



Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 06:10 am BST

PDB ID : 4UH9
Title : Structure of bovine endothelial nitric oxide synthase heme domain in complex with N1-(3-(2-(6-Amino-4-methylpyridin-2-yl)ethyl)-5- fluorophenyl)-N1,N2-dimethylethane-1,2-diamine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2015-03-23
Resolution : 2.14 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 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 : 2.11
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) : 2.11

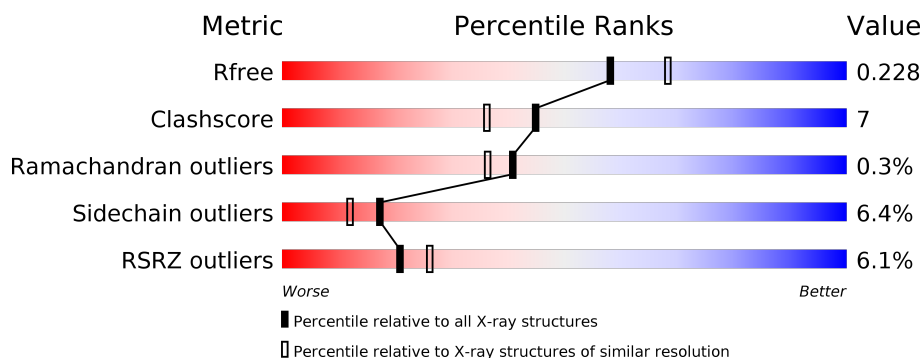
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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 on 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	443	 6% 77% 12% • 9%
1	B	443	 5% 77% 12% • 9%

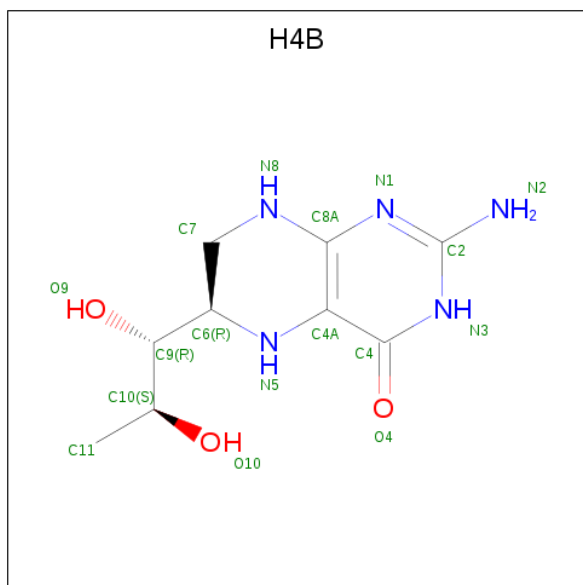
The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	GOL	A	880	-	-	-	X

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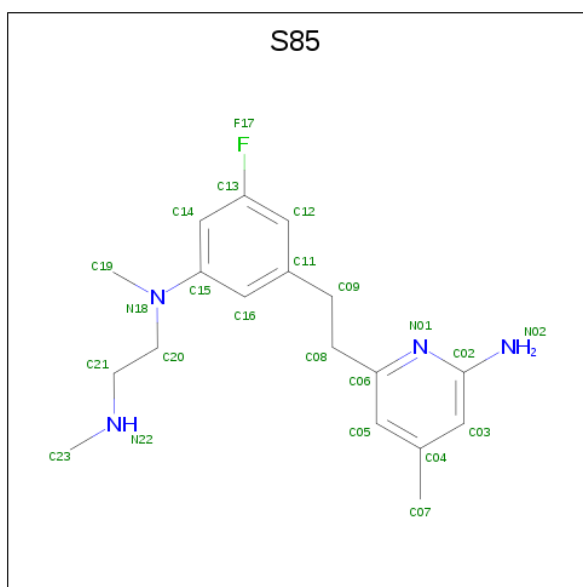
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Fe	N			O
2	B	1	43	34	1	4	4	0	0

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



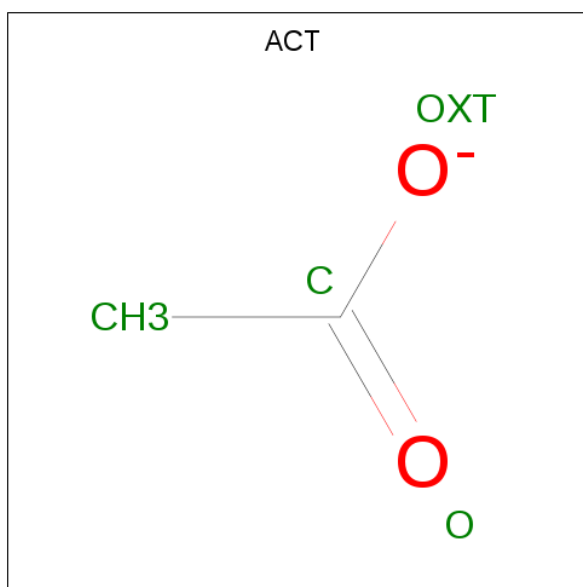
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	17	9	5	3	0	0
3	B	1	17	9	5	3	0	0

- Molecule 4 is N1-(3-(2-(6-AMINO-4-METHYLPYRIDIN-2-YL)ETHYL)-5-FLUOROPHENYL)-N1,N2-DIMETHYLETHANE-1,2-DIAMINE (three-letter code: S85) (formula: $C_{18}H_{25}FN_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	F	N		
4	A	1	23	18	1	4	0	0
4	A	1	23	18	1	4	0	0
4	B	1	23	18	1	4	0	0

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



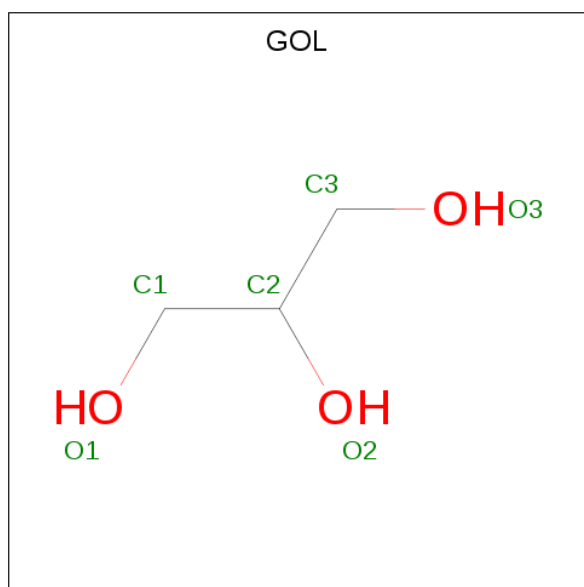
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	4	2	2	0	0

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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		
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	134	Total	O	0	0
			134	134		

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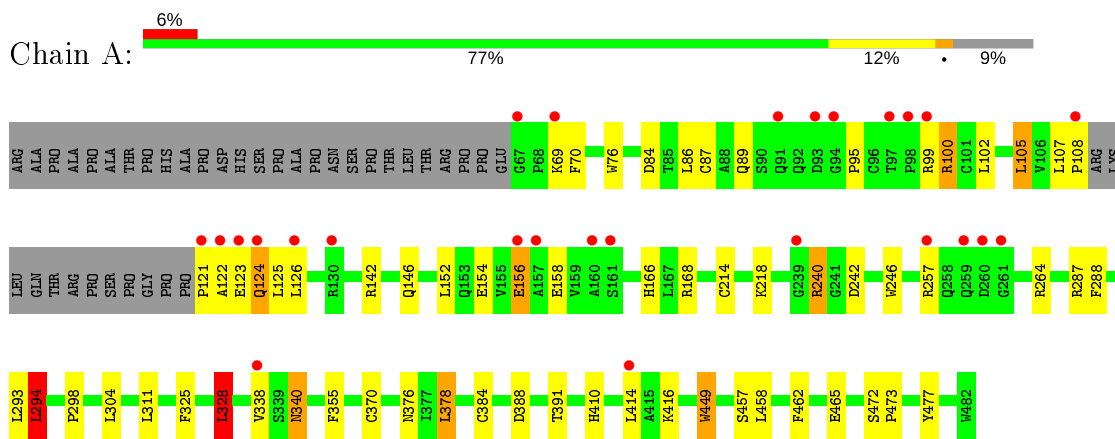
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	109	Total 109	O 109	0	0

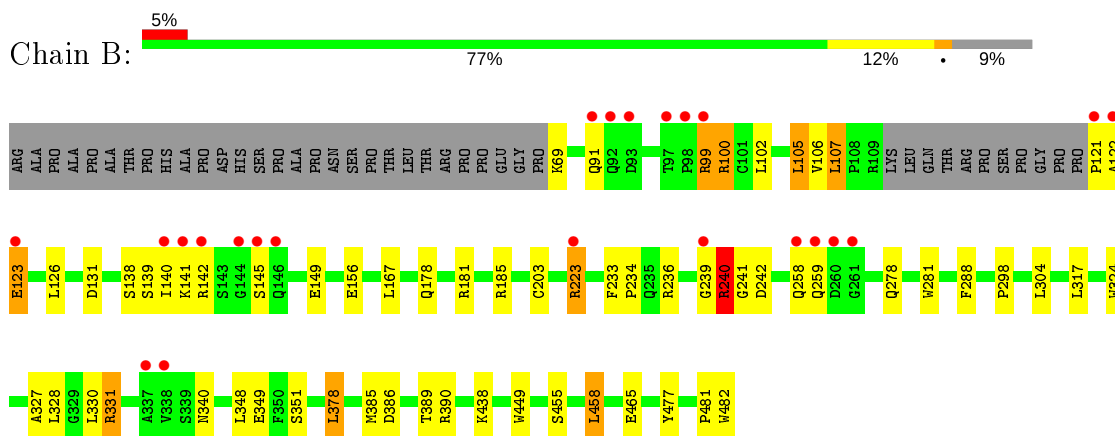
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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, ENDOTHELIAL



- Molecule 1: NITRIC OXIDE SYNTHASE, ENDOTHELIAL



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.22Å 106.78Å 157.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.46 – 2.14 39.48 – 2.14	Depositor EDS
% Data completeness (in resolution range)	98.2 (88.46-2.14) 98.3 (39.48-2.14)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 2.14Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.174 , 0.227 0.174 , 0.228	Depositor DCC
R_{free} test set	2701 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtrriage
Anisotropy	0.490	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6885	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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: GOL, ZN, H4B, CAS, S85, ACT, HEM

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	0.88	2/3292 (0.1%)	0.94	10/4483 (0.2%)
1	B	0.82	0/3291	0.91	3/4480 (0.1%)
All	All	0.85	2/6583 (0.0%)	0.92	13/8963 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	449	TRP	CE3-CZ3	5.55	1.47	1.38
1	A	288	PHE	CG-CD1	5.36	1.46	1.38

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	240	ARG	NE-CZ-NH1	14.22	127.41	120.30
1	B	240	ARG	NE-CZ-NH2	-13.56	113.52	120.30
1	A	240	ARG	NE-CZ-NH2	-10.74	114.93	120.30
1	A	240	ARG	NE-CZ-NH1	9.80	125.20	120.30
1	A	168	ARG	NE-CZ-NH1	6.94	123.77	120.30
1	A	168	ARG	NE-CZ-NH2	-6.58	117.01	120.30
1	A	328	LEU	CB-CG-CD1	6.08	121.34	111.00
1	A	242	ASP	CB-CG-OD1	5.88	123.59	118.30
1	A	294	LEU	CB-CG-CD1	5.47	120.30	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	388	ASP	CB-CG-OD1	5.40	123.16	118.30
1	A	378	LEU	CA-CB-CG	5.28	127.45	115.30
1	A	414	LEU	CB-CG-CD2	-5.25	102.07	111.00
1	B	378	LEU	CB-CG-CD1	5.19	119.82	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	239	GLY	Peptide

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	3212	0	3114	50	0
1	B	3212	0	3117	35	1
2	A	43	0	30	5	0
2	B	43	0	30	4	0
3	A	17	0	15	1	0
3	B	17	0	15	1	0
4	A	46	0	50	3	0
4	B	23	0	25	3	0
5	A	8	0	6	0	0
5	B	8	0	6	0	0
6	A	6	0	8	0	0
6	B	6	0	8	0	0
7	A	1	0	0	0	0
8	A	134	0	0	5	1
8	B	109	0	0	2	0
All	All	6885	0	6424	85	1

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 7.

All (85) 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:384:CAS:AS	1:A:384:CAS:SG	2.52	1.27
1:A:107:LEU:HD12	1:A:108:PRO:HD2	1.35	1.04
1:A:158:GLU:OE2	1:A:166:HIS:HD2	1.49	0.94
1:A:257:ARG:HG3	1:A:257:ARG:HH11	1.33	0.93
1:A:121:PRO:HB3	1:A:124:GLN:HG2	1.59	0.84
1:B:99:ARG:NH1	1:B:100:ARG:HD2	1.99	0.77
2:A:500:HEM:HBB2	2:A:500:HEM:HHC	1.66	0.77
1:B:223:ARG:NH1	1:B:223:ARG:HB2	1.99	0.76
1:B:99:ARG:HH11	1:B:100:ARG:HD2	1.49	0.75
1:B:236:ARG:HD3	1:B:351:SER:HB3	1.69	0.74
1:A:158:GLU:OE2	1:A:166:HIS:CD2	2.39	0.73
1:A:294:LEU:HD13	1:A:304:LEU:HD13	1.73	0.70
1:B:106:VAL:HG12	1:B:107:LEU:HD13	1.72	0.70
1:A:107:LEU:HD12	1:A:108:PRO:CD	2.17	0.70
1:A:105:LEU:HD13	1:B:465:GLU:OE1	1.93	0.69
1:A:257:ARG:NH1	1:A:257:ARG:HG3	2.03	0.69
1:B:281:TRP:HB2	1:B:304:LEU:HD21	1.75	0.68
1:A:240:ARG:HD3	1:A:298:PRO:HB3	1.75	0.68
1:B:236:ARG:HD2	1:B:242:ASP:OD1	1.95	0.66
1:A:384:CAS:CE2	1:A:384:CAS:SG	2.85	0.64
4:B:800:S85:H231	8:B:2107:HOH:O	1.96	0.63
1:B:481:PRO:HD2	1:B:482:TRP:CE3	2.37	0.60
1:A:121:PRO:HB3	1:A:124:GLN:CG	2.29	0.60
1:B:223:ARG:HH11	1:B:223:ARG:HB2	1.67	0.60
1:B:324:TRP:O	1:B:327:ALA:HB3	2.07	0.55
1:A:95:PRO:HB3	1:A:108:PRO:HB2	1.89	0.54
2:B:500:HEM:C1C	4:B:800:S85:H073	2.42	0.54
1:A:87:CYS:SG	1:B:99:ARG:NH1	2.81	0.53
1:A:465:GLU:HB3	1:B:105:LEU:HD22	1.91	0.53
1:B:167:LEU:HG	1:B:348:LEU:HD12	1.91	0.52
2:A:500:HEM:CBB	2:A:500:HEM:HHC	2.38	0.52
1:A:264:ARG:HD3	8:A:2064:HOH:O	2.10	0.51
1:A:340:ASN:HD22	1:A:340:ASN:H	1.58	0.51
1:A:376:ASN:ND2	8:A:2092:HOH:O	2.41	0.50
1:A:154:GLU:CG	4:A:801:S85:H092	2.42	0.49
1:A:76:TRP:HH2	1:B:107:LEU:HD22	1.78	0.49
1:A:384:CAS:CB	1:A:384:CAS:AS	3.21	0.48
1:B:317:LEU:HG	1:B:331:ARG:HA	1.95	0.48
1:A:214:CYS:SG	8:A:2043:HOH:O	2.56	0.48
1:A:214:CYS:O	1:A:218:LYS:HG3	2.14	0.47
1:A:152:LEU:O	1:A:156:GLU:HG2	2.14	0.47
1:B:455:SER:HB3	1:B:458:LEU:HD22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:ARG:CZ	1:B:223:ARG:HB2	2.42	0.47
1:B:178:GLN:HE22	1:B:181:ARG:HH11	1.61	0.47
1:A:246:TRP:HB2	1:A:294:LEU:HB3	1.96	0.47
1:B:390:ARG:HB2	1:B:390:ARG:HE	1.23	0.46
1:B:385:MET:O	1:B:386:ASP:HB3	2.15	0.46
1:A:257:ARG:CG	1:A:257:ARG:NH1	2.74	0.46
1:A:105:LEU:N	1:A:105:LEU:CD2	2.79	0.45
1:A:100:ARG:HD2	8:B:2008:HOH:O	2.16	0.45
1:A:338:VAL:HG21	4:A:800:S85:C13	2.46	0.45
1:A:287:ARG:NH1	8:A:2070:HOH:O	2.30	0.45
1:B:449:TRP:HA	3:B:600:H4B:N1	2.31	0.44
1:A:449:TRP:HA	3:A:600:H4B:N1	2.32	0.44
1:A:70:PHE:HB3	1:A:84:ASP:O	2.17	0.44
1:A:457:SER:HA	1:A:462:PHE:CG	2.53	0.44
1:A:477:TYR:OH	2:A:500:HEM:O2D	2.26	0.44
1:A:126:LEU:HA	1:A:126:LEU:HD12	1.74	0.44
1:B:185:ARG:HD3	1:B:449:TRP:CD2	2.53	0.44
1:B:288:PHE:CB	1:B:331:ARG:HD3	2.48	0.44
1:A:142:ARG:HA	1:A:142:ARG:HD3	1.79	0.43
1:A:294:LEU:HD13	1:A:304:LEU:CD1	2.47	0.43
1:A:338:VAL:HG23	4:A:800:S85:H05	1.99	0.43
1:B:140:ILE:C	1:B:141:LYS:HG2	2.35	0.43
1:A:86:LEU:O	1:A:89:GLN:HB2	2.18	0.43
2:B:500:HEM:CBA	4:B:800:S85:H092	2.48	0.43
1:A:410:HIS:ND1	8:A:2104:HOH:O	2.35	0.43
1:A:449:TRP:HZ3	2:A:500:HEM:O2A	2.00	0.43
1:B:481:PRO:HD2	1:B:482:TRP:CZ3	2.54	0.43
1:B:121:PRO:HD2	1:B:123:GLU:OE1	2.19	0.43
1:A:457:SER:HA	1:A:462:PHE:CB	2.50	0.42
1:B:233:PHE:HB3	1:B:234:PRO:CD	2.49	0.42
1:B:477:TYR:OH	2:B:500:HEM:O1D	2.25	0.42
1:A:340:ASN:HD22	1:A:340:ASN:N	2.17	0.42
1:A:355:PHE:CD1	2:A:500:HEM:CAC	3.02	0.42
1:B:142:ARG:O	1:B:145:SER:OG	2.29	0.42
1:B:122:ALA:O	1:B:126:LEU:HB2	2.20	0.41
1:A:472:SER:HA	1:A:473:PRO:C	2.40	0.41
1:B:241:GLY:O	1:B:298:PRO:HB3	2.20	0.41
1:A:370:CYS:SG	1:A:378:LEU:HD13	2.60	0.41
1:A:76:TRP:CH2	1:B:107:LEU:HD22	2.56	0.41
1:B:236:ARG:HG3	1:B:349:GLU:HB2	2.03	0.41
1:A:325:PHE:O	1:A:328:LEU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:CYS:SG	1:B:99:ARG:CZ	3.10	0.40
2:B:500:HEM:HBB2	2:B:500:HEM:HHC	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:ARG:NH2	8:A:2039:HOH:O[2_555]	2.19	0.01

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	399/443 (90%)	387 (97%)	11 (3%)	1 (0%)	41 36
1	B	398/443 (90%)	382 (96%)	15 (4%)	1 (0%)	41 36
All	All	797/886 (90%)	769 (96%)	26 (3%)	2 (0%)	41 36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	328	LEU
1	A	122	ALA

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	342/375 (91%)	324 (95%)	18 (5%)	22	18
1	B	342/375 (91%)	316 (92%)	26 (8%)	13	7
All	All	684/750 (91%)	640 (94%)	44 (6%)	17	12

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	LYS
1	A	99	ARG
1	A	100	ARG
1	A	102	LEU
1	A	105	LEU
1	A	123	GLU
1	A	124	GLN
1	A	125	LEU
1	A	146	GLN
1	A	156	GLU
1	A	293	LEU
1	A	294	LEU
1	A	311	LEU
1	A	328	LEU
1	A	340	ASN
1	A	391	THR
1	A	416	LYS
1	A	458	LEU
1	B	69	LYS
1	B	91	GLN
1	B	99	ARG
1	B	100	ARG
1	B	102	LEU
1	B	105	LEU
1	B	107	LEU
1	B	123	GLU
1	B	131	ASP
1	B	138	SER
1	B	139	SER
1	B	149	GLU
1	B	156	GLU
1	B	203	CYS
1	B	223	ARG
1	B	240	ARG
1	B	258	GLN

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Mol	Chain	Res	Type
1	B	259	GLN
1	B	278	GLN
1	B	330	LEU
1	B	331	ARG
1	B	340	ASN
1	B	378	LEU
1	B	389	THR
1	B	438	LYS
1	B	458	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	GLN
1	A	146	GLN
1	A	166	HIS
1	A	191	GLN
1	A	340	ASN
1	A	376	ASN
1	A	413	GLN
1	A	468	ASN
1	B	178	GLN
1	B	191	GLN
1	B	222	ASN
1	B	225	ASN
1	B	258	GLN
1	B	340	ASN
1	B	376	ASN
1	B	405	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](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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
1	CAS	A	384	1	5,8,9	1.79	1 (20%)	1,9,11	0.66	0
1	CAS	B	384	1	5,8,9	1.35	2 (40%)	1,9,11	0.85	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
1	CAS	A	384	1	-	0/0/7/9	-
1	CAS	B	384	1	-	0/0/7/9	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	384	CAS	AS-CE1	3.60	2.05	1.96
1	B	384	CAS	AS-CE2	2.23	2.01	1.96
1	B	384	CAS	AS-CE1	2.00	2.01	1.96

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	384	CAS	3	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 1 is monoatomic - leaving 13 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	-	1,3,3	0.35	0	0,3,3	0.00	-
2	HEM	A	500	1	27,50,50	1.00	1 (3%)	17,82,82	2.06	8 (47%)
5	ACT	A	861	-	1,3,3	4.13	1 (100%)	0,3,3	0.00	-
3	H4B	A	600	-	16,18,18	1.16	2 (12%)	11,26,26	3.25	7 (63%)
5	ACT	B	860	-	1,3,3	1.24	0	0,3,3	0.00	-
6	GOL	B	880	-	5,5,5	0.29	0	5,5,5	0.85	0
4	S85	A	800	-	24,24,24	1.33	2 (8%)	32,32,32	2.21	10 (31%)
4	S85	B	800	-	24,24,24	0.95	1 (4%)	32,32,32	1.96	10 (31%)
4	S85	A	801	-	24,24,24	1.21	1 (4%)	32,32,32	1.77	5 (15%)
5	ACT	B	861	-	1,3,3	2.70	1 (100%)	0,3,3	0.00	-
3	H4B	B	600	-	16,18,18	1.21	2 (12%)	11,26,26	2.72	6 (54%)
6	GOL	A	880	-	5,5,5	0.71	0	5,5,5	0.75	0
2	HEM	B	500	1	27,50,50	1.18	4 (14%)	17,82,82	1.73	1 (5%)

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	A	500	1	-	2/6/54/54	-
3	H4B	A	600	-	-	0/8/17/17	0/2/2/2
6	GOL	B	880	-	-	0/4/4/4	-
4	S85	A	800	-	-	3/13/13/13	0/2/2/2
4	S85	B	800	-	-	3/13/13/13	0/2/2/2
4	S85	A	801	-	-	3/13/13/13	0/2/2/2
3	H4B	B	600	-	-	3/8/17/17	0/2/2/2
6	GOL	A	880	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	B	500	1	-	0/6/54/54	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	861	ACT	CH3-C	4.13	1.54	1.48
3	A	600	H4B	C2-N2	2.75	1.39	1.33
5	B	861	ACT	CH3-C	2.70	1.52	1.48
4	B	800	S85	C14-C13	2.64	1.42	1.37
3	B	600	H4B	C7-C6	2.61	1.54	1.52
2	B	500	HEM	C4D-C3D	2.59	1.48	1.42
2	B	500	HEM	C3B-C2B	-2.52	1.36	1.40
4	A	800	S85	C14-C13	2.51	1.41	1.37
4	A	801	S85	C05-C04	2.43	1.43	1.39
4	A	800	S85	C03-C02	2.24	1.43	1.39
2	A	500	HEM	C3B-C2B	-2.21	1.37	1.40
2	B	500	HEM	CAA-C2A	-2.14	1.48	1.52
3	B	600	H4B	C4-N3	2.11	1.36	1.33
2	B	500	HEM	CAD-C3D	2.08	1.55	1.52
3	A	600	H4B	C7-C6	2.03	1.54	1.52

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	HEM	CBA-CAA-C2A	-5.90	101.61	112.49
4	A	800	S85	C02-N01-C06	5.84	122.52	118.10
3	A	600	H4B	N3-C2-N1	-5.28	117.14	125.42
4	A	801	S85	C02-N01-C06	5.15	122.01	118.10
4	B	800	S85	C02-N01-C06	5.12	121.98	118.10
3	A	600	H4B	C4-N3-C2	4.93	123.76	115.93
4	A	800	S85	C09-C11-C12	-4.80	112.66	120.54
4	B	800	S85	C05-C06-N01	-4.63	117.99	122.90
3	A	600	H4B	C4-C4A-C8A	4.19	118.29	114.57
3	B	600	H4B	C4-N3-C2	4.10	122.44	115.93
3	B	600	H4B	N3-C2-N1	-4.09	119.00	125.42
3	A	600	H4B	C4-C4A-N5	3.97	122.46	119.12
2	A	500	HEM	CBD-CAD-C3D	3.94	119.74	112.48
4	A	800	S85	C15-C14-C13	3.89	122.50	118.06
4	A	801	S85	C20-C21-N22	3.88	121.38	111.04
4	A	800	S85	C12-C13-C14	-3.71	118.83	123.52
3	B	600	H4B	C4-C4A-C8A	3.69	117.85	114.57
3	A	600	H4B	C2-N1-C8A	3.44	122.25	114.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	800	S85	C14-C15-N18	-3.29	117.52	121.33
4	A	800	S85	F17-C13-C14	3.25	122.90	118.25
4	A	801	S85	C21-C20-N18	-3.16	100.85	112.31
2	A	500	HEM	C1D-C2D-C3D	-3.15	104.80	107.00
4	A	800	S85	C05-C06-N01	-3.11	119.60	122.90
3	B	600	H4B	C4-C4A-N5	3.11	121.73	119.12
2	A	500	HEM	CMC-C2C-C3C	3.09	130.46	124.68
4	B	800	S85	C12-C13-C14	-3.05	119.67	123.52
3	A	600	H4B	N2-C2-N1	2.92	121.80	117.25
4	B	800	S85	C09-C08-C06	2.81	119.30	112.99
2	A	500	HEM	CBA-CAA-C2A	-2.80	107.32	112.49
3	B	600	H4B	C2-N1-C8A	2.79	120.80	114.54
3	B	600	H4B	N2-C2-N1	2.79	121.59	117.25
4	A	800	S85	C09-C11-C16	2.79	125.12	120.54
4	B	800	S85	C08-C06-N01	2.74	120.03	115.95
4	B	800	S85	C09-C11-C12	-2.73	116.05	120.54
4	A	800	S85	C16-C15-N18	2.73	124.48	121.33
4	B	800	S85	F17-C13-C14	2.69	122.10	118.25
2	A	500	HEM	CMA-C3A-C2A	2.56	129.77	124.94
2	A	500	HEM	CMA-C3A-C4A	-2.48	124.65	128.46
4	A	801	S85	C05-C06-N01	-2.43	120.32	122.90
3	A	600	H4B	N2-C2-N3	2.40	120.98	117.25
4	A	800	S85	C16-C11-C12	2.36	122.22	118.98
4	B	800	S85	C14-C15-N18	-2.29	118.68	121.33
2	A	500	HEM	CAA-CBA-CGA	2.24	116.44	112.67
4	B	800	S85	C21-C20-N18	-2.24	104.17	112.31
2	A	500	HEM	C4A-C3A-C2A	-2.22	105.45	107.00
4	B	800	S85	C15-C14-C13	2.20	120.57	118.06
4	A	801	S85	C15-C14-C13	2.19	120.56	118.06

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	HEM	C2D-C3D-CAD-CBD
2	A	500	HEM	C4D-C3D-CAD-CBD
4	B	800	S85	N18-C20-C21-N22
4	A	801	S85	N18-C20-C21-N22
4	A	800	S85	C20-C21-N22-C23
3	B	600	H4B	C7-C6-C9-O9
3	B	600	H4B	C7-C6-C9-C10
4	A	800	S85	C06-C08-C09-C11

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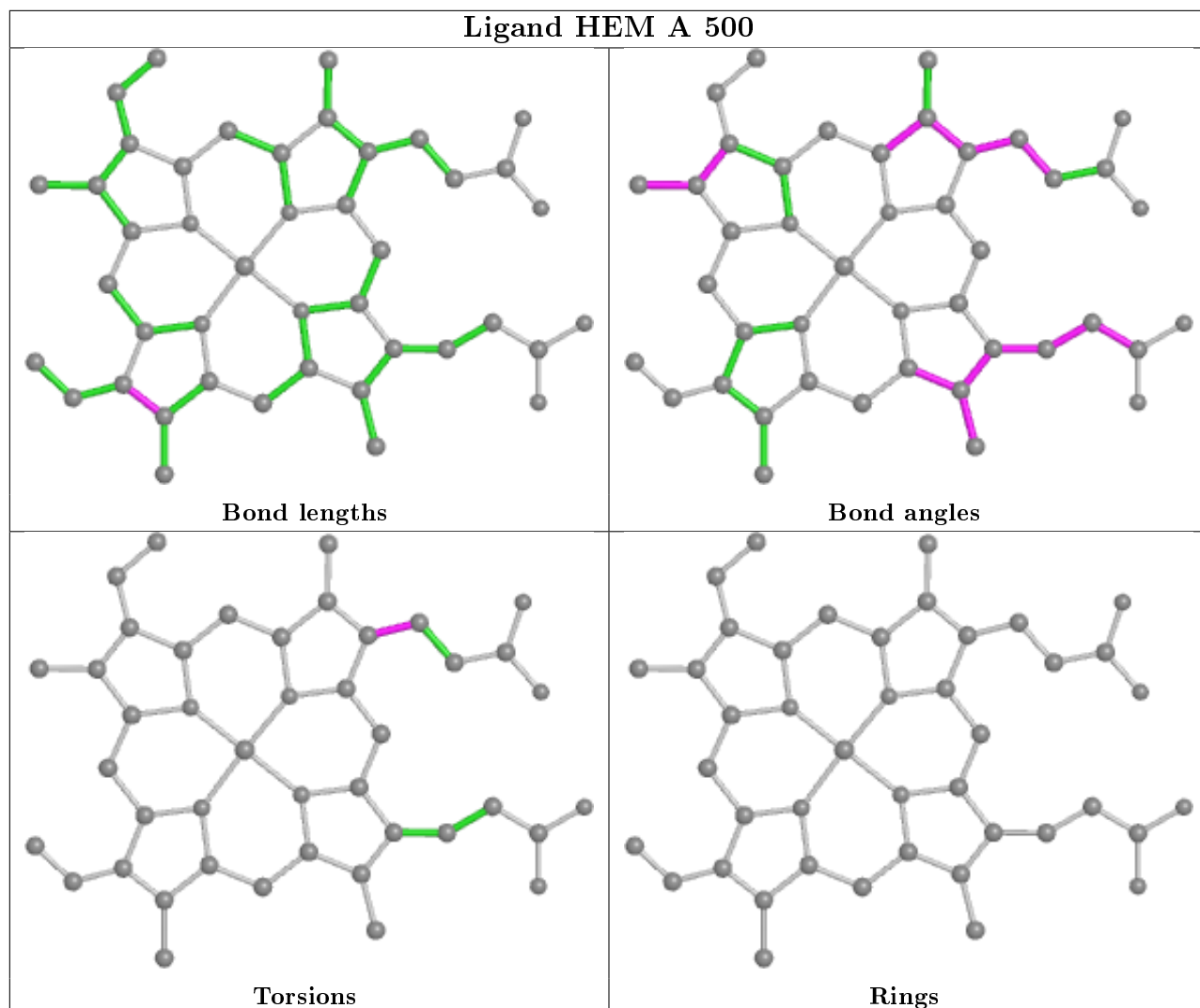
Mol	Chain	Res	Type	Atoms
4	A	800	S85	C21-C20-N18-C19
4	A	801	S85	C21-C20-N18-C19
4	A	801	S85	C20-C21-N22-C23
4	B	800	S85	C06-C08-C09-C11
4	B	800	S85	C16-C15-N18-C19
3	B	600	H4B	N5-C6-C9-O9

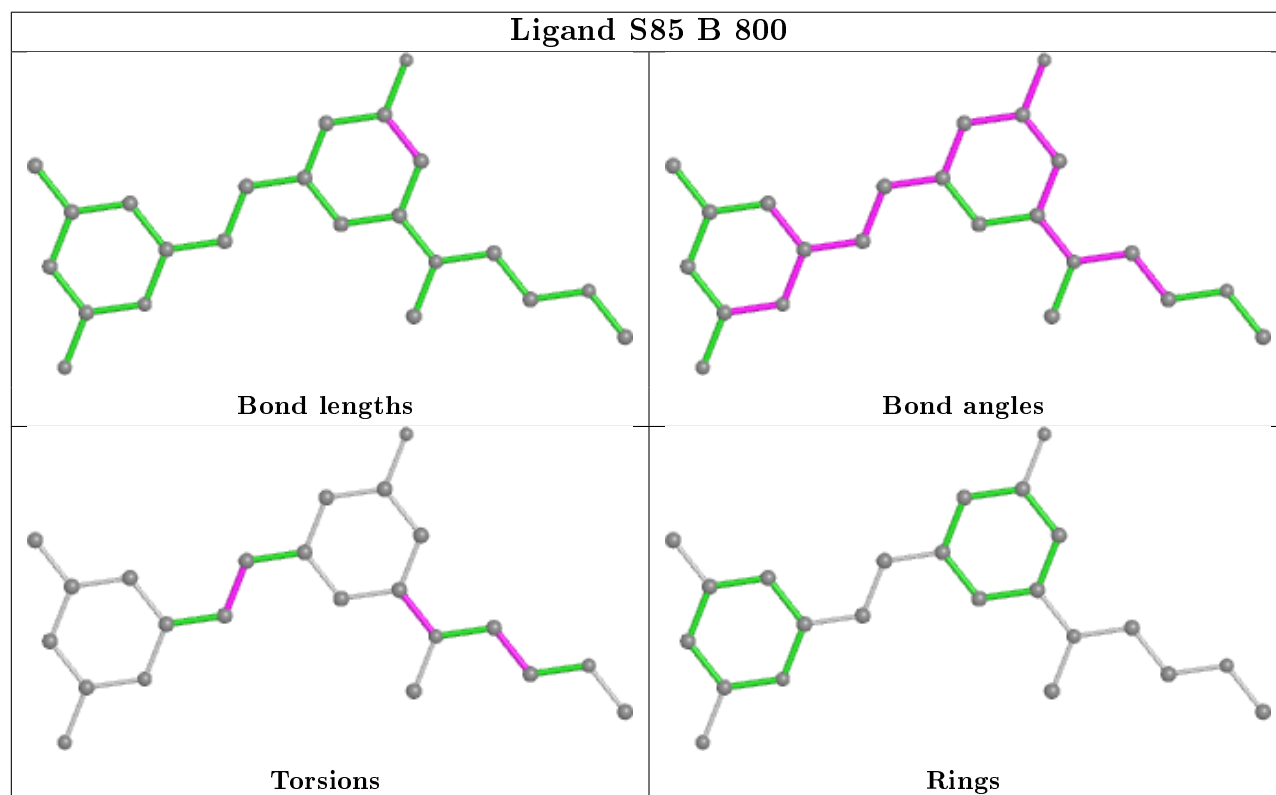
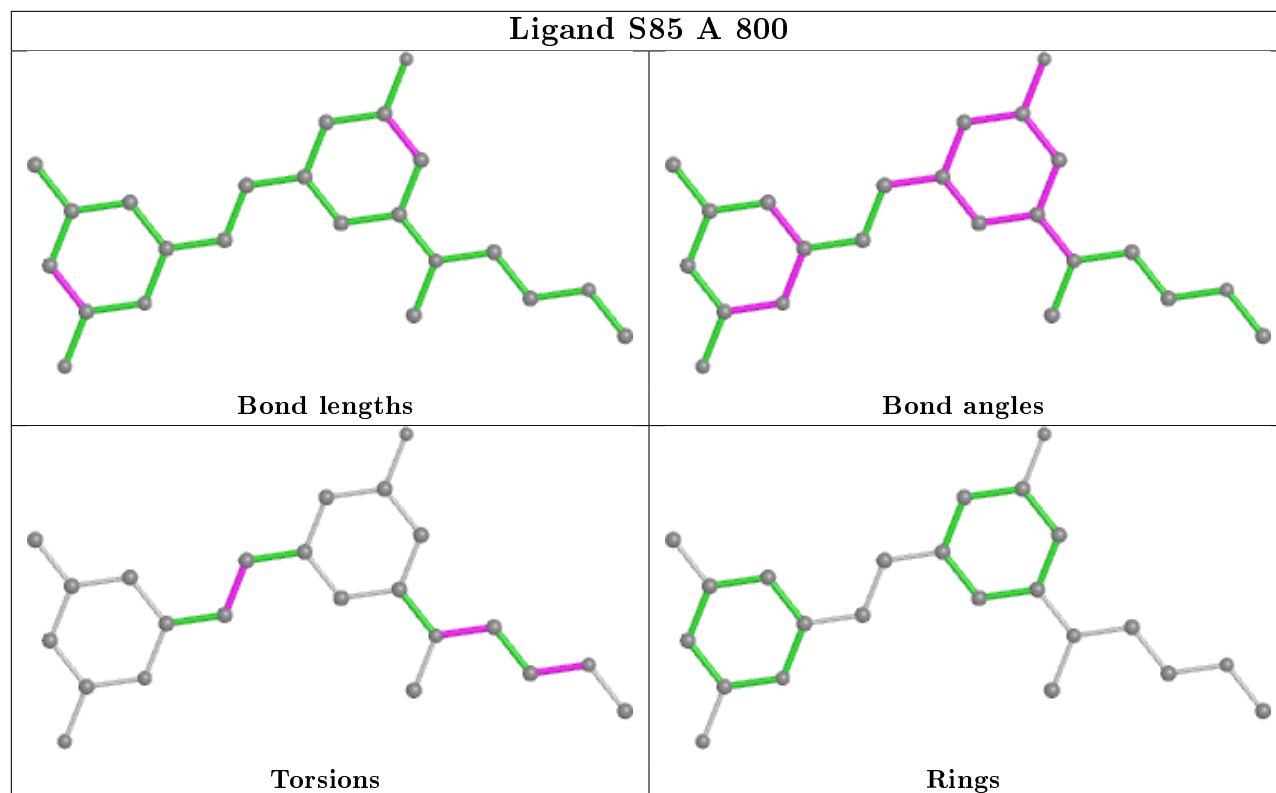
There are no ring outliers.

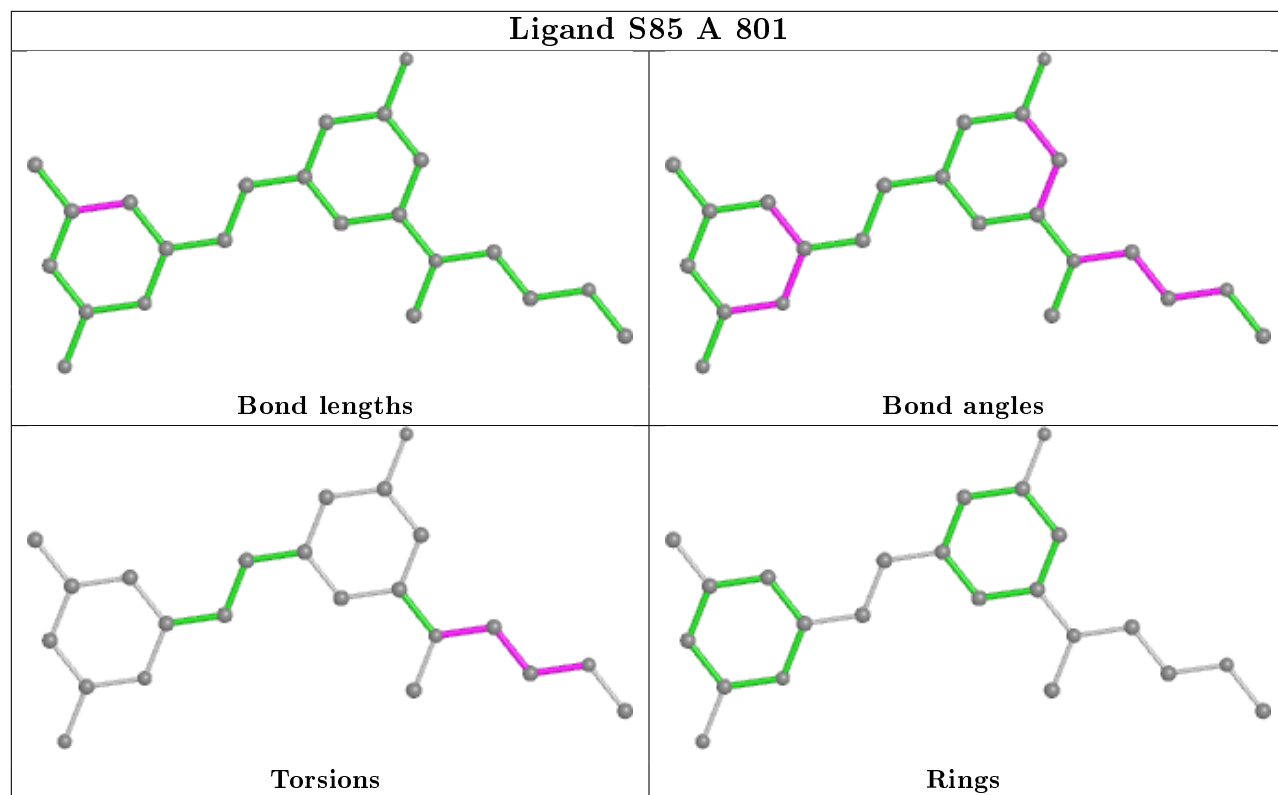
7 monomers are involved in 15 short contacts:

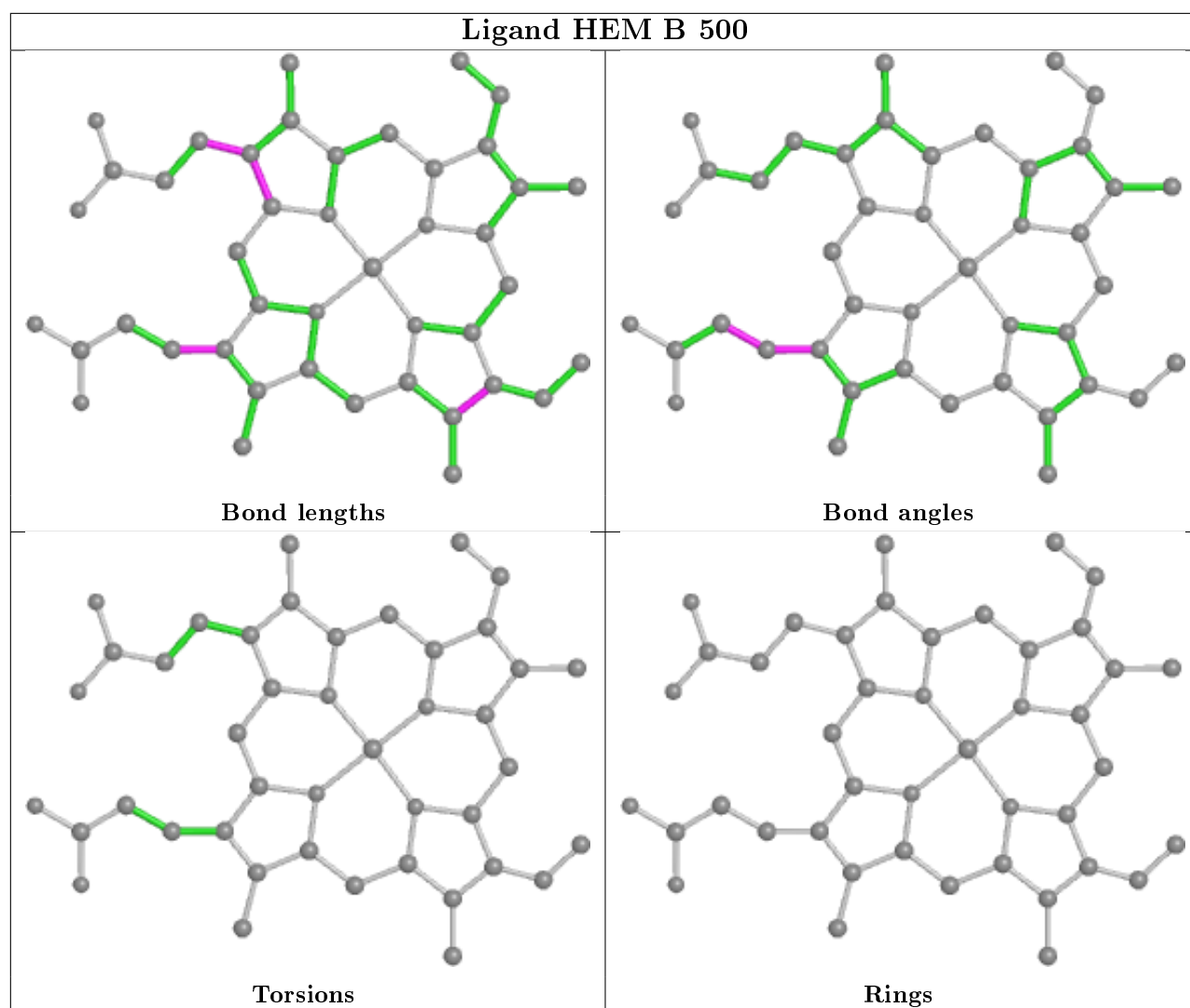
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	HEM	5	0
3	A	600	H4B	1	0
4	A	800	S85	2	0
4	B	800	S85	3	0
4	A	801	S85	1	0
3	B	600	H4B	1	0
2	B	500	HEM	4	0

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	403/443 (90%)	0.10	26 (6%) 18 23	32, 45, 78, 109	0
1	B	402/443 (90%)	0.09	23 (5%) 23 30	33, 49, 84, 119	0
All	All	805/886 (90%)	0.09	49 (6%) 21 26	32, 47, 82, 119	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	91	GLN	6.5
1	B	122	ALA	5.3
1	B	259	GLN	5.3
1	A	123	GLU	5.2
1	A	160	ALA	5.2
1	A	67	GLY	4.8
1	B	121	PRO	4.7
1	A	259	GLN	4.6
1	A	121	PRO	4.5
1	B	98	PRO	4.4
1	B	123	GLU	4.3
1	A	122	ALA	4.2
1	A	69	LYS	4.1
1	A	91	GLN	4.1
1	A	126	LEU	3.9
1	B	146	GLN	3.4
1	B	93	ASP	3.4
1	B	142	ARG	3.3
1	A	98	PRO	3.3
1	A	157	ALA	3.3
1	A	124	GLN	3.2
1	A	338	VAL	3.2
1	B	260	ASP	3.0
1	B	99	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	261	GLY	3.0
1	A	130	ARG	2.9
1	B	92	GLN	2.8
1	A	97	THR	2.7
1	A	260	ASP	2.7
1	B	145	SER	2.7
1	A	99	ARG	2.6
1	A	239	GLY	2.5
1	A	156	GLU	2.5
1	B	239	GLY	2.5
1	B	144	GLY	2.4
1	B	223	ARG	2.4
1	B	258	GLN	2.4
1	A	93	ASP	2.4
1	B	140	ILE	2.4
1	B	97	THR	2.2
1	B	141	LYS	2.2
1	A	161	SER	2.2
1	A	257	ARG	2.2
1	B	338	VAL	2.1
1	A	414	LEU	2.1
1	A	108	PRO	2.1
1	B	337	ALA	2.0
1	B	261	GLY	2.0
1	A	94	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CAS	A	384	9/10	0.95	0.09	39,42,80,81	0
1	CAS	B	384	9/10	0.97	0.13	55,60,112,112	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands

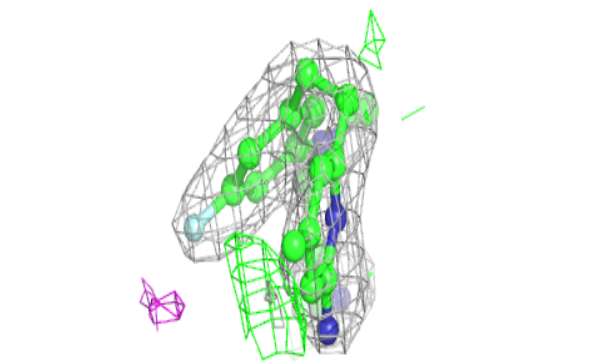
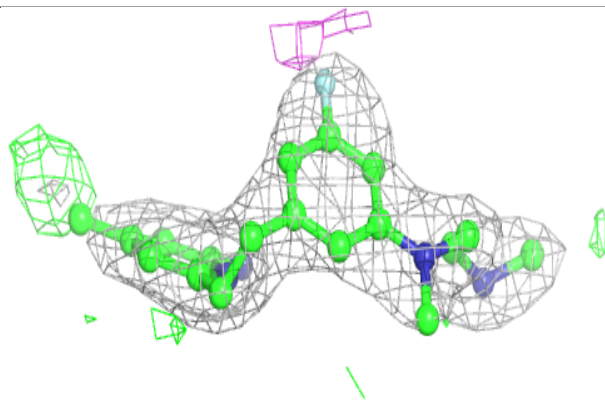
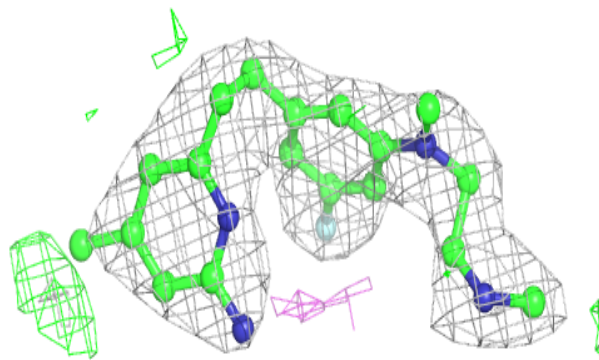
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	GOL	A	880	6/6	0.78	0.42	59,85,87,91	0
4	S85	A	801	23/23	0.86	0.16	42,68,75,76	0
6	GOL	B	880	6/6	0.92	0.30	69,76,78,79	0
4	S85	B	800	23/23	0.92	0.25	44,60,95,109	0
4	S85	A	800	23/23	0.95	0.25	29,55,82,94	0
5	ACT	A	860	4/4	0.95	0.12	40,47,47,53	0
3	H4B	A	600	17/17	0.96	0.17	40,49,53,55	0
5	ACT	A	861	4/4	0.96	0.21	41,44,47,49	0
3	H4B	B	600	17/17	0.97	0.14	43,47,55,57	0
2	HEM	A	500	43/43	0.98	0.19	22,30,65,72	0
5	ACT	B	861	4/4	0.98	0.18	43,45,51,54	0
2	HEM	B	500	43/43	0.98	0.14	35,41,52,64	0
7	ZN	A	1483	1/1	0.99	0.04	64,64,64,64	0
5	ACT	B	860	4/4	0.99	0.17	46,50,52,53	0

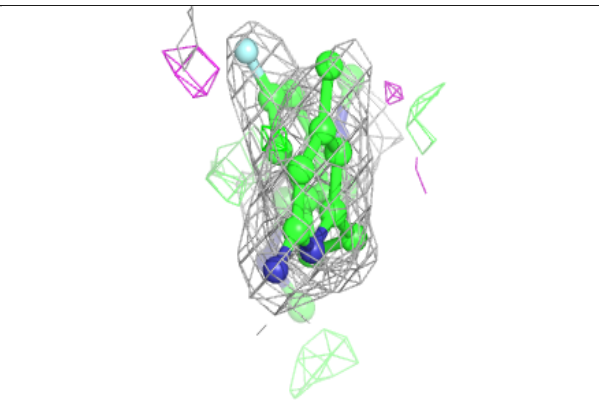
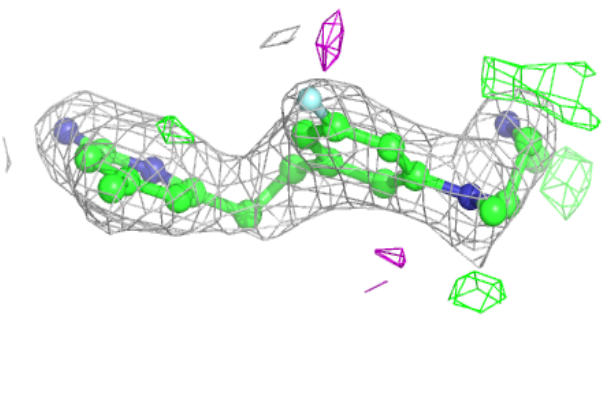
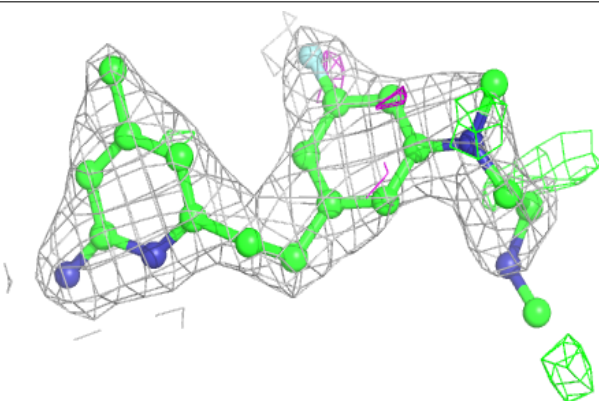
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around S85 A 801:

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

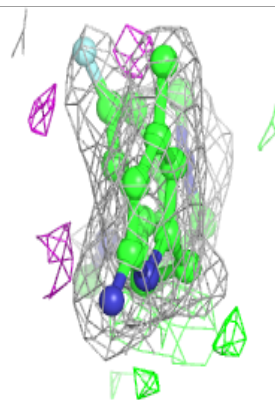
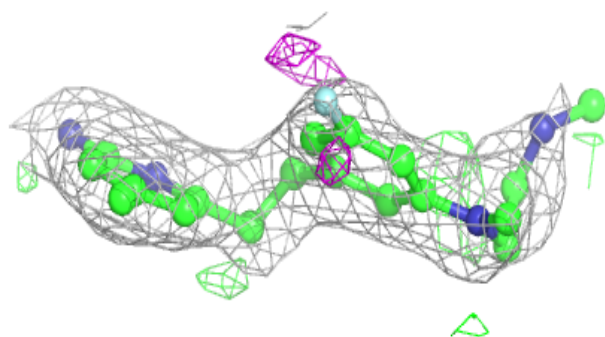
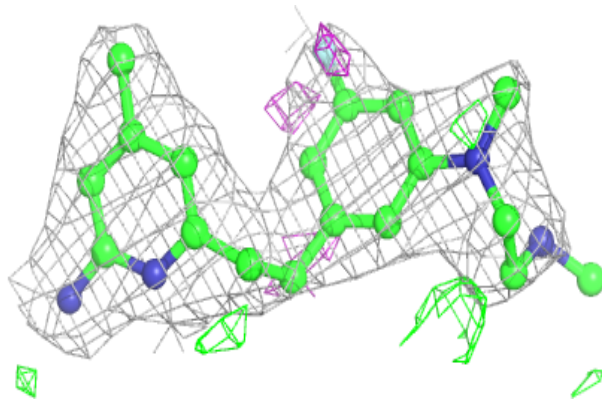
**Electron density around S85 B 800:**

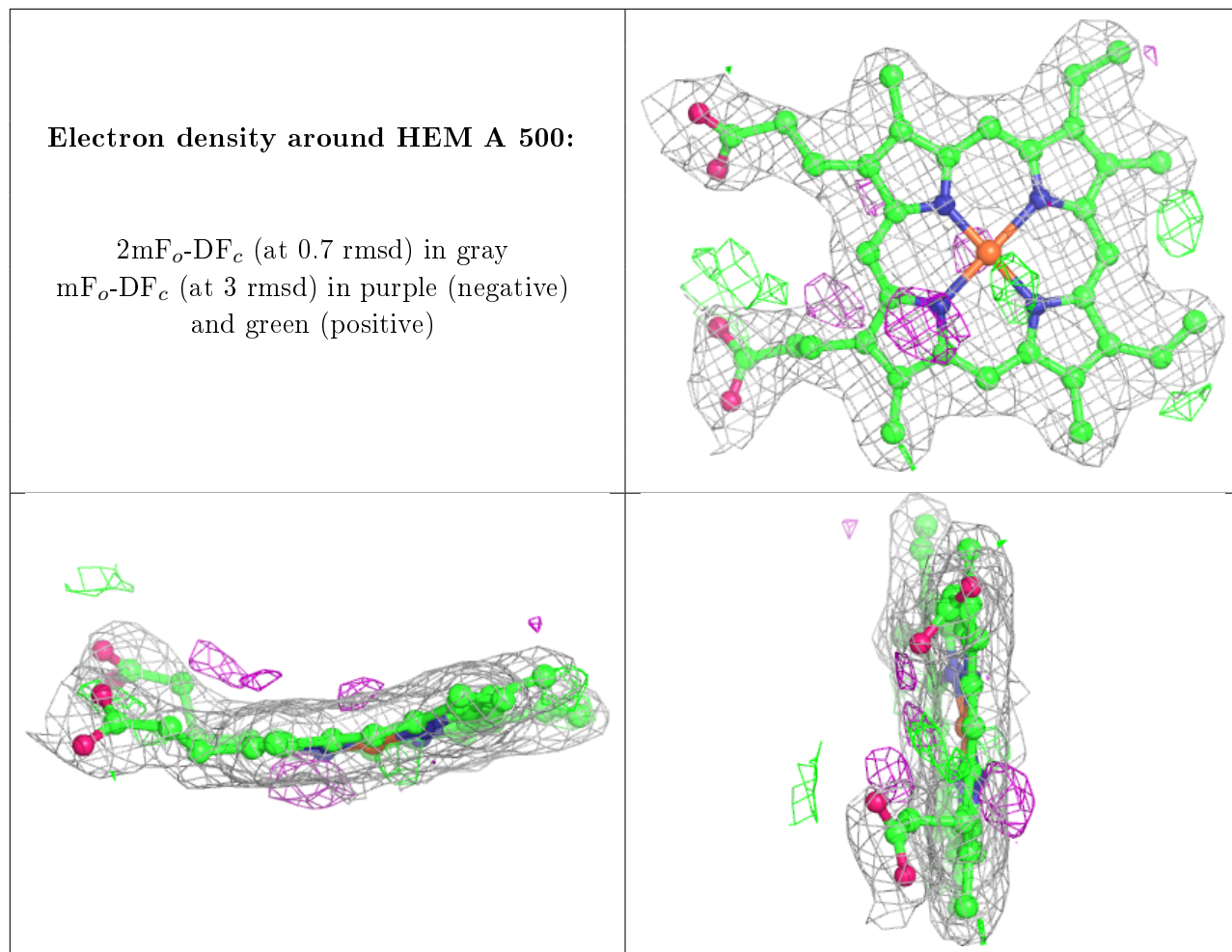
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

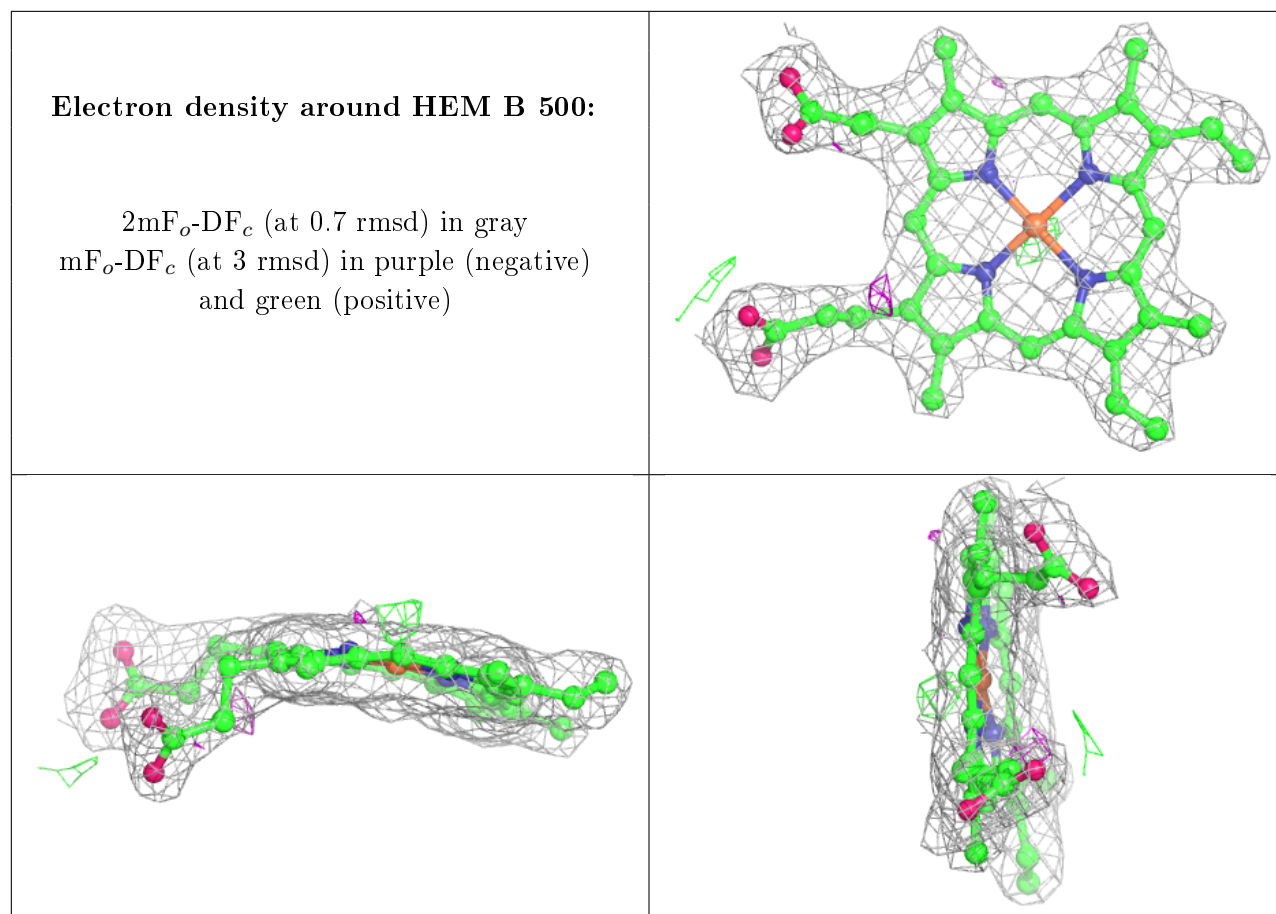


Electron density around S85 A 800:

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







6.5 Other polymers [i](#)

There are no such residues in this entry.