

Appendix S1 in Supporting Information:

Table 1. Sequences of the PCR primers used (Primer3 web resource; <http://bioinfo.ut.ee/primer3/>).

Gene name	Sequence (5'→3')	bp	Tm (°C)	Phytozome no.
<i>PRUPE_S16 96 for</i>	ATGGCGGCTCCTGCAATA	18	54	<i>PRUPE_ppa012996mg</i>
<i>PRUPE_S16 96-98 rev</i>	TCAACGGTAAGACTTCTGGAAC	22		
<i>PRUPE_ACO1 for</i>	ATGGAGAACTTCCCAATCATCAAC	24	55	<i>PRUPE_ppa008791mg</i>
<i>PRUPE_ACO1 rev</i>	TTAAGCTGTTGCAATTGGACCC	22		
<i>PRUPE_CAD sc6₁₋₅ for</i>	ATGGTGGTTTCTACAGAGCAAG	22	55	<i>PRUPE_ppa016455mg</i>
<i>PRUPE_CAD sc6₁₋₅ rev</i>	TTAAGAGCTAGACTTCAGTGTGTTT	25		<i>PRUPE_ppa007668mg</i>
				<i>PRUPE_ppa007613mg</i>
				<i>PRUPE_ppa007226mg</i>
				<i>PRUPE_ppa007622mg</i>
<i>PRUPE_CAD sc8_{1,2} deg for</i>	ATGGKTAGCCTTGARGTGGA	20	51	<i>PRUPE_ppa007749mg/</i>
<i>PRUPE_CAD sc8_{1,2} deg rev</i>	CTATKGATKAAGATTGCTGSC	21		<i>PRUPE_ppa007636mg</i>

Appendix S2 in Supporting Information:

Figure 1. Alignment of the 24 deduced PRUPE_CADs of *Prunus persica* and reciprocal identity scores as determined by CLUSTAL W 2.1 multiple sequence alignment. Sequences of Zn1, Zn2 and coenzyme binding motifs are shown in boxes; the conserved amino acids in these binding motifs are evidenced in gray.

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CADsc1_PRUPE_ppa007634m ---MAQTPPNHTQTVSGWAAHD-SSGKITPFIFKRRENGINDVTIEVLVYCGICHTDLHHV 56
CADsc3_PRUPE_ppa024217m -MSENTEGANGNDCLGWAATD-ESGILSPYKFSRRSLQNDVSVKITHCGICYADLVFP 58
CADsc4_PRUPE_ppq007678m --MAKSPREEHPEKAFGWAARD-TSGILSPFRFSRRENADDDVTIKVLYCGVCHSDVHSV 57
CADsc5_PRUPE_ppa007789m ----MSSESANENCLGYAARD-PSGVLSEYKFSRRALGIDDISIKITHCGVCYADVIWA 54
CADsc61_PRUPE_ppa016455m --MVKSQEHEHPKAFGWAARD-SSGVLSPFNFSRRETGEKDVTFKVLVYCGICHTDLHMV 57
CADsc62_PRUPE_ppa007668m --MVTPTQEHEHPKAFGWAARD-SSGVLSPFKFSRRETGEKDVFSFKVLVYCGICHDLHMV 57
CADsc63_PRUPE_ppa007613m --MVVSTQEHEHPKAFGWAARD-SSGVLSPFKFSRRETGEKDVFSFKVLVYCGICHDLHMV 57
CADsc64_PRUPE_ppa007226m --MVVSTQEHEHPKAFGWAARD-SSGVLSPFKFSRRETGEKDVFSFKVLVYCGICHDLHMV 57
CADsc65_PRUPE_ppa007622m --MVVSTQEHEHPKAFGWAARD-SSGVLSPFKFSRRETGEKDVFSFKVLVYCGICHDLHMV 57
CADsc66_PRUPE_ppa007615m --MAVPEQEHPKAFGWAARD-SSGVLSPFKFSRRETGEKDVTFKVLVYCGICHTDLSML 57
CADsc67_PRUPE_ppa007627m --MAVPEQEHPKAFGWAARD-SSGVLSPFRFSRRATGENDVTFKVLVYCGICHTDLHMV 57
CADsc68_PRUPE_ppa007605m --MAKSPREEHPKAFGWAARD-TSGHLSPFHFRRATGDEDVRFKVLVYCGICHDLHSI 57
CADsc69_PRUPE_ppa021232m --MAVCPQEHPKAFGWAARD-SSGVLSPFKFSRRATGKNDVTFKVLVYCGICHTDLSML 57
CADsc610_PRUPE_ppa021536m --MAKPEQEHPKAFGWAARD-STSGHLSPFNFRRATGDEDVRFKVLFCGICHSDLHSI 58
CADsc611_PRUPE_ppa022917m --MAKSQEQQHPKAFGWAARD-SSGVLSPFNFSRR-----HFNLGY- 33
CADsc612_PRUPE_ppa022697m -----MEGRKAFGWAARD-TSGILSPYSFNLKRTGSEDVVLKVLVYCGVDHTDLHQM 50
CADsc613_PRUPE_ppa022409m -----KTGEKDALRVLYCGICHSDLHVM 24
CADsc614_PRUPE_ppa022088m -MTKAASEAKSPVNAYGWAARD-SSGVLSPFHFRANSDDDIIVKILYCGICHSDIHLV 58
CADsc615_PRUPE_ppa023056m --MAKSQEQQHPKAFGWAARN-SSGVLSPFNFSRRLYSPSNLVSFYLFH----HFNLGY- 53
CADsc616_PRUPE_ppa026085m --MVKTPEQEHLVEAFGWAARY-TTGHLSPFNFSRSIK----- 35
CADsc617_PRUPE_ppa027148m MSQELTGAEQAVKAYGWAARD-SSGVLSPFHFRNGNDNISMKILYCGICHSDLHLA 59
CADsc618_PRUPE_ppa018829m ----MSTQEHEHPKAFGWAARD-SSGVLSPFNFSRRETGEKDVTFKVLVYCGICHSDLHLI 55
CADsc81_PRUPE_ppa007749m ----MVSLEVERTTTGWAARD-SSGILSPYTYTLRNTGPEDVYIKVLCGVCHTDTHQA 54
CADsc82_PRUPE_ppa007736m ----MGSLEVERTTTGWAARD-SSGILSPYTYTLRNTGPEDVYVVKVLSGICHSDLHQV 54

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	Zn 1 binding motif	Zn 2 binding motif				
CADsc1_PRUPE_ppa007634m	RN----DWGITMYPVVP	GHEITGVITKVGSNV	KEFKV	GDRVGVGC	-----	97
CADsc3_PRUPE_ppa024217m	RN----KHGNAKYPMVP	GHEIAGIVQEVGSNV	RGFKV	GDHVGIGT	-----	99
CADsc4_PRUPE_ppq007678m	KN----EWGFTNYPIVP	GHEIVGVVTKAGKNV	EKFKV	GDRVGVGV	-----	98
CADsc5_PRUPE_ppa007789m	RN----KHGDSKYPLVP	GHEIAGIVKEVGSNV	LRFKV	GDHIGVGT	-----	95
CADsc61_PRUPE_ppa016455m	KN----DWGFSTYPLVP	GHEIVGVVTEVGSNV	EKFKV	GDKVGVGC	-----	98
CADsc62_PRUPE_ppa007668m	KN----EWFDFSTYPLVP	GHEIVGVVTEVGSNV	QKFSV	GDKVGVGC	-----	98
CADsc63_PRUPE_ppa007613m	KN----EWGSSTYPLVP	GHEIVGVVTEVGSNV	EKFKV	GDKVGVGC	-----	98
CADsc64_PRUPE_ppa007226m	KN----EWGSSTYPLVP	GHEIVGVVTEVGSNV	EKFKV	GDKVGVGC	-----	98
CADsc65_PRUPE_ppa007622m	KN----EWGSSTYPLVP	GHEIVGVVTEVGSNV	EKFKV	GDKVGVGC	-----	98
CADsc66_PRUPE_ppa007615m	KN----EWGISMYPLLP	GHEIVGQVTEVGSNV	EKFKV	GDSVGVGY	-----	98
CADsc67_PRUPE_ppa007627m	KN----EWGLSTYPLIP	GHEIVGVVTVQVGSNV	EKLKV	GDHVGVGY	-----	98
CADsc68_PRUPE_ppa007605m	KN----EWGFSVYPMVP	GHEIVGEVTEVGSNV	KKVKV	GDKVGVGC	-----	98
CADsc69_PRUPE_ppa021232m	KN----EWGFSMYPLLP	GHEIVGQVTEVGSNV	EKFKV	GDSVGVGY	-----	98
CADsc610_PRUPE_ppa021536m	KN----DWGFSIYPIVP	GHEIVGEVTEVGSNV	KKVKV	GKVGKVGCV	-----	99
CADsc611_PRUPE_ppa022917m	-----	HEIVGVVTEVGSRV	QKYEY	GDKVGVGC	-----	60
CADsc612_PRUPE_ppa022697m	RN----EIHNNTYPLVP	GHEVVGEVVELGSEV	KKFRV	GDLVGVGC	-----	91
CADsc613_PRUPE_ppa022409m	KN----EWGTTSYPIVPG	YEVVGVVTELGSKV	EKFKV	GDKVGVGC	-----	65
CADsc614_PRUPE_ppa022088m	KN----KIWPPLYPTVP	GHEIVGQVTRTGKNV	TKFRV	GDIAGVGC	-----	99
CADsc615_PRUPE_ppa023056m	WFFVFFYLEWEITTYPLVP	GHEIVGVVTEVGSRV	LKYEY	GDKVGVGC	-----	99
CADsc616_PRUPE_ppa026085m	-N-----EWGICTYPIVP	GHELVEVTEVGNKV	KTKKV	GDRVGVGAF	QQGVVRPLLSQRGS	89
CADsc617_PRUPE_ppa027148m	KD----EVGMTIYPIVP	GHEIVGEVTVKGRNV	TKFKV	GDIAGVGC	-----	100
CADsc618_PRUPE_ppa018829m	KNELESTEWGASTYPLVP	GHEIVGVVTEVGSNV	EKFKV	GDKVGVGC	-----	101
CADsc81_PRUPE_ppa007749m	KN----HLGMSKYPMVP	GHEVVGEVVEVGSNV	SKFIV	GDVVGVL	-----	95
CADsc82_PRUPE_ppa007736m	KN----DLGRSNYPMVP	GHEVVGEVLEVGSDV	TKFRV	GDVVGVL	-----	95

	Zn 2 binding motif	
CADsc1_PRUPE_ppa007634m	LAATCLECDFCKDSQENY	DQ-VQFTYNGIFWDGSIYGGYSKMLVADHRYVWHIPA 153
CADsc3_PRUPE_ppa024217m	YVNSCRNCDYCGDGLFIFC	EKGAVFTYNNVDEDGTTIQGGFSSYIVAHQGYCFRIPD 156
CADsc4_PRUPE_ppq007678m	IVGSCMKCEYCDQDLLENY	PR-TIFTYNSLDHTRTKTYGGYSDMIIVHHRVYLRFPD 154
CADsc5_PRUPE_ppa007789m	YVNSCRDCEYCNFGEFVY	AKGSVYTFNGVDADGTTIKGGYSSHIVHHERYCFKIPD 152
CADsc61_PRUPE_ppa016455m	VVGSQSCDNKANNLENY	PK-YILTYGAKYHDVTTIYGGYSDFMVADEHFVICVPD 154
CADsc62_PRUPE_ppa007668m	MVGSCTSCDSCANNLENY	PK-YILTYGAKYHDGTTIYGGYSDFMVADEHFVIRVPD 154
CADsc63_PRUPE_ppa007613m	MVGSCHSCDSCANNLENY	PK-MILTYGSKYLDGTTTYGGYSDFMVADEHFVIRVPD 154
CADsc64_PRUPE_ppa007226m	MVGSCHSCDSCANNLENY	PK-MILTYGSKYLDGTTTYGGYSDFMVADEHFVIRVPD 154

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Fig. 1

CADsc65_PRUPE_ppa007622m	---MVGSC HS CDSCANNLENYC	PK-MILTYGSKYLDGTTTYGGYSDIMVADEHFVVRVPD	154
CADsc66_PRUPE_ppa007615m	---LVGSC Q SCDNCNGNNAENYC	PE-MIFTSGAKYHDGSTTYGGYSNIMVADEHFVVRIPD	154
CADsc67_PRUPE_ppa007627m	---MIGAC Q SCDSCSNNAENYC	PE-MIPTSGAKYHDGTTTYGGYSDIMVANEHFVVRVPD	154
CADsc68_PRUPE_ppa007605m	---LVGAC H ACDNCNNDLENYC	PK-MLLTYNSVYTDGTLTYGGYSDSMVANEHYLVRFPE	154
CADsc69_PRUPE_ppa021232m	---LVGSC Q SCDSCSNNAENYC	PE-MILTGAKYDYGSTTYGGYSNIMVADEHFVIRIPD	154
CADsc610_PRUPE_ppa021536m	---MVGAC D SCESCNNHLENYC	PK-MILTYGAIYHDGTITYGGYSDTMVASERYIVRFPE	155
CADsc611_PRUPE_ppa022917m	---LVGSC Q SCDRCANNLENYC	PG-LILTYGAKYHDGIP-----PRMEHFVIRIPD	107
CADsc612_PRUPE_ppa022697m	---IVGSC G ECLSCQSNMEQYC	HN-KIVTYNDNTKDGSPTRGGFSSAMVVHQRFVVRIPD	147
CADsc613_PRUPE_ppa022409m	---MVGSC Q SCDSCANNFENYC	PE-LILTYGEKYHDGTITYGGYSDFMVDEHFTVRI PD	121
CADsc614_PRUPE_ppa022088m	---LVGSC G SCDNCCKQDLENYC	PK-MLWTFQGGHEDGTRAFGGYSDNMVVEERYAVLIPN	155
CADsc615_PRUPE_ppa023056m	---LVGSC Q SCDRCANNLENYWPR	LILTYGAKYHDGIP-----PRMEHFVIRIPD	146
CADsc616_PRUPE_ppa026085m	ATGVVGA C HDCDNCNNDLEIYC	PK-MVLTYSIIYHDGTVTYGGYSDTMVANERYIVHFPD	148
CADsc617_PRUPE_ppa027148m	---MVGSC R SCDNCCTQDLENYC	PK-MVWTYNKKHEDGSRFTGGYSDKIVVDEHFVQIPK	156
CADsc618_PRUPE_ppa018829m	---MVGSC H SCDNCANNLENYC	PR-WIPTFGGKYHDGTTTYGGYSDIMVADEHFVNNIPD	157
CADsc81_PRUPE_ppa007749m	---IVGC R RNCNPKCTDNEQYC	NK-KIWITYSDVYTDGKLTQGGFSAALVIDQKFAVKIPD	151
CADsc82_PRUPE_ppa007736m	---LVGCC R RSCNPKCTDNEQYC	NK-KIWSYNDTYSDGKPTQGGFAGALVADQKFFVVKIPD	151

NADPH binding motif

CADsc1_PRUPE_ppa007634m	NLPLDATAPLLCAGVTVFSPMKDHNHLQAPGKKIGVV	GLGGLG HVAVKFGKAFGHHVTVI	213
CADsc3_PRUPE_ppa024217m	GYPLASAAPLLCAGITVYTPMIRHKMN-QPGKSLGVI	GLGGLG HLAVKFGKAFGLNVTVF	215
CADsc4_PRUPE_ppq007678m	NLALDAGAPLLCAGITVYSPMKYYGMT-EPGKHLGVA	GLGGLG HVAVKIKGAFGLKVTVI	213
CADsc5_PRUPE_ppa007789m	NYPLASAAPLLCAGITVYAPMKRHKMN-QPGKSLGVI	GLGGLG HMAVKFGKAFGLHVTVF	211
CADsc61_PRUPE_ppa016455m	NLPLDGAAPLLCAGITTYALSALRYGGLD-KPGMHVGVV	GLGGLG HVAVKFAKALGVRVTVI	213
CADsc62_PRUPE_ppa007668m	NLPLDGAAPLLCAGITTYSPRLRYGGLD-KPGMHVGVV	GLGGLG HVAVKFAKAMGVKVTVI	213
CADsc63_PRUPE_ppa007613m	SLPLDGAAPLLCAGITTYSPRLRYGGLD-KPGMHVGVV	GLGGLG HVAVKFAKAMGVKVTVI	213
CADsc64_PRUPE_ppa007226m	SLPLDGAAPLLCAGITTYSPRLRYGGLD-KPGMHVGVV	GLGGLG HVAVKFAKAMGVKVTVI	213
CADsc65_PRUPE_ppa007622m	SLPLDGAAPLLCAGITTYSPRLRYGGLD-KPGMHVGVV	GLGGLG HVAVKFAKAMGVKVTVI	213
CADsc66_PRUPE_ppa007615m	NLPLDGAAPLLCAGVTTYSPRLRYGGLD-KPGMHVGVV	GAGGLG HVAIKFAKAMGVKVTVI	213
CADsc67_PRUPE_ppa007627m	NLPLHGAAPLLCAGVTTYSPRLRYGGLD-KPGMHVGVV	GVGGLG HVAVKFAKAMGVKVTVI	213
CADsc68_PRUPE_ppa007605m	NMPLDAGAPLLCAGITVYSPKLYFGLA-EPGKHVGI	GLGGLG HVGVKFAKALGAKVTVI	213
CADsc69_PRUPE_ppa021232m	NLPLDGAAPLLCAGVTTYSPRLRYGGLD-KPGMHVGVV	GVGGLG HVAVKFAKAMGVKVTVI	213
CADsc610_PRUPE_ppa021536m	NMPLDAGAPLLCAGITVYSPKLYFGLG-EPGKHVGI	GLGGLG HVGVKFAKALGAKVTVI	214
CADsc611_PRUPE_ppa022917m	KLPLEGAAPLLCAGITTYSPRLRYGGLD-KPGMHVGVV	GLGGLG HVAVKFAKAMGVRVTAI	166
CADsc612_PRUPE_ppa022697m	KLALDGAAPLLCAGVTAYSPLKQFMGS-NKVLKAGIL	GLGGVG HLGV-----	193
CADsc613_PRUPE_ppa022409m	NLPLDGAAPLLCAGITTYSPRLRYFELD-KPGMHVGVV	GLGGVG HLAVKFAKAMGVKVTVI	180
CADsc614_PRUPE_ppa022088m	GFALAGTAPLLCAGITVYSPKLFHGLS-KSTHHLGVV	GLGGLG HMAVKFAKAFGVKVTVV	214
CADsc615_PRUPE_ppa023056m	KLPLEGAAPLLCAGITTYSPRLRYGGLD-KPGMHVGVV	GLGGLG HVAVKFAKAKGVRVTAI	205
CADsc616_PRUPE_ppa026085m	NMPLDGGAPLLCAGITMYSPLKYFGLA-EAGKHIGIV	GLGGLG HVGVKFAKAFGAKVTVL	207
CADsc617_PRUPE_ppa027148m	NLPLQGTAPMLCAGITVYSPMRYFGLM-EPGKHLGVV	GLGGLG HMAVKFAKAVGAKVTVI	215
CADsc618_PRUPE_ppa018829m	NLPLDGAAPLLCAGITTYSPRLRYGGLD-KPGMHVGVV	GLGGLG HVAVKFAKAMGVKVTVI	216
CADsc81_PRUPE_ppa007749m	GMVLEQAAPLLCAGVTVYSPRLRQFGLN-VSGLRGGIL	GLGGVG HMGVKIAKAMEHHVTVI	210
CADsc82_PRUPE_ppa007736m	GMAWEQAAPLLCAGVTVYSPLNHFGLN-LSGLRGGIL	GLGGVG HMGVKIAKAMGHHTVI	210

CADsc1_PRUPE_ppa007634m	STSPSKEEAKERLGADDFLVSTDAQQLKKGMRTLDFI	-----LNTVS	256
CADsc3_PRUPE_ppa024217m	STSTSKKEEALTLGADNFVVSNNLEQMTALAKSLDFI	-----IDTAS	258
CADsc4_PRUPE_ppq007678m	SSSPGKDEEAVKRLGADSFLLSDPAKLAAMGTM DYI	-----IDTAS	256
CADsc5_PRUPE_ppa007789m	STSVSKKEEALEILGADFFVVSDDQEQMTALVKS LDFL	-----IDTAS	254
CADsc61_PRUPE_ppa016455m	STSPNKKKEAIEHLRADFLVSRDQDQMAAVGTM DGI	-----IDTAS	256
CADsc62_PRUPE_ppa007668m	STSPNKKKEAIEHLCADSFVSRDQDQMAAVGTM DGI	-----IDTAS	256
CADsc63_PRUPE_ppa007613m	STSPNKKKEAIDHLHADSFLVSRDEDQMAALGTM DGI	-----IDTAS	256
CADsc64_PRUPE_ppa007226m	STSPNKKKEAIDHLHADSFLVSRDEDQMAALGTM DGI	-----IDTAS	256
CADsc65_PRUPE_ppa007622m	STSPNKKKEAIDHLHADSFLVSRDQDQMAALGTM DGI	-----IDTAS	256
CADsc66_PRUPE_ppa007615m	STSPNKKKEAIEHLGADSFVSRDNGQMAAMGTM DGI	-----IDTAS	256
CADsc67_PRUPE_ppa007627m	STSPNKKKEAIEHLGADSFVSRDNGQMAAMGTM DGI	-----IDTAS	256
CADsc68_PRUPE_ppa007605m	STSPSKKDEALNQLGADSFVSRDQDQMAAMGTL DGI	-----IDTAS	256
CADsc69_PRUPE_ppa021232m	STSPNKKKEAIEHLGADSFVSRDNGQMAAMGTM DGI	-----IDTAS	256
CADsc610_PRUPE_ppa021536m	STSPSKKDEALNHLGADDFLVRDQDQLQAAMGTF DGI	-----IDTAS	257
CADsc611_PRUPE_ppa022917m	STSPSKKKEAIEHLKADSFVSRDQDQMLAAMGTM DGI	-----IDTAS	209
CADsc612_PRUPE_ppa022697m	-SSDKKKEEALEILGADFFVVSNNLEQMTALAKSL DFI	-----LDTVP	235
CADsc613_PRUPE_ppa022409m	STSPNKKKEAIEHLHADSFLVSRDQDQMAAMGTM DGI	-----IDTVF	223
CADsc614_PRUPE_ppa022088m	SSSPSKKKEAIEHLGADSFVSRDQDQMAAMGTM DGI	-----IDTAS	257
CADsc615_PRUPE_ppa023056m	STSPSKKKEAIEHLKADSFVSRDQDQMLAAMGTM DGI	-----IDTAS	248
CADsc616_PRUPE_ppa026085m	STSPSKKDEALNQLGADSFVSRDQDQMAAMGTL DGI	-----IDTAS	267
CADsc617_PRUPE_ppa027148m	STSPNKKKEAIEHLGADSFVSRDQDQMAAMGTM DGI	-----IDTAS	258
CADsc618_PRUPE_ppa018829m	STSPGKKEEAIEHLHADSFLVSRDEDQMAAMGTM DGI	-----IDTAS	259
CADsc81_PRUPE_ppa007749m	SSSDKKRVEAMEHIGADEYLISSDATKMQEAADSL DDI	-----IDTVP	253
CADsc82_PRUPE_ppa007736m	SSSDRKKKEEAIEHLGADDFLVSRDQDQMAAMGTL DGI	-----IDTVP	253

CADsc1_PRUPE_ppa007634m	AKHSLGPLLELLKVNVTMVVVVGAPDQPFELPSPFPMIFGKRAVKGSVIGGMRDTEKEMMELC	316
CADsc3_PRUPE_ppa024217m	GDHPFDPYMSLLKTAGVLVLVVGAPSEV-KLSPLSLIGMKSIGSATGGTKQTQEMLDFC	317
CADsc4_PRUPE_ppq007678m	AVHALAPLIGLLKLNGLKLVTVGLPDKPLELPVFPLVLGRKLVGSDIGGVKQEQEMLDFC	316
CADsc5_PRUPE_ppa007789m	GDHPFDPYMALLKTGGTLVLVGFSEV-KFSPASLNLGMKTIISGSVTGGTKDTQEMIDFC	313
CADsc61_PRUPE_ppa016455m	AVHPLLPLIALLKSNGLKVMVGAPEKPLELPVFPFLMGRKMVAGSNIGGMKETQEMIDFA	316
CADsc62_PRUPE_ppa007668m	AVHPLLPLIALLKSNGLKLVVGAPEKPLELPVFPFLMGRKMVAGSNIGGMKETQEMIDFA	316
CADsc63_PRUPE_ppa007613m	AVHPLLPLIGLLKSHGKLVVGAPEKPLELPVFPFLMGRKIVAGSCVGGMKETQEMIDFA	316
CADsc64_PRUPE_ppa007226m	AVHPLLPLIGLLKSHGKLVVGAPEKPLELPVFPFLMGRKILGSCIGGMKETQEMIDFA	316
CADsc65_PRUPE_ppa007622m	AVHPLLPLIGLLKSHGKLVVGAPEKPLELPVFPFLMGRKIVGSGCIGGMKETQEMIDFA	316
CADsc66_PRUPE_ppa007615m	AVHPLLPLIGLLKSNGLKLVVGAPEKPLELPVFPFLMGRKIVAGSNIGGMKETQEMIDFA	316
CADsc67_PRUPE_ppa007627m	AVHPLLPLIGLLKNNGLKLVVGAPEKPLELPVFPFLMGRKIMAGSVVGGMKETQEMIDFA	316
CADsc68_PRUPE_ppa007605m	AVHPVPLIGLLKSHGKLIILVGAPEKPLELPVFPVPLIVGRKVLVAGSGIGGMKETQEMIDFA	316
CADsc69_PRUPE_ppa021232m	AVHPLLPLIGLLKSNGLKLVVGAPEKPLELPVFPVPLISGRKIVAGSTVGGKQEQEMIDFA	316
CADsc610_PRUPE_ppa021828m	AVHPVPLIGLLKSHGKLIILVGAPEKPLELPVFPVPLITGRKIVAGSGIGGMKETQEMIDFA	317
CADsc611_PRUPE_ppa022917m	AVHPVPLIRLLKSNGLKLVVGAPEKPLELPVFPVPLMGRKMVAGSNIGGVKQEQEMIDFA	269
CADsc612_PRUPE_ppa022697m	ALHPLRLYLSLLKVDGKLIIVAAVPKPLQDAVDIILGKRTITGSLIGSMEETREILEFW	295
CADsc613_PRUPE_ppa022409m	AAHPLLPLIGLLKSNGLKVMVTAPEKNIQIPAFSLLMGRKMVAGSRIGGMKETQEMVDF	283
CADsc614_PRUPE_ppa022088m	SPHPLLPLIGLLKSNGLKLVVGAPEKPLELPVFPVPLIMGRKIVAGSNIGGMKETQEMIDFA	317
CADsc615_PRUPE_ppa023056m	AVHPVPLIRLLKSNGLKLVVGAPEKPLELPVFPVPLMGRKMVAGSNIGGVKQEQEMIDFA	308
CADsc616_PRUPE_ppa026085m	AVHAISPLIDLKSHGKLIIMVGAPEKPLELPVFPVPLMGRKLVAGSAVGGMKETQKIDFA	327
CADsc617_PRUPE_ppa027148m	AAHPLLHLVGLLKTNGKLIILVGAPEKPLELPVFPVPLILGRKLVAGSATGGMKETQEMIDFA	318
CADsc618_PRUPE_ppa018829m	ANHPLLPIIDLLKSHGKLIILVGAPEKPLELPVFPVPLMGRKIVAGSCVGGMKETQEMIDFA	319
CADsc81_PRUPE_ppa007749m	VVHPLEPYLSLLKLDGKLIILMGAINDPLQFVSPMLMLGRKTIITGSFVSGMKETEEMLEFC	313
CADsc82_PRUPE_ppa007736m	VVHPLEPYLSLLRLDGKLIILMVGIVGAPLQFVSPMMLGRKTIITGSFVSGMKETEEMLEFC	313

CADsc1_PRUPE_ppa007634m	GKHNITCDIEVTPHKLDAALDRVAKNDVRYRFVIDITAGLPSNL-----	361
CADsc3_PRUPE_ppa024217m	AAHKIYPNIEIPIQYVNEALERLIKRDVKYRFVIDVSSLK-----	359
CADsc4_PRUPE_ppq007678m	AKHNITSDIELIRMDYINTAMERIAKSDVRYRFVIDVGNLSLTQ-----	359
CADsc5_PRUPE_ppa007789m	AAHEIHPMIEIPIQYATEALERLVKKDVKYRFVIDIENSLK-----	355
CADsc61_PRUPE_ppa016455m	AKHNITAQVEVIVPVDYLNNTAMERLAKTDVKYRFVIDVGNLTKST-----	360
CADsc62_PRUPE_ppa007668m	AKHNITAQVEVIVPIDYLNNTAMERLAKTDVKYRFVIDIGNTLKST-----	360
CADsc63_PRUPE_ppa007613m	AKHNVTADIEVIVPIDYVNTAMERLAKTDVRYRFVIDIGNTLKPS-----	361
CADsc64_PRUPE_ppa007226m	AKHNITADIEVIVPIDYLNNTAMERLVKADVRYRFVIDIGNTLKSS-----	361
CADsc65_PRUPE_ppa007622m	AKHNITADIEVIVPIDYLNNTAMERLVKADVRYRFVIDIGNTLKSS-----	361
CADsc66_PRUPE_ppa007615m	GKHNITANIELIPIIDYVNTAMERLIKADVRYRFVIDIANTLKSS-----	361
CADsc67_PRUPE_ppa007627m	GKHNITANVEVIVPVDYVNTAMERLIKTDVKYRFVIDIANTLKSS-----	361
CADsc68_PRUPE_ppa007605m	AKHNITAEIEVISMVYVNTAMERLAKNDVRYRFVIDVGNLTKS-----	362
CADsc69_PRUPE_ppa021232m	GKHNITANVEVIVPIDYVNTAMERLIKADVRYRFVIDIANTLKSS-----	361
CADsc610_PRUPE_ppa021536m	AKHNITAEIELISMDYLNNTALERLAKNDVRYRFVIDIGNTLAATK-----	363
CADsc611_PRUPE_ppa022917m	AKHNITAEVEVIVPIDYVNTAMERLAKADVRYRFVIDVGNLTKPPDSCNRN-----	319
CADsc612_PRUPE_ppa022697m	ADKGLKSFIEIVKMDYLNNEAFERMERNDVRFVLDVAGSDLE-----	338
CADsc613_PRUPE_ppa022409m	VKHNITADIEVIVPVDYLNNTAMERLAKSDVKYRFVIDIGNTLKST-----	328
CADsc614_PRUPE_ppa022088m	AKHNITADVEVVPMDYVNTALDRLDKGDVKYRFVIDVAKTINNHDSEASP-----	366
CADsc615_PRUPE_ppa023056m	AKHNITAEVELLITQGRNLEGNHSLPRHNGFDE-----	341
CADsc616_PRUPE_ppa026085m	AKHNITAEIEVISMVYVNTTLKRLVKNNVRYRFVIDIGNTLAATK-----	373
CADsc617_PRUPE_ppa027148m	AKHNITADVEVIVPMDYVNTALERVAKTDVKYRFVIDVANTIKSPY-----	363
CADsc618_PRUPE_ppa018829m	AKHNVTADIEVIVPIDYVNTAMERLAKTDVRYRFVIDIGNTLKPS-----	364
CADsc81_PRUPE_ppa007749m	KEKGLKTMIEVVKMEYINTAFERLEKNDVRYRFVVDVAASNHLQ-----	357
CADsc82_PRUPE_ppa007736m	KEKGLTSMIEVVKMDYVNTAFERLEKNDVRYRFVVDVAGSNLNP-----	357

CADsc1_PRUPE_ppa007634m	LPSNL-----	361
CADsc3_PRUPE_ppa024217m	LK-----	359
CADsc4_PRUPE_ppq007678m	LTQ-----	359
CADsc5_PRUPE_ppa007789m	LK-----	355
CADsc61_PRUPE_ppa016455m	LKST-----	360
CADsc62_PRUPE_ppa007668m	LKST-----	360
CADsc63_PRUPE_ppa007613m	LKPSS-----	361
CADsc64_PRUPE_ppa007226m	LKSSS-----	361
CADsc65_PRUPE_ppa007622m	LKSSS-----	361
CADsc66_PRUPE_ppa007615m	LKSSS-----	361
CADsc67_PRUPE_ppa007627m	LKSSS-----	361
CADsc68_PRUPE_ppa007605m	LAATKS-----	362
CADsc69_PRUPE_ppa021232m	LKSSS-----	361
CADsc610_PRUPE_ppa021536m	LAATKP-----	363
CADsc611_PRUPE_ppa022917m	LKPPDSCNRN-----	319
CADsc612_PRUPE_ppa022697m	DLE-----	338
CADsc613_PRUPE_ppa022409m	LKSTS-----	328
CADsc614_PRUPE_ppa022088m	INNHDSEASP-----	366
CADsc615_PRUPE_ppa023056m	HLPRHNGFDE-----	341
CADsc616_PRUPE_ppa026085m	LAATKP-----	373
CADsc617_PRUPE_ppa027148m	IKSPY-----	363

CADsc6₁₈_PRUPE_ppa018829m LKPSS----- 364
 CADsc8₁_PRUPE_ppa007749m NLHQ----- 357
 CADsc8₂_PRUPE_ppa007736m NLNP----- 357

CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to Protein
 Sequence format is Pearson

Sequence 1: CADsc1_PRUPE_ppa007634m 361 aa
 Sequence 2: CADsc3_PRUPE_ppa024217m 359 aa
 Sequence 3: CADsc4_PRUPE_ppa007678m 359 aa
 Sequence 4: CADsc5_PRUPE_ppa007789m 355 aa
 Sequence 5: CADsc6₁_PRUPE_ppa016455m 360 aa
 Sequence 6: CADsc6₂_PRUPE_ppa007668m 360 aa
 Sequence 7: CADsc6₃_PRUPE_ppa007613m 361 aa
 Sequence 8: CADsc6₄_PRUPE_ppa007226m 361 aa
 Sequence 9: CADsc6₅_PRUPE_ppa007622m 361 aa
 Sequence 10: CADsc6₆_PRUPE_ppa007615m 361 aa
 Sequence 11: CADsc6₇_PRUPE_ppa007627m 361 aa
 Sequence 12: CADsc6₈_PRUPE_ppa007605m 362 aa
 Sequence 13: CADsc6₉_PRUPE_ppa021232m 361 aa
 Sequence 14: CADsc6₁₀_PRUPE_ppa021536m 363 aa
 Sequence 15: CADsc6₁₁_PRUPE_ppa022917m 319 aa
 Sequence 16: CADsc6₁₂_PRUPE_ppa022697m 338 aa
 Sequence 17: CADsc6₁₃_PRUPE_ppa022409m 328 aa
 Sequence 18: CADsc6₁₄_PRUPE_ppa022088m 366 aa
 Sequence 19: CADsc6₁₅_PRUPE_ppa023056m 341 aa
 Sequence 20: CADsc6₁₆_PRUPE_ppa026085m 373 aa
 Sequence 21: CADsc6₁₇_PRUPE_ppa027148m 363 aa
 Sequence 22: CADsc6₁₈_PRUPE_ppa018829m 364 aa
 Sequence 23: CADsc8₁_PRUPE_ppa007749m 357 aa
 Sequence 24: CADsc8₂_PRUPE_ppa007736m 373 aa

Pairwise alignments

Sequence 1: CADsc1 PRUPE ppa007634m

Sequences (1:2) Aligned. Score: 46.52
 Sequences (1:3) Aligned. Score: 57.10
 Sequences (1:4) Aligned. Score: 47.04
 Sequences (1:5) Aligned. Score: 55.83
 Sequences (1:6) Aligned. Score: 55.56
 Sequences (1:7) Aligned. Score: 54.29
 Sequences (1:8) Aligned. Score: 54.85
 Sequences (1:9) Aligned. Score: 55.12
 Sequences (1:10) Aligned. Score: 56.51
 Sequences (1:11) Aligned. Score: 54.29
 Sequences (1:12) Aligned. Score: 54.02
 Sequences (1:13) Aligned. Score: 55.68
 Sequences (1:14) Aligned. Score: 54.85
 Sequences (1:15) Aligned. Score: 49.84
 Sequences (1:16) Aligned. Score: 44.38
 Sequences (1:17) Aligned. Score: 53.96
 Sequences (1:18) Aligned. Score: 51.52
 Sequences (1:19) Aligned. Score: 44.57
 Sequences (1:20) Aligned. Score: 47.65
 Sequences (1:21) Aligned. Score: 54.85
 Sequences (1:22) Aligned. Score: 54.57
 Sequences (1:23) Aligned. Score: 43.42
 Sequences (1:24) Aligned. Score: 44.54

Sequence 2: CADsc3 PRUPE ppa024217m

Sequences (2:3) Aligned. Score: 50.70
 Sequences (2:4) Aligned. Score: 76.06
 Sequences (2:5) Aligned. Score: 49.58
 Sequences (2:6) Aligned. Score: 50.42
 Sequences (2:7) Aligned. Score: 50.97
 Sequences (2:8) Aligned. Score: 50.97
 Sequences (2:9) Aligned. Score: 50.97
 Sequences (2:10) Aligned. Score: 50.70
 Sequences (2:11) Aligned. Score: 48.19
 Sequences (2:12) Aligned. Score: 50.70
 Sequences (2:13) Aligned. Score: 50.14
 Sequences (2:14) Aligned. Score: 49.03
 Sequences (2:15) Aligned. Score: 49.53
 Sequences (2:16) Aligned. Score: 44.67

Sequences (2:17) Aligned. Score: 47.26
Sequences (2:18) Aligned. Score: 50.42
Sequences (2:19) Aligned. Score: 41.06
Sequences (2:20) Aligned. Score: 43.73
Sequences (2:21) Aligned. Score: 50.97
Sequences (2:22) Aligned. Score: 49.86
Sequences (2:23) Aligned. Score: 46.22
Sequences (2:24) Aligned. Score: 46.78
Sequence 3: CADsc4 PRUPE ppq007678m
Sequences (3:4) Aligned. Score: 52.11
Sequences (3:5) Aligned. Score: 67.13
Sequences (3:6) Aligned. Score: 66.85
Sequences (3:7) Aligned. Score: 67.13
Sequences (3:8) Aligned. Score: 67.41
Sequences (3:9) Aligned. Score: 67.69
Sequences (3:10) Aligned. Score: 65.46
Sequences (3:11) Aligned. Score: 65.18
Sequences (3:12) Aligned. Score: 69.08
Sequences (3:13) Aligned. Score: 64.07
Sequences (3:14) Aligned. Score: 69.08
Sequences (3:15) Aligned. Score: 64.26
Sequences (3:16) Aligned. Score: 50.59
Sequences (3:17) Aligned. Score: 62.50
Sequences (3:18) Aligned. Score: 61.56
Sequences (3:19) Aligned. Score: 55.43
Sequences (3:20) Aligned. Score: 59.05
Sequences (3:21) Aligned. Score: 64.62
Sequences (3:22) Aligned. Score: 66.57
Sequences (3:23) Aligned. Score: 49.02
Sequences (3:24) Aligned. Score: 49.58
Sequence 4: CADsc5 PRUPE ppa007789m
Sequences (4:5) Aligned. Score: 50.99
Sequences (4:6) Aligned. Score: 52.39
Sequences (4:7) Aligned. Score: 51.27
Sequences (4:8) Aligned. Score: 51.83
Sequences (4:9) Aligned. Score: 52.11
Sequences (4:10) Aligned. Score: 50.99
Sequences (4:11) Aligned. Score: 49.30
Sequences (4:12) Aligned. Score: 51.27
Sequences (4:13) Aligned. Score: 50.99
Sequences (4:14) Aligned. Score: 50.99
Sequences (4:15) Aligned. Score: 48.59
Sequences (4:16) Aligned. Score: 41.42
Sequences (4:17) Aligned. Score: 48.17
Sequences (4:18) Aligned. Score: 51.27
Sequences (4:19) Aligned. Score: 40.76
Sequences (4:20) Aligned. Score: 45.35
Sequences (4:21) Aligned. Score: 53.24
Sequences (4:22) Aligned. Score: 51.83
Sequences (4:23) Aligned. Score: 45.92
Sequences (4:24) Aligned. Score: 45.07
Sequence 5: CADsc6₁ PRUPE ppa016455m
Sequences (5:6) Aligned. Score: 92.50
Sequences (5:7) Aligned. Score: 87.50
Sequences (5:8) Aligned. Score: 87.50
Sequences (5:9) Aligned. Score: 87.78
Sequences (5:10) Aligned. Score: 80.56
Sequences (5:11) Aligned. Score: 83.33
Sequences (5:12) Aligned. Score: 75.28
Sequences (5:13) Aligned. Score: 80.56
Sequences (5:14) Aligned. Score: 76.11
Sequences (5:15) Aligned. Score: 82.45
Sequences (5:16) Aligned. Score: 48.22
Sequences (5:17) Aligned. Score: 82.01
Sequences (5:18) Aligned. Score: 63.89
Sequences (5:19) Aligned. Score: 70.97
Sequences (5:20) Aligned. Score: 64.17
Sequences (5:21) Aligned. Score: 69.44
Sequences (5:22) Aligned. Score: 85.00
Sequences (5:23) Aligned. Score: 50.42
Sequences (5:24) Aligned. Score: 51.82
Sequence 6: CADsc6₂ PRUPE ppa007668m
Sequences (6:7) Aligned. Score: 89.72
Sequences (6:8) Aligned. Score: 89.72
Sequences (6:9) Aligned. Score: 90.00

Sequences (6:10)	Aligned.	Score: 80.83
Sequences (6:11)	Aligned.	Score: 83.61
Sequences (6:12)	Aligned.	Score: 75.00
Sequences (6:13)	Aligned.	Score: 81.94
Sequences (6:14)	Aligned.	Score: 76.67
Sequences (6:15)	Aligned.	Score: 81.50
Sequences (6:16)	Aligned.	Score: 49.41
Sequences (6:17)	Aligned.	Score: 82.62
Sequences (6:18)	Aligned.	Score: 63.61
Sequences (6:19)	Aligned.	Score: 70.67
Sequences (6:20)	Aligned.	Score: 63.89
Sequences (6:21)	Aligned.	Score: 70.00
Sequences (6:22)	Aligned.	Score: 84.72
Sequences (6:23)	Aligned.	Score: 50.70
Sequences (6:24)	Aligned.	Score: 52.38

Sequence 7: CADsc6₃ PRUPE ppa007613m

Sequences (7:8)	Aligned.	Score: 97.78
Sequences (7:9)	Aligned.	Score: 97.51
Sequences (7:10)	Aligned.	Score: 82.83
Sequences (7:11)	Aligned.	Score: 85.60
Sequences (7:12)	Aligned.	Score: 77.56
Sequences (7:13)	Aligned.	Score: 83.66
Sequences (7:14)	Aligned.	Score: 77.01
Sequences (7:15)	Aligned.	Score: 80.56
Sequences (7:16)	Aligned.	Score: 49.41
Sequences (7:17)	Aligned.	Score: 82.32
Sequences (7:18)	Aligned.	Score: 63.99
Sequences (7:19)	Aligned.	Score: 68.62
Sequences (7:20)	Aligned.	Score: 66.48
Sequences (7:21)	Aligned.	Score: 69.53
Sequences (7:22)	Aligned.	Score: 91.41
Sequences (7:23)	Aligned.	Score: 51.82
Sequences (7:24)	Aligned.	Score: 53.78

Sequence 8: CADsc6₄ PRUPE ppa007226m

Sequences (8:9)	Aligned.	Score: 99.17
Sequences (8:10)	Aligned.	Score: 83.10
Sequences (8:11)	Aligned.	Score: 85.04
Sequences (8:12)	Aligned.	Score: 77.56
Sequences (8:13)	Aligned.	Score: 83.38
Sequences (8:14)	Aligned.	Score: 77.01
Sequences (8:15)	Aligned.	Score: 80.56
Sequences (8:16)	Aligned.	Score: 50.00
Sequences (8:17)	Aligned.	Score: 82.62
Sequences (8:18)	Aligned.	Score: 63.71
Sequences (8:19)	Aligned.	Score: 69.21
Sequences (8:20)	Aligned.	Score: 65.93
Sequences (8:21)	Aligned.	Score: 68.70
Sequences (8:22)	Aligned.	Score: 89.20
Sequences (8:23)	Aligned.	Score: 51.54
Sequences (8:24)	Aligned.	Score: 53.22

Sequence 9: CADsc6₅ PRUPE ppa007622m

Sequences (9:10)	Aligned.	Score: 83.10
Sequences (9:11)	Aligned.	Score: 84.76
Sequences (9:12)	Aligned.	Score: 77.29
Sequences (9:13)	Aligned.	Score: 83.38
Sequences (9:14)	Aligned.	Score: 77.29
Sequences (9:15)	Aligned.	Score: 80.88
Sequences (9:16)	Aligned.	Score: 50.30
Sequences (9:17)	Aligned.	Score: 83.54
Sequences (9:18)	Aligned.	Score: 63.71
Sequences (9:19)	Aligned.	Score: 69.50
Sequences (9:20)	Aligned.	Score: 66.20
Sequences (9:21)	Aligned.	Score: 68.98
Sequences (9:22)	Aligned.	Score: 88.92
Sequences (9:23)	Aligned.	Score: 51.54
Sequences (9:24)	Aligned.	Score: 53.22

Sequence 10: CADsc6₆ PRUPE ppa007615m

Sequences (10:11)	Aligned.	Score: 87.26
Sequences (10:12)	Aligned.	Score: 72.02
Sequences (10:13)	Aligned.	Score: 95.29
Sequences (10:14)	Aligned.	Score: 73.13
Sequences (10:15)	Aligned.	Score: 77.74
Sequences (10:16)	Aligned.	Score: 49.70
Sequences (10:17)	Aligned.	Score: 75.00
Sequences (10:18)	Aligned.	Score: 63.43

Sequences (10:19) Aligned. Score: 66.57
Sequences (10:20) Aligned. Score: 60.39
Sequences (10:21) Aligned. Score: 68.70
Sequences (10:22) Aligned. Score: 80.33
Sequences (10:23) Aligned. Score: 50.70
Sequences (10:24) Aligned. Score: 52.66
Sequence 11: CADsc6₇ PRUPE ppa007627m
Sequences (11:12) Aligned. Score: 73.13
Sequences (11:13) Aligned. Score: 88.09
Sequences (11:14) Aligned. Score: 73.13
Sequences (11:15) Aligned. Score: 76.80
Sequences (11:16) Aligned. Score: 47.63
Sequences (11:17) Aligned. Score: 77.13
Sequences (11:18) Aligned. Score: 63.43
Sequences (11:19) Aligned. Score: 65.98
Sequences (11:20) Aligned. Score: 61.50
Sequences (11:21) Aligned. Score: 67.87
Sequences (11:22) Aligned. Score: 82.27
Sequences (11:23) Aligned. Score: 50.14
Sequences (11:24) Aligned. Score: 51.54
Sequence 12: CADsc6₈ PRUPE ppa007605m
Sequences (12:13) Aligned. Score: 71.75
Sequences (12:14) Aligned. Score: 88.40
Sequences (12:15) Aligned. Score: 71.47
Sequences (12:16) Aligned. Score: 50.30
Sequences (12:17) Aligned. Score: 69.21
Sequences (12:18) Aligned. Score: 63.81
Sequences (12:19) Aligned. Score: 60.41
Sequences (12:20) Aligned. Score: 74.03
Sequences (12:21) Aligned. Score: 68.78
Sequences (12:22) Aligned. Score: 73.76
Sequences (12:23) Aligned. Score: 53.22
Sequences (12:24) Aligned. Score: 53.78
Sequence 13: CADsc6₉ PRUPE ppa021232m
Sequences (13:14) Aligned. Score: 72.58
Sequences (13:15) Aligned. Score: 78.06
Sequences (13:16) Aligned. Score: 49.41
Sequences (13:17) Aligned. Score: 75.00
Sequences (13:18) Aligned. Score: 64.27
Sequences (13:19) Aligned. Score: 65.98
Sequences (13:20) Aligned. Score: 60.11
Sequences (13:21) Aligned. Score: 68.98
Sequences (13:22) Aligned. Score: 80.06
Sequences (13:23) Aligned. Score: 50.98
Sequences (13:24) Aligned. Score: 52.94
Sequence 14: CADsc6₁₀ PRUPE ppa021536m
Sequences (14:15) Aligned. Score: 70.85
Sequences (14:16) Aligned. Score: 50.00
Sequences (14:17) Aligned. Score: 70.43
Sequences (14:18) Aligned. Score: 62.53
Sequences (14:19) Aligned. Score: 61.29
Sequences (14:20) Aligned. Score: 73.55
Sequences (14:21) Aligned. Score: 66.94
Sequences (14:22) Aligned. Score: 73.55
Sequences (14:23) Aligned. Score: 51.26
Sequences (14:24) Aligned. Score: 52.94
Sequence 15: CADsc6₁₁ PRUPE ppa022917m
Sequences (15:16) Aligned. Score: 42.32
Sequences (15:17) Aligned. Score: 66.46
Sequences (15:18) Aligned. Score: 62.70
Sequences (15:19) Aligned. Score: 85.58
Sequences (15:20) Aligned. Score: 62.70
Sequences (15:21) Aligned. Score: 65.52
Sequences (15:22) Aligned. Score: 79.31
Sequences (15:23) Aligned. Score: 45.45
Sequences (15:24) Aligned. Score: 47.65
Sequence 16: CADsc6₁₂ PRUPE ppa022697m
Sequences (16:17) Aligned. Score: 46.65
Sequences (16:18) Aligned. Score: 47.04
Sequences (16:19) Aligned. Score: 37.87
Sequences (16:20) Aligned. Score: 41.72
Sequences (16:21) Aligned. Score: 46.15
Sequences (16:22) Aligned. Score: 48.82
Sequences (16:23) Aligned. Score: 61.54
Sequences (16:24) Aligned. Score: 61.83

Sequence 17: CADsc6₁₃ PRUPE ppa022409m
 Sequences (17:18) Aligned. Score: 60.98
 Sequences (17:19) Aligned. Score: 57.93
 Sequences (17:20) Aligned. Score: 58.54
 Sequences (17:21) Aligned. Score: 67.38
 Sequences (17:22) Aligned. Score: 80.49
 Sequences (17:23) Aligned. Score: 49.09
 Sequences (17:24) Aligned. Score: 50.00
Sequence 18: CADsc6₁₄ PRUPE ppa022088m
 Sequences (18:19) Aligned. Score: 54.55
 Sequences (18:20) Aligned. Score: 54.10
 Sequences (18:21) Aligned. Score: 73.83
 Sequences (18:22) Aligned. Score: 63.46
 Sequences (18:23) Aligned. Score: 48.18
 Sequences (18:24) Aligned. Score: 50.14
Sequence 19: CADsc6₁₅ PRUPE ppa023056m
 Sequences (19:20) Aligned. Score: 54.25
 Sequences (19:21) Aligned. Score: 55.13
 Sequences (19:22) Aligned. Score: 67.74
 Sequences (19:23) Aligned. Score: 37.83
 Sequences (19:24) Aligned. Score: 39.00
Sequence 20: CADsc6₁₆ PRUPE ppa026085m
 Sequences (20:21) Aligned. Score: 57.58
 Sequences (20:22) Aligned. Score: 62.91
 Sequences (20:23) Aligned. Score: 43.98
 Sequences (20:24) Aligned. Score: 44.54
Sequence 21: CADsc6₁₇ PRUPE ppa027148m
 Sequences (21:22) Aligned. Score: 68.04
 Sequences (21:23) Aligned. Score: 50.14
 Sequences (21:24) Aligned. Score: 51.82
Sequence 22: CADsc6₁₈ PRUPE ppa018829m
 Sequences (22:23) Aligned. Score: 50.98
 Sequences (22:24) Aligned. Score: 52.66
Sequence 23: CADsc8₁ PRUPE ppa007749m
 Sequences (23:24) Aligned. Score: 85.71

Appendix S3 in Supporting Information:

Table 2: Identity scores of the 24 deduced PRUPE_CADs of *Prunus persica* against strawberry FaCAD (AAK28509.1) as determined by CLUSTAL W 2.1 multiple sequence alignment reported in Supporting Information Fig. 1.

Name	NCBI reference number	Identity score
PRUPE_CAD sc65	PRUPE_ppa007622m	88.58
PRUPE_CAD sc64	PRUPE_ppa007226m	88.30
PRUPE_CAD sc63	PRUPE_ppa007613m	87.47
PRUPE_CAD sc618	PRUPE_ppa018829m	86.07
PRUPE_CAD sc62	PRUPE_ppa007668m	85.24
PRUPE_CAD sc61	PRUPE_ppa016455m	84.12
PRUPE_CAD sc67	PRUPE_ppa007627m	80.50
PRUPE_CAD sc66	PRUPE_ppa007615m	79.94
PRUPE_CAD sc69	PRUPE_ppa021232m	79.94
PRUPE_CAD sc613	PRUPE_ppa022409m	78.96
PRUPE_CAD sc611	PRUPE_ppa022917m	78.68
PRUPE_CAD sc610	PRUPE_ppa021536m	77.16
PRUPE_CAD sc68	PRUPE_ppa007605m	75.77
PRUPE_CAD sc617	PRUPE_ppa027148m	68.80
PRUPE_CAD sc4	PRUPE_ppa007678m	67.69
PRUPE_CAD sc615	PRUPE_ppa023056m	66.86
PRUPE_CAD sc616	PRUPE_ppa026085m	66.02
PRUPE_CAD sc614	PRUPE_ppa022088m	64.35
PRUPE_CAD sc1	PRUPE_ppa007634m	55.43
PRUPE_CAD sc82	PRUPE_ppa007736m	53.50
PRUPE_CAD sc5	PRUPE_ppa007789m	52.39
PRUPE_CAD sc81	PRUPE_ppa007749m	52.38
PRUPE_CAD sc612	PRUPE_ppa022697m	51.18
PRUPE_CAD sc3	PRUPE_ppa024217m	50.97

Appendix S4 in Supporting Information:

Table 3: Deduced molecular weights (Mw) and pIs of the putative *P. persica* PRUPE_CADs as determined by ExPASy database (http://www.expasy.org/proteomics/protein_characterisation_and_function).

Reference to the text	Name	Mw	pI
PRUPE_CAD sc1	PRUPE_ppa007634m	39.28	7.24
PRUPE_CAD sc3	PRUPE_ppa024217m	38.42	6.14
PRUPE_CAD sc4	PRUPE_ppa007678m	39.04	6.60
PRUPE_CAD sc5	PRUPE_ppa007789m	38.43	6.46
PRUPE_CAD sc6 ₁	PRUPE_ppa016455m	39.10	6.86
PRUPE_CAD sc6 ₂	PRUPE_ppa007668m	39.02	6.79
PRUPE_CAD sc6 ₃	PRUPE_ppa007613m	38.92	6.23
PRUPE_CAD sc6 ₄	PRUPE_ppa007226m	38.92	6.23
PRUPE_CAD sc6 ₅	PRUPE_ppa007622m	38.88	6.35
PRUPE_CAD sc6 ₆	PRUPE_ppa007615m	38.51	6.75
PRUPE_CAD sc6 ₇	PRUPE_ppa007627m	38.58	6.86
PRUPE_CAD sc6 ₈	PRUPE_ppa007605m	38.88	6.27
PRUPE_CAD sc6 ₉	PRUPE_ppa021232m	38.44	6.71
PRUPE_CAD sc6 ₁₀	PRUPE_ppa021536m	38.98	6.36
PRUPE_CAD sc6 ₁₁	PRUPE_ppa022917m	34.64	8.73
PRUPE_CAD sc6 ₁₂	PRUPE_ppa022697m	36.80	5.57
PRUPE_CAD sc6 ₁₃	PRUPE_ppa022409m	35.62	5.88
PRUPE_CAD sc6 ₁₄	PRUPE_ppa022088m	39.19	6.63
PRUPE_CAD sc6 ₁₅	PRUPE_ppa023056m	37.73	8.82
PRUPE_CAD sc6 ₁₆	PRUPE_ppa026085m	40.48	8.57
PRUPE_CAD sc6 ₁₇	PRUPE_ppa027148m	39.23	6.35
PRUPE_CAD sc6 ₁₈	PRUPE_ppa018829m	39.39	5.86
PRUPE_CAD sc8 ₁	PRUPE_ppa007749m	39.00	5.83
PRUPE_CAD sc8 ₂	PRUPE_ppa007736m	38.72	5.43