

wwPDB X-ray Structure Validation Summary Report (i)

Oct 31, 2021 – 09:58 AM EDT

PDB ID : 1IO8

Title: Thermophilic cytochrome P450 (CYP119) from sulfolobus solfataricus: High

resolution structural origin of its thermostability and functional properties

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Genomics/Proteomics Initiative (RSGI)

Deposited on : 2001-02-08

Resolution : 2.00 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 $\begin{array}{c} \text{A user guide is available at} \\ \text{https://www.wwpdb.org/validation/2017/XrayValidationReportHelp} \\ \text{with specific help available everywhere you see the (i) symbol.} \end{array}$

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED

EDS : NOT EXECUTED

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

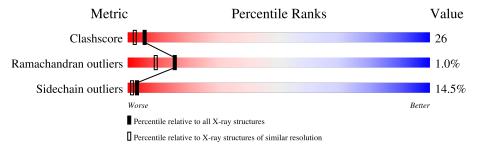
Validation Pipeline (wwPDB-VP) : 2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 2.00 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	Similar resolution		
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$		
Clashscore	141614	9178 (2.00-2.00)		
Ramachandran outliers	138981	9054 (2.00-2.00)		
Sidechain outliers	138945	9053 (2.00-2.00)		

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain					
1	A	368	54%	38%	7% •			
1	В	368	52%	35%	10% •			



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6334 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.

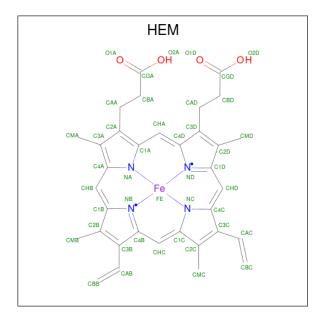
• Molecule 1 is a protein called CYTOCHROME P450 CYP119.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	366	Total 3007	C 1925	N 517	O 559	S 6	0	0	0
1	В	359	Total 2958	C 1893	N 509	O 550	S 6	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	LEU	PHE	engineered mutation	UNP Q55080
В	524	LEU	PHE	engineered mutation	UNP Q55080

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



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	В	1	Total	С	Fe	N	О	0	0
_	В	1	43	34	1	4	4		

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	132	Total O 132 132	0	0
3	В	151	Total O 151 151	0	0

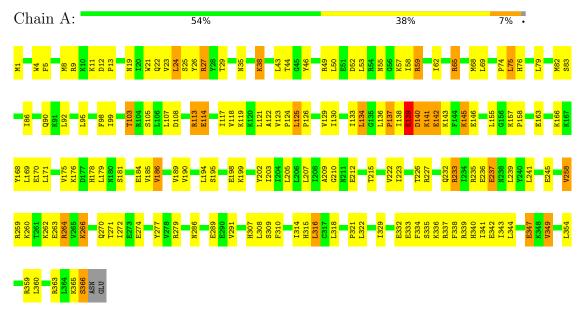


3 Residue-property plots (i)

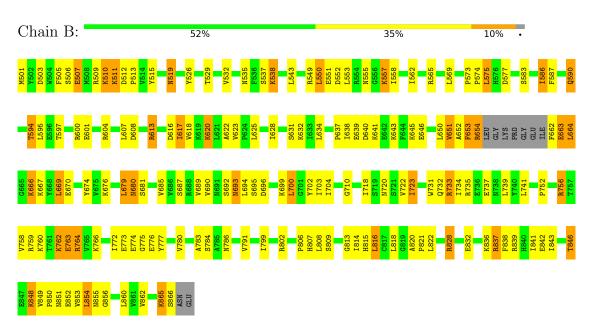
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

Note EDS was not executed.

• Molecule 1: CYTOCHROME P450 CYP119



• Molecule 1: CYTOCHROME P450 CYP119





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 43 21 2	Depositor	
Cell constants	85.52Å 85.52Å 221.46Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	20.00 - 2.00	Depositor	
% Data completeness	94.5 (20.00-2.00)	Depositor	
(in resolution range)	34.9 (20.00 2.00)		
R_{merge}	0.06	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	X-PLOR 3.851	Depositor	
R, R_{free}	0.230 , 0.307	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	6334	wwPDB-VP	
Average B, all atoms (Å ²)	35.0	wwPDB-VP	



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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.41	0/3070	0.65	0/4149	
1	В	0.44	0/3019	0.64	0/4079	
All	All	0.43	0/6089	0.64	0/8228	

There are no bond length outliers.

There are no bond angle outliers.

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	3007	0	3043	156	0
1	В	2958	0	2985	157	0
2	A	43	0	30	3	0
2	В	43	0	30	1	0
3	A	132	0	0	7	0
3	В	151	0	0	15	0
All	All	6334	0	6088	312	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 26.

The worst 5 of 312 close contacts within the same asymmetric unit are listed below, sorted by



their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:851:ASN:ND2	1:B:853:VAL:H	1.60	0.99
1:B:613:ARG:HH11	1:B:613:ARG:HB3	1.26	0.98
1:B:764:ARG:HH11	1:B:764:ARG:HB2	1.24	0.98
1:B:586:ILE:HD11	1:B:818:LEU:HD21	1.47	0.97
1:A:223:ILE:HD11	1:A:360:LEU:HD11	1.48	0.96

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	364/368 (99%)	338 (93%)	22 (6%)	4 (1%)	14 8
1	В	355/368~(96%)	333 (94%)	19 (5%)	3 (1%)	19 13
All	All	719/736~(98%)	671 (93%)	41 (6%)	7 (1%)	15 9

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	GLU
1	В	653	PHE
1	A	139	GLU
1	В	513	PRO
1	A	137	PRO

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.

\mathbf{Mol}	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	336/338 (99%)	290 (86%)	46 (14%)	3 2
1	В	331/338 (98%)	280 (85%)	51 (15%)	2 1
All	All	$667/676 \ (99\%)$	570 (86%)	97 (14%)	3 1

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	586	ILE
1	В	664	LEU
1	В	594	THR
1	В	631	SER
1	В	680	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	693	ASN
1	В	729	ASN
1	В	855	ASN
1	В	807	HIS
1	В	851	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	Trme	Chain	Pog Link		Bo	ond leng	ths	В	ond ang	cles
MIOI	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	A	401	3,1	27,50,50	1.97	9 (33%)	17,82,82	1.30	3 (17%)
2	HEM	В	901	3,1	27,50,50	1.83	9 (33%)	17,82,82	1.76	5 (29%)

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.

\mathbf{Mol}	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	401	3,1	-	0/6/54/54	-
2	HEM	В	901	3,1	-	0/6/54/54	-

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
2	A	401	HEM	C3B-CAB	-4.03	1.39	1.47
2	A	401	HEM	C3C-CAC	-4.00	1.39	1.47
2	A	401	HEM	C4D-C3D	3.86	1.51	1.42
2	В	901	HEM	C3B-CAB	-3.75	1.40	1.47
2	В	901	HEM	C3C-CAC	-3.25	1.41	1.47

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	901	HEM	CBD-CAD-C3D	-4.10	104.93	112.48
2	В	901	HEM	C4A-C3A-C2A	-3.33	104.68	107.00
2	В	901	HEM	CMD-C2D-C1D	-2.98	123.89	128.46
2	A	401	HEM	CMD-C2D-C1D	-2.91	124.00	128.46
2	A	401	HEM	C4A-C3A-C2A	-2.41	105.32	107.00

There are no chirality outliers.



There are no torsion outliers.

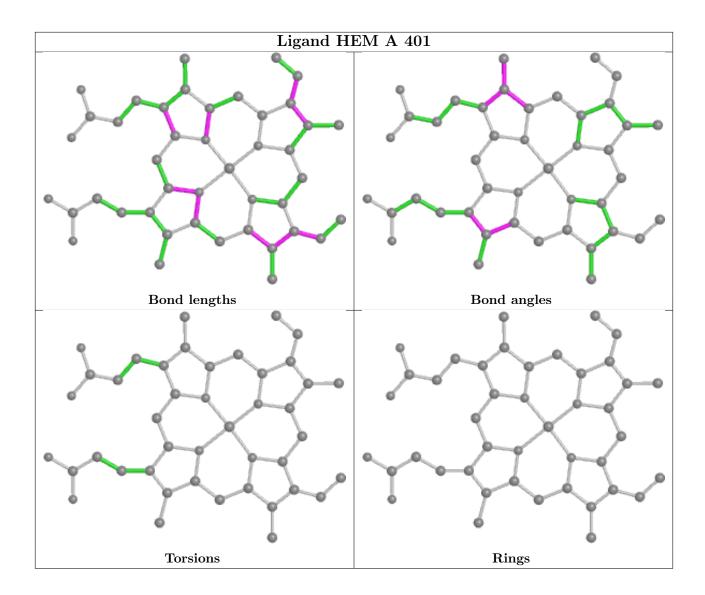
There are no ring outliers.

2 monomers are involved in 4 short contacts:

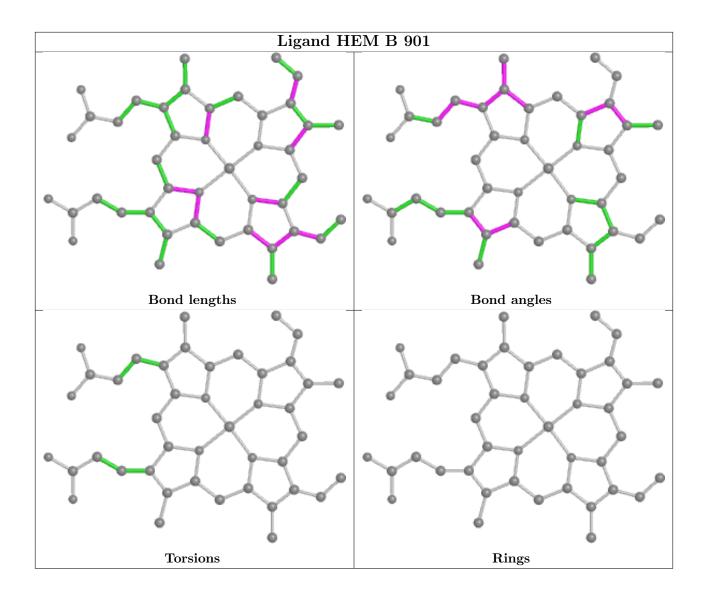
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	HEM	3	0
2	В	901	HEM	1	0

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 then 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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

