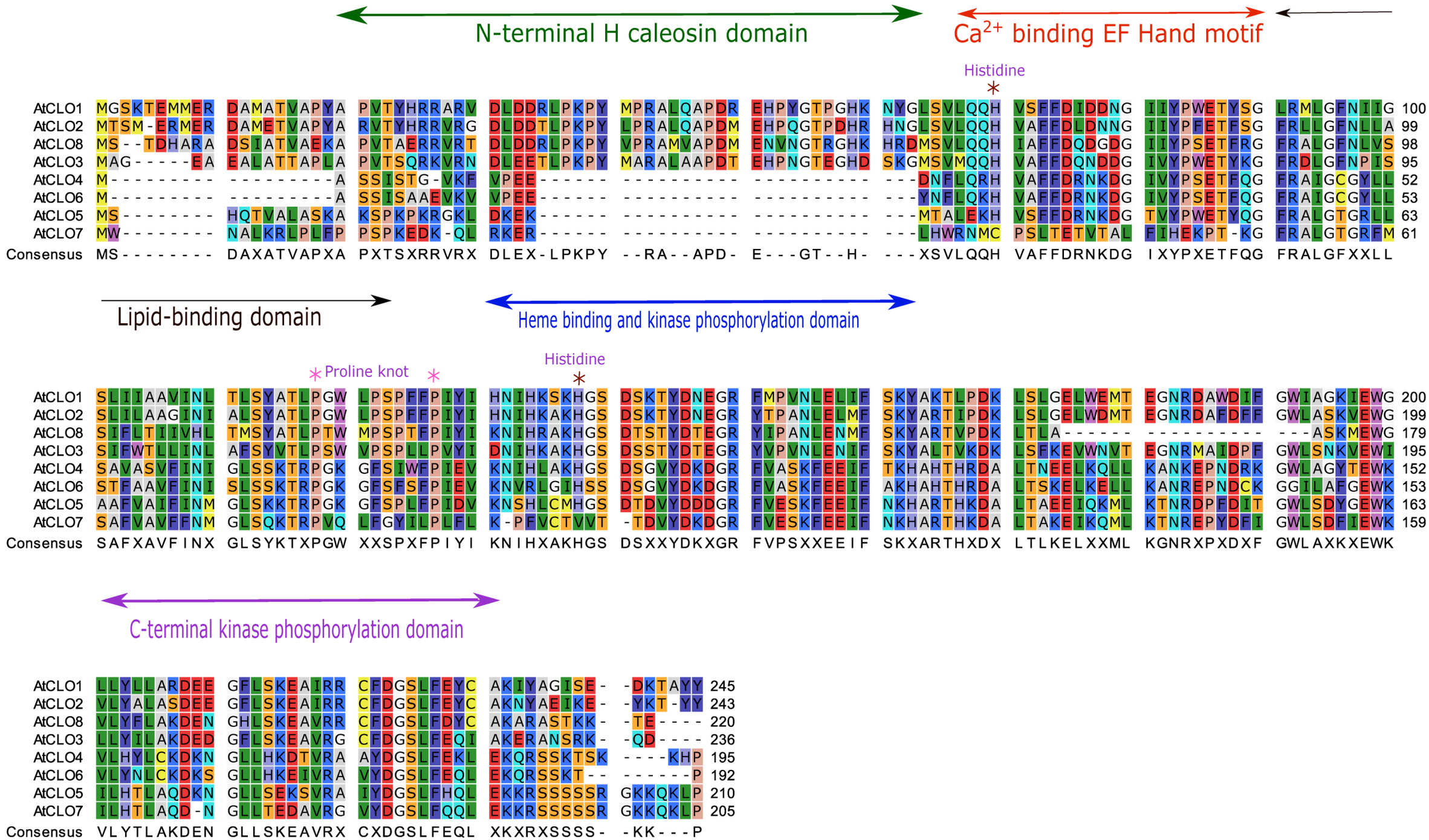
C


N-terminal H caleosin domain
Ca2+ binding EF Hand motif
Histidine
AtCLO1 MGSKTEMMER DAMATVAPYA PVTYHRRARV DLDDRLPKPY MPRALQAPDR EHPYGTPGHK NYGLSVLQQH VSFFDIDDNG IIYPWETYSG LRMLGFNIIG 100
AtCLO2 MTSM-ERMER DAMETVAPYA RVTYHRRVRG DLDDTLPKPY LPRALQAPDM EHPQGTPDHR HNGLSVLQQH VAFFDLDNNG IIYPFETFSG FRLLGFNLLA 99
AtCLO8 MS--TDHARA DSIATVAEKA PVTAERRVRT DLDDRLPKPY VPRAMVAPDM ENVNGTRGHK HRDMSVLQQH IAFFDQDGDG IIYPSETFRG FRALGFNLVS 98
AtCLO3 MAG-----EA EALATTAPLA PVTSQRKVRN DLEETLPKPY MARALAAPDT EHPNGTEGHD SKGMSVMQQH VAFFDQNDDG IVYPWETYKG FRDLGFNPIS 95
AtCLO4 M--------- ---------A SSISTG-VKF VPEE------ ---------- ---------- ---DNFLQRH VAFFDRNKDG IVYPSETFQG FRAIGCGYLL 52
AtCLO6 M--------- ---------A SSISAAEVKV VPEE------ ---------- ---------- ---YNFLQKH VAFFDRNKDG IVYPSETFQG FRAIGCGYLL 53
AtCLO5 MS-------- HQTVALASKA KSPKPKRGKL DKEK------ ---------- ---------- ---MTALEKH VSFFDRNKDG TVYPWETYQG FRALGTGRLL 63
AtCLO7 MW-------- NALKRLPLFP PSPKEDK-QL RKER------ ---------- ---------- ---LHWRNMC PSLTETVTAL FIHEKPT-KG FRALGTGRFM 61
Consensus MS-------- DAXATVAPXA PXTSXRRVRX DLEX-LPKPY --RA--APD- E---GT--H- ---XSVLQQH VAFFDRNKDG IXYPXETFQG FRALGFXXLL
Lipid-binding domain
Heme binding and kinase phosphorylation domain
Proline knot
Histidine
AtCLO1 SLIIAAVINL TLSYATLPGW LPSPFFPIYI HNIHKSKHGS DSKTYDNEGR FMPVNLELIF SKYAKTLPDK LSLGELWEMT EGNRDAWDIF GWIAGKIEWG 200
AtCLO2 SLILAAGINI ALSYATLPGW LPSPFFPIYI HNIHKAKHGS DSKTYDNEGR YTPANLELMF SKYARTIPDK LSLGELWDMT EGNRDAFDFF GWLASKVEWG 199
AtCLO8 SIFLTIIVHL TMSYATLPTW MPSPTFPIYI KNIHRAKHGS DTSTYDTEGR YIPANLENMF SKYARTVPDK LTLA------ ---------- ---ASKMEWG 179
AtCLO3 SIFWTLLINL AFSYVTLPSW VPSPLLPVYI DNIHKAKHGS DSSTYDTEGR YVPVNLENIF SKYALTVKDK LSFKEVWNVT EGNRMAIDPF GWLSNKVEWI 195
AtCLO4 SAVASVFINI GLSSKTRPGK GFSIWFPIEV KNIHLAKHGS DSGVYDKDGR FVASKFEEIF TKHAHTHRDA LTNEELKQLL KANKEPNDRK GWLAGYTEWK 152
AtCLO6 STFAAVFINI SLSSKTRPGK GFSFSFPIEV KNVRLGIHSS DSGVYDKDGR FVASKFEEIF AKHAHTHRDA LTSKELKELL KANREPNDCK GGILAFGEWK 153
AtCLO5 AAFVAIFINM GLSKKTRPGK GFSPLFPIDV KNSHLCMHGS DTDVYDDDGR FVESKFEEIF NKHARTHKDA LTAEEIQKML KTNRDPFDIT GWLSDYGEWK 163
AtCLO7 SAFVAVFFNM GLSQKTRPVQ LFGYILPLFL K-PFVCTVVT -TDVYDKDGR FVESKFEEIF NKHARTHKDA LTAKEIKQML KTNREPYDFI GWLSDFIEWK 159
Consensus SAFXAVFINX GLSYKTXPGW XXSPXFPIYI KNIHXAKHGS DSXXYDKXGR FVPSXXEEIF SKXARTHXDX LTLKELXXML KGNRXPXDXF GWLAXKXEWK
C-terminal kinase phosphorylation domain
AtCLO1 LLYLLARDEE GFLSKEAIRR CFDGSLFEYC AKIYAGISE- -DKTAYY 245
AtCLO2 VLYALASDEE GFLSKEAIRR CFDGSLFEYC AKNYAEIKE- -YKT-YY 243
AtCLO8 VLYFLAKDEN GHLSKEAVRR CFDGSLFDYC AKARASTKK- -TE---- 220
AtCLO3 LLYILAKDED GFLSKEAVRG CFDGSLFEQI AKERANSRK- -QD---- 236
AtCLO4 VLHYLCKDKN GLLHKDTVRA AYDGSLFEKL EKQRSSKTSK ----KHP 195
AtCLO6 VLYNLCKDKS GLLHKEIVRA VYDGSLFEQL EKQRSSKT-- ------P 192
AtCLO5 ILHTLAQDKN GLLSEKSVRA IYDGSLFHQL EKKRSSSSSR GKKQKLP 210
AtCLO7 ILHTLAQD-N GLLTEDAVRG VYDGSLFQQL EKKRSSSSSR GKKQKLP 205
Consensus VLYTLAKDEN GLLSKEAVRX CXDGSLFEQL XKXRXSSSS- -KK---P