



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:34 AM GMT

PDB ID : 2RAN
Title : RAT ANNEXIN V CRYSTAL STRUCTURE: CA2+-INDUCED CONFORMATIONAL CHANGES
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Deposited on : 1994-09-01
Resolution : 1.89 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 : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

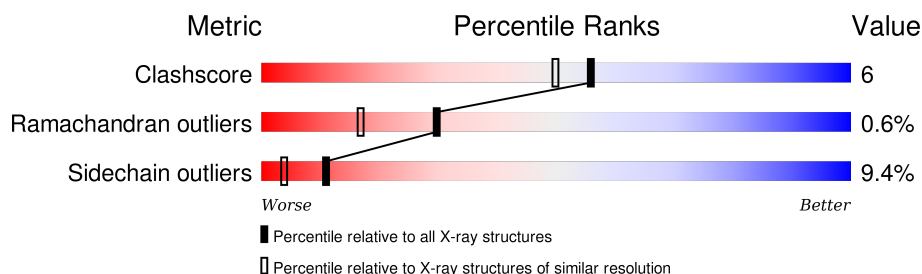
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	316	 71% 24% . .

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
3	SO4	A	327	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3185 atoms, of which 573 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.

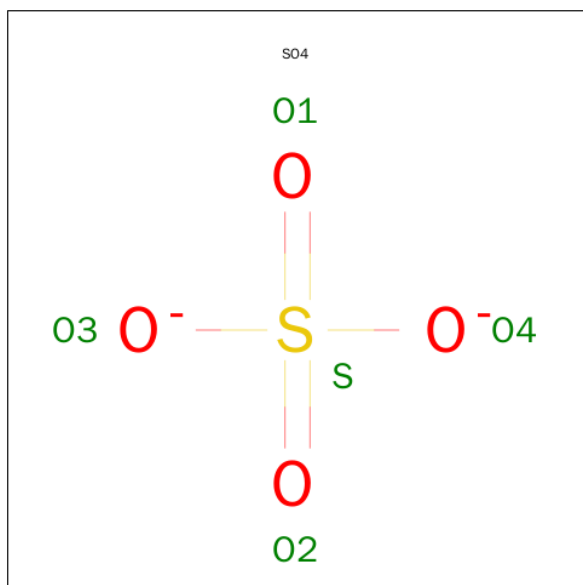
- Molecule 1 is a protein called ANNEXIN V.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	316	Total	C	H	N	O	S	0	0	0
			3060	1564	573	423	492	8			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	Ca	0	0
			7	7		

- Molecule 3 is SULFATE ION (three-letter code: 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.

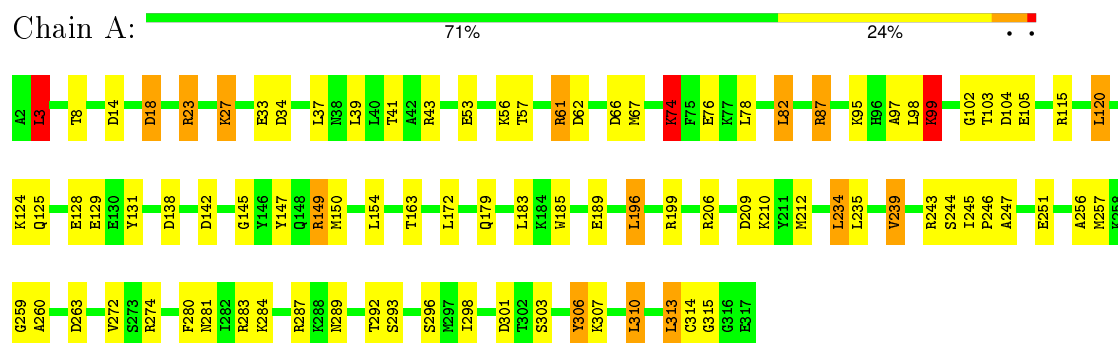
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	108	Total 108	O 108	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

• Molecule 1: ANNEXIN V



4 Data and refinement statistics

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

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	156.90 Å 156.90 Å 37.03 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	21.32 – 1.89	Depositor
% Data completeness (in resolution range)	83.0 (21.32-1.89)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.212 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3185	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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	0.94	2/2519 (0.1%)	1.64	42/3391 (1.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3	LEU	C-N	-7.81	1.16	1.34
1	A	315	GLY	C-N	-7.54	1.19	1.33

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	ARG	NE-CZ-NH1	10.80	125.70	120.30
1	A	274	ARG	NE-CZ-NH1	9.98	125.29	120.30
1	A	206	ARG	NE-CZ-NH1	9.43	125.02	120.30
1	A	37	LEU	CA-CB-CG	8.61	135.10	115.30
1	A	274	ARG	NE-CZ-NH2	-8.42	116.09	120.30
1	A	185	TRP	CD1-CG-CD2	8.18	112.84	106.30
1	A	283	ARG	NE-CZ-NH1	8.14	124.37	120.30
1	A	99	LYS	CA-C-N	-7.67	100.86	116.20
1	A	185	TRP	CE2-CD2-CG	-7.43	101.36	107.30
1	A	43	ARG	NE-CZ-NH1	7.38	123.99	120.30
1	A	287	ARG	NE-CZ-NH1	7.19	123.90	120.30
1	A	257	MET	CG-SD-CE	-6.63	89.59	100.20
1	A	199	ARG	NE-CZ-NH2	-6.41	117.10	120.30
1	A	150	MET	CG-SD-CE	6.29	110.27	100.20
1	A	142	ASP	CB-CG-OD2	6.22	123.90	118.30
1	A	87	ARG	NE-CZ-NH2	-6.11	117.24	120.30
1	A	23	ARG	CB-CG-CD	6.08	127.41	111.60
1	A	310	LEU	CB-CG-CD2	-6.05	100.71	111.00
1	A	172	LEU	CA-CB-CG	6.03	129.16	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	149	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	A	185	TRP	CG-CD2-CE3	5.81	139.13	133.90
1	A	61	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	A	76	GLU	OE1-CD-OE2	-5.66	116.50	123.30
1	A	189	GLU	OE1-CD-OE2	-5.52	116.67	123.30
1	A	14	ASP	CB-CG-OD1	5.47	123.23	118.30
1	A	43	ARG	NE-CZ-NH2	-5.45	117.57	120.30
1	A	99	LYS	N-CA-C	5.42	125.64	111.00
1	A	104	ASP	CB-CG-OD1	5.39	123.15	118.30
1	A	23	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	66	ASP	CB-CG-OD1	5.25	123.03	118.30
1	A	33	GLU	CB-CA-C	-5.25	99.90	110.40
1	A	306	TYR	CB-CG-CD2	-5.25	117.85	121.00
1	A	102	GLY	CA-C-N	-5.24	105.68	117.20
1	A	74	LYS	CA-CB-CG	5.20	124.83	113.40
1	A	105	GLU	OE1-CD-OE2	-5.13	117.14	123.30
1	A	239	VAL	CG1-CB-CG2	-5.12	102.71	110.90
1	A	185	TRP	CG-CD1-NE1	-5.07	105.03	110.10
1	A	18	ASP	CB-CG-OD1	5.05	122.85	118.30
1	A	105	GLU	CA-CB-CG	-5.05	102.28	113.40
1	A	310	LEU	CB-CG-CD1	5.05	119.58	111.00
1	A	115	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	A	251	GLU	CA-CB-CG	5.00	124.41	113.40

There are no chirality outliers.

There are no planarity outliers.

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	2487	573	2493	31	0
2	A	7	0	0	0	0
3	A	10	0	0	2	0
4	A	108	0	0	2	0
All	All	2612	573	2493	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:209:ASP:O	1:A:212:MET:HB3	1.95	0.66
1:A:27:LYS:NZ	3:A:327:SO4:S	2.73	0.61
1:A:18:ASP:HB3	1:A:39:LEU:HD21	1.83	0.60
1:A:196:LEU:HD23	1:A:235:LEU:HD22	1.82	0.59
1:A:99:LYS:HA	1:A:99:LYS:HE2	1.88	0.56
1:A:298:ILE:HD12	1:A:314:CYS:SG	2.45	0.56
1:A:98:LEU:HD13	1:A:138:ASP:HB3	1.90	0.54
1:A:244:SER:HB3	1:A:247:ALA:HB3	1.91	0.52
1:A:147:TYR:CD1	1:A:234:LEU:HD12	2.44	0.52
1:A:245:ILE:HB	1:A:246:PRO:HD3	1.92	0.51
1:A:239:VAL:O	1:A:243:ARG:HG3	2.11	0.51
1:A:128:GLU:HG2	4:A:507:HOH:O	2.09	0.51
1:A:97:ALA:O	1:A:103:THR:HA	2.12	0.49
1:A:120:LEU:O	1:A:124:LYS:HG3	2.12	0.49
1:A:74:LYS:HG2	1:A:306:TYR:CE2	2.49	0.47
1:A:56:LYS:HE3	1:A:62:ASP:HA	1.97	0.47
1:A:3:LEU:HA	1:A:281:ASN:OD1	2.14	0.47
1:A:82:LEU:HD13	1:A:272:VAL:HG22	1.97	0.46
1:A:256:ALA:HB1	1:A:263:ASP:HB3	1.99	0.45
1:A:145:GLY:O	1:A:149:ARG:HD3	2.18	0.43
1:A:78:LEU:O	1:A:82:LEU:HB2	2.19	0.43
1:A:147:TYR:HD1	1:A:234:LEU:HD12	1.83	0.42
1:A:61:ARG:NH2	4:A:403:HOH:O	2.51	0.42
1:A:280:PHE:CE2	1:A:284:LYS:HE2	2.54	0.42
1:A:41:THR:HB	1:A:313:LEU:HD13	2.02	0.41
1:A:95:LYS:HG2	1:A:131:TYR:CE1	2.56	0.41
1:A:303:SER:HA	1:A:307:LYS:HD3	2.02	0.41
1:A:27:LYS:NZ	3:A:327:SO4:O1	2.52	0.41
1:A:82:LEU:HD12	1:A:82:LEU:HA	1.90	0.41
1:A:179:GLN:HA	1:A:183:LEU:HB2	2.02	0.40
1:A:293:SER:HB3	1:A:296:SER:OG	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	314/316 (99%)	303 (96%)	9 (3%)	2 (1%)	30	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	259	GLY
1	A	260	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	266/266 (100%)	241 (91%)	25 (9%)	11	4

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	8	THR
1	A	23	ARG
1	A	27	LYS
1	A	34	ASP
1	A	53	GLU
1	A	57	THR
1	A	67	MET
1	A	74	LYS

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Mol	Chain	Res	Type
1	A	82	LEU
1	A	87	ARG
1	A	99	LYS
1	A	120	LEU
1	A	125	GLN
1	A	129	GLU
1	A	154	LEU
1	A	163	THR
1	A	196	LEU
1	A	210	LYS
1	A	234	LEU
1	A	289	ASN
1	A	292	THR
1	A	301	ASP
1	A	310	LEU
1	A	313	LEU

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

Mol	Chain	Res	Type
1	A	125	GLN
1	A	158	ASN
1	A	175	GLN
1	A	179	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 7 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	327	-	4,4,4	1.51	0	6,6,6	0.40	0
3	SO4	A	328	-	4,4,4	1.08	0	6,6,6	0.52	0

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
3	SO4	A	327	-	-	0/0/0/0	0/0/0/0
3	SO4	A	328	-	-	0/0/0/0	0/0/0/0

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 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	327	SO4	2	0

5.7 Other polymers

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.