Full wwPDB X-ray Structure Validation Report (i)

Dec 4, 2023 – 12:15 PM JST

PDB ID	:	8HOR
Title	:	Crystal structure of the P450 BM3 heme domain mutant F87A in complex with Im-C6-Phe(4CH3)-Tyr
Authors	:	Jiang, Y.; Dong, S.; Feng, Y.; Cong, Z.
Deposited on	:	2022-12-10
Resolution	:	1.95 Å(reported)

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

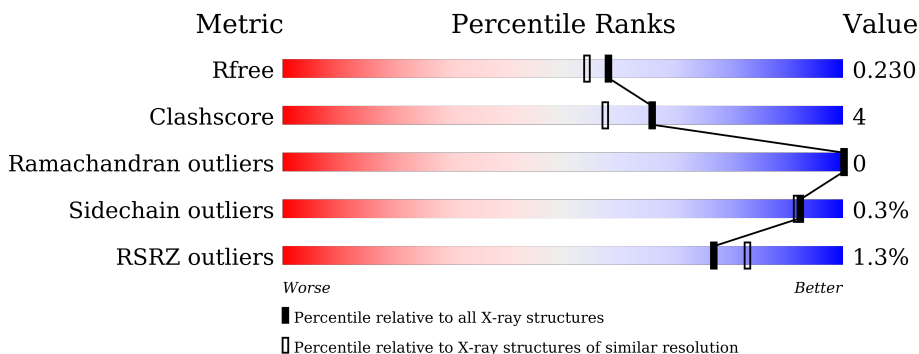|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.95 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	Percentile Ranks	Value
Rfree		0.230
Clashscore		4
Ramachandran outliers		0
Sidechain outliers		0.3%
RSRZ outliers		1.3%

Worse   *Better*

▌Percentile relative to all X-ray structures

◻Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	465	.% 88% 8% •
1	B	465	2% 88% 10% •
2	C	3	100%
2	D	3	33% 67%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8079 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 Bifunctional cytochrome P450/NADPH–P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total 3548	C 2270	N 603	O 658	S 17	0	1	0
1	B	453	Total 3596	C 2301	N 611	O 667	S 17	0	1	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP A0A1Q8UP87
A	87	ALA	PHE	engineered mutation	UNP A0A1Q8UP87
A	456	LEU	-	expression tag	UNP A0A1Q8UP87
A	457	GLU	-	expression tag	UNP A0A1Q8UP87
A	458	HIS	-	expression tag	UNP A0A1Q8UP87
A	459	HIS	-	expression tag	UNP A0A1Q8UP87
A	460	HIS	-	expression tag	UNP A0A1Q8UP87
A	461	HIS	-	expression tag	UNP A0A1Q8UP87
A	462	HIS	-	expression tag	UNP A0A1Q8UP87
A	463	HIS	-	expression tag	UNP A0A1Q8UP87
B	-1	GLY	-	expression tag	UNP A0A1Q8UP87
B	87	ALA	PHE	engineered mutation	UNP A0A1Q8UP87
B	456	LEU	-	expression tag	UNP A0A1Q8UP87
B	457	GLU	-	expression tag	UNP A0A1Q8UP87
B	458	HIS	-	expression tag	UNP A0A1Q8UP87
B	459	HIS	-	expression tag	UNP A0A1Q8UP87
B	460	HIS	-	expression tag	UNP A0A1Q8UP87
B	461	HIS	-	expression tag	UNP A0A1Q8UP87
B	462	HIS	-	expression tag	UNP A0A1Q8UP87
B	463	HIS	-	expression tag	UNP A0A1Q8UP87

- Molecule 2 is a protein called Im-C6-Phe(4CH3)-Tyr.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total 37	C 28	N 4	O 5	0	0	0
2	D	3	Total 37	C 28	N 4	O 5	0	0	0

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).

HEM

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	391	Total 391	O 391	0	0
4	B	379	Total 379	O 379	0	0
4	C	1	Total 1	O 1	0	0
4	D	4	Total 4	O 4	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: Bifunctional cytochrome P450/NADPH–P450 reductase

Chain A:

• Molecule 1: Bifunctional cytochrome P450/NADPH–P450 reductase

Chain B:

• Molecule 2: Im-C6-Phe(4CH3)-Tyr

Chain C:

There are no outlier residues recorded for this chain.

• Molecule 2: Im-C6-Phe(4CH3)-Tyr

Chain D:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	58.69Å 147.65Å 64.72Å 90.00° 100.01° 90.00°	Depositor
Resolution (Å)	73.82 – 1.95 73.82 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.2 (73.82-1.95) 97.2 (73.82-1.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.05 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.18.2	Depositor
R, R_{free}	0.212 , 0.230 0.212 , 0.230	Depositor DCC
R_{free} test set	2436 reflections (3.18%)	wwPDB-VP
Wilson B-factor (Å^2)	25.0	Xtriage
Anisotropy	0.493	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 46.9	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	8079	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.04% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: I7X, HEM, 4PH

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	0.32	0/3632	0.44	0/4919
1	B	0.35	0/3683	0.45	0/4989
2	C	0.80	0/13	1.45	0/15
2	D	1.65	0/13	1.58	0/15
All	All	0.34	0/7341	0.45	0/9938

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3548	0	3463	25	0
1	B	3596	0	3531	32	0
2	C	37	0	20	0	0
2	D	37	0	20	1	0
3	A	43	0	30	1	0
3	B	43	0	30	1	0
4	A	391	0	0	6	0
4	B	379	0	0	5	0
4	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	4	0	0	2	0
All	All	8079	0	7094	57	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 4.

All (57) 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:288:GLN:NE2	4:B:601:HOH:O	2.21	0.73
1:B:202:LYS:HE2	4:B:606:HOH:O	1.89	0.70
1:B:388:HIS:HA	1:B:391:LYS:HD3	1.77	0.67
1:A:76:LYS:NZ	4:A:606:HOH:O	2.29	0.65
1:A:98:LYS:HD2	4:A:605:HOH:O	1.98	0.63
1:B:370:ASP:O	1:B:378:ARG:NH2	2.30	0.63
1:A:148:LEU:HD21	1:A:413:VAL:HG21	1.83	0.60
1:A:104:LEU:HD21	1:B:383:SER:HB3	1.84	0.59
1:A:158:PHE:HD2	1:A:219:ILE:HG21	1.66	0.59
1:B:202:LYS:NZ	4:B:619:HOH:O	2.37	0.57
1:B:158:PHE:HD2	1:B:219:ILE:HG21	1.71	0.54
1:A:367:TRP:HB2	1:A:371:VAL:HG12	1.91	0.53
1:A:388:HIS:HA	1:A:391:LYS:HD3	1.91	0.52
1:B:153:ILE:HD11	1:B:261:PHE:HB3	1.91	0.51
1:B:434:LYS:HB2	1:B:442:GLU:HB2	1.93	0.51
1:B:264:ALA:HB1	4:D:101:HOH:O	2.10	0.50
1:A:81:PHE:HB3	1:A:209:ILE:HG12	1.94	0.49
1:A:58:ILE:HD12	1:A:360:LEU:HD13	1.94	0.49
1:A:124:VAL:HG13	1:A:455:LEU:HD13	1.94	0.49
1:B:148:LEU:HD21	1:B:413:VAL:HG21	1.93	0.48
1:B:153:ILE:HG23	1:B:262:LEU:HD23	1.96	0.48
1:A:393:PHE:HB3	1:A:400:CYS:HB3	1.95	0.48
1:A:375:ARG:HD2	4:A:634:HOH:O	2.13	0.47
1:B:298:LEU:HD22	1:B:303:PRO:HB3	1.97	0.47
1:B:124:VAL:HG13	1:B:455:LEU:HD13	1.96	0.47
1:B:149:THR:O	1:B:153:ILE:HG22	2.15	0.47
1:A:173:PHE:CE1	1:A:262:LEU:HD13	2.50	0.47
1:A:422:ASP:OD2	4:A:601:HOH:O	2.20	0.47
1:B:267:GLU:HA	1:B:270:SER:OG	2.16	0.46
1:B:43:GLU:HG2	1:B:48:VAL:HG22	1.96	0.46
1:A:126:LEU:HD22	1:A:148:LEU:HD13	1.98	0.46
1:A:179:ARG:NH2	1:A:208:ASP:OD1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:MET:SD	1:B:436:THR:HA	2.56	0.46
1:B:434:LYS:NZ	4:B:625:HOH:O	2.41	0.46
1:B:387:GLN:HG2	1:B:388:HIS:CD2	2.51	0.46
1:A:266:HIS:CG	1:A:267:GLU:N	2.84	0.45
1:B:366:ILE:HG21	1:B:389:ALA:HB1	1.98	0.45
1:A:400:CYS:HB2	3:A:501:HEM:NA	2.32	0.45
2:D:1:I7X:N34	4:D:101:HOH:O	2.36	0.45
1:B:253:ASN:O	1:B:257:GLN:HG2	2.18	0.44
1:B:81:PHE:HB3	1:B:209:ILE:HG12	2.00	0.44
1:A:243:PRO:HG2	4:A:925:HOH:O	2.18	0.44
1:B:120:VAL:HG11	1:B:302:VAL:HG13	2.00	0.44
1:A:370:ASP:O	1:A:378:ARG:NH2	2.44	0.43
1:B:266:HIS:CG	1:B:267:GLU:N	2.85	0.43
1:A:434:LYS:HB2	1:A:442:GLU:HB2	2.00	0.43
1:A:189:GLN:NE2	4:A:631:HOH:O	2.50	0.42
1:B:173:PHE:CE1	1:B:262:LEU:HD13	2.55	0.42
1:A:368:GLY:O	1:A:371:VAL:HG13	2.20	0.42
1:B:400:CYS:HB2	3:B:501:HEM:NA	2.34	0.41
1:A:68:ASP:HB3	1:A:334:TYR:CE1	2.55	0.41
1:B:15:LYS:HD2	1:B:43:GLU:HB3	2.01	0.41
1:B:367:TRP:HB2	1:B:371:VAL:HG12	2.03	0.41
1:B:393:PHE:HB3	1:B:400:CYS:HB3	2.02	0.41
1:A:253:ASN:O	1:A:257:GLN:HG2	2.21	0.41
1:B:375:ARG:NH2	4:B:629:HOH:O	2.43	0.41
1:B:407:LEU:HD23	1:B:407:LEU:HA	1.93	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	446/465 (96%)	435 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	452/465 (97%)	439 (97%)	13 (3%)	0	100	100
All	All	898/930 (97%)	874 (97%)	24 (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	A	374/407 (92%)	373 (100%)	1 (0%)	92	92
1	B	382/407 (94%)	381 (100%)	1 (0%)	92	92
2	C	1/1 (100%)	1 (100%)	0	100	100
2	D	1/1 (100%)	1 (100%)	0	100	100
All	All	758/816 (93%)	756 (100%)	2 (0%)	92	92

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	148	LEU
1	B	148	LEU

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 ⓘ

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
2	4PH	D	2	2	11,12,13	1.41	2 (18%)	12,15,17	0.94	1 (8%)
2	4PH	C	2	2	11,12,13	0.38	0	12,15,17	0.57	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4PH	D	2	2	-	0/5/6/8	0/1/1/1
2	4PH	C	2	2	-	0/5/6/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	4PH	CA-N	-2.76	1.39	1.48
2	D	2	4PH	O-C	-2.03	1.11	1.19

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	2	4PH	CG-CB-CA	2.56	119.29	114.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 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	#$|Z| > 2$
3	HEM	A	501	-	41,50,50	1.46	5 (12%)	45,82,82	1.50	6 (13%)
3	HEM	B	501	1	41,50,50	1.46	4 (9%)	45,82,82	1.47	8 (17%)

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	HEM	A	501	-	-	2/12/54/54	-
3	HEM	B	501	1	-	2/12/54/54	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	HEM	C3C-CAC	3.84	1.55	1.47
3	A	501	HEM	C3C-CAC	3.79	1.55	1.47
3	A	501	HEM	C3C-C2C	-3.70	1.35	1.40
3	B	501	HEM	C3C-C2C	-3.68	1.35	1.40
3	A	501	HEM	CAB-C3B	3.00	1.55	1.47
3	B	501	HEM	CAB-C3B	2.96	1.55	1.47
3	A	501	HEM	CMB-C2B	2.13	1.55	1.50
3	B	501	HEM	CMB-C2B	2.10	1.55	1.50
3	A	501	HEM	FE-NB	2.03	2.06	1.96

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	HEM	C4D-ND-C1D	3.33	108.51	105.07
3	B	501	HEM	C4D-ND-C1D	3.13	108.31	105.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	501	HEM	CBA-CAA-C2A	-3.12	107.30	112.62
3	A	501	HEM	C4C-CHD-C1D	3.03	126.55	122.56
3	A	501	HEM	C1B-NB-C4B	2.90	108.07	105.07
3	B	501	HEM	C1B-NB-C4B	2.89	108.06	105.07
3	B	501	HEM	CBA-CAA-C2A	-2.80	107.85	112.62
3	B	501	HEM	C4C-CHD-C1D	2.78	126.22	122.56
3	B	501	HEM	C4B-CHC-C1C	2.61	126.00	122.56
3	A	501	HEM	C4B-CHC-C1C	2.41	125.73	122.56
3	A	501	HEM	C3D-C4D-ND	-2.30	107.60	110.17
3	B	501	HEM	C3D-C4D-ND	-2.17	107.75	110.17
3	B	501	HEM	CMC-C2C-C3C	2.15	128.70	124.68
3	B	501	HEM	C3B-C2B-C1B	2.00	107.97	106.49

There are no chirality outliers.
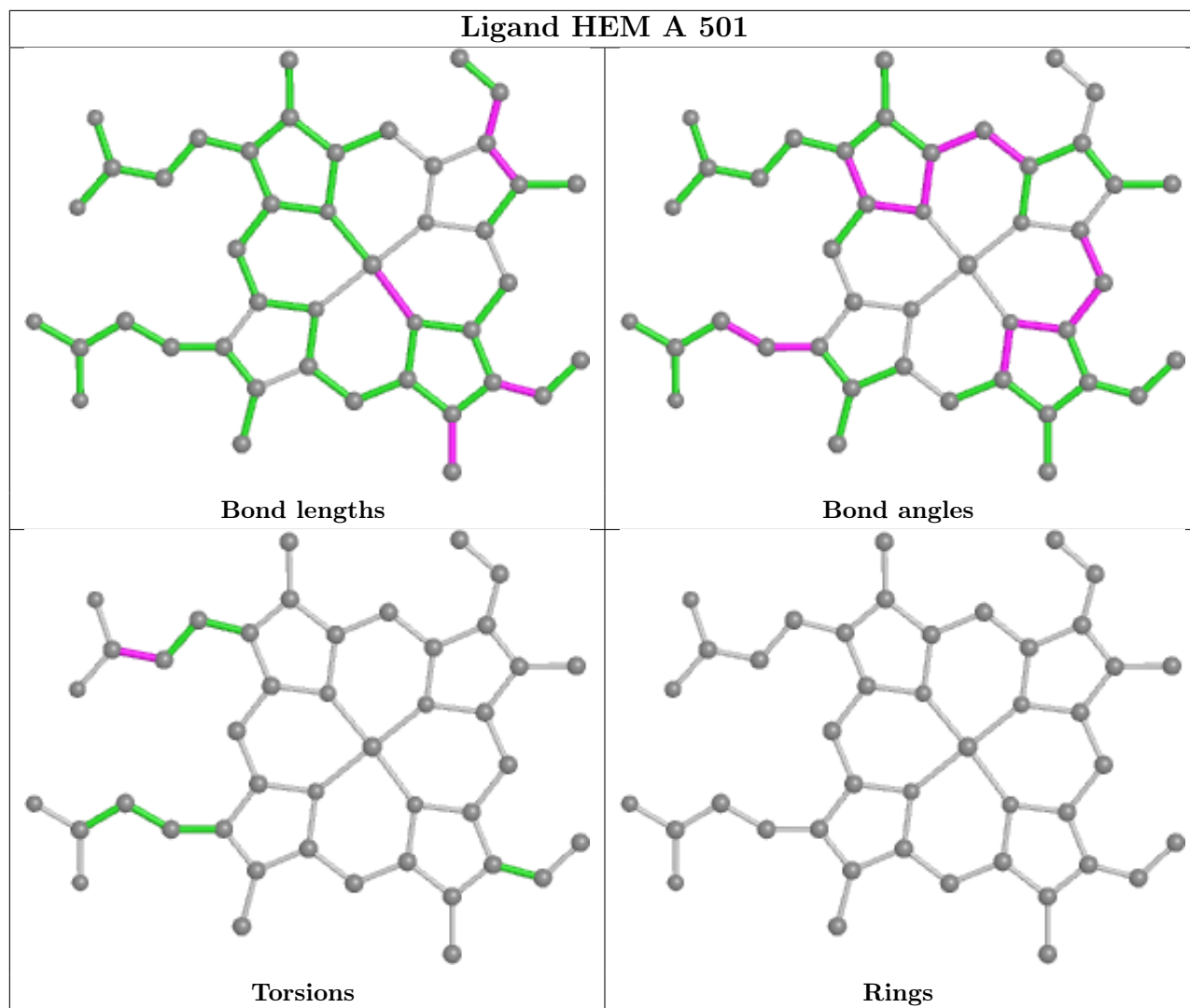
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501	HEM	CAD-CBD-CGD-O1D
3	A	501	HEM	CAD-CBD-CGD-O1D
3	B	501	HEM	CAD-CBD-CGD-O2D
3	A	501	HEM	CAD-CBD-CGD-O2D

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	HEM	1	0
3	B	501	HEM	1	0

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

Ligand HEM A 501

Bond lengths

Bond angles

Torsions

Rings

Ligand HEM B 501

Bond lengths

Bond angles

Torsions

Rings
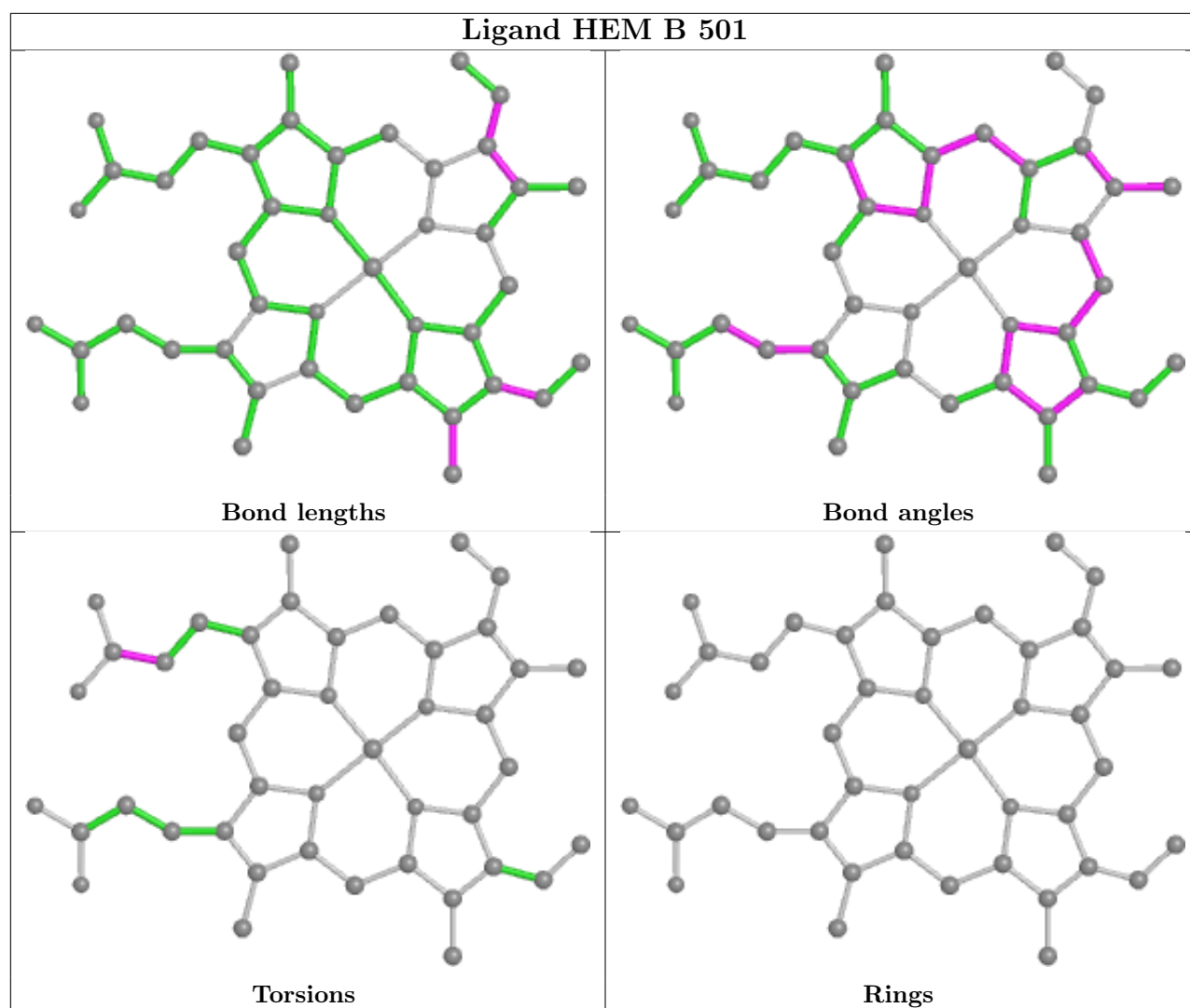
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	449/465 (96%)	0.13	4 (0%)	84	89	17, 26, 44, 62	0
1	B	453/465 (97%)	0.17	8 (1%)	68	76	18, 27, 46, 59	0
2	C	1/3 (33%)	0.00	0	100	100	23, 23, 23, 23	0
2	D	1/3 (33%)	-0.23	0	100	100	24, 24, 24, 24	0
All	All	904/936 (96%)	0.15	12 (1%)	77	83	17, 27, 45, 62	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	384	ALA	4.5
1	B	383	SER	2.8
1	B	191	ALA	2.7
1	A	201	ASN	2.4
1	B	369	ASP	2.3
1	B	302	VAL	2.2
1	A	205	PHE	2.1
1	B	193	PRO	2.1
1	A	178	VAL	2.1
1	A	226	SER	2.0
1	B	196	PRO	2.0
1	B	153	ILE	2.0

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

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.

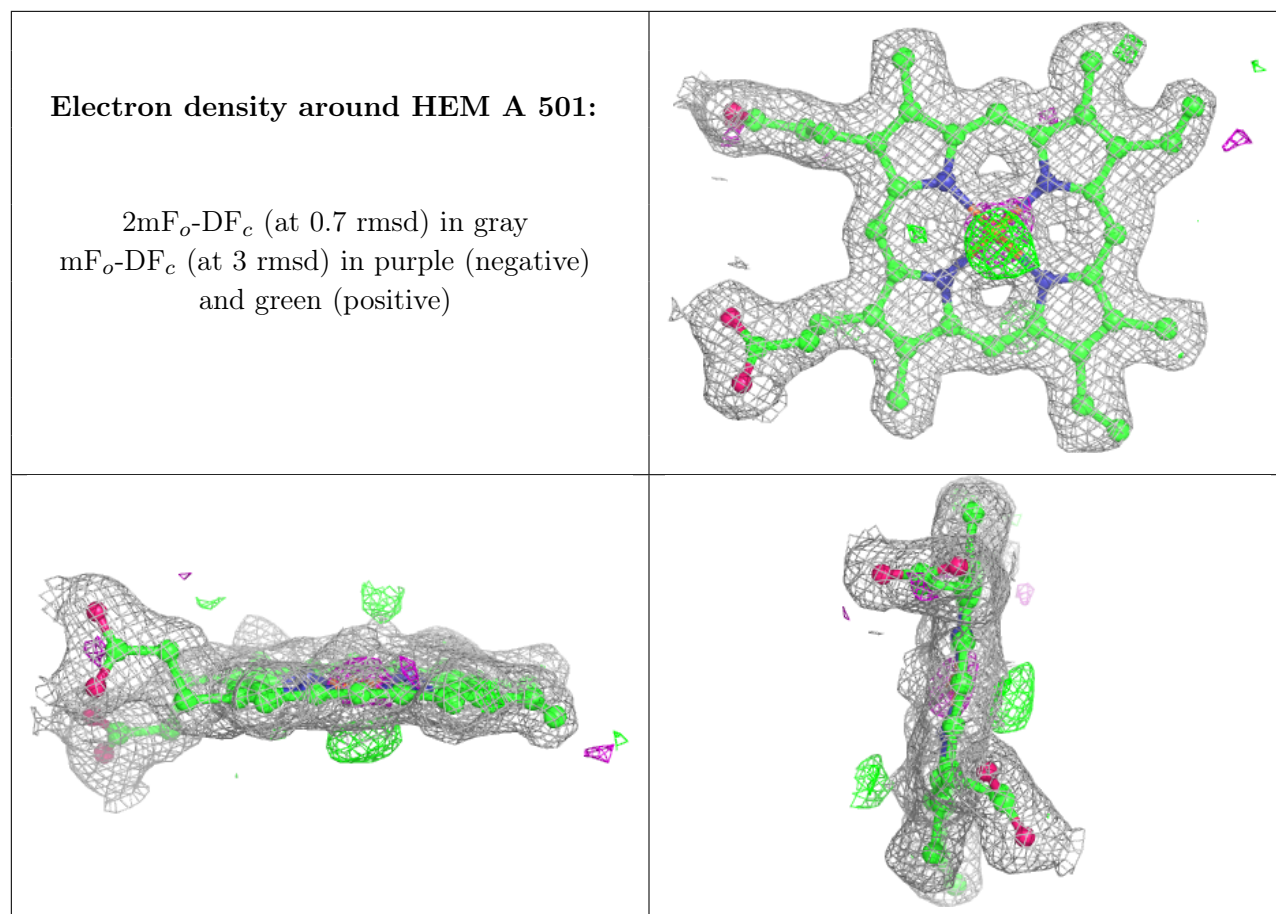| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	4PH	C	2	12/13	0.92	0.12	19,20,26,27	0
2	4PH	D	2	12/13	0.95	0.10	19,23,26,27	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

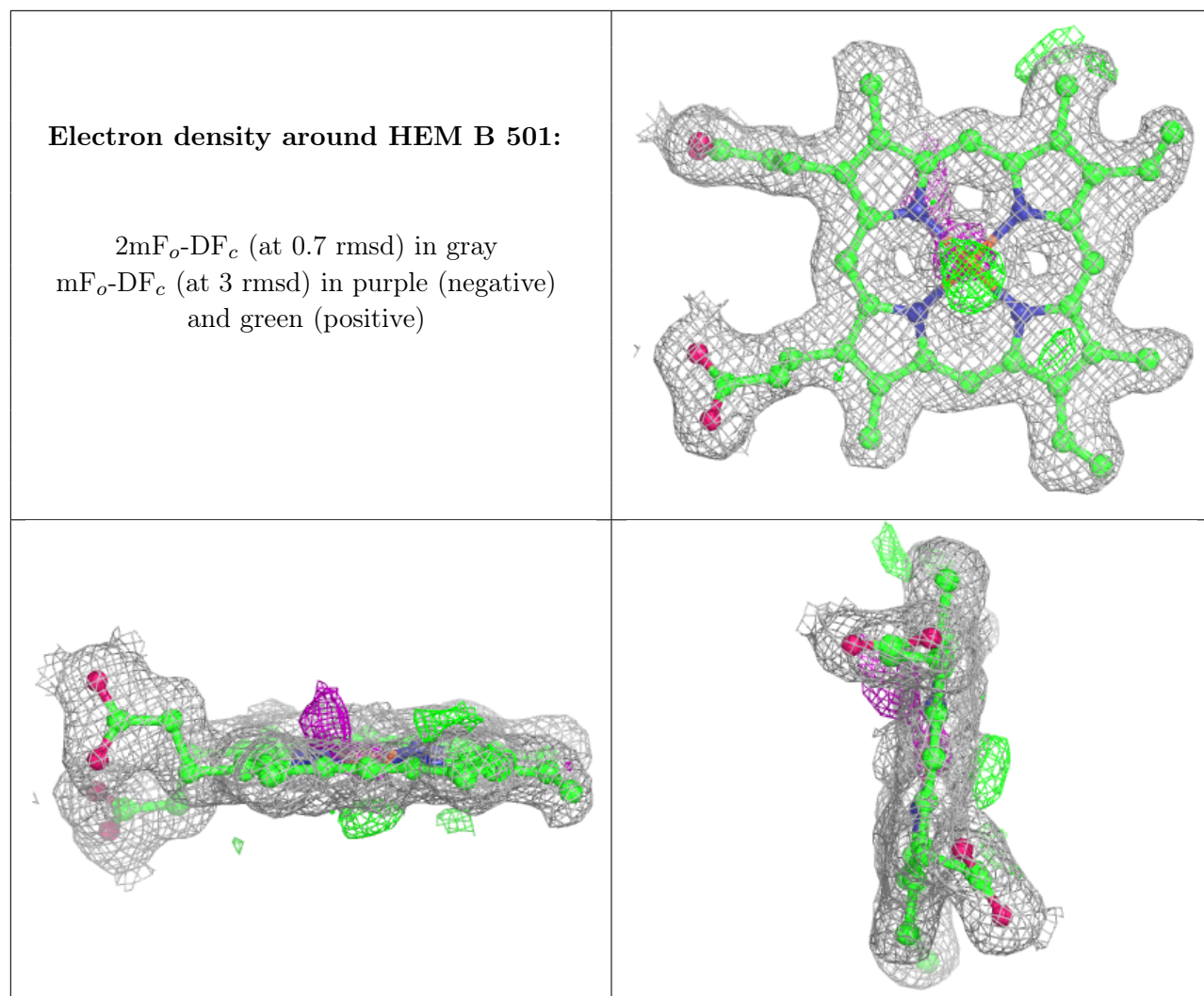## 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
3	HEM	A	501	43/43	0.95	0.12	15,19,22,28	0
3	HEM	B	501	43/43	0.96	0.12	13,19,22,28	0

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

Electron density around HEM A 501:

$2mF_o$-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 501:

$2mF_o$-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.