



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 4, 2023 – 02:48 AM EDT

PDB ID : 6POC
Title : Structure of human neuronal nitric oxide synthase R354A/G357D mutant heme domain in complex with 7-(3-(Aminomethyl)-4-(oxazol-4-ylmethoxy)phenyl)-4-methylquinolin-2-amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2019-07-03
Resolution : 2.00 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 : 2.35.1
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) : 2.35.1

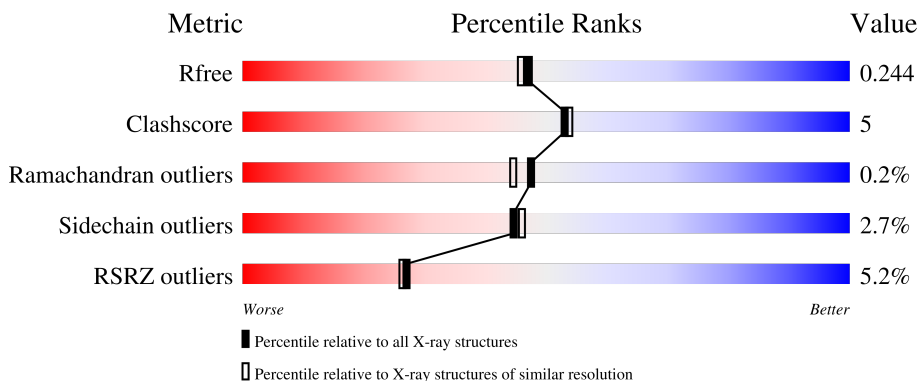
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.



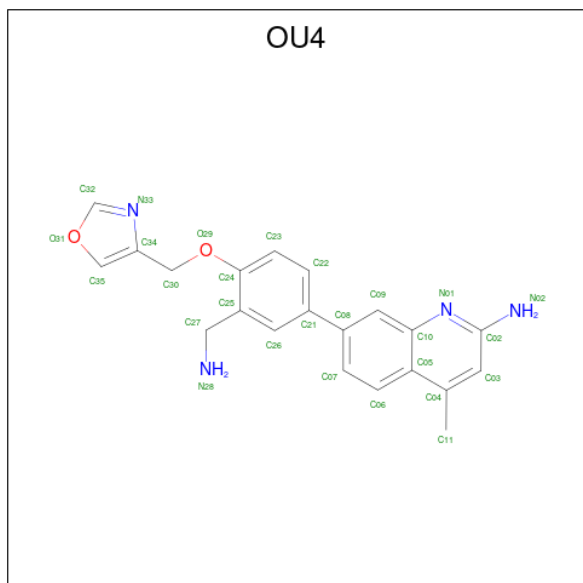
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	421	 4% 85% 13% ..
1	B	421	 6% 85% 13% .

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is 7-{3-(aminomethyl)-4-[(1,3-oxazol-4-yl)methoxy]phenyl}-4-methylquinolin-2-amine (three-letter code: OU4) (formula: C₂₁H₂₀N₄O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			27	21	4	2		
3	A	1	Total	C	N	O	0	0
			27	21	4	2		
3	B	1	Total	C	N	O	0	0
			27	21	4	2		
3	B	1	Total	C	N	O	0	0
			27	21	4	2		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Zn 1 1	0	0

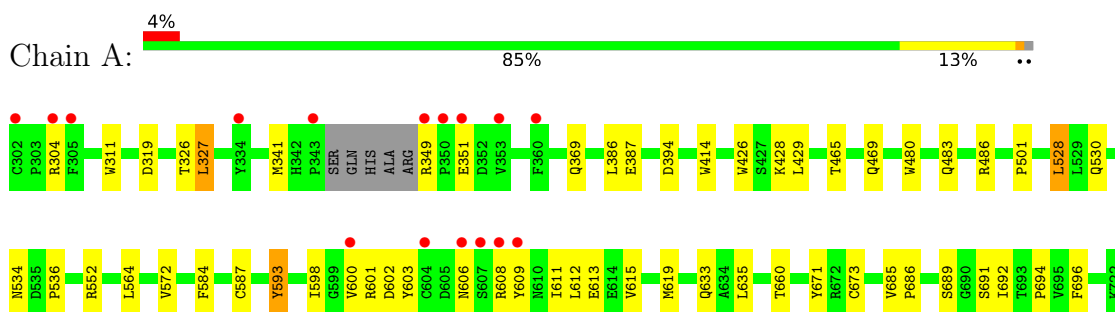
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	242	Total O 242 242	0	0
6	B	184	Total O 184 184	0	0

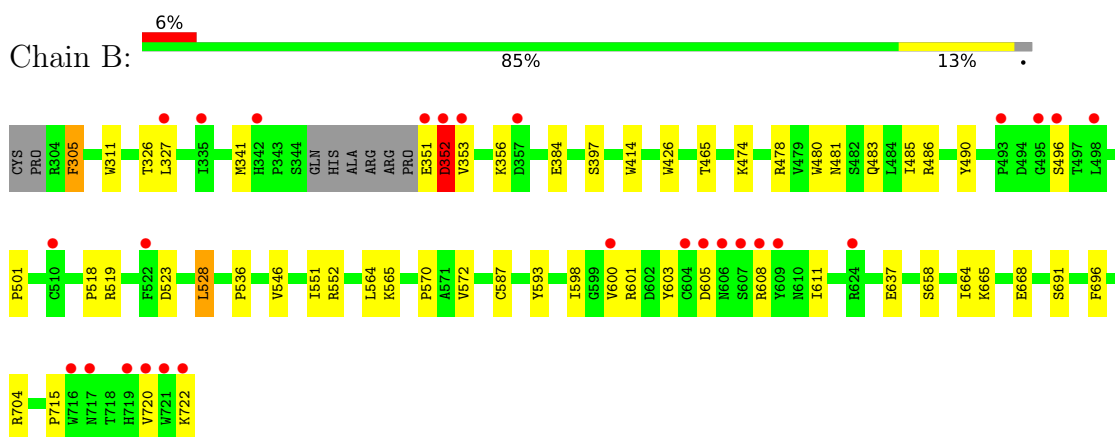
3 Residue-property plots [i](#)

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: Nitric oxide synthase, brain



- Molecule 1: Nitric oxide synthase, brain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.13Å 122.26Å 164.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.31 – 2.00 61.13 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.7 (57.31-2.00) 98.9 (61.13-2.00)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	0.20	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.00Å)	Xtrriage
Refinement program	PHENIX (1.11.1-2575_1496: ???)	Depositor
R, R_{free}	0.193 , 0.241 0.194 , 0.244	Depositor DCC
R_{free} test set	3511 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtrriage
Anisotropy	0.838	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7657	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.91% 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: HEM, GOL, OU4, 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	0.38	0/3633	0.54	0/4930
1	B	0.38	0/3602	0.51	0/4885
All	All	0.38	0/7235	0.53	0/9815

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.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	593	TYR	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	3522	0	3427	41	0
1	B	3496	0	3394	32	0
2	A	43	0	30	3	0
2	B	43	0	30	2	0
3	A	54	0	0	3	0
3	B	54	0	0	3	0
4	A	12	0	16	2	0
4	B	6	0	8	0	0
5	B	1	0	0	0	0
6	A	242	0	0	3	0
6	B	184	0	0	2	0
All	All	7657	0	6905	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 5.

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:528:LEU:HD22	1:A:536:PRO:HB2	1.58	0.86
1:B:528:LEU:HD22	1:B:536:PRO:HB2	1.71	0.72
1:A:480:TRP:HB2	1:A:528:LEU:HB3	1.73	0.71
2:B:802:HEM:HHC	2:B:802:HEM:HBB2	1.74	0.69
1:A:387:GLU:OE1	6:A:901:HOH:O	2.13	0.66
1:A:429:LEU:O	4:A:805:GOL:H12	1.97	0.64
1:A:428:LYS:NZ	6:A:903:HOH:O	2.30	0.64
1:A:609[B]:TYR:HD1	1:A:613:GLU:HB3	1.62	0.64
1:A:606[B]:ASN:ND2	1:A:609[B]:TYR:HB2	2.14	0.61
1:B:664:ILE:O	1:B:668[B]:GLU:HG2	2.01	0.60
1:B:356:LYS:HG2	1:B:397:SER:HA	1.84	0.58
1:B:572:VAL:HG21	3:B:803:OU4:C07	2.35	0.57
1:A:593:TYR:CD1	1:A:598[A]:ILE:HD11	2.40	0.56
1:A:483:GLN:HB2	1:A:486:ARG:HG2	1.87	0.56
1:A:601[A]:ARG:HG3	6:A:1042:HOH:O	2.05	0.56
1:A:564:LEU:HD11	1:A:611[A]:ILE:HD13	1.87	0.56
1:A:606[B]:ASN:HD21	1:A:609[B]:TYR:HB2	1.71	0.55
1:B:605[A]:ASP:HB2	1:B:608[A]:ARG:HG2	1.90	0.54
1:A:572:VAL:HG21	3:A:802:OU4:C07	2.38	0.53
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.89	0.53
2:A:801:HEM:HBB2	2:A:801:HEM:HHC	1.91	0.52
1:A:414:TRP:CE3	1:A:426:TRP:HA	2.44	0.52
1:B:564:LEU:HD11	1:B:611[A]:ILE:HD13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:485:ILE:HD13	1:B:546:VAL:HG13	1.93	0.50
3:B:804:OU4:O29	3:B:804:OU4:N28	2.45	0.50
1:A:691:SER:HA	1:A:696:PHE:CG	2.47	0.50
1:B:691:SER:HA	1:B:696:PHE:CG	2.47	0.49
1:B:490:TYR:CE1	1:B:519:ARG:HA	2.47	0.49
1:A:660:THR:OG1	1:A:694:PRO:HD2	2.13	0.49
1:B:601[A]:ARG:HG3	6:B:1041:HOH:O	2.11	0.49
1:A:598[A]:ILE:HA	1:A:602[A]:ASP:HB2	1.96	0.48
1:A:341:MET:HE3	1:B:311:TRP:CE2	2.49	0.47
1:B:551:ILE:HG12	1:B:565:LYS:HA	1.97	0.47
1:B:327:LEU:HD12	1:B:704:ARG:HG2	1.97	0.46
1:B:341:MET:HE1	3:B:804:OU4:C22	2.45	0.46
1:A:465:THR:O	1:A:587:CYS:HA	2.15	0.46
1:B:478:ARG:CZ	1:B:715:PRO:HG3	2.46	0.46
1:B:564:LEU:HD11	1:B:611[B]:ILE:HD12	1.97	0.46
1:B:603[B]:TYR:O	1:B:611[B]:ILE:HG12	2.16	0.46
1:A:469:GLN:HB3	1:A:584:PHE:CE2	2.51	0.45
1:A:319:ASP:HB2	1:A:671:TYR:CE2	2.52	0.45
1:A:349:ARG:HG2	1:A:351:GLU:H	1.82	0.44
1:A:633:GLN:NE2	1:B:637:GLU:OE2	2.49	0.44
1:B:465:THR:O	1:B:587:CYS:HA	2.18	0.44
1:B:570:PRO:HB3	1:B:593:TYR:CZ	2.52	0.44
1:B:351:GLU:HG3	1:B:352:ASP:OD1	2.18	0.44
1:A:602[A]:ASP:OD1	1:A:608[A]:ARG:NH2	2.50	0.43
1:B:305:PHE:HD1	1:B:305:PHE:N	2.16	0.43
1:A:609[B]:TYR:HA	1:A:613:GLU:OE1	2.19	0.43
1:B:305:PHE:N	1:B:305:PHE:CD1	2.85	0.43
1:B:501:PRO:HG2	1:B:608[A]:ARG:O	2.19	0.43
1:A:615:VAL:O	1:A:619:MET:HG3	2.18	0.43
1:B:593:TYR:CD1	1:B:598[A]:ILE:HD11	2.53	0.43
1:B:691:SER:HA	1:B:696:PHE:CB	2.49	0.42
1:A:689:SER:HB3	1:A:692:ILE:HD11	2.00	0.42
1:A:685:VAL:HA	1:A:686:PRO:HD3	1.92	0.42
1:A:341:MET:HE1	3:A:803:OU4:C22	2.50	0.42
1:B:483:GLN:HB2	1:B:486:ARG:CG	2.50	0.42
1:A:530:GLN:HG3	1:A:534:ASN:O	2.20	0.42
1:A:311:TRP:CE2	1:B:341:MET:HE3	2.55	0.41
1:A:600[A]:VAL:HG13	1:A:635:LEU:HD11	2.02	0.41
1:A:601[A]:ARG:HH22	3:A:803:OU4:C26	2.32	0.41
1:A:601[B]:ARG:HA	1:A:611[B]:ILE:HB	2.03	0.41
1:B:414:TRP:CE3	1:B:426:TRP:HA	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:518:PRO:HG2	1:B:523:ASP:CG	2.41	0.41
1:A:603[B]:TYR:O	1:A:611[B]:ILE:HG12	2.20	0.41
1:A:612:LEU:HD23	1:A:612:LEU:HA	1.90	0.41
1:B:480:TRP:HB2	1:B:528:LEU:HB3	2.02	0.41
1:A:600[A]:VAL:HG22	1:A:635:LEU:HD11	2.03	0.41
1:A:326:THR:OG1	1:A:327:LEU:HD23	2.21	0.41
1:A:501:PRO:HG2	1:A:608[A]:ARG:HA	2.03	0.41
2:A:801:HEM:HHC	2:A:801:HEM:CBB	2.51	0.41
1:B:600[A]:VAL:HG12	1:B:601[A]:ARG:HD2	2.01	0.41
2:B:802:HEM:O1A	6:B:901:HOH:O	2.22	0.41
1:A:528:LEU:HD23	1:A:528:LEU:HA	1.85	0.40
1:A:369:GLN:HG3	4:A:804:GOL:H2	2.02	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	430/421 (102%)	418 (97%)	12 (3%)	0	100	100
1	B	426/421 (101%)	408 (96%)	16 (4%)	2 (0%)	29	23
All	All	856/842 (102%)	826 (96%)	28 (3%)	2 (0%)	47	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	352	ASP
1	B	496	SER

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	389/376 (104%)	381 (98%)	8 (2%)	53	57
1	B	385/376 (102%)	372 (97%)	13 (3%)	37	36
All	All	774/752 (103%)	753 (97%)	21 (3%)	44	46

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	304	ARG
1	A	327	LEU
1	A	386	LEU
1	A	394	ASP
1	A	528	LEU
1	A	552	ARG
1	A	673[A]	CYS
1	A	673[B]	CYS
1	B	305	PHE
1	B	326	THR
1	B	352	ASP
1	B	353	VAL
1	B	384	GLU
1	B	474	LYS
1	B	481	ASN
1	B	528	LEU
1	B	552	ARG
1	B	658	SER
1	B	665	LYS
1	B	720	VAL
1	B	722	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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
3	OU4	B	803	-	25,30,30	0.96	1 (4%)	35,42,42	1.51	6 (17%)
3	OU4	B	804	-	25,30,30	0.96	0	35,42,42	1.40	6 (17%)
3	OU4	A	803	-	25,30,30	0.92	0	35,42,42	1.31	4 (11%)
4	GOL	A	804	-	5,5,5	0.41	0	5,5,5	0.25	0
4	GOL	B	805	-	5,5,5	0.40	0	5,5,5	0.11	0
2	HEM	B	802	1	41,50,50	1.52	5 (12%)	45,82,82	1.80	11 (24%)
3	OU4	A	802	-	25,30,30	0.98	1 (4%)	35,42,42	1.51	8 (22%)
2	HEM	A	801	1	41,50,50	1.45	6 (14%)	45,82,82	1.36	6 (13%)
4	GOL	A	805	-	5,5,5	0.49	0	5,5,5	0.53	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OU4	B	803	-	-	3/9/11/11	0/4/4/4
3	OU4	B	804	-	-	4/9/11/11	0/4/4/4
3	OU4	A	803	-	-	4/9/11/11	0/4/4/4
4	GOL	A	804	-	-	4/4/4/4	-
4	GOL	B	805	-	-	2/4/4/4	-
2	HEM	B	802	1	-	0/12/54/54	-
3	OU4	A	802	-	-	1/9/11/11	0/4/4/4
2	HEM	A	801	1	-	0/12/54/54	-
4	GOL	A	805	-	-	4/4/4/4	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	802	HEM	C3C-C2C	-4.18	1.34	1.40
2	A	801	HEM	C3C-C2C	-3.65	1.35	1.40
2	B	802	HEM	C3C-CAC	3.17	1.54	1.47
2	B	802	HEM	CAB-C3B	3.03	1.55	1.47
2	A	801	HEM	C3C-CAC	3.00	1.54	1.47
2	A	801	HEM	CAB-C3B	2.59	1.54	1.47
2	A	801	HEM	CMD-C2D	2.48	1.56	1.50
2	A	801	HEM	C3B-C2B	-2.38	1.32	1.37
3	A	802	OU4	C02-N01	2.35	1.36	1.33
2	A	801	HEM	CMB-C2B	2.13	1.55	1.50
3	B	803	OU4	C02-N01	2.08	1.36	1.33
2	B	802	HEM	C3B-C2B	-2.08	1.33	1.37
2	B	802	HEM	CMD-C2D	2.07	1.55	1.50

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	802	HEM	C4B-CHC-C1C	4.70	128.76	122.56
2	B	802	HEM	CBA-CAA-C2A	-3.78	106.17	112.62
3	B	803	OU4	C05-C10-N01	-3.51	119.08	122.81
3	A	803	OU4	O29-C24-C25	3.48	120.33	115.78
3	B	804	OU4	O29-C24-C25	3.48	120.33	115.78
3	A	802	OU4	N02-C02-N01	3.43	121.10	118.26
2	A	801	HEM	C4B-CHC-C1C	3.43	127.08	122.56
3	B	803	OU4	O29-C24-C25	3.42	120.25	115.78
3	A	803	OU4	C04-C05-C10	3.41	119.86	118.01
2	B	802	HEM	CHD-C1D-ND	3.31	128.03	124.43
3	B	804	OU4	C04-C05-C10	3.26	119.78	118.01
2	B	802	HEM	C3D-C4D-ND	-3.13	106.68	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	803	OU4	C04-C05-C10	3.11	119.69	118.01
3	A	802	OU4	C05-C10-N01	-2.99	119.64	122.81
2	B	802	HEM	CAD-C3D-C2D	-2.98	122.34	127.88
3	B	803	OU4	C30-C34-C35	-2.92	125.49	129.99
2	B	802	HEM	CMA-C3A-C4A	-2.84	124.10	128.46
3	B	803	OU4	C30-O29-C24	2.80	123.27	117.76
2	B	802	HEM	CAD-CBD-CGD	-2.77	107.63	113.60
2	A	801	HEM	CMC-C2C-C3C	2.77	129.86	124.68
3	A	802	OU4	C30-O29-C24	2.65	122.98	117.76
3	A	802	OU4	C26-C21-C08	-2.64	116.50	120.86
2	B	802	HEM	C4D-ND-C1D	2.59	107.75	105.07
2	B	802	HEM	C3B-C2B-C1B	2.57	108.39	106.49
2	A	801	HEM	CHA-C4D-ND	2.47	127.44	124.38
2	A	801	HEM	CBA-CAA-C2A	-2.40	108.52	112.62
2	B	802	HEM	CAD-C3D-C4D	2.36	128.79	124.66
3	A	802	OU4	C30-C34-C35	-2.34	126.39	129.99
3	A	803	OU4	C30-O29-C24	2.33	122.36	117.76
3	A	802	OU4	C03-C04-C05	2.21	119.95	117.78
3	B	803	OU4	C03-C04-C05	2.19	119.94	117.78
2	B	802	HEM	C1B-NB-C4B	2.16	107.31	105.07
3	A	803	OU4	C30-C34-C35	-2.12	126.72	129.99
3	B	804	OU4	C08-C09-C10	-2.10	119.60	121.44
2	A	801	HEM	CHD-C1D-ND	2.09	126.70	124.43
3	B	804	OU4	C26-C21-C08	-2.08	117.42	120.86
3	A	802	OU4	O29-C24-C25	2.08	118.49	115.78
3	A	802	OU4	C04-C05-C10	2.07	119.13	118.01
3	B	804	OU4	C05-C10-N01	-2.06	120.63	122.81
3	B	804	OU4	O29-C30-C34	2.01	114.82	109.42
2	A	801	HEM	CMA-C3A-C4A	-2.00	125.39	128.46

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	803	OU4	C24-C25-C27-N28
3	B	804	OU4	C24-C25-C27-N28
4	A	804	GOL	O1-C1-C2-C3
4	A	805	GOL	O1-C1-C2-O2
4	A	805	GOL	O1-C1-C2-C3
4	A	805	GOL	C1-C2-C3-O3
4	B	805	GOL	O1-C1-C2-C3
4	B	805	GOL	O1-C1-C2-O2

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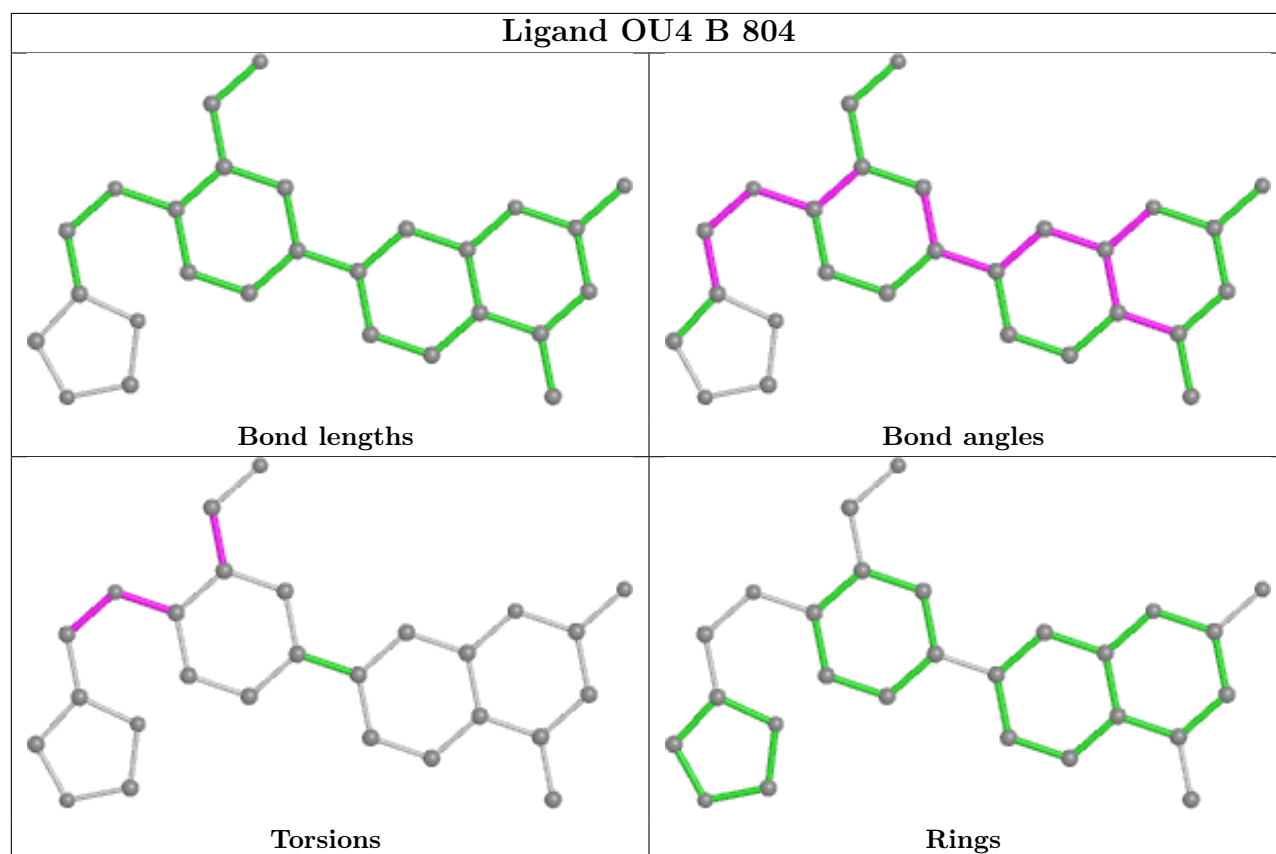
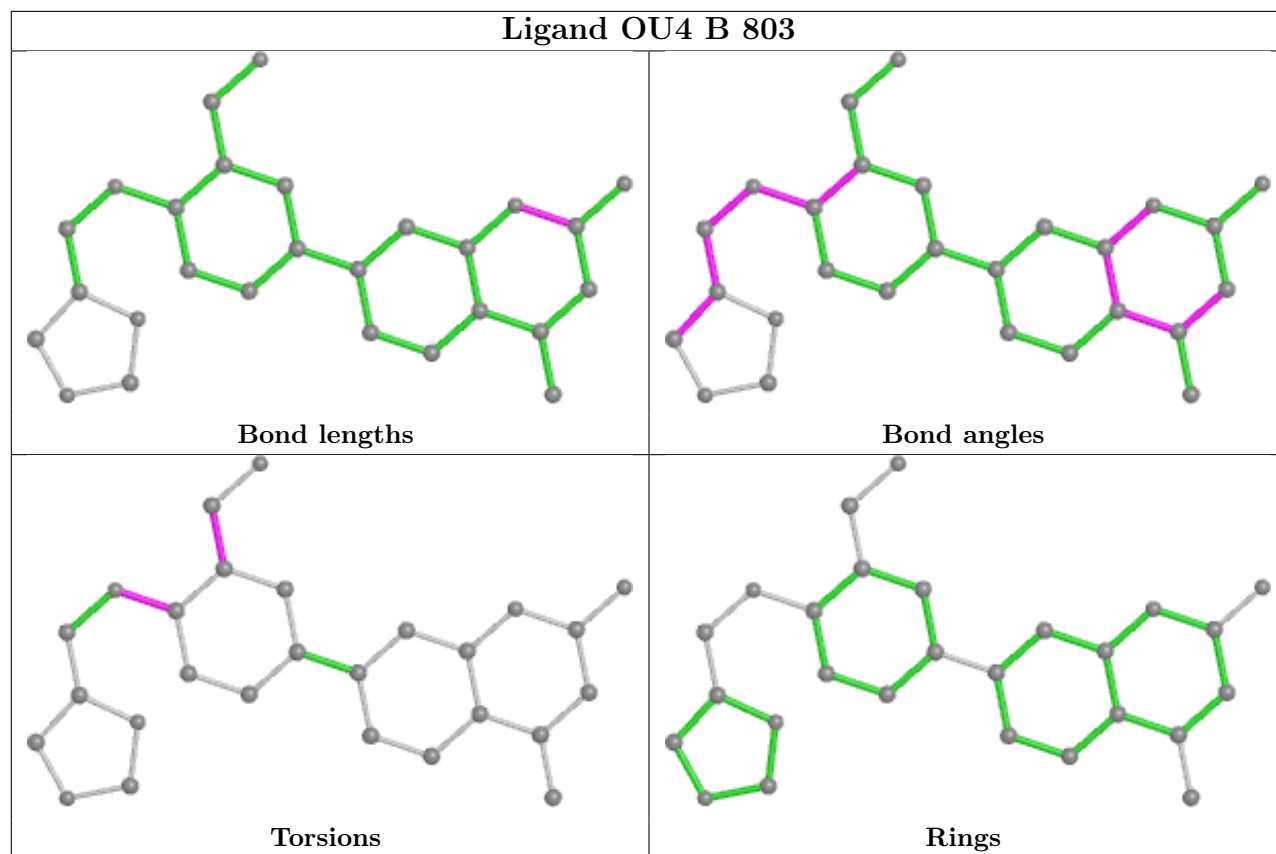
Mol	Chain	Res	Type	Atoms
3	A	803	OU4	C34-C30-O29-C24
4	A	804	GOL	O1-C1-C2-O2
4	A	805	GOL	O2-C2-C3-O3
3	A	803	OU4	C23-C24-O29-C30
3	B	803	OU4	C25-C24-O29-C30
3	B	803	OU4	C24-C25-C27-N28
3	B	803	OU4	C23-C24-O29-C30
3	A	803	OU4	C25-C24-O29-C30
4	A	804	GOL	O2-C2-C3-O3
3	B	804	OU4	C34-C30-O29-C24
3	B	804	OU4	C23-C24-O29-C30
3	B	804	OU4	C25-C24-O29-C30
4	A	804	GOL	C1-C2-C3-O3
3	A	802	OU4	C24-C25-C27-N28

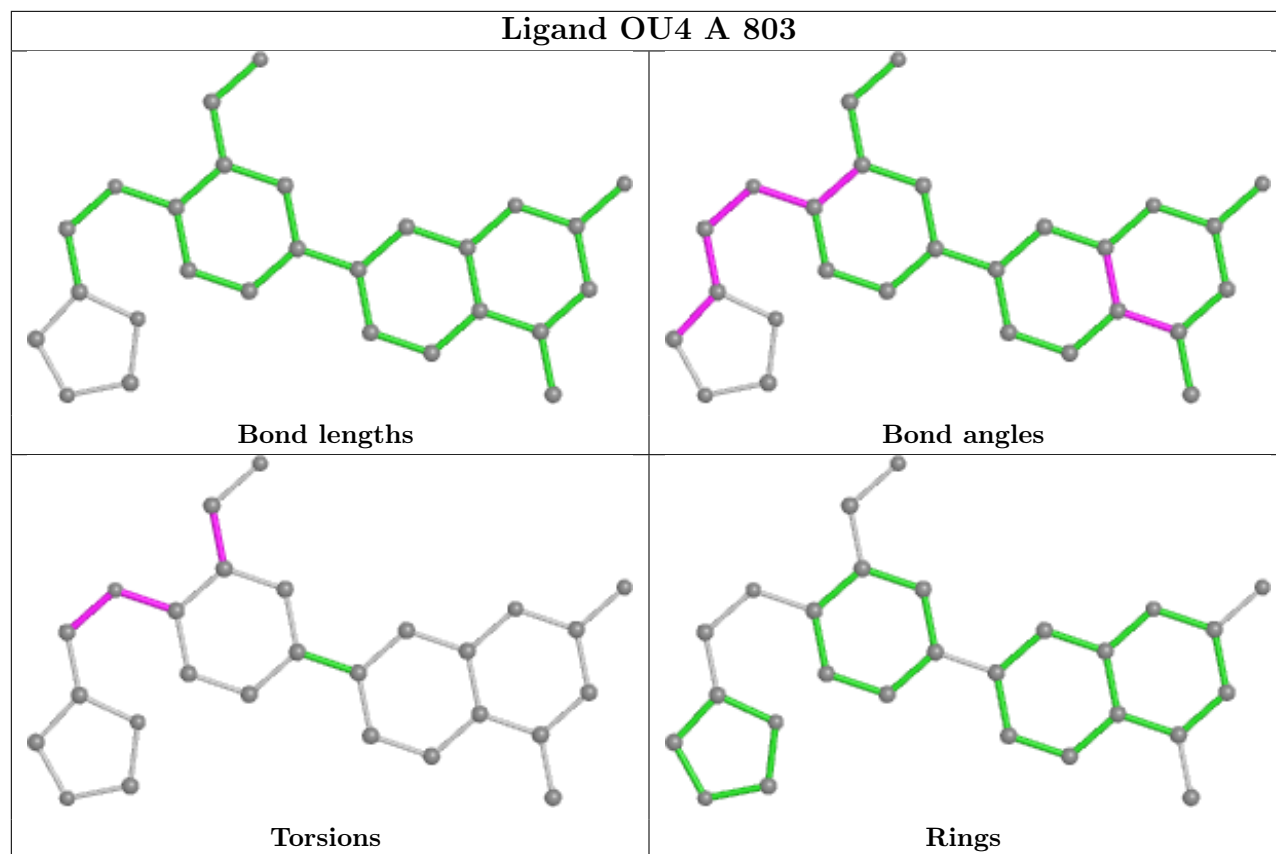
There are no ring outliers.

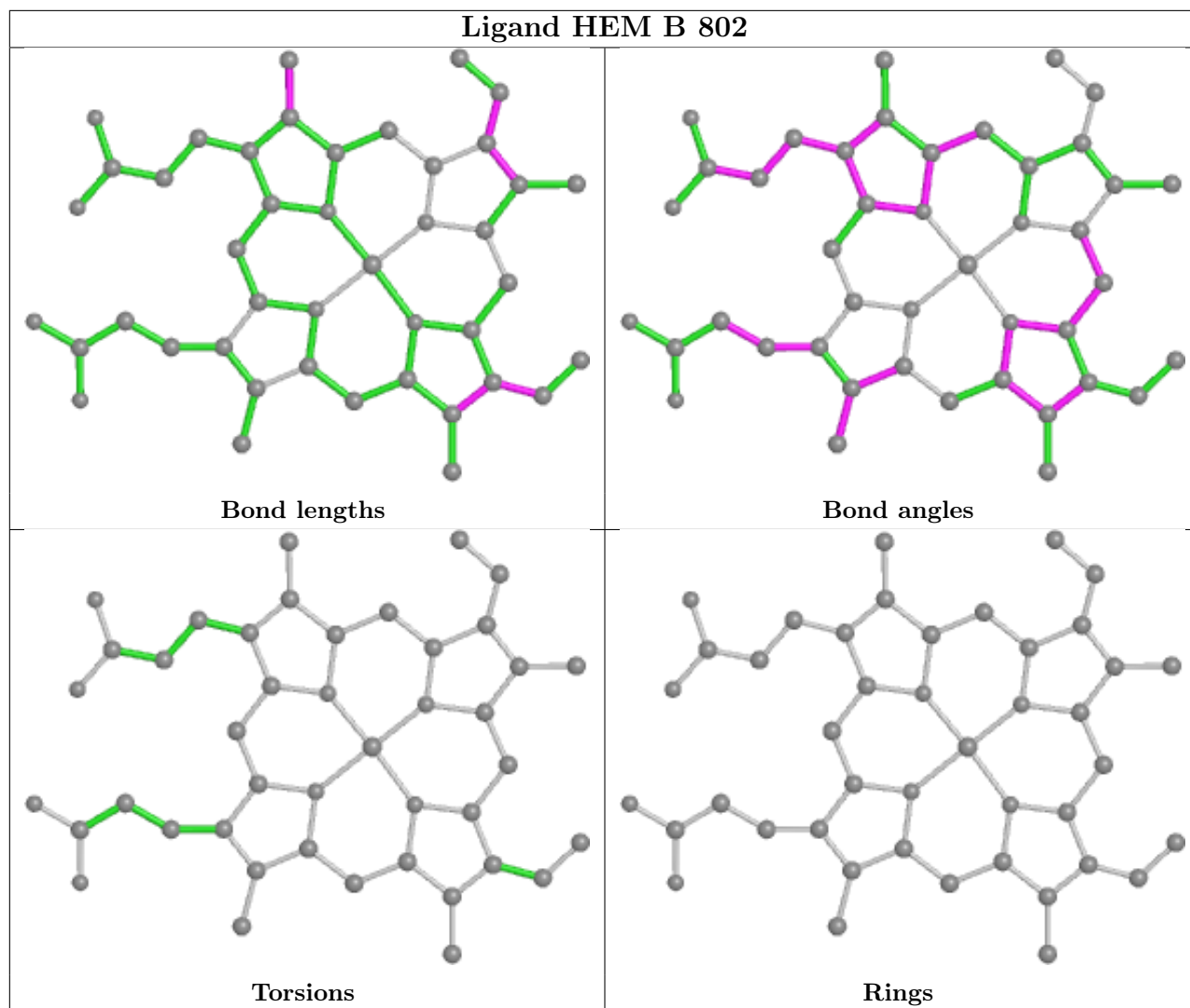
8 monomers are involved in 13 short contacts:

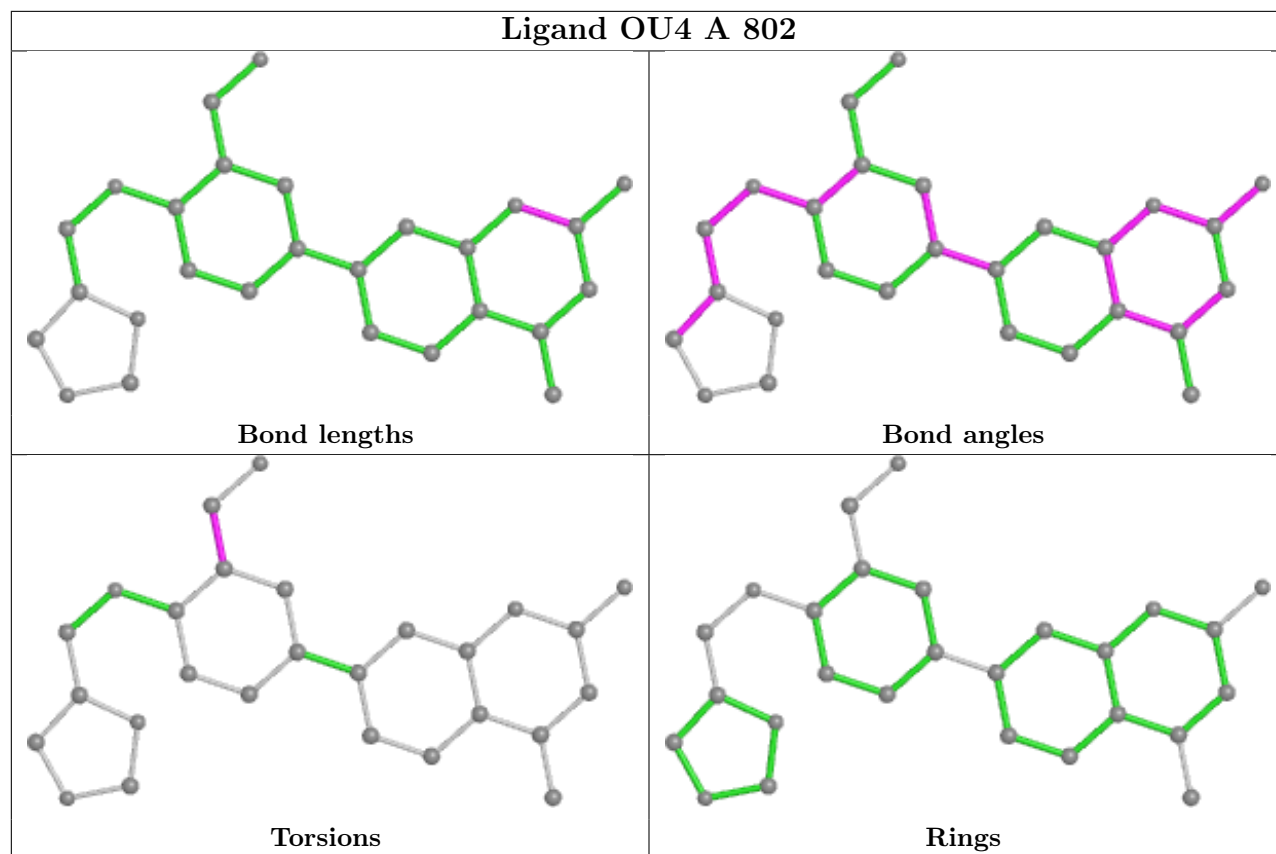
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	803	OU4	1	0
3	B	804	OU4	2	0
3	A	803	OU4	2	0
4	A	804	GOL	1	0
2	B	802	HEM	2	0
3	A	802	OU4	1	0
2	A	801	HEM	3	0
4	A	805	GOL	1	0

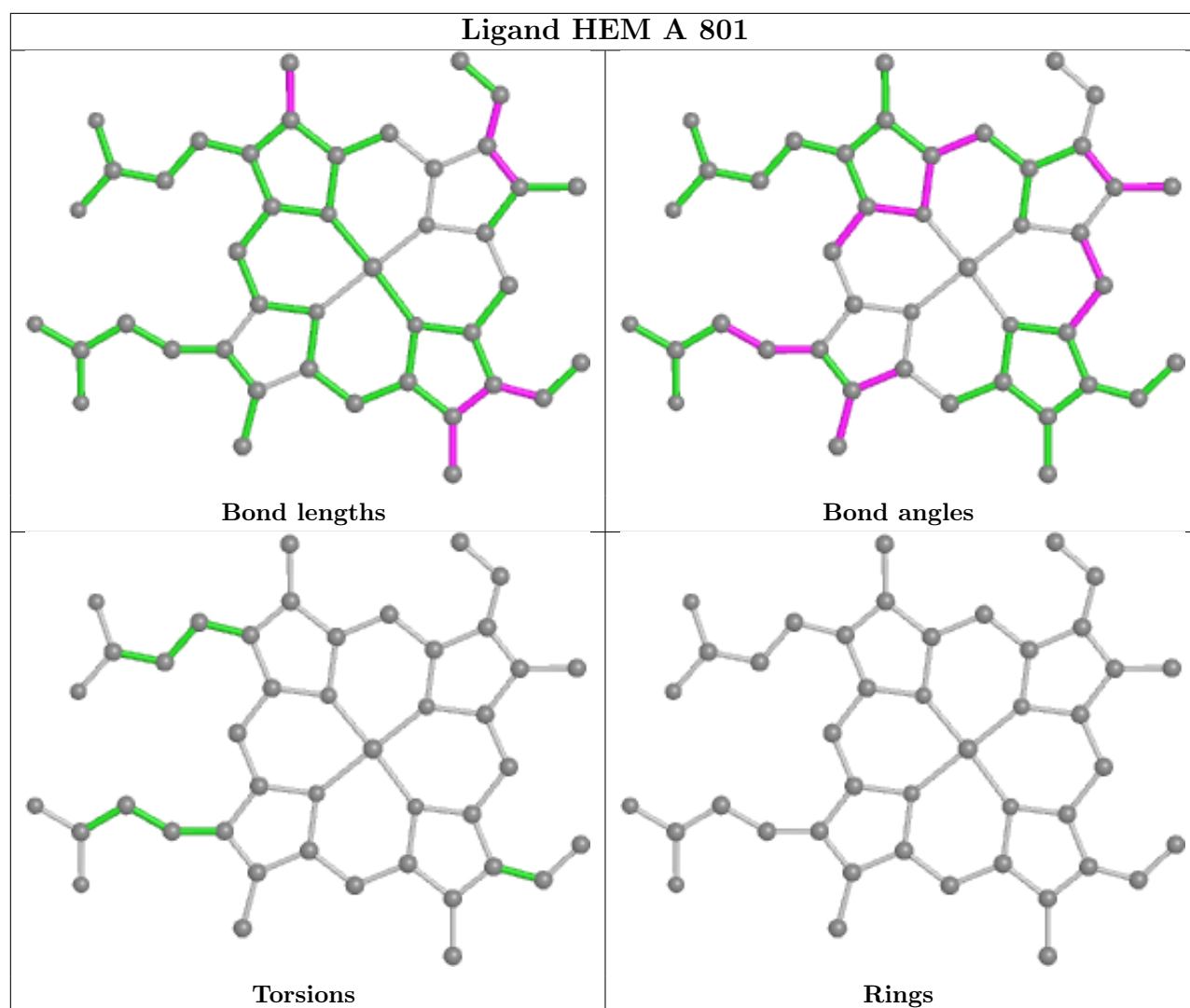
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 [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	416/421 (98%)	0.59	16 (3%) 40 39	35, 50, 83, 146	0
1	B	413/421 (98%)	0.70	27 (6%) 18 18	38, 55, 97, 147	0
All	All	829/842 (98%)	0.65	43 (5%) 27 26	35, 53, 91, 147	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	350	PRO	7.9
1	B	720	VAL	7.0
1	B	351	GLU	6.9
1	A	608[A]	ARG	5.6
1	B	721	TRP	5.5
1	B	352	ASP	5.4
1	B	327	LEU	5.3
1	A	351	GLU	5.1
1	A	302	CYS	4.6
1	A	604[A]	CYS	4.0
1	B	510	CYS	3.9
1	A	609[A]	TYR	3.7
1	B	607[A]	SER	3.6
1	A	607[A]	SER	3.4
1	B	353	VAL	3.3
1	A	606[A]	ASN	3.2
1	B	608[A]	ARG	3.2
1	B	719	HIS	3.1
1	B	716	TRP	3.0
1	B	496	SER	2.9
1	B	605[A]	ASP	2.9
1	A	349	ARG	2.9
1	A	305	PHE	2.8
1	B	606[A]	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	609[A]	TYR	2.7
1	B	335	ILE	2.7
1	B	498	LEU	2.7
1	B	722	LYS	2.7
1	B	342	HIS	2.7
1	B	493	PRO	2.6
1	B	600[A]	VAL	2.6
1	A	343	PRO	2.6
1	A	600[A]	VAL	2.5
1	B	522	PHE	2.5
1	B	357	ASP	2.4
1	A	353	VAL	2.4
1	A	360	PHE	2.3
1	B	495	GLY	2.3
1	A	334	TYR	2.2
1	B	717	ASN	2.2
1	B	624	ARG	2.2
1	B	604[A]	CYS	2.1
1	A	304	ARG	2.1

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 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, 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.

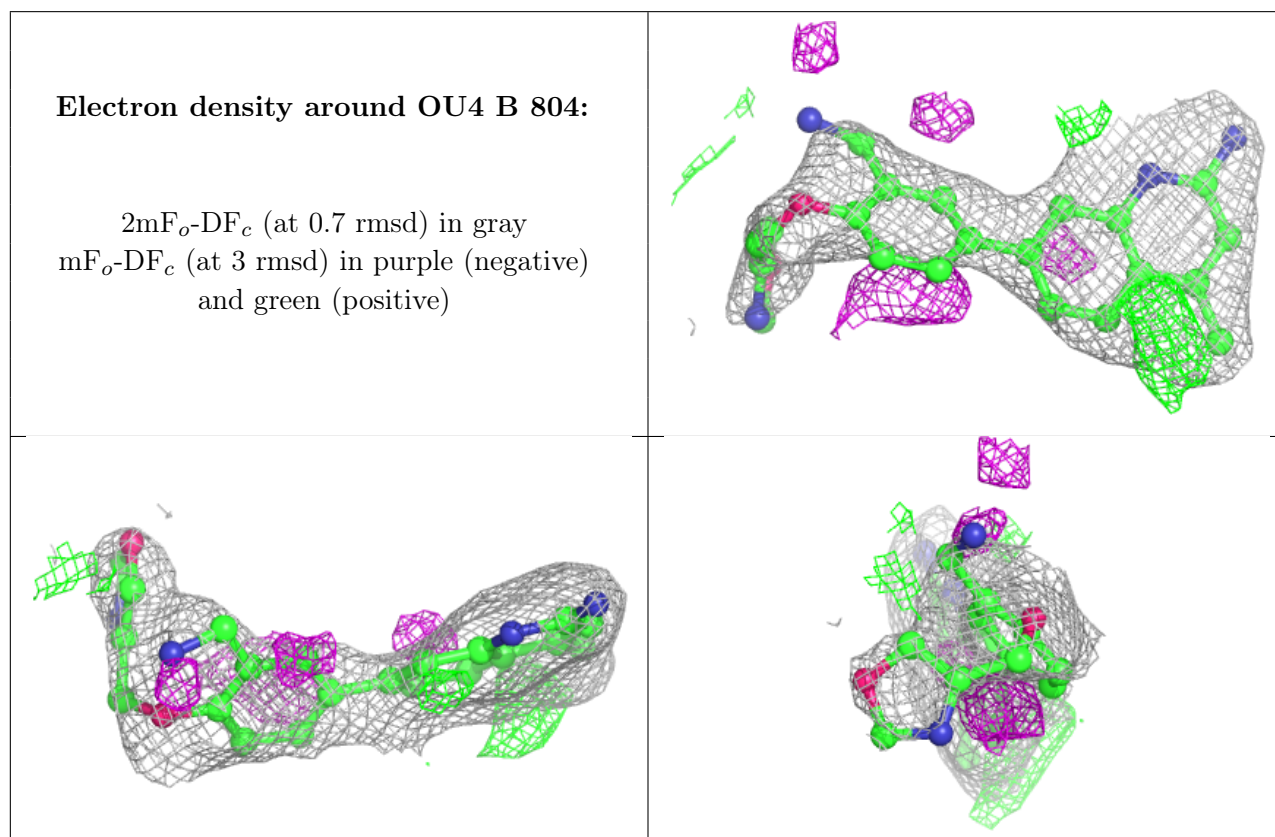
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	A	804	6/6	0.76	0.24	62,64,70,73	0
4	GOL	A	805	6/6	0.87	0.20	43,62,72,82	0
4	GOL	B	805	6/6	0.87	0.14	76,77,81,84	0
3	OU4	B	804	27/27	0.88	0.24	43,95,133,134	0

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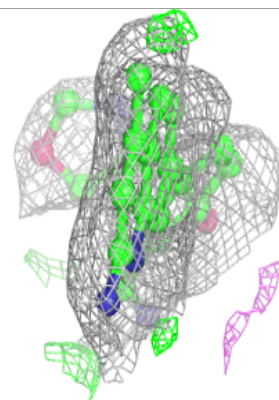
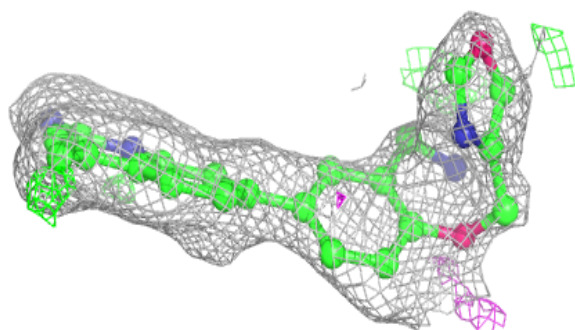
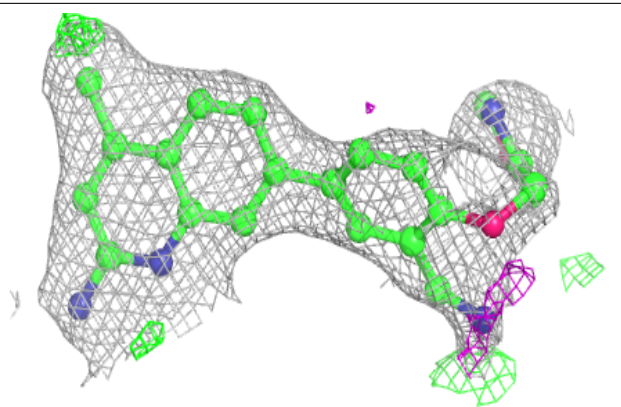
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	OU4	A	803	27/27	0.88	0.16	35,89,117,118	0
3	OU4	B	803	27/27	0.93	0.21	32,61,124,126	0
3	OU4	A	802	27/27	0.94	0.17	31,60,137,141	0
2	HEM	B	802	43/43	0.96	0.14	34,43,59,73	0
2	HEM	A	801	43/43	0.97	0.12	29,40,64,68	0
5	ZN	B	801	1/1	0.99	0.11	50,50,50,50	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.

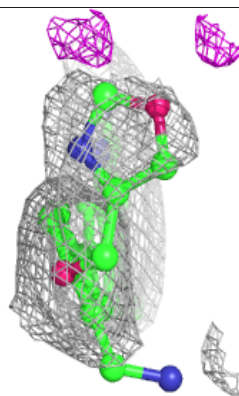
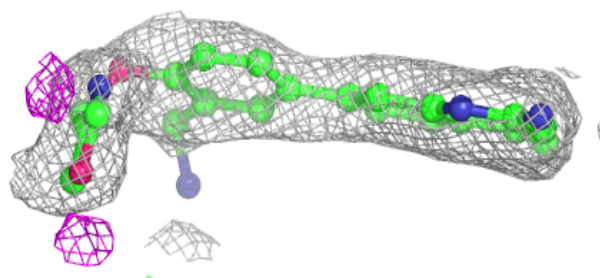
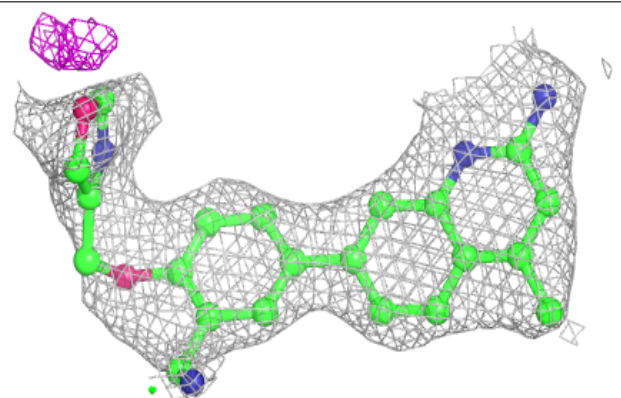


Electron density around OU4 A 803:

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

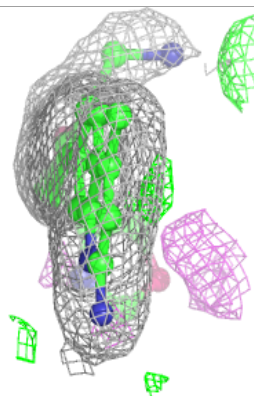
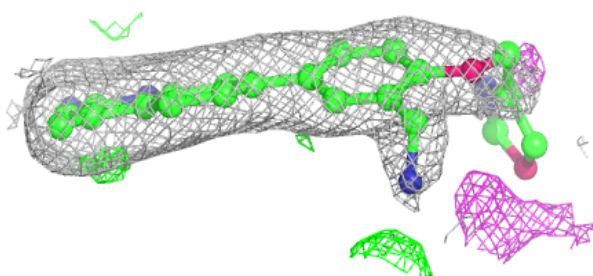
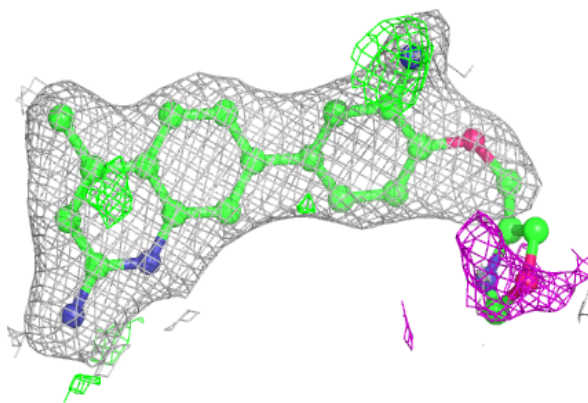
**Electron density around OU4 B 803:**

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



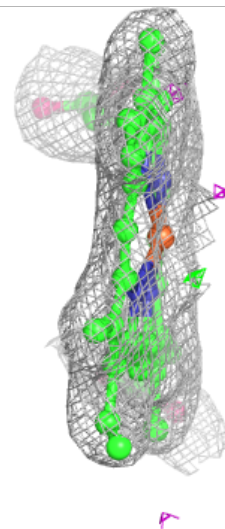
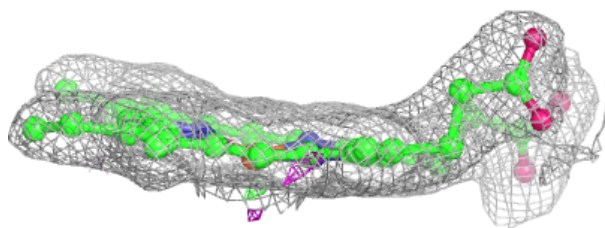
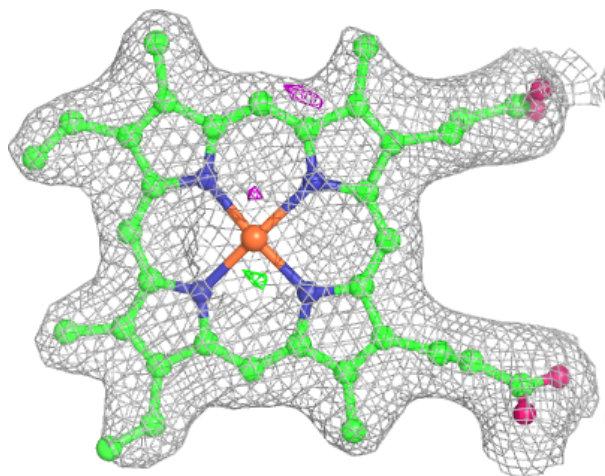
Electron density around OU4 A 802:

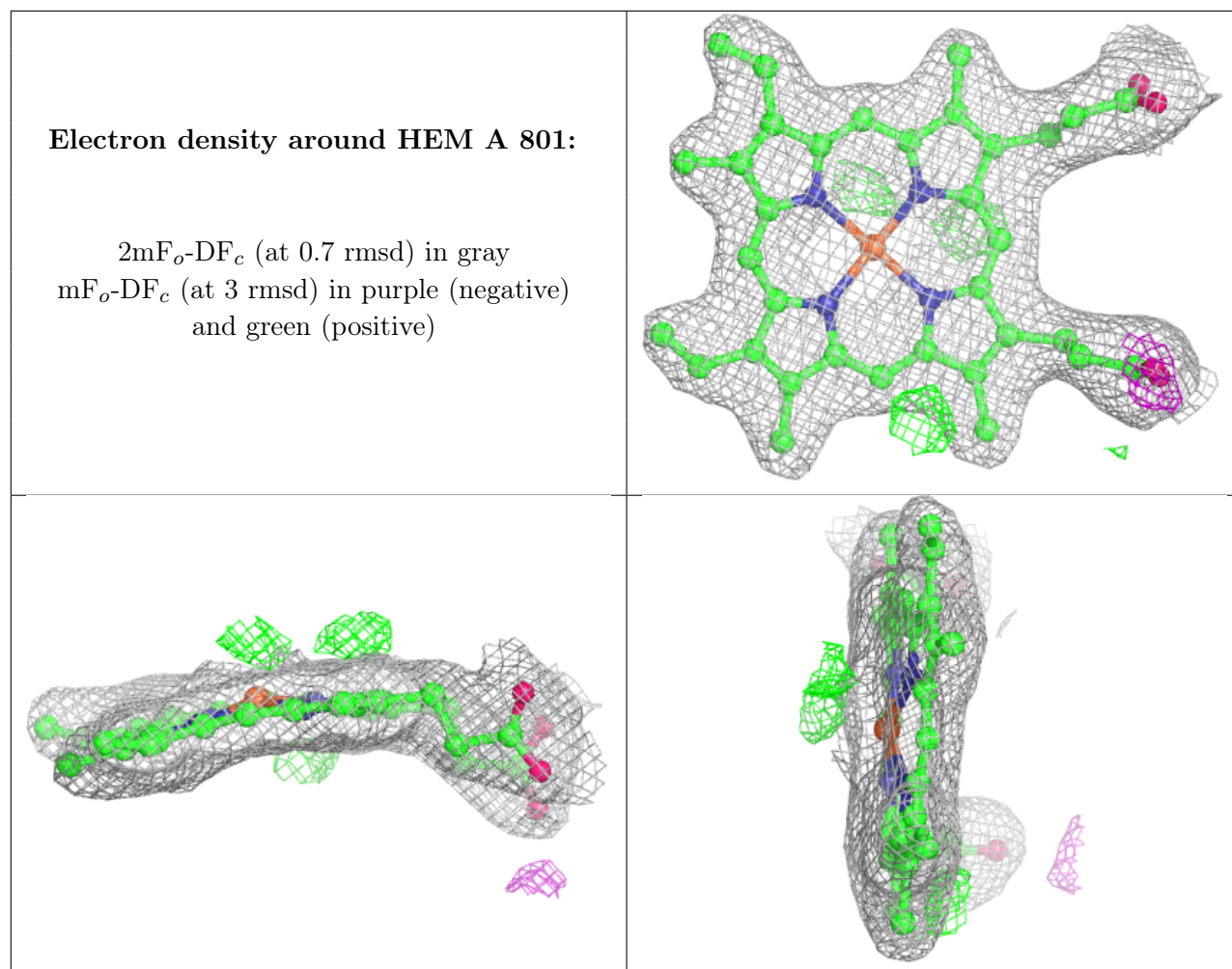
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 802:

$2mF_o-DF_c$ (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.