



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 10:59 PM UTC

PDB ID : 2J0D / pdb_00002j0d
Title : Crystal structure of human P450 3A4 in complex with erythromycin
Authors : Sjogren, T.; Ekroos, M.
Deposited on : 2006-08-02
Resolution : 2.75 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 : 4-5-2 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

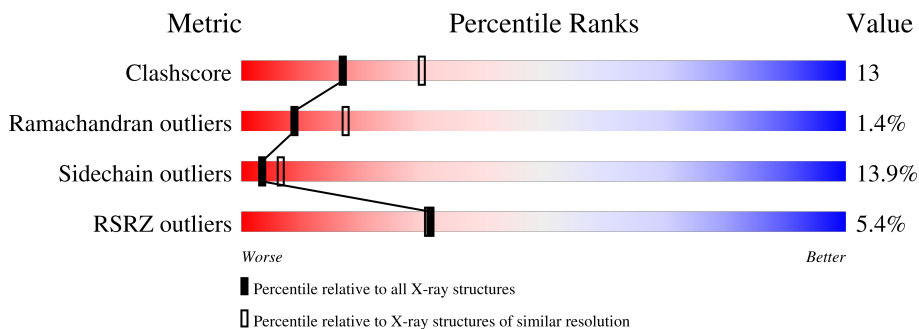
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	485	3% 61% 26% 5% 8%
1	B	485	7% 59% 26% 7% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7326 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.

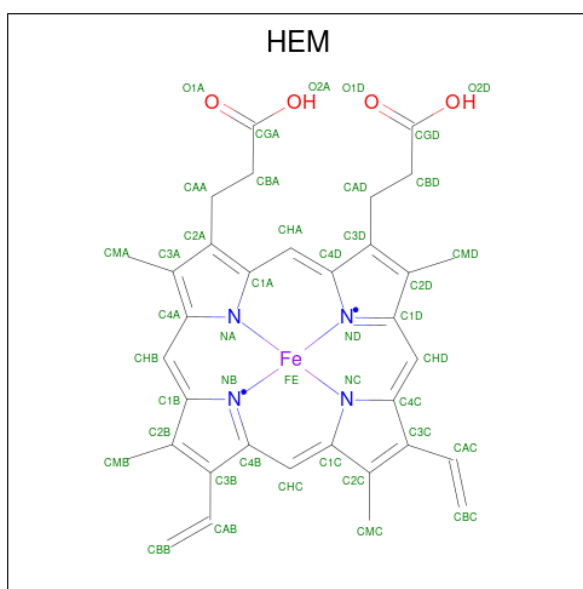
- Molecule 1 is a protein called CYTOCHROME P450 3A4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	0	0
			3578	2331	588	635	24			
1	B	445	Total	C	N	O	S	0	0	0
			3562	2320	585	633	24			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	392	VAL	TRP	conflict	UNP P08684
B	392	VAL	TRP	conflict	UNP P08684

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



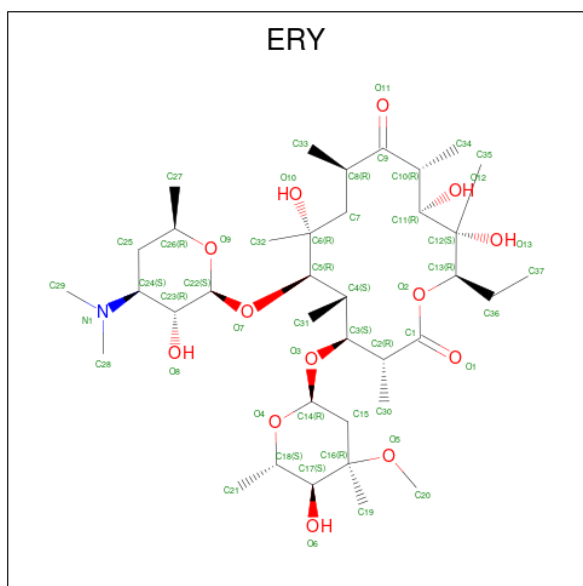
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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

- Molecule 3 is ERYTHROMYCIN A (CCD ID: ERY) (formula: $C_{37}H_{67}NO_{13}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			51	37	1	13		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	27	Total	O	0	0
			27	27		
4	B	22	Total	O	0	0
			22	22		

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.

Chain A:

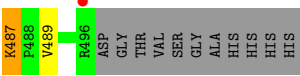
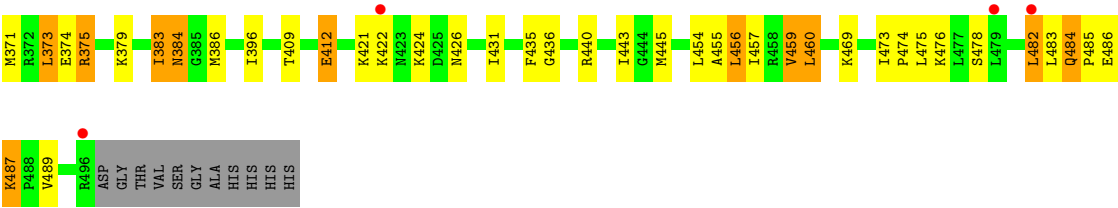
3% 61% 26% 5% 8%

MET ALA TYR GLY THR HIS S29 T42 K67 Y68 G89 K70 V71 D76 G77 Q78 P80 V81 L82 A83 I84 T85 M89 Y93 L94 E97 V101 F102 R105 R106 P107 F108 G109 P110 V111 G112 PRD F113 S116 A117 I118 S119 I120 R130 S131 L132 L133 S134 P135 T136 E144 I148 Q151 R161 E165 V170 T171 L172 Y179 V183 I184 T187 V191 D194 S195 LEU ASN N198 P199 Q200 D201 P202 P203 V204 E205 L210 L211 R212 F213 ASP PHE LEU ASP PRD F219 S222 I223 F226 L229 I232 L233 E234 V271 T238 F241 P242 R243 F244 V245 L249 V253 M256 K257 R260 LEU GLU ASP THR GLN LYS HIS ARG VAL ASP F271 L272 L273 L274 L275 L276 D277 N280 S281 LYS GLU THR GLU SER H287 K288 E289 L290 L293 E294 I300 F302 I303 F316 L317 M318 L331 G335 E333 E334 I335 L339 P344 P345 T349 V350 L351 Q352 M353 Y355 L356 D357 M358 T363 L364 R365 T369 L373 E374 R375 V381 N384 L388 P389 K390 I396 L401 H402 E410 P411 E412 K413 N426 I431 F435 C436 S437 G438 C442 F447

Chain B:

7% 59% 26% 7% 8%

Met
Ala
Tyr
G26
G31
L32
K35
L44
I50
Y53
H54
K55
C58
H65
K70
D76
L82
T85
D86
P87
D88
M89
I90
V93
L94
E97
C98
Y99
S100
F101
F102
R106
P107
F108
G109
P110
V111
G112
F113
M114
K115
I120
D123
E124
E125
W126
A127
R128
L129
S131
S134
K135
L144
I150
Y152
L156
L160
R161
R162
E163
A164
E165
L166
G167
R168
L172
K173
D174
F175
F176
Y179
S180
M181
I184
T185
S186
T187
S188
F189
G190
L191
G192
L193
D194
S195
A196
D198
S200



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	67.25Å 210.71Å 161.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.75 30.00 – 2.75	Depositor EDS
% Data completeness (in resolution range)	97.3 (30.00-2.75) 97.2 (30.00-2.75)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.87 (at 2.76Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.238 , 0.315 0.233 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.333	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7326	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% 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, ERY

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	0.59	0/3662	0.93	3/4948 (0.1%)
1	B	0.57	0/3647	0.94	1/4929 (0.0%)
All	All	0.58	0/7309	0.94	4/9877 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	123	ASP	N-CA-C	5.51	116.16	108.00
1	A	438	GLY	CA-C-N	5.33	126.50	119.84
1	A	438	GLY	C-N-CA	5.33	126.50	119.84
1	A	111	VAL	N-CA-C	5.18	118.70	113.47

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	3578	0	3665	90	0
1	B	3562	0	3646	92	0
2	A	43	0	30	9	0
2	B	43	0	30	1	0
3	A	51	0	67	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	27	0	0	0	0
4	B	22	0	0	0	0
All	All	7326	0	7438	189	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 13.

The worst 5 of 189 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)
2:A:1497:HEM:HMB1	2:A:1497:HEM:HBB2	1.24	1.11
2:A:1497:HEM:HBB2	2:A:1497:HEM:CMB	1.86	1.02
1:A:117:ALA:HB1	1:A:301:ILE:HG13	1.54	0.90
1:B:355:TYR:HA	1:B:358:MET:HE3	1.54	0.87
1:A:108:PHE:HE1	1:A:120:ILE:HD12	1.40	0.86

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	436/485 (90%)	398 (91%)	32 (7%)	6 (1%)	9	17
1	B	435/485 (90%)	395 (91%)	34 (8%)	6 (1%)	9	17
All	All	871/970 (90%)	793 (91%)	66 (8%)	12 (1%)	9	17

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	202	PRO
1	A	354	GLU

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Mol	Chain	Res	Type
1	B	201	ASP
1	A	199	PRO
1	A	290	LEU

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	A	405/441 (92%)	355 (88%)	50 (12%)	4	8
1	B	403/441 (91%)	341 (85%)	62 (15%)	2	4
All	All	808/882 (92%)	696 (86%)	112 (14%)	3	6

5 of 112 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	94	LEU
1	B	483	LEU
1	B	203	PHE
1	B	482	LEU
1	B	412	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	151	GLN
1	B	206	ASN
1	B	451	ASN
1	B	384	ASN
1	B	423	ASN

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](#)

3 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$
3	ERY	A	1498	-	53,53,53	0.74	0	82,82,82	2.32	22 (26%)
2	HEM	B	1497	1	50,50,50	2.14	9 (18%)	67,82,82	1.16	3 (4%)
2	HEM	A	1497	1	50,50,50	2.41	16 (32%)	67,82,82	1.89	18 (26%)

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
3	ERY	A	1498	-	-	9/72/107/107	0/3/3/3
2	HEM	B	1497	1	-	2/14/54/54	-
2	HEM	A	1497	1	-	0/14/54/54	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1497	HEM	C3D-C2D	7.50	1.52	1.36
2	B	1497	HEM	FE-NC	7.39	2.19	1.95
2	A	1497	HEM	C3D-C2D	6.95	1.51	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1497	HEM	FE-ND	6.94	2.16	1.94
2	A	1497	HEM	CAD-C3D	5.69	1.66	1.51

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1498	ERY	O7-C5-C6	11.43	120.03	106.40
3	A	1498	ERY	C22-O7-C5	6.65	127.59	116.26
3	A	1498	ERY	C13-O2-C1	6.27	129.15	118.20
2	A	1497	HEM	C3B-C4B-NB	-5.46	105.55	109.47
2	B	1497	HEM	C4D-ND-C1D	5.02	111.15	105.21

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

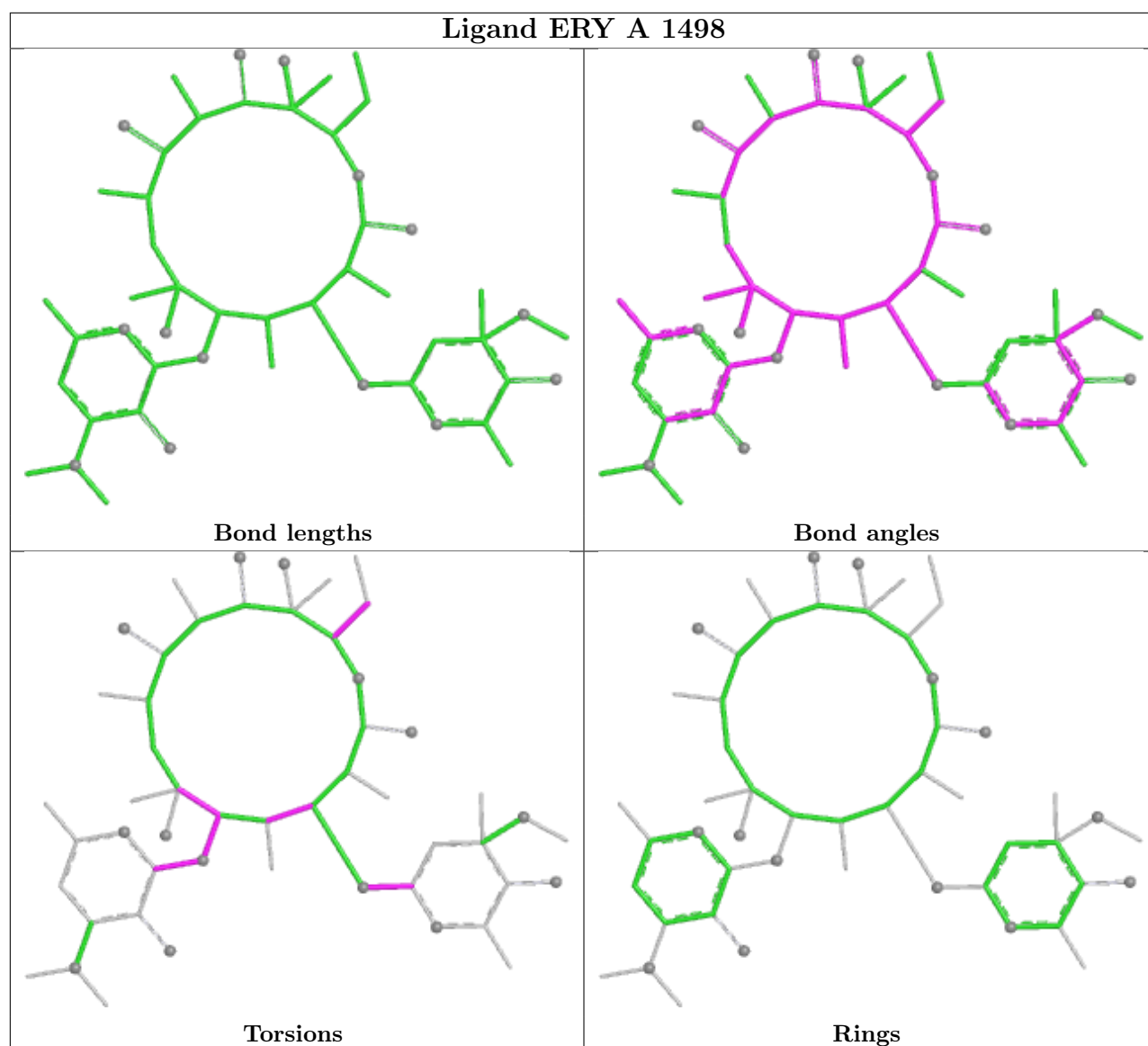
Mol	Chain	Res	Type	Atoms
3	A	1498	ERY	O7-C5-C6-C7
3	A	1498	ERY	C6-C5-O7-C22
3	A	1498	ERY	C15-C14-O3-C3
2	B	1497	HEM	C2C-C3C-CAC-CBC
3	A	1498	ERY	O9-C22-O7-C5

There are no ring outliers.

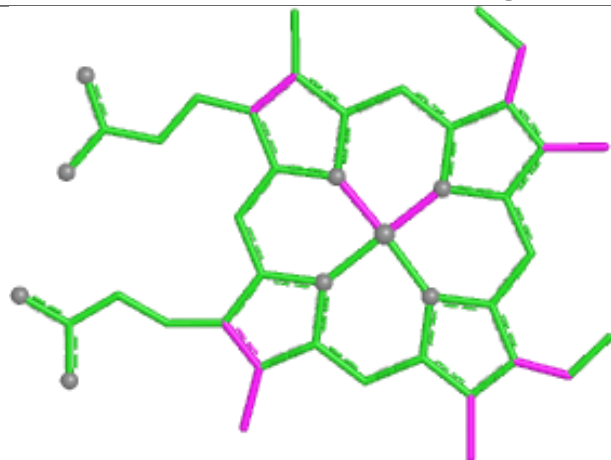
3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1498	ERY	3	0
2	B	1497	HEM	1	0
2	A	1497	HEM	9	0

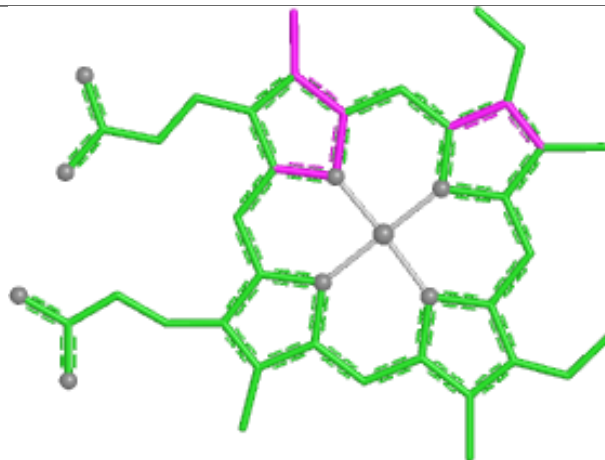
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



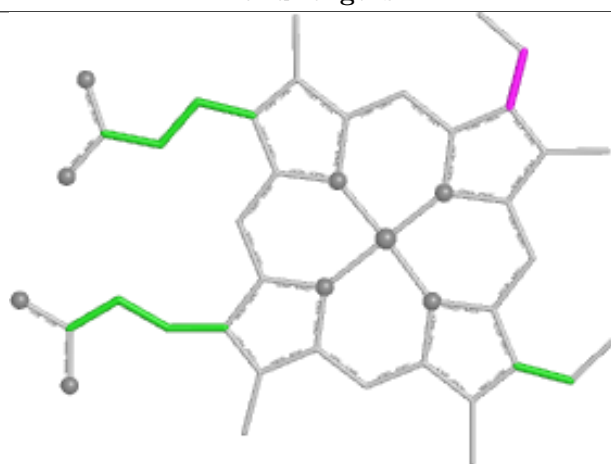
Ligand HEM B 1497



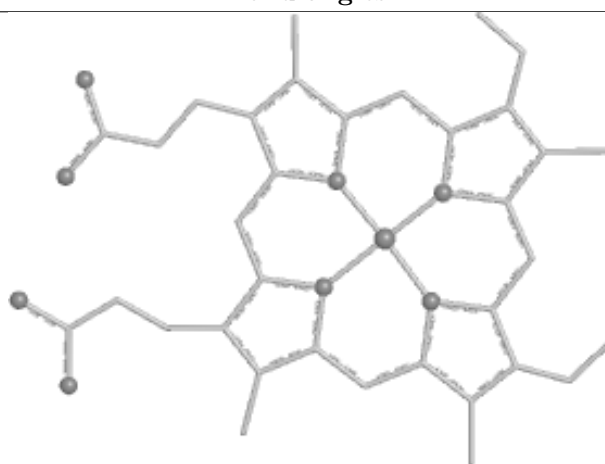
Bond lengths



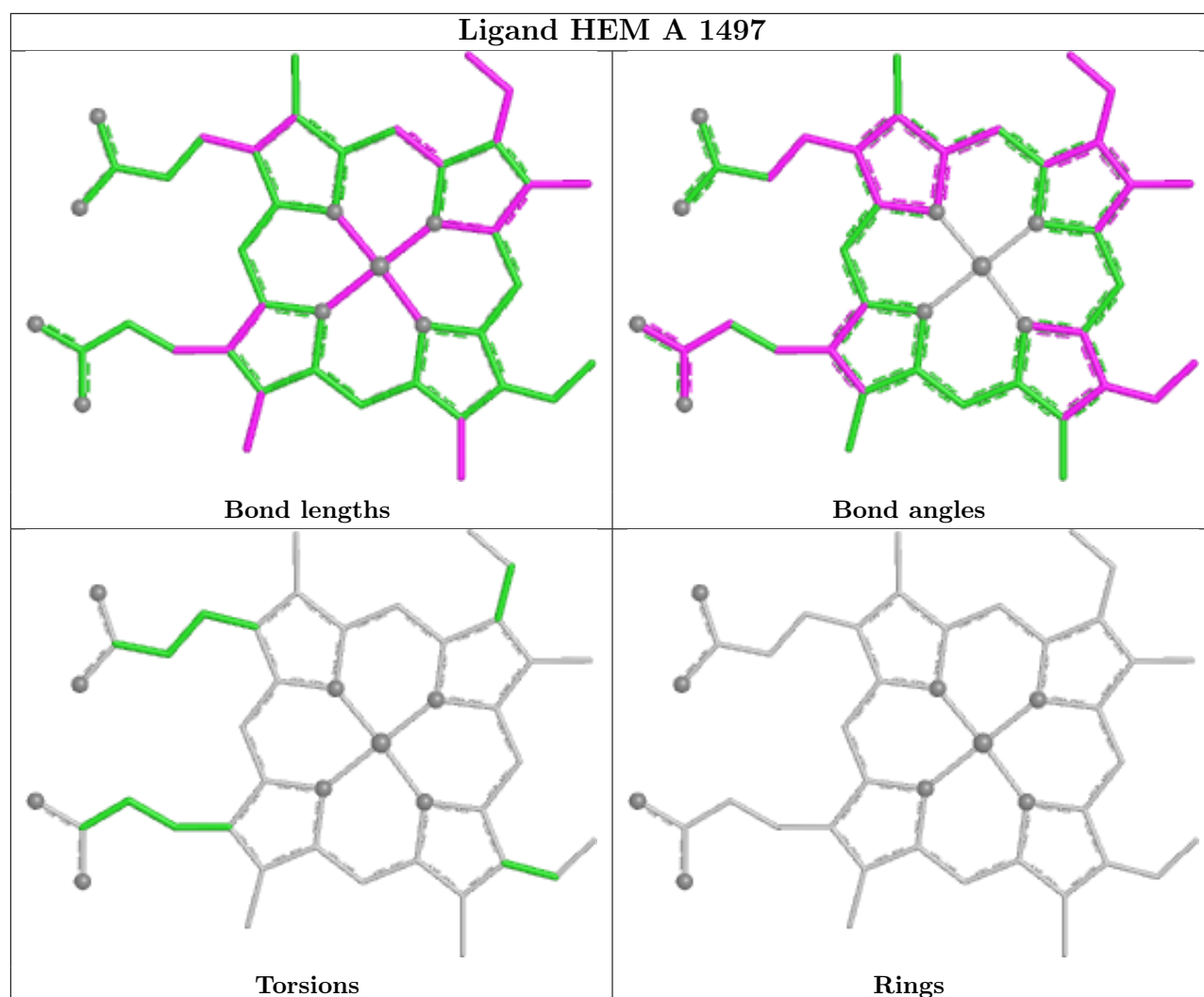
Bond angles



Torsions



Rings



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	446/485 (91%)	0.34	15 (3%) 48 46	22, 47, 71, 79	0
1	B	445/485 (91%)	0.62	33 (7%) 20 20	22, 56, 93, 105	0
All	All	891/970 (91%)	0.48	48 (5%) 31 31	22, 51, 83, 105	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	290	LEU	4.0
1	B	189	PHE	3.6
1	B	165	GLU	3.6
1	A	110	PRO	3.5
1	B	203	PHE	3.2

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 [i](#)

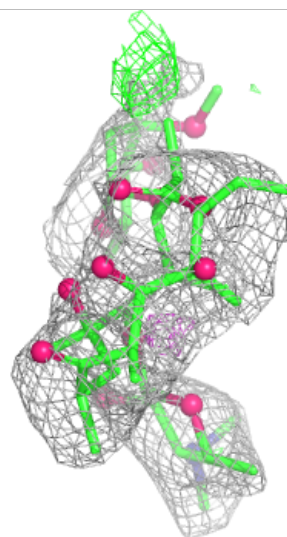
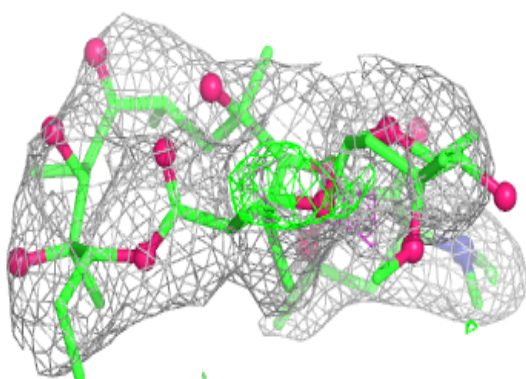
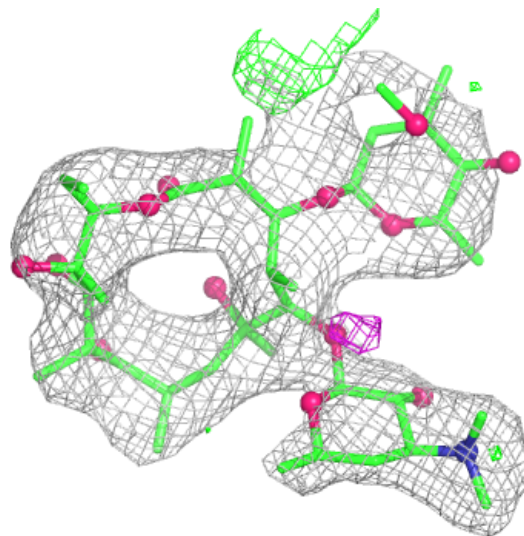
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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
3	ERY	A	1498	51/51	0.80	0.23	88,93,100,100	0
2	HEM	A	1497	43/43	0.95	0.10	22,24,31,36	0
2	HEM	B	1497	43/43	0.97	0.09	27,29,33,35	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.

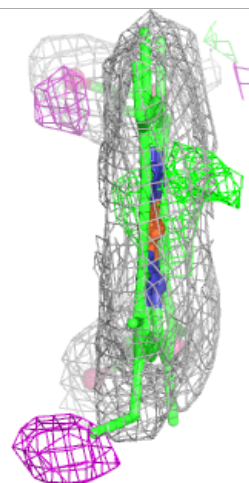
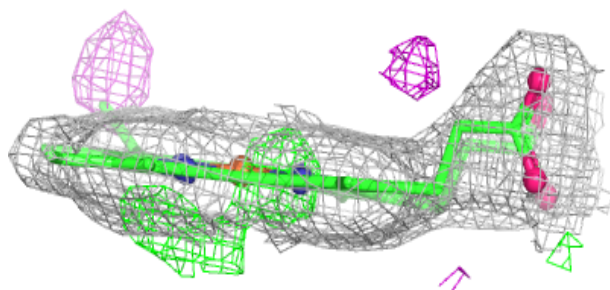
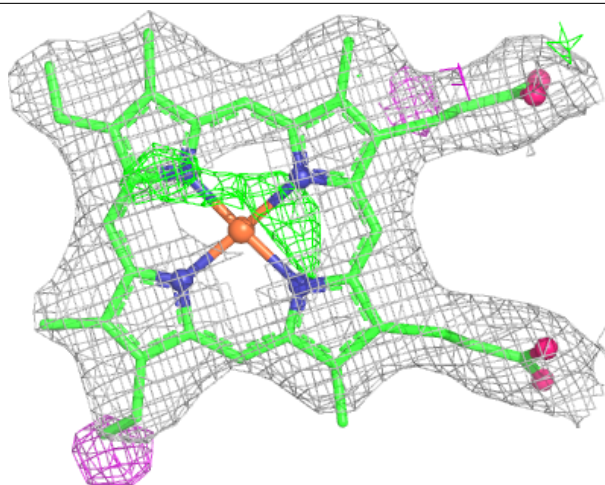
Electron density around ERY A 1498:

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



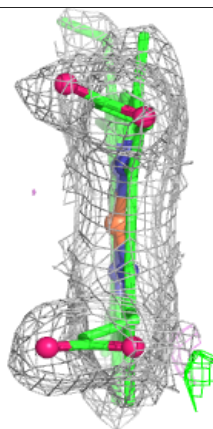
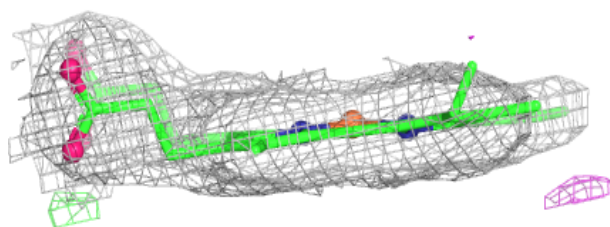
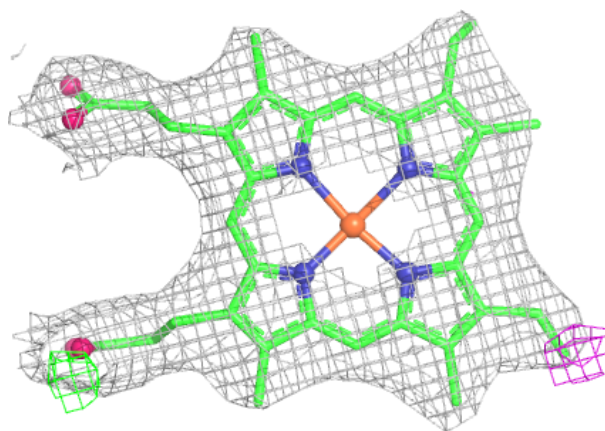
Electron density around HEM A 1497:

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



Electron density around HEM B 1497:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.