

## Supporting Information

# **Structural insights into a novel ARM repeat protein CTNNBL1 and its association with the hPrp19/CDC5L complex**

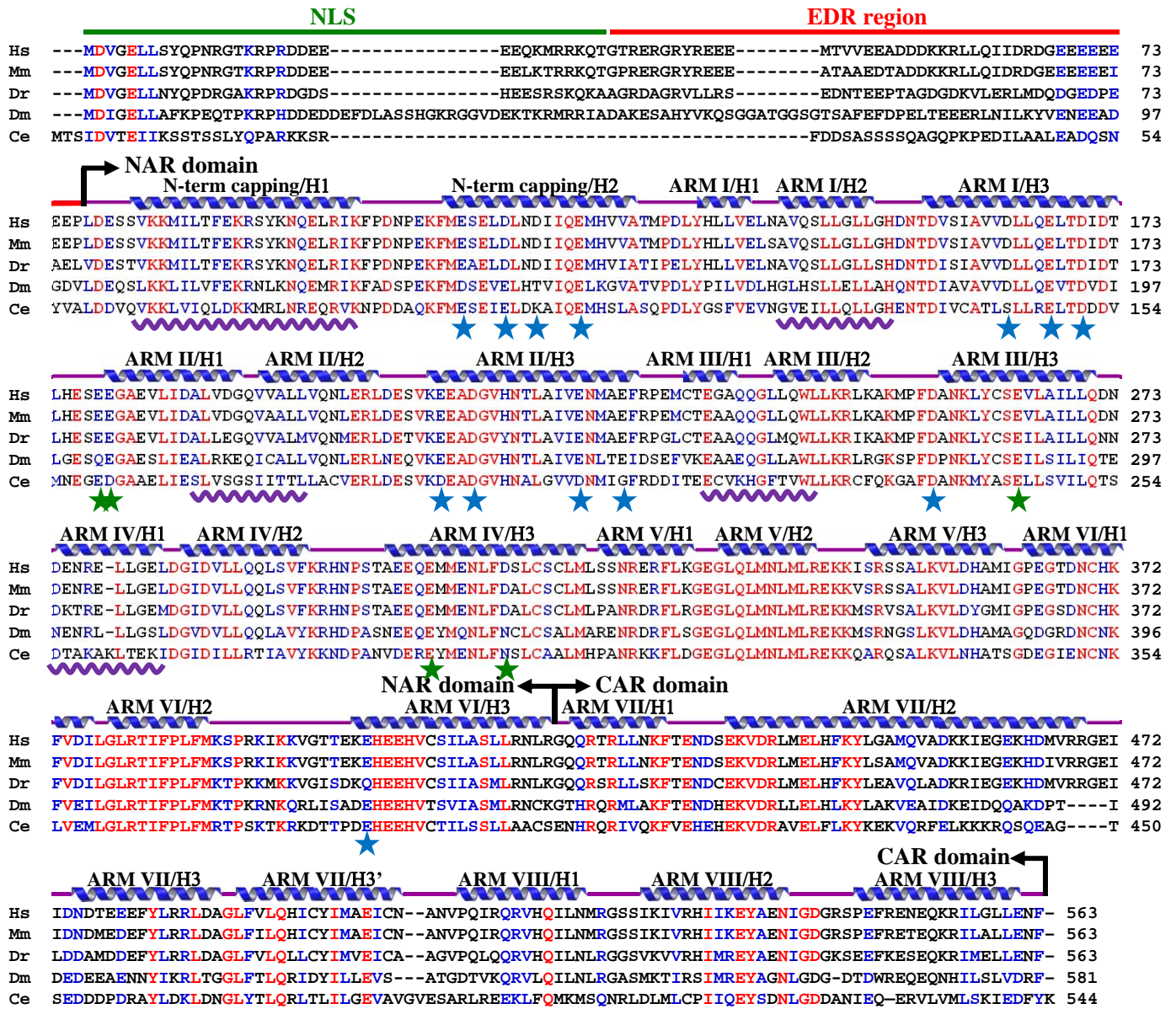
Jae-Woo Ahn, Sangwoo Kim, Eun-Jung Kim, Yeo-Jin Kim and Kyung-Jin Kim\*

\*Correspondence should be addressed to: Email: [kkim@knu.ac.kr](mailto:kkim@knu.ac.kr)

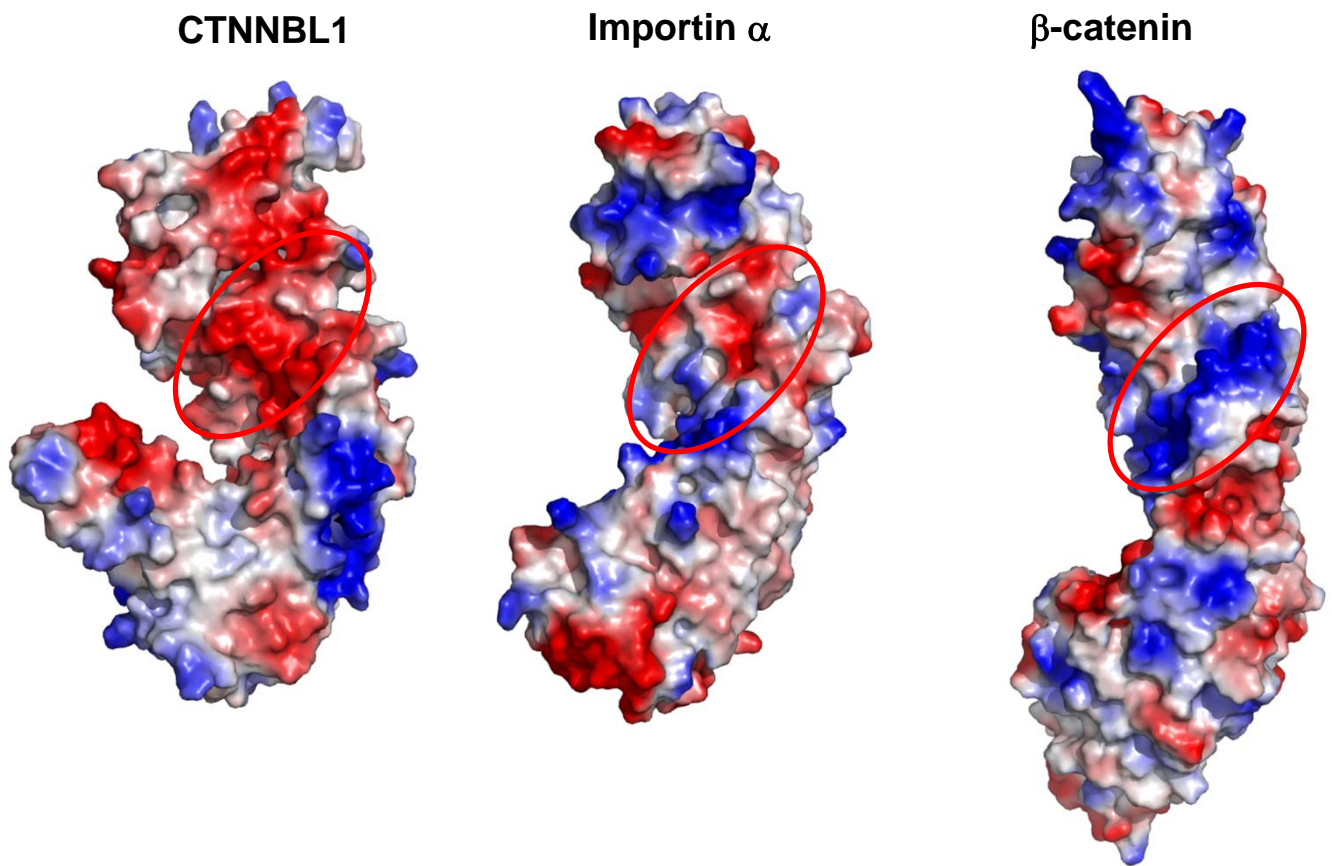
This PDF file includes:

Supporting Figures S1 to S3

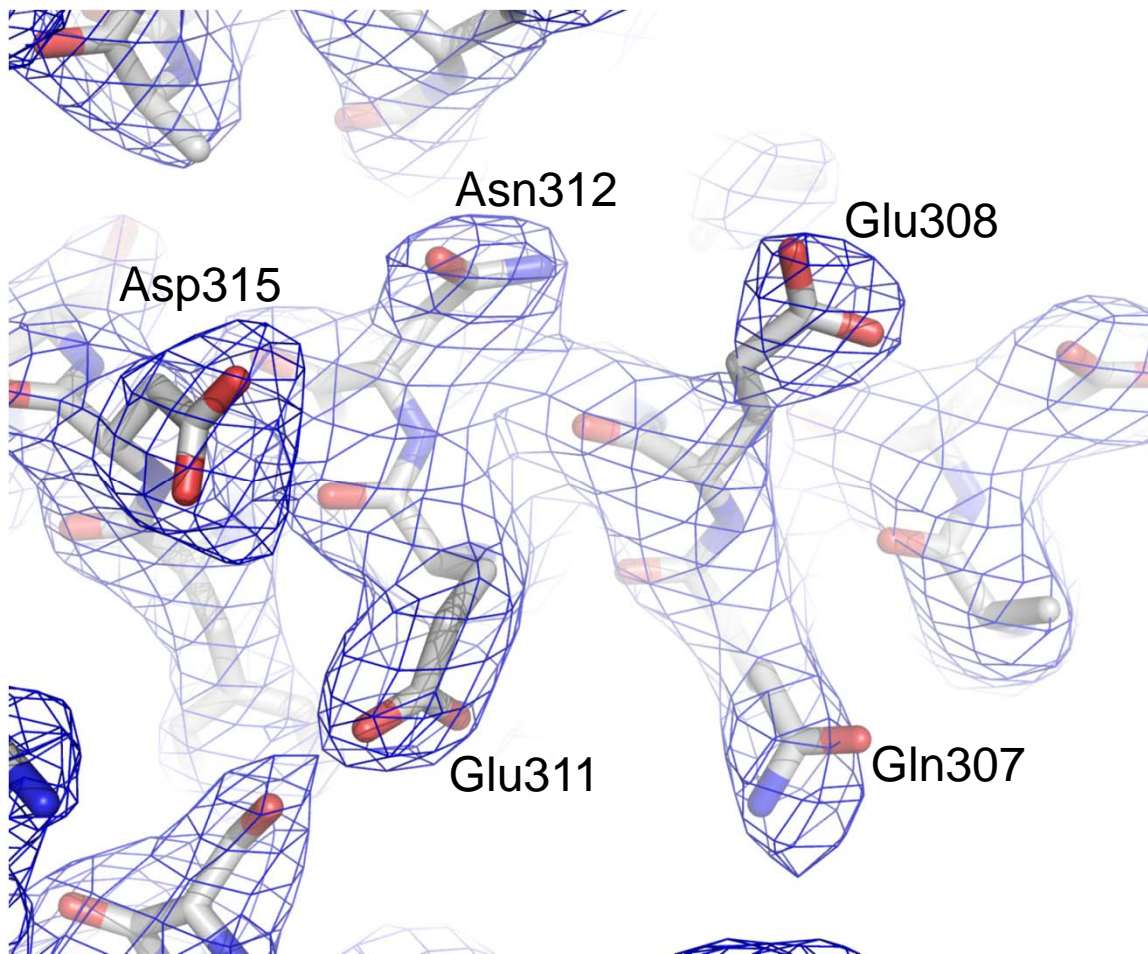
Supporting Tables S1 and S2



**Supporting Figure S1.** Amino acid sequence alignment of CTNNB1. Secondary structure elements are shown based on the crystal structure of CTNNB1. Identical and highly conserved residues are presented in red and blue colored characters, respectively. The NLS and EDR region were indicated by green and red colored lines, respectively, and the NAR and the CAR domains were labeled. The residues involved in the formation of the negative-charged patch are indicated with asterisks, and the residues whose simultaneous mutations abolish the binding with CDC5L were distinguished with green colored asterisks. Hs, Mm, Dr, Dm, and Ce are abbreviations for *Homo sapiens*, *Mus musculus*, *Danio rerio*, *Drosophila melanogaster*, and *Caenorhabditis elegans*, respectively.



**Supporting Figure S2.** Charge comparison of the CDC5L binding site of CTNNBL1 with the ligand binding sites of Importin  $\alpha$  and  $\beta$ -catenin. Structures of CTNNBL1, Importin  $\alpha$  and  $\beta$ -catenin are presented as surface electrostatic potential models, and the binding sites of the proteins are indicated with red-colored circle.



**Supporting Figure S3.** Electron density map of the CTNNBL1 structure. In order to show the quality of the electron density map of the CTNNBL1 structure, residues in the H3 helix of the ARM IV are shown in a stick model, and their omit electron densities (blue mesh) are contoured at  $2.0 \sigma$ .

**Supporting Table S1.** Primer oligonucleotide sequences used for the cloning of CTNNBL1 and CDC5L.

<b>Gene</b>	<b>Cloning primer</b>	<b>Restriction site</b>	<b>Primer sequence</b>
CTNNBL1	33_Forward	Nde I	5'-GCGCGCATATGACTGGTACTCGAGAACGCGGCC-3'
	77_Forward	Nde I	5'-GCGCGCATATGCCATTGGATGAAAGCTCAGTGAAG-3'
	563_Reverse	Sal I	5'-GCGCGGTCGACCTAGAAGTTCTCCAGCAAGCCCAG-3'
CDC5L	141_Forward	Nde I	5'-GCGCGCATATGCCAATTGATATGGATG-3'
	377_Reverse	Xho I	5'-GCGCGCTCGAGGGTGTCCACATTG-3'



**Supporting Table S2.** Primer oligonucleotide sequences used for the mutation of CTNNBL1.

<b>CTNNBL1 mutation primer</b>	<b>Primer sequence</b>
E167R_Forward	5'-GGTCGATTTGCTTCAGCGATTAACAGATATAGACACCC-3'
E167R_Reverse	5'-GGGTGTCTATATCTGTTAATCGCTGAAGCAAATCGACC-3'
E178R/E179R_Forward	5'-CCCTCCATGAGAGTCGACGGGGAGCAGAAGTGCTC-3'
E178R/E179R_Reverse	5'-GAGCACTTCTGCTCCCCGTCGACTCTCATGGAGGG-3'
D213R_Forward	5'-CTGTGAAAGAGGAGGCACGGGGCGTCCACAACAC-3'
D213R_Reverse	5'-GTGTTGTGGACGCCCCGTGCCTCCTCTTTCACAG-3'
D256R_Forward	5'-GAAGGCAAAGATGCCTTTTCGTGCCAACAACTGTATTG-3'
D256R_Reverse	5'-CAATACAGTTTGTGGCACGAAAAGGCATCTTTCCTTC-3'
E308R_Forward	5'-CGGCTGAGGAGCAGCGGATGATGGAGAATCTGTTTG-3'
E308R_Reverse	5'-CAAACAGATTCTCCATCATCCGCTGCTCCTCAGCCG-3'
E402R_Forward	5'-GGGAACCACTGAGAAGCGACATGAAGAGCATGTCTG-3'
E402R_Reverse	5'-CAGACATGCTCTTCATGTCGCTTCTCAGTGGTTCCC-3'
E223R_Forward	5'-GGCTATTGTGCGCAACATGGCTG-3'
E223R_Reverse	5'-CAGCCATGTTGCGCACAATAGCC-3'
E264R_Forward	5'-CTGTATTGCAGTCGCGTGCTGGCC-3'
E264R_Reverse	5'-GGCCAGCACGCGACTGCAATACAG-3'
D315R_Forward	5'-GAGAATCTGTTTCGTTCCCTCTGC-3'
D315R_Reverse	5'-GCAGAGGGAACGAAACAGATTCTC-3'