Full wwPDB X-ray Structure Validation Report (i)

Apr 30, 2024 – 08:42 pm BST

PDB ID	:	5ADD
Title	:	Structure of rat neuronal nitric oxide synthase d597n m336v mutant heme domain in complex with 7-((3-(methylamino)methyl) phenoxy)methyl)quinol in-2-amine
Authors	:	Li, H.; Poulos, T.L.
Deposited on	:	2015-08-20
Resolution	:	2.10 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 (i) 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 (i)) were used in the production of this report:

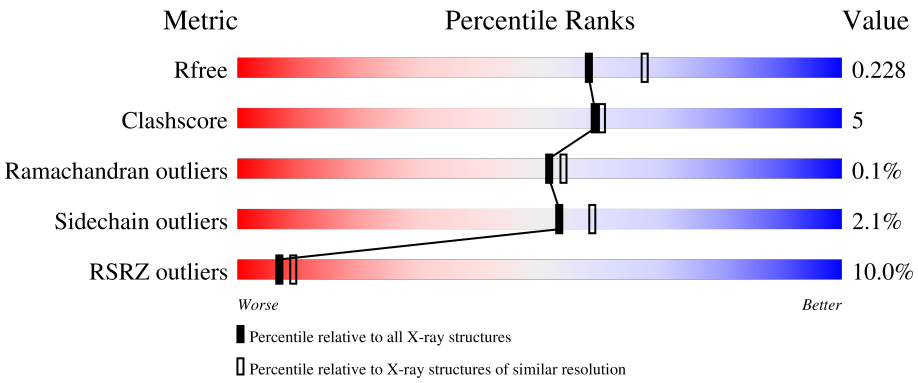
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	422	14% 82% 14% ·
1	B	422	5% 87% 10% ·

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7209 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.

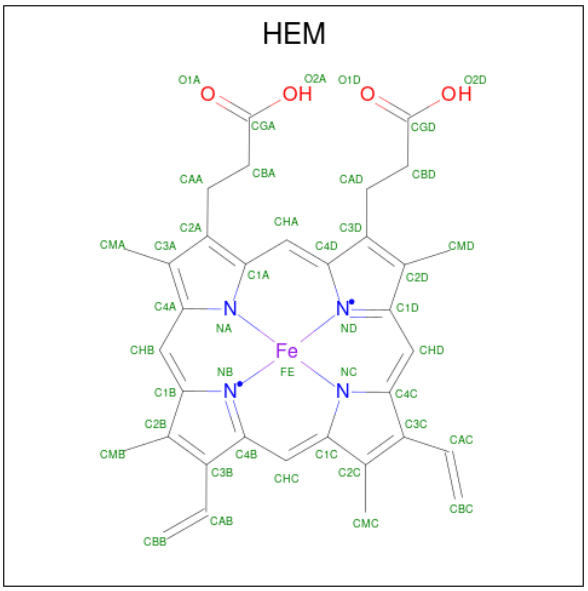
- Molecule 1 is a protein called NITRIC OXIDE SYNTHASE, BRAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	408	3326	2130	568	607	21	0	3	1
1	B	411	3356	2148	575	613	20	0	3	0

There are 4 discrepancies between the modelled and reference sequences:

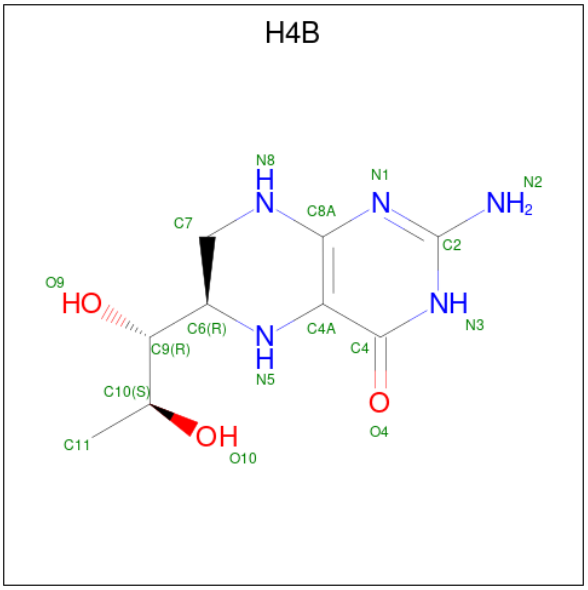
Chain	Residue	Modelled	Actual	Comment	Reference
A	336	VAL	MET	engineered mutation	UNP P29476
A	597	ASN	ASP	engineered mutation	UNP P29476
B	336	VAL	MET	engineered mutation	UNP P29476
B	597	ASN	ASP	engineered mutation	UNP P29476

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



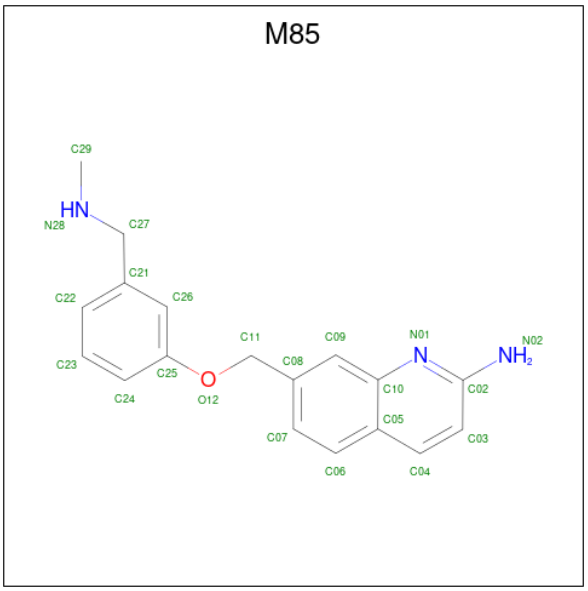
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	A	1	43	34	1	4	4	0	0
2	B	1	43	34	1	4	4	0	0

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).



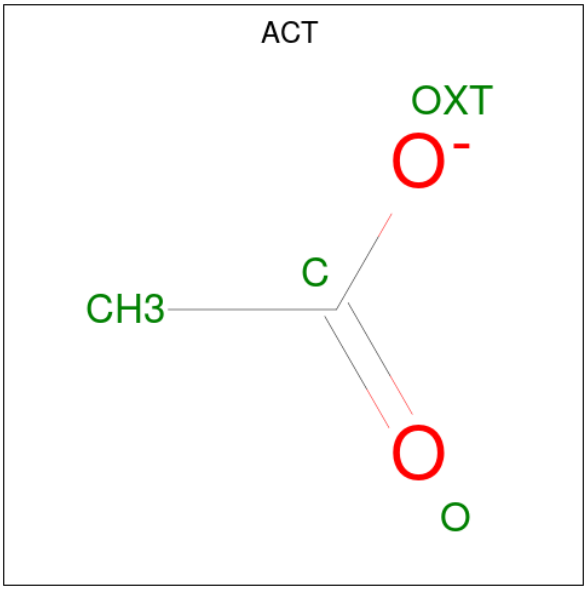
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	17	9	5	3	0	0
3	B	1	17	9	5	3	0	0

- Molecule 4 is 7-[[3-(methylaminomethyl)phenoxy]methyl]quinolin-2-amine (three-letter code: M85) (formula: $C_{18}H_{19}N_3O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	22	18	3	1	0	0
			Total	C	N	O		
4	B	1	22	18	3	1	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
6	A	1	1	1	0	0

- Molecule 7 is water.

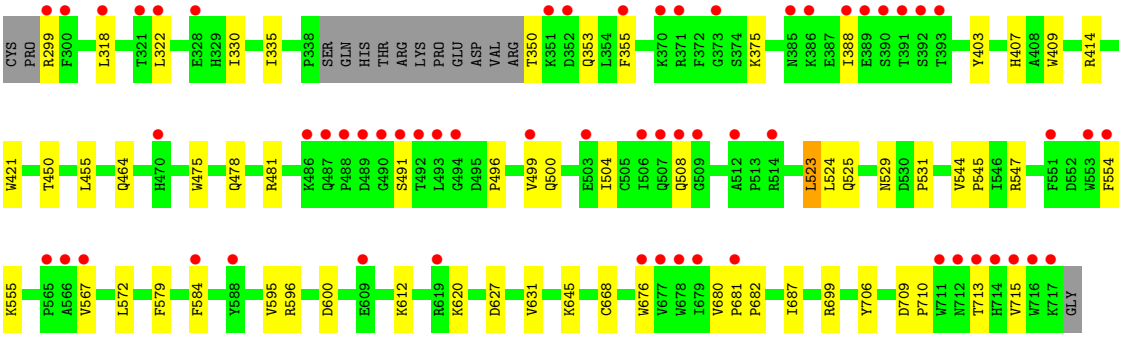
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	154	154	154	0	0
			Total	O		
7	B	200	200	200	0	0

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.

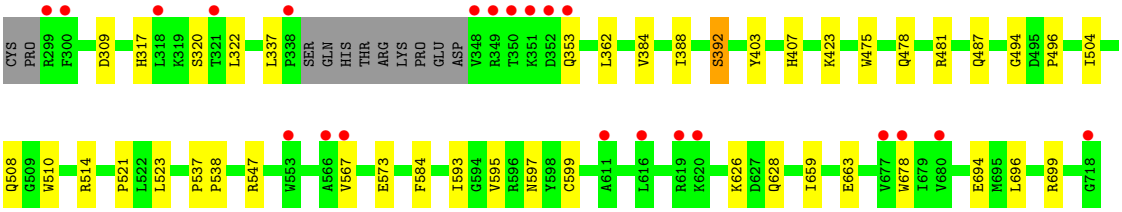
• Molecule 1: NITRIC OXIDE SYNTHASE, BRAIN

Chain A:



• Molecule 1: NITRIC OXIDE SYNTHASE, BRAIN

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	51.83Å 110.84Å 165.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.81 – 2.10 40.81 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.81-2.10) 99.6 (40.81-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.40 (at 2.10Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.187 , 0.231 0.184 , 0.228	Depositor DCC
R_{free} test set	2774 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	32.2	Xtriage
Anisotropy	0.753	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 56.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7209	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: H4B, HEM, ZN, ACT, M85

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	0.42	0/3428	0.53	0/4654
1	B	0.43	0/3458	0.52	0/4689
All	All	0.43	0/6886	0.52	0/9343

There are no bond length outliers.

There are no bond angle outliers.

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	3326	0	3241	41	0
1	B	3356	0	3277	23	0
2	A	43	0	30	3	0
2	B	43	0	30	2	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	22	0	19	2	0
4	B	22	0	19	3	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	154	0	0	2	0
7	B	200	0	0	0	0
All	All	7209	0	6652	63	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 (63) 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:523:LEU:HD22	1:A:531:PRO:HB2	1.58	0.82
2:B:750:HEM:HMC2	2:B:750:HEM:HBC2	1.71	0.72
2:B:750:HEM:HHC	2:B:750:HEM:HBB2	1.75	0.67
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.80	0.64
1:A:322:LEU:HD13	1:A:699:ARG:HH21	1.66	0.61
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.85	0.59
1:B:567:VAL:HG21	4:B:800:M85:C07	2.33	0.58
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.87	0.56
1:A:668[B]:CYS:SG	7:A:2136:HOH:O	2.58	0.56
1:A:567:VAL:HG21	4:A:800:M85:C07	2.38	0.53
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.90	0.53
1:A:350:THR:N	1:A:353:GLN:OE1	2.42	0.53
1:A:706:TYR:OH	2:A:750:HEM:O2D	2.21	0.52
1:A:322:LEU:HD13	1:A:699:ARG:NH2	2.26	0.51
1:A:687:ILE:HD12	1:B:626:LYS:HB3	1.92	0.51
1:A:322:LEU:HB2	1:A:699:ARG:HB2	1.93	0.51
1:A:475:TRP:CZ2	1:A:531:PRO:HG3	2.45	0.51
1:B:487:GLN:OE1	1:B:514:ARG:NH2	2.44	0.50
1:A:584:PHE:HE1	4:A:800:M85:H06	1.77	0.49
1:A:450:THR:HA	1:A:455:LEU:HD22	1.94	0.49
1:A:631:VAL:HG11	1:B:628:GLN:HG3	1.95	0.49
1:B:584:PHE:HE1	4:B:800:M85:H06	1.78	0.49
1:A:330:ILE:HD11	1:B:696:LEU:HB3	1.95	0.48
1:B:595:VAL:O	1:B:599:CYS:HB2	2.14	0.48
1:A:596:ARG:O	1:A:600:ASP:HB2	2.14	0.48
1:A:508:GLN:HE21	1:A:531:PRO:HG2	1.79	0.47
1:A:676:TRP:CE2	1:A:680:VAL:HG21	2.50	0.47
1:B:593:ILE:HA	1:B:597:ASN:HB2	1.97	0.46
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.97	0.46
1:B:403:TYR:CE2	1:B:407:HIS:CE1	3.03	0.46
1:A:525:GLN:HG3	1:A:529:ASN:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:ARG:NH1	1:A:706:TYR:OH	2.49	0.46
1:A:572:LEU:HB3	1:A:579:PHE:HB2	2.00	0.43
1:A:620:LYS:HB2	1:A:620:LYS:NZ	2.33	0.43
1:A:544:VAL:HA	1:A:545:PRO:HD2	1.91	0.43
1:A:627:ASP:O	1:A:631:VAL:HG23	2.19	0.42
1:B:475:TRP:HB2	1:B:523:LEU:HB3	2.01	0.42
1:A:464:GLN:HB3	1:A:579:PHE:CE1	2.55	0.42
1:A:496:PRO:HA	1:A:499:VAL:HG23	2.02	0.42
1:A:554:PHE:HB3	7:A:2103:HOH:O	2.19	0.42
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.01	0.42
1:A:676:TRP:CZ2	1:A:680:VAL:HG21	2.54	0.42
2:A:750:HEM:HMC1	2:A:750:HEM:HBC2	2.01	0.42
1:B:659:ILE:O	1:B:663:GLU:HG3	2.20	0.42
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.55	0.41
1:A:335:ILE:HD13	1:B:694:GLU:HB3	2.03	0.41
1:A:524:LEU:O	1:A:531:PRO:HA	2.20	0.41
1:B:494:GLY:O	1:B:496:PRO:HD3	2.21	0.41
1:A:299:ARG:HE	1:A:318:LEU:HD13	1.85	0.41
1:A:403:TYR:CE2	1:A:407:HIS:CE1	3.09	0.41
1:A:523:LEU:HD23	1:A:523:LEU:HA	1.86	0.41
1:A:595:VAL:HG11	1:A:682:PRO:HB2	2.03	0.41
1:A:709:ASP:HA	1:A:710:PRO:HD3	1.88	0.41
1:B:322:LEU:HD13	1:B:699:ARG:NH2	2.35	0.41
1:A:355:PHE:HD1	1:A:388:ILE:HD12	1.85	0.41
1:B:317:HIS:O	1:B:320:SER:HB3	2.20	0.41
1:A:680:VAL:HA	1:A:681:PRO:HD3	1.93	0.40
1:B:510:TRP:CE2	1:B:521:PRO:HD3	2.56	0.40
1:B:678:TRP:HH2	4:B:800:M85:HN28	1.69	0.40
1:B:388:ILE:O	1:B:392:SER:N	2.51	0.40
1:B:504:ILE:O	1:B:508:GLN:HG2	2.21	0.40
1:A:500:GLN:O	1:A:504:ILE:HG13	2.21	0.40
1:B:537:PRO:HA	1:B:538:PRO:HD3	1.97	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	407/422 (96%)	388 (95%)	18 (4%)	1 (0%)	47	49
1	B	410/422 (97%)	404 (98%)	6 (2%)	0	100	100
All	All	817/844 (97%)	792 (97%)	24 (3%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	491	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	366/377 (97%)	358 (98%)	8 (2%)	52	57
1	B	369/377 (98%)	362 (98%)	7 (2%)	57	63
All	All	735/754 (98%)	720 (98%)	15 (2%)	53	60

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	375	LYS
1	A	523	LEU
1	A	547	ARG
1	A	555	LYS
1	A	612	LYS
1	A	645	LYS
1	A	713	THR
1	A	715	VAL
1	B	309	ASP
1	B	337	LEU
1	B	353	GLN

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Mol	Chain	Res	Type
1	B	392	SER
1	B	423	LYS
1	B	547	ARG
1	B	573	GLU

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

Mol	Chain	Res	Type
1	A	508	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	ACT	A	860	-	3,3,3	0.77	0	3,3,3	0.73	0
3	H4B	A	760	-	16,18,18	0.92	0	11,26,26	2.52	5 (45%)
5	ACT	B	860	-	3,3,3	0.68	0	3,3,3	1.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	H4B	B	760	-	16,18,18	1.12	1 (6%)	11,26,26	2.38	5 (45%)
4	M85	B	800	-	24,24,24	0.89	0	30,32,32	1.06	1 (3%)
2	HEM	A	750	1	41,50,50	2.03	8 (19%)	45,82,82	2.30	13 (28%)
4	M85	A	800	-	24,24,24	0.91	0	30,32,32	0.97	1 (3%)
2	HEM	B	750	1	41,50,50	2.02	8 (19%)	45,82,82	1.96	11 (24%)

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
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
4	M85	B	800	-	-	0/7/8/8	0/3/3/3
2	HEM	A	750	1	-	3/12/54/54	-
4	M85	A	800	-	-	0/7/8/8	0/3/3/3
2	HEM	B	750	1	-	4/12/54/54	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	750	HEM	C3D-C2D	8.03	1.53	1.36
2	A	750	HEM	C3D-C2D	7.94	1.53	1.36
2	B	750	HEM	C3C-CAC	3.90	1.55	1.47
2	A	750	HEM	C3C-CAC	3.83	1.55	1.47
2	A	750	HEM	FE-NB	3.59	2.14	1.96
2	B	750	HEM	C3C-C2C	-3.48	1.35	1.40
2	A	750	HEM	C3C-C2C	-3.14	1.36	1.40
2	B	750	HEM	FE-NB	3.14	2.12	1.96
2	A	750	HEM	FE-ND	3.12	2.12	1.96
2	A	750	HEM	CAB-C3B	3.08	1.55	1.47
2	B	750	HEM	CAB-C3B	3.02	1.55	1.47
2	B	750	HEM	CMD-C2D	2.71	1.56	1.50
2	B	750	HEM	CMB-C2B	2.60	1.56	1.50
2	B	750	HEM	FE-ND	2.54	2.09	1.96
2	A	750	HEM	CMD-C2D	2.23	1.55	1.50
3	B	760	H4B	C4-N3	2.15	1.36	1.33
2	A	750	HEM	CMB-C2B	2.12	1.55	1.50

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	750	HEM	C4D-ND-C1D	7.26	112.58	105.07
2	A	750	HEM	CBA-CAA-C2A	-7.24	100.27	112.62
2	B	750	HEM	C4D-ND-C1D	6.41	111.70	105.07
3	B	760	H4B	C8A-C4A-C4	5.40	119.36	114.57
2	B	750	HEM	CBA-CAA-C2A	-4.95	104.17	112.62
3	A	760	H4B	C8A-C4A-C4	4.82	118.85	114.57
2	A	750	HEM	C4C-CHD-C1D	3.99	127.82	122.56
2	B	750	HEM	C4B-CHC-C1C	3.94	127.76	122.56
3	A	760	H4B	N1-C2-N3	-3.62	119.74	125.42
2	A	750	HEM	C4B-CHC-C1C	3.48	127.16	122.56
2	A	750	HEM	CMD-C2D-C1D	3.44	130.28	125.04
2	A	750	HEM	CAD-CBD-CGD	-3.41	106.26	113.60
2	A	750	HEM	C1B-NB-C4B	3.18	108.36	105.07
3	A	760	H4B	C2-N3-C4	3.16	120.94	115.93
2	B	750	HEM	C4C-CHD-C1D	3.10	126.65	122.56
3	A	760	H4B	C2-N1-C8A	3.06	121.39	114.54
3	B	760	H4B	N1-C2-N3	-3.03	120.67	125.42
2	B	750	HEM	CAD-CBD-CGD	-2.95	107.26	113.60
2	A	750	HEM	C3B-C2B-C1B	2.85	108.60	106.49
2	B	750	HEM	CMD-C2D-C1D	2.85	129.37	125.04
3	B	760	H4B	C2-N1-C8A	2.71	120.60	114.54
2	B	750	HEM	C1D-C2D-C3D	-2.56	104.26	106.96
2	A	750	HEM	CHC-C4B-C3B	2.56	128.49	124.57
2	B	750	HEM	CHC-C4B-C3B	2.56	128.48	124.57
4	A	800	M85	C11-O12-C25	2.41	123.61	117.65
2	B	750	HEM	C1B-NB-C4B	2.35	107.50	105.07
2	A	750	HEM	C3D-C4D-ND	-2.35	107.56	110.17
3	B	760	H4B	C2-N3-C4	2.32	119.61	115.93
2	A	750	HEM	C2C-C3C-C4C	2.27	108.48	106.90
2	A	750	HEM	CHA-C4D-ND	2.26	127.17	124.38
3	A	760	H4B	N2-C2-N1	2.25	120.76	117.25
2	B	750	HEM	C3D-C4D-ND	-2.14	107.79	110.17
4	B	800	M85	C11-O12-C25	2.04	122.69	117.65
2	A	750	HEM	C3C-C4C-NC	-2.03	107.11	110.94
2	B	750	HEM	CHA-C4D-ND	2.02	126.88	124.38
3	B	760	H4B	N2-C2-N1	2.00	120.37	117.25

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	750	HEM	C4B-C3B-CAB-CBB
2	B	750	HEM	C4B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
2	A	750	HEM	CAD-CBD-CGD-O1D
2	A	750	HEM	CAD-CBD-CGD-O2D
2	B	750	HEM	CAA-CBA-CGA-O2A
2	B	750	HEM	CAA-CBA-CGA-O1A
2	B	750	HEM	CAD-CBD-CGD-O1D

There are no ring outliers.

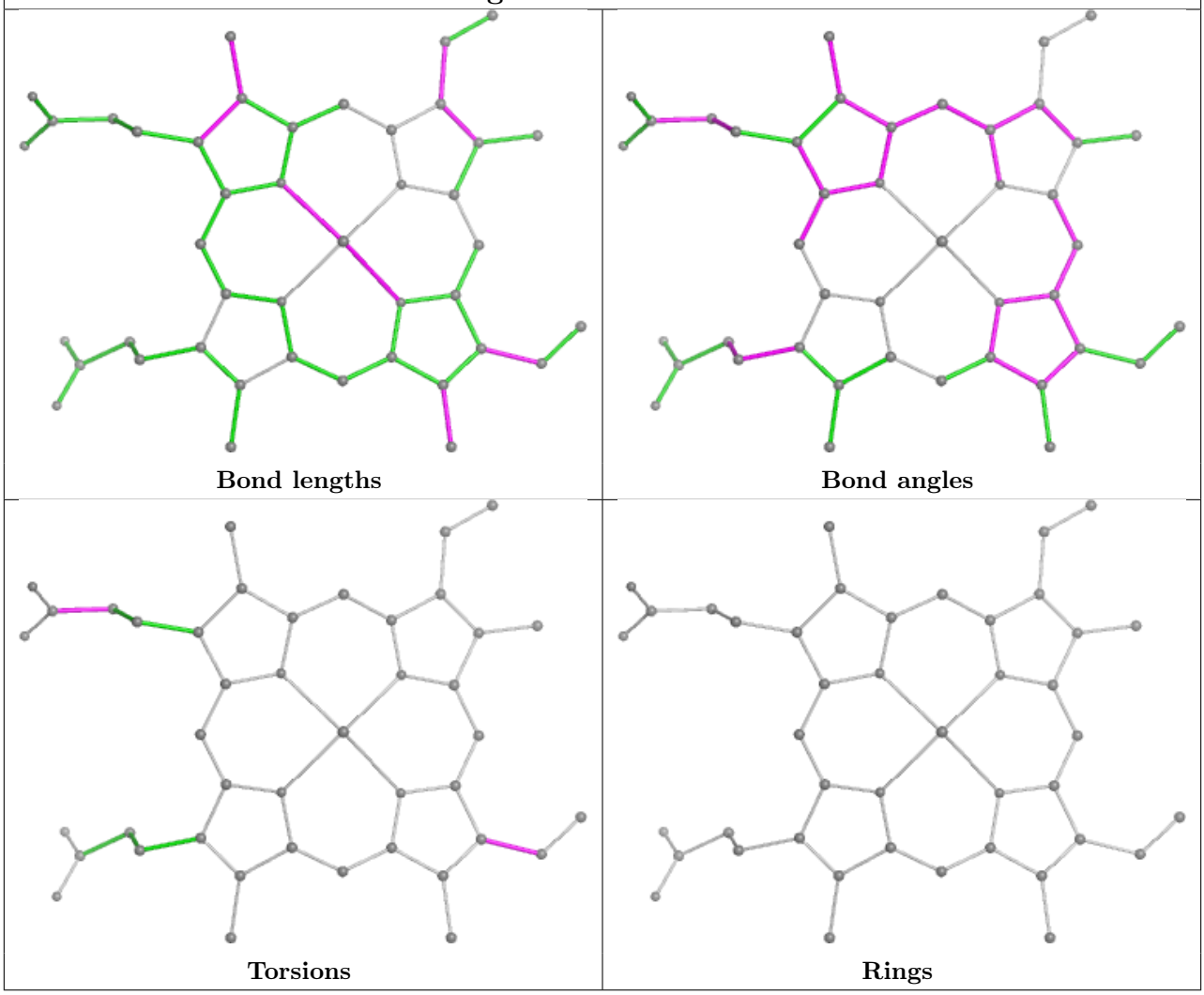
4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	800	M85	3	0
2	A	750	HEM	3	0
4	A	800	M85	2	0
2	B	750	HEM	2	0

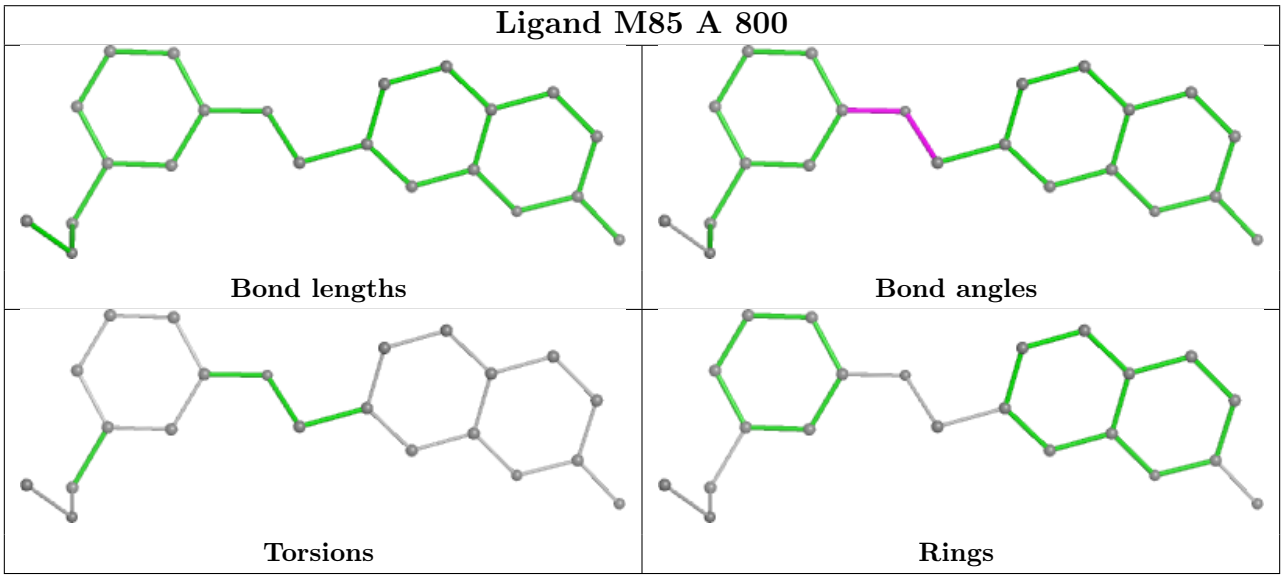
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

Ligand M85 B 800

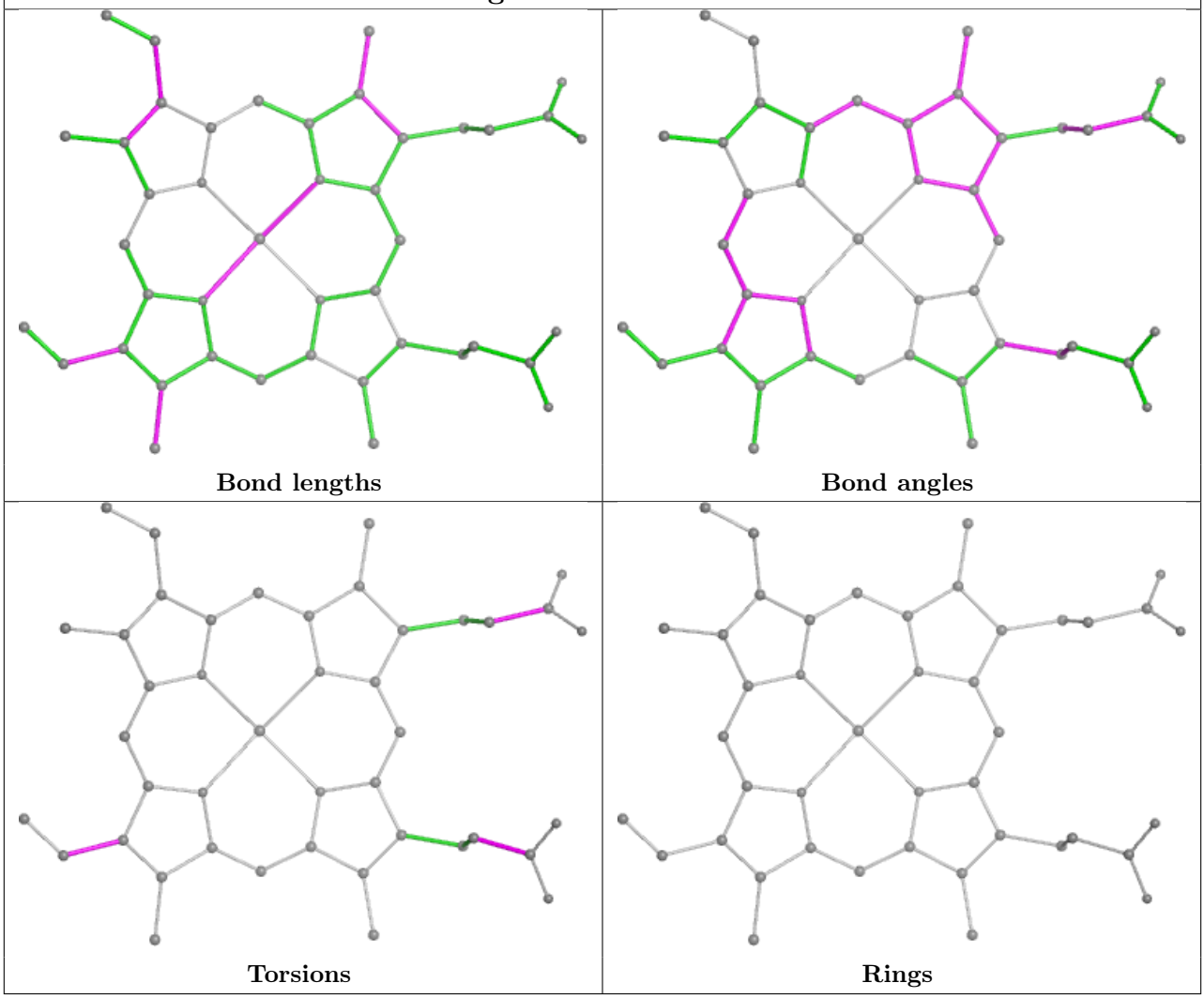
Ligand HEM A 750



Ligand M85 A 800



Ligand HEM B 750



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	408/422 (96%)	0.84	60 (14%) 2 3	25, 51, 97, 148	0
1	B	411/422 (97%)	0.35	22 (5%) 25 31	24, 42, 74, 119	0
All	All	819/844 (97%)	0.59	82 (10%) 7 9	24, 45, 92, 148	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	717	LYS	12.8
1	A	715	VAL	8.5
1	B	350	THR	7.8
1	B	348	VAL	7.6
1	A	716	TRP	7.4
1	B	300	PHE	6.0
1	B	718	GLY	5.9
1	A	352	ASP	5.5
1	A	488	PRO	5.4
1	A	714	HIS	4.6
1	A	507	GLN	4.4
1	A	388	ILE	4.3
1	B	352	ASP	3.9
1	A	355	PHE	3.8
1	A	551	PHE	3.8
1	B	619	ARG	3.8
1	A	712	ASN	3.7
1	A	713	THR	3.7
1	A	390	SER	3.7
1	A	300	PHE	3.7
1	A	486	LYS	3.6
1	A	711	TRP	3.6
1	A	489	ASP	3.5
1	A	503	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	318	LEU	3.3
1	A	553	TRP	3.3
1	B	349	ARG	3.2
1	A	373	GLY	3.1
1	A	508	GLN	3.1
1	A	491	SER	3.1
1	A	391	THR	3.0
1	B	299	ARG	3.0
1	A	389	GLU	3.0
1	A	678	TRP	2.9
1	A	493	LEU	2.9
1	A	554	PHE	2.9
1	A	567	VAL	2.8
1	A	499	VAL	2.8
1	B	351	LYS	2.8
1	B	616	LEU	2.8
1	A	506	ILE	2.7
1	A	393	THR	2.7
1	A	386	LYS	2.7
1	A	299	ARG	2.7
1	A	514	ARG	2.7
1	A	490	GLY	2.7
1	B	321	THR	2.7
1	B	677	VAL	2.7
1	A	487	GLN	2.6
1	A	584	PHE	2.6
1	A	392	SER	2.5
1	A	492	THR	2.5
1	A	512	ALA	2.5
1	A	351	LYS	2.5
1	A	318	LEU	2.4
1	A	679	ILE	2.4
1	A	566	ALA	2.4
1	A	370	LYS	2.4
1	A	677	VAL	2.3
1	A	565	PRO	2.3
1	A	385	ASN	2.3
1	A	588	TYR	2.2
1	B	620	LYS	2.2
1	A	609	GLU	2.2
1	A	321	THR	2.2
1	B	567	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	371	ARG	2.2
1	A	619	ARG	2.2
1	B	566	ALA	2.2
1	B	553	TRP	2.2
1	B	680	VAL	2.2
1	A	509	GLY	2.2
1	B	353	GLN	2.2
1	A	470	HIS	2.2
1	A	328	GLU	2.2
1	B	611	ALA	2.2
1	A	676	TRP	2.1
1	B	338	PRO	2.1
1	B	678	TRP	2.1
1	A	681	PRO	2.0
1	A	322	LEU	2.0
1	A	494	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
5	ACT	A	860	4/4	0.87	0.21	57,61,62,63	0
4	M85	B	800	22/22	0.88	0.26	29,50,80,83	0
3	H4B	A	760	17/17	0.92	0.18	24,37,43,49	0
4	M85	A	800	22/22	0.93	0.24	32,45,82,83	0
3	H4B	B	760	17/17	0.94	0.18	26,37,47,50	0
5	ACT	B	860	4/4	0.94	0.15	50,58,59,62	0
2	HEM	B	750	43/43	0.97	0.18	19,32,48,59	0

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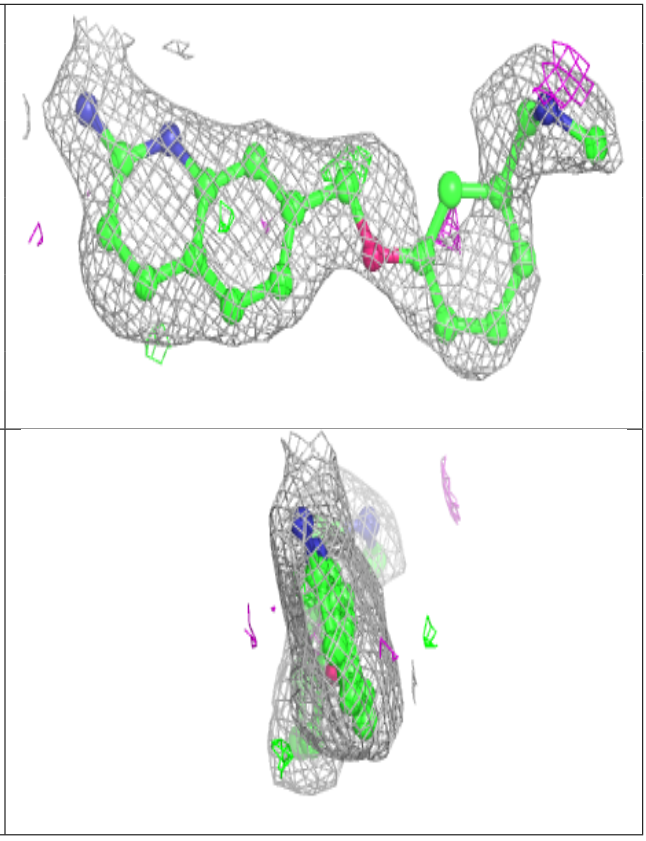
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	HEM	A	750	43/43	0.98	0.20	23,35,54,56	0
6	ZN	A	1717	1/1	1.00	0.10	36,36,36,36	0

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.

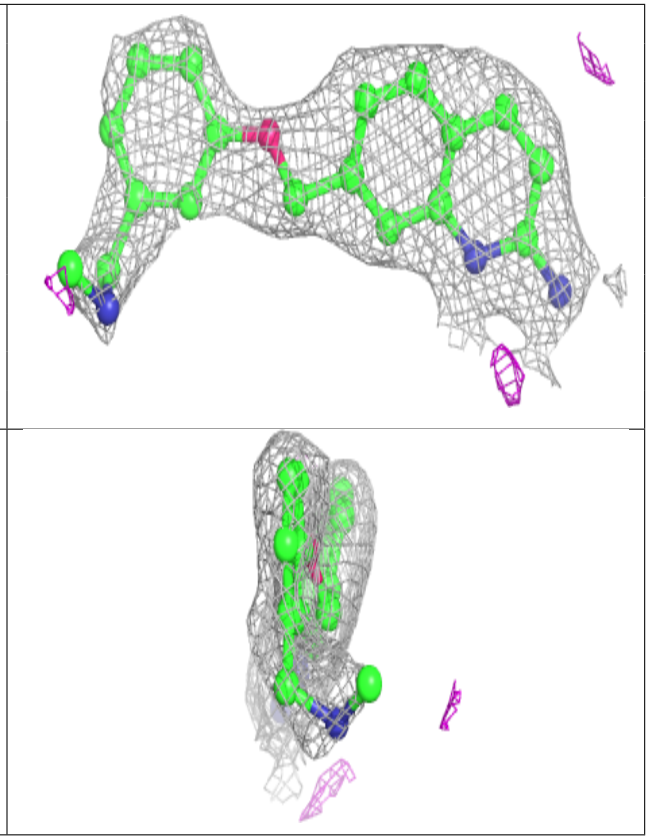
Electron density around M85 B 800:

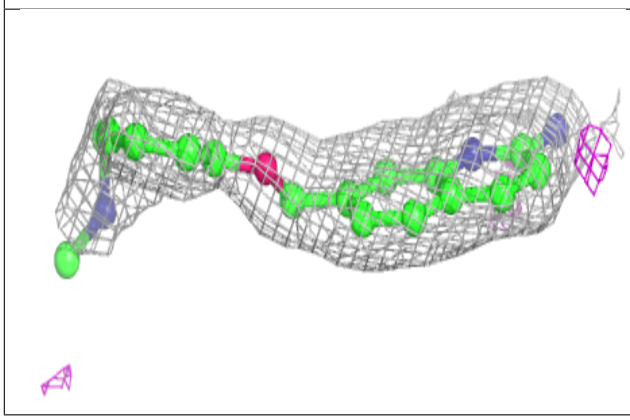
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



Electron density around M85 A 800:

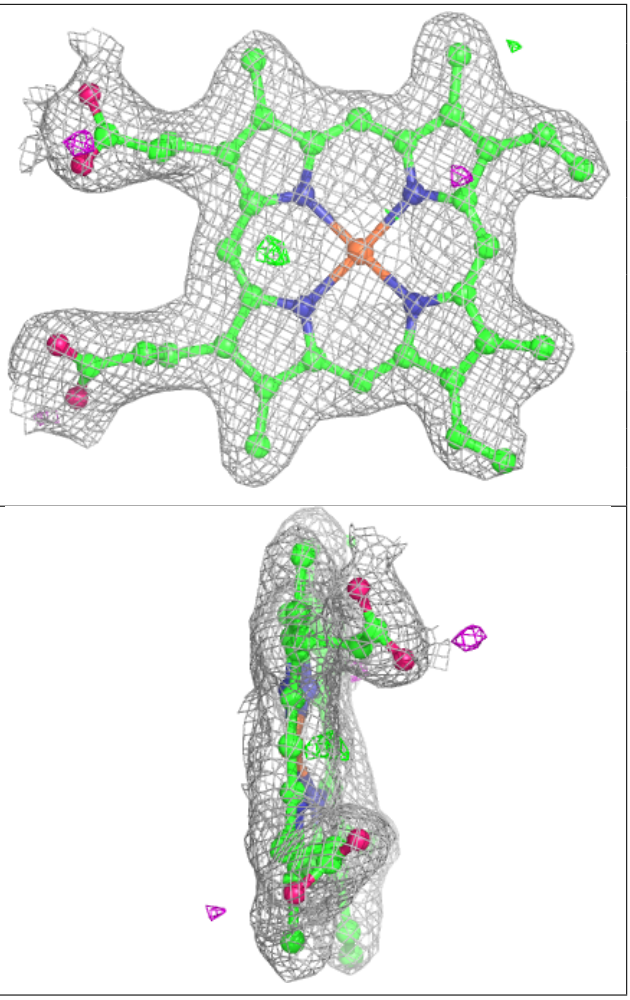
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





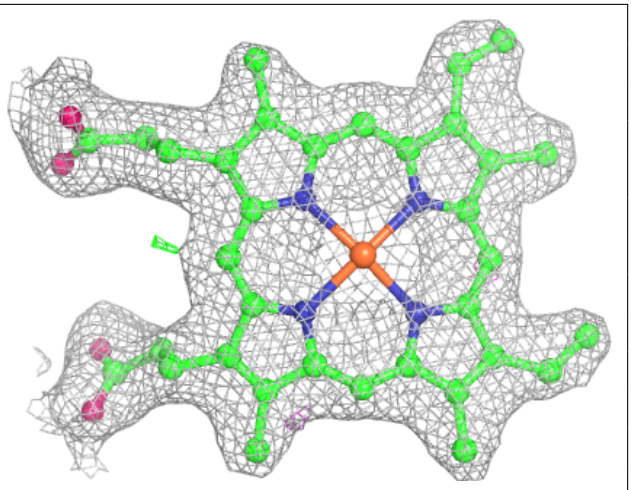
Electron density around HEM B 750:

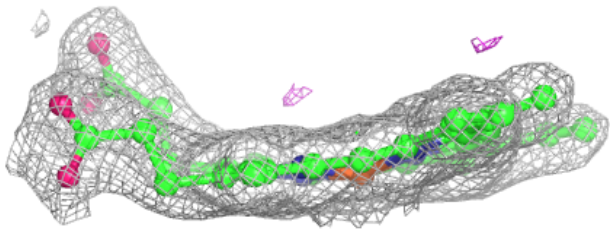
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

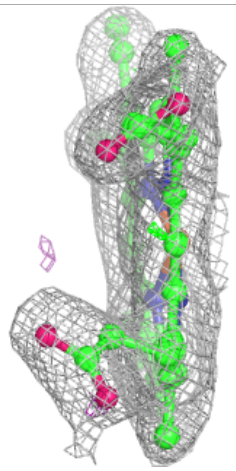


Electron density around HEM A 750:

$2mF_o$-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.