



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2023 – 06:06 pm BST

PDB ID : 8ADR
Title : Crystal structure of a staphylococcal orthologue of CYP134A1 (CYPX) in complex with a fragment
Authors : Snee, M.; Katariya, M.; Levy, C.
Deposited on : 2022-07-11
Resolution : 1.92 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.34
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) : 2.34

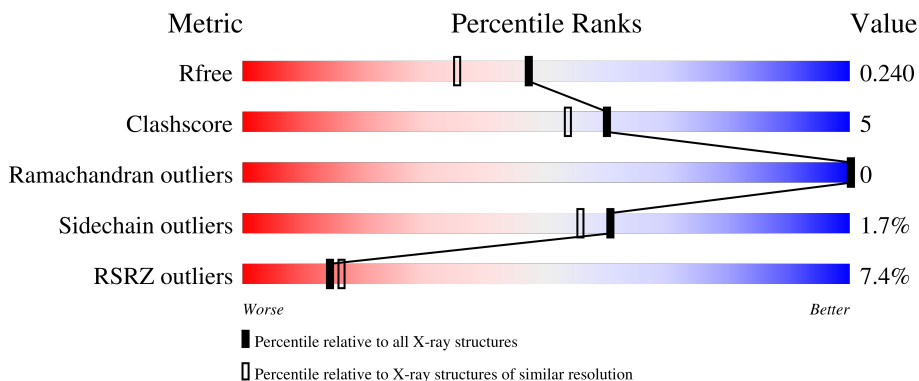
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 1.92 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	400	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6724 atoms, of which 3278 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 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	391	6443	2047	3242	530	611	13	0	7	0

There are 139 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A0A380DQV1
A	1	SER	-	expression tag	UNP A0A380DQV1
A	2	LEU	-	expression tag	UNP A0A380DQV1
A	3	LYS	-	expression tag	UNP A0A380DQV1
A	4	VAL	-	expression tag	UNP A0A380DQV1
A	5	TYR	-	expression tag	UNP A0A380DQV1
A	6	ASN	-	expression tag	UNP A0A380DQV1
A	7	SER	-	expression tag	UNP A0A380DQV1
A	8	ILE	-	expression tag	UNP A0A380DQV1
A	9	PHE	-	expression tag	UNP A0A380DQV1
A	10	ASP	-	expression tag	UNP A0A380DQV1
A	11	GLN	-	expression tag	UNP A0A380DQV1
A	12	ALA	-	expression tag	UNP A0A380DQV1
A	13	TYR	-	expression tag	UNP A0A380DQV1
A	14	GLU	-	expression tag	UNP A0A380DQV1
A	15	ILE	-	expression tag	UNP A0A380DQV1
A	16	ASP	-	expression tag	UNP A0A380DQV1
A	17	PRO	-	expression tag	UNP A0A380DQV1
A	18	ILE	-	expression tag	UNP A0A380DQV1
A	19	PRO	-	expression tag	UNP A0A380DQV1
A	20	TYR	-	expression tag	UNP A0A380DQV1
A	21	PHE	-	expression tag	UNP A0A380DQV1
A	22	ASN	-	expression tag	UNP A0A380DQV1
A	23	PHE	-	expression tag	UNP A0A380DQV1
A	24	LEU	-	expression tag	UNP A0A380DQV1
A	25	ARG	-	expression tag	UNP A0A380DQV1
A	26	LYS	-	expression tag	UNP A0A380DQV1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	27	HIS	-	expression tag	UNP A0A380DQV1
A	28	ASP	-	expression tag	UNP A0A380DQV1
A	29	PRO	-	expression tag	UNP A0A380DQV1
A	30	VAL	-	expression tag	UNP A0A380DQV1
A	31	HIS	-	expression tag	UNP A0A380DQV1
A	32	TYR	-	expression tag	UNP A0A380DQV1
A	33	GLU	-	expression tag	UNP A0A380DQV1
A	34	GLU	-	expression tag	UNP A0A380DQV1
A	35	SER	-	expression tag	UNP A0A380DQV1
A	36	ILE	-	expression tag	UNP A0A380DQV1
A	37	ASP	-	expression tag	UNP A0A380DQV1
A	38	ALA	-	expression tag	UNP A0A380DQV1
A	39	TYR	-	expression tag	UNP A0A380DQV1
A	40	PHE	-	expression tag	UNP A0A380DQV1
A	41	VAL	-	expression tag	UNP A0A380DQV1
A	42	SER	-	expression tag	UNP A0A380DQV1
A	43	LYS	-	expression tag	UNP A0A380DQV1
A	44	TYR	-	expression tag	UNP A0A380DQV1
A	45	LYS	-	expression tag	UNP A0A380DQV1
A	46	ASP	-	expression tag	UNP A0A380DQV1
A	47	VAL	-	expression tag	UNP A0A380DQV1
A	48	LYS	-	expression tag	UNP A0A380DQV1
A	49	TYR	-	expression tag	UNP A0A380DQV1
A	50	ILE	-	expression tag	UNP A0A380DQV1
A	51	LEU	-	expression tag	UNP A0A380DQV1
A	52	LYS	-	expression tag	UNP A0A380DQV1
A	53	ASN	-	expression tag	UNP A0A380DQV1
A	54	ASN	-	expression tag	UNP A0A380DQV1
A	55	ASP	-	expression tag	UNP A0A380DQV1
A	56	ILE	-	expression tag	UNP A0A380DQV1
A	57	PHE	-	expression tag	UNP A0A380DQV1
A	58	ASN	-	expression tag	UNP A0A380DQV1
A	59	THR	-	expression tag	UNP A0A380DQV1
A	60	LYS	-	expression tag	UNP A0A380DQV1
A	61	THR	-	expression tag	UNP A0A380DQV1
A	62	LEU	-	expression tag	UNP A0A380DQV1
A	63	ALA	-	expression tag	UNP A0A380DQV1
A	64	LYS	-	expression tag	UNP A0A380DQV1
A	65	ARG	-	expression tag	UNP A0A380DQV1
A	66	ALA	-	expression tag	UNP A0A380DQV1
A	67	GLU	-	expression tag	UNP A0A380DQV1
A	68	PRO	-	expression tag	UNP A0A380DQV1

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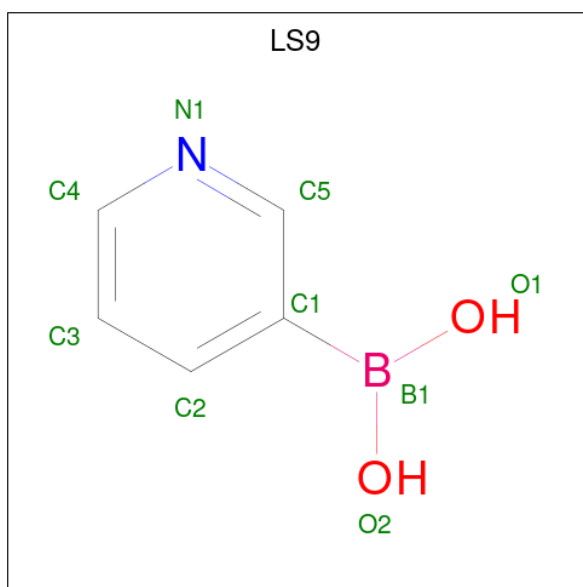
Chain	Residue	Modelled	Actual	Comment	Reference
A	69	VAL	-	expression tag	UNP A0A380DQV1
A	70	MET	-	expression tag	UNP A0A380DQV1
A	71	LYS	-	expression tag	UNP A0A380DQV1
A	72	ASP	-	expression tag	UNP A0A380DQV1
A	73	ARG	-	expression tag	UNP A0A380DQV1
A	74	VAL	-	expression tag	UNP A0A380DQV1
A	75	LEU	-	expression tag	UNP A0A380DQV1
A	76	ALA	-	expression tag	UNP A0A380DQV1
A	77	GLN	-	expression tag	UNP A0A380DQV1
A	78	MET	-	expression tag	UNP A0A380DQV1
A	79	SER	-	expression tag	UNP A0A380DQV1
A	80	GLY	-	expression tag	UNP A0A380DQV1
A	81	GLN	-	expression tag	UNP A0A380DQV1
A	82	GLU	-	expression tag	UNP A0A380DQV1
A	83	HIS	-	expression tag	UNP A0A380DQV1
A	84	LYS	-	expression tag	UNP A0A380DQV1
A	85	SER	-	expression tag	UNP A0A380DQV1
A	86	LYS	-	expression tag	UNP A0A380DQV1
A	87	LYS	-	expression tag	UNP A0A380DQV1
A	88	LYS	-	expression tag	UNP A0A380DQV1
A	89	ALA	-	expression tag	UNP A0A380DQV1
A	90	ILE	-	expression tag	UNP A0A380DQV1
A	91	LEU	-	expression tag	UNP A0A380DQV1
A	92	LYS	-	expression tag	UNP A0A380DQV1
A	93	GLY	-	expression tag	UNP A0A380DQV1
A	94	MET	-	expression tag	UNP A0A380DQV1
A	95	THR	-	expression tag	UNP A0A380DQV1
A	96	GLY	-	expression tag	UNP A0A380DQV1
A	97	LYS	-	expression tag	UNP A0A380DQV1
A	98	TYR	-	expression tag	UNP A0A380DQV1
A	99	LEU	-	expression tag	UNP A0A380DQV1
A	100	GLU	-	expression tag	UNP A0A380DQV1
A	101	ASN	-	expression tag	UNP A0A380DQV1
A	102	LEU	-	expression tag	UNP A0A380DQV1
A	103	MET	-	expression tag	UNP A0A380DQV1
A	104	PRO	-	expression tag	UNP A0A380DQV1
A	105	ILE	-	expression tag	UNP A0A380DQV1
A	106	LEU	-	expression tag	UNP A0A380DQV1
A	107	GLU	-	expression tag	UNP A0A380DQV1
A	108	LYS	-	expression tag	UNP A0A380DQV1
A	109	ARG	-	expression tag	UNP A0A380DQV1
A	110	THR	-	expression tag	UNP A0A380DQV1

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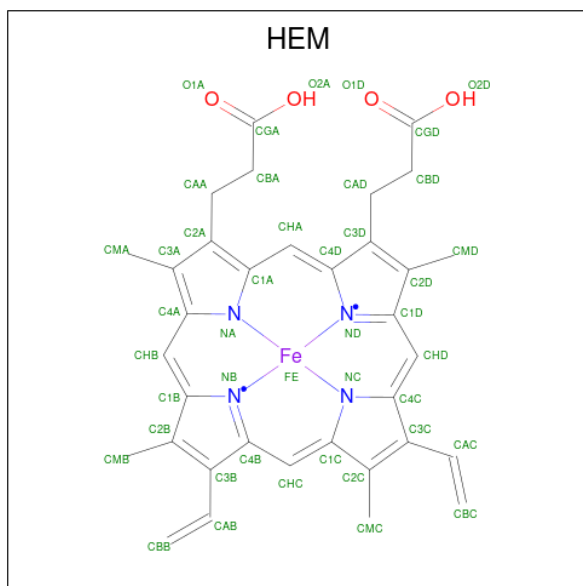
Chain	Residue	Modelled	Actual	Comment	Reference
A	111	ASN	-	expression tag	UNP A0A380DQV1
A	112	ASP	-	expression tag	UNP A0A380DQV1
A	113	ILE	-	expression tag	UNP A0A380DQV1
A	114	ILE	-	expression tag	UNP A0A380DQV1
A	115	ASN	-	expression tag	UNP A0A380DQV1
A	116	LYS	-	expression tag	UNP A0A380DQV1
A	117	HIS	-	expression tag	UNP A0A380DQV1
A	118	ILE	-	expression tag	UNP A0A380DQV1
A	119	GLU	-	expression tag	UNP A0A380DQV1
A	120	LYS	-	expression tag	UNP A0A380DQV1
A	121	LYS	-	expression tag	UNP A0A380DQV1
A	122	GLU	-	expression tag	UNP A0A380DQV1
A	123	ILE	-	expression tag	UNP A0A380DQV1
A	124	ASP	-	expression tag	UNP A0A380DQV1
A	125	ILE	-	expression tag	UNP A0A380DQV1
A	126	VAL	-	expression tag	UNP A0A380DQV1
A	127	ASN	-	expression tag	UNP A0A380DQV1
A	128	ASP	-	expression tag	UNP A0A380DQV1
A	129	PHE	-	expression tag	UNP A0A380DQV1
A	130	GLY	-	expression tag	UNP A0A380DQV1
A	131	LYS	-	expression tag	UNP A0A380DQV1
A	132	VAL	-	expression tag	UNP A0A380DQV1
A	133	PHE	-	expression tag	UNP A0A380DQV1
A	134	ALA	-	expression tag	UNP A0A380DQV1
A	135	VAL	-	expression tag	UNP A0A380DQV1
A	136	GLN	-	expression tag	UNP A0A380DQV1
A	137	SER	-	expression tag	UNP A0A380DQV1
A	138	SER	-	expression tag	UNP A0A380DQV1

- Molecule 2 is pyridin-3-ylboronic acid (three-letter code: LS9) (formula: C₅H₆BNO₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	B	C	H	N			O
2	A	1	15	1	5	6	1	2	0	0

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	Fe	H	N			O
3	A	1	73	34	1	30	4	4	0	0

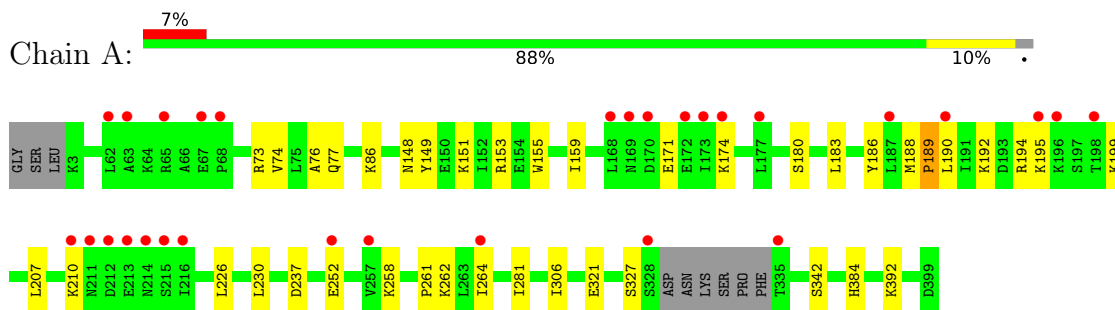
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	193	Total 193	O 193	0	0

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 protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	81.02Å 108.24Å 105.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.89 – 1.92 52.89 – 1.92	Depositor EDS
% Data completeness (in resolution range)	98.7 (52.89-1.92) 86.7 (52.89-1.92)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 1.92Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.210 , 0.241 0.210 , 0.240	Depositor DCC
R_{free} test set	1779 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtrriage
Anisotropy	0.970	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6724	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.68% 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, LS9

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	0.44	0/3280	0.55	2/4422 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	189	PRO	N-CD-CG	-9.17	89.44	103.20
1	A	189	PRO	CA-N-CD	-6.94	101.79	111.50

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	3201	3242	3235	26	0
2	A	9	6	0	0	0
3	A	43	30	30	5	0
4	A	193	0	0	3	0
All	All	3446	3278	3265	30	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 5.

All (30) 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:281:ILE:HD12	1:A:306:ILE:HD11	1.76	0.67
1:A:252:GLU:OE1	4:A:501:HOH:O	2.14	0.64
1:A:183:LEU:HD23	1:A:226:LEU:HD21	1.79	0.63
3:A:402:HEM:HMB2	3:A:402:HEM:HBB2	1.82	0.61
1:A:210:LYS:NZ	4:A:502:HOH:O	2.34	0.60
1:A:186:TYR:O	1:A:190:LEU:HD23	2.01	0.60
1:A:392:LYS:HA	1:A:392:LYS:HE2	1.84	0.59
3:A:402:HEM:HBC2	3:A:402:HEM:HMC2	1.85	0.59
1:A:148:ASN:OD1	1:A:151:LYS:HB2	2.09	0.52
1:A:159:ILE:CG2	1:A:230:LEU:HD11	2.42	0.48
1:A:384[B]:HIS:CG	1:A:392:LYS:HZ1	2.33	0.47
1:A:74:VAL:HG12	1:A:76:ALA:H	1.80	0.47
3:A:402:HEM:HBC2	3:A:402:HEM:CMC	2.45	0.46
1:A:155:TRP:HE3	1:A:183:LEU:HD13	1.81	0.45
1:A:261:PRO:O	1:A:264:ILE:HG22	2.16	0.45
3:A:402:HEM:HBB2	3:A:402:HEM:CMB	2.45	0.45
1:A:86:LYS:NZ	4:A:511:HOH:O	2.49	0.44
1:A:171:GLU:HG3	1:A:174:LYS:HE2	2.00	0.43
1:A:183:LEU:HD23	1:A:226:LEU:CD2	2.48	0.42
1:A:392:LYS:HE2	1:A:392:LYS:CA	2.49	0.42
1:A:192:LYS:N	1:A:192:LYS:HD3	2.34	0.42
1:A:188:MET:HB3	1:A:189:PRO:HD2	2.01	0.42
1:A:342:SER:O	3:A:402:HEM:HMA1	2.20	0.42
1:A:153:ARG:O	1:A:153:ARG:HD3	2.19	0.41
1:A:159:ILE:HG21	1:A:230:LEU:HD11	2.02	0.41
1:A:73:ARG:HG2	1:A:77:GLN:OE1	2.20	0.41
1:A:159:ILE:HD11	1:A:180:SER:HA	2.02	0.41
1:A:194:ARG:CZ	1:A:199:LYS:HD3	2.51	0.41
1:A:195:LYS:CD	1:A:207:LEU:HD22	2.51	0.41
1:A:159:ILE:HG22	1:A:230:LEU:HD11	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	394/400 (98%)	384 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	365/368 (99%)	358 (98%)	7 (2%)	57	51

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	149	TYR
1	A	237	ASP
1	A	258	LYS
1	A	262	LYS
1	A	321[A]	GLU
1	A	321[B]	GLU
1	A	327	SER

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	53	ASN
1	A	127	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	HEM	A	402	2,1	41,50,50	1.41	5 (12%)	45,82,82	1.25	5 (11%)
2	LS9	A	401	3	9,9,9	0.33	0	9,11,11	0.88	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
3	HEM	A	402	2,1	-	2/12/54/54	-
2	LS9	A	401	3	-	0/4/4/4	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	HEM	C3C-C2C	-3.49	1.35	1.40
3	A	402	HEM	C3C-CAC	3.36	1.54	1.47
3	A	402	HEM	CAA-C2A	3.16	1.56	1.52
3	A	402	HEM	C3D-C2D	-2.21	1.32	1.36
3	A	402	HEM	CAB-C3B	2.06	1.53	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	HEM	C4B-CHC-C1C	3.27	126.87	122.56
3	A	402	HEM	CMA-C3A-C4A	-2.66	124.38	128.46
3	A	402	HEM	C4C-CHD-C1D	2.32	125.62	122.56
3	A	402	HEM	CMC-C2C-C3C	2.13	128.67	124.68
3	A	402	HEM	O1A-CGA-CBA	-2.06	116.48	123.08

There are no chirality outliers.

All (2) torsion outliers are listed below:

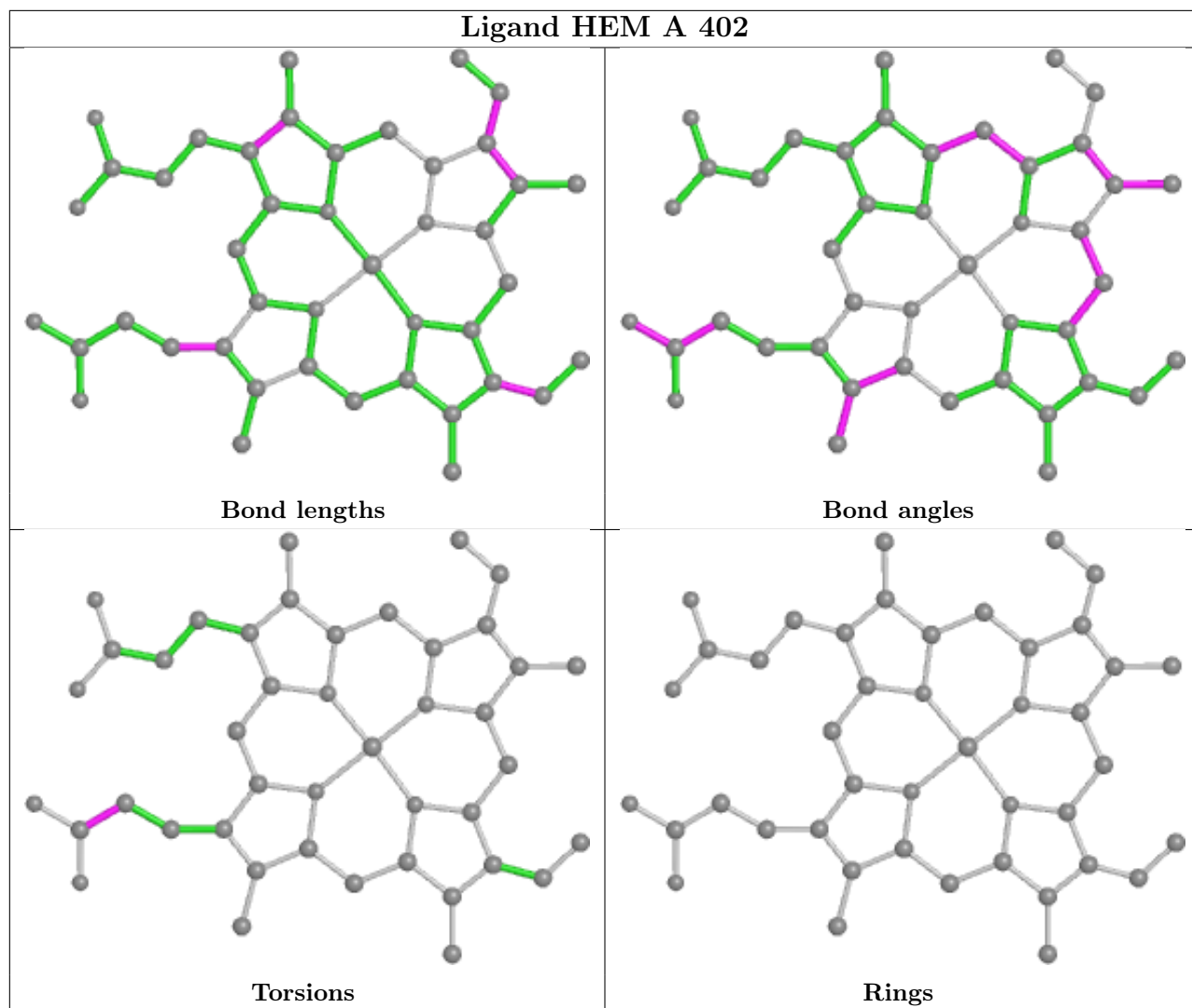
Mol	Chain	Res	Type	Atoms
3	A	402	HEM	CAA-CBA-CGA-O1A
3	A	402	HEM	CAA-CBA-CGA-O2A

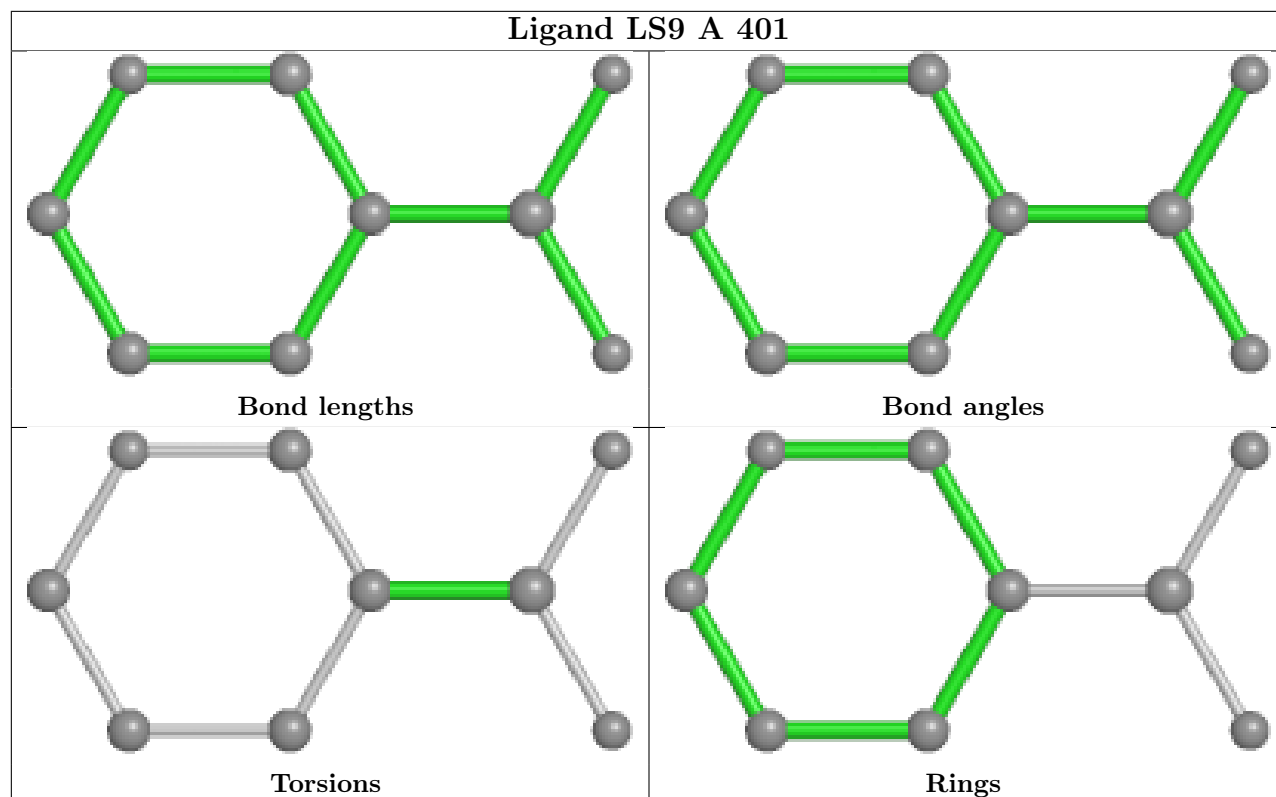
There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	HEM	5	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	391/400 (97%)	0.55	29 (7%) 14 16	28, 43, 95, 133	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	213	GLU	7.4
1	A	212	ASP	5.3
1	A	168	LEU	5.1
1	A	65	ARG	4.8
1	A	335	THR	4.7
1	A	190	LEU	4.5
1	A	177	LEU	4.3
1	A	196	LYS	4.3
1	A	173	ILE	4.2
1	A	67	GLU	3.8
1	A	328	SER	3.7
1	A	195	LYS	3.6
1	A	214	ASN	3.5
1	A	216	ILE	3.4
1	A	215	SER	3.4
1	A	198	THR	3.1
1	A	210	LYS	2.6
1	A	68	PRO	2.6
1	A	63	ALA	2.6
1	A	187	LEU	2.5
1	A	211	ASN	2.5
1	A	172	GLU	2.3
1	A	257	VAL	2.2
1	A	170	ASP	2.1
1	A	264	ILE	2.1
1	A	62	LEU	2.1
1	A	169	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	252	GLU	2.1
1	A	174	LYS	2.1

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 monosaccharides in this entry.

6.4 Ligands [i](#)

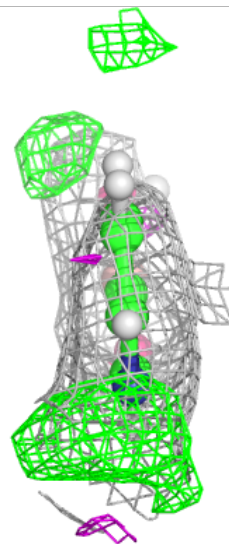
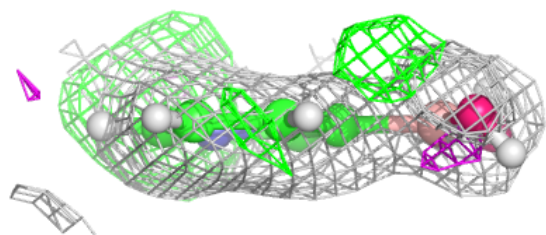
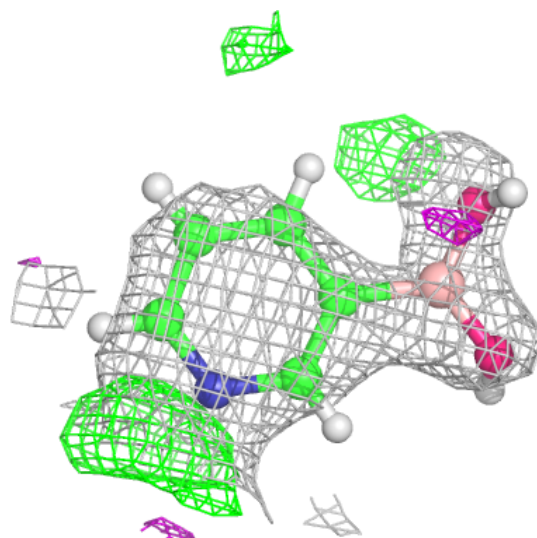
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

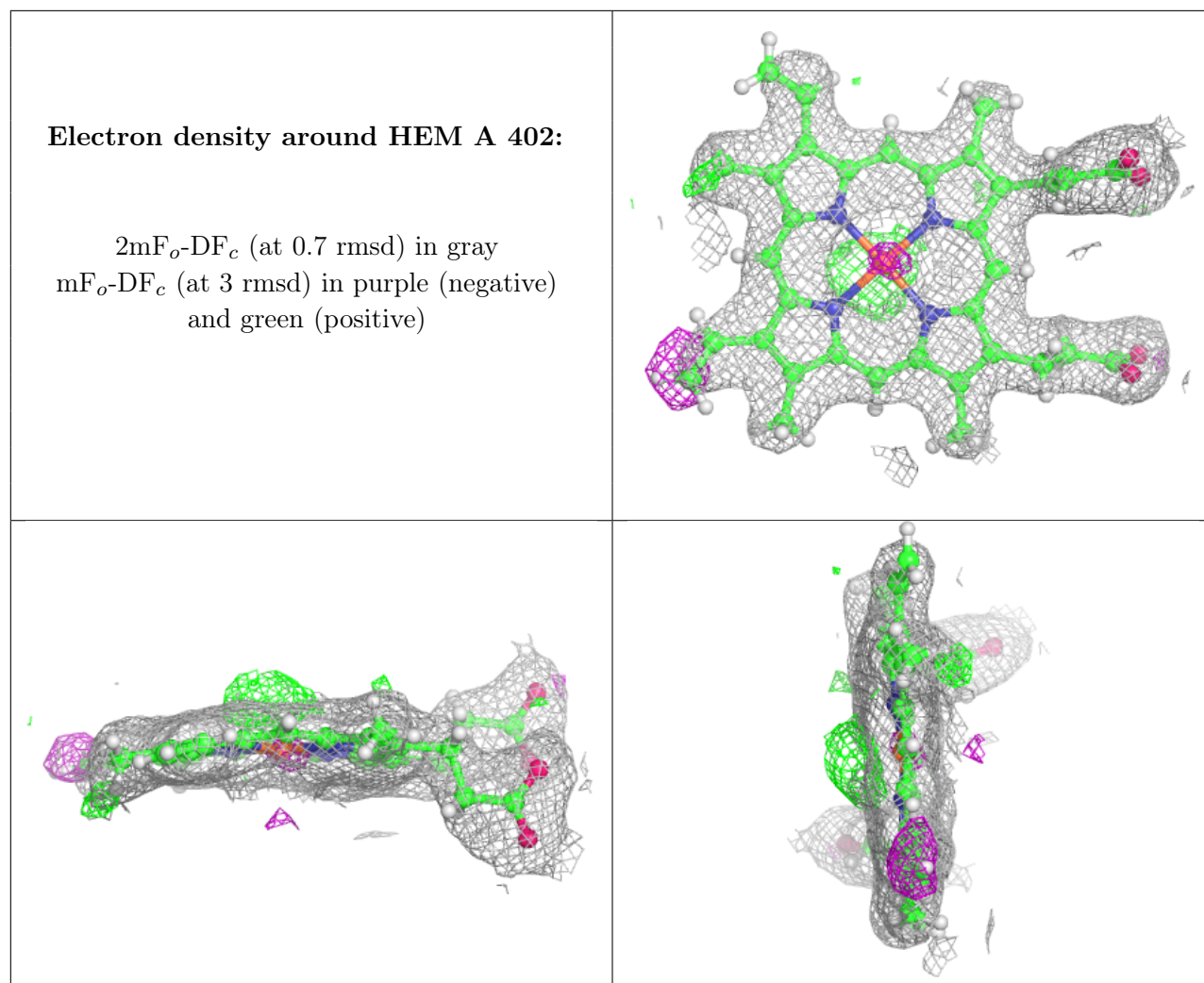
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
2	LS9	A	401	9/9	0.74	0.24	35,43,52,56	15
3	HEM	A	402	43/43	0.97	0.13	29,35,44,51	0

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 LS9 A 401:

$2mF_o-DF_c$ (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.