



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2021 – 11:13 PM EDT

PDB ID : 1P0W
Title : F393W mutant heme domain of flavocytochrome P450 BM3
Authors : Ost, T.W.B.; Clark, J.; Miles, C.S.; Walkinshaw, M.D.; Reid, G.A.; Chapman, S.K.; Daff, S.; Mowat, C.G.
Deposited on : 2003-04-11
Resolution : 2.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

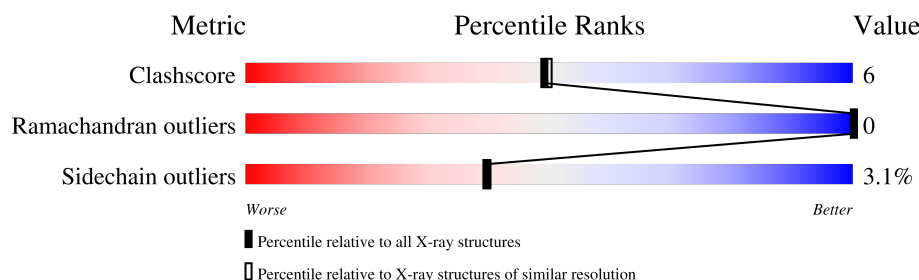
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	455	 83% 12% . .
1	B	455	 83% 13% . . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8593 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 P-450:NADPH-P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	0	0	0
			3508	2252	593	646	17			
1	B	448	Total	C	N	O	S	0	0	0
			3579	2294	604	664	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	393	TRP	PHE	engineered mutation	UNP P14779
B	393	TRP	PHE	engineered mutation	UNP P14779

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: 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		

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

- Molecule 3 is water.

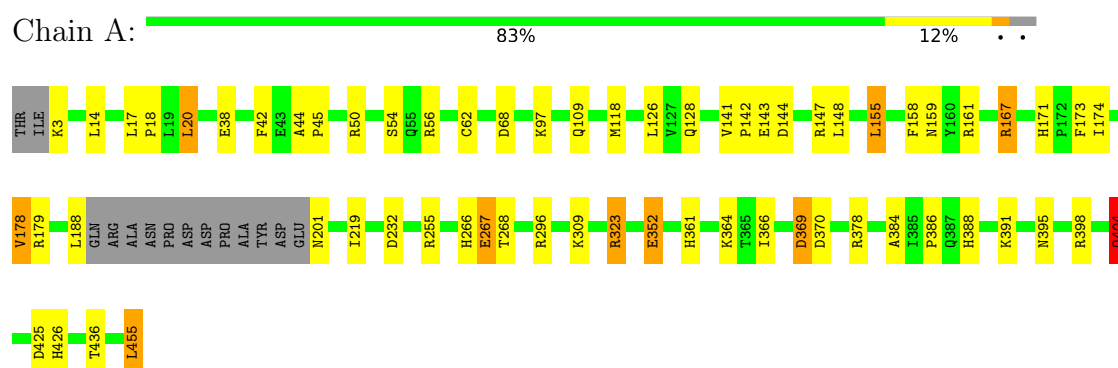
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	671	Total	O	0	0
			671	671		
3	B	749	Total	O	0	0
			749	749		

3 Residue-property plots

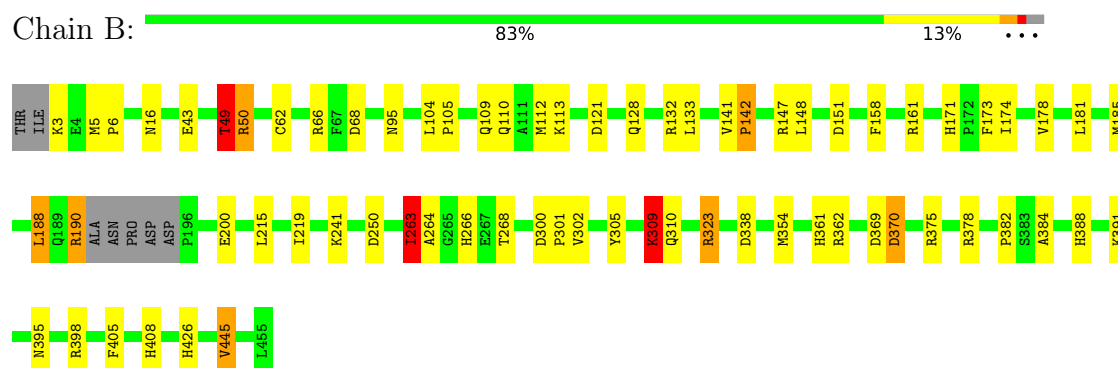
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

- Molecule 1: Bifunctional P-450:NADPH-P450 reductase



- Molecule 1: Bifunctional P-450:NADPH-P450 reductase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.91Å 153.54Å 61.43Å 90.00° 94.42° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.159 , 0.221	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8593	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.61	0/3590	1.31	30/4862 (0.6%)
1	B	0.63	0/3663	1.37	29/4957 (0.6%)
All	All	0.62	0/7253	1.34	59/9819 (0.6%)

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

There are no bond length outliers.

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	50	ARG	NE-CZ-NH2	-20.07	110.27	120.30
1	B	50	ARG	NE-CZ-NH1	15.40	128.00	120.30
1	A	50	ARG	NE-CZ-NH1	-13.37	113.61	120.30
1	A	50	ARG	NE-CZ-NH2	12.55	126.58	120.30
1	B	369	ASP	CB-CG-OD2	11.17	128.35	118.30
1	B	66	ARG	NE-CZ-NH1	10.93	125.77	120.30
1	A	68	ASP	CB-CG-OD1	10.56	127.80	118.30
1	B	147	ARG	NE-CZ-NH2	-9.76	115.42	120.30
1	A	167	ARG	NE-CZ-NH1	9.65	125.12	120.30
1	B	323	ARG	NE-CZ-NH1	9.64	125.12	120.30
1	B	147	ARG	NE-CZ-NH1	9.36	124.98	120.30
1	B	190	ARG	NE-CZ-NH2	-9.33	115.64	120.30
1	B	378	ARG	NE-CZ-NH2	-8.05	116.27	120.30
1	A	296	ARG	NE-CZ-NH2	-8.05	116.28	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	ARG	NE-CZ-NH1	7.80	124.20	120.30
1	A	161	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	A	323	ARG	NE-CZ-NH1	7.58	124.09	120.30
1	A	296	ARG	NE-CZ-NH1	7.35	123.97	120.30
1	A	352	GLU	OE1-CD-OE2	7.33	132.09	123.30
1	B	445	VAL	N-CA-CB	-7.21	95.64	111.50
1	B	398	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	A	167	ARG	CG-CD-NE	7.18	126.87	111.80
1	B	250	ASP	CB-CG-OD1	7.09	124.68	118.30
1	B	66	ARG	NE-CZ-NH2	-7.05	116.77	120.30
1	B	323	ARG	NE-CZ-NH2	-7.05	116.78	120.30
1	A	143	GLU	OE1-CD-OE2	-6.94	114.97	123.30
1	B	309	LYS	CD-CE-NZ	6.61	126.89	111.70
1	A	147	ARG	NE-CZ-NH2	-6.58	117.01	120.30
1	B	263	ILE	CA-CB-CG2	6.55	124.01	110.90
1	B	151	ASP	CB-CG-OD1	6.48	124.14	118.30
1	A	161	ARG	NE-CZ-NH1	6.45	123.52	120.30
1	B	378	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	B	151	ASP	CB-CG-OD2	-6.39	112.55	118.30
1	A	267	GLU	CA-CB-CG	6.31	127.28	113.40
1	A	50	ARG	CD-NE-CZ	6.28	132.39	123.60
1	A	179	ARG	NE-CZ-NH1	6.23	123.41	120.30
1	B	370	ASP	CB-CG-OD1	6.20	123.88	118.30
1	B	68	ASP	CB-CG-OD2	-6.12	112.80	118.30
1	B	49	THR	CA-CB-CG2	-6.10	103.86	112.40
1	A	398	ARG	NE-CZ-NH2	5.91	123.26	120.30
1	A	369	ASP	CB-CG-OD2	5.89	123.61	118.30
1	A	455	LEU	CA-CB-CG	5.80	128.64	115.30
1	B	445	VAL	CG1-CB-CG2	5.77	120.13	110.90
1	A	144	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	B	121	ASP	CB-CG-OD1	5.68	123.42	118.30
1	A	425	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	56	ARG	NE-CZ-NH1	5.57	123.08	120.30
1	A	323	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	B	132	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	A	167	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	A	255	ARG	NE-CZ-NH1	-5.49	117.56	120.30
1	A	370	ASP	CB-CG-OD2	5.41	123.17	118.30
1	B	338	ASP	CB-CG-OD1	-5.38	113.46	118.30
1	A	56	ARG	CD-NE-CZ	5.26	130.97	123.60
1	A	404	GLN	CB-CG-CD	5.25	125.25	111.60
1	A	179	ARG	CD-NE-CZ	5.24	130.93	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	378	ARG	NE-CZ-NH1	-5.23	117.69	120.30
1	B	161	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	B	362	ARG	NE-CZ-NH2	-5.04	117.78	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	436	THR	Mainchain

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	3508	0	3440	38	0
1	B	3579	0	3517	45	0
2	A	43	0	30	1	0
2	B	43	0	30	2	0
3	A	671	0	0	9	0
3	B	749	0	0	10	0
All	All	8593	0	7017	84	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 6.

All (84) 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:16:ASN:HD22	1:B:43:GLU:H	1.22	0.87
1:B:361:HIS:HE1	1:B:391:LYS:H	1.25	0.82
1:A:361:HIS:HE1	1:A:391:LYS:H	1.27	0.80
1:B:49:THR:HG21	1:B:354:MET:HG2	1.64	0.79
1:B:171:HIS:HD2	1:B:173:PHE:H	1.32	0.74
1:A:384:ALA:HB3	3:A:916:HOH:O	1.88	0.73
1:A:171:HIS:HD2	1:A:173:PHE:H	1.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:GLN:HG3	3:A:879:HOH:O	1.94	0.68
1:A:391:LYS:HZ1	1:A:395:ASN:HD22	1.46	0.64
1:A:391:LYS:NZ	1:A:395:ASN:HD22	1.95	0.63
1:B:109:GLN:HE22	1:B:309:LYS:HZ3	1.47	0.62
1:A:364:LYS:HD3	1:A:369:ASP:HA	1.82	0.62
1:B:49:THR:HG22	1:B:50:ARG:H	1.65	0.60
1:B:370:ASP:OD2	1:B:375:ARG:NH1	2.31	0.60
1:B:109:GLN:HE22	1:B:309:LYS:NZ	2.00	0.60
1:A:158:PHE:CE2	1:A:219:ILE:HD13	2.38	0.59
1:B:171:HIS:CD2	1:B:173:PHE:H	2.17	0.58
1:A:109:GLN:HE22	1:A:309:LYS:HZ2	1.52	0.58
1:A:174:ILE:O	1:A:178:VAL:HG13	2.03	0.58
1:A:109:GLN:HE22	1:A:309:LYS:NZ	2.02	0.58
1:A:118:MET:HE1	3:A:1081:HOH:O	2.04	0.57
1:A:267:GLU:HG2	3:A:722:HOH:O	2.05	0.56
1:A:232:ASP:HB3	3:A:1042:HOH:O	2.06	0.56
1:B:3:LYS:HD2	3:B:1093:HOH:O	2.05	0.56
1:A:141:VAL:HB	1:A:142:PRO:HD3	1.87	0.55
2:B:460:HEM:HBC2	2:B:460:HEM:HMC2	1.88	0.55
1:A:62:CYS:HB3	1:A:395:ASN:ND2	2.22	0.55
1:A:266:HIS:CE1	1:A:267:GLU:HG3	2.42	0.55
1:B:174:ILE:O	1:B:178:VAL:HG13	2.07	0.54
1:A:267:GLU:HG2	3:A:1070:HOH:O	2.06	0.54
1:B:109:GLN:NE2	1:B:309:LYS:HZ3	2.04	0.54
1:A:17:LEU:HB3	1:A:18:PRO:HD3	1.90	0.53
1:A:158:PHE:HE2	1:A:219:ILE:HD13	1.75	0.51
1:A:171:HIS:CD2	1:A:173:PHE:H	2.24	0.51
1:A:201:ASN:N	3:A:592:HOH:O	2.42	0.51
1:A:44:ALA:HB1	1:A:45:PRO:HD2	1.93	0.50
1:A:38:GLU:HB2	1:A:54:SER:HB3	1.94	0.50
1:B:384:ALA:HB3	3:B:1111:HOH:O	2.12	0.49
1:A:109:GLN:NE2	1:A:309:LYS:HZ2	2.10	0.49
1:B:266:HIS:HE1	3:B:731:HOH:O	1.95	0.49
1:B:388:HIS:HD2	1:B:391:LYS:HZ3	1.61	0.49
1:A:388:HIS:HA	1:A:391:LYS:HD3	1.95	0.48
1:B:16:ASN:ND2	1:B:43:GLU:H	2.01	0.48
1:B:49:THR:HG22	1:B:50:ARG:N	2.27	0.48
1:B:300:ASP:HB3	1:B:301:PRO:HD2	1.95	0.48
1:A:97:LYS:HB2	3:A:1003:HOH:O	2.12	0.48
1:B:110:GLN:HE22	1:B:113:LYS:NZ	2.12	0.47
1:A:366:ILE:HD12	1:A:386:PRO:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:GLN:HG2	3:B:1172:HOH:O	2.14	0.47
1:B:141:VAL:HB	1:B:142:PRO:HD3	1.97	0.46
1:B:391:LYS:NZ	1:B:395:ASN:HD22	2.14	0.46
1:A:118:MET:HB3	1:A:155:LEU:HD13	1.96	0.46
1:A:3:LYS:HA	1:A:3:LYS:HD3	1.79	0.45
1:B:215:LEU:O	1:B:219:ILE:HG12	2.16	0.45
1:B:323:ARG:HA	1:B:361:HIS:CD2	2.52	0.45
1:B:104:LEU:HB2	1:B:105:PRO:HD3	2.00	0.44
1:A:118:MET:SD	1:A:155:LEU:HD13	2.58	0.44
1:A:126:LEU:C	1:A:126:LEU:HD13	2.38	0.44
1:B:185:MET:O	1:B:188:LEU:HB2	2.17	0.44
1:A:323:ARG:HA	1:A:361:HIS:CD2	2.53	0.44
1:B:268:THR:HB	2:B:460:HEM:C3B	2.53	0.43
1:B:310:GLN:HG3	3:B:866:HOH:O	2.19	0.43
1:B:5:MET:HA	1:B:6:PRO:HD3	1.85	0.43
1:B:171:HIS:HD2	1:B:173:PHE:N	2.10	0.43
1:B:95:ASN:HD22	1:B:95:ASN:HA	1.69	0.42
1:B:200:GLU:OE2	1:B:200:GLU:HA	2.20	0.42
1:B:62:CYS:SG	1:B:391:LYS:HE2	2.59	0.42
1:B:112:MET:SD	1:B:405:PHE:HA	2.60	0.42
1:A:361:HIS:CE1	1:A:391:LYS:H	2.18	0.42
1:B:190:ARG:HG3	3:B:1118:HOH:O	2.20	0.42
1:B:241:LYS:HD3	3:B:1021:HOH:O	2.20	0.41
1:A:268:THR:HB	2:A:460:HEM:C3B	2.55	0.41
1:B:388:HIS:HD2	1:B:391:LYS:NZ	2.18	0.41
1:A:20:LEU:HD22	1:A:42:PHE:CE2	2.56	0.41
1:B:178:VAL:HG22	3:B:710:HOH:O	2.20	0.41
1:B:309:LYS:NZ	1:B:408:HIS:ND1	2.68	0.41
1:B:263:ILE:HG13	1:B:264:ALA:N	2.36	0.41
1:B:300:ASP:HB3	1:B:301:PRO:CD	2.51	0.41
1:B:361:HIS:HE1	1:B:391:LYS:N	2.06	0.41
1:B:382:PRO:HG2	3:B:1038:HOH:O	2.20	0.41
1:B:426:HIS:HE1	3:B:636:HOH:O	2.02	0.41
1:A:171:HIS:HD2	1:A:173:PHE:N	2.15	0.41
1:B:305:TYR:CZ	1:B:309:LYS:HD3	2.57	0.40
1:A:426:HIS:HE1	3:A:585:HOH:O	2.04	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	437/455 (96%)	428 (98%)	9 (2%)	0	100	100
1	B	444/455 (98%)	432 (97%)	12 (3%)	0	100	100
All	All	881/910 (97%)	860 (98%)	21 (2%)	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	371/399 (93%)	359 (97%)	12 (3%)	39	38
1	B	382/399 (96%)	371 (97%)	11 (3%)	42	43
All	All	753/798 (94%)	730 (97%)	23 (3%)	40	40

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	20	LEU
1	A	128	GLN
1	A	148	LEU
1	A	155	LEU
1	A	159	ASN
1	A	167	ARG
1	A	178	VAL

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Mol	Chain	Res	Type
1	A	188	LEU
1	A	352	GLU
1	A	404	GLN
1	A	455	LEU
1	B	49	THR
1	B	133	LEU
1	B	142	PRO
1	B	148	LEU
1	B	158	PHE
1	B	181	LEU
1	B	188	LEU
1	B	263	ILE
1	B	302	VAL
1	B	309	LYS
1	B	445	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	95	ASN
1	A	109	GLN
1	A	110	GLN
1	A	128	GLN
1	A	159	ASN
1	A	171	HIS
1	A	266	HIS
1	A	361	HIS
1	A	395	ASN
1	A	426	HIS
1	B	7	GLN
1	B	16	ASN
1	B	21	ASN
1	B	95	ASN
1	B	109	GLN
1	B	110	GLN
1	B	128	GLN
1	B	171	HIS
1	B	201	ASN
1	B	266	HIS
1	B	285	HIS
1	B	361	HIS

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Mol	Chain	Res	Type
1	B	387	GLN
1	B	388	HIS
1	B	395	ASN
1	B	426	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
2	HEM	B	460	3,1	27,50,50	2.09	6 (22%)	17,82,82	1.63	4 (23%)
2	HEM	A	460	3,1	27,50,50	1.87	5 (18%)	17,82,82	1.69	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
2	HEM	B	460	3,1	-	0/6/54/54	-
2	HEM	A	460	3,1	-	0/6/54/54	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	460	HEM	C3B-C2B	-5.30	1.33	1.40
2	A	460	HEM	C3C-C2C	-5.06	1.33	1.40
2	B	460	HEM	C3C-C2C	-4.73	1.33	1.40
2	A	460	HEM	C3B-C2B	-4.20	1.34	1.40
2	B	460	HEM	CAA-C2A	3.58	1.57	1.52
2	A	460	HEM	CAA-C2A	2.81	1.56	1.52
2	B	460	HEM	C3B-CAB	2.63	1.53	1.47
2	B	460	HEM	C3C-CAC	2.56	1.53	1.47
2	A	460	HEM	C3C-CAC	2.40	1.52	1.47
2	A	460	HEM	CMA-C3A	2.30	1.56	1.51
2	B	460	HEM	CAD-C3D	2.20	1.56	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	460	HEM	CAA-CBA-CGA	3.41	118.39	112.67
2	B	460	HEM	CMA-C3A-C4A	-3.11	123.69	128.46
2	A	460	HEM	CMB-C2B-C3B	2.85	130.01	124.68
2	A	460	HEM	CMA-C3A-C4A	-2.81	124.14	128.46
2	B	460	HEM	CAD-CBD-CGD	2.57	116.99	112.67
2	B	460	HEM	CMD-C2D-C1D	-2.35	124.85	128.46
2	A	460	HEM	CMD-C2D-C1D	-2.23	125.03	128.46
2	B	460	HEM	CBD-CAD-C3D	-2.02	108.75	112.48

There are no chirality outliers.

There are no torsion outliers.

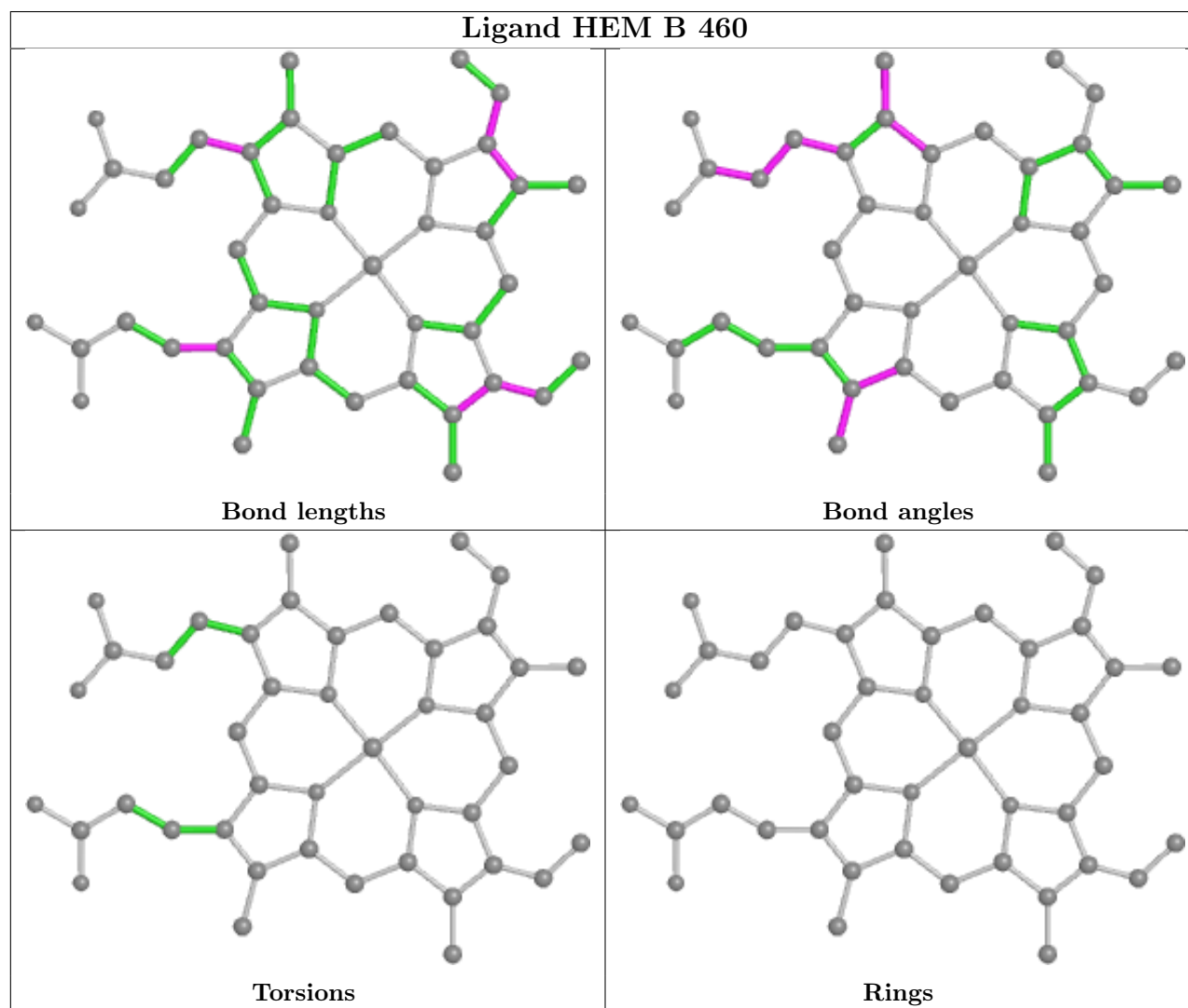
There are no ring outliers.

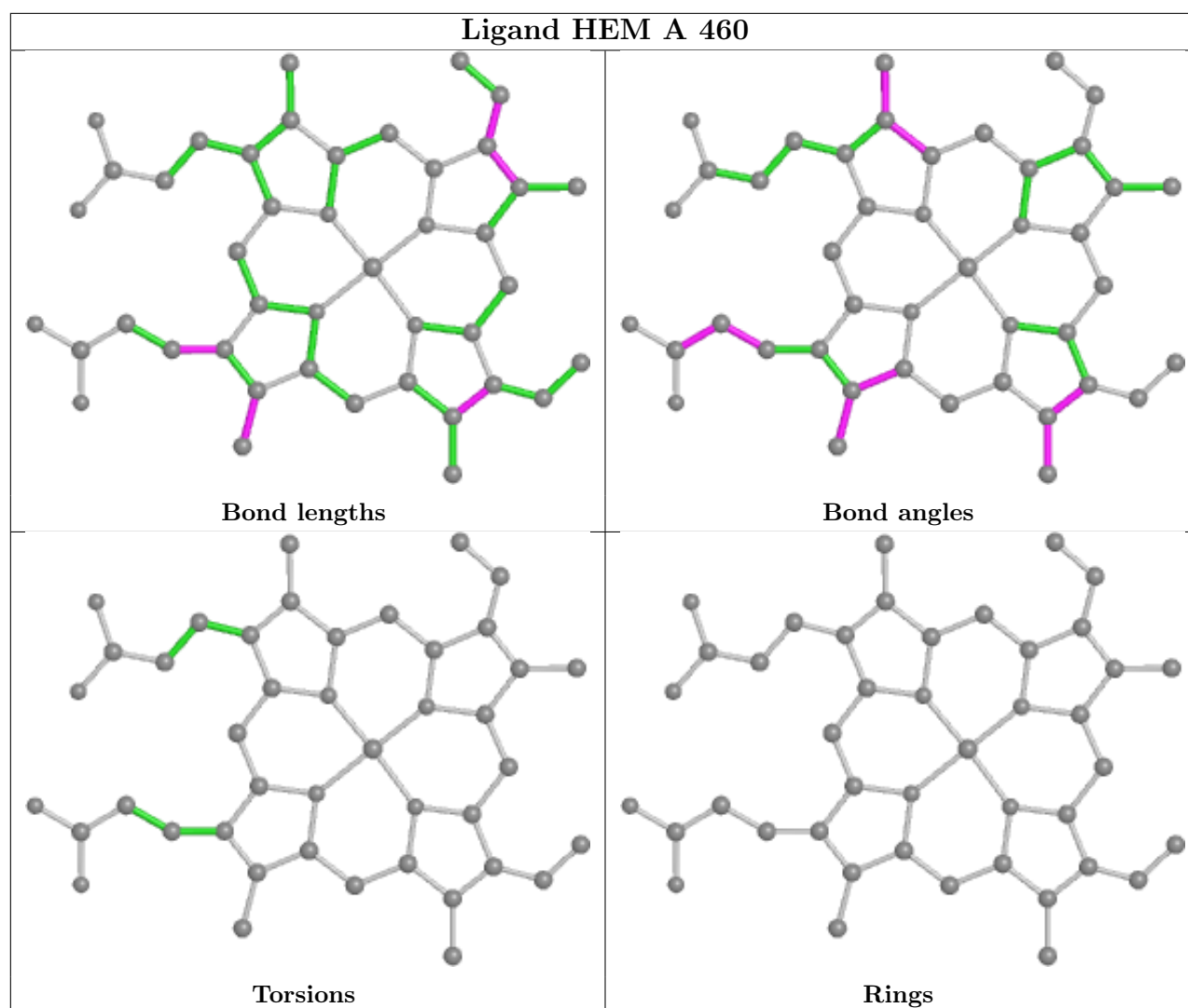
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	460	HEM	2	0
2	A	460	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.