



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:41 AM GMT

PDB ID : 2DZW  
Title : Structure of mutant tryptophan synthase alpha-subunit (E244A) from a hyperthermophile, *Pyrococcus furiosus*  
Authors : Ogasahara, K.; Yamagata, Y.; Yutani, K.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2006-09-30  
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

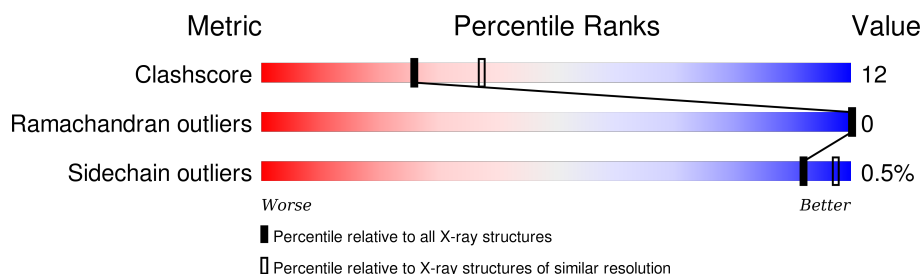
# 1 Overall quality at a glance

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))
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	248	 76% 23% .
1	B	248	 75% 23% .

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4259 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 Tryptophan synthase alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	0	0	0
			1911	1234	324	349	4			
1	B	245	Total	C	N	O	S	0	0	0
			1918	1238	325	351	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	244	ALA	GLU	ENGINEERED	UNP Q8U094
B	244	ALA	GLU	ENGINEERED	UNP Q8U094

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	242	Total	O	0	0
			242	242		
2	B	188	Total	O	0	0
			188	188		



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.11Å 77.64Å 166.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.68 – 2.40	Depositor
% Data completeness (in resolution range)	84.3 (19.68-2.40)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.192 , 0.258	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4259	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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	0.36	0/1947	0.61	0/2626
1	B	0.36	0/1954	0.59	0/2636
All	All	0.36	0/3901	0.60	0/5262

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	1911	0	1968	50	0
1	B	1918	0	1975	47	0
2	A	242	0	0	16	0
2	B	188	0	0	15	0
All	All	4259	0	3943	96	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 12.

All (96) 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:20:SER:OG	1:A:232:ARG:HG2	1.78	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:LYS:O	1:A:243:GLU:HG3	1.79	0.81
1:A:236:GLU:H	1:A:236:GLU:CD	1.85	0.79
1:B:90:ASN:HB3	1:B:91:PRO:HD3	1.64	0.79
1:A:90:ASN:HB3	1:A:91:PRO:HD3	1.66	0.77
1:A:167:GLY:HA3	2:A:314:HOH:O	1.89	0.72
1:B:235:THR:HB	1:B:236:GLU:OE1	1.90	0.72
1:B:239:LYS:O	1:B:243:GLU:HG3	1.94	0.68
1:A:86:MET:HG2	2:A:452:HOH:O	1.96	0.66
1:B:59:LEU:HD12	2:B:396:HOH:O	1.95	0.65
1:A:176:PRO:HB2	1:A:178:THR:HG22	1.79	0.65
1:B:236:GLU:CD	1:B:236:GLU:H	2.00	0.64
1:A:166:TYR:CE1	1:A:178:THR:HG21	2.37	0.60
1:B:173:GLU:HB3	2:B:254:HOH:O	2.01	0.59
1:A:5:GLY:HA2	1:A:210:LEU:HD22	1.85	0.59
1:B:150:LYS:HE3	1:B:154:ASP:OD2	2.03	0.58
1:B:75:PHE:CD2	1:B:83:ILE:HD11	2.39	0.57
1:B:54:SER:HB3	1:B:224:VAL:CG1	2.36	0.55
1:A:75:PHE:CD2	1:A:83:ILE:HD11	2.40	0.55
1:B:121:HIS:HA	2:B:351:HOH:O	2.06	0.55
1:A:166:TYR:CB	1:A:176:PRO:HG3	2.37	0.54
1:B:41:PHE:O	1:B:44:PRO:HD3	2.07	0.54
1:A:18:LYS:HE2	2:A:476:HOH:O	2.06	0.54
1:A:28:LEU:HD22	1:A:242:VAL:HG21	1.89	0.54
1:A:204:GLU:HG2	2:A:268:HOH:O	2.07	0.54
1:B:44:PRO:HA	1:B:88:TYR:CZ	2.44	0.52
1:B:64:LYS:NZ	2:B:432:HOH:O	2.42	0.52
1:B:67:GLU:O	1:B:71:ILE:HG13	2.09	0.52
1:A:235:THR:HB	1:A:236:GLU:OE2	2.10	0.52
1:A:88:TYR:O	1:A:91:PRO:HD2	2.10	0.51
1:A:166:TYR:HB2	2:A:358:HOH:O	2.10	0.51
1:B:88:TYR:O	1:B:91:PRO:HD2	2.11	0.51
1:A:41:PHE:O	1:A:44:PRO:HD3	2.10	0.51
1:A:44:PRO:HA	1:A:88:TYR:CZ	2.46	0.50
1:A:123:LYS:HG2	2:A:424:HOH:O	2.11	0.50
1:B:117:LEU:HB3	2:B:402:HOH:O	2.11	0.50
1:A:142:PRO:HD3	1:A:163:VAL:O	2.12	0.49
1:B:208:SER:O	1:B:212:GLU:HG2	2.13	0.49
1:B:151:VAL:HA	2:B:263:HOH:O	2.13	0.49
1:A:150:LYS:HE3	1:A:154:ASP:OD2	2.13	0.49
1:B:142:PRO:HD3	1:B:163:VAL:O	2.13	0.48
1:A:139:LEU:C	1:A:139:LEU:HD23	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:239:LYS:NZ	1:B:239:LYS:HB3	2.29	0.48
1:B:168:THR:HB	2:B:254:HOH:O	2.13	0.48
1:A:59:LEU:HD12	2:A:254:HOH:O	2.14	0.47
1:A:67:GLU:O	1:A:71:ILE:HG13	2.14	0.47
1:A:191:ARG:HG2	1:B:2:PHE:HA	1.96	0.47
1:B:195:ALA:HA	1:B:216:GLY:O	2.14	0.47
1:B:90:ASN:O	1:B:94:ARG:HG3	2.15	0.47
1:B:236:GLU:N	1:B:236:GLU:OE1	2.39	0.47
1:A:124:GLU:HG3	2:A:457:HOH:O	2.14	0.47
1:A:168:THR:HB	1:A:173:GLU:C	2.35	0.46
1:A:165:LEU:HD23	1:A:165:LEU:O	2.15	0.46
1:A:60:LYS:HE2	2:A:362:HOH:O	2.15	0.46
1:A:240:LYS:HD3	1:A:240:LYS:HA	1.73	0.46
1:B:139:LEU:HD23	1:B:139:LEU:C	2.36	0.46
1:B:66:ARG:HH11	1:B:66:ARG:HG3	1.81	0.46
1:A:61:ASN:N	1:A:61:ASN:HD22	2.14	0.45
1:A:166:TYR:HB3	1:A:176:PRO:HG3	1.97	0.45
1:A:77:ARG:HG2	1:A:77:ARG:HH11	1.81	0.45
1:A:66:ARG:HH11	1:A:66:ARG:HG3	1.82	0.44
1:A:40:PRO:HG2	1:A:63:PHE:CD1	2.52	0.44
1:B:151:VAL:HG13	2:B:263:HOH:O	2.18	0.44
1:A:175:ILE:HG22	1:A:179:ALA:HB3	2.00	0.44
1:A:8:ILE:O	1:A:218:VAL:HA	2.19	0.43
1:B:8:ILE:O	1:B:218:VAL:HA	2.18	0.43
1:B:87:THR:HA	2:B:365:HOH:O	2.18	0.43
1:B:28:LEU:HD22	1:B:242:VAL:HG21	2.00	0.43
1:B:77:ARG:HH11	1:B:77:ARG:HG2	1.83	0.43
1:B:177:LYS:HG2	2:B:278:HOH:O	2.17	0.43
1:A:236:GLU:CD	1:A:236:GLU:N	2.64	0.43
1:B:40:PRO:HG2	1:B:63:PHE:CD1	2.53	0.43
1:A:178:THR:HG23	2:A:358:HOH:O	2.18	0.42
1:B:17:ASP:HA	2:B:361:HOH:O	2.18	0.42
1:B:56:TYR:O	1:B:60:LYS:HG2	2.20	0.42
1:B:243:GLU:HG2	1:B:248:ILE:HD11	2.01	0.42
1:A:77:ARG:HA	2:A:375:HOH:O	2.19	0.42
1:B:61:ASN:N	1:B:61:ASN:HD22	2.15	0.42
1:B:90:ASN:OD1	1:B:94:ARG:HD2	2.20	0.42
1:B:202:LYS:O	1:B:205:HIS:HB2	2.20	0.42
1:A:90:ASN:OD1	1:A:94:ARG:HD2	2.20	0.41
1:A:56:TYR:HD2	2:A:254:HOH:O	2.03	0.41
1:A:97:VAL:HB	2:A:339:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:LEU:HD22	1:A:35:ILE:HG21	2.02	0.41
1:A:173:GLU:N	2:A:291:HOH:O	2.54	0.41
1:A:155:MET:HG3	2:A:288:HOH:O	2.21	0.41
1:B:25:LEU:HD22	1:B:35:ILE:HG21	2.03	0.41
1:B:127:GLU:HB3	2:B:436:HOH:O	2.20	0.41
1:B:106:ALA:HA	2:B:311:HOH:O	2.19	0.41
1:B:174:GLU:N	2:B:254:HOH:O	2.54	0.41
1:A:90:ASN:O	1:A:94:ARG:HG3	2.20	0.41
1:A:240:LYS:HD2	2:A:344:HOH:O	2.21	0.41
1:B:139:LEU:HB3	2:B:267:HOH:O	2.20	0.41
1:B:227:ILE:HG13	1:B:238:LEU:HD21	2.03	0.41
1:B:66:ARG:NH1	1:B:66:ARG:HG3	2.36	0.40
1:A:87:THR:OG1	1:A:88:TYR:N	2.55	0.40

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	240/248 (97%)	225 (94%)	15 (6%)	0	100	100
1	B	241/248 (97%)	228 (95%)	13 (5%)	0	100	100
All	All	481/496 (97%)	453 (94%)	28 (6%)	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.

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	202/204 (99%)	202 (100%)	0	100	100
1	B	203/204 (100%)	201 (99%)	2 (1%)	82	93
All	All	405/408 (99%)	403 (100%)	2 (0%)	92	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	200	VAL
1	B	236	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	23	ASN
1	A	52	GLN
1	A	61	ASN
1	A	99	ASN
1	B	19	GLN
1	B	23	ASN
1	B	52	GLN
1	B	61	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.