



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2017 – 06:41 PM EDT

PDB ID : 4YB5
Title : Adenosine triphosphate phosphoribosyltransferase from *Campylobacter jejuni*
in complex with the allosteric inhibitor histidine
Authors : Mittelstaedt, G.; Moggre, G.-J.; Parker, E.J.
Deposited on : unknown
Resolution : 2.24 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 : **FAILED**
Mogul : 1.7.2 (RC1), CSD as538be (2017)
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

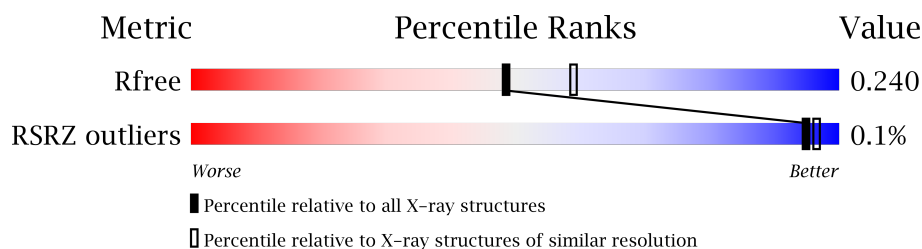
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.24 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	1804 (2.26-2.22)
RSRZ outliers	101464	1809 (2.26-2.22)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SCN	A	302	-	-	-	X
2	SCN	E	302	-	-	-	X
2	SCN	F	302	-	-	-	X
5	PGE	C	302	-	-	-	X
6	PEG	D	301	-	-	-	X
6	PEG	F	303	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13442 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 ATP phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	0	0
			2187	1388	376	410	13			
1	B	295	Total	C	N	O	S	0	0	0
			2228	1416	387	412	13			
1	C	295	Total	C	N	O	S	0	0	0
			2207	1402	381	411	13			
1	D	292	Total	C	N	O	S	0	0	0
			2215	1406	381	415	13			
1	E	290	Total	C	N	O	S	0	0	0
			2171	1380	370	408	13			
1	F	290	Total	C	N	O	S	0	0	0
			2187	1389	375	410	13			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q5HSJ4
B	0	GLY	-	expression tag	UNP Q5HSJ4
C	0	GLY	-	expression tag	UNP Q5HSJ4
D	0	GLY	-	expression tag	UNP Q5HSJ4
E	0	GLY	-	expression tag	UNP Q5HSJ4
F	0	GLY	-	expression tag	UNP Q5HSJ4

- Molecule 2 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).

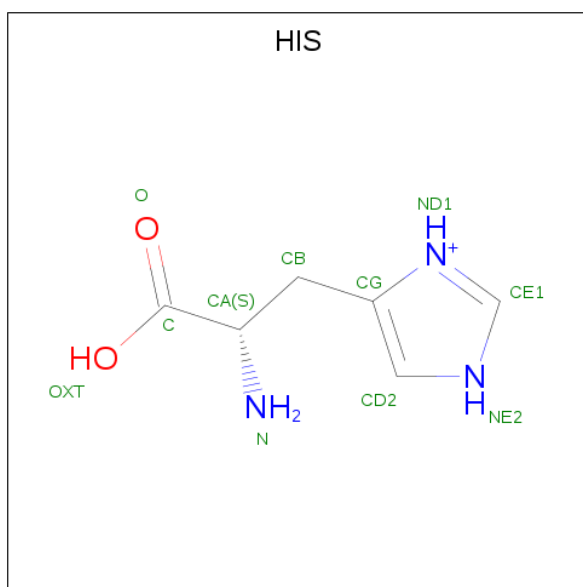


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	S	0	0
			3	1	1	1		
2	A	1	Total	C	N	S	0	0
			3	1	1	1		
2	B	1	Total	C	N	S	0	0
			3	1	1	1		
2	C	1	Total	C	N	S	0	0
			3	1	1	1		
2	E	1	Total	C	N	S	0	0
			3	1	1	1		
2	E	1	Total	C	N	S	0	0
			3	1	1	1		
2	F	1	Total	C	N	S	0	0
			3	1	1	1		
2	F	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	K	0	0
			1	1		
3	A	2	Total	K	0	0
			2	2		
3	C	2	Total	K	0	0
			2	2		

- Molecule 4 is HISTIDINE (three-letter code: HIS) (formula: C₆H₁₀N₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			11	6	3	2		
4	B	1	Total	C	N	O	0	0
			11	6	3	2		
4	C	1	Total	C	N	O	0	0
			11	6	3	2		
4	D	1	Total	C	N	O	0	0
			11	6	3	2		
4	E	1	Total	C	N	O	0	0
			11	6	3	2		
4	F	1	Total	C	N	O	0	0
			11	6	3	2		

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			7	4	3		
6	F	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	19	Total 19	O 19	0	0
7	B	21	Total 21	O 21	0	0
7	C	18	Total 18	O 18	0	0
7	D	27	Total 27	O 27	0	0
7	E	22	Total 22	O 22	0	0
7	F	21	Total 21	O 21	0	0

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3 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.14Å 123.22Å 95.70Å 90.00° 110.66° 90.00°	Depositor
Resolution (Å)	48.04 – 2.24 48.04 – 2.24	Depositor EDS
% Data completeness (in resolution range)	98.9 (48.04-2.24) 98.9 (48.04-2.24)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.209 , 0.239 0.209 , 0.240	Depositor DCC
R_{free} test set	4728 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	43.8	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 26.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13442	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

4.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

4.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 5 are monoatomic - leaving 17 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	$\# Z > 2$
2	SCN	A	301	-	1,2,2	0.20	0	0,1,1	0.00	-
2	SCN	A	302	-	1,2,2	0.17	0	0,1,1	0.00	-
4	HIS	A	304	-	3,11,11	0.52	0	3,14,14	1.35	1 (33%)
2	SCN	B	301	-	1,2,2	0.11	0	0,1,1	0.00	-
4	HIS	B	303	-	3,11,11	0.60	0	3,14,14	1.30	0
2	SCN	C	301	-	1,2,2	0.20	0	0,1,1	0.00	-
5	PGE	C	302	-	9,9,9	0.96	0	8,8,8	1.10	1 (12%)
4	HIS	C	304	-	3,11,11	0.59	0	3,14,14	1.26	0
6	PEG	D	301	-	6,6,6	0.78	0	5,5,5	1.09	0
4	HIS	D	302	-	3,11,11	0.42	0	3,14,14	1.37	1 (33%)
2	SCN	E	301	-	1,2,2	0.13	0	0,1,1	0.00	-
2	SCN	E	302	-	1,2,2	0.15	0	0,1,1	0.00	-
4	HIS	E	303	-	3,11,11	0.45	0	3,14,14	1.31	0
2	SCN	F	301	-	1,2,2	0.14	0	0,1,1	0.00	-
2	SCN	F	302	-	1,2,2	0.22	0	0,1,1	0.00	-
6	PEG	F	303	-	6,6,6	0.67	0	5,5,5	0.89	0
4	HIS	F	304	-	3,11,11	0.47	0	3,14,14	1.30	1 (33%)

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
2	SCN	A	301	-	-	0/0/0/0	0/0/0/0
2	SCN	A	302	-	-	0/0/0/0	0/0/0/0
4	HIS	A	304	-	-	0/4/8/8	0/1/1/1
2	SCN	B	301	-	-	0/0/0/0	0/0/0/0
4	HIS	B	303	-	-	0/4/8/8	0/1/1/1
2	SCN	C	301	-	-	0/0/0/0	0/0/0/0
5	PGE	C	302	-	-	0/7/7/7	0/0/0/0
4	HIS	C	304	-	-	0/4/8/8	0/1/1/1
6	PEG	D	301	-	-	0/4/4/4	0/0/0/0
4	HIS	D	302	-	-	0/4/8/8	0/1/1/1
2	SCN	E	301	-	-	0/0/0/0	0/0/0/0
2	SCN	E	302	-	-	0/0/0/0	0/0/0/0
4	HIS	E	303	-	-	0/4/8/8	0/1/1/1
2	SCN	F	301	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SCN	F	302	-	-	0/0/0/0	0/0/0/0
6	PEG	F	303	-	-	0/4/4/4	0/0/0/0
4	HIS	F	304	-	-	0/4/8/8	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	C	302	PGE	O2-C3-C4	2.03	119.70	110.41
4	F	304	HIS	CD2-NE2-CE1	2.05	108.98	105.78
4	D	302	HIS	CD2-NE2-CE1	2.09	109.04	105.78
4	A	304	HIS	CD2-NE2-CE1	2.14	109.11	105.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

5.1 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	291/300 (97%)	-0.34	0	100 100	29, 46, 70, 104	0
1	B	295/300 (98%)	-0.33	0	100 100	31, 49, 74, 97	0
1	C	295/300 (98%)	-0.31	0	100 100	31, 48, 69, 105	0
1	D	292/300 (97%)	-0.29	0	100 100	29, 48, 76, 106	0
1	E	290/300 (96%)	-0.25	1 (0%)	93 94	31, 49, 72, 105	0
1	F	290/300 (96%)	-0.28	0	100 100	31, 48, 71, 100	0
All	All	1753/1800 (97%)	-0.30	1 (0%)	95 96	29, 48, 73, 106	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	35	HIS	3.3

5.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.4 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
6	PEG	D	301	7/7	0.81	0.30	6.97	46,59,63,66	0
2	SCN	A	302	3/3	0.86	0.29	6.79	56,56,69,73	0
5	PGE	C	302	10/10	0.76	0.31	5.97	54,65,75,79	0
2	SCN	F	302	3/3	0.94	0.16	3.30	57,57,59,63	0
6	PEG	F	303	7/7	0.87	0.19	3.26	45,52,62,65	0
2	SCN	E	302	3/3	0.97	0.18	3.17	60,60,66,68	0
4	HIS	B	303	11/11	0.97	0.15	1.24	35,37,39,40	0
2	SCN	B	301	3/3	0.98	0.15	0.87	51,51,52,53	0
2	SCN	A	301	3/3	0.97	0.14	0.70	51,51,57,64	0
4	HIS	A	304	11/11	0.96	0.13	0.41	31,33,36,38	0
2	SCN	C	301	3/3	0.96	0.14	0.37	52,52,60,61	0
4	HIS	D	302	11/11	0.98	0.11	0.06	28,31,34,35	0
2	SCN	E	301	3/3	0.97	0.15	-0.05	59,59,61,62	0
4	HIS	F	304	11/11	0.96	0.12	-0.34	31,33,35,39	0
4	HIS	E	303	11/11	0.97	0.12	-0.39	29,31,33,33	0
3	K	B	302	1/1	0.94	0.11	-0.43	80,80,80,80	0
2	SCN	F	301	3/3	0.96	0.12	-0.48	67,67,67,71	0
3	K	C	305	1/1	0.97	0.10	-0.64	75,75,75,75	0
4	HIS	C	304	11/11	0.97	0.09	-1.12	34,35,40,41	0
3	K	A	303	1/1	0.93	0.09	-1.61	77,77,77,77	0
3	K	A	305	1/1	0.97	0.07	-1.80	70,70,70,70	0
3	K	C	303	1/1	0.99	0.02	-2.94	63,63,63,63	0

5.5 Other polymers ⓘ

There are no such residues in this entry.