



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 05:47 pm BST

PDB ID : 3UTM  
Title : Crystal structure of a mouse Tankyrase-Axin complex  
Authors : Cheng, Z.; Morrone, S.; Xu, W.  
Deposited on : 2011-11-26  
Resolution : 2.00 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

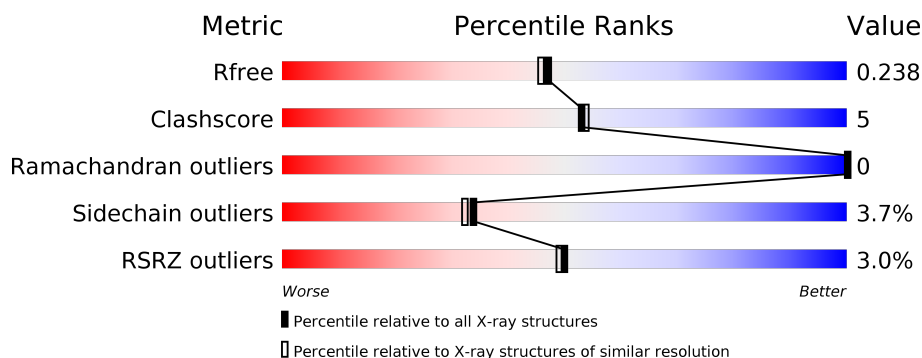
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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  $\geq 3$ , 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	351	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>11%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	351	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>9%</div> <div>•</div> <div>13%</div> </div> </div>
2	C	83	<div> <div>8%</div> <div> <div></div> <div>30%</div> <div>8%</div> <div>61%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5263 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 Tankyrase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	0	0
			2446	1527	450	455	14			
1	B	307	Total	C	N	O	S	0	0	0
			2353	1469	436	434	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	GLY	-	EXPRESSION TAG	UNP Q6PFX9
A	306	GLU	-	EXPRESSION TAG	UNP Q6PFX9
A	307	PHE	-	EXPRESSION TAG	UNP Q6PFX9
B	305	GLY	-	EXPRESSION TAG	UNP Q6PFX9
B	306	GLU	-	EXPRESSION TAG	UNP Q6PFX9
B	307	PHE	-	EXPRESSION TAG	UNP Q6PFX9

- Molecule 2 is a protein called Axin-1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	32	Total	C	N	O	0	0	0
			237	143	41	53			

There are 3 discrepancies between the modelled and reference sequences:

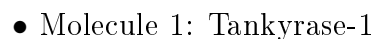
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	SER	-	EXPRESSION TAG	UNP O35625
C	-1	HIS	-	EXPRESSION TAG	UNP O35625
C	0	MET	-	EXPRESSION TAG	UNP O35625

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	111	Total 111	O 111	0	0
3	B	112	Total 112	O 112	0	0
3	C	4	Total 4	O 4	0	0



- Molecule 1: Tankyrase-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	131.67Å 106.54Å 73.43Å 90.00° 105.76° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 29.93 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.00) 99.5 (29.93-1.95)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.84 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.207 , 0.238 0.207 , 0.238	Depositor DCC
$R_{free}$ test set	3573 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.0	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 49.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5263	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.82% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.53	1/2490 (0.0%)	0.60	0/3368
1	B	0.53	0/2395	0.62	0/3238
2	C	0.35	0/243	0.54	0/331
All	All	0.52	1/5128 (0.0%)	0.61	0/6937

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	427	TRP	CD2-CE2	5.18	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

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	2446	0	2470	27	0
1	B	2353	0	2381	26	0
2	C	237	0	212	6	0
3	A	111	0	0	2	0
3	B	112	0	0	2	0
3	C	4	0	0	1	0
All	All	5263	0	5063	54	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 5.

All (54) 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:B:532:GLN:H	1:B:532:GLN:HE21	1.05	0.94
1:A:578:ASN:HD21	1:A:609:ASP:H	1.08	0.90
1:B:397:VAL:H	1:B:400:HIS:HD2	1.29	0.80
1:B:532:GLN:HE21	1:B:532:GLN:N	1.82	0.76
1:A:553:THR:H	1:A:556:HIS:HD2	1.33	0.74
1:A:545:ASN:HD21	1:A:576:LYS:H	1.36	0.74
1:B:553:THR:H	1:B:556:HIS:HD2	1.37	0.70
1:A:578:ASN:ND2	1:A:609:ASP:H	1.88	0.70
1:B:406:GLY:CA	1:B:440:ARG:HG2	2.22	0.69
1:A:497:LYS:O	1:A:501:THR:HG23	1.93	0.68
1:A:361:ARG:NH2	3:A:80:HOH:O	2.28	0.67
1:B:457:VAL:HG13	1:B:461:GLY:HA2	1.79	0.65
1:B:497:LYS:O	1:B:501:THR:HG23	1.97	0.64
1:B:397:VAL:H	1:B:400:HIS:CD2	2.15	0.62
1:B:532:GLN:H	1:B:532:GLN:NE2	1.89	0.60
1:A:373:ASN:HB2	1:A:407:HIS:CE1	2.38	0.59
1:B:441:VAL:HG12	1:B:473:LEU:HD13	1.86	0.58
1:B:553:THR:H	1:B:556:HIS:CD2	2.23	0.55
2:C:18:GLU:HG3	2:C:20:ALA:H	1.71	0.55
1:B:547:LYS:HB3	1:B:551:PHE:HA	1.89	0.55
1:A:364:THR:H	1:A:367:HIS:HD2	1.55	0.54
1:B:543:ASN:HB3	3:B:20:HOH:O	2.08	0.54
1:A:364:THR:H	1:A:367:HIS:CD2	2.26	0.53
1:B:457:VAL:CG1	1:B:461:GLY:HA2	2.38	0.53
1:A:553:THR:H	1:A:556:HIS:CD2	2.22	0.52
1:B:406:GLY:HA3	1:B:440:ARG:HG2	1.92	0.52
1:B:344:LEU:HG	1:B:377:ILE:HD13	1.91	0.51
1:B:373:ASN:ND2	3:B:16:HOH:O	2.43	0.51
1:A:361:ARG:HD3	2:C:26:PRO:HD3	1.93	0.50
1:A:545:ASN:ND2	1:A:576:LYS:H	2.07	0.50
1:A:488:GLN:NE2	1:A:491:ARG:HH11	2.10	0.50
1:A:367:HIS:HE1	1:A:396:LEU:O	1.95	0.50
1:A:579:ALA:HB3	3:A:660:HOH:O	2.12	0.49
1:A:348:LEU:HD11	1:A:353:VAL:HG23	1.93	0.49
1:B:332:LEU:HD12	1:B:344:LEU:HD22	1.95	0.48
1:A:578:ASN:HD21	1:A:609:ASP:N	1.91	0.48
1:A:374:ARG:HB3	1:A:377:ILE:HB	1.95	0.47
1:A:604:LEU:HD11	1:A:632:LEU:HD23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:406:GLY:HA2	1:B:440:ARG:HG2	1.96	0.47
1:A:562:ALA:HB2	1:A:596:HIS:CG	2.50	0.47
1:A:426:LEU:HB3	3:C:304:HOH:O	2.16	0.46
1:B:400:HIS:HE1	1:B:429:PHE:O	1.98	0.46
2:C:68:LEU:HA	2:C:68:LEU:HD23	1.87	0.44
1:B:460:HIS:HE1	2:C:66:LEU:HD13	1.83	0.44
1:B:429:PHE:HE1	2:C:68:LEU:HD22	1.83	0.43
1:B:367:HIS:HD2	1:B:401:ASN:HD21	1.67	0.43
1:B:397:VAL:HG22	1:B:400:HIS:CD2	2.54	0.43
1:A:545:ASN:HD21	1:A:575:ALA:HA	1.85	0.42
1:A:547:LYS:HB3	1:A:551:PHE:HA	2.02	0.42
1:A:363:SER:HB3	1:A:367:HIS:HB2	2.02	0.41
1:A:543:ASN:ND2	1:A:545:ASN:H	2.19	0.41
1:A:361:ARG:NH1	2:C:23:PRO:O	2.53	0.41
1:A:493:ALA:HB3	1:B:527:HIS:HB2	2.03	0.40
1:B:454:PRO:HB2	1:B:465:VAL:HG23	2.02	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	318/351 (91%)	316 (99%)	2 (1%)	0	100	100
1	B	305/351 (87%)	299 (98%)	6 (2%)	0	100	100
2	C	28/83 (34%)	27 (96%)	1 (4%)	0	100	100
All	All	651/785 (83%)	642 (99%)	9 (1%)	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	261/285 (92%)	252 (97%)	9 (3%)	37	36
1	B	251/285 (88%)	241 (96%)	10 (4%)	31	29
2	C	26/71 (37%)	25 (96%)	1 (4%)	33	31
All	All	538/641 (84%)	518 (96%)	20 (4%)	34	32

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	332	LEU
1	A	334	GLU
1	A	374	ARG
1	A	442	GLU
1	A	531	LYS
1	A	543	ASN
1	A	552	MET
1	A	569	VAL
1	A	635	SER
1	B	383	GLN
1	B	388	VAL
1	B	440	ARG
1	B	445	SER
1	B	457	VAL
1	B	500	LYS
1	B	513	GLN
1	B	532	GLN
1	B	597	LEU
1	B	602	LEU
2	C	19	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	367	HIS

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Mol	Chain	Res	Type
1	A	383	GLN
1	A	384	HIS
1	A	401	ASN
1	A	460	HIS
1	A	488	GLN
1	A	513	GLN
1	A	543	ASN
1	A	545	ASN
1	A	556	HIS
1	A	578	ASN
1	A	598	GLN
1	B	373	ASN
1	B	400	HIS
1	B	401	ASN
1	B	460	HIS
1	B	513	GLN
1	B	532	GLN
1	B	556	HIS

### 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 carbohydrates 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	320/351 (91%)	-0.22	9 (2%)	53	51	41, 59, 89, 124	0
1	B	307/351 (87%)	-0.19	4 (1%)	77	76	39, 58, 83, 112	0
2	C	32/83 (38%)	1.26	7 (21%)	0	0	78, 95, 128, 146	0
All	All	659/785 (83%)	-0.13	20 (3%)	50	49	39, 59, 95, 146	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	635	SER	6.4
1	A	327	TYR	5.1
2	C	60	THR	5.0
2	C	64	SER	4.8
2	C	65	ASP	4.1
1	A	318	SER	4.1
2	C	19	ASP	4.1
1	A	319	ALA	3.5
1	B	500	LYS	3.2
1	A	320	LYS	3.1
2	C	30	GLY	2.6
1	A	323	LEU	2.5
1	A	322	VAL	2.4
1	A	321	ALA	2.4
1	B	397	VAL	2.3
1	B	359	ASP	2.2
1	B	416	LYS	2.1
1	A	316	ASP	2.1
2	C	66	LEU	2.1
2	C	63	ARG	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 carbohydrates 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.