



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:51 PM UTC

PDB ID : 1GJY / pdb_00001gjy
Title : The X-ray structure of the Sorcin Calcium Binding Domain (SCBD) provides insight into the phosphorylation and calcium dependent processes
Authors : Ilari, A.; Johnson, K.A.; Nastopoulos, V.; Tsernoglou, D.; Chiancone, E.
Deposited on : 2001-08-06
Resolution : 2.20 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)	:	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

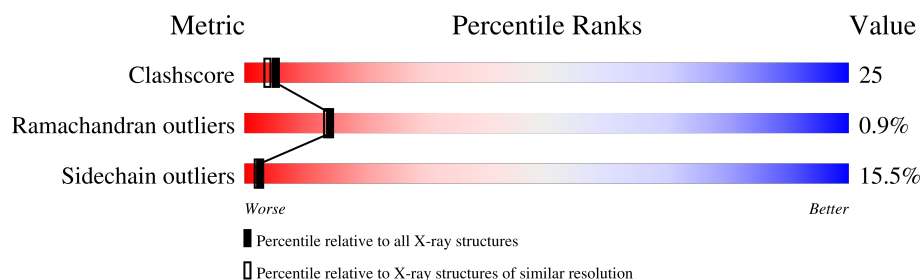
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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	167	
1	B	167	
1	C	167	
1	D	167	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5615 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 SORCIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	167	Total	C	N	O	S	0	0	0
			1321	826	227	255	13			
1	B	167	Total	C	N	O	S	0	0	0
			1321	826	227	255	13			
1	C	167	Total	C	N	O	S	0	0	0
			1321	826	227	255	13			
1	D	167	Total	C	N	O	S	0	0	0
			1321	826	227	255	13			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

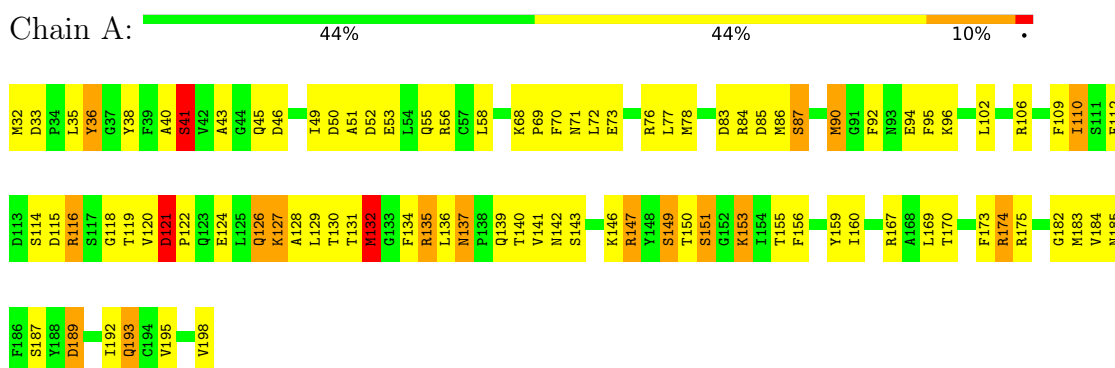
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	61	Total	O	0	0
			61	61		
3	B	62	Total	O	0	0
			62	62		
3	C	86	Total	O	0	0
			86	86		
3	D	97	Total	O	0	0
			97	97		

3 Residue-property plots

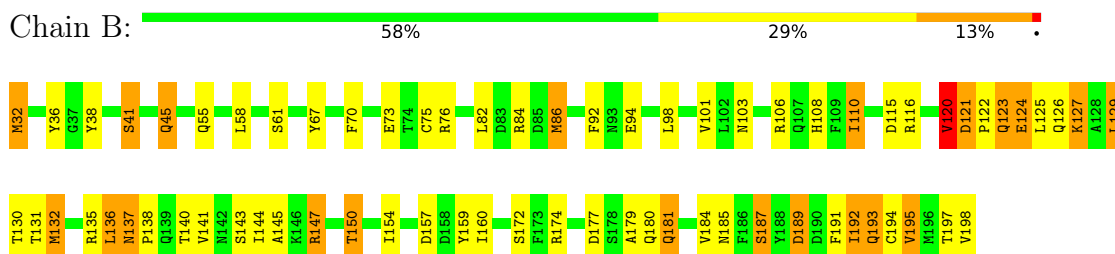
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

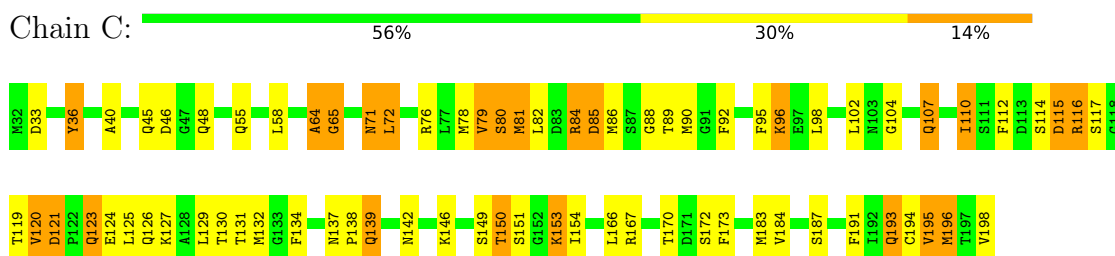
• Molecule 1: SORCIN



• Molecule 1: SORCIN



• Molecule 1: SORCIN



• Molecule 1: SORCIN



M32		Y36		I49		E53		R56		C57		L58		T59		Q60		S61		G62		I63		A64		N71		L72		E73		T74		C75		R76		L77		M78		V79		L82		D83		R84		D85		M86		M90		G91		F92		L98		V101		L102		M103		R106		F109		I110		S114		D115		R116		T119		V120		D121		F122		Q123		E124		L125
Q126		R127		A128		T131		M132		G133		F134		N137		P138		Q139		T140		V141		N142		S143		K153		L154		T155		F156		K165		D171		S172		F173		R174		R175		R176		D177		S178		A179		Q180		G182		M183		V184		S187		F191		I192		Q193		C194		V195		M196		T197		V198												

4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	130.93Å 103.85Å 78.55Å 90.00° 117.96° 90.00°	Depositor
Resolution (Å)	14.00 – 2.20	Depositor
% Data completeness (in resolution range)	85.0 (14.00-2.20)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.232 , 0.296	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5615	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

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: 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	0.75	1/1346 (0.1%)	1.20	12/1812 (0.7%)
1	B	0.88	4/1346 (0.3%)	1.23	15/1812 (0.8%)
1	C	0.75	0/1346	1.07	8/1812 (0.4%)
1	D	0.82	0/1346	1.13	9/1812 (0.5%)
All	All	0.80	5/5384 (0.1%)	1.16	44/7248 (0.6%)

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	1
1	C	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	180	GLN	CA-C	7.98	1.63	1.52
1	B	180	GLN	C-O	-7.73	1.14	1.24
1	A	90	MET	SD-CE	-6.52	1.63	1.79
1	B	181	GLN	CA-C	-5.14	1.45	1.52
1	B	32	MET	SD-CE	-5.05	1.67	1.79

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	MET	N-CA-C	-8.97	102.10	113.23
1	B	187	SER	N-CA-C	-8.61	96.80	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	182	GLY	N-CA-C	-8.49	102.98	115.63
1	A	187	SER	N-CA-C	-8.20	98.32	110.46
1	B	58	LEU	N-CA-C	-7.52	103.16	111.36

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	36	TYR	Sidechain
1	C	36	TYR	Sidechain

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	1321	0	1271	82	0
1	B	1321	0	1271	73	0
1	C	1321	0	1271	67	0
1	D	1321	0	1271	55	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	10	0	0	0	0
2	D	5	0	0	1	0
3	A	61	0	0	3	1
3	B	62	0	0	3	0
3	C	86	0	0	2	0
3	D	97	0	0	3	1
All	All	5615	0	5084	255	1

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 25.

The worst 5 of 255 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:C:132:MET:HE2	1:C:166:LEU:HD23	1.37	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:137:ASN:HB3	1:C:139:GLN:NE2	1.75	1.00
1:C:132:MET:HE3	1:C:134:PHE:HE2	1.31	0.95
1:B:123:GLN:H	1:B:123:GLN:HE21	1.12	0.88
1:C:194:CYS:O	1:C:198:VAL:HG23	1.74	0.86

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2003:HOH:O	3:D:2092:HOH:O[4_546]	1.56	0.64

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	165/167 (99%)	151 (92%)	13 (8%)	1 (1%)	21	23
1	B	165/167 (99%)	149 (90%)	14 (8%)	2 (1%)	10	8
1	C	165/167 (99%)	157 (95%)	7 (4%)	1 (1%)	21	23
1	D	165/167 (99%)	158 (96%)	5 (3%)	2 (1%)	10	8
All	All	660/668 (99%)	615 (93%)	39 (6%)	6 (1%)	14	14

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	179	ALA
1	D	84	ARG
1	A	85	ASP
1	D	85	ASP
1	C	65	GLY

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	144/144 (100%)	117 (81%)	27 (19%)	1	1
1	B	144/144 (100%)	126 (88%)	18 (12%)	4	4
1	C	144/144 (100%)	121 (84%)	23 (16%)	2	2
1	D	144/144 (100%)	123 (85%)	21 (15%)	3	2
All	All	576/576 (100%)	487 (84%)	89 (16%)	2	2

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	120	VAL
1	D	71	ASN
1	C	123	GLN
1	C	172	SER
1	D	106	ARG

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	C	137	ASN
1	D	48	GLN
1	C	193	GLN
1	D	60	GLN
1	B	45	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](#)

5 ligands are modelled in this entry.

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	$\# Z > 2$
2	SO4	C	200	-	4,4,4	0.46	0	6,6,6	0.32	0
2	SO4	C	201	-	4,4,4	0.63	0	6,6,6	0.68	0
2	SO4	B	200	-	4,4,4	1.63	1 (25%)	6,6,6	1.38	1 (16%)
2	SO4	A	200	-	4,4,4	0.49	0	6,6,6	0.49	0
2	SO4	D	200	-	4,4,4	0.24	0	6,6,6	0.49	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	200	SO4	O1-S	2.62	1.60	1.44

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	200	SO4	O4-S-O2	2.62	123.27	109.56

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
2	D	200	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

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.