



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:41 PM GMT

PDB ID : 1Q62  
Title : PKA double mutant model of PKB  
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Deposited on : 2003-08-12  
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](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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

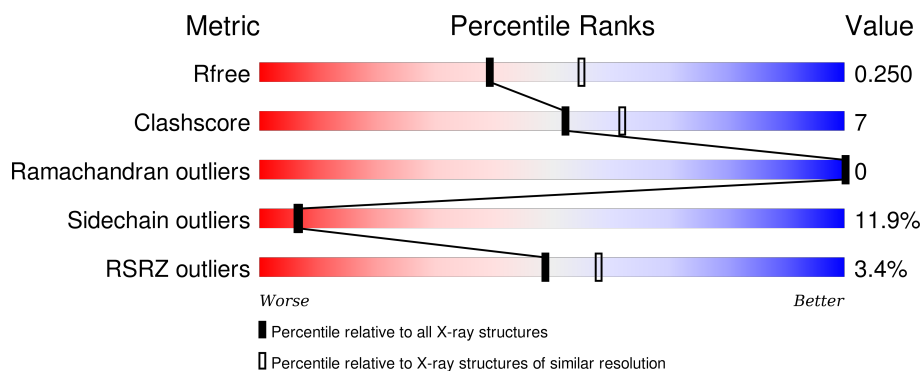
# 1 Overall quality at a glance

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))
$R_{free}$	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (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  $\geq 3$ , 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	350	 3% 75% 19% ...
2	I	20	 10% 85% 10% 5%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3057 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 cAMP-dependent protein kinase, alpha-catalytic subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	P	S	66	0	0
			2793	1808	468	505	2	10			

There are 4 discrepancies between the modelled and reference sequences:

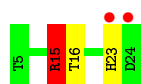
Chain	Residue	Modelled	Actual	Comment	Reference
A	123	ALA	VAL	ENGINEERED	UNP P00517
A	173	MET	LEU	ENGINEERED	UNP P00517
A	197	TPO	THR	MODIFIED RESIDUE	UNP P00517
A	338	SEP	SER	MODIFIED RESIDUE	UNP P00517

- Molecule 2 is a protein called cAMP-dependent protein kinase inhibitor, alpha form.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	20	Total	C	N	O	3	0	0
			157	94	32	31			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	95	Total	O	0	0
			95	95		
3	I	12	Total	O	0	0
			12	12		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.30Å 75.27Å 80.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.30 8.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.2 (8.00-2.30) 97.2 (8.00-2.30)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.91 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.185 , 0.252 0.196 , 0.250	Depositor DCC
$R_{free}$ test set	1970 reflections (11.45%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.8	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.1	EDS
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 19181 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3057	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.40% 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, 0.375 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: TPO, SEP

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	0.91	1/2843 (0.0%)	0.98	11/3828 (0.3%)
2	I	1.01	0/159	1.22	2/212 (0.9%)
All	All	0.91	1/3002 (0.0%)	0.99	13/4040 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	230	GLU	CD-OE2	-5.83	1.19	1.25

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	ARG	NE-CZ-NH1	9.33	124.97	120.30
1	A	133	ARG	NE-CZ-NH2	-9.32	115.64	120.30
1	A	328	ASP	CB-CG-OD2	8.55	126.00	118.30
1	A	184	ASP	CB-CG-OD2	7.76	125.29	118.30
2	I	15	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	A	104	VAL	CB-CA-C	-6.99	98.13	111.40
2	I	15	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	A	191	VAL	CB-CA-C	-5.72	100.53	111.40
1	A	339	ILE	CB-CG1-CD1	5.59	129.56	113.90
1	A	175	ASP	CB-CG-OD1	5.53	123.28	118.30
1	A	308	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	A	308	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	A	267	ASP	CB-CG-OD2	5.01	122.81	118.30

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	2793	0	2766	38	0
2	I	157	0	146	4	0
3	A	95	0	0	3	0
3	I	12	0	0	0	0
All	All	3057	0	2912	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 7.

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)
1:A:56:ARG:HH12	1:A:333:GLU:HB2	1.55	0.71
1:A:56:ARG:NH1	1:A:333:GLU:HB2	2.08	0.69
1:A:208:GLU:HG3	1:A:277:LEU:HD11	1.78	0.66
1:A:208:GLU:HG2	1:A:277:LEU:HD21	1.77	0.65
1:A:41:ASP:O	1:A:63:MET:CE	2.48	0.62
1:A:56:ARG:HD3	3:A:388:HOH:O	2.00	0.61
1:A:198:LEU:HD23	1:A:209:ILE:HG22	1.86	0.58
1:A:210:ILE:HD13	1:A:247:TYR:HB3	1.85	0.57
1:A:158:HIS:HE1	1:A:220:ASP:OD2	1.88	0.56
1:A:56:ARG:HH12	1:A:333:GLU:CB	2.18	0.56
1:A:104:VAL:HG22	1:A:182:VAL:O	2.05	0.56
1:A:41:ASP:O	1:A:63:MET:HE1	2.08	0.53
1:A:54:PHE:CZ	2:I:23:HIS:CE1	2.97	0.53
1:A:198:LEU:HD23	1:A:209:ILE:CG2	2.39	0.52
1:A:54:PHE:HZ	2:I:23:HIS:CE1	2.28	0.51
1:A:56:ARG:NH2	1:A:333:GLU:HB2	2.25	0.51
1:A:242:GLN:HG2	1:A:245:GLN:OE1	2.12	0.50
1:A:139:SER:HB2	1:A:141:PRO:HD2	1.95	0.49
1:A:56:ARG:NH1	1:A:333:GLU:CB	2.76	0.48
1:A:56:ARG:HH22	1:A:333:GLU:HB2	1.77	0.48
1:A:208:GLU:CG	1:A:277:LEU:HD21	2.43	0.48
1:A:56:ARG:CZ	1:A:333:GLU:HB2	2.42	0.48
1:A:203:GLU:OE2	2:I:15:ARG:HD3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:GLY:O	1:A:56:ARG:HB2	2.14	0.47
1:A:195:THR:OG1	1:A:197:TPO:O2P	2.26	0.46
1:A:133:ARG:HD2	2:I:16:THR:O	2.17	0.44
1:A:271:ASN:HB3	1:A:281:PHE:CD1	2.52	0.44
1:A:104:VAL:HG13	1:A:181:GLN:CD	2.38	0.43
1:A:43:PHE:HB3	1:A:60:VAL:HG13	2.01	0.43
1:A:126:GLY:HA2	1:A:327:PHE:CZ	2.54	0.43
1:A:277:LEU:CD2	3:A:442:HOH:O	2.68	0.42
1:A:104:VAL:HG13	1:A:181:GLN:OE1	2.19	0.42
1:A:74:LEU:HD21	1:A:118:MET:HE2	2.01	0.41
1:A:288:VAL:HG22	1:A:288:VAL:O	2.20	0.41
1:A:77:GLN:NE2	3:A:408:HOH:O	2.52	0.40
1:A:342:LYS:HD3	1:A:342:LYS:HA	1.78	0.40
1:A:142:HIS:CD2	1:A:146:TYR:CE2	3.09	0.40
1:A:191:VAL:O	1:A:217:LYS:NZ	2.49	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	334/350 (95%)	318 (95%)	16 (5%)	0	100	100
2	I	18/20 (90%)	17 (94%)	1 (6%)	0	100	100
All	All	352/370 (95%)	335 (95%)	17 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	296/302 (98%)	260 (88%)	36 (12%)	6	6
2	I	15/15 (100%)	14 (93%)	1 (7%)	20	26
All	All	311/317 (98%)	274 (88%)	37 (12%)	6	7

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	SER
1	A	16	LYS
1	A	17	GLU
1	A	19	LEU
1	A	27	LEU
1	A	32	ASN
1	A	40	LEU
1	A	51	THR
1	A	53	SER
1	A	54	PHE
1	A	56	ARG
1	A	59	LEU
1	A	64	GLU
1	A	74	LEU
1	A	83	LYS
1	A	95	LEU
1	A	104	VAL
1	A	114	SER
1	A	160	LEU
1	A	162	LEU
1	A	191	VAL
1	A	198	LEU
1	A	210	ILE
1	A	229	TYR
1	A	244	ILE
1	A	268	LEU
1	A	269	LEU
1	A	272	LEU
1	A	278	THR
1	A	285	LYS
1	A	295	LYS

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Mol	Chain	Res	Type
1	A	299	THR
1	A	311	GLU
1	A	317	LYS
1	A	318	PHE
1	A	339	ILE
2	I	15	ARG

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

Mol	Chain	Res	Type
1	A	62	HIS
1	A	67	ASN
1	A	77	GLN
1	A	113	ASN
1	A	158	HIS
1	A	176	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	TPO	A	197	1	8,10,11	0.93	0	7,14,16	1.30	1 (14%)
1	SEP	A	338	1	8,9,10	1.50	1 (12%)	8,12,14	2.13	3 (37%)

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
1	TPO	A	197	1	-	0/8/11/13	0/0/0/0
1	SEP	A	338	1	-	0/6/8/10	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	338	SEP	P-O1P	3.22	1.61	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	338	SEP	O-C-CA	-2.11	119.99	125.49
1	A	197	TPO	O3P-P-O2P	2.29	116.09	107.38
1	A	338	SEP	O2P-P-OG	2.62	114.10	106.56
1	A	338	SEP	OG-CB-CA	4.22	111.87	108.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	197	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates 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, 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	336/350 (96%)	-0.04	10 (2%) 54 63	29, 44, 66, 73	23 (6%)
2	I	20/20 (100%)	-0.04	2 (10%) 9 14	33, 36, 66, 73	2 (10%)
All	All	356/370 (96%)	-0.04	12 (3%) 49 58	29, 44, 66, 73	25 (7%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	13	GLU	6.8
2	I	24	ASP	3.9
1	A	321	PRO	3.7
1	A	31	GLU	3.3
1	A	17	GLU	2.9
1	A	14	SER	2.8
1	A	20	ALA	2.8
1	A	253	GLY	2.8
1	A	24	GLU	2.8
2	I	23	HIS	2.6
1	A	340	ASN	2.5
1	A	318	PHE	2.4

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

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(Å <sup>2</sup> )	Q<0.9
1	SEP	A	338	10/11	0.91	0.16	-	65,65,67,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	TPO	A	197	11/12	0.97	0.10	-	28,30,32,33	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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.