

wwPDB X-ray Structure Validation Summary Report (i)

Dec 12, 2023 – 06:43 pm GMT

PDB ID	:	3ZTQ
Title	:	Hexagonal crystal form P61 of the Aquifex aeolicus nucleoside diphosphate
		kinase
Authors	:	Boissier, F.; Georgescauld, F.; Moynie, L.; Dupuy, JW.; Sarger, C.; Podar,
		M.; Lascu, I.; Giraud, MF.; Dautant, A.
Deposited on	:	2011-07-12
Resolution	:	2.10 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

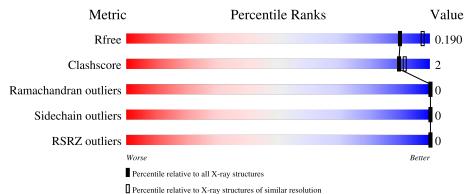
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.10 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	5197(2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 of 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% 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	А	142	95%	
1	В	142	96% •••	- 1
1	С	142	95% ••	
1	D	142	94% 5% •	
1	Е	142	96%	••

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Mol	Chain	Length	Quality of chain
1	F	142	94% 5% •
1	G	142	95% .
1	Н	142	94%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10299 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	٨	1 / 1	Total	С	Ν	0	S	0	3	0
1	А	141	1129	723	191	210	5	0	0	0
1	В	141	Total	С	Ν	0	S	0	2	0
	D	141	1125	720	190	210	5	0	2	0
1	С	141	Total	С	Ν	0	S	0	3	0
	C	141	1133	725	191	211	6	0	9	U
1	D	141	Total	С	Ν	0	S	0	3	0
	D	141	1135	726	191	212	6	0	5	0
1	Е	141	Total	С	Ν	0	S	0	3	0
	Ľ	141	1132	724	191	212	5	0	3	0
1	F	141	Total	С	Ν	0	S	0	1	0
	Г	141	1118	716	189	208	5	0	1	0
1	G	141	Total	С	Ν	0	S	0	3	0
	G	141	1132	725	191	210	6	0	0	U
1	Н	141	Total	С	Ν	0	S	0	2	0
	11	141	1126	721	190	209	6			U

• Molecule 1 is a protein called NUCLEOSIDE DIPHOSPHATE KINASE.

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	173	Total O 173 173	0	0
2	В	169	Total O 169 169	0	0
2	С	173	Total O 173 173	0	0
2	D	133	Total O 133 133	0	0
2	Е	173	Total O 173 173	0	0
2	F	155	Total O 155 155	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	154	Total O 154 154	0	0
2	Н	139	Total O 139 139	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: NUCLEOSIDE DIPHOSPHATE KINASE

Chain A:	95%	
MET A2 D25 R26 R26 R26 R285 R85	1100 1133 1142	
• Molecule 1	: NUCLEOSIDE DIPHOSPHATE KINASE	
Chain B:	96%	• •
MET A2 R26 R57 R57 I106		
• Molecule 1	: NUCLEOSIDE DIPHOSPHATE KINASE	
Chain C:	95%	
MET A2 R26 Y52 V53 H54 R55	<mark>4133 - 10 - 10 - 10 - 10 - 10 - 10 - 10 -</mark>	
• Molecule 1	: NUCLEOSIDE DIPHOSPHATE KINASE	
Chain D:	94%	5% •
MET A2 R26 Y52 R55 R55	E65 1106 1106 1133 1142	
• Molecule 1	: NUCLEOSIDE DIPHOSPHATE KINASE	
Chain E:	96%	• ••
MET A2 R26 V53 R85	1106 1413 1413	
• Molecule 1	: NUCLEOSIDE DIPHOSPHATE KINASE	
Chain F:	94%	5%•

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• Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

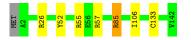
Chain G: 95% · ·



• Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain H:

94%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants	116.36Å 116.36 Å 247.32 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.09 - 2.10	Depositor
Resolution (A)	38.09 - 2.00	EDS
% Data completeness	97.2 (38.09-2.10)	Depositor
(in resolution range)	91.7 (38.09-2.00)	EDS
R _{merge}	0.09	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.88 (at 2.00 \text{\AA})$	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
D D.	0.170 , 0.199	Depositor
R, R_{free}	0.189 , 0.190	DCC
R_{free} test set	5854 reflections (5.01%)	wwPDB-VP
Wilson B-factor $(Å^2)$	16.2	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33 , 37.5	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.467 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10299	wwPDB-VP
Average B, all atoms $(Å^2)$	24.0	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 48.38 % 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 8.6761e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

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.



¹Intensities estimated from amplitudes.

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	Bond	lengths	Bond angles		
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.47	0/1160	0.57	2/1558~(0.1%)	
1	В	0.47	0/1150	0.56	0/1545	
1	С	0.51	0/1158	0.57	0/1555	
1	D	0.48	0/1160	0.55	0/1557	
1	Ε	0.46	0/1160	0.57	2/1558~(0.1%)	
1	F	0.46	0/1143	0.54	0/1535	
1	G	0.48	0/1160	0.55	0/1557	
1	Н	0.47	0/1151	0.67	4/1545~(0.3%)	
All	All	0.48	0/9242	0.57	8/12410~(0.1%)	

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	Н	57	ARG	NE-CZ-NH2	-7.90	116.35	120.30
1	Н	57	ARG	NE-CZ-NH1	7.17	123.88	120.30
1	Н	85	ARG	NE-CZ-NH2	-7.10	116.75	120.30
1	Е	85	ARG	NE-CZ-NH2	-6.98	116.81	120.30
1	Н	85	ARG	NE-CZ-NH1	6.85	123.72	120.30

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	1129	0	1134	4	0
1	В	1125	0	1126	4	0
1	С	1133	0	1134	4	0
1	D	1135	0	1133	6	0
1	Е	1132	0	1131	5	0
1	F	1118	0	1120	6	0
1	G	1132	0	1136	5	0
1	Н	1126	0	1128	6	0
2	А	173	0	0	1	0
2	В	169	0	0	1	0
2	С	173	0	0	1	0
2	D	133	0	0	2	0
2	Е	173	0	0	2	0
2	F	155	0	0	1	0
2	G	154	0	0	1	0
2	Н	139	0	0	2	0
All	All	10299	0	9042	33	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 2.

The worst 5 of 33 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:H:85:ARG:HD2	2:H:2095:HOH:O	1.87	0.74
1:F:26:ARG:HG2	1:F:106:ILE:HD11	1.70	0.73
1:B:26:ARG:HG2	1:B:106:ILE:HD11	1.71	0.70
1:A:85:ARG:HD2	2:A:2125:HOH:O	1.92	0.69
1:E:85:ARG:HD2	2:E:2128:HOH:O	1.94	0.68

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	Perce	Percentiles	
1	А	142/142~(100%)	138~(97%)	4(3%)	0	100	100	
1	В	141/142~(99%)	137~(97%)	4(3%)	0	100	100	
1	С	142/142~(100%)	140 (99%)	2(1%)	0	100	100	
1	D	142/142~(100%)	139~(98%)	3~(2%)	0	100	100	
1	Е	142/142~(100%)	138~(97%)	4 (3%)	0	100	100	
1	F	140/142~(99%)	136~(97%)	4 (3%)	0	100	100	
1	G	142/142~(100%)	139~(98%)	3~(2%)	0	100	100	
1	Н	141/142~(99%)	138 (98%)	3(2%)	0	100	100	
All	All	1132/1136~(100%)	1105 (98%)	27~(2%)	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	А	120/118~(102%)	120 (100%)	0	100 100
1	В	119/118 (101%)	119 (100%)	0	100 100
1	С	120/118~(102%)	120 (100%)	0	100 100
1	D	120/118~(102%)	120 (100%)	0	100 100
1	Ε	120/118~(102%)	120 (100%)	0	100 100
1	F	118/118~(100%)	118 (100%)	0	100 100
1	G	120/118~(102%)	120 (100%)	0	100 100
1	Н	119/118 (101%)	119 (100%)	0	100 100
All	All	956/944~(101%)	956 (100%)	0	100 100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains identified.



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 monosaccharides 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)

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, 95^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2		Z>2	$OWAB(Å^2)$	Q < 0.9
1	А	141/142~(99%)	-1.02	0	100	100	11, 18, 42, 71	0
1	В	141/142~(99%)	-0.96	0	100	100	11, 17, 42, 72	0
1	С	141/142~(99%)	-0.96	0	100	100	11, 18, 41, 74	0
1	D	141/142~(99%)	-0.97	0	100	100	11, 19, 42, 74	0
1	Ε	141/142~(99%)	-0.97	0	100	100	12, 19, 42, 72	0
1	F	141/142~(99%)	-0.94	0	100	100	12, 17, 43, 71	0
1	G	141/142~(99%)	-0.93	0	100	100	12, 19, 41, 74	0
1	Н	141/142~(99%)	-0.94	0	100	100	12, 20, 42, 74	0
All	All	1128/1136~(99%)	-0.96	0	100	100	11, 18, 44, 74	0

There are no RSRZ outliers to report.

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 monosaccharides 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.

