

CmaACS1	MTETRRFFNRNRSKSNKEEPTTSDCGGTANFVI VPLQCI VCGSGCVVLGSLI PCVLFYFL(LYLKRNRS)ETEDPPSPFEVESP CNSSSPSSNCSVLESP	100
CmaACS2	0
CmaACS3	0
CmaACS4	0
CmaACS5	0
CmaACS6	0
CmaACS7	0
CmaACS8	0
CmaACS9	MT(NRL)PTFRNSKPIEEFE SATS CCGRAANRVVPLQSVV(CGRGCVVLGSLI PCVLFYFL(LYLKRNRS)DTRD)SPSPDAESS CNSSLSNCLVLETV	100
CmaACS10	0
CmaACS11	M
CmaACS12	0
CmaACS13	0
I		
CmaACS1	LPRTLRTFLSSRSNGPVCSCRANSI AKVCESSIFVYAKKFEEDPFLELNPITGII QLSIFENKLSSTLVCLVLEFNGRDAILCGGNENELSVACTVS	200
CmaACS2	82
CmaACS3	90
CmaACS4	82
CmaACS5	82
CmaACS6	82
CmaACS7	90
CmaACS8	86
CmaACS9	LPRTLRTFLSSRSNGPVCSCRANSI AKVCESSIFVYAKKFEEDPFLELNPITGII QLSVAKNLSSTLVCLVLEFNGRDAILCGGNENELSVACTVS	200
CmaACS10	91
CmaACS11	FTLNSCI PHKCE (ET)SAGLSTKATCNSEGGCLSSYHLCVVEYKKNPYEIRPNQII QGLAENCLCFDLVEFVLEENPDAAFC. KRDCKSI FRELALF	99
CmaACS12	92
CmaACS13	92
II		
CmaACS1	QPSIDGLADKLAVASFSCAVCNVSII PSCLVFTNVCSSAII TLSFCIDAGHFAFLPTPY. ...	295
CmaACS2	QDVHGIPAFKKALVF...EIRGNKVTEANNIVLTGAT SANITLAFCLAE GAFILPTPY. ...	177
CmaACS3	QDVHGIPFENAVANF...CKVRCDRVKDPDRVVASG GATCAHIVAFCLAE GAFILPTPY. ...	185
CmaACS4	QDVHGIPAFKKALVF...SEIRGNRVINPDEHIVLTGAT SANITLAFCLAE GAFILPTPY. ...	177
CmaACS5	QDVHGIPAFKKALVF...EIRGNKVTDVNNIVLTGAT SANITLAFCLAE GAFILPTPY. ...	177
CmaACS6	QDVHGIPAFKKALVF...EIRGNKVTEANNIVLTGAT SANITLAFCLAE GAFILPTPY. ...	177
CmaACS7	QDVHGILSFRITACF...EIRGGRARDPNRFVLTGAT AANLITLILANGLILPTPY. ...	185
CmaACS8	QDVHGILSFRITACF...EIRGGRARDPNRFVLTGAT AANLITLILANGLILPTPY. ...	181
CmaACS9	QPSIDGLADKLAVASFSCAVCNVSII PSCLVFTNVCSSAII TLSFCIDAGHFAFLPTPY. ...	295
CmaACS10	QDVHGIPCFRNVANF...AKVRGNRVCDPDRVVASG GATCAHIVAFCLAE GAFILPTPY. ...	186
CmaACS11	QDVHGIPAFKKALVF...SEIRGNKVTDVNNIVLTGAT SANITLAFCLAE GAFILPTPY. ...	194
CmaACS12	QDVHGILLEFCALASF...EKVRGGRVNDPSRIVAGCGATCSSITVI FCLADLGAFLSI FLENSTNSLSKFD	192
CmaACS13	QDVHGILLEFCALASF...EKVRGGRVNDPSRIVAGCGATCSSITVI FCLADLGAFLSI FLENSTNSLSKFD	187
III		
CmaACS1	LDFAFEFCRSRGLKVRGIIISNPSIPGNCLEFETIKLLHARDKNIIISNII FVCGSTVCSFEFVSMAEMDLESD. ...	391
CmaACS2	IEQVHVEFCARNLRKGVLTINPSPIGTTASRHEILDLVFEITSRGIIISNII FVCGSTVCFPGVSMAEVLRRSSSCIEFVVRKRVHVSLSKLGIP	277
CmaACS3	IEFAAEKCESNIKIKQLIINPSPIGTYDRCTIETAVAFINCKRGIIVCIEIAATVETEPGII SI SEVIENDTECD. ...	282
CmaACS4	LLFAVCSCSRDLKVRGVLINPSPIGTTITTTCEINLLLGIAASKNIIISNII FVCGSTVFNPGVSVAEILNCSYKHNDI RCQVHVSLSKLGIP	277
CmaACS5	MEFAERFELNLRKGVLTINPSPIGTTASRBEILNVFEITSRGIIISNII FVCGSTVETPKRTIMDDLKES. ...	273
CmaACS6	IEQVHVEFCARNLRKGVLTINPSPIGTTANRIEILNVFEITSRGIIISNII FVCGSTVCFPGVSMAEVLRRSSSCIEFVVRKRVHVSLSKLGIP	277
CmaACS7	IEAANNIAI ANLNRKGVLTINPSPIGATI CRSTIEEILDFVTRKNIIISNII FVCGSVFSSAEIISVAEVLASRGYKL. ...	282
CmaACS8	IEAANNIAI ANLNRKGVLTINPSPIGLTI CRSTIEEVLFDVTRKNIIISNII FVCGSVFSSAEIISVAGVLESRGKN. ...	278
CmaACS9	LDFAFEFCARNLRKGVLTINPSIPGNCLEFETIKLLHARDKNIIISNII FVCGSTVCSFEFVSMAEMDLESD. ...	391
CmaACS10	MEFAVEFEKSGIKVQLIINPSPIGTYVYDKKITEITAVFINKNIIISNII FVCGSTVCFPGVSVAEILNCSYKHNDI RCQVHVSLSKLGIP	283
CmaACS11	LLFAVCSARNLRKGVLTINPSPIGTTITTTCEINLLLGIAASKNIIISNII FVCGSTVCFPGVSVAEILNCSYKHNDI RCQVHVSLSKLGIP	294
CmaACS12	IEFAVKKCEANI KVRGIIINPSPIGTYDRDITKTLVTVNCHDIIICDII SATVFKAPTII SIACI VEEFECK. ...	289
CmaACS13	IEFAVKKCEANI KVRGIIINPSPIGTYDRDITKTLVTVNCHDIIICDII SATVFKAPTII SIACI VEEFECK. ...	284
IV		
CmaACS1	CFRVAATVSNENILAAAGKLARSSTSAITGNLSSMSHACIKFI CINKRKLCEANSKFVAGHLELII KYAFSSNGPFCVADACNITR. SYSSEK	489
CmaACS2	CFRVAATVSNDDAVVAATRASSGLVSSCTGYLLSAM SIKKTIIRNYI SENCKRLKCFCKMLVSCAKQICLCLNSNA CLFQVADARHLK. SDFTES	375
CmaACS3	CFRVGITVSNDDAVNCAARAASSGLVSSCTGHLLASMSIDDEIASEFLVGSARKLAARHNRITRQACQICYLFGSGCLFLMDLRHLK. EKTLEA	380
CmaACS4	CFRVAATVSNDDVVAATRASSGLVSSCTGYLLSAM SIKKTIIRNYI SENCKRLKCFCKMLVSCAKQICKEFGNA CLFQVADARHLK. ANTFFS	375
CmaACS5	CFRVGITVSNPKVVAATRASSGLVSSCTGYLLSAM SIKKTIIRNYI SENCKRLKCFCKMLVSCAKQICLCLNSNA CLFQVADARHLK. SCSTFE	371
CmaACS6	CFRVAATVSNDDVVAATRASSGLVSSCTGYLLSAM SIKKTIIRNYI SENCKRLKCFCKMLVSCAKQICLCLNSNA CLFQVADARHLK. SDFTES	375
CmaACS7	CFRVGITVSNDDVVTARRASSITLISCTGRFLASMSNRKCIIRKRI KANRDLKRYEYIIEQRTAQICLCLNSNA CLFQVADARHLK. DCKKTTNT	382
CmaACS8	CFRVGITVSNDDVVTARRASSITLISCTGRFLASMSNRKCIIRKRI KANRDLKRYEYIIEQRTAQICLCLNSNA CLFQVADARHLK. KNPTFRE	377
CmaACS9	CFRVAATVSNENILAAAGKLARSSTSAITGNLSSMSIKKCIIRCFRI RIRREELCEANRRFAAGHLELII KCIENSGCFQVADASNTI. G. SYSEKA	489
CmaACS10	CFRVGITVSNDDAVCAARAASSGLVSSCTGYLLASMSIDDAVDRFLAGSAEKLATRRNRITKQACQICYLEGSGCLFLMDLRHLK. EKTLEA	381
CmaACS11	CFRVGITVSNDDVVAATRASSGLVSSCTGYLLSAM SIKKTIIRNYI SENCKRLKCFCKMLVSCAKQICKEFGNA CLFQVADARHLK. ANTFFS	392
CmaACS12	CFRVGITVSNDDVVTARRASSITLISCTGHLLAAMSTIEIDVDFLANSKRLCEHARFTKELDEKQITCLNSNA CLFQVADARHLK. DCTFRA	387
CmaACS13	CFRVGITVSNDDVVTARRASSITLISCTGHLLAAMSTIEIDVDFLANSKRLCEHARFTKELDEKQITCLNSNA CLFQVADARHLK. DCTFRA	382
V		
CmaACS1	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	549
CmaACS2	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	473
CmaACS3	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	473
CmaACS4	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	468
CmaACS5	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	442
CmaACS6	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	470
CmaACS7	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	445
CmaACS8	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	441
CmaACS9	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	549
CmaACS10	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	473
CmaACS11	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	492
CmaACS12	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	464
CmaACS13	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	482
VI		
CmaACS1	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	549
CmaACS2	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	473
CmaACS3	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	473
CmaACS4	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	468
CmaACS5	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	442
CmaACS6	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	470
CmaACS7	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	445
CmaACS8	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	441
CmaACS9	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	549
CmaACS10	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	473
CmaACS11	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	492
CmaACS12	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	464
CmaACS13	EVLEVDKLLDI GKVEVIFGSCCNCIEFGVFGCHITTLIDEEIPI VMIRRTISEACKSYT. ...	482
VII		
CmaACS1	LP(PS)MLRAT	549
CmaACS2	LP(PS)MLRAT	478
CmaACS3	LP(PS)MLRAT	483
CmaACS4	LP(PS)MLRAT	469
CmaACS5	LP(PS)MLRAT	442
CmaACS6	LP(PS)MLRAT	475
CmaACS7	LP(PS)MLRAT	445
CmaACS8	LP(PS)MLRAT	441
CmaACS9	LP(PS)MLRAT	549
CmaACS10	LP(PS)MLRAT	483
CmaACS11	LP(PS)MLRAT	496
CmaACS12	LP(PS)MLRAT	464
CmaACS13	LP(PS)MLRAT	492

Figure S1. Amino acid sequence alignment of *CmaACS* genes. The conserved glutamate residue (E) marked with an arrowhead is involved in substrate specificity. Ser residues implicated in calcium-dependent protein kinase (CDPK) and mitogen-activated protein kinase (MPK6) phosphorylation are marked by asterisks and a black dot, respectively. The seven highly conserved regions (I–VII) among all ACC synthases are underlined.