



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 05:41 am BST

PDB ID : 2B3R
Title : Crystal structure of the C2 domain of class II phosphatidylinositide 3-kinase C2
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Deposited on : 2005-09-20
Resolution : 2.30 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 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) : **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) : 2.11

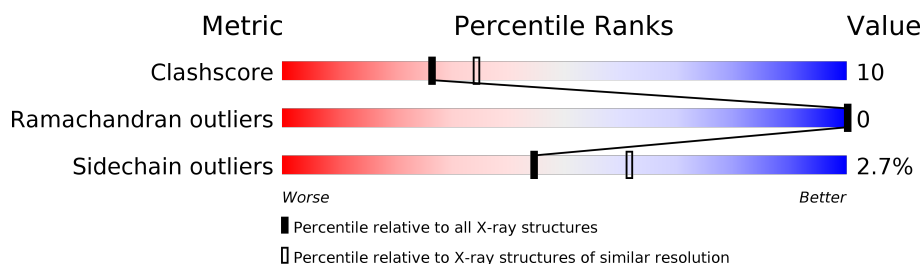
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 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	134	
1	B	134	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	302	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2252 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 3-kinase C2 domain-containing alpha polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	124	Total	C	N	O	S	0	0	0
			997	637	171	186	3			
1	B	124	Total	C	N	O	S	0	0	0
			997	637	171	186	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	CLONING ARTIFACT	UNP Q61194
A	-7	HIS	-	CLONING ARTIFACT	UNP Q61194
A	-6	HIS	-	CLONING ARTIFACT	UNP Q61194
A	-5	HIS	-	CLONING ARTIFACT	UNP Q61194
A	-4	HIS	-	CLONING ARTIFACT	UNP Q61194
A	-3	HIS	-	CLONING ARTIFACT	UNP Q61194
A	-2	GLY	-	CLONING ARTIFACT	UNP Q61194
A	-1	SER	-	CLONING ARTIFACT	UNP Q61194
B	-8	HIS	-	CLONING ARTIFACT	UNP Q61194
B	-7	HIS	-	CLONING ARTIFACT	UNP Q61194
B	-6	HIS	-	CLONING ARTIFACT	UNP Q61194
B	-5	HIS	-	CLONING ARTIFACT	UNP Q61194
B	-4	HIS	-	CLONING ARTIFACT	UNP Q61194
B	-3	HIS	-	CLONING ARTIFACT	UNP Q61194
B	-2	GLY	-	CLONING ARTIFACT	UNP Q61194
B	-1	SER	-	CLONING ARTIFACT	UNP Q61194

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 3 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total	O	0	0
			117	117		
3	B	111	Total	O	0	0
			111	111		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

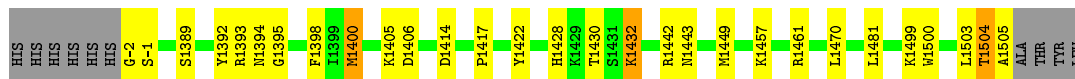
- Molecule 1: Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing alpha polypeptide

Chain A: 



- Molecule 1: Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing alpha polypeptide

Chain B: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	53.37Å 53.37Å 200.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (47.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.197 , 0.232	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2252	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

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	0.52	0/1016	0.76	0/1370
1	B	0.46	0/1016	0.73	1/1370 (0.1%)
All	All	0.49	0/2032	0.75	1/2740 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1504	THR	N-CA-C	-5.66	95.73	111.00

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	997	0	1028	14	0
1	B	997	0	1028	27	0
2	A	15	0	0	1	1
2	B	15	0	0	0	1
3	A	117	0	0	3	1
3	B	111	0	0	7	1
All	All	2252	0	2056	42	2

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 10.

All (42) 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)
2:A:302:SO4:O1	3:A:65:HOH:O	1.85	0.93
1:B:1504:THR:HG22	1:B:1505:ALA:HB3	1.65	0.79
1:A:1406:ASP:H	1:A:1443:ASN:ND2	1.82	0.78
1:A:1403:HIS:HB3	1:A:1445:THR:HA	1.67	0.76
1:B:1504:THR:CG2	1:B:1505:ALA:HB3	2.20	0.72
1:B:1504:THR:HG22	1:B:1505:ALA:CB	2.21	0.71
1:B:1389:SER:HB3	1:B:1400:MET:HB3	1.76	0.65
1:B:1504:THR:HG22	1:B:1505:ALA:C	2.17	0.65
1:A:1406:ASP:H	1:A:1443:ASN:HD21	1.46	0.64
1:B:1406:ASP:H	1:B:1443:ASN:ND2	1.98	0.61
1:A:1405:LYS:HA	1:A:1443:ASN:HD22	1.66	0.61
1:B:1504:THR:HA	1:B:1505:ALA:HB3	1.81	0.60
1:B:1398:PHE:HB3	1:B:1449:MET:SD	2.42	0.60
1:A:1417:PRO:HD2	1:A:1438:SER:O	2.02	0.59
1:B:1442:ARG:NH1	3:B:150:HOH:O	2.37	0.58
1:B:1461:ARG:NH1	3:B:225:HOH:O	2.37	0.57
1:B:1432:LYS:NZ	3:B:110:HOH:O	2.36	0.57
1:B:1405:LYS:HE3	1:B:1500:TRP:CH2	2.41	0.56
1:B:1428:HIS:HB2	1:B:1430:THR:HG22	1.88	0.54
1:A:1393:ARG:HH11	1:A:1394:ASN:HD22	1.56	0.54
1:B:1392:TYR:OH	1:B:1395:GLY:HA2	2.07	0.54
1:B:1406:ASP:H	1:B:1443:ASN:HD21	1.55	0.53
1:B:1393:ARG:HE	1:B:1394:ASN:ND2	2.07	0.53
1:B:1504:THR:CA	1:B:1505:ALA:HB3	2.40	0.52
1:A:1436:LYS:HE3	3:B:95:HOH:O	2.11	0.49
1:B:-1:SER:HA	3:B:179:HOH:O	2.11	0.49
1:A:1424:LEU:HA	1:A:1425:PRO:C	2.33	0.49
1:B:-2:GLY:HA3	1:B:1481:LEU:O	2.13	0.48
1:B:1393:ARG:HE	1:B:1394:ASN:HD21	1.61	0.48
1:A:1389:SER:HB3	1:A:1400:MET:HB3	1.96	0.48
1:B:1405:LYS:HA	1:B:1443:ASN:HD22	1.79	0.47
1:A:1467:LEU:HD23	1:A:1467:LEU:C	2.36	0.46
1:A:1440:LYS:HE2	3:A:140:HOH:O	2.16	0.46
1:A:1423:LEU:HA	1:A:1423:LEU:HD12	1.87	0.45
1:A:1392:TYR:OH	1:A:1395:GLY:HA2	2.17	0.45
1:B:1422:TYR:OH	1:B:1432:LYS:HG3	2.17	0.44
1:B:1417:PRO:HA	1:B:1470:LEU:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1499:LYS:NZ	3:B:158:HOH:O	2.50	0.43
1:B:1392:TYR:CZ	1:B:1395:GLY:HA2	2.54	0.42
1:A:1453:SER:HB2	3:A:186:HOH:O	2.19	0.41
1:B:1457:LYS:O	1:B:1461:ARG:HG3	2.21	0.41
1:B:1414:ASP:HB2	3:B:187:HOH:O	2.21	0.40

All (2) 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)
2:B:301:SO4:O1	3:B:56:HOH:O[8_665]	1.36	0.84
2:A:302:SO4:O4	3:A:65:HOH:O[8_665]	1.91	0.29

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	122/134 (91%)	116 (95%)	6 (5%)	0	100	100
1	B	122/134 (91%)	117 (96%)	5 (4%)	0	100	100
All	All	244/268 (91%)	233 (96%)	11 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	113/122 (93%)	110 (97%)	3 (3%)	44	61
1	B	113/122 (93%)	110 (97%)	3 (3%)	44	61
All	All	226/244 (93%)	220 (97%)	6 (3%)	44	61

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1403	HIS
1	A	1423	LEU
1	A	1494	SER
1	B	1400	MET
1	B	1432	LYS
1	B	1503	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1394	ASN
1	A	1443	ASN
1	A	1447	ASN
1	B	1394	ASN
1	B	1428	HIS
1	B	1443	ASN
1	B	1447	ASN
1	B	1502	GLN

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](#)

6 ligands are 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	B	305	-	4,4,4	0.48	0	6,6,6	0.24	0
2	SO4	A	302	-	4,4,4	0.67	0	6,6,6	0.83	0
2	SO4	A	303	-	4,4,4	0.43	0	6,6,6	0.23	0
2	SO4	B	306	-	4,4,4	0.46	0	6,6,6	0.32	0
2	SO4	A	304	-	4,4,4	0.40	0	6,6,6	0.14	0
2	SO4	B	301	-	4,4,4	0.33	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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	302	SO4	1	1
2	B	301	SO4	0	1

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.