



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:04 PM UTC

PDB ID : 2EXE / pdb_00002exe
Title : Crystal structure of the phosphorylated CLK3
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Deposited on : 2005-11-08
Resolution : 2.35 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
Xtrriage (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

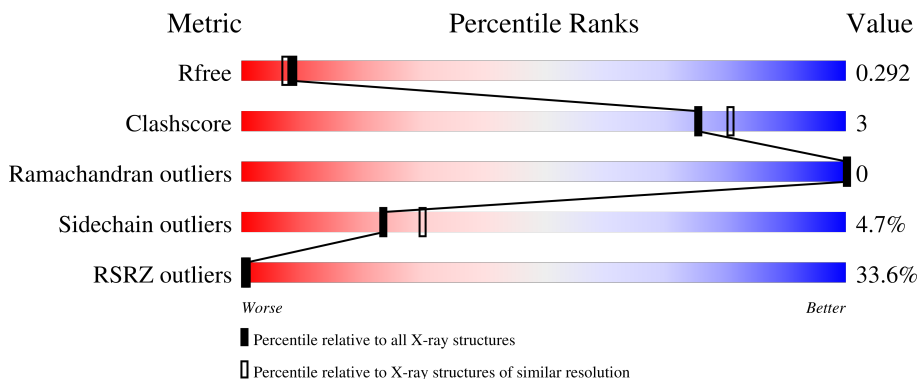
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	357	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2195 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 Dual specificity protein kinase CLK3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	262	2097	1356	355	373	13	0	2	0

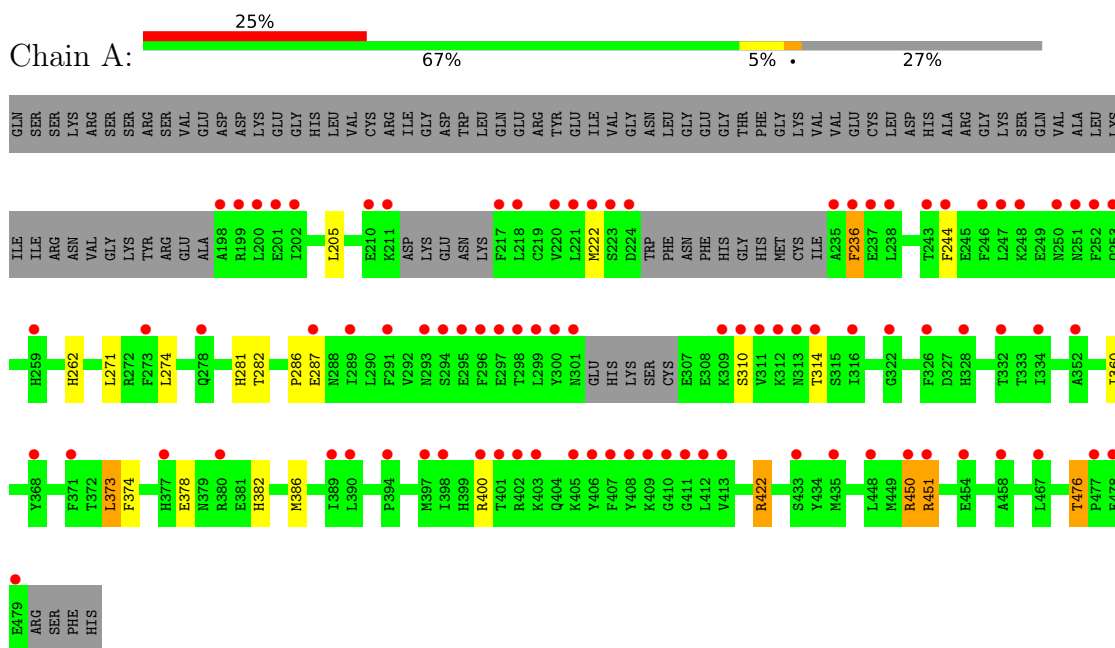
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	96	Total	O	0	2
			98	98		

3 Residue-property plots [i](#)

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: Dual specificity protein kinase CLK3



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	62.18Å 111.00Å 161.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.82 – 2.35 32.82 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.7 (32.82-2.35) 99.6 (32.82-2.35)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.31Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.225 , 0.260 (Not available) , 0.292	Depositor DCC
R_{free} test set	1237 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	40.2	Xtrriage
Anisotropy	0.656	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	2195	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.57	0/2159	0.83	2/2928 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	476	THR	OG1-CB-CG2	6.56	122.42	109.30
1	A	476	THR	CA-CB-CG2	6.06	120.80	110.50

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	476	THR	CB

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	2097	0	1968	12	0
2	A	98	0	0	0	0
All	All	2195	0	1968	12	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 3.

All (12) 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:262:HIS:ND1	1:A:314:THR:HG23	2.11	0.65
1:A:236:PHE:CD1	1:A:236:PHE:N	2.71	0.58
1:A:422:ARG:HH11	1:A:422:ARG:HA	1.69	0.58
1:A:271:LEU:HD13	1:A:360:ILE:HD11	1.88	0.56
1:A:373:LEU:HD13	1:A:374:PHE:CE2	2.47	0.49
1:A:244:PHE:HB2	1:A:286:PRO:HB2	1.95	0.48
1:A:450:ARG:HD3	1:A:451:ARG:HG2	1.95	0.48
1:A:281:HIS:O	1:A:282:THR:OG1	2.33	0.45
1:A:205:LEU:HD13	1:A:222:MET:HG3	1.98	0.45
1:A:382:HIS:CD2	1:A:386:MET:HE3	2.54	0.42
1:A:262:HIS:ND1	1:A:314:THR:CG2	2.81	0.42
1:A:287[B]:GLU:H	1:A:287[B]:GLU:CD	2.27	0.41

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	256/357 (72%)	246 (96%)	10 (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	214/323 (66%)	204 (95%)	10 (5%)	23 30

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

Mol	Chain	Res	Type
1	A	236	PHE
1	A	274	LEU
1	A	310	SER
1	A	373	LEU
1	A	378	GLU
1	A	400	ARG
1	A	422	ARG
1	A	450	ARG
1	A	451	ARG
1	A	476	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	328	HIS
1	A	427	ASN

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 [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, 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	262/357 (73%)	1.71	88 (33%) 1 0	33, 55, 76, 107	2 (0%)

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	300	TYR	7.8
1	A	198	ALA	7.5
1	A	235	ALA	7.5
1	A	217	PHE	6.3
1	A	224	ASP	6.2
1	A	477	PRO	5.5
1	A	243	THR	4.7
1	A	296	PHE	4.5
1	A	328	HIS	4.2
1	A	297	GLU	4.1
1	A	278	GLN	4.0
1	A	301	ASN	3.8
1	A	252	PHE	3.7
1	A	389	ILE	3.7
1	A	237	GLU	3.6
1	A	410	GLY	3.6
1	A	298	THR	3.5
1	A	236	PHE	3.5
1	A	380	ARG	3.5
1	A	202	ILE	3.4
1	A	200	LEU	3.3
1	A	406	TYR	3.3
1	A	211	LYS	3.3
1	A	408	TYR	3.3
1	A	401	THR	3.2
1	A	402	ARG	3.2
1	A	397	MET	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	394	PRO	3.1
1	A	314	THR	3.1
1	A	310	SER	3.1
1	A	313	ASN	3.1
1	A	299	LEU	3.1
1	A	223	SER	3.0
1	A	294	SER	3.0
1	A	311	VAL	3.0
1	A	248	LYS	3.0
1	A	291	PHE	3.0
1	A	244	PHE	2.9
1	A	289	ILE	2.9
1	A	312	LYS	2.9
1	A	450	ARG	2.9
1	A	411	GLY	2.8
1	A	435	MET	2.7
1	A	400	ARG	2.7
1	A	222	MET	2.7
1	A	218	LEU	2.7
1	A	246	PHE	2.7
1	A	250	ASN	2.7
1	A	293	ASN	2.7
1	A	413	VAL	2.7
1	A	221	LEU	2.6
1	A	295	GLU	2.6
1	A	478	GLU	2.6
1	A	409	LYS	2.6
1	A	407	PHE	2.4
1	A	405	LYS	2.4
1	A	451	ARG	2.4
1	A	247	LEU	2.4
1	A	259	HIS	2.4
1	A	377	HIS	2.4
1	A	287[A]	GLU	2.3
1	A	251	ASN	2.3
1	A	199	ARG	2.3
1	A	238	LEU	2.3
1	A	368	TYR	2.3
1	A	332	THR	2.3
1	A	398	ILE	2.3
1	A	467	LEU	2.2
1	A	352	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	334	ILE	2.2
1	A	454	GLU	2.2
1	A	210	GLU	2.2
1	A	403	LYS	2.2
1	A	458	ALA	2.2
1	A	220	VAL	2.2
1	A	371	PHE	2.2
1	A	390	LEU	2.1
1	A	201	GLU	2.1
1	A	309	LYS	2.1
1	A	253	GLN	2.1
1	A	433	SER	2.1
1	A	412	LEU	2.1
1	A	448	LEU	2.1
1	A	322	GLY	2.1
1	A	326	PHE	2.1
1	A	316	ILE	2.0
1	A	273	PHE	2.0
1	A	479	GLU	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.