



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4HND  
Title : Crystal structure of the catalytic domain of Selenomethionine substituted human PI4KIIalpha in complex with ADP  
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Deposited on : 2012-10-19  
Resolution : 3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<http://wwpdb.org/validation/2016/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  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028442  
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-20028442

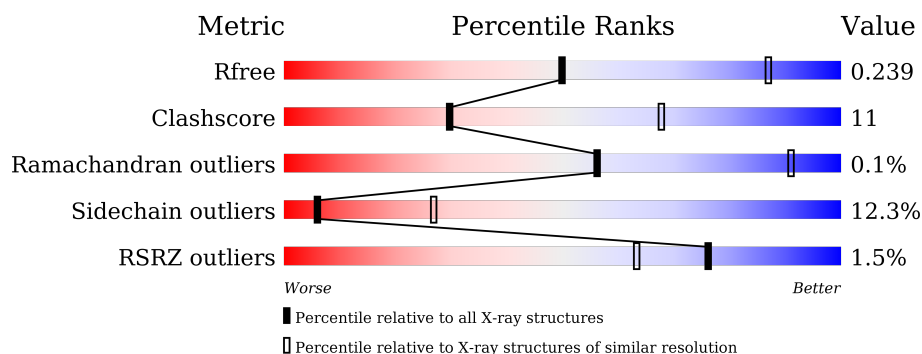
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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. 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	384	<div> <div> <div></div> <div>64%</div> <div>23%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	384	<div> <div> <div>2%</div> <div>64%</div> <div>22%</div> <div>•</div> <div>12%</div> </div> </div>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5649 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.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	Se	4	0	0
			2867	1853	498	511	3	2			
1	B	337	Total	C	N	O	S	Se	12	0	0
			2728	1763	467	493	3	2			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	70	GLY	-	EXPRESSION TAG	UNP Q9BTU6
A	71	PRO	-	EXPRESSION TAG	UNP Q9BTU6
A	72	LEU	-	EXPRESSION TAG	UNP Q9BTU6
A	73	GLY	-	EXPRESSION TAG	UNP Q9BTU6
A	74	SER	-	EXPRESSION TAG	UNP Q9BTU6
A	75	PRO	-	EXPRESSION TAG	UNP Q9BTU6
A	76	GLU	-	EXPRESSION TAG	UNP Q9BTU6
A	77	PHE	-	EXPRESSION TAG	UNP Q9BTU6
A	174	SER	CYS	ENGINEERED MUTATION	UNP Q9BTU6
A	175	SER	CYS	ENGINEERED MUTATION	UNP Q9BTU6
A	177	SER	CYS	ENGINEERED MUTATION	UNP Q9BTU6
A	178	SER	CYS	ENGINEERED MUTATION	UNP Q9BTU6
B	70	GLY	-	EXPRESSION TAG	UNP Q9BTU6
B	71	PRO	-	EXPRESSION TAG	UNP Q9BTU6
B	72	LEU	-	EXPRESSION TAG	UNP Q9BTU6
B	73	GLY	-	EXPRESSION TAG	UNP Q9BTU6
B	74	SER	-	EXPRESSION TAG	UNP Q9BTU6
B	75	PRO	-	EXPRESSION TAG	UNP Q9BTU6
B	76	GLU	-	EXPRESSION TAG	UNP Q9BTU6
B	77	PHE	-	EXPRESSION TAG	UNP Q9BTU6
B	174	SER	CYS	ENGINEERED MUTATION	UNP Q9BTU6
B	175	SER	CYS	ENGINEERED MUTATION	UNP Q9BTU6
B	177	SER	CYS	ENGINEERED MUTATION	UNP Q9BTU6
B	178	SER	CYS	ENGINEERED MUTATION	UNP Q9BTU6

- # ADP

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 27	C 10	N 5	O 10	P 2	0	0
2	B	1	Total 27	C 10	N 5	O 10	P 2	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	192.95Å 192.95Å 157.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	136.44 – 3.20 45.48 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (136.44-3.20) 99.8 (45.48-3.20)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.78 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.193 , 0.238 0.195 , 0.239	Depositor DCC
$R_{free}$ test set	1256 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	74.6	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 36.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5649	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP

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	0.59	5/2941 (0.2%)	0.64	0/3983
1	B	0.53	3/2799 (0.1%)	0.62	0/3796
All	All	0.56	8/5740 (0.1%)	0.63	0/7779

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	366	TRP	CD2-CE2	5.72	1.48	1.41
1	A	359	TRP	CD2-CE2	5.65	1.48	1.41
1	A	314	TRP	CD2-CE2	5.31	1.47	1.41
1	A	366	TRP	CD2-CE2	5.27	1.47	1.41
1	A	169	TRP	CD2-CE2	5.14	1.47	1.41

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	2867	0	2856	61	0
1	B	2728	0	2698	65	1
2	A	27	0	12	0	0
2	B	27	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5649	0	5578	125	1

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 11.

The worst 5 of 125 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:B:129:ARG:HD2	1:B:134:SER:O	1.42	1.19
1:A:280:GLU:HG2	1:A:280:GLU:O	1.48	1.08
1:B:130:ILE:CD1	1:B:139:PHE:CE2	2.42	1.02
1:A:402:TYR:O	1:A:406:LYS:HG2	1.64	0.95
1:B:130:ILE:CD1	1:B:139:PHE:CZ	2.51	0.93

All (1) 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)
1:B:361:ALA:O	1:B:361:ALA:O[8_555]	1.86	0.34

## 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	345/384 (90%)	331 (96%)	13 (4%)	1 (0%)	46	85
1	B	329/384 (86%)	312 (95%)	17 (5%)	0	100	100
All	All	674/768 (88%)	643 (95%)	30 (4%)	1 (0%)	56	91

All (1) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	164	PRO

### 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	303/329 (92%)	262 (86%)	41 (14%)	5	22
1	B	289/329 (88%)	257 (89%)	32 (11%)	8	32
All	All	592/658 (90%)	519 (88%)	73 (12%)	6	27

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	383	LEU
1	A	449	VAL
1	B	383	LEU
1	A	430	LEU
1	B	104	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	445	GLN
1	B	102	ASN
1	B	347	ASN
1	A	437	ASN
1	B	419	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

2 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	ADP	A	500	-	24,29,29	1.09	1 (4%)	23,45,45	1.90	4 (17%)
2	ADP	B	500	-	24,29,29	1.04	1 (4%)	23,45,45	1.83	1 (4%)

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	ADP	A	500	-	-	0/12/32/32	0/3/3/3
2	ADP	B	500	-	-	0/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	ADP	C5-C4	3.31	1.48	1.40
2	A	500	ADP	C5-C4	3.38	1.48	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	B	500	ADP	N3-C2-N1	-6.89	123.46	128.87
2	A	500	ADP	N3-C2-N1	-6.23	123.98	128.87
2	A	500	ADP	O3B-PB-O2B	2.21	115.55	107.44
2	A	500	ADP	O5'-C5'-C4'	2.48	118.05	109.09
2	A	500	ADP	C4'-O4'-C1'	3.20	113.03	109.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	351/384 (91%)	-0.19	4 (1%)	82 72	41, 68, 138, 202	1 (0%)
1	B	335/384 (87%)	-0.00	6 (1%)	71 58	41, 76, 151, 226	3 (0%)
All	All	686/768 (89%)	-0.10	10 (1%)	76 63	41, 72, 150, 226	4 (0%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	452	GLU	5.1
1	B	451	VAL	4.8
1	B	133	GLY	4.7
1	A	169	TRP	3.7
1	B	134	SER	2.9

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	ADP	A	500	27/27	0.84	0.29	1.21	72,79,140,146	0
2	ADP	B	500	27/27	0.81	0.28	0.76	104,109,138,149	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.