



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:51 PM UTC

PDB ID : 1WVE / pdb_00001wve
Title : p-Cresol Methylhydroxylase: Alteration of the Structure of the Flavoprotein Subunit upon its Binding to the Cytochrome Subunit
Authors : Cunane, L.M.; Chen, Z.-W.; McIntire, W.S.; Mathews, F.S.
Deposited on : 2004-12-15
Resolution : 1.85 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)	:	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

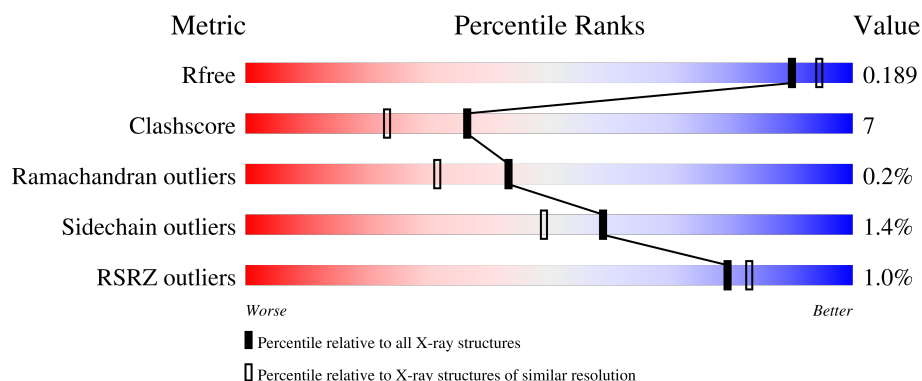
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	520	% 84% 14% ..
1	B	520	% 84% 13% ..
2	C	80	% 88% 5% 6%
2	D	80	% 81% 11% 6%

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
5	TRS	A	2705	-	X	-	-
5	TRS	B	2704	-	X	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 10692 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 4-cresol dehydrogenase [hydroxylating] flavoprotein subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	515	Total	C	N	O	S	0	7	0
			4082	2596	696	760	30			
1	B	515	Total	C	N	O	S	0	11	0
			4123	2619	705	767	32			

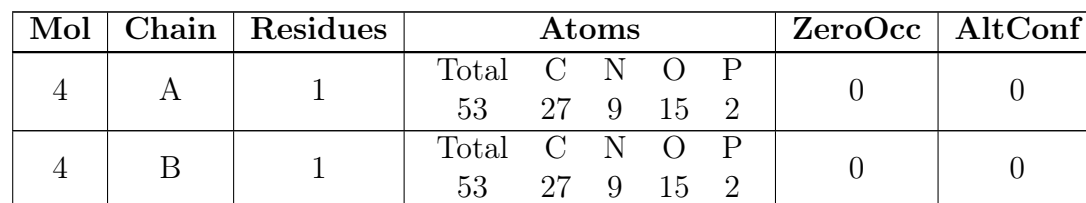
- Molecule 2 is a protein called 4-cresol dehydrogenase [hydroxylating] cytochrome c subunit.

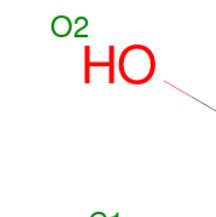
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	75	Total	C	N	O	S	0	0	0
			571	363	97	108	3			
2	D	75	Total	C	N	O	S	0	0	0
			571	363	97	108	3			

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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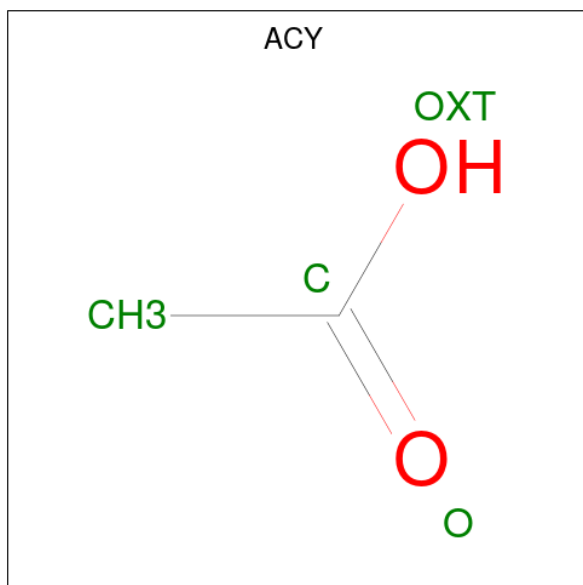
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			8	4	1	3		



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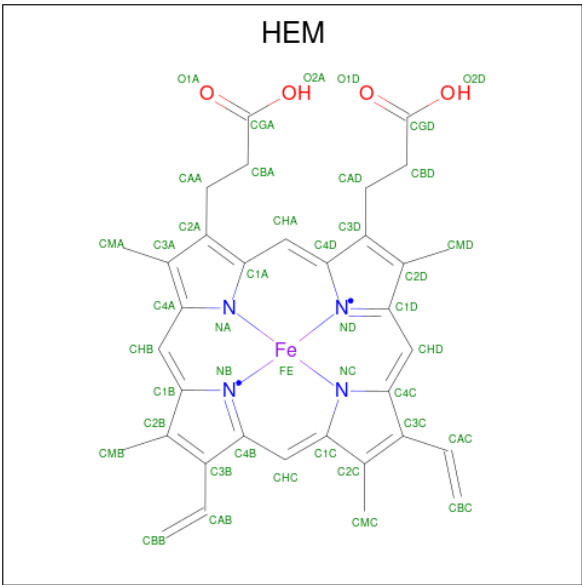
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			8	4	1	3		
5	B	1	Total	C	N	O	0	0
			8	4	1	3		
5	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 6 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

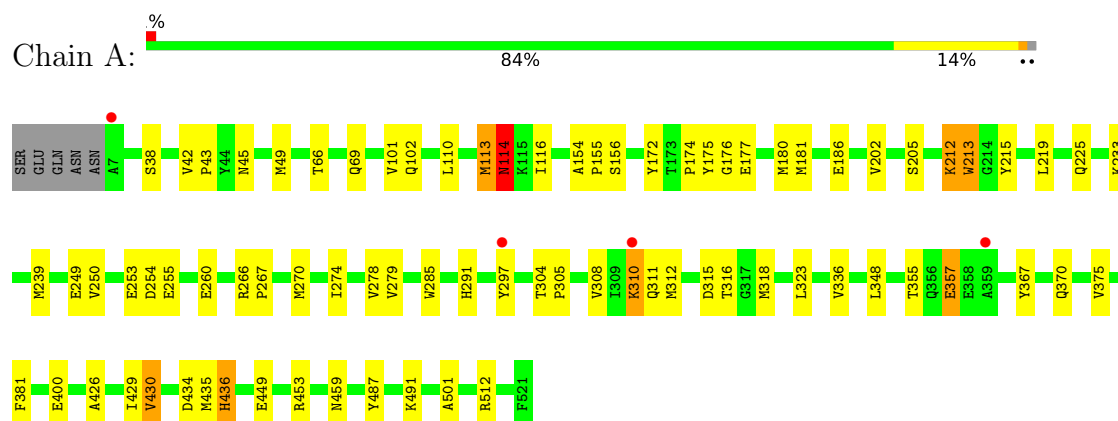
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	499	Total	O	0	0
			499	499		
8	C	83	Total	O	0	0
			83	83		
8	B	441	Total	O	0	0
			441	441		
8	D	80	Total	O	0	0
			80	80		

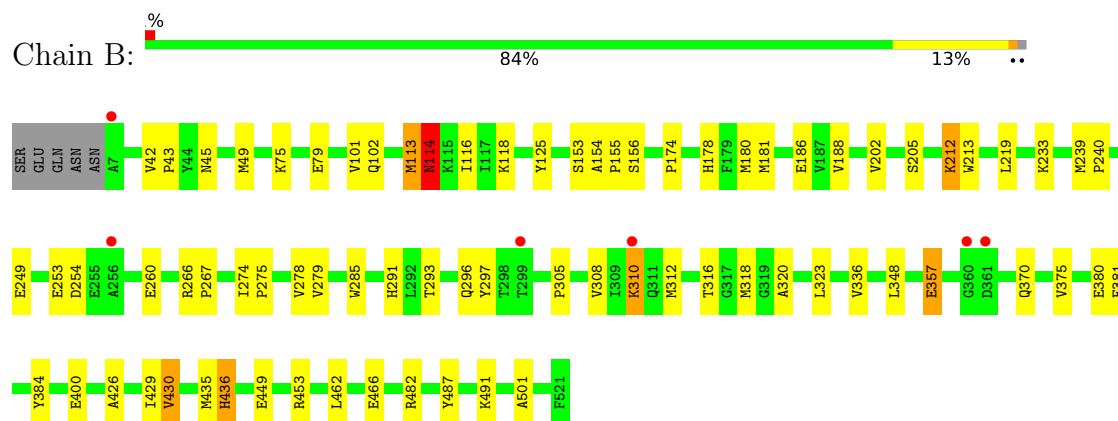
3 Residue-property plots

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.

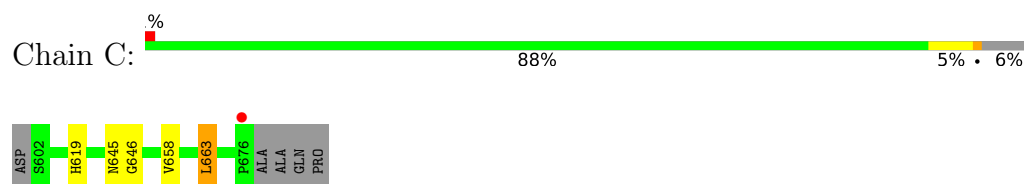
- Molecule 1: 4-cresol dehydrogenase [hydroxylating] flavoprotein subunit



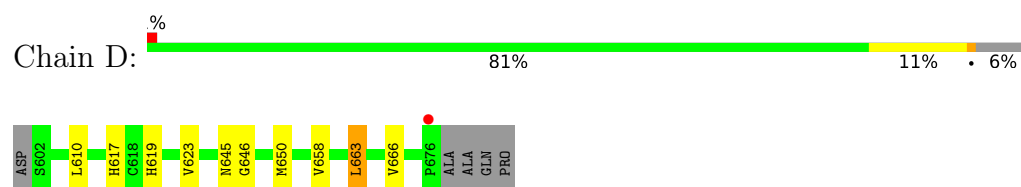
- Molecule 1: 4-cresol dehydrogenase [hydroxylating] flavoprotein subunit



- Molecule 2: 4-cresol dehydrogenase [hydroxylating] cytochrome c subunit



- Molecule 2: 4-cresol dehydrogenase [hydroxylating] cytochrome c subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.83Å 118.60Å 136.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.85 30.00 – 1.85	Depositor EDS
% Data completeness (in resolution range)	91.7 (30.00-1.85) 91.7 (30.00-1.85)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 1.80Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.159 , 0.194 0.154 , 0.189	Depositor DCC
R_{free} test set	9705 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10692	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.88% 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: ACY, CL, HEM, FAD, TRS

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	0.49	0/4180	0.99	20/5669 (0.4%)
1	B	0.49	0/4221	0.97	19/5720 (0.3%)
2	C	0.70	2/587 (0.3%)	1.10	5/798 (0.6%)
2	D	0.70	2/587 (0.3%)	1.10	5/798 (0.6%)
All	All	0.52	4/9575 (0.0%)	1.00	49/12985 (0.4%)

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	B	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	619	HIS	CE1-NE2	10.83	1.43	1.32
2	C	619	HIS	CE1-NE2	10.17	1.42	1.32
2	C	619	HIS	ND1-CE1	5.68	1.38	1.32
2	D	619	HIS	ND1-CE1	5.67	1.38	1.32

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	619	HIS	ND1-CG-CD2	13.74	119.84	106.10
2	C	619	HIS	ND1-CG-CD2	13.71	119.81	106.10
1	B	274	ILE	N-CA-C	-10.29	96.59	107.60
1	A	212	LYS	N-CA-C	9.86	121.72	110.97
1	A	430	VAL	N-CA-C	9.85	123.30	108.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	213	TRP	N-CA-C	9.63	121.86	111.36
1	A	213	TRP	N-CA-C	9.62	121.85	111.36
1	A	274	ILE	N-CA-C	-9.59	97.33	107.60
1	B	430	VAL	N-CA-C	9.57	122.87	108.23
1	B	212	LYS	N-CA-C	9.30	121.11	110.97
2	C	619	HIS	CB-CG-CD2	-9.01	119.49	131.20
2	D	619	HIS	CB-CG-CD2	-9.00	119.50	131.20
1	A	219	LEU	N-CA-C	8.92	124.41	113.17
1	A	436	HIS	N-CA-C	-8.29	94.03	108.20
1	B	219	LEU	N-CA-C	8.28	123.61	113.17
1	A	114	ASN	N-CA-C	7.80	122.70	111.56
1	B	436	HIS	N-CA-C	-7.45	93.89	107.75
1	A	116	ILE	N-CA-C	-7.31	96.32	107.73
1	B	116	ILE	N-CA-C	-7.12	96.62	107.73
1	B	114	ASN	N-CA-C	7.08	122.71	111.81
2	C	619	HIS	CG-CD2-NE2	-6.94	100.26	107.20
2	D	619	HIS	CG-CD2-NE2	-6.88	100.32	107.20
2	C	646	GLY	N-CA-C	-6.79	101.74	112.61
1	A	253	GLU	N-CA-C	6.44	120.34	112.23
1	B	285	TRP	N-CA-C	-6.16	104.49	111.14
2	D	646	GLY	N-CA-C	-6.12	102.81	112.61
1	A	285	TRP	N-CA-C	-5.94	104.72	111.14
1	B	291	HIS	N-CA-C	5.91	119.79	112.58
1	A	172	TYR	N-CA-C	5.84	120.00	112.41
1	A	254	ASP	N-CA-C	5.68	118.74	109.59
1	B	178	HIS	N-CA-C	5.63	117.86	111.11
2	C	619	HIS	N-CA-C	5.62	120.20	113.23
1	B	254	ASP	N-CA-C	5.59	118.60	109.59
1	B	253	GLU	N-CA-C	5.56	120.19	112.90
1	A	400	GLU	N-CA-C	-5.51	102.73	110.50
2	D	619	HIS	N-CA-C	5.48	120.03	113.23
1	B	426	ALA	N-CA-C	5.43	117.05	108.96
1	A	426	ALA	N-CA-C	5.38	116.98	108.96
1	B	320	ALA	N-CA-C	-5.38	105.53	111.71
1	A	113[A]	MET	N-CA-C	-5.32	101.64	109.62
1	A	113[B]	MET	N-CA-C	-5.32	101.64	109.62
1	B	113[A]	MET	N-CA-C	-5.31	101.65	109.62
1	B	113[B]	MET	N-CA-C	-5.31	101.65	109.62
1	A	176	GLY	N-CA-C	5.30	120.56	113.61
1	B	188	VAL	N-CA-C	-5.26	100.83	108.36
1	B	400	GLU	N-CA-C	-5.25	103.09	110.50
1	A	291	HIS	N-CA-C	5.23	118.96	112.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	304	THR	CA-C-N	5.11	125.11	119.90
1	A	304	THR	C-N-CA	5.11	125.11	119.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	384	TYR	Sidechain

5.2 Too-close contacts [i](#)

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	4082	0	4007	71	0
1	B	4123	0	4044	61	0
2	C	571	0	550	3	0
2	D	571	0	550	7	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	53	0	28	1	0
4	B	53	0	28	2	0
5	A	16	0	24	0	0
5	B	16	0	24	0	0
6	A	12	0	9	2	0
6	B	4	0	3	1	0
7	C	43	0	30	1	0
7	D	43	0	30	2	0
8	A	499	0	0	11	0
8	B	441	0	0	7	0
8	C	83	0	0	0	0
8	D	80	0	0	0	0
All	All	10692	0	9327	137	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 7.

All (137) 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:174:PRO:HB2	1:A:239:MET:HE1	1.63	0.80
1:A:357:GLU:H	1:A:357:GLU:CD	1.97	0.73
1:B:174:PRO:HB2	1:B:239[A]:MET:HE1	1.72	0.71
1:A:212:LYS:NZ	8:A:3162:HOH:O	2.23	0.69
1:B:42:VAL:HG13	1:B:43:PRO:HD3	1.74	0.69
1:A:355:THR:HB	1:A:357:GLU:OE2	1.92	0.69
1:A:266:ARG:HB3	1:A:267:PRO:HD3	1.76	0.67
1:B:174:PRO:CG	1:B:239[A]:MET:HE1	2.23	0.67
1:A:501:ALA:HB2	1:B:501:ALA:HB2	1.78	0.66
1:A:180[A]:MET:HE3	1:A:181:MET:HE3	1.78	0.66
1:B:180[A]:MET:HE3	1:B:181:MET:HE3	1.77	0.65
1:A:154:ALA:HB2	8:A:3190:HOH:O	1.98	0.64
1:B:118:LYS:HE2	8:B:3103:HOH:O	1.98	0.63
1:B:174:PRO:CB	1:B:239[A]:MET:HE1	2.29	0.63
1:A:180[B]:MET:HG3	8:A:3056:HOH:O	1.99	0.62
1:A:174:PRO:CB	1:A:239:MET:HE1	2.28	0.61
1:B:357:GLU:H	1:B:357:GLU:CD	2.08	0.61
1:B:212:LYS:NZ	8:B:3088:HOH:O	2.30	0.61
1:A:38:SER:O	1:A:42[B]:VAL:HG23	2.02	0.59
1:B:462:LEU:O	1:B:466[B]:GLU:HG3	2.03	0.58
1:A:180[A]:MET:HG2	1:A:181:MET:HE3	1.84	0.58
1:B:174:PRO:HB2	1:B:239[A]:MET:CE	2.34	0.57
1:B:266:ARG:HB3	1:B:267:PRO:HD3	1.87	0.55
1:B:466[B]:GLU:CD	1:B:482:ARG:HH22	2.13	0.55
1:B:180[A]:MET:HG2	1:B:181:MET:CE	2.37	0.55
1:A:174:PRO:HB2	1:A:239:MET:CE	2.34	0.55
1:A:180[B]:MET:HE2	1:B:212:LYS:HE3	1.88	0.54
1:B:180[A]:MET:HG2	1:B:181:MET:HE3	1.90	0.54
1:B:381:PHE:CD1	7:D:699:HEM:HBC1	2.43	0.54
1:A:180[A]:MET:HG2	1:A:181:MET:CE	2.38	0.53
8:A:3056:HOH:O	1:B:180[B]:MET:HG3	2.08	0.53
1:B:430:VAL:HG22	1:B:435:MET:SD	2.49	0.53
1:A:174:PRO:CG	1:A:239:MET:HE1	2.39	0.52
1:A:180[A]:MET:CE	1:A:181:MET:HE3	2.39	0.52
1:B:75:LYS:O	1:B:79[A]:GLU:HG3	2.10	0.52
1:A:260[A]:GLU:HB3	1:A:348:LEU:HD11	1.93	0.51
1:A:323:LEU:C	1:A:323:LEU:HD23	2.35	0.51
1:B:153:SER:HB2	1:B:155:PRO:HD2	1.92	0.51
1:B:42:VAL:HG13	1:B:43:PRO:CD	2.40	0.51
1:B:174:PRO:HG2	1:B:239[A]:MET:HE1	1.93	0.51
1:B:180[A]:MET:CE	1:B:181:MET:HE3	2.41	0.51
1:A:355:THR:OG1	1:A:357:GLU:HG2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:GLU:HB3	1:A:233:LYS:HB2	1.93	0.51
2:C:658:VAL:HG12	2:C:663:LEU:HD13	1.93	0.51
1:A:336:VAL:HG21	1:B:336:VAL:HG21	1.92	0.50
1:B:316:THR:OG1	1:B:318:MET:HG3	2.11	0.50
1:B:305:PRO:HB2	1:B:308:VAL:HG23	1.94	0.50
1:A:370:GLN:HB3	1:A:375:VAL:HB	1.93	0.49
8:A:2818:HOH:O	1:B:491:LYS:HE3	2.11	0.49
2:D:658:VAL:HG12	2:D:663:LEU:HD13	1.93	0.49
1:A:316:THR:OG1	1:A:318:MET:HG3	2.12	0.49
1:B:293:THR:OG1	1:B:296:GLN:HG3	2.13	0.49
1:B:487:TYR:HB3	1:B:491:LYS:HD3	1.95	0.48
1:B:101:VAL:HG13	1:B:102:GLN:HG3	1.95	0.48
1:B:429:ILE:HB	1:B:436:HIS:HB2	1.95	0.48
1:A:202:VAL:HB	1:A:205:SER:HB2	1.94	0.48
1:B:323:LEU:HD23	1:B:323:LEU:C	2.38	0.48
6:B:1702:ACY:H1	8:B:3130:HOH:O	2.12	0.48
1:B:449:GLU:OE2	1:B:453:ARG:NE	2.37	0.48
1:A:381:PHE:CD1	7:C:699:HEM:HBC1	2.49	0.48
2:D:650:MET:HB2	7:D:699:HEM:C1D	2.49	0.47
1:A:491:LYS:HE3	8:B:2831:HOH:O	2.13	0.47
4:A:599:FAD:O5B	4:A:599:FAD:H8A	2.14	0.47
1:B:202:VAL:HB	1:B:205:SER:HB2	1.97	0.47
1:A:110:LEU:HD13	1:A:113[B]:MET:CE	2.44	0.47
1:A:212:LYS:HE3	1:A:213:TRP:CZ3	2.49	0.47
1:A:42[B]:VAL:HG11	2:C:645:ASN:OD1	2.15	0.46
1:A:225:GLN:HA	1:A:512:ARG:NH2	2.29	0.46
1:A:429:ILE:HB	1:A:436:HIS:HB2	1.98	0.46
1:B:42:VAL:CG1	1:B:43:PRO:HD3	2.45	0.46
1:B:186:GLU:HB3	1:B:233:LYS:HB2	1.96	0.46
1:A:181:MET:HA	1:A:181:MET:HE2	1.96	0.46
1:A:297:TYR:CE2	1:A:312:MET:HG2	2.50	0.46
1:A:110:LEU:HD13	1:A:113[B]:MET:HE1	1.97	0.46
1:A:310:LYS:HB3	1:A:310:LYS:NZ	2.31	0.46
1:A:430:VAL:HG22	1:A:435:MET:SD	2.55	0.45
1:A:487:TYR:HB3	1:A:491:LYS:HD3	1.98	0.45
1:B:310:LYS:HB3	1:B:310:LYS:NZ	2.30	0.45
1:A:113[A]:MET:HE2	8:A:2759:HOH:O	2.16	0.45
1:A:249:GLU:HG2	1:A:250:VAL:N	2.32	0.45
1:A:278:VAL:HG12	1:A:279:VAL:N	2.30	0.45
4:B:599:FAD:O5B	4:B:599:FAD:H8A	2.16	0.45
1:B:174:PRO:CD	1:B:239[A]:MET:HE1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:VAL:CG2	1:B:336:VAL:HG21	2.46	0.45
1:A:305:PRO:HB2	1:A:308:VAL:HG23	1.99	0.45
1:A:42[A]:VAL:CG1	1:A:43:PRO:HD3	2.46	0.45
1:B:449:GLU:HG2	8:B:3067:HOH:O	2.17	0.44
1:B:278:VAL:HG12	1:B:279:VAL:N	2.32	0.44
1:A:174:PRO:HG2	1:A:239:MET:HE1	2.00	0.44
1:A:180[A]:MET:O	1:A:181:MET:HE2	2.17	0.44
1:A:260[B]:GLU:HB3	1:A:348:LEU:HD11	2.00	0.44
1:B:154:ALA:N	1:B:155:PRO:CD	2.81	0.44
1:A:311:GLN:HE21	1:A:315:ASP:CG	2.26	0.43
1:A:449:GLU:OE2	1:A:453:ARG:NE	2.33	0.43
1:A:42[A]:VAL:HG13	1:A:43:PRO:HD3	2.00	0.43
1:B:174:PRO:HD2	1:B:239[A]:MET:HE1	1.99	0.43
1:B:42:VAL:HG21	2:D:645:ASN:OD1	2.19	0.43
2:D:658:VAL:CG1	2:D:663:LEU:HD13	2.49	0.43
1:A:66:THR:OG1	1:A:69:GLN:HG3	2.19	0.42
1:A:180[A]:MET:C	1:A:181:MET:HE2	2.44	0.42
1:A:215:TYR:HB3	1:B:487:TYR:CE2	2.54	0.42
1:A:255:GLU:HG3	8:A:3067:HOH:O	2.18	0.42
1:B:113[A]:MET:HE2	8:B:2749:HOH:O	2.19	0.42
1:B:260:GLU:HB3	1:B:348:LEU:HD11	2.01	0.42
6:A:2701:ACY:H2	8:A:3201:HOH:O	2.18	0.42
1:A:114:ASN:HD22	1:A:114:ASN:N	2.16	0.42
1:B:297:TYR:CE2	1:B:312:MET:HG2	2.54	0.42
1:A:357:GLU:CD	1:A:357:GLU:N	2.71	0.42
2:C:663:LEU:HD12	2:C:663:LEU:HA	1.88	0.42
1:B:249:GLU:HA	1:B:323:LEU:O	2.19	0.42
1:A:110:LEU:HB3	1:A:113[B]:MET:HE2	2.02	0.41
1:A:459[B]:ASN:ND2	8:A:2837:HOH:O	2.39	0.41
1:B:153:SER:CB	1:B:155:PRO:HD2	2.50	0.41
2:D:663:LEU:HD12	2:D:663:LEU:HA	1.87	0.41
2:D:617:HIS:O	2:D:623:VAL:HG11	2.20	0.41
1:A:175:TYR:CD2	1:A:239:MET:HE3	2.55	0.41
1:A:180[B]:MET:O	1:A:181:MET:HE2	2.19	0.41
1:A:270:MET:CG	1:B:240:PRO:HG2	2.51	0.41
1:B:49:MET:HG2	8:B:2822:HOH:O	2.19	0.41
1:A:154:ALA:N	1:A:155:PRO:CD	2.83	0.41
1:A:180[B]:MET:C	1:A:181:MET:HE2	2.46	0.41
1:A:278:VAL:CG1	1:A:279:VAL:N	2.84	0.41
1:A:49:MET:HG2	8:A:2846:HOH:O	2.21	0.41
1:B:380:GLU:OE2	4:B:599:FAD:H6	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:610:LEU:HD23	2:D:666:VAL:HB	2.01	0.41
1:A:279:VAL:O	1:A:323:LEU:HA	2.20	0.40
1:B:125:TYR:CD1	1:B:125:TYR:C	2.99	0.40
1:B:278:VAL:CG1	1:B:279:VAL:N	2.84	0.40
1:A:101:VAL:HG13	1:A:102:GLN:HG3	2.03	0.40
1:A:270:MET:HG2	1:B:240:PRO:CG	2.51	0.40
1:A:336:VAL:HG21	1:B:336:VAL:CG2	2.51	0.40
6:A:1701:ACY:H1	8:A:3184:HOH:O	2.21	0.40
1:B:370:GLN:HB3	1:B:375:VAL:HB	2.03	0.40

There are no symmetry-related clashes.

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	520/520 (100%)	510 (98%)	9 (2%)	1 (0%)	43	31
1	B	524/520 (101%)	514 (98%)	9 (2%)	1 (0%)	43	31
2	C	73/80 (91%)	69 (94%)	4 (6%)	0	100	100
2	D	73/80 (91%)	71 (97%)	2 (3%)	0	100	100
All	All	1190/1200 (99%)	1164 (98%)	24 (2%)	2 (0%)	43	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	156	SER
1	B	156	SER

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	434/432 (100%)	426 (98%)	8 (2%)	51	40
1	B	438/432 (101%)	433 (99%)	5 (1%)	65	57
2	C	61/64 (95%)	60 (98%)	1 (2%)	55	44
2	D	61/64 (95%)	60 (98%)	1 (2%)	55	44
All	All	994/992 (100%)	979 (98%)	15 (2%)	59	47

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	114	ASN
1	A	177[A]	GLU
1	A	177[B]	GLU
1	A	310	LYS
1	A	357	GLU
1	A	367	TYR
1	A	434	ASP
2	C	663	LEU
1	B	45	ASN
1	B	114	ASN
1	B	275	PRO
1	B	310	LYS
1	B	357	GLU
2	D	663	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	114	ASN
1	A	142	GLN
1	A	272	ASN

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Mol	Chain	Res	Type
1	A	311	GLN
1	A	313	GLN
1	A	331	GLN
1	A	518	ASN
2	C	665	GLN
1	B	19	ASN
1	B	23	GLN
1	B	114	ASN
1	B	311	GLN
1	B	313	GLN
1	B	505	ASN
2	D	665	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 for Mogul analysis.

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	FAD	B	599	1	58,58,58	2.26	20 (34%)	85,89,89	1.62	15 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	TRS	A	2705	-	7,7,7	0.67	0	9,9,9	1.66	3 (33%)
7	HEM	C	699	2	50,50,50	1.63	10 (20%)	67,82,82	0.92	3 (4%)
4	FAD	A	599	1	58,58,58	2.36	21 (36%)	85,89,89	1.64	15 (17%)
5	TRS	B	2704	-	7,7,7	0.67	0	9,9,9	1.50	3 (33%)
5	TRS	A	1704	-	7,7,7	0.60	0	9,9,9	1.47	3 (33%)
6	ACY	A	2702	-	3,3,3	1.31	1 (33%)	3,3,3	1.16	0
7	HEM	D	699	2	50,50,50	1.64	11 (22%)	67,82,82	0.94	3 (4%)
6	ACY	B	1702	-	3,3,3	1.17	0	3,3,3	1.29	0
6	ACY	A	1701	-	3,3,3	1.08	0	3,3,3	1.16	0
6	ACY	A	2701	-	3,3,3	1.44	1 (33%)	3,3,3	1.17	0
5	TRS	B	1705	-	7,7,7	0.62	0	9,9,9	1.45	3 (33%)

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	FAD	B	599	1	-	4/34/50/50	0/6/6/6
5	TRS	A	2705	-	-	9/9/9/9	-
4	FAD	A	599	1	-	3/34/50/50	0/6/6/6
5	TRS	B	2704	-	-	8/9/9/9	-
5	TRS	A	1704	-	-	0/9/9/9	-
7	HEM	D	699	2	-	6/14/54/54	-
7	HEM	C	699	2	-	4/14/54/54	-
5	TRS	B	1705	-	-	3/9/9/9	-

All (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	599	FAD	C1'-C2'	6.80	1.62	1.52
4	B	599	FAD	C1'-C2'	6.20	1.61	1.52
7	C	699	HEM	CBB-CAB	5.32	1.56	1.30
7	D	699	HEM	CBC-CAC	5.21	1.55	1.30
7	C	699	HEM	CBC-CAC	5.17	1.55	1.30
4	B	599	FAD	C10-N10	5.11	1.48	1.37
4	A	599	FAD	C10-N10	5.04	1.48	1.37
4	A	599	FAD	O2'-C2'	-4.99	1.32	1.43
7	D	699	HEM	CBB-CAB	4.96	1.54	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	599	FAD	C8M-C8	-4.51	1.42	1.51
4	A	599	FAD	C8M-C8	-4.28	1.43	1.51
4	A	599	FAD	C2'-C3'	4.27	1.60	1.53
4	B	599	FAD	O2'-C2'	-4.22	1.34	1.43
4	A	599	FAD	C6-C5X	4.11	1.46	1.40
4	A	599	FAD	C9A-C5X	4.06	1.47	1.41
4	B	599	FAD	C9A-C5X	4.06	1.47	1.41
4	B	599	FAD	C4X-N5	4.05	1.39	1.30
4	A	599	FAD	C4A-N3A	3.99	1.41	1.34
4	A	599	FAD	C9A-N10	3.95	1.48	1.41
4	A	599	FAD	C4X-N5	3.93	1.39	1.30
4	B	599	FAD	C4A-N3A	3.86	1.41	1.34
4	B	599	FAD	C6-C5X	3.82	1.45	1.40
4	B	599	FAD	C2'-C3'	3.74	1.60	1.53
4	B	599	FAD	C9A-N10	3.51	1.47	1.41
4	B	599	FAD	C8-C7	3.23	1.48	1.40
4	B	599	FAD	O3'-C3'	-3.13	1.35	1.43
4	A	599	FAD	C8-C7	3.07	1.48	1.40
4	B	599	FAD	C10-N1	3.03	1.39	1.33
4	A	599	FAD	C10-N1	2.91	1.39	1.33
4	A	599	FAD	O3'-C3'	-2.83	1.35	1.43
7	C	699	HEM	FE-NA	2.79	2.04	1.95
4	A	599	FAD	C8A-N7A	-2.74	1.26	1.31
7	D	699	HEM	CAB-C3B	2.72	1.54	1.47
4	B	599	FAD	C9-C8	-2.67	1.36	1.39
7	C	699	HEM	CMD-C2D	2.66	1.56	1.50
4	B	599	FAD	C1B-N9A	2.63	1.53	1.46
7	C	699	HEM	CMC-C2C	2.60	1.56	1.50
7	D	699	HEM	FE-NB	2.57	2.02	1.94
4	A	599	FAD	C2A-N3A	2.55	1.38	1.33
4	A	599	FAD	C1B-N9A	2.52	1.53	1.46
7	D	699	HEM	FE-NA	2.50	2.03	1.95
4	A	599	FAD	C9-C8	-2.49	1.36	1.39
4	B	599	FAD	C2A-N3A	2.49	1.38	1.33
4	A	599	FAD	C4-N3	2.46	1.43	1.38
7	D	699	HEM	CAC-C3C	2.37	1.53	1.47
4	A	599	FAD	C4'-C3'	2.35	1.57	1.53
7	D	699	HEM	CMC-C2C	2.28	1.55	1.50
7	D	699	HEM	C2A-C3A	-2.28	1.33	1.38
6	A	2701	ACY	O-C	2.25	1.32	1.22
4	A	599	FAD	C2A-N1A	2.24	1.37	1.33
7	D	699	HEM	O2A-CGA	-2.20	1.23	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	599	FAD	C8A-N7A	-2.18	1.27	1.31
7	C	699	HEM	CAC-C3C	2.17	1.53	1.47
6	A	2702	ACY	O-C	2.12	1.31	1.22
7	C	699	HEM	O1A-CGA	2.11	1.29	1.22
4	B	599	FAD	O4B-C1B	2.09	1.46	1.42
4	B	599	FAD	C1'-N10	2.09	1.52	1.47
7	C	699	HEM	CMB-C2B	2.09	1.55	1.50
7	C	699	HEM	O2A-CGA	-2.09	1.23	1.30
7	C	699	HEM	FE-NC	2.09	2.02	1.95
7	D	699	HEM	O2D-CGD	-2.08	1.23	1.30
4	B	599	FAD	C4'-C3'	2.02	1.57	1.53
7	D	699	HEM	CMD-C2D	2.02	1.54	1.50
4	A	599	FAD	C1'-N10	2.01	1.52	1.47

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	599	FAD	O4'-C4'-C5'	5.00	121.01	109.99
4	B	599	FAD	C1'-C2'-C3'	4.60	122.14	109.66
4	A	599	FAD	O4'-C4'-C5'	4.54	119.99	109.99
4	B	599	FAD	O5'-C5'-C4'	-4.43	97.55	109.36
4	A	599	FAD	C1'-C2'-C3'	4.42	121.64	109.66
4	A	599	FAD	O5'-C5'-C4'	-4.39	97.64	109.36
4	B	599	FAD	O4'-C4'-C3'	-3.98	99.94	109.25
4	A	599	FAD	O4'-C4'-C3'	-3.84	100.26	109.25
4	A	599	FAD	C4A-N9A-C8A	-3.58	101.98	105.74
4	B	599	FAD	C8M-C8-C9	-3.17	113.99	119.57
5	A	2705	TRS	O1-C1-C	3.09	119.48	110.88
4	A	599	FAD	C8M-C8-C9	-3.05	114.19	119.57
4	A	599	FAD	C9A-C5X-N5	3.03	125.67	122.45
4	B	599	FAD	C9A-C5X-N5	2.96	125.60	122.45
7	C	699	HEM	O1A-CGA-CBA	-2.86	114.02	123.09
4	B	599	FAD	C4A-N9A-C8A	-2.84	102.75	105.74
7	D	699	HEM	O1A-CGA-CBA	-2.83	114.11	123.09
7	C	699	HEM	CBB-CAB-C3B	-2.75	113.76	127.53
4	A	599	FAD	C5X-N5-C4X	-2.75	113.63	118.09
4	B	599	FAD	O3'-C3'-C2'	-2.74	102.71	108.93
4	B	599	FAD	O4B-C1B-N9A	2.72	113.31	108.09
4	B	599	FAD	N3-C2-N1	-2.71	113.74	119.50
4	A	599	FAD	O3'-C3'-C2'	-2.71	102.78	108.93
7	D	699	HEM	CBB-CAB-C3B	-2.71	114.01	127.53
5	A	2705	TRS	O2-C2-C	2.69	118.36	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	599	FAD	N3-C2-N1	-2.66	113.86	119.50
4	B	599	FAD	C5X-N5-C4X	-2.65	113.80	118.09
5	B	2704	TRS	O2-C2-C	2.62	118.17	110.88
7	D	699	HEM	CBC-CAC-C3C	-2.55	114.81	127.53
5	B	2704	TRS	O1-C1-C	2.54	117.94	110.88
4	A	599	FAD	O4B-C1B-N9A	2.53	112.95	108.09
5	A	1704	TRS	O2-C2-C	2.49	117.81	110.88
5	A	2705	TRS	O3-C3-C	2.48	117.80	110.88
4	A	599	FAD	C4-C4X-N5	-2.47	114.79	118.21
4	B	599	FAD	C10-N1-C2	2.47	122.19	116.85
4	A	599	FAD	C5'-C4'-C3'	-2.46	107.58	112.22
5	B	1705	TRS	O3-C3-C	2.45	117.72	110.88
5	A	1704	TRS	O3-C3-C	2.45	117.69	110.88
4	A	599	FAD	C10-N1-C2	2.44	122.13	116.85
5	B	1705	TRS	O1-C1-C	2.40	117.57	110.88
5	A	1704	TRS	O1-C1-C	2.36	117.45	110.88
7	C	699	HEM	CBC-CAC-C3C	-2.33	115.86	127.53
5	B	1705	TRS	O2-C2-C	2.33	117.37	110.88
5	B	2704	TRS	O3-C3-C	2.31	117.32	110.88
4	B	599	FAD	O2'-C2'-C3'	2.17	114.33	109.25
4	B	599	FAD	C5'-C4'-C3'	-2.13	108.20	112.22
4	B	599	FAD	C4-C4X-N5	-2.09	115.31	118.21
4	A	599	FAD	C10-C4X-N5	2.03	128.95	124.81

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	2705	TRS	C1-C-C2-O2
5	A	2705	TRS	N-C-C2-O2
7	C	699	HEM	C2B-C3B-CAB-CBB
7	C	699	HEM	C2C-C3C-CAC-CBC
7	D	699	HEM	C2B-C3B-CAB-CBB
7	D	699	HEM	C2C-C3C-CAC-CBC
4	A	599	FAD	O4'-C4'-C5'-O5'
4	B	599	FAD	O4'-C4'-C5'-O5'
5	A	2705	TRS	C3-C-C2-O2
7	C	699	HEM	C4B-C3B-CAB-CBB
7	D	699	HEM	C4B-C3B-CAB-CBB
5	A	2705	TRS	C2-C-C1-O1
5	A	2705	TRS	C3-C-C1-O1
5	A	2705	TRS	N-C-C3-O3

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Mol	Chain	Res	Type	Atoms
5	B	1705	TRS	N-C-C2-O2
5	B	2704	TRS	C2-C-C1-O1
5	B	2704	TRS	C3-C-C1-O1
5	B	2704	TRS	N-C-C2-O2
5	B	2704	TRS	C1-C-C3-O3
5	B	2704	TRS	N-C-C3-O3
7	C	699	HEM	C4C-C3C-CAC-CBC
7	D	699	HEM	C4C-C3C-CAC-CBC
4	B	599	FAD	C4'-C5'-O5'-P
5	A	2705	TRS	C1-C-C3-O3
5	A	2705	TRS	C2-C-C3-O3
5	B	1705	TRS	C3-C-C2-O2
5	B	2704	TRS	C2-C-C3-O3
4	A	599	FAD	C4'-C5'-O5'-P
5	A	2705	TRS	N-C-C1-O1
5	B	1705	TRS	C1-C-C2-O2
5	B	2704	TRS	N-C-C1-O1
4	B	599	FAD	O3'-C3'-C4'-O4'
5	B	2704	TRS	C1-C-C2-O2
7	D	699	HEM	CAD-CBD-CGD-O2D
4	A	599	FAD	C3'-C4'-C5'-O5'
4	B	599	FAD	C3'-C4'-C5'-O5'
7	D	699	HEM	CAD-CBD-CGD-O1D

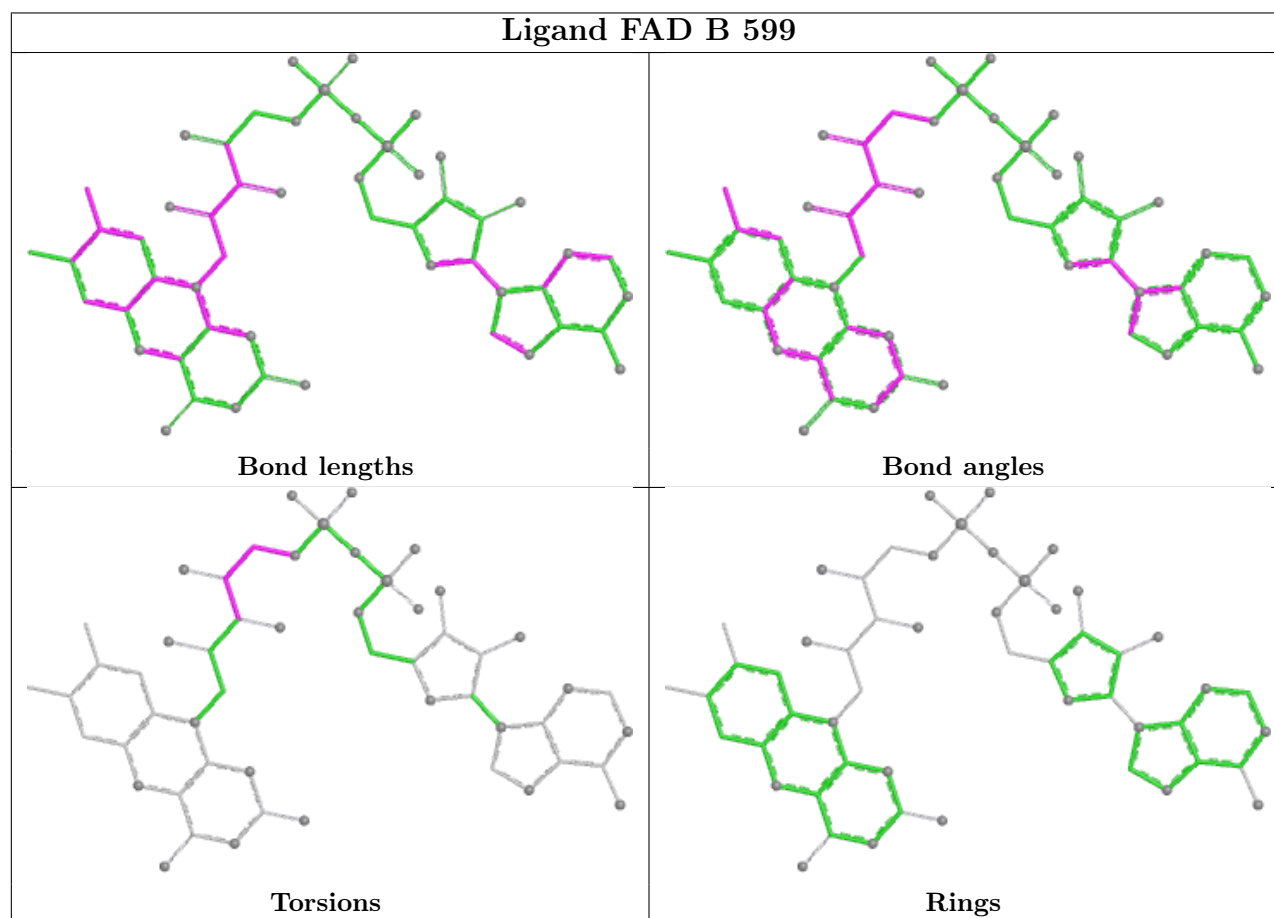
There are no ring outliers.

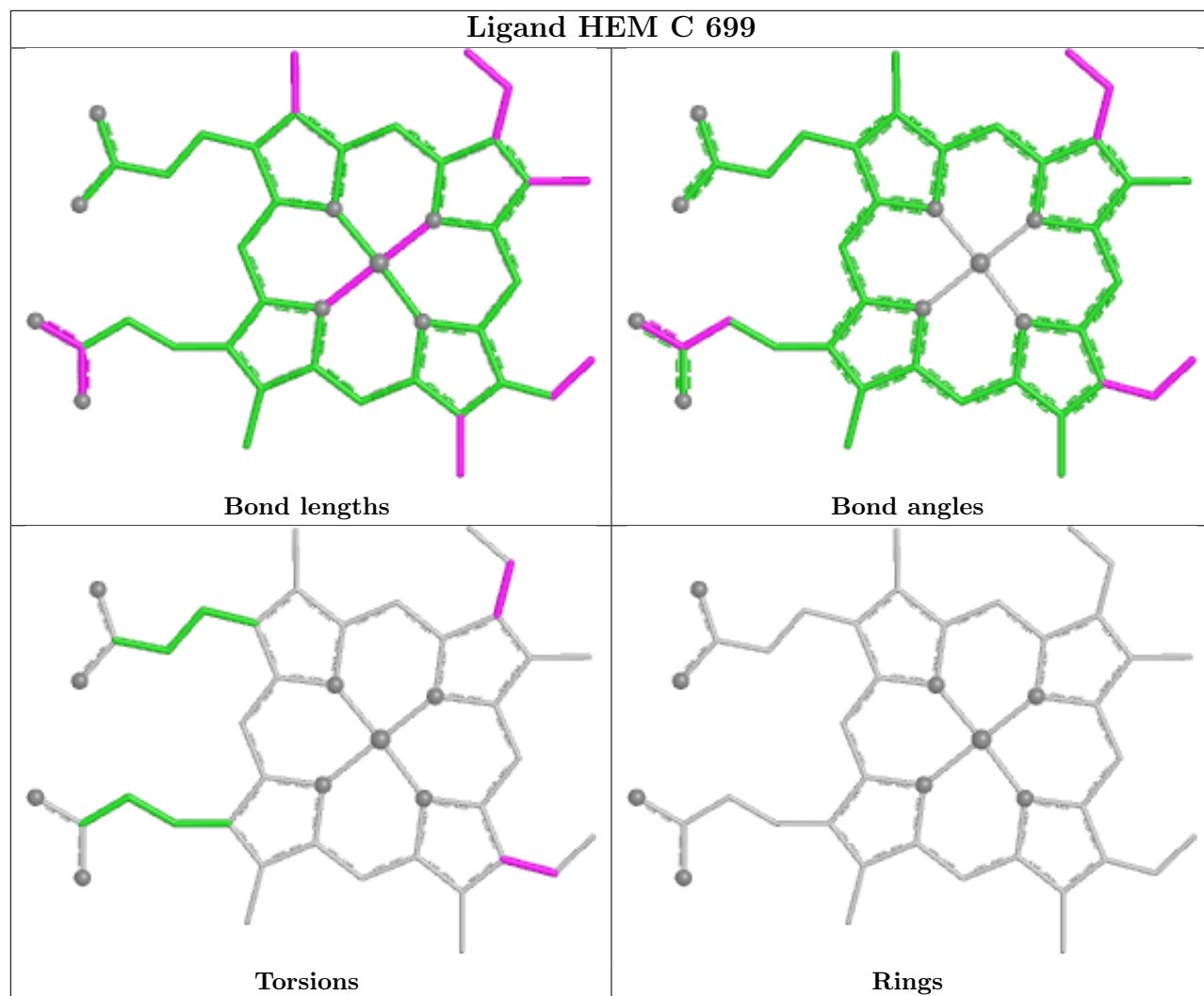
7 monomers are involved in 9 short contacts:

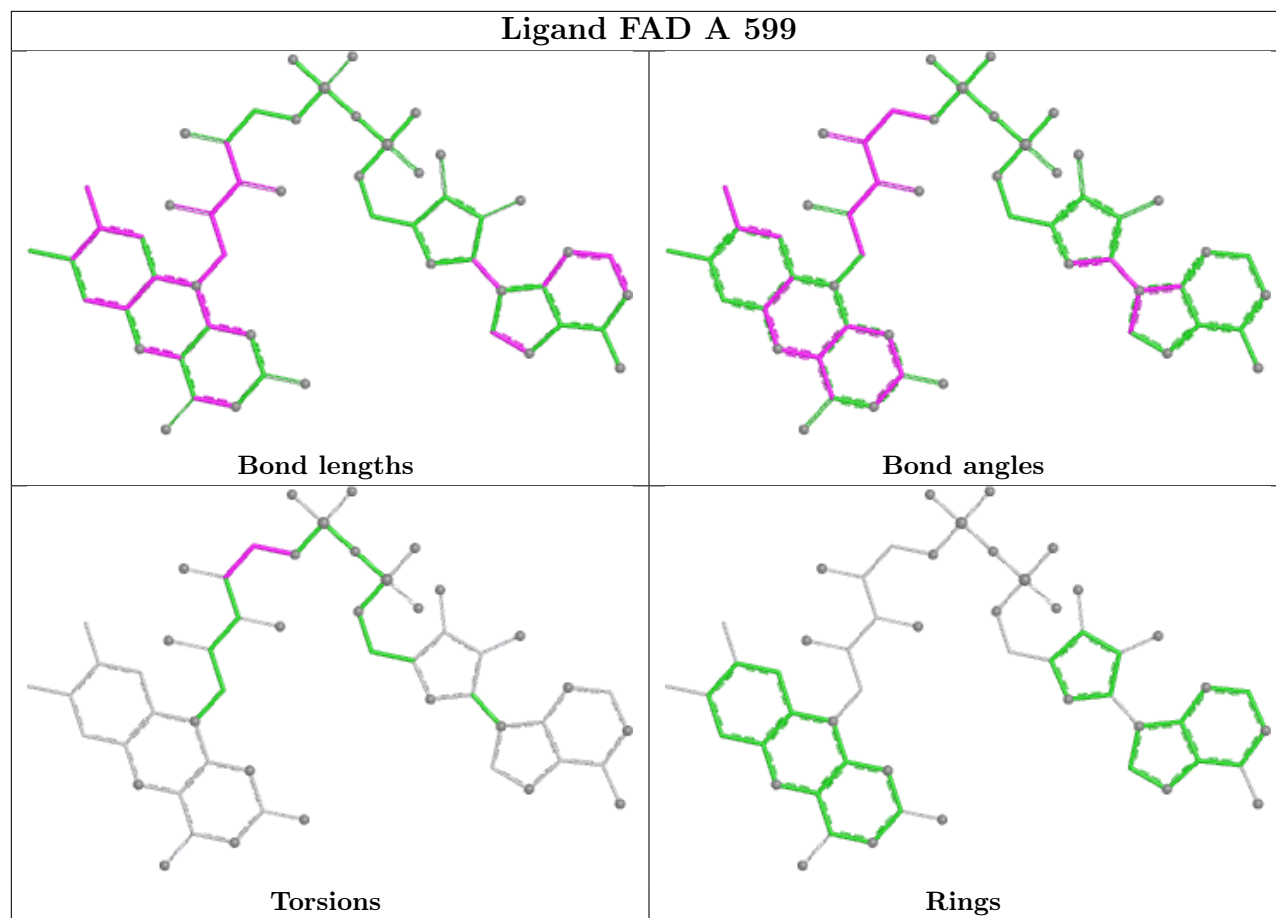
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	599	FAD	2	0
7	C	699	HEM	1	0
4	A	599	FAD	1	0
7	D	699	HEM	2	0
6	B	1702	ACY	1	0
6	A	1701	ACY	1	0
6	A	2701	ACY	1	0

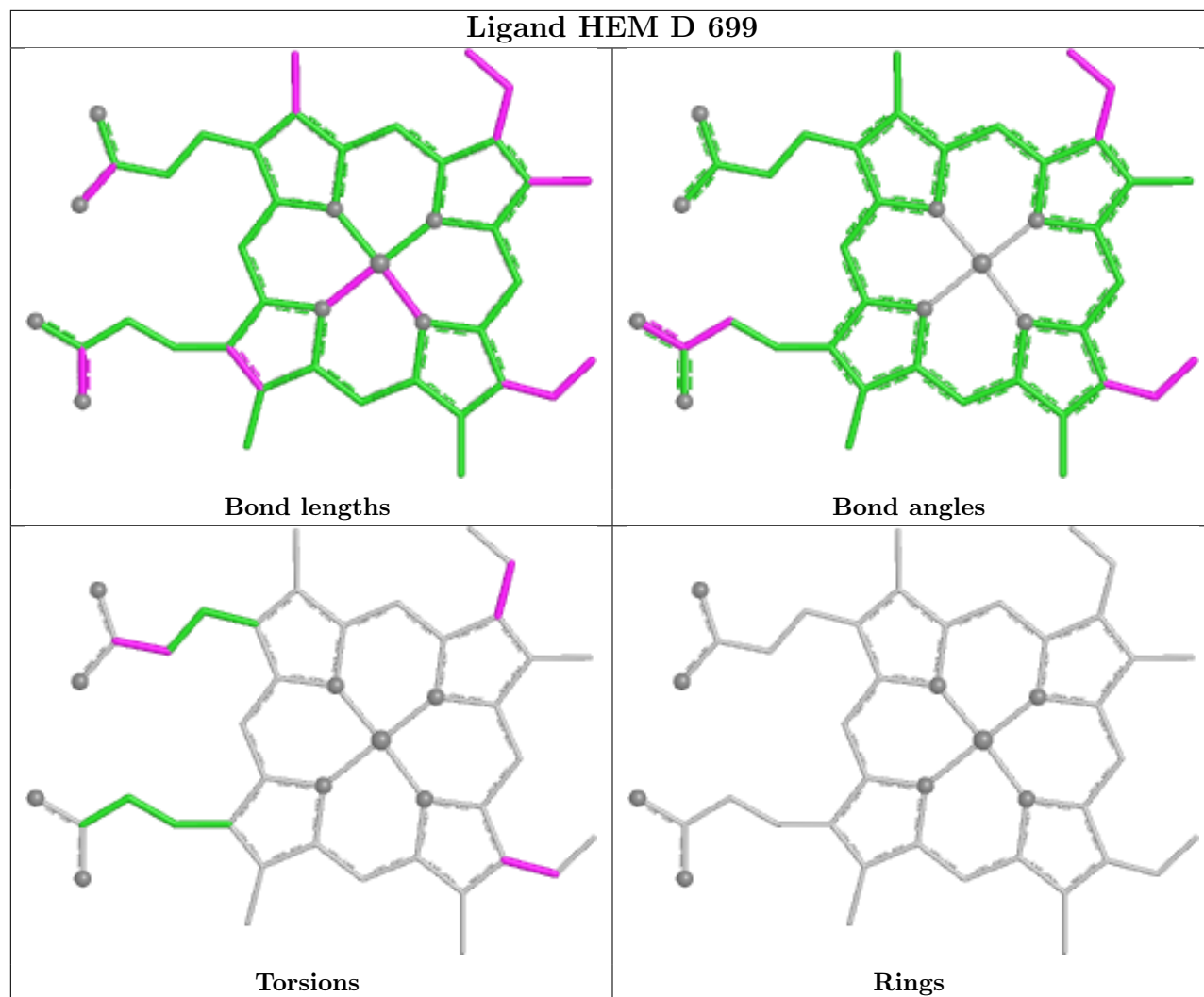
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 [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	515/520 (99%)	-0.47	4 (0%) 82 86	6, 19, 39, 52	7 (1%)
1	B	515/520 (99%)	-0.45	6 (1%) 76 80	7, 19, 39, 53	11 (2%)
2	C	75/80 (93%)	-0.39	1 (1%) 75 79	14, 21, 32, 50	0
2	D	75/80 (93%)	-0.31	1 (1%) 75 79	16, 22, 32, 50	0
All	All	1180/1200 (98%)	-0.44	12 (1%) 79 83	6, 19, 39, 53	18 (1%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	7	ALA	3.3
1	A	359	ALA	2.7
1	B	310	LYS	2.7
2	D	676	PRO	2.6
1	B	361	ASP	2.4
1	B	360	GLY	2.3
2	C	676	PRO	2.2
1	B	7	ALA	2.2
1	B	256	ALA	2.1
1	A	297	TYR	2.1
1	A	310	LYS	2.1
1	B	299	THR	2.0

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

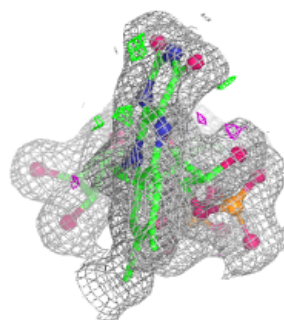
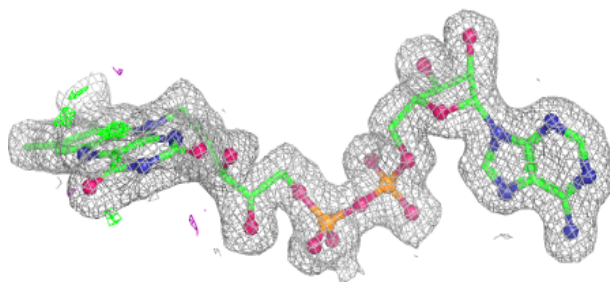
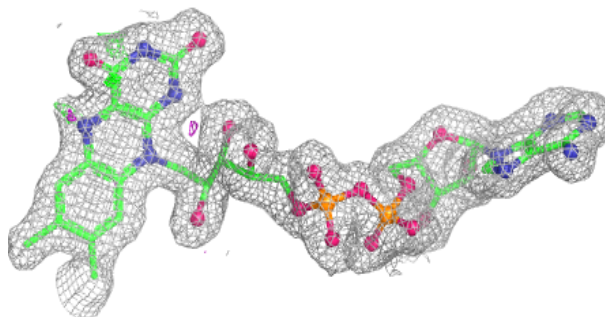
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
6	ACY	A	2701	4/4	0.72	0.20	47,47,48,48	0
6	ACY	A	2702	4/4	0.76	0.15	50,51,51,52	0
6	ACY	A	1701	4/4	0.83	0.13	28,28,30,34	0
5	TRS	A	2705	8/8	0.85	0.11	29,34,36,38	0
6	ACY	B	1702	4/4	0.89	0.10	31,31,33,33	0
5	TRS	B	1705	8/8	0.91	0.09	25,33,35,36	0
5	TRS	A	1704	8/8	0.93	0.07	30,31,31,31	0
5	TRS	B	2704	8/8	0.93	0.08	18,30,35,35	0
4	FAD	A	599	53/53	0.98	0.04	8,14,20,26	0
4	FAD	B	599	53/53	0.98	0.04	11,14,21,27	0
7	HEM	C	699	43/43	0.98	0.05	11,15,23,27	0
7	HEM	D	699	43/43	0.98	0.05	13,16,22,26	0
3	CL	B	1703	1/1	0.99	0.03	15,15,15,15	0
3	CL	A	2703	1/1	1.00	0.01	17,17,17,17	0

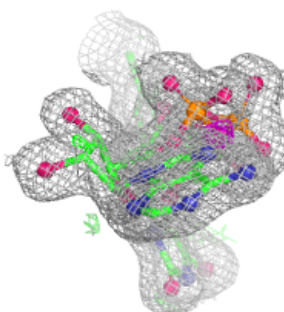
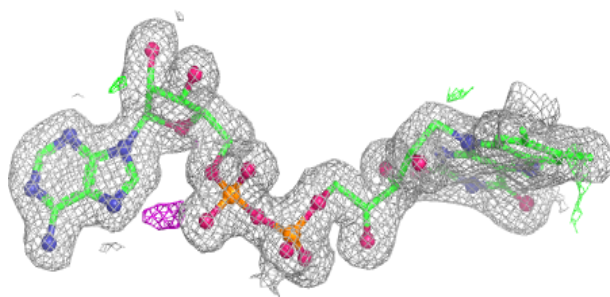
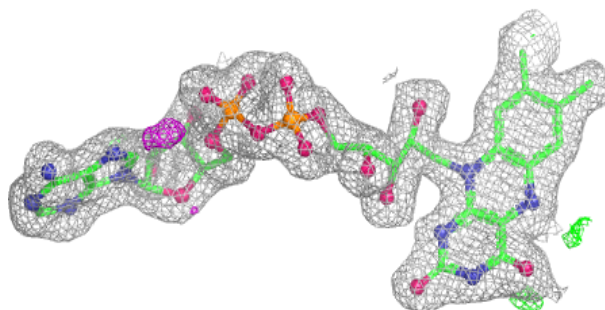
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD A 599:

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

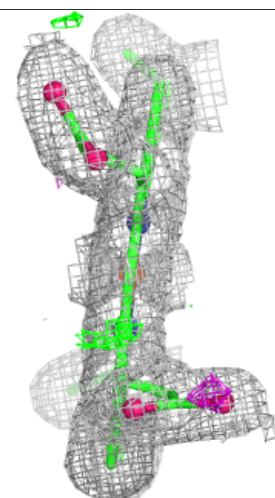
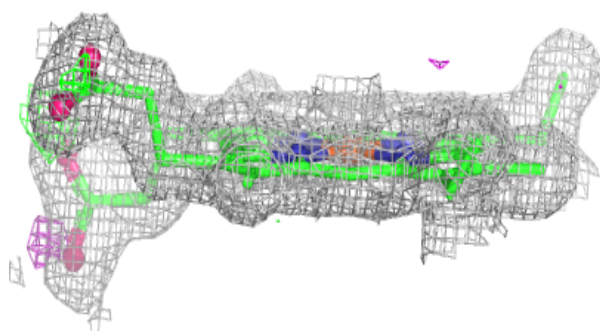
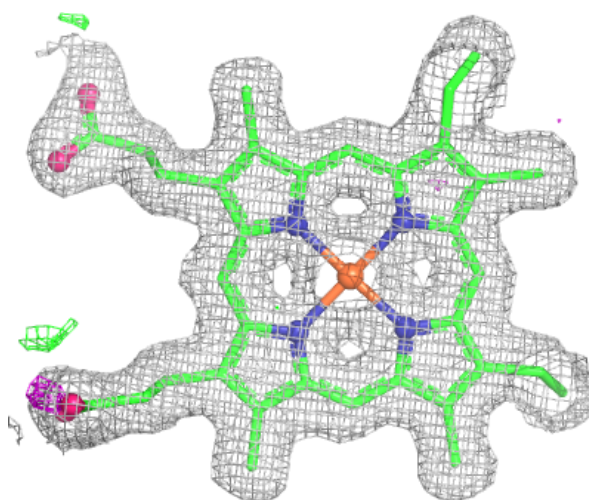
**Electron density around FAD B 599:**

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



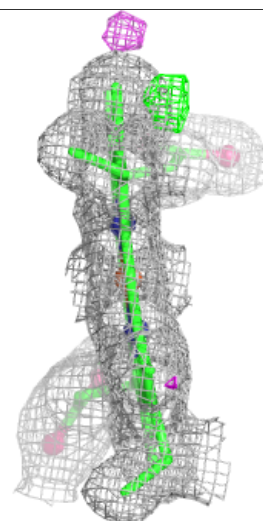
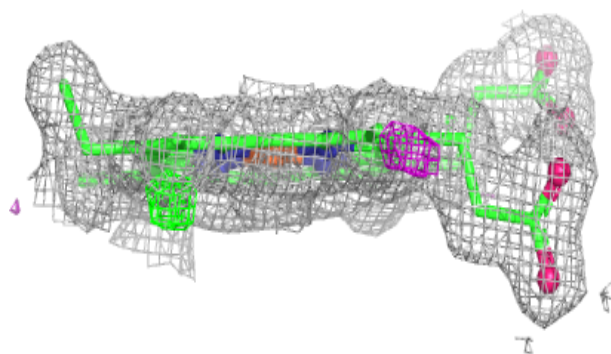
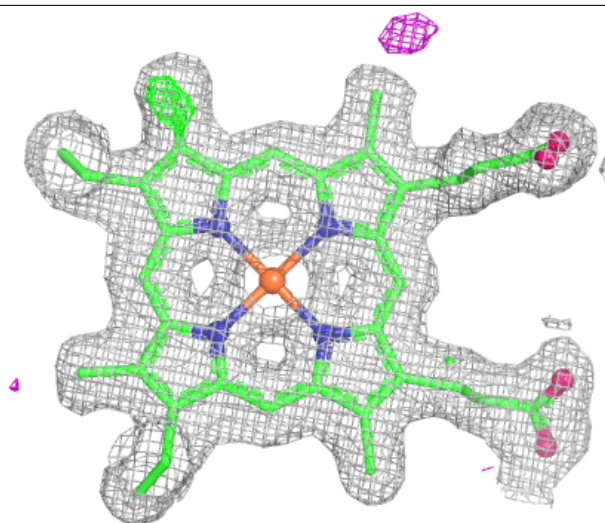
Electron density around HEM C 699:

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



Electron density around HEM D 699:

$2mF_o-DF_c$ (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.