



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:29 PM UTC

PDB ID : 7LU7 / pdb_00007lu7
Title : Human TDO (hTDO) in complex with NLG919 analog
Authors : Yeh, S.-R.
Deposited on : 2021-02-21
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

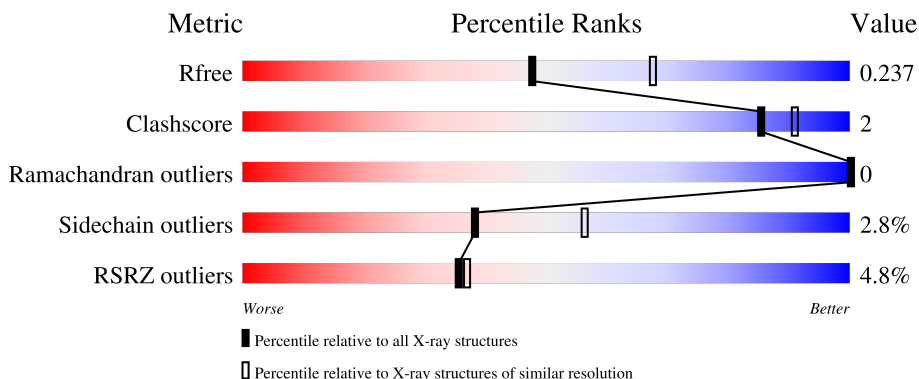
1 Overall quality at a glance

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	AAA	380	2% 83% 6% 10%
1	BBB	380	3% 82% 6% 12%
1	CCC	380	8% 77% 7% 15%
1	DDD	380	4% 83% 7% 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23726 atoms, of which 11645 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 Tryptophan 2,3-dioxygenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	341	Total	C	H	N	O	S	77	0	0
			5791	1865	2895	503	517	11			
1	BBB	334	Total	C	H	N	O	S	69	0	0
			5655	1816	2834	488	506	11			
1	CCC	323	Total	C	H	N	O	S	71	0	0
			5480	1764	2742	475	488	11			
1	DDD	343	Total	C	H	N	O	S	76	0	0
			5819	1869	2910	510	519	11			

There are 32 discrepancies between the modelled and reference sequences:

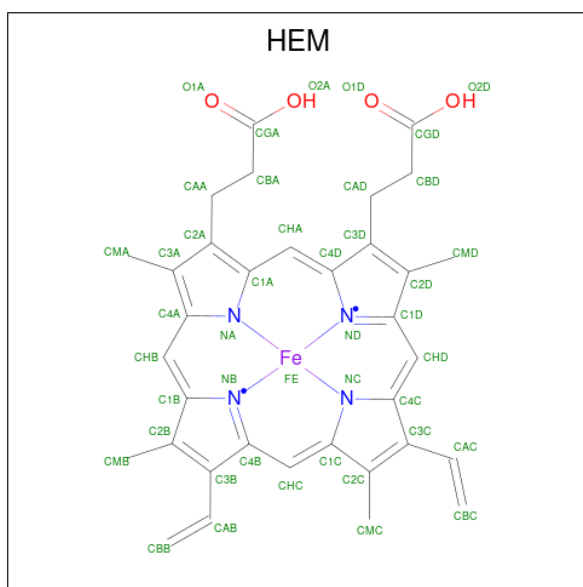
Chain	Residue	Modelled	Actual	Comment	Reference
AAA	17	MET	-	initiating methionine	UNP P48775
AAA	390	GLU	-	expression tag	UNP P48775
AAA	391	HIS	-	expression tag	UNP P48775
AAA	392	HIS	-	expression tag	UNP P48775
AAA	393	HIS	-	expression tag	UNP P48775
AAA	394	HIS	-	expression tag	UNP P48775
AAA	395	HIS	-	expression tag	UNP P48775
AAA	396	HIS	-	expression tag	UNP P48775
BBB	17	MET	-	initiating methionine	UNP P48775
BBB	390	GLU	-	expression tag	UNP P48775
BBB	391	HIS	-	expression tag	UNP P48775
BBB	392	HIS	-	expression tag	UNP P48775
BBB	393	HIS	-	expression tag	UNP P48775
BBB	394	HIS	-	expression tag	UNP P48775
BBB	395	HIS	-	expression tag	UNP P48775
BBB	396	HIS	-	expression tag	UNP P48775
CCC	17	MET	-	initiating methionine	UNP P48775
CCC	390	GLU	-	expression tag	UNP P48775
CCC	391	HIS	-	expression tag	UNP P48775
CCC	392	HIS	-	expression tag	UNP P48775
CCC	393	HIS	-	expression tag	UNP P48775

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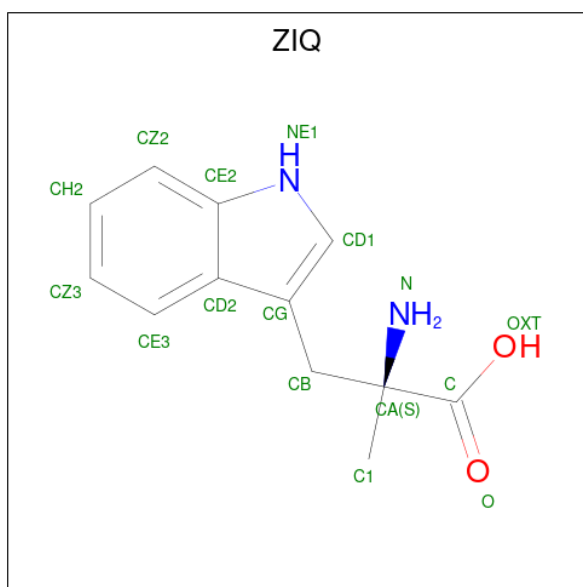
Chain	Residue	Modelled	Actual	Comment	Reference
CCC	394	HIS	-	expression tag	UNP P48775
CCC	395	HIS	-	expression tag	UNP P48775
CCC	396	HIS	-	expression tag	UNP P48775
DDD	17	MET	-	initiating methionine	UNP P48775
DDD	390	GLU	-	expression tag	UNP P48775
DDD	391	HIS	-	expression tag	UNP P48775
DDD	392	HIS	-	expression tag	UNP P48775
DDD	393	HIS	-	expression tag	UNP P48775
DDD	394	HIS	-	expression tag	UNP P48775
DDD	395	HIS	-	expression tag	UNP P48775
DDD	396	HIS	-	expression tag	UNP P48775

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



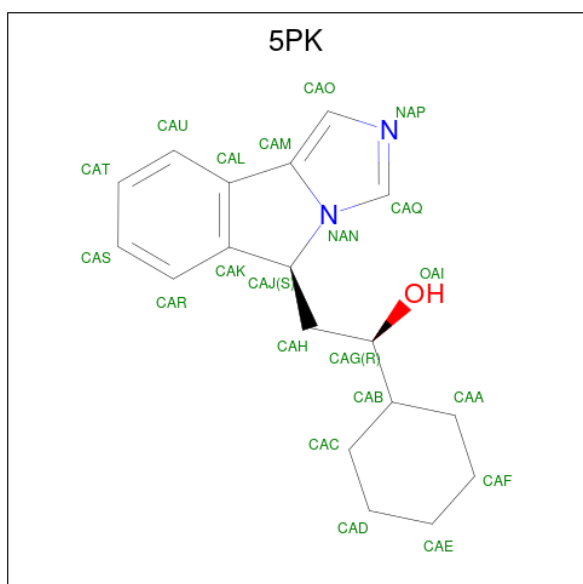
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	AAA	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
2	BBB	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
2	CCC	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
2	DDD	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0

- Molecule 3 is alpha-methyl-L-tryptophan (CCD ID: ZIQ) (formula: $C_{12}H_{14}N_2O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	AAA	1	Total	C	H	N	O	0	0
			30	12	14	2	2		
3	BBB	1	Total	C	H	N	O	0	0
			30	12	14	2	2		
3	CCC	1	Total	C	H	N	O	0	0
			30	12	14	2	2		
3	DDD	1	Total	C	H	N	O	0	0
			30	12	14	2	2		

- Molecule 4 is (1 {R})-1-cyclohexyl-2-[(5 {S})-5 {H}-imidazo[1,5-b]isoindol-5-yl]ethanol (CCD ID: 5PK) (formula: C₁₈H₂₂N₂O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	AAA	1	Total	C	H	N	O	0	0
			43	18	22	2	1		
4	AAA	1	Total	C	H	N	O	0	0
			43	18	22	2	1		
4	CCC	1	Total	C	H	N	O	0	0
			43	18	22	2	1		
4	DDD	1	Total	C	H	N	O	0	0
			43	18	22	2	1		

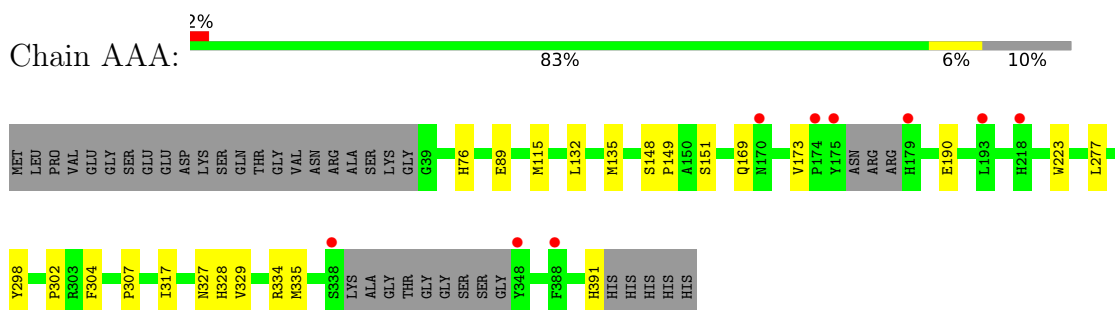
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AAA	93	Total	O	0	0
			93	93		
5	BBB	123	Total	O	0	0
			123	123		
5	CCC	77	Total	O	0	0
			77	77		
5	DDD	104	Total	O	0	0
			104	104		

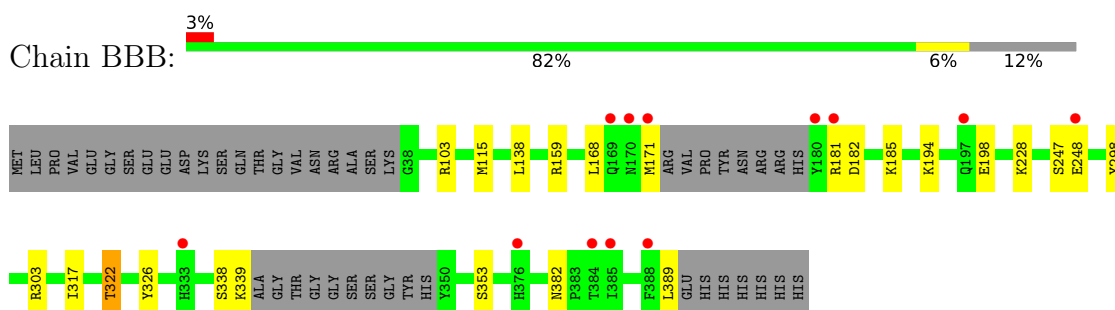
3 Residue-property plots [i](#)

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.

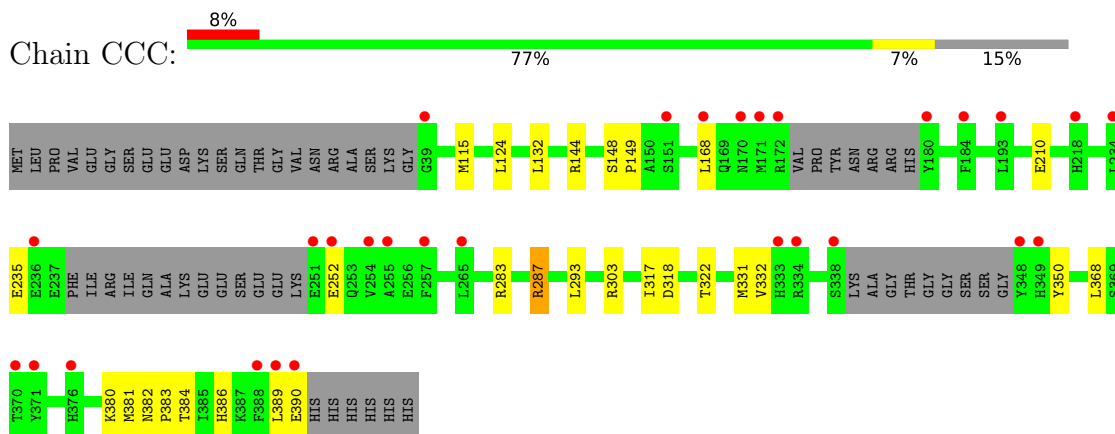
- Molecule 1: Tryptophan 2,3-dioxygenase



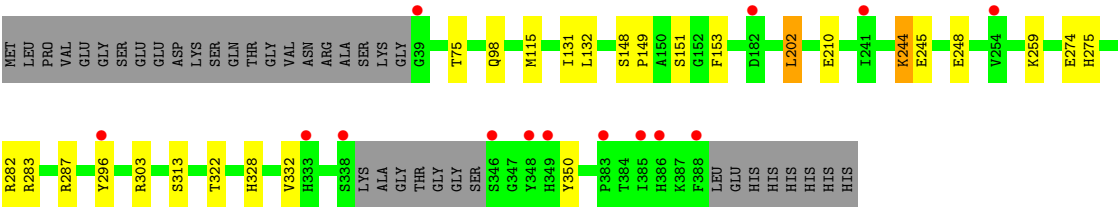
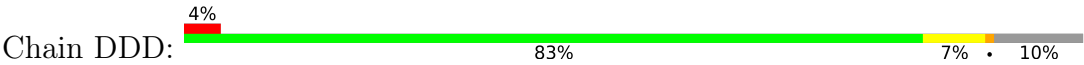
- Molecule 1: Tryptophan 2,3-dioxygenase



- Molecule 1: Tryptophan 2,3-dioxygenase



- Molecule 1: Tryptophan 2,3-dioxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	143.26 Å 153.81 Å 87.97 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.95 – 2.30 29.95 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.95-2.30) 99.0 (29.95-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.29 Å)	Xtriage
Refinement program	REFMAC 5.8.0267, REFMAC 5.8.0267	Depositor
R, R_{free}	0.189 , 0.236 0.189 , 0.237	Depositor DCC
R_{free} test set	4304 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	39.8	Xtriage
Anisotropy	0.307	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 28.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	23726	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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: HEM, ZIQ, 5PK

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	AAA	1.05	1/2964 (0.0%)	1.42	8/3989 (0.2%)
1	BBB	1.01	0/2883	1.41	3/3876 (0.1%)
1	CCC	1.01	0/2800	1.46	0/3767
1	DDD	1.02	0/2977	1.43	3/4006 (0.1%)
All	All	1.02	1/11624 (0.0%)	1.43	14/15638 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	328	HIS	CE1-NE2	5.02	1.37	1.32

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	322	THR	CB-CA-C	5.86	121.92	110.67
1	DDD	275	HIS	CA-CB-CG	5.52	119.32	113.80
1	BBB	298	TYR	CA-C-N	5.49	127.90	120.38
1	BBB	298	TYR	C-N-CA	5.49	127.90	120.38
1	AAA	89	GLU	CA-C-N	5.32	127.36	120.44

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	AAA	2896	2895	2876	11	0
1	BBB	2821	2834	2818	8	0
1	CCC	2738	2742	2724	14	0
1	DDD	2909	2910	2893	11	0
2	AAA	43	30	30	5	0
2	BBB	43	30	30	2	0
2	CCC	43	30	30	3	0
2	DDD	43	30	30	3	0
3	AAA	16	14	0	0	0
3	BBB	16	14	0	1	0
3	CCC	16	14	0	0	0
3	DDD	16	14	0	0	0
4	AAA	42	44	44	6	0
4	CCC	21	22	22	1	0
4	DDD	21	22	22	2	0
5	AAA	93	0	0	0	0
5	BBB	123	0	0	0	0
5	CCC	77	0	0	0	0
5	DDD	104	0	0	0	0
All	All	12081	11645	11519	52	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 2.

The worst 5 of 52 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AAA:401:HEM:C4A	4:AAA:403:5PK:H21	2.29	0.67
1:DDD:210:GLU:HG2	1:DDD:287:ARG:HB3	1.85	0.59
2:DDD:401:HEM:HBC2	2:DDD:401:HEM:HHH	1.84	0.57
4:AAA:404:5PK:H21	2:BBB:401:HEM:C4A	2.40	0.56
1:CCC:115:MET:HE3	1:CCC:317:ILE:CD1	2.36	0.55

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	AAA	335/380 (88%)	327 (98%)	8 (2%)	0	100	100
1	BBB	328/380 (86%)	319 (97%)	9 (3%)	0	100	100
1	CCC	315/380 (83%)	303 (96%)	12 (4%)	0	100	100
1	DDD	339/380 (89%)	332 (98%)	7 (2%)	0	100	100
All	All	1317/1520 (87%)	1281 (97%)	36 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	AAA	318/348 (91%)	312 (98%)	6 (2%)	50	69
1	BBB	310/348 (89%)	301 (97%)	9 (3%)	37	55
1	CCC	301/348 (86%)	293 (97%)	8 (3%)	39	58
1	DDD	319/348 (92%)	307 (96%)	12 (4%)	29	44
All	All	1248/1392 (90%)	1213 (97%)	35 (3%)	38	56

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	DDD	202	LEU
1	DDD	244	LYS
1	DDD	282	ARG
1	BBB	322	THR
1	BBB	248	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

12 ligands 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	$\# Z > 2$
2	HEM	BBB	401	1,4	50,50,50	1.70	11 (22%)	67,82,82	1.69	17 (25%)
3	ZIQ	DDD	402	-	14,17,17	0.70	0	20,25,25	0.87	1 (5%)
3	ZIQ	AAA	402	-	14,17,17	0.54	0	20,25,25	1.06	1 (5%)
3	ZIQ	BBB	402	-	14,17,17	0.60	0	20,25,25	0.98	1 (5%)
2	HEM	DDD	401	1,4	50,50,50	1.60	12 (24%)	67,82,82	1.83	21 (31%)
4	5PK	DDD	403	2	24,24,24	0.75	0	27,34,34	0.58	0
4	5PK	AAA	403	2	24,24,24	1.02	1 (4%)	27,34,34	0.75	0
4	5PK	CCC	403	2	24,24,24	1.09	2 (8%)	27,34,34	0.64	0
3	ZIQ	CCC	402	-	14,17,17	0.58	0	20,25,25	1.01	1 (5%)
2	HEM	CCC	401	1,4	50,50,50	1.67	7 (14%)	67,82,82	1.82	15 (22%)
4	5PK	AAA	404	2	24,24,24	0.87	1 (4%)	27,34,34	0.60	0
2	HEM	AAA	401	1,4	50,50,50	1.62	10 (20%)	67,82,82	1.79	17 (25%)

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	BBB	401	1,4	-	3/14/54/54	-
3	ZIQ	DDD	402	-	-	4/11/11/11	0/2/2/2
3	ZIQ	AAA	402	-	-	4/11/11/11	0/2/2/2
3	ZIQ	BBB	402	-	-	1/11/11/11	0/2/2/2
2	HEM	DDD	401	1,4	-	4/14/54/54	-
4	5PK	DDD	403	2	-	4/8/28/28	0/4/4/4
4	5PK	AAA	403	2	-	3/8/28/28	0/4/4/4
4	5PK	CCC	403	2	-	1/8/28/28	0/4/4/4
3	ZIQ	CCC	402	-	-	2/11/11/11	0/2/2/2
2	HEM	CCC	401	1,4	-	2/14/54/54	-
4	5PK	AAA	404	2	-	3/8/28/28	0/4/4/4
2	HEM	AAA	401	1,4	-	2/14/54/54	-

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	CCC	401	HEM	FE-NC	4.98	2.11	1.95
2	BBB	401	HEM	FE-NB	4.46	2.08	1.94
2	CCC	401	HEM	FE-NB	4.43	2.08	1.94
2	AAA	401	HEM	FE-NB	4.32	2.08	1.94
2	AAA	401	HEM	FE-NC	4.22	2.09	1.95

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	CCC	401	HEM	CHC-C4B-NB	5.47	130.31	124.42
2	CCC	401	HEM	CBD-CAD-C3D	-5.27	97.95	112.53
2	DDD	401	HEM	CHC-C4B-NB	4.80	129.59	124.42
2	AAA	401	HEM	CHC-C4B-NB	4.70	129.48	124.42
2	DDD	401	HEM	CBD-CAD-C3D	-4.67	99.61	112.53

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	DDD	401	HEM	C2A-CAA-CBA-CGA
3	DDD	402	ZIQ	O-C-CA-C1
3	DDD	402	ZIQ	OXT-C-CA-C1

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Mol	Chain	Res	Type	Atoms
4	AAA	403	5PK	CAC-CAB-CAG-OAI
4	AAA	403	5PK	CAC-CAB-CAG-CAH

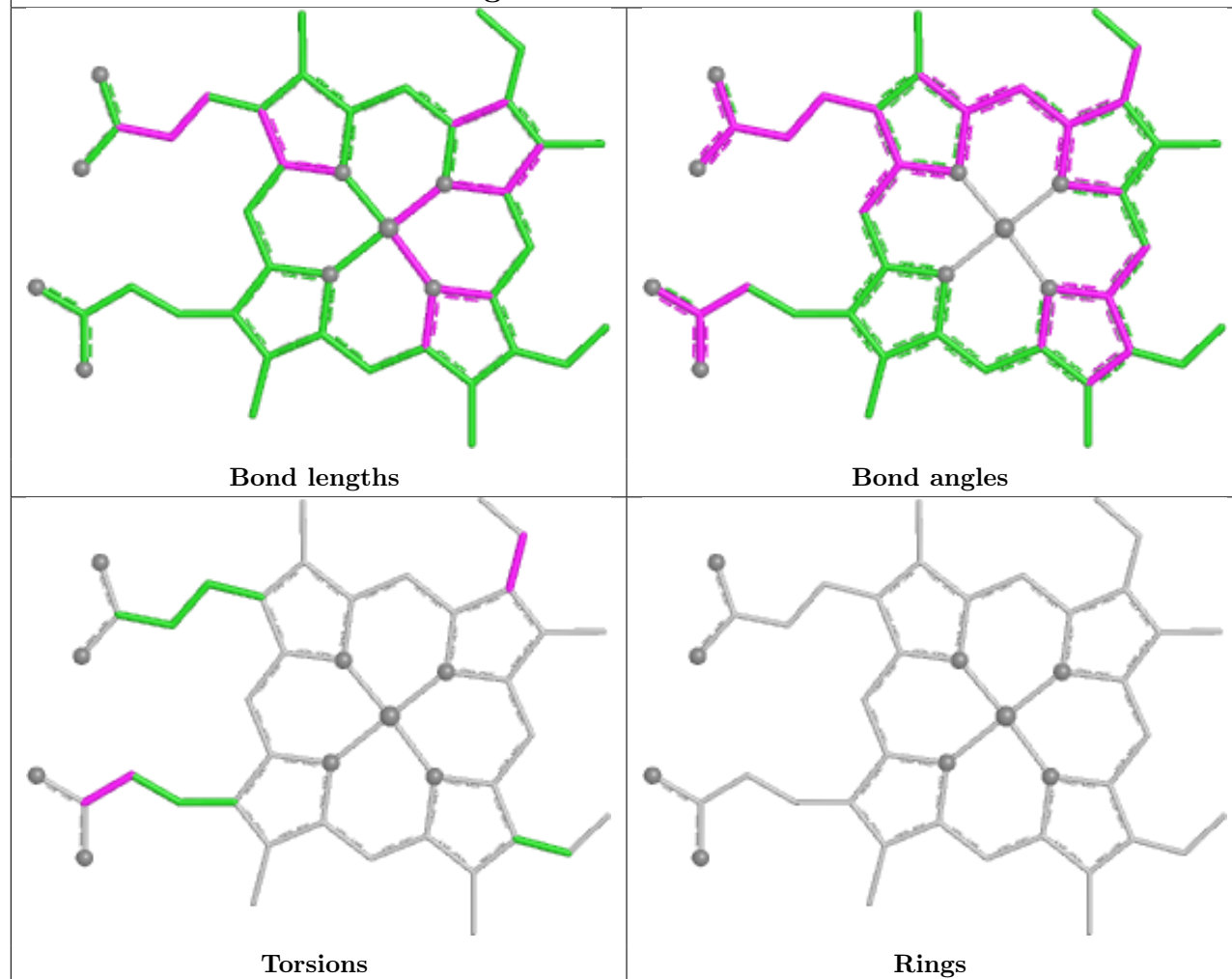
There are no ring outliers.

9 monomers are involved in 16 short contacts:

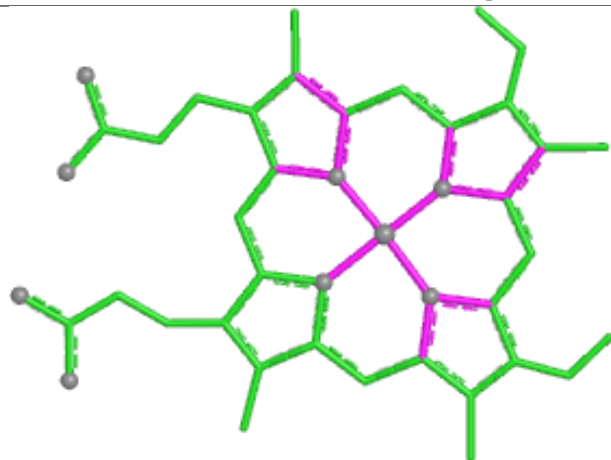
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BBB	401	HEM	2	0
3	BBB	402	ZIQ	1	0
2	DDD	401	HEM	3	0
4	DDD	403	5PK	2	0
4	AAA	403	5PK	5	0
4	CCC	403	5PK	1	0
2	CCC	401	HEM	3	0
4	AAA	404	5PK	1	0
2	AAA	401	HEM	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

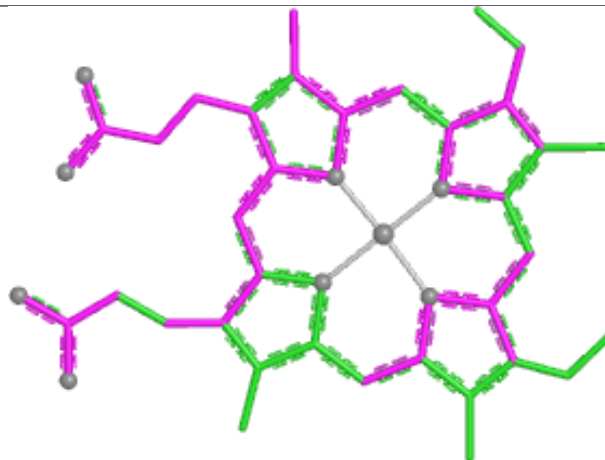
Ligand HEM BBB 401



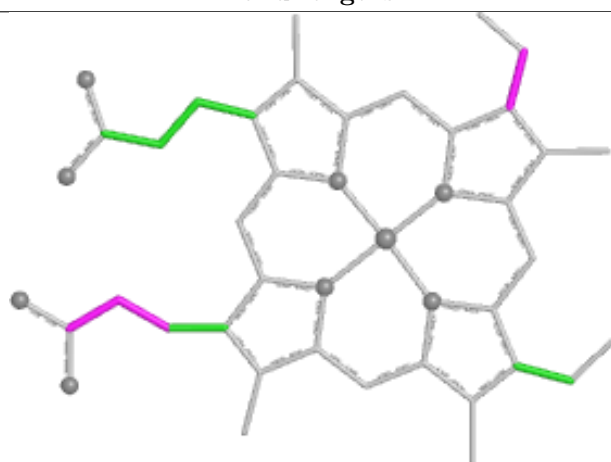
Ligand HEM DDD 401



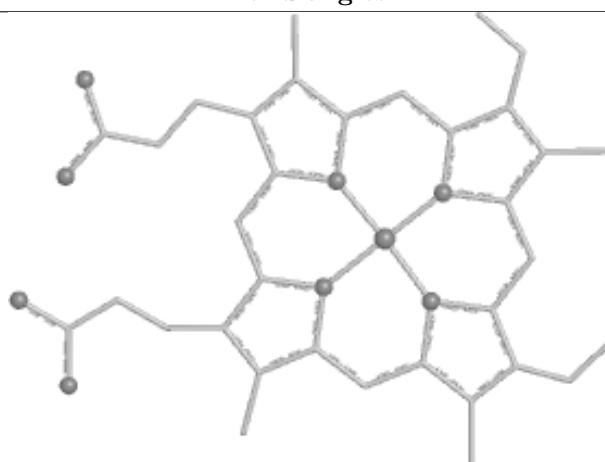
Bond lengths



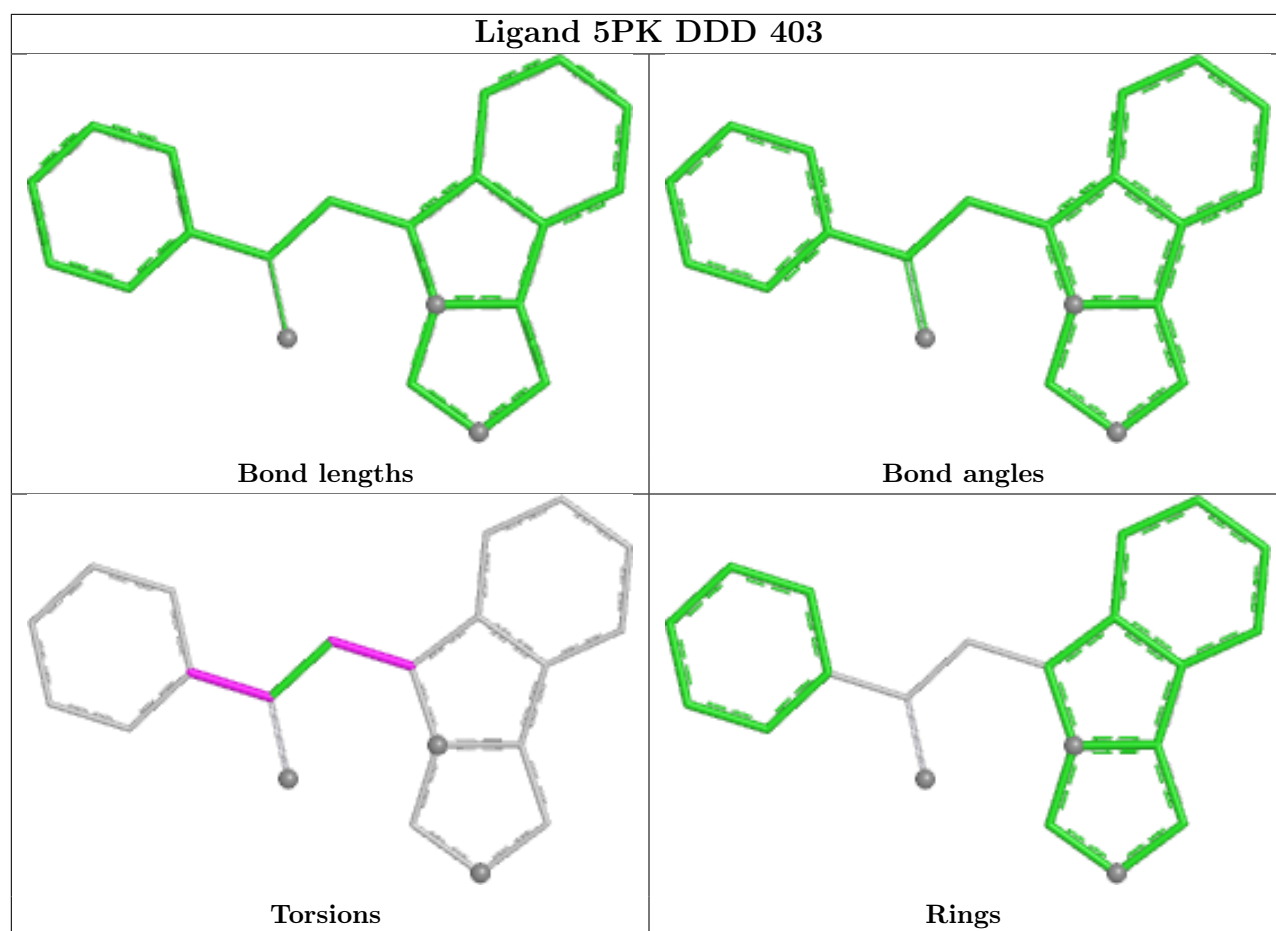
Bond angles



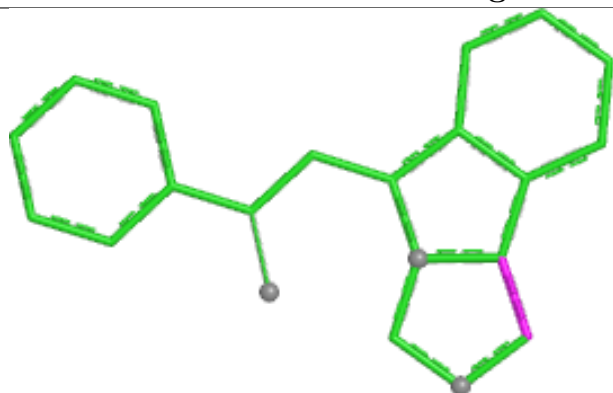
Torsions



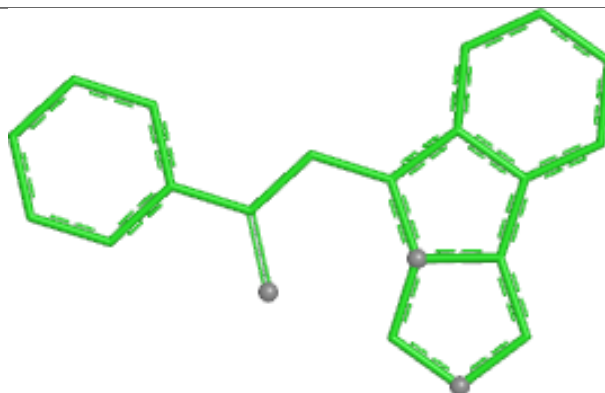
Rings



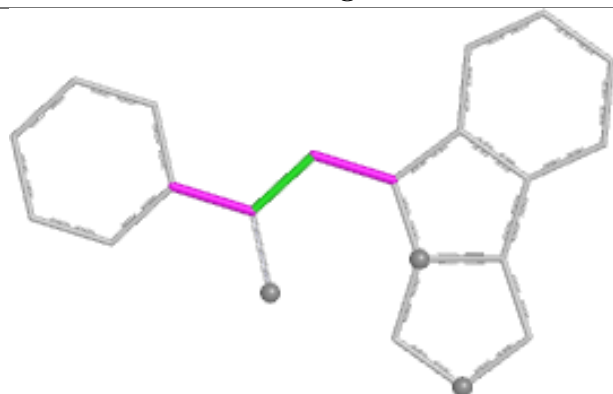
Ligand 5PK AAA 403



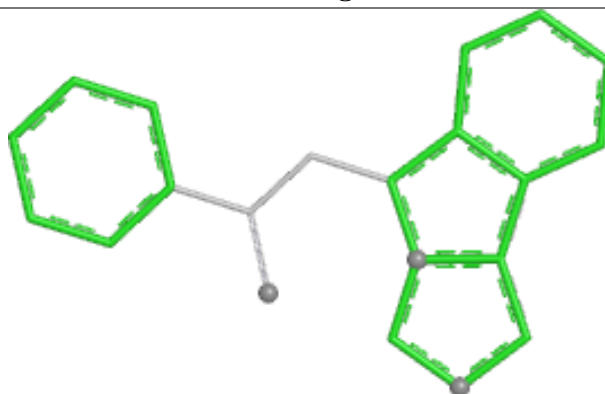
Bond lengths



Bond angles

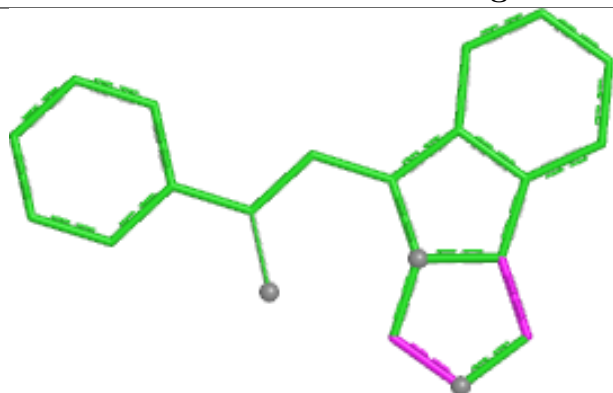


Torsions

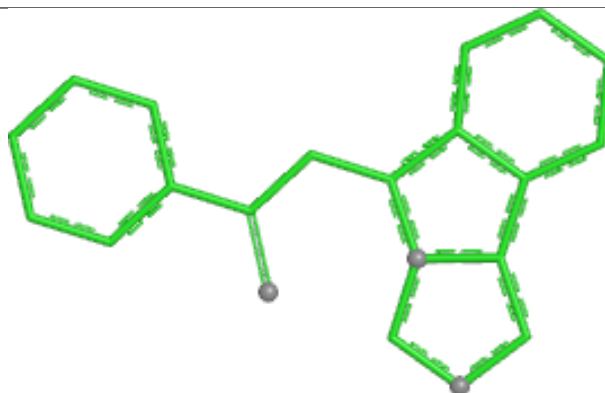


Rings

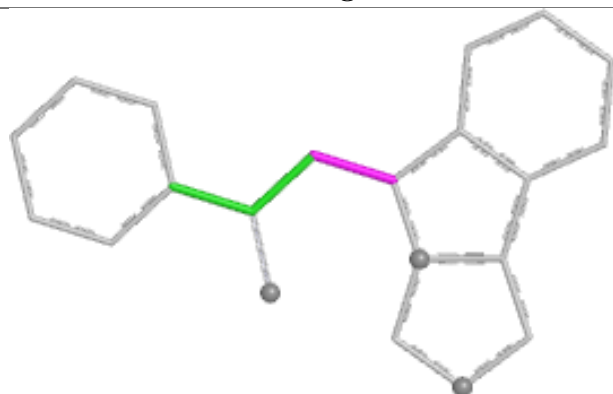
Ligand 5PK CCC 403



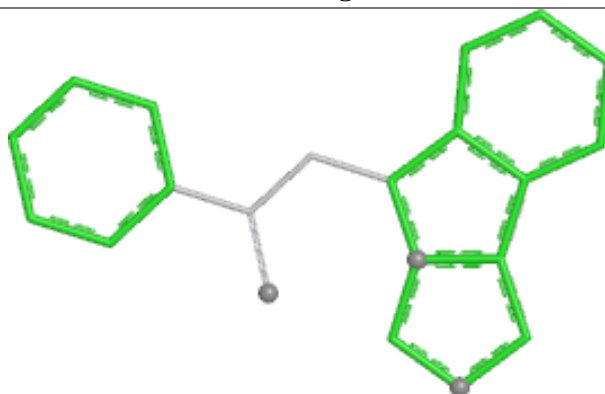
Bond lengths



Bond angles

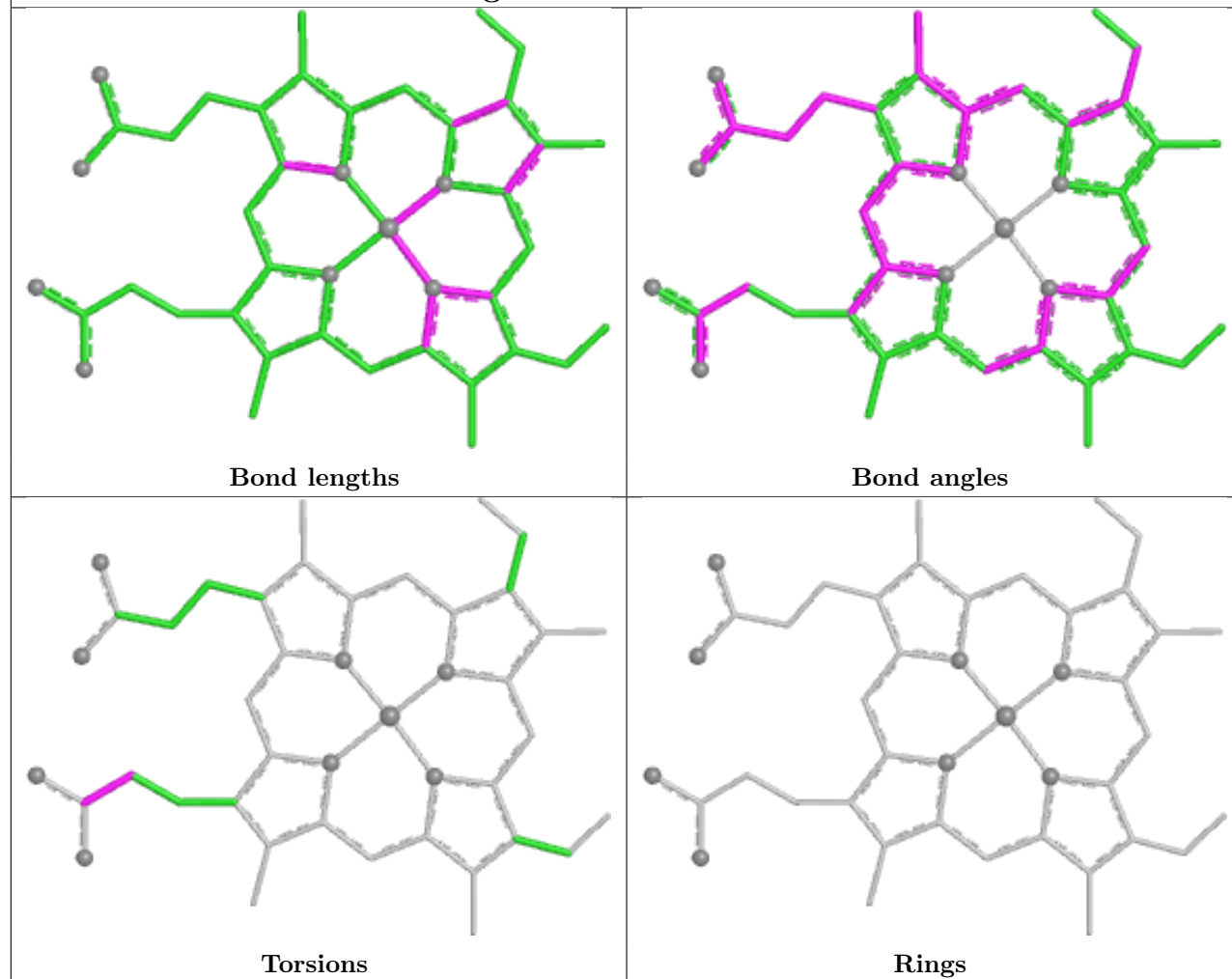


Torsions

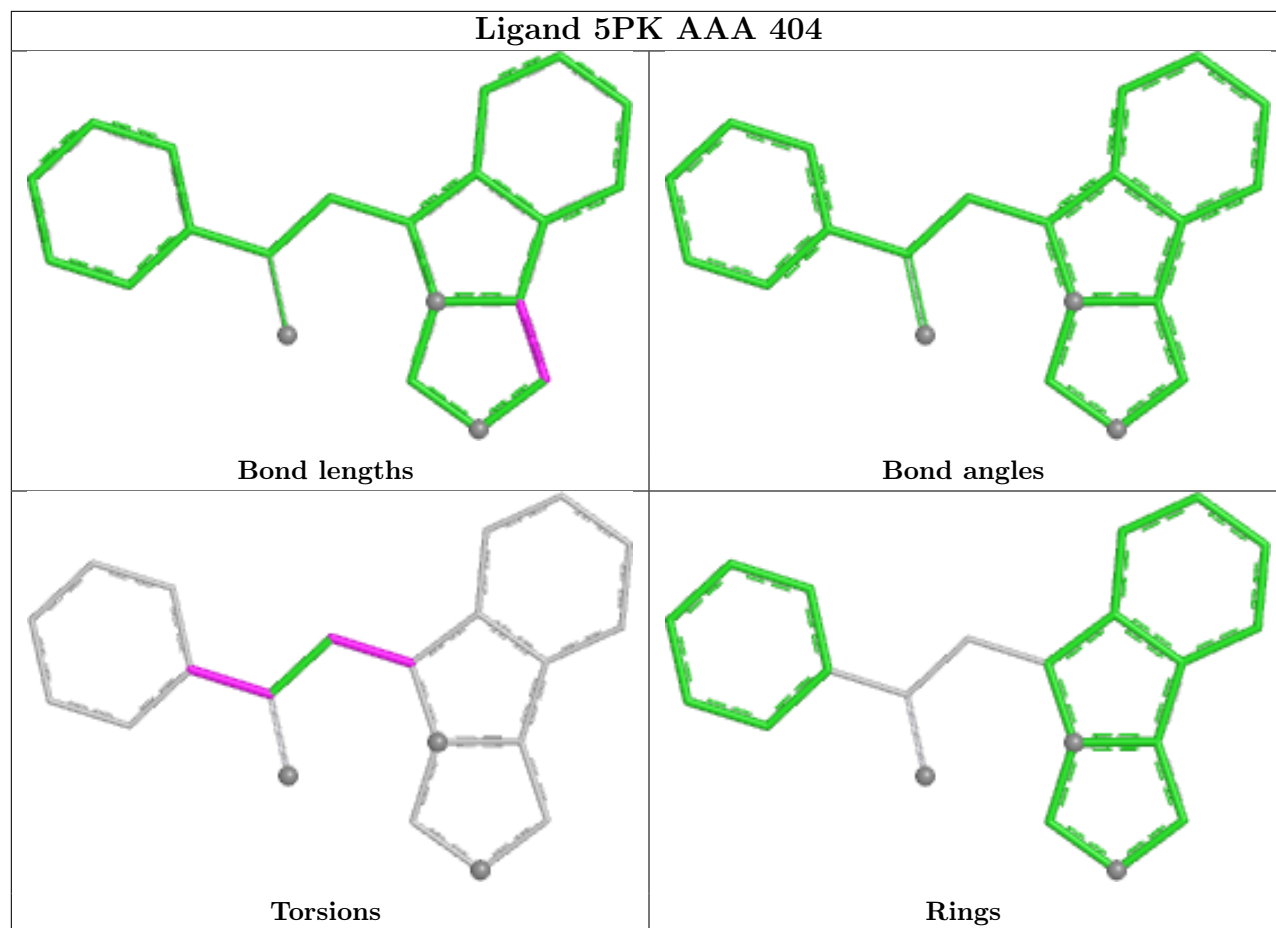


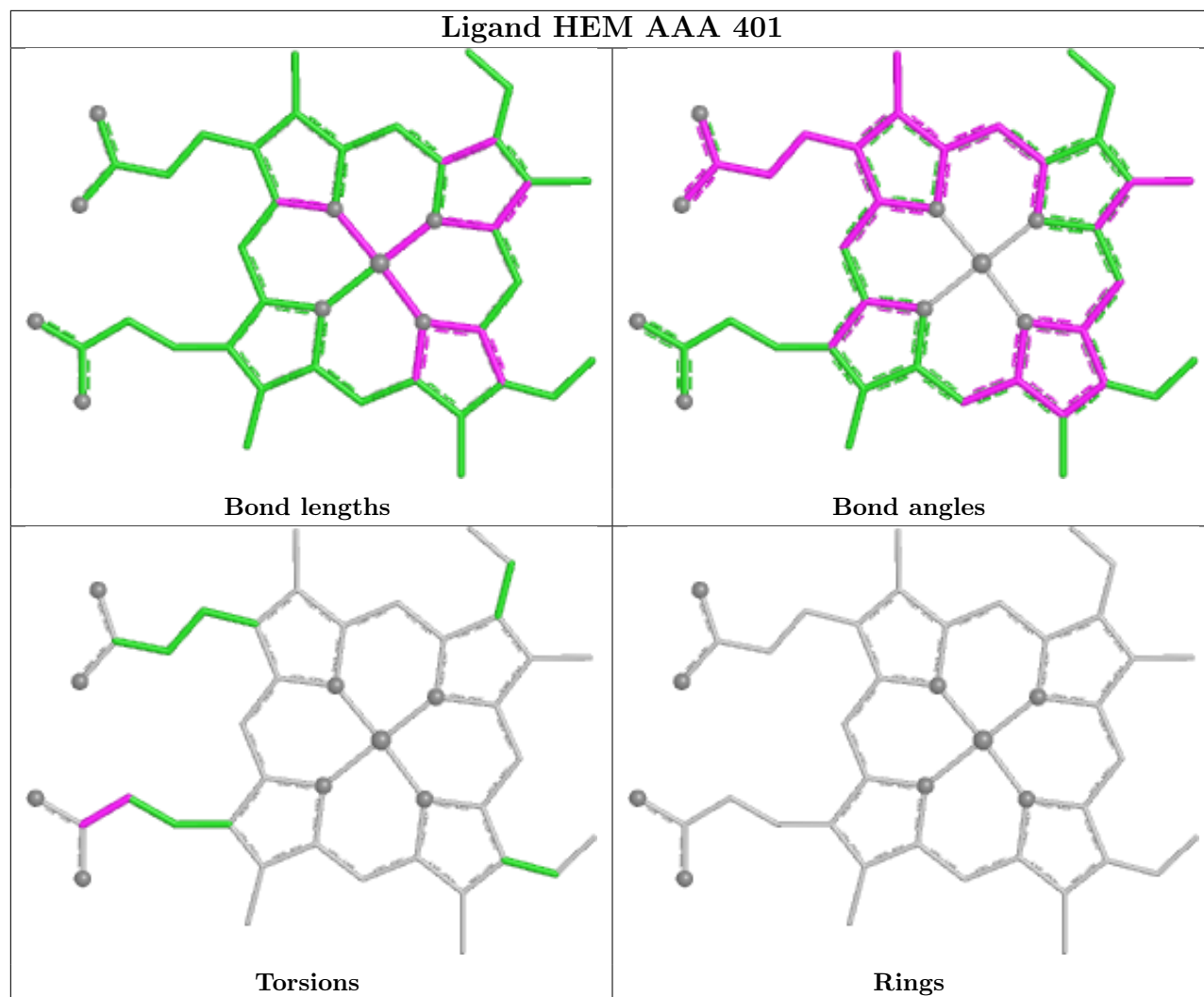
Rings

Ligand HEM CCC 401



Ligand 5PK AAA 404





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	AAA	341/380 (89%)	-0.13	9 (2%) 57 59	26, 45, 94, 123	0
1	BBB	334/380 (87%)	-0.26	12 (3%) 46 48	24, 40, 94, 125	0
1	CCC	323/380 (85%)	0.35	29 (8%) 15 16	29, 56, 116, 151	0
1	DDD	343/380 (90%)	-0.08	14 (4%) 41 43	29, 48, 99, 145	0
All	All	1341/1520 (88%)	-0.03	64 (4%) 35 37	24, 46, 103, 151	0

The worst 5 of 64 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	180	TYR	5.6
1	CCC	348	TYR	4.4
1	AAA	175	TYR	4.1
1	DDD	385	ILE	3.8
1	CCC	172	ARG	3.7

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](#)

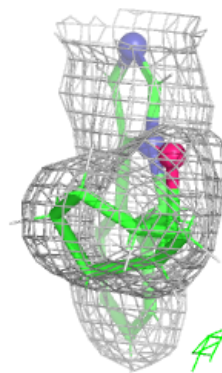
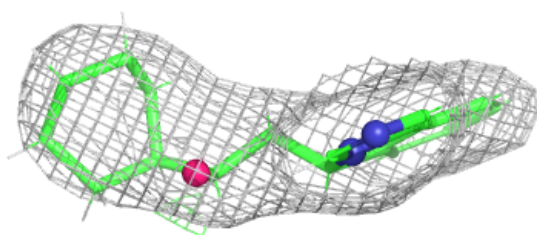
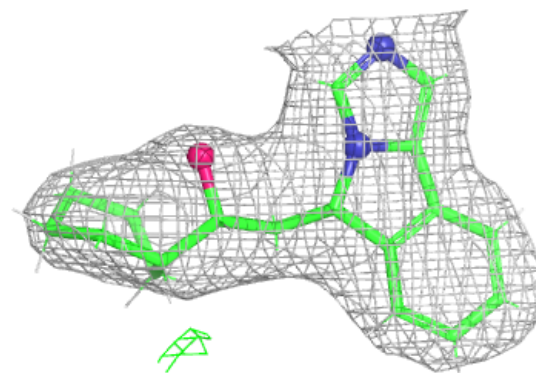
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZIQ	CCC	402	16/16	0.95	0.08	39,45,55,63	0
3	ZIQ	DDD	402	16/16	0.96	0.06	37,41,48,50	0
4	5PK	AAA	403	21/21	0.96	0.08	45,57,73,74	0
4	5PK	CCC	403	21/21	0.96	0.09	38,50,74,75	0
4	5PK	DDD	403	21/21	0.96	0.07	45,50,59,60	0
3	ZIQ	BBB	402	16/16	0.97	0.05	33,35,38,42	0
4	5PK	AAA	404	21/21	0.97	0.06	33,45,62,65	0
2	HEM	CCC	401	43/43	0.97	0.08	45,51,67,81	0
3	ZIQ	AAA	402	16/16	0.97	0.05	29,35,42,46	0
2	HEM	DDD	401	43/43	0.98	0.06	33,40,52,68	0
2	HEM	BBB	401	43/43	0.98	0.07	32,39,56,68	0
2	HEM	AAA	401	43/43	0.98	0.06	37,43,58,70	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.

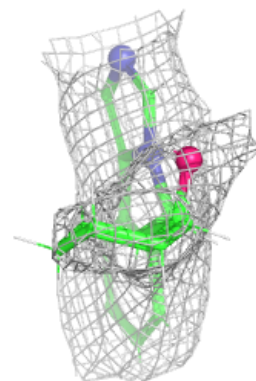
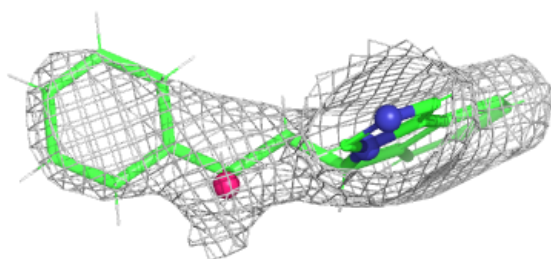
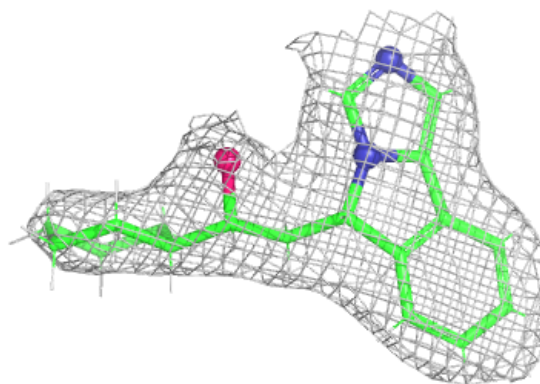
Electron density around 5PK AAA 403:

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

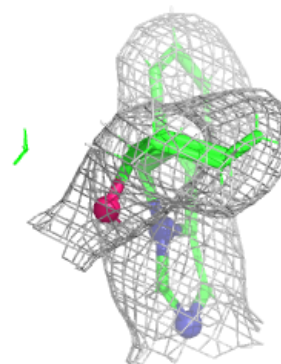
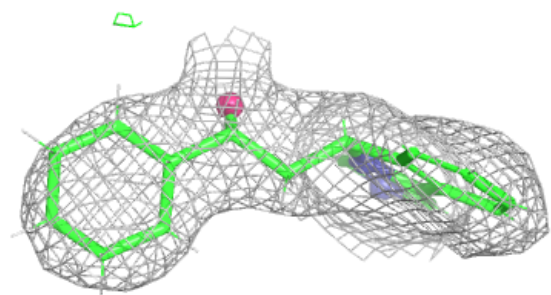
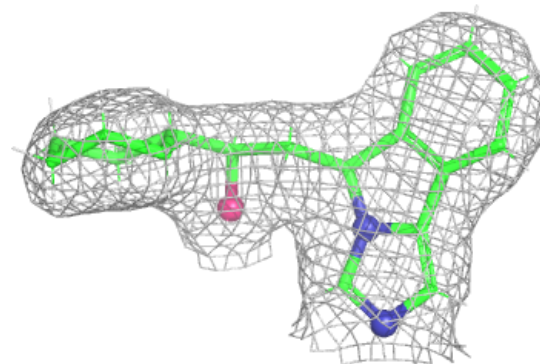


Electron density around 5PK CCC 403:

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

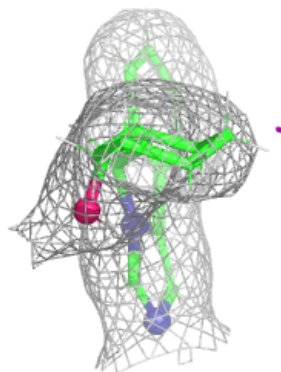
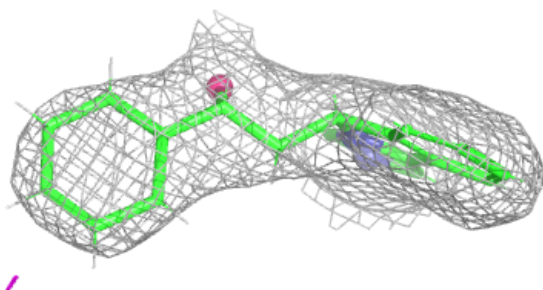
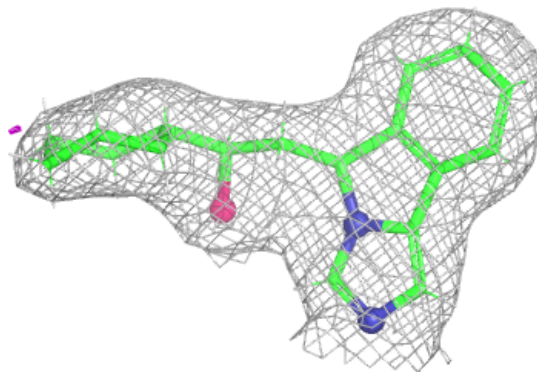
**Electron density around 5PK DDD 403:**

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



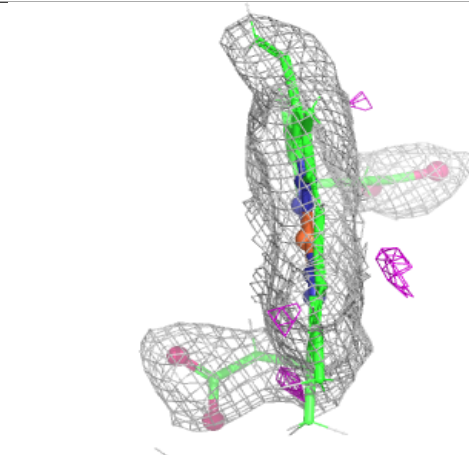
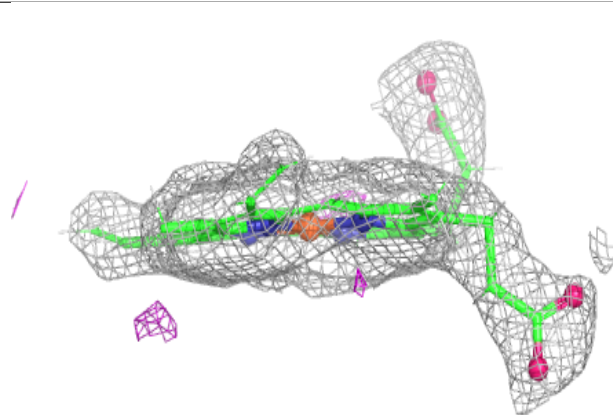
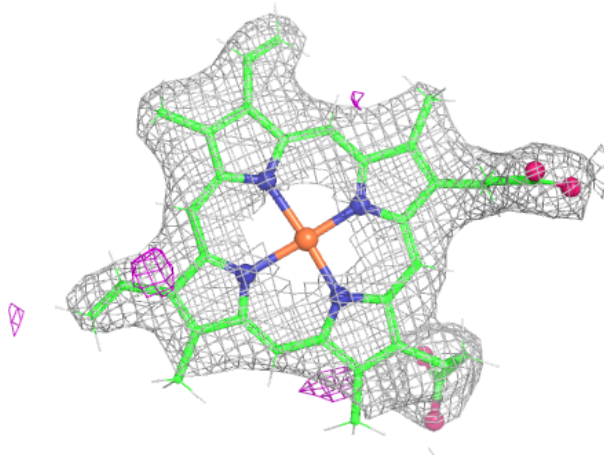
Electron density around 5PK AAA 404:

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



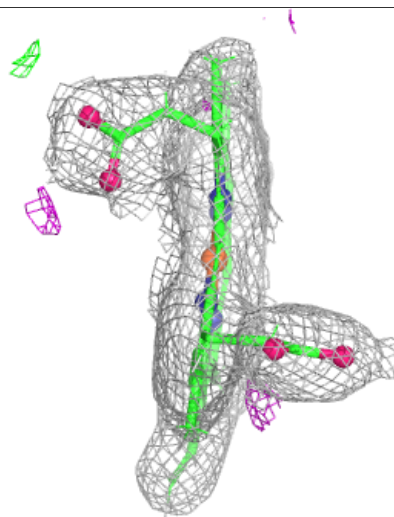
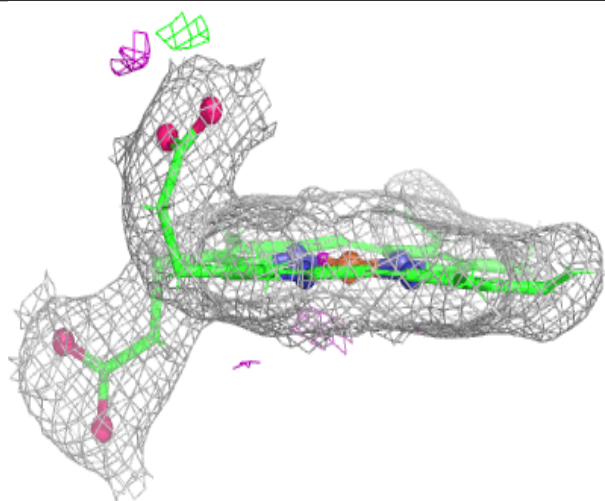
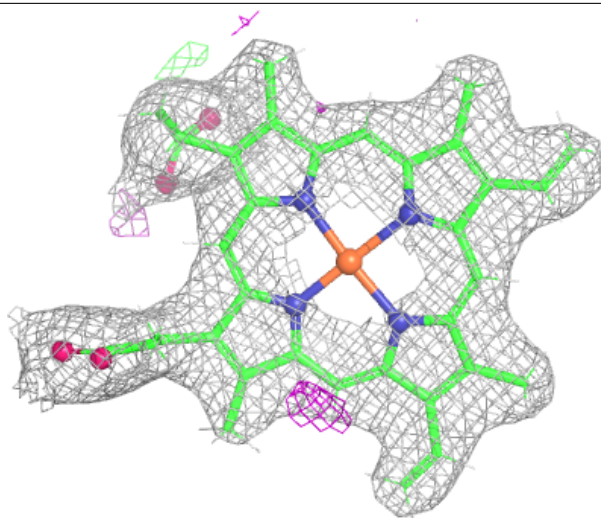
Electron density around HEM CCC 401:

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



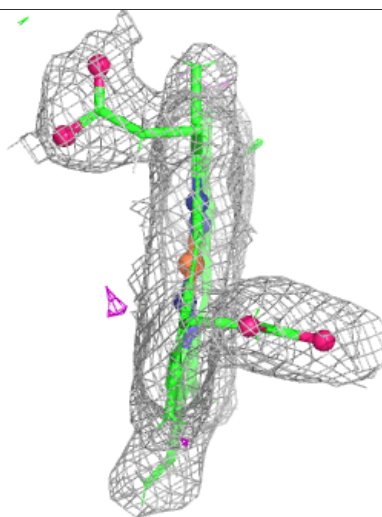
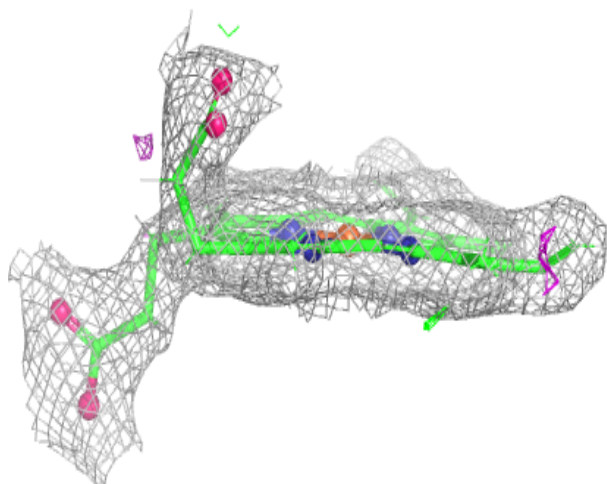
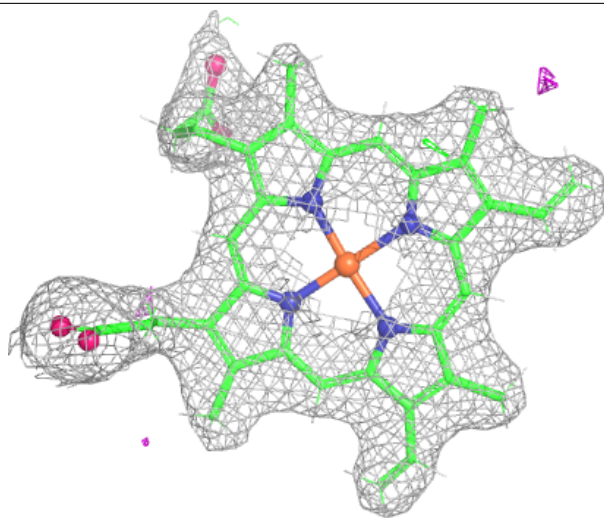
Electron density around HEM DDD 401:

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



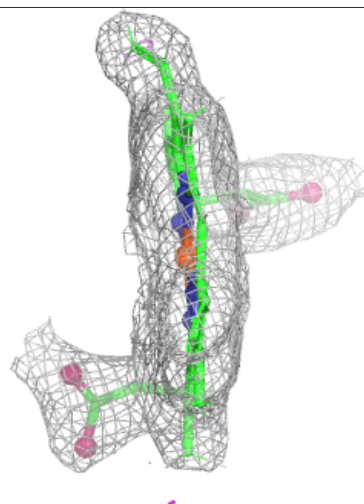
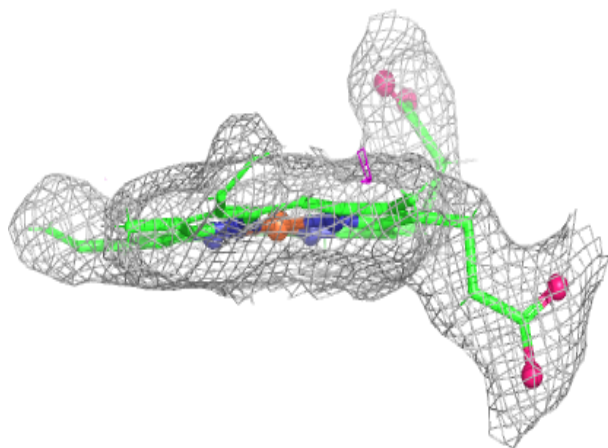
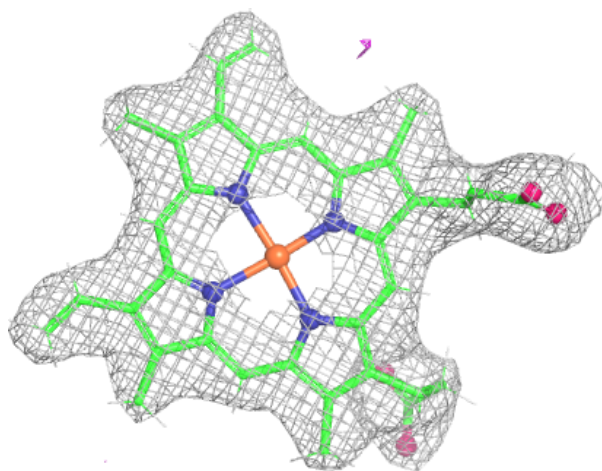
Electron density around HEM BBB 401:

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



Electron density around HEM AAA 401:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.