



Full wwPDB X-ray Structure Validation Report i

Feb 27, 2014 – 11:51 AM GMT

PDB ID : 4CB8
Title : Structural and mutational analysis reveals that CTNNBL1 binds NLSs in a manner distinct from that of its closest armadillo-relative, karyopherin alpha
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Deposited on : 2013-10-10
Resolution : 2.90 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

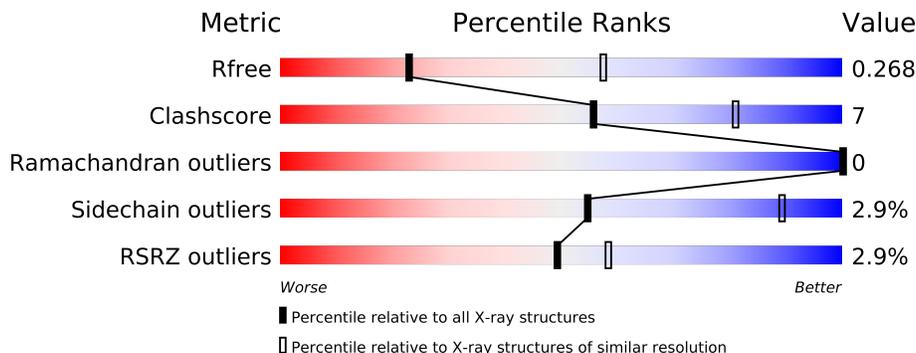
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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}	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

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 hydrogen and 0 are deuterium.

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.

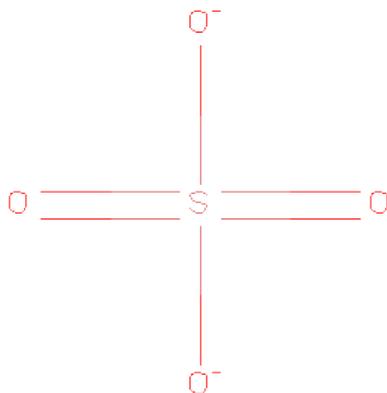
- Molecule 1 is a protein called BETA-CATENIN-LIKE PROTEIN 1.

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 (three-letter code: 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.

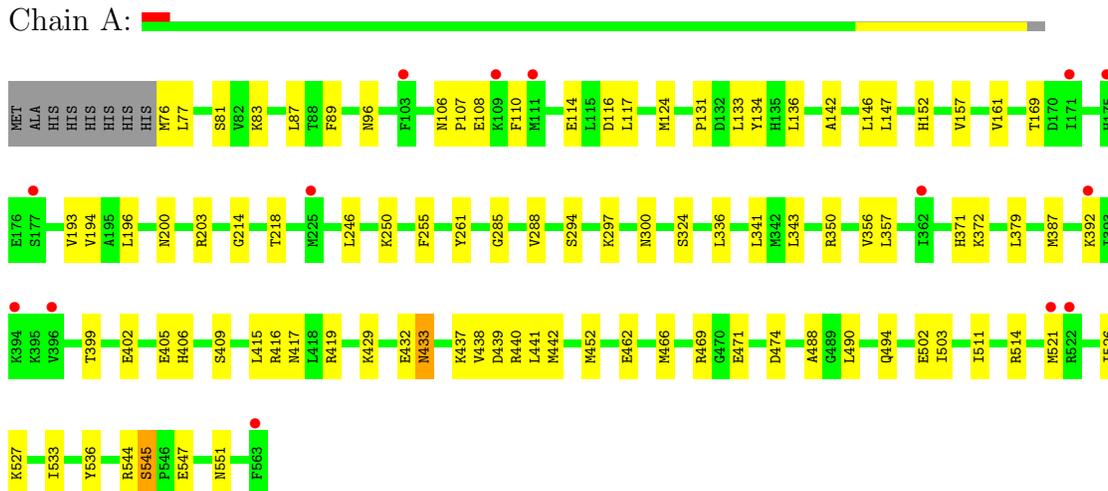
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		

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.

- Molecule 1: BETA-CATENIN-LIKE PROTEIN 1

Chain A:



4 Data and refinement statistics (i)

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 52.16 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.5 (52.21-2.90) 96.5 (52.16-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.24 (at 2.91Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.191 , 0.269 0.196 , 0.268	Depositor DCC
R_{free} test set	805 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	67.7	Xtrriage
Anisotropy	0.058	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.3	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Outliers	0 of 15836 reflections	Xtrriage
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

Xtrriage'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.

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	0.54	0/3975	0.72	0/5342

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.

There are no bond angle outliers.

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 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3924	0	3968	52	0
2	A	10	0	0	0	0
3	A	6	0	0	2	0
All	All	3940	0	3968	52	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (52) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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:214:GLY:O	1:A:218:THR:HG23	1.99	0.62
1:A:452:MET:HE1	1:A:488:ALA:HB3	1.81	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: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: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:89:PHE:HB2	1:A:124:MET:HE2	1.96	0.47
1:A:83:LYS:O	1:A:87:LEU:HG	2.14	0.47
1:A:96:ASN:HD21	1:A:152:HIS:HE2	1.62	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:440:ARG:O	1:A:441:LEU:C	2.54	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:N	1:A:433:ASN:OD1	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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:131:PRO:HA	1:A:134:TYR:CE1	2.54	0.43
1:A:142:ALA:O	1:A:146:LEU:HB2	2.17	0.43
1:A:107:PRO:HA	1:A:110:PHE:CZ	2.53	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:356:VAL:O	1:A:357:LEU:C	2.56	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:544:ARG:CG	1:A:545:SER:H	2.34	0.41
1:A:402:GLU:O	1:A:405:GLU:HB2	2.21	0.41
1:A:89:PHE:CE1	1:A:117:LEU:HD11	2.56	0.41
1:A:474:ASP:C	1:A:474:ASP:OD1	2.60	0.41
1:A:294:SER:O	1:A:297:LYS:HG2	2.21	0.41
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%)	428 (97%)	13 (3%)	55 89

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	SER
1	A	114	GLU
1	A	116	ASP
1	A	169	THR
1	A	261	TYR
1	A	300	ASN
1	A	324	SER
1	A	350	ARG
1	A	392	LYS
1	A	433	ASN
1	A	521	MET
1	A	527	LYS
1	A	545	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	ASN
1	A	166	GLN
1	A	217	ASN
1	A	239	GLN
1	A	258	ASN
1	A	292	GLN
1	A	371	HIS
1	A	417	ASN
1	A	551	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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	1564	-	4,4,4	0.44	0	6,6,6	0.71	0
2	SO4	A	1565	-	4,4,4	0.68	0	6,6,6	0.90	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
2	SO4	A	1564	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1565	-	-	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.

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

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%)	0.24	14 (2%) 49 58	38, 63, 105, 130	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	521	MET	3.7
1	A	103	PHE	3.3
1	A	563	PHE	2.8
1	A	396	VAL	2.6
1	A	171	ILE	2.5
1	A	109	LYS	2.4
1	A	522	ARG	2.4
1	A	225	MET	2.4
1	A	177	SER	2.1
1	A	362	ILE	2.1
1	A	394	LYS	2.1
1	A	111	MET	2.0
1	A	392	LYS	2.0
1	A	175	HIS	2.0

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	A	1564	5/5	0.20	0.03	43,49,52,53	0
2	SO4	A	1565	5/5	0.16	-1.33	67,69,76,80	0

6.5 Other polymers

There are no such residues in this entry.