



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 06:13 AM EDT

PDB ID : 1WYE
Title : Crystal structure of 2-keto-3-deoxygluconate kinase (form 1) from Sulfolobus Tokodaii
Authors : Toyoda, T.; Suzuki, K.; Hossain, M.T.; Koike, I.; Sekiguchi, T.; Takenaka, A.
Deposited on : 2005-02-12
Resolution : 2.80 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 : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

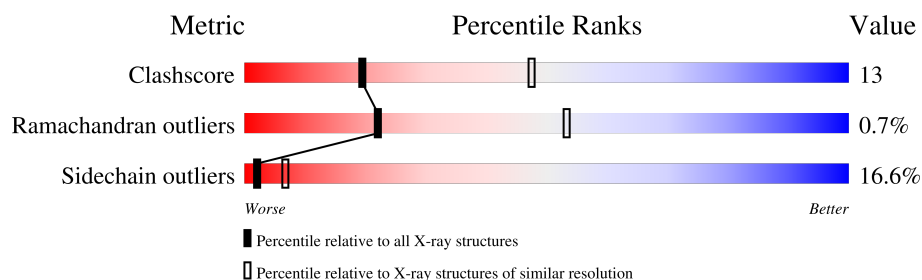
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	311	61% 31% 8% .
1	B	311	61% 31% 7% ..
1	C	311	63% 31% 5% .
1	D	311	63% 31% 6% .
1	E	311	60% 34% 5% ..
1	F	311	65% 28% 6% .

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 14836 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 2-keto-3-deoxygluconate kinase.

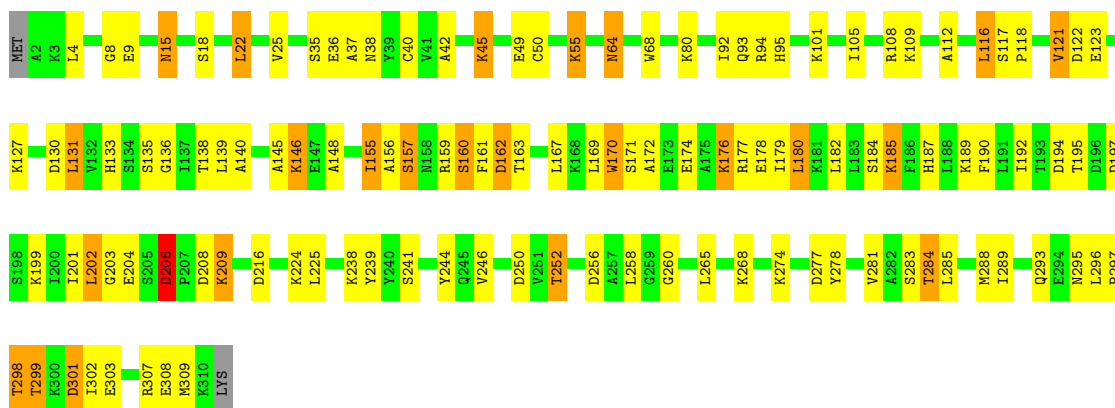
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	0	0
			2410	1548	389	466	7			
1	B	309	Total	C	N	O	S	0	0	0
			2410	1548	389	466	7			
1	C	309	Total	C	N	O	S	0	0	0
			2410	1548	389	466	7			
1	D	309	Total	C	N	O	S	0	0	0
			2410	1548	389	466	7			
1	E	309	Total	C	N	O	S	0	0	0
			2410	1548	389	466	7			
1	F	309	Total	C	N	O	S	0	0	0
			2406	1545	388	466	7			

- Molecule 2 is water.

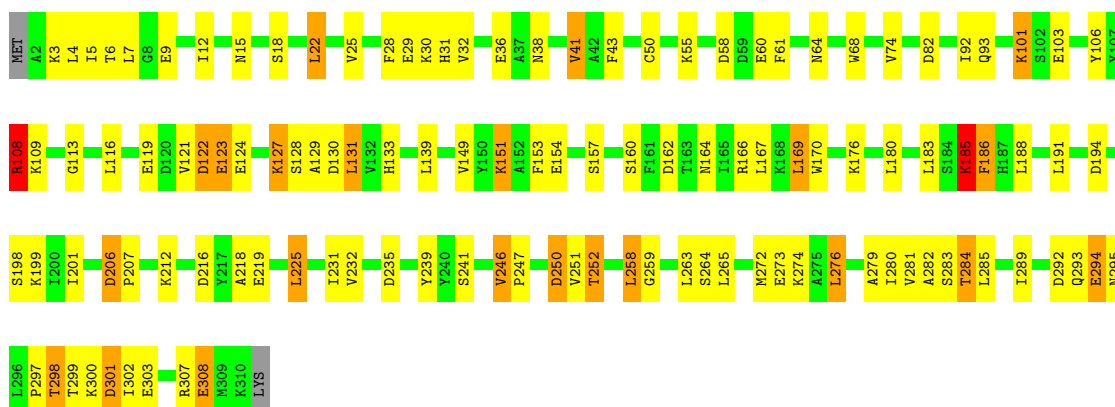
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	55	Total	O	0	0
			55	55		
2	B	45	Total	O	0	0
			45	45		
2	C	71	Total	O	0	0
			71	71		
2	D	79	Total	O	0	0
			79	79		
2	E	76	Total	O	0	0
			76	76		
2	F	54	Total	O	0	0
			54	54		

Note EDS was not executed.

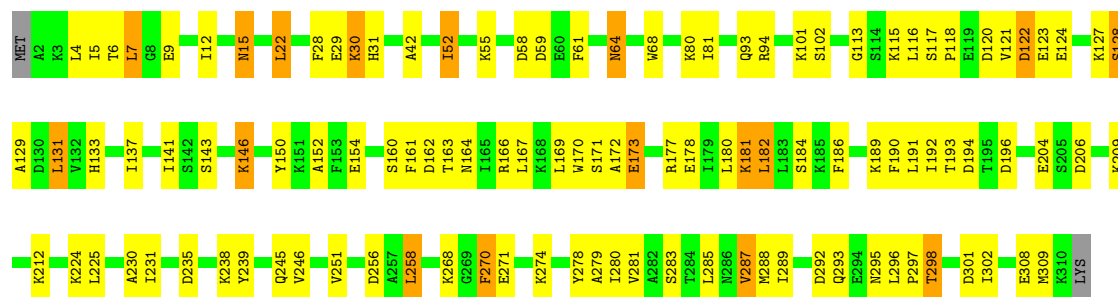
- Chain A:  61% 31% 8%



- Chain B: 61% 31% 7% . . .

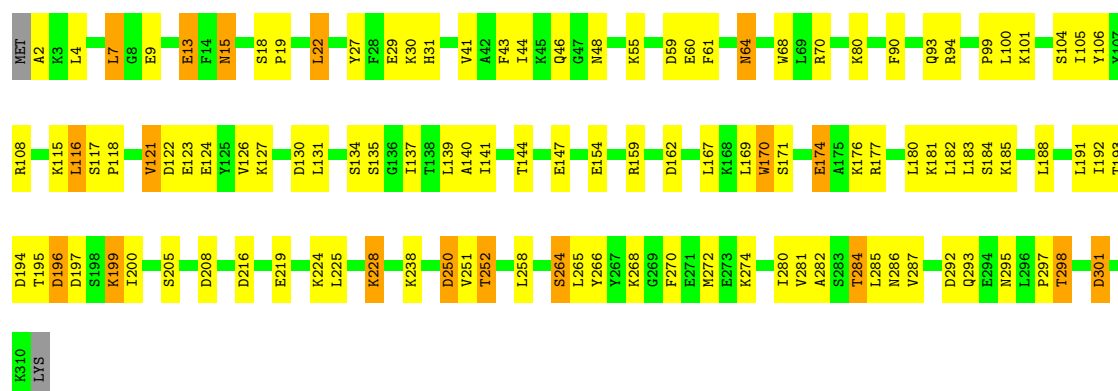


- Chain C: 63% 31% 5%



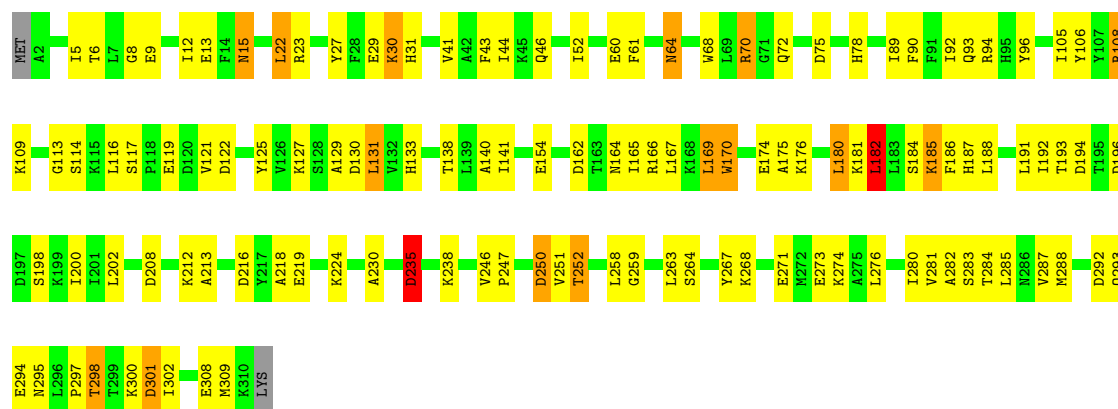
• Molecule 1: 2-keto-3-deoxygluconate kinase

Chain D: 63% 31% 6% •



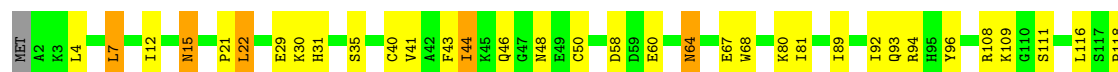
• Molecule 1: 2-keto-3-deoxygluconate kinase

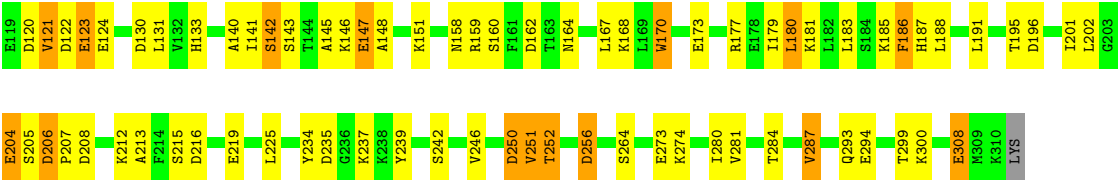
Chain E: 60% 34% 5% ••



• Molecule 1: 2-keto-3-deoxygluconate kinase

Chain F: 65% 28% 6% •





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.67Å 149.10Å 161.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80	Depositor
% Data completeness (in resolution range)	99.8 (50.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.179 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14836	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

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	0/2461	0.94	10/3324 (0.3%)
1	B	0.78	0/2461	0.93	12/3324 (0.4%)
1	C	0.81	0/2461	0.95	7/3324 (0.2%)
1	D	0.80	0/2461	0.97	8/3324 (0.2%)
1	E	0.79	0/2461	0.96	12/3324 (0.4%)
1	F	0.73	0/2457	0.94	8/3320 (0.2%)
All	All	0.78	0/14762	0.95	57/19940 (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	A	0	1
1	F	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	122	ASP	CB-CG-OD2	8.20	125.68	118.30
1	F	162	ASP	CB-CG-OD2	7.92	125.43	118.30
1	A	216	ASP	CB-CG-OD2	7.89	125.40	118.30
1	F	250	ASP	CB-CG-OD2	7.87	125.38	118.30
1	A	206	ASP	CB-CG-OD2	7.43	124.99	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	155	ILE	Peptide
1	F	234	TYR	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	2410	0	2392	63	0
1	B	2410	0	2392	65	0
1	C	2410	0	2392	61	0
1	D	2410	0	2392	70	0
1	E	2410	0	2392	67	0
1	F	2406	0	2381	57	0
2	A	55	0	0	3	0
2	B	45	0	0	3	0
2	C	71	0	0	3	0
2	D	79	0	0	5	0
2	E	76	0	0	3	0
2	F	54	0	0	2	0
All	All	14836	0	14341	369	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 13.

The worst 5 of 369 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:C:30:LYS:HE2	1:C:64:ASN:OD1	1.44	1.17
1:E:184:SER:O	1:E:185:LYS:HG2	1.56	1.05
1:A:146:LYS:HE2	1:A:178:GLU:OE1	1.56	1.04
1:A:15:ASN:HD21	1:A:94:ARG:HD3	1.23	1.00
1:D:258:LEU:HD11	1:D:280:ILE:HD13	1.42	1.00

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	307/311 (99%)	283 (92%)	22 (7%)	2 (1%)	22	53
1	B	307/311 (99%)	292 (95%)	12 (4%)	3 (1%)	15	44
1	C	307/311 (99%)	295 (96%)	11 (4%)	1 (0%)	41	72
1	D	307/311 (99%)	291 (95%)	16 (5%)	0	100	100
1	E	307/311 (99%)	293 (95%)	11 (4%)	3 (1%)	15	44
1	F	307/311 (99%)	284 (92%)	19 (6%)	4 (1%)	12	36
All	All	1842/1866 (99%)	1738 (94%)	91 (5%)	13 (1%)	22	53

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	186	PHE
1	C	128	SER
1	E	185	LYS
1	F	142	SER
1	F	186	PHE

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	257/260 (99%)	211 (82%)	46 (18%)	2	5
1	B	257/260 (99%)	208 (81%)	49 (19%)	1	4
1	C	257/260 (99%)	217 (84%)	40 (16%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	257/260 (99%)	216 (84%)	41 (16%)	2	7
1	E	257/260 (99%)	218 (85%)	39 (15%)	3	8
1	F	256/260 (98%)	215 (84%)	41 (16%)	2	7
All	All	1541/1560 (99%)	1285 (83%)	256 (17%)	2	7

5 of 256 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	164	ASN
1	F	195	THR
1	C	22	LEU
1	B	308	GLU
1	F	208	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	286	ASN
1	E	78	HIS
1	D	293	GLN
1	E	31	HIS
1	E	286	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 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](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.