WORLDWIDE PDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Aug 12, 2014 – 11:00 PM EDT

PDB ID   :   4MLU
Title   :   Peptides Containing Mono-anionic Phosphothreonine Esters That Exhibit High Plk1 Polo-box Domain-binding Affinities and Potent Antiproliferative Effects in HeLa Cells
Authors   :   Qian, W.-J.; Park, J.-E.; Lim, D.C.; Park, S.-Y.; Lee, K.-W.; Yaffe, M.B.; Lee, K.S.; Burke, T.R.
Deposited on :   2013-09-06
Resolution :   1.45 Å(reported)

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 1.45 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	Percentile Ranks	Value
Rfree		0.220
Clashscore		8
Ramachandran outliers		0
Sidechain outliers		3.5%
RSRZ outliers		2.3%

Worse   *Better*

▮ Percentile relative to all X–ray structures

▯ Percentile relative to X–ray structures of similar resolution
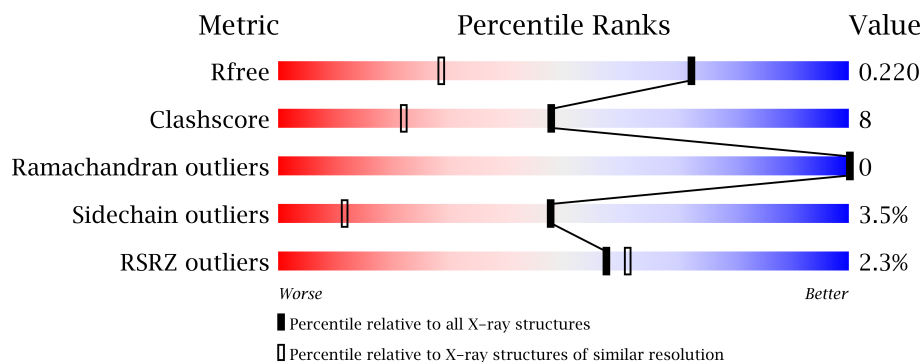
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1819 (1.48-1.40)
Clashscore	79885	2050 (1.48-1.40)
Ramachandran outliers	78287	2002 (1.48-1.40)
Sidechain outliers	78261	2001 (1.48-1.40)
RSRZ outliers	66119	1819 (1.48-1.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	237	
2	B	7	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2044 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Serine/threonine-proteinkinase PLK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total 1770	C 1123	N 312	O 325	S 10	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	367	GLY	-	EXPRESSION TAG	UNP P53350
A	368	ALA	-	EXPRESSION TAG	UNP P53350
A	369	HIS	-	EXPRESSION TAG	UNP P53350
A	370	MET	-	EXPRESSION TAG	UNP P53350

- Molecule 2 is a protein called Phosphothreonine ester-containing peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	7	Total 73	C 48	N 8	O 16	P 1	0	1	1

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	187	Total 187	O 187	0	0
3	B	14	Total 14	O 14	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Serine/threonine-proteinkinase PLK1

Chain A:

- Molecule 2: Phosphothreonine ester-containing peptide

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	35.82Å 51.27Å 58.01Å 90.00° 101.19° 90.00°	Depositor
Resolution (Å)	14.86 – 1.45 14.86 – 1.45	Depositor EDS
% Data completeness (in resolution range)	96.1 (14.86-1.45) 94.1 (14.86-1.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.78 (at 1.45Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.191 , 0.222 0.190 , 0.220	Depositor DCC
R_{free} test set	1958 reflections (5.66%)	DCC
Wilson B-factor (Å^2)	19.6	Xtriage
Anisotropy	0.396	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 41.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Outliers	0 of 35358 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	2044	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.10% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 28X, NH2, ACE, 56A

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	0.35	0/1813	0.55	0/2448
2	B	0.61	0/21	1.30	0/27
All	All	0.35	0/1834	0.56	0/2475

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1770	0	1766	24	0
2	B	73	0	71	15	0
3	A	187	0	0	6	1
3	B	14	0	0	0	0
All	All	2044	0	1837	29	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

All (29) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:493:ALA:HB2	2:B:6[B]:28X:H71	1.53	0.91
1:A:560:ARG:NH1	3:A:872:HOH:O	2.18	0.77
1:A:540:LYS:HE2	2:B:6[B]:28X:H70	1.68	0.75
1:A:457:ASP:OD1	3:A:884:HOH:O	2.11	0.68
1:A:540:LYS:CE	2:B:6[B]:28X:H70	2.33	0.59
1:A:384:VAL:HA	1:A:568:GLU:HG2	1.89	0.55
1:A:556:LYS:NZ	1:A:558:ASP:OD2	2.40	0.54
1:A:493:ALA:CB	2:B:6[B]:28X:H71	2.33	0.53
1:A:540:LYS:HE2	2:B:6[B]:28X:C67	2.36	0.52
1:A:493:ALA:HB2	2:B:6[B]:28X:C67	2.34	0.52
1:A:557[A]:ARG:NE	2:B:6[A]:28X:H70	2.25	0.52
1:A:560:ARG:NH2	3:A:781:HOH:O	2.41	0.51
1:A:584:ARG:NE	1:A:588:ASP:OD2	2.42	0.51
1:A:373:HIS:N	3:A:848:HOH:O	2.42	0.51
2:B:4:56A:HD2	2:B:5:SER:O	2.12	0.49
3:A:704:HOH:O	2:B:6[A]:28X:H71	2.16	0.45
1:A:557[A]:ARG:HE	2:B:6[A]:28X:H70	1.81	0.45
1:A:404:ALA:O	1:A:500:ARG:NH1	2.50	0.44
1:A:414:TRP:CD1	2:B:5:SER:HB3	2.52	0.44
1:A:388:LYS:HD2	1:A:391:GLU:OE2	2.18	0.42
1:A:512:ARG:HG3	1:A:513:THR:HG23	2.02	0.42
1:A:567:LEU:HD22	1:A:572:CYS:HB3	2.00	0.42
3:A:710:HOH:O	2:B:6[B]:28X:H66	2.19	0.42
1:A:557[A]:ARG:HH21	2:B:6[A]:28X:H68	1.84	0.42
1:A:444:LEU:HD23	1:A:483:ARG:HD2	2.02	0.42
1:A:472:LEU:HD23	1:A:472:LEU:HA	1.93	0.41
1:A:432:VAL:HG22	1:A:444:LEU:HB3	2.03	0.40

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	Distance(Å)	Clash(Å)
3:A:829:HOH:O	3:A:871:HOH:O[2_556]	2.19	0.01

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	213/237 (90%)	207 (97%)	6 (3%)	0	100	100
2	B	3/7 (43%)	3 (100%)	0	0	100	100
All	All	216/244 (88%)	210 (97%)	6 (3%)	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	198/212 (93%)	191 (96%)	7 (4%)	48	11
2	B	3/3 (100%)	3 (100%)	0	100	100
All	All	201/215 (94%)	194 (96%)	7 (4%)	48	11

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	379	GLN
1	A	417	TYR
1	A	456	ARG
1	A	463	LEU
1	A	512	ARG
1	A	584	ARG
1	A	591	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

3 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	#$|Z| > 2$
2	56A	B	4	2	25,25,26	3.37	1 (4%)	28,30,32	1.80	5 (17%)
2	28X	B	6[A]	-	6,6,17	0.66	0	6,6,23	1.59	1 (16%)
2	28X	B	6[B]	-	6,6,17	0.66	0	6,6,23	1.34	2 (33%)

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	56A	B	4	2	-	0/15/17/19	0/2/2/2
2	28X	B	6[A]	-	-	0/5/5/22	0/0/0/0
2	28X	B	6[B]	-	-	0/5/5/22	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	4	56A	O-C	16.62	1.22	1.11

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	4	56A	C-CA-N	-7.60	106.24	113.83
2	B	6[A]	28X	C63-C64-C67	-2.96	105.09	111.80
2	B	4	56A	C28-C27-ND1	-2.31	107.88	112.43
2	B	4	56A	CD2-NE2-CE1	2.30	109.32	105.79
2	B	6[B]	28X	O68-C67-C64	2.21	120.17	110.37
2	B	4	56A	CE1-ND1-CG	-2.18	106.60	110.40
2	B	6[B]	28X	O61-C62-C63	-2.06	106.82	114.21
2	B	4	56A	CB-CG-CD2	-2.02	126.95	130.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 ⓘ

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	216/237 (91%)	0.15	5 (2%)	57	61	10, 17, 28, 38	0
2	B	5/7 (71%)	-0.21	0	100	100	14, 18, 21, 24	0
All	All	221/244 (90%)	0.14	5 (2%)	57	61	10, 18, 27, 38	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	456	ARG	3.7
1	A	500	ARG	3.4
1	A	507	ARG	3.2
1	A	499	PRO	2.6
1	A	393	GLY	2.5

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, 95th 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	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	28X	B	6[A]	7/18	0.15	4.54	13,14,22,23	7
2	28X	B	6[B]	7/18	0.15	4.54	6,15,18,19	7
2	56A	B	4	24/25	0.09	0.75	15,18,22,25	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

W O R L D W I D E
wwPDB
PROTEIN DATA BANK

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.