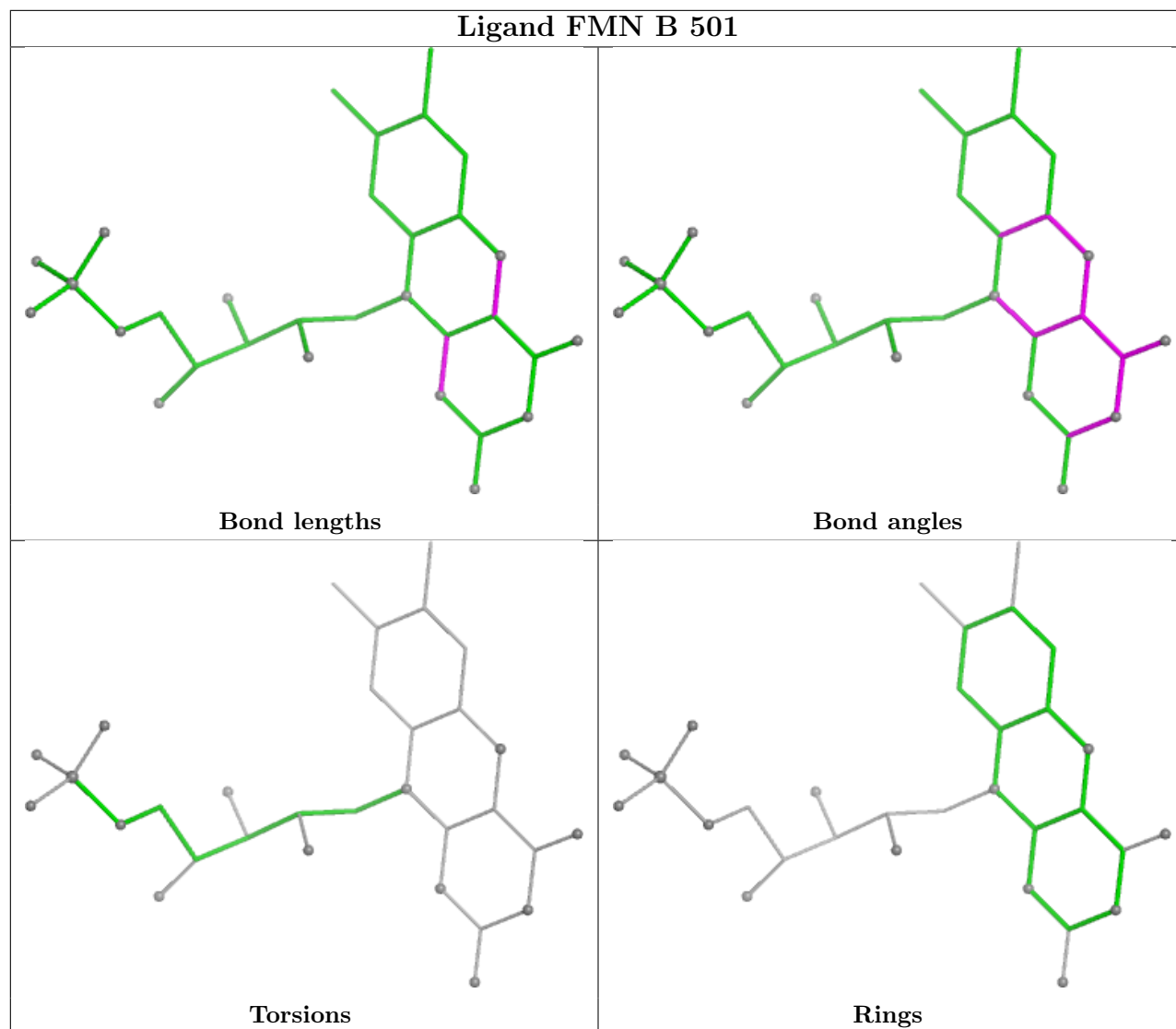
There are no ring outliers.

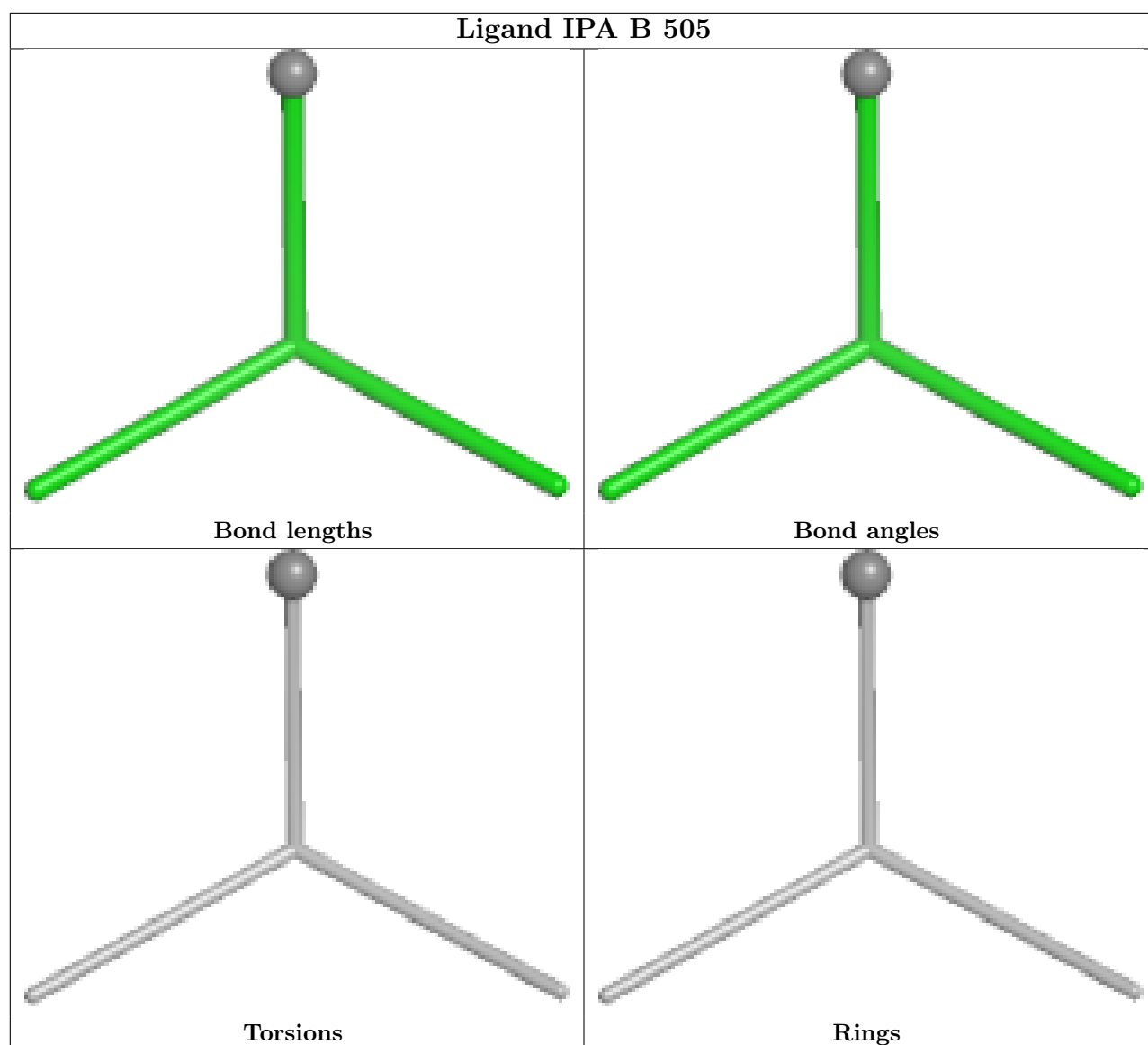
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	FMN	1	0
2	B	501	FMN	1	0
6	B	505	IPA	2	0

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.







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, 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	400/479 (83%)	0.41	12 (3%) 52 58	10, 19, 31, 57	1 (0%)
1	B	400/479 (83%)	0.58	16 (4%) 42 47	12, 22, 34, 53	2 (0%)
All	All	800/958 (83%)	0.50	28 (3%) 47 53	10, 20, 32, 57	3 (0%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	401	LEU	5.4
1	A	401	LEU	5.2
1	B	22	PHE	4.0
1	B	400	PRO	3.6
1	A	399	ALA	3.6
1	B	278	GLU	3.6
1	A	22	PHE	3.1
1	A	400	PRO	3.0
1	A	398	LEU	2.7
1	A	281	PRO	2.7
1	B	57	ARG	2.7
1	B	90	GLU	2.6
1	B	336	ARG	2.6
1	B	399	ALA	2.5
1	B	376[A]	ARG	2.5
1	B	394	ARG	2.5
1	A	90	GLU	2.4
1	B	68	ASP	2.4
1	B	277	ALA	2.3
1	A	278	GLU	2.3
1	B	194	TYR	2.3
1	A	282	ARG	2.3
1	A	82	GLU	2.2
1	B	240	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	272	ILE	2.2
1	B	294	ASP	2.2
1	B	83	ASP	2.1
1	A	327	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 [i](#)

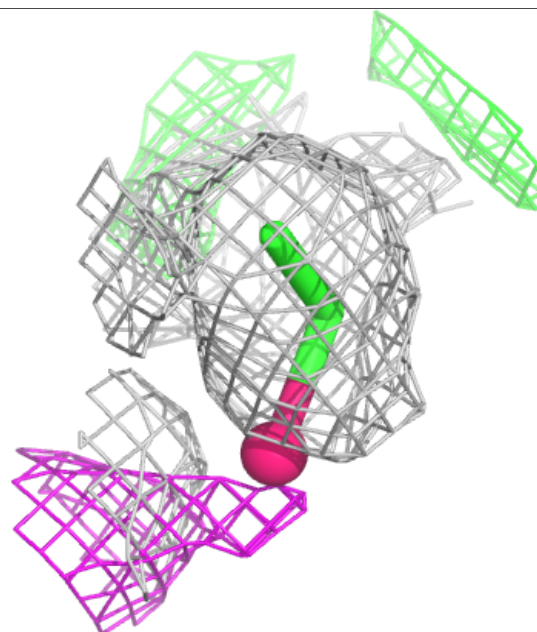
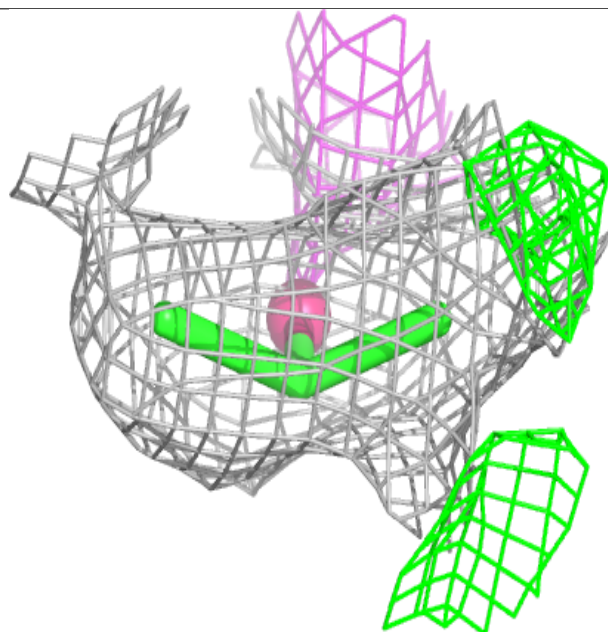
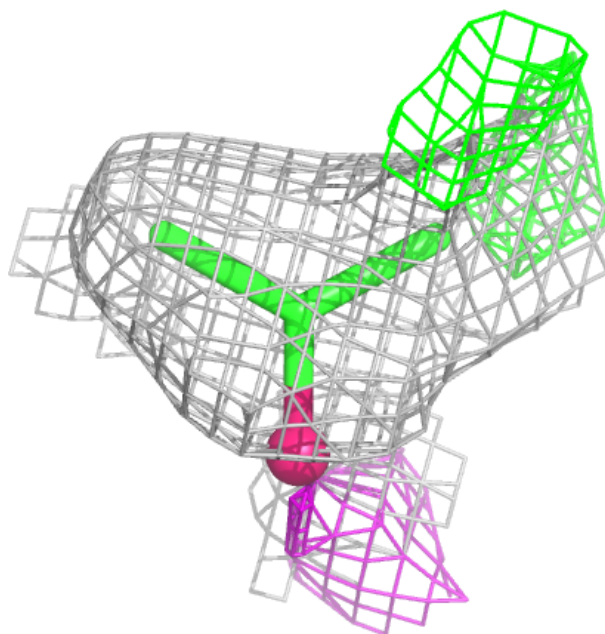
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	IPA	B	505	4/4	0.48	0.23	32,33,33,34	0
5	OXY	A	505	2/2	0.70	0.14	32,32,32,33	0
4	O	A	504	1/1	0.92	0.14	46,46,46,46	0
2	FMN	B	501	31/31	0.93	0.08	12,15,17,18	0
2	FMN	A	501	31/31	0.94	0.07	11,14,16,17	0
4	O	B	504	1/1	0.95	0.12	42,42,42,42	0
3	FE	A	502	1/1	0.97	0.11	32,32,32,32	0
3	FE	B	502	1/1	0.98	0.14	31,31,31,31	0
3	FE	B	503	1/1	0.98	0.06	33,33,33,33	0
3	FE	A	503	1/1	0.99	0.07	34,34,34,34	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.

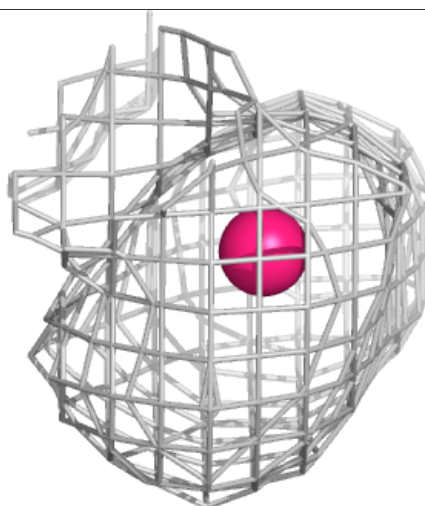
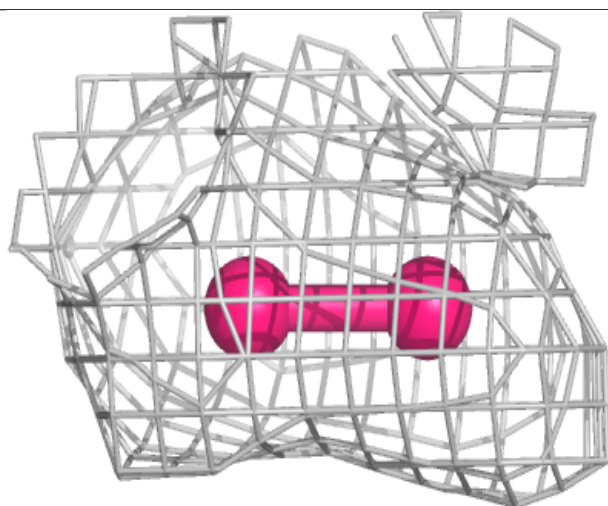
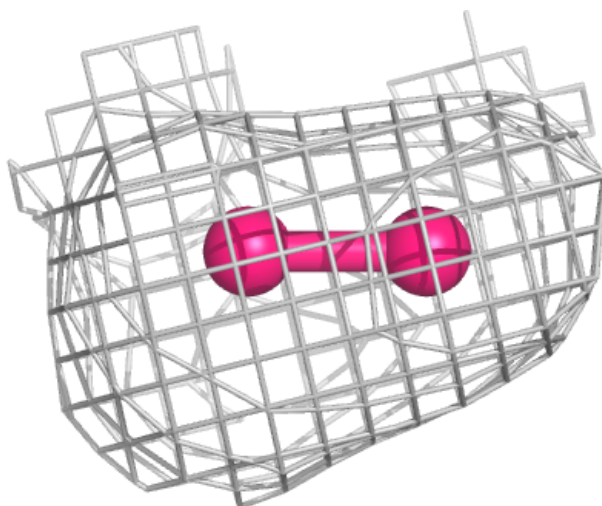
Electron density around IPA B 505:

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



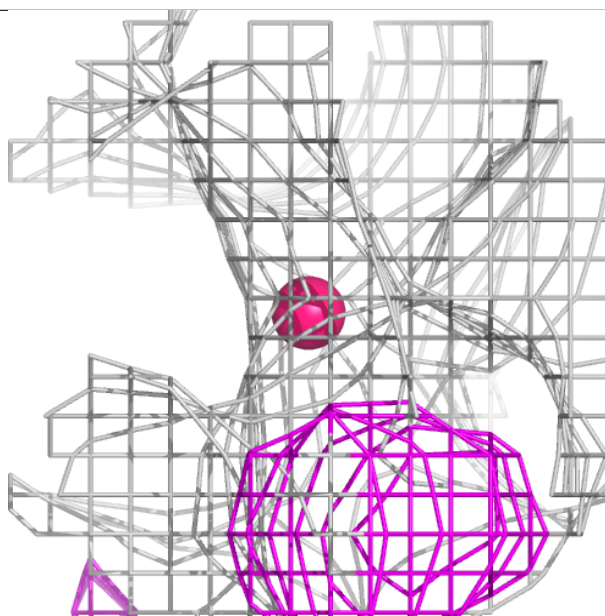
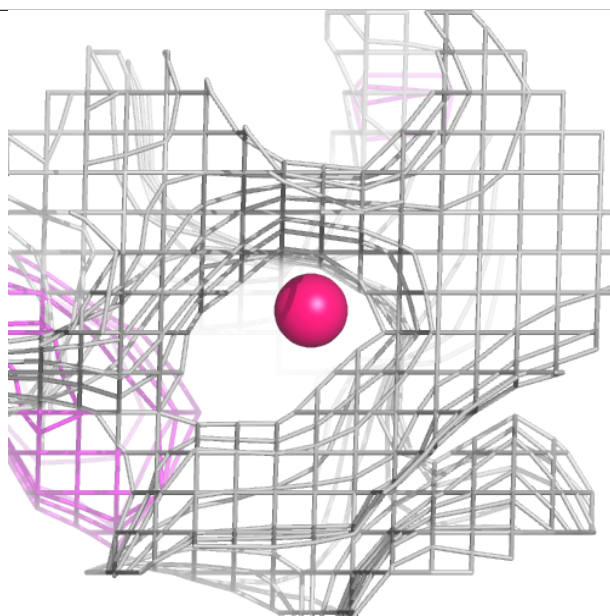
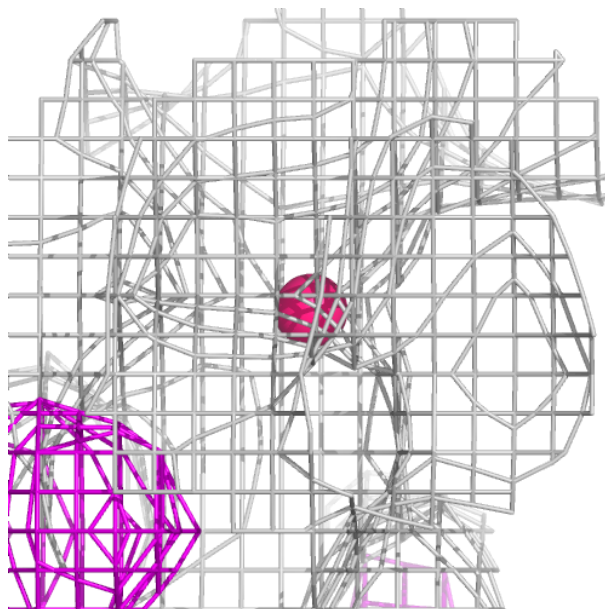
Electron density around OXY A 505:

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



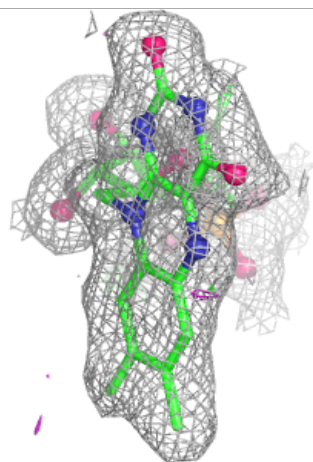
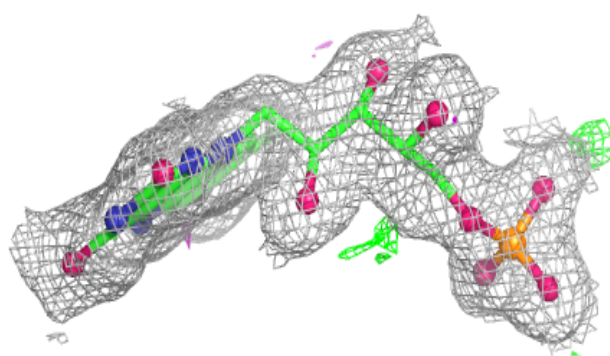
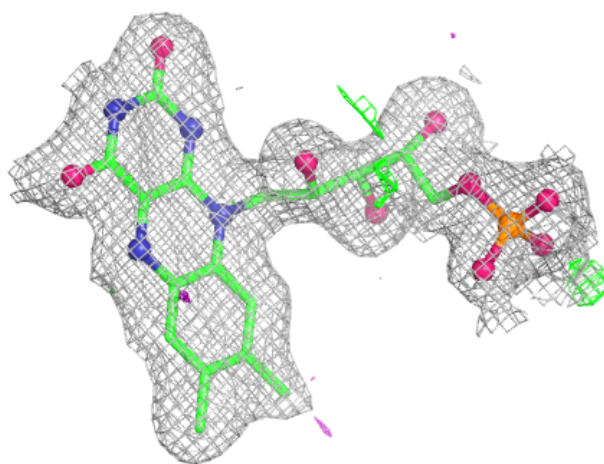
Electron density around O A 504:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



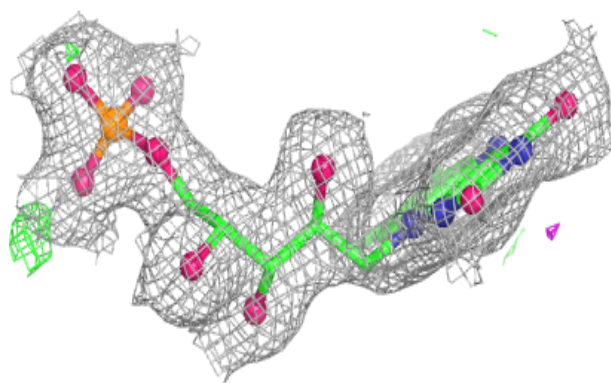
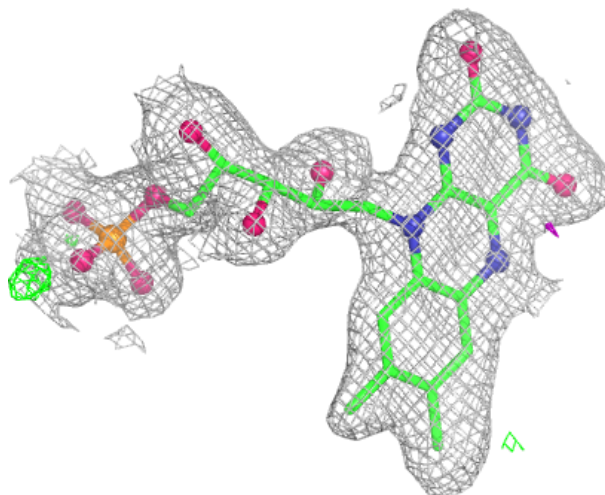
Electron density around FMN B 501:

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and green (positive)



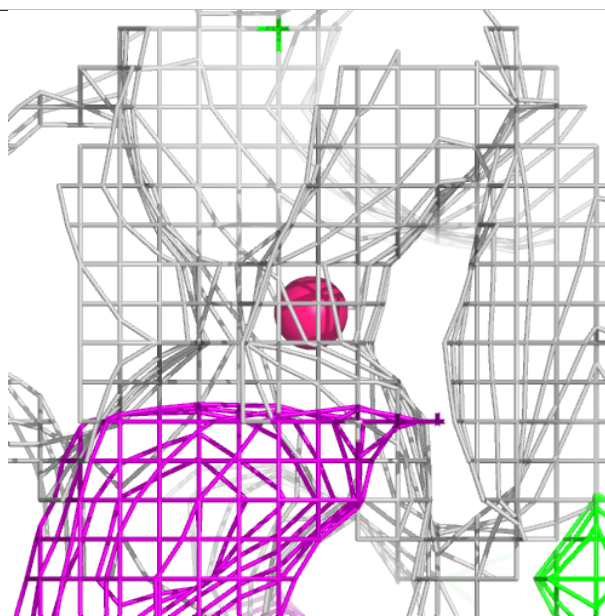
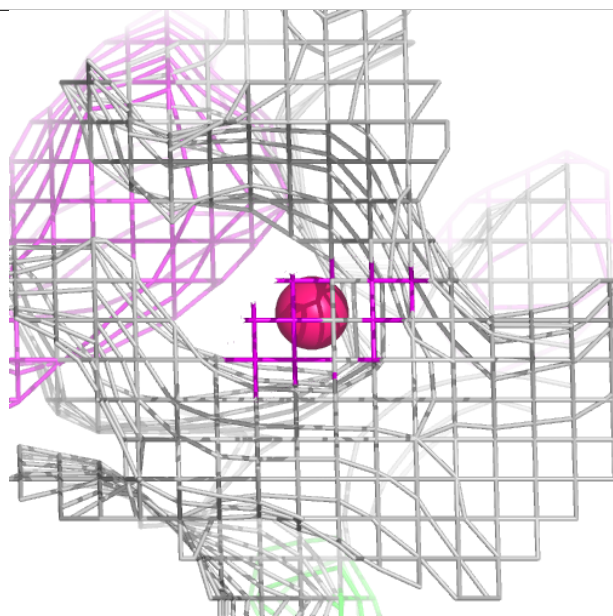
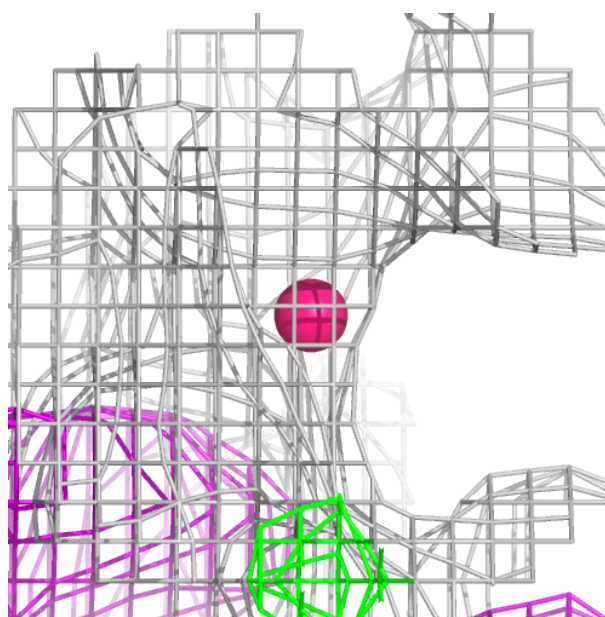
Electron density around FMN A 501:

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and green (positive)



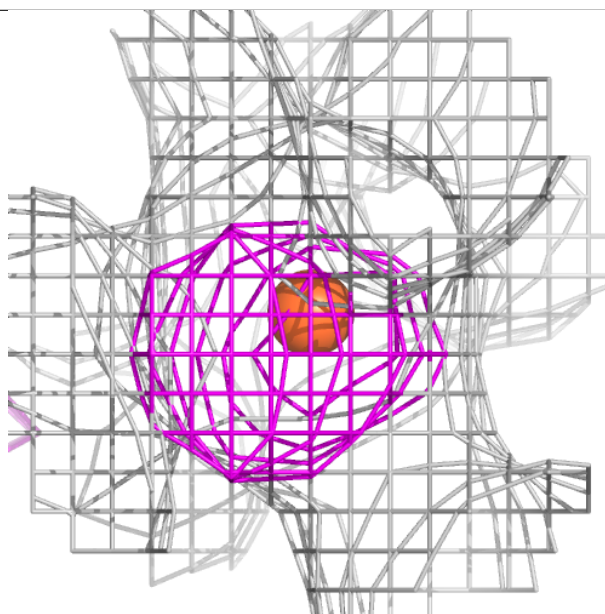
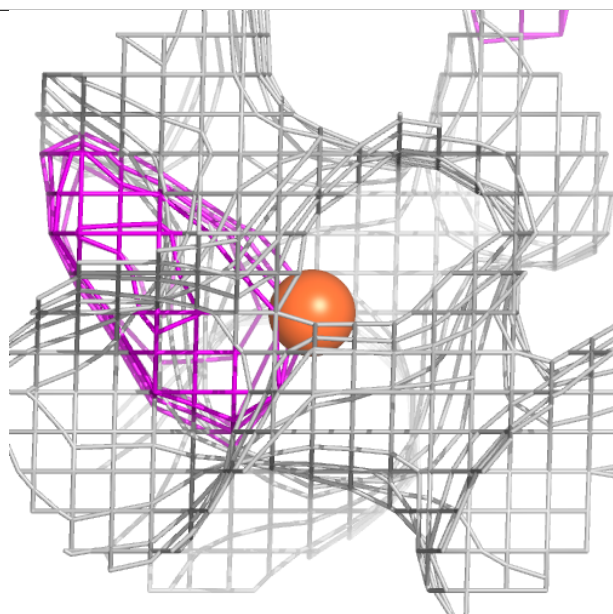
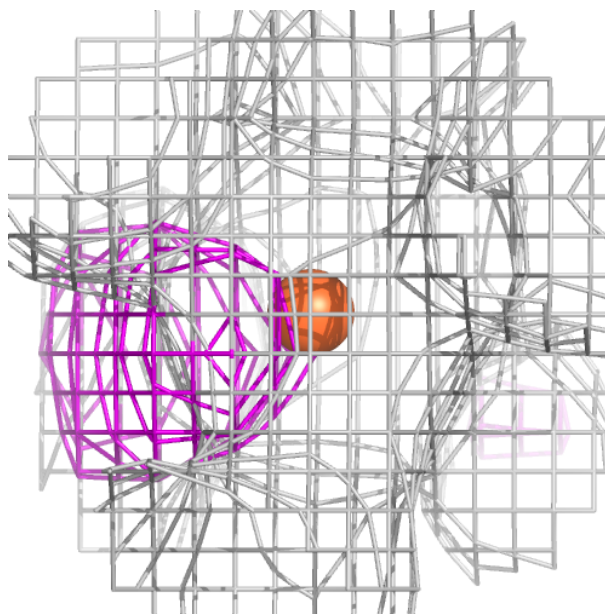
Electron density around O B 504:

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and green (positive)



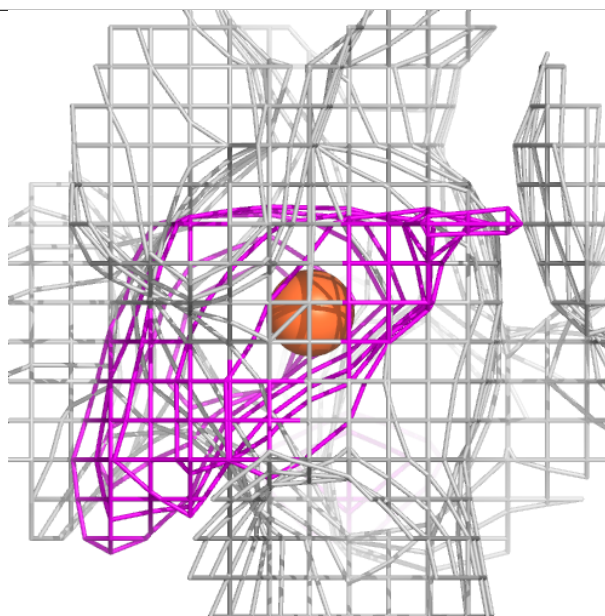
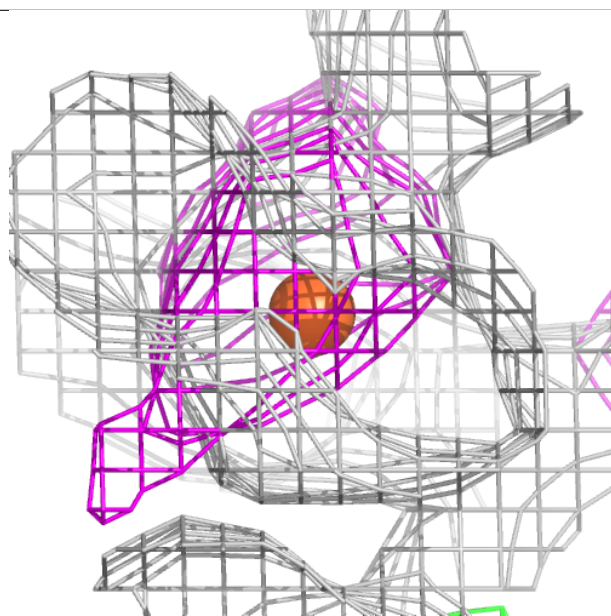
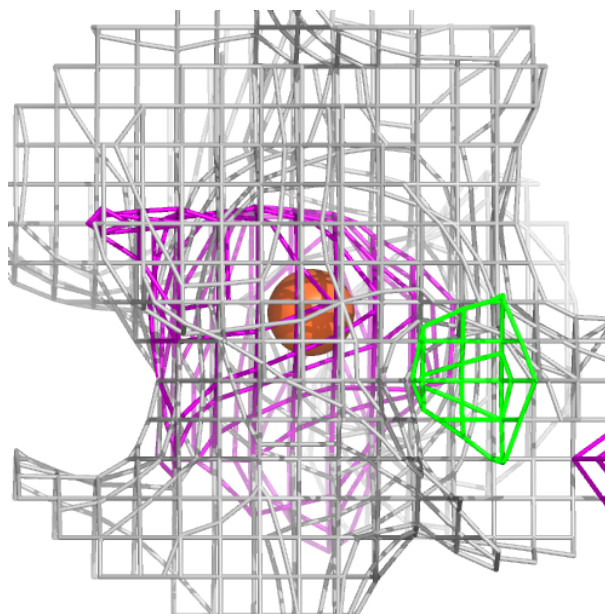
Electron density around FE A 502:

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and green (positive)



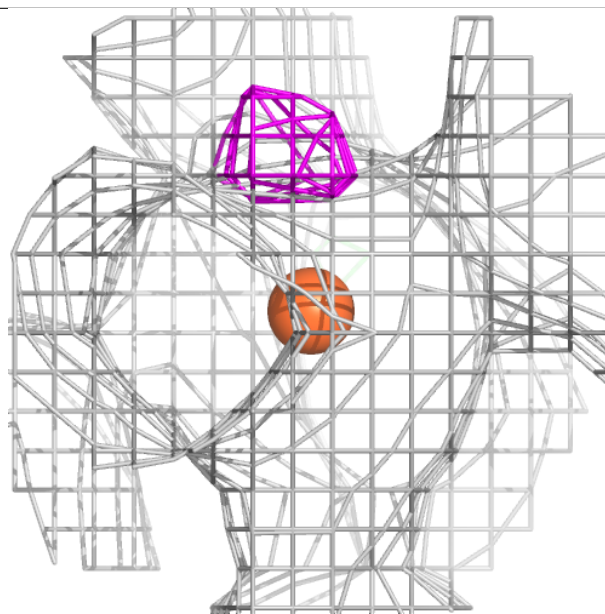
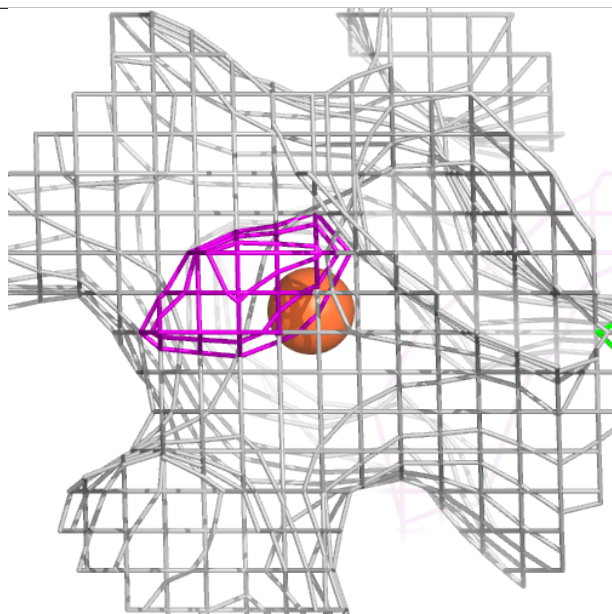
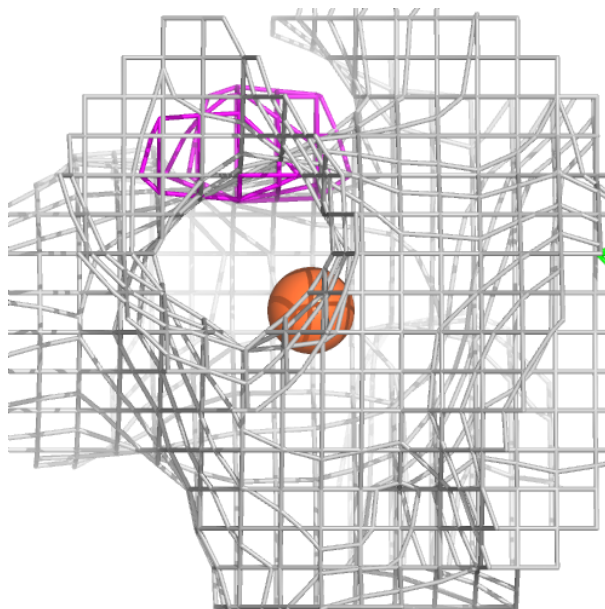
Electron density around FE B 502:

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and green (positive)



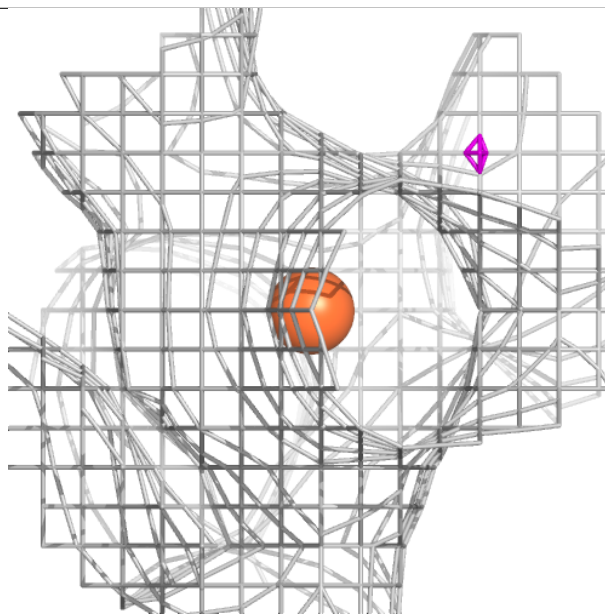
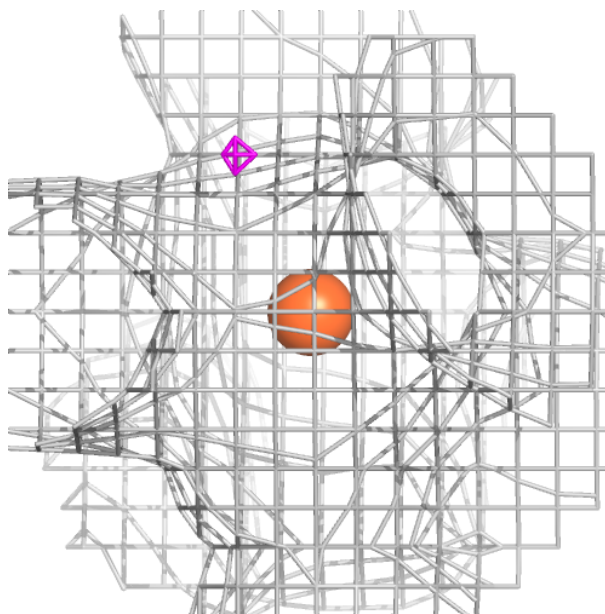
Electron density around FE B 503:

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and green (positive)



Electron density around FE A 503:

$2mF_o-DF_c$ (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.