



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2021 – 09:57 AM EDT

PDB ID : 1BC3  
Title : RECOMBINANT RAT ANNEXIN V, TRIPLE MUTANT (T72K, S144K, S228K)  
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Deposited on : 1998-05-04  
Resolution : 1.95 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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
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) : 2.23.2

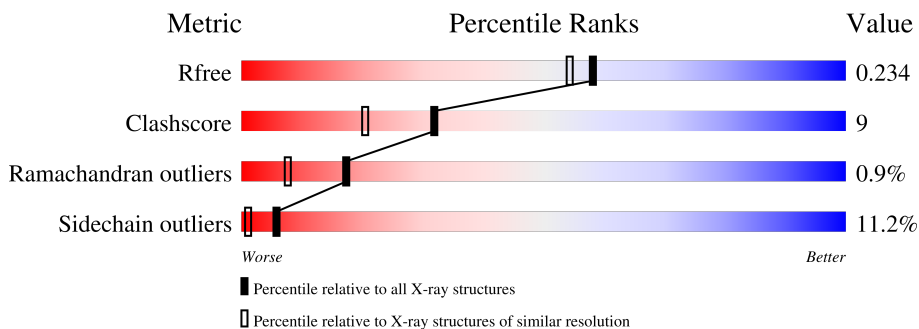
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)

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  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	319	 76% 19% .

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2629 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 ANNEXIN V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	318	2510	1580	428	494	8	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	LYS	THR	engineered mutation	UNP P14668
A	144	LYS	SER	engineered mutation	UNP P14668
A	228	LYS	SER	engineered mutation	UNP P14668

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	Ca	0	0
			5	5		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		


- Molecule 4 is water.

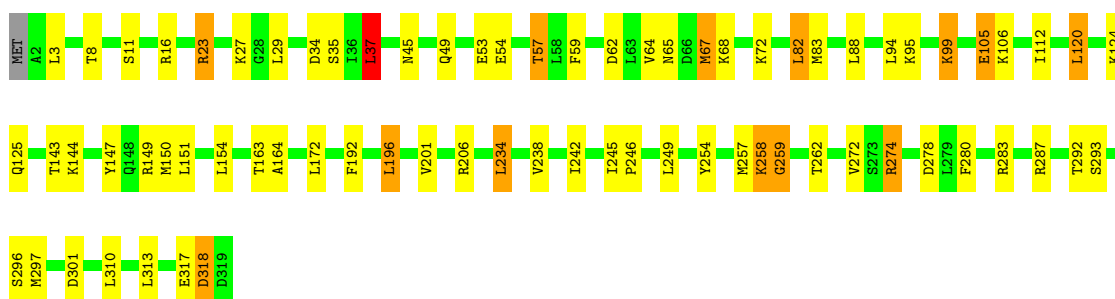
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	109	Total	O	0	0
			109	109		

### 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. 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. 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: ANNEXIN V

Chain A:  76% 19%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.34Å 157.34Å 37.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 1.95 45.42 – 1.86	Depositor EDS
% Data completeness (in resolution range)	83.7 (10.00-1.95) 74.2 (45.42-1.86)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 1.86Å)	Xtrriage
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.259 , 0.211 0.198 , 0.234	Depositor DCC
$R_{free}$ test set	1061 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.1	Xtrriage
Anisotropy	0.462	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 63.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2629	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.64% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, SO4

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	0.31	0/2542	0.58	1/3419 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	LEU	CA-CB-CG	6.15	129.45	115.30

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	2510	0	2525	45	0
2	A	5	0	0	0	0
3	A	5	0	0	1	0
4	A	109	0	0	1	0
All	All	2629	0	2525	45	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 9.

All (45) 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:95:LYS:HE2	1:A:99:LYS:HD3	1.48	0.92
1:A:163:THR:HG22	1:A:164:ALA:H	1.51	0.76
1:A:317:GLU:O	1:A:318:ASP:HB3	1.88	0.70
1:A:95:LYS:CE	1:A:99:LYS:HD3	2.26	0.64
1:A:99:LYS:NZ	1:A:99:LYS:HA	2.13	0.64
1:A:3:LEU:HG	1:A:278:ASP:HB3	1.82	0.61
1:A:23:ARG:HG3	1:A:59:PHE:CE2	2.37	0.59
1:A:53:GLU:O	1:A:57:THR:HG23	2.04	0.58
1:A:201:VAL:HG22	1:A:242:ILE:CD1	2.34	0.57
1:A:201:VAL:HG22	1:A:242:ILE:HD12	1.89	0.54
1:A:82:LEU:HD21	1:A:313:LEU:HD11	1.90	0.54
1:A:64:VAL:HG12	1:A:68:LYS:HE3	1.91	0.52
1:A:274:ARG:HD3	1:A:278:ASP:OD1	2.10	0.52
1:A:27:LYS:HA	3:A:450:SO4:O3	2.10	0.52
1:A:258:LYS:O	1:A:259:GLY:O	2.28	0.52
1:A:45:ASN:O	1:A:49:GLN:HG2	2.09	0.52
1:A:99:LYS:HD2	1:A:99:LYS:N	2.24	0.52
1:A:249:LEU:HD13	1:A:274:ARG:HD2	1.91	0.51
1:A:245:ILE:HB	1:A:246:PRO:HD3	1.93	0.50
1:A:249:LEU:CD1	1:A:274:ARG:HD2	2.42	0.50
1:A:317:GLU:O	1:A:318:ASP:CB	2.58	0.50
1:A:150:MET:CG	1:A:234:LEU:HD13	2.41	0.49
1:A:82:LEU:HD13	1:A:272:VAL:HG22	1.94	0.49
1:A:112:ILE:HD12	1:A:151:LEU:HD22	1.96	0.48
1:A:23:ARG:HG3	1:A:59:PHE:CZ	2.49	0.47
1:A:99:LYS:HA	1:A:99:LYS:HZ3	1.80	0.46
1:A:120:LEU:O	1:A:124:LYS:HG3	2.16	0.46
1:A:280:PHE:O	1:A:283:ARG:HB2	2.16	0.46
1:A:72:LYS:HE3	4:A:600:HOH:O	2.16	0.45
1:A:62:ASP:HB3	1:A:65:ASN:HB2	1.98	0.45
1:A:163:THR:HG22	1:A:164:ALA:N	2.26	0.45
1:A:257:MET:O	1:A:258:LYS:C	2.56	0.44
1:A:23:ARG:HG3	1:A:59:PHE:CD2	2.53	0.44
1:A:192:PHE:O	1:A:196:LEU:HB2	2.18	0.44
1:A:105:GLU:HG2	1:A:147:TYR:CE2	2.53	0.44
1:A:254:TYR:O	1:A:258:LYS:HB2	2.18	0.44
1:A:37:LEU:C	1:A:37:LEU:HD23	2.38	0.43
1:A:293:SER:HB3	1:A:296:SER:OG	2.19	0.43
1:A:67:MET:HE1	1:A:83:MET:HG3	2.00	0.42
1:A:257:MET:CE	1:A:297:MET:HG2	2.50	0.42
1:A:257:MET:HE3	1:A:297:MET:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:THR:C	1:A:144:LYS:HG3	2.40	0.41
1:A:245:ILE:N	1:A:246:PRO:CD	2.84	0.41
1:A:54:GLU:OE1	1:A:54:GLU:HA	2.21	0.40
1:A:238:VAL:O	1:A:242:ILE:HG12	2.21	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	316/319 (99%)	303 (96%)	10 (3%)	3 (1%)	<b>17</b> <b>8</b>

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	258	LYS
1	A	259	GLY
1	A	318	ASP

### 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	268/269 (100%)	238 (89%)	30 (11%)	<b>6</b> <b>1</b>

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	THR
1	A	11	SER
1	A	16	ARG
1	A	23	ARG
1	A	29	LEU
1	A	34	ASP
1	A	35	SER
1	A	37	LEU
1	A	57	THR
1	A	67	MET
1	A	82	LEU
1	A	88	LEU
1	A	94	LEU
1	A	99	LYS
1	A	105	GLU
1	A	106	LYS
1	A	120	LEU
1	A	125	GLN
1	A	149	ARG
1	A	154	LEU
1	A	172	LEU
1	A	196	LEU
1	A	206	ARG
1	A	234	LEU
1	A	262	THR
1	A	274	ARG
1	A	287	ARG
1	A	292	THR
1	A	301	ASP
1	A	310	LEU

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	125	GLN
1	A	148	GLN
1	A	175	GLN
1	A	179	GLN
1	A	218	GLN
1	A	289	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 5 are 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	$\# Z  > 2$
3	SO4	A	450	-	4,4,4	0.83	0	6,6,6	0.59	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	450	SO4	1	0

## 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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.