



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 06:57 am BST

PDB ID : 3A4Z
Title : Structure of cytochrome P450 Vdh mutant (Vdh-K1) obtained by directed evolution
Authors : Yasutake, Y.; Fujii, Y.; Cheon, W.K.; Arisawa, A.; Tamura, T.
Deposited on : 2009-07-24
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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) : 1.13
EDS : 2.11
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) : 2.11

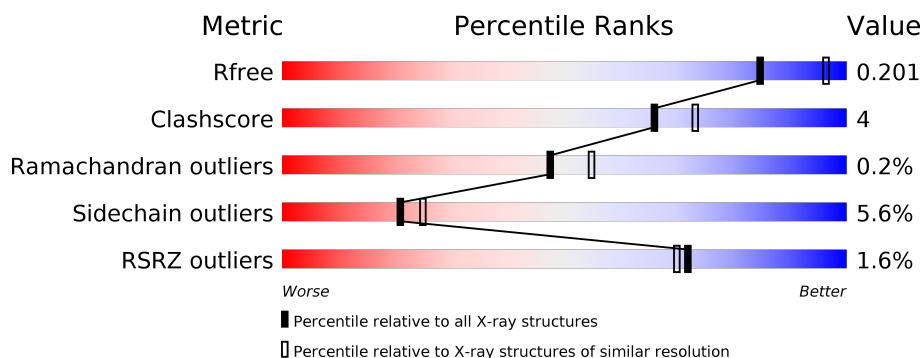
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 on 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	411	<div> <div>91%</div> <div>6% ..</div> </div>
1	B	411	<div> <div>2%</div> <div>86%</div> <div>9% ..</div> </div>
1	C	411	<div> <div>4%</div> <div>83%</div> <div>13% ..</div> </div>
1	D	411	<div> <div>%</div> <div>83%</div> <div>12% ..</div> </div>
1	E	411	<div> <div>%</div> <div>87%</div> <div>9% ..</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16621 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 Vitamin D hydroxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	402	Total	C	N	O	S	0	0	0
			3113	1958	549	589	17			
1	B	402	Total	C	N	O	S	0	0	0
			3113	1958	549	589	17			
1	C	401	Total	C	N	O	S	0	0	0
			3108	1955	548	588	17			
1	D	401	Total	C	N	O	S	0	0	0
			3108	1955	548	588	17			
1	E	401	Total	C	N	O	S	0	0	0
			3108	1955	548	588	17			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	70	ARG	THR	ENGINEERED MUTATION	UNP C4B644
A	156	LEU	VAL	ENGINEERED MUTATION	UNP C4B644
A	216	MET	GLU	ENGINEERED MUTATION	UNP C4B644
A	384	ARG	GLU	ENGINEERED MUTATION	UNP C4B644
A	404	LEU	-	EXPRESSION TAG	UNP C4B644
A	405	GLU	-	EXPRESSION TAG	UNP C4B644
A	406	HIS	-	EXPRESSION TAG	UNP C4B644
A	407	HIS	-	EXPRESSION TAG	UNP C4B644
A	408	HIS	-	EXPRESSION TAG	UNP C4B644
A	409	HIS	-	EXPRESSION TAG	UNP C4B644
A	410	HIS	-	EXPRESSION TAG	UNP C4B644
A	411	HIS	-	EXPRESSION TAG	UNP C4B644
B	70	ARG	THR	ENGINEERED MUTATION	UNP C4B644
B	156	LEU	VAL	ENGINEERED MUTATION	UNP C4B644
B	216	MET	GLU	ENGINEERED MUTATION	UNP C4B644
B	384	ARG	GLU	ENGINEERED MUTATION	UNP C4B644
B	404	LEU	-	EXPRESSION TAG	UNP C4B644
B	405	GLU	-	EXPRESSION TAG	UNP C4B644
B	406	HIS	-	EXPRESSION TAG	UNP C4B644

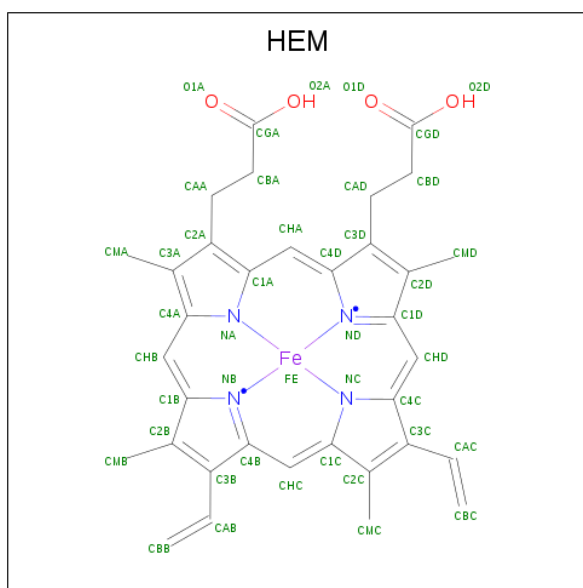
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Chain	Residue	Modelled	Actual	Comment	Reference
B	407	HIS	-	EXPRESSION TAG	UNP C4B644
B	408	HIS	-	EXPRESSION TAG	UNP C4B644
B	409	HIS	-	EXPRESSION TAG	UNP C4B644
B	410	HIS	-	EXPRESSION TAG	UNP C4B644
B	411	HIS	-	EXPRESSION TAG	UNP C4B644
C	70	ARG	THR	ENGINEERED MUTATION	UNP C4B644
C	156	LEU	VAL	ENGINEERED MUTATION	UNP C4B644
C	216	MET	GLU	ENGINEERED MUTATION	UNP C4B644
C	384	ARG	GLU	ENGINEERED MUTATION	UNP C4B644
C	404	LEU	-	EXPRESSION TAG	UNP C4B644
C	405	GLU	-	EXPRESSION TAG	UNP C4B644
C	406	HIS	-	EXPRESSION TAG	UNP C4B644
C	407	HIS	-	EXPRESSION TAG	UNP C4B644
C	408	HIS	-	EXPRESSION TAG	UNP C4B644
C	409	HIS	-	EXPRESSION TAG	UNP C4B644
C	410	HIS	-	EXPRESSION TAG	UNP C4B644
C	411	HIS	-	EXPRESSION TAG	UNP C4B644
D	70	ARG	THR	ENGINEERED MUTATION	UNP C4B644
D	156	LEU	VAL	ENGINEERED MUTATION	UNP C4B644
D	216	MET	GLU	ENGINEERED MUTATION	UNP C4B644
D	384	ARG	GLU	ENGINEERED MUTATION	UNP C4B644
D	404	LEU	-	EXPRESSION TAG	UNP C4B644
D	405	GLU	-	EXPRESSION TAG	UNP C4B644
D	406	HIS	-	EXPRESSION TAG	UNP C4B644
D	407	HIS	-	EXPRESSION TAG	UNP C4B644
D	408	HIS	-	EXPRESSION TAG	UNP C4B644
D	409	HIS	-	EXPRESSION TAG	UNP C4B644
D	410	HIS	-	EXPRESSION TAG	UNP C4B644
D	411	HIS	-	EXPRESSION TAG	UNP C4B644
E	70	ARG	THR	ENGINEERED MUTATION	UNP C4B644
E	156	LEU	VAL	ENGINEERED MUTATION	UNP C4B644
E	216	MET	GLU	ENGINEERED MUTATION	UNP C4B644
E	384	ARG	GLU	ENGINEERED MUTATION	UNP C4B644
E	404	LEU	-	EXPRESSION TAG	UNP C4B644
E	405	GLU	-	EXPRESSION TAG	UNP C4B644
E	406	HIS	-	EXPRESSION TAG	UNP C4B644
E	407	HIS	-	EXPRESSION TAG	UNP C4B644
E	408	HIS	-	EXPRESSION TAG	UNP C4B644
E	409	HIS	-	EXPRESSION TAG	UNP C4B644
E	410	HIS	-	EXPRESSION TAG	UNP C4B644
E	411	HIS	-	EXPRESSION TAG	UNP C4B644

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

mula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Ca		
			3	3	0	0
3	D	1	Total	Ca		
			1	1	0	0
3	C	1	Total	Ca		
			1	1	0	0
3	E	1	Total	Ca		
			1	1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



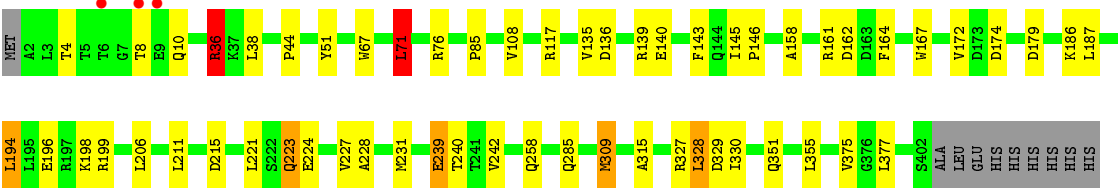
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is water.

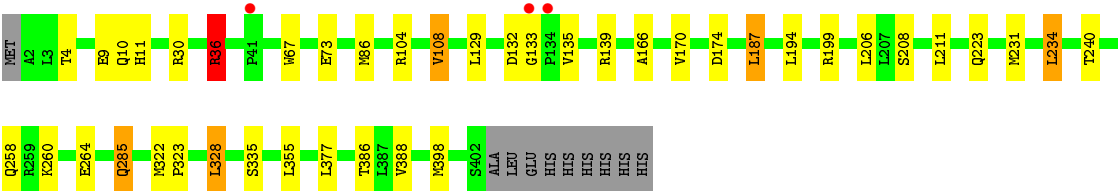
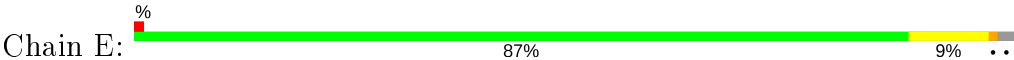
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	257	Total	O	0	0
			257	257		
6	B	127	Total	O	0	0
			127	127		
6	C	128	Total	O	0	0
			128	128		
6	D	148	Total	O	0	0
			148	148		
6	E	154	Total	O	0	0
			154	154		

- Molecule 1: Vitamin D hydroxylase





• Molecule 1: Vitamin D hydroxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	77.38Å 172.47Å 189.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.27 – 2.20 49.24 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.27-2.20) 99.9 (49.24-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.201 , 0.244 0.202 , 0.201	Depositor DCC
R_{free} test set	6458 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16621	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CA, ACT, 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	0.76	0/3179	0.82	3/4325 (0.1%)
1	B	0.66	0/3179	0.74	5/4325 (0.1%)
1	C	0.69	0/3174	0.79	2/4318 (0.0%)
1	D	0.68	0/3174	0.77	3/4318 (0.1%)
1	E	0.71	0/3174	0.80	6/4318 (0.1%)
All	All	0.70	0/15880	0.78	19/21604 (0.1%)

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	36	ARG	NE-CZ-NH2	-12.37	114.12	120.30
1	C	97	ARG	NE-CZ-NH2	-12.35	114.12	120.30
1	A	36	ARG	NE-CZ-NH1	10.81	125.70	120.30
1	C	97	ARG	NE-CZ-NH1	10.09	125.35	120.30
1	E	234	LEU	CA-CB-CG	7.96	133.61	115.30

There are no chirality outliers.

There are no planarity outliers.

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	3113	0	3095	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3113	0	3095	24	0
1	C	3108	0	3090	33	0
1	D	3108	0	3090	32	0
1	E	3108	0	3090	20	0
2	A	43	0	30	0	0
2	B	43	0	30	0	0
2	C	43	0	30	8	0
2	D	43	0	30	1	0
2	E	43	0	30	1	0
3	A	3	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
4	A	4	0	3	0	0
4	C	8	0	6	0	0
4	D	4	0	3	0	0
4	E	8	0	6	0	0
5	A	12	0	15	0	0
6	A	257	0	0	2	0
6	B	127	0	0	2	0
6	C	128	0	0	2	0
6	D	148	0	0	1	0
6	E	154	0	0	3	0
All	All	16621	0	15643	126	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.

The worst 5 of 126 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:187:LEU:HD13	1:A:231:MET:HG3	1.44	0.98
1:C:363:ARG:HH21	1:C:363:ARG:HG3	1.34	0.92
1:C:258:GLN:HG3	1:C:328:LEU:HD13	1.53	0.90
1:C:150:ILE:HG12	1:C:237:GLY:HA3	1.60	0.84
1:C:329:ASP:OD1	1:C:331:THR:HG22	1.77	0.84

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	400/411 (97%)	385 (96%)	14 (4%)	1 (0%)	41	46
1	B	400/411 (97%)	385 (96%)	15 (4%)	0	100	100
1	C	399/411 (97%)	383 (96%)	15 (4%)	1 (0%)	41	46
1	D	399/411 (97%)	381 (96%)	17 (4%)	1 (0%)	41	46
1	E	399/411 (97%)	383 (96%)	16 (4%)	0	100	100
All	All	1997/2055 (97%)	1917 (96%)	77 (4%)	3 (0%)	47	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	174	ASP
1	C	377	LEU
1	D	174	ASP

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	334/343 (97%)	322 (96%)	12 (4%)	35	45
1	B	334/343 (97%)	315 (94%)	19 (6%)	20	24
1	C	334/343 (97%)	307 (92%)	27 (8%)	11	12
1	D	334/343 (97%)	315 (94%)	19 (6%)	20	24
1	E	334/343 (97%)	317 (95%)	17 (5%)	24	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1670/1715 (97%)	1576 (94%)	94 (6%)	21	25

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	135	VAL
1	C	333	ASP
1	E	208	SER
1	C	169	SER
1	C	211	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	238	HIS
1	C	285	GLN
1	D	285	GLN
1	C	223	GLN
1	E	10	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 6 are monoatomic - leaving 13 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	ACT	A	4006	-	1,3,3	2.63	1 (100%)	0,3,3	0.00	-
2	HEM	E	412	1	27,50,50	2.24	9 (33%)	17,82,82	1.92	5 (29%)
5	GOL	A	3001	-	5,5,5	0.57	0	5,5,5	0.27	0
2	HEM	A	412	1	27,50,50	2.21	11 (40%)	17,82,82	1.67	4 (23%)
4	ACT	E	4008	-	1,3,3	1.42	0	0,3,3	0.00	-
4	ACT	E	4005	3	1,3,3	2.06	1 (100%)	0,3,3	0.00	-
2	HEM	D	412	1	27,50,50	2.19	9 (33%)	17,82,82	1.60	5 (29%)
4	ACT	C	4004	3	1,3,3	1.74	0	0,3,3	0.00	-
5	GOL	A	3002	3	5,5,5	0.32	0	5,5,5	1.72	1 (20%)
2	HEM	B	412	1	27,50,50	2.08	7 (25%)	17,82,82	1.88	6 (35%)
4	ACT	D	4001	-	1,3,3	2.89	1 (100%)	0,3,3	0.00	-
4	ACT	C	4007	-	1,3,3	2.58	1 (100%)	0,3,3	0.00	-
2	HEM	C	412	1	27,50,50	2.15	8 (29%)	17,82,82	1.81	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	E	412	1	-	0/6/54/54	-
2	HEM	A	412	1	-	0/6/54/54	-
2	HEM	D	412	1	-	0/6/54/54	-
5	GOL	A	3001	-	-	0/4/4/4	-
5	GOL	A	3002	3	-	2/4/4/4	-
2	HEM	B	412	1	-	0/6/54/54	-
2	HEM	C	412	1	-	0/6/54/54	-

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	412	HEM	C3C-C2C	-5.46	1.32	1.40
2	B	412	HEM	C3D-C2D	5.45	1.53	1.37
2	D	412	HEM	C3D-C2D	5.43	1.53	1.37
2	A	412	HEM	C3D-C2D	5.34	1.53	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	412	HEM	C3D-C2D	5.08	1.52	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	412	HEM	CBD-CAD-C3D	-4.52	104.15	112.48
2	C	412	HEM	CMA-C3A-C4A	-3.56	123.00	128.46
2	B	412	HEM	CBD-CAD-C3D	-3.51	106.01	112.48
2	D	412	HEM	C4C-C3C-C2C	3.45	109.31	106.90
2	E	412	HEM	C4C-C3C-C2C	3.28	109.19	106.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

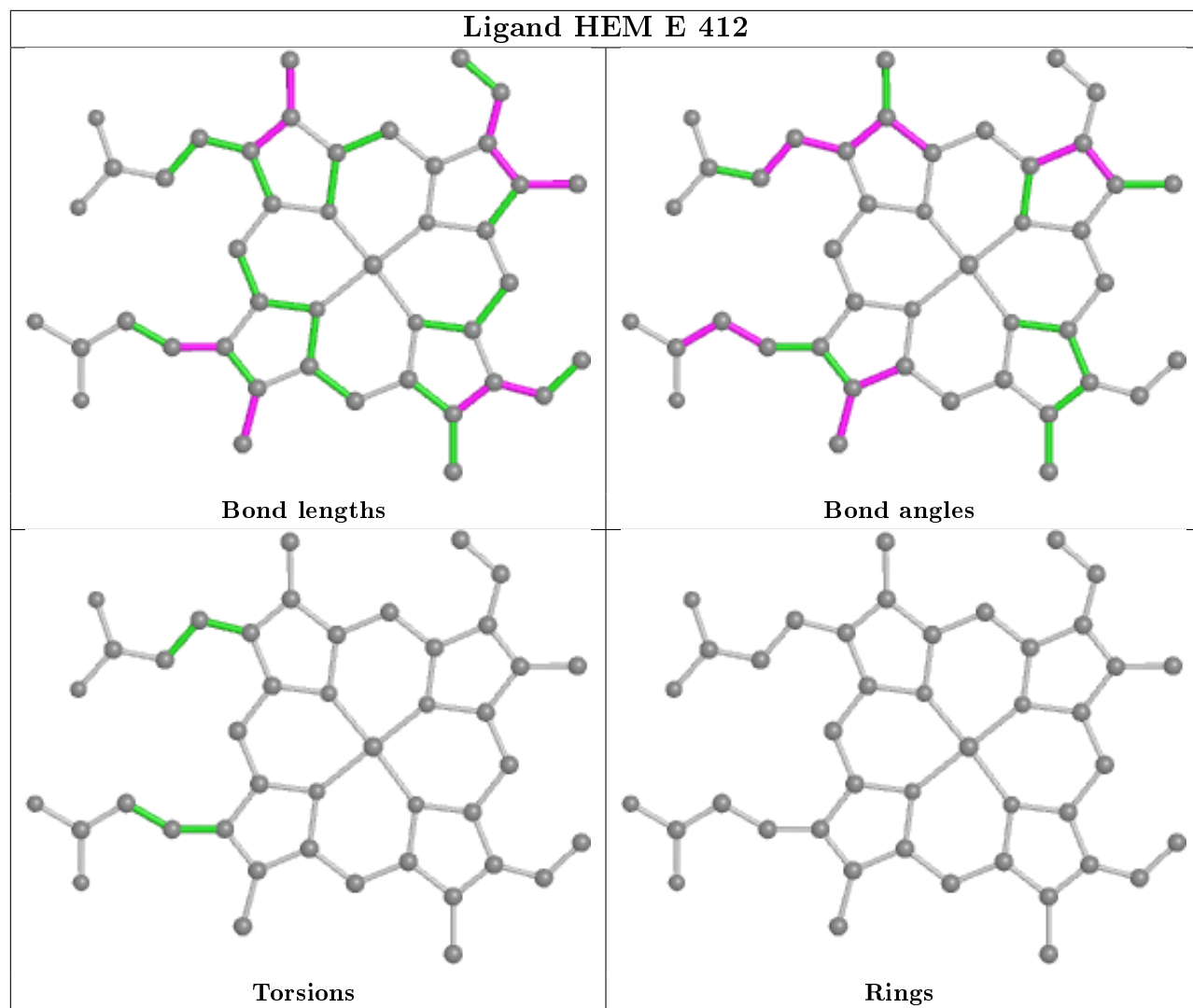
Mol	Chain	Res	Type	Atoms
5	A	3002	GOL	O1-C1-C2-C3
5	A	3002	GOL	O2-C2-C3-O3

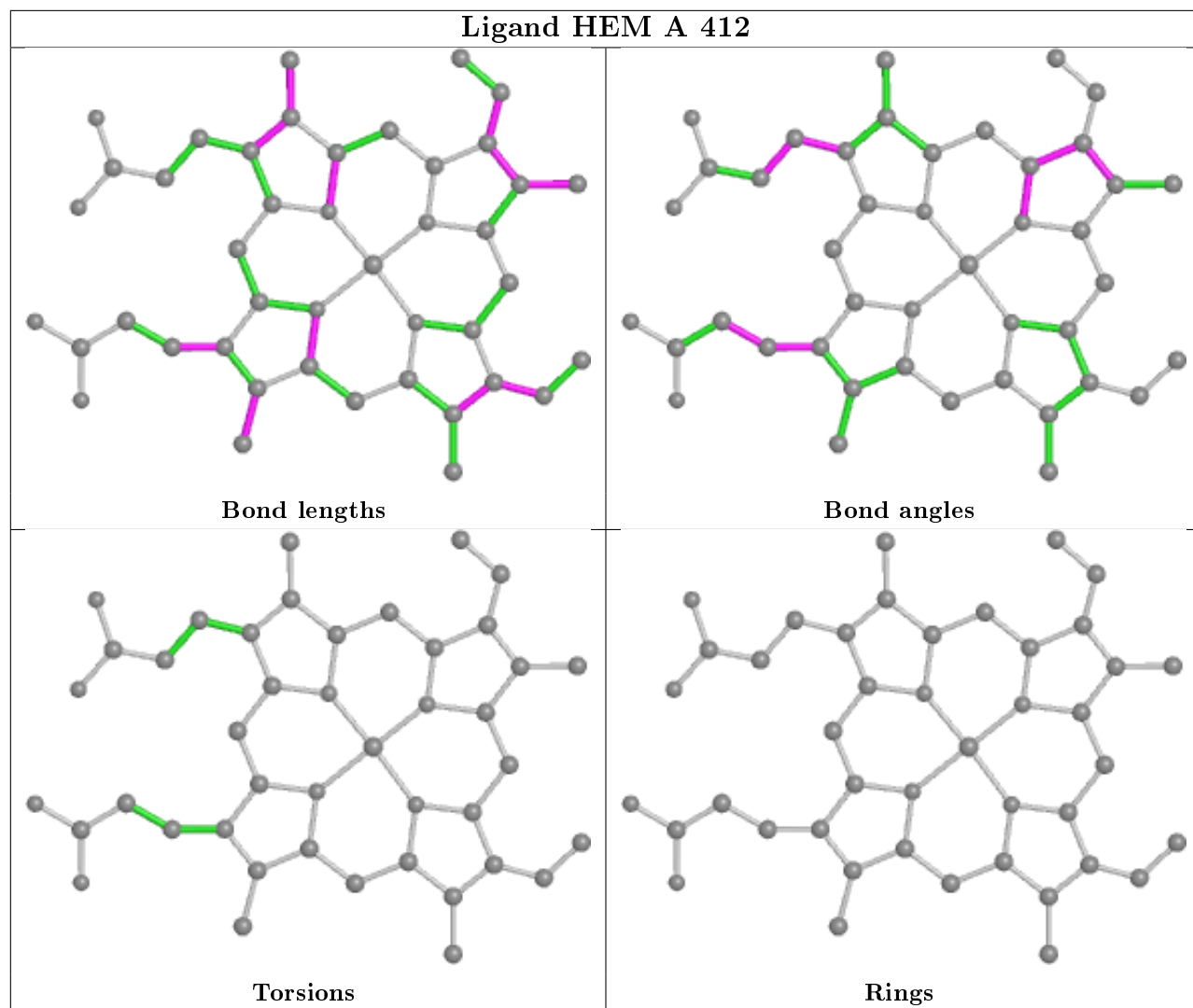
There are no ring outliers.

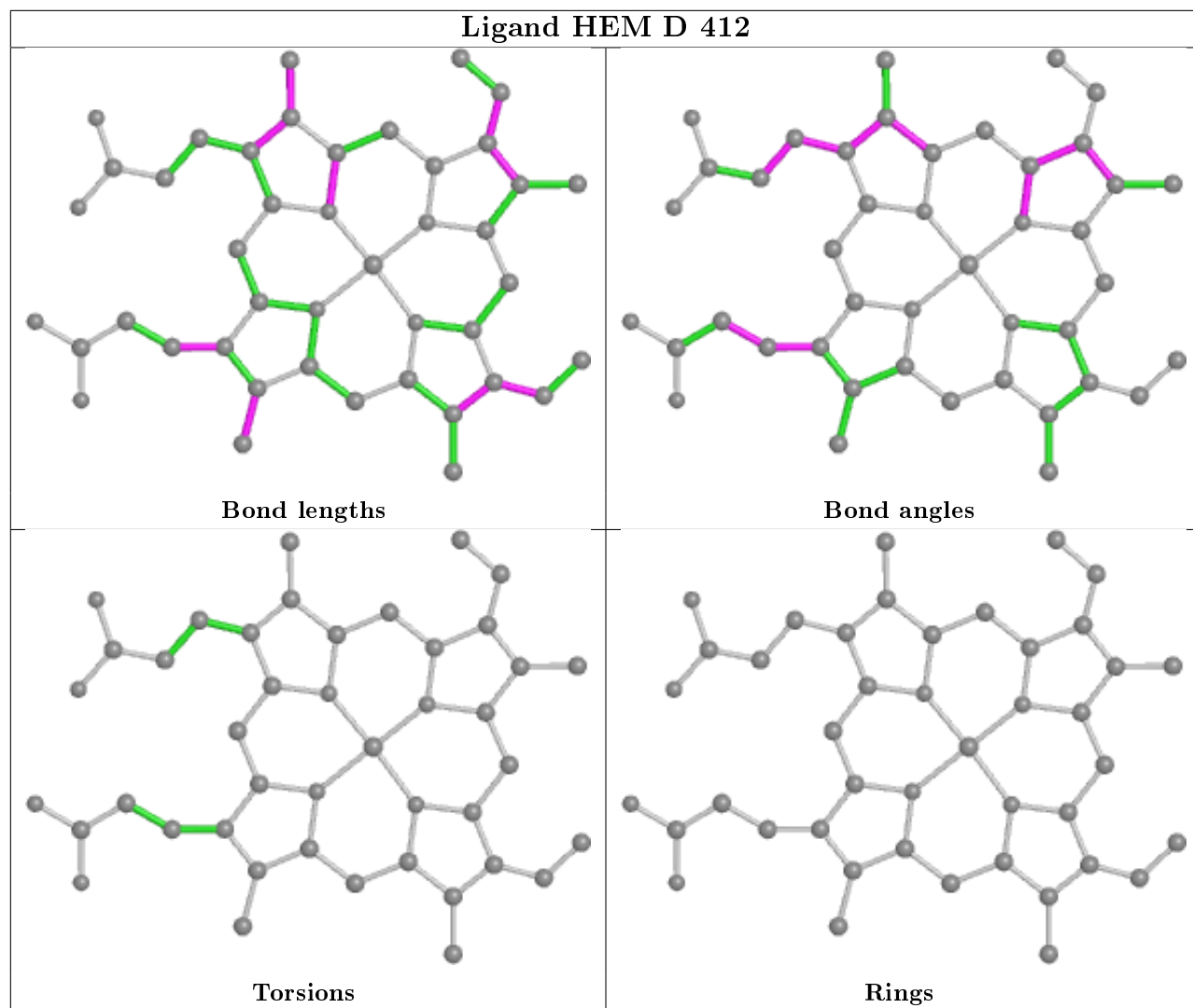
3 monomers are involved in 10 short contacts:

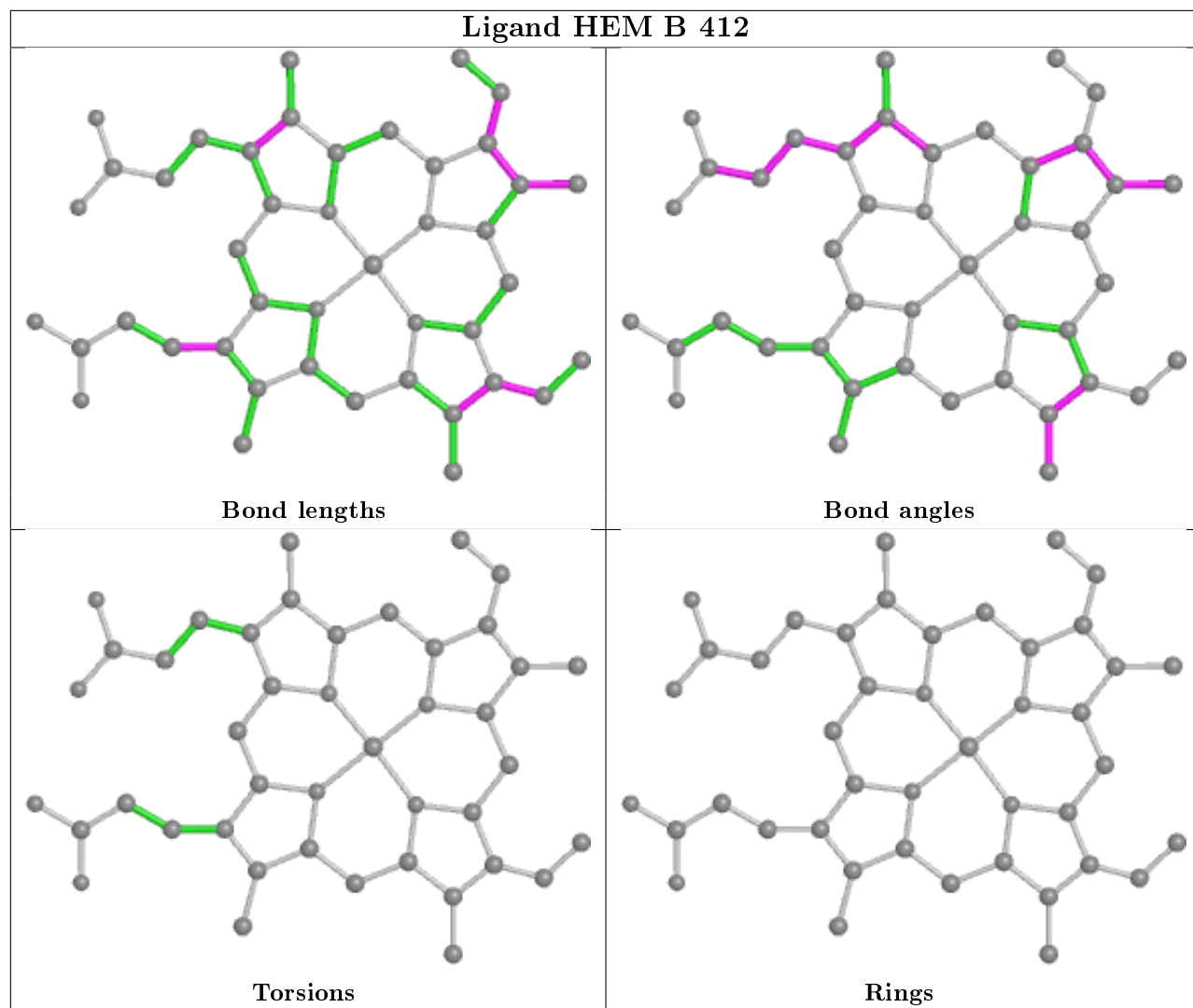
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	412	HEM	1	0
2	D	412	HEM	1	0
2	C	412	HEM	8	0

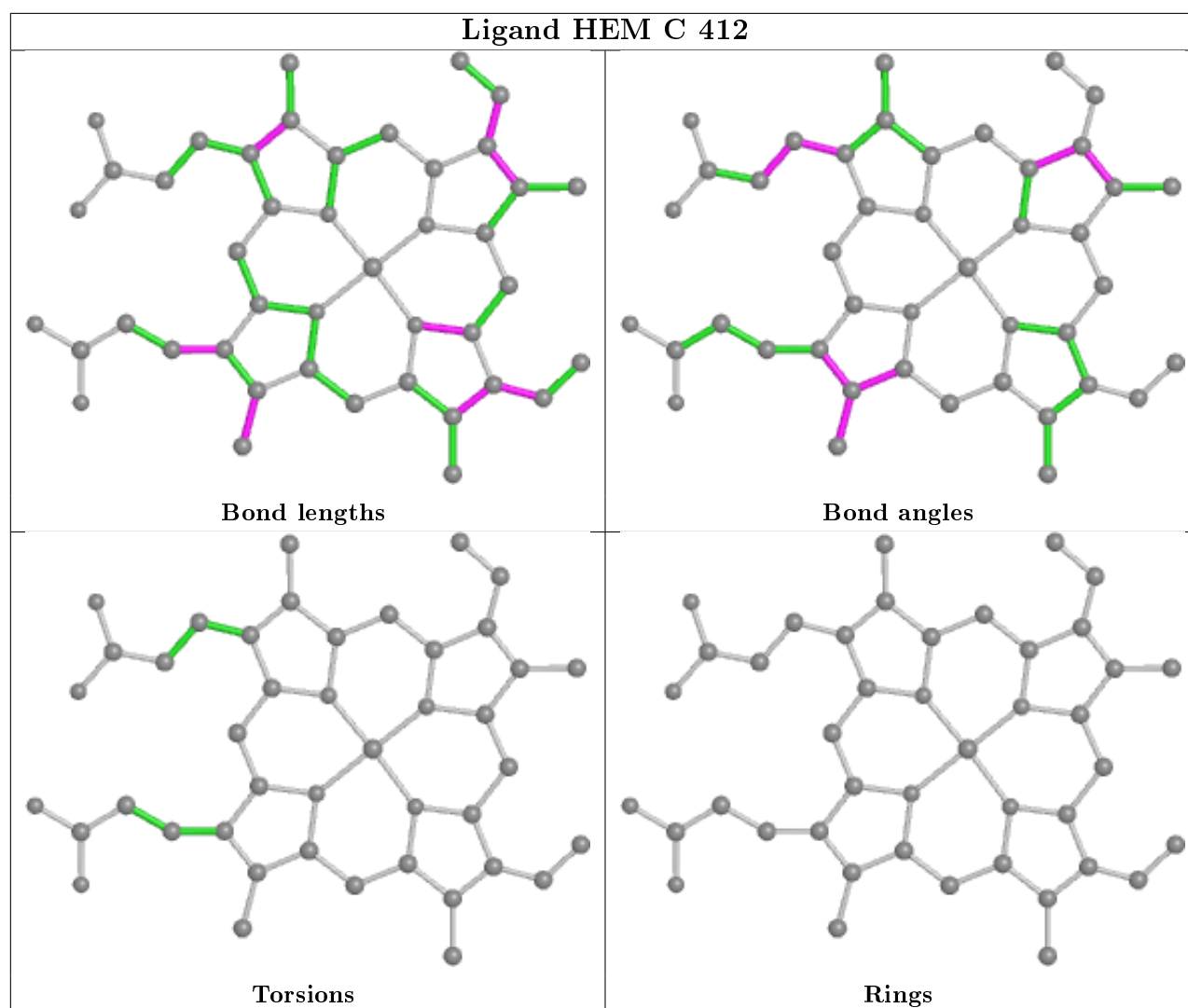
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 ⓘ

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	402/411 (97%)	-0.19	1 (0%) 95 94	15, 26, 42, 53	0
1	B	402/411 (97%)	-0.06	10 (2%) 57 55	23, 36, 62, 75	0
1	C	401/411 (97%)	-0.17	15 (3%) 41 39	20, 35, 58, 69	0
1	D	401/411 (97%)	-0.28	3 (0%) 87 86	17, 35, 55, 64	0
1	E	401/411 (97%)	-0.36	3 (0%) 87 86	22, 32, 47, 59	0
All	All	2007/2055 (97%)	-0.21	32 (1%) 72 70	15, 33, 55, 75	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	399	GLY	4.7
1	D	8	THR	4.5
1	C	134	PRO	4.2
1	C	6	THR	3.9
1	A	403	ALA	3.6

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates 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,

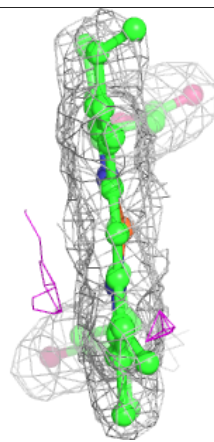
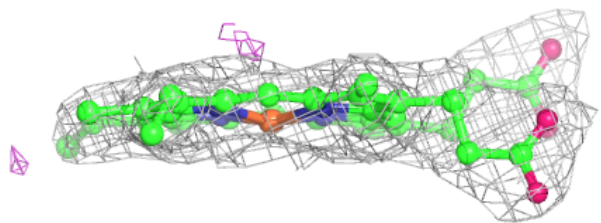
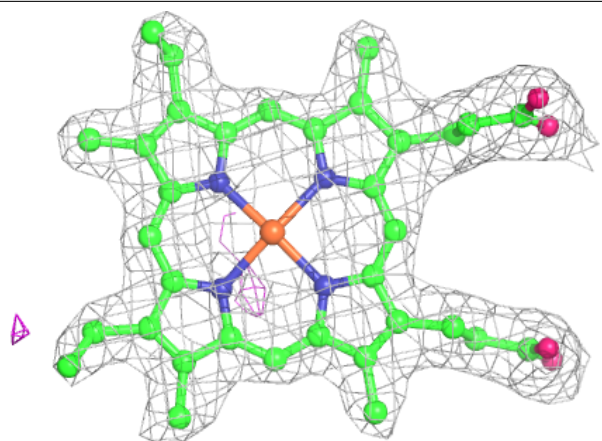
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	ACT	E	4005	4/4	0.82	0.14	47,48,48,48	0
4	ACT	C	4004	4/4	0.85	0.14	49,50,50,50	0
3	CA	A	2506	1/1	0.87	0.12	50,50,50,50	0
4	ACT	C	4007	4/4	0.91	0.12	34,35,35,36	0
3	CA	D	2502	1/1	0.94	0.12	44,44,44,44	0
5	GOL	A	3002	6/6	0.94	0.16	36,38,39,45	0
5	GOL	A	3001	6/6	0.95	0.11	24,27,29,30	0
2	HEM	B	412	43/43	0.96	0.12	27,31,34,36	0
3	CA	C	2503	1/1	0.96	0.10	43,43,43,43	0
3	CA	A	2505	1/1	0.97	0.06	37,37,37,37	0
2	HEM	C	412	43/43	0.97	0.12	14,21,24,30	0
4	ACT	A	4006	4/4	0.98	0.11	22,23,23,23	0
3	CA	E	2504	1/1	0.98	0.12	43,43,43,43	0
2	HEM	D	412	43/43	0.98	0.11	19,21,23,26	0
4	ACT	D	4001	4/4	0.98	0.11	23,23,23,24	0
2	HEM	A	412	43/43	0.98	0.13	15,19,20,26	0
4	ACT	E	4008	4/4	0.98	0.12	32,32,33,33	0
2	HEM	E	412	43/43	0.99	0.13	20,22,24,29	0
3	CA	A	2501	1/1	0.99	0.12	39,39,39,39	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.

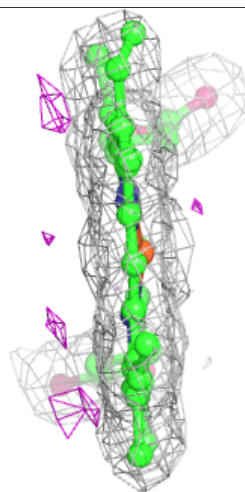
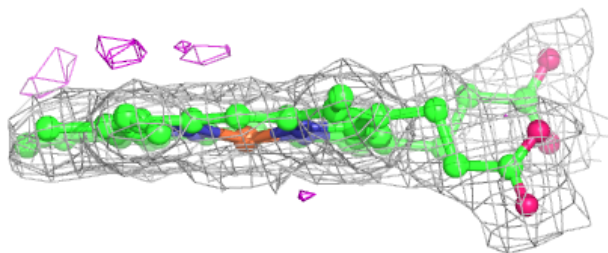
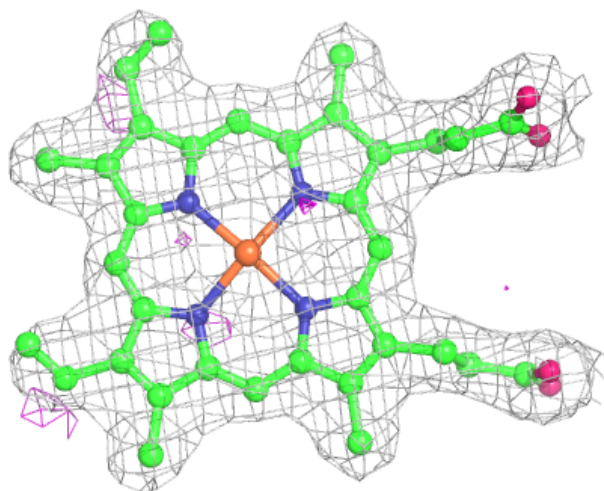
Electron density around HEM B 412:

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



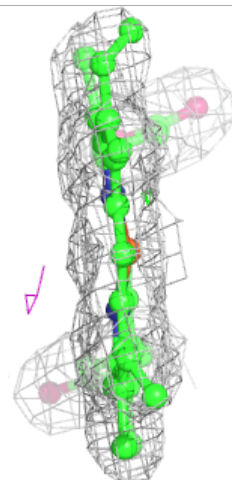
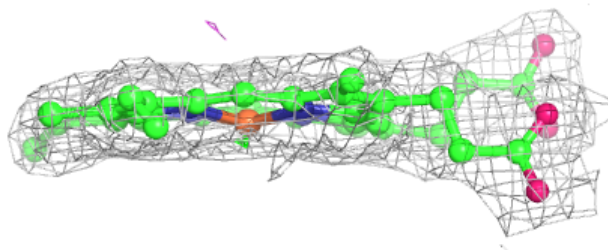
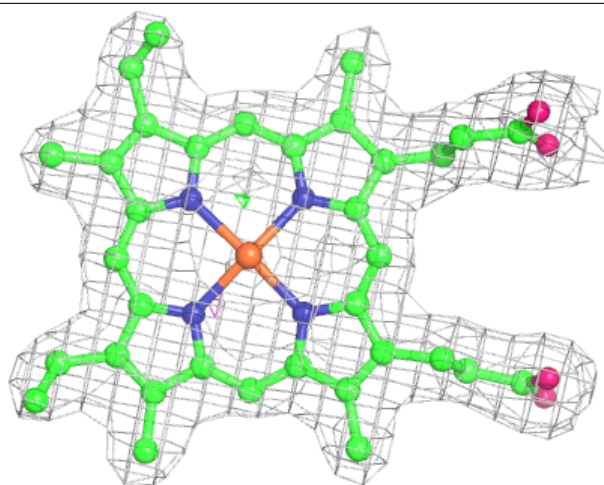
Electron density around HEM C 412:

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



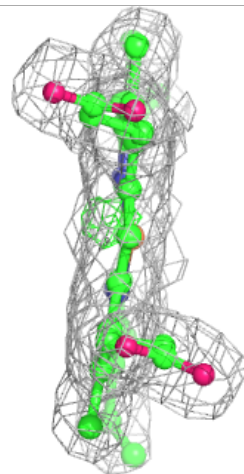
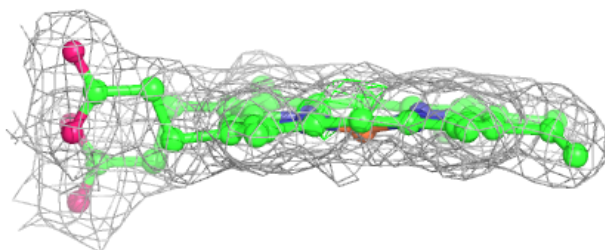
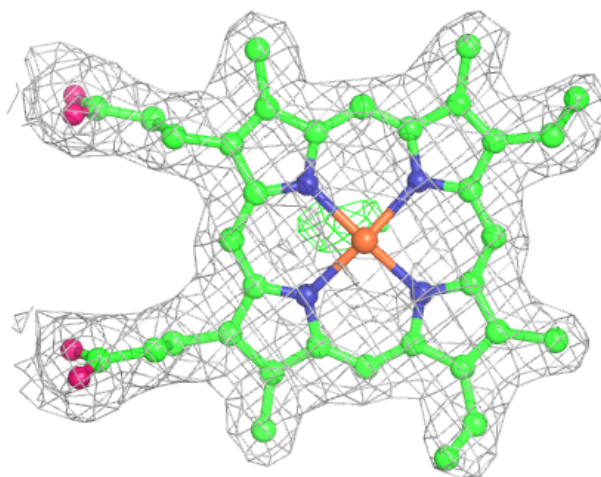
Electron density around HEM D 412:

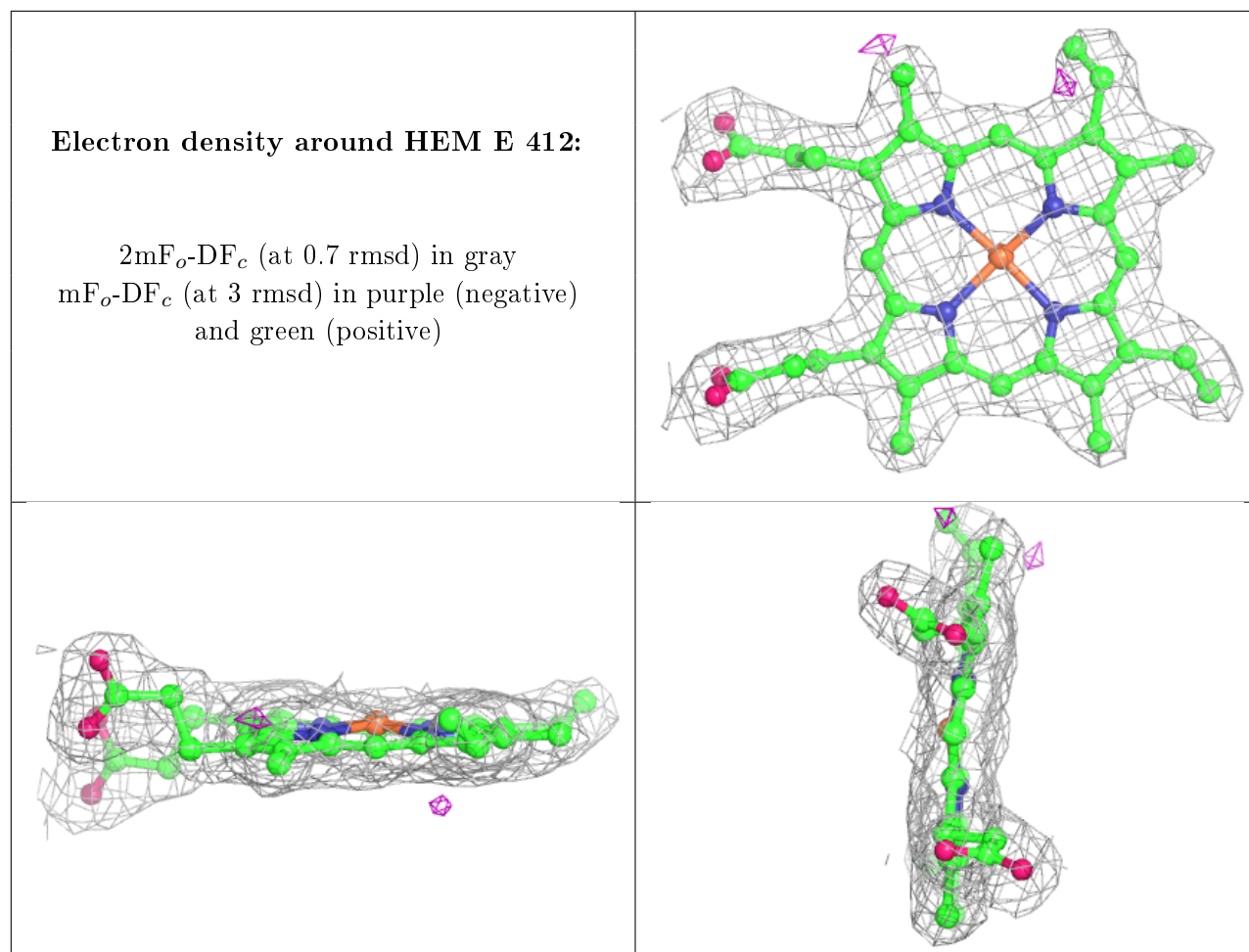
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 412:

$2mF_o-DF_c$ (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.