



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 27, 2017 – 03:02 AM EDT

PDB ID : 1O4U
Title : Crystal structure of a nicotinate nucleotide pyrophosphorylase (tm1645) from thermotoga maritima at 2.50 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : unknown
Resolution : 2.50 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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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	:	rb-20030345
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)	:	rb-20030345

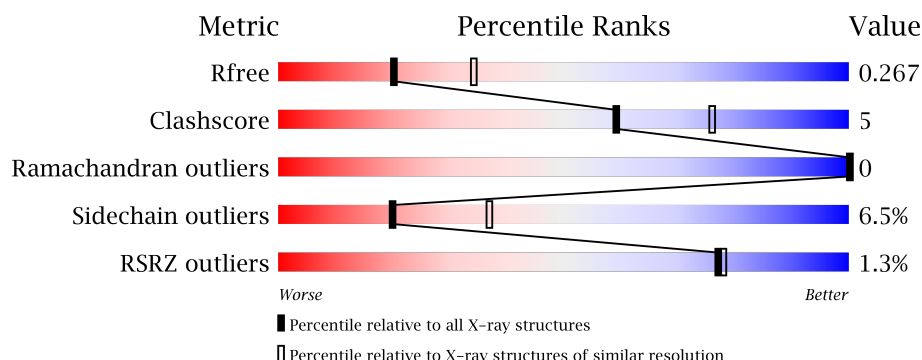
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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. 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	285	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 15%, green 76%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 76% 15% 7% </div> </div>
1	B	285	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 14%, green 78%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 78% 14% 7% </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4204 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 Type II quinolic acid phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	1	0
			2046	1296	343	398	9			
1	B	266	Total	C	N	O	S	0	2	0
			2045	1291	347	398	9			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	LEADER SEQUENCE	UNP Q9X1X8
A	-10	GLY	-	LEADER SEQUENCE	UNP Q9X1X8
A	-9	SER	-	LEADER SEQUENCE	UNP Q9X1X8
A	-8	ASP	-	LEADER SEQUENCE	UNP Q9X1X8
A	-7	LYS	-	LEADER SEQUENCE	UNP Q9X1X8
A	-6	ILE	-	LEADER SEQUENCE	UNP Q9X1X8
A	-5	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
A	-4	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
A	-3	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
A	-2	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
A	-1	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
A	0	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
B	-11	MET	-	LEADER SEQUENCE	UNP Q9X1X8
B	-10	GLY	-	LEADER SEQUENCE	UNP Q9X1X8
B	-9	SER	-	LEADER SEQUENCE	UNP Q9X1X8
B	-8	ASP	-	LEADER SEQUENCE	UNP Q9X1X8
B	-7	LYS	-	LEADER SEQUENCE	UNP Q9X1X8
B	-6	ILE	-	LEADER SEQUENCE	UNP Q9X1X8
B	-5	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
B	-4	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
B	-3	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
B	-2	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
B	-1	HIS	-	LEADER SEQUENCE	UNP Q9X1X8
B	0	HIS	-	LEADER SEQUENCE	UNP Q9X1X8

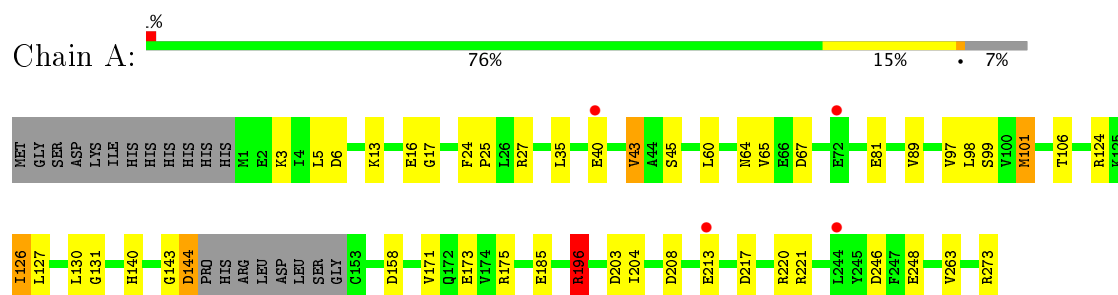
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	53	Total 53	O 53	0	0
2	B	60	Total 60	O 60	0	0

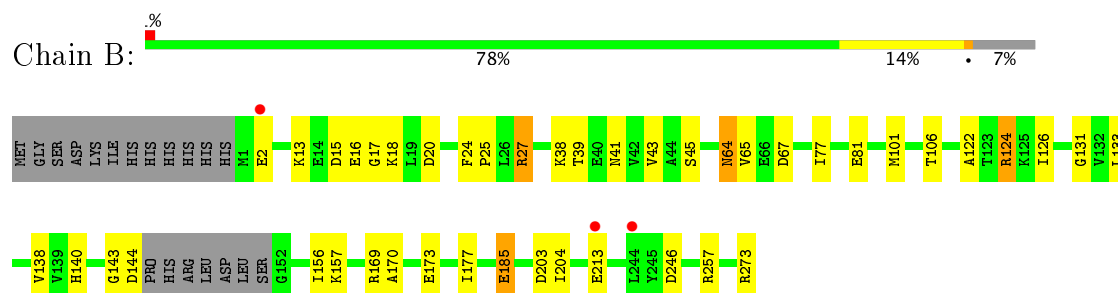
3 Residue-property plots

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.

- Molecule 1: Type II quinolic acid phosphoribosyltransferase



- Molecule 1: Type II quinolic acid phosphoribosyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	96.37Å 126.12Å 138.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.29 – 2.50 38.29 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.0 (38.29-2.50) 99.0 (38.29-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.51Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.213 , 0.272 0.212 , 0.267	Depositor DCC
R_{free} test set	1510 reflections (5.45%)	DCC
Wilson B-factor (Å ²)	49.9	Xtriage
Anisotropy	0.387	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 32.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4204	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	0.77	1/2071 (0.0%)	0.90	9/2794 (0.3%)
1	B	0.76	0/2075	0.89	7/2798 (0.3%)
All	All	0.77	1/4146 (0.0%)	0.89	16/5592 (0.3%)

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	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101	MET	SD-CE	-5.42	1.47	1.77

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	203	ASP	CB-CG-OD2	7.99	125.49	118.30
1	A	196	ARG	NE-CZ-NH2	7.68	124.14	120.30
1	B	246	ASP	CB-CG-OD2	7.19	124.77	118.30
1	A	144	ASP	CB-CG-OD2	6.69	124.32	118.30
1	A	208	ASP	CB-CG-OD2	6.40	124.06	118.30
1	A	217	ASP	CB-CG-OD2	6.37	124.03	118.30
1	A	246	ASP	CB-CG-OD2	6.09	123.78	118.30
1	B	67	ASP	CB-CG-OD2	5.71	123.44	118.30
1	A	158	ASP	CB-CG-OD2	5.58	123.33	118.30
1	B	20	ASP	CB-CG-OD2	5.52	123.27	118.30
1	B	27[A]	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	B	27[B]	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	A	67	ASP	CB-CG-OD2	5.37	123.13	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	ASP	CB-CG-OD2	5.27	123.04	118.30
1	B	203	ASP	CB-CG-OD2	5.18	122.96	118.30
1	B	15	ASP	CB-CG-OD2	5.13	122.91	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	16	GLU	Peptide
1	B	39	THR	Peptide
1	B	41	ASN	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	2046	0	2094	24	0
1	B	2045	0	2089	21	0
2	A	53	0	0	3	0
2	B	60	0	0	3	0
All	All	4204	0	4183	45	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 5.

All (45) 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:196:ARG:HH21	1:A:196:ARG:HG3	1.44	0.82
1:A:45:SER:HB2	1:A:140:HIS:CD2	2.16	0.81
1:A:97:VAL:HG13	1:A:101:MET:CE	2.15	0.75
1:B:45:SER:HB2	1:B:140:HIS:HD2	1.50	0.74
1:B:43:VAL:HG12	1:B:106:THR:HA	1.70	0.72
1:B:126:ILE:HD12	1:B:131:GLY:HA3	1.72	0.69
1:A:220:ARG:NH2	2:A:306:HOH:O	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:LEU:HB2	1:A:130:LEU:HD11	1.74	0.69
1:A:45:SER:HB2	1:A:140:HIS:HD2	1.60	0.66
1:A:196:ARG:NH2	1:A:196:ARG:HG3	2.08	0.65
1:B:38:LYS:NZ	2:B:322:HOH:O	2.30	0.65
1:B:13:LYS:O	1:B:17:GLY:HA2	1.99	0.63
1:A:97:VAL:HG13	1:A:101:MET:HE2	1.81	0.63
1:B:45:SER:HB2	1:B:140:HIS:CD2	2.33	0.62
1:A:196:ARG:HH21	1:A:196:ARG:CG	2.13	0.62
1:B:185:GLU:HG2	1:B:204:ILE:HB	1.83	0.59
1:B:64:ASN:HD21	1:B:77:ILE:HA	1.69	0.58
1:A:185:GLU:HG2	1:A:204:ILE:HB	1.86	0.57
1:A:143:GLY:O	1:A:144:ASP:CB	2.54	0.56
1:B:143:GLY:O	1:B:144:ASP:HB2	2.05	0.56
1:A:221:ARG:HD3	2:A:277:HOH:O	2.05	0.56
1:B:101:MET:HE1	1:B:133:LEU:HD22	1.86	0.56
1:B:27[B]:ARG:NH1	2:B:298:HOH:O	2.40	0.55
1:A:126:ILE:HD12	1:A:131:GLY:HA3	1.88	0.55
1:A:43:VAL:CG1	1:A:106:THR:HA	2.37	0.55
1:B:24:PHE:HB3	1:B:25:PRO:HD3	1.91	0.53
1:A:24:PHE:HB3	1:A:25:PRO:HD3	1.93	0.51
1:B:101:MET:CE	1:B:133:LEU:HD22	2.41	0.51
1:A:40:GLU:HB2	2:A:297:HOH:O	2.12	0.50
1:A:16:GLU:HB3	1:A:17:GLY:HA2	1.93	0.49
1:A:60:LEU:N	1:A:60:LEU:HD12	2.28	0.48
1:B:143:GLY:O	1:B:144:ASP:CB	2.62	0.48
1:A:99:SER:HB3	1:A:263:VAL:HG11	1.96	0.47
1:B:43:VAL:CG1	1:B:106:THR:HA	2.43	0.47
1:B:124:ARG:NE	2:B:331:HOH:O	2.48	0.46
1:A:130:LEU:HD12	1:A:130:LEU:C	2.35	0.46
1:B:64:ASN:ND2	1:B:77:ILE:HA	2.31	0.45
1:B:122:ALA:HB2	1:B:138:VAL:HG21	1.98	0.45
1:A:43:VAL:HG12	1:A:106:THR:HA	1.98	0.45
1:A:16:GLU:HB3	1:A:17:GLY:CA	2.48	0.44
1:A:171:VAL:O	1:A:175:ARG:HB2	2.17	0.43
1:B:126:ILE:CD1	1:B:131:GLY:HA3	2.46	0.43
1:A:35:LEU:HD21	1:A:98:LEU:CD1	2.49	0.43
1:B:156:ILE:HD13	1:B:170:ALA:HB1	2.02	0.41
1:B:18:LYS:HG2	1:B:18:LYS:H	1.78	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	262/285 (92%)	251 (96%)	11 (4%)	0	100	100
1	B	264/285 (93%)	255 (97%)	9 (3%)	0	100	100
All	All	526/570 (92%)	506 (96%)	20 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	226/248 (91%)	210 (93%)	16 (7%)	17	32
1	B	225/248 (91%)	212 (94%)	13 (6%)	23	43
All	All	451/496 (91%)	422 (94%)	29 (6%)	20	38

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	5	LEU
1	A	13	LYS
1	A	27	ARG
1	A	43	VAL
1	A	64	ASN
1	A	65	VAL
1	A	81	GLU

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Mol	Chain	Res	Type
1	A	89	VAL
1	A	124	ARG
1	A	126	ILE
1	A	173	GLU
1	A	196	ARG
1	A	213	GLU
1	A	248	GLU
1	A	273	ARG
1	B	2	GLU
1	B	64	ASN
1	B	65	VAL
1	B	81	GLU
1	B	124	ARG
1	B	157	LYS
1	B	169	ARG
1	B	173	GLU
1	B	177	ILE
1	B	185	GLU
1	B	213	GLU
1	B	257	ARG
1	B	273	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	HIS
1	B	64	ASN
1	B	140	HIS

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 [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, 95th 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 ²)	Q<0.9
1	A	265/285 (92%)	0.04	4 (1%) 74 75	25, 39, 53, 71	0
1	B	266/285 (93%)	-0.01	3 (1%) 80 81	26, 39, 53, 72	0
All	All	531/570 (93%)	0.01	7 (1%) 77 78	25, 39, 53, 72	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	72	GLU	3.5
1	A	244	LEU	2.9
1	B	213	GLU	2.7
1	B	244	LEU	2.4
1	A	40	GLU	2.2
1	A	213	GLU	2.1
1	B	2	GLU	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.