



# Full wwPDB X-ray Structure Validation Report

May 14, 2020 – 07:50 am BST

PDB ID : 5EUT  
Title : Crystal structure of phosphatidyl inositol 4-kinase II alpha in the apo state  
Authors : Baumlova, A.; Boura, E.  
Deposited on : 2015-11-19  
Resolution : 2.80 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](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  
Xtrriage (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

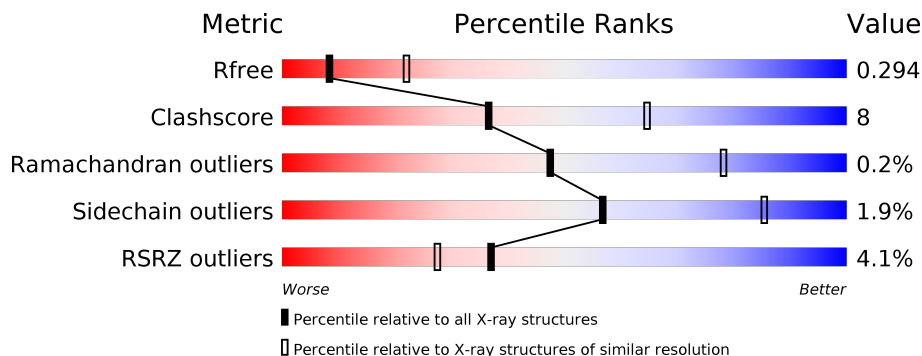
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 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	556	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3894 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 Phosphatidylinositol 4-kinase type 2-alpha,Endolysin,Phosphatidylinositol 4-kinase type 2-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	485	3894	2500	673	713	8	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	GLY	-	expression tag	UNP Q9BTU6
A	73	ALA	-	expression tag	UNP Q9BTU6
A	74	MET	-	expression tag	UNP Q9BTU6
A	75	GLY	-	expression tag	UNP Q9BTU6
A	1001	GLY	-	linker	UNP Q9BTU6
A	1002	THR	-	linker	UNP Q9BTU6
A	1003	GLY	-	linker	UNP Q9BTU6
A	1014	GLY	ARG	conflict	UNP P00720
A	1056	THR	CYS	conflict	UNP P00720
A	1099	ALA	CYS	conflict	UNP P00720
A	1139	ARG	ILE	conflict	UNP P00720
A	1166	LEU	PHE	conflict	UNP Q9BTU6



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.01Å 101.52Å 78.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.97 – 2.80 48.97 – 2.79	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.97-2.80) 87.3 (48.97-2.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.52 (at 2.81Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.246 , 0.289 0.258 , 0.294	Depositor DCC
$R_{free}$ test set	811 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.9	Xtrriage
Anisotropy	0.522	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 31.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.034 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	3894	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% 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](#)

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	0.24	0/3984	0.47	0/5403

There are no bond length outliers.

There are no bond angle outliers.

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	A	3894	0	3870	61	0
All	All	3894	0	3870	61	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 8.

All (61) 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:A:162:LEU:O	1:A:222:ASN:ND2	2.19	0.75
1:A:155:ASN:HD21	1:A:256:LYS:HE2	1.52	0.73
1:A:1013:GLU:OE2	1:A:1147:ARG:NH1	2.19	0.70
1:A:1042:ASN:HA	1:A:1045:LYS:HB3	1.76	0.66
1:A:1012:ASP:OD1	1:A:1150:ARG:NH1	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:ARG:HG3	1:A:123:ARG:HH11	1.62	0.64
1:A:130:ILE:HG22	1:A:132:GLN:H	1.62	0.64
1:A:164:PRO:O	1:A:167:THR:OG1	2.16	0.63
1:A:192:SER:HB3	1:A:348:GLY:HA2	1.81	0.62
1:A:1038:SER:HG	1:A:1040:SER:HG	1.47	0.61
1:A:299:VAL:HG11	1:A:384:ILE:HD13	1.84	0.60
1:A:228:ARG:O	1:A:231:SER:OG	2.21	0.58
1:A:291:LEU:O	1:A:295:GLU:HG3	2.04	0.56
1:A:222:ASN:O	1:A:256:LYS:NZ	2.34	0.56
1:A:1094:ASP:OD2	1:A:1097:ARG:NH1	2.32	0.56
1:A:130:ILE:HG22	1:A:132:GLN:N	2.20	0.56
1:A:1130:GLU:O	1:A:1133:VAL:HG22	2.06	0.56
1:A:1086:LEU:HD23	1:A:1120:LEU:HD21	1.88	0.55
1:A:130:ILE:H	1:A:130:ILE:HD12	1.73	0.53
1:A:1127:ARG:HB2	1:A:1130:GLU:HB2	1.92	0.52
1:A:140:VAL:HB	1:A:149:ALA:HB3	1.92	0.51
1:A:1054:ARG:HH12	1:A:1056:THR:HA	1.75	0.50
1:A:1103:ASN:OD1	1:A:1147:ARG:NH2	2.39	0.49
1:A:377:SER:O	1:A:380:ILE:HG22	2.13	0.49
1:A:191:LEU:HD11	1:A:408:ASP:HB2	1.94	0.49
1:A:202:LYS:HD3	1:A:397:LEU:HD13	1.95	0.49
1:A:102:ASN:HD21	1:A:215:TYR:H	1.60	0.49
1:A:129:ARG:HB2	1:A:138:TYR:CE1	2.48	0.48
1:A:197:SER:OG	1:A:210:ARG:NH1	2.46	0.48
1:A:380:ILE:HG13	1:A:384:ILE:HD12	1.94	0.48
1:A:1054:ARG:NH1	1:A:1056:THR:HA	2.29	0.48
1:A:154:LYS:O	1:A:157:GLU:HB2	2.15	0.47
1:A:1010:ARG:NH2	1:A:1066:GLU:OE1	2.37	0.47
1:A:381:LYS:O	1:A:385:LEU:HB2	2.15	0.47
1:A:1045:LYS:HE3	1:A:1057:ASN:H	1.79	0.47
1:A:438:LYS:HD3	1:A:442:HIS:HB3	1.95	0.47
1:A:1133:VAL:O	1:A:1136:ALA:HB3	2.15	0.46
1:A:1127:ARG:HD3	1:A:1130:GLU:HG3	1.97	0.46
1:A:1034:LEU:HD21	1:A:1037:LYS:HE3	1.97	0.46
1:A:408:ASP:OD2	1:A:410:GLY:N	2.50	0.44
1:A:1140:TRP:O	1:A:1141:TYR:HB3	2.16	0.44
1:A:381:LYS:HG2	1:A:434:LEU:HD22	2.00	0.43
1:A:123:ARG:CG	1:A:123:ARG:HH11	2.30	0.43
1:A:221:PHE:HB2	1:A:223:TYR:CE2	2.53	0.43
1:A:1089:VAL:HG21	1:A:1120:LEU:HB3	2.01	0.43
1:A:267:TYR:HB3	1:A:315:LEU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:LYS:O	1:A:422:VAL:HG23	2.19	0.43
1:A:271:ASP:HB2	1:A:311:ASN:HB3	2.00	0.43
1:A:305:ARG:HG3	1:A:305:ARG:O	2.19	0.42
1:A:339:VAL:HG12	1:A:340:ILE:HG13	2.02	0.42
1:A:1137:LYS:HB3	1:A:1137:LYS:HE2	1.89	0.42
1:A:136:GLY:O	1:A:153:PRO:HD2	2.20	0.42
1:A:407:LYS:HE3	1:A:407:LYS:HB2	1.76	0.42
1:A:1128:TRP:HB3	1:A:1156:ARG:HA	2.01	0.41
1:A:353:LEU:HD21	1:A:415:GLN:HG2	2.01	0.41
1:A:1157:THR:OG1	1:A:1159:THR:HG22	2.20	0.41
1:A:157:GLU:O	1:A:160:GLY:N	2.47	0.41
1:A:1140:TRP:CG	1:A:1141:TYR:N	2.89	0.40
1:A:226:ILE:HG22	1:A:230:LYS:HE3	2.04	0.40
1:A:381:LYS:HE2	1:A:381:LYS:HB3	1.84	0.40
1:A:1122:MET:HE1	1:A:1130:GLU:HB3	2.02	0.40

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	479/556 (86%)	462 (96%)	16 (3%)	1 (0%)	47 78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1003	GLY



### 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	413/473 (87%)	405 (98%)	8 (2%)	57 85

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	GLU
1	A	131	TYR
1	A	157	GLU
1	A	167	THR
1	A	1029	ILE
1	A	1036	THR
1	A	1042	ASN
1	A	334	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains 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 carbohydrates 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<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	485/556 (87%)	0.43	20 (4%) 37 27	45, 74, 111, 122	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	169	TRP	5.7
1	A	1057	ASN	3.7
1	A	331	ASP	3.5
1	A	1135	LEU	3.5
1	A	1152	ILE	3.4
1	A	1161	ASP	3.2
1	A	166	TRP	3.1
1	A	171	GLN	3.0
1	A	1156	ARG	3.0
1	A	131	TYR	2.9
1	A	1155	PHE	2.8
1	A	134	SER	2.6
1	A	251	ILE	2.5
1	A	1105	VAL	2.5
1	A	1129	ASP	2.4
1	A	1153	THR	2.4
1	A	1160	TRP	2.4
1	A	182	ASP	2.1
1	A	1004	ASN	2.0
1	A	1054	ARG	2.0

### 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](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.