



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:48 AM UTC

PDB ID : 5AD6 / pdb_00005ad6
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with
7-((3-(Dimethylamino)methyl)phenoxy)methyl)quinolin-2- amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2015-08-20
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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
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

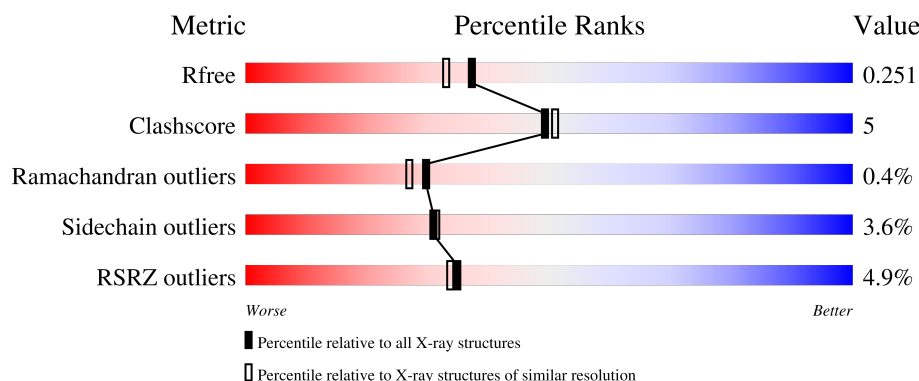
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

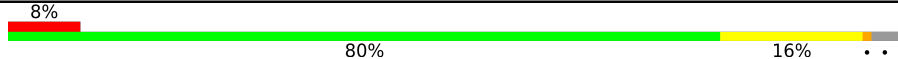
The reported resolution of this entry is 2.00 Å.

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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

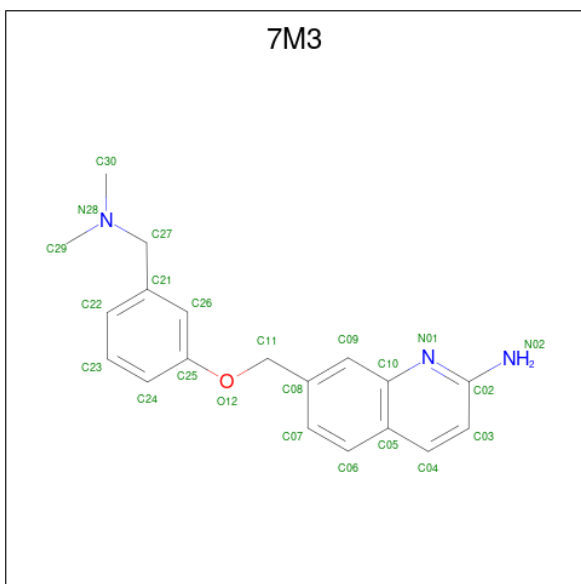
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	422	
1	B	422	



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

- Molecule 4 is 7-[[3-[(dimethylamino)methyl]phenoxy]methyl]quinolin-2-amine (CCD ID: 7M3) (formula: C₁₉H₂₁N₃O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			23	19	3	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			23	19	3	1		

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

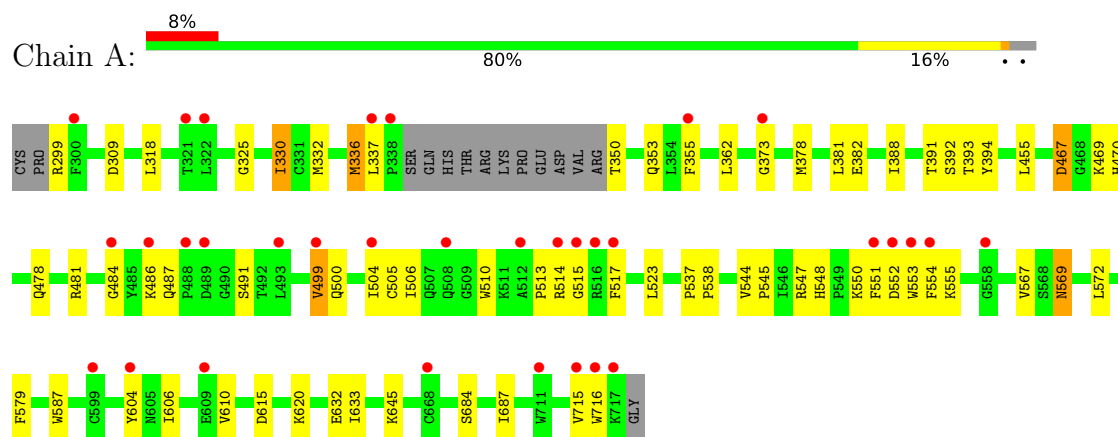
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	199	Total	O	0	0
			199	199		
7	B	235	Total	O	0	0
			235	235		

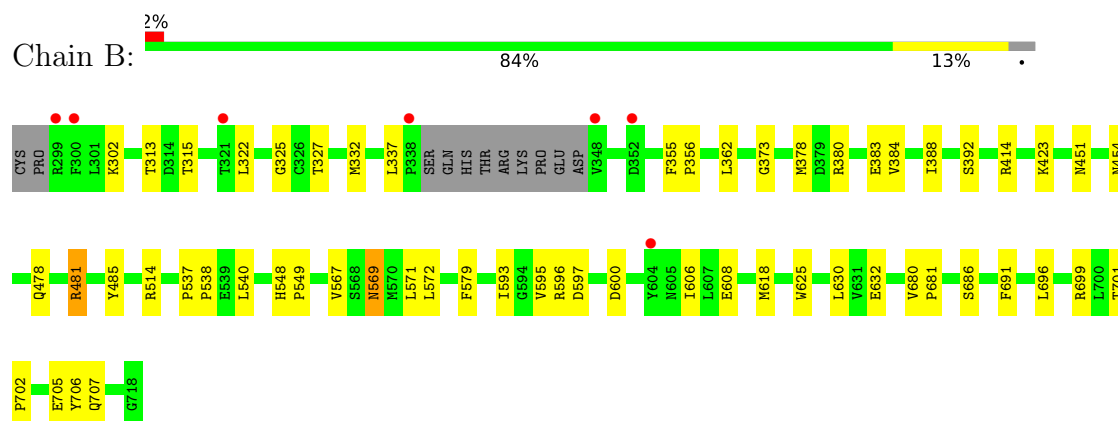
3 Residue-property plots [i](#)

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	51.76Å 111.67Å 164.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.16 – 2.00 39.16 – 2.00	Depositor EDS
% Data completeness (in resolution range)	78.3 (39.16-2.00) 78.3 (39.16-2.00)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 2.00Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.192 , 0.251 0.193 , 0.251	Depositor DCC
R_{free} test set	2487 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7286	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, 7M3, H4B, HEM, 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	0.48	1/3422 (0.0%)	0.85	0/4643
1	B	0.52	0/3453	0.84	0/4681
All	All	0.50	1/6875 (0.0%)	0.84	0/9324

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	716	TRP	C-N	-6.93	1.23	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3323	0	3232	34	0
1	B	3354	0	3270	34	0
2	A	43	0	30	2	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	23	0	21	1	0
4	B	23	0	21	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	B	1	0	0	0	0
7	A	199	0	0	0	0
7	B	235	0	0	2	0
All	All	7286	0	6640	73	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 (73) 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)
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.67	0.76
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.71	0.72
2:B:750:HEM:HHC	2:B:750:HEM:HBB2	1.73	0.70
1:B:699:ARG:NH2	1:B:705:GLU:OE1	2.28	0.66
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.79	0.65
4:B:800:7M3:H07	4:B:800:7M3:H24	1.80	0.64
1:A:373:GLY:HA2	1:A:378:MET:HE3	1.80	0.63
2:B:750:HEM:HMC2	2:B:750:HEM:HBC2	1.83	0.61
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.83	0.60
1:A:567:VAL:HG21	4:A:800:7M3:C07	2.32	0.60
1:B:593:ILE:HA	1:B:597:ASP:HB2	1.86	0.58
1:A:569:ASN:HD22	1:A:569:ASN:H	1.51	0.56
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.88	0.56
1:A:355:PHE:HD1	1:A:388:ILE:HD12	1.75	0.52
1:A:545:PRO:HG2	1:A:547:ARG:NH1	2.25	0.52
1:B:569:ASN:H	1:B:569:ASN:HD22	1.58	0.52
1:A:486:LYS:HE2	1:A:499:VAL:HG11	1.93	0.51
1:B:325:GLY:O	1:B:332:MET:HG3	2.12	0.50
1:B:322:LEU:HB2	1:B:699:ARG:HB2	1.95	0.49
1:B:388:ILE:O	1:B:392:SER:N	2.42	0.49
1:B:485:TYR:CZ	1:B:514:ARG:HA	2.49	0.48
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.96	0.48
1:A:606:ILE:O	1:A:610:VAL:HG23	2.14	0.47
1:A:325:GLY:O	1:A:332:MET:HG3	2.13	0.47
1:A:500:GLN:O	1:A:504:ILE:HG13	2.14	0.47
1:B:380:ARG:NH1	1:B:383:GLU:OE1	2.41	0.47
1:A:391:THR:O	1:A:392:SER:OG	2.29	0.47
1:A:572:LEU:HB3	1:A:579:PHE:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:706:TYR:OH	2:B:750:HEM:O1D	2.29	0.46
1:A:469:LYS:HE3	1:A:470:HIS:HE1	1.80	0.46
1:A:393:THR:OG1	1:A:394:TYR:N	2.48	0.46
1:B:686:SER:HA	1:B:691:PHE:CG	2.51	0.46
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.49	0.46
1:B:606:ILE:HA	7:B:2203:HOH:O	2.16	0.46
1:B:572:LEU:HB3	1:B:579:PHE:HB2	1.97	0.45
1:B:548:HIS:CG	1:B:549:PRO:HD2	2.51	0.45
1:B:596:ARG:O	1:B:600:ASP:HB2	2.16	0.45
1:A:505:CYS:O	1:A:510:TRP:N	2.43	0.45
1:A:299:ARG:HG2	1:A:318:LEU:HD11	1.99	0.45
1:B:414:ARG:NH1	1:B:706:TYR:OH	2.49	0.45
1:A:517:PHE:HE1	1:A:604:TYR:CZ	2.36	0.44
1:B:302:LYS:HE3	1:B:302:LYS:HB2	1.42	0.44
1:B:567:VAL:HG21	4:B:800:7M3:C07	2.47	0.44
1:A:484:GLY:O	1:A:499:VAL:HA	2.18	0.44
1:A:469:LYS:HE3	1:A:470:HIS:CE1	2.52	0.44
1:A:610:VAL:HG21	1:A:633:ILE:HD11	1.98	0.44
1:A:513:PRO:O	1:A:515:GLY:N	2.50	0.44
1:A:548:HIS:NE2	1:A:632:GLU:OE1	2.47	0.44
1:B:595:VAL:HG13	1:B:630:LEU:HD11	2.00	0.43
1:B:680:VAL:HA	1:B:681:PRO:HD3	1.89	0.43
1:B:355:PHE:N	1:B:356:PRO:HD2	2.33	0.43
1:A:350:THR:N	1:A:353:GLN:OE1	2.52	0.43
1:A:569:ASN:HD22	1:A:569:ASN:N	2.14	0.43
1:B:618:MET:HA	1:B:625:TRP:CD1	2.53	0.43
1:A:548:HIS:HB2	1:A:554:PHE:CG	2.54	0.43
1:B:537:PRO:HA	1:B:538:PRO:HD3	1.88	0.43
1:B:569:ASN:HD21	4:B:800:7M3:C22	2.31	0.42
1:B:569:ASN:HD21	4:B:800:7M3:C23	2.32	0.42
1:A:362:LEU:HD23	1:A:362:LEU:HA	1.85	0.42
1:A:684:SER:HB3	1:A:687:ILE:HD11	2.02	0.42
1:B:608:GLU:HB2	7:B:2202:HOH:O	2.20	0.42
1:B:569:ASN:HD22	1:B:569:ASN:N	2.18	0.41
1:A:537:PRO:HA	1:A:538:PRO:HD3	1.86	0.41
1:B:571:LEU:HD12	1:B:707:GLN:OE1	2.19	0.41
1:A:467:ASP:OD1	1:A:467:ASP:N	2.54	0.41
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.02	0.41
1:B:701:THR:HA	1:B:702:PRO:C	2.45	0.41
1:A:336:MET:HE2	1:A:336:MET:HB3	1.70	0.41
1:B:373:GLY:HA2	1:B:378:MET:HE3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:451:ASN:HB3	1:B:454:ASN:O	2.21	0.40
1:A:544:VAL:HA	1:A:545:PRO:HD2	1.89	0.40
1:A:551:PHE:HB3	1:A:553:TRP:CE2	2.57	0.40
2:B:750:HEM:HBA2	4:B:800:7M3:H111	2.04	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	406/422 (96%)	382 (94%)	21 (5%)	3 (1%)	18	14
1	B	409/422 (97%)	395 (97%)	14 (3%)	0	100	100
All	All	815/844 (97%)	777 (95%)	35 (4%)	3 (0%)	30	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	514	ARG
1	A	491	SER
1	A	309	ASP

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	365/377 (97%)	347 (95%)	18 (5%)	22	20
1	B	368/377 (98%)	360 (98%)	8 (2%)	45	50
All	All	733/754 (97%)	707 (96%)	26 (4%)	31	32

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	330	ILE
1	A	336	MET
1	A	337	LEU
1	A	381	LEU
1	A	382	GLU
1	A	467	ASP
1	A	487	GLN
1	A	499	VAL
1	A	506	ILE
1	A	523	LEU
1	A	550	LYS
1	A	552	ASP
1	A	555	LYS
1	A	569	ASN
1	A	615	ASP
1	A	620	LYS
1	A	645	LYS
1	A	715	VAL
1	B	313	THR
1	B	315	THR
1	B	327	THR
1	B	337	LEU
1	B	423	LYS
1	B	481	ARG
1	B	540	LEU
1	B	569	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	385	ASN
1	A	440	ASN
1	A	478	GLN
1	A	500	GLN

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Mol	Chain	Res	Type
1	A	569	ASN
1	A	601	ASN
1	B	364	GLN
1	B	395	GLN
1	B	478	GLN
1	B	507	GLN
1	B	569	ASN
1	B	664	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
2	HEM	B	750	1	50,50,50	2.03	11 (22%)	67,82,82	1.33	7 (10%)
5	ACT	B	860	-	3,3,3	0.78	0	3,3,3	0.92	0
3	H4B	A	760	-	17,18,18	0.74	0	14,26,26	1.95	5 (35%)
3	H4B	B	760	-	17,18,18	0.82	0	14,26,26	1.95	5 (35%)
4	7M3	A	800	-	25,25,25	1.00	1 (4%)	33,34,34	1.01	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	A	750	1	50,50,50	2.11	9 (18%)	67,82,82	1.37	8 (11%)
5	ACT	A	860	-	3,3,3	0.79	0	3,3,3	0.87	0
4	7M3	B	800	-	25,25,25	0.91	1 (4%)	33,34,34	1.13	3 (9%)

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	HEM	B	750	1	-	4/14/54/54	-
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
3	H4B	B	760	-	-	2/8/17/17	0/2/2/2
4	7M3	A	800	-	-	3/9/9/9	0/3/3/3
2	HEM	A	750	1	-	5/14/54/54	-
4	7M3	B	800	-	-	5/9/9/9	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3D-C2D	7.82	1.53	1.36
2	B	750	HEM	C3D-C2D	7.72	1.53	1.36
2	A	750	HEM	FE-NA	6.20	2.15	1.95
2	B	750	HEM	FE-NB	5.88	2.13	1.94
2	A	750	HEM	FE-ND	5.76	2.12	1.94
2	B	750	HEM	FE-NA	5.10	2.12	1.95
2	A	750	HEM	FE-NB	4.95	2.10	1.94
2	B	750	HEM	FE-ND	3.83	2.06	1.94
2	B	750	HEM	CAC-C3C	3.20	1.55	1.47
2	B	750	HEM	FE-NC	3.06	2.05	1.95
2	A	750	HEM	CAB-C3B	2.85	1.55	1.47
2	A	750	HEM	CAC-C3C	2.84	1.55	1.47
2	B	750	HEM	CAB-C3B	2.58	1.54	1.47
2	B	750	HEM	CMD-C2D	2.38	1.55	1.50
2	A	750	HEM	CMC-C2C	2.31	1.55	1.50
4	A	800	7M3	C06-C07	2.26	1.41	1.36
2	B	750	HEM	CMB-C2B	2.24	1.55	1.50
2	B	750	HEM	CMA-C3A	2.19	1.55	1.50
2	A	750	HEM	CMA-C3A	2.17	1.55	1.50
2	B	750	HEM	CMC-C2C	2.17	1.55	1.50
2	A	750	HEM	C2A-C3A	-2.09	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	800	7M3	C06-C07	2.02	1.41	1.36

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	750	HEM	C4D-ND-C1D	5.44	111.65	105.21
2	B	750	HEM	C4D-ND-C1D	4.52	110.56	105.21
3	A	760	H4B	C2-N1-C8A	4.46	121.24	113.36
3	B	760	H4B	C2-N1-C8A	4.32	120.99	113.36
3	B	760	H4B	O4-C4-C4A	-3.24	119.45	127.26
2	A	750	HEM	CHA-C4D-ND	3.13	128.24	124.37
4	A	800	7M3	C11-O12-C25	3.02	124.80	117.62
2	B	750	HEM	CBA-CAA-C2A	-3.02	104.19	112.53
2	B	750	HEM	CHA-C4D-ND	3.02	128.10	124.37
3	B	760	H4B	C4A-C4-N3	2.84	119.94	112.13
2	B	750	HEM	C3B-C4B-NB	-2.81	107.45	109.47
3	A	760	H4B	C4A-C4-N3	2.71	119.58	112.13
2	B	750	HEM	C1D-C2D-C3D	-2.68	104.16	106.98
2	B	750	HEM	CAD-CBD-CGD	-2.64	106.67	113.67
4	B	800	7M3	C21-C27-N28	-2.60	108.30	113.17
3	A	760	H4B	O4-C4-C4A	-2.58	121.04	127.26
2	A	750	HEM	C3B-C2B-C1B	2.55	108.32	106.41
3	B	760	H4B	C2-N3-C4	-2.42	120.72	125.11
3	A	760	H4B	C2-N3-C4	-2.40	120.76	125.11
2	B	750	HEM	C2A-C1A-NA	-2.37	107.53	110.15
2	A	750	HEM	CAD-CBD-CGD	-2.33	107.50	113.67
2	A	750	HEM	C1D-C2D-C3D	-2.29	104.58	106.98
4	A	800	7M3	C03-C02-N01	-2.25	119.39	122.09
2	A	750	HEM	C1B-NB-C4B	2.14	107.74	105.21
2	A	750	HEM	C3B-C4B-NB	-2.12	107.95	109.47
3	A	760	H4B	C4-C4A-N5	2.11	122.03	116.27
4	B	800	7M3	C03-C02-N01	-2.08	119.60	122.09
2	A	750	HEM	CBD-CAD-C3D	-2.07	106.81	112.53
4	B	800	7M3	C11-O12-C25	2.02	122.43	117.62
3	B	760	H4B	N3-C2-N1	-2.00	119.65	123.32

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	800	7M3	C21-C27-N28-C29
4	B	800	7M3	C21-C27-N28-C30

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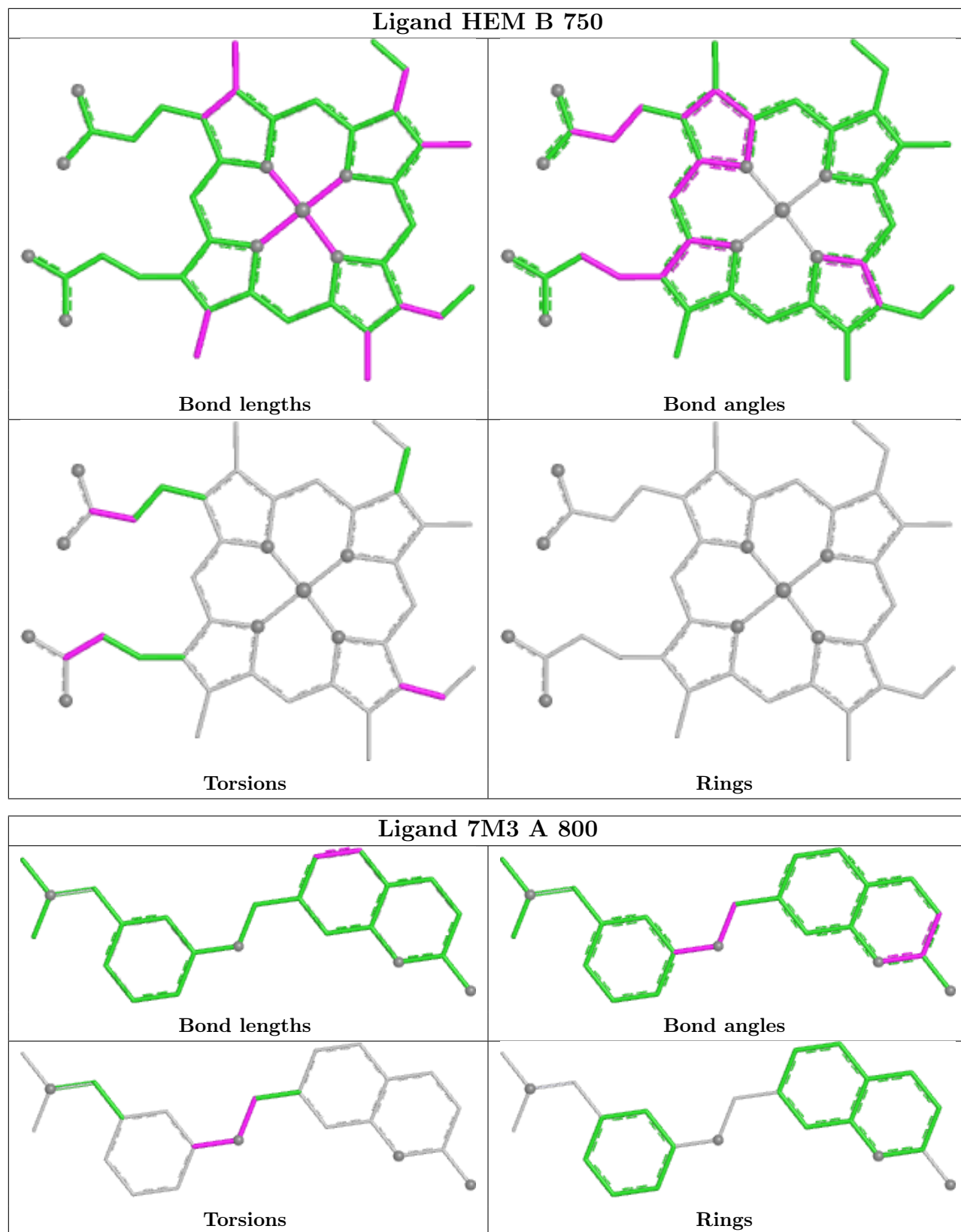
Mol	Chain	Res	Type	Atoms
4	B	800	7M3	C26-C25-O12-C11
4	B	800	7M3	C24-C25-O12-C11
2	A	750	HEM	C2A-CAA-CBA-CGA
4	A	800	7M3	C08-C11-O12-C25
4	A	800	7M3	C26-C25-O12-C11
4	A	800	7M3	C24-C25-O12-C11
2	A	750	HEM	C1A-C2A-CAA-CBA
4	B	800	7M3	C08-C11-O12-C25
2	A	750	HEM	C4B-C3B-CAB-CBB
2	B	750	HEM	C4B-C3B-CAB-CBB
3	B	760	H4B	C11-C10-C9-O9
2	A	750	HEM	CAD-CBD-CGD-O2D
2	A	750	HEM	CAD-CBD-CGD-O1D
2	B	750	HEM	CAA-CBA-CGA-O2A
2	B	750	HEM	CAA-CBA-CGA-O1A
3	B	760	H4B	O10-C10-C9-O9
2	B	750	HEM	CAD-CBD-CGD-O2D

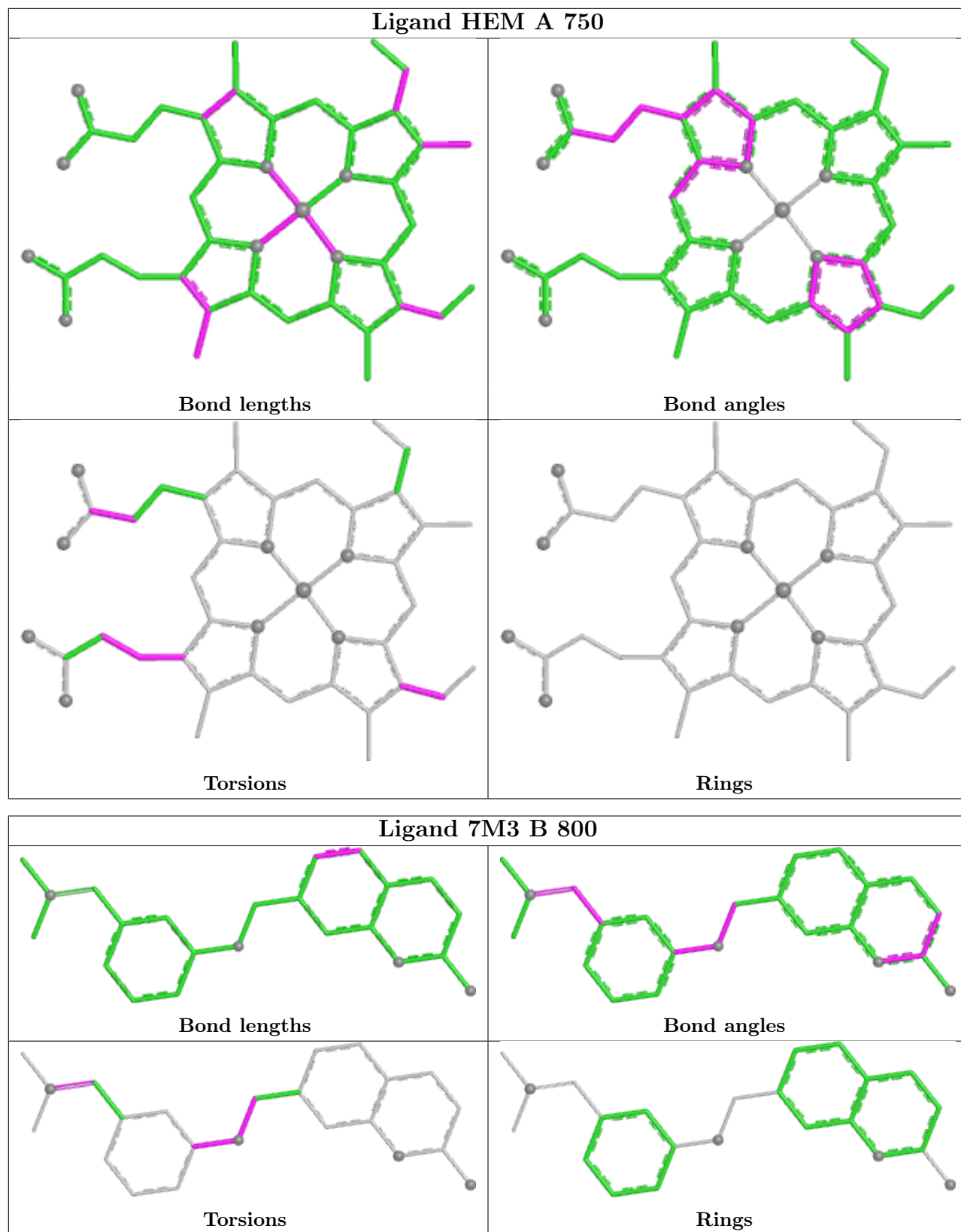
There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	750	HEM	4	0
4	A	800	7M3	1	0
2	A	750	HEM	2	0
4	B	800	7M3	5	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	408/422 (96%)	0.22	33 (8%) 18 17	15, 39, 85, 119	2 (0%)
1	B	411/422 (97%)	-0.19	7 (1%) 69 68	12, 31, 64, 94	2 (0%)
All	All	819/844 (97%)	0.01	40 (4%) 35 34	12, 35, 77, 119	4 (0%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	348	VAL	5.3
1	A	515	GLY	4.3
1	A	716	TRP	3.5
1	A	338	PRO	3.3
1	B	338	PRO	3.3
1	A	488	PRO	3.1
1	A	321	THR	3.0
1	A	300	PHE	3.0
1	A	558	GLY	3.0
1	A	551	PHE	2.9
1	A	486	LYS	2.8
1	A	514	ARG	2.8
1	A	717	LYS	2.7
1	A	322	LEU	2.6
1	A	499	VAL	2.6
1	A	516	ARG	2.6
1	B	321	THR	2.6
1	A	715	VAL	2.5
1	B	352	ASP	2.5
1	B	300	PHE	2.5
1	A	554	PHE	2.4
1	A	355	PHE	2.3
1	A	553	TRP	2.3
1	A	493	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	508	GLN	2.3
1	A	517	PHE	2.3
1	A	711	TRP	2.3
1	A	512	ALA	2.2
1	B	604	TYR	2.2
1	A	604	TYR	2.2
1	A	337	LEU	2.1
1	A	552	ASP	2.1
1	A	609	GLU	2.1
1	B	299	ARG	2.1
1	A	599	CYS	2.1
1	A	489	ASP	2.1
1	A	504	ILE	2.1
1	A	373	GLY	2.1
1	A	484	GLY	2.1
1	A	668[A]	CYS	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(Å ²)	Q<0.9
4	7M3	B	800	23/23	0.88	0.18	12,39,95,98	0
3	H4B	B	760	17/17	0.89	0.11	26,42,55,56	0
4	7M3	A	800	23/23	0.90	0.16	19,33,99,100	0
5	ACT	B	860	4/4	0.91	0.11	33,40,45,60	0
5	ACT	A	860	4/4	0.93	0.10	30,45,46,52	0
3	H4B	A	760	17/17	0.93	0.08	31,44,55,58	0
2	HEM	A	750	43/43	0.99	0.06	9,22,49,61	0

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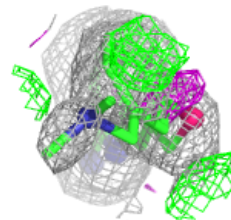
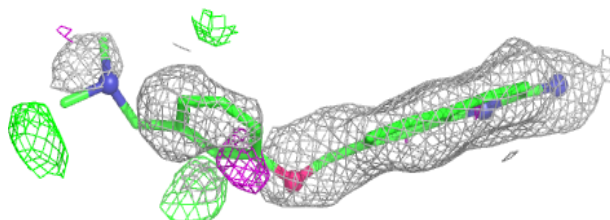
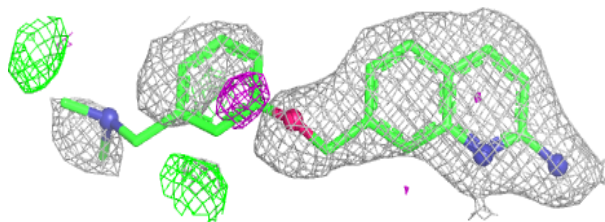
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	HEM	B	750	43/43	0.99	0.06	9,22,44,62	0
6	ZN	B	900	1/1	0.99	0.01	26,26,26,26	0

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.

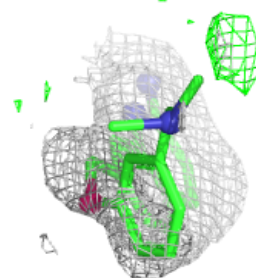
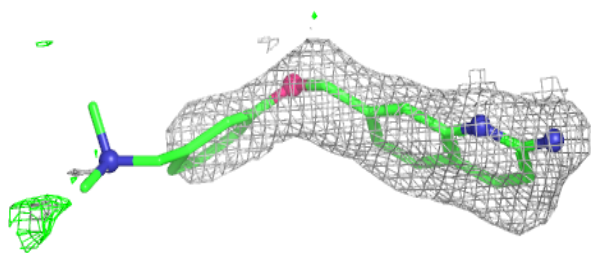
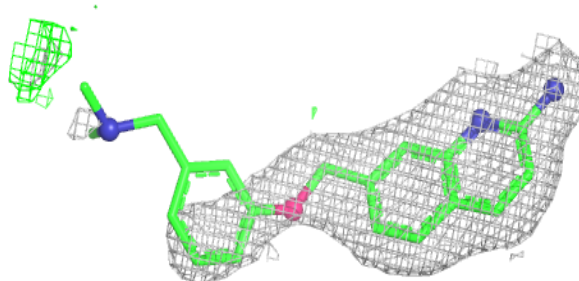
Electron density around 7M3 B 800:

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



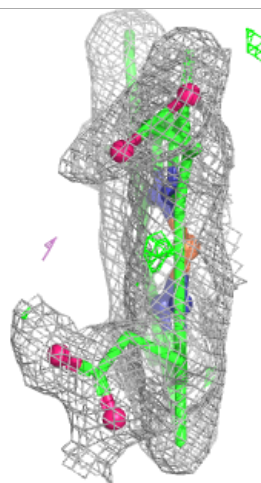
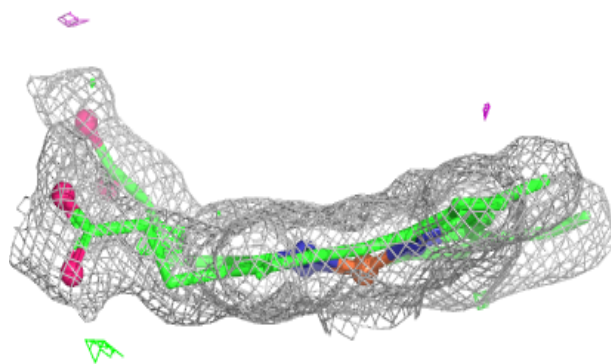
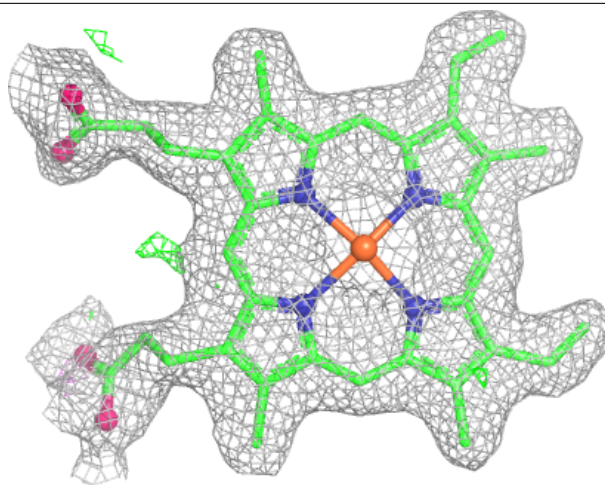
Electron density around 7M3 A 800:

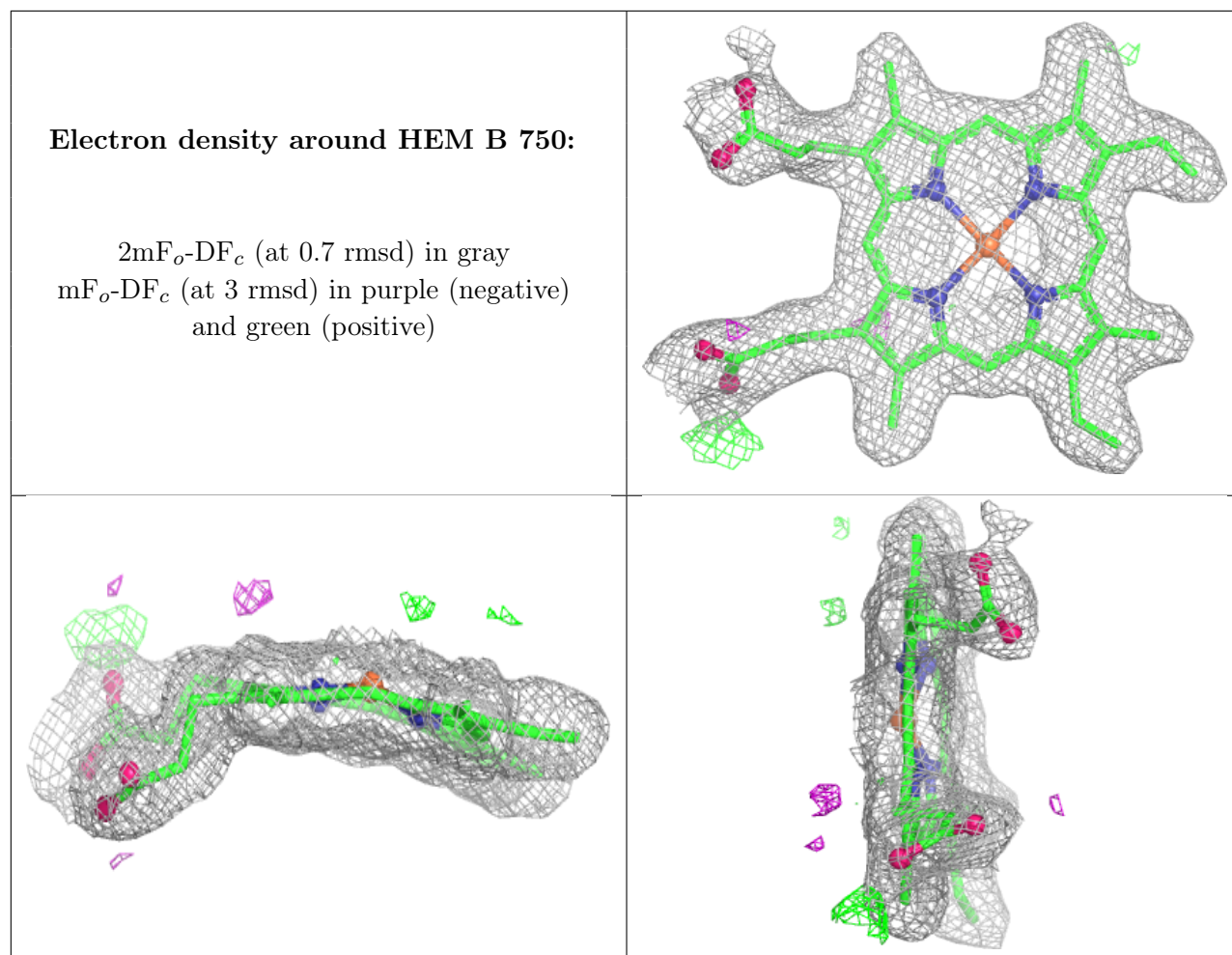
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM 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.