



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2023 – 10:31 AM EDT

PDB ID : 2RGZ
Title : Ensemble refinement of the protein crystal structure of human heme oxygenase-2 C127A (HO-2) with bound heme
Authors : Bianchetti, C.M.; Bingman, C.A.; Bitto, E.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on : 2007-10-05
Resolution : 2.61 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 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

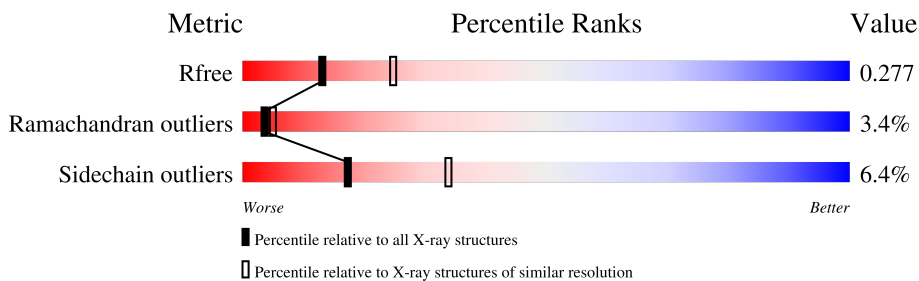
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	3797 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	1-A	264	
1	1-B	264	
1	10-A	264	
1	10-B	264	
1	11-A	264	
1	11-B	264	
1	12-A	264	
1	12-B	264	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain		
1	13-A	264	72%	9%	19%
1	13-B	264	76%	7%	17%
1	14-A	264	72%	9%	19%
1	14-B	264	72%	11%	17%
1	15-A	264	72%	9%	19%
1	15-B	264	73%	9%	17%
1	16-A	264	73%	7%	19%
1	16-B	264	71%	12%	17%
1	2-A	264	76%	5%	19%
1	2-B	264	79%	.	17%
1	3-A	264	75%	6%	19%
1	3-B	264	73%	9%	17%
1	4-A	264	73%	8%	19%
1	4-B	264	77%	6%	17%
1	5-A	264	75%	6%	19%
1	5-B	264	76%	7%	17%
1	6-A	264	76%	5%	19%
1	6-B	264	74%	9%	17%
1	7-A	264	75%	6%	19%
1	7-B	264	77%	6%	17%
1	8-A	264	77%	.	19%
1	8-B	264	74%	8%	17%
1	9-A	264	74%	7%	19%
1	9-B	264	77%	6%	17%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 58291 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 Heme oxygenase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	2-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	3-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	4-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	5-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	6-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	7-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	8-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	9-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	10-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	11-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	12-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	13-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	14-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	15-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0
1	16-A	214	Total 1758	C 1118	N 299	O 333	S 8	0	0	0

Continued on next page...

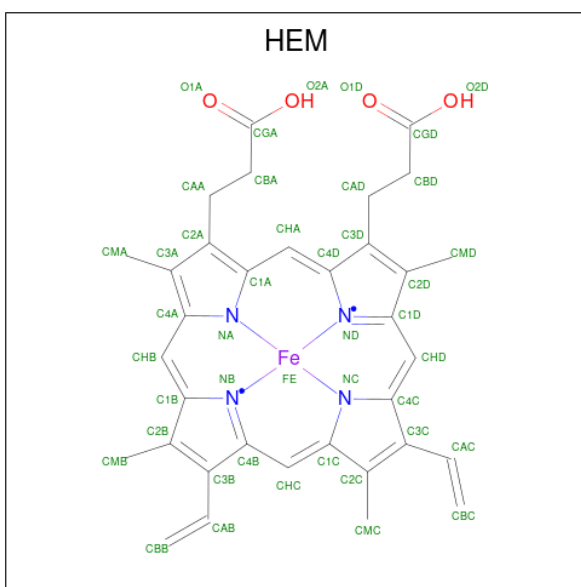
Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	2-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	3-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	4-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	5-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	6-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	7-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	8-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	9-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	10-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	11-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	12-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	13-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	14-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	15-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0
1	16-B	219	Total 1794	C 1140	N 304	O 342	S 8	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	ALA	CYS	engineered mutation	UNP P30519
B	127	ALA	CYS	engineered mutation	UNP P30519

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	1-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	2-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	3-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	4-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	5-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	6-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	7-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	8-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	9-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	10-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	11-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	12-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	13-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	14-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	15-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	16-A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	1-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	2-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	3-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	4-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	5-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	6-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	7-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	8-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	9-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	10-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	11-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	12-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	13-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	14-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	15-B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	16-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	1-A	49	Total	O	0	0
			49	49		

Continued on next page...


Continued from previous page...

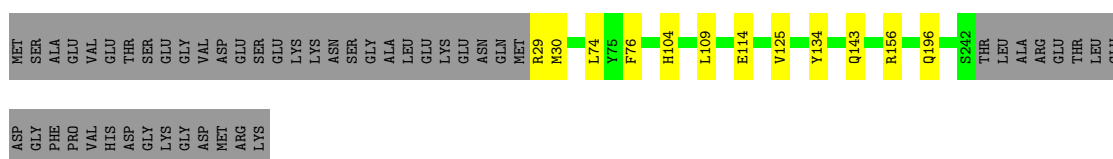
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	1-B	34	Total	O	0	0
			34	34		

3 Residue-property plots [i](#)


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.

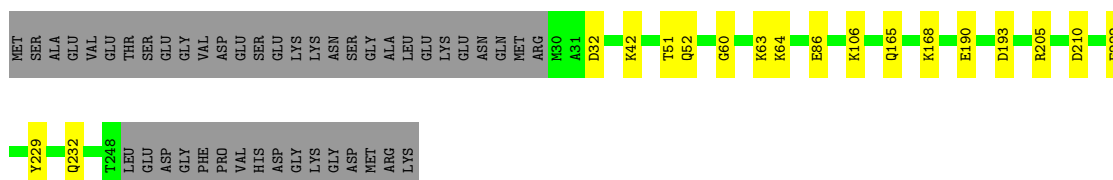
- Molecule 1: Heme oxygenase 2

Chain 1-A: 




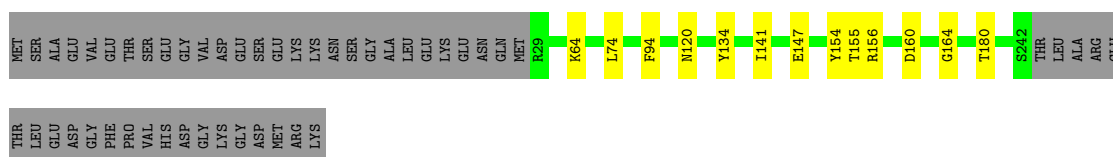
- Molecule 1: Heme oxygenase 2

Chain 1-B: 




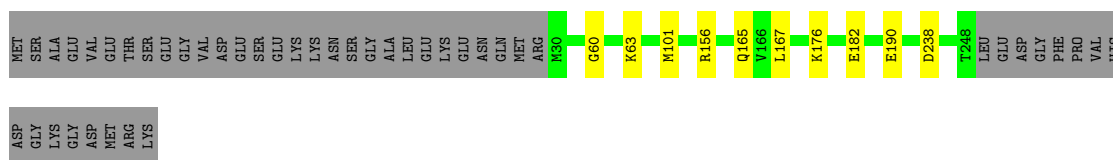
- Molecule 1: Heme oxygenase 2

Chain 2-A: 




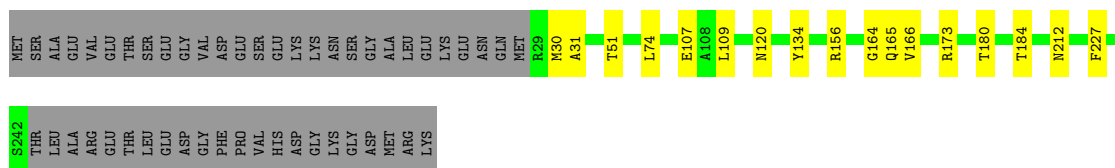
- Molecule 1: Heme oxygenase 2

Chain 2-B: 




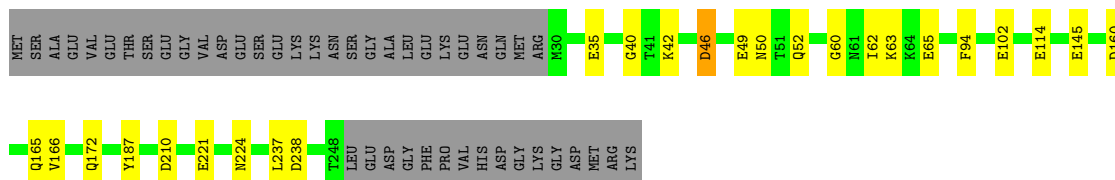
- Molecule 1: Heme oxygenase 2

Chain 3-A:  75% 6% 19%




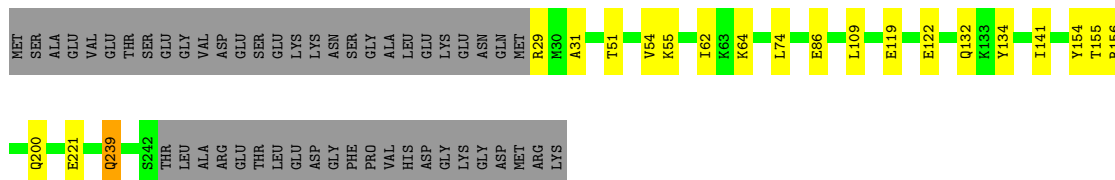
- Molecule 1: Heme oxygenase 2

Chain 3-B:  73% 9% 17%




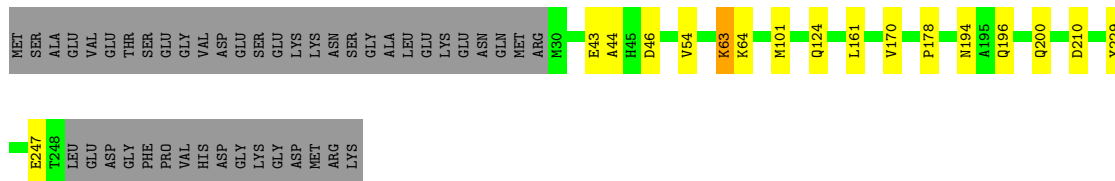
- Molecule 1: Heme oxygenase 2

Chain 4-A:  73% 8% 19%




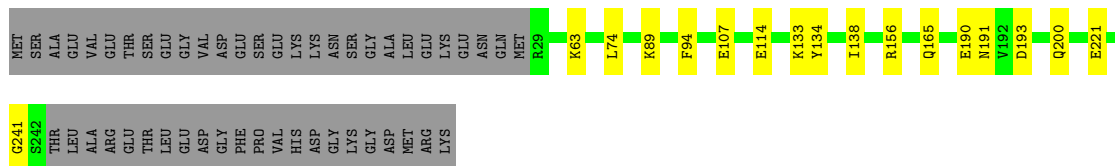
- Molecule 1: Heme oxygenase 2

Chain 4-B:  77% 6% 17%




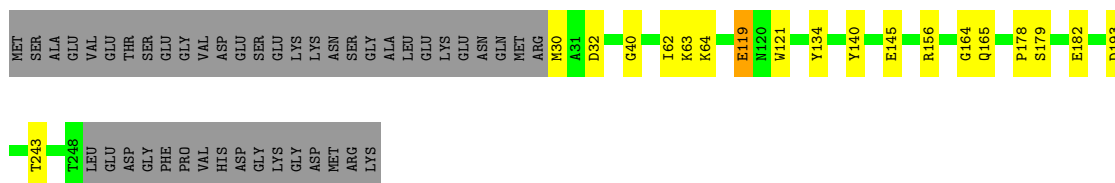
- Molecule 1: Heme oxygenase 2

Chain 5-A:  75% 6% 19%




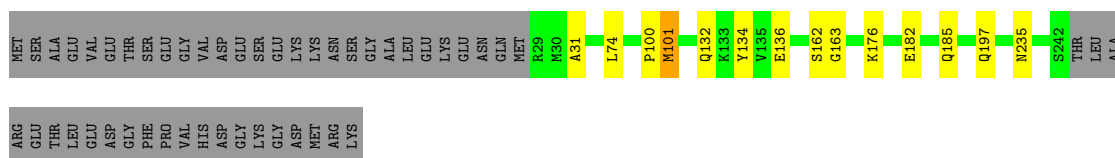
- Molecule 1: Heme oxygenase 2

Chain 5-B:  76% 7% 17%




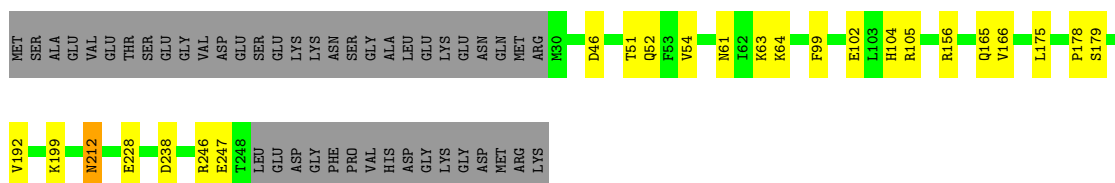
• Molecule 1: Heme oxygenase 2

Chain 6-A:  76% 5% 19%




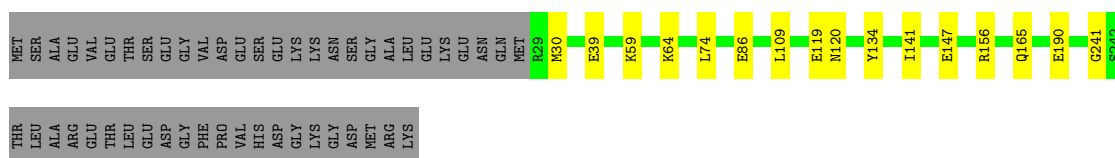
• Molecule 1: Heme oxygenase 2

Chain 6-B:  74% 9% 17%




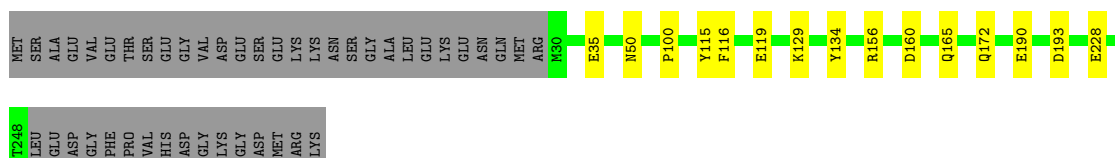
• Molecule 1: Heme oxygenase 2

Chain 7-A:  75% 6% 19%




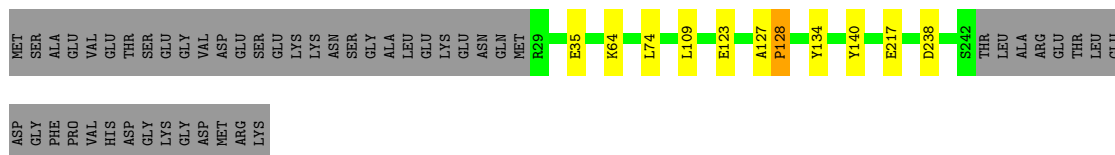
• Molecule 1: Heme oxygenase 2

Chain 7-B:  77% 6% 17%

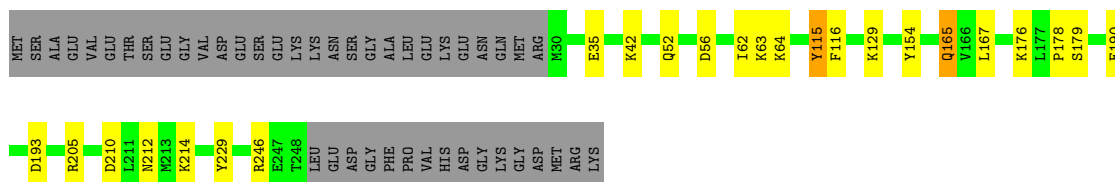
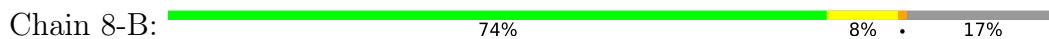


• Molecule 1: Heme oxygenase 2

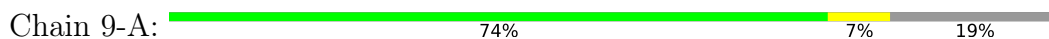
Chain 8-A:  77% 6% 19%



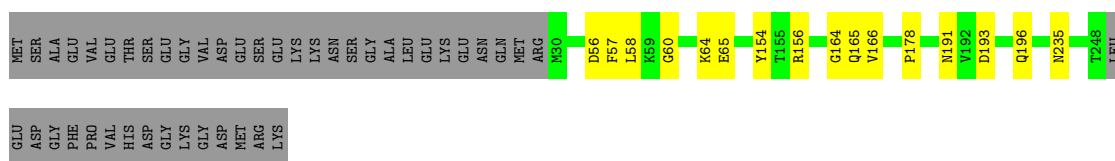
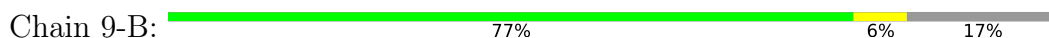
• Molecule 1: Heme oxygenase 2



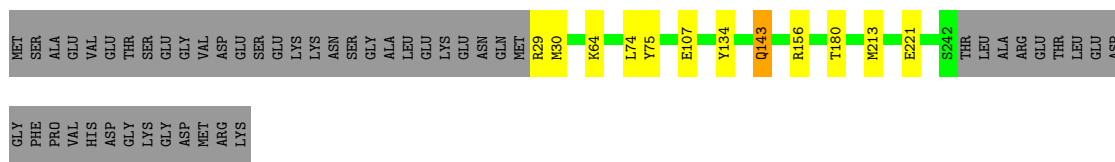
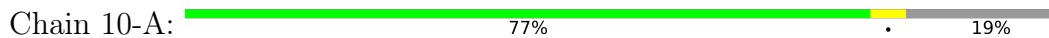
• Molecule 1: Heme oxygenase 2



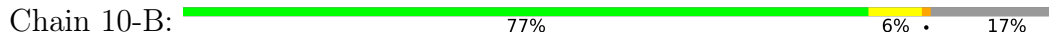
• Molecule 1: Heme oxygenase 2

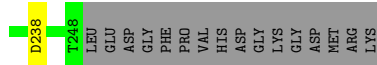
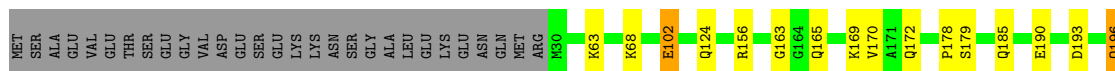


• Molecule 1: Heme oxygenase 2

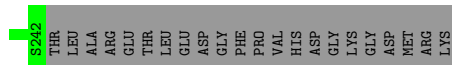
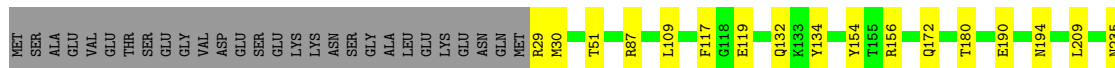
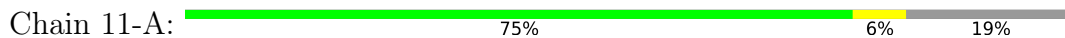


• Molecule 1: Heme oxygenase 2

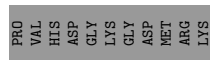
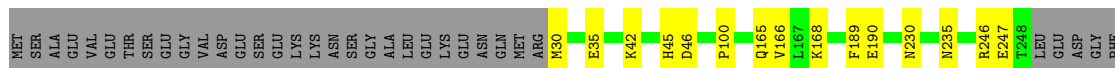
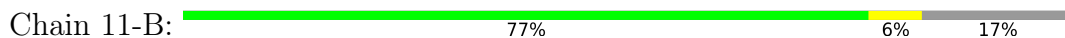




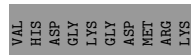
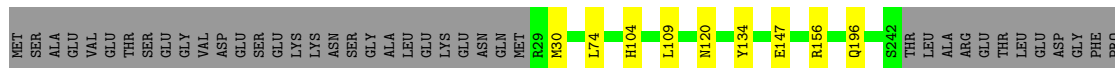
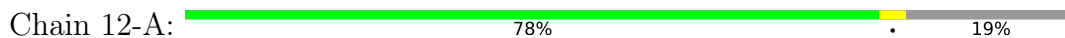
● Molecule 1: Heme oxygenase 2



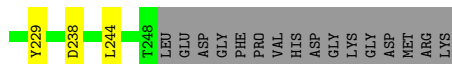
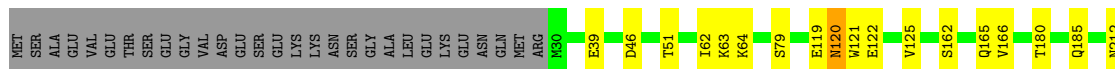
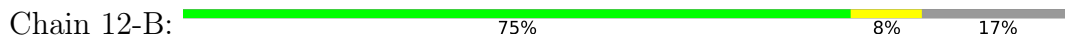
● Molecule 1: Heme oxygenase 2



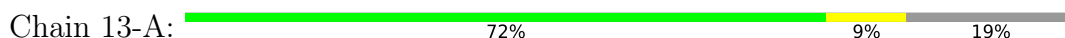
● Molecule 1: Heme oxygenase 2

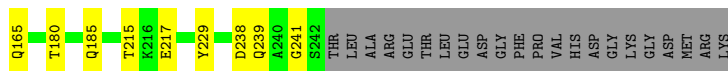
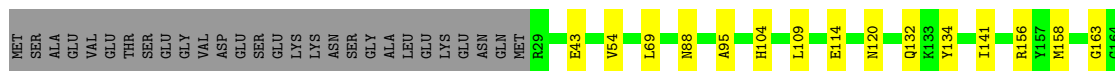


● Molecule 1: Heme oxygenase 2



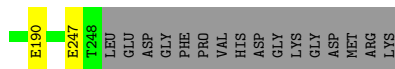
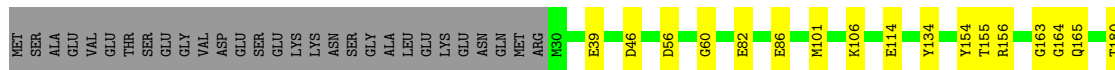
● Molecule 1: Heme oxygenase 2





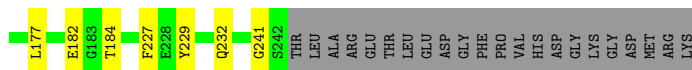
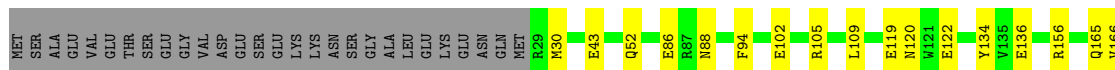
- Molecule 1: Heme oxygenase 2

Chain 13-B: 76% 7% 17%



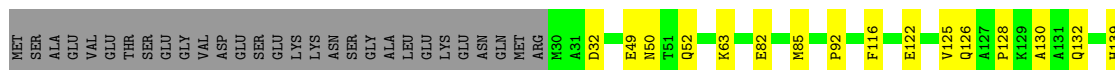
- Molecule 1: Heme oxygenase 2

Chain 14-A: 72% 9% 19%



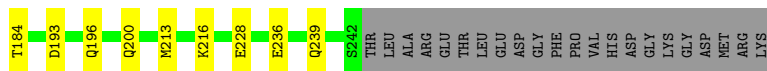
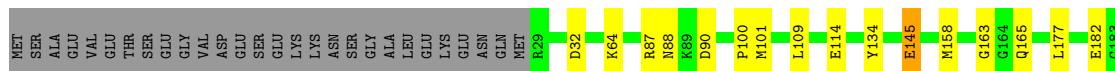
- Molecule 1: Heme oxygenase 2

Chain 14-B: 72% 11% 17%



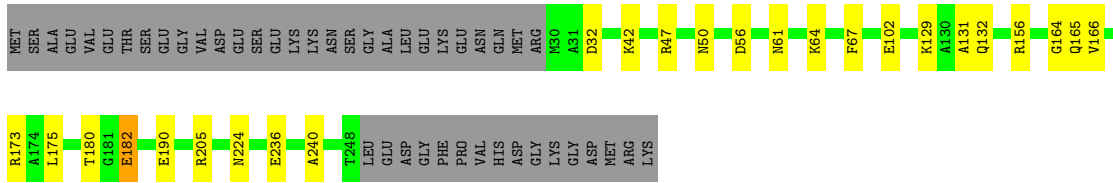
- Molecule 1: Heme oxygenase 2

Chain 15-A: 72% 9% 19%

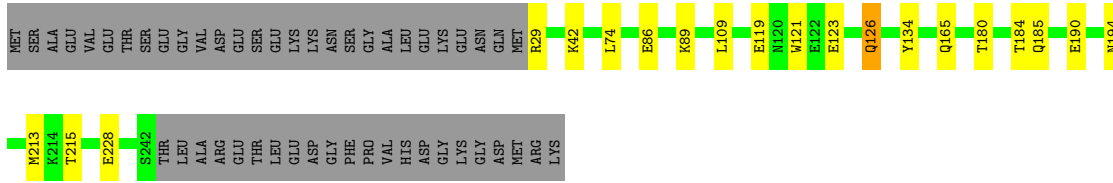
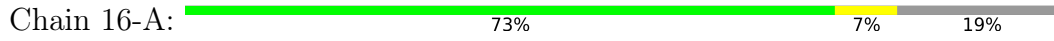


- Molecule 1: Heme oxygenase 2

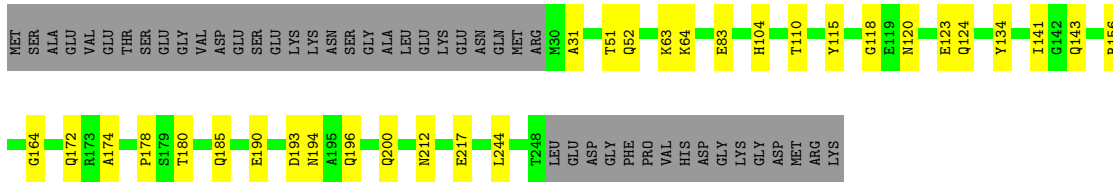
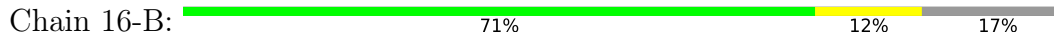
Chain 15-B: 73% 9% 17%



• Molecule 1: Heme oxygenase 2



• Molecule 1: Heme oxygenase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.98Å 85.09Å 97.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.02 – 2.61 39.02 – 2.61	Depositor EDS
% Data completeness (in resolution range)	99.3 (39.02-2.61) 99.4 (39.02-2.61)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.30 (at 2.61Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.161 , 0.249 0.205 , 0.277	Depositor DCC
R_{free} test set	1005 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	66.1	Xtrriage
Anisotropy	0.048	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 158.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	58291	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.90% 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: 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	1-A	0.43	0/1794	0.57	0/2410
1	1-B	0.39	0/1830	0.54	0/2460
1	2-A	0.43	0/1794	0.56	0/2410
1	2-B	0.40	0/1830	0.54	0/2460
1	3-A	0.43	0/1794	0.57	0/2410
1	3-B	0.39	0/1830	0.56	0/2460
1	4-A	0.44	0/1794	0.58	0/2410
1	4-B	0.39	0/1830	0.56	0/2460
1	5-A	0.43	0/1794	0.58	1/2410 (0.0%)
1	5-B	0.39	0/1830	0.54	0/2460
1	6-A	0.42	0/1794	0.56	0/2410
1	6-B	0.40	0/1830	0.55	0/2460
1	7-A	0.42	0/1794	0.57	0/2410
1	7-B	0.39	0/1830	0.54	0/2460
1	8-A	0.44	0/1794	0.57	0/2410
1	8-B	0.39	0/1830	0.55	0/2460
1	9-A	0.43	0/1794	0.57	0/2410
1	9-B	0.39	0/1830	0.54	0/2460
1	10-A	0.43	0/1794	0.57	0/2410
1	10-B	0.40	0/1830	0.55	0/2460
1	11-A	0.43	0/1794	0.56	0/2410
1	11-B	0.40	0/1830	0.55	0/2460
1	12-A	0.43	0/1794	0.55	0/2410
1	12-B	0.40	0/1830	0.55	0/2460
1	13-A	0.47	0/1794	0.63	0/2410
1	13-B	0.43	0/1830	0.55	0/2460
1	14-A	0.48	0/1794	0.61	0/2410
1	14-B	0.44	0/1830	0.58	0/2460
1	15-A	0.50	0/1794	0.64	0/2410
1	15-B	0.43	0/1830	0.60	0/2460
1	16-A	0.49	0/1794	0.64	0/2410
1	16-B	0.42	0/1830	0.57	0/2460

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.42	0/57984	0.57	1/77920 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5-A	156	ARG	NE-CZ-NH2	-5.48	117.56	120.30

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	1-A	1758	0	1717	0	0
1	1-B	1794	0	1753	0	0
1	2-A	1758	0	1717	0	0
1	2-B	1794	0	1753	0	0
1	3-A	1758	0	1717	0	0
1	3-B	1794	0	1753	0	0
1	4-A	1758	0	1717	0	0
1	4-B	1794	0	1753	0	0
1	5-A	1758	0	1717	0	0
1	5-B	1794	0	1753	0	0
1	6-A	1758	0	1717	0	0
1	6-B	1794	0	1753	0	0
1	7-A	1758	0	1717	0	0
1	7-B	1794	0	1753	0	0
1	8-A	1758	0	1717	0	0
1	8-B	1794	0	1753	0	0
1	9-A	1758	0	1717	0	0
1	9-B	1794	0	1753	0	0
1	10-A	1758	0	1717	0	0
1	10-B	1794	0	1753	0	0
1	11-A	1758	0	1717	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	11-B	1794	0	1753	0	0
1	12-A	1758	0	1717	0	0
1	12-B	1794	0	1753	0	0
1	13-A	1758	0	1717	0	0
1	13-B	1794	0	1753	0	0
1	14-A	1758	0	1717	0	0
1	14-B	1794	0	1753	0	0
1	15-A	1758	0	1717	0	0
1	15-B	1794	0	1753	0	0
1	16-A	1758	0	1717	0	0
1	16-B	1794	0	1753	0	0
2	1-A	43	0	30	0	0
2	1-B	43	0	30	0	0
2	2-A	43	0	30	0	0
2	2-B	43	0	30	0	0
2	3-A	43	0	30	0	0
2	3-B	43	0	30	0	0
2	4-A	43	0	30	0	0
2	4-B	43	0	30	0	0
2	5-A	43	0	30	0	0
2	5-B	43	0	30	0	0
2	6-A	43	0	30	0	0
2	6-B	43	0	30	0	0
2	7-A	43	0	30	0	0
2	7-B	43	0	30	0	0
2	8-A	43	0	30	0	0
2	8-B	43	0	30	0	0
2	9-A	43	0	30	0	0
2	9-B	43	0	30	0	0
2	10-A	43	0	30	0	0
2	10-B	43	0	30	0	0
2	11-A	43	0	30	0	0
2	11-B	43	0	30	0	0
2	12-A	43	0	30	0	0
2	12-B	43	0	30	0	0
2	13-A	43	0	30	0	0
2	13-B	43	0	30	0	0
2	14-A	43	0	30	0	0
2	14-B	43	0	30	0	0
2	15-A	43	0	30	0	0
2	15-B	43	0	30	0	0
2	16-A	43	0	30	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	16-B	43	0	30	0	0
3	1-A	49	0	0	0	0
3	1-B	34	0	0	0	0
All	All	58291	0	56480	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	1-A	212/264 (80%)	185 (87%)	23 (11%)	4 (2%)	8	14
1	1-B	217/264 (82%)	190 (88%)	19 (9%)	8 (4%)	3	4
1	2-A	212/264 (80%)	184 (87%)	23 (11%)	5 (2%)	6	9
1	2-B	217/264 (82%)	183 (84%)	30 (14%)	4 (2%)	8	15
1	3-A	212/264 (80%)	192 (91%)	17 (8%)	3 (1%)	11	21
1	3-B	217/264 (82%)	174 (80%)	33 (15%)	10 (5%)	2	2
1	4-A	212/264 (80%)	188 (89%)	17 (8%)	7 (3%)	4	5
1	4-B	217/264 (82%)	175 (81%)	35 (16%)	7 (3%)	4	5
1	5-A	212/264 (80%)	189 (89%)	18 (8%)	5 (2%)	6	9
1	5-B	217/264 (82%)	186 (86%)	22 (10%)	9 (4%)	3	3
1	6-A	212/264 (80%)	181 (85%)	25 (12%)	6 (3%)	5	7
1	6-B	217/264 (82%)	167 (77%)	38 (18%)	12 (6%)	2	1
1	7-A	212/264 (80%)	182 (86%)	26 (12%)	4 (2%)	8	14
1	7-B	217/264 (82%)	183 (84%)	28 (13%)	6 (3%)	5	7

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	8-A	212/264 (80%)	187 (88%)	21 (10%)	4 (2%)	8	14
1	8-B	217/264 (82%)	183 (84%)	21 (10%)	13 (6%)	1	1
1	9-A	212/264 (80%)	179 (84%)	24 (11%)	9 (4%)	3	3
1	9-B	217/264 (82%)	184 (85%)	23 (11%)	10 (5%)	2	2
1	10-A	212/264 (80%)	189 (89%)	20 (9%)	3 (1%)	11	21
1	10-B	217/264 (82%)	185 (85%)	23 (11%)	9 (4%)	3	3
1	11-A	212/264 (80%)	185 (87%)	24 (11%)	3 (1%)	11	21
1	11-B	217/264 (82%)	184 (85%)	28 (13%)	5 (2%)	6	10
1	12-A	212/264 (80%)	198 (93%)	12 (6%)	2 (1%)	17	33
1	12-B	217/264 (82%)	174 (80%)	33 (15%)	10 (5%)	2	2
1	13-A	212/264 (80%)	186 (88%)	21 (10%)	5 (2%)	6	9
1	13-B	217/264 (82%)	182 (84%)	26 (12%)	9 (4%)	3	3
1	14-A	212/264 (80%)	176 (83%)	30 (14%)	6 (3%)	5	7
1	14-B	217/264 (82%)	165 (76%)	35 (16%)	17 (8%)	1	1
1	15-A	212/264 (80%)	176 (83%)	26 (12%)	10 (5%)	2	2
1	15-B	217/264 (82%)	171 (79%)	36 (17%)	10 (5%)	2	2
1	16-A	212/264 (80%)	177 (84%)	32 (15%)	3 (1%)	11	21
1	16-B	217/264 (82%)	172 (79%)	28 (13%)	17 (8%)	1	1
All	All	6864/8448 (81%)	5812 (85%)	817 (12%)	235 (3%)	3	5

5 of 235 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-B	64	LYS
1	2-A	64	LYS
1	3-B	46	ASP
1	3-B	52	GLN
1	3-B	65	GLU

5.3.2 Protein sidechains [i](#)

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	1-A	182/224 (81%)	174 (96%)	8 (4%)	28	52
1	1-B	186/224 (83%)	176 (95%)	10 (5%)	22	42
1	2-A	182/224 (81%)	174 (96%)	8 (4%)	28	52
1	2-B	186/224 (83%)	180 (97%)	6 (3%)	39	63
1	3-A	182/224 (81%)	168 (92%)	14 (8%)	13	24
1	3-B	186/224 (83%)	170 (91%)	16 (9%)	10	19
1	4-A	182/224 (81%)	167 (92%)	15 (8%)	11	21
1	4-B	186/224 (83%)	175 (94%)	11 (6%)	19	37
1	5-A	182/224 (81%)	171 (94%)	11 (6%)	19	37
1	5-B	186/224 (83%)	175 (94%)	11 (6%)	19	37
1	6-A	182/224 (81%)	173 (95%)	9 (5%)	25	46
1	6-B	186/224 (83%)	173 (93%)	13 (7%)	15	29
1	7-A	182/224 (81%)	170 (93%)	12 (7%)	16	32
1	7-B	186/224 (83%)	177 (95%)	9 (5%)	25	47
1	8-A	182/224 (81%)	174 (96%)	8 (4%)	28	52
1	8-B	186/224 (83%)	173 (93%)	13 (7%)	15	29
1	9-A	182/224 (81%)	173 (95%)	9 (5%)	25	46
1	9-B	186/224 (83%)	180 (97%)	6 (3%)	39	63
1	10-A	182/224 (81%)	172 (94%)	10 (6%)	21	41
1	10-B	186/224 (83%)	176 (95%)	10 (5%)	22	42
1	11-A	182/224 (81%)	168 (92%)	14 (8%)	13	24
1	11-B	186/224 (83%)	176 (95%)	10 (5%)	22	42
1	12-A	182/224 (81%)	175 (96%)	7 (4%)	33	57
1	12-B	186/224 (83%)	174 (94%)	12 (6%)	17	33
1	13-A	182/224 (81%)	163 (90%)	19 (10%)	7	12
1	13-B	186/224 (83%)	176 (95%)	10 (5%)	22	42
1	14-A	182/224 (81%)	164 (90%)	18 (10%)	8	14
1	14-B	186/224 (83%)	175 (94%)	11 (6%)	19	37
1	15-A	182/224 (81%)	166 (91%)	16 (9%)	10	18
1	15-B	186/224 (83%)	170 (91%)	16 (9%)	10	19
1	16-A	182/224 (81%)	164 (90%)	18 (10%)	8	14

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	16-B	186/224 (83%)	172 (92%)	14 (8%)	13	25
All	All	5888/7168 (82%)	5514 (94%)	374 (6%)	17	34

5 of 374 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	11-B	230	ASN
1	14-A	102	GLU
1	12-A	147	GLU
1	13-A	134	TYR
1	14-B	52	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 175 such sidechains are listed below:

Mol	Chain	Res	Type
1	10-B	124	GLN
1	13-A	144	ASN
1	10-B	185	GLN
1	11-B	196	GLN
1	14-A	197	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 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	12-A	300	1	41,50,50	1.38	5 (12%)	45,82,82	1.00	1 (2%)
2	HEM	12-B	265	1	41,50,50	1.41	5 (12%)	45,82,82	1.01	2 (4%)
2	HEM	2-A	300	1	41,50,50	1.34	5 (12%)	45,82,82	0.99	0
2	HEM	9-A	300	1	41,50,50	1.43	5 (12%)	45,82,82	0.95	0
2	HEM	5-A	300	1	41,50,50	1.29	5 (12%)	45,82,82	1.04	2 (4%)
2	HEM	2-B	265	1	41,50,50	1.48	5 (12%)	45,82,82	0.98	2 (4%)
2	HEM	1-B	265	1	41,50,50	1.47	5 (12%)	45,82,82	0.95	1 (2%)
2	HEM	5-B	265	1	41,50,50	1.43	5 (12%)	45,82,82	0.97	2 (4%)
2	HEM	16-A	300	1	41,50,50	1.33	5 (12%)	45,82,82	1.01	1 (2%)
2	HEM	3-A	300	1	41,50,50	1.35	5 (12%)	45,82,82	1.03	1 (2%)
2	HEM	8-B	265	1	41,50,50	1.43	5 (12%)	45,82,82	0.97	1 (2%)
2	HEM	15-B	265	1	41,50,50	1.44	5 (12%)	45,82,82	1.02	2 (4%)
2	HEM	7-B	265	1	41,50,50	1.45	5 (12%)	45,82,82	0.95	2 (4%)
2	HEM	3-B	265	1	41,50,50	1.39	5 (12%)	45,82,82	1.03	1 (2%)
2	HEM	6-B	265	1	41,50,50	1.42	5 (12%)	45,82,82	0.96	3 (6%)
2	HEM	4-A	300	1	41,50,50	1.44	5 (12%)	45,82,82	0.97	2 (4%)
2	HEM	11-A	300	1	41,50,50	1.38	5 (12%)	45,82,82	0.99	1 (2%)
2	HEM	13-A	300	1	41,50,50	1.44	5 (12%)	45,82,82	0.92	1 (2%)
2	HEM	7-A	300	1	41,50,50	1.35	5 (12%)	45,82,82	1.01	0
2	HEM	9-B	265	1	41,50,50	1.48	5 (12%)	45,82,82	0.99	2 (4%)
2	HEM	13-B	265	1	41,50,50	1.45	5 (12%)	45,82,82	0.96	2 (4%)
2	HEM	6-A	300	1	41,50,50	1.38	5 (12%)	45,82,82	1.00	1 (2%)
2	HEM	10-A	300	1	41,50,50	1.29	5 (12%)	45,82,82	1.01	1 (2%)
2	HEM	14-A	300	1	41,50,50	1.44	7 (17%)	45,82,82	0.95	1 (2%)
2	HEM	4-B	265	1	41,50,50	1.42	5 (12%)	45,82,82	1.00	2 (4%)
2	HEM	16-B	265	1	41,50,50	1.52	5 (12%)	45,82,82	1.01	2 (4%)
2	HEM	15-A	300	1	41,50,50	1.28	5 (12%)	45,82,82	1.07	1 (2%)
2	HEM	11-B	265	1	41,50,50	1.43	5 (12%)	45,82,82	0.99	2 (4%)
2	HEM	10-B	265	1	41,50,50	1.48	5 (12%)	45,82,82	0.97	2 (4%)
2	HEM	1-A	300	1	41,50,50	1.31	5 (12%)	45,82,82	1.00	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	8-A	300	1	41,50,50	1.33	5 (12%)	45,82,82	1.04	1 (2%)
2	HEM	14-B	265	1	41,50,50	1.52	5 (12%)	45,82,82	1.10	3 (6%)

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	12-A	300	1	-	5/12/54/54	-
2	HEM	12-B	265	1	-	8/12/54/54	-
2	HEM	2-A	300	1	-	5/12/54/54	-
2	HEM	9-A	300	1	-	5/12/54/54	-
2	HEM	5-A	300	1	-	2/12/54/54	-
2	HEM	2-B	265	1	-	5/12/54/54	-
2	HEM	1-B	265	1	-	7/12/54/54	-
2	HEM	5-B	265	1	-	6/12/54/54	-
2	HEM	16-A	300	1	-	5/12/54/54	-
2	HEM	3-A	300	1	-	7/12/54/54	-
2	HEM	8-B	265	1	-	6/12/54/54	-
2	HEM	15-B	265	1	-	6/12/54/54	-
2	HEM	7-B	265	1	-	6/12/54/54	-
2	HEM	3-B	265	1	-	8/12/54/54	-
2	HEM	6-B	265	1	-	4/12/54/54	-
2	HEM	4-A	300	1	-	6/12/54/54	-
2	HEM	11-A	300	1	-	4/12/54/54	-
2	HEM	13-A	300	1	-	4/12/54/54	-
2	HEM	7-A	300	1	-	3/12/54/54	-
2	HEM	9-B	265	1	-	5/12/54/54	-
2	HEM	13-B	265	1	-	4/12/54/54	-
2	HEM	6-A	300	1	-	5/12/54/54	-
2	HEM	10-A	300	1	-	2/12/54/54	-
2	HEM	14-A	300	1	-	4/12/54/54	-
2	HEM	4-B	265	1	-	8/12/54/54	-
2	HEM	16-B	265	1	-	9/12/54/54	-
2	HEM	15-A	300	1	-	2/12/54/54	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	11-B	265	1	-	4/12/54/54	-
2	HEM	10-B	265	1	-	7/12/54/54	-
2	HEM	1-A	300	1	-	3/12/54/54	-
2	HEM	8-A	300	1	-	2/12/54/54	-
2	HEM	14-B	265	1	-	3/12/54/54	-

The worst 5 of 162 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	9-A	300	HEM	C3C-CAC	-4.49	1.38	1.47
2	14-B	265	HEM	C3C-CAC	-4.42	1.38	1.47
2	6-A	300	HEM	C3C-CAC	-4.41	1.38	1.47
2	11-A	300	HEM	C3C-CAC	-4.40	1.38	1.47
2	4-A	300	HEM	C3C-CAC	-4.37	1.38	1.47

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	8-B	265	HEM	C4B-CHC-C1C	2.44	125.78	122.56
2	12-B	265	HEM	C4C-CHD-C1D	2.33	125.64	122.56
2	16-B	265	HEM	C4C-CHD-C1D	2.30	125.59	122.56
2	2-B	265	HEM	C4C-CHD-C1D	2.29	125.58	122.56
2	13-A	300	HEM	C4C-CHD-C1D	2.29	125.58	122.56

There are no chirality outliers.

5 of 160 torsion outliers are listed below:

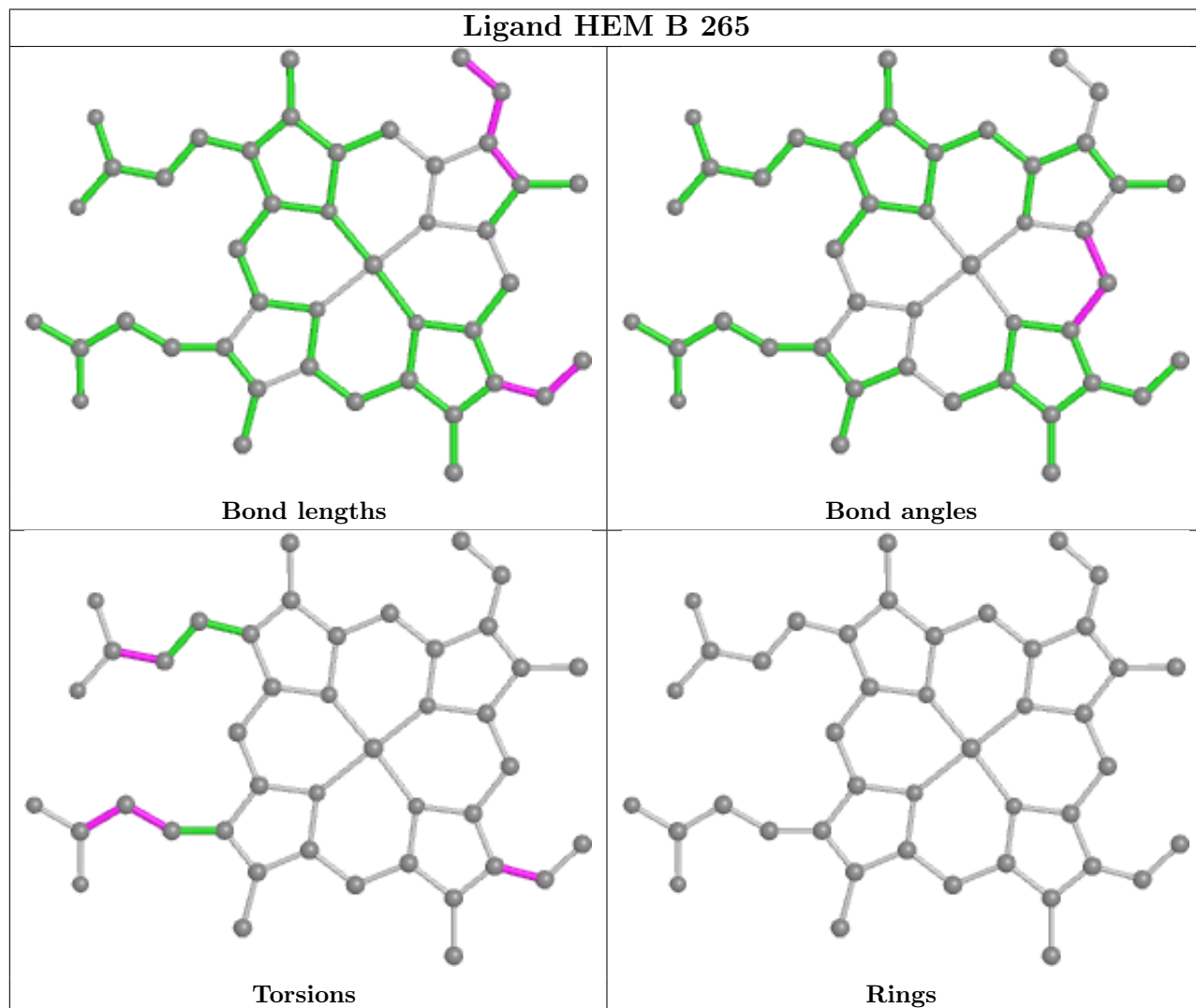
Mol	Chain	Res	Type	Atoms
2	2-A	300	HEM	C1A-C2A-CAA-CBA
2	4-A	300	HEM	C4B-C3B-CAB-CBB
2	16-A	300	HEM	C1A-C2A-CAA-CBA
2	1-B	265	HEM	C2B-C3B-CAB-CBB
2	1-B	265	HEM	C4B-C3B-CAB-CBB

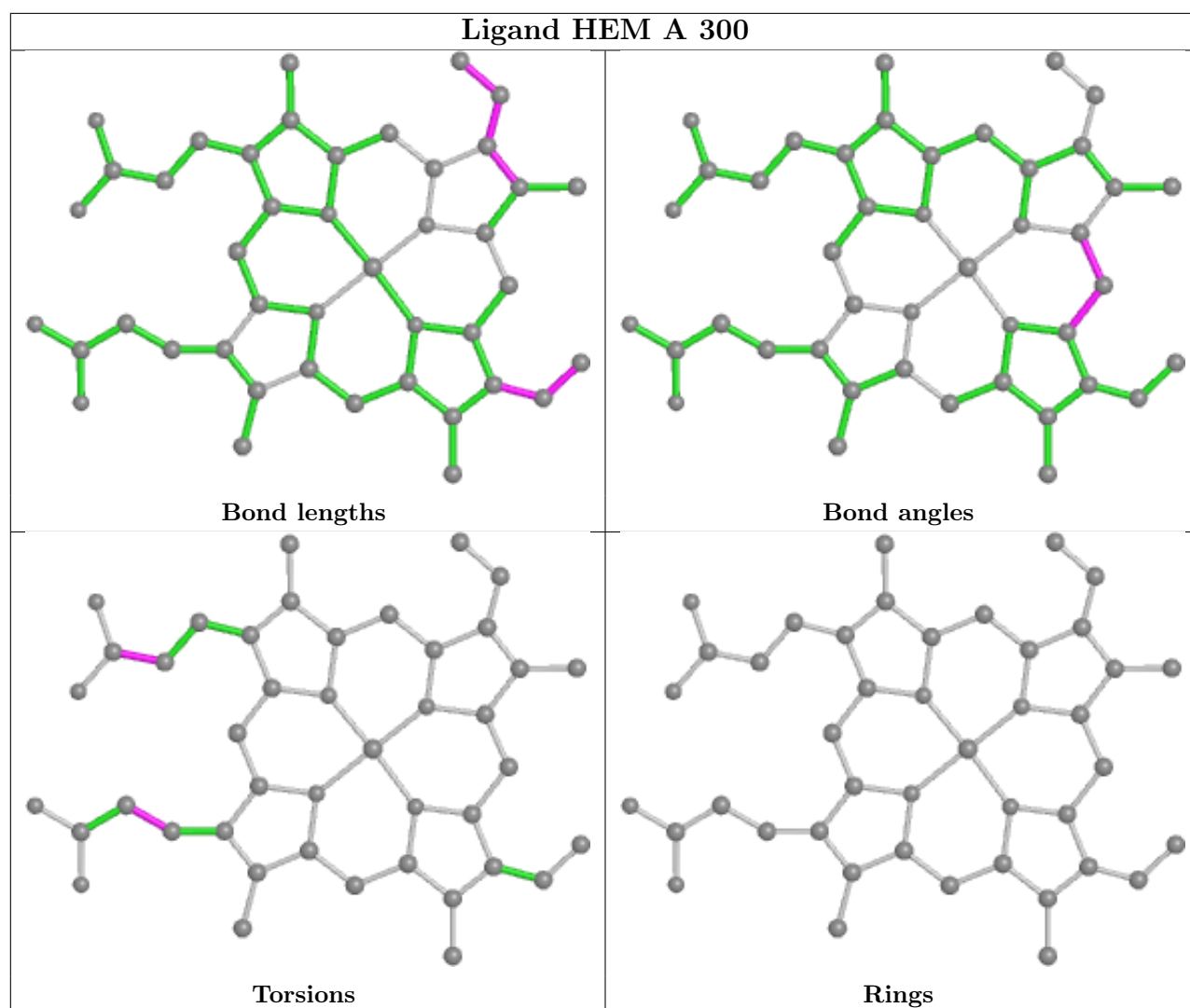
There are no ring outliers.

No monomer is involved in short contacts.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

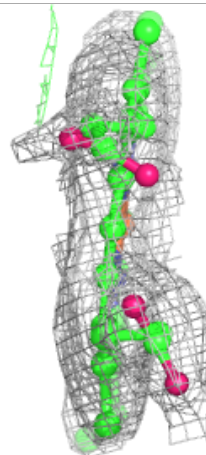
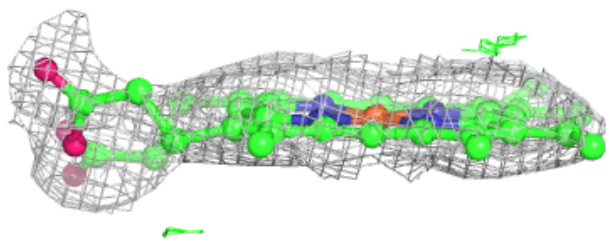
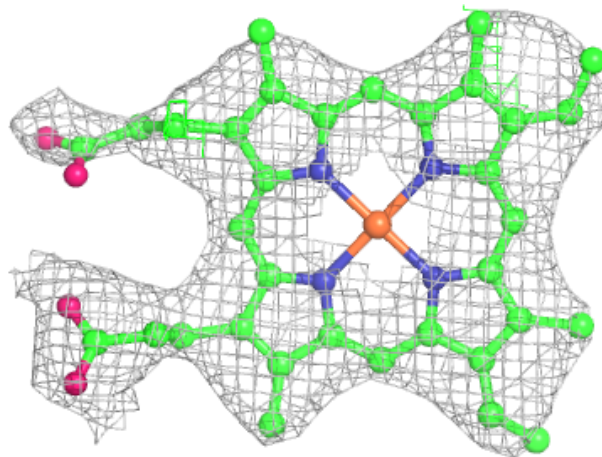
6.4 Ligands

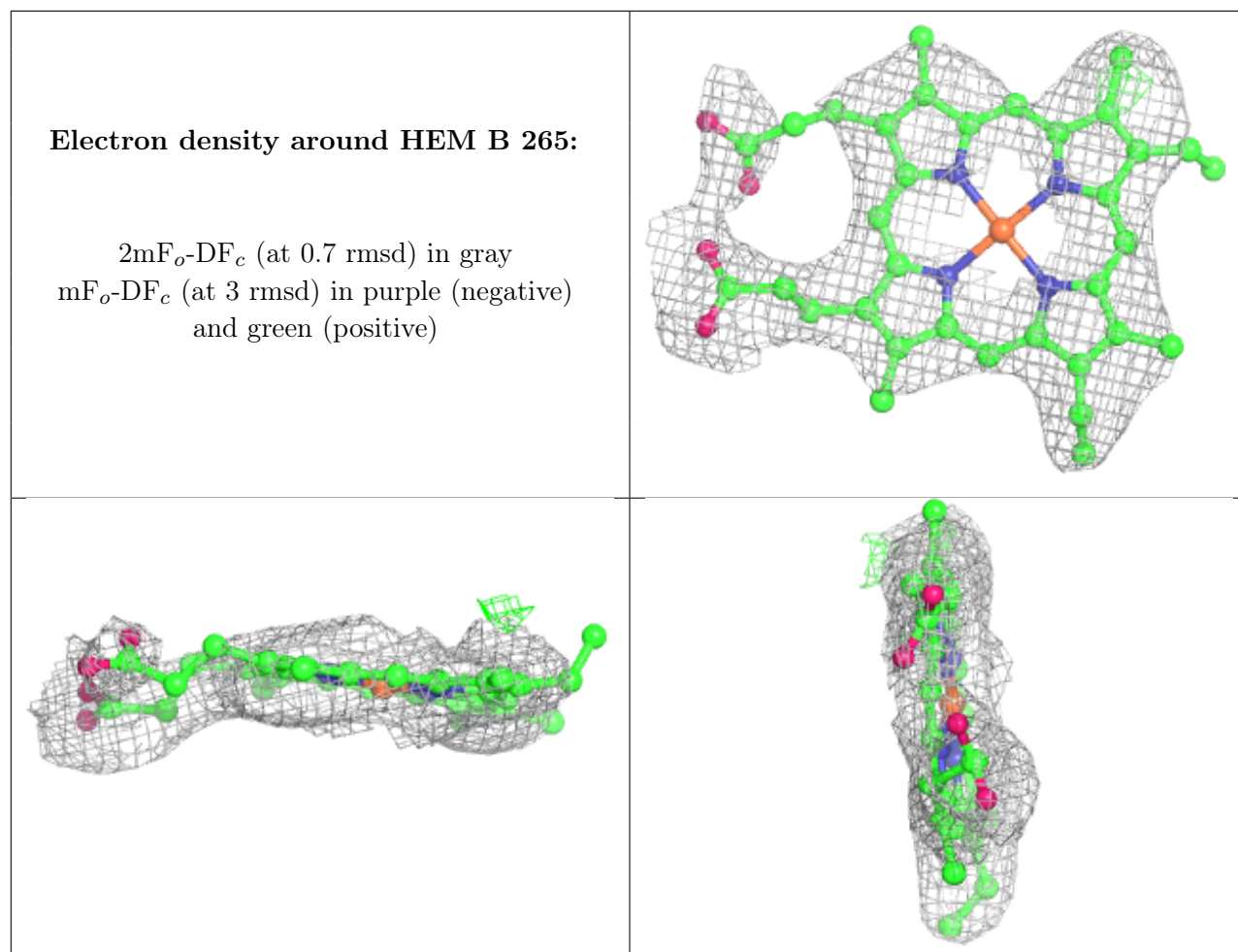
Unable to reproduce the depositors R factor - this section is therefore empty.

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

Electron density around HEM A 300:

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





6.5 Other polymers [\(i\)](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.