



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 07:44 PM UTC

PDB ID : 2OZ0 / pdb_00002oz0
Title : Mechanistic and Structural Studies of H373Q Flavocytochrome b2: Effects of Mutating the Active Site Base
Authors : Tsai, C.-L.; Gokulan, K.; Sobrado, P.; Sacchettini, J.C.; Fitzpatrick, P.F.
Deposited on : 2007-02-23
Resolution : 2.80 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

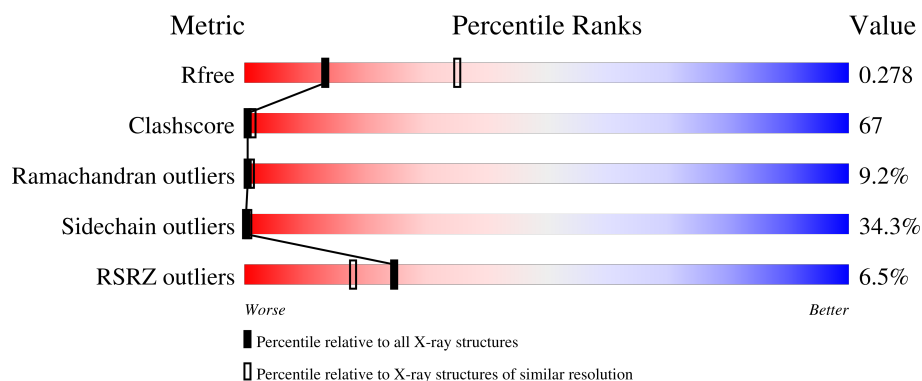
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	511	7% 8% 29% 39% 20% .
1	B	511	5% 6% 22% 28% 22% 23%

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
3	FMN	A	569	X	-	X	-
3	FMN	B	570	-	-	X	-
4	PYR	B	571	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7042 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.

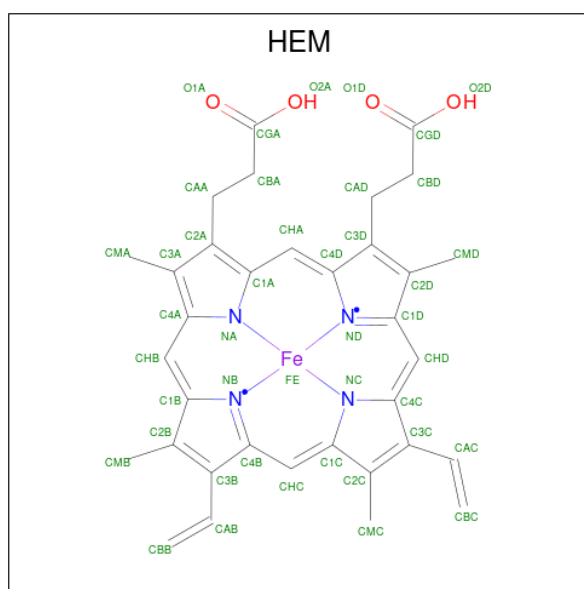
- Molecule 1 is a protein called Cytochrome b2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	492	Total	C	N	O	S	0	0	0
			3833	2441	649	728	15			
1	B	396	Total	C	N	O	S	0	0	0
			3081	1953	524	593	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	373	GLN	HIS	engineered mutation	UNP P00175
B	373	GLN	HIS	engineered mutation	UNP P00175

- 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	C	Fe	N	O	0	0
			43	34	1	4	4		

-
- The chemical structure of FMN (Flavin Mononucleotide) is shown. It consists of an isoalloxazine ring system (a fused bicyclic system with two nitrogen atoms) attached to a ribitol chain. The ribitol chain is a five-carbon chain with hydroxyl groups at C2, C3, and C4. The C1 of the ribitol chain is attached to the N10 of the isoalloxazine ring. The C5 of the ribitol chain is attached to a phosphate group (O1P, O2P, O3P, O4P, O5P). The isoalloxazine ring system is labeled with atoms N1, N5, N10, C2, C4A, C5A, C6, C7, C8, C9, C10, and C4. The ribitol chain is labeled with atoms C1, C2, C3, C4, and C5. The phosphate group is labeled with atoms O1P, O2P, O3P, O4P, and O5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 31	C 17	N 4	O 9	P 1	0	0
3	B	1	Total 31	C 17	N 4	O 9	P 1	0	0

-

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	7	Total 7	O 7	0	0
5	B	10	Total 10	O 10	0	0

L483	K484	A485	R486	T487	Y488	G489	Y490	P491	N492	D493	Y494	L495	Y496	N497	E498	Y499	Y500	E501	T504	L505	T506	E507	F508	E509	D510	ALA																																		
L422	C423	L424	G425	A426	K427	G428	G429	G430	L431	G432	R433	L436	Y437	A438	N439	S440	C441	Y442	G443	R444	N445	G446	Y447	E448	K449	A450	I451	E452	I453	L454	R455	L456	E457	I458	E459	M460	S461	M462	R463	L464	L465	G466	V467	T468	S469	I470	A471	E472	L473	K474	P475	D476	L477	L478	D479	L480	S481	T482		
E362	I363	G364	V365	S366	G367	V368	V369	L370	S371	N372	Q373	G374	G375	Q376	Q377	L378	D379	F380	S381	R382	A383	P384	I385	E386	V387	L388	A389	E390	T391	M392	P393	I394	L395	E396	Q397	R398	N399	L400	K401	D402	K403	L404	E405	V406	F407	V408	D409	G410	G411	V412	R413	R414	G415	T416	D417	V418	L419	K420	A421	
ALA	GLY	PRO	LYS	ALA	MET	LYS	LYS	THR	ASN	VAL	GLU	GLU	SER	GLN	G317	A318	S319	R320	A321	L322	S323	K324	D263	D264	L265	V266	K267	N268	L330	T331	W332	K333	D334	I335	E336	E337	L338	K339	K340	K341	T342	K343	L344	P345	I346	V347	I348	K349	G350	V351	Q352	R353	T354	E355	D356	V357	I358	K359	A360	A361
A241	A242	P243	S244	D245	K246	Q247	I248	Q249	W250	Y251	Q252	L253	Y254	V255	N256	S257	D258	R259	K260	L261	T262	D263	D264	L265	V266	K267	N268	V269	E270	K271	L272	G273	V274	A275	A276	L277	F278	V279	T280	V281	D282	A283	P284	S285	L286	I287	R289	E290	K291	D292	M293	K294	L295	D296	F297	S298	N299	THR	LYS	
T181	D182	M183	L184	G185	S186	H187	V188	D189	Y190	P191	F192	Y193	V194	S195	A196	T197	A198	L199	C200	K201	L202	G203	N204	P205	L206	E207	G208	E209	K210	D211	V212	A213	R214	G215	C216	G217	Q218	G219	V220	T221	K222	V223	P224	Q225	K226	I227	S228	T229	L230	K231	S232	C233	S234	P235	E236	E237	I238	I239	E240	
N121	I122	I123	N124	L125	Y126	D127	F128	E129	Y130	L131	A132	S133	Q134	T135	L136	T137	K138	Q139	A140	W141	A142	Y143	Y144	S145	S146	G147	A148	N149	D150	F151	V152	T153	H154	R155	E156	M157	H158	N159	A160	Y161	H162	R163	I164	F165	F166	K167	P168	K169	L170	L171	V172	D173	S174	R175	K176	V177	D178	I179	S180	
ILE	PHE	GLU	PRO	LEU	HIS	ALA	PRO	ASN	VAL	ILE	ASP	LYS	TYR	ILE	ALA	PRO	GLU	LYS	LYS	LEU	GLY	PRO	LEU	GLN	GLY	SER	MET	PRO	PRO	GLU	LEU	VAL	CYS	PRO	PRO	TYR	A98	P99	G100	T101	T102	K103	E104	D105	I106	A107	R108	K109	E110	Q111	L112	K113	S114	L115	L116	P117	P118	I119	D120	

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	163.69Å 163.69Å 112.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.80 50.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	87.6 (50.00-2.80) 87.5 (50.00-2.80)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.206 , 0.278 0.227 , 0.278	Depositor DCC
R_{free} test set	2123 reflections (3.33%)	wwPDB-VP
Wilson B-factor (Å ²)	62.3	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 64.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7042	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, HEM, PYR

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	2.46	200/3907 (5.1%)	3.24	535/5291 (10.1%)
1	B	2.32	130/3130 (4.2%)	3.18	424/4230 (10.0%)
All	All	2.40	330/7037 (4.7%)	3.21	959/9521 (10.1%)

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	A	2	57
1	B	4	64
All	All	6	121

The worst 5 of 330 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	421	ALA	CA-CB	-14.29	1.30	1.53
1	A	248	ILE	CA-CB	-13.07	1.35	1.54
1	A	223	VAL	C-O	12.90	1.33	1.24
1	A	89	PRO	C-N	-12.78	1.19	1.33
1	A	61	ILE	C-O	-11.71	1.11	1.23

The worst 5 of 959 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	382	ARG	O-C-N	-36.59	81.14	122.85
1	A	89	PRO	CA-C-N	28.72	153.30	119.98
1	A	89	PRO	C-N-CA	28.72	153.30	119.98
1	A	395	LEU	O-C-N	-28.28	92.14	122.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	317	GLY	CA-C-N	24.00	167.38	121.54

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	11	ILE	CA
1	A	298	SER	CA
1	B	102	THR	CB
1	B	149	ASN	CA
1	B	272	LEU	CA

5 of 121 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	10	LYS	Mainchain
1	A	11	ILE	Peptide
1	A	31	GLY	Peptide
1	A	47	GLN	Peptide
1	A	50	ILE	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	3833	0	3894	441	1
1	B	3081	0	3140	519	1
2	A	43	0	30	15	0
3	A	31	0	17	14	0
3	B	31	0	18	14	0
4	B	6	0	0	1	0
5	A	7	0	0	0	0
5	B	10	0	0	1	0
All	All	7042	0	7099	948	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 67.

The worst 5 of 948 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:175:ARG:CD	1:B:175:ARG:CG	1.77	1.63
1:A:413:ARG:CD	1:A:413:ARG:CG	1.78	1.61
1:A:343:LYS:CB	1:A:343:LYS:CG	1.79	1.60
1:A:286:LEU:CD1	1:A:286:LEU:CG	1.78	1.59
1:B:106:ILE:CD1	1:B:106:ILE:CG1	1.75	1.59

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:A:353:ARG:NH2	1:B:169:LYS:CG[6_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	488/511 (96%)	381 (78%)	67 (14%)	40 (8%)	0	1
1	B	392/511 (77%)	273 (70%)	78 (20%)	41 (10%)	0	1
All	All	880/1022 (86%)	654 (74%)	145 (16%)	81 (9%)	0	1

5 of 81 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	11	ILE
1	A	20	ASN
1	A	37	THR
1	A	48	ASP

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	424/440 (96%)	282 (66%)	142 (34%)	0	1
1	B	340/440 (77%)	220 (65%)	120 (35%)	0	0
All	All	764/880 (87%)	502 (66%)	262 (34%)	0	0

5 of 262 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	397	GLN
1	B	423	CYS
1	B	504	THR
1	A	346	ILE
1	A	340	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	372	ASN
1	B	497	ASN
1	A	497	ASN
1	B	268	ASN
1	A	439	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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$
4	PYR	B	571	-	5,5,5	3.49	3 (60%)	3,6,6	0.71	0
3	FMN	A	569	-	33,33,33	0.98	1 (3%)	48,50,50	2.17	15 (31%)
3	FMN	B	570	-	33,33,33	1.09	2 (6%)	48,50,50	2.24	15 (31%)
2	HEM	A	560	1	50,50,50	2.48	19 (38%)	67,82,82	2.50	23 (34%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PYR	B	571	-	-	4/4/4/4	-
3	FMN	A	569	-	1/1/4/4	3/18/18/18	0/3/3/3
3	FMN	B	570	-	-	5/18/18/18	0/3/3/3
2	HEM	A	560	1	-	9/14/54/54	-

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	560	HEM	C3D-C2D	7.30	1.52	1.36
2	A	560	HEM	FE-ND	7.27	2.17	1.94
4	B	571	PYR	CA-C	-5.51	1.36	1.54
4	B	571	PYR	O-C	4.78	1.34	1.22
2	A	560	HEM	FE-NA	4.34	2.09	1.95

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	570	FMN	C4'-C3'-C2'	6.53	124.44	113.57
2	A	560	HEM	CHC-C4B-NB	6.52	131.44	124.42
2	A	560	HEM	CAA-CBA-CGA	6.36	130.53	113.67
3	B	570	FMN	O5'-P-O1P	6.29	123.43	106.44
3	A	569	FMN	C4'-C3'-C2'	6.12	123.75	113.57

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	569	FMN	C2'

5 of 21 torsion outliers are listed below:

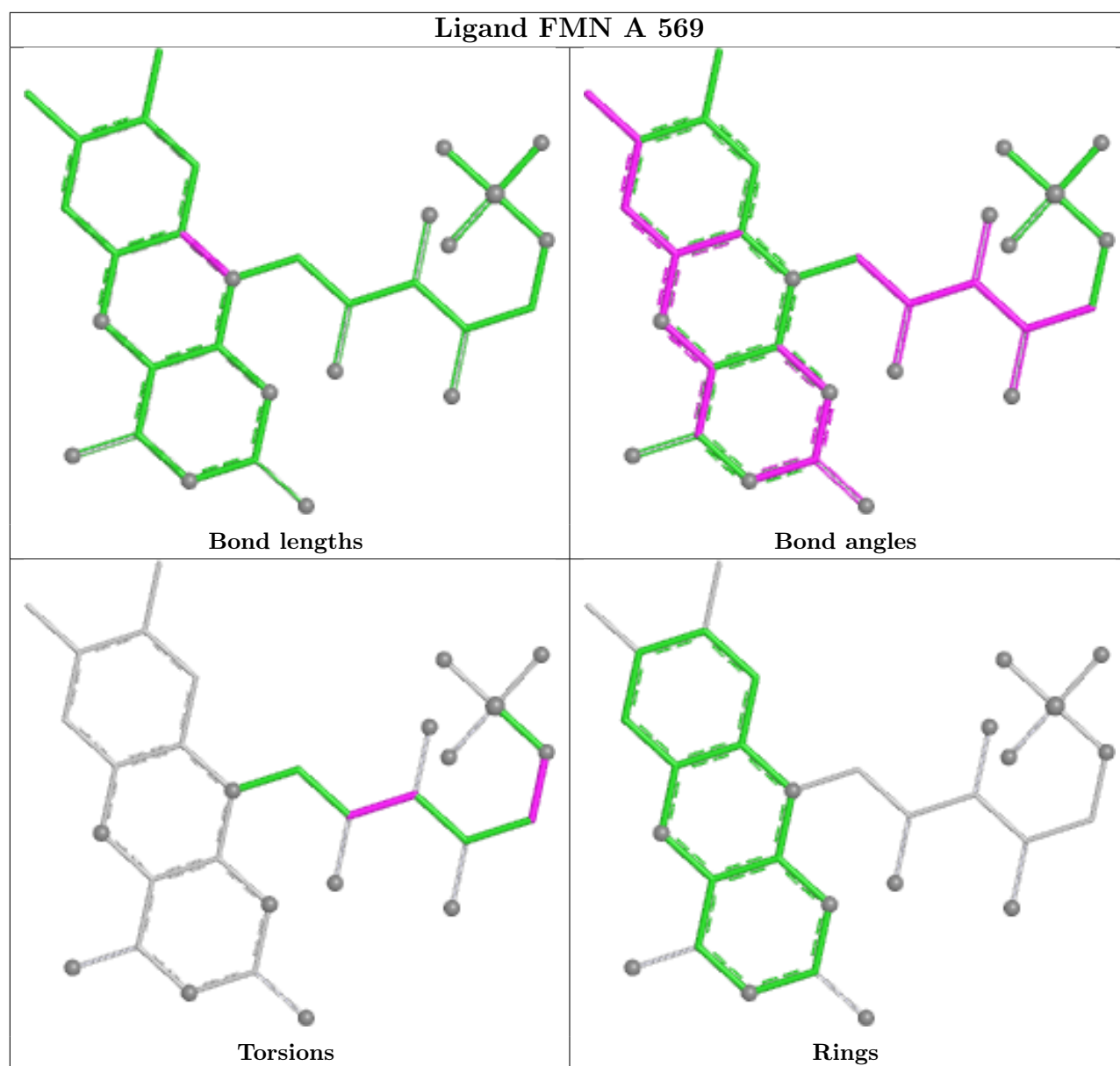
Mol	Chain	Res	Type	Atoms
2	A	560	HEM	C3D-CAD-CBD-CGD
4	B	571	PYR	O-C-CA-O3
4	B	571	PYR	OXT-C-CA-O3
3	A	569	FMN	O2'-C2'-C3'-C4'
3	A	569	FMN	O2'-C2'-C3'-O3'

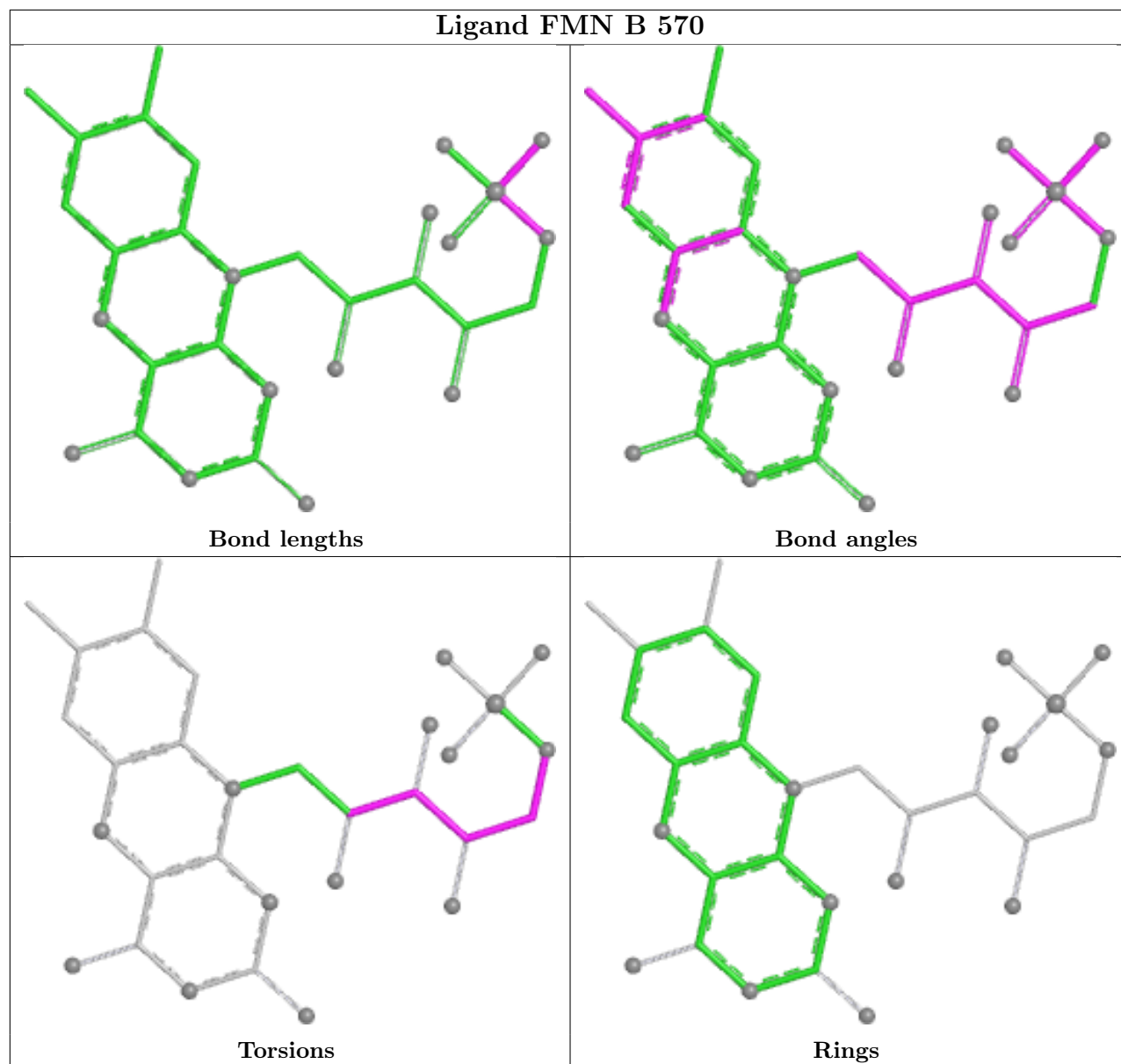
There are no ring outliers.

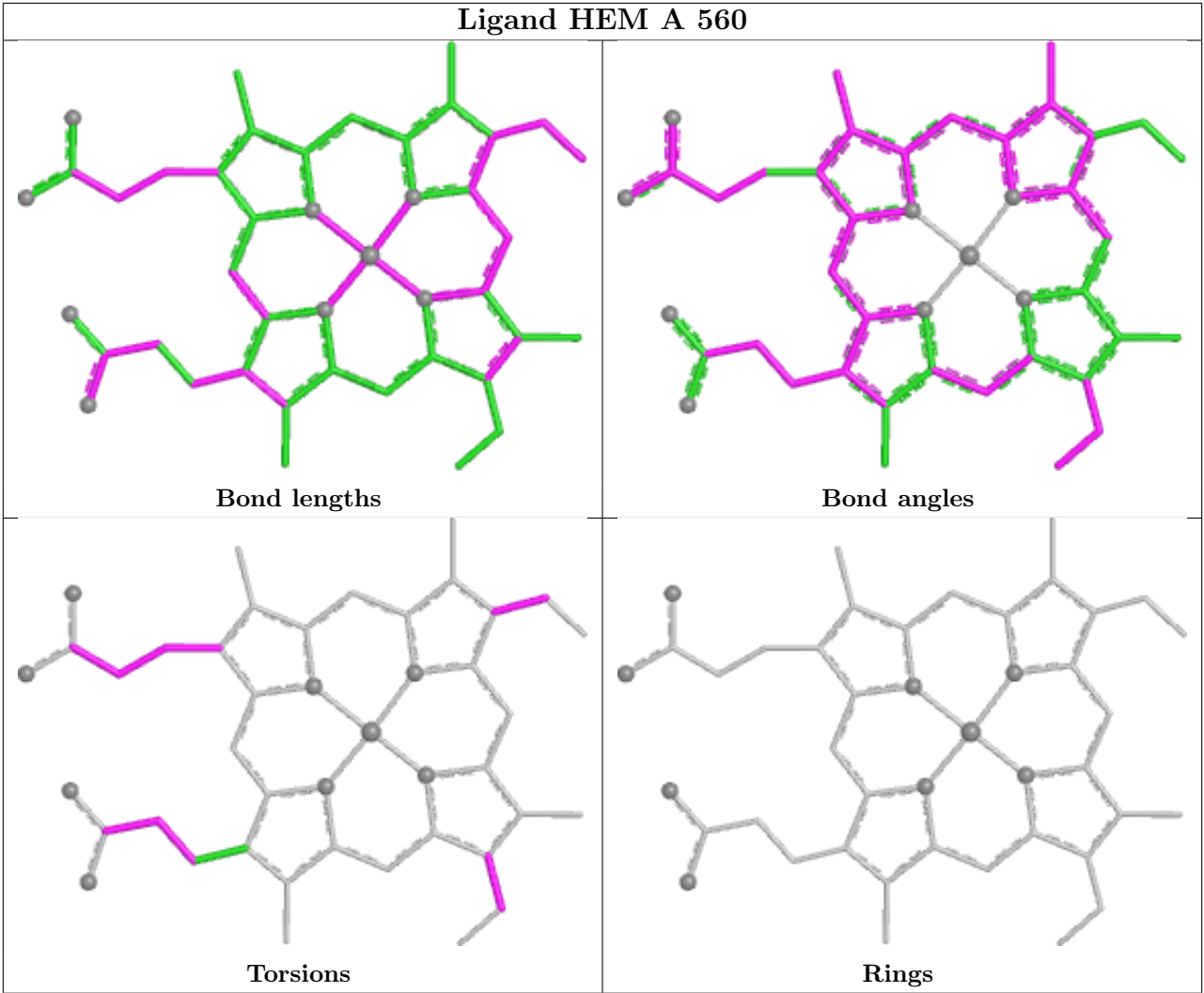
4 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	571	PYR	1	0
3	A	569	FMN	14	0
3	B	570	FMN	14	0
2	A	560	HEM	15	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	89:PRO	C	90:PRO	N	1.19

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	492/511 (96%)	0.15	35 (7%)	22 16	19, 52, 147, 183	0
1	B	396/511 (77%)	0.34	23 (5%)	29 22	18, 65, 107, 171	0
All	All	888/1022 (86%)	0.23	58 (6%)	25 18	18, 58, 138, 183	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	491	PRO	5.6
1	B	98	ALA	5.6
1	B	321	ALA	5.4
1	B	317	GLY	5.1
1	B	323	SER	5.1

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](#)

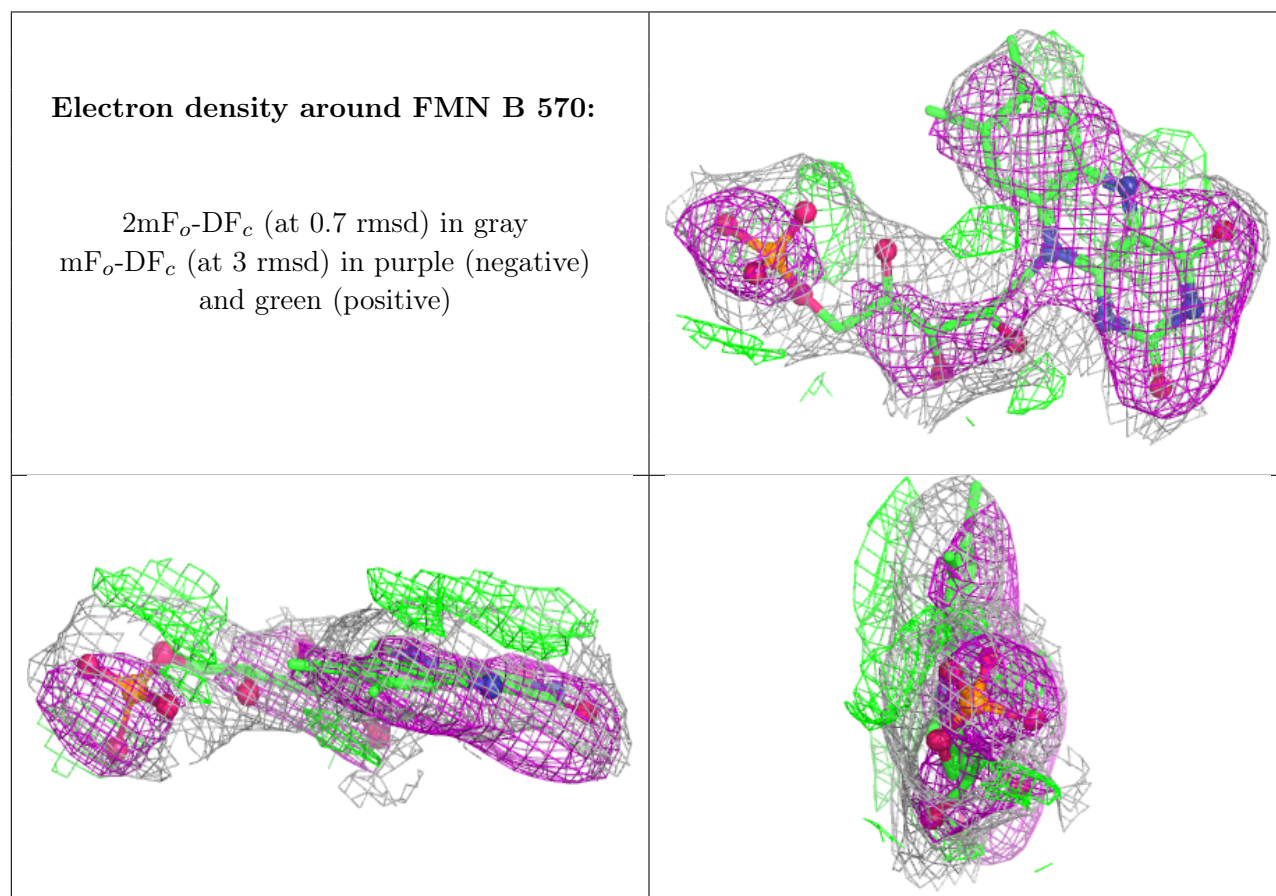
There are no oligosaccharides in this entry.

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.

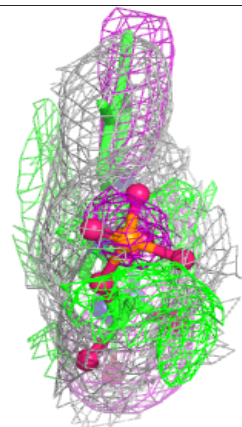
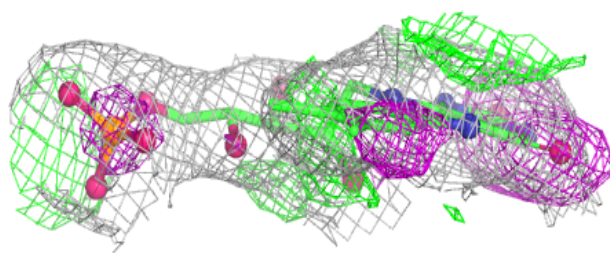
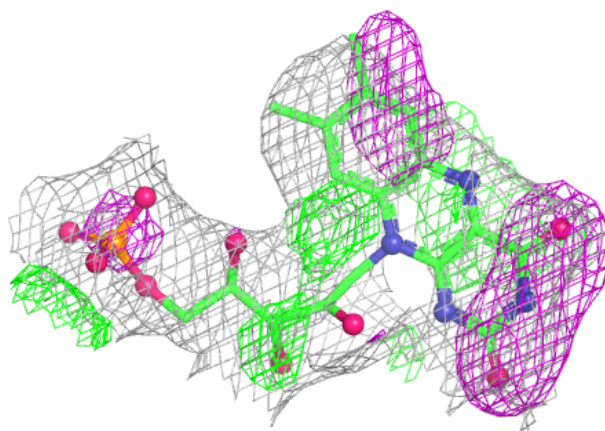
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	PYR	B	571	6/6	0.81	0.37	120,125,128,133	0
3	FMN	B	570	31/31	0.86	0.13	16,21,24,26	0
3	FMN	A	569	31/31	0.91	0.10	10,14,17,18	0
2	HEM	A	560	43/43	0.95	0.13	90,98,116,122	0

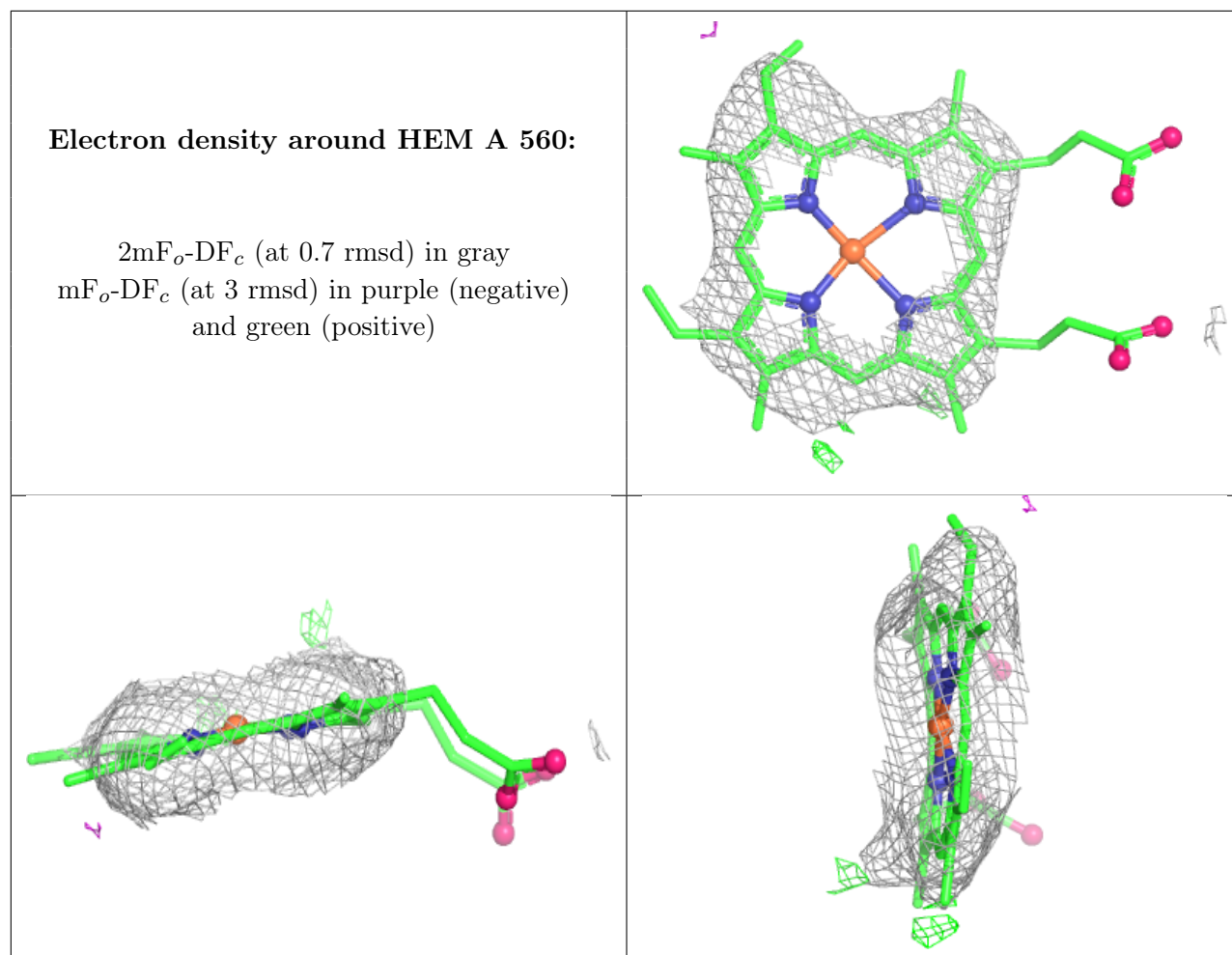
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



Electron density around FMN A 569:

$2mF_o-DF_c$ (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.