



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:07 PM GMT

PDB ID : 1IWI
Title : Putidaredoxin-Binding Stabilizes an Active Conformer of Cytochrome P450cam in its Reduced State; Crystal Structure of Cytochrome P450cam
Authors : Nagano, S.; Shimada, H.; Tarumi, A.; Hishiki, T.; Kimata-Ariga, Y.; Egawa, T.; Park, S.-Y.; Adachi, S.; Shiro, Y.; Ishimura, Y.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2002-05-15
Resolution : 2.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

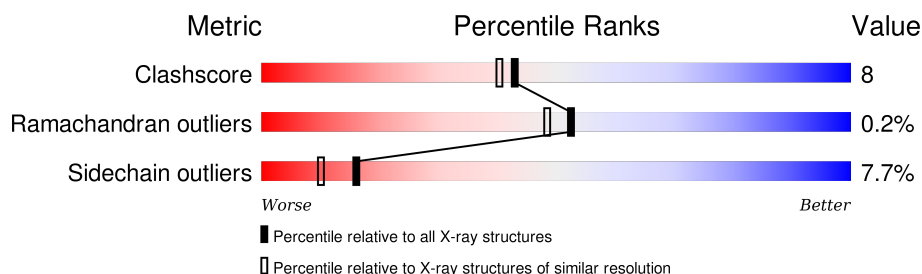
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	415	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3388 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-CAM.

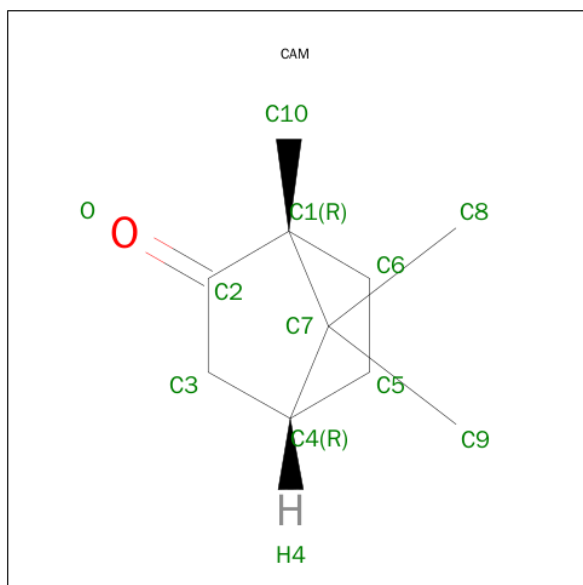
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	0	0
			3208	2033	560	597	18			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: 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		

- Molecule 3 is CAMPHOR (three-letter code: CAM) (formula: $C_{10}H_{16}O$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	10	1		

- Molecule 4 is water.

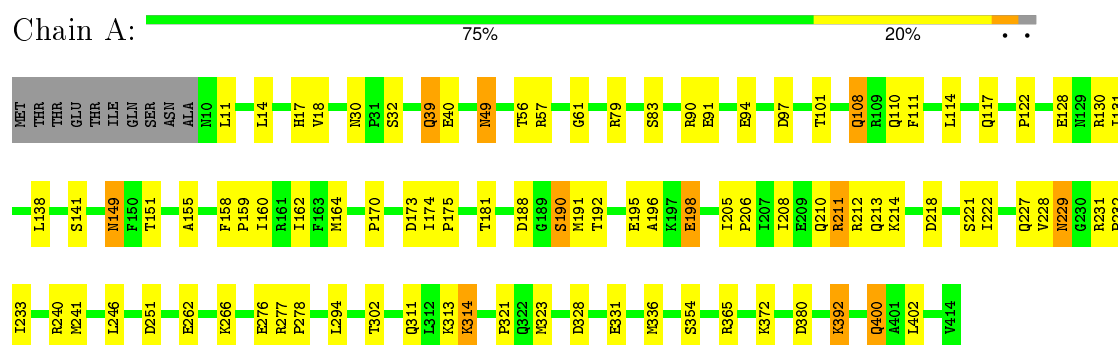
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	126	Total	O	0	0
			126	126		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

• Molecule 1: CYTOCHROME P450-CAM



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	109.16 Å 104.33 Å 36.18 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.00	Depositor
% Data completeness (in resolution range)	94.5 (15.00-2.00)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.177 , 0.182	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3388	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, CAM

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	0.31	0/3287	0.54	0/4465

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

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	3208	0	3156	53	0
2	A	43	0	30	0	0
3	A	11	0	16	0	0
4	A	126	0	0	2	0
All	All	3388	0	3202	53	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 8.

All (53) 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:49:ASN:H	1:A:49:ASN:HD22	1.36	0.73
1:A:158:PHE:HB3	1:A:159:PRO:HD3	1.70	0.72
1:A:208:ILE:O	1:A:212:ARG:HG3	1.91	0.71
1:A:392:LYS:HD3	1:A:400:GLN:HE21	1.61	0.65
1:A:294:LEU:HD23	1:A:294:LEU:H	1.61	0.65
1:A:328:ASP:HB3	1:A:331:GLU:HG3	1.82	0.62
1:A:188:ASP:HB3	1:A:190:SER:OG	2.00	0.62
1:A:392:LYS:HD3	1:A:400:GLN:NE2	2.15	0.61
1:A:218:ASP:O	1:A:222:ILE:HG12	2.01	0.60
1:A:211:ARG:HG3	1:A:221:SER:OG	2.01	0.59
1:A:111:PHE:HB3	1:A:241:MET:HE2	1.86	0.56
1:A:170:PRO:HG2	1:A:173:ASP:OD1	2.07	0.55
1:A:114:LEU:O	1:A:117:GLN:HB2	2.07	0.55
1:A:131:ILE:HG12	1:A:162:ILE:HD13	1.89	0.55
1:A:294:LEU:HD23	1:A:294:LEU:N	2.20	0.55
1:A:97:ASP:O	1:A:240:ARG:HD2	2.07	0.54
1:A:83:SER:HB3	1:A:101:THR:O	2.09	0.52
1:A:11:LEU:HG	1:A:57:ARG:HB2	1.92	0.51
1:A:90:ARG:O	1:A:94:GLU:HG3	2.10	0.51
1:A:191:MET:HE1	1:A:196:ALA:HA	1.91	0.51
1:A:108:GLN:HE22	1:A:354:SER:HB2	1.75	0.51
1:A:56:THR:O	1:A:61:GLY:HA2	2.12	0.50
1:A:14:LEU:HD11	1:A:18:VAL:CG1	2.42	0.50
1:A:205:ILE:HB	1:A:206:PRO:HD3	1.94	0.49
1:A:17:HIS:CD2	1:A:313:LYS:HG3	2.48	0.49
1:A:149:ASN:ND2	1:A:402:LEU:H	2.10	0.49
1:A:174:ILE:HB	1:A:175:PRO:HD3	1.97	0.47
1:A:149:ASN:HD21	1:A:402:LEU:H	1.62	0.46
1:A:210:GLN:HA	1:A:213:GLN:HE21	1.80	0.46
1:A:198:GLU:OE1	1:A:198:GLU:HA	2.15	0.46
1:A:40:GLU:HG3	1:A:336:MET:CE	2.45	0.45
1:A:110:GLN:NE2	1:A:229:ASN:HA	2.31	0.45
1:A:211:ARG:CG	1:A:211:ARG:HH21	2.29	0.45
1:A:231:ARG:HB2	1:A:232:PRO:CD	2.47	0.45
1:A:192:THR:OG1	1:A:195:GLU:HG3	2.16	0.45
1:A:91:GLU:H	1:A:91:GLU:CD	2.20	0.45
1:A:39:GLN:NE2	1:A:39:GLN:H	2.15	0.45
1:A:49:ASN:ND2	1:A:49:ASN:H	2.08	0.45
1:A:191:MET:CE	1:A:196:ALA:HA	2.48	0.44
1:A:262:GLU:O	1:A:266:LYS:HD3	2.18	0.43
1:A:181:THR:CG2	1:A:251:ASP:HB2	2.48	0.43
1:A:122:PRO:HD2	4:A:531:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:GLN:HE21	1:A:108:GLN:HB3	1.53	0.42
1:A:181:THR:HG21	1:A:251:ASP:HB2	2.00	0.42
1:A:231:ARG:H	1:A:231:ARG:HG3	1.70	0.41
1:A:30:ASN:ND2	4:A:536:HOH:O	2.53	0.41
1:A:276:GLU:C	1:A:278:PRO:HD3	2.41	0.41
1:A:212:ARG:NH2	1:A:233:ILE:O	2.54	0.41
1:A:14:LEU:HD11	1:A:18:VAL:HG11	2.03	0.41
1:A:151:THR:HA	1:A:155:ALA:HB3	2.02	0.41
1:A:302:THR:O	1:A:314:LYS:HG3	2.21	0.40
1:A:294:LEU:CD2	1:A:294:LEU:N	2.83	0.40
1:A:160:ILE:O	1:A:164:MET:HG2	2.21	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	403/415 (97%)	394 (98%)	8 (2%)	1 (0%)	52 48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	321	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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	350/359 (98%)	323 (92%)	27 (8%)	16	10

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	SER
1	A	39	GLN
1	A	49	ASN
1	A	79	ARG
1	A	108	GLN
1	A	128	GLU
1	A	130	ARG
1	A	138	LEU
1	A	141	SER
1	A	149	ASN
1	A	190	SER
1	A	198	GLU
1	A	211	ARG
1	A	214	LYS
1	A	227	GLN
1	A	228	VAL
1	A	229	ASN
1	A	246	LEU
1	A	277	ARG
1	A	311	GLN
1	A	314	LYS
1	A	323	MET
1	A	365	ARG
1	A	372	LYS
1	A	380	ASP
1	A	392	LYS
1	A	400	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
1	A	39	GLN
1	A	46	GLN
1	A	49	ASN
1	A	59	ASN
1	A	69	GLN

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Mol	Chain	Res	Type
1	A	108	GLN
1	A	110	GLN
1	A	129	ASN
1	A	149	ASN
1	A	213	GLN
1	A	225	ASN
1	A	229	ASN
1	A	388	GLN
1	A	400	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 carbohydrates 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	$\# Z > 2$
2	HEM	A	417	1	30,50,50	2.37	10 (33%)	24,82,82	2.17	9 (37%)
3	CAM	A	418	-	12,12,12	2.39	4 (33%)	21,21,21	1.59	3 (14%)

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	A	417	1	-	0/10/54/54	0/0/8/8
3	CAM	A	418	-	-	0/0/31/31	0/0/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	417	HEM	C3C-CAC	-6.16	1.39	1.51
2	A	417	HEM	C2D-C3D	-5.89	1.36	1.54
2	A	417	HEM	C3B-CAB	-5.70	1.40	1.51
2	A	417	HEM	C2C-C1C	-3.17	1.46	1.52
2	A	417	HEM	C3D-C4D	-3.11	1.47	1.51
2	A	417	HEM	C3B-C4B	-2.93	1.49	1.51
2	A	417	HEM	C2D-C1D	-2.00	1.45	1.51
2	A	417	HEM	CHC-C1C	2.00	1.41	1.36
3	A	418	CAM	C8-C7	2.09	1.59	1.53
2	A	417	HEM	C1C-NC	2.15	1.38	1.36
3	A	418	CAM	C3-C4	2.23	1.59	1.53
3	A	418	CAM	C5-C4	2.26	1.59	1.53
2	A	417	HEM	C4C-NC	3.16	1.39	1.36
3	A	418	CAM	C1-C2	6.39	1.61	1.53

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	418	CAM	C9-C7-C8	-3.29	99.91	107.52
2	A	417	HEM	C3C-CAC-CBC	-2.18	121.11	124.46
2	A	417	HEM	CMA-C3A-C4A	-2.14	124.82	128.36
2	A	417	HEM	C3B-CAB-CBB	2.23	127.88	124.46
3	A	418	CAM	O-C2-C3	2.59	131.74	126.40
2	A	417	HEM	CMD-C2D-C3D	2.76	126.57	114.35
3	A	418	CAM	C6-C1-C2	2.76	107.63	102.93
2	A	417	HEM	C2D-C3D-C4D	2.94	106.48	101.50
2	A	417	HEM	CMC-C2C-C3C	3.86	126.17	116.53
2	A	417	HEM	CAD-C3D-C4D	4.21	127.31	112.47
2	A	417	HEM	CMB-C2B-C3B	4.33	127.33	116.53
2	A	417	HEM	CAD-C3D-C2D	4.51	126.18	113.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.