Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	4WHL
Title	:	A New Class of Peptidomimetics Targeting the Polo-box Domain of Polo-like kinase 1
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Deposited on	:	2014-09-23
Resolution	:	2.71 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 (i) 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 (i)) were used in the production of this report:

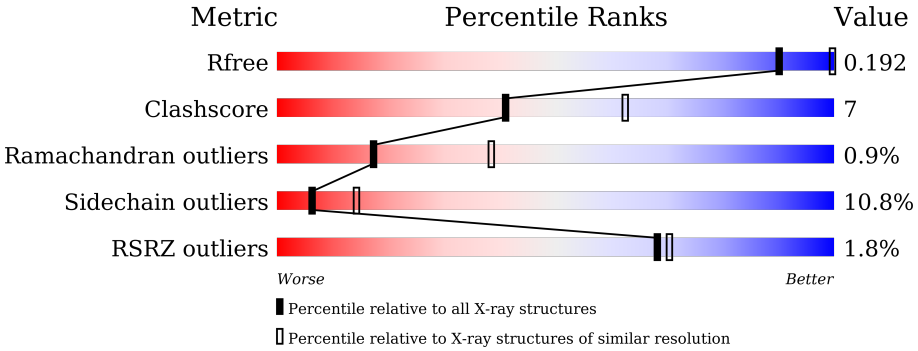
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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}	130704	3359 (2.74-2.70)
Clashscore	141614	3686 (2.74-2.70)
Ramachandran outliers	138981	3622 (2.74-2.70)
Sidechain outliers	138945	3623 (2.74-2.70)
RSRZ outliers	127900	3276 (2.74-2.70)

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 <=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	237	2%, 71%, 18%, • 9%
2	B	5	40%, 20%, 40%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	TPO	B	4	X	-	-	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1782 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 Serine/threonine-protein kinase PLK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	216	1725	1103	286	325	11	0	3	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 C6H5(CH2)8-DERIVATIZED PEPTIDE INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	5	56	38	7	10	1	0	0	1

- Molecule 3 is water.

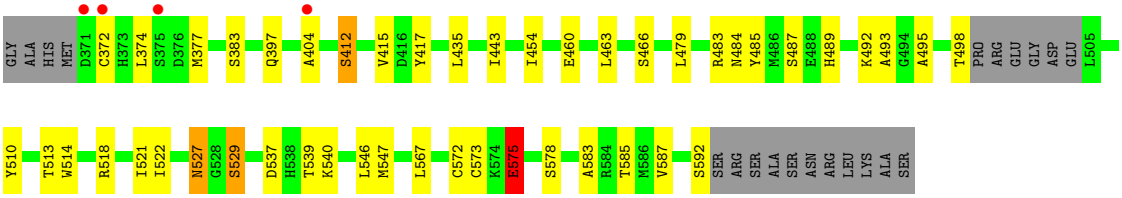
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	1	1	1	0	0

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.

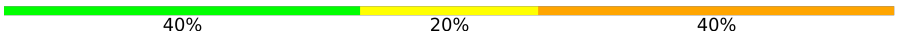
• Molecule 1: Serine/threonine-protein kinase PLK1

Chain A:



• Molecule 2: C6H5(CH2)8-DERIVATIZED PEPTIDE INHIBITOR

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	57.76Å 57.76Å 137.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.71 35.91 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.71) 100.0 (35.91-2.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.38 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.182 , 0.245 0.192 , 0.192	Depositor DCC
R_{free} test set	327 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å^2)	50.5	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 33.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1782	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.47% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: 56A, TPO, NH2, KAC

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	0.63	0/1773	0.77	0/2402
2	B	0.57	0/5	1.87	0/5
All	All	0.63	0/1778	0.77	0/2407

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
2	B	1	0

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	4	TPO	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	1725	0	1671	25	0
2	B	56	0	45	3	0
3	A	1	0	0	0	0
All	All	1782	0	1716	25	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 (25) 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:527:ASN:HD21	1:A:529:SER:HB2	1.56	0.70
1:A:537:ASP:OD1	1:A:539:THR:HG23	1.93	0.69
1:A:527:ASN:ND2	1:A:529:SER:HB2	2.16	0.61
1:A:479:LEU:O	1:A:479:LEU:HD23	2.06	0.55
1:A:415:VAL:HG11	2:B:2:56A:H30	1.88	0.55
1:A:537:ASP:OD1	1:A:539:THR:CG2	2.55	0.54
1:A:454:ILE:HD13	1:A:510:TYR:CD2	2.43	0.52
1:A:479:LEU:HD23	1:A:479:LEU:C	2.28	0.52
1:A:492:LYS:O	1:A:495:ALA:HB2	2.11	0.51
1:A:521:ILE:C	1:A:522:ILE:HD12	2.34	0.48
1:A:397:GLN:NE2	1:A:573:CYS:H	2.14	0.46
1:A:435:LEU:HD23	1:A:514:TRP:HD1	1.81	0.45
1:A:377:MET:CE	1:A:587:VAL:HG21	2.48	0.44
1:A:573:CYS:SG	1:A:575:GLU:HB2	2.57	0.43
1:A:522:ILE:HD12	1:A:522:ILE:N	2.34	0.43
1:A:583:ALA:O	1:A:587:VAL:HG23	2.19	0.43
1:A:415:VAL:CG1	2:B:2:56A:H30	2.48	0.42
1:A:483:ARG:HH21	1:A:484:ASN:HD21	1.66	0.42
1:A:435:LEU:HD23	1:A:514:TRP:CD1	2.55	0.42
1:A:540:LYS:NZ	2:B:4:TPO:O3P	2.43	0.42
1:A:412:SER:HA	1:A:493:ALA:HB3	2.02	0.41
1:A:443:ILE:HD11	1:A:510:TYR:CB	2.51	0.41
1:A:485:TYR:CD1	1:A:489:HIS:CD2	3.09	0.41
1:A:567:LEU:HD22	1:A:572:CYS:HB3	2.03	0.41
1:A:412:SER:HB2	1:A:492:LYS:HG3	2.03	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	215/237 (91%)	194 (90%)	19 (9%)	2 (1%)	17 38
2	B	1/5 (20%)	0	1 (100%)	0	100 100
All	All	216/242 (89%)	194 (90%)	20 (9%)	2 (1%)	17 38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	575	GLU
1	A	404	ALA

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	188/212 (89%)	166 (88%)	22 (12%)	5 12
2	B	1/1 (100%)	1 (100%)	0	100 100
All	All	189/213 (89%)	167 (88%)	22 (12%)	6 12

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	372	CYS
1	A	374	LEU
1	A	383	SER
1	A	412	SER

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Mol	Chain	Res	Type
1	A	417	TYR
1	A	460	GLU
1	A	463	LEU
1	A	466	SER
1	A	487[A]	SER
1	A	487[B]	SER
1	A	498	THR
1	A	513	THR
1	A	518	ARG
1	A	527	ASN
1	A	529	SER
1	A	546	LEU
1	A	547	MET
1	A	575	GLU
1	A	578[A]	SER
1	A	578[B]	SER
1	A	585	THR
1	A	592	SER

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

Mol	Chain	Res	Type
1	A	385	ASN
1	A	397	GLN
1	A	452	GLN
1	A	484	ASN
1	A	489	HIS
1	A	527	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)

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	2	2	21,25,26	1.28	1 (4%)	22,30,32	1.15	2 (9%)
2	KAC	B	1	2	14,14,15	1.48	1 (7%)	16,16,18	1.46	2 (12%)
2	TPO	B	4	2	8,10,11	1.64	1 (12%)	10,14,16	1.18	1 (10%)

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	2	2	-	2/16/17/19	0/2/2/2
2	KAC	B	1	2	-	2/9/10/11	0/1/1/1
2	TPO	B	4	2	1/1/3/4	1/9/11/13	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	KAC	CBW-CBS	-5.19	1.39	1.50
2	B	2	56A	C34-C35	-4.64	1.38	1.51
2	B	4	TPO	P-O2P	3.79	1.69	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	KAC	CBE-N-CBS	-3.90	113.19	122.08
2	B	1	KAC	CBE-CBC-CBG	-3.18	103.44	112.87
2	B	2	56A	NE2-CE1-ND1	-2.68	108.28	112.26
2	B	4	TPO	OG1-P-O1P	2.67	119.69	109.39
2	B	2	56A	C27-ND1-CG	2.39	128.73	124.72

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	4	TPO	CB

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	4	TPO	O-C-CA-CB
2	B	1	KAC	CBG-CBC-CBE-N
2	B	1	KAC	CBE-CBC-CBG-C
2	B	2	56A	CA-CB-CG-CD2
2	B	2	56A	C31-C32-C33-C34

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	56A	2	0
2	B	4	TPO	1	0

5.5 Carbohydrates (i)

There are no monosaccharides 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	216/237 (91%)	-0.22	4 (1%) 66 69	29, 46, 74, 102	0
2	B	1/5 (20%)	-0.07	0 100 100	39, 39, 39, 39	0
All	All	217/242 (89%)	-0.22	4 (1%) 68 70	29, 46, 74, 102	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	372	CYS	3.0
1	A	404	ALA	2.5
1	A	371	ASP	2.1
1	A	375	SER	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (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. 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	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	KAC	B	1	14/15	0.95	0.18	39,46,51,56	0
2	56A	B	2	24/25	0.95	0.14	34,36,41,43	0
2	TPO	B	4	11/12	0.96	0.12	36,41,46,47	0

6.3 Carbohydrates (i)

There are no monosaccharides 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.