



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:52 AM GMT

PDB ID : 2OK8  
Title : Ferredoxin-NADP+ reductase from Plasmodium falciparum  
Authors : Milani, M.; Mastrangelo, E.; Bolognesi, M.  
Deposited on : 2007-01-16  
Resolution : 2.40 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

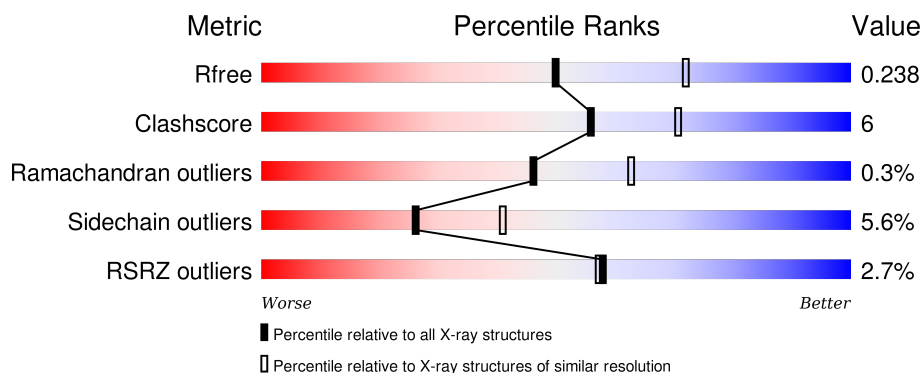
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	316	
1	B	316	
1	C	316	
1	D	316	

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
2	FLC	A	9002	-	-	-	X

## 2 Entry composition [i](#)

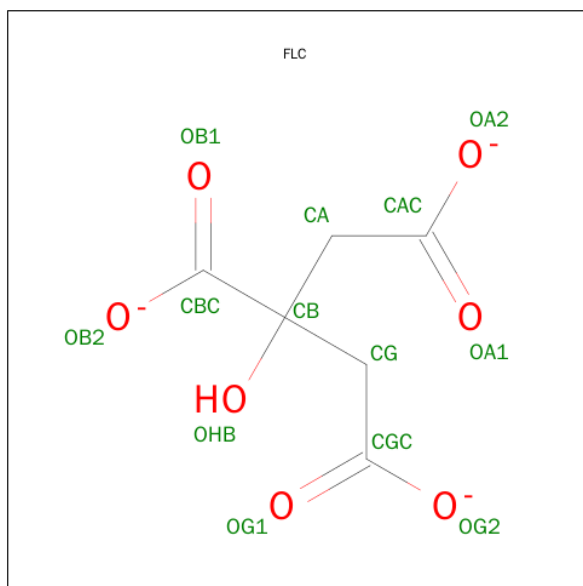
There are 4 unique types of molecules in this entry. The entry contains 9261 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Putative ferredoxin–NADP reductase.

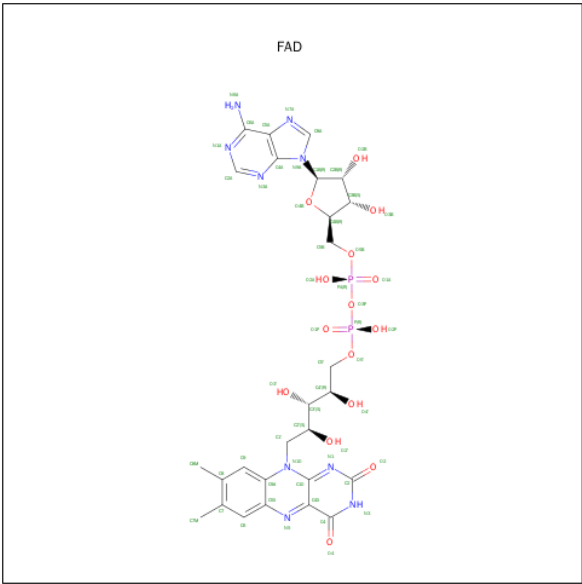
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	0	0
			2201	1427	361	404	9			
1	B	262	Total	C	N	O	S	0	1	0
			2199	1430	358	402	9			
1	C	257	Total	C	N	O	S	0	0	0
			2146	1397	349	391	9			
1	D	261	Total	C	N	O	S	0	0	0
			2186	1423	357	397	9			

- Molecule 2 is CITRATE ANION (three-letter code: FLC) (formula:  $C_6H_5O_7$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			13	6	7		
2	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	91	Total	O	0	0
			91	91		
4	B	88	Total	O	0	0
			88	88		
4	C	73	Total	O	0	0
			73	73		
4	D	39	Total	O	0	0
			39	39		



Chain D:

3% 66% 15% 17%

LYS GLU GLU ASN N5 K13 K17 I24 I25 L26 V27 R28 P29 H37 L38 E62 LEU ASP ASN ASN PRO ASN ASN GLN ILE ASN LYS ASP HIS ASN ILE ILE ILE ASN THR THR ASN HIS THR THR ASN ASN HIS ASN ASN ILE ALA LEU SER HIS ILE LYS LYS GLN R98 R101

N110 M111 E112 S115 V116 Y123 GLU GLN THR GLU ASN ALA PRO R28 ILE THR N134 Y135 G138 L145 K146 I147 N148 D149 D150 I151 Y152 N164 D165 A166 K169 N172 D196 LYS ASN ASN L200 Y201 Y210 E220 Q233 I240 N241 I242 Y245 Q260

D261 E262 M272 L273 F274 C279 E280 L281 H286 K287 S288 I289 R290 Y291 K292 V293 M294 K298 SER HIS ASP Q302 V311 E314 V315 Y316

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	138.04Å 138.04Å 147.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.40 69.02 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (20.00-2.40) 99.4 (69.02-2.40)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.26 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.195 , 0.246 0.190 , 0.238	Depositor DCC
$R_{free}$ test set	3191 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	41.7	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 52.9	EDS
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63382 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9261	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% of the height of the origin peak. No significant pseudotranslation is detected.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 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: FLC, FAD

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	0.52	0/2256	0.62	0/3045
1	B	0.52	0/2254	0.63	0/3043
1	C	0.50	0/2199	0.59	0/2967
1	D	0.48	0/2240	0.60	0/3022
All	All	0.50	0/8949	0.61	0/12077

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	154	THR	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	2201	0	2144	22	0
1	B	2199	0	2150	24	0
1	C	2146	0	2101	34	0
1	D	2186	0	2136	25	0
2	A	13	0	5	0	0
2	B	13	0	5	0	0
3	A	53	0	31	0	0
3	B	53	0	31	2	0
3	C	53	0	31	3	0
3	D	53	0	31	0	0
4	A	91	0	0	0	0
4	B	88	0	0	6	0
4	C	73	0	0	3	0
4	D	39	0	0	2	0
All	All	9261	0	8665	109	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 6.

The worst 5 of 109 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:165:ASP:HB3	1:A:169:LYS:HG3	1.36	1.05
1:A:245:VAL:HG22	1:A:262:GLU:HG3	1.61	0.83
1:C:172:ASN:HD22	1:C:210:TYR:H	1.26	0.81
1:D:245:VAL:HG22	1:D:262:GLU:HG3	1.64	0.80
1:B:272:ASN:HB3	4:B:9033:HOH:O	1.81	0.78

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	255/316 (81%)	252 (99%)	3 (1%)	0	100	100
1	B	255/316 (81%)	247 (97%)	7 (3%)	1 (0%)	39	56
1	C	247/316 (78%)	234 (95%)	13 (5%)	0	100	100
1	D	251/316 (79%)	240 (96%)	9 (4%)	2 (1%)	24	35
All	All	1008/1264 (80%)	973 (96%)	32 (3%)	3 (0%)	46	63

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	156	ALA
1	D	166	ALA
1	D	29	PRO

### 5.3.2 Protein sidechains ⓘ

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	244/295 (83%)	231 (95%)	13 (5%)	28	44
1	B	244/295 (83%)	227 (93%)	17 (7%)	19	29
1	C	238/295 (81%)	228 (96%)	10 (4%)	36	56
1	D	241/295 (82%)	227 (94%)	14 (6%)	25	39
All	All	967/1180 (82%)	913 (94%)	54 (6%)	26	41

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	252	SER
1	C	13	LYS
1	D	240	ILE
1	B	253	ASP
1	B	287	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	260	GLN
1	B	300	HIS
1	C	241	ASN
1	B	172	ASN
1	B	241	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](#)

6 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	FAD	A	415	-	48,58,58	1.23	6 (12%)	54,89,89	2.46	12 (22%)
2	FLC	A	9002	-	3,12,12	0.82	0	3,17,17	1.15	0
3	FAD	B	415	-	48,58,58	1.31	5 (10%)	54,89,89	2.49	13 (24%)
2	FLC	B	9001	-	3,12,12	0.77	0	3,17,17	2.25	2 (66%)
3	FAD	C	415	-	48,58,58	1.27	6 (12%)	54,89,89	2.36	10 (18%)
3	FAD	D	415	-	48,58,58	1.33	7 (14%)	54,89,89	2.26	12 (22%)

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	FAD	A	415	-	-	0/30/50/50	0/6/6/6
2	FLC	A	9002	-	-	0/6/16/16	0/0/0/0
3	FAD	B	415	-	-	0/30/50/50	0/6/6/6
2	FLC	B	9001	-	-	0/6/16/16	0/0/0/0
3	FAD	C	415	-	-	0/30/50/50	0/6/6/6
3	FAD	D	415	-	-	0/30/50/50	0/6/6/6

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	415	FAD	C4'-C3'	-2.30	1.48	1.53
3	A	415	FAD	C4'-C3'	-2.19	1.49	1.53
3	D	415	FAD	C4'-C3'	-2.14	1.49	1.53
3	D	415	FAD	C10-N1	2.15	1.39	1.35
3	A	415	FAD	C5X-N5	2.16	1.38	1.35

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	415	FAD	N3A-C2A-N1A	-12.92	119.00	128.89
3	B	415	FAD	N3A-C2A-N1A	-12.50	119.32	128.89
3	A	415	FAD	N3A-C2A-N1A	-12.19	119.56	128.89
3	D	415	FAD	N3A-C2A-N1A	-12.01	119.70	128.89
3	A	415	FAD	C4X-C4-N3	-3.37	118.98	123.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	415	FAD	2	0
3	C	415	FAD	3	0

## 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](#)

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	263/316 (83%)	0.13	0 100 100	17, 31, 58, 93	0
1	B	262/316 (82%)	0.26	11 (4%) 40 41	18, 35, 72, 115	1 (0%)
1	C	257/316 (81%)	0.30	7 (2%) 58 57	21, 41, 69, 94	1 (0%)
1	D	261/316 (82%)	0.38	10 (3%) 44 45	32, 54, 86, 124	2 (0%)
All	All	1043/1264 (82%)	0.27	28 (2%) 58 57	17, 40, 78, 124	4 (0%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	98	ARG	5.5
1	D	200	LEU	4.7
1	D	123	TYR	4.3
1	B	299	SER	4.1
1	B	301	ASP	4.0

### 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	FLC	A	9002	13/13	0.59	0.48	13.02	45,59,62,65	12
3	FAD	B	415	53/53	0.97	0.16	-0.20	14,23,43,45	0
3	FAD	D	415	53/53	0.96	0.18	-0.26	25,39,84,85	0
3	FAD	C	415	53/53	0.96	0.15	-0.36	25,37,68,68	0
3	FAD	A	415	53/53	0.98	0.14	-0.77	17,24,59,60	0
2	FLC	B	9001	13/13	0.97	0.13	-1.59	42,44,48,48	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.