



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 09:28 PM GMT

PDB ID : 5AE8
Title : Crystal structure of mouse PI3 kinase delta in complex with GSK2269557
Authors : Down, K.D.; Amour, A.; Baldwin, I.R.; Cooper, A.W.J.; Deakin, A.M.; Felton, L.M.; Guntrip, S.B.; Hardy, C.; Harrison, Z.A.; Jones, K.L.; Jones, P.; Keeling, S.E.; Le, J.; Livia, S.; Lucas, F.; Lunniss, C.J.; Parr, N.J.; Robinson, E.; Rowland, P.; Smith, S.; Thomas, D.A.; Vitulli, G.; Washio, Y.; Hamblin, N.
Deposited on : 2015-08-26
Resolution : 2.42 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

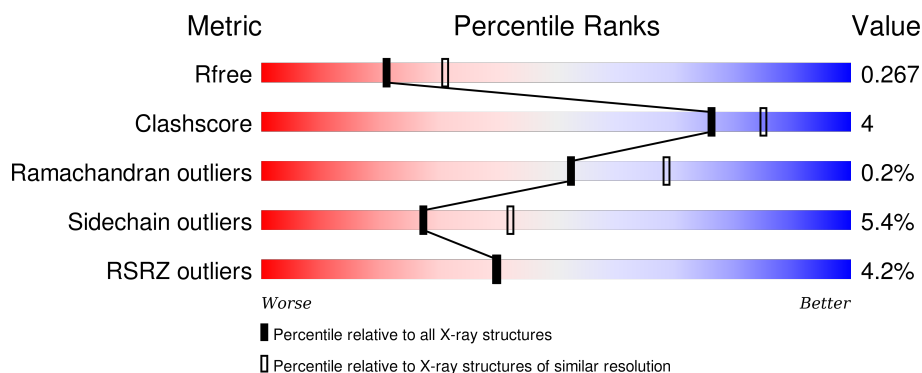
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.42 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}	91344	3386 (2.44-2.40)
Clashscore	102246	3897 (2.44-2.40)
Ramachandran outliers	100387	3837 (2.44-2.40)
Sidechain outliers	100360	3838 (2.44-2.40)
RSRZ outliers	91569	3396 (2.44-2.40)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	940	<div> <div>4%</div> <div>78%</div> <div>13%</div> <div>9%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7450 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.

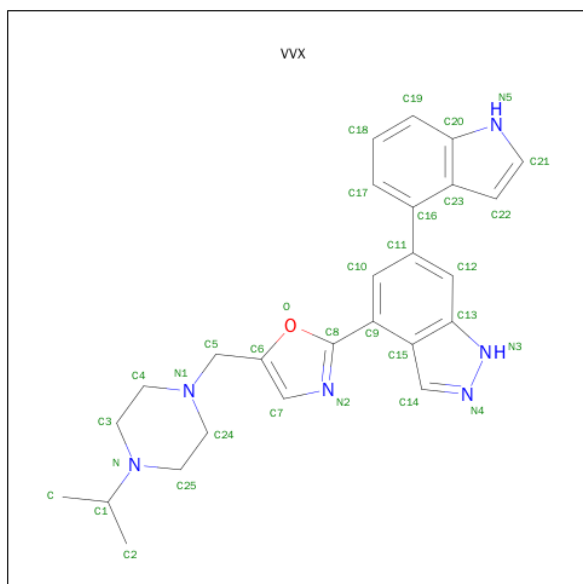
- Molecule 1 is a protein called PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE 3-KINASE CATALYTIC SUBUNIT DELTA ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	856	Total	C	N	O	S	0	0	0
			6910	4416	1184	1256	54			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	GLY	-	EXPRESSION TAG	UNP Q3UDT3

- Molecule 2 is 6-(1H-INDOL-4-YL)-4-(5-{[4-(1-METHYLETHYL)-1-PIPERAZINYL]METHYL}-1,3-OXAZOL-2-YL)-1H-INDAZOLE (three-letter code: VVX) (formula: C₂₆H₂₈N₆O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			33	26	6	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	507	Total 507	O 507	0	0

- Molecule 1: PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE 3-KINASE CATALYTIC SUB-UNIT DELTA ISOFORM



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	142.96Å 64.40Å 116.80Å 90.00° 103.17° 90.00°	Depositor
Resolution (Å)	47.17 – 2.42 66.49 – 2.42	Depositor EDS
% Data completeness (in resolution range)	95.7 (47.17-2.42) 96.2 (66.49-2.42)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.42Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.190 , 0.250 0.201 , 0.267	Depositor DCC
R_{free} test set	1521 reflections (4.16%)	DCC
Wilson B-factor (Å ²)	46.7	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 70.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 38078 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7450	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.62% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: VVX

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	0.51	0/7060	0.68	0/9530

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	6910	0	6894	52	0
2	A	33	0	28	2	0
3	A	507	0	0	0	0
All	All	7450	0	6922	52	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 4.

All (52) 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:641:ARG:HH12	1:A:737:PRO:HB2	1.47	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:ILE:HB	1:A:472:VAL:HG23	1.71	0.73
1:A:224:LYS:HD3	1:A:232:LEU:HD21	1.77	0.67
1:A:271:THR:O	1:A:273:HIS:HD2	1.77	0.66
1:A:978:PHE:CD2	1:A:998:LEU:HD11	2.32	0.66
1:A:194:VAL:HG21	1:A:216:LEU:HD21	1.84	0.59
1:A:329:GLU:HG2	1:A:472:VAL:HG22	1.85	0.58
1:A:205:PHE:CZ	1:A:220:ALA:HA	2.40	0.56
1:A:534:MET:O	1:A:538:VAL:HG23	2.07	0.55
1:A:886:THR:HA	1:A:891:ILE:HD12	1.90	0.54
1:A:271:THR:O	1:A:273:HIS:CD2	2.58	0.53
1:A:600:LEU:HD22	1:A:603:LEU:HD11	1.90	0.53
1:A:135:GLU:HG2	1:A:625:LEU:HD12	1.90	0.53
1:A:371:TRP:HB3	1:A:373:GLN:HG2	1.89	0.53
1:A:328:ILE:HD11	1:A:474:TYR:HB2	1.90	0.52
1:A:583:LEU:HD11	1:A:600:LEU:HD11	1.90	0.52
1:A:895:HIS:H	1:A:898:ASN:HD21	1.57	0.52
1:A:523:LEU:HD21	1:A:548:ARG:HD3	1.93	0.51
1:A:349:HIS:HB2	1:A:354:LEU:HD21	1.94	0.50
1:A:621:TYR:CZ	1:A:983:ALA:HB2	2.47	0.50
1:A:859:LEU:HD21	1:A:905:GLY:HA2	1.94	0.49
1:A:247:HIS:CD2	1:A:740:LEU:HD21	2.47	0.49
1:A:917:GLY:HA2	1:A:930:VAL:HG23	1.95	0.49
1:A:700:LYS:HE2	1:A:756:MET:O	2.12	0.49
1:A:786:GLN:HE22	1:A:988:GLU:HB2	1.80	0.47
1:A:617:GLN:OE1	1:A:984:ALA:HA	2.15	0.47
1:A:895:HIS:H	1:A:898:ASN:ND2	2.12	0.47
1:A:894:ARG:HA	1:A:898:ASN:HD21	1.79	0.47
1:A:209:THR:HB	1:A:257:CYS:HB3	1.97	0.46
1:A:786:GLN:NE2	1:A:988:GLU:HB2	2.31	0.46
1:A:1008:GLU:O	1:A:1012:LEU:HB2	2.16	0.46
1:A:326:GLU:HB3	1:A:474:TYR:HB3	1.97	0.45
1:A:340:LYS:HE3	1:A:362:GLU:HB3	1.99	0.45
1:A:752:MET:HB2	1:A:758:PRO:HD2	1.99	0.44
1:A:895:HIS:CE1	1:A:897:ASP:HB2	2.52	0.44
1:A:325:ILE:HD11	1:A:375:LEU:HD12	2.00	0.44
1:A:938:PHE:N	1:A:938:PHE:CD1	2.83	0.44
1:A:609:PHE:HE1	1:A:646:PHE:CD2	2.36	0.44
1:A:387:MET:HG3	1:A:588:PRO:O	2.17	0.44
1:A:637:ALA:HB1	1:A:644:GLY:HA2	2.00	0.43
1:A:765:SER:HB3	1:A:772:GLY:HA3	1.99	0.43
1:A:492:LEU:O	1:A:496:ARG:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:TRP:HA	1:A:382:CYS:HB2	2.01	0.43
1:A:419:ALA:HB1	1:A:441:MET:HB3	2.02	0.42
1:A:975:LEU:HD11	1:A:1004:LEU:HD23	2.01	0.42
1:A:245:GLY:HA3	1:A:768:ALA:HB2	2.02	0.42
1:A:341:LEU:HG	1:A:365:VAL:HG22	2.02	0.42
1:A:614:GLN:HG3	1:A:981:MET:HG2	2.01	0.41
1:A:779:LYS:NZ	2:A:2033:VVX:H18	2.35	0.41
1:A:255:PRO:HG2	1:A:258:HIS:CD2	2.56	0.41
1:A:870:ARG:O	1:A:874:GLU:HG2	2.21	0.41
1:A:825:ILE:HG21	2:A:2033:VVX:C22	2.51	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	842/940 (90%)	814 (97%)	26 (3%)	2 (0%)	52 69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	229	ARG
1	A	911	ASP

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	759/827 (92%)	718 (95%)	41 (5%)	27	42

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	SER
1	A	188	ARG
1	A	200	GLU
1	A	233	VAL
1	A	264	SER
1	A	290	SER
1	A	333	VAL
1	A	336	ASP
1	A	352	GLU
1	A	368	GLU
1	A	397	VAL
1	A	423	LEU
1	A	437	ARG
1	A	466	GLU
1	A	475	LEU
1	A	490	LYS
1	A	506	GLU
1	A	509	LEU
1	A	523	LEU
1	A	525	GLU
1	A	530	LEU
1	A	541	HIS
1	A	560	ASP
1	A	601	ARG
1	A	710	GLN
1	A	713	GLU
1	A	722	GLU
1	A	731	LEU
1	A	786	GLN
1	A	795	GLN
1	A	847	THR
1	A	869	ASP
1	A	897	ASP
1	A	898	ASN
1	A	915	PHE
1	A	928	GLU
1	A	933	ILE
1	A	937	ASP

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Mol	Chain	Res	Type
1	A	955	ARG
1	A	994	ASP
1	A	1004	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	155	GLN
1	A	258	HIS
1	A	273	HIS
1	A	508	GLN
1	A	558	HIS
1	A	710	GLN
1	A	780	ASN
1	A	786	GLN
1	A	898	ASN
1	A	918	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	VVX	A	2033	-	32,38,38	0.75	0	37,55,55	0.97	2 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	VVX	A	2033	-	-	0/11/26/26	0/5/6/6

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2033	VVX	C6-C5-N1	2.12	117.14	113.02
2	A	2033	VVX	C5-C6-C7	4.52	137.28	128.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2033	VVX	2	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	856/940 (91%)	0.19	36 (4%) 40 40	28, 61, 107, 149	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	501	GLY	6.9
1	A	395	TYR	6.2
1	A	205	PHE	4.7
1	A	509	LEU	4.3
1	A	317	TRP	3.6
1	A	381	VAL	3.6
1	A	371	TRP	3.6
1	A	323	PHE	3.5
1	A	472	VAL	3.4
1	A	991	CYS	3.4
1	A	470	ALA	3.3
1	A	506	GLU	3.2
1	A	515	LEU	3.1
1	A	512	ARG	3.0
1	A	1032	ASN	3.0
1	A	370	VAL	2.8
1	A	1017	VAL	2.8
1	A	396	ALA	2.6
1	A	437	ARG	2.6
1	A	445	VAL	2.5
1	A	233	VAL	2.5
1	A	591	TYR	2.4
1	A	232	LEU	2.3
1	A	318	SER	2.3
1	A	537	GLU	2.3
1	A	473	ILE	2.3
1	A	109	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	488	LEU	2.2
1	A	190	LEU	2.2
1	A	329	GLU	2.2
1	A	330	GLY	2.1
1	A	207	VAL	2.1
1	A	503	ILE	2.1
1	A	502	ARG	2.1
1	A	592	VAL	2.1
1	A	471	LEU	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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(Å ²)	Q<0.9
2	VVX	A	2033	33/33	0.97	0.15	0.54	31,36,59,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.