



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 10:19 PM UTC

PDB ID : 8TS7 / pdb_00008ts7
Title : Human PI3K p85alpha/p110alpha
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Deposited on : 2023-08-11
Resolution : 2.71 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

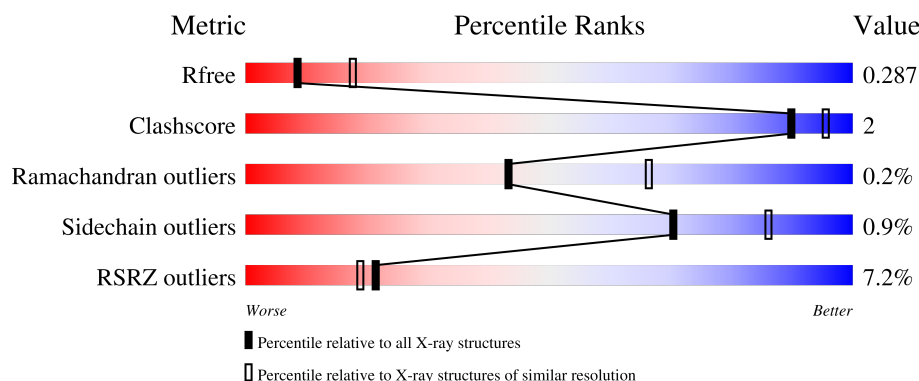
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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}	180053	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

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	1063	5% 88% 5% 6%
2	B	300	13% 84% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20858 atoms, of which 10434 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 alpha isoform.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	997	Total	C	H	N	O	S	114	0	0
			16361	5224	8196	1399	1474	68			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	GLY	-	expression tag	UNP P42336
A	-8	SER	-	expression tag	UNP P42336
A	-7	PRO	-	expression tag	UNP P42336
A	-6	GLY	-	expression tag	UNP P42336
A	-5	ILE	-	expression tag	UNP P42336
A	-4	SER	-	expression tag	UNP P42336
A	-3	GLY	-	expression tag	UNP P42336
A	-2	GLY	-	expression tag	UNP P42336
A	-1	GLY	-	expression tag	UNP P42336
A	0	GLY	-	expression tag	UNP P42336
A	1	GLY	-	expression tag	UNP P42336

- Molecule 2 is a protein called Phosphatidylinositol 3-kinase regulatory subunit alpha.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	266	Total	C	H	N	O	S	141	0	0
			4497	1414	2238	403	435	7			

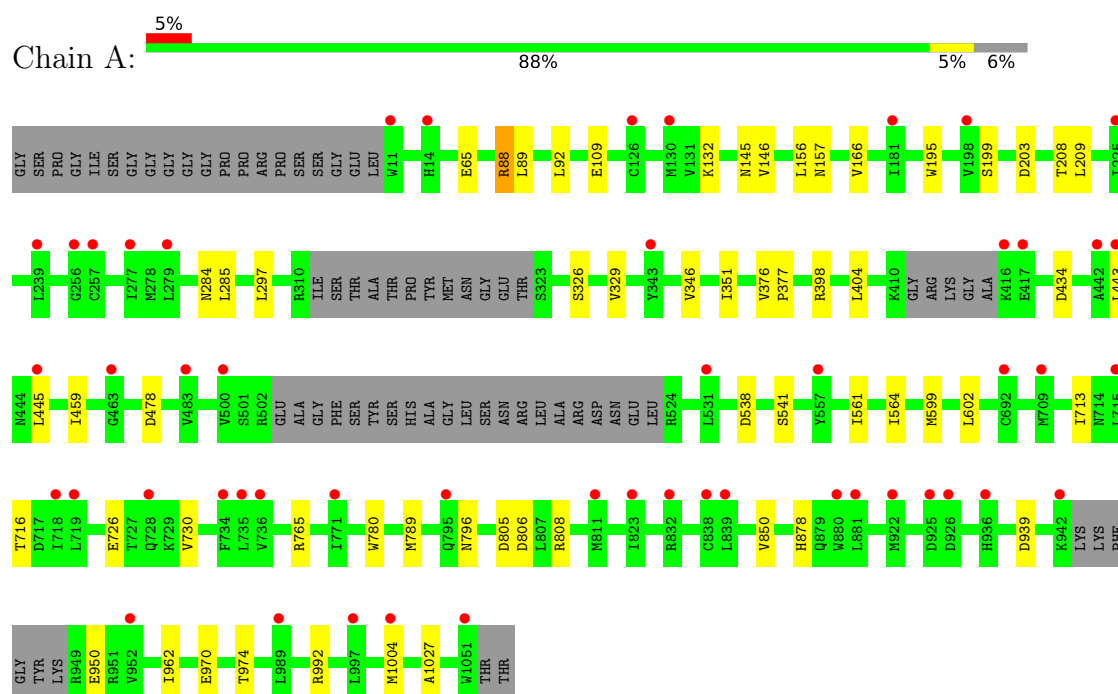
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	316	GLY	-	expression tag	UNP P27986
B	317	PRO	-	expression tag	UNP P27986

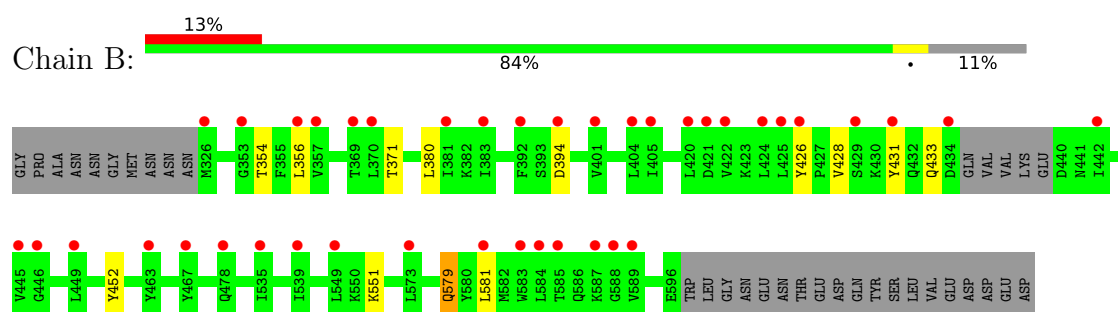
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

- Molecule 1: Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform



- Molecule 2: Phosphatidylinositol 3-kinase regulatory subunit alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.99Å 120.33Å 190.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.79 – 2.71 74.79 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.9 (74.79-2.71) 99.9 (74.79-2.71)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 2.73Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.259 , 0.288 0.261 , 0.287	Depositor DCC
R_{free} test set	2773 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	99.7	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 78.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20858	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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

5.1 Standard geometry

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	0.11	0/8347	0.26	0/11278
2	B	0.12	0/2296	0.24	0/3072
All	All	0.11	0/10643	0.25	0/14350

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

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	8165	8196	8189	32	0
2	B	2259	2238	2236	6	0
All	All	10424	10434	10425	38	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 2.

All (38) 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:B:433:GLN:OE1	2:B:579:GLN:NE2	2.27	0.68
1:A:805:ASP:N	1:A:805:ASP:OD1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:ASN:C	1:A:285:LEU:HD12	2.31	0.55
1:A:346:VAL:HG21	1:A:351:ILE:HD13	1.88	0.55
1:A:806:ASP:OD2	1:A:808:ARG:NH1	2.40	0.55
1:A:109:GLU:N	1:A:109:GLU:OE1	2.41	0.54
1:A:398:ARG:NH1	1:A:434:ASP:OD1	2.42	0.52
1:A:166:VAL:HG11	1:A:297:LEU:HD22	1.93	0.51
1:A:285:LEU:HD12	1:A:285:LEU:N	2.28	0.49
1:A:992:ARG:NH1	1:A:1027:ALA:O	2.46	0.49
1:A:195:TRP:CD2	1:A:789:MET:HE1	2.47	0.48
1:A:376:VAL:HG22	1:A:377:PRO:HD2	1.96	0.48
1:A:765:ARG:NH1	1:A:796:ASN:OD1	2.46	0.48
2:B:354:THR:HG22	2:B:426:TYR:HB2	1.94	0.48
1:A:199:SER:OG	1:A:203:ASP:OD1	2.18	0.48
2:B:356:LEU:HD11	2:B:428:VAL:HG21	1.96	0.46
1:A:599:MET:CE	1:A:1004:MET:HE1	2.46	0.46
1:A:209:LEU:HD12	1:A:209:LEU:N	2.31	0.46
1:A:404:LEU:C	1:A:404:LEU:HD12	2.41	0.46
2:B:371:THR:HG22	2:B:380:LEU:CD2	2.46	0.46
1:A:780:TRP:CH2	1:A:850:VAL:HG21	2.51	0.45
1:A:459:ILE:HG22	1:A:459:ILE:O	2.16	0.45
1:A:713:ILE:HA	1:A:716:THR:HG22	1.97	0.45
1:A:88:ARG:O	1:A:92:LEU:HD13	2.17	0.45
1:A:538:ASP:OD1	1:A:541:SER:OG	2.32	0.45
1:A:561:ILE:O	1:A:561:ILE:HG23	2.16	0.45
1:A:443:LEU:HD22	1:A:445:LEU:HD23	1.99	0.45
1:A:726:GLU:HB3	1:A:730:VAL:HG13	1.99	0.44
1:A:346:VAL:HG21	1:A:351:ILE:CD1	2.48	0.43
1:A:208:THR:C	1:A:209:LEU:HD12	2.43	0.43
2:B:394:ASP:OD1	2:B:394:ASP:N	2.47	0.43
1:A:561:ILE:O	1:A:564:ILE:HG22	2.19	0.43
2:B:581:LEU:O	2:B:581:LEU:HD23	2.20	0.42
1:A:326:SER:O	1:A:329:VAL:HG22	2.20	0.42
1:A:878:HIS:HB2	1:A:962:ILE:HD12	2.03	0.41
1:A:970:GLU:O	1:A:974:THR:HG23	2.20	0.41
1:A:156:LEU:O	1:A:157:ASN:HB2	2.20	0.40
1:A:145:ASN:OD1	1:A:146:VAL:N	2.54	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	987/1063 (93%)	953 (97%)	32 (3%)	2 (0%)	43	66
2	B	262/300 (87%)	254 (97%)	8 (3%)	0	100	100
All	All	1249/1363 (92%)	1207 (97%)	40 (3%)	2 (0%)	43	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	939	ASP
1	A	950	GLU

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	916/963 (95%)	910 (99%)	6 (1%)	76	89
2	B	247/277 (89%)	243 (98%)	4 (2%)	55	78
All	All	1163/1240 (94%)	1153 (99%)	10 (1%)	70	86

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	GLU
1	A	88	ARG
1	A	89	LEU
1	A	132	LYS

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Mol	Chain	Res	Type
1	A	478	ASP
1	A	602	LEU
2	B	431	TYR
2	B	452	TYR
2	B	551	LYS
2	B	579	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	444	ASN
1	A	556	HIS
1	A	682	GLN
1	A	917	HIS
2	B	406	ASN
2	B	478	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 oligosaccharides 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 ⓘ

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	997/1063 (93%)	0.53	51 (5%)	33 30	37, 118, 171, 229	9 (0%)
2	B	266/300 (88%)	1.01	40 (15%)	5 5	41, 152, 220, 244	12 (4%)
All	All	1263/1363 (92%)	0.63	91 (7%)	21 19	37, 122, 193, 244	21 (1%)

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	838	CYS	6.8
1	A	277	ILE	6.5
2	B	420	LEU	6.3
1	A	181	ILE	6.0
1	A	811	MET	5.7
2	B	401	VAL	5.5
2	B	405	ILE	5.3
2	B	422	VAL	5.1
1	A	719	LEU	4.9
1	A	531	LEU	4.5
1	A	417	GLU	4.3
1	A	692	CYS	4.2
2	B	584	LEU	4.0
1	A	257	CYS	3.9
1	A	14	HIS	3.8
2	B	404	LEU	3.7
1	A	11	TRP	3.6
2	B	357	VAL	3.6
1	A	728	GLN	3.5
2	B	445	VAL	3.5
1	A	126	CYS	3.5
1	A	1004	MET	3.5
1	A	942	LYS	3.3
2	B	353	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
2	B	589	VAL	3.2
1	A	989	LEU	3.1
2	B	370	LEU	3.0
1	A	709	MET	3.0
1	A	416	LYS	3.0
2	B	392	PHE	2.9
2	B	446	GLY	2.9
1	A	922	MET	2.8
1	A	997	LEU	2.8
2	B	426	TYR	2.8
1	A	279	LEU	2.8
1	A	839	LEU	2.8
2	B	421	ASP	2.8
1	A	736	VAL	2.7
2	B	478	GLN	2.6
2	B	431	TYR	2.6
2	B	424	LEU	2.5
2	B	588	GLY	2.5
1	A	734	PHE	2.5
1	A	735	LEU	2.5
2	B	394	ASP	2.5
2	B	549	LEU	2.5
2	B	463	TYR	2.5
1	A	771	ILE	2.5
2	B	449	LEU	2.5
1	A	925	ASP	2.4
1	A	225	ILE	2.4
1	A	715	LEU	2.4
2	B	539	ILE	2.4
1	A	442	ALA	2.4
2	B	442	ILE	2.3
2	B	425	LEU	2.3
1	A	718	ILE	2.3
2	B	429	SER	2.3
1	A	1051	TRP	2.3
1	A	239	LEU	2.3
1	A	443	LEU	2.3
2	B	356	LEU	2.3
2	B	581	LEU	2.3
1	A	952	VAL	2.3
1	A	926	ASP	2.2
2	B	326	MET	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	381	ILE	2.2
1	A	795	GLN	2.2
1	A	445	LEU	2.2
2	B	535	ILE	2.2
2	B	583	TRP	2.2
2	B	587	LYS	2.2
1	A	881	LEU	2.2
1	A	880	TRP	2.1
1	A	256	GLY	2.1
2	B	434	ASP	2.1
1	A	343	TYR	2.1
1	A	483	VAL	2.1
2	B	383	ILE	2.1
1	A	130	MET	2.1
1	A	832	ARG	2.0
2	B	369	THR	2.0
2	B	585	THR	2.0
1	A	463	GLY	2.0
1	A	823	ILE	2.0
2	B	467	TYR	2.0
2	B	573	LEU	2.0
1	A	936	HIS	2.0
1	A	198	VAL	2.0
1	A	500	VAL	2.0
1	A	557	TYR	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 oligosaccharides 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.