



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 09:10 PM UTC

PDB ID : 4CB8 / pdb_00004cb8
Title : Structural and mutational analysis reveals that CTNNBL1 binds NLSs in a manner distinct from that of its closest armadillo-relative, karyopherin alpha
Authors : Ganesh, K.; vanMaldegem, F.; Telerman, S.B.; Simpson, P.; Johnson, C.M.; Williams, R.L.; Neuberger, M.S.; Rada, C.
Deposited on : 2013-10-10
Resolution : 2.90 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)	:	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

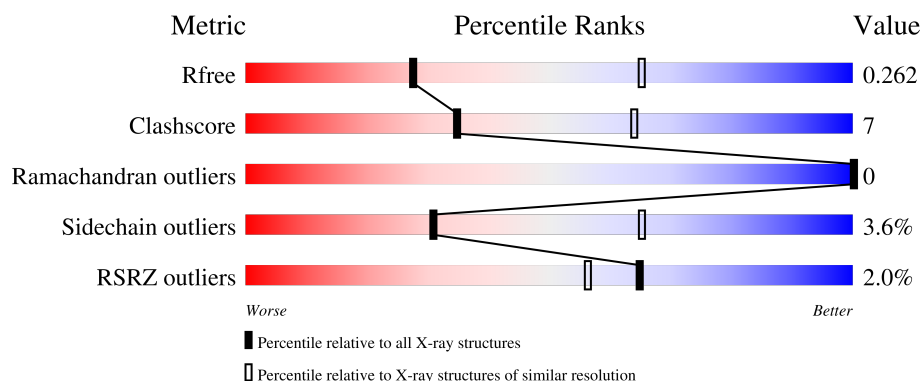
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

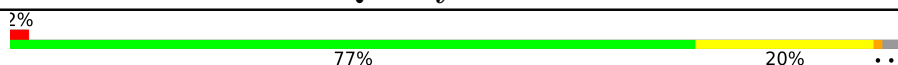
The reported resolution of this entry is 2.90 Å.

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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 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	496	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3940 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.

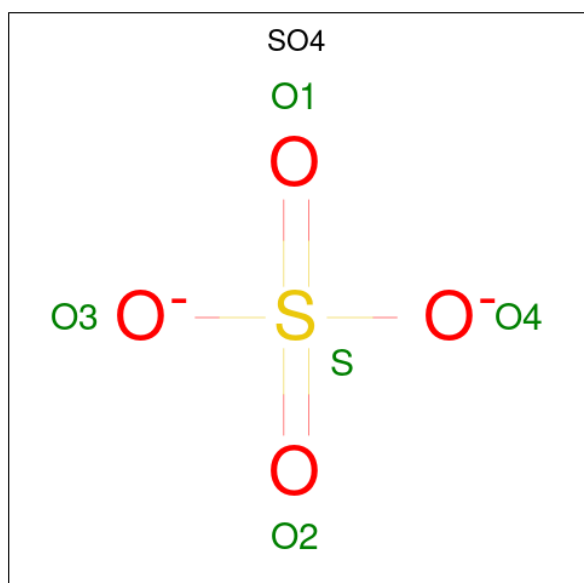
- Molecule 1 is a protein called BETA-CATENIN-LIKE PROTEIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	488	3924	2461	685	750	28	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68	MET	-	expression tag	UNP Q8WYA6
A	69	ALA	-	expression tag	UNP Q8WYA6
A	70	HIS	-	expression tag	UNP Q8WYA6
A	71	HIS	-	expression tag	UNP Q8WYA6
A	72	HIS	-	expression tag	UNP Q8WYA6
A	73	HIS	-	expression tag	UNP Q8WYA6
A	74	HIS	-	expression tag	UNP Q8WYA6
A	75	HIS	-	expression tag	UNP Q8WYA6
A	76	MET	-	expression tag	UNP Q8WYA6

- 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	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		

i

- Molecule 1: BETA-CATENIN-LIKE PROTEIN 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.10Å 92.69Å 121.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.21 – 2.90 52.21 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.5 (52.21-2.90) 96.5 (52.21-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.24 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.191 , 0.269 (Not available) , 0.262	Depositor DCC
R_{free} test set	829 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	67.7	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3940	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% 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: 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	0.76	0/3975	0.98	5/5342 (0.1%)

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	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	396	VAL	N-CA-C	6.87	117.66	110.72
1	A	362	ILE	N-CA-C	6.42	116.58	110.42
1	A	229	ARG	CA-C-N	6.08	126.25	119.32
1	A	229	ARG	C-N-CA	6.08	126.25	119.32
1	A	551	ASN	N-CA-C	6.02	117.51	111.07

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	255	PHE	Peptide
1	A	432	GLU	Peptide

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	3924	0	3968	59	0
2	A	10	0	0	0	0
3	A	6	0	0	2	0
All	All	3940	0	3968	59	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 7.

All (59) 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:200:ASN:O	1:A:203:ARG:HG2	1.84	0.76
1:A:437:LYS:HG2	3:A:2004:HOH:O	1.86	0.74
1:A:106:ASN:HB3	1:A:108:GLU:OE1	1.89	0.72
1:A:469:ARG:NE	1:A:471:GLU:OE2	2.31	0.63
1:A:526:ILE:H	1:A:526:ILE:HD12	1.64	0.62
1:A:193:VAL:HG11	1:A:225:MET:HE1	1.82	0.62
1:A:214:GLY:O	1:A:218:THR:HG23	1.99	0.62
1:A:416:ARG:HE	1:A:417:ASN:HD21	1.46	0.61
1:A:399:THR:HG23	1:A:402:GLU:H	1.64	0.61
1:A:415:LEU:HB3	1:A:502:GLU:HG2	1.84	0.60
1:A:157:VAL:O	1:A:161:VAL:HG23	2.02	0.59
1:A:439:ASP:OD1	1:A:514:ARG:NH2	2.33	0.58
1:A:343:LEU:HD11	1:A:357:LEU:CD1	2.36	0.55
1:A:490:LEU:O	1:A:494:GLN:HG3	2.08	0.54
1:A:452:MET:HE1	1:A:485:ARG:O	2.09	0.53
1:A:503:ILE:HG23	1:A:511:ILE:HG21	1.92	0.50
1:A:452:MET:CE	1:A:488:ALA:HB3	2.41	0.50
1:A:440:ARG:O	1:A:441:LEU:C	2.54	0.50
1:A:387:MET:SD	1:A:437:LYS:HD3	2.52	0.50
1:A:147:LEU:HB3	1:A:196:LEU:HD13	1.94	0.49
1:A:356:VAL:O	1:A:357:LEU:C	2.56	0.48
1:A:83:LYS:O	1:A:87:LEU:HG	2.14	0.47
1:A:452:MET:HE2	1:A:488:ALA:HB3	1.96	0.47
1:A:96:ASN:HD21	1:A:152:HIS:HE2	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ILE:HA	1:A:124:MET:HE3	1.96	0.47
1:A:285:GLY:O	1:A:288:VAL:HB	2.15	0.47
1:A:89:PHE:CZ	1:A:146:LEU:HD13	2.51	0.45
1:A:474:ASP:OD1	1:A:474:ASP:C	2.60	0.45
1:A:76:MET:HG2	1:A:77:LEU:N	2.31	0.45
1:A:547:GLU:O	1:A:551:ASN:ND2	2.49	0.45
1:A:297:LYS:HB2	1:A:341:LEU:HD23	1.98	0.45
1:A:371:HIS:CE1	1:A:419:ARG:H	2.35	0.45
1:A:416:ARG:NE	1:A:417:ASN:HD21	2.14	0.44
1:A:433:ASN:OD1	1:A:433:ASN:N	2.49	0.44
1:A:406:HIS:O	1:A:409:SER:HB3	2.17	0.44
1:A:371:HIS:HE1	1:A:419:ARG:H	1.64	0.44
1:A:379:LEU:HG	3:A:2002:HOH:O	2.17	0.44
1:A:131:PRO:HA	1:A:134:TYR:CE1	2.54	0.43
1:A:107:PRO:HA	1:A:110:PHE:CZ	2.53	0.43
1:A:142:ALA:O	1:A:146:LEU:HB2	2.17	0.43
1:A:309:MET:O	1:A:310:MET:C	2.61	0.43
1:A:533:ILE:O	1:A:536:TYR:HB3	2.19	0.43
1:A:250:LYS:HD3	1:A:288:VAL:HG22	2.00	0.43
1:A:193:VAL:HG13	1:A:194:VAL:N	2.34	0.43
1:A:336:LEU:CD1	1:A:372:LYS:HB3	2.49	0.42
1:A:429:LYS:O	1:A:437:LYS:HG3	2.19	0.42
1:A:462:GLU:O	1:A:466:MET:HG3	2.20	0.42
1:A:89:PHE:HB2	1:A:124:MET:CE	2.51	0.41
1:A:438:VAL:O	1:A:442:MET:HG2	2.20	0.41
1:A:94:TYR:O	1:A:95:LYS:C	2.63	0.41
1:A:448:TYR:O	1:A:449:LEU:C	2.63	0.41
1:A:544:ARG:CG	1:A:545:SER:H	2.34	0.41
1:A:89:PHE:CE1	1:A:117:LEU:HD11	2.56	0.41
1:A:402:GLU:O	1:A:405:GLU:HB2	2.21	0.41
1:A:89:PHE:HB2	1:A:124:MET:HE1	2.02	0.41
1:A:294:SER:O	1:A:297:LYS:HG2	2.21	0.41
1:A:221:ILE:CG2	1:A:225:MET:HE3	2.52	0.40
1:A:246:LEU:HD23	1:A:246:LEU:HA	1.96	0.40
1:A:133:LEU:O	1:A:136:LEU:HB2	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	486/496 (98%)	464 (96%)	22 (4%)	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	441/448 (98%)	425 (96%)	16 (4%)	31	65

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

Mol	Chain	Res	Type
1	A	81	SER
1	A	108	GLU
1	A	114	GLU
1	A	116	ASP
1	A	169	THR
1	A	300	ASN
1	A	324	SER
1	A	351	SER
1	A	392	LYS
1	A	394	LYS
1	A	433	ASN
1	A	452	MET
1	A	503	ILE

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Mol	Chain	Res	Type
1	A	521	MET
1	A	527	LYS
1	A	545	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	ASN
1	A	135	HIS
1	A	166	GLN
1	A	217	ASN
1	A	239	GLN
1	A	258	ASN
1	A	292	GLN
1	A	340	ASN
1	A	371	HIS
1	A	417	ASN
1	A	453	GLN
1	A	551	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](#)

2 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	A	1565	-	4,4,4	0.58	0	6,6,6	0.73	0
2	SO4	A	1564	-	4,4,4	0.29	0	6,6,6	0.44	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 [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	488/496 (98%)	-0.10	10 (2%) 65 56	38, 63, 105, 130	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	545	SER	4.9
1	A	300	ASN	3.4
1	A	103	PHE	3.4
1	A	521	MET	3.4
1	A	393	ILE	3.2
1	A	76	MET	3.0
1	A	522	ARG	2.8
1	A	91	LYS	2.7
1	A	362	ILE	2.4
1	A	544	ARG	2.2

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($\text{\AA}^2$)	Q<0.9
2	SO4	A	1565	5/5	0.92	0.10	67,69,76,80	0
2	SO4	A	1564	5/5	0.98	0.06	43,49,52,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.