

# wwPDB X-ray Structure Validation Summary Report (i)

#### May 17, 2020 - 07:49 am BST

PDB ID	:	1VB5
Title	:	Crystal Structure Analysis of the Pyrococcus horikoshii OT3 translation initi-
		ation factor eIF-2B
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Deposited on	:	2004-02-22
$\operatorname{Resolution}$	:	2.20  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 A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

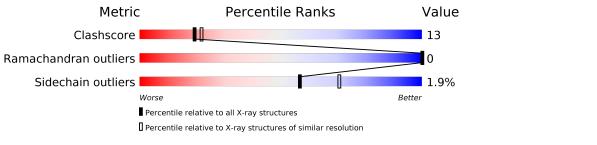
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
$\mathrm{EDS}$	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503(2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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 respectively. 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	А	276	76%	22%	••
1	В	276	75%	24%	



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4594 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 translation initiation factor eIF-2B.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Δ	274	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0
	А	214	2188	1397	378	403	10	0	0	0
1	В	275	Total	С	Ν	Ο	S	0	0	0
	D	215	2198	1402	380	406	10	0	0	0

• Molecule 2 is water.

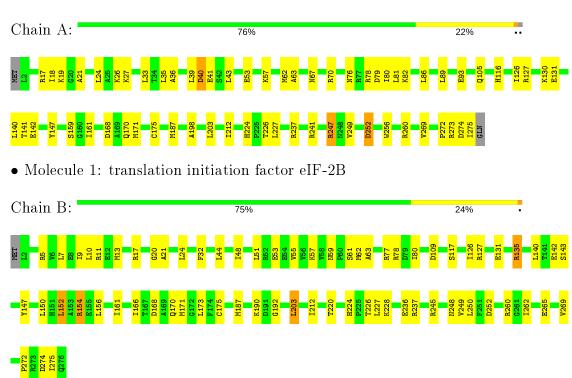
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	120	Total O 120 120	0	0
2	В	88	Total O 88 88	0	0



# 3 Residue-property plots (i)

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. Residues are colorcoded 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. 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: translation initiation factor eIF-2B



## 4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 63 2 2	Depositor	
Cell constants	158.44Å 158.44Å 151.49Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor	
Resolution (Å)	50.00 - 2.20	Depositor	
% Data completeness	(Not available) (50.00-2.20)	Depositor	
(in resolution range)		-	
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	CNS	Depositor	
$R, R_{free}$	0.209 , $0.234$	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	4594	wwPDB-VP	
Average B, all atoms $(Å^2)$	28.0	wwPDB-VP	



# 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	Bo	nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.34	0/2222	0.60	0/2996	
1	В	0.35	1/2232~(0.0%)	0.61	1/3008~(0.0%)	
All	All	0.35	1/4454~(0.0%)	0.61	1/6004~(0.0%)	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	В	109	ASP	C-N	-5.84	1.22	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	109	ASP	C-N-CA	-5.83	110.05	122.30

There are no chirality outliers.

There are no planarity outliers.

### 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	А	2188	0	2257	60	0
1	В	2198	0	2265	60	0
2	А	120	0	0	2	0
2	В	88	0	0	6	1
All	All	4594	0	4522	114	1



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 13.

The worst 5 of 114 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:269:VAL:HG23	1:B:274:ASP:HB2	1.47	0.95
1:A:247:ARG:HH11	1:A:247:ARG:HB3	1.37	0.88
1:B:135:ARG:HB2	1:B:135:ARG:HH11	1.36	0.87
1:B:150:LEU:O	1:B:154:ARG:HD3	1.74	0.87
1:A:269:VAL:HG13	1:A:274:ASP:HB2	1.58	0.85

All (1) 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-1 Atom-2		Clash overlap (Å)	
2:B:364:HOH:O	2:B:364:HOH:O[10_775]	1.05	1.15	

### 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	Percen	tiles
1	А	272/276~(99%)	265~(97%)	7(3%)	0	100	100
1	В	273/276~(99%)	264~(97%)	9~(3%)	0	100	100
All	All	545/552~(99%)	529~(97%)	16(3%)	0	100	100

There are no Ramachandran outliers to report.

#### 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.



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	236/238~(99%)	232~(98%)	4 (2%)	60 74
1	В	237/238~(100%)	232~(98%)	5 (2%)	53 67
All	All	473/476~(99%)	464 (98%)	9 (2%)	57 71

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

5 of 9 residues with a non-rotameric side chain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	В	135	ARG
1	В	272	PRO
1	В	154	ARG
1	А	247	ARG
1	В	152	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	116	HIS
1	А	170	GLN
1	А	224	HIS
1	В	170	GLN
1	В	224	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)

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)

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.

