



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 03:07 AM UTC

PDB ID : 1P0V / pdb_00001p0v
Title : F393A 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 : 2.05 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

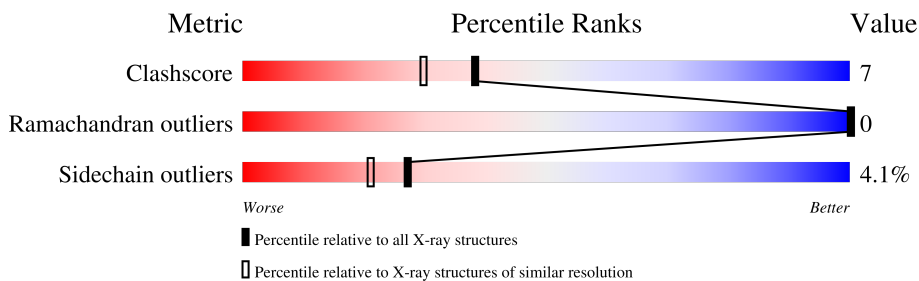
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)

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	 77% 16% . . .
1	B	455	 74% 20% . . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8552 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
			3510	2249	595	649	17			
1	B	444	Total	C	N	O	S	0	0	0
			3547	2271	596	663	17			

There are 2 discrepancies between the modelled and reference sequences:

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

- 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		

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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	644	Total	O	0	0
			644	644		
3	B	765	Total	O	0	0
			765	765		

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	58.69Å 152.91Å 61.20Å 90.00° 94.64° 90.00°	Depositor
Resolution (Å)	20.00 – 2.05	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.05)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.169 , 0.237	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8552	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	0.86	1/3589 (0.0%)	1.84	58/4856 (1.2%)
1	B	0.85	0/3628	1.75	67/4908 (1.4%)
All	All	0.86	1/7217 (0.0%)	1.80	125/9764 (1.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	167	ARG	CD-NE	-5.71	1.38	1.46

All (125) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	ARG	CG-CD-NE	28.47	174.63	112.00
1	A	132	ARG	NH1-CZ-NH2	-25.39	86.29	119.30
1	A	132	ARG	NE-CZ-NH2	24.54	141.29	119.20
1	A	132	ARG	CD-NE-CZ	-16.10	101.87	124.40
1	B	296	ARG	CD-NE-CZ	14.94	145.31	124.40
1	A	21	ASN	CA-CB-CG	14.66	127.26	112.60
1	A	132	ARG	NE-CZ-NH1	10.53	132.03	121.50
1	A	50	ARG	NE-CZ-NH1	-10.30	111.19	121.50
1	B	403	GLN	CG-CD-NE2	9.76	131.04	116.40
1	A	50	ARG	CD-NE-CZ	9.52	137.72	124.40
1	B	223	ARG	CD-NE-CZ	9.23	137.33	124.40
1	B	403	GLN	OE1-CD-NE2	-8.90	113.70	122.60
1	A	50	ARG	NE-CZ-NH2	8.81	127.13	119.20
1	B	223	ARG	NE-CZ-NH2	-8.79	111.29	119.20
1	B	47	ARG	N-CA-C	8.66	119.69	108.34
1	B	329	PRO	N-CA-C	8.39	124.34	113.86
1	A	87	PHE	CA-CB-CG	8.25	122.05	113.80
1	A	167	ARG	CA-CB-CG	8.16	130.42	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	445	VAL	N-CA-CB	-8.12	97.33	112.36
1	B	250	ASP	CA-CB-CG	8.10	120.70	112.60
1	B	50	ARG	NE-CZ-NH2	-7.94	112.05	119.20
1	B	446	VAL	N-CA-CB	-7.92	97.90	110.96
1	B	302	VAL	N-CA-CB	-7.86	100.20	111.21
1	B	158	PHE	CA-CB-CG	7.78	121.58	113.80
1	B	357	ILE	O-C-N	-7.30	115.75	120.42
1	A	255	ARG	NE-CZ-NH1	-7.12	114.38	121.50
1	A	379	PHE	CA-CB-CG	-6.93	106.87	113.80
1	B	430	GLU	CB-CG-CD	6.90	124.33	112.60
1	A	94	LYS	CA-C-O	-6.80	113.29	120.63
1	A	158	PHE	CA-CB-CG	6.79	120.59	113.80
1	B	46	GLY	N-CA-C	6.76	120.84	112.73
1	A	70	ASN	OD1-CG-ND2	6.68	129.28	122.60
1	B	296	ARG	NE-CZ-NH1	6.62	128.12	121.50
1	B	87	PHE	CA-CB-CG	6.61	120.41	113.80
1	A	86	LEU	N-CA-C	6.58	118.45	111.28
1	A	56	ARG	CD-NE-CZ	6.50	133.50	124.40
1	A	404	GLN	N-CA-CB	6.48	119.75	110.16
1	B	433	ILE	N-CA-C	6.45	117.02	107.15
1	B	403	GLN	CB-CG-CD	6.45	123.56	112.60
1	B	226	SER	CA-C-O	6.42	126.49	119.24
1	A	167	ARG	N-CA-C	6.40	118.79	109.07
1	A	255	ARG	NE-CZ-NH2	6.18	124.77	119.20
1	A	395	ASN	N-CA-C	6.16	118.77	109.23
1	B	280	LEU	CA-C-O	-6.12	114.07	120.55
1	B	445	VAL	CB-CA-C	6.11	120.63	110.30
1	B	253	ASN	CA-CB-CG	-6.04	106.56	112.60
1	A	404	GLN	O-C-N	6.02	129.01	122.15
1	A	437	LEU	N-CA-C	-5.99	104.88	111.82
1	A	41	LYS	CA-CB-CG	5.97	126.04	114.10
1	A	49	THR	N-CA-CB	5.92	122.53	111.52
1	B	374	PHE	CA-CB-CG	-5.92	107.88	113.80
1	A	21	ASN	OD1-CG-ND2	-5.91	116.69	122.60
1	B	49	THR	N-CA-CB	5.88	121.15	111.62
1	B	238	LEU	CA-C-O	-5.85	114.22	120.42
1	B	309	LYS	CB-CG-CD	5.84	124.73	111.30
1	A	136	ASP	CB-CG-OD1	5.83	131.80	118.40
1	B	56	ARG	CA-C-O	-5.80	114.40	120.55
1	A	357	ILE	CA-C-O	-5.77	114.33	118.71
1	B	249	LEU	CA-C-O	-5.76	115.28	121.56
1	A	317	VAL	CA-C-N	5.75	127.99	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	317	VAL	C-N-CA	5.75	127.99	120.28
1	A	403	GLN	CG-CD-NE2	5.67	124.90	116.40
1	B	49	THR	OG1-CB-CG2	5.65	120.60	109.30
1	B	205	PHE	CA-CB-CG	5.64	119.44	113.80
1	B	379	PHE	CA-CB-CG	-5.63	108.17	113.80
1	A	360	LEU	CA-C-O	5.61	126.50	120.55
1	B	106	SER	CA-CB-OG	-5.61	99.87	111.10
1	A	323	ARG	NE-CZ-NH2	-5.56	114.20	119.20
1	A	361	HIS	CA-CB-CG	5.54	119.34	113.80
1	B	345	TYR	CA-C-N	5.53	125.70	119.90
1	B	345	TYR	C-N-CA	5.53	125.70	119.90
1	B	368	GLY	N-CA-C	-5.50	105.68	112.33
1	B	369	ASP	CB-CG-OD2	5.49	131.02	118.40
1	B	423	PHE	CA-CB-CG	-5.48	108.32	113.80
1	B	171	HIS	CA-C-N	5.48	125.57	119.32
1	B	171	HIS	C-N-CA	5.48	125.57	119.32
1	B	27	GLN	OE1-CD-NE2	-5.48	117.12	122.60
1	B	140	GLU	CA-C-O	-5.48	114.72	120.58
1	B	47	ARG	CA-C-O	5.46	127.76	121.32
1	A	423	PHE	CA-CB-CG	-5.45	108.35	113.80
1	A	250	ASP	CA-CB-CG	-5.45	107.15	112.60
1	A	423	PHE	CA-C-N	-5.44	115.31	122.99
1	A	423	PHE	C-N-CA	-5.44	115.31	122.99
1	B	366	ILE	CB-CA-C	-5.44	105.38	111.80
1	B	159	ASN	OD1-CG-ND2	-5.43	117.17	122.60
1	B	214	ASP	CA-CB-CG	-5.42	107.18	112.60
1	B	53	SER	CB-CA-C	-5.39	100.73	109.13
1	A	317	VAL	O-C-N	-5.36	116.58	121.94
1	B	55	GLN	CA-C-O	5.35	126.22	120.55
1	A	283	ASN	CA-C-N	5.31	125.63	119.47
1	A	283	ASN	C-N-CA	5.31	125.63	119.47
1	B	437	LEU	N-CA-C	-5.31	105.67	111.82
1	A	366	ILE	CB-CA-C	-5.29	105.56	111.80
1	A	263	ILE	CB-CA-C	-5.28	105.21	111.97
1	B	446	VAL	CA-CB-CG1	5.28	119.38	110.40
1	B	24	LYS	O-C-N	-5.28	116.64	121.34
1	A	326	PRO	N-CA-C	-5.26	102.92	111.03
1	B	23	ASP	N-CA-C	-5.26	106.45	112.92
1	A	404	GLN	CA-C-O	-5.26	114.85	120.42
1	B	428	ASN	CA-C-O	5.25	127.93	121.84
1	A	204	GLN	CA-C-N	5.25	127.31	120.28
1	A	204	GLN	C-N-CA	5.25	127.31	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	136	ASP	OD1-CG-OD2	-5.24	110.33	122.90
1	B	154	GLY	CA-C-N	5.20	127.51	120.44
1	B	154	GLY	C-N-CA	5.20	127.51	120.44
1	A	38	GLU	N-CA-C	5.18	119.23	113.01
1	A	357	ILE	CA-C-N	5.18	124.98	119.28
1	A	357	ILE	C-N-CA	5.18	124.98	119.28
1	A	34	ASP	CB-CA-C	-5.18	102.53	110.81
1	B	17	LEU	CA-C-N	5.14	124.86	119.82
1	B	17	LEU	C-N-CA	5.14	124.86	119.82
1	A	405	PHE	CA-CB-CG	5.13	118.93	113.80
1	B	360	LEU	CA-C-O	5.10	126.35	120.90
1	A	413	VAL	N-CA-C	5.08	115.31	110.53
1	B	226	SER	N-CA-C	-5.08	107.64	113.88
1	B	451	LYS	N-CA-C	-5.05	106.89	113.16
1	B	408	HIS	CA-CB-CG	-5.05	108.75	113.80
1	B	436	THR	N-CA-C	-5.04	100.05	110.80
1	B	134	ASN	CA-C-N	5.04	127.35	120.54
1	B	134	ASN	C-N-CA	5.04	127.35	120.54
1	A	420	HIS	CA-C-O	-5.04	113.71	119.60
1	B	85	GLY	N-CA-C	-5.03	104.81	112.51
1	A	93	GLU	N-CA-CB	5.02	117.74	109.95
1	B	362	ARG	CD-NE-CZ	5.02	131.43	124.40
1	A	362	ARG	CD-NE-CZ	5.01	131.41	124.40

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	3510	0	3453	42	4
1	B	3547	0	3491	54	1
2	A	43	0	30	0	0
2	B	43	0	30	2	0
3	A	644	0	0	12	0
3	B	765	0	0	11	3

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8552	0	7004	97	4

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 7.

All (97) 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:A:59:LYS:CE	1:A:59:LYS:CG	2.50	0.90
1:B:116:HIS:HD2	1:B:408:HIS:HE2	1.20	0.88
1:A:116:HIS:HD2	1:A:408:HIS:HE2	1.22	0.85
1:B:361:HIS:HE1	1:B:391:LYS:H	1.28	0.82
1:B:16:ASN:HD22	1:B:43:GLU:H	1.28	0.82
1:A:361:HIS:HE1	1:A:391:LYS:H	1.26	0.81
1:A:118:MET:HG3	3:A:694:HOH:O	1.82	0.80
1:B:49:THR:HG21	1:B:354:MET:HG2	1.68	0.74
1:B:171:HIS:HD2	1:B:173:PHE:H	1.34	0.74
1:B:174:ILE:O	1:B:178:VAL:HG13	1.95	0.67
1:B:223:ARG:NH2	1:B:232:ASP:OD2	2.28	0.66
1:A:141:VAL:HB	1:A:142:PRO:HD3	1.77	0.66
1:B:100:HIS:HD2	3:B:560:HOH:O	1.80	0.65
1:B:370:ASP:OD2	1:B:375:ARG:NH2	2.28	0.62
1:B:43:GLU:HG2	1:B:48:VAL:HG22	1.81	0.62
1:B:35:GLU:HG2	1:B:36:LEU:HD23	1.82	0.61
1:B:201:ASN:HD22	1:B:201:ASN:H	1.49	0.61
1:B:391:LYS:NZ	1:B:395:ASN:HD22	1.99	0.60
1:A:126:LEU:C	1:A:126:LEU:HD13	2.27	0.60
1:A:167:ARG:HG3	1:A:169:GLN:O	2.00	0.60
1:A:17:LEU:HB3	1:A:18:PRO:HD3	1.84	0.60
1:B:3:LYS:HD2	3:B:1119:HOH:O	2.02	0.60
1:A:109:GLN:NE2	1:A:309:LYS:HZ2	2.01	0.59
1:B:57:LEU:HD21	3:B:1013:HOH:O	2.02	0.59
1:B:16:ASN:ND2	1:B:43:GLU:H	2.00	0.57
1:A:404:GLN:HG2	3:A:862:HOH:O	2.05	0.57
1:B:116:HIS:CD2	1:B:408:HIS:HE2	2.12	0.57
1:A:109:GLN:HE22	1:A:309:LYS:NZ	2.02	0.56
1:B:171:HIS:CD2	1:B:173:PHE:H	2.20	0.56
1:B:223:ARG:HD3	3:B:730:HOH:O	2.04	0.56
1:A:109:GLN:HE22	1:A:309:LYS:HZ2	1.52	0.55
1:A:74:ALA:HB1	1:A:185:MET:HE1	1.89	0.55
1:B:388:HIS:HD2	1:B:391:LYS:HZ3	1.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:LYS:HB2	3:A:857:HOH:O	2.07	0.54
1:A:158:PHE:CE2	1:A:219:ILE:HD13	2.41	0.54
1:A:174:ILE:O	1:A:178:VAL:HG13	2.08	0.53
1:A:118:MET:SD	1:A:155:LEU:HD13	2.47	0.53
1:A:391:LYS:NZ	1:A:395:ASN:HD22	2.07	0.53
1:B:391:LYS:HE3	1:B:394:GLY:O	2.09	0.52
1:B:323:ARG:HA	1:B:361:HIS:CD2	2.44	0.52
1:B:391:LYS:HZ3	1:B:395:ASN:HD22	1.56	0.52
1:B:300:ASP:HB3	1:B:301:PRO:HD2	1.92	0.52
1:B:198:TYR:HA	1:B:201:ASN:ND2	2.23	0.52
1:A:62:CYS:HB3	1:A:395:ASN:ND2	2.26	0.51
1:B:148:LEU:HD21	1:B:413:VAL:HG21	1.93	0.51
1:B:388:HIS:HD2	1:B:391:LYS:NZ	2.09	0.51
1:B:116:HIS:HE1	1:B:303:PRO:O	1.94	0.51
1:A:302:VAL:HG22	3:A:917:HOH:O	2.11	0.50
2:B:460:HEM:HBC2	2:B:460:HEM:HMC2	1.93	0.50
1:B:109:GLN:HE22	1:B:309:LYS:NZ	2.10	0.50
1:B:201:ASN:H	1:B:201:ASN:ND2	2.09	0.50
1:B:452:LYS:HE2	3:B:807:HOH:O	2.11	0.50
1:B:132:ARG:NH2	3:B:517:HOH:O	2.46	0.49
1:B:39:ILE:HA	1:B:51:TYR:O	2.12	0.49
1:B:49:THR:HG22	1:B:50:ARG:H	1.77	0.49
1:A:14:LEU:HD12	3:A:955:HOH:O	2.12	0.48
1:B:3:LYS:HD3	1:B:3:LYS:HA	1.79	0.47
1:A:403:GLN:HG2	3:A:1098:HOH:O	2.15	0.47
1:B:60:GLU:OE2	1:B:342:GLY:HA2	2.16	0.46
1:B:298:LEU:HD22	1:B:303:PRO:HB3	1.98	0.46
1:B:58:ILE:HD13	1:B:355:VAL:HG13	1.97	0.46
1:B:300:ASP:HB3	1:B:301:PRO:CD	2.46	0.46
1:B:185:MET:O	1:B:188:LEU:HB2	2.16	0.46
1:B:253:ASN:O	1:B:257:GLN:HG2	2.16	0.46
1:A:118:MET:HB3	1:A:155:LEU:HD13	1.98	0.45
1:A:118:MET:HE1	3:A:912:HOH:O	2.16	0.45
1:B:178:VAL:HG22	3:B:732:HOH:O	2.16	0.45
1:B:306:LYS:HE3	3:B:1171:HOH:O	2.17	0.44
1:B:110:GLN:HG2	3:B:1069:HOH:O	2.16	0.44
1:A:24:LYS:HE2	1:A:433:ILE:O	2.17	0.44
1:B:150:LEU:HD13	1:B:174:ILE:HD13	1.99	0.44
1:A:361:HIS:HE1	1:A:391:LYS:N	2.03	0.44
1:A:116:HIS:CD2	1:A:408:HIS:HE2	2.14	0.43
1:A:342:GLY:O	1:A:344:GLU:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:GLU:HG2	3:A:1095:HOH:O	2.18	0.42
1:B:17:LEU:HD23	3:B:1057:HOH:O	2.19	0.42
1:A:52:LEU:HD11	1:A:353:LEU:HD13	2.01	0.42
1:A:426:HIS:HE1	3:A:520:HOH:O	2.01	0.42
1:B:138:HIS:CD2	1:B:445:VAL:HG22	2.55	0.42
1:B:288:GLN:O	1:B:292:GLU:HG3	2.19	0.42
1:B:138:HIS:HD2	1:B:445:VAL:HG22	1.85	0.42
1:A:206:GLN:HG2	3:A:877:HOH:O	2.20	0.41
1:A:366:ILE:HG21	1:A:389:ALA:HB1	2.03	0.41
1:B:382:PRO:HD2	3:B:744:HOH:O	2.20	0.41
1:A:44:ALA:O	1:A:45:PRO:C	2.62	0.41
1:B:268:THR:HB	2:B:460:HEM:C3B	2.55	0.41
1:A:298:LEU:HD22	1:A:303:PRO:HB3	2.03	0.41
1:A:49:THR:HG23	1:A:352:GLU:HB2	2.02	0.41
1:A:141:VAL:HB	1:A:142:PRO:CD	2.49	0.41
1:A:223:ARG:HG3	3:A:544:HOH:O	2.21	0.41
1:A:116:HIS:HE1	1:A:303:PRO:O	2.04	0.41
1:B:426:HIS:CE1	1:B:445:VAL:HG13	2.56	0.41
1:B:370:ASP:OD2	1:B:375:ARG:NH1	2.49	0.40
1:A:20:LEU:HG	1:A:42:PHE:HZ	1.86	0.40
1:A:226:SER:OG	1:A:228:GLU:HG2	2.21	0.40
1:B:391:LYS:HE2	1:B:395:ASN:HB2	2.03	0.40
1:A:136:ASP:CG	3:A:642:HOH:O	2.65	0.40

All (4) 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:132:ARG:NH1	3:B:485:HOH:O[2_656]	1.86	0.34
1:A:132:ARG:NH2	1:B:166:TYR:OH[2_656]	1.96	0.24
1:A:132:ARG:NE	3:B:485:HOH:O[2_656]	1.99	0.21
1:A:132:ARG:CZ	3:B:485:HOH:O[2_656]	2.01	0.19

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	164/455 (36%)	161 (98%)	3 (2%)	0	100	100
1	B	440/455 (97%)	428 (97%)	12 (3%)	0	100	100
All	All	604/910 (66%)	589 (98%)	15 (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	373/398 (94%)	356 (95%)	17 (5%)	24	18
1	B	381/398 (96%)	367 (96%)	14 (4%)	30	25
All	All	754/796 (95%)	723 (96%)	31 (4%)	27	21

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	45	PRO
1	A	49	THR
1	A	75	LEU
1	A	97	LYS
1	A	126	LEU
1	A	148	LEU
1	A	155	LEU
1	A	158	PHE
1	A	167	ARG
1	A	178	VAL
1	A	182	ASP
1	A	188	LEU
1	A	230	SER
1	A	312	LYS

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Mol	Chain	Res	Type
1	A	430	GLU
1	A	452	LYS
1	B	49	THR
1	B	103	LEU
1	B	110	GLN
1	B	148	LEU
1	B	178	VAL
1	B	181	LEU
1	B	188	LEU
1	B	201	ASN
1	B	223	ARG
1	B	302	VAL
1	B	309	LYS
1	B	403	GLN
1	B	445	VAL
1	B	446	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	70	ASN
1	A	95	ASN
1	A	109	GLN
1	A	110	GLN
1	A	116	HIS
1	A	169	GLN
1	A	201	ASN
1	A	236	HIS
1	A	266	HIS
1	A	285	HIS
1	A	319	ASN
1	A	359	GLN
1	A	361	HIS
1	A	395	ASN
1	A	404	GLN
1	A	426	HIS
1	B	7	GLN
1	B	16	ASN
1	B	70	ASN
1	B	73	GLN
1	B	95	ASN

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Mol	Chain	Res	Type
1	B	100	HIS
1	B	109	GLN
1	B	110	GLN
1	B	116	HIS
1	B	171	HIS
1	B	201	ASN
1	B	213	ASN
1	B	236	HIS
1	B	266	HIS
1	B	285	HIS
1	B	319	ASN
1	B	361	HIS
1	B	388	HIS
1	B	395	ASN
1	B	404	GLN

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 ⓘ

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	1	50,50,50	1.40	10 (20%)	67,82,82	0.78	1 (1%)
2	HEM	A	460	1,3	50,50,50	1.38	7 (14%)	67,82,82	0.82	1 (1%)

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	1	-	2/14/54/54	-
2	HEM	A	460	1,3	-	2/14/54/54	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	460	HEM	CMC-C2C	3.00	1.56	1.50
2	B	460	HEM	FE-NB	2.68	2.03	1.94
2	A	460	HEM	FE-NC	2.63	2.03	1.95
2	B	460	HEM	CAA-C2A	2.61	1.58	1.51
2	B	460	HEM	CMD-C2D	2.60	1.56	1.50
2	A	460	HEM	CMD-C2D	2.52	1.55	1.50
2	A	460	HEM	CAC-C3C	2.44	1.53	1.47
2	A	460	HEM	FE-ND	2.44	2.02	1.94
2	B	460	HEM	CAB-C3B	2.42	1.53	1.47
2	B	460	HEM	CAC-C3C	2.35	1.53	1.47
2	A	460	HEM	CMB-C2B	2.34	1.55	1.50
2	B	460	HEM	CMC-C2C	2.25	1.55	1.50
2	B	460	HEM	CMB-C2B	2.18	1.55	1.50
2	B	460	HEM	FE-NA	2.17	2.02	1.95
2	B	460	HEM	C3B-C2B	-2.16	1.32	1.37
2	B	460	HEM	FE-ND	2.15	2.01	1.94
2	A	460	HEM	CMA-C3A	2.08	1.55	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	460	HEM	C3B-C2B-C1B	3.10	108.74	106.41
2	B	460	HEM	C3B-C2B-C1B	2.34	108.17	106.41

There are no chirality outliers.

All (4) torsion outliers are listed below:

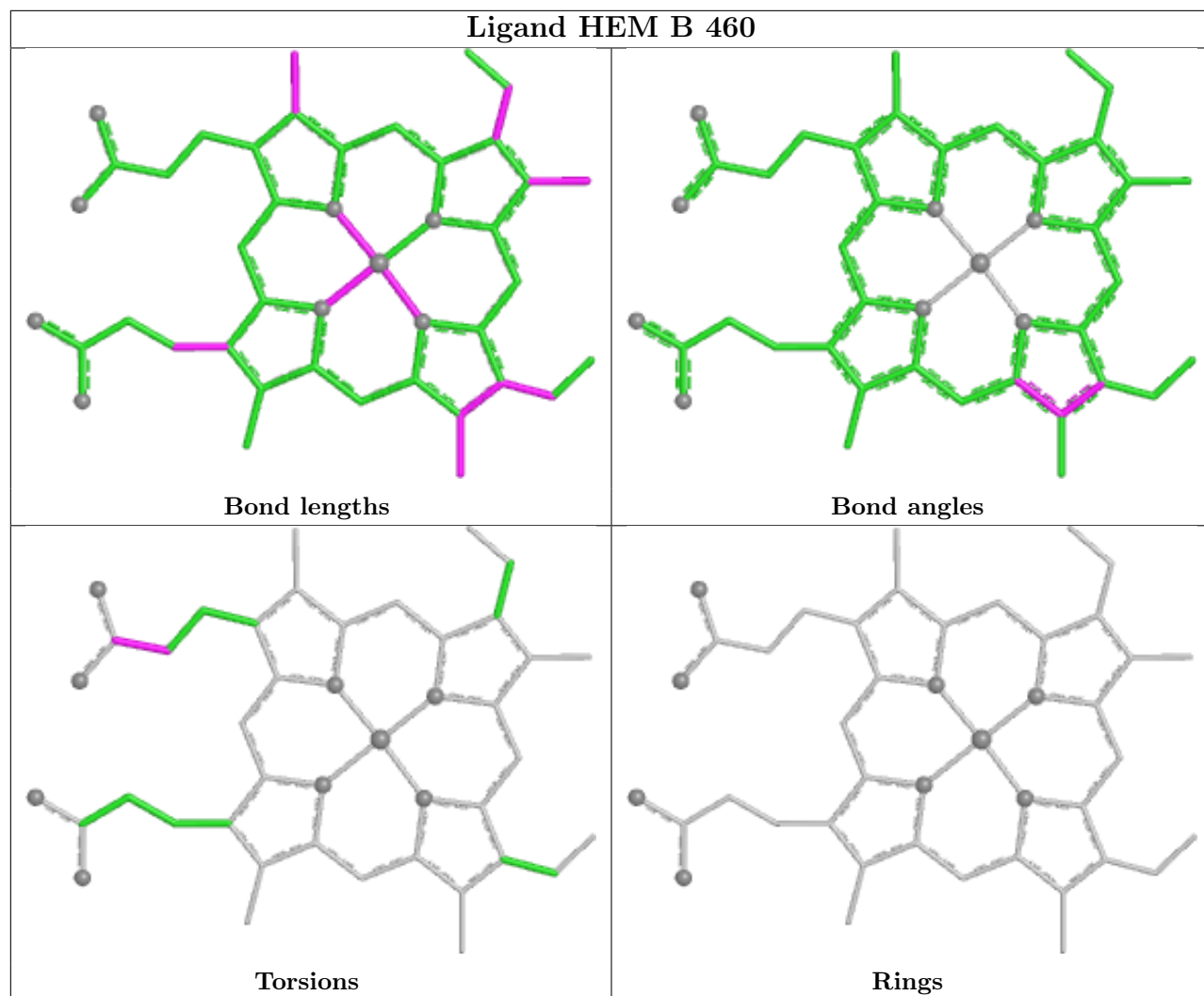
Mol	Chain	Res	Type	Atoms
2	B	460	HEM	CAD-CBD-CGD-O1D
2	B	460	HEM	CAD-CBD-CGD-O2D
2	A	460	HEM	CAD-CBD-CGD-O1D
2	A	460	HEM	CAD-CBD-CGD-O2D

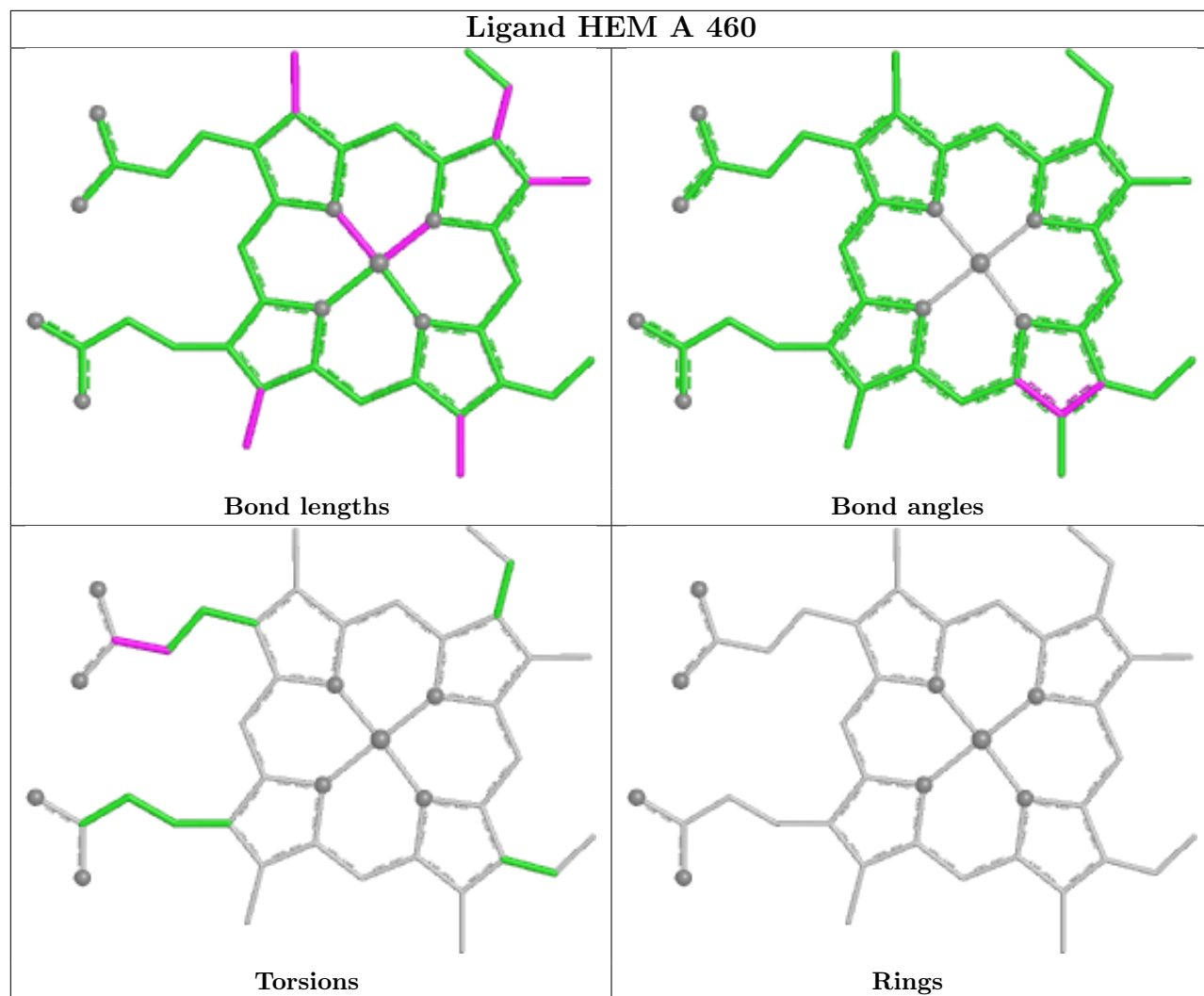
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	460	HEM	2	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.