



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 10:21 PM UTC

PDB ID : 7TS8 / pdb_00007ts8
Title : Structure of human neuronal nitric oxide synthase R354A/G357D mutant heme domain in complex with 4-chloro-6-((5-(2-(dimethylamino)ethyl)-2,3-difluorophenyl)ethynyl)pyridin-2-amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2022-01-31
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

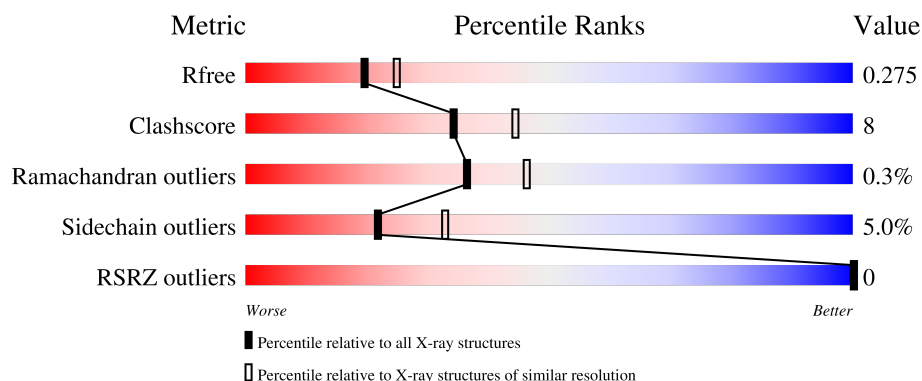
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	423	 72% 24% ..
1	B	423	 76% 20% ..
1	C	423	 75% 20% ..
1	D	423	 79% 18% ..

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14213 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.

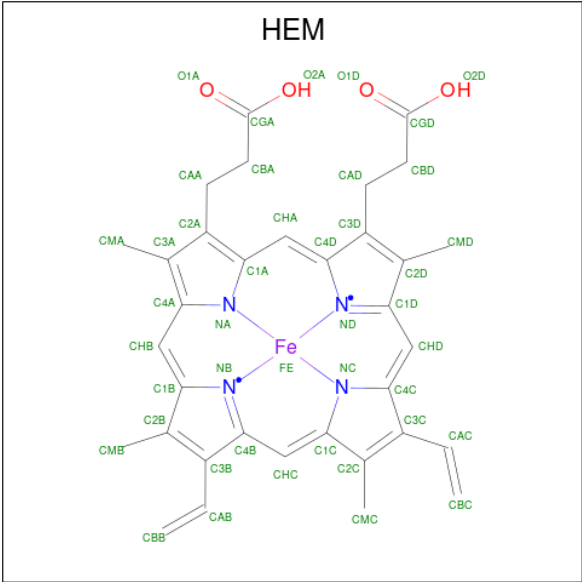
- Molecule 1 is a protein called Nitric oxide synthase, brain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	4	0
			3386	2169	575	620	22			
1	B	411	Total	C	N	O	S	0	2	0
			3355	2150	572	612	21			
1	C	412	Total	C	N	O	S	0	3	0
			3365	2156	571	617	21			
1	D	413	Total	C	N	O	S	0	2	0
			3371	2161	574	615	21			

There are 16 discrepancies between the modelled and reference sequences:

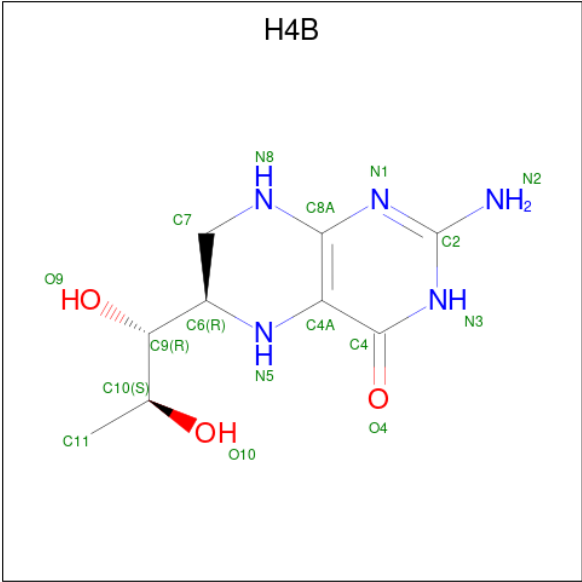
Chain	Residue	Modelled	Actual	Comment	Reference
A	354	ALA	ARG	engineered mutation	UNP P29475
A	357	ASP	GLY	engineered mutation	UNP P29475
A	723	LEU	-	expression tag	UNP P29475
A	724	VAL	-	expression tag	UNP P29475
B	354	ALA	ARG	engineered mutation	UNP P29475
B	357	ASP	GLY	engineered mutation	UNP P29475
B	723	LEU	-	expression tag	UNP P29475
B	724	VAL	-	expression tag	UNP P29475
C	354	ALA	ARG	engineered mutation	UNP P29475
C	357	ASP	GLY	engineered mutation	UNP P29475
C	723	LEU	-	expression tag	UNP P29475
C	724	VAL	-	expression tag	UNP P29475
D	354	ALA	ARG	engineered mutation	UNP P29475
D	357	ASP	GLY	engineered mutation	UNP P29475
D	723	LEU	-	expression tag	UNP P29475
D	724	VAL	-	expression tag	UNP P29475

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



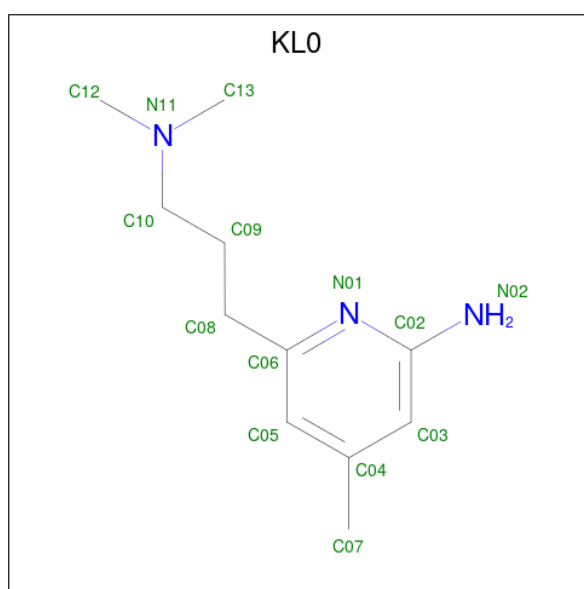
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (CCD ID: H4B) (formula: C₉H₁₅N₅O₃).



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

- Molecule 4 is 6-[3-(dimethylamino)propyl]-4-methylpyridin-2-amine (CCD ID: KL0) (formula: C₁₁H₁₉N₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			14	11	3		
4	B	1	Total	C	N	0	0
			14	11	3		
4	C	1	Total	C	N	0	0
			14	11	3		
4	D	1	Total	C	N	0	0
			14	11	3		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

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

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	83	Total	O	0	0
			83	83		

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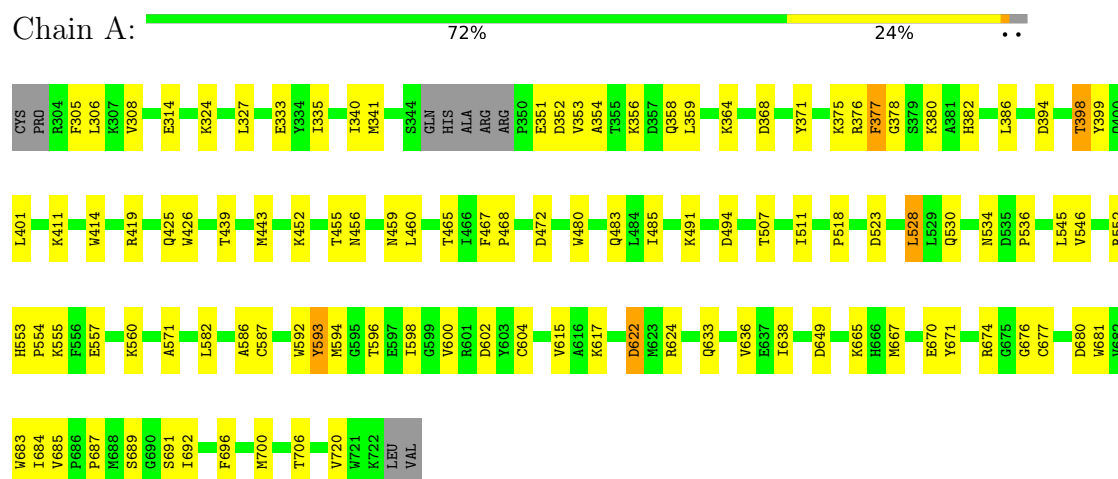
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	121	Total 121	O 121	0	0
7	C	88	Total 88	O 88	0	0
7	D	110	Total 110	O 110	0	0

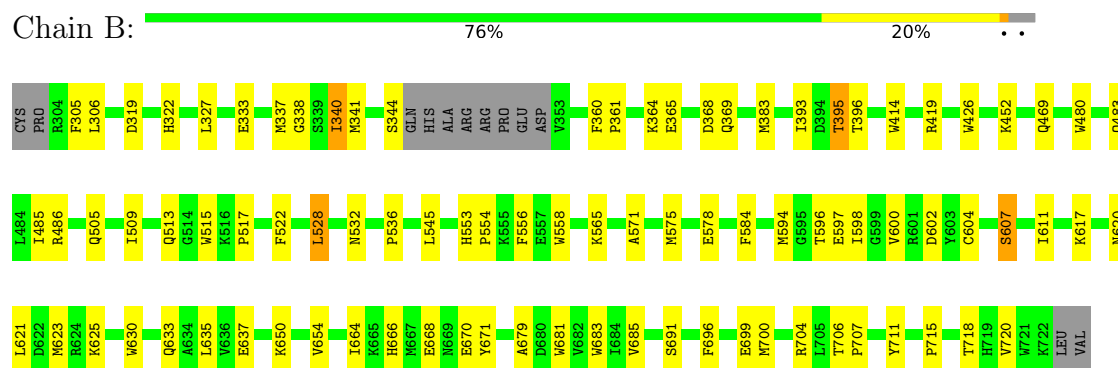
3 Residue-property plots

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.

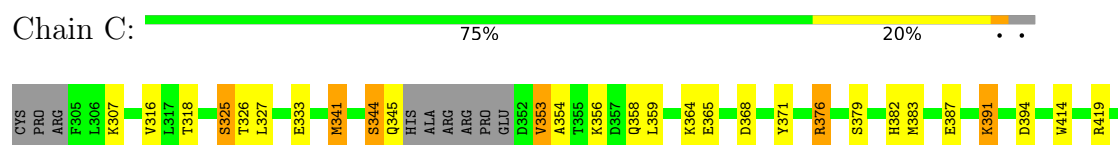
- Molecule 1: Nitric oxide synthase, brain



- Molecule 1: Nitric oxide synthase, brain



- Molecule 1: Nitric oxide synthase, brain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.91Å 163.78Å 118.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	67.35 – 2.30 67.35 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (67.35-2.30) 99.8 (67.35-2.30)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.219 , 0.283 0.208 , 0.275	Depositor DCC
R_{free} test set	4301 reflections (2.62%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.946	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 28.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.447 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14213	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% 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: H4B, ZN, KL0, HEM, GOL

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	0.34	0/3494	0.53	0/4742
1	B	0.36	0/3456	0.56	0/4689
1	C	0.35	0/3469	0.56	0/4709
1	D	0.38	0/3472	0.56	0/4710
All	All	0.36	0/13891	0.55	0/18850

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	A	0	1
1	C	0	1
1	D	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	593	TYR	Peptide
1	C	593	TYR	Peptide
1	D	723	LEU	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	3386	0	3301	57	0
1	B	3355	0	3271	50	0
1	C	3365	0	3277	56	0
1	D	3371	0	3291	39	0
2	A	43	0	30	4	0
2	B	43	0	30	3	0
2	C	43	0	30	3	0
2	D	43	0	30	3	0
3	A	34	0	30	1	0
3	C	17	0	15	1	0
3	D	17	0	15	1	0
4	A	14	0	0	1	0
4	B	14	0	0	1	0
4	C	14	0	0	0	0
4	D	14	0	0	0	0
5	A	12	0	16	2	0
5	B	6	0	8	0	0
5	C	12	0	16	1	0
5	D	6	0	8	0	0
6	A	1	0	0	0	0
6	D	1	0	0	0	0
7	A	83	0	0	0	0
7	B	121	0	0	2	0
7	C	88	0	0	2	0
7	D	110	0	0	0	0
All	All	14213	0	13368	206	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 8.

All (206) 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:B:327:LEU:HB3	1:B:704:ARG:HD3	1.61	0.82
1:C:528:LEU:HD22	1:C:536:PRO:HB2	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:528:LEU:HD22	1:A:536:PRO:HB2	1.60	0.81
1:A:356:LYS:HE2	1:A:394:ASP:HA	1.62	0.81
1:C:354:ALA:HB1	1:C:358:GLN:HB2	1.63	0.78
2:D:802:HEM:HBB2	2:D:802:HEM:HHC	1.64	0.78
1:A:687:PRO:HB2	1:B:691:SER:HB3	1.70	0.73
1:A:557:GLU:O	1:A:560:LYS:NZ	2.22	0.72
2:A:801:HEM:HBB2	2:A:801:HEM:HHC	1.72	0.71
1:C:711:TYR:OH	2:C:801:HEM:O1D	2.03	0.70
1:B:679:ALA:HB3	1:B:700:MET:HB3	1.74	0.70
2:C:801:HEM:HHC	2:C:801:HEM:HBB2	1.75	0.67
2:D:802:HEM:HMC2	2:D:802:HEM:HBC2	1.77	0.67
1:A:376:ARG:O	1:A:378:GLY:N	2.28	0.67
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.78	0.65
1:C:327:LEU:HD13	1:C:345:GLN:HE22	1.60	0.65
1:B:528:LEU:HD22	1:B:536:PRO:HB2	1.79	0.64
2:B:801:HEM:HMC2	2:B:801:HEM:HBC2	1.79	0.64
2:C:801:HEM:HBC2	2:C:801:HEM:HMC2	1.80	0.63
1:D:480:TRP:HB2	1:D:528:LEU:HB3	1.81	0.61
1:D:528:LEU:HD22	1:D:536:PRO:HB2	1.83	0.61
1:B:414:TRP:CE3	1:B:426:TRP:HA	2.36	0.61
1:D:686:PRO:HG2	1:D:693:THR:HG21	1.83	0.61
1:C:494:ASP:OD2	1:C:495:GLY:N	2.34	0.60
1:B:664:ILE:O	1:B:668:GLU:HG3	2.02	0.60
1:C:430:GLN:HA	5:C:805:GOL:H31	1.84	0.59
1:D:414:TRP:CE3	1:D:426:TRP:HA	2.37	0.59
1:C:478:ARG:NH2	7:C:902:HOH:O	2.32	0.59
1:C:598:ILE:HA	1:C:602:ASP:HB2	1.84	0.59
1:A:600:VAL:O	1:A:604:CYS:HB2	2.03	0.59
1:B:607:SER:OG	7:B:901:HOH:O	2.16	0.58
1:C:689:SER:HB3	1:C:692:ILE:HD11	1.86	0.58
1:C:542:PRO:HD2	1:C:545:LEU:HD12	1.85	0.58
1:D:679:ALA:HB3	1:D:700:MET:HB3	1.85	0.57
1:B:360:PHE:HB2	1:B:361:PRO:HD3	1.86	0.57
1:A:507:THR:O	1:A:511:ILE:HG13	2.05	0.57
1:B:598:ILE:HA	1:B:602:ASP:HB2	1.86	0.57
1:A:615:VAL:HG21	1:A:638:ILE:HD11	1.87	0.56
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.88	0.56
1:D:419:ARG:HD3	1:D:683:TRP:CD2	2.41	0.56
1:C:507:THR:O	1:C:511:ILE:HG13	2.06	0.56
1:C:616:ALA:HA	1:C:621:LEU:HD12	1.87	0.56
1:C:419:ARG:HD3	1:C:683:TRP:CD2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:689:SER:HB3	1:A:692:ILE:HD11	1.87	0.56
1:D:341:MET:HE2	3:D:803:H4B:H9	1.88	0.55
1:C:376:ARG:HB3	1:C:376:ARG:NH2	2.22	0.55
1:B:575:MET:HE3	1:B:711:TYR:CD2	2.42	0.55
1:C:353:VAL:HG11	1:C:472:ASP:HA	1.88	0.55
1:B:483:GLN:HB2	1:B:486:ARG:HG3	1.88	0.55
1:D:598:ILE:HA	1:D:602:ASP:HB2	1.89	0.55
1:C:593:TYR:CD1	1:C:598:ILE:HD11	2.42	0.55
1:B:556:PHE:HB3	1:B:558:TRP:CE2	2.43	0.54
1:A:398:THR:OG1	1:A:399:TYR:N	2.41	0.53
1:A:480:TRP:HB2	1:A:528:LEU:HB3	1.89	0.53
1:A:593:TYR:CD1	1:A:598:ILE:HD11	2.44	0.53
1:A:691:SER:HA	1:A:696:PHE:CG	2.44	0.53
1:C:691:SER:HA	1:C:696:PHE:CG	2.44	0.53
1:A:354:ALA:HB1	1:A:358:GLN:HB2	1.90	0.53
1:D:327:LEU:HG	1:D:328:GLU:H	1.73	0.53
1:C:551:ILE:HG12	1:C:565:LYS:HA	1.91	0.53
1:A:353:VAL:HG11	1:A:472:ASP:HA	1.91	0.52
1:C:600:VAL:O	1:C:604:CYS:HB2	2.09	0.52
1:B:419:ARG:HD3	1:B:683:TRP:CD2	2.45	0.52
1:B:522:PHE:HB2	1:B:565:LYS:HE3	1.92	0.52
1:A:622:ASP:OD2	1:A:624:ARG:HB2	2.10	0.52
1:B:681:TRP:CZ2	1:B:685:VAL:HG21	2.45	0.52
1:C:368:ASP:OD1	1:C:382:HIS:NE2	2.42	0.51
1:A:340:ILE:HD13	1:B:699:GLU:HB3	1.91	0.51
1:A:351:GLU:C	1:A:353:VAL:H	2.17	0.51
1:A:485:ILE:HD13	1:A:546:VAL:HG13	1.93	0.51
1:A:306:LEU:HD13	1:B:337:MET:HE2	1.93	0.51
1:D:623:MET:HA	1:D:630:TRP:CD1	2.46	0.51
1:B:480:TRP:CE2	1:B:715:PRO:HB2	2.45	0.51
1:C:364:LYS:NZ	1:C:368:ASP:OD2	2.43	0.51
1:B:600:VAL:HG22	1:B:635:LEU:HD11	1.91	0.50
1:C:376:ARG:HB2	1:C:379:SER:HB3	1.91	0.50
1:A:419:ARG:HD3	1:A:683:TRP:CD2	2.46	0.50
1:A:364:LYS:NZ	1:A:368:ASP:OD2	2.45	0.50
1:D:485:ILE:HD13	1:D:546:VAL:HG13	1.92	0.50
1:D:646:PHE:CG	1:D:653:ILE:HD12	2.47	0.50
1:C:681:TRP:CZ2	1:C:685:VAL:HG21	2.46	0.50
1:C:613:GLU:HG3	1:C:623:MET:HE1	1.93	0.50
1:A:414:TRP:CE3	1:A:426:TRP:HA	2.47	0.49
1:A:552:ARG:HH12	1:A:649:ASP:CG	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:414:TRP:CE3	1:C:426:TRP:HA	2.47	0.49
1:D:706:THR:HA	1:D:707:PRO:C	2.37	0.49
1:B:337:MET:HB3	1:B:340:ILE:HG13	1.94	0.49
1:A:633:GLN:NE2	1:B:637:GLU:OE2	2.45	0.49
1:A:530:GLN:HG3	1:A:534:ASN:O	2.13	0.49
1:B:600:VAL:O	1:B:604:CYS:HB2	2.12	0.49
1:C:326:THR:HG21	1:C:706[A]:THR:HG22	1.95	0.49
1:C:327:LEU:HD11	1:C:704:ARG:NH2	2.28	0.49
1:C:480:TRP:HB2	1:C:528:LEU:HB3	1.93	0.49
1:C:484:LEU:HB2	1:C:571:ALA:HB3	1.96	0.48
1:D:515:TRP:CZ3	1:D:517:PRO:HB3	2.49	0.48
1:B:469:GLN:HB3	1:B:584:PHE:CE2	2.48	0.48
1:C:667:MET:HE1	1:C:700:MET:HG2	1.95	0.48
1:D:646:PHE:CD2	1:D:653:ILE:HD12	2.50	0.47
1:A:598:ILE:O	1:A:602:ASP:HB2	2.13	0.47
1:A:594:MET:HE3	1:A:596:THR:OG1	2.14	0.47
1:C:356:LYS:NZ	1:C:394:ASP:OD2	2.37	0.47
1:A:671:TYR:CE2	1:A:676:GLY:HA2	2.50	0.47
1:A:375:LYS:HA	1:A:377:PHE:CE2	2.50	0.47
1:B:452:LYS:HD2	1:B:545:LEU:HD21	1.97	0.47
1:C:505:GLN:O	1:C:509:ILE:HG13	2.15	0.47
1:A:592:TRP:O	4:A:803:KL0:N02	2.48	0.46
1:C:679:ALA:HB3	1:C:700:MET:HB3	1.96	0.46
1:A:354:ALA:HB3	1:A:359:LEU:HB2	1.98	0.46
1:A:667:MET:HE1	1:A:700:MET:HG2	1.97	0.46
1:A:371:TYR:CD2	1:A:382:HIS:HB2	2.50	0.46
1:A:674:ARG:HE	5:A:804:GOL:H31	1.81	0.46
1:B:305:PHE:O	1:B:306:LEU:HD23	2.15	0.46
1:D:600:VAL:O	1:D:604:CYS:HB2	2.15	0.46
1:B:691:SER:HA	1:B:696:PHE:CG	2.51	0.46
1:A:518:PRO:HG2	1:A:523:ASP:CG	2.41	0.45
1:D:691:SER:HA	1:D:696:PHE:CG	2.52	0.45
1:C:307:LYS:HD3	1:C:316:VAL:HG11	1.98	0.45
1:A:353:VAL:CG1	1:A:472:ASP:HA	2.47	0.45
1:B:522:PHE:CB	1:B:565:LYS:HE3	2.46	0.45
1:C:687:PRO:HB2	1:D:691:SER:HB3	1.99	0.45
1:C:327:LEU:HD13	1:C:345:GLN:NE2	2.31	0.44
1:D:364:LYS:NZ	1:D:368:ASP:OD2	2.50	0.44
1:D:547:LEU:HD21	1:D:651:VAL:HG22	1.99	0.44
1:D:600:VAL:HG22	1:D:635:LEU:HD11	2.00	0.44
1:D:601:ARG:O	1:D:605:ASP:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:341:MET:HE2	1:C:341:MET:HB2	1.81	0.44
1:A:411:LYS:HE3	5:A:805:GOL:H2	2.00	0.44
1:A:689:SER:HB3	1:A:692:ILE:CG1	2.48	0.44
1:C:376:ARG:HB3	1:C:376:ARG:HH21	1.82	0.44
1:C:622:ASP:OD2	1:C:624:ARG:HB2	2.18	0.44
1:B:364:LYS:NZ	1:B:368:ASP:OD2	2.51	0.44
1:B:706:THR:HA	1:B:707:PRO:C	2.42	0.44
1:C:455:THR:HA	1:C:460:LEU:HD22	2.00	0.44
2:A:801:HEM:HBC2	2:A:801:HEM:CMC	2.46	0.44
1:C:465:THR:O	1:C:587:CYS:HA	2.18	0.43
1:C:554:PRO:HD3	1:C:644:TYR:CD2	2.53	0.43
1:A:368:ASP:OD1	1:A:382:HIS:NE2	2.50	0.43
2:B:801:HEM:HBB2	2:B:801:HEM:CHC	2.47	0.43
1:D:600:VAL:HA	1:D:635:LEU:HD11	2.00	0.43
1:A:483:GLN:HA	1:A:571:ALA:O	2.18	0.43
1:B:419:ARG:HD3	1:B:683:TRP:CE2	2.53	0.43
1:C:371:TYR:HD2	1:C:376:ARG:HG3	1.83	0.43
1:D:722:LYS:HB3	1:D:722:LYS:HE2	1.83	0.43
1:A:681:TRP:CZ2	1:A:685:VAL:HG21	2.53	0.43
1:A:333:GLU:H	1:A:333:GLU:CD	2.27	0.43
1:A:455:THR:HA	1:A:460:LEU:HD22	2.01	0.43
1:B:414:TRP:CZ3	1:B:426:TRP:HA	2.53	0.43
1:B:509:ILE:O	1:B:513:GLN:HG2	2.19	0.43
3:A:807:H4B:H9	1:B:341:MET:HE2	2.01	0.43
1:C:664:ILE:HG13	1:C:694:PRO:HB2	2.01	0.43
1:D:681:TRP:CZ2	1:D:685:VAL:HG21	2.53	0.43
1:A:687:PRO:CB	1:B:691:SER:HB3	2.42	0.43
1:B:553:HIS:CG	1:B:554:PRO:HD2	2.54	0.43
1:A:553:HIS:CG	1:A:554:PRO:HD2	2.54	0.42
1:A:680:ASP:O	1:A:684:ILE:HG12	2.19	0.42
1:B:483:GLN:HB2	1:B:486:ARG:CG	2.49	0.42
1:B:594:MET:HE3	1:B:596:THR:OG1	2.20	0.42
1:C:483:GLN:HB2	1:C:486:ARG:HG2	2.01	0.42
1:D:509:ILE:O	1:D:513:GLN:HG2	2.19	0.42
1:B:360:PHE:CE1	1:B:393:ILE:HB	2.54	0.42
1:D:621:LEU:HD23	1:D:621:LEU:HA	1.86	0.42
1:C:624:ARG:NH2	7:C:911:HOH:O	2.52	0.42
1:A:636:VAL:HG11	1:B:633:GLN:HG3	2.00	0.42
1:B:306:LEU:HG	1:B:322:HIS:CE1	2.55	0.42
1:C:325:SER:HB2	1:C:703:TYR:HB2	2.01	0.42
1:B:483:GLN:HA	1:B:571:ALA:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:623:MET:HA	1:B:630:TRP:CD1	2.55	0.42
1:C:623:MET:HE3	1:C:630:TRP:CZ3	2.55	0.42
1:B:597:GLU:OE2	4:B:802:KL0:N02	2.53	0.42
1:D:723:LEU:HD23	1:D:723:LEU:HA	1.78	0.41
2:D:802:HEM:HBB2	2:D:802:HEM:CHC	2.43	0.41
1:C:600:VAL:HA	1:C:635:LEU:HD11	2.01	0.41
1:A:401:LEU:HG	1:A:582:LEU:HD12	2.02	0.41
1:B:395:THR:HB	1:B:396:THR:HG23	2.01	0.41
1:D:439:THR:O	1:D:443:MET:HG3	2.19	0.41
1:C:391:LYS:HA	1:C:394:ASP:HB2	2.01	0.41
1:D:542:PRO:HA	1:D:543:PRO:HD3	1.96	0.41
1:B:515:TRP:CZ3	1:B:517:PRO:HB3	2.56	0.41
1:B:594:MET:HA	1:B:654:VAL:O	2.21	0.41
1:C:671:TYR:CE2	1:C:676:GLY:HA2	2.56	0.41
1:D:515:TRP:CE2	1:D:526:PRO:HD3	2.55	0.41
1:D:334:TYR:C	1:D:335:ILE:HG13	2.46	0.41
1:D:556:PHE:HB3	1:D:558:TRP:CE2	2.56	0.41
1:D:689:SER:HB3	1:D:692:ILE:HG12	2.01	0.41
1:C:471:THR:OG1	1:C:472:ASP:N	2.53	0.41
2:A:801:HEM:HBB2	2:A:801:HEM:CHC	2.46	0.41
1:B:611:ILE:HA	7:B:904:HOH:O	2.21	0.41
1:C:327:LEU:HD11	1:C:704:ARG:HH22	1.85	0.41
1:C:601:ARG:HH12	3:C:802:H4B:C4	2.34	0.41
1:D:480:TRP:CE2	1:D:715:PRO:HB2	2.55	0.41
1:A:467:PHE:HB3	1:A:468:PRO:CD	2.52	0.41
1:B:621:LEU:HD23	1:B:621:LEU:HA	1.79	0.41
1:C:636:VAL:HG11	1:D:633:GLN:HG3	2.01	0.40
1:A:419:ARG:HD3	1:A:683:TRP:CE2	2.56	0.40
1:A:439:THR:O	1:A:443:MET:HG3	2.20	0.40
1:A:465:THR:O	1:A:587:CYS:HA	2.21	0.40
1:B:666:HIS:CE1	1:B:670:GLU:HG3	2.57	0.40
1:C:689:SER:HB3	1:C:692:ILE:CG1	2.50	0.40
1:D:553:HIS:CG	1:D:554:PRO:HD2	2.56	0.40
1:A:452:LYS:HB2	1:A:545:LEU:HD22	2.03	0.40
1:A:467:PHE:HB2	1:A:586:ALA:HB3	2.03	0.40
1:D:337:MET:HB3	1:D:340:ILE:HG13	2.03	0.40
1:A:456:ASN:HB3	1:A:459:ASN:O	2.22	0.40
1:A:670:GLU:HB2	1:A:677:CYS:HB2	2.03	0.40
1:B:319:ASP:HB2	1:B:671:TYR:HE2	1.85	0.40
1:D:450:HIS:CD2	1:D:450:HIS:C	2.99	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	414/423 (98%)	387 (94%)	24 (6%)	3 (1%)	18	23
1	B	409/423 (97%)	396 (97%)	12 (3%)	1 (0%)	43	55
1	C	411/423 (97%)	384 (93%)	26 (6%)	1 (0%)	43	55
1	D	411/423 (97%)	398 (97%)	13 (3%)	0	100	100
All	All	1645/1692 (97%)	1565 (95%)	75 (5%)	5 (0%)	36	46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	377	PHE
1	C	344	SER
1	A	352	ASP
1	A	622	ASP
1	B	338	GLY

5.3.2 Protein sidechains

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	374/378 (99%)	354 (95%)	20 (5%)	20	30
1	B	369/378 (98%)	350 (95%)	19 (5%)	21	32
1	C	371/378 (98%)	354 (95%)	17 (5%)	24	36
1	D	371/378 (98%)	352 (95%)	19 (5%)	21	32
All	All	1485/1512 (98%)	1410 (95%)	75 (5%)	22	32

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305	PHE
1	A	308	VAL
1	A	314	GLU
1	A	324	LYS
1	A	327	LEU
1	A	335	ILE
1	A	341	MET
1	A	380	LYS
1	A	386	LEU
1	A	398	THR
1	A	425	GLN
1	A	491	LYS
1	A	494	ASP
1	A	528	LEU
1	A	555	LYS
1	A	617	LYS
1	A	665	LYS
1	A	706[A]	THR
1	A	706[B]	THR
1	A	720	VAL
1	B	333	GLU
1	B	340	ILE
1	B	344	SER
1	B	365	GLU
1	B	369	GLN
1	B	383	MET
1	B	395	THR
1	B	485	ILE
1	B	505	GLN
1	B	528	LEU
1	B	532	ASN
1	B	578	GLU
1	B	607	SER
1	B	617	LYS
1	B	620	ASN
1	B	625	LYS
1	B	650	LYS
1	B	718	THR
1	B	720	VAL
1	C	318	THR
1	C	325	SER
1	C	333	GLU

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Mol	Chain	Res	Type
1	C	341	MET
1	C	344	SER
1	C	353	VAL
1	C	359	LEU
1	C	365	GLU
1	C	376	ARG
1	C	383	MET
1	C	387	GLU
1	C	391	LYS
1	C	474	LYS
1	C	491	LYS
1	C	528	LEU
1	C	552	ARG
1	C	560	LYS
1	D	314	GLU
1	D	353	VAL
1	D	365	GLU
1	D	369	GLN
1	D	372	SER
1	D	383	MET
1	D	396	THR
1	D	485	ILE
1	D	528	LEU
1	D	578	GLU
1	D	607	SER
1	D	613	GLU
1	D	618	LYS
1	D	625	LYS
1	D	650	LYS
1	D	658	SER
1	D	708	SER
1	D	720	VAL
1	D	724	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	513	GLN
1	A	719	HIS
1	B	412	HIS
1	B	430	GLN
1	B	469	GLN

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Mol	Chain	Res	Type
1	C	345	GLN
1	C	400	GLN
1	C	606	ASN
1	D	430	GLN
1	D	666	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 2 are monoatomic - leaving 18 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	$\# Z > 2$
3	H4B	D	803	-	17,18,18	0.86	1 (5%)	14,26,26	1.94	5 (35%)
5	GOL	A	805	-	5,5,5	0.35	0	5,5,5	0.29	0
5	GOL	C	805	-	5,5,5	0.39	0	5,5,5	0.34	0
4	KL0	A	803	-	14,14,14	0.55	0	17,18,18	1.55	1 (5%)
3	H4B	A	802	-	17,18,18	0.82	1 (5%)	14,26,26	1.83	4 (28%)
2	HEM	B	801	1	50,50,50	1.44	6 (12%)	67,82,82	1.32	8 (11%)
2	HEM	C	801	1	50,50,50	1.48	7 (14%)	67,82,82	1.13	3 (4%)
5	GOL	C	804	-	5,5,5	0.34	0	5,5,5	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	D	802	1	50,50,50	1.61	6 (12%)	67,82,82	1.42	6 (8%)
5	GOL	B	803	-	5,5,5	0.37	0	5,5,5	0.43	0
5	GOL	A	804	-	5,5,5	0.31	0	5,5,5	0.32	0
5	GOL	D	805	-	5,5,5	0.34	0	5,5,5	0.43	0
4	KL0	D	804	-	14,14,14	0.42	0	17,18,18	1.97	3 (17%)
4	KL0	C	803	-	14,14,14	0.58	0	17,18,18	1.67	3 (17%)
2	HEM	A	801	1	50,50,50	1.48	9 (18%)	67,82,82	1.32	8 (11%)
3	H4B	A	807	-	17,18,18	0.96	1 (5%)	14,26,26	1.84	4 (28%)
3	H4B	C	802	-	17,18,18	0.87	1 (5%)	14,26,26	1.89	5 (35%)
4	KL0	B	802	-	14,14,14	0.40	0	17,18,18	1.70	4 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	H4B	D	803	-	-	1/8/17/17	0/2/2/2
5	GOL	A	805	-	-	2/4/4/4	-
5	GOL	C	805	-	-	0/4/4/4	-
4	KL0	A	803	-	-	3/6/6/6	0/1/1/1
3	H4B	A	802	-	-	0/8/17/17	0/2/2/2
2	HEM	B	801	1	-	2/14/54/54	-
2	HEM	C	801	1	-	3/14/54/54	-
5	GOL	C	804	-	-	2/4/4/4	-
2	HEM	D	802	1	-	1/14/54/54	-
5	GOL	B	803	-	-	0/4/4/4	-
5	GOL	A	804	-	-	2/4/4/4	-
5	GOL	D	805	-	-	0/4/4/4	-
4	KL0	D	804	-	-	3/6/6/6	0/1/1/1
4	KL0	C	803	-	-	3/6/6/6	0/1/1/1
2	HEM	A	801	1	-	3/14/54/54	-
3	H4B	A	807	-	-	0/8/17/17	0/2/2/2
3	H4B	C	802	-	-	0/8/17/17	0/2/2/2
4	KL0	B	802	-	-	3/6/6/6	0/1/1/1

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	802	HEM	FE-ND	5.51	2.11	1.94
2	D	802	HEM	FE-NA	5.11	2.12	1.95
2	A	801	HEM	FE-NA	4.21	2.09	1.95
2	B	801	HEM	FE-NA	4.19	2.09	1.95
2	C	801	HEM	FE-NA	4.07	2.08	1.95
2	B	801	HEM	FE-ND	3.77	2.06	1.94
2	A	801	HEM	FE-NB	3.36	2.05	1.94
2	D	802	HEM	FE-NC	3.24	2.05	1.95
2	C	801	HEM	FE-ND	3.24	2.04	1.94
2	B	801	HEM	CAB-C3B	3.19	1.55	1.47
2	A	801	HEM	CAB-C3B	3.15	1.55	1.47
2	C	801	HEM	FE-NC	3.10	2.05	1.95
2	D	802	HEM	CAB-C3B	3.02	1.55	1.47
2	C	801	HEM	CAB-C3B	2.99	1.55	1.47
2	A	801	HEM	FE-NC	2.98	2.05	1.95
2	B	801	HEM	CAC-C3C	2.91	1.55	1.47
2	C	801	HEM	CAC-C3C	2.87	1.55	1.47
2	B	801	HEM	FE-NC	2.85	2.04	1.95
2	D	802	HEM	CAC-C3C	2.83	1.55	1.47
2	A	801	HEM	FE-ND	2.76	2.03	1.94
2	A	801	HEM	CAC-C3C	2.64	1.54	1.47
3	C	802	H4B	C4-N3	-2.48	1.34	1.38
2	D	802	HEM	CMB-C2B	2.42	1.55	1.50
3	D	803	H4B	C4-N3	-2.34	1.34	1.38
2	C	801	HEM	FE-NB	2.33	2.02	1.94
2	C	801	HEM	CMD-C2D	2.33	1.55	1.50
2	A	801	HEM	CMD-C2D	2.27	1.55	1.50
2	B	801	HEM	CMB-C2B	2.27	1.55	1.50
3	A	807	H4B	C4-N3	-2.23	1.34	1.38
2	A	801	HEM	CMB-C2B	2.15	1.55	1.50
2	A	801	HEM	CMA-C3A	2.05	1.55	1.50
3	A	802	H4B	C4-N3	-2.04	1.35	1.38

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	804	KL0	C02-N01-C06	5.73	122.35	118.07
4	B	802	KL0	C02-N01-C06	4.46	121.40	118.07
4	C	803	KL0	C02-N01-C06	4.26	121.26	118.07
2	D	802	HEM	CHD-C1D-ND	4.01	128.74	124.42
3	C	802	H4B	C2-N1-C8A	3.98	120.38	113.36
4	A	803	KL0	C02-N01-C06	3.97	121.04	118.07
3	D	803	H4B	C2-N1-C8A	3.81	120.08	113.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	HEM	CBA-CAA-C2A	-3.78	102.08	112.53
2	D	802	HEM	CBA-CAA-C2A	-3.70	102.31	112.53
3	A	802	H4B	C2-N1-C8A	3.64	119.78	113.36
3	A	807	H4B	O4-C4-C4A	-3.55	118.70	127.26
3	A	807	H4B	C2-N1-C8A	3.53	119.59	113.36
4	D	804	KL0	C08-C06-N01	3.51	121.38	116.06
2	C	801	HEM	CBA-CAA-C2A	-3.50	102.86	112.53
4	D	804	KL0	C05-C06-N01	-3.39	118.86	122.73
4	C	803	KL0	C08-C06-N01	3.12	120.78	116.06
3	A	802	H4B	O4-C4-C4A	-3.08	119.83	127.26
2	D	802	HEM	C2A-C1A-NA	-3.00	106.82	110.15
4	C	803	KL0	C05-C06-N01	-2.97	119.34	122.73
4	B	802	KL0	C08-C06-N01	2.94	120.51	116.06
3	A	802	H4B	C2-N3-C4	-2.91	119.83	125.11
3	C	802	H4B	C4A-C4-N3	2.87	120.01	112.13
3	D	803	H4B	C4A-C4-N3	2.83	119.91	112.13
3	A	807	H4B	C2-N3-C4	-2.78	120.07	125.11
2	B	801	HEM	CHA-C4D-ND	2.76	127.78	124.37
2	B	801	HEM	CHD-C1D-ND	2.74	127.38	124.42
3	A	807	H4B	C4A-C4-N3	2.71	119.58	112.13
2	B	801	HEM	CAD-CBD-CGD	-2.71	106.49	113.67
3	A	802	H4B	C4A-C4-N3	2.71	119.56	112.13
3	D	803	H4B	C2-N3-C4	-2.65	120.31	125.11
3	D	803	H4B	O4-C4-C4A	-2.63	120.92	127.26
2	B	801	HEM	CBA-CAA-C2A	-2.63	105.26	112.53
2	A	801	HEM	C3B-C4B-NB	-2.58	107.61	109.47
3	C	802	H4B	O4-C4-C4A	-2.58	121.04	127.26
2	B	801	HEM	C1B-NB-C4B	2.57	108.25	105.21
4	B	802	KL0	C05-C06-N01	-2.55	119.82	122.73
2	A	801	HEM	C2A-C1A-NA	-2.53	107.35	110.15
2	B	801	HEM	C3B-C2B-C1B	2.43	108.23	106.41
2	A	801	HEM	CAD-CBD-CGD	-2.42	107.24	113.67
2	C	801	HEM	C3B-C4B-NB	-2.35	107.78	109.47
2	B	801	HEM	C4C-CHD-C1D	-2.32	121.09	126.02
2	B	801	HEM	C3B-C4B-NB	-2.32	107.80	109.47
2	C	801	HEM	C3B-C2B-C1B	2.31	108.14	106.41
3	C	802	H4B	C4-C4A-N5	2.30	122.54	116.27
3	D	803	H4B	C4-C4A-N5	2.21	122.29	116.27
2	A	801	HEM	C3D-C4D-ND	-2.20	107.76	110.17
2	D	802	HEM	CHD-C1D-C2D	-2.15	121.63	125.03
2	A	801	HEM	C1B-NB-C4B	2.15	107.76	105.21
2	D	802	HEM	C4A-CHB-C1B	-2.12	121.25	126.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	802	HEM	CHC-C4B-NB	2.12	126.70	124.42
2	A	801	HEM	O1D-CGD-CBD	-2.11	116.40	123.09
3	C	802	H4B	C2-N3-C4	-2.10	121.30	125.11
2	A	801	HEM	CBD-CAD-C3D	-2.09	106.76	112.53
4	B	802	KL0	C07-C04-C05	-2.05	118.14	120.92

There are no chirality outliers.

All (28) torsion outliers are listed below:

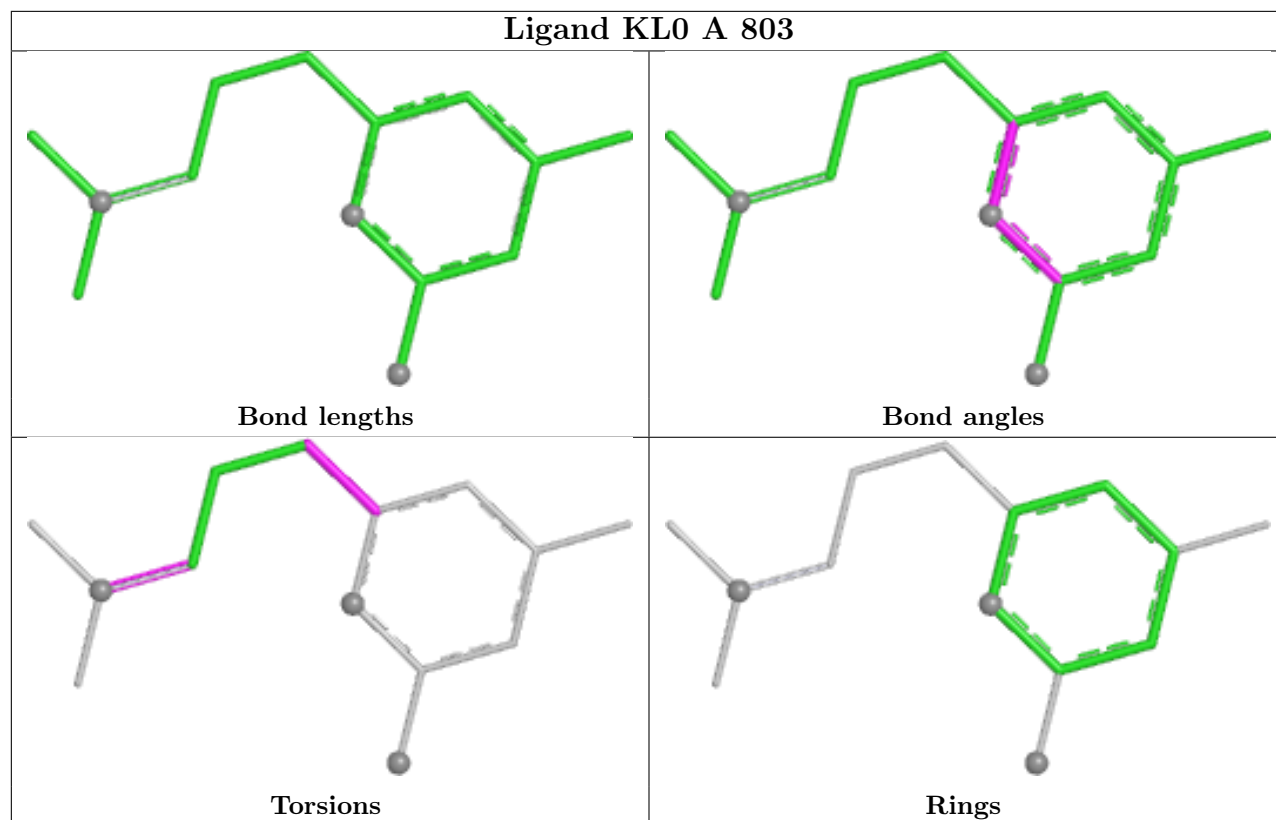
Mol	Chain	Res	Type	Atoms
5	A	804	GOL	O1-C1-C2-C3
5	C	804	GOL	O1-C1-C2-C3
4	C	803	KL0	C09-C10-N11-C13
4	D	804	KL0	C09-C10-N11-C12
4	B	802	KL0	C09-C10-N11-C12
4	B	802	KL0	C09-C10-N11-C13
4	C	803	KL0	C09-C10-N11-C12
4	D	804	KL0	C09-C10-N11-C13
5	A	804	GOL	O1-C1-C2-O2
5	C	804	GOL	O1-C1-C2-O2
5	A	805	GOL	C1-C2-C3-O3
2	B	801	HEM	C4B-C3B-CAB-CBB
2	C	801	HEM	C4B-C3B-CAB-CBB
5	A	805	GOL	O2-C2-C3-O3
4	A	803	KL0	C09-C10-N11-C12
2	A	801	HEM	C4B-C3B-CAB-CBB
2	D	802	HEM	C4B-C3B-CAB-CBB
2	B	801	HEM	C2A-CAA-CBA-CGA
2	A	801	HEM	CAA-CBA-CGA-O2A
2	A	801	HEM	CAA-CBA-CGA-O1A
2	C	801	HEM	CAA-CBA-CGA-O2A
4	A	803	KL0	N01-C06-C08-C09
2	C	801	HEM	CAA-CBA-CGA-O1A
4	B	802	KL0	C06-C08-C09-C10
4	C	803	KL0	C06-C08-C09-C10
4	D	804	KL0	C06-C08-C09-C10
3	D	803	H4B	N5-C6-C9-O9
4	A	803	KL0	C05-C06-C08-C09

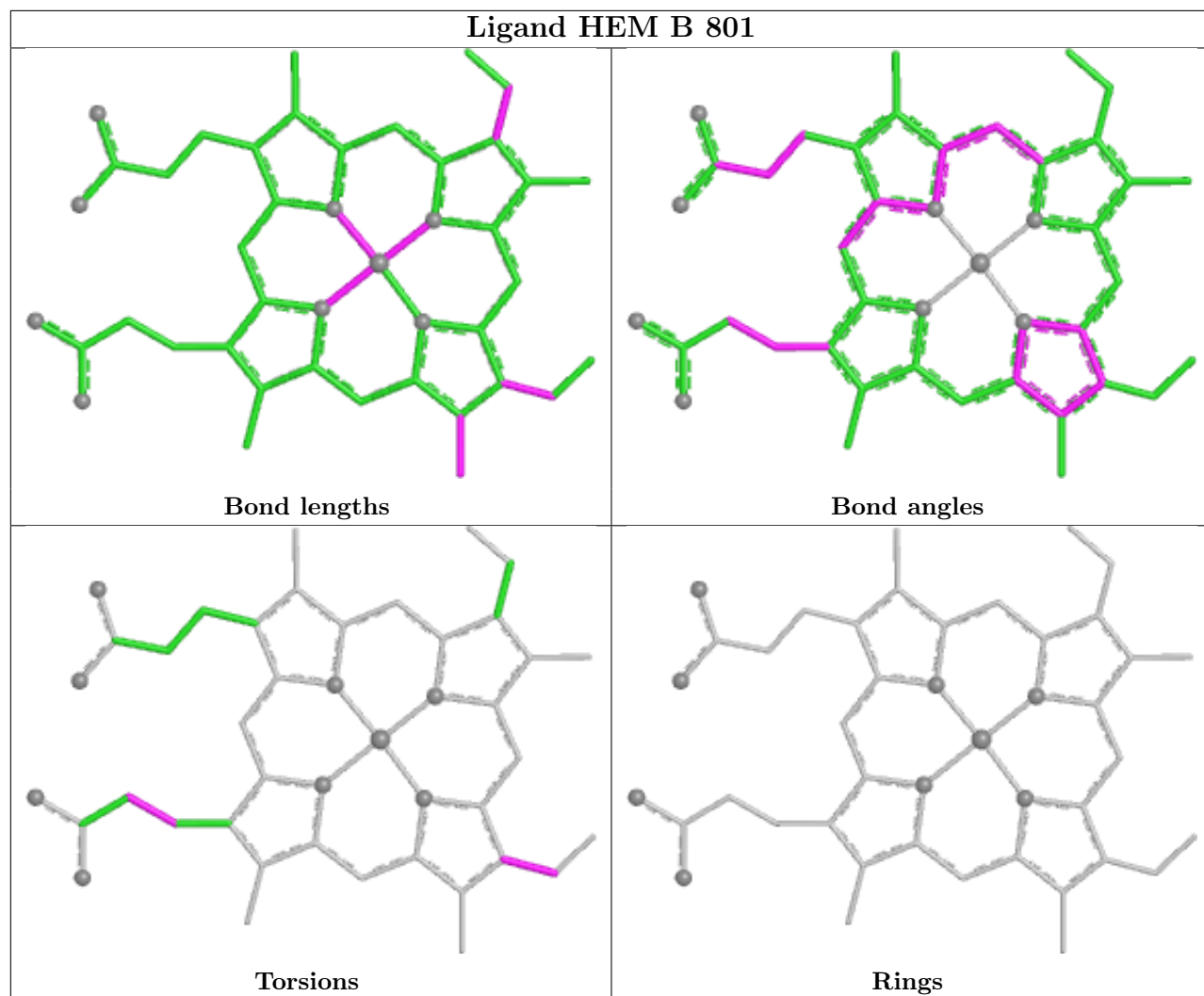
There are no ring outliers.

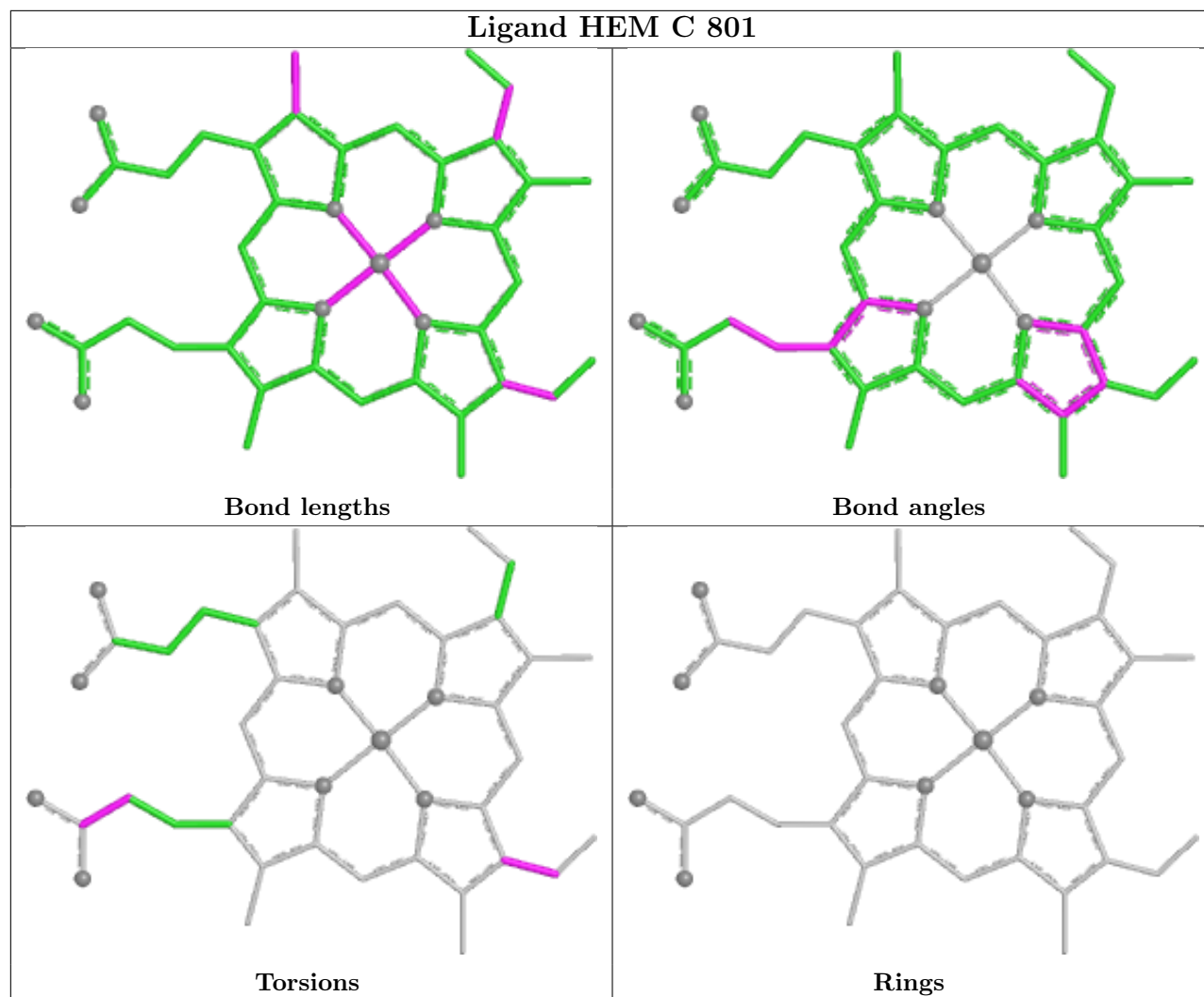
12 monomers are involved in 21 short contacts:

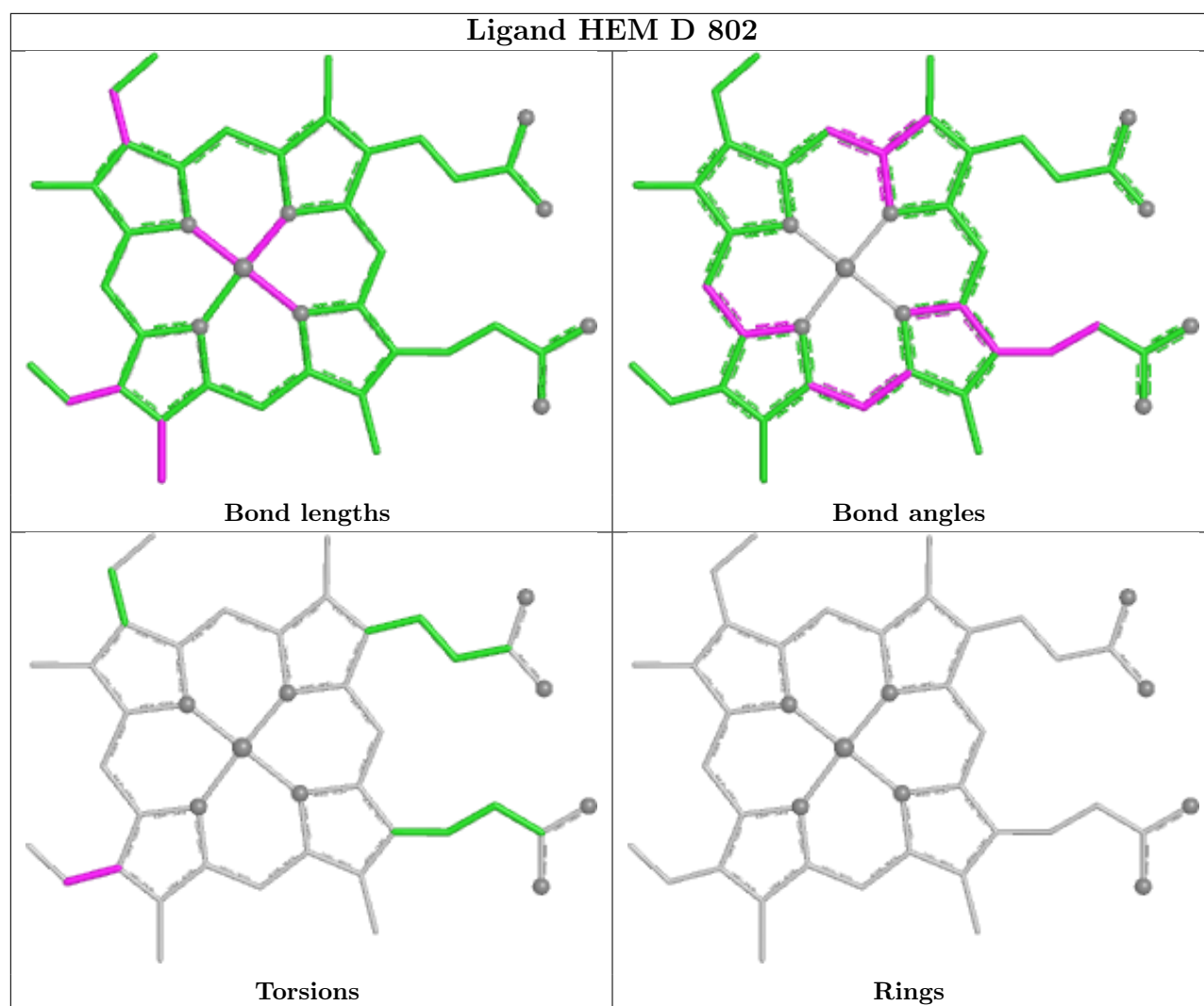
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	803	H4B	1	0
5	A	805	GOL	1	0
5	C	805	GOL	1	0
4	A	803	KL0	1	0
2	B	801	HEM	3	0
2	C	801	HEM	3	0
2	D	802	HEM	3	0
5	A	804	GOL	1	0
2	A	801	HEM	4	0
3	A	807	H4B	1	0
3	C	802	H4B	1	0
4	B	802	KL0	1	0

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 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.

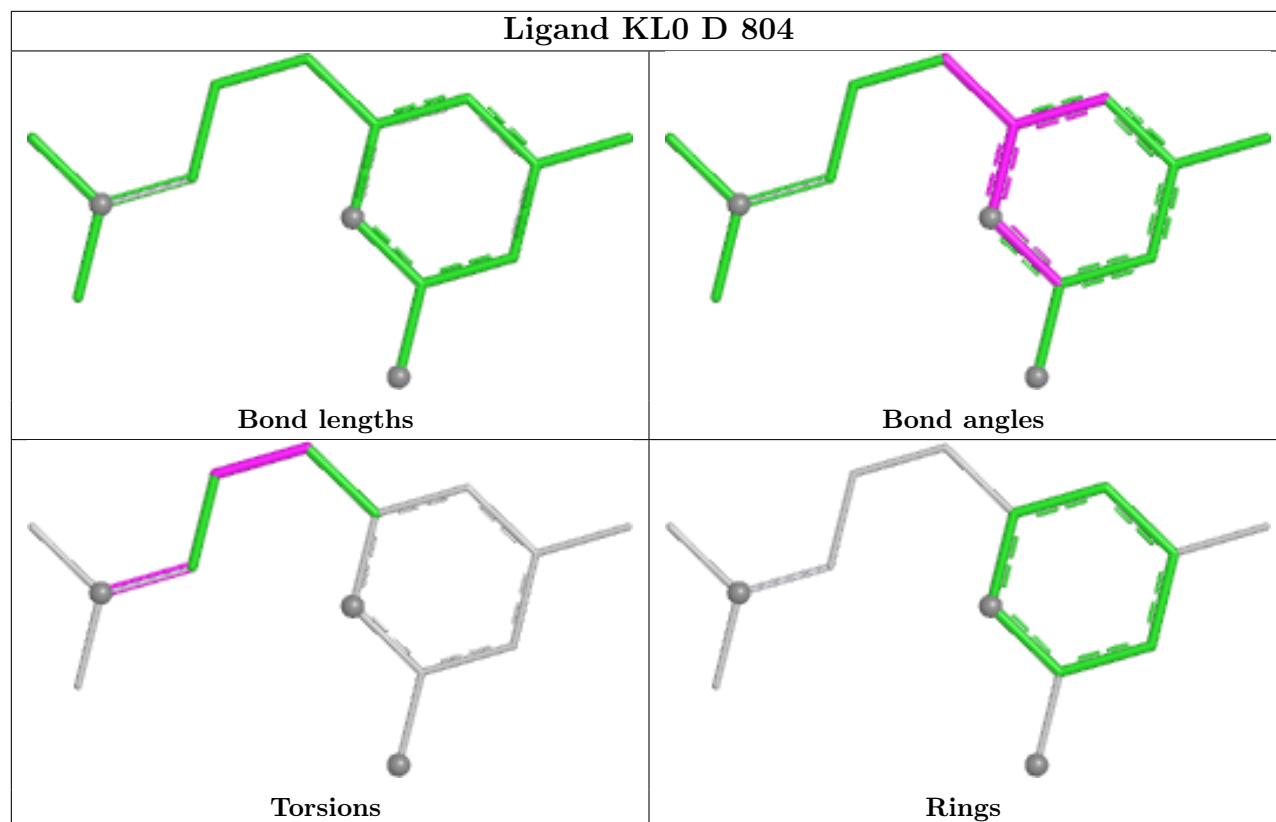




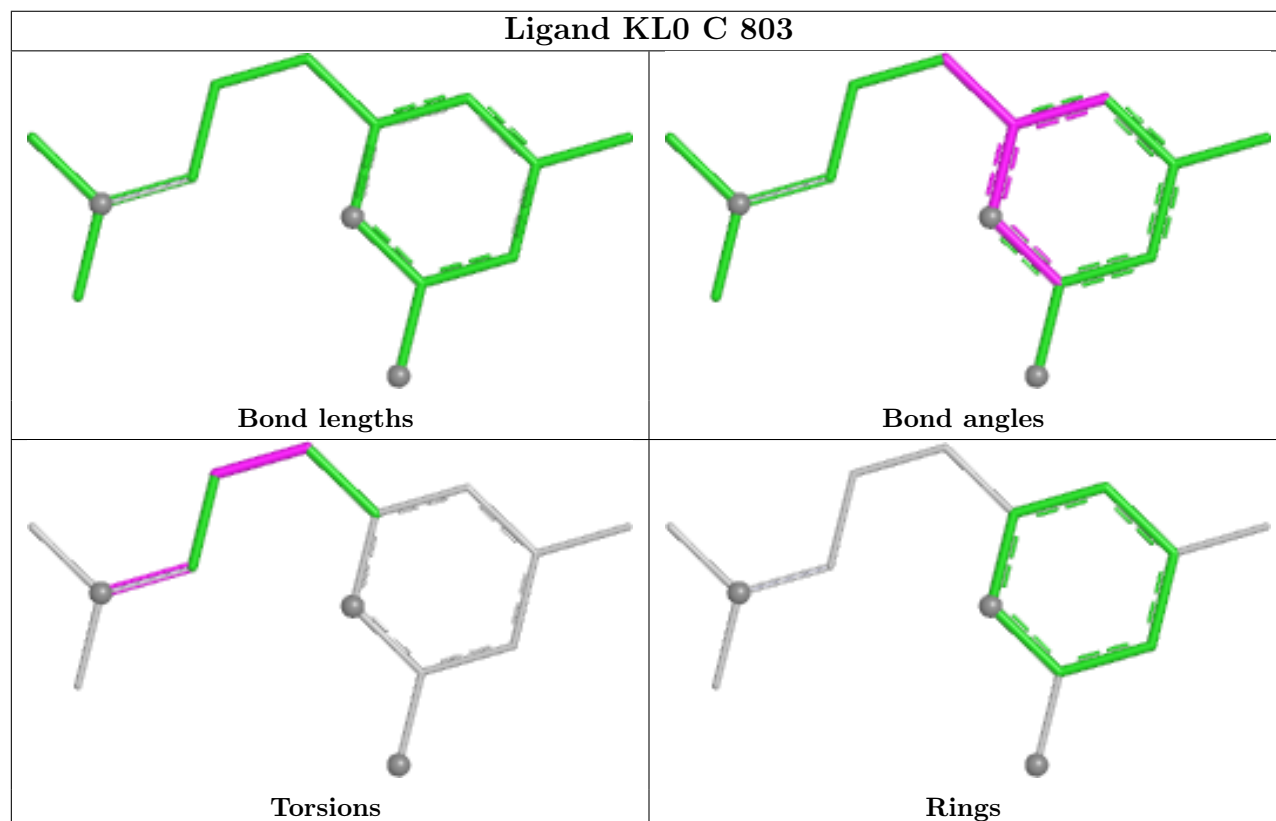


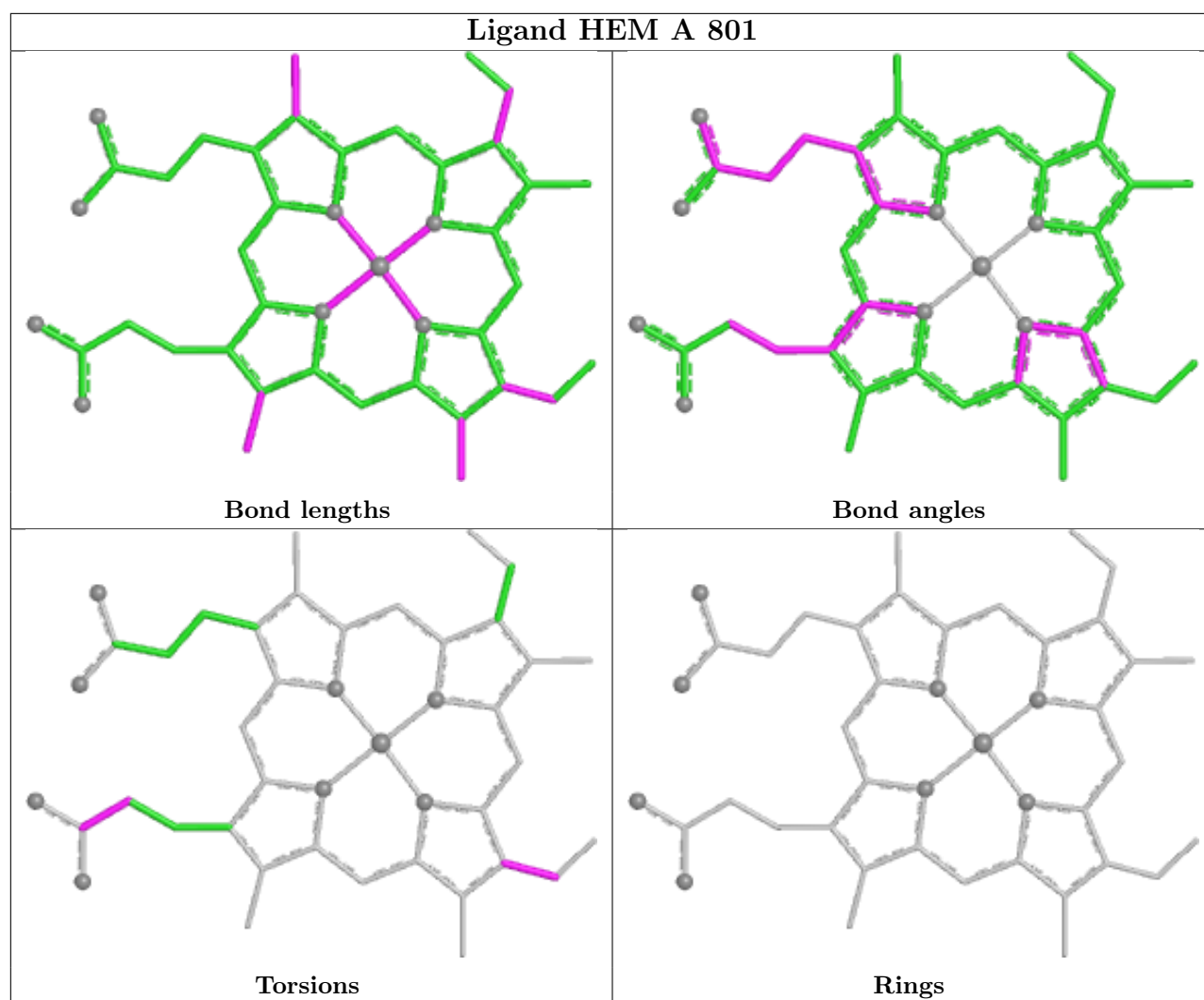


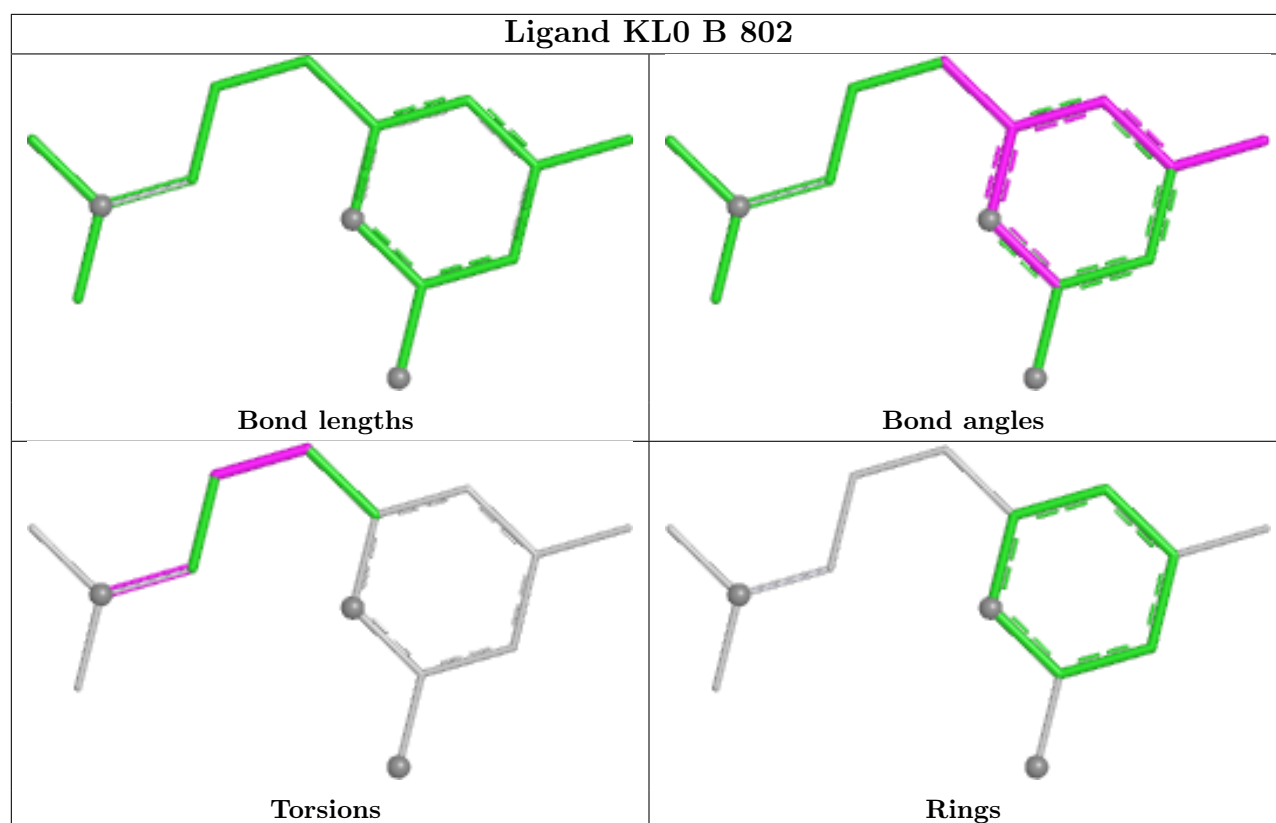
Ligand KL0 D 804



Ligand KL0 C 803







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	414/423 (97%)	-1.08	0 100 100	24, 53, 94, 145	4 (0%)
1	B	411/423 (97%)	-1.18	0 100 100	22, 46, 74, 95	2 (0%)
1	C	412/423 (97%)	-1.13	0 100 100	24, 52, 86, 120	3 (0%)
1	D	413/423 (97%)	-1.19	0 100 100	23, 45, 76, 97	2 (0%)
All	All	1650/1692 (97%)	-1.14	0 100 100	22, 49, 83, 145	11 (0%)

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	GOL	B	803	6/6	0.98	0.06	58,62,66,68	0
5	GOL	C	804	6/6	0.98	0.07	95,98,99,100	0
5	GOL	C	805	6/6	0.98	0.07	61,64,69,75	0
5	GOL	D	805	6/6	0.98	0.08	71,77,78,80	0

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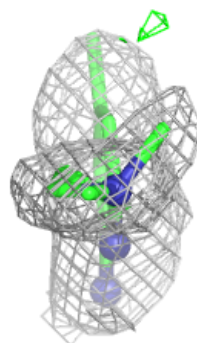
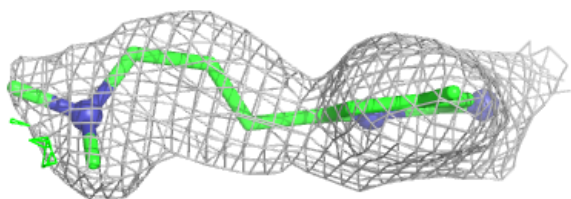
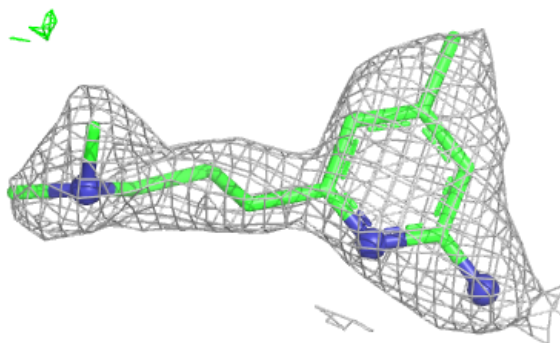
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	H4B	D	803	17/17	0.99	0.04	26,46,51,57	0
4	KL0	A	803	14/14	0.99	0.05	26,46,58,62	0
4	KL0	B	802	14/14	0.99	0.05	46,57,62,64	0
4	KL0	C	803	14/14	0.99	0.05	30,38,55,56	0
4	KL0	D	804	14/14	0.99	0.05	40,55,67,68	0
5	GOL	A	804	6/6	0.99	0.07	80,88,95,96	0
5	GOL	A	805	6/6	0.99	0.04	60,65,69,76	0
2	HEM	B	801	43/43	0.99	0.04	27,39,58,61	0
3	H4B	A	802	17/17	0.99	0.04	44,53,60,61	0
3	H4B	A	807	17/17	0.99	0.04	40,45,60,65	0
3	H4B	C	802	17/17	0.99	0.04	37,48,58,65	0
2	HEM	D	802	43/43	1.00	0.03	20,33,55,60	0
2	HEM	A	801	43/43	1.00	0.04	32,44,55,67	0
2	HEM	C	801	43/43	1.00	0.04	21,40,58,63	0
6	ZN	A	806	1/1	1.00	0.01	49,49,49,49	0
6	ZN	D	801	1/1	1.00	0.01	51,51,51,51	0

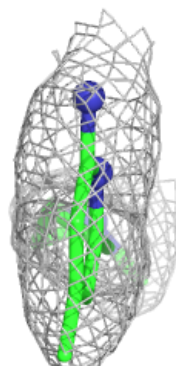
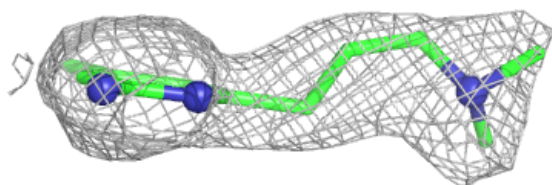
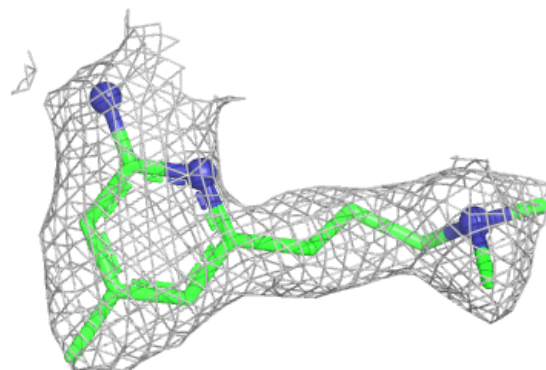
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around KL0 A 803:

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

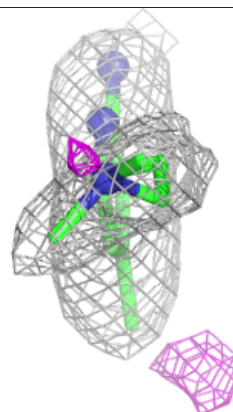
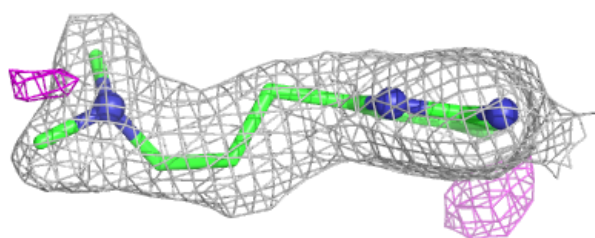
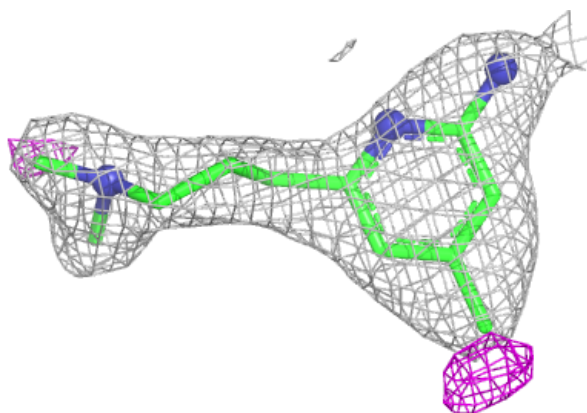
**Electron density around KL0 B 802:**

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

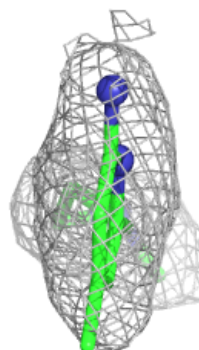
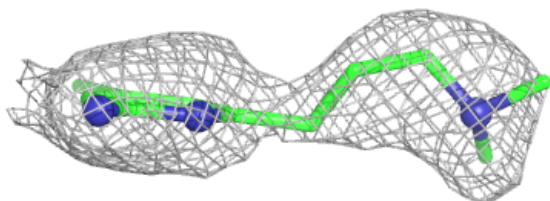
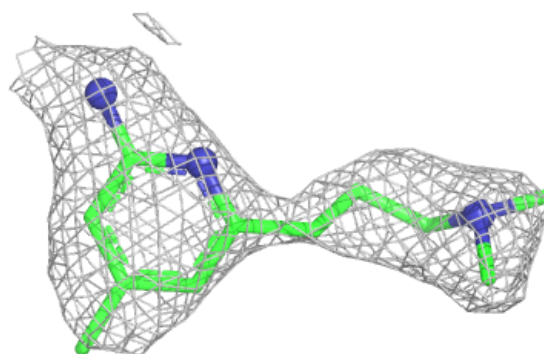


Electron density around KL0 C 803:

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

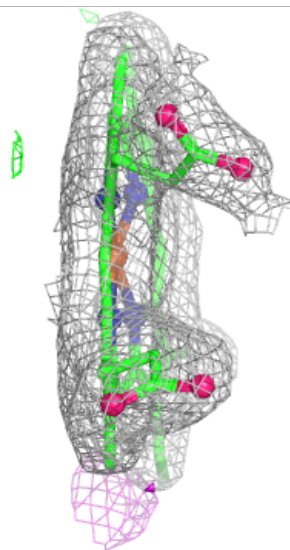
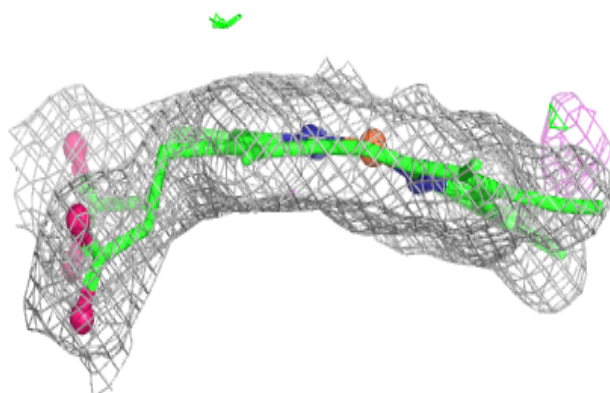
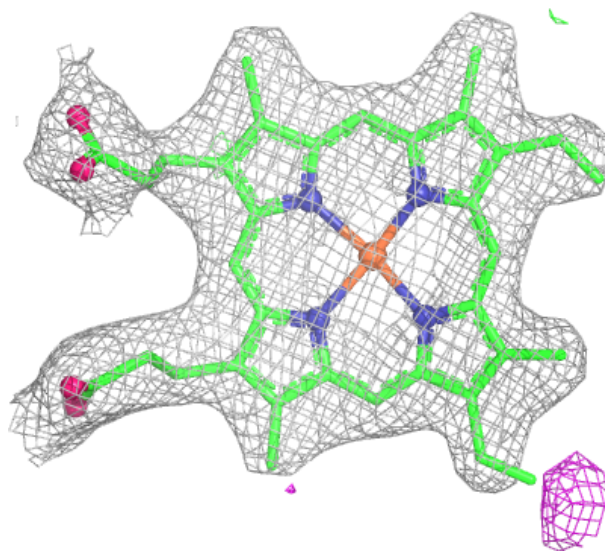
**Electron density around KL0 D 804:**

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



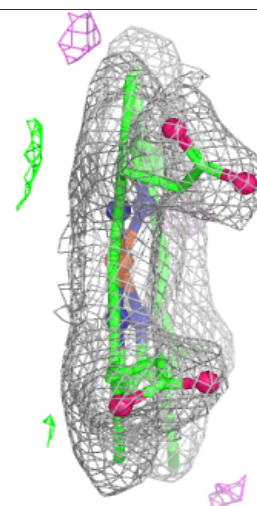
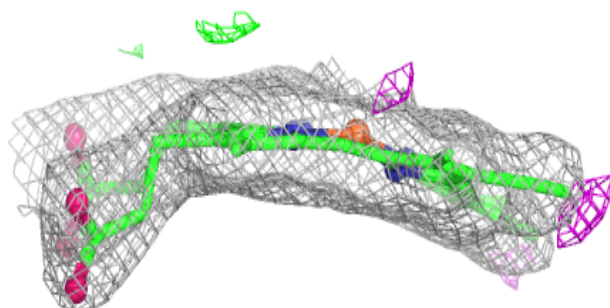
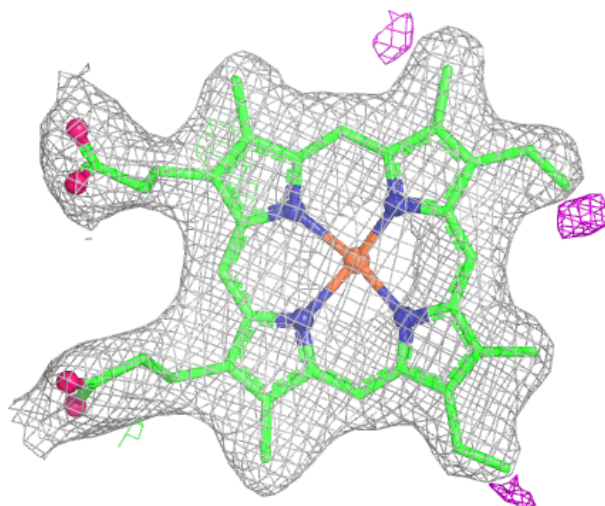
Electron density around HEM B 801:

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



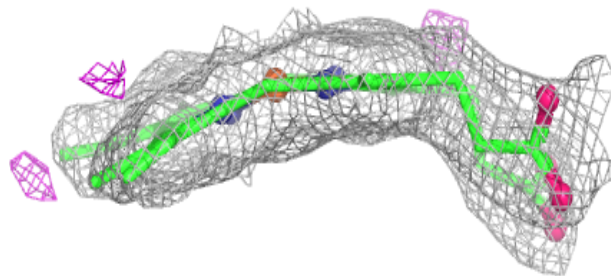
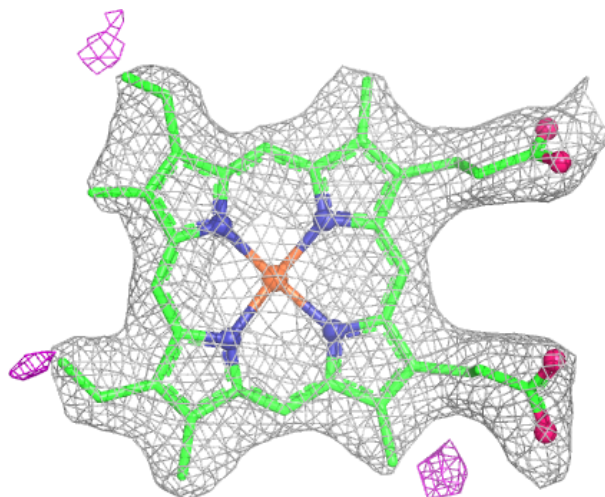
Electron density around HEM D 802:

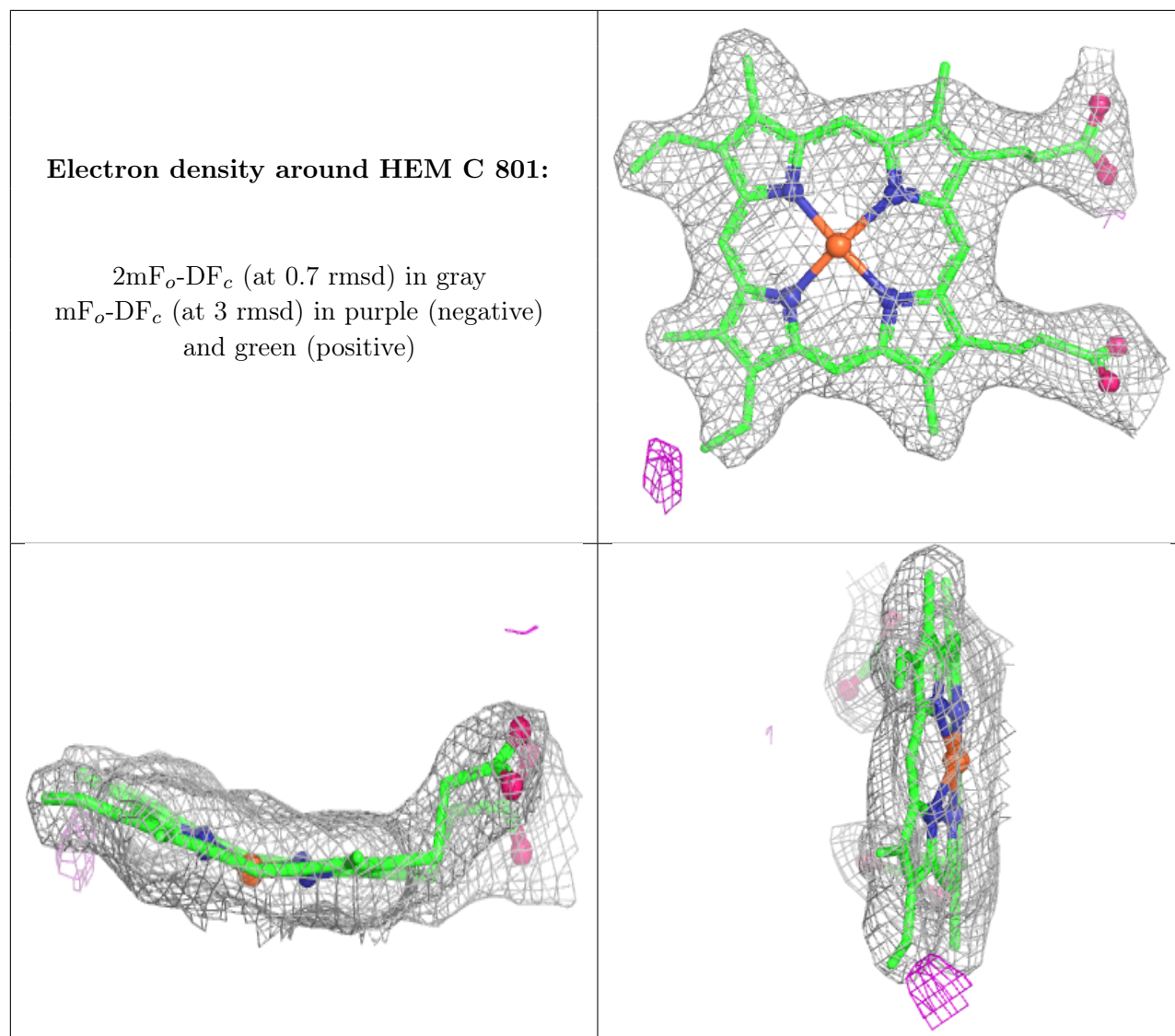
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 801:

$2mF_o-DF_c$ (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.