



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:39 AM GMT

PDB ID : 2I14
Title : Crystal structure of nicotinate-nucleotide pyrophosphorylase from *Pyrococcus furiosus*
Authors : Shin, D.H.; Kim, R.; Kim, S.-H.; Berkeley Structural Genomics Center (BSGC)
Deposited on : 2006-08-12
Resolution : 2.90 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
<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:

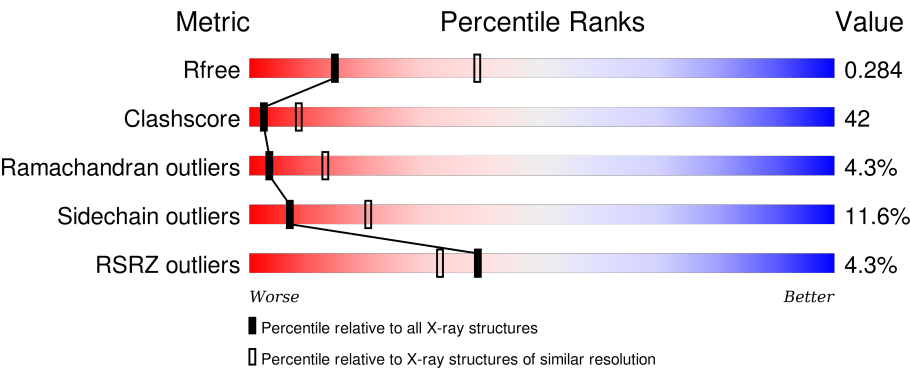
MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : 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 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	395	<div><div>3%</div><div><div></div><div>41%</div><div>50%</div><div>7%</div><div>..</div></div></div>
1	B	395	<div><div>6%</div><div><div></div><div>39%</div><div>50%</div><div>9%</div><div>..</div></div></div>
1	C	395	<div><div>5%</div><div><div></div><div>41%</div><div>49%</div><div>8%</div><div>..</div></div></div>
1	D	395	<div><div>4%</div><div><div></div><div>39%</div><div>50%</div><div>8%</div><div>..</div></div></div>
1	E	395	<div><div>4%</div><div><div></div><div>39%</div><div>50%</div><div>8%</div><div>..</div></div></div>

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Mol	Chain	Length	Quality of chain
1	F	395	<div><div></div><div>4%</div><div>37%</div><div>52%</div><div>8%</div><div>••</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18539 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 Nicotinate-nucleotide pyrophosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	0	0
			3055	1974	517	551	13			
1	B	389	Total	C	N	O	S	0	0	0
			3055	1974	517	551	13			
1	C	389	Total	C	N	O	S	0	0	0
			3055	1974	517	551	13			
1	D	389	Total	C	N	O	S	0	0	0
			3055	1974	517	551	13			
1	E	389	Total	C	N	O	S	0	0	0
			3055	1974	517	551	13			
1	F	389	Total	C	N	O	S	0	0	0
			3055	1974	517	551	13			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
A	-4	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
A	-3	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
A	-2	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
A	-1	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
A	0	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
B	395	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
B	396	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
B	397	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
B	398	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
B	399	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
B	400	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
C	995	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
C	996	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
C	997	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
C	998	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
C	999	GLY	-	CLONING ARTIFACT	UNP Q8TZS9

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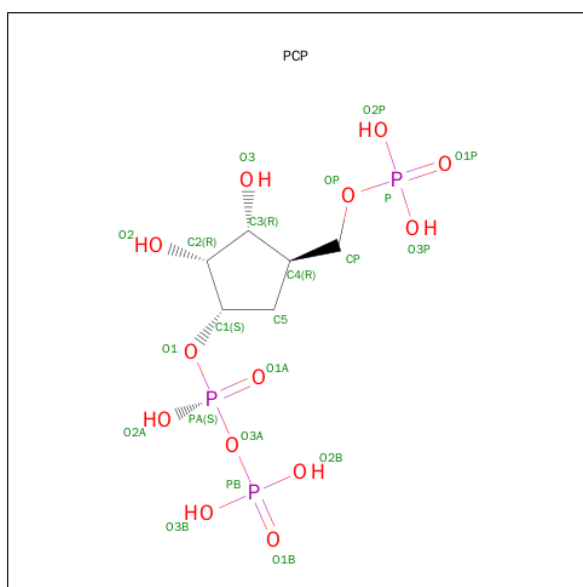
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Chain	Residue	Modelled	Actual	Comment	Reference
C	1000	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
D	1395	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
D	1396	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
D	1397	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
D	1398	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
D	1399	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
D	1400	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
E	1995	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
E	1996	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
E	1997	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
E	1998	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
E	1999	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
E	2000	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
F	2395	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
F	2396	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
F	2397	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
F	2398	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
F	2399	GLY	-	CLONING ARTIFACT	UNP Q8TZS9
F	2400	GLY	-	CLONING ARTIFACT	UNP Q8TZS9

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	2	Total 2	Zn 2	0	0
2	E	2	Total 2	Zn 2	0	0
2	B	2	Total 2	Zn 2	0	0
2	C	2	Total 2	Zn 2	0	0
2	A	2	Total 2	Zn 2	0	0
2	F	2	Total 2	Zn 2	0	0

- Molecule 3 is 1-ALPHA-PYROPHOSPHORYL-2-ALPHA,3-ALPHA-DIHYDROXY-4-BETA-CYCLOPENTANE-METHANOL-5-PHOSPHATE (three-letter code: PCP) (formula: C₆H₁₅O₁₃P₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			22	6	13	3		
3	B	1	Total	C	O	P	0	0
			22	6	13	3		
3	C	1	Total	C	O	P	0	0
			22	6	13	3		
3	D	1	Total	C	O	P	0	0
			22	6	13	3		
3	E	1	Total	C	O	P	0	0
			22	6	13	3		
3	F	1	Total	C	O	P	0	0
			22	6	13	3		

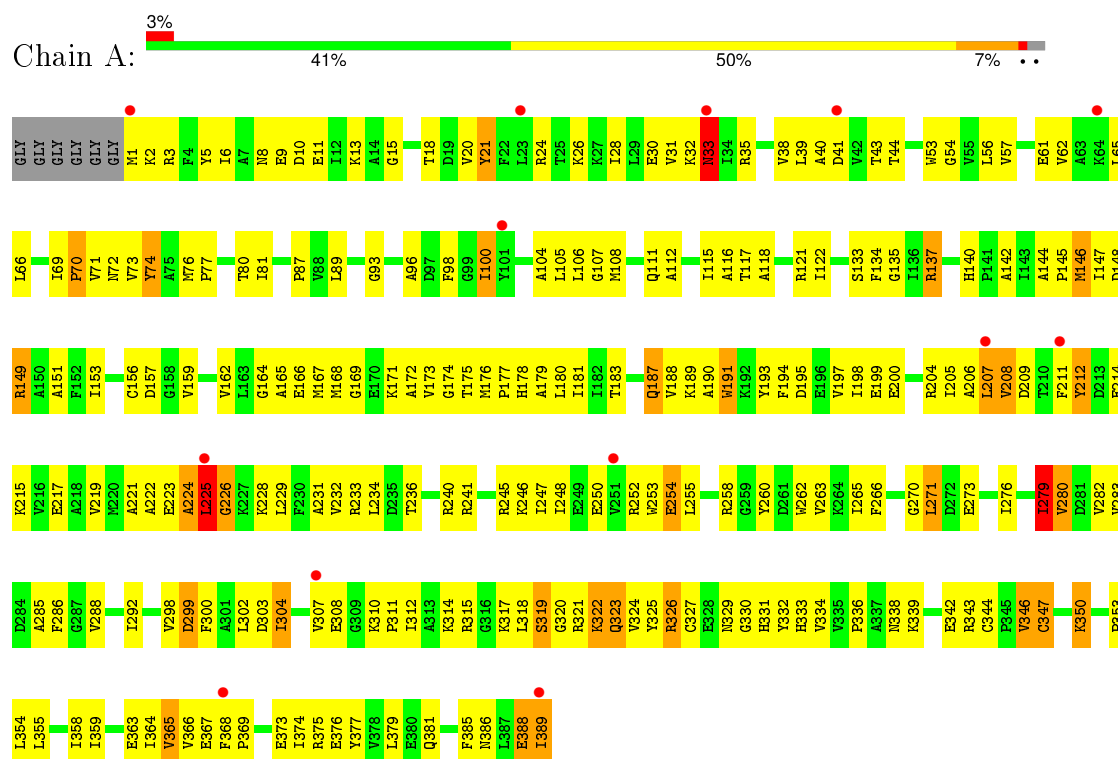
- Molecule 4 is water.

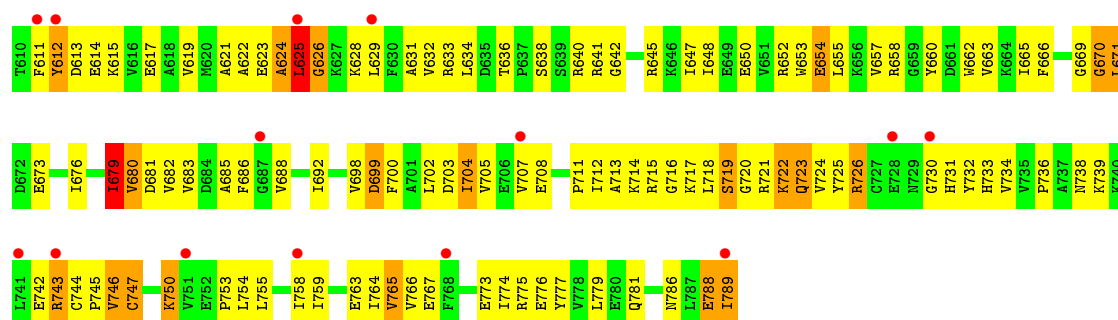
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	10	Total	O	0	0
			10	10		
4	C	9	Total	O	0	0
			9	9		
4	D	10	Total	O	0	0
			10	10		
4	E	16	Total	O	0	0
			16	16		
4	F	12	Total	O	0	0
			12	12		

3 Residue-property plots

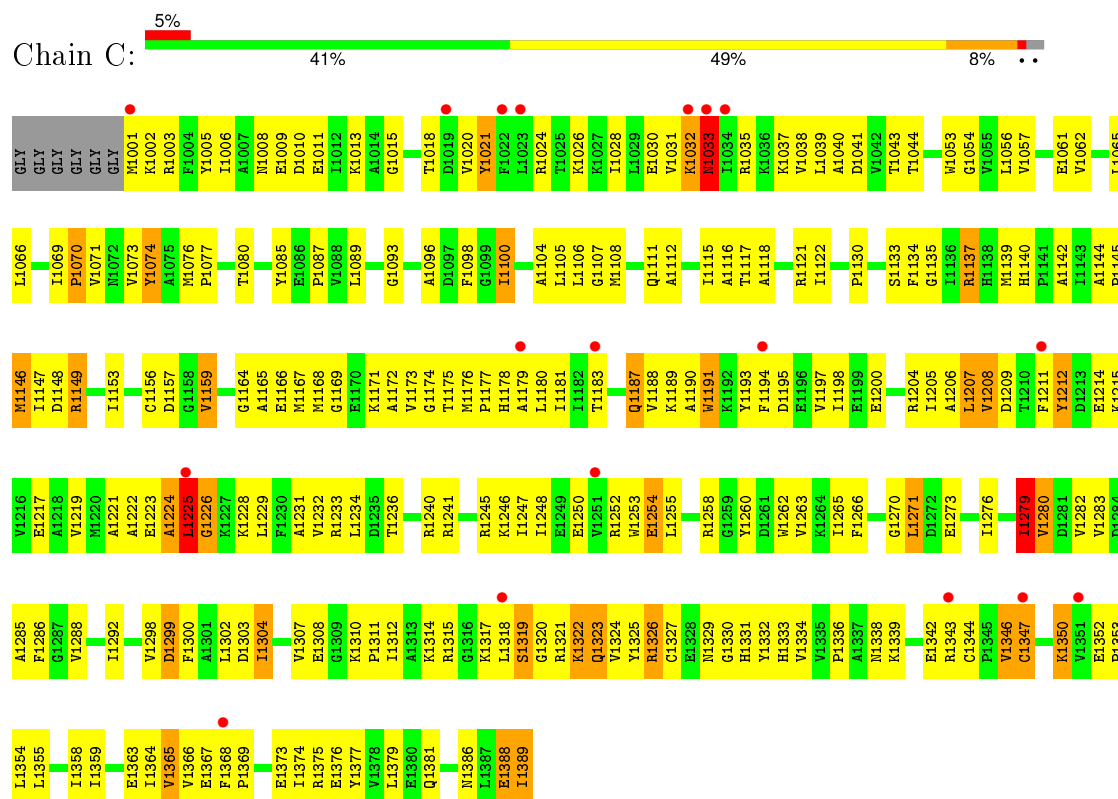
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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: Nicotinate-nucleotide pyrophosphorylase

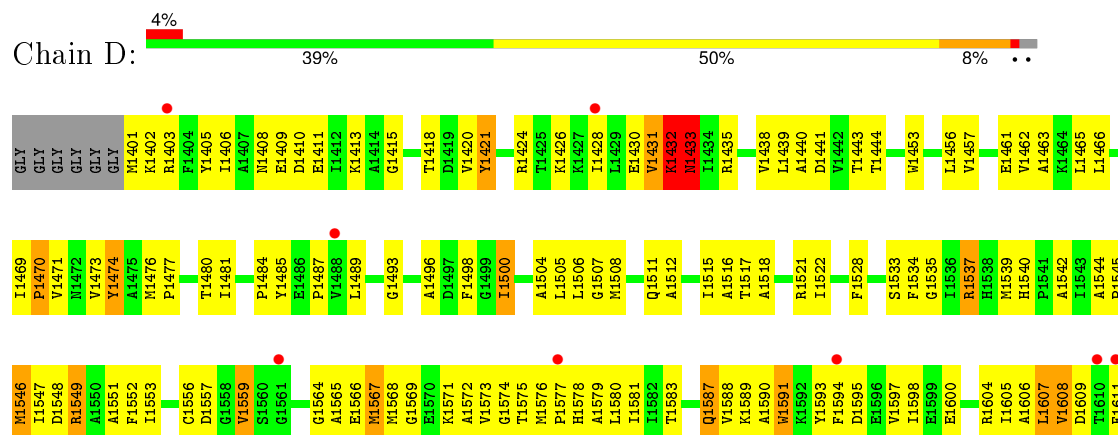


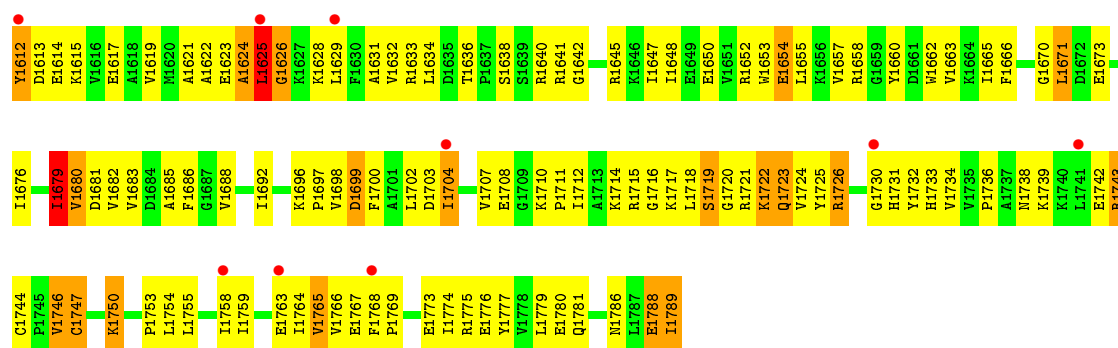


• Molecule 1: Nicotinate-nucleotide pyrophosphorylase

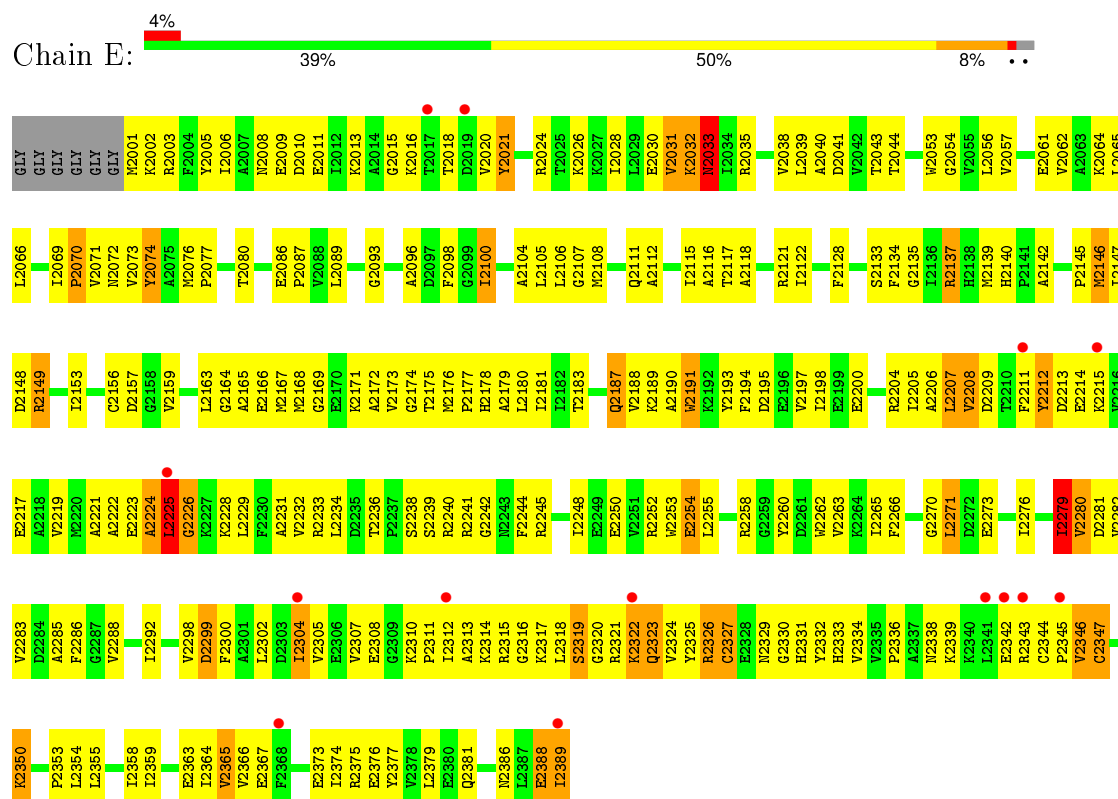


• Molecule 1: Nicotinate-nucleotide pyrophosphorylase

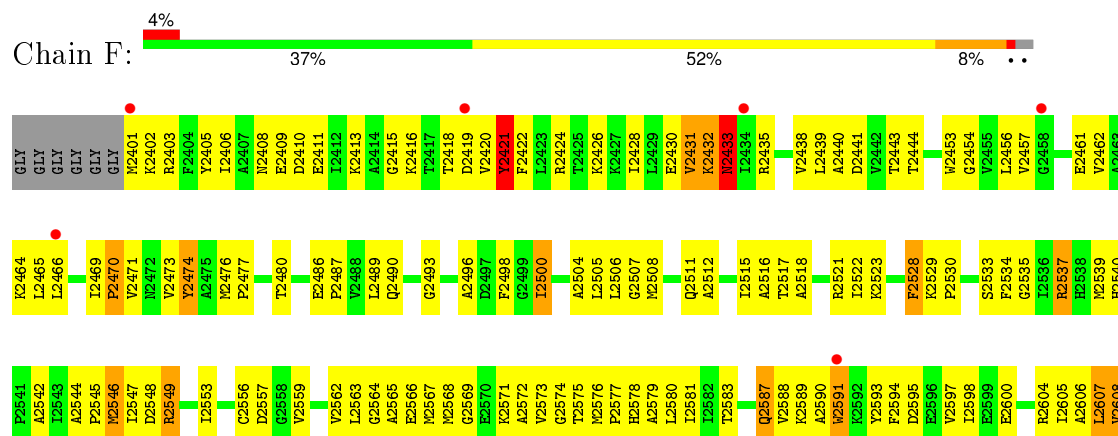




• Molecule 1: Nicotinate-nucleotide pyrophosphorylase



• Molecule 1: Nicotinate-nucleotide pyrophosphorylase





4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	111.48Å 111.48Å 178.26Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.99 – 2.90 48.27 – 2.90	Depositor EDS
% Data completeness (in resolution range)	85.3 (19.99-2.90) 94.9 (48.27-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.91Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.247 , 0.282 0.250 , 0.284	Depositor DCC
R_{free} test set	5299 reflections (10.18%)	DCC
Wilson B-factor (Å ²)	68.0	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.0	EDS
Estimated twinning fraction	0.000 for -h,-k,l 0.478 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 54946 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	18539	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.79 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.2409e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PCP

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	0.44	0/3117	0.66	2/4211 (0.0%)
1	B	0.46	0/3117	0.67	2/4211 (0.0%)
1	C	0.44	0/3117	0.66	2/4211 (0.0%)
1	D	0.45	0/3117	0.67	2/4211 (0.0%)
1	E	0.46	0/3117	0.67	2/4211 (0.0%)
1	F	0.47	0/3117	0.67	2/4211 (0.0%)
All	All	0.45	0/18702	0.67	12/25266 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1135	GLY	N-CA-C	5.59	127.08	113.10
1	B	535	GLY	N-CA-C	5.49	126.83	113.10
1	E	2135	GLY	N-CA-C	5.45	126.72	113.10
1	D	1535	GLY	N-CA-C	5.43	126.67	113.10
1	F	2535	GLY	N-CA-C	5.42	126.66	113.10

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	3055	0	3140	283	0
1	B	3055	0	3138	287	0
1	C	3055	0	3137	283	1
1	D	3055	0	3138	292	1
1	E	3055	0	3138	295	1
1	F	3055	0	3138	301	1
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
3	A	22	0	10	2	0
3	B	22	0	10	1	0
3	C	22	0	10	1	0
3	D	22	0	10	2	0
3	E	22	0	10	1	0
3	F	22	0	10	1	0
4	A	8	0	0	0	0
4	B	10	0	0	0	0
4	C	9	0	0	2	0
4	D	10	0	0	0	0
4	E	16	0	0	1	0
4	F	12	0	0	0	0
All	All	18539	0	18889	1578	2

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 42.

The worst 5 of 1578 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:322:LYS:HG3	1:A:336:PRO:HA	1.23	1.19
1:E:2322:LYS:HG3	1:E:2336:PRO:HA	1.23	1.15
1:B:722:LYS:HG3	1:B:736:PRO:HA	1.21	1.14
1:F:2722:LYS:HG3	1:F:2736:PRO:HA	1.23	1.11
1:A:157:ASP:HA	1:A:375:ARG:HH12	1.16	1.09

All (2) 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-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2376:GLU:OE1	1:F:2776:GLU:OE1[3_884]	1.90	0.30
1:C:1373:GLU:OE2	1:D:1780:GLU:OE1[2_865]	2.17	0.03

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	387/395 (98%)	329 (85%)	44 (11%)	14 (4%)	4	18
1	B	387/395 (98%)	328 (85%)	40 (10%)	19 (5%)	3	10
1	C	387/395 (98%)	329 (85%)	45 (12%)	13 (3%)	5	19
1	D	387/395 (98%)	329 (85%)	41 (11%)	17 (4%)	3	12
1	E	387/395 (98%)	330 (85%)	40 (10%)	17 (4%)	3	12
1	F	387/395 (98%)	326 (84%)	42 (11%)	19 (5%)	3	10
All	All	2322/2370 (98%)	1971 (85%)	252 (11%)	99 (4%)	3	13

5 of 99 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	346	VAL
1	B	746	VAL
1	C	1346	VAL
1	D	1746	VAL
1	E	2346	VAL

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	321/321 (100%)	285 (89%)	36 (11%)	7	22
1	B	321/321 (100%)	283 (88%)	38 (12%)	6	19
1	C	321/321 (100%)	284 (88%)	37 (12%)	7	21
1	D	321/321 (100%)	283 (88%)	38 (12%)	6	19
1	E	321/321 (100%)	283 (88%)	38 (12%)	6	19
1	F	321/321 (100%)	284 (88%)	37 (12%)	7	21
All	All	1926/1926 (100%)	1702 (88%)	224 (12%)	7	20

5 of 224 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1319	SER
1	D	1559	VAL
1	F	2654	GLU
1	C	1326	ARG
1	D	1413	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1187	GLN
1	D	1483	HIS
1	F	2540	HIS
1	C	1333	HIS
1	D	1408	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

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 for Mogul analysis.

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	PCP	A	392	-	20,22,22	1.27	3 (15%)	31,35,35	1.44	1 (3%)
3	PCP	B	792	-	20,22,22	1.26	3 (15%)	31,35,35	1.45	2 (6%)
3	PCP	C	1392	-	20,22,22	1.26	3 (15%)	31,35,35	1.42	1 (3%)
3	PCP	D	1792	-	20,22,22	1.29	3 (15%)	31,35,35	1.47	2 (6%)
3	PCP	E	2392	-	20,22,22	1.25	3 (15%)	31,35,35	1.46	2 (6%)
3	PCP	F	2792	-	20,22,22	1.24	3 (15%)	31,35,35	1.49	2 (6%)

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	PCP	A	392	-	-	0/17/33/33	0/1/1/1
3	PCP	B	792	-	-	0/17/33/33	0/1/1/1
3	PCP	C	1392	-	-	0/17/33/33	0/1/1/1
3	PCP	D	1792	-	-	0/17/33/33	0/1/1/1
3	PCP	E	2392	-	-	0/17/33/33	0/1/1/1
3	PCP	F	2792	-	-	0/17/33/33	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	2392	PCP	PB-O2B	-2.65	1.45	1.54
3	D	1792	PCP	PB-O2B	-2.64	1.45	1.54
3	A	392	PCP	PB-O2B	-2.60	1.45	1.54
3	B	792	PCP	PB-O2B	-2.50	1.45	1.54
3	F	2792	PCP	PB-O2B	-2.49	1.45	1.54

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	E	2392	PCP	O2A-PA-O3A	2.01	114.21	105.09
3	F	2792	PCP	O2A-PA-O3A	2.03	114.31	105.09
3	D	1792	PCP	O2A-PA-O3A	2.07	114.50	105.09
3	B	792	PCP	O2A-PA-O3A	2.07	114.50	105.09
3	C	1392	PCP	C4-C5-C1	5.91	112.97	103.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	392	PCP	2	0
3	B	792	PCP	1	0
3	C	1392	PCP	1	0
3	D	1792	PCP	2	0
3	E	2392	PCP	1	0
3	F	2792	PCP	1	0

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, 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	389/395 (98%)	0.45	13 (3%)	50	42	32, 65, 86, 105	0
1	B	389/395 (98%)	0.53	22 (5%)	27	21	34, 66, 86, 106	0
1	C	389/395 (98%)	0.49	18 (4%)	36	30	31, 65, 85, 105	0
1	D	389/395 (98%)	0.48	17 (4%)	38	32	35, 66, 86, 106	0
1	E	389/395 (98%)	0.47	14 (3%)	46	38	32, 65, 86, 106	0
1	F	389/395 (98%)	0.50	17 (4%)	38	32	32, 65, 86, 106	0
All	All	2334/2370 (98%)	0.49	101 (4%)	39	32	31, 65, 87, 106	0

The worst 5 of 101 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	2741	LEU	6.0
1	E	2341	LEU	5.4
1	C	1211	PHE	4.8
1	D	1741	LEU	4.6
1	B	625	LEU	4.6

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](#)

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, 95th 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(Å ²)	Q<0.9
3	PCP	F	2792	22/22	0.80	0.30	1.78	103,109,112,112	0
3	PCP	C	1392	22/22	0.74	0.29	1.04	104,110,112,113	0
3	PCP	B	792	22/22	0.82	0.28	0.73	103,109,112,112	0
3	PCP	E	2392	22/22	0.75	0.27	0.57	103,109,112,112	0
3	PCP	A	392	22/22	0.73	0.26	0.55	103,109,112,112	0
3	PCP	D	1792	22/22	0.80	0.26	0.42	102,109,112,113	0
2	ZN	D	1793	1/1	0.92	0.12	-1.05	84,84,84,84	0
2	ZN	A	393	1/1	0.94	0.09	-1.53	76,76,76,76	0
2	ZN	B	793	1/1	0.86	0.09	-1.77	85,85,85,85	0
2	ZN	C	1391	1/1	0.96	0.11	-2.15	62,62,62,62	0
2	ZN	F	2791	1/1	0.97	0.08	-2.20	83,83,83,83	0
2	ZN	C	1393	1/1	0.95	0.09	-2.37	85,85,85,85	0
2	ZN	A	391	1/1	0.98	0.11	-2.64	57,57,57,57	0
2	ZN	F	2793	1/1	0.99	0.09	-2.71	77,77,77,77	0
2	ZN	E	2393	1/1	0.96	0.09	-2.90	77,77,77,77	0
2	ZN	E	2391	1/1	0.96	0.05	-3.21	82,82,82,82	0
2	ZN	D	1791	1/1	0.98	0.08	-3.43	77,77,77,77	0
2	ZN	B	791	1/1	0.96	0.08	-3.68	78,78,78,78	0

6.5 Other polymers [i](#)

There are no such residues in this entry.