

SoPIP2;1	-----MSKEVSEEA-QAHQH---GKDYVDP---PPAPFFDLGELKLWSEWR	
CePIP1;1	MEAKEQDVQLGANKFAERQPIGTAAQSQD---EGKDYKEP---PPAPFFEPGELSSWSFYR	
CePIP1;2	MEDKEQDVRGLGANKFSESRQPIGTAAQVVD---KDYHDS---PATPLDFPSELGWSFYR	
CePIP1;3	MQAKDEDVGLGANKFSESRQPIGTAAQSQDQVQDKDYKEP---PPAPLFEPGELKWSFYR	
CePIP2;1	-----MGKDTEIGVEPSSYSG---KDYTDP---PPAPLIDVEELGKWSLYR	
CePIP2;2	-----MELQVKEAAGQSSSKL---PPLSTLKRPPAPFLGLDELKWSPLYR	
CePIP2;3	-----ME---DPSNGHARSPL---AKFETP---PPAPFLGAHELKWSLYR	
CePIP2;4	-----MAKDVE---GGEYTT---KDYTDP---PPAPLFDVEEITKWSLYR	
CePIP2;5	-----MAKDVEAGT---GGEYTT---KDYIDP---LPAPFVLDLEEITKWSLYR	
CePIP2;6	-----MAKDIEAGT---GIEYAI---KDYTDP---PPAPLVDLEEITKWSLYR	
CePIP2;7	-----MAKDVEA---VADSGT---RDYDTP---PPAPLVDEBELTWSLYR	
CePIP2;8	-----MSKEVSEEA-EHHHAP---AKDYTDP---PPAPLFDMAELKLSFYR	
CePIP2;9	-----MSKHVTVEEVESGKKP---YNEP---KPTPLLYMGELSKWSLYR	
CePIP2;10	-----MSKVDAGVKGLEGGAKK---WSLIKPFGEFTWSLYR	
CePIP2;11	-----MSKADAGVEELEGGAKK---YFEP---KPTPLIDAGEFTWSLYR	
	::*	
	TM1	TM2
SoPIP2;1	AAIAEFATLLFLYITVATVIG--H-SK-----ETVVOGSVGLLGIAWAFGGMI FVLVYC	
CePIP1;1	AGIAEFMATFLFLYITILVTMGMVNN-----SPSKASVGIQGIAWAFGGMI FALVYC	
CePIP1;2	AGIAEFMATFLFLYITVLTVMGVVK-----SPTKSTVGIQGIAWAFGGMI FALVYC	
CePIP1;3	AGIAEFVATFLFLYITILVTMGMVSK-----SSSKATVGIQGIAWAFGGMI FALVYC	
CePIP2;1	AVIAEFATLLFLYITVATVIGYKHQSDAAVNGTDAACSGVGLGIAWAFGGMI FVLVYC	
CePIP2;2	ATITEFTATLLFLYITILVTIGYGHQNDK---PNSPCGGVGVGIAWAFGGMI FVLVYC	
CePIP2;3	AVLTFEAVTFLLFLYVLALTVIGYSHQSDAKA-FPSAPCGSVGLQGIAWAFGGMI FVLVYC	
CePIP2;4	AVIAEFATLLFLYITVATVIGYKHQSDPNVNTTDAACSGVGLGIAWAFGGMI FVLVYC	
CePIP2;5	AVIAEFVATLLFLYITVATVIGYKHQSDPNVNTTDAACSGVGLGIAWAFGGMI FVLVYC	
CePIP2;6	AVIAEFVATMLFLYITVATVIGYKHQSDPNVNTTDAACSGVGLGIAWAFGGMI FVLVYC	
CePIP2;7	AVIAEFVATMLFLYITVATVIGYKHQSDPNVPADAAACSGVGLGIAWAFGGMI FVLVYC	
CePIP2;8	ALIAEFATLLFLYISIAITVIGYKV---QIQADQACSGVGLGIAWAFGGMI FVLVYC	
CePIP2;9	AVIAEFVATLLFLYISIAITVIGYKNS-----RADSTGIFLGVAVAFGASIFVLVYC	
CePIP2;10	AAIAEFVATLLFLYISIAITVIGYKNS-----SAEANGVGLGVAVAFGASIFVLVYC	
CePIP2;11	AAIAEFVATLLFLYISIAITVIGYKNS-----SAEANGVGLGVAVAFGASIFVLVYC	
	::*	
	HB	TM3
SoPIP2;1	TAGISGGHINPAVTFGLFLARKVLLRALVYMIACLGAICGVGLVKAFMKGPFYNGFQQGG	
CePIP1;1	TAGISGGHINPAVTFGLFLARKLTLTRAVFYVMQCLGAICGAGVVKGYQKGLYQSTGGG	
CePIP1;2	TAGISGGHINPAVTFGLFLARKLLTRAVFYIMQCLGAICGAGVVKGFQKGLYENNGGG	
CePIP1;3	TAGISGGHINPAVTFGLFLARKLTLTRALFYVMQCLGAICGAGVVKGFQKGLYENNGGG	
CePIP2;1	TAGISGGHINPAVTFGLFLARKVLLRALYMIACLGAICGVGLVKAFMKGPFYNGFQQGG	
CePIP2;2	TAGISGGHINPAVTFGLFLGRKVLLRALFYIVAQMLGAICGVGLVKGFQKSLFNRYGGG	
CePIP2;3	TAGISGGHINPAVTFGLFLGRKVLIRALLYMLAVAGAIAGVGLVKGFQKELFNRYGGA	
CePIP2;4	TAGISGGHINPAVTFGLFLARKVLLRAVLYIIAACLGAICGVGLVKGFQKSFYVRYGGG	
CePIP2;5	TAGISGGHINPAVTFGLFLARKVLLRAVLYIIAACLGAICGVGLVKGFQKSFYVRYGGG	
CePIP2;6	TAGISGGHINPAVTFGLFLARKVLLRALYMIACLGAICGVGLVKGFQKSFYVRYGGG	
CePIP2;7	TAGISGGHINPAVTFGLFLARKVLLRALYIIAACLGAICGVGLVKGFQKRAFYVRYGGG	
CePIP2;8	TAGISGGHINPAVTFGLFLARKVLLRAVLYIIAACLGAICGVGVKGMKHPYNSLGGG	
CePIP2;9	TAGISGGHINPAVTFGLVGRKLLARAVLYIIAACLGAICGAGIVKGMKHPYNSLGGG	
CePIP2;10	INGISGDHINPAVTFGLVGRKLLRAVLYIIVQCLGAICGAGIVKGMKHPYNSLGGG	
CePIP2;11	IGGISGGHINPAVTFGLVGRKLLGRAVLYIIVQCLGAICGAGIVKGMKHPYNSLGGG	
	::*	
	TM4	TM5
SoPIP2;1	ANSVALGYNKGTALGAEIIGTFVLVYTVFSATDPKRLARDSHVPI LAPLPIGFAVFMVHL	
CePIP1;1	ANVVAHGYTKGSGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPI LAPLPIGFAVFLVHL	
CePIP1;2	ANVVAPGYTKGDGLGAEIIGTFVLVYTVFSATDAKRNARDSHVPI LAPLPIGFAVFLVHL	
CePIP1;3	ANVUNPGYTKGDGLGAEIIGTFILVYTVFSATDAKRNARDSHVPI LAPLPIGFAVFLVHL	
CePIP2;1	ANLSSGYSKGTGLGAEIIGTFVLVYTVFSATDPKRNARDSHI PVLAPLPIGFAVFMVHL	
CePIP2;2	ANFVHEGYTKGTALGAEIIGTFVLVYTVFSATDEKRRARDSHVPI LAPLPIGSFVLVHL	
CePIP2;3	TNTVSSGSYSRATGLGAEIIGTFVLVYTVFSATDDKRRARDSHVPI LAPLPIGSFVIVHL	
CePIP2;4	ANLSSGSYSHGTGLAEEIIGTFVLVYTVFSATDPKRNARDSHVPLAPLPIGFAVFMVHL	
CePIP2;5	ANLSSGSYSHGTGLAEEIIGTFVLVYTVFSATDPKRNARDSHI PVLAPLPIGFAVFMVHL	
CePIP2;6	ANLSSGSYNGTGLAEEIIGTFVLVYTVFSATDPKRNARDSHI PVLAPLPIGFAVFMVHL	
CePIP2;7	ANLSSGSYSGTGVGAEIIGTFVLVYTVFSATDPKRNARDSHVPLAPLPIGFAVFMVHL	
CePIP2;8	ANLSSGSYSRGTALGAEIIGTFVLVYTVFSATDPKRLARDSHVPLAPLPIGFAVFMVHL	
CePIP2;9	TNSVSEGYSKGAAALGAEIIGTFVLVYTVFSATDPKRTARDSEFVPLVPLPIGFAVFAIHL	
CePIP2;10	ANSVADGYSKAGALGAEIIGTFVLVYTVFSATDRKRTAQEPFVPLVPLPIGFAVFAIHL	
CePIP2;11	ANSVADGYSKAGALGAEIIGTFVLVYTVFSATDPKRTARDSEFVPLVPLPIGFAVFAIHL	
	::*	
	HE	TM6
SoPIP2;1	ATIPITGTGINPARSFGAALVFNENKVDWDDQWIFWVGPFIGAAIAAYHQVILRAAAIKA	
CePIP1;1	ATIPITGTGINPARSLGAAIINYKDHAWDDMHI FWVGPFIGAAIAAYHQVIRAI PFKS	
CePIP1;2	ATIPITGTGINPARSLGAAIINYKQAWNDHWHI FWVGPFIGAAIAAYHQVIRAI PFKS	
CePIP1;3	ATIPITGTGINPARSLGAAIINYNRDHWDDHWHI FWVGPFIGAAIAAYHQVIRAI PFKT	
CePIP2;1	ATIPITGTGINPARSFGAALVILGSKAWDDQWIFWVGPFIGAAIAAYHQVILRAGAVKA	
CePIP2;2	ATIPITGTGINPARSFGAALVINYNDKFWDDHWHI FWLGPFI GAAIAAYEYVLRGSALKA	
CePIP2;3	ATIPITGTGINPARSLGAAIINYNEKAWDDQWIFWVGPLVGAIAAYEYVILKASALKA	
CePIP2;4	ATIPITGTGINPARSFGAALVINYNDKAWDDHWHI FWVGPFI GAAIAAYHQVILRSTTKA	
CePIP2;5	ATIPITGTGINPARSFGAALVINYNDKAWDDHWHI FWVGPFVGAIAAYVHQVILRASAACA	
CePIP2;6	ATIPITGTGINPARSLGAAIINYNDKFWNDHWHI FWVGPFAGAAIAAYHQVILRASAACA	
CePIP2;7	ATIPITGTGINPARSLGAAVYVNHETTWDHWHI FWVGPFAGAAIAAYHQVILRASAACA	
CePIP2;8	ATIPITGTGINPARSLGAAIINYNDKAWDDHWHI FWVGPLVGAIAAYVHQVILRAAAIKA	
CePIP2;9	ATIPITGTGINPARSLGAAVYVYQKQIWDHWHI FWVGPLVGAAIAAYVHQVILRGGAVKA	
CePIP2;10	ATIPITGTGINPARSLGAAVYVYQKAIWDDHWHI FWAGPLIGALLAAYVYQVFLRGAACA	
CePIP2;11	ATIPITGTGINPARSLGAAVYVYQKTIWDDHWHI FWVGPFI GALLAAYVYQVFLRGGAAKA	
	::*	
SoPIP2;1	LG-----FRS NPTN	
CePIP1;1	R-----	
CePIP1;2	KDYY-----	
CePIP1;3	KS-----	
CePIP2;1	-----LGRFRINA--	
CePIP2;2	LGSFKWS--FRKGELA--	
CePIP2;3	MGSFKRSTFR TNGS--	
CePIP2;4	-----MGSYRINA--	
CePIP2;5	-----MGSYRIRT--	
CePIP2;6	I-----MGSYRGN--	
CePIP2;7	-----NGSYRM--	
CePIP2;8	LG-----FRS SQHN	
CePIP2;9	LN-----FRSTTV	
CePIP2;10	SG-----SRSTTV	
CePIP2;11	LG-----FRSTTV	

Supplemental Fig. S1 Multiple sequence alignment and structural features of 14 CePIPs. Sequence alignment was performed using MUSCLE. Transmembrane helices (TM1–TM6) and the two half helices forming the two NPAs (HB and HE) (shaded), NPA motifs (shown in red), ar/R filter residues (shown in green), and six Froger’s positions (shown in blue) are indicated. The highly conserved cysteine residues in LA are shown in gold, whereas the residues at the position corresponding to H¹⁹³ in SoPIP2;1 (PDB accession number 1Z98) are shown in brown. The residues at the position corresponding to S⁹⁶, S¹¹⁵, S¹⁸⁸, S²⁷⁴, and S²⁷⁶ in SoPIP2;1 are highlighted in bright green, whereas the residues at the position corresponding to L¹⁹⁷ in SoPIP2;1 are underlined. (Abbreviations: Ce: *C. esculentus*; HB: half helix in loop B; HE: half helix in loop E; So: *S. oleracea*; PIP: plasma membrane intrinsic protein; TM: transmembrane helix)