



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:59 PM UTC

PDB ID : 4D6Z / pdb_00004d6z
Title : Cytochrome P450 3A4 bound to imidazole and an inhibitor
Authors : Sevrioukova, I.; Poulos, T.
Deposited on : 2014-11-19
Resolution : 1.93 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

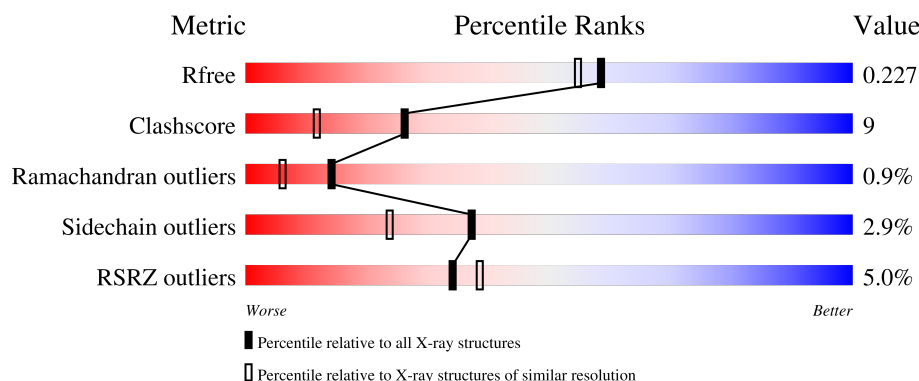
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	487	5% 80% 13% 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
3	PK9	A	1600	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4044 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.

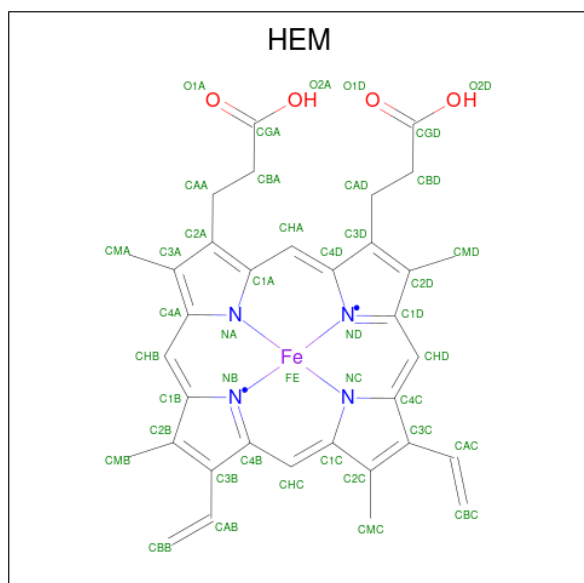
- Molecule 1 is a protein called CYTOCHROME P450 3A4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	460	3759	2449	615	669	26	0	10	0

There are 8 discrepancies between the modelled and reference sequences:

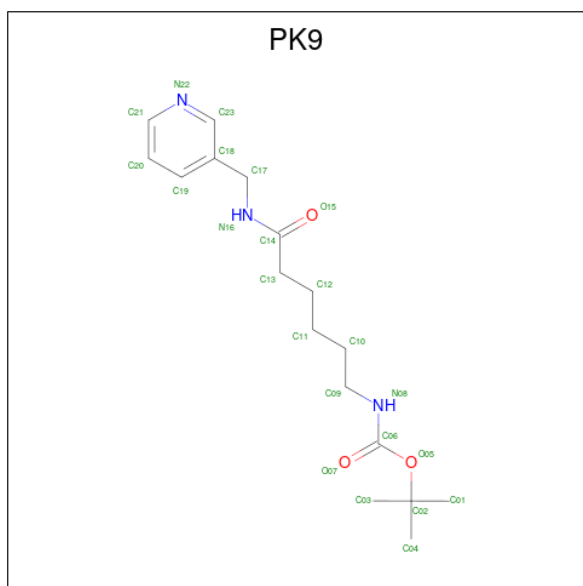
Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MET	-	expression tag	UNP P08684
A	22	ALA	-	expression tag	UNP P08684
A	504	HIS	-	expression tag	UNP P08684
A	505	HIS	-	expression tag	UNP P08684
A	506	HIS	-	expression tag	UNP P08684
A	507	HIS	-	expression tag	UNP P08684
A	282	ALA	LYS	engineered mutation	UNP P08684
A	285	ALA	GLU	engineered mutation	UNP P08684

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



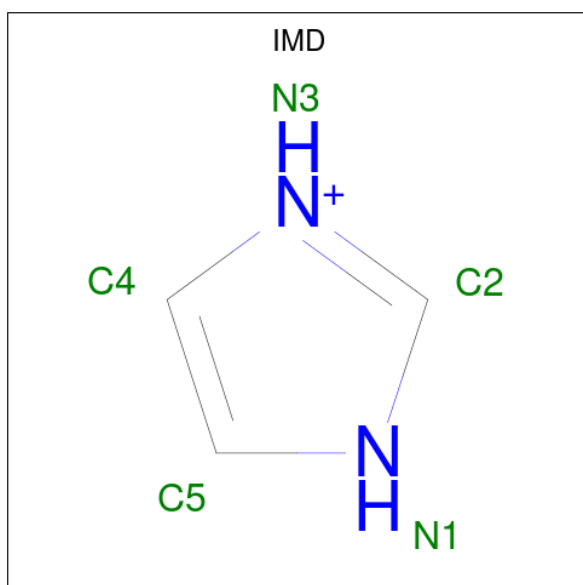
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
							0	0

- Molecule 3 is tert-butyl {6-oxo-6-[(pyridin-3-ylmethyl)amino]hexyl}carbamate (CCD ID: PK9) (formula: $C_{17}H_{27}N_3O_3$).



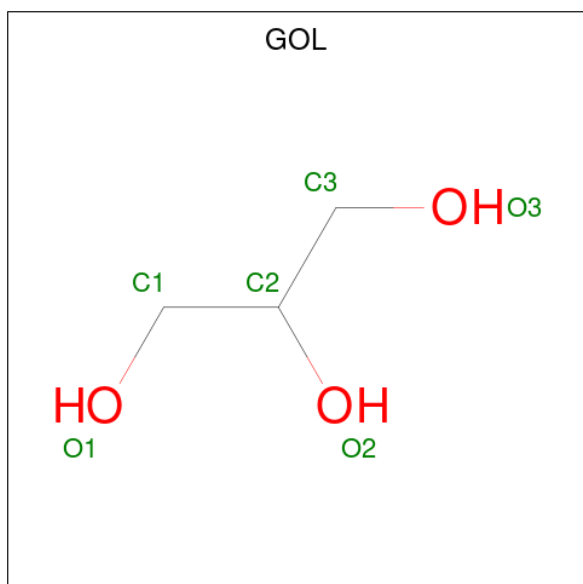
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O		
			23	17	3	3		
							0	0

- Molecule 4 is IMIDAZOLE (CCD ID: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			5	3	2		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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		
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		

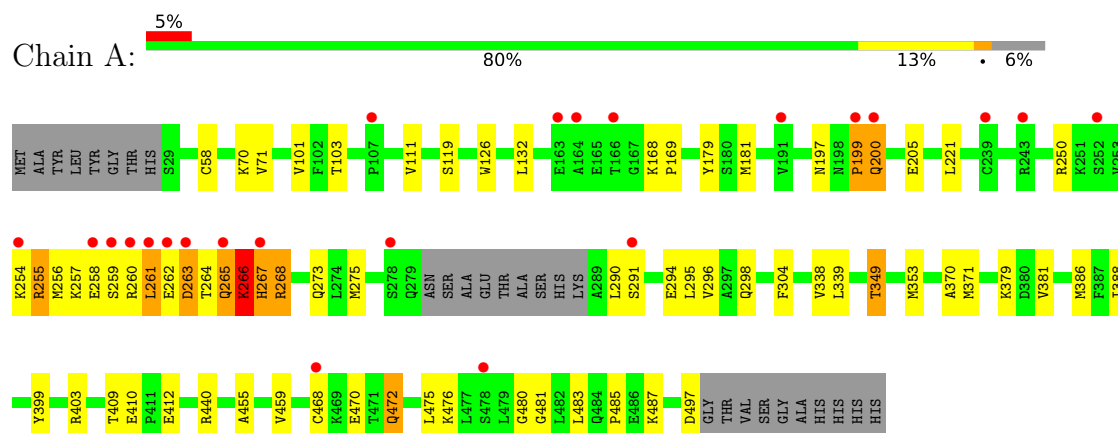
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	190	Total	O	0	0
			190	190		

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 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: CYTOCHROME P450 3A4



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	77.05Å 99.40Å 133.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.49 – 1.93 38.49 – 1.93	Depositor EDS
% Data completeness (in resolution range)	98.9 (38.49-1.93) 98.9 (38.49-1.93)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 1.94Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.180 , 0.227 0.182 , 0.227	Depositor DCC
R_{free} test set	1935 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	37.2	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 55.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4044	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: IMD, HEM, GOL, PK9

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	0.50	0/3870	0.80	4/5234 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	PRO	CA-C-N	-6.56	112.82	122.86
1	A	199	PRO	C-N-CA	-6.56	112.82	122.86
1	A	388	ILE	CA-C-N	5.08	124.98	119.85
1	A	388	ILE	C-N-CA	5.08	124.98	119.85

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	3759	0	3870	69	0
2	A	43	0	30	0	0
3	A	23	0	27	11	0
4	A	5	0	4	3	0
5	A	24	0	32	3	0
6	A	190	0	0	3	0
All	All	4044	0	3963	73	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 9.

All (73) 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:266:LYS:HE2	1:A:268:ARG:HH11	1.40	0.85
1:A:472:GLN:HE21	1:A:487:LYS:HG3	1.48	0.77
1:A:403:ARG:HH22	5:A:1605:GOL:H11	1.52	0.75
3:A:1600:PK9:H013	4:A:1601:IMD:H4	1.70	0.74
1:A:266:LYS:CE	1:A:268:ARG:HH11	2.01	0.74
1:A:371[B]:MET:HE3	1:A:483:LEU:HB2	1.73	0.69
1:A:255:ARG:HA	1:A:258:GLU:HB2	1.76	0.67
1:A:250:ARG:O	1:A:254:LYS:HG3	1.96	0.66
1:A:267:HIS:O	1:A:268:ARG:HB2	1.96	0.65
1:A:267:HIS:O	1:A:268:ARG:CB	2.45	0.63
1:A:266:LYS:HE2	1:A:268:ARG:HD3	1.82	0.61
1:A:254:LYS:O	1:A:258:GLU:N	2.34	0.60
1:A:339:LEU:HD21	1:A:349[A]:THR:HG21	1.83	0.60
1:A:268:ARG:CB	1:A:273:GLN:HG3	2.34	0.58
1:A:304:PHE:CE2	3:A:1600:PK9:H19	2.39	0.58
1:A:71[A]:VAL:HG11	1:A:386:MET:HE1	1.86	0.57
1:A:256:MET:O	1:A:260:ARG:HB2	2.04	0.57
1:A:259:SER:O	1:A:262:GLU:HB2	2.05	0.57
1:A:470:GLU:N	1:A:470:GLU:OE1	2.38	0.57
1:A:263:ASP:O	1:A:264:THR:HB	2.03	0.56
1:A:254:LYS:O	1:A:258:GLU:HB2	2.05	0.56
1:A:275:MET:HE2	1:A:295:LEU:HG	1.87	0.56
1:A:119[B]:SER:HB3	3:A:1600:PK9:H121	1.87	0.55
1:A:119[A]:SER:HB2	3:A:1600:PK9:H121	1.87	0.55
1:A:472:GLN:NE2	1:A:487:LYS:HG3	2.18	0.54
1:A:268:ARG:HB2	1:A:273:GLN:HG3	1.88	0.54
1:A:266:LYS:CE	1:A:268:ARG:NH1	2.69	0.54
1:A:294:GLU:O	1:A:298:GLN:HG2	2.08	0.54
1:A:58:CYS:SG	1:A:371[B]:MET:HE2	2.48	0.54
1:A:412:GLU:HG2	6:A:2156:HOH:O	2.08	0.53
1:A:379:LYS:O	1:A:381[B]:VAL:HG23	2.10	0.51
1:A:409:THR:HG22	1:A:410:GLU:HG3	1.91	0.51
3:A:1600:PK9:H013	4:A:1601:IMD:C4	2.40	0.51
1:A:261:LEU:HD12	1:A:261:LEU:O	2.10	0.51
1:A:265:GLN:O	1:A:266:LYS:HB2	2.10	0.51
1:A:119[B]:SER:CB	3:A:1600:PK9:H16	2.24	0.50
1:A:472:GLN:OE1	1:A:476:LYS:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:ARG:HG2	1:A:296:VAL:HG11	1.95	0.49
1:A:169:PRO:HB3	1:A:468:CYS:SG	2.52	0.49
1:A:371[B]:MET:HE1	5:A:1602:GOL:C3	2.42	0.48
1:A:266:LYS:HE2	1:A:268:ARG:NH1	2.18	0.48
1:A:126:TRP:CZ2	1:A:440[B]:ARG:HG2	2.49	0.48
1:A:119[B]:SER:HB2	3:A:1600:PK9:H16	1.79	0.48
1:A:261:LEU:C	1:A:263:ASP:H	2.23	0.47
1:A:268:ARG:HB3	1:A:273:GLN:HG3	1.97	0.47
1:A:259:SER:O	1:A:262:GLU:N	2.48	0.45
1:A:266:LYS:NZ	1:A:268:ARG:NH1	2.64	0.45
1:A:371[A]:MET:HE1	1:A:481:GLY:O	2.16	0.45
3:A:1600:PK9:H132	4:A:1601:IMD:C2	2.47	0.45
1:A:370:ALA:C	1:A:371[B]:MET:HG3	2.40	0.45
1:A:119[A]:SER:CB	3:A:1600:PK9:H16	2.28	0.45
1:A:257:LYS:O	1:A:258:GLU:C	2.58	0.45
1:A:221:LEU:HD23	1:A:221:LEU:HA	1.83	0.45
1:A:70:LYS:NZ	6:A:2031:HOH:O	2.50	0.44
1:A:103:THR:O	1:A:440[B]:ARG:HD2	2.18	0.44
1:A:58:CYS:HB3	1:A:399:TYR:CD1	2.53	0.43
1:A:267:HIS:O	1:A:268:ARG:CG	2.66	0.43
1:A:475[A]:LEU:HD11	1:A:485:PRO:HB3	2.01	0.43
1:A:132:LEU:HD13	1:A:290:LEU:HG	1.99	0.43
1:A:101:VAL:HG22	1:A:379:LYS:HE2	2.00	0.43
1:A:254:LYS:O	1:A:258:GLU:CA	2.66	0.43
1:A:304:PHE:HE2	3:A:1600:PK9:H19	1.81	0.43
1:A:179:TYR:CZ	1:A:455:ALA:HB2	2.54	0.43
1:A:197:ASN:C	1:A:199:PRO:HD3	2.44	0.43
1:A:266:LYS:NZ	1:A:268:ARG:HH11	2.18	0.42
1:A:71[B]:VAL:HG11	1:A:386:MET:HE1	2.02	0.42
1:A:181[B]:MET:HE3	1:A:181[B]:MET:HB2	1.81	0.42
3:A:1600:PK9:H092	6:A:2150:HOH:O	2.18	0.42
1:A:260:ARG:HA	1:A:260:ARG:HD2	1.63	0.41
1:A:480:GLY:O	5:A:1602:GOL:H32	2.20	0.41
1:A:200:GLN:HG3	1:A:205:GLU:CD	2.46	0.41
1:A:338:VAL:HB	1:A:353:MET:HE2	2.03	0.41
1:A:275:MET:HE1	1:A:295:LEU:HA	2.03	0.40

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	466/487 (96%)	443 (95%)	19 (4%)	4 (1%)	14 6

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	LYS
1	A	268	ARG
1	A	265	GLN
1	A	267	HIS

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	431/441 (98%)	418 (97%)	13 (3%)	36 22

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	111	VAL
1	A	168	LYS
1	A	200	GLN
1	A	255	ARG
1	A	261	LEU
1	A	263	ASP
1	A	266	LYS

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Mol	Chain	Res	Type
1	A	291	SER
1	A	349[A]	THR
1	A	349[B]	THR
1	A	459	VAL
1	A	472	GLN
1	A	497	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	200	GLN
1	A	273	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](#)

7 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	PK9	A	1600	-	23,23,23	1.39	2 (8%)	29,29,29	1.55	5 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GOL	A	1604	-	5,5,5	0.46	0	5,5,5	0.25	0
5	GOL	A	1602	-	5,5,5	0.44	0	5,5,5	0.59	0
2	HEM	A	1500	1,4	50,50,50	1.89	10 (20%)	67,82,82	1.36	9 (13%)
5	GOL	A	1605	-	5,5,5	0.36	0	5,5,5	0.27	0
5	GOL	A	1603	-	5,5,5	0.37	0	5,5,5	0.48	0
4	IMD	A	1601	2	5,5,5	0.64	0	5,5,5	0.51	0

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
5	GOL	A	1604	-	-	2/4/4/4	-
3	PK9	A	1600	-	-	14/19/19/19	0/1/1/1
5	GOL	A	1602	-	-	2/4/4/4	-
2	HEM	A	1500	1,4	-	1/14/54/54	-
5	GOL	A	1605	-	-	2/4/4/4	-
5	GOL	A	1603	-	-	4/4/4/4	-
4	IMD	A	1601	2	-	-	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1500	HEM	C3D-C2D	7.31	1.52	1.36
3	A	1600	PK9	O05-C06	5.81	1.45	1.34
2	A	1500	HEM	FE-NB	4.44	2.08	1.94
2	A	1500	HEM	CAC-C3C	3.73	1.57	1.47
2	A	1500	HEM	FE-NA	3.61	2.07	1.95
2	A	1500	HEM	FE-NC	3.47	2.06	1.95
2	A	1500	HEM	FE-ND	3.23	2.04	1.94
2	A	1500	HEM	CAB-C3B	3.12	1.55	1.47
3	A	1600	PK9	O05-C02	-2.89	1.43	1.48
2	A	1500	HEM	CMD-C2D	2.38	1.55	1.50
2	A	1500	HEM	CMC-C2C	2.30	1.55	1.50
2	A	1500	HEM	CMB-C2B	2.13	1.55	1.50

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1600	PK9	O05-C06-N08	4.81	116.83	110.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1500	HEM	C4D-ND-C1D	4.70	110.77	105.21
3	A	1600	PK9	O05-C06-O07	-3.44	119.52	125.64
2	A	1500	HEM	C1B-NB-C4B	2.76	108.48	105.21
2	A	1500	HEM	CHD-C1D-ND	2.68	127.31	124.42
2	A	1500	HEM	CBD-CAD-C3D	-2.47	105.70	112.53
3	A	1600	PK9	C18-C17-N16	-2.38	108.06	113.07
2	A	1500	HEM	C3B-C4B-NB	-2.35	107.78	109.47
3	A	1600	PK9	C21-N22-C23	2.34	120.95	116.85
2	A	1500	HEM	C3B-C2B-C1B	2.33	108.16	106.41
2	A	1500	HEM	CAD-C3D-C4D	2.20	128.52	124.70
2	A	1500	HEM	CMB-C2B-C1B	-2.17	121.65	125.03
3	A	1600	PK9	C19-C18-C23	2.04	120.10	117.10
2	A	1500	HEM	CHB-C1B-NB	2.02	126.87	124.37

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1600	PK9	O15-C14-N16-C17
3	A	1600	PK9	C13-C14-N16-C17
5	A	1602	GOL	O1-C1-C2-C3
5	A	1603	GOL	C1-C2-C3-O3
5	A	1604	GOL	C1-C2-C3-O3
5	A	1604	GOL	O2-C2-C3-O3
5	A	1605	GOL	C1-C2-C3-O3
3	A	1600	PK9	O07-C06-O05-C02
3	A	1600	PK9	C03-C02-O05-C06
3	A	1600	PK9	C01-C02-O05-C06
3	A	1600	PK9	N08-C06-O05-C02
3	A	1600	PK9	C04-C02-O05-C06
3	A	1600	PK9	N08-C09-C10-C11
5	A	1603	GOL	O1-C1-C2-O2
5	A	1603	GOL	O2-C2-C3-O3
5	A	1603	GOL	O1-C1-C2-C3
5	A	1602	GOL	O1-C1-C2-O2
5	A	1605	GOL	O2-C2-C3-O3
3	A	1600	PK9	C12-C13-C14-N16
3	A	1600	PK9	C12-C13-C14-O15
3	A	1600	PK9	C09-C10-C11-C12
3	A	1600	PK9	O05-C06-N08-C09
3	A	1600	PK9	O07-C06-N08-C09
3	A	1600	PK9	C18-C17-N16-C14

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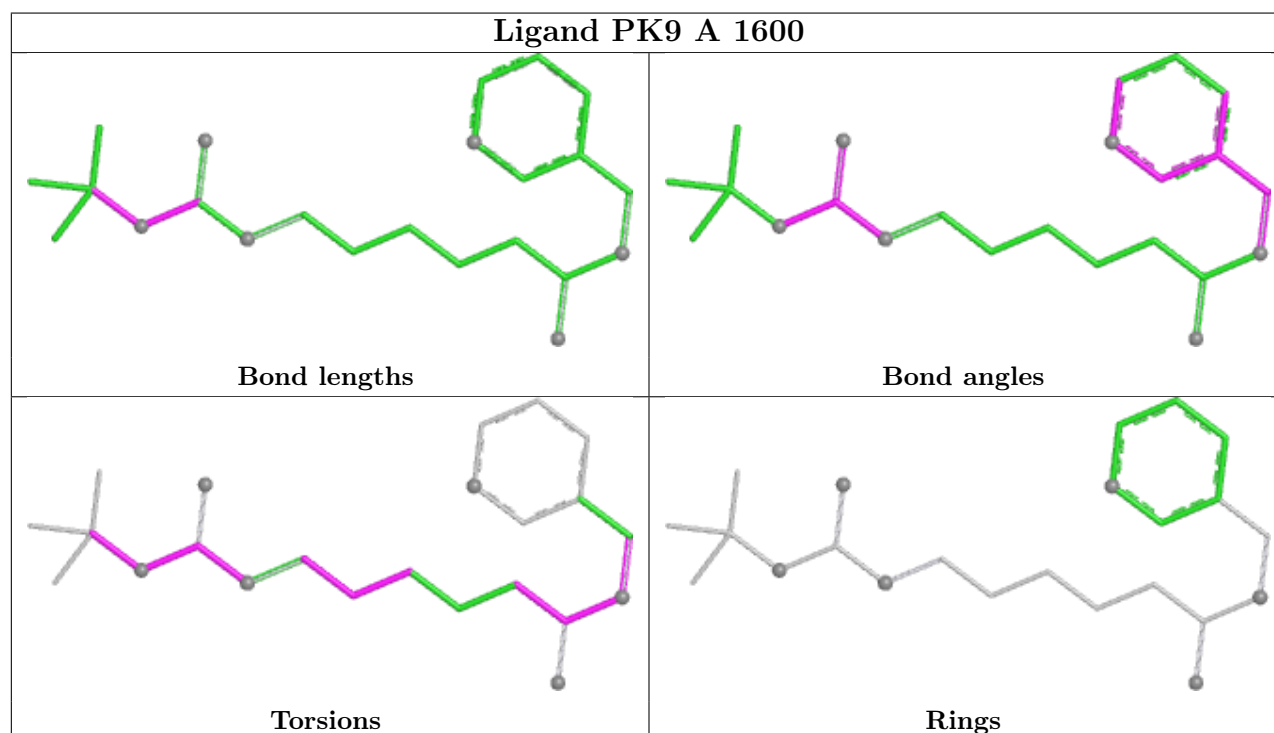
Mol	Chain	Res	Type	Atoms
2	A	1500	HEM	CAA-CBA-CGA-O2A

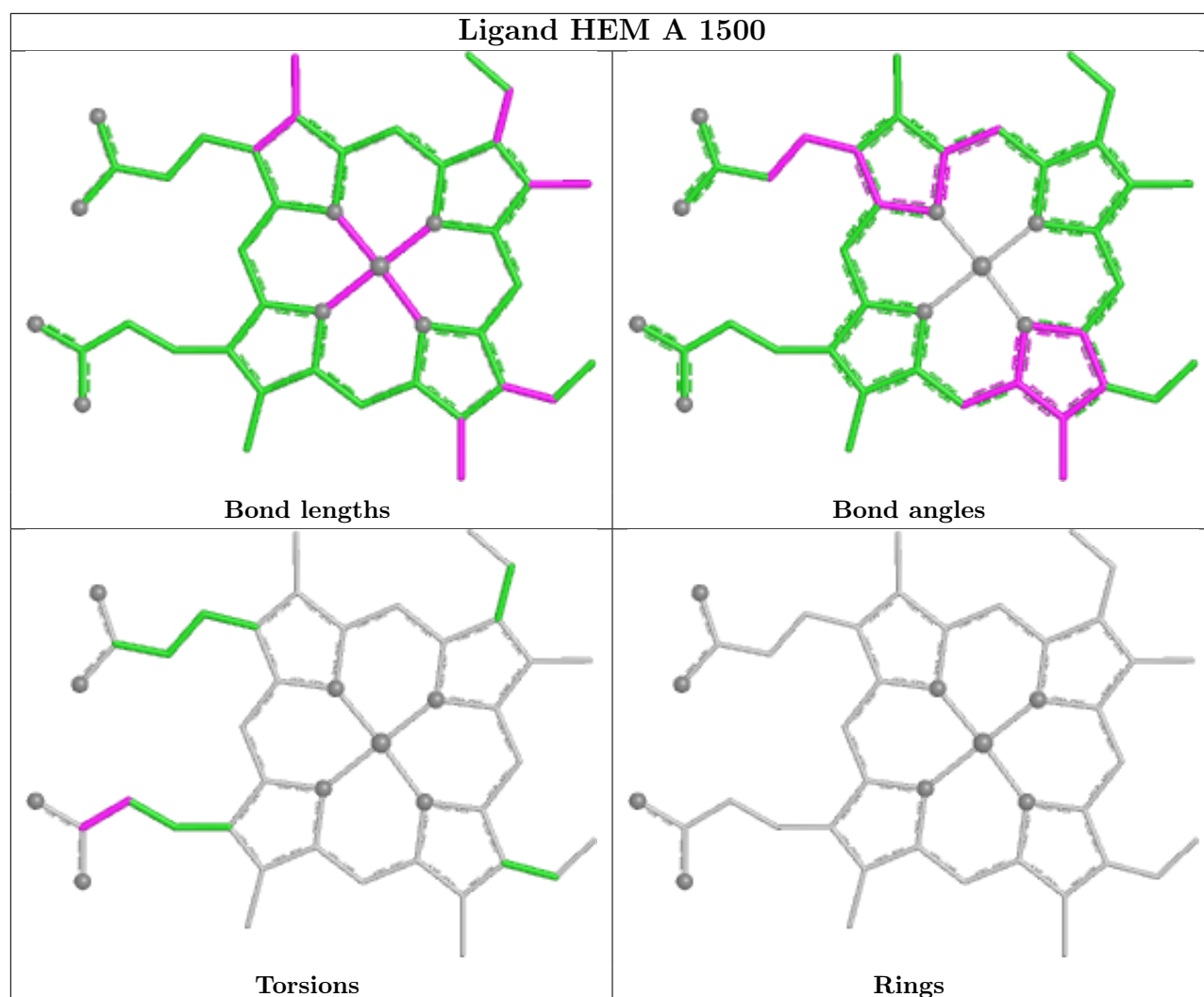
There are no ring outliers.

4 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1600	PK9	11	0
5	A	1602	GOL	2	0
5	A	1605	GOL	1	0
4	A	1601	IMD	3	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	460/487 (94%)	0.32	23 (5%)	34 38	17, 46, 85, 165	10 (2%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	261	LEU	7.3
1	A	259	SER	3.5
1	A	468	CYS	3.2
1	A	107	PRO	2.9
1	A	265	GLN	2.8
1	A	262	GLU	2.7
1	A	267	HIS	2.7
1	A	164	ALA	2.6
1	A	166	THR	2.5
1	A	254	LYS	2.4
1	A	478	SER	2.4
1	A	278[A]	SER	2.4
1	A	263	ASP	2.3
1	A	239	CYS	2.2
1	A	252	SER	2.2
1	A	163	GLU	2.1
1	A	243	ARG	2.1
1	A	258	GLU	2.1
1	A	200	GLN	2.1
1	A	260	ARG	2.1
1	A	191	VAL	2.0
1	A	291	SER	2.0
1	A	199	PRO	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 [i](#)

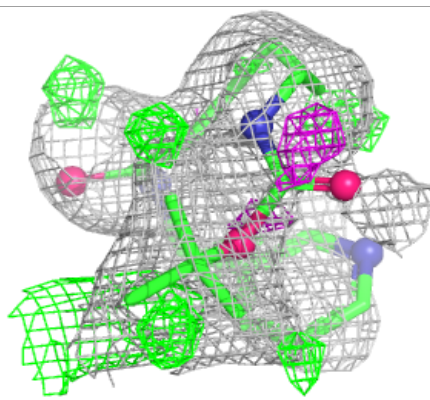
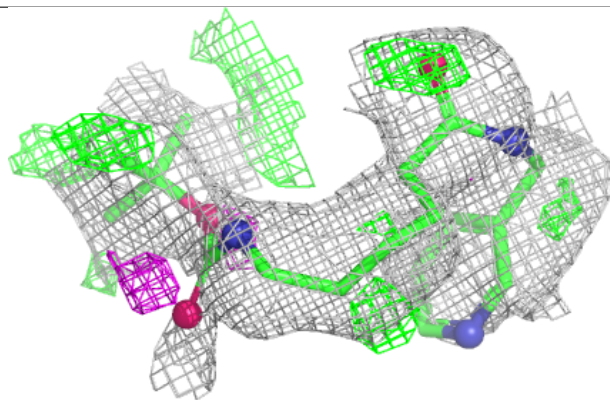
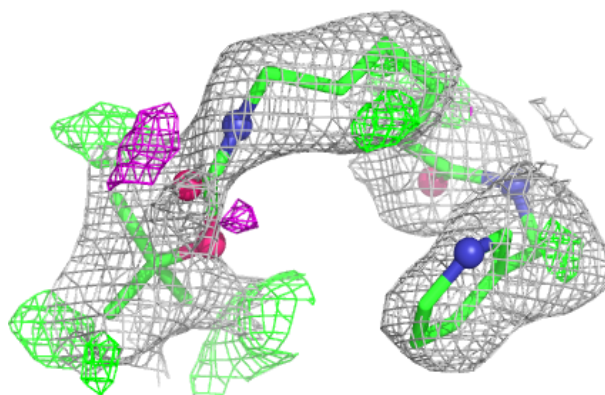
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	PK9	A	1600	23/23	0.75	0.18	65,92,107,111	0
5	GOL	A	1605	6/6	0.82	0.13	73,83,84,87	0
5	GOL	A	1602	6/6	0.91	0.11	37,47,54,58	0
4	IMD	A	1601	5/5	0.91	0.16	57,57,68,72	0
5	GOL	A	1603	6/6	0.92	0.11	51,61,73,74	0
5	GOL	A	1604	6/6	0.94	0.09	37,54,65,80	0
2	HEM	A	1500	43/43	0.99	0.05	25,30,36,49	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.

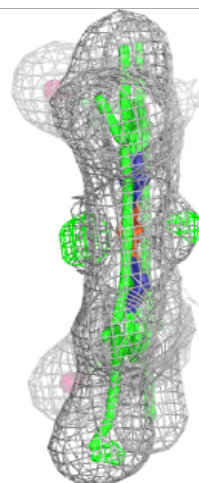
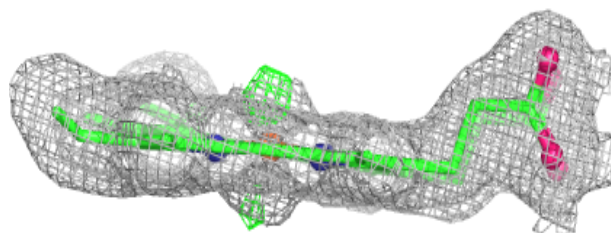
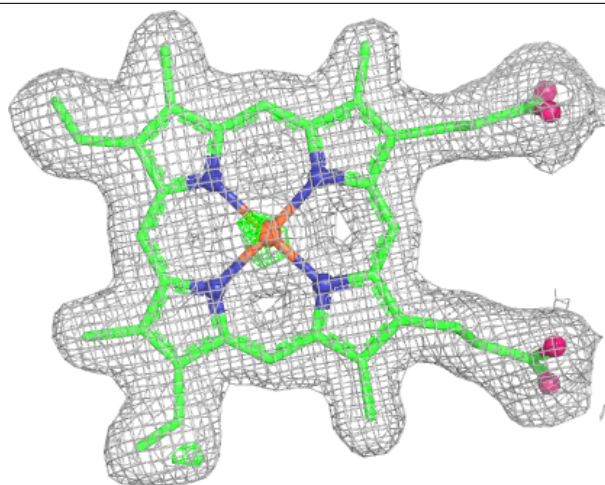
Electron density around PK9 A 1600:

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



Electron density around HEM A 1500:

$2mF_o-DF_c$ (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.