Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2023 – 01:40 AM EDT

PDB ID	:	2G6N
Title	:	Strcture of rat nNOS heme domain (BH2 bound) complexed with CO
Authors	:	Li, H.; Igarashi, J.; Jamal, J.; Yang, W.; Poulos, T.L.
Deposited on	:	2006-02-24
Resolution	:	1.90 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:

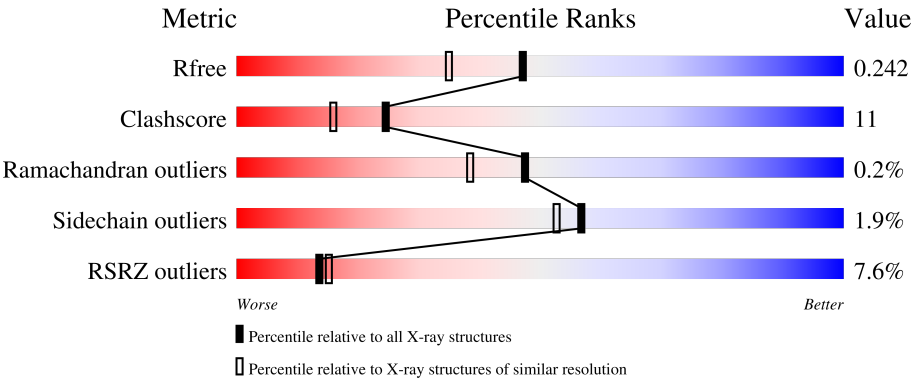
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	420	12% 71% 25%
1	B	420	3% 81% 16%

2 Entry composition

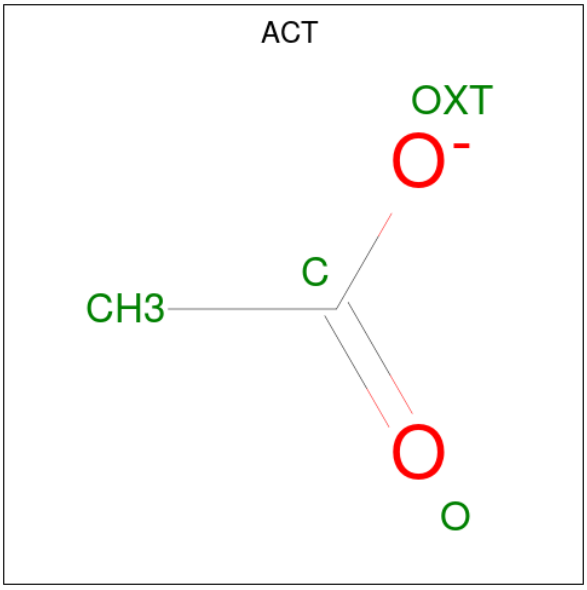
There are 8 unique types of molecules in this entry. The entry contains 7283 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	409	Total	C	N	O	S	0	0	0
			3331	2132	571	607	21			
1	B	411	Total	C	N	O	S	0	0	0
			3345	2140	574	610	21			

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).

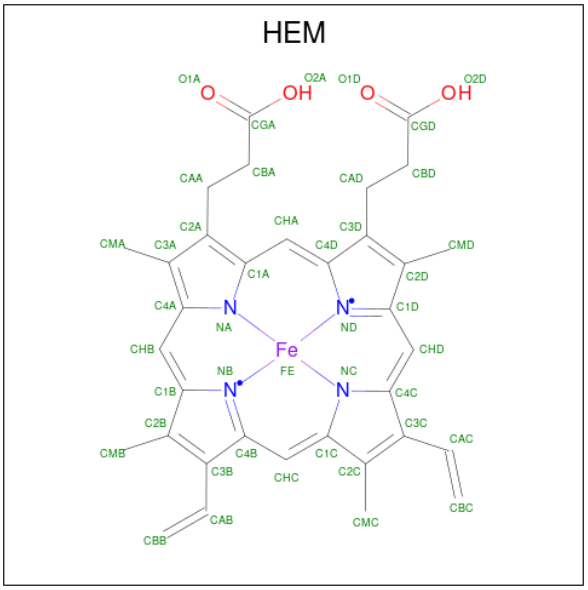


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

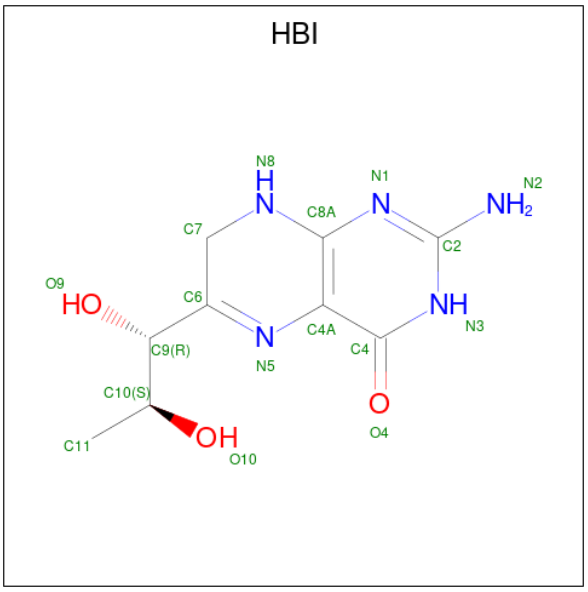
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	0

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



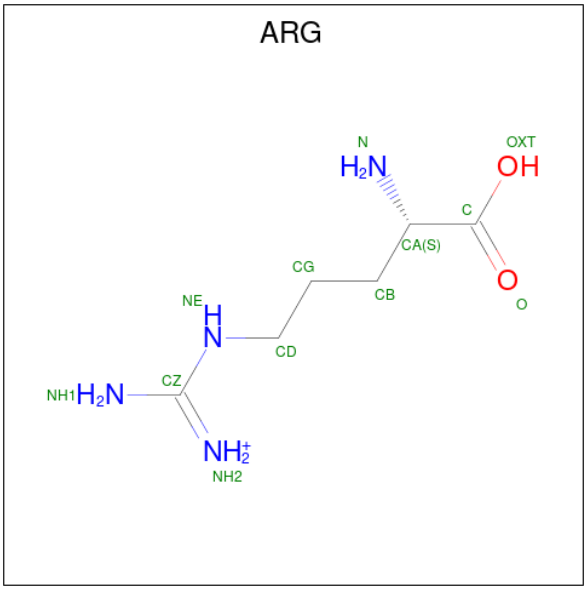
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C Fe N O 43 34 1 4 4	0	0
4	B	1	Total C Fe N O 43 34 1 4 4	0	0

- Molecule 5 is 7,8-DIHYDROBIOPTERIN (three-letter code: HBI) (formula: $C_9H_{13}N_5O_3$).



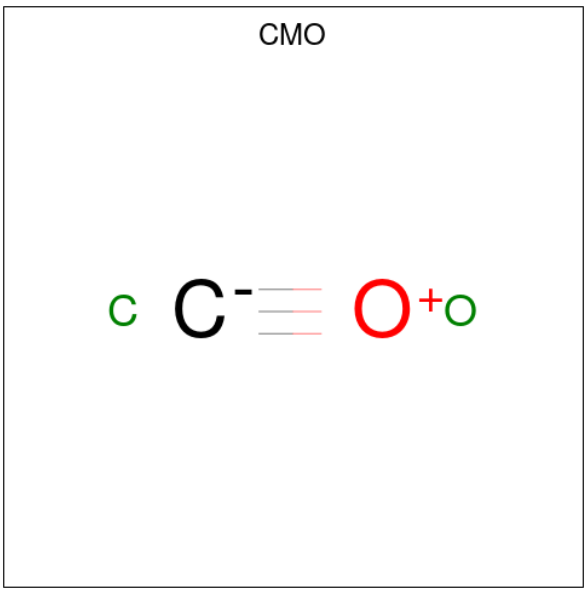
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O 17 9 5 3	0	0
5	B	1	Total C N O 17 9 5 3	0	0

- Molecule 6 is ARGININE (three-letter code: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N O 12 6 4 2	0	0
6	B	1	Total C N O 12 6 4 2	0	0

- Molecule 7 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).



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

- Molecule 8 is water.

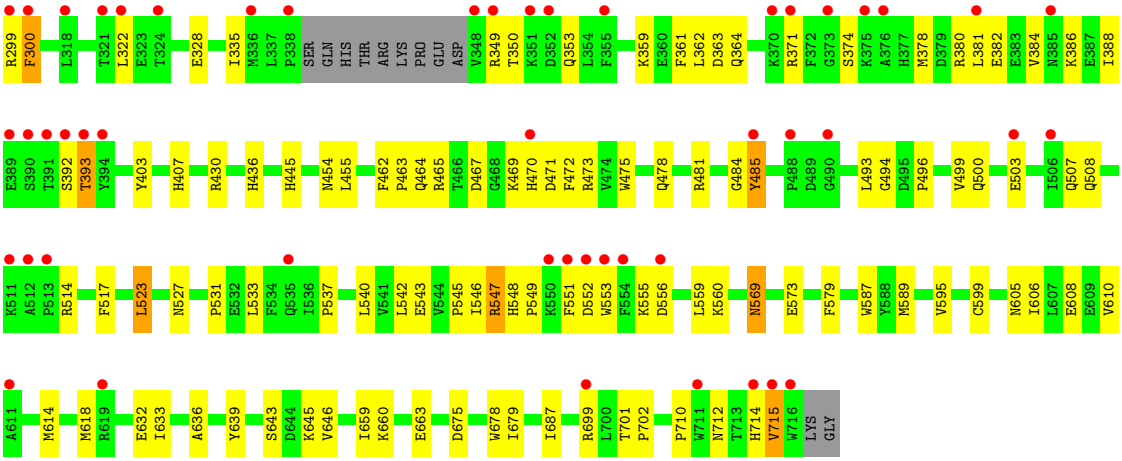
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	183	Total O 183 183	0	0
8	B	267	Total O 267 267	0	0

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.

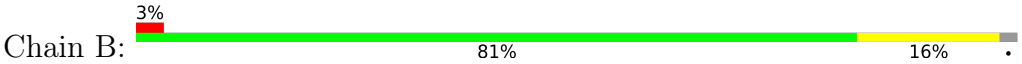
• Molecule 1: Nitric-oxide synthase, brain

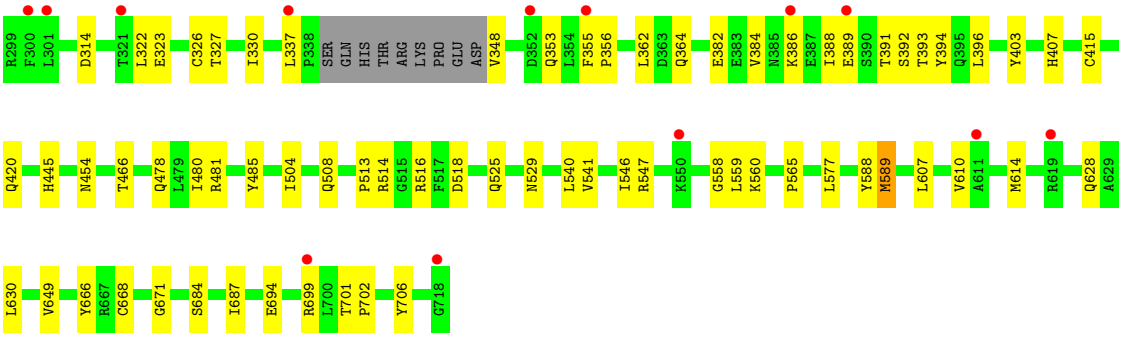
Chain A:



• 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	51.97Å 111.53Å 164.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.55 – 1.90 49.55 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.3 (49.55-1.90) 98.4 (49.55-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	0.89 (at 1.90Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.227 , 0.262 0.213 , 0.242	Depositor DCC
R_{free} test set	3745 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	28.6	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 50.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7283	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 4.67% 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

5.1 Standard geometry

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

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	0/3424	0.60	1/4645 (0.0%)
1	B	0.41	0/3438	0.63	2/4661 (0.0%)
All	All	0.40	0/6862	0.62	3/9306 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	326	CYS	CA-CB-SG	6.53	125.76	114.00
1	A	589	MET	N-CA-C	-5.58	95.92	111.00
1	B	589	MET	N-CA-C	-5.43	96.35	111.00

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	3331	0	3243	99	0
1	B	3345	0	3259	50	0
2	A	4	0	3	0	0
2	B	4	0	3	1	0
3	A	1	0	0	0	0
4	A	43	0	30	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	43	0	30	3	0
5	A	17	0	13	1	0
5	B	17	0	13	0	0
6	A	12	0	12	0	0
6	B	12	0	12	0	0
7	A	2	0	0	0	0
7	B	2	0	0	0	0
8	A	183	0	0	9	0
8	B	267	0	0	5	0
All	All	7283	0	6618	147	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 11.

All (147) 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	1.31	1.06
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.58	0.86
1:A:473:ARG:NH2	1:A:710:PRO:HD3	1.95	0.82
1:A:549:PRO:HG3	1:A:639:TYR:CG	2.15	0.81
1:A:382:GLU:HG3	1:A:386:LYS:HE3	1.69	0.74
1:A:496:PRO:HA	1:A:499:VAL:HG23	1.68	0.73
1:A:523:LEU:CD2	1:A:531:PRO:HB2	2.17	0.72
1:A:322:LEU:HD13	1:A:699:ARG:NH2	2.05	0.71
1:A:556:ASP:O	8:A:1075:HOH:O	2.12	0.68
1:A:485:TYR:CZ	1:A:514:ARG:HA	2.30	0.67
1:A:608:GLU:N	8:A:1079:HOH:O	2.07	0.66
1:A:467:ASP:OD2	1:A:469:LYS:HB2	1.95	0.66
1:B:559:LEU:HD23	8:B:1082:HOH:O	1.96	0.66
1:A:508:GLN:NE2	1:A:508:GLN:HA	2.11	0.65
1:A:508:GLN:HA	1:A:508:GLN:HE21	1.62	0.64
1:B:355:PHE:HB2	1:B:356:PRO:HD3	1.80	0.64
1:B:323:GLU:O	1:B:699:ARG:HD3	1.98	0.63
1:A:322:LEU:HB2	1:A:699:ARG:HB2	1.81	0.63
1:A:687:ILE:HG13	1:B:630:LEU:HD22	1.81	0.62
1:A:552:ASP:HB3	8:A:1042:HOH:O	2.00	0.62
1:A:499:VAL:O	1:A:503:GLU:HG3	2.00	0.61
1:A:699:ARG:HD2	8:A:1021:HOH:O	1.99	0.61
1:A:545:PRO:HG2	1:A:547:ARG:NH2	2.16	0.60
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:GLN:HB2	1:A:481:ARG:CG	2.31	0.59
1:A:508:GLN:HE21	1:A:508:GLN:CA	2.13	0.58
1:B:382:GLU:HG3	1:B:386:LYS:NZ	2.20	0.57
1:B:516:ARG:NH1	8:B:1082:HOH:O	2.37	0.57
1:A:714:HIS:CG	1:A:715:VAL:H	2.23	0.57
1:A:371:ARG:HH11	1:A:371:ARG:HG2	1.69	0.56
1:A:715:VAL:O	1:A:715:VAL:HG13	2.06	0.56
1:A:484:GLY:O	1:A:499:VAL:HA	2.06	0.56
1:A:610:VAL:O	1:A:614:MET:HG3	2.06	0.56
1:A:659:ILE:O	1:A:663:GLU:HG3	2.05	0.55
1:B:322:LEU:HD13	1:B:699:ARG:HH21	1.72	0.55
1:A:465:ARG:NH1	1:A:471:ASP:OD2	2.40	0.54
1:A:322:LEU:CB	1:A:699:ARG:HE	2.20	0.54
1:B:684:SER:HB3	1:B:687:ILE:CG1	2.37	0.54
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.90	0.54
1:A:643:SER:OG	8:A:1083:HOH:O	2.19	0.54
1:A:555:LYS:HE2	8:A:1042:HOH:O	2.08	0.53
1:A:374:SER:O	1:A:378:MET:HG2	2.08	0.53
1:A:606:ILE:O	1:A:610:VAL:HG23	2.09	0.53
1:A:687:ILE:CG1	1:B:630:LEU:HD22	2.38	0.53
1:B:546:ILE:HG12	1:B:560:LYS:HA	1.91	0.52
1:A:322:LEU:HB3	1:A:699:ARG:HH21	1.75	0.52
1:A:470:HIS:HA	1:A:527:ASN:O	2.10	0.52
1:A:436:HIS:HB2	8:A:976:HOH:O	2.09	0.51
1:A:371:ARG:HG2	1:A:371:ARG:NH1	2.26	0.51
1:A:359:LYS:HG2	1:A:363:ASP:OD2	2.11	0.51
1:A:382:GLU:O	1:A:386:LYS:HG3	2.11	0.51
1:A:714:HIS:CG	1:A:715:VAL:N	2.79	0.51
1:A:485:TYR:CE1	1:A:514:ARG:HA	2.46	0.50
1:A:545:PRO:HG2	1:A:547:ARG:HH21	1.74	0.50
1:A:551:PHE:HB3	1:A:553:TRP:CE2	2.46	0.50
1:A:687:ILE:HD12	1:B:607:LEU:HD11	1.94	0.50
1:B:684:SER:HB3	1:B:687:ILE:HD11	1.94	0.50
1:A:549:PRO:HG3	1:A:639:TYR:CD1	2.47	0.50
1:A:546:ILE:HG12	1:A:560:LYS:HA	1.94	0.50
1:B:355:PHE:HZ	1:B:389:GLU:CG	2.24	0.49
1:A:384:VAL:O	1:A:388:ILE:HG13	2.12	0.49
1:B:415:CYS:HB2	4:B:750:HEM:ND	2.27	0.49
1:A:322:LEU:HD13	1:A:699:ARG:HH21	1.79	0.48
1:A:508:GLN:NE2	1:A:508:GLN:CA	2.73	0.48
1:A:632:GLU:OE2	1:B:628:GLN:NE2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:396:LEU:HG	1:B:577:LEU:HD12	1.96	0.48
1:B:513:PRO:HG2	1:B:518:ASP:CG	2.33	0.48
1:A:543:GLU:O	8:A:1073:HOH:O	2.19	0.48
1:B:560:LYS:NZ	8:B:1168:HOH:O	2.46	0.48
1:A:430:ARG:O	1:A:463:PRO:HG3	2.14	0.47
1:A:361:PHE:O	1:A:364:GLN:HG2	2.14	0.47
1:A:608:GLU:HA	1:A:618:MET:HE3	1.95	0.47
1:A:322:LEU:HB2	1:A:699:ARG:HE	1.79	0.47
1:A:493:LEU:HD21	1:A:514:ARG:O	2.14	0.47
1:A:537:PRO:HB2	1:A:540:LEU:HG	1.97	0.47
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.03	0.47
1:A:465:ARG:CZ	1:A:471:ASP:OD2	2.63	0.47
1:A:463:PRO:HB2	1:A:472:PHE:CE1	2.49	0.47
1:B:337:LEU:HD22	1:B:706:TYR:CD1	2.50	0.47
1:A:300:PHE:HD1	1:A:300:PHE:H	1.64	0.46
1:B:382:GLU:HG3	1:B:386:LYS:HZ3	1.80	0.46
1:A:349:ARG:HH11	1:A:349:ARG:HG3	1.80	0.46
1:B:485:TYR:CE1	1:B:514:ARG:HA	2.50	0.46
1:A:378:MET:HA	1:A:378:MET:CE	2.46	0.46
1:B:388:ILE:O	1:B:392:SER:N	2.44	0.46
1:B:391:THR:O	1:B:392:SER:HB2	2.16	0.45
1:B:327:THR:OG1	1:B:330:ILE:HG22	2.16	0.45
1:B:480:ILE:HD13	1:B:541:VAL:HG13	1.97	0.45
1:A:300:PHE:CD1	1:A:300:PHE:N	2.85	0.45
1:B:364:GLN:NE2	8:B:1133:HOH:O	2.50	0.45
4:B:750:HEM:HMC1	4:B:750:HEM:HBC2	1.99	0.45
1:A:542:LEU:HD21	1:A:646:VAL:HG22	1.97	0.45
1:A:464:GLN:HB3	1:A:579:PHE:CE2	2.52	0.45
1:B:445:HIS:C	1:B:445:HIS:CD2	2.90	0.45
1:A:701:THR:HA	1:A:702:PRO:C	2.38	0.44
1:A:710:PRO:C	1:A:712:ASN:H	2.20	0.44
4:A:750:HEM:HBB2	4:A:750:HEM:HHC	1.99	0.44
1:A:462:PHE:HB3	1:A:463:PRO:CD	2.48	0.44
1:A:614:MET:CE	1:A:632:GLU:HG3	2.48	0.44
1:A:678:TRP:HA	5:A:760:HBI:N1	2.32	0.44
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.99	0.44
1:A:455:LEU:HD12	1:A:587:TRP:CB	2.47	0.44
1:A:350:THR:OG1	1:A:353:GLN:HG3	2.18	0.44
1:B:684:SER:HB3	1:B:687:ILE:HG12	1.98	0.44
1:A:548:HIS:ND1	1:A:549:PRO:HD2	2.32	0.44
1:B:666:TYR:HA	1:B:671:GLY:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:548:HIS:HA	1:A:549:PRO:HD3	1.90	0.44
1:A:362:LEU:HD11	1:A:384:VAL:HG21	2.00	0.43
1:A:569:ASN:ND2	1:A:569:ASN:H	2.16	0.43
1:B:610:VAL:O	1:B:614:MET:HG3	2.18	0.43
1:B:353:GLN:H	1:B:353:GLN:HG2	1.63	0.43
1:B:701:THR:HA	1:B:702:PRO:C	2.38	0.43
1:B:348:VAL:HG21	1:B:466:THR:O	2.18	0.43
1:A:322:LEU:HB3	1:A:699:ARG:HE	1.83	0.43
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.00	0.43
1:B:393:THR:HG23	1:B:394:TYR:N	2.33	0.43
1:B:322:LEU:HD13	1:B:699:ARG:NH2	2.32	0.43
1:B:504:ILE:O	1:B:508:GLN:HG2	2.19	0.43
1:A:335:ILE:HD13	1:B:694:GLU:HB3	2.01	0.42
1:A:500:GLN:O	1:A:503:GLU:N	2.52	0.42
1:B:355:PHE:HZ	1:B:389:GLU:HG3	1.84	0.42
1:B:355:PHE:HZ	1:B:389:GLU:HG2	1.84	0.42
1:A:380:ARG:O	1:A:384:VAL:HG23	2.19	0.42
1:A:595:VAL:O	1:A:599:CYS:HB2	2.19	0.42
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.08	0.42
1:A:494:GLY:O	1:A:496:PRO:HD3	2.20	0.42
1:A:523:LEU:HG	1:A:533:LEU:CD2	2.50	0.42
4:B:750:HEM:HBC2	4:B:750:HEM:CMC	2.49	0.42
1:A:614:MET:HE1	1:A:632:GLU:HG3	2.02	0.42
1:A:381:LEU:HD12	1:A:381:LEU:O	2.19	0.41
1:A:392:SER:O	1:A:393:THR:HB	2.20	0.41
1:A:445:HIS:CD2	1:A:445:HIS:C	2.93	0.41
1:B:525:GLN:HG3	1:B:529:ASN:O	2.19	0.41
1:B:684:SER:HB3	1:B:687:ILE:CD1	2.51	0.41
1:B:558:GLY:C	8:B:1082:HOH:O	2.58	0.41
1:A:660:LYS:HE3	8:A:1090:HOH:O	2.21	0.41
1:B:314:ASP:HB2	1:B:666:TYR:HE2	1.86	0.41
1:B:485:TYR:CZ	1:B:514:ARG:HA	2.56	0.41
1:A:569:ASN:H	1:A:569:ASN:HD22	1.68	0.41
1:A:349:ARG:NH2	1:A:573:GLU:OE2	2.53	0.40
1:A:299:ARG:HB3	1:A:300:PHE:H	1.68	0.40
1:A:633:ILE:O	1:A:636:ALA:HB3	2.21	0.40
1:A:517:PHE:HZ	1:A:559:LEU:HD23	1.85	0.40
1:B:420:GLN:HG2	2:B:861:ACT:H2	2.02	0.40
1:B:565:PRO:HB3	1:B:588:TYR:CZ	2.57	0.40
1:B:589:MET:HA	1:B:649:VAL:O	2.22	0.40
1:A:675:ASP:O	1:A:679:ILE:HG12	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	405/420 (96%)	372 (92%)	31 (8%)	2 (0%)	29 18
1	B	407/420 (97%)	393 (97%)	14 (3%)	0	100 100
All	All	812/840 (97%)	765 (94%)	45 (6%)	2 (0%)	47 38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	715	VAL
1	A	393	THR

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	365/375 (97%)	355 (97%)	10 (3%)	44 38
1	B	366/375 (98%)	362 (99%)	4 (1%)	73 73
All	All	731/750 (98%)	717 (98%)	14 (2%)	57 53

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	300	PHE

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Mol	Chain	Res	Type
1	A	328	GLU
1	A	454	ASN
1	A	485	TYR
1	A	507	GLN
1	A	523	LEU
1	A	547	ARG
1	A	569	ASN
1	A	605	ASN
1	A	645	LYS
1	B	454	ASN
1	B	540	LEU
1	B	547	ARG
1	B	668	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	364	GLN
1	A	425	GLN
1	A	454	ASN
1	A	508	GLN
1	A	527	ASN
1	A	569	ASN
1	A	605	ASN
1	A	697	ASN
1	B	364	GLN
1	B	385	ASN
1	B	425	GLN
1	B	454	ASN
1	B	507	GLN
1	B	527	ASN
1	B	535	GLN
1	B	601	ASN
1	B	605	ASN
1	B	642	GLN
1	B	697	ASN

5.3.3 RNA

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 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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	ACT	B	861	-	3,3,3	0.93	0	3,3,3	0.73	0
6	ARG	B	771	-	10,11,11	0.78	0	11,13,13	0.82	0
6	ARG	A	770	-	10,11,11	0.85	0	11,13,13	0.80	0
5	HBI	A	760	-	13,18,18	3.10	5 (38%)	14,26,26	3.32	6 (42%)
4	HEM	B	750	7,1	41,50,50	1.36	6 (14%)	45,82,82	1.49	6 (13%)
7	CMO	B	920	4	0,1,1	-	-	-		
2	ACT	A	860	-	3,3,3	0.89	0	3,3,3	0.87	0
5	HBI	B	761	-	13,18,18	3.25	4 (30%)	14,26,26	3.36	6 (42%)
7	CMO	A	920	4	0,1,1	-	-	-		
4	HEM	A	750	7,1	41,50,50	1.39	5 (12%)	45,82,82	1.27	5 (11%)

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
6	ARG	B	771	-	-	1/11/11/11	-
6	ARG	A	770	-	-	0/11/11/11	-
5	HBI	A	760	-	-	0/4/17/17	0/2/2/2
4	HEM	B	750	7,1	-	0/12/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	HBI	B	761	-	-	0/4/17/17	0/2/2/2
4	HEM	A	750	7,1	-	1/12/54/54	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	761	HBI	C6-N5	8.70	1.39	1.28
5	A	760	HBI	C6-N5	8.32	1.39	1.28
5	B	761	HBI	C4-N3	5.35	1.42	1.33
5	A	760	HBI	C4-N3	5.22	1.42	1.33
5	B	761	HBI	C7-N8	4.29	1.52	1.45
4	A	750	HEM	C3C-CAC	-4.03	1.39	1.47
5	A	760	HBI	C7-N8	3.86	1.52	1.45
4	B	750	HEM	CHB-C1B	3.15	1.43	1.35
4	B	750	HEM	C3C-CAC	-3.01	1.41	1.47
5	B	761	HBI	C8A-N1	2.75	1.39	1.34
4	A	750	HEM	CHA-C4D	2.70	1.41	1.35
4	A	750	HEM	CHB-C1B	2.48	1.41	1.35
4	B	750	HEM	FE-ND	2.47	2.09	1.96
5	A	760	HBI	C8A-N1	2.45	1.39	1.34
4	A	750	HEM	CAB-C3B	-2.44	1.40	1.47
4	B	750	HEM	CAB-C3B	-2.28	1.41	1.47
4	B	750	HEM	CHA-C4D	2.18	1.40	1.35
4	A	750	HEM	FE-ND	2.18	2.07	1.96
4	B	750	HEM	C3C-C2C	-2.17	1.37	1.40
5	A	760	HBI	C2-N3	2.15	1.39	1.35

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	761	HBI	C8A-C4A-C4	7.56	119.48	114.53
5	A	760	HBI	C8A-C4A-C4	7.44	119.40	114.53
5	A	760	HBI	N1-C2-N3	-5.19	117.28	125.42
5	B	761	HBI	N1-C2-N3	-5.14	117.35	125.42
5	B	761	HBI	C2-N3-C4	5.00	123.88	115.93
5	A	760	HBI	C2-N3-C4	4.80	123.55	115.93
5	B	761	HBI	C4A-C4-N3	-4.50	117.28	123.43
5	A	760	HBI	C4A-C4-N3	-4.37	117.45	123.43
4	B	750	HEM	C4C-CHD-C1D	4.36	128.31	122.56
4	B	750	HEM	C4B-CHC-C1C	4.07	127.93	122.56
4	B	750	HEM	CBA-CAA-C2A	-3.79	106.15	112.62
5	A	760	HBI	C2-N1-C8A	3.77	122.99	114.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	761	HBI	C2-N1-C8A	3.64	122.70	114.54
4	A	750	HEM	C4B-CHC-C1C	3.62	127.33	122.56
5	B	761	HBI	N2-C2-N1	3.62	122.88	117.25
5	A	760	HBI	N2-C2-N1	3.33	122.43	117.25
4	B	750	HEM	CMA-C3A-C4A	-2.91	124.00	128.46
4	A	750	HEM	C4C-CHD-C1D	2.85	126.31	122.56
4	A	750	HEM	CMC-C2C-C3C	2.73	129.79	124.68
4	B	750	HEM	CMA-C3A-C2A	2.70	130.03	124.94
4	A	750	HEM	CHC-C4B-C3B	2.14	127.85	124.57
4	A	750	HEM	CAB-C3B-C2B	-2.12	121.63	128.60
4	B	750	HEM	C4A-C3A-C2A	-2.03	105.58	107.00

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	750	HEM	C4B-C3B-CAB-CBB
6	B	771	ARG	O-C-CA-N

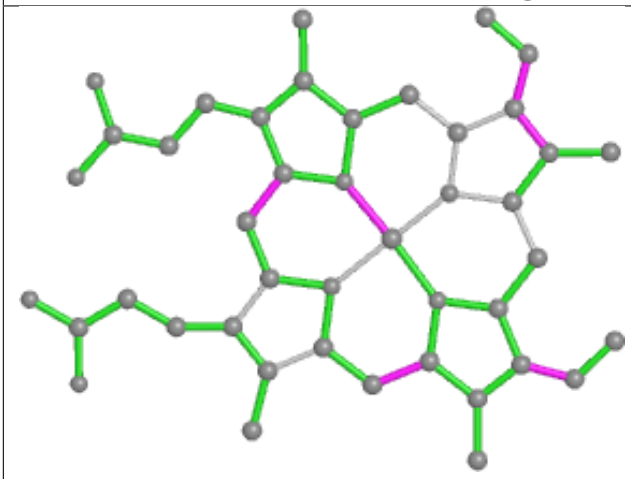
There are no ring outliers.

4 monomers are involved in 6 short contacts:

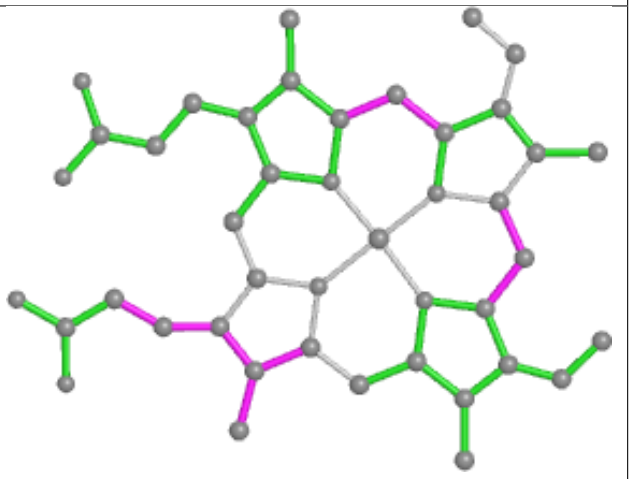
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	861	ACT	1	0
5	A	760	HBI	1	0
4	B	750	HEM	3	0
4	A	750	HEM	1	0

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 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.

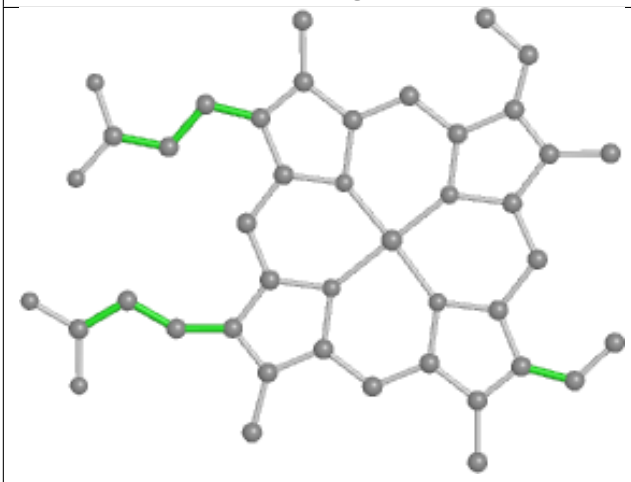
Ligand HEM B 750



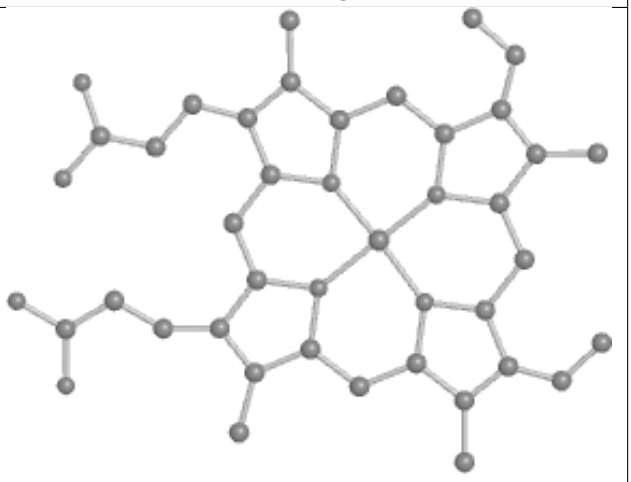
Bond lengths



Bond angles

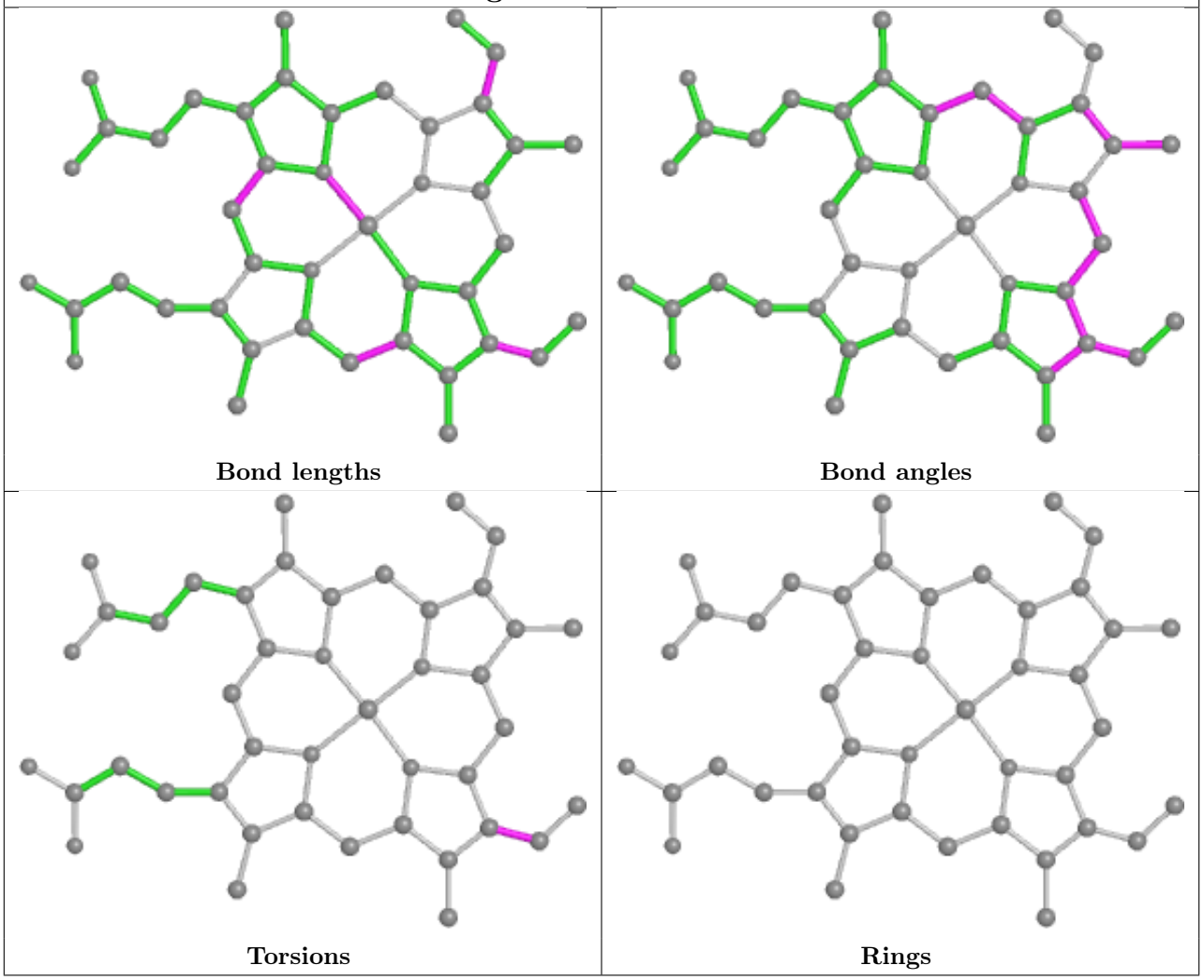


Torsions



Rings

Ligand HEM A 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

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, 95^{th} 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	409/420 (97%)	0.78	49 (11%) 4 4	19, 42, 69, 85	0
1	B	411/420 (97%)	0.29	13 (3%) 47 50	20, 32, 56, 74	0
All	All	820/840 (97%)	0.53	62 (7%) 13 15	19, 36, 65, 85	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	716	TRP	7.8
1	B	300	PHE	6.0
1	B	321	THR	5.9
1	A	506	ILE	5.7
1	A	488	PRO	4.9
1	A	355	PHE	4.8
1	A	352	ASP	4.3
1	A	391	THR	4.1
1	A	373	GLY	4.0
1	A	554	PHE	3.9
1	A	551	PHE	3.9
1	A	321	THR	3.9
1	A	322	LEU	3.7
1	B	352	ASP	3.6
1	A	511	LYS	3.5
1	A	348	VAL	3.5
1	B	718	GLY	3.4
1	A	385	ASN	3.2
1	A	324	THR	3.2
1	A	470	HIS	3.1
1	A	503	GLU	3.1
1	A	552	ASP	3.1
1	A	390	SER	3.0
1	A	619	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	337	LEU	2.8
1	A	394	TYR	2.8
1	A	512	ALA	2.8
1	A	376	ALA	2.7
1	A	375	LYS	2.7
1	A	490	GLY	2.7
1	B	355	PHE	2.7
1	B	386	LYS	2.6
1	A	351	LYS	2.6
1	A	318	LEU	2.6
1	A	381	LEU	2.6
1	A	714	HIS	2.6
1	A	550	LYS	2.6
1	A	392	SER	2.5
1	A	715	VAL	2.5
1	A	349	ARG	2.5
1	A	513	PRO	2.4
1	A	699	ARG	2.4
1	A	299	ARG	2.4
1	B	619	ARG	2.4
1	B	611	ALA	2.3
1	A	556	ASP	2.3
1	B	389	GLU	2.3
1	A	393	THR	2.3
1	A	711	TRP	2.2
1	A	553	TRP	2.2
1	A	336	MET	2.2
1	A	300	PHE	2.2
1	A	611	ALA	2.2
1	B	550	LYS	2.2
1	B	699	ARG	2.2
1	A	535	GLN	2.0
1	A	370	LYS	2.0
1	A	389	GLU	2.0
1	A	485	TYR	2.0
1	A	371	ARG	2.0
1	A	338	PRO	2.0
1	B	301	LEU	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)

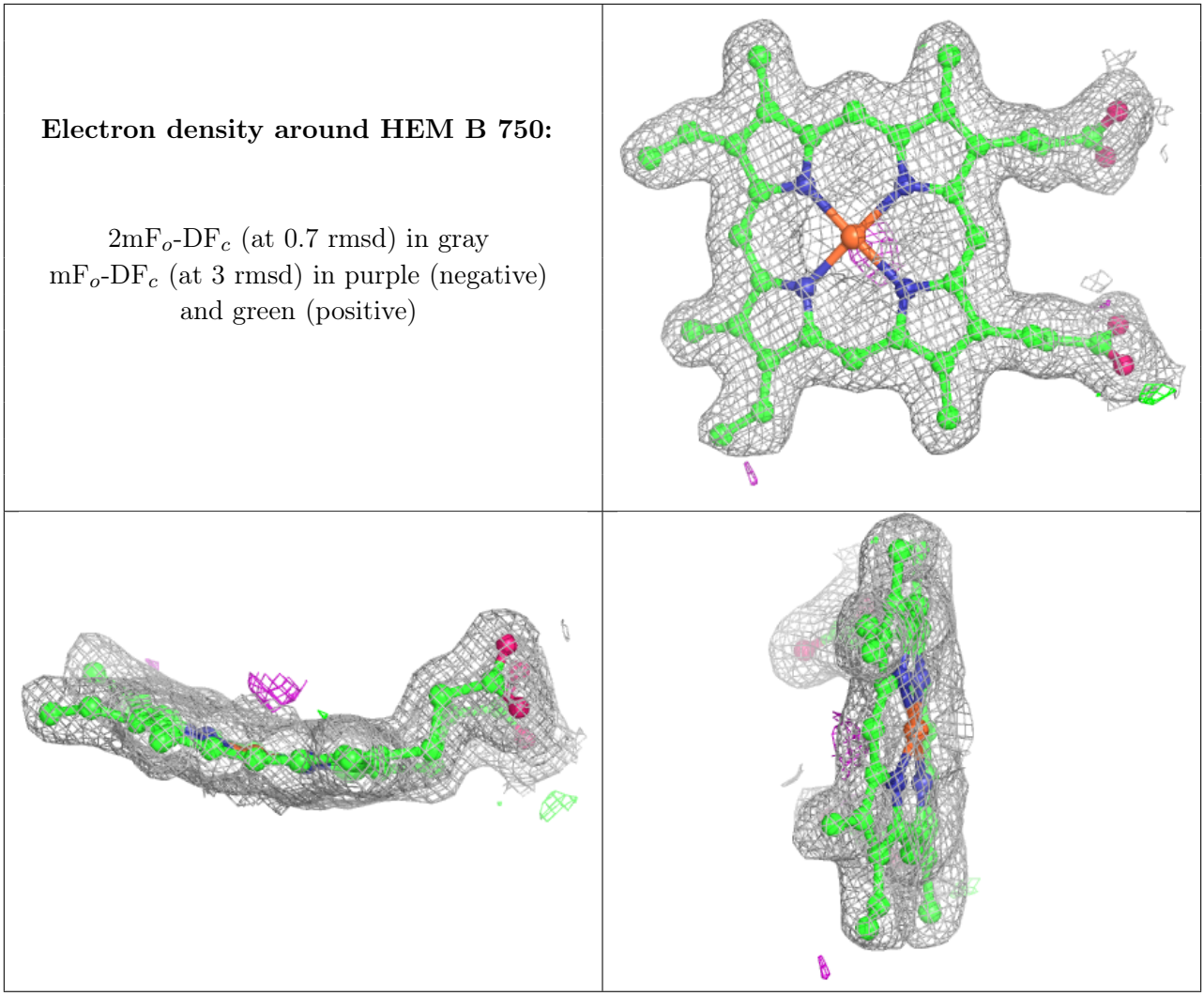
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
2	ACT	A	860	4/4	0.86	0.30	55,56,57,57	0
2	ACT	B	861	4/4	0.90	0.26	46,49,49,50	0
7	CMO	A	920	2/2	0.93	0.23	31,31,31,32	0
6	ARG	A	770	12/12	0.96	0.10	23,27,29,31	0
6	ARG	B	771	12/12	0.96	0.12	20,24,28,29	0
5	HBI	B	761	17/17	0.96	0.12	18,20,28,30	0
5	HBI	A	760	17/17	0.97	0.10	21,23,28,28	0
4	HEM	B	750	43/43	0.98	0.13	17,22,27,29	0
4	HEM	A	750	43/43	0.98	0.11	18,23,27,29	0
3	ZN	A	900	1/1	0.99	0.05	36,36,36,36	0
7	CMO	B	920	2/2	0.99	0.23	32,32,32,32	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.

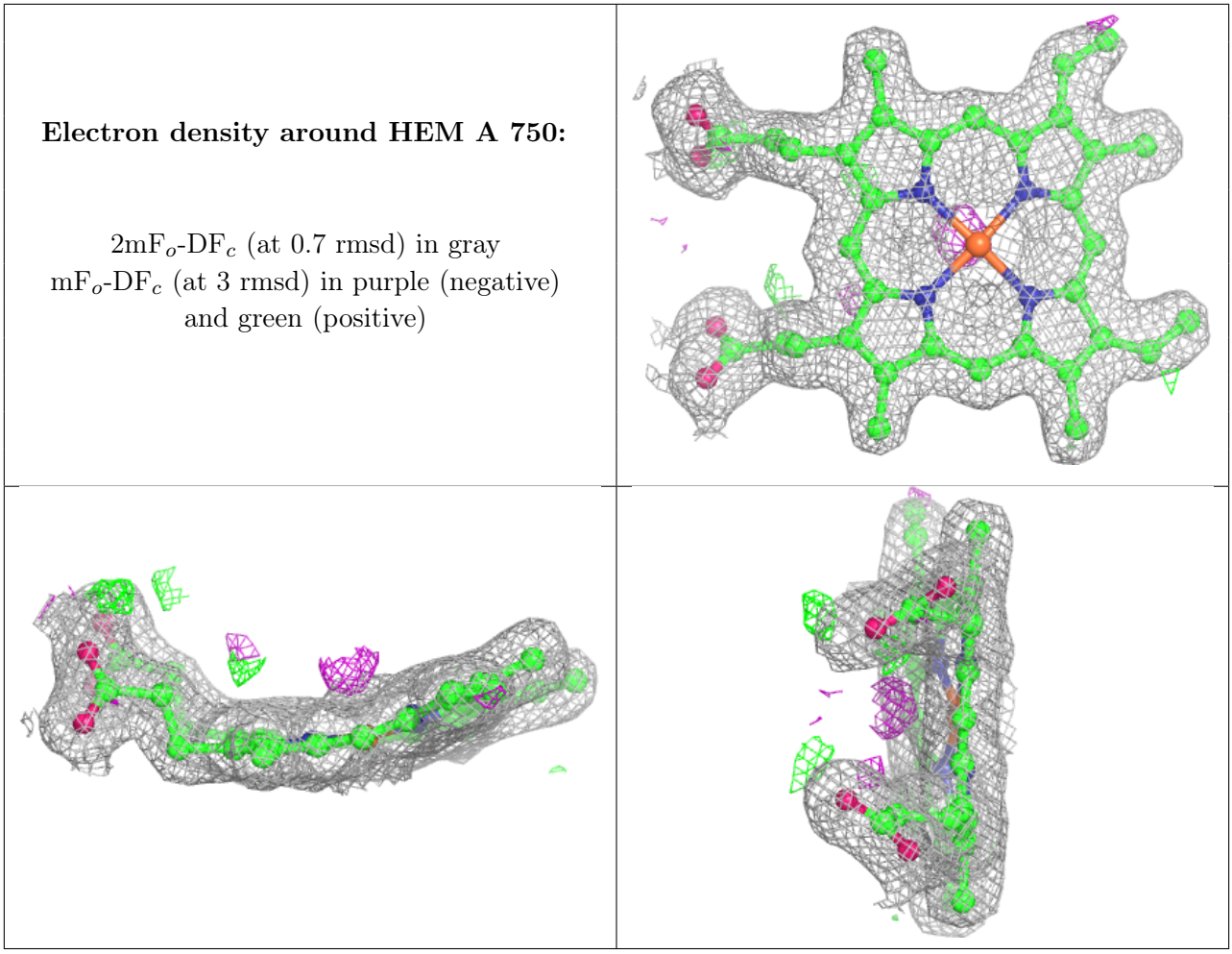
Electron density around HEM B 750:

$2mF_o$-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.