



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2017 – 06:51 PM EDT

PDB ID : 3MVH
Title : Crystal structure of Akt-1-inhibitor complexes
Authors : Pandit, J.
Deposited on : unknown
Resolution : 2.01 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 : **FAILED**
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

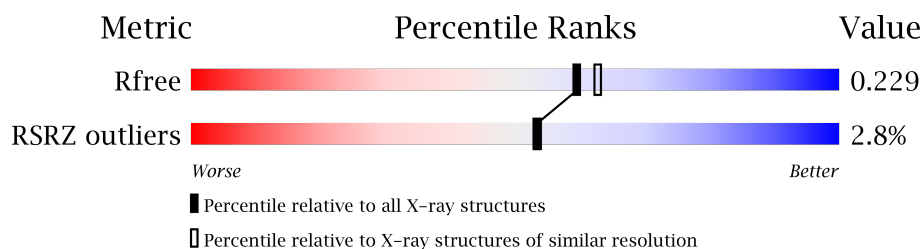
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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}	100719	6609 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2962 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 v-akt murine thymoma viral oncogene homolog 1 (AKT1).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	P	S	0	9	0
			2606	1674	435	480	1	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	139	GLY	-	EXPRESSION TAG	UNP B2RAM5
A	140	ALA	-	EXPRESSION TAG	UNP B2RAM5
A	141	MET	-	EXPRESSION TAG	UNP B2RAM5
A	142	ASP	-	EXPRESSION TAG	UNP B2RAM5
A	143	PRO	-	EXPRESSION TAG	UNP B2RAM5
A	473	ASP	SER	ENGINEERED	UNP B2RAM5

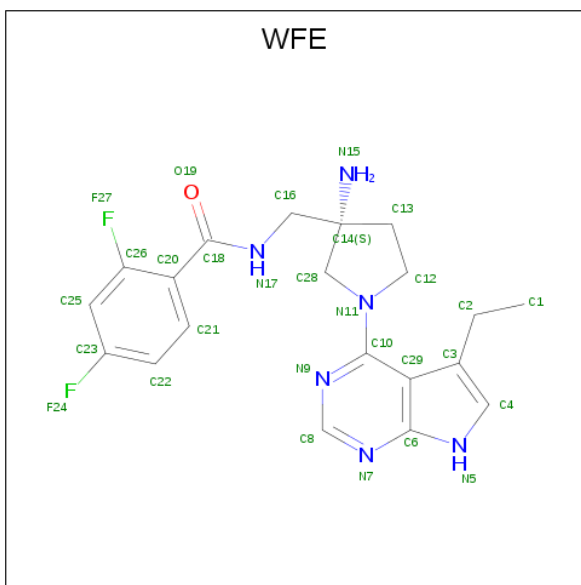
- Molecule 2 is a protein called GSK3-beta peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	10	Total	C	N	O	0	0	0
			79	47	16	16			

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 4 is N-[[[(3S)-3-amino-1-(5-ethyl-7H-pyrrolo[2,3-d]pyrimidin-4-yl)pyrrolidin-3-yl]methyl]-2,4-difluorobenzamide (three-letter code: WFE) (formula: C₂₀H₂₂F₂N₆O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			29	20	2	6	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	230	Total O 230 230	0	0
5	B	17	Total O 17 17	0	0

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3 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.35Å 55.26Å 92.31Å 90.00° 102.64° 90.00°	Depositor
Resolution (Å)	50.00 – 2.01 34.91 – 2.01	Depositor EDS
% Data completeness (in resolution range)	99.3 (50.00-2.01) 99.3 (34.91-2.01)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.07 (at 2.01Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.178 , 0.230 0.176 , 0.229	Depositor DCC
R_{free} test set	1391 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2962	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.19% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

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4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is 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	308	1	9,10,11	1.75	2 (22%)	10,14,16	1.61	2 (20%)

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	308	1	-	0/8/11/13	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	308	TPO	CA-C	2.62	1.53	1.50
1	A	308	TPO	P-OG1	3.66	1.66	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	308	TPO	OG1-P-O1P	-2.96	97.67	109.26
1	A	308	TPO	O3P-P-O1P	3.08	122.53	110.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

4.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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
4	WFE	A	999	-	30,32,32	1.46	5 (16%)	32,47,47	3.16	14 (43%)

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
4	WFE	A	999	-	-	0/15/27/27	0/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	999	WFE	C13-C14	-4.23	1.49	1.54
4	A	999	WFE	C28-N11	-3.49	1.42	1.46
4	A	999	WFE	C29-C6	-2.04	1.37	1.43
4	A	999	WFE	C12-N11	2.30	1.50	1.47
4	A	999	WFE	C3-C29	2.85	1.45	1.41

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	999	WFE	N7-C8-N9	-11.91	118.48	128.86
4	A	999	WFE	C2-C3-C4	-3.86	122.87	128.04
4	A	999	WFE	C25-C26-C20	-3.71	119.86	123.62
4	A	999	WFE	C3-C29-C6	-3.62	104.15	110.22
4	A	999	WFE	C26-C20-C18	-3.56	116.48	124.84
4	A	999	WFE	N9-C10-N11	-2.65	110.98	116.85
4	A	999	WFE	C1-C2-C3	-2.13	110.24	115.03
4	A	999	WFE	C26-C25-C23	2.13	118.98	116.65
4	A	999	WFE	C20-C18-N17	2.40	122.21	117.45
4	A	999	WFE	C8-N7-C6	2.61	119.46	113.33
4	A	999	WFE	C28-C14-C16	3.65	116.72	112.83
4	A	999	WFE	C21-C20-C26	3.85	121.13	116.64
4	A	999	WFE	C29-C10-N11	4.25	129.74	121.13
4	A	999	WFE	C8-N9-C10	4.79	123.58	111.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data ⓘ

5.1 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	311/342 (90%)	-0.31	9 (2%) 52 52	11, 24, 52, 61	0
2	B	10/10 (100%)	-0.32	0 100 100	17, 21, 38, 39	0
All	All	321/352 (91%)	-0.31	9 (2%) 53 53	11, 23, 51, 61	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	220	HIS	4.3
1	A	188	ALA	2.9
1	A	444	ALA	2.5
1	A	161	PHE	2.4
1	A	184	GLU	2.1
1	A	221	ASP	2.1
1	A	304	ALA	2.1
1	A	158	LYS	2.1
1	A	148	ASN	2.0

5.2 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	TPO	A	308	11/12	0.98	0.07	-	18,22,27,34	0

5.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.4 Ligands [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. 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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	WFE	A	999	29/29	0.92	0.15	0.18	25,30,55,56	0
3	MN	A	1	1/1	0.99	0.04	-	29,29,29,29	0

5.5 Other polymers [i](#)

There are no such residues in this entry.