

Table S1. ScanProsite Score hits by 1 profile (pattern PS00018*)			
Loop	HsCaNB-1	TcCaNB	LsppCaNB
1	8181	None	9855
2	12840	8544	9018
3	14402	13202	13621
4	13286	10915	12589

*EF-hand calcium-binding domain.

Table S2. Myristoylator results			
HsCaNB-1 = The protein is predicted as myristoylated			
	Positive	Negative	Score
Average response of 25 neural networks	0.994907	0.00506406	0.98984294
TcCaNB = The protein is predicted as non-myristoylated			
	Positive	Negative	Score
Average response of 25 neural networks	0.426957	0.573101	-0.146144

A

Query = HsCaNB-1
Sbjct = TcCaNB

Score	Expect	Method	Identities	Positives	Gaps
138 bits(348)	6e-47	Compositional matrix adjust.	72/159(45%)	99/159(62%)	6/159(3%)
Query 1	MGNEASY-PEM-----	CSHFDADEIKRLGKRFKLDLDSGSLSVVEEFMSLPQLQNPL	54		
Sbjct 1	MGEGSSFTPEEMRQLREATAFSEAQIVRLQKRFATLAQGGGRLTAEALSSISSVASNPL	60			
Query 55	VQRFIDFDTGNGEVDFFKEFIEGVSVQSVKDGKEQKLRFAFRIYDMKDGYSINGELFQ	114			
Sbjct 61	LGRVLAVLDTSGDGKIDFMTFAKALAVFSQADKRLRFTFKMYDVGDDGKISNKDLFE	120			
Query 115	VLKMMVGNLKDQTLQQLQIVDKTIINADKDGGRISFEFF	153			
Sbjct 121	TLTIMGVTNLGVQLQQLQIVDKTFIEVDLNRDGYITFEFF	159			

B

Query = HsCaNB-1
Sbjct = LsppCaNB

Score	Expect	Method	Identities	Positives	Gaps
149 bits(376)	3e-51	Compositional matrix adjust.	75/148(51%)	99/148(66%)	0/148(0%)
Query 19	EIKRLGKRFKLDLDSGSLSVVEEFMSLPQLQNPLVQRFIDFDTGNGEVDFFKEFIEG	78			
Sbjct 24	QVQRLYKSFSLNKKSGKITRAEFNSIPALASNPLVDRVLAVMDTDGSDTVDFGDFVRA	83			
Query 79	VSQFSVKGDKKEQKLRFAFRIYDMKDGYSINGELFQVLKMMVGNLKDQTLQQLQIVDKTII	138			
Sbjct 84	LAVLSSATSKEDKRLRFTFKMYDIDGGRISNKDLFQMLSINVGVLNSQMLQQLQIVDKTFI	143			
Query 139	NADKDGGRISFEFFCAVVGGLDIHKM	166			
Sbjct 144	EADVDRDGYITFEFFQALAVNSDFGRL	171			

Figure S1. BLAST protein comparison of *HsCaNB-1* with *TcCaNB* (A) and *HsCaNB-1* with *LsppCaNB* (B) using Blast 2 sequences interface (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&BLAST_SPEC=blast2seq&LINK_LOC=blasttab&LAST_PAGE=blastp&BLAST_INIT=blast2seq)

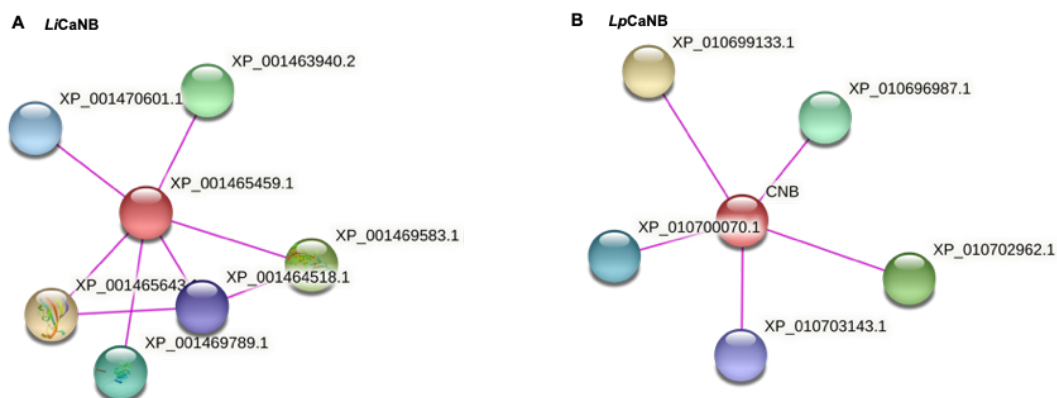


Figure S2. Protein-protein interaction network of the *Leishmania infantum* (LiCaNB) and *Leishmania panamensis* (LpCaNB) CaNB proteins (STRING V.11.0). The line indicates the type of interaction evidence (experimentally determined). Parameters: Score (high confidence 0.7), sources of interaction used: experimental and databases. In A: XP_001465459.1 (Calcineurin B subunit, putative), XP_001470601.1 (Serine/threonine protein phosphatase, putative), XP_001463940.2 (Uncharacterized protein), XP_001465643.1 (Peptidylprolyl isomerase, Fk506-binding protein 1-like protein), XP_001469789.1 (Serine/threonine protein phosphatase 2B catalytic subunit A2, putative), XP_001464518.1 (Uncharacterized protein) and in B: CNB (Calcineurin B subunit, putative), XP_010699133.1 (Peptidylprolyl isomerase), XP_010696987.1 (Serine/threonine-specific protein phosphatase, putative), XP_010700070.1 (Serine/threonine-protein phosphatase), XP_010703143.1 (Serine/threonine protein phosphatase 2B catalytic subunit A2, putative) and XP_010702962.1 (Peptidylprolyl isomerase).

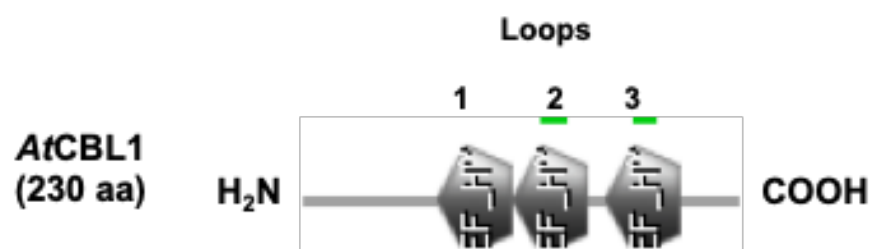


Figure S3. Protein domain architecture of calcineurin B-like of *Arabidopsis thaliana* (AtCBL1)