

	(1)	1	10	20	30	46
AtCAM1 NP_001154755	(1)	-----	-----	-----	-----	-----
OsCaM LOC_Os05g41210	(1)	-----	-----	-----	-----	-----
AtCAM2 NP_001189724	(1)	-----	-----	-----	-----	-----
OsCaM3 LOC_Os01g17190	(1)	-----	-----	-----	-----	-----
CeCaM NP_503386	(1)	-----	-----	-----	-----	-----
DrCaM BC164893	(1)	-----	-----	-----	-----	-----
HsCML3 NP_005176	(1)	-----	-----	-----	-----	-----
ScCaM NP_009667	(1)	-----	-----	-----	-----	-----
MmCam4 NP_064420	(1)	-----	-----	-----	-----	-----
AtCBL4 AF192886	(1)	-----	-----	-----	-----	-----
OsCBL4 ABA54179	(1)	-----	-----	-----	-----	-----
TaCBL4	(1)	-----	-----	-----	-----	-----
OsCBL7 ABA54182	(1)	-----	-----	-----	-----	-----
TaCBL7	(1)	-----	-----	-----	-----	-----
OsCBL9 ABA54184	(1)	MESGYGFRFS	DDDDVESAS	SLTVGERLCA	AFLPFVAIAE	AVFFALTD
TaCBL9	(1)	MASRFNSRIS	SGDLRSGSSL	TVGERLCAVVL	PFVAIAEFVFF	ALTD
AtCBL1 AAC26008	(1)	-----	-----	-----	-----	-----
AtCBL9 AF411958_1	(1)	-----	-----	-----	-----	-----
OsCBL1 ABA54176	(1)	-----	-----	-----	-----	-----
TaCBL1	(1)	-----	-----	-----	-----	-----
AtCBL7 AF290434_1	(1)	-----	-----	-----	-----	-----
AtCBL6 AF192884_1	(1)	-----	-----	-----	-----	-----MMMQ
AtCBL2 AAC26009	(1)	-----	-----	-----	-----	-----MSQ
AtCBL3 AAC26010	(1)	-----	-----	-----	-----	-----MSQ
OsCBL2 ABA54177	(1)	-----	-----	-----	-----	-----MVQ
OsCBL3 ABA99199	(1)	-----	-----	-----	-----	-----MVQ
TaCBL2	(1)	-----	-----	-----	-----	-----MVQ
TaCBL3	(1)	-----	-----	-----	-----	-----MLQ
OsCBL6 ABA54181	(1)	-----	-----	-----	-----	-----MVD
TaCBL6	(1)	-----	-----	-----	-----	-----MVD
Consensus	(1)	-----	-----	-----	-----	-----

	(47)	47	60	70	80	92
AtCAM1 NP_001154755	(1)	-----	-----	-----	-----	-----
OsCaM LOC_Os05g41210	(1)	-----	-----	-----	-----	-----
AtCAM2 NP_001189724	(1)	-----	-----	-----	-----	-----
OsCaM3 LOC_Os01g17190	(1)	-----	-----	-----	-----	-----
CeCaM NP_503386	(1)	-----	-----	-----	-----	-----
DrCaM BC164893	(1)	-----	-----	-----	-----	-----
HsCML3 NP_005176	(1)	-----	-----	-----	-----	-----
ScCaM NP_009667	(1)	-----	-----	-----	-----	-----
MmCam4 NP_064420	(1)	-----	-----	-----	-----	-----
AtCBL4 AF192886	(1)	-----M	GCSVSK-----	-----K	KKKNAMR-PP	G-----
OsCBL4 ABA54179	(1)	-----M	GCASS-----	-----K	QFKR-PP	G-----
TaCBL4	(1)	-----M	GCVLSS-----	-----P	-----RRSR-TP	G-----
OsCBL7 ABA54182	(1)	-----M	GCISS-----	-----K	QFKR-AAE	-----
TaCBL7	(1)	-----M	GCVSS-----	-----K	QFRR-APP	-----
OsCBL9 ABA54184	(47)	CLADLLPPS	AAAS---R	HRRSAA	SSYLA	AVAR--KWNHQQRGRVG
TaCBL9	(47)	CLAGICSPP	SASSSSHP	RRDPS	APSFFLT	AKKCSHHHHHLLRRRVA
AtCBL1 AAC26008	(1)	-----M	GCFHSK-----	-----A	AKEF----	RC-----
AtCBL9 AF411958_1	(1)	-----M	GCFHST-----	-----A	AAREF----	PD-----
OsCBL1 ABA54176	(1)	-----M	GCFQST-----	-----A	RRP--R--	PG-----
TaCBL1	(1)	-----M	GCIQST-----	-----P	KRRQHP--	AG-----
AtCBL7 AF290434_1	(1)	-MDSTRNS	SASNST---	-----G	CFTDQK-	-----
AtCBL6 AF192884_1	(5)	CLDGLKH	LALILLT---	-----C	CDADPP--	KV-----
AtCBL2 AAC26009	(4)	CVDGIKHL	CTSVLG---	-----C	FDLDLYKQ	SGG-----
AtCBL3 AAC26010	(4)	CIDGFKH	VCSFFR---	-----C	FDIDIYKQ	SGG-----
OsCBL2 ABA54177	(4)	CLDGVRQ	LAVVFK---	-----C	CDLELK-Q	PRG-----
OsCBL3 ABA99199	(4)	CLDGVRQ	LAVVFK---	-----C	CDLELK-Q	PRG-----
TaCBL2	(4)	CLDGVKH	LAVLFK---	-----C	CDLELK-Q	PRG-----
TaCBL3	(4)	CLEGVRH	LGGVLLK---	-----C	CDIDLK-Q	PKG-----
OsCBL6 ABA54181	(4)	SSEGLRR	LAAALLFK---	-----C	CSLDS	SNRPNG-----
TaCBL6	(4)	FPEGLRR	LAAALLFK---	-----C	CDLDI	PNRPKG-----
Consensus	(47)		M			G

	(93)	93	100	110	120	138
AtCAM1 NP_001154755	(1)	-----	MADQLTDEQ	ISEFKEAFS	LFDKDGDVFF	LSDLG
OsCaM LOC_Os05g41210	(1)	-----	MADQLTDEQ	IAEFKEAFS	LFDKDG	-----
AtCAM2 NP_001189724	(1)	-----	MADQLTDDQ	ISEFKEAFS	LFDKDGDG	-----
OsCaM3 LOC_Os01g17190	(1)	-----	MADQLTDDQ	IAEFKEAFS	LFDKDG	-----
CeCaM NP_503386	(1)	-----	MADQLTEEQ	IAEFKEAFS	LFDKDG	-----
DrCaM BC164893	(1)	-----	MADQLTEEQ	IAEFKEAFS	LFDKDG	-----
HsCML3 NP_005176	(1)	-----	MADQLTEEQ	VTEFKEAFS	LFDKDG	-----
ScCaM NP_009667	(1)	-----	MSSNLTEEQ	IAEFKEAF	ALFDKDN	-----
MmCam4 NP_064420	(1)	-----	MSHGF	TKEEVAE	FQAAFNR	FDKKN
AtCBL4 AF192886	(19)	-----	YEDPELLASV	TPFTVEEVEALY	ELFKKLS	SII
OsCBL4 ABA54179	(15)	-----	YEEPAVLLAQ	TTFTVNEVEALRELY	NKMSY	SII
TaCBL4	(17)	-----	YEEPTVLA	SQTSFTVNEVEALY	ELFKKLS	SIF
OsCBL7 ABA54182	(15)	-----	HEDPAIILAKE	TTFSVSEVEALY	ELFKKISH	SIF
TaCBL7	(15)	-----	HEDAALLAKE	TTFSLNEVEALY	ELFKKIS	SIF
OsCBL9 ABA54184	(87)	IGCTS	LTLRQLARL	LADESRC	FSVNEVEALFELY	EKTS
TaCBL9	(93)	PGCSS	LSFRDLARL	LADESRC	FSVNEVEALFELY	KKIS
AtCBL1 AAC26008	(15)	-----	HEDPVKLA	SETAFSVSEVEALFELFKS	ISS	SVV
AtCBL9 AF411958_1	(15)	-----	HENPVKLA	SETAFSVSEVEALYELFKS	ISS	SVV
OsCBL1 ABA54176	(15)	-----	YEDPVGLA	SETAFSVSEVEALFELFKS	IS	SVI
TaCBL1	(17)	-----	YEDPVHLLA	SQTAFSVSEVEALFELFKS	IS	SVI
AtCBL7 AF290434_1	(21)	-----	KRK---	ALYEVFKKLS	GVDCQRNEGNV	VEGVTC
AtCBL6 AF192884_1	(28)	-----	RQNP	KDVARGTVFTVNE	TEALYELFKS	IS
AtCBL2 AAC26009	(30)	-----	LGDPELLA	RDTVFSVSETEALYELFKKIS	SAVI	-----
AtCBL3 AAC26010	(30)	-----	LGDPELLA	RDTVFSVSETEALYELFKKIS	SAVI	-----
OsCBL2 ABA54177	(29)	-----	LEDQPVLARE	TVFSVSEVEALYELFKKIS	SAVI	-----
OsCBL3 ABA99199	(29)	-----	LEDQPVLARE	TVFSVSEVEALYELFKKIS	SAVI	-----
TaCBL2	(29)	-----	LEDQPVLARE	TVFSVSEVEALYELFKKIS	SAVI	-----
TaCBL3	(29)	-----	LEDPEVLARE	TVFSVSEVEALYELFKKIS	SAVI	-----
OsCBL6 ABA54181	(30)	-----	LQDPERLARE	TVFNVNE	TEALYELFKKIS	SAVV
TaCBL6	(30)	-----	LEDPERLARE	TVFSVNE	TEALYELFKKIS	SAVV
Consensus	(93)		EDPMLA	TFSVSEVEALFELFKKIS	SVI	

EF hand 1

	(139)	139	150	160	170	184
AtCAM1 NP_001154755	(34)	FDFKRLSNCL	ETTPELSH	GCITTKEL	LGTVMRSLGQNPTEAELQDMI	
OsCaM LOC_Os05g41210	(25)	-----	-----	DGCITTKEL	LGTVMRSLGQNPTEAELQDMI	
AtCAM2 NP_001189724	(27)	-----	MLHPPFP	SIIVG	GCITTKEL	LGTVMRSLGQNPTEAELQDMI
OsCaM3 LOC_Os01g17190	(25)	-----	-----	-----	DGCITTKEL	LGTVMRSLGQNPTEAELQDMI
CeCaM NP_503386	(25)	-----	-----	-----	DGTITTKEL	LGTVMRSLGQNPTEAELQDMI
DrCaM BC164893	(25)	-----	-----	-----	DGTITTKEL	LGTVMRSLGQNPTEAELQDMI
HsCML3 NP_005176	(25)	-----	-----	-----	DGCITTKREL	LGTVMRSLGQNPTEAELRDMM
ScCaM NP_009667	(25)	-----	-----	-----	NGSISSE	LATVMRSLGLSPSEAEVNDLM
MmCam4 NP_064420	(25)	-----	-----	-----	DGHSVVEE	LGDMKQLGK
AtCBL4 AF192886	(52)	-----	-----	-----	DDGLIHKEEFQALALFR	NRN
OsCBL4 ABA54179	(48)	-----	-----	-----	KDGLIHKEEFQALALFR	NSRK
TaCBL4	(50)	-----	-----	-----	KDGLIHKEEFRLALFR	TSK
OsCBL7 ABA54182	(48)	-----	-----	-----	KDGLIHKEEFQALALFR	NSNK
TaCBL7	(48)	-----	-----	-----	KDGLIHKEEFQALALFR	NSNR
OsCBL9 ABA54184	(128)	-----	-----	-----	DDGLTHKEEPQALALFR	TPSG
TaCBL9	(134)	-----	-----	-----	NDGLIHKEELQALALFK	TPSG
AtCBL1 AAC26008	(48)	-----	-----	-----	DDGLINKEEFQALALFK	SRKR
AtCBL9 AF411958_1	(48)	-----	-----	-----	DDGLINKEEFQALALFK	NRKK
OsCBL1 ABA54176	(48)	-----	-----	-----	DDGLINKEEFRLALFK	NRKK
TaCBL1	(50)	-----	-----	-----	DDGLINKEEFQALALFK	NTRK
AtCBL7 AF290434_1	(51)	-----	-----	-----	YYGEMNKQFHVAIF	QTDKN
AtCBL6 AF192884_1	(57)	-----	-----	-----	KNGLIDKEQFQLVLF	KMNT
AtCBL2 AAC26009	(63)	-----	-----	-----	DDGLINKEEFQALALFK	TNKK
AtCBL3 AAC26010	(63)	-----	-----	-----	DDGLINKEEFQALALFK	TNKK
OsCBL2 ABA54177	(62)	-----	-----	-----	DDGLINKEEFQALALFK	TSKK
OsCBL3 ABA99199	(62)	-----	-----	-----	DDGLINKEEFQALALFK	TSKK
TaCBL2	(62)	-----	-----	-----	DDGLINKEEFQALALFK	TSKK
TaCBL3	(62)	-----	-----	-----	DDGLINKEEFQALALFK	TSKK
OsCBL6 ABA54181	(63)	-----	-----	-----	DDGLINKEEFQALALFK	TNRK
TaCBL6	(63)	-----	-----	-----	DDGVINKEEFQALALFK	TNRK
Consensus	(139)			DGLI	KEEFQALALFK	KK

EF hand 1

EF hand 2

	(185)	185	190	200	210	220	230
AtCAM1 NP_001154755	(80)	NEV	DADGNGTIDFPEFLNLMAKMKMDTDSSEELKEAFRVFDKDQNG				
OsCaM LOC_Os05g41210	(54)	NEV	DADGNGTIDFPEFLNLMAKMKMDTDSSEELKEAFRVFDKDQNG				
AtCAM2 NP_001189724	(66)	NEV	DADGNGTIDFPEFLNLMAKMKMDTDSSEELKEAFRVFDKDQNG				
OsCaM3 LOC_Os01g17190	(54)	NEV	DADGNGTIDFPEFLNLMAKMKMDTDSSEELKEAFRVFDKDQNG				
CeCaM NP_503386	(54)	NEV	DADGNGTIDFPEFLTMARKMKDTDSSEELIREAFRVFDKDGNG				
DrCaM BC164893	(54)	NEV	DADGNGTIDFPEFLTMARKMKDTDSSEELIREAFRVFDKDGNG				
HsCML3 NP_005176	(54)	SEI	DRDNGTIDFPEFLGMARKMKDTDSSEELIREAFRVFDKDGNG				
ScCaM NP_009667	(54)	NEI	DVDGNHQIEFSEFLALMSRQLKSNDSSEQLLEAFKVFDDKNGDG				
MmCam4 NP_064420	(54)	SKL	TDGDGKISFEFLTAIEKYKKGHRAG-ELRAVFNVLDDQNGDG				
AtCBL4 AF192886	(81)	DMFD	VKRNGVIEFGEFVRSLSGVFHPSPAPVHEKVKFAFKLYDLRQTG				
OsCBL4 ABA54179	(77)	DLFD	LKRNGVIEFGEFVRSLSVFHPKAPKSEKTAFAFKLYDLRGTG				
TaCBL4	(79)	DLFD	LKRNGVIEFGEFVRSLSIFHPKAPSEKTAFAFKLYDLRGTG				
OsCBL7 ABA54182	(77)	DLFD	LKRNGVIDFGEFVRSLSIFHPKAPSEKTAFAFKLYDLRGTG				
TaCBL7	(77)	DLFD	LKRNGVIEFEEFVRSLSHIFHPDTPMADKIAFAFRLYDLRGTG				
OsCBL9 ABA54184	(157)	DLFDE	EKKNGVIEFDEFIHALSVFHP LAPLEDKINFAFRLYDLRQTG				
TaCBL9	(163)	DLFDE	EKKNGVIEFEEFIHALSVFHP LAPVEDKINFAFRLYDLRQTG				
AtCBL1 AAC26008	(77)	DMFD	VKRKGVIDFGDFVRSLSNVFHPNASLEDKIDFTFRLYDMDCGT				
AtCBL9 AF411958_1	(77)	DLFD	VKRKGVIDFGDFVRSLSNVFHPNASLEEKTDFTFRLYDMDCGT				
OsCBL1 ABA54176	(77)	DLFD	VKKRGVIDFGDFVRSLSNVFHPNIPMEEKIDFSFKLYDMDN TG				
TaCBL1	(79)	DLFD	VKKRGVIDFGDFVRSLSNVFHPNIPVEEKIDFSFKLYDMDGTG				
AtCBL7 AF290434_1	(80)	DLFD	TNHDLGLGFEEFARALS VFHSPAPIDDKIDLSFQLYDLKQQG				
AtCBL6 AF192884_1	(86)	DLFD	TKNTGILDFEAFARALS VFHPNAKFDKIEFSFKLYDLNQQG				
AtCBL2 AAC26009	(92)	DLFD	TKHNGILGFEEFARALS VFHPNAPIDDKIHFSFQLYDLKQQG				
AtCBL3 AAC26010	(92)	DLFD	TKHNGILGFEEFARALS VFHPNAPIEDKIDFSFQLYDLKQQG				
OsCBL2 ABA54177	(91)	DLFD	TKHNGILGFDFEFARALS VFHSPAPLDEKIDFSFQLYDLKQQG				
OsCBL3 ABA99199	(91)	DLFD	TKHNGILGFDFEFARALS VFHSPAPLDEKIDFSFQLYDLKQQG				
TaCBL2	(91)	DLFD	TKHNGILGFEEFARALS VFHPNASVEEKIDFSFQLYDLKQQG				
TaCBL3	(91)	DLFD	TKHNGILGFEEFARALS VFHSPAPPEEKIDFSFQLYDLKQQG				
OsCBL6 ABA54181	(92)	DLFD	TKHNGILGFEEFARALS VFHPNAPIDDKIDFAFKLYDLKQQG				
TaCBL6	(92)	DLFD	TKHNGILEFEEFVRSLS VFHPNAPVDDKIDFAFKLYDLKQQG				
Consensus (185)		DLFD	K NGVIDF EFVRSLSVFHP APLEEKI FAFRLYDLKQQG				

EF hand 2

EF hand 3

	(231)	231	240	250	260	276
AtCAM1 NP_001154755	(126)	FISAAELRHVMTNLG-----EKL TDEE--VDEMIREADV DGDGQI				
OsCaM LOC_Os05g41210	(100)	FISAAELRHVMTNLG-----EKL TDEE--VDEMIREADV DGDGQI				
AtCAM2 NP_001189724	(112)	FISAAELRHVMTNLG-----EKL TDEE--VDEMIK EADV DGDGQI				
OsCaM3 LOC_Os01g17190	(100)	FISAAELRHVMTNLG-----EKL TDEE--VDEMIREADV DGDGQI				
CeCaM NP_503386	(100)	FISAAELRHVMTNLG-----EKL TDEE--VDEMIREADV DGDGQV				
DrCaM BC164893	(100)	YISAAELRHVMTNLG-----EKL TDEE--VDEMIREADV DGDGQV				
HsCML3 NP_005176	(100)	FVSAAELRHVMTNLG-----EKL SDEE--VDEMIRAADTDGDGQV				
ScCaM NP_009667	(100)	LISAAELKHVLTSLG-----EKL TDAE--VDMLREVS-DGSGEI				
MmCam4 NP_064420	(99)	YITVDELKESLSKLG-----E SLSQEE--LEDMIRVADV DQDGKV				
AtCBL4 AF192886	(127)	FIEREELKEMVVALHSEELVLS EDMIEMVVDKAFVQADRKNDGKI				
OsCBL4 ABA54179	(123)	YIEKEELREMVALLDES DLHLSECAVEAIVDNTFSQADSNGDGRI				
TaCBL4	(125)	YIEKEELREMVALLDES DLCLSDSAVEAIVDNTFSQADSNGDRI				
OsCBL7 ABA54182	(123)	YIEREELYEMVLATLINES DILLSDDAVEQIVDQTFKQADLNSDGKI				
TaCBL7	(123)	SIEREELKEMVLATLINES DILLSDDAVQQIVDQTFKQADLNSDGRI				
OsCBL9 ABA54184	(203)	FIEREVVMQVIAILLSESDMKLSEELLEAIIDKTFE DADADR DGKI				
TaCBL9	(209)	FIEREVVMQVIAILLSESHVELSHDLLEAILDKTFE DADTD RDGKI				
AtCBL1 AAC26008	(123)	YIERQEVKQMLIAILLCESEMKLADDTIETIILDKTFE DADVNDGKI				
AtCBL9 AF411958_1	(123)	FIERQEVKQMLIAILLCESEMKLADDTIEMILDQTFE DADVDR DGKI				
OsCBL1 ABA54176	(123)	FIERKEVKQMLIAILLGESEMRLSDEIETIILDKTFE DADTNQDGRI				
TaCBL1	(125)	FIERKEVKQMLIAILLGESEMRLSDEIVEITLDKAFSDADTNQDGKI				
AtCBL7 AF290434_1	(126)	FIERQGVKQLVVATLAESGMSQSDIEVESIIDKTFEADTKHLDGMI				
AtCBL6 AF192884_1	(132)	YIKRQEVKQMVVRLTAESGMNLS DHVIESIIDKTFEADTKLDGKI				
AtCBL2 AAC26009	(138)	FIERQEVKQMVVATLAESGMNLSKDTVIEDIIDKTFEADTKHDGKI				
AtCBL3 AAC26010	(138)	FIERQEVKQMVVATLAESGMNLSDEIIESIIDKTFEADTKHDGRI				
OsCBL2 ABA54177	(137)	YIERQEVKQMVVATLAESGMNLSDEIIESIIDKTFEADTKHDGRI				
OsCBL3 ABA99199	(137)	YIERQEVKQMVVATLAESGMNLSDEIIESIIDKTFEADTKHDGRI				
TaCBL2	(137)	FIERQEVKQMVVATLAESGMNLSDEIENIIDKTFEADTKHDGKI				
TaCBL3	(137)	FIERQEVKQMVVATLAESGMNLSDEVIIESIIDKTFEADTKHDGKI				
OsCBL6 ABA54181	(138)	FIERQEVKQMVVATLAESGMNLSDEIIEGIIIDKTFEADTKHDGKI				
TaCBL6	(138)	FIERQEVKQMVVATLAESGMNLSDEVIIEGIIIDKTFEADTKHDGKI				
Consensus (231)		FIER	EVKQMVVALL ES M LSDEIIE IVDKTFE ADT DGKI			

EF hand 3

EF hand 4

	(277)	<u>277</u>		290		300		310		322
AtCAM1 NP_001154755 (164)	NY	EEF	VK	IM	MAK	-----	-----	-----	-----	-----
OsCaM LOC_Os05g41210 (138)	NY	EEF	VK	V	MAK	-----	-----	-----	-----	-----
AtCAM2 NP_001189724 (150)	NY	EEF	VK	V	MAK	-----	-----	-----	-----	-----
OsCaM3 LOC_Os01g17190 (138)	NY	DEF	VK	V	MAK	-----	-----	-----	-----	-----
CeCaM NP_503386 (138)	NY	EEF	V	T	M	T	T	K	-----	-----
DrCaM BC164893 (138)	NY	EEF	V	Q	M	T	A	K	-----	-----
HsCML3 NP_005176 (138)	NY	EEF	V	R	V	L	V	S	K	-----
ScCaM NP_009667 (137)	NI	QQ	F	A	A	L	I	S	K	-----
MmCam4 NP_064420 (137)	KY	EEF	V	R	L	H	V	E	N	-----
AtCBL4 AF192886 (173)	DI	DEW	K	D	F	V	S	L	N	P
OsCBL4 ABA54179 (169)	DP	EEW	E	E	F	V	K	A	N	P
TaCBL4 (171)	DP	KEE	E	E	F	V	K	K	N	P
OsCBL7 ABA54182 (169)	DP	DEW	K	A	F	A	S	K	N	P
TaCBL7 (169)	DP	DEW	K	E	F	A	S	K	N	P
OsCBL9 ABA54184 (249)	NQ	QEW	K	E	F	V	L	R	H	P
TaCBL9 (255)	CQ	EEW	K	E	F	V	L	R	H	P
AtCBL1 AAC26008 (169)	DK	LEW	S	D	E	V	N	K	N	P
AtCBL9 AF411958_1 (169)	DK	T	E	W	S	N	F	V	I	K
OsCBL1 ABA54176 (169)	DR	T	E	W	E	N	F	V	S	R
TaCBL1 (171)	DR	T	E	W	E	N	F	V	S	R
AtCBL7 AF290434_1 (172)	DE	EEW	M	D	L	V	F	R	H	P
AtCBL6 AF192884_1 (178)	DK	EEW	R	S	L	V	L	R	H	P
AtCBL2 AAC26009 (184)	DK	EEW	R	S	L	V	L	R	H	P
AtCBL3 AAC26010 (184)	DK	EEW	R	T	L	V	L	R	H	P
OsCBL2 ABA54177 (183)	DK	EEW	R	N	L	V	L	R	H	P
OsCBL3 ABA99199 (183)	DK	EEW	R	N	L	V	L	R	H	P
TaCBL2 (183)	DR	EEW	H	N	L	V	L	R	H	P
TaCBL3 (183)	DK	EEW	R	N	L	V	L	R	H	P
OsCBL6 ABA54181 (184)	DK	EEW	R	N	L	V	L	R	H	P
TaCBL6 (184)	DK	EEW	R	N	L	V	L	R	H	P
Consensus (277)	D	EEW	L	V	L	R	P	S	L	L

EF hand 4

	(323)	<u>323</u>	<u>326</u>
AtCAM1 NP_001154755 (176)	----	----	----
OsCaM LOC_Os05g41210 (150)	----	----	----
AtCAM2 NP_001189724 (162)	----	----	----
OsCaM3 LOC_Os01g17190 (150)	----	----	----
CeCaM NP_503386 (150)	----	----	----
DrCaM BC164893 (150)	----	----	----
HsCML3 NP_005176 (150)	----	----	----
ScCaM NP_009667 (148)	----	----	----
MmCam4 NP_064420 (149)	----	----	----
AtCBL4 AF192886 (219)	NV	S	S
OsCBL4 ABA54179 (211)	----	----	----
TaCBL4 (217)	SK	--	----
OsCBL7 ABA54182 (214)	----	----	----
TaCBL7 (214)	----	----	----
OsCBL9 ABA54184 (291)	----	----	----
TaCBL9 (297)	----	----	----
AtCBL1 AAC26008 (214)	----	----	----
AtCBL9 AF411958_1 (214)	----	----	----
OsCBL1 ABA54176 (214)	----	----	----
TaCBL1 (216)	----	----	----
AtCBL7 AF290434_1 (215)	----	----	----
AtCBL6 AF192884_1 (224)	LDG	--	----
AtCBL2 AAC26009 (227)	----	----	----
AtCBL3 AAC26010 (227)	----	----	----
OsCBL2 ABA54177 (226)	----	----	----
OsCBL3 ABA99199 (226)	----	----	----
TaCBL2 (226)	----	----	----
TaCBL3 (226)	----	----	----
OsCBL6 ABA54181 (227)	----	----	----
TaCBL6 (227)	----	----	----
Consensus (323)	----	----	----

Additional file 5: Analysis of EF-hand motifs in calcium binding proteins of representative species. Multiple sequence alignment was performed using the ClustalX1.83. Identical amino acids are shaded in yellow, conservative amino acids are shaded in light blue and similar amino acids are shaded in green. The four EF-hand motifs are indicated in the figure.