



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2024 – 04:07 PM EDT

PDB ID : 4TZ7
Title : Crystal structure of type I phosphatidylinositol 4-phosphate 5-kinase alpha from Zebrafish
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Deposited on : 2014-07-09
Resolution : 3.31 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

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)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

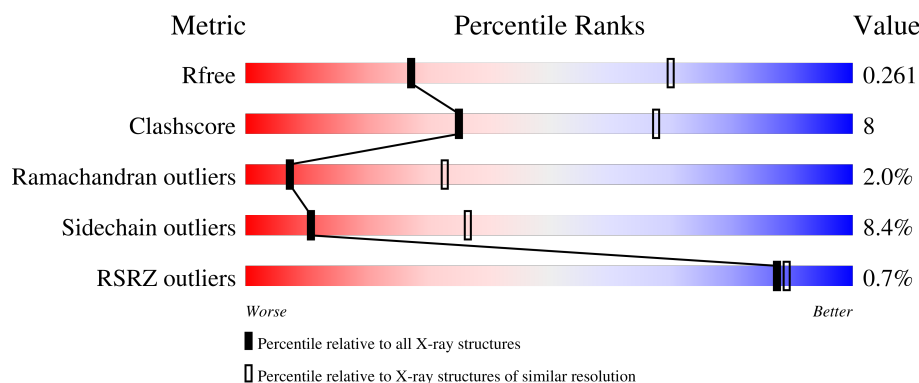
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.31 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	1089 (3.36-3.28)
Clashscore	141614	1137 (3.36-3.28)
Ramachandran outliers	138981	1115 (3.36-3.28)
Sidechain outliers	138945	1114 (3.36-3.28)
RSRZ outliers	127900	1059 (3.36-3.28)

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	394	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2290 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-phosphate 5-kinase, type I, alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2290	1468	386	421	15			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	MET	-	expression tag	UNP Q503I3
A	47	ALA	-	expression tag	UNP Q503I3
A	48	SER	-	expression tag	UNP Q503I3
A	432	LEU	-	expression tag	UNP Q503I3
A	433	GLU	-	expression tag	UNP Q503I3
A	434	HIS	-	expression tag	UNP Q503I3
A	435	HIS	-	expression tag	UNP Q503I3
A	436	HIS	-	expression tag	UNP Q503I3
A	437	HIS	-	expression tag	UNP Q503I3
A	438	HIS	-	expression tag	UNP Q503I3
A	439	HIS	-	expression tag	UNP Q503I3

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	88.95Å 88.95Å 157.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.31 – 3.31 33.31 – 3.31	Depositor EDS
% Data completeness (in resolution range)	99.0 (33.31-3.31) 99.2 (33.31-3.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.78 (at 3.32Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.207 , 0.268 0.203 , 0.261	Depositor DCC
R_{free} test set	982 reflections (9.96%)	wwPDB-VP
Wilson B-factor (Å ²)	114.8	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 86.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2290	wwPDB-VP
Average B, all atoms (Å ²)	119.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [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	0.50	0/2343	0.71	0/3174

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	420	CYS	Peptide

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	2290	0	2097	36	0
All	All	2290	0	2097	36	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 (36) 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:181:LEU:HD23	1:A:206:LEU:HD22	1.78	0.65
1:A:73:SER:OG	1:A:118:THR:HG21	1.97	0.64
1:A:293:GLN:HE21	1:A:409:SER:HA	1.67	0.59
1:A:226:PRO:O	1:A:227:ARG:HB3	2.02	0.58
1:A:100:SER:O	1:A:101:GLN:CB	2.54	0.55
1:A:83:ARG:NH2	1:A:89:ASP:OD2	2.35	0.54
1:A:90:PHE:CD2	1:A:186:PRO:HG3	2.42	0.54
1:A:360:ILE:CB	1:A:372:VAL:O	2.55	0.54
1:A:187:GLY:HA3	1:A:295:PHE:HZ	1.73	0.53
1:A:119:TYR:HD2	1:A:206:LEU:HG	1.73	0.52
1:A:224:LEU:HD11	1:A:375:GLY:N	2.25	0.51
1:A:225:LEU:HD13	1:A:231:MET:HG2	1.91	0.51
1:A:241:THR:O	1:A:244:ARG:HB3	2.11	0.51
1:A:119:TYR:CD2	1:A:206:LEU:HG	2.47	0.49
1:A:245:ARG:HG2	1:A:261:LEU:HD12	1.96	0.47
1:A:62:LEU:HD22	1:A:161:TYR:CZ	2.50	0.47
1:A:226:PRO:O	1:A:227:ARG:CB	2.62	0.47
1:A:407:ARG:HB3	1:A:408:PRO:HD3	1.96	0.47
1:A:142:LEU:HD22	1:A:170:ILE:HD11	1.97	0.46
1:A:224:LEU:HD11	1:A:375:GLY:CA	2.45	0.46
1:A:103:SER:O	1:A:104:SER:CB	2.64	0.46
1:A:117:LYS:CE	1:A:208:CYS:SG	3.04	0.45
1:A:223:ASN:O	1:A:224:LEU:C	2.54	0.45
1:A:244:ARG:HG2	1:A:260:ASP:HB2	1.98	0.45
1:A:272:LEU:O	1:A:273:LEU:HD12	2.17	0.45
1:A:158:SER:HA	1:A:172:THR:HG21	1.99	0.44
1:A:380:LEU:O	1:A:381:GLN:HG3	2.18	0.44
1:A:93:VAL:HG22	1:A:119:TYR:HD1	1.82	0.43
1:A:71:THR:HG23	1:A:143:CYS:CB	2.49	0.42
1:A:62:LEU:C	1:A:62:LEU:HD23	2.39	0.42
1:A:83:ARG:O	1:A:125:ARG:NH2	2.53	0.42
1:A:149:GLU:HG3	1:A:161:TYR:CE1	2.56	0.41
1:A:241:THR:HG22	1:A:261:LEU:HD21	2.03	0.41
1:A:179:GLU:O	1:A:182:GLN:HB3	2.21	0.40
1:A:88:GLN:H	1:A:88:GLN:CD	2.24	0.40
1:A:208:CYS:SG	1:A:217:ARG:HG2	2.62	0.40

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	295/394 (75%)	257 (87%)	32 (11%)	6 (2%)	7	33

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	GLN
1	A	104	SER
1	A	227	ARG
1	A	111	HIS
1	A	146	PRO
1	A	224	LEU

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	226/350 (65%)	207 (92%)	19 (8%)	11	36

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	THR
1	A	83	ARG
1	A	118	THR
1	A	147	LEU
1	A	148	ILE

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Mol	Chain	Res	Type
1	A	165	ASP
1	A	166	ASP
1	A	184	LEU
1	A	197	ARG
1	A	241	THR
1	A	244	ARG
1	A	260	ASP
1	A	267	MET
1	A	272	LEU
1	A	301	SER
1	A	379	ILE
1	A	407	ARG
1	A	409	SER
1	A	424	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	GLN
1	A	293	GLN
1	A	364	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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(Å ²)	Q<0.9
1	A	303/394 (76%)	-0.26	2 (0%) 87 89	72, 118, 171, 203	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	402	THR	4.6
1	A	403	VAL	2.8

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.