



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 4, 2023 – 09:47 PM EDT

PDB ID : 3UFP
Title : Structure of rat nitric oxide synthase heme domain in complex with 6-(((3R,4R)-4-((5-(3-fluorophenyl)pentyl)oxy)pyrrolidin-3-yl)methyl)-4-methylpyridin-2-amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2011-11-01
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 ⓘ 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
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

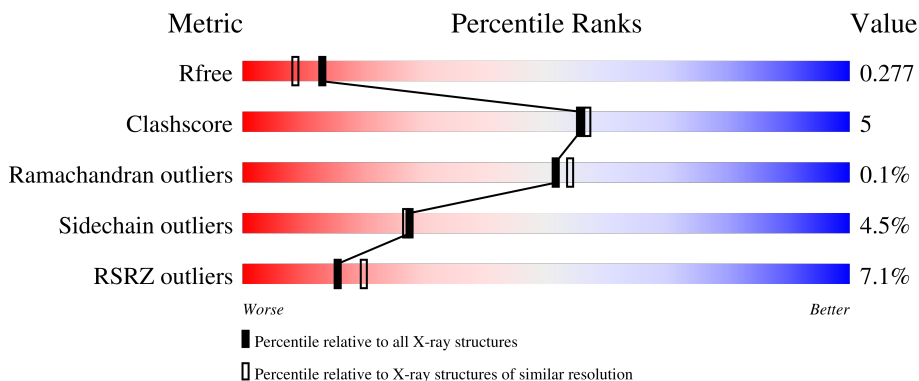
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


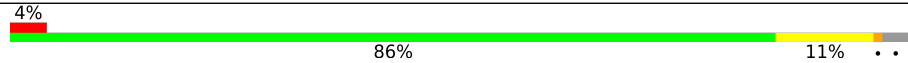
The reported resolution of this entry is 2.10 Å.

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)

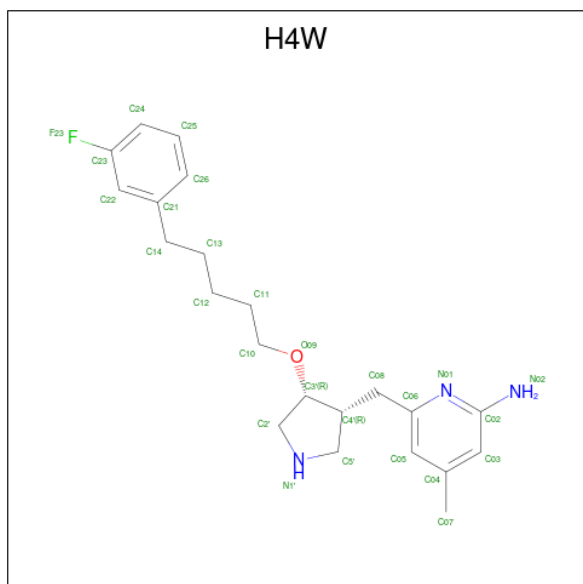
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. 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	 10% 81% 14% ..
1	B	422	 4% 86% 11% ..



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 6-[[[(3R,4R)-4-[[5-(3-fluorophenyl)pentyl]oxy]pyrrolidin-3-yl]methyl]-4-methylpyridin-2-amine (three-letter code: H4W) (formula: C₂₂H₃₀FN₃O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
4	A	1	27	22	1	3	1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
4	B	1	27	22	1	3	1	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

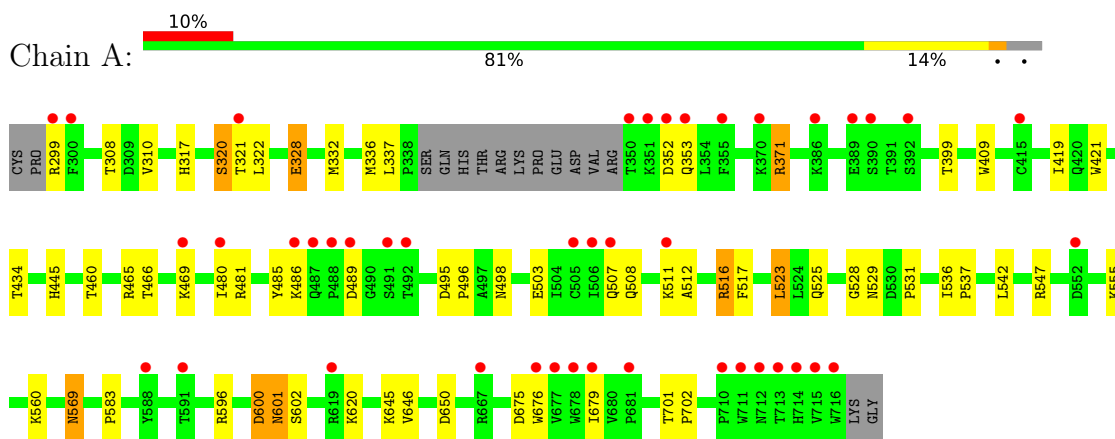
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	100	100	100	0	0
7	B	159	159	159	0	0

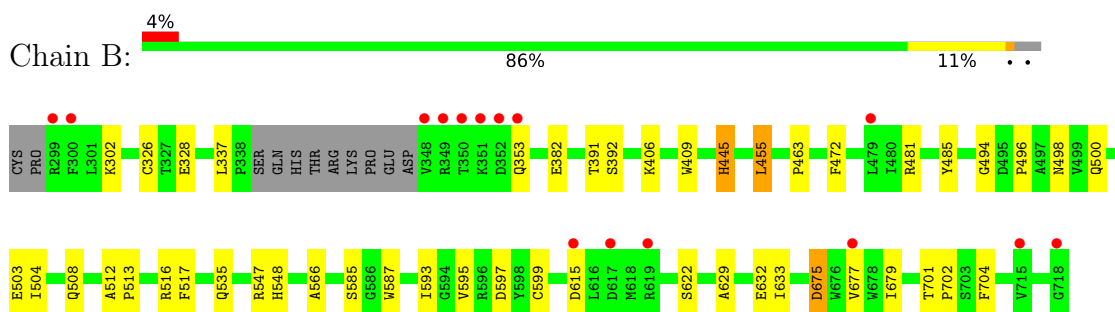
3 Residue-property plots

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 i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.04Å 110.90Å 164.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.99 – 2.10 38.99 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (38.99-2.10) 99.4 (38.99-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.10Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.208 , 0.262 0.225 , 0.277	Depositor DCC
R_{free} test set	2772 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	32.9	Xtrriage
Anisotropy	0.294	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7103	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% 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: H4B, ZN, HEM, H4W, ACT

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	0.69	0/3406	0.71	0/4621
1	B	0.77	1/3444 (0.0%)	0.76	1/4669 (0.0%)
All	All	0.73	1/6850 (0.0%)	0.73	1/9290 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	704	PHE	CE2-CZ	5.33	1.47	1.37

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	675	ASP	CB-CG-OD1	5.14	122.93	118.30

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	3313	0	3221	39	0
1	B	3348	0	3264	28	0
2	A	43	0	30	1	0
2	B	43	0	30	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	27	0	30	1	0
4	B	27	0	30	4	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	1	0	0	0	0
7	A	100	0	0	5	0
7	B	159	0	0	1	0
All	All	7103	0	6641	69	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 (69) 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:701:THR:HB	7:A:22:HOH:O	1.60	0.99
1:A:371:ARG:CG	1:A:371:ARG:HH21	1.95	0.79
1:B:615:ASP:HA	7:B:94:HOH:O	1.84	0.77
1:B:391:THR:O	1:B:392:SER:HB2	1.85	0.76
1:A:596:ARG:O	1:A:600:ASP:HB2	1.89	0.73
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.73	0.70
1:B:593:ILE:HA	1:B:597:ASP:HB2	1.75	0.69
1:A:317:HIS:O	1:A:320:SER:HB3	1.95	0.67
1:A:371:ARG:HH21	1:A:371:ARG:HG2	1.59	0.66
1:A:516:ARG:HB3	1:A:517:PHE:CD1	2.32	0.64
1:A:517:PHE:HB2	1:A:560:LYS:HE3	1.81	0.62
1:A:371:ARG:HG2	1:A:371:ARG:NH2	2.15	0.60
1:B:675:ASP:O	1:B:679:ILE:HG12	2.02	0.60
1:B:587:TRP:H	2:B:750:HEM:HAB	1.67	0.58
1:B:595:VAL:O	1:B:599:CYS:HB2	2.03	0.58
1:A:480:ILE:HA	7:A:106:HOH:O	2.06	0.55
1:A:419:ILE:O	1:A:419:ILE:HG12	2.07	0.55
1:A:371:ARG:HH21	1:A:371:ARG:HG3	1.74	0.53
1:A:371:ARG:CG	1:A:371:ARG:NH2	2.62	0.53
1:A:399:THR:HG23	7:A:240:HOH:O	2.09	0.53
1:A:525:GLN:HG3	1:A:529:ASN:O	2.08	0.53
1:B:504:ILE:O	1:B:508:GLN:HG2	2.09	0.53
1:B:481:ARG:NH1	1:B:498:ASN:OD1	2.43	0.52
1:A:701:THR:CB	7:A:22:HOH:O	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.47	0.50
1:A:321:THR:HG23	1:A:322:LEU:HG	1.94	0.50
1:A:328:GLU:HB3	1:B:326:CYS:O	2.11	0.50
1:A:460:THR:O	1:A:583:PRO:HD2	2.12	0.50
1:A:525:GLN:HE21	1:A:528:GLY:HA2	1.77	0.49
1:B:337:LEU:HD21	4:B:800:H4W:H4	1.95	0.49
4:B:800:H4W:H8	4:B:800:H4W:H13	1.55	0.48
1:B:409:TRP:CZ3	2:B:750:HEM:HMC3	2.49	0.47
1:B:302:LYS:HB2	1:B:302:LYS:HE3	1.48	0.47
1:B:445:HIS:C	1:B:445:HIS:CD2	2.89	0.46
1:B:500:GLN:O	1:B:503:GLU:HB2	2.15	0.46
1:A:507:GLN:HB2	7:A:135:HOH:O	2.16	0.46
1:A:328:GLU:H	1:A:328:GLU:CD	2.20	0.45
1:A:517:PHE:CB	1:A:560:LYS:HE3	2.45	0.45
1:A:569:ASN:HD22	1:A:569:ASN:H	1.63	0.45
1:B:516:ARG:HG2	1:B:517:PHE:CE1	2.51	0.45
2:A:750:HEM:C1C	4:A:800:H4W:H30	2.51	0.45
1:B:701:THR:HA	1:B:702:PRO:C	2.36	0.45
1:B:463:PRO:HD2	1:B:472:PHE:CD2	2.52	0.43
1:B:455:LEU:HD23	1:B:587:TRP:HB3	2.01	0.43
2:B:750:HEM:CMC	2:B:750:HEM:HBC2	2.48	0.43
1:B:494:GLY:O	1:B:496:PRO:HD3	2.17	0.43
4:B:800:H4W:C2'	4:B:800:H4W:C11	2.95	0.43
1:B:485:TYR:HE2	1:B:512:ALA:HB1	1.82	0.43
1:A:542:LEU:HD21	1:A:646:VAL:HG22	2.00	0.43
1:A:536:ILE:O	1:A:537:PRO:C	2.56	0.43
1:B:485:TYR:CE2	1:B:512:ALA:HB1	2.53	0.43
1:A:445:HIS:C	1:A:445:HIS:CD2	2.92	0.42
1:A:481:ARG:HD3	1:A:498:ASN:HD21	1.84	0.42
1:B:391:THR:O	1:B:392:SER:CB	2.62	0.42
1:A:569:ASN:H	1:A:569:ASN:ND2	2.18	0.42
1:A:495:ASP:HA	1:A:496:PRO:HD3	1.90	0.41
1:A:465:ARG:HG3	1:A:466:THR:N	2.35	0.41
1:A:650:ASP:OD1	1:B:622:SER:HB3	2.21	0.41
1:A:601:ASN:HD22	1:A:601:ASN:HA	1.65	0.41
1:A:701:THR:OG1	1:A:702:PRO:HA	2.21	0.41
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.53	0.41
1:A:676:TRP:CZ3	1:B:677:VAL:HG13	2.56	0.41
1:A:675:ASP:O	1:A:679:ILE:HG12	2.21	0.41
1:B:629:ALA:O	1:B:633:ILE:HD12	2.21	0.40
1:B:512:ALA:HA	1:B:513:PRO:HD2	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:THR:HB	1:A:310:VAL:HG23	2.01	0.40
1:B:566:ALA:HB2	1:B:585:SER:HB3	2.03	0.40
2:B:750:HEM:O2D	4:B:800:H4W:H1	2.21	0.40
1:A:485:TYR:HE2	1:A:512:ALA:HB1	1.86	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	403/422 (96%)	383 (95%)	19 (5%)	1 (0%)	47	49
1	B	408/422 (97%)	393 (96%)	15 (4%)	0	100	100
All	All	811/844 (96%)	776 (96%)	34 (4%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	555	LYS

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	363/377 (96%)	338 (93%)	25 (7%)	15	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	367/377 (97%)	359 (98%)	8 (2%)	52	57
All	All	730/754 (97%)	697 (96%)	33 (4%)	27	27

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	299	ARG
1	A	320	SER
1	A	328	GLU
1	A	332	MET
1	A	336	MET
1	A	337	LEU
1	A	352	ASP
1	A	353	GLN
1	A	371	ARG
1	A	434	THR
1	A	469	LYS
1	A	486	LYS
1	A	489	ASP
1	A	503	GLU
1	A	508	GLN
1	A	511	LYS
1	A	516	ARG
1	A	523	LEU
1	A	547	ARG
1	A	569	ASN
1	A	600	ASP
1	A	601	ASN
1	A	602	SER
1	A	620	LYS
1	A	645	LYS
1	B	328	GLU
1	B	353	GLN
1	B	382	GLU
1	B	406	LYS
1	B	445	HIS
1	B	455	LEU
1	B	535	GLN
1	B	547	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	353	GLN
1	A	569	ASN
1	A	601	ASN
1	A	605	ASN
1	A	642	GLN
1	A	697	ASN
1	B	364	GLN
1	B	454	ASN
1	B	527	ASN
1	B	601	ASN
1	B	605	ASN
1	B	642	GLN
1	B	697	ASN

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
4	H4W	B	800	-	28,29,29	0.88	1 (3%)	32,38,38	1.91	9 (28%)
5	ACT	B	860	-	3,3,3	0.59	0	3,3,3	1.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	A	750	1	41,50,50	1.86	8 (19%)	45,82,82	2.04	11 (24%)
3	H4B	A	760	-	16,18,18	1.16	1 (6%)	11,26,26	3.16	8 (72%)
3	H4B	B	760	-	16,18,18	1.11	0	11,26,26	3.05	7 (63%)
4	H4W	A	800	-	28,29,29	0.81	1 (3%)	32,38,38	1.37	7 (21%)
2	HEM	B	750	1	41,50,50	2.01	9 (21%)	45,82,82	1.61	9 (20%)
5	ACT	A	860	-	3,3,3	0.64	0	3,3,3	1.11	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
4	H4W	B	800	-	-	8/13/23/23	0/3/3/3
2	HEM	A	750	1	-	1/12/54/54	-
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	H4W	A	800	-	-	7/13/23/23	0/3/3/3
2	HEM	B	750	1	-	2/12/54/54	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	750	HEM	C3D-C2D	7.75	1.53	1.36
2	A	750	HEM	C3D-C2D	7.24	1.52	1.36
2	B	750	HEM	C3C-C2C	-5.02	1.33	1.40
2	A	750	HEM	C3C-C2C	-4.09	1.34	1.40
2	B	750	HEM	C3C-CAC	3.27	1.54	1.47
3	A	760	H4B	C4A-C4	-2.86	1.37	1.41
2	B	750	HEM	CMB-C2B	2.80	1.56	1.50
2	A	750	HEM	C3C-CAC	2.77	1.53	1.47
2	A	750	HEM	CAB-C3B	2.70	1.54	1.47
2	B	750	HEM	CMD-C2D	2.59	1.56	1.50
2	A	750	HEM	CAA-C2A	2.43	1.55	1.52
2	B	750	HEM	CMC-C2C	2.38	1.57	1.51
2	A	750	HEM	C3B-C2B	-2.36	1.32	1.37
2	B	750	HEM	CAA-C2A	2.32	1.55	1.52
4	A	800	H4W	C24-C23	2.29	1.41	1.37
2	B	750	HEM	C4A-NA	2.29	1.40	1.36
2	A	750	HEM	CMD-C2D	2.18	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	CMC-C2C	2.14	1.56	1.51
2	B	750	HEM	CAB-C3B	2.12	1.53	1.47
4	B	800	H4W	C24-C23	2.07	1.41	1.37

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	760	H4B	C4-C4A-N5	6.08	124.23	119.12
2	A	750	HEM	C4D-ND-C1D	5.90	111.16	105.07
3	B	760	H4B	C8A-C4A-C4	5.15	119.15	114.57
3	B	760	H4B	C4-C4A-N5	4.75	123.11	119.12
4	B	800	H4W	C02-N01-C06	4.68	121.65	118.10
2	A	750	HEM	C2C-C3C-C4C	4.67	110.16	106.90
3	B	760	H4B	C2-N3-C4	4.37	122.87	115.93
3	A	760	H4B	C8A-C4A-C4	4.31	118.40	114.57
4	B	800	H4W	C24-C23-C22	-4.29	117.72	123.29
2	A	750	HEM	CHA-C4D-ND	4.19	129.56	124.38
2	A	750	HEM	CMD-C2D-C1D	4.00	131.13	125.04
3	A	760	H4B	N2-C2-N3	3.92	123.35	117.25
2	B	750	HEM	C4D-ND-C1D	3.88	109.08	105.07
2	B	750	HEM	C4B-CHC-C1C	3.79	127.56	122.56
4	B	800	H4W	C05-C06-N01	-3.75	118.93	122.90
2	B	750	HEM	CMD-C2D-C1D	3.67	130.63	125.04
3	B	760	H4B	N1-C2-N3	-3.43	120.04	125.42
2	B	750	HEM	CHC-C4B-NB	3.13	127.84	124.43
4	A	800	H4W	C24-C23-C22	-3.06	119.31	123.29
4	A	800	H4W	C5'-N1'-C2'	3.06	112.65	105.42
4	B	800	H4W	C21-C22-C23	3.05	121.58	118.81
3	A	760	H4B	C2-N1-C8A	3.01	121.28	114.54
2	A	750	HEM	CBD-CAD-C3D	-2.95	104.43	112.63
2	B	750	HEM	C2C-C3C-C4C	2.90	108.92	106.90
3	A	760	H4B	N1-C2-N3	-2.88	120.89	125.42
2	A	750	HEM	O1A-CGA-CBA	-2.80	114.08	123.08
4	A	800	H4W	C05-C06-N01	-2.80	119.93	122.90
4	B	800	H4W	C5'-N1'-C2'	2.64	111.65	105.42
3	A	760	H4B	O9-C9-C6	-2.61	102.75	108.98
2	B	750	HEM	C4B-C3B-C2B	2.60	109.18	107.11
2	B	750	HEM	C1D-C2D-C3D	-2.58	104.25	106.96
3	B	760	H4B	C4A-C4-N3	-2.48	116.96	124.01
3	A	760	H4B	C4A-N5-C6	-2.46	114.45	121.16
4	A	800	H4W	C21-C22-C23	2.43	121.02	118.81
3	B	760	H4B	N2-C2-N3	2.40	120.98	117.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	800	H4W	C5'-C4'-C3'	2.39	106.44	103.40
4	B	800	H4W	N02-C02-N01	2.35	120.20	116.49
4	B	800	H4W	C07-C04-C05	-2.33	117.48	120.94
2	A	750	HEM	C3C-C4C-NC	-2.29	106.62	110.94
3	A	760	H4B	C2-N3-C4	2.28	119.55	115.93
3	B	760	H4B	C2-N1-C8A	2.27	119.64	114.54
2	B	750	HEM	C4C-CHD-C1D	2.26	125.54	122.56
2	B	750	HEM	CHA-C4D-ND	2.19	127.08	124.38
2	A	750	HEM	CBA-CAA-C2A	-2.18	108.89	112.62
2	A	750	HEM	C4C-CHD-C1D	2.13	125.37	122.56
4	A	800	H4W	F23-C23-C24	2.13	122.15	118.54
2	A	750	HEM	CMA-C3A-C4A	-2.10	125.24	128.46
4	A	800	H4W	C08-C06-C05	-2.09	116.59	121.04
4	B	800	H4W	C06-C08-C4'	-2.07	108.72	115.55
2	A	750	HEM	CAD-CBD-CGD	-2.06	109.16	113.60
4	A	800	H4W	C02-N01-C06	2.04	119.64	118.10

There are no chirality outliers.

All (20) torsion outliers are listed below:

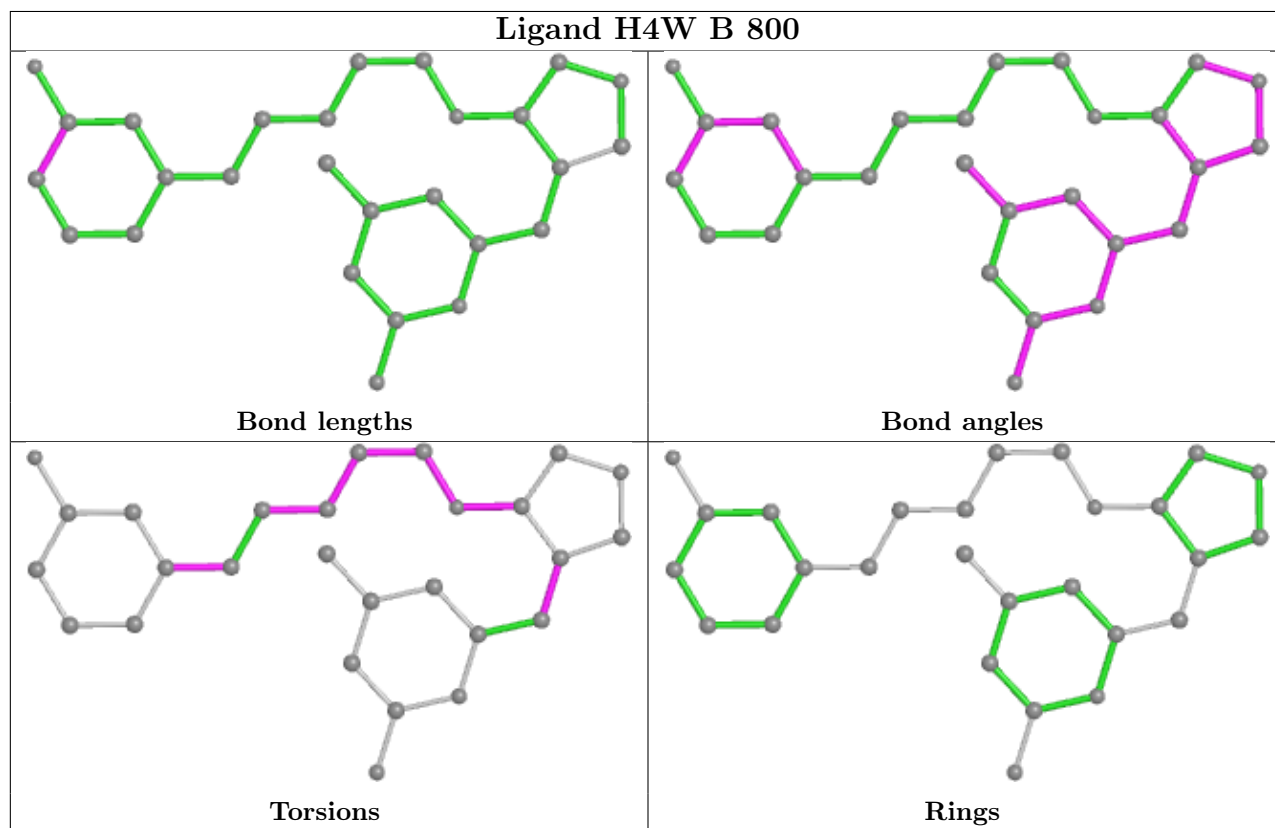
Mol	Chain	Res	Type	Atoms
2	B	750	HEM	C2B-C3B-CAB-CBB
2	B	750	HEM	C4B-C3B-CAB-CBB
4	B	800	H4W	C11-C10-O09-C3'
4	B	800	H4W	C2'-C3'-O09-C10
4	B	800	H4W	C06-C08-C4'-C5'
4	B	800	H4W	C10-C11-C12-C13
4	B	800	H4W	O09-C10-C11-C12
4	B	800	H4W	C11-C12-C13-C14
4	A	800	H4W	C10-C11-C12-C13
4	A	800	H4W	C2'-C3'-O09-C10
4	A	800	H4W	C4'-C3'-O09-C10
4	A	800	H4W	C06-C08-C4'-C5'
4	A	800	H4W	C11-C10-O09-C3'
4	A	800	H4W	C13-C14-C21-C22
4	A	800	H4W	C13-C14-C21-C26
3	B	760	H4B	C7-C6-C9-O9
4	B	800	H4W	C13-C14-C21-C22
3	B	760	H4B	N5-C6-C9-O9
2	A	750	HEM	CAD-CBD-CGD-O2D
4	B	800	H4W	C13-C14-C21-C26

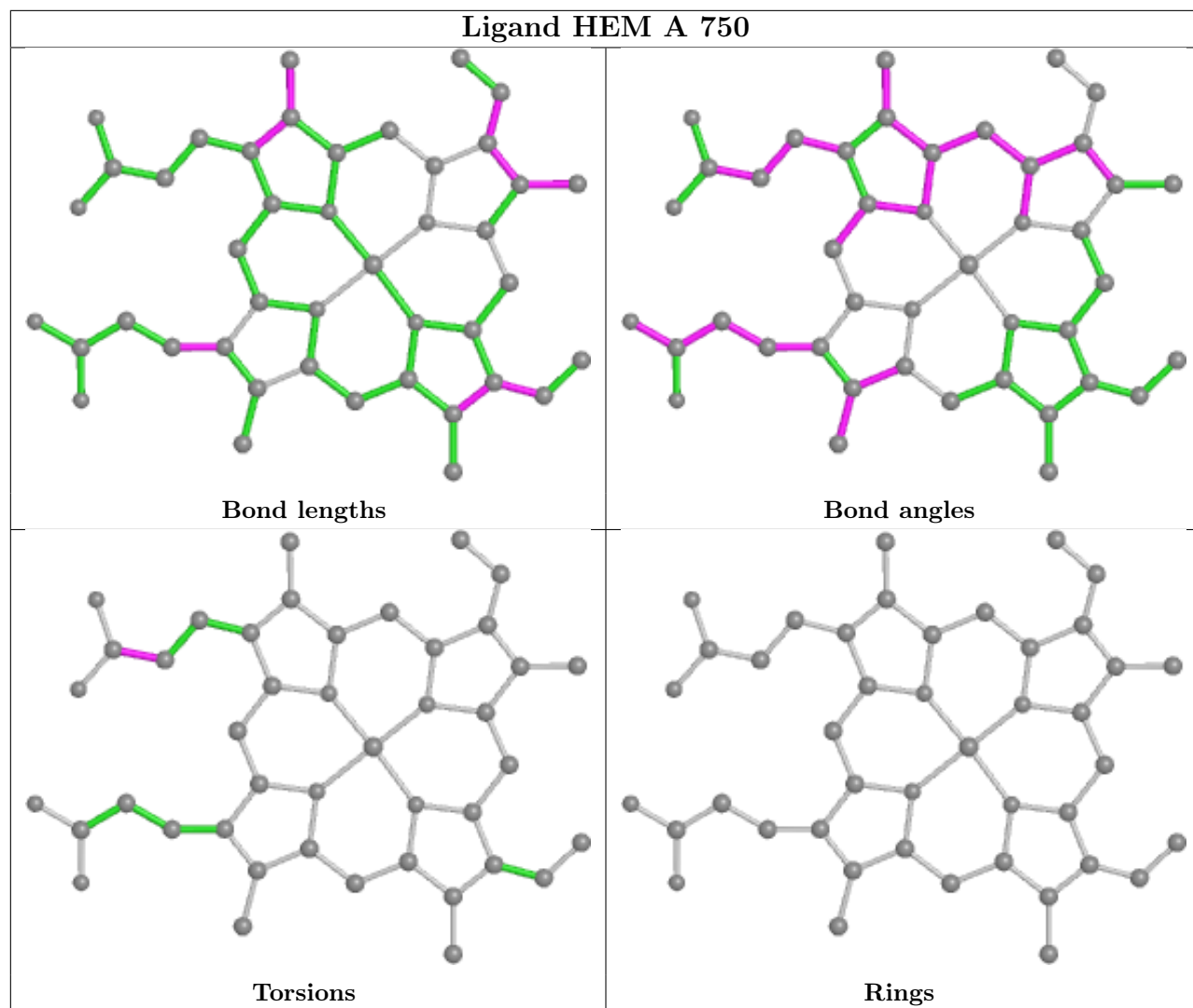
There are no ring outliers.

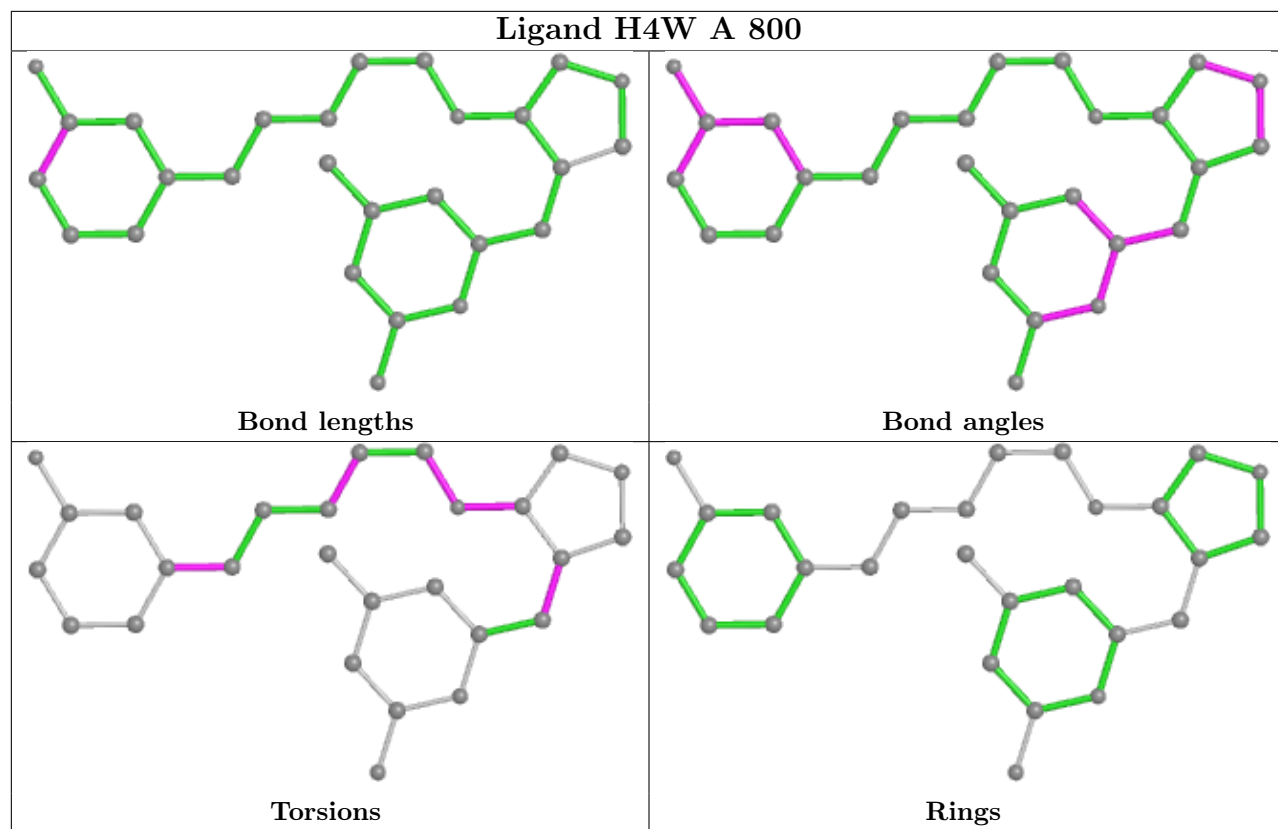
4 monomers are involved in 8 short contacts:

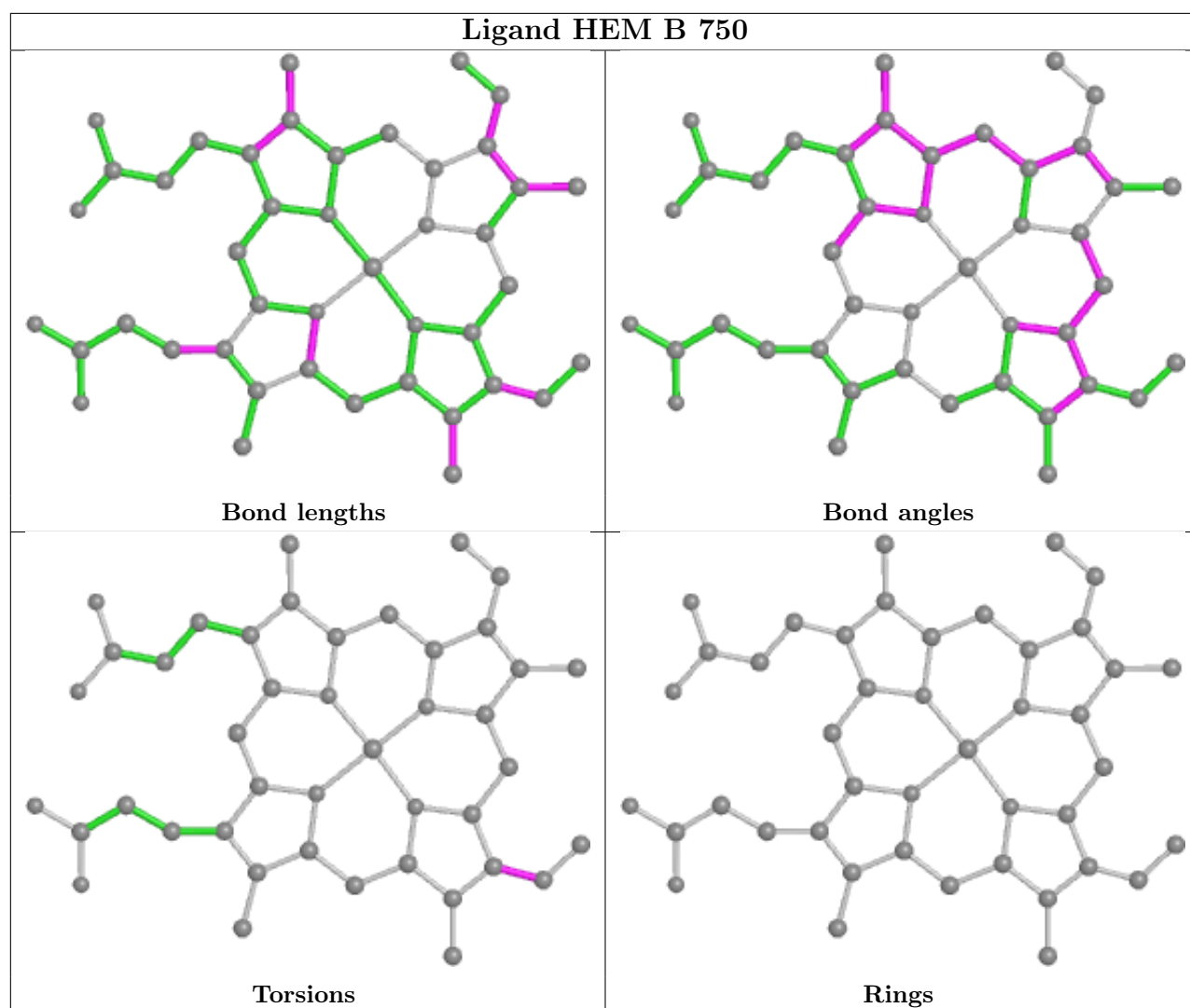
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	800	H4W	4	0
2	A	750	HEM	1	0
4	A	800	H4W	1	0
2	B	750	HEM	4	0

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	407/422 (96%)	0.57	43 (10%) 6 7	23, 49, 87, 114	0
1	B	411/422 (97%)	0.14	15 (3%) 42 49	19, 38, 64, 86	0
All	All	818/844 (96%)	0.36	58 (7%) 16 20	19, 43, 83, 114	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	6.5
1	B	348	VAL	6.5
1	B	718	GLY	6.5
1	A	352	ASP	5.8
1	A	716	TRP	5.1
1	A	488	PRO	5.0
1	B	619	ARG	4.9
1	A	713	THR	4.7
1	B	350	THR	4.5
1	A	355	PHE	4.0
1	A	351	LYS	3.9
1	A	715	VAL	3.8
1	A	486	LYS	3.8
1	A	299	ARG	3.5
1	A	469	LYS	3.4
1	B	352	ASP	3.4
1	A	619	ARG	3.3
1	A	350	THR	3.3
1	A	714	HIS	3.3
1	B	351	LYS	3.2
1	A	506	ILE	2.9
1	A	480	ILE	2.8
1	A	511	LYS	2.8
1	B	299	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	300	PHE	2.8
1	A	392	SER	2.8
1	A	677	VAL	2.7
1	A	507	GLN	2.7
1	B	677	VAL	2.7
1	B	349	ARG	2.6
1	A	389	GLU	2.6
1	A	712	ASN	2.5
1	A	711	TRP	2.5
1	B	615	ASP	2.5
1	A	487	GLN	2.5
1	B	715	VAL	2.5
1	A	588	TYR	2.4
1	A	710	PRO	2.4
1	A	491	SER	2.4
1	A	505	CYS	2.3
1	B	617	ASP	2.3
1	A	678	TRP	2.3
1	A	415	CYS	2.3
1	A	321	THR	2.2
1	A	489	ASP	2.2
1	A	676	TRP	2.2
1	B	353	GLN	2.2
1	A	667	ARG	2.2
1	B	479	LEU	2.2
1	A	386	LYS	2.1
1	A	681	PRO	2.1
1	A	353	GLN	2.1
1	A	370	LYS	2.1
1	A	552	ASP	2.1
1	A	492	THR	2.1
1	A	591	THR	2.1
1	A	679	ILE	2.0
1	A	390	SER	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](#)

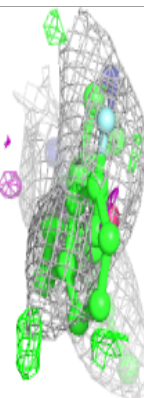
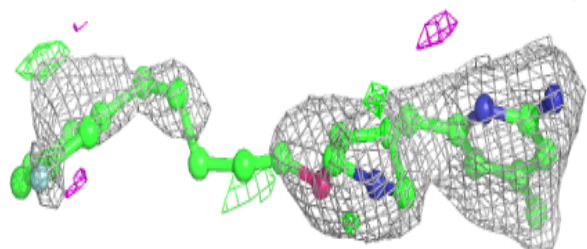
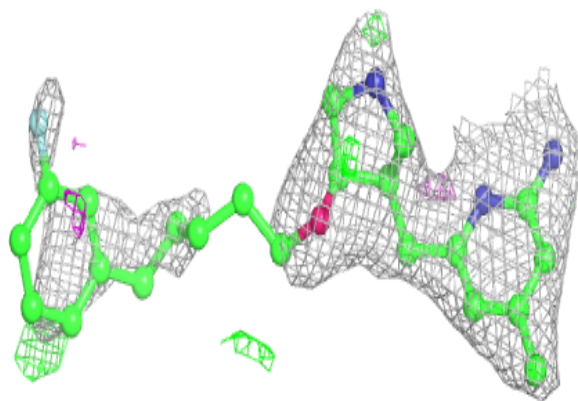
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	H4W	A	800	27/27	0.86	0.33	26,56,87,87	0
4	H4W	B	800	27/27	0.86	0.24	27,54,64,65	0
5	ACT	A	860	4/4	0.90	0.26	53,53,53,55	0
5	ACT	B	860	4/4	0.90	0.15	55,56,56,56	0
3	H4B	A	760	17/17	0.92	0.19	27,32,39,42	0
3	H4B	B	760	17/17	0.94	0.19	27,31,37,38	0
2	HEM	A	750	43/43	0.96	0.22	25,29,37,45	0
2	HEM	B	750	43/43	0.97	0.16	19,24,39,47	0
6	ZN	A	900	1/1	0.99	0.10	34,34,34,34	0

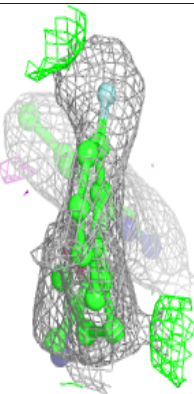
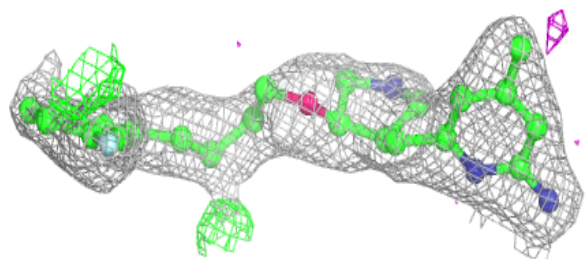
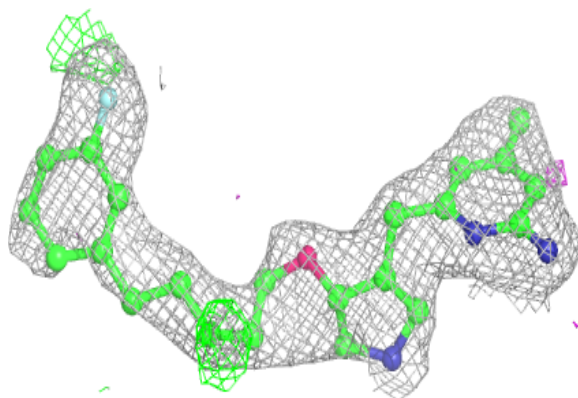
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around H4W 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)

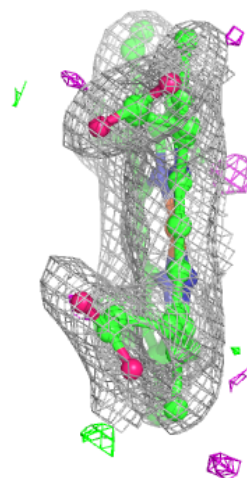
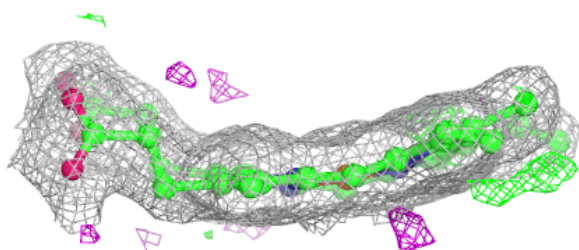
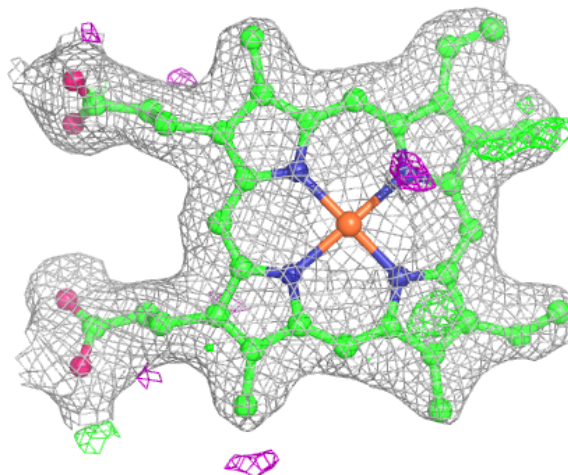
**Electron density around H4W B 800:**

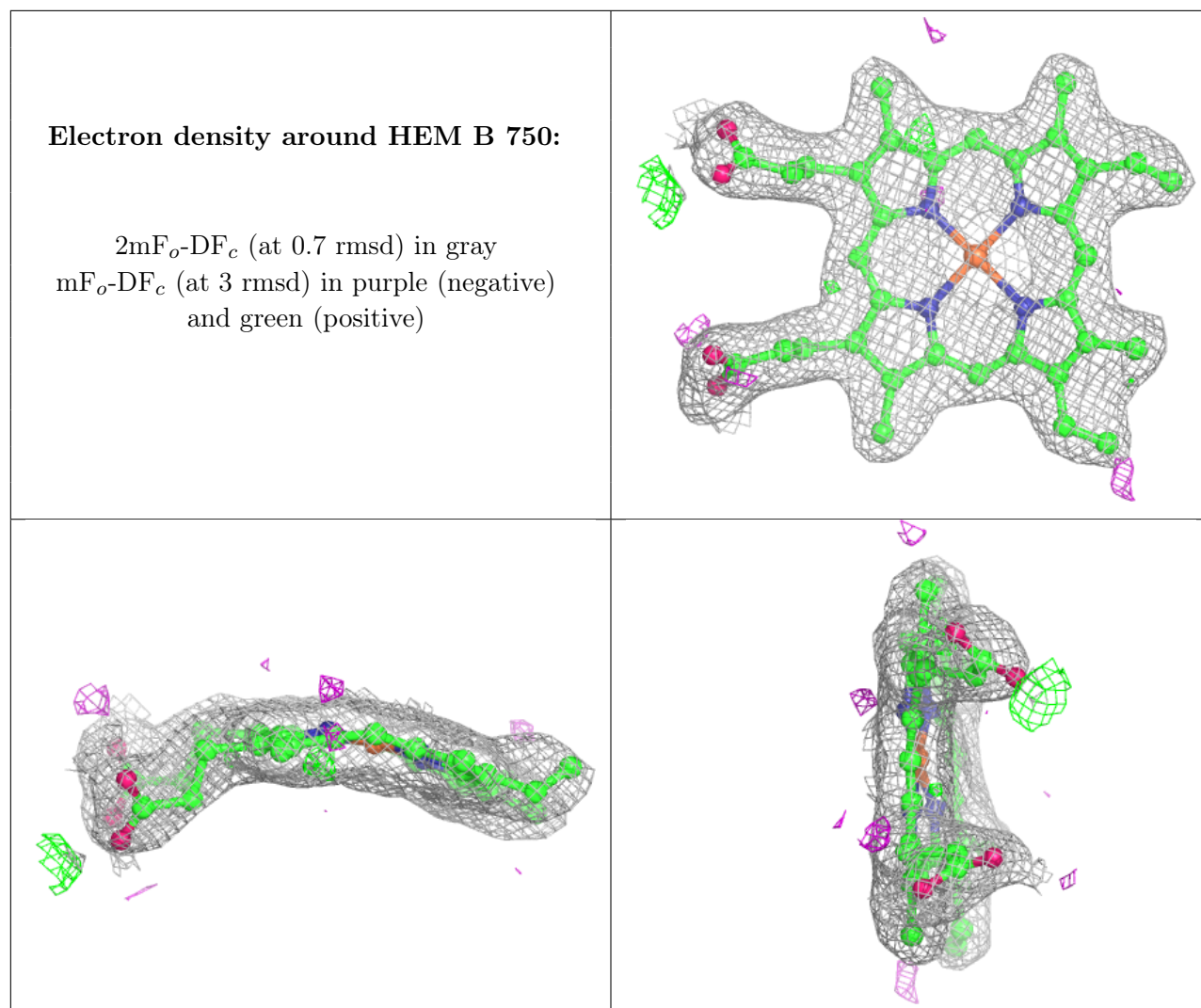
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 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.