



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:46 PM GMT

PDB ID : 1QL6
Title : THE CATALYTIC MECHANISM OF PHOSPHORYLASE KINASE
PROBED BY MUTATIONAL STUDIES
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Johnson, L.N.
Deposited on : 1999-08-24
Resolution : 2.40 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 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

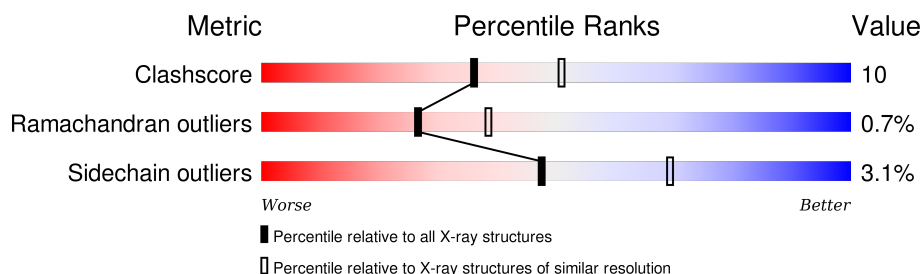
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	298	 60% 32% •• 6%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2412 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.

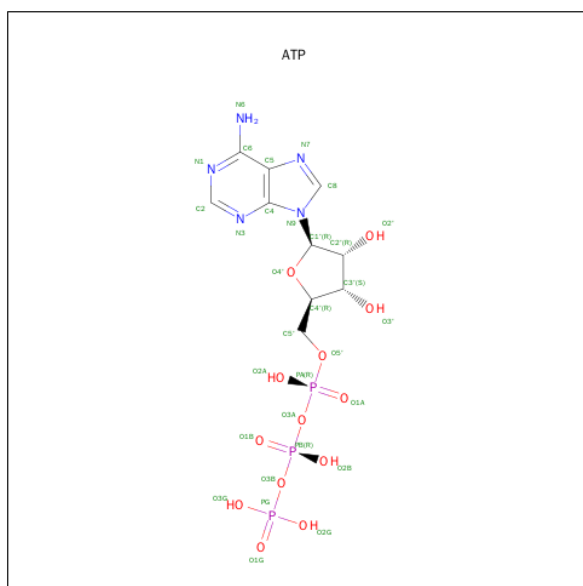
- Molecule 1 is a protein called PHOSPHORYLASE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	281	2270	1453	377	424	16	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	182	SER	GLU	ENGINEERED	UNP P00518

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mn	0	0
			2	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	98	Total	O	0	0
			98	98		
5	B	5	Total	O	0	0
			5	5		
5	C	1	Total	O	0	0
			1	1		

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	47.56 Å 68.17 Å 112.47 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40	Depositor
% Data completeness (in resolution range)	86.6 (20.00-2.40)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.05	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.240 , 0.330	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2412	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MN, SO4, ATP

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	0.65	0/2322	1.79	43/3137 (1.4%)

There are no bond length outliers.

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	ARG	NE-CZ-NH2	-18.77	110.91	120.30
1	A	127	ARG	NE-CZ-NH1	-13.93	113.34	120.30
1	A	175	ASP	CB-CG-OD1	12.50	129.55	118.30
1	A	275	ARG	CD-NE-CZ	10.56	138.38	123.60
1	A	35	ARG	NE-CZ-NH1	-10.55	115.03	120.30
1	A	275	ARG	NE-CZ-NH1	9.62	125.11	120.30
1	A	266	ARG	NE-CZ-NH2	-8.49	116.06	120.30
1	A	178	GLU	OE1-CD-OE2	-8.45	113.17	123.30
1	A	127	ARG	NH1-CZ-NH2	8.35	128.59	119.40
1	A	27	ARG	NE-CZ-NH2	8.33	124.47	120.30
1	A	34	ARG	NE-CZ-NH1	8.33	124.46	120.30
1	A	167	ASP	CB-CG-OD1	7.84	125.36	118.30
1	A	260	VAL	CB-CA-C	-7.84	96.51	111.40
1	A	148	ARG	NE-CZ-NH2	-7.68	116.46	120.30
1	A	16	TYR	CB-CG-CD2	7.19	125.32	121.00
1	A	93	TYR	CB-CG-CD1	-7.04	116.78	121.00
1	A	35	ARG	NH1-CZ-NH2	7.04	127.14	119.40
1	A	44	GLU	OE1-CD-OE2	-6.83	115.10	123.30
1	A	23	GLU	OE1-CD-OE2	-6.82	115.12	123.30
1	A	275	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	A	158	ASP	CB-CG-OD2	6.37	124.03	118.30
1	A	249	GLY	N-CA-C	6.37	129.03	113.10
1	A	114	TYR	CB-CG-CD1	6.14	124.68	121.00
1	A	59	SER	N-CA-CB	6.10	119.64	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	THR	N-CA-CB	6.07	121.83	110.30
1	A	178	GLU	CA-CB-CG	5.95	126.49	113.40
1	A	131	ARG	NE-CZ-NH1	-5.89	117.35	120.30
1	A	131	ARG	CD-NE-CZ	5.87	131.82	123.60
1	A	125	GLU	OE1-CD-OE2	-5.73	116.42	123.30
1	A	20	GLU	OE1-CD-OE2	-5.66	116.51	123.30
1	A	91	ASP	CB-CG-OD2	5.62	123.36	118.30
1	A	256	TYR	CB-CG-CD2	5.56	124.34	121.00
1	A	141	HIS	CB-CA-C	5.55	121.50	110.40
1	A	173	GLN	CA-CB-CG	5.35	125.16	113.40
1	A	279	GLU	OE1-CD-OE2	5.23	129.57	123.30
1	A	262	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	153	GLU	CG-CD-OE1	5.20	128.71	118.30
1	A	27	ARG	NE-CZ-NH1	-5.16	117.72	120.30
1	A	35	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	A	268	LEU	C-N-CA	5.10	134.46	121.70
1	A	224	ALA	CB-CA-C	-5.08	102.47	110.10
1	A	193	GLU	OE1-CD-OE2	-5.08	117.20	123.30
1	A	132	ALA	N-CA-CB	5.03	117.14	110.10

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	2270	0	2253	44	0
2	B	31	0	12	0	0
3	B	2	0	0	0	0
4	C	5	0	0	0	0
5	A	98	0	0	1	0
5	B	5	0	0	0	0
5	C	1	0	0	0	0
All	All	2412	0	2265	44	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 10.

All (44) 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:250:SER:HB3	1:A:251:PRO:CD	1.99	0.92
1:A:250:SER:HB3	1:A:251:PRO:HD3	1.49	0.91
1:A:175:ASP:HB3	1:A:176:PRO:HD2	1.72	0.70
1:A:12:THR:OG1	1:A:95:THR:HG21	1.93	0.69
1:A:219:MET:HG2	1:A:264:VAL:HG22	1.73	0.69
1:A:230:TRP:HA	1:A:237:MET:HE2	1.74	0.69
1:A:11:SER:OG	1:A:95:THR:HG22	1.93	0.68
1:A:250:SER:CB	1:A:251:PRO:CD	2.72	0.67
1:A:260:VAL:HG13	1:A:286:PHE:CE1	2.30	0.67
1:A:284:HIS:CG	1:A:285:PRO:HD2	2.35	0.61
1:A:154:ASN:O	1:A:166:THR:HG22	2.03	0.59
1:A:251:PRO:HD2	1:A:252:GLU:OE1	2.02	0.59
1:A:138:CYS:O	1:A:142:LYS:HG3	2.04	0.58
1:A:33:VAL:HG22	1:A:48:LYS:HB2	1.86	0.57
1:A:218:ILE:O	1:A:222:LEU:HG	2.07	0.55
1:A:72:LYS:HG2	5:A:2062:HOH:O	2.06	0.55
1:A:181:ARG:NH2	1:A:203:HIS:O	2.39	0.54
1:A:175:ASP:HB3	1:A:176:PRO:CD	2.38	0.54
1:A:41:THR:O	1:A:42:CYS:HB2	2.08	0.54
1:A:48:LYS:HE2	1:A:50:ILE:HD11	1.91	0.53
1:A:52:VAL:HG22	1:A:97:THR:O	2.11	0.51
1:A:13:HIS:O	1:A:17:GLU:N	2.37	0.51
1:A:156:LEU:O	1:A:163:ILE:HA	2.10	0.50
1:A:51:ASP:OD2	1:A:55:GLY:N	2.43	0.50
1:A:59:SER:O	1:A:60:ALA:C	2.51	0.48
1:A:15:PHE:CZ	1:A:47:VAL:HG21	2.48	0.48
1:A:231:HIS:ND1	1:A:232:ARG:N	2.62	0.48
1:A:174:LEU:HD21	1:A:180:LEU:HD11	1.96	0.47
1:A:266:ARG:O	1:A:276:TYR:HB2	2.14	0.47
1:A:187:PRO:HA	1:A:190:LEU:HD12	1.97	0.46
1:A:138:CYS:SG	1:A:279:GLU:HG2	2.55	0.45
1:A:271:GLN:OE1	1:A:273:GLN:OE1	2.36	0.44
1:A:83:HIS:CG	1:A:84:PRO:HD2	2.52	0.44
1:A:87:ILE:HD12	1:A:87:ILE:HA	1.74	0.43
1:A:53:THR:HG22	1:A:56:GLY:H	1.83	0.43
1:A:27:ARG:HG2	1:A:32:VAL:HG22	2.00	0.43
1:A:233:LYS:HE2	1:A:233:LYS:HB3	1.83	0.43
1:A:183:VAL:HG21	1:A:198:SER:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:PRO:HA	1:A:288:GLN:HG2	2.02	0.42
1:A:220:TYR:CD1	1:A:228:PRO:HD3	2.55	0.42
1:A:230:TRP:HA	1:A:237:MET:CE	2.47	0.42
1:A:67:ARG:CZ	1:A:71:LEU:HD11	2.50	0.41
1:A:271:GLN:HB3	1:A:273:GLN:OE1	2.20	0.41
1:A:157:LEU:HD13	1:A:161:MET:CE	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	279/298 (94%)	262 (94%)	15 (5%)	2 (1%)	26	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	59	SER
1	A	250	SER

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	254/268 (95%)	246 (97%)	8 (3%)	47	69

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	GLU
1	A	66	LEU
1	A	88	GLN
1	A	96	ASN
1	A	138	CYS
1	A	260	VAL
1	A	276	TYR
1	A	291	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	271	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 ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	ATP	B	381	3	24,33,33	1.40	3 (12%)	31,52,52	1.99	7 (22%)
4	SO4	C	401	-	4,4,4	1.00	0	6,6,6	0.43	0

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	ATP	B	381	3	-	0/18/38/38	0/3/3/3
4	SO4	C	401	-	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	381	ATP	C8-N7	-2.78	1.29	1.34
2	B	381	ATP	C5-N7	-2.46	1.31	1.39
2	B	381	ATP	C2-N1	3.03	1.39	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	381	ATP	N3-C2-N1	-5.01	125.06	128.89
2	B	381	ATP	O3A-PA-O5'	-2.06	97.46	102.94
2	B	381	ATP	C4'-O4'-C1'	2.05	111.97	109.72
2	B	381	ATP	O3'-C3'-C2'	2.41	119.66	111.83
2	B	381	ATP	C4-C5-N7	3.15	112.38	109.48
2	B	381	ATP	O4'-C1'-N9	4.56	117.64	108.10
2	B	381	ATP	C1'-N9-C4	5.25	134.86	126.94

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 ⓘ

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.