



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:02 PM UTC

PDB ID : 2ZHO / pdb_00002zho
Title : Crystal structure of the regulatory subunit of aspartate kinase from *Thermus thermophilus* (ligand free form)
Authors : Yoshida, A.; Tomita, T.; Kuzuyama, T.; Nishiyama, M.
Deposited on : 2008-02-06
Resolution : 2.98 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

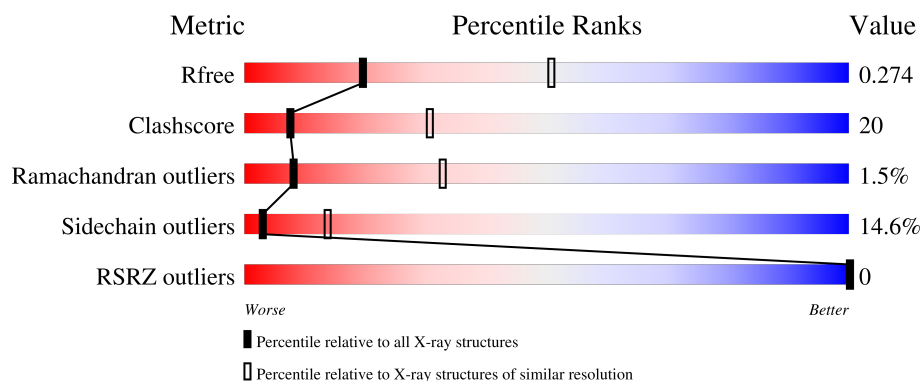
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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}	180053	3580 (3.00-2.96)
Clashscore	190562	3904 (3.00-2.96)
Ramachandran outliers	187476	3761 (3.00-2.96)
Sidechain outliers	187428	3764 (3.00-2.96)
RSRZ outliers	180081	3579 (3.00-2.96)

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 $\leq 5\%$. 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	167	
1	B	167	
1	C	167	
1	D	167	
1	E	167	

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Mol	Chain	Length	Quality of chain
1	F	167	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: green (60%), yellow (22%), orange (7%), and grey (11%).

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6532 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 Aspartokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	151	Total	C	N	O	S	0	0	0
			1087	694	181	208	4			
1	B	147	Total	C	N	O	S	0	0	0
			1065	680	177	204	4			
1	C	151	Total	C	N	O	S	0	0	0
			1088	693	183	208	4			
1	D	149	Total	C	N	O	S	0	0	0
			1061	680	173	204	4			
1	E	150	Total	C	N	O	S	0	0	0
			1088	694	184	206	4			
1	F	148	Total	C	N	O	S	0	0	0
			1064	681	175	204	4			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	162	HIS	-	expression tag	UNP P61489
A	163	HIS	-	expression tag	UNP P61489
A	164	HIS	-	expression tag	UNP P61489
A	165	HIS	-	expression tag	UNP P61489
A	166	HIS	-	expression tag	UNP P61489
A	167	HIS	-	expression tag	UNP P61489
B	162	HIS	-	expression tag	UNP P61489
B	163	HIS	-	expression tag	UNP P61489
B	164	HIS	-	expression tag	UNP P61489
B	165	HIS	-	expression tag	UNP P61489
B	166	HIS	-	expression tag	UNP P61489
B	167	HIS	-	expression tag	UNP P61489
C	162	HIS	-	expression tag	UNP P61489
C	163	HIS	-	expression tag	UNP P61489
C	164	HIS	-	expression tag	UNP P61489
C	165	HIS	-	expression tag	UNP P61489
C	166	HIS	-	expression tag	UNP P61489

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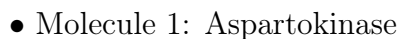
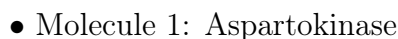
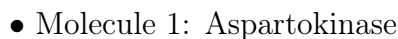
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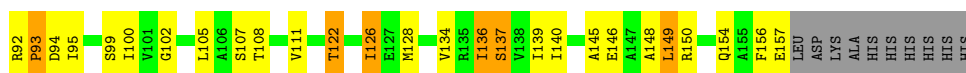
Chain	Residue	Modelled	Actual	Comment	Reference
C	167	HIS	-	expression tag	UNP P61489
D	162	HIS	-	expression tag	UNP P61489
D	163	HIS	-	expression tag	UNP P61489
D	164	HIS	-	expression tag	UNP P61489
D	165	HIS	-	expression tag	UNP P61489
D	166	HIS	-	expression tag	UNP P61489
D	167	HIS	-	expression tag	UNP P61489
E	162	HIS	-	expression tag	UNP P61489
E	163	HIS	-	expression tag	UNP P61489
E	164	HIS	-	expression tag	UNP P61489
E	165	HIS	-	expression tag	UNP P61489
E	166	HIS	-	expression tag	UNP P61489
E	167	HIS	-	expression tag	UNP P61489
F	162	HIS	-	expression tag	UNP P61489
F	163	HIS	-	expression tag	UNP P61489
F	164	HIS	-	expression tag	UNP P61489
F	165	HIS	-	expression tag	UNP P61489
F	166	HIS	-	expression tag	UNP P61489
F	167	HIS	-	expression tag	UNP P61489

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	11	Total O 11 11	0	0
2	B	13	Total O 13 13	0	0
2	C	17	Total O 17 17	0	0
2	D	7	Total O 7 7	0	0
2	E	20	Total O 20 20	0	0
2	F	11	Total O 11 11	0	0

- Molecule 1: Aspartokinase

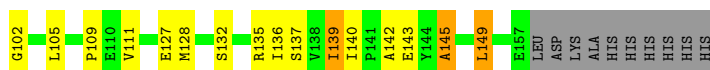
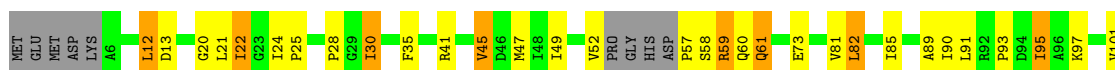




● Molecule 1: Aspartokinase



● Molecule 1: Aspartokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	107.18Å 107.18Å 87.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.41 – 2.98 46.41 – 2.98	Depositor EDS
% Data completeness (in resolution range)	99.6 (46.41-2.98) 99.7 (46.41-2.98)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 3.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.244 , 0.266 0.228 , 0.274	Depositor DCC
R_{free} test set	1168 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	66.2	Xtriage
Anisotropy	0.422	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.003 for -h,-k,l 0.215 for h,-h-k,-l 0.018 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6532	wwPDB-VP
Average B, all atoms (Å ²)	56.0	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 24.40 % 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 3.8631e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.64	0/1101	0.95	2/1499 (0.1%)
1	B	0.70	1/1078 (0.1%)	1.01	6/1466 (0.4%)
1	C	0.66	0/1101	1.00	3/1494 (0.2%)
1	D	0.65	0/1076	0.97	0/1467
1	E	0.67	0/1102	0.98	2/1497 (0.1%)
1	F	0.65	0/1077	0.94	1/1465 (0.1%)
All	All	0.66	1/6535 (0.0%)	0.98	14/8888 (0.2%)

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	1
1	C	0	1
1	D	0	3
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	157	GLU	C-N	7.82	1.44	1.33

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	53	PRO	N-CA-CB	11.47	110.45	102.65
1	B	157	GLU	O-C-N	-9.36	110.15	122.59
1	C	58	SER	O-C-N	-7.52	112.59	122.59
1	F	57	PRO	N-CA-CB	7.22	110.94	103.00
1	C	57	PRO	N-CA-CB	6.84	110.52	103.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	157	GLU	Mainchain
1	C	58	SER	Mainchain
1	D	14	LEU	Peptide
1	D	80	PRO	Peptide
1	D	91	LEU	Peptide

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	1087	0	1097	59	0
1	B	1065	0	1084	31	0
1	C	1088	0	1100	47	0
1	D	1061	0	1066	50	0
1	E	1088	0	1117	51	0
1	F	1064	0	1080	39	0
2	A	11	0	0	1	0
2	B	13	0	0	0	0
2	C	17	0	0	0	0
2	D	7	0	0	0	0
2	E	20	0	0	2	0
2	F	11	0	0	0	0
All	All	6532	0	6544	262	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 20.

The worst 5 of 262 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:E:48:ILE:HD13	1:E:64:PHE:HB3	1.28	1.12
1:A:91:LEU:HB3	1:F:90:ILE:HD12	1.30	1.11
1:E:24:ILE:HD11	1:E:61:GLN:HA	1.15	1.11
1:D:80:PRO:HB2	1:D:81:VAL:HA	1.15	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:16:HIS:HB3	1:D:68:LYS:HG2	1.25	1.08

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	147/167 (88%)	133 (90%)	12 (8%)	2 (1%)	9	34
1	B	143/167 (86%)	131 (92%)	10 (7%)	2 (1%)	9	34
1	C	147/167 (88%)	135 (92%)	11 (8%)	1 (1%)	18	50
1	D	145/167 (87%)	125 (86%)	16 (11%)	4 (3%)	4	19
1	E	146/167 (87%)	136 (93%)	9 (6%)	1 (1%)	18	50
1	F	144/167 (86%)	134 (93%)	7 (5%)	3 (2%)	5	25
All	All	872/1002 (87%)	794 (91%)	65 (8%)	13 (2%)	8	33

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	80	PRO
1	D	93	PRO
1	F	59	ARG
1	B	51	GLY
1	C	121	SER

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	107/127 (84%)	91 (85%)	16 (15%)	3	13
1	B	106/127 (84%)	89 (84%)	17 (16%)	2	11
1	C	106/127 (84%)	87 (82%)	19 (18%)	2	9
1	D	104/127 (82%)	85 (82%)	19 (18%)	2	8
1	E	109/127 (86%)	97 (89%)	12 (11%)	6	24
1	F	105/127 (83%)	95 (90%)	10 (10%)	8	29
All	All	637/762 (84%)	544 (85%)	93 (15%)	3	14

5 of 93 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	60	GLN
1	E	12	LEU
1	D	76	GLU
1	D	122	THR
1	E	36	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	61	GLN
1	F	153	HIS
1	C	27	GLN
1	C	61	GLN
1	D	72	GLN

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 [i](#)

There are no oligosaccharides 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, 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(Å²)	Q<0.9	
1	A	151/167 (90%)	-1.11	0	100100	35, 64, 81, 88	0
1	B	147/167 (88%)	-1.18	0	100100	25, 48, 68, 94	0
1	C	151/167 (90%)	-1.20	0	100100	23, 47, 73, 90	0
1	D	149/167 (89%)	-1.05	0	100100	46, 69, 85, 102	0
1	E	150/167 (89%)	-1.18	0	100100	19, 43, 71, 88	0
1	F	148/167 (88%)	-1.14	0	100100	39, 61, 77, 94	0
All	All	896/1002 (89%)	-1.14	0	100100	19, 56, 80, 102	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 oligosaccharides 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.