



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:22 PM UTC

PDB ID : 1AVR / pdb_00001avr
Title : CRYSTAL AND MOLECULAR STRUCTURE OF HUMAN ANNEXIN V AFTER REFINEMENT. IMPLICATIONS FOR STRUCTURE, MEMBRANE BINDING AND ION CHANNEL FORMATION OF THE ANNEXIN FAMILY OF PROTEINS
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Deposited on : 1991-10-17
Resolution : 2.30 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

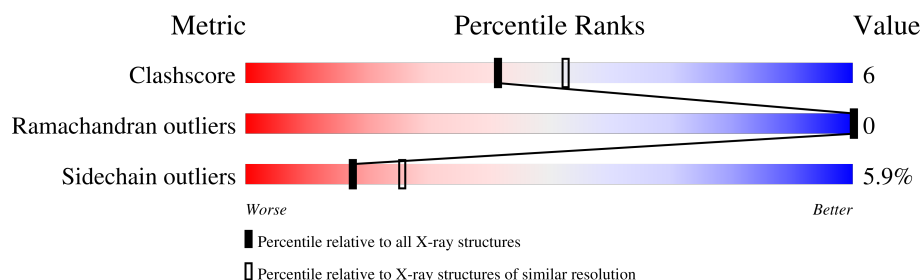
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	320	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2714 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.

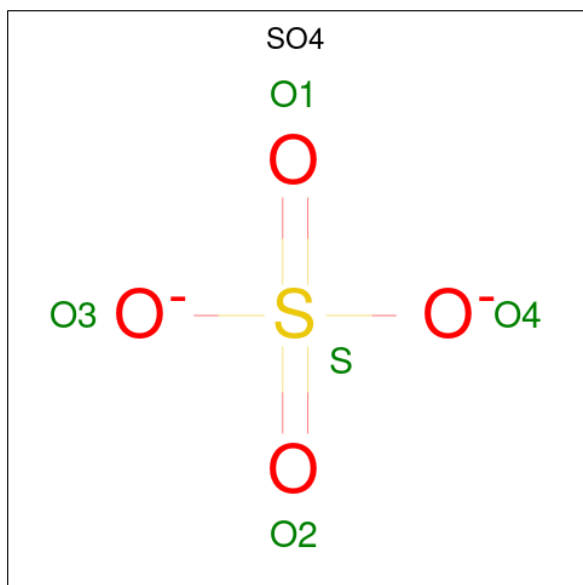
- Molecule 1 is a protein called ANNEXIN V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	62	0	1
			2497	1574	421	494	8			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is water.

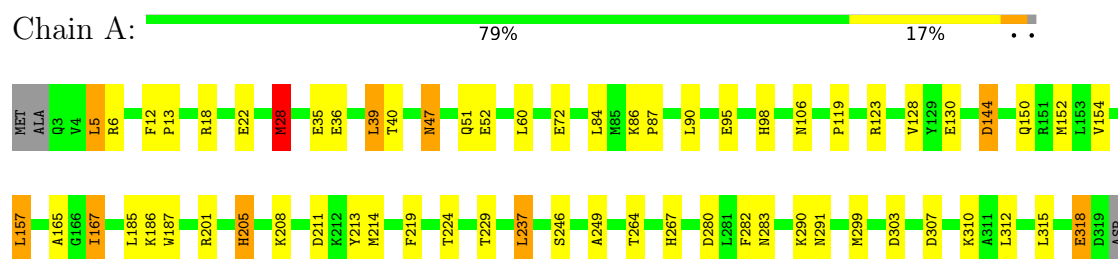
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	202	Total 202	O 202	0	0

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. 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.

Note EDS was not executed.

• Molecule 1: ANNEXIN V



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	99.70Å 99.70Å 96.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	EREF	Depositor
R, R_{free}	0.184 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2714	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	1.11	8/2531 (0.3%)	1.48	8/3407 (0.2%)

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
1	A	0	3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98	HIS	ND1-CE1	9.45	1.42	1.32
1	A	98	HIS	CE1-NE2	9.21	1.41	1.32
1	A	187	TRP	NE1-CE2	-9.04	1.27	1.37
1	A	267	HIS	CE1-NE2	8.84	1.41	1.32
1	A	205	HIS	CE1-NE2	8.82	1.41	1.32
1	A	205	HIS	ND1-CE1	8.33	1.40	1.32
1	A	267	HIS	ND1-CE1	7.62	1.40	1.32
1	A	165	ALA	C-N	-5.24	1.31	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	144	ASP	CA-CB-CG	-7.69	104.91	112.60
1	A	39	LEU	N-CA-CB	-6.72	99.93	109.94
1	A	98	HIS	CA-CB-CG	-6.62	107.18	113.80
1	A	291	ASN	CA-CB-CG	-6.34	106.25	112.60
1	A	28	MET	N-CA-CB	-6.13	102.16	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	95	GLU	N-CA-CB	-6.08	100.86	110.28
1	A	211	ASP	O-C-N	5.70	128.25	122.09
1	A	47	ASN	CA-CB-CG	-5.34	107.26	112.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	167	ILE	Mainchain
1	A	229	THR	Mainchain
1	A	318	GLU	Mainchain

5.2 Too-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 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	2497	0	2506	31	0
2	A	5	0	0	0	0
3	A	10	0	0	0	0
4	A	202	0	0	0	0
All	All	2714	0	2506	31	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 6.

All (31) 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:6:ARG:H	1:A:283:ASN:HD21	1.24	0.84
1:A:28:MET:HG3	1:A:72:GLU:HG3	1.62	0.80
1:A:167:ILE:HD13	1:A:208:LYS:HG3	1.69	0.74
1:A:5:LEU:HG	1:A:280:ASP:HB3	1.68	0.74
1:A:6:ARG:H	1:A:283:ASN:ND2	1.90	0.69
1:A:28:MET:CG	1:A:72:GLU:HG3	2.27	0.64
1:A:213:TYR:OH	1:A:224:THR:HG21	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:MET:HE2	1:A:237:LEU:HD12	1.88	0.56
1:A:47:ASN:O	1:A:51:GLN:HG2	2.09	0.52
1:A:106:ASN:HD22	1:A:106:ASN:C	2.16	0.52
1:A:152:MET:HE2	1:A:237:LEU:CD1	2.40	0.51
1:A:90:LEU:HD23	1:A:128:VAL:CG1	2.41	0.50
1:A:150:GLN:O	1:A:154:VAL:HG23	2.12	0.49
1:A:6:ARG:HD2	1:A:282:PHE:CG	2.49	0.47
1:A:119:PRO:O	1:A:123:ARG:HG3	2.15	0.47
1:A:36:GLU:H	1:A:36:GLU:CD	2.23	0.47
1:A:84:LEU:HD21	1:A:315:LEU:HD11	1.96	0.46
1:A:307:ASP:HA	1:A:310:LYS:HD2	1.98	0.45
1:A:86:LYS:HD3	1:A:87:PRO:HD2	1.98	0.45
1:A:90:LEU:HD23	1:A:128:VAL:HG11	1.98	0.45
1:A:35:GLU:O	1:A:39:LEU:HB2	2.17	0.45
1:A:315:LEU:HD23	1:A:315:LEU:HA	1.79	0.44
1:A:28:MET:HG3	1:A:72:GLU:CG	2.42	0.44
1:A:205:HIS:O	1:A:208:LYS:HB2	2.18	0.43
1:A:18:ARG:O	1:A:22:GLU:HG3	2.19	0.43
1:A:201:ARG:HH11	1:A:201:ARG:HD3	1.71	0.42
1:A:214:MET:HA	1:A:219:PHE:O	2.19	0.42
1:A:246:SER:HB3	1:A:249:ALA:HB3	2.02	0.42
1:A:12:PHE:HA	1:A:13:PRO:HD2	1.90	0.42
1:A:157:LEU:HD12	1:A:157:LEU:HA	1.89	0.40
1:A:36:GLU:O	1:A:40:THR:HG23	2.21	0.40

There are no symmetry-related clashes.

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	315/320 (98%)	308 (98%)	7 (2%)	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	269/272 (99%)	253 (94%)	16 (6%)	18	26

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	28	MET
1	A	52	GLU
1	A	60	LEU
1	A	130	GLU
1	A	144	ASP
1	A	157	LEU
1	A	185	LEU
1	A	186	LYS
1	A	237	LEU
1	A	264	THR
1	A	290	LYS
1	A	299	MET
1	A	303	ASP
1	A	312	LEU
1	A	318	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	232	ASN
1	A	235	GLN
1	A	283	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 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	551	-	4,4,4	0.83	0	6,6,6	0.18	0
3	SO4	A	550	-	4,4,4	0.77	0	6,6,6	0.28	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.

No monomer is involved in short contacts.

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.