

A Sequence alignment of CCB1 orthologues

```

                *           20           *           40           *           60           *           80           *           100
CCB1-Cm : MPRHAWSLAQDSRSNVNVLRVASVMASNGIHASARAMFCSFTAIKWQGTHVHRLQQQRCLFRLHAEQTPALVRKQRSHNRVEQALPLPTRDLAQLFAYG : 100
CCB1-Tp : ----- : -
CCB1-Av : ----- : -
CCB1-Se : ----- : -
CCB1-Syn : ----- : -
CCB1-At : ----- -MATKLISPPPLSCPWVTSREVIILKGLPRRRREWMVTKRNRVSAVTAMIVEPLSVVSSSAIQIHQWWE : 66
CCB1-Os : ----- MEATAAATRLLLPPLRAPPPSLAGAAAAAGGGGR -WRGAVPRRARARRAVVPPRASLVDSSG-----G : 63
CCB1-Cr : ----- MLATQTSR---RCATSRSSRVVFFAAQAPRRCVRLAAARNGQAEQASAVESLGLKLSMPALASFVSFL : 64

```

```

                *           120           *           140           *           160           *           180           *           200
CCB1-Cm : CVGVPAVAHASVTTTAEVANTTAPRIYGGITFLLLTIVGFVRFMVASGGRRIEQTNITFIDTKE--SDIVTTEKLVGDVLTARKYVPRERE-ASRVLVER : 196
CCB1-Tp : -----YSKASYYTTLA--LYAASFPGWSQIKRSTKAKVKRKTIVSAGEAAEGGKELRQQAGEIMAYMKANNYEVVAEAG---ETITFR : 78
CCB1-Av : -----MDTAILPSTFL--LTLLLAVGLLFFIRASTKDRTEMMQLISEQEESE-----VLMPLQLEFYFRSRSYRVAEVDHEKNQVTFE : 74
CCB1-Se : -----MSDRVTLASVFF--ITLLPVIGVVFIRSGFKDRITTTQLTESDLDRP-----TLIARLQDYFRSRYRVAEVDHEKNQVTFE : 75
CCB1-Syn : -----MDVMDLPVLGSTYF--FTIFSLIGLIFIRSSVKDRITQIRAWIDNPEA-----GLDEIKTYENNRAMRITNIDPVQQAITFE : 77
CCB1-At : QNPNSLLLMTEATG--GYSLASYYTSLG--LFVISVPGWLSLIKRSVKSKIVRKTIVVNDVK---KEPKQVAGEILSFFTRNENITDRG---ETITFE : 155
CCB1-Os : AAAAVALLLDAAVAGATGYSQASYYTSLG--LFVLSVPGWLSLIKRSVKSKVVKQTFVKEEGQT---MAPNQVAGEILSFFTRNENITDRG---EVIITFE : 155
CCB1-Cr : AMDAPAMALEATNPFEGVQSNLSLYVTLA--LFLMSVPGWLSLVKRAPQAACKRLTFEVPGPVAVEGAMSLDDRARQIFRYFKRYNDVKETG---EVIITFE : 159

```

```

                *           220           *           240           *           260           *           280           *           300
CCB1-Cm : GRTQPSVAIGAFIVFCAAGGLYGFALAAKVLLPGNSDWNVAIILLSPLMWFVYNTNQREEEFRFRVDPVSSDS---KAIIVYKGRPDETEAMESEKIV : 293
CCB1-Tp : CLVARSTSQAFFLTFCTALGMASLALVLCIQFQDVFDFNFIYTLTLLSPYAGIYYWRSGDRVDDMKVKLAANDDDT---LNETHEGNDDEIERMWRITDQLQ : 175
CCB1-Av : GFVKPSIFLAVPLTLLASAGLVCLSLVFAALLFRFGNIFLGLVLFAPLSGLFYWKAGRLEKVVKLKLESLANQPQL-FSKITVVAHRDELLELQKAPLK : 173
CCB1-Se : GIVAPSLFLAVFVATLAATGLGCLGLVVVATATGSSPOLALIPATLAPIAGRLVYQAKRPERVTAFATAADR-----SDLTVAHRDELITLQSLPIR : 169
CCB1-Syn : GNVQASPFLLAVPLSLLAALCLLCLALVLAVFWPQRCFLFFFLWLAPLAGTFYVQKAAARVEAITLEFGDPDQPSHPGQYPLTITTAHRDELRELAQAFPLD : 177
CCB1-At : GKMPSPRGOAALLTFCTCISLASVGLVITITVPDFGNNWFITLLSPLAGVYVYKASRKEETKVKMVMVGSKGR---LDEIVVQGGDDVQVEEMRKEITQLN : 252
CCB1-Os : GIMVPSRGOAALLTFCTCISLGSVGLVLSIAPVEGNNWFVWMTLSPLAGVYVYKASRKEETKVKMILSDDGN---VSEILVRCDDVQVEEMRKEITKFS : 252
CCB1-Cr : GIYAADKGOAALTTFYTFVGMASVALVLSILVPOVGNWVYGTALSPAYAYVMQRTGRPEQFRVKMVTATDDQ---TTDTIVEGDKEEIERFWKEELGIV : 256

```

```

                *
CCB1-Cm : RNRPEE----- : 299
CCB1-Tp : EKG MVKVEGIL---- : 186
CCB1-Av : PNE----- : 176
CCB1-Se : ALES----- : 173
CCB1-Syn : WQGGSSH----- : 184
CCB1-At : EKG MVYVKGLFERSS : 267
CCB1-Os : EKG MIYVKGIFET-- : 265
CCB1-Cr : EKG KVYVKGMLEA-- : 269

```

B Sequence alignment of CCB3 orthologues

```

                *      20      *      40      *      60      *      80      *      100
CCB3-Cm : MFLLYTGCVLRRDIRFGVCSKLNAGARTQHYGSVRSGSTWWRKSL LPRGRYPVFTGYAAEQQRAPSKRCLCESLVMVTDVASTWMAFAWGAVTGSALTT : 100
CCB3-Tp : -----
CCB3-Av : -----
CCB3-Se : -----
CCB3-Syn : -----
CCB3-At : -----MT-TVTTSF-----VSFSPALMIFQKSRSSPNFRNRSTS---LPIVSATLS-----HIEEAATTTNLRQTNSISESL-R : 67
CCB3-Os : -----MEASMSRTVSM LFSARRCIVASAAKDIEIAQGGRRRRSNDVKQQRGSHGQLAVAAATTAAMTGQCHAAAAAAPERQWQVEAEWVCR : 88
CCB3-Cr : -----MMASSMLHSSARCAAFKAGPLRSPQFALRPRATVSLSAVKSSSEASSSACSTSERQAHPLARLEVATVASLLASGALAGSCLAA : 85

```

```

                *      120      *      140      *      160      *      180      *      200
CCB3-Cm : PTVANSVQVPAPFVAPLRGLTSLVFTTYTVLFLRFVTPWFPQINAGRPPWSIVVLATEGLLRPTRRRIIPQGGVDITPLVWLAITSLSQELLVGSQGIIT : 200
CCB3-Tp : --MVLSETDPWVQPLAL-VLGFPLNLF SFAMLCRIVLSWYPTANVNEVPENIVVWPTEPLLRLV RGSVPPAFGVDITPVVWLVGFTFVN EILLGQOGLLT : 97
CCB3-Av : -----MTGVNLSVWILGPFVGVMTFLFIFRIILTWYPQVDENR LPE NLIAWPTEPFLLIPLRKIIPPIGGVDITPIVCVGFISLLREVLLGQOGLLT : 91
CCB3-Se : -----MQPLLWFSWILCGVLAGMTLLFFIFRIILTWYPQVDLQQGPPYRAIALPTEPFLLAPTRRLIPPLGGVDISPIIWWALISLLREILLGQOGLLT : 91
CCB3-Syn : -----MNYAAIVGQGLGILAVMTVLFIFRIILTWYPQVELTKWPWKLIALPTEPLLIPTRKLVPPICGGVDLAPILWVFICTFLREILLGQOGLIT : 91
CCB3-At : NISLA-DLDPGTAKLAIGLGPALSAFGFLFIRIVMSWYPKLPVDFPYPVAYAPTEPILVQTRKVIPLAGVDVTPVWVFGLVSELS EILVGPQGLLV : 166
CCB3-Os : AVAVVGELDPATAKAAIGVAGPALSAFGFLFIARIVMSWYPRLPVREFPYPVAYAPTEPLLAVTRKVIPLAGVDVTPVWVFGLVSELS EILVGPQGLLV : 188
CCB3-Cr : DSPENAEQTVQLAALAANTLRPAFNIETLLYIIRVPMTWYPEIDGKKMPWALAYAPTEPVL SVARKVVPLLSGVDVSPIVMIAFITFSN EILLGPQGLLT : 185

```

```

CCB3-Cm : LITR---- : 204
CCB3-Tp : MKMKYGI- : 104
CCB3-Av : MLARMS-- : 97
CCB3-Se : MVLEQG-- : 97
CCB3-Syn : MASRLQ-- : 97
CCB3-At : LVSQQQVN : 174
CCB3-Os : LLSQQKP- : 195
CCB3-Cr : LIQQRGGL : 193

```

C Sequence alignment of CCB2 and CCB4 in vascular plants and *C. reinhardtii*

```

                *           20           *           40           *           60           *           80           *           100
CCB2-At : --MSIQTCNFP-----FHPK FALQPRQRSTR--IFARTENDSPQSKTSDQQLNLSLRLRFTFGIPGFDESYLPRWIGYGFGSLLLNLNHFSSASAP : 85
CCB4-At : MEARIILRLRIQIPWSAN-----RQFSHPPLDFPRFIRASSSSTSQKPKTYE-GPKPRKNLVADEISKNDLDRSLPIYVGGASLLAVLFNRTVSGIAP : 92
CCB2-Os : --MPLLARAPPPPPPLRHRGRLLPFTSSSSPRRRRRPFAARVRASGSDPPPQQQQQVNLSLRFTLGLIPGLDESYLPRWIGLGFGLVNLNHLSPSP : 98
CCB4-Os : MEMTRSITLVPLPATLRPASAACRFRRRRRGLPFGALFSPSPPSNQQQEMHIRALQPRQDWVGEVVRSDNTLVRGLPILGGASLLAVLNRVAVSGIAA : 100
CCB2-Cr : -MSQALLANRLIGSRLCPLRQRAEQAAPCKPPVLSRRTSTQVRAETQRRGLGDDIDVAVFRFTLGLIPGFDDRFIPRVVGLALGALLVNHVLGADP : 99
CCB4-Cr : --MTSLLRGRSHQAAVLR-----QGRVRPFLPAQQCFPLRIVHVAAKSGE-AVEPDOSFG--LVAQQAEFFRALPLYAGGAGVASLLNRLSGIAP : 87

                *           120          *           140          *           160          *           180          *           200
CCB2-At : ISESMRSEALGUSLAAFSTIALPYICKFLKGS-VVEQRSPEEEGEQ---VFVHSSNIG--DSLKEDLAWATYVLLRNTSTIAVLIISVQELCYR----- : 173
CCB4-At : VADASSSQSRADLLALGLAVTNLLTGLVWLSIRPKSITPVNPKGVE---CKVVESDLP--ASMVSELLWAWESLKVATCCKSLVIVYNICLLIQ----- : 181
CCB2-Os : TP-AQLRSEALGLCLAAFSATLPYLGRFLEGAGAAERVLPPEGSRQ---VFAMSDLS--AAQKEDMAWASYVLLRNTNTTSVLIISIGNQLCTR----- : 186
CCB4-Os : VADASSSQSRADILLALSVTDILAGLVWLSIRPKSISPVVPRGVE---CKRVGTGVL--DSALRELLWTWDSLTTATCCKSLVVVYGENCVLIQ----- : 189
CCB2-Cr : TPEAQVRCEWLGALLASLCVLPDIEERLREAMPGRGRQKAAEAIEGSANGFFLEPSLQ--EAAKKEAWASFSLLKNTNCCGVAVAAGSRVLMARGALG : 197
CCB4-Cr : VVDASSSQSRADVLGIVLSAVLLLTGLQWLALKPREVAAVDLEGST---VDFVEPGLKPYAALLREFAWARDAMFSTTRCKSLVLLYKERTLFH----- : 178

                *           220          *           240          *           260          *           280          *           300
CCB2-At : GYWNCPE-----QMSKAQLHDWFKKKVDEIGLADVKETLYFPQYA---GSALSLDILPDGTRSLFVQPLVQN---TNEPQKVNCFLLVASTAGYA : 257
CCB4-At : IGMVAESPEDKKTIVIKTDKLMQGSVYRGMKSKAQSYLANLSLYP-----GRSELP-FLPANTQAVILQPLGDK-----GIAVIGGNTIRG : 262
CCB2-Os : GYWDPE-----DISKYAMIEWFKSQMQEAGIVDREDLYFPFTFS---DTQLG-KLFPQGILSVLAQPVLLNNPDPTNSEIKAEGFILLASNSSYA : 272
CCB4-Os : IGVAAGSPEDGNAVVMVDAQKFMQGSLYRSAMESKKQSYLANLALYP-----GRTELP-FLPANTQALILQPIGDK-----GIAVIGGDTIRG : 270
CCB2-Cr : SGVVAPGNAAASLAAMSKDLSAVSGSSKVAEALAGAAAGSQQLWLPDRGGFGGSGAGSLALLPAGACLVLQHIPLP-----GGGPAALIVFSERPRA : 290
CCB4-Cr : YGFITKG-----VKPGNVVPGICTQAMRDSQGNYLANLVLYP-----GRPEFTAFLEPENTQGMVQPVGKD-----GVIVAGTDTVRG : 252

                *           320          *           340          *
CCB2-At : YSDKDRAWIGAMAEKFRG----- : 275
CCB4-At : FTSSDQAWISSIIEKLDATLGRYFVDSDEISRVTV----- : 297
CCB2-Os : YSEKHRVWIRTVANKFQCT----- : 291
CCB4-Os : FTNLDQAWIAMIADKLDATLSKS----- : 293
CCB2-Cr : LADREGRVVAAVANKLAAFV----- : 310
CCB4-Cr : FSRLDQAWLSTIADKLEVSLEGVALPQAGVGFGGSGSSSSGAKASGKQPAAR : 306

```

D Sequence alignment of CCB2 orthologues

```

*          20          *          40          *          60          *          80          *          100
CCB2/4-Av : -----MTKPDDPNRVLRRRPEVVGGLG-----AILLLLNRRLLTPEELT : 36
CCB2/4-Se : -----MASDSAVLWLRRPLIAGAIG-----GTLLLMVNRALTPEELL : 35
CCB2/4-Syn : -----MSAADPNRIVRLLPLGASSLG-----GLLLLLNRRLLSTPMLN : 35
CCB2-At : -MSIQICNFP-----FHPKFALQPRAQRSTR--IFARTENDSPQSKTSDQQLNLSVLRRFTFGIPGFDESYLPRWIGYGFSLLLLNHFSASAPI : 86
CCB2-Os : -MPLLARAPPPPPLRHRGRLLPRFTSSSSPRRRRRPRAARVRASGSDPPQQQQQQQVNLSVRFFTLGIPGLDESYLPRWIGLGFCALVLLNHLLSSPST : 99
CCB2-Cr : MSQALLANRLIGSRLCPLRQRALRQAPCKPPVLSRRTSTQVRAETQRRGLGLGDDDIDVAVFFRFTLGIPGFDDRFIPRVVGLALCALLVVNHVLGADPT : 100

*          120          *          140          *          160          *          180          *          200
CCB2/4-Av : N-SCARGDVLGVILSAVLLLTGLIWQQVQPR-----SPDSVELIGDEGEVLSADLPEAVKTELAWASHLLLLTNTVTRSLVVYYQGKVLLRGILGS-- : 126
CCB2/4-Se : P-TQSRSSDALGILLSALLLLSGLLWQRVQPV-----PPEMVVLEGEEGFELDDQLPEASRQELAWASKLLLLTNTITGSLLIWYDGOVLLRGILAP-- : 125
CCB2/4-Syn : P-SCARSDVVGVILGMLVCVWLIWQRIQPK-----SPEAVVLEGEKEGFDLLDSLPQEIKTELAWASHLLLLTNTVTQTMVVYYDROVLLRGILSE-- : 125
CCB2-At : SESQMRSEALGLSLAFSALPYIGKFLKGS-----VVEQRSLPEEGEQVVISSNIGSLSKEDLAWATYVLLRNTSTIAVVLISVQGELCVR-GYWNC-- : 178
CCB2-Os : P-AQLRSEALGLCLAAFSATLPYLGRFLEGAG---AAERVPLPEGSRQVEAMSSDSLSAAOKEDMAWASYVLLRNTITSVLISIGNQLCIR-GYWDP-- : 191
CCB2-Cr : PEAOVRCEWLGALLSLCVLVPDIEERLREAMPGRGRQKAAEAIEGSANCFFLEPSLQEAAKKELAWASFSLLKNTNCCGVAVAAGRVLMARGALGSGV : 200

*          220          *          240          *          260          *          280          *          300
CCB2/4-Av : ---KAEVTPGAIVKRVLEKQQPVYLVAL-----NVVYPC-----RIEFDYLPENTGVICQPIGNE-----GVLLILGANAPRSYTK : 193
CCB2/4-Se : ---PVPVQPGPIVERVLKTGKAVYLVDL-----KLLYPC-----RIEFNYLPANSQGLICQPLGNR-----GVLLLLAARAPRSYTQ : 192
CCB2/4-Syn : ---QKEVKPGPIVERVMQTQKPVYLVNL-----FLLYPC-----RVEFDYLPANTQGLICQPLDDR-----GVLLILGANIPRSYTK : 192
CCB2-At : ---PDQMSKAQLHDWFKKVDEIGLADVKE-----TLYFPQYAGS---ALSLDILPDGTRSLFVQPLVQN---TNEPQKVNSFLVVASTAGYAYSD : 260
CCB2-Os : ---PEDLSKYAMIEWFKSQMQEAGIVDLRE-----DLYFPTESDT---QLG-KLLPQGILSVLAQPVLNNPDPTNSEIKAEGFILLASNSSYAYSE : 275
CCB2-Cr : VAPGNAAASLAAMSKDLSAVSGSSKVAEALAGAAAGSQQLWLLPDRGCFGGSGAGSLALLLPAGAQCLLVQHIPLP-----GGGPAALLVFSERPRALAD : 293

*          320
CCB2/4-Av : QDENWIAGIADKLAVTLKNSHG----- : 215
CCB2/4-Se : QDERWIAGIADKLQSLSRSAAAIAVEQP : 221
CCB2/4-Syn : QDENWVTGIADKIAHSLSLMPINA----- : 215
CCB2-At : KDRANIGAMAEKFRG----- : 275
CCB2-Os : KHRVWIRTVANKFQCT----- : 291
CCB2-Cr : RERGWVAAVANKLAAFV----- : 310

```

E Sequence alignment of CCB4 orthologues

```

                *           20           *           40           *           60           *           80           *           100
CCB2/4-Av : -----MTK---PDPNRVLRRLRFVVGGLGAILLLNRLLT----- : 32
CCB2/4-Se : -----MA---SDSAVWLRRLPIAGAI GGTL LMVNRALT----- : 31
CCB2/4-Syn : -----MS---ADPNRIVRLPLI GAGSLGGILLLNRLST----- : 31
CCB4-At : MEARIILLRIQIPWSAN-----RQFSHPPLDFPRFIRASSSSTSQPKTYE-GPKPRKNLVADFISKNDDLVRSLPIYVGGASL LAVL FNRTVSGIAP : 92
CCB4-Os : MEMTRSLTLVPLPATLRPASAACRRRRRRRGLPF GALFSPSPSPSNQQQEMHIRALQPRQDWWGEWVRSNDTLVRGLPI LGGGASL LAVL NRAVSGIAA : 100
CCB4-Cr : -----MTSLLGRSHQA AVL RQGRV RFLPAQQCRPLRIVHVAAKKSGEAVEPDQSFGLVAQQA EFRALPLIYAGGAGVAS LLLNRLLSGIAP : 87

                *           120          *           140          *           160          *           180          *           200
CCB2/4-Av : -PELTNSQARGDVLGVTL SAVL IITGLI WQQVQPS PDSVELIGDEGFVLSADLP--EAVKTELAWASHLLLNINVTLSLVVYYQCKVLRRGITLGS--- : 126
CCB2/4-Se : -PELLPTQSRSDALGILLSALLILSGLLWQRVQVPPEMVVLEGE GGFELDDQLP--EASRQELAWASKLLLNITGSLLIWYDGOVLRRGILAP--- : 125
CCB2/4-Syn : -PMLNPSQARSDVVGVTLAGMLVCVWLIWQRVQPKSPEAVVLEKGGFDLDSL P--QETKTELAWASHLLLNINVTQTMVVYYDRQVLRRGILSE--- : 125
CCB4-At : VADASSSQSRADLLALGLAVTNLLTGLVWLSIRPKSITPVNPKGVCKRVVESDLP--ASMVSELLWAWESLKVA TCCRSLVIVYNGICLLIQIGMVAESPE : 190
CCB4-Os : VADASSSQSRADILLTALSVTDILAGLVWLSIRPKSISPVVPRGVCKRVGTGVL--DSALRELLWTDWLSLTATCCRSLVVVYGGNCVLIQIGVAAGSPE : 198
CCB4-Cr : VVDASSSQSRADVLGIVLSAVL LLLTGLQWLALKPEVAAVDLEGSTVDFVEPGLKPYAALLREFAWARDAMFSTTRCKSLVLLYKCRITLFHYGFTTKG-- : 185

                *           220          *           240          *           260          *           280          *           300
CCB2/4-Av : -----KA EVT PGATV KRVLEKQQPVYLVAENVYPGRIEFD-YLPENTQGVICQPIGNEGVLLILGANAPRSYTKQDENWIAGIADKLA VTL----- : 210
CCB2/4-Se : -----PVPVQPGPIVERVILKTGKAVYLVLDKLYPGRIEFN-YLPANSQGLICQPLGNRGVLLLAARAPRSYTQQDERWIAGIADKLDQSL----- : 209
CCB2/4-Syn : -----QKEVKPGPIVERVMQTKQPVYLVNPLYPGRVEFD-YLPANTQGLICQPLDDRGVLLGANIPRSYTKQDENWVTGIADKLAHSL----- : 209
CCB4-At : DKKTIVIVKTDKLMQGSVYRGVMKSKAQSYLANISLYPGRSELP-FLPANTQAVILOPLDKGIAVIGGNTIRGFTSSDQAWISSIGEKLDATLG----- : 283
CCB4-Os : DGNAMVMDAQKFMQGSLYRSAMESKKQSYLANLALYPGRTELP-FLPANTQALILQPIGDKGIAVIGGDTIRGFTNLDQAWIAMIADKLDATLS----- : 291
CCB4-Cr : -----VKPGNVVPGETCTQAMRDSQGNYLANISLYPGRPEFTAFLPENTQGV MVQPVKDGVI VAGTDTV RGFSLDQAWLSTIADKLE VSLGEGVALP : 279

                *           320
CCB2/4-Av : -----KNSHG----- : 215
CCB2/4-Se : -----SRSAAAI AVEQP----- : 221
CCB2/4-Syn : -----SMPINA----- : 215
CCB4-At : -----RYFVDSDEISRVTV-- : 297
CCB4-Os : -----KS----- : 293
CCB4-Cr : QAGVGFGGSGGSSSSGAKASGKQPAAR : 306

```

F Sequence alignment of CCB2/4 orthologues

```

*          20          *          40          *          60          *          80          *          100
CCB2/4-Cm : ----MEAQERSVDDAKDTCIGQKLSKRRPVGCSVDCALGFSAPSGPPTVPLRRVLLPASRVRTPPCREASRSG--TVCSTRNVPGIARIACKSRGALRAR : 94
CCB2/4-Pt : MKRTRLAIYAAVTLQSTTLTLALMPSSAAFSCSRTRDYRLRSTVKPPLHQFGKLRTPPKAPKSQSHILSTNKCLVSLRSSNSDDELLSTTTTTSKAKVRFS : 100
CCB2/4-Tp : -----MTCTRCDPGSSVPLLAFAQHSTHGVTTRQRQFANTKRISYPAQLENTNNNE-ESQSSFLSTSKATVQFKSNRNN----- : 76
CCB2/4-Av : ----- : -
CCB2/4-Se : ----- : -
CCB2/4-Syn : ----- : -

*          120          *          140          *          160          *          180          *          200
CCB2/4-Cm : KIGTQRAVIVLRHAQRPELLWGKPSPALVFGGLGTLAAALVWNRLLANLTVVEG-----TRARADLVCAIASALLLYAVSAWQIEVRSTAPVRI : 183
CCB2/4-Pt : TSKVSSPGEASNSLLDSILSWITSDVGSVILGFSGLTALLVGRLLLSLSSDDTIASSPDAQSEETRANLLAFATGAVLLNGISKLDVESALAPLVEL : 200
CCB2/4-Tp : --NNASNKNLANLTPIDSLLLNLTSDRTSLLLSGSLGILLNRLLSFPEGEDAILYEAS-----RSRIDLLGVFAAGSVLLNGITKLDVESAKSERVVL : 169
CCB2/4-Av : -----MTKPDPNRVLRRPFPVVGGLGAILLLNRLLTPELINS-----QARGDVLGVILSAVLLITGLIWQQVQPRSPDSVEL : 73
CCB2/4-Se : -----MASDSAVWLRRLPLIAGAIGGTLMLVNRALTPELPT-----QSRSDALGILLALLILSGLLWQRVQPVPPEMVEL : 72
CCB2/4-Syn : -----MSADPNRIVRLLPLGAGSLGGLLLNRLSTPMNPS-----QARSDVVGVLVLAGMLVVCVWLIWQRVQPKSPBAVVL : 72

*          220          *          240          *          260          *          280          *          300
CCB2/4-Cm : RDG-----HHLEQETETIAGGELETAALWLLIDTVFGACANVTAVVWLTGDNTRIVAQRG-----MVKAAALG : 245
CCB2/4-Pt : SCQ-----KLSEPVVGVDES-QSTAAQIGWTLKALLAATPAQSAVILLATTLHPFNSNSVVKSPSSVGVQVVALAGIVPSVS-----PSLPT : 280
CCB2/4-Tp : ECRNSFEFGSGGIVWNKNGDNKPEGGDQVVENFQSTVEALGSFIKCTPARTAVLLASTATATSENKQHR----WEPVAMAGILPLDTRCTSIPDSTA : 264
CCB2/4-Av : ICD-----EGFVLSADLPEAVKTELAWASHLLTNTVTRSLVYYQGVLLRGIILGS-----KAETV : 131
CCB2/4-Se : EGE-----EGFELDDQPEASRQELAWASKLLLTNTITGSLIWIYDGVLLRGIILAP-----PVPVQ : 130
CCB2/4-Syn : EK-----EGFDLLDSLPQEIKTELAWASHLLTNTVVTQIMVYYDRQVLLRGIILSE-----QKEVK : 130

*          320          *          340          *          360          *          380          *          400
CCB2/4-Cm : SQVDLRRFEELG-----VLNLRDPVSSRYFADLKTVPKRSLEWQQLPADTQSAWLGTFKAPLQRD-GSQPAQSCFLLILGCNKIRGFLD : 328
CCB2/4-Pt : GTA LDRFR-----NSATESTDETYLPTLQALPGRTEFT-YLPPNTQAVLLVPVRLQQQS--IDGRDTVTYALVLLGGNRARVFTP : 357
CCB2/4-Tp : STP LDRMLRYDGSIKGGSVAGSDVVGRRPKKNVPKESYLP TLQALPGRVEET-YLPTNAQEAFLVPVSTTETTNVAVAGCSATYFAVVLGGDTAKSFTP : 363
CCB2/4-Av : PGA VKRVLE-----KQQPVYLVALNVYPGRIEFD-YLPENTQGVLCQPIGN-----EGVLLIGANAPRSYTK : 193
CCB2/4-Se : PGP VERVLK-----TGKAVYLVDLKLYPGRTEFN-YLPANSQGLICQPLGN-----RGVLLLAARAPRSYTK : 192
CCB2/4-Syn : PGP VERVMQ-----TQKPVYLVNLPYLPGRVEED-YLPANTQGLICQPLDD-----RGVLLIGANIPRSYTK : 192

*          420
CCB2/4-Cm : K D L E M L A C F Q Q Q W M P ----- : 343
CCB2/4-Pt : K D I S W C Q S V A Q R I G R D L S V D ----- : 377
CCB2/4-Tp : K D I A W C R E I S S W I G D S C E ----- : 381
CCB2/4-Av : Q D E N W I A G I A D K I A V T L K N S H G ----- : 215
CCB2/4-Se : Q D E R W I A G I A D K I D Q S L S R S A A I A V E Q P : 221
CCB2/4-Syn : Q D E N W V T G I A D K I A H S L S M P I N A ----- : 215

```