



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 04:00 am GMT

PDB ID : 2H7S  
Title : L244A mutant of Cytochrome P450cam  
Authors : Verras, A.; Alian, A.; Montellano, P.R.  
Deposited on : 2006-06-02  
Resolution : 2.15 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

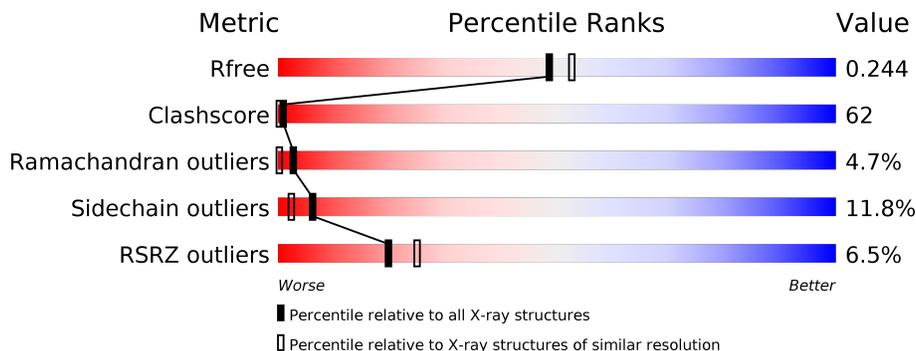
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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))
$R_{free}$	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

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  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	A	414	
1	C	414	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6696 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.

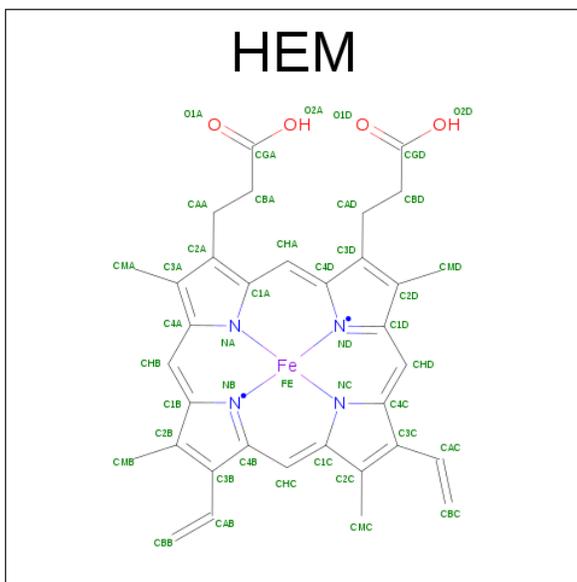
- Molecule 1 is a protein called Cytochrome P450-cam.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	405	Total 3201	C 2029	N 560	O 595	S 17	0	0	0
1	C	405	Total 3199	C 2026	N 559	O 597	S 17	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	244	ALA	LEU	ENGINEERED	UNP P00183
A	334	ALA	CYS	ENGINEERED	UNP P00183
C	244	ALA	LEU	ENGINEERED	UNP P00183
C	334	ALA	CYS	ENGINEERED	UNP P00183

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

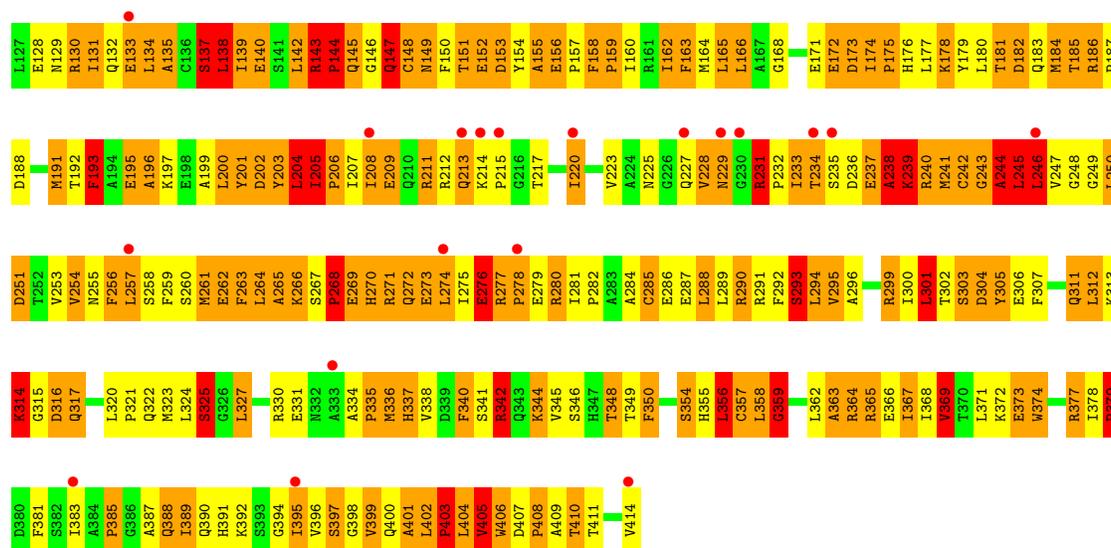


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	111	Total	O	25	0
			111	111		
3	C	99	Total	O	24	0
			99	99		





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.70Å 59.85Å 114.12Å 90.00° 104.69° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 45.43 – 2.15	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.15) 80.3 (45.43-2.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.77 (at 2.14Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.235 , 0.249 0.237 , 0.244	Depositor DCC
$R_{free}$ test set	3262 reflections (10.90%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.3	Xtriage
Anisotropy	0.370	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 14.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.407 for h,-k,-h-l	Xtriage
Reported twinning fraction	0.391 for h,-k,-h-l	Depositor
Outliers	1 of 37909 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6696	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.41 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to  $4.8801e-05$ . The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

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	2.85	278/3280 (8.5%)	2.29	173/4456 (3.9%)
1	C	2.87	289/3278 (8.8%)	2.43	180/4454 (4.0%)
All	All	2.86	567/6558 (8.6%)	2.36	353/8910 (4.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8
1	C	0	9
All	All	0	17

The worst 5 of 567 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	399	VAL	CB-CG2	16.70	1.88	1.52
1	A	95	ALA	CA-CB	-15.72	1.19	1.52
1	C	373	GLU	CD-OE1	15.07	1.42	1.25
1	C	401	ALA	C-O	13.02	1.48	1.23
1	A	40	GLU	CD-OE1	13.00	1.40	1.25

The worst 5 of 353 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	290	ARG	NE-CZ-NH1	-24.41	108.09	120.30
1	C	130	ARG	NE-CZ-NH1	-23.85	108.37	120.30
1	A	77	ASP	CB-CG-OD2	20.89	137.10	118.30
1	C	130	ARG	NE-CZ-NH2	20.79	130.70	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	377	ARG	NE-CZ-NH1	-19.19	110.70	120.30

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	GLU	Peptide
1	A	108	GLN	Peptide
1	A	120	GLY	Peptide
1	A	258	SER	Mainchain
1	A	81	PHE	Peptide

## 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	0	3148	417	11
1	C	3199	0	3137	391	12
2	A	43	0	30	17	0
2	C	43	0	30	7	0
3	A	111	0	0	9	0
3	C	99	0	0	9	0
All	All	6696	0	6345	793	23

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 62.

The worst 5 of 793 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:C:356:LEU:CG	1:C:356:LEU:CD1	1.74	1.61
1:A:404:LEU:CD1	1:A:404:LEU:CG	1.76	1.58
1:A:151:THR:CB	1:A:151:THR:CG2	1.75	1.58
1:C:373:GLU:CB	1:C:373:GLU:CG	1.75	1.58
1:C:131:ILE:CB	1:C:131:ILE:CG2	1.78	1.56

The worst 5 of 23 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ARG:NH2	1:A:176:HIS:CB[2_545]	1.02	1.18
1:C:109:ARG:NH2	1:C:176:HIS:CB[2_546]	1.05	1.15
1:C:107:GLU:OE2	1:C:410:THR:CG2[1_455]	1.48	0.72
1:C:110:GLN:OE1	1:C:176:HIS:ND1[2_546]	1.54	0.66
1:A:110:GLN:OE1	1:A:176:HIS:ND1[2_545]	1.59	0.61

### 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	403/414 (97%)	345 (86%)	38 (9%)	20 (5%)	2	0
1	C	403/414 (97%)	336 (83%)	49 (12%)	18 (4%)	3	0
All	All	806/828 (97%)	681 (84%)	87 (11%)	38 (5%)	3	0

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	ARG
1	A	246	LEU
1	A	278	PRO
1	A	282	PRO
1	A	293	SER

#### 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	347/356 (98%)	309 (89%)	38 (11%)	7	3
1	C	347/356 (98%)	303 (87%)	44 (13%)	5	1
All	All	694/712 (98%)	612 (88%)	82 (12%)	6	2

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	412	LYS
1	C	99	ILE
1	C	325	SER
1	C	16	PRO
1	C	79	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	317	GLN
1	C	30	ASN
1	C	149	ASN
1	A	343	GLN
1	A	355	HIS

### 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	415	1,3	28,50,50	3.38	14 (50%)	17,82,82	3.15	7 (41%)
2	HEM	C	415	1,3	28,50,50	4.38	19 (67%)	17,82,82	4.39	10 (58%)

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	415	1,3	-	0/6/54/54	0/0/8/8
2	HEM	C	415	1,3	-	0/6/54/54	0/0/8/8

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	415	HEM	C3B-C2B	-9.80	1.27	1.40
2	A	415	HEM	C3B-C2B	-8.69	1.28	1.40
2	C	415	HEM	C4C-NC	-7.77	1.27	1.36
2	C	415	HEM	C4B-NB	-7.68	1.19	1.36
2	C	415	HEM	C1B-NB	-6.77	1.28	1.36

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	415	HEM	CMA-C3A-C4A	-8.13	115.96	128.46
2	C	415	HEM	CMB-C2B-C3B	-6.92	112.06	124.89
2	C	415	HEM	CMA-C3A-C4A	-4.65	121.32	128.46
2	A	415	HEM	C3B-C4B-NB	-4.59	103.28	109.21
2	C	415	HEM	CAA-C2A-C3A	-4.44	116.32	129.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	415	HEM	17	0
2	C	415	HEM	7	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	405/414 (97%)	0.77	30 (7%) 15 19	8, 24, 36, 49	0
1	C	405/414 (97%)	0.73	23 (5%) 24 32	11, 24, 34, 44	0
All	All	810/828 (97%)	0.75	53 (6%) 20 25	8, 24, 36, 49	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	414	VAL	7.6
1	A	214	LYS	6.0
1	C	246	LEU	5.9
1	C	229	ASN	5.9
1	C	19	PRO	4.4

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	HEM	A	415	43/43	0.94	0.16	0.10	13,15,17,18	0
2	HEM	C	415	43/43	0.94	0.14	-0.35	13,18,20,21	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.