



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 01:44 am GMT

PDB ID : 2B98  
Title : Crystal Structure of an archaeal pentameric riboflavin synthase  
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Deposited on : 2005-10-11  
Resolution : 2.30 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  
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

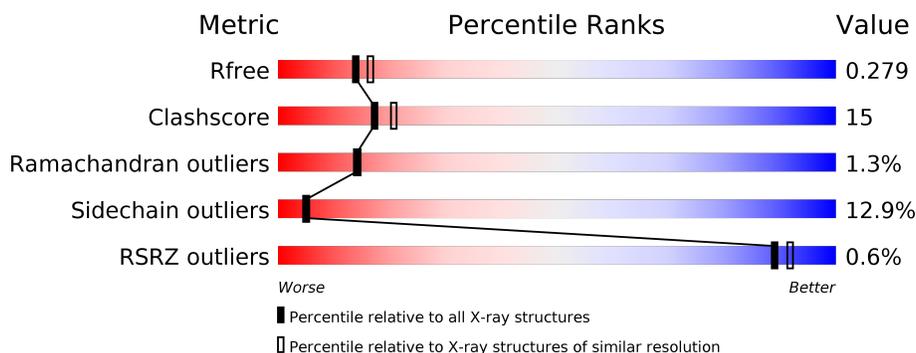
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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	156	 % 53% 28% 8% • 10%
1	B	156	 % 49% 32% 6% • 10%
1	C	156	 % 63% 28% 6% •
1	D	156	 % 53% 32% • • 10%
1	E	156	 % 56% 34% 6% • •

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5989 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.

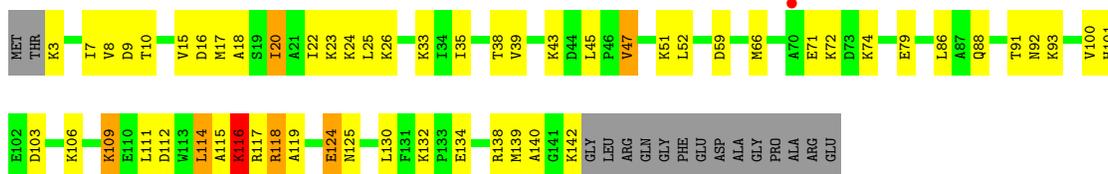
- Molecule 1 is a protein called Riboflavin synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	141	1106	707	188	202	9	63	0	0
1	B	141	1109	709	188	203	9	94	0	0
1	C	152	1189	758	203	219	9	72	0	0
1	D	140	1102	705	187	201	9	66	0	0
1	E	152	1189	758	203	219	9	57	0	0

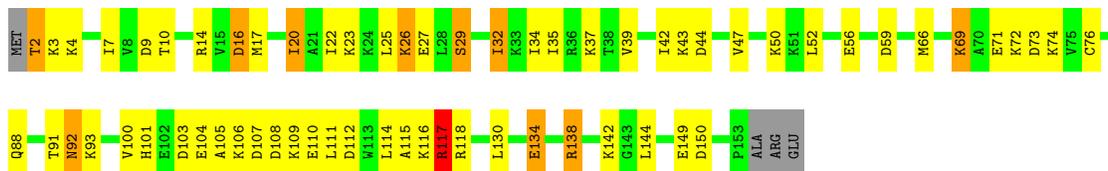
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	64	Total	O	0	0
			64	64		
2	B	62	Total	O	0	0
			62	62		
2	C	61	Total	O	0	0
			61	61		
2	D	52	Total	O	0	0
			52	52		
2	E	55	Total	O	0	0
			55	55		





• Molecule 1: Riboflavin synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.77Å 72.69Å 72.70Å 68.48° 74.61° 74.90°	Depositor
Resolution (Å)	20.00 – 2.30 20.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.30) 84.9 (20.00-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.24 (at 2.30Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.208 , 0.276 0.212 , 0.279	Depositor DCC
$R_{free}$ test set	1677 reflections (5.51%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.5	Xtrriage
Anisotropy	0.099	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 33.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	0.095 for h,h-k,h-l 0.257 for -h,-l,-k 0.089 for -h,-h+l,-h+k	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5989	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.12% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	2.50	11/1122 (1.0%)	1.64	23/1504 (1.5%)
1	B	5.55	17/1125 (1.5%)	2.54	34/1509 (2.3%)
1	C	1.94	8/1207 (0.7%)	1.37	21/1619 (1.3%)
1	D	1.90	13/1118 (1.2%)	1.56	23/1499 (1.5%)
1	E	1.84	14/1207 (1.2%)	1.33	22/1619 (1.4%)
All	All	3.07	63/5779 (1.1%)	1.74	123/7750 (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
1	B	0	3
1	C	0	1
1	D	0	1
All	All	0	7

The worst 5 of 63 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	134	GLU	CD-OE1	161.56	3.03	1.25
1	B	134	GLU	CD-OE2	70.17	2.02	1.25
1	D	124	GLU	CG-CD	50.00	2.27	1.51
1	A	71	GLU	CG-CD	48.47	2.24	1.51
1	E	74	LYS	CD-CE	41.81	2.55	1.51

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	134	GLU	OE1-CD-OE2	-64.04	46.45	123.30
1	B	141	GLY	O-C-N	-42.17	55.23	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	124	GLU	CG-CD-OE2	-28.90	60.49	118.30
1	A	71	GLU	CG-CD-OE2	-24.92	68.45	118.30
1	C	148	PHE	CB-CG-CD1	-23.05	104.67	120.80

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	31	ASN	Sidechain
1	A	71	GLU	Sidechain
1	B	102	GLU	Sidechain
1	B	134	GLU	Sidechain
1	B	141	GLY	Mainchain

## 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	1106	0	1162	43	0
1	B	1109	0	1166	33	0
1	C	1189	0	1238	40	0
1	D	1102	0	1159	30	0
1	E	1189	0	1238	42	0
2	A	64	0	0	3	0
2	B	62	0	0	2	0
2	C	61	0	0	5	0
2	D	52	0	0	8	0
2	E	55	0	0	8	0
All	All	5989	0	5963	166	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 15.

The worst 5 of 166 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:47:VAL:HG21	1:E:88:GLN:HB3	1.24	1.11
1:A:88:GLN:HB3	1:E:47:VAL:HG21	1.25	1.09
1:E:7:ILE:HG22	2:E:196:HOH:O	1.60	1.02
1:A:47:VAL:HG21	1:B:88:GLN:HB3	1.35	1.02
1:E:20:ILE:HD13	1:E:20:ILE:H	1.25	1.00

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	139/156 (89%)	132 (95%)	4 (3%)	3 (2%)	8	6
1	B	139/156 (89%)	136 (98%)	2 (1%)	1 (1%)	25	30
1	C	150/156 (96%)	144 (96%)	6 (4%)	0	100	100
1	D	138/156 (88%)	131 (95%)	5 (4%)	2 (1%)	13	13
1	E	150/156 (96%)	143 (95%)	4 (3%)	3 (2%)	9	7
All	All	716/780 (92%)	686 (96%)	21 (3%)	9 (1%)	14	14

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	107	ASP
1	E	92	ASN
1	D	140	ALA
1	A	92	ASN
1	A	142	LYS

### 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	119/130 (92%)	100 (84%)	19 (16%)	3	3
1	B	120/130 (92%)	106 (88%)	14 (12%)	6	7
1	C	127/130 (98%)	116 (91%)	11 (9%)	12	14
1	D	119/130 (92%)	104 (87%)	15 (13%)	5	5
1	E	127/130 (98%)	107 (84%)	20 (16%)	3	3
All	All	612/650 (94%)	533 (87%)	79 (13%)	5	5

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	24	LYS
1	D	20	ILE
1	E	114	LEU
1	C	25	LEU
1	C	118	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	88	GLN
1	C	92	ASN
1	E	88	GLN
1	B	122	HIS
1	B	125	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](#)

There are no ligands in this entry.

## 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	141/156 (90%)	-0.44	1 (0%) 87 90	25, 34, 43, 46	18 (12%)
1	B	141/156 (90%)	-0.40	2 (1%) 75 80	24, 34, 41, 60	25 (17%)
1	C	152/156 (97%)	-0.45	0 100 100	25, 33, 44, 48	21 (13%)
1	D	140/156 (89%)	-0.50	1 (0%) 87 90	24, 33, 42, 69	18 (12%)
1	E	152/156 (97%)	-0.48	0 100 100	25, 34, 41, 46	16 (10%)
All	All	726/780 (93%)	-0.45	4 (0%) 89 92	24, 34, 42, 69	98 (13%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	70	ALA	3.0
1	A	12	PHE	2.7
1	B	35	ILE	2.6
1	B	12	PHE	2.6

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.