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AP3          MARGKIQIKRIENQTNRQVTYSKRRNGLFKKAHELTVLCDARVSIIMFSS-SNKLHEYIS [59]
DeAP3        ------------------------AGIMKKARELTVLCDAEVSLIMFSS-TGKFSEYIS [34]
DEF          MARGKIQIKRIENQTNRQVTYSKRRNGLFKKAHELSVLCDAKVSIIMISS-TQKLHEYIS [59]
GDEF1        MGRGKIEIKKIENNTNRQVTYSKRRNGIFKKAHELTVLCDAKVSLIMFSN-TGKFHEYIS [59]
GDEF2        MARGKIQIKKIENSTNRQVTYSKRRNGLFKKASELTVLCDAKVSIIMVSC-TDKLHEYIS [59]
Gu.ti.AP3 _4      -------------------------QELTVLCDAKVSIIMISNGSNKCHEYTS [32]
Gu.ti.AP3_5       -----------------------LKKAQELTVLCDAKVSLIMISIGSNKCHEYTS [32]
HmAP3        ------------------------NGLFKKANELTVLCDAKVSIIMFST-TNKLHEYIS [34]
HmTM6        ------------------------NGIIKKAQELTVLCDAKVSLIMIST-TGKFHEYTS [34]
HPDEF1       MARGKIQIKKIENSTNRQVTYSKRRNGLFKKASELTVLCDAKVSIIMVSC-TDKLHEYIS [59]
HPDEF2       MARGKIQIKKIENSTNRQVTYSKRRNGLFKKASELTVLCDAKVSIIMVSC-TDKLHEYIS [59]
JrAP3        ---------IENETNRQVTYSKRRKGLFKKAHELTVLCDAKVSLIMISS-NKKLRDYVS [49]
TAP3         ------------------------NGLFKKANELTVLCDAKVSIVMISS-TGKLHEFIS [34]
TM6          ---GKIEIKKIENSTNRQVTYSKRRNGIFKKRELTVLCDAKISLIMLSS-TRKYHEYTS [56]
MASAKO_B3    MGRGKIEIKLIENQTNRQVTYSKRRNGIFKKAQELTVLCDAQVSLIMQSS-TDKIHEYIS [59]
MdMADS13     MGRGKIEIKLIENQTNRQVTYSKRRNGIFKKAQELTVLCDAKVSLIMLSN-TNKMHEYIS [59]
MdTM6        MGRGKIEIKLIENQTNRQVTYSKRRNGIFKKAQELTVLCDAKVSLIMLSN-TSKMHEYIS [59]
NMH7         MARGKIQIKRIENTTNRQVIYSKRRNGLFKKANELTVLCDAKVSIIMFSS-TGKLHEYIS [59]
NTDEF        MARGKIQIKRIENQTNRQVTYSKRRNGLFKKANELTVLCDAKVSIIMISS-TGKLHEFIS [59]
NTTM6        ----------------------------------------AKISLLMLSS-TRKFHEYTS [19]
PcAP3        ----------IENPTNRQVTYSKRRSGIFKKAKELTILCDAQVCLIMFSN-TGKVCEYVS [49]
PhDEF        MARGKIQIKRIENQTNRQVTYSKRRNGLFKKANELTVLCDAKVSIIMISS-TGKLHEFIS [59]
PhTM6        MGRGKIEIKKIENSTNRQVTYSKRRNGLFKKAKELTVLCDAKICLIMLSS-TRKFHEYTS [59]
PnAP3_1      ------------------------SGIFKKAKELTILCDAQVCLIMFSN-TGKVCEYVS [34]
PnAP3_2      MGRGKIEIKRIENATNRQVTYSKRRSGILKKAKELTVLCDAEVSLIMFSS-TGKMTEYLS [59]
PtAP3_1      ------------------------NGIFKKALELSVLCDAKVSIIMVAT-NRKLHEYTS [34]
PtAP3_2      ------------------------NGIFKKAKELSVLCDAKVSIIMVAT-NRKLHEYTS [34]
PTD          ------------------------NGIIKKAQELTVLCDAKVSLIMIST-TGKFHEYTS [34]
RAD1         MARGKIQIKRIENDTNRQVTYSKRRSGLFKKAKELTILCDAKVSIIMISN-TNKLHEFIS [59]
RAD2         MTRGQIQIRRIENITNRQVTYSKRRNGLFKKAQELVVLCDAKVSIIMISS-RNKLHEFTT [59]
RbAP3_1      ------------------------AGIIKKAQELTVLCDAEVSLIMVSS-SGKCVDFIS [34]
RbAP3_2      ------------------------AGIMKKAQELTVLCDAKVALLMISNNTHKISEYVS [35]
Ri.sa.AP3_1      --------------------NGLFKKATELTVLCDAKVSIIMFSS-TNKLHEYLS [34]
Ri.sa.AP3_2      --------------------NGLFKKATELTVLCDAKVSIIMFSS-TNKLHEYLS [34]
SLM3         MARRKIQIKKIENLTNRQVTYSKRRNGLFKKANELTVLCDATVSIIMLSS-NLKLHEFLS [59]
STDEF        MARGKIQIKKIENQTNRQVTYSKRRNGLFKKANELTVLCDAKVSIVMISS-TGKLHEFIS [59]


AP3          PN--TTTKEIVDLYQTISDVDVWATQYERMQETKRKLLETNRNLRTQIKQR-LGECLDEL [116]
DeAP3        PSAT--TKRMFDRYQQVSGVNLWNSHYERMQDNLNKQKEINNKLRREIRQR-MGEDLNDL [91]
DEF          PT--TATKQLFDQYQKAVGVDLWSSHYEKMQEHLKKLNEVNRNLRREIRQR-MGESLNDL [116]
GDEF1        PS--TTTKKMYDQYQSTVGFDLWSSHYERMKETMKKLKDTNNKLRREIRQRVLGEDFDGL [117]
GDEF2        PS--ITTKQFFDQYQKASGIDLWNSHYEKMQEELRQLKEVNRNLRRQIRQR-LGDCLEDL [116]
Gu.ti.AP3_4  SS--TSTKSIYDQYQKASGIDLWSSHYEKMQDSLRKLKDTNNRLRKEMRQR-MGEDLDDL [89]
Gu.ti.AP3_5  SS--TSTKSVYDQYQKASGIDLWSSHYEKMQDSLRKLKDTNNRLRKEMRQR-MGEDLDDL [89]
HmAP3        PS--ISTKELFDLYQTTMGIDLWSSHYERMQENLKKLKDVNRNLRMEIRQR-MGESLNDL [91]
HmTM6        PS--TTTKQIYDQYQKTLDIDLWSTHYERMQEHLRKLKEVNNKLRREIRQR-LGEDLNDL [91]
HPDEF1       PS--TTTKQFFDQYQKAAGIDLWNSHYEKMQEELRQLKEVNKNLRRQIRQR-LGDCLEHL [116]
HPDEF2       PS--TTTKQFFDQYQKAAGIDLWNSHYEKMQEELRQLKEVNKNLRRQIRQR-LGDCLEHL [116]
JrAP3        PS--TTTKQIFDQYQHTMGVDLWSSHYERMQEELKKLNDVNRSLRREIRHR-RGESLIDL [106]
TAP3         PS--ITTKQLFDLYQKTIGVDIWTTHYEKMQEQLRKLKDVNRNLRKEIRQR-MGESLNDL [91]
TM6          PN--TTTKKMIDQYQSALGVDIWSIHYEKMQENLKRLKEINNKLRREIRQR-TGEDMSGL [113]
MASAKO_B3    PT--TTTKKMFDLYQKNLQIDLWSSHYEAMKENLWKLKEVNNKLRRDIRQR-LGHDLNGL [116]
MdMADS13     PT--TTTKSMYDDYQKTMGIDLWRTHEESMKDTLWKLKEINNKLRREIRQR-LGHDLNGL [116]
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MdTM6         PT--TTTKSMYDDYQKTMGIDLWRTHYESMKDTLWKLKEINNKLRREIRQR-LGHDLNGL [116]
NMH7          PS--ASTKQFFDQYQTTVGIDLWNSHYENMQENLKKLKDVNRNLRKEIRQG-MGECLNDL [116]
NTDEF         PS--VTTKQLFDLYQKTVGVDLWNSHYEKMQEQLRKLKDVNRNLRREIRQR-MGESLNDL [116]
NTTM6         PN--TTQKKMIDQYQRTLGVDIWSTHYERMLENLKRLKEINNKLRREIRQR-TGEDMSGL [76]
PcAP3         PS--TTMKEFFDRFRRVTNIDLWASQYETLQEELKKQKEINSRLKKEIRQRTGQDDLNEL [107]
PhDEF         PS--ITTKQLFDLYQKTVGVDLWNSHYEKMQEQLRKLKEVNRNLRKEIRQR-MGESLNDL [116]
PhTM6         PN--TTTKKMIDLYQRTLGVDIWNKHYEKMQENLNRLKDINNKLRREIRQR-TGEDMSGL [116]
PnAP3_1       PS--TTMKEFFDRFRRITNIDLWASQYETLQEELKTQKEINNKLKKEIRQRTGQDDLSEL [92]
PnAP3_2       PSLNGNTKRVYDKYQQLSGISLWNSHYESLQNALNKQKEINRRLRREIRQR-MGEDLDEL [118]
PtAP3_1       PH--TTTKELYDLYQKASGKSLWNSHYERMNDNLNKLKEINNKLRTEIRQR-MGEDLNEL [91]
PtAP3_2       PH--TTTKDLYDLYQKASGNSLWNSHYERMKDNLNKLKDINNKLRTEIRQR-MGEDLNDL [91]
PTD           PS--TTTKQIYDQYQKTLDIDLWSTHYERMQEHLRKLKEVNNKLRREIRQR-LGEDLNDL [91]
RAD1          PN--ITTKQVYDAYQTTFSPDLWTSHYAKMEQELRNLNEVNRQIRKEIRRR-MGCCLEDM [116]
RAD2          PG--TTTKQIYDMYQQLSGNDVWSSQYAMMLEELRKIKEANGNIRKEIRRR-MGFSMEDM [116]
RbAP3_1       PT--ISQKEFYDKYQKITKQDLWKSQYDEMQERFKHLMETNRKLRREIGQRVG-EDLEGL [91]
RbAP3_2       PG--TSFKAIYDQYEKTSGVSLWDSEYERMQRNLKKVKEDNNKLRKEIRQR-QGDDLDGL [92]
Ri.sa.AP3_1   PF--ISTKQVFDQYQNKLGIDLWQTHYERMQEHLKQLKDVNNNLRMEIRHR-MGASLDGL [91]
Ri.sa.AP3_2   PF--ISTKQVFDQYQNNLQIDLWQTHYERMQEHLKQLKDVNNNLRMEIRHR-MGASLDGL [91]
SLM3          PGSNLTTKDVYDRYQKALGVDIWVTHEKRMQDDLQKLNELNRKLQTDIRQR-MGDCLEDL [118]
STDEF         PS--ITTKQLFDLYQKTIGVDIWTSHYEKMQEQLRKLKDVNRNLRKEIRQR-MGESLNDL [116]
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AP3           DIQELRRLEDEMENTFKLVRERKFKSLGNQIETTKKKNKSQQDIQKNLIHE---LELRAE [173]
DeAP3         SIEELRGLEQNMDNSLKIVRDRKYHVITTQTETYRKKLRNLHETHNNLLREFE-----GR [146]
DEF           GYEQIVNLIEDMDNSLKLIRERKYKVISNQIDTSKKKVRNVEEIHRNLVLE---FDARRE [173]
GDEF1         DMNDLTSLEQHMQDSLTLVRERKYHVIKTQTDTCRKRVRNLEQRNGNLRLDYET------ [171]
GDEF2         GFEEFLDLEKESQEAVYIIRERKLKVIGNKLETSKKKVRSAQDVYKKLMHE---FDIRGE [173]
Gu.ti.AP3_4   RFDQIVALKVKTISSITSIRERKFHVIKNQIGTTNKKVKNLEEIQRNLLLD---LEAKCE [146]
Gu.ti.AP3_5   RFDQIVALIVKAISSITSIRERKFHVIKTKTHTCGKKVRNLKEIQRNLLLD---LEAKCE [146]
HmAP3         SWKDLRGLEQEMDSSVKIIRERKYRVLGNQIDTHRKKVRNAEEIHRYIIHE---FEVKEE [148]
HmTM6         NLNELRDLEQKSAASTAVIRERKYHVLKTQTETCRKKVRNLEERYGNLFLD---WEGKCE [148]
HPDEF1        GFEKLLDLEKESQEAVYIIRERKLKVIGNKLETSKKKVRSAQDVYKKLMHE---FGIRGE [173]
HPDEF2        GFEKLLDLEKESQEAVYIIRERKLKVIGNKLETSKKKVRSAQDVYKKLMHE---FGIRGE [173]
JrAP3         NLEELYHLEQNVESAVKVIRDRKYHVIGKKTDILKKKKKRAESIHKVLLHE---LVARDE [163]
TAP3          NYEQLEELMENVDNSLKLIRERKFKVIGNQIETYRKKVRNVEEINRNLLLE---FDARQE [148]
TM6           NLQELCHLQENITESVAEIRERKYHVIKNQTDTCKKKARNLEEQNGTLVLD---LEAKCE [170]
MASAKO_B3     SYAELQDLEETMSQSVQIIRDRKYHVLKTQAETTRKKVKNLEERNSNLMHGYG--APGNE [174]
MdMADS13      SFDELASLDDEMQSSLDAIRQRKYHVIKTQTETTKKKVKNLEQRRGNMLHGYFDQEAAGE [176]
MdTM6         SYDDLRSLEDKMQSSLDAIRERKYHVIKTQTETTKKKVKNLEERRGNMLHG---YEAASE [173]
NMH7          SMEELRLLEDEMDKALKAIRERKYKVITNQIDTQRKKFNNEREVDNRLLRD---LDARAE [173]
NTDEF         NYEQLEELNENVDNSLKLIRERKYKVIGNQIDTYKKKVRNVEEIHRNLLLE---FDARQE [173]
NTTM6         NLQELCRLQENISESVAEIRERKYHVIKTQTDTFKKKVKNLEEQHGNLVLD---LEAKSE [133]
PcAP3         TFEELRSLEANLLSSVEIVRLRKFHVLGSHTETSKKRNKAMEETHKNLLRATYSQADRDE [167]
PhDEF         NYEQLEELMENVDNSLKLIRERKYKVIGNQIETFKKKVRNVEEIHRNLLLE---FDARQE [173]
PhTM6         NLQELCHLQGNVSDSLAEIRERKYHVIKTQTDTCRKRVRNLEEQHGSLVHD---LEAKSE [173]
PnAP3_1       SLDEMRILEKNLIDSADIVRNRKNHVLNSHTETSKKRNKAQEETYKNLVRALHSQADREE [152]
PnAP3_2       TIEELRSLEQNLEASVKVVRDRKYHVIITQTETTRKKLRNHTEQNHGLLREFEPI--LDE [176]
PtAP3_1       RLDELRGLEQNMEECLKNIRDRKEHQLRNQIGTSKKKTRNAEEINRKLIRR---LDGMDD [148]
PtAP3_2       RLEELRGLEQNIQESLMIVGDRKEHQLRNQIGTYKKKSRNAEEINRKLLRR---LDGIDD [148]
PTD           NLNELRDLEQKSAASTAVIRERKYHVLKTQTETCRKKVRNLEERYGNLFLD---WEGKCE [148]
RAD1          SYQELVFLQQDMENAVTNLSERKYKVLSNQIETGKKKLRNVQGIRQNLMQA---YDALRE [173]
RAD2          SFRELVILQQDMQDSVAKISERKYKAIANQIETTRKKLRNSHGIHRSLVHA---FGALNL [173]
RbAP3_1       GIHELRSLEQDLRNSAKVVRLRKFGLLSSQGETQKKKIKNLAGINGSLWQEY----QERV [147]
RbAP3_2       SFAELRGLEQNMHSSVERVRHRKEHVIRTQTDTTNKKIKSHEETQRTLLAEYDVMDK--A [150]
Ri.sa.AP3_1   SLAELRNLEEEMDGTLDIILERKRRVIGNQIDTLKKKVRNSEEVNRKLVHE---FDVRCE [148]
Ri.sa.AP3_2   SLAELRNLEEEMDGSVDIIRERKRRVIGNQIDTLRKKVRNSEEVNRKLVHE---FDVRSE [148]
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SLM3            SFEELCRLGQEMQEAVTLIRERKYKKIDNQIDTTKKKVRNGQEVHKGLLQE---FEIPKD [175]
STDEF           NFEQLEELMENVDNSLKLIRERKYKVIGNQIETYRKKVRNVEEIHRNLLLE---FDARQE [173]



AP3            DPHYGLV-------------------------------------------------- [180]
DeAP3          D-------------------------------------------------------- [147]
DEF            DPHFGLVD------------------------------------------------- [181]
GDEF1          --------------------------------------------------------- [171]
GDEF2          DPQYGMI-------------------------------------------------- [180]
Gu.ti.AP3_4    D-------------------------------------------------------- [147]
Gu.ti.AP3_5    DPQYGMV-------------------------------------------------- [153]
HmAP3          DPHYGLVDNGGN-YD------------------------------------------- [162]
HmTM6          DPQYGLVE-------------------------------------------------- [156]
HPDEF1         DPQFGMIEDGEYD--------------------------------------------- [186]
HPDEF2         DPQFGMIEDGEYDAVYGYP--------------------------------------- [192]
JrAP3          DP-YGLVDNGGG---------------------------------------------- [174]
TAP3           DPYGGLVEHDG----------------------------------------------- [159]
TM6            DPKYGVVENEGH --------------------------------------------- [182]
MASAKO_B3      DPQYGYVDNEGDYESAVALANGASNLYFFNRVHNNHNLDHGH----------- [216]
MdMADS13       DPQYGYEDNEGD---------------------------------------------- [188]
MdTM6          NPQYCYVDNEGDYESALVLANGANNLYTFQL--------------------- [204]
NMH7           DPRFEMMDNGGE-YESVIGFSNLGPRMFALSL-------------------- [204]
NTDEF          DPYGLVEQEG------------------------------------------------ [183]
NTTM6          DPKYGTVENEG----------------------------------------------- [144]
PcAP3          -EFLFYAIPADREGDHNRDYLSSSSSMRTLSINGG-DCENSQIT--------- [209]
PhDEF          DPYGLVEQEGDYNSVL------------------------------------------ [189]
PhTM6          DPTYGVVENEGHF--------------------------------------------- [186]
PnAP3_1        QEFHFYAIPADTEGDHHRDYLSSSSSMRRLSISGGGDCE-------------- [191]
PnAP3_2        DPHYVIAHQEEDYESAIELAHGG----------------------------- [199]
PtAP3_1_       DSQYGLEDDGVDDEPAIALTNGNSHIFAFRLHP------------------- [181]
PtAP3_2        DSQYGLEDDGGDDESAIALTNGNSHIFAFR---------------------- [178]
PTD            DPQYGLVE-------------------------------------------------- [156]
RAD1           DPHCGLVYNG------------------------------------------------ [183]
RAD2           N-----EYG------------------------------------------------- [177]
RbAP3_1        EEEYIAS---GMSELE------------------------------------------ [160]
RbAP3_2        GSQYSFVQQD------------------------------------------------ [160]
Ri.sa.AP3_1    HPHFGLVDNGGRE--------------------------------------------- [161]
Ri.sa.AP3_2    DPHFGLVDNGGSEYDTVLEY-------------------------------------- [168]
SLM3           EPPYGLVDNGDYSN-------------------------------------------- [189]
STDEF          DPYGGLV-------------------------------------------------- [180]
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