



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:21 AM UTC

PDB ID : 3ACO / pdb_00003aco
Title : Crystal structure of the EFC/F-BAR domain of human PACSIN2/Syndapin II (2.7 Å)
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Deposited on : 2010-01-07
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

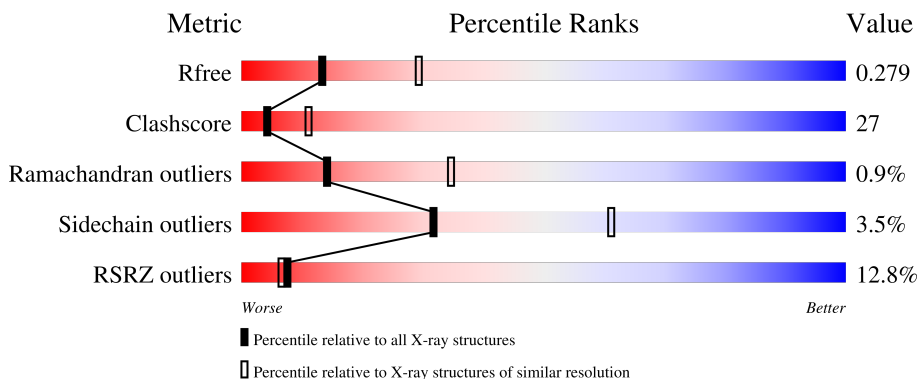
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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 $\leq 5\%$. 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	350	
1	B	350	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4983 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 Protein kinase C and casein kinase substrate in neurons protein 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	284	2354	1481	424	434	5	10	0	0	0
1	B	284	2354	1481	424	434	5	10	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP Q9UNF0
A	-5	SER	-	expression tag	UNP Q9UNF0
A	-4	SER	-	expression tag	UNP Q9UNF0
A	-3	GLY	-	expression tag	UNP Q9UNF0
A	-2	SER	-	expression tag	UNP Q9UNF0
A	-1	SER	-	expression tag	UNP Q9UNF0
A	0	GLY	-	expression tag	UNP Q9UNF0
B	-6	GLY	-	expression tag	UNP Q9UNF0
B	-5	SER	-	expression tag	UNP Q9UNF0
B	-4	SER	-	expression tag	UNP Q9UNF0
B	-3	GLY	-	expression tag	UNP Q9UNF0
B	-2	SER	-	expression tag	UNP Q9UNF0
B	-1	SER	-	expression tag	UNP Q9UNF0
B	0	GLY	-	expression tag	UNP Q9UNF0

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

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	122	Total 122	O 122	0	0
3	B	151	Total 151	O 151	0	0

LEU
SER
ARG
ARG
GLU
LYS
LYS
LYS
ALA
THR
ASP
GLY
VAL
THR
LEU
THR
GLY
ILE
ASN
GLN
THR
GLY
ASP
GLN
SER
LEU
PRO
SER
SER
LYS
PRO
SER
SER

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	31.61Å 84.65Å 357.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.88 – 2.70 39.88 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.2 (39.88-2.70) 96.2 (39.88-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.63 (at 2.69Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.226 , 0.279 0.226 , 0.279	Depositor DCC
R_{free} test set	1327 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	37.8	Xtrriage
Anisotropy	0.349	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 86.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4983	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.06% 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.

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

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	0.39	0/2393	0.87	10/3186 (0.3%)
1	B	0.40	0/2393	0.89	8/3186 (0.3%)
All	All	0.39	0/4786	0.88	18/6372 (0.3%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	ARG	N-CA-C	-6.90	103.84	111.36
1	A	98	LEU	N-CA-C	-6.47	105.25	113.01
1	A	291	GLY	CA-C-N	6.47	126.40	119.28
1	A	291	GLY	C-N-CA	6.47	126.40	119.28
1	B	67	ARG	N-CA-C	-5.93	104.90	111.36

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	2354	0	2324	138	0
1	B	2354	0	2324	132	0
2	A	2	0	0	0	0
3	A	122	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	151	0	0	11	0
All	All	4983	0	4648	254	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 27.

The worst 5 of 254 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:177:LYS:HA	1:A:182:LEU:HD21	1.49	0.94
1:B:211:SER:HA	1:B:214:GLU:HB2	1.55	0.88
1:A:143:LYS:H	1:A:144:PRO:HD2	1.37	0.88
1:A:58:GLN:HG2	1:B:51:ILE:HG12	1.56	0.86
1:B:152:VAL:HG22	1:B:211:SER:HB2	1.58	0.84

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	282/350 (81%)	253 (90%)	26 (9%)	3 (1%)	11	29
1	B	282/350 (81%)	256 (91%)	24 (8%)	2 (1%)	18	41
All	All	564/700 (81%)	509 (90%)	50 (9%)	5 (1%)	14	35

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	21	VAL
1	A	119	ALA
1	A	181	SER

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Mol	Chain	Res	Type
1	A	143	LYS
1	B	144	PRO

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	246/292 (84%)	236 (96%)	10 (4%)	27	56
1	B	246/292 (84%)	239 (97%)	7 (3%)	38	68
All	All	492/584 (84%)	475 (96%)	17 (4%)	32	61

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	173	GLU
1	B	270	LEU
1	A	257	LEU
1	A	270	LEU
1	A	296	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	175	ASN
1	B	191	GLN
1	B	186	GLN
1	B	217	GLN
1	A	228	GLN

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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	274/350 (78%)	0.71	38 (13%) 6 5	10, 54, 166, 190	0
1	B	274/350 (78%)	0.44	32 (11%) 9 7	9, 42, 156, 196	0
All	All	548/700 (78%)	0.57	70 (12%) 7 6	9, 48, 159, 196	0

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	259	ASN	5.2
1	A	297	ASN	4.6
1	B	158	ALA	4.6
1	A	144	PRO	4.0
1	A	202	LEU	3.9

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 oligosaccharides in this entry.

6.4 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. 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	B-factors(\AA^2)	Q<0.9
2	CA	A	400	1/1	0.83	0.11	57,57,57,57	0
2	CA	A	401	1/1	0.92	0.08	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.