



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 21, 2018 – 01:28 pm GMT

PDB ID : 1LCO  
Title : X-RAY STRUCTURE OF TWO COMPLEXES OF THE Y143F FLAVO-CYTOCHROME B2 MUTANT CRYSTALLIZED IN THE PRESENCE OF LACTATE OR PHENYL-LACTATE  
Authors : Tegoni, M.; Cambillau, C.  
Deposited on : 1995-03-30  
Resolution : 2.90 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

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

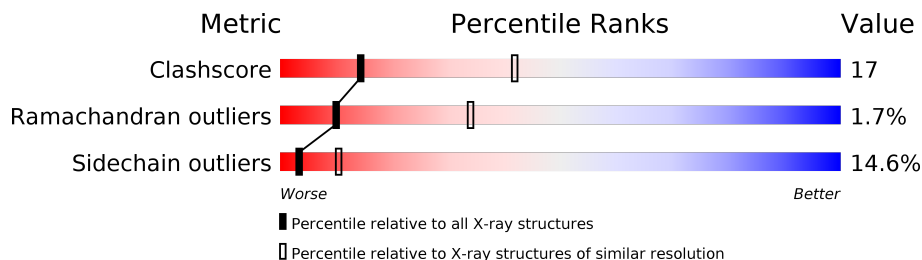
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	122078	1924 (2.90-2.90)
Ramachandran outliers	120005	1884 (2.90-2.90)
Sidechain outliers	119972	1886 (2.90-2.90)

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 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	511	
1	B	511	

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	FMN	A	570	X	-	-	-
3	FMN	B	570	X	-	-	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8915 atoms, of which 1840 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 L-LACTATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	480	Total	C	H	N	O	S	0	0	0
			4547	2384	811	631	707	14			
1	B	391	Total	C	H	N	O	S	0	0	0
			3732	1930	687	521	583	11			

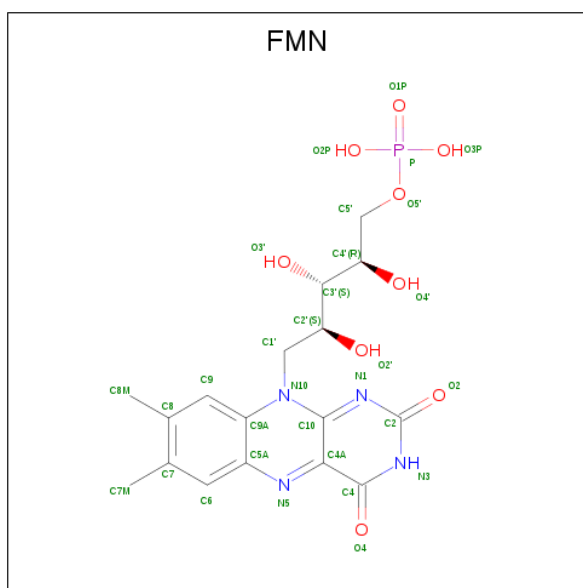
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	PHE	TYR	CONFLICT	UNP P00175
B	143	PHE	TYR	CONFLICT	UNP P00175

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

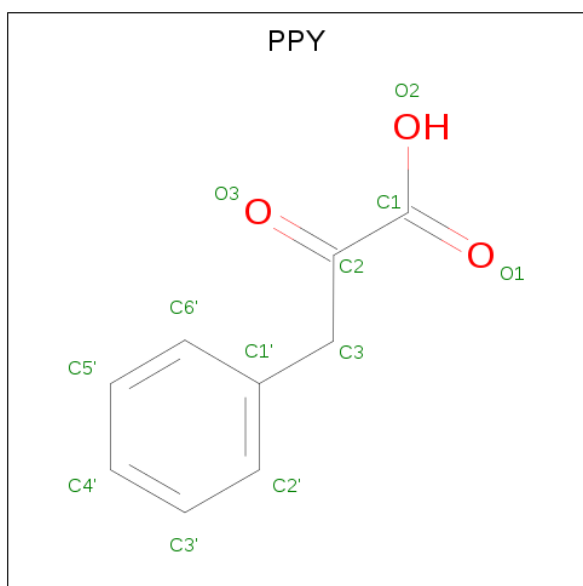


- Molecule 3 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula:  $C_{17}H_{21}N_4O_9P$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	0	0
			35	17	4	4	9	1		
3	B	1	Total	C	H	N	O	P	0	0
			35	17	4	4	9	1		

- Molecule 4 is 3-PHENYLPYRUVIC ACID (three-letter code: PPY) (formula:  $C_9H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	9	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			12	9	3		

- Molecule 5 is water.

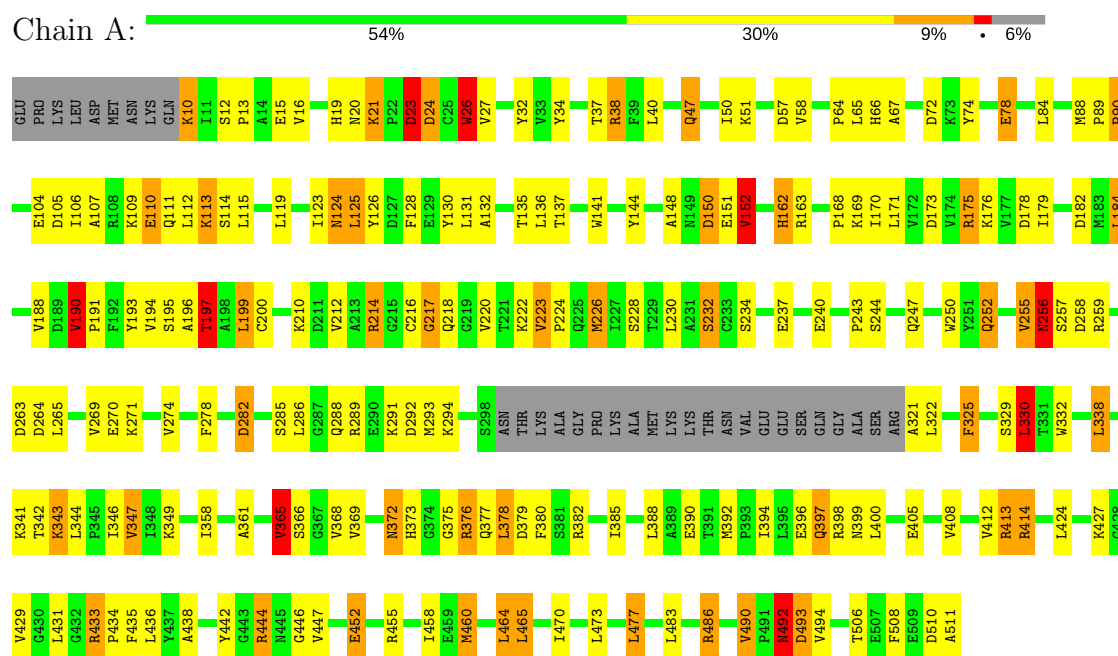
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	152	Total	H	O	0	0
			456	304	152		
5	B	13	Total	H	O	0	0
			39	26	13		

### 3 Residue-property plots

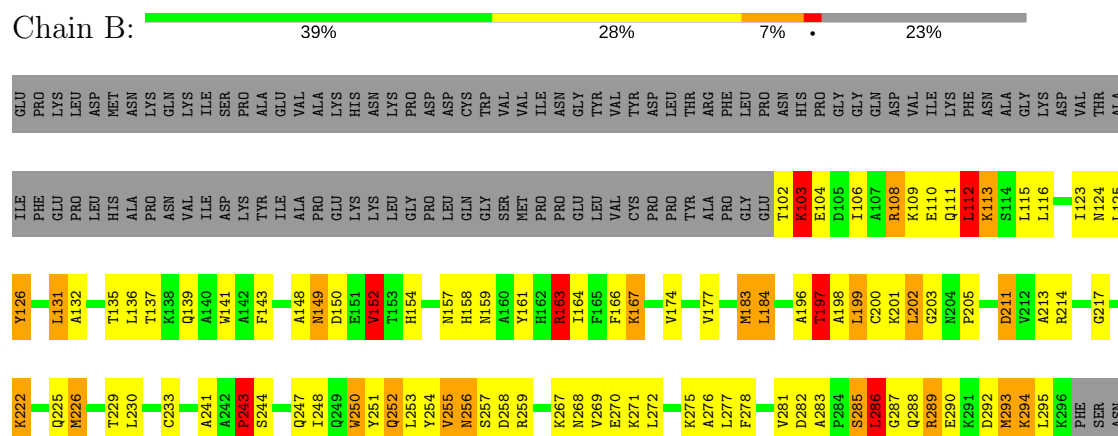
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

Note EDS was not executed.

#### • Molecule 1: L-LACTATE DEHYDROGENASE



#### • Molecule 1: L-LACTATE DEHYDROGENASE





## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	164.50Å 164.50Å 114.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.90)	Depositor
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.186 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8915	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	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: FMN, HEM, PPY

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	0.98	2/3810 (0.1%)	1.85	78/5161 (1.5%)
1	B	0.97	0/3093	1.86	71/4177 (1.7%)
All	All	0.98	2/6903 (0.0%)	1.86	149/9338 (1.6%)

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	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	413	ARG	CZ-NH1	5.40	1.40	1.33
1	A	382	ARG	CZ-NH1	5.07	1.39	1.33

The worst 5 of 149 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	414	ARG	NE-CZ-NH1	16.62	128.61	120.30
1	A	382	ARG	NE-CZ-NH2	-14.70	112.95	120.30
1	B	251	TYR	CB-CG-CD1	-13.46	112.93	121.00
1	B	289	ARG	NE-CZ-NH2	-13.10	113.75	120.30
1	A	492	ASN	CA-C-N	-12.82	89.00	117.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	ASP	Peptide
1	A	492	ASN	Mainchain

## 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	3736	811	3793	117	0
1	B	3045	687	3112	125	0
2	A	43	4	30	3	0
3	A	31	4	19	3	0
3	B	31	4	19	6	0
4	A	12	0	7	1	0
4	B	12	0	7	2	0
5	A	152	304	0	9	0
5	B	13	26	0	0	0
All	All	7075	1840	6987	230	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 17.

The worst 5 of 230 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:B:143:PHE:HA	1:B:289:ARG:HH22	1.45	0.79
1:B:290:GLU:HA	1:B:293:MET:HG3	1.64	0.79
1:A:40:LEU:HG	1:A:47:GLN:HB2	1.67	0.76
1:B:197:THR:HG21	1:B:436:LEU:HG	1.67	0.75
1:A:291:LYS:HD2	5:A:754:HOH:O	1.87	0.73

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	476/511 (93%)	428 (90%)	39 (8%)	9 (2%)	9	31
1	B	387/511 (76%)	348 (90%)	33 (8%)	6 (2%)	11	35
All	All	863/1022 (84%)	776 (90%)	72 (8%)	15 (2%)	10	34

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	149	ASN
1	A	104	GLU
1	A	114	SER
1	A	119	LEU
1	A	493	ASP

### 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	412/440 (94%)	350 (85%)	62 (15%)	3	10
1	B	336/440 (76%)	289 (86%)	47 (14%)	4	11
All	All	748/880 (85%)	639 (85%)	109 (15%)	3	10

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	372	ASN

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Mol	Chain	Res	Type
1	A	506	THR
1	B	429	VAL
1	A	378	LEU
1	A	460	MET

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	377	GLN
1	A	497	ASN
1	B	492	ASN
1	A	439	ASN
1	A	492	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

5 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	560	1	27,50,50	1.75	6 (22%)	17,82,82	1.59	4 (23%)
3	FMN	A	570	-	30,33,33	3.23	6 (20%)	38,50,50	3.19	19 (50%)
4	PPY	A	580	-	9,12,12	1.42	2 (22%)	10,15,15	1.54	2 (20%)
3	FMN	B	570	-	30,33,33	2.95	8 (26%)	38,50,50	3.08	14 (36%)
4	PPY	B	580	-	9,12,12	1.64	1 (11%)	10,15,15	0.70	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
2	HEM	A	560	1	-	0/6/54/54	0/0/8/8
3	FMN	A	570	-	2/2/4/4	0/16/18/18	0/3/3/3
4	PPY	A	580	-	-	0/4/8/8	0/1/1/1
3	FMN	B	570	-	2/2/4/4	0/16/18/18	0/3/3/3
4	PPY	B	580	-	-	0/4/8/8	0/1/1/1

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	570	FMN	C1'-N10	-14.77	1.33	1.48
3	B	570	FMN	C1'-N10	-13.24	1.34	1.48
3	A	570	FMN	C2'-C3'	-4.60	1.44	1.53
2	A	560	HEM	C3C-CAC	-4.44	1.38	1.47
3	A	570	FMN	C6-C5A	-4.25	1.35	1.41

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	570	FMN	C9A-N10-C10	-4.24	116.12	121.77
3	A	570	FMN	C9A-N10-C10	-3.87	116.61	121.77
4	A	580	PPY	C1'-C3-C2	-3.64	105.99	114.61
3	A	570	FMN	C7M-C7-C6	-3.63	111.41	120.36
3	A	570	FMN	C6-C5A-N5	-3.49	114.95	118.95

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	570	FMN	C4'

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Mol	Chain	Res	Type	Atom
3	B	570	FMN	C2'
3	A	570	FMN	C4'
3	A	570	FMN	C2'

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	560	HEM	3	0
3	A	570	FMN	3	0
4	A	580	PPY	1	0
3	B	570	FMN	6	0
4	B	580	PPY	2	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](#)

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.