



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2QG7  
Title : Plasmodium vivax ethanolamine kinase Pv091845  
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Deposited on : 2007-06-28  
Resolution : 2.41 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

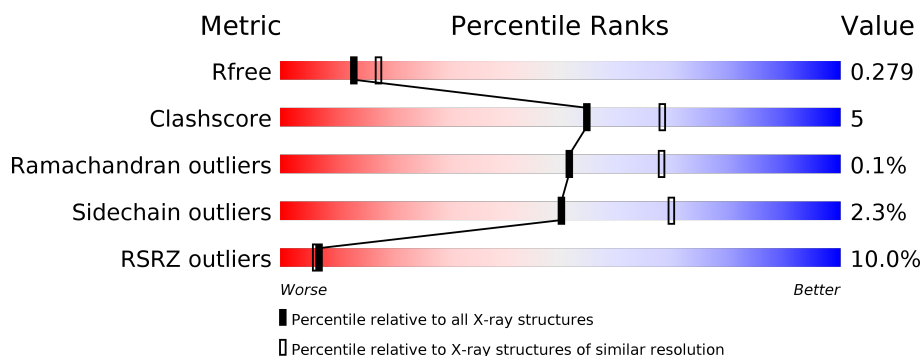
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.41 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))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	458	<div> <div>5%</div> <div> <div></div> <div>69%</div> <div>11%</div> <div>20%</div> </div> </div>
1	B	458	<div> <div>6%</div> <div> <div></div> <div>65%</div> <div>14%</div> <div>21%</div> </div> </div>
1	D	458	<div> <div>13%</div> <div> <div></div> <div>64%</div> <div>16%</div> <div>20%</div> </div> </div>
1	E	458	<div> <div>8%</div> <div> <div></div> <div>70%</div> <div>10%</div> <div>19%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12638 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 ethanolamine kinase Pv091845.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	2	0
			3057	1969	504	567	17			
1	B	363	Total	C	N	O	S	0	1	0
			3021	1944	500	560	17			
1	D	367	Total	C	N	O	S	0	0	0
			3041	1958	503	563	17			
1	E	369	Total	C	N	O	S	0	1	0
			3058	1973	501	566	18			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	Cloning Artifact	UNP A5K4Q6
A	2	SER	-	Cloning Artifact	UNP A5K4Q6
B	1	GLY	-	Cloning Artifact	UNP A5K4Q6
B	2	SER	-	Cloning Artifact	UNP A5K4Q6
D	1	GLY	-	Cloning Artifact	UNP A5K4Q6
D	2	SER	-	Cloning Artifact	UNP A5K4Q6
E	1	GLY	-	Cloning Artifact	UNP A5K4Q6
E	2	SER	-	Cloning Artifact	UNP A5K4Q6

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	162	Total	O	0	0
			162	162		
3	B	101	Total	O	0	0
			101	101		
3	D	87	Total	O	0	0
			87	87		
3	E	106	Total	O	0	0
			106	106		



- Molecule 1: ethanolamine kinase Pv091845



[illegible]

Chain E:

8% 70% 10% 19%

GLY SER GLU GLN LYS ARG LEU GLU GLY THR ALA ASN VAL ALA GLU SER SER PRO PHE PRO LEU ARG SER LYS THR VAL GLY THR GLU THR LYS ASN LYS GLN GLY VAL Y50 T53 E54 S55 G62 E63 D64 R65

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.03 Å 172.70 Å 93.35 Å 90.00° 110.72° 90.00°	Depositor
Resolution (Å)	24.93 – 2.41 24.93 – 2.41	Depositor EDS
% Data completeness (in resolution range)	96.1 (24.93-2.41) 96.2 (24.93-2.41)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 2.41 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.230 , 0.290 0.223 , 0.279	Depositor DCC
$R_{free}$ test set	4237 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.7	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 51.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12638	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.83	2/3121 (0.1%)	0.72	0/4207
1	B	0.84	2/3082 (0.1%)	0.70	1/4149 (0.0%)
1	D	0.81	3/3105 (0.1%)	0.67	2/4182 (0.0%)
1	E	0.81	4/3121 (0.1%)	0.69	1/4203 (0.0%)
All	All	0.82	11/12429 (0.1%)	0.70	4/16741 (0.0%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	213	LYS	CD-CE	10.60	1.77	1.51
1	E	128	LYS	CE-NZ	7.18	1.67	1.49
1	B	85	LYS	CE-NZ	7.17	1.67	1.49
1	D	126	LYS	CE-NZ	6.51	1.65	1.49
1	A	74	LYS	CD-CE	6.49	1.67	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	65	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	D	213	LYS	CD-CE-NZ	-5.35	99.40	111.70
1	D	213	LYS	CG-CD-CE	-5.23	96.20	111.90
1	B	190	ARG	NE-CZ-NH1	5.11	122.85	120.30

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	3057	0	3025	30	0
1	B	3021	0	3004	34	0
1	D	3041	0	3024	42	0
1	E	3058	0	3043	23	0
2	A	5	0	0	1	0
3	A	162	0	0	3	1
3	B	101	0	0	0	1
3	D	87	0	0	2	0
3	E	106	0	0	1	0
All	All	12638	0	12096	127	1

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 5.

The worst 5 of 127 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:D:213:LYS:CE	1:D:213:LYS:CD	1.77	1.61
1:D:213:LYS:CE	1:D:213:LYS:CG	2.54	0.84
1:A:232:ARG:HH21	1:A:232:ARG:HG2	1.45	0.80
1:E:207:LYS:HG3	1:E:394:TYR:O	1.82	0.80
1:A:64:ASP:HB3	1:A:67:GLU:HG2	1.63	0.79

All (1) 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)
3:A:655:HOH:O	3:B:520:HOH:O[2_656]	2.13	0.07

## 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	360/458 (79%)	349 (97%)	11 (3%)	0	100	100
1	B	354/458 (77%)	343 (97%)	11 (3%)	0	100	100
1	D	357/458 (78%)	341 (96%)	15 (4%)	1 (0%)	41	55
1	E	360/458 (79%)	343 (95%)	16 (4%)	1 (0%)	41	55
All	All	1431/1832 (78%)	1376 (96%)	53 (4%)	2 (0%)	51	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	133	GLN
1	E	227	LYS

### 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	342/407 (84%)	333 (97%)	9 (3%)	46	66
1	B	340/407 (84%)	333 (98%)	7 (2%)	53	72
1	D	342/407 (84%)	331 (97%)	11 (3%)	39	59
1	E	343/407 (84%)	338 (98%)	5 (2%)	65	80
All	All	1367/1628 (84%)	1335 (98%)	32 (2%)	50	70

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	298	LEU
1	D	123	ILE
1	E	215	ASN
1	D	109	ASP
1	D	127	VAL

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

Mol	Chain	Res	Type
1	B	411	GLN
1	D	122	ASN
1	D	301	ASN
1	B	404	ASN
1	D	375	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	SO4	A	600	-	4,4,4	0.38	0	6,6,6	0.24	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	SO4	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	368/458 (80%)	0.22	23 (6%)	20 18	34, 48, 78, 92	0
1	B	363/458 (79%)	0.48	28 (7%)	13 12	37, 58, 91, 127	0
1	D	367/458 (80%)	0.77	58 (15%)	2 1	40, 66, 114, 120	0
1	E	369/458 (80%)	0.46	37 (10%)	7 6	36, 59, 97, 104	0
All	All	1467/1832 (80%)	0.48	146 (9%)	7 6	34, 58, 100, 127	0

The worst 5 of 146 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	433	SER	7.0
1	D	134	ALA	6.9
1	E	131	SER	6.8
1	D	231	THR	6.8
1	E	130[A]	MET	6.5

### 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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	A	600	5/5	0.96	0.09	86,87,88,88	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.