

MIDA_HUMAN (5309) AAEMWQSYLILTAPLSQRLCEELRLILEPTQAAKLGDYRTGKRLNIRKVIPIYIASQFRKDKIWLRRTPKSKRQY
MIDA_YEAST (4629) SRELWHKSEISTADLVSRIGEQLRLILEPTLATKLKGDYKTGKRLNMKRIPIYIASQFRKDKIWLRRTPKSKRQY
MIDA_GIARD (4554) GNHLLDLLIKQTSAAAFSLAERLRIILEPTVTSDLKGFRTGKKLNLRRIIPFIIASEFQKDKIWLRRTPKSKRVY
BCHD_RHOCA (306) AGQEQ--IGNRRGRPLPSRKGLLEDDAKIDL VATLRS AAPWQGLRRRQAPAGTERVLLVSSDIHIKRRKEMSDR
BCHD_CHLFL (370) -GSRG-TISGQRGRHIRSVPGK-PAQGRLDVIATLRAAAPWQIRIRAAEYHPHRRGRIHLRADDLHIKKYRSKAGT
CHLD_ARATH (501) GRAKNVIFSEDGRGYIKPMLPK-GPVKRLAVDATLRAAAPYQKLRREKDISG-TRKVFVEKTDMAKRMARKAGA
ITAM_HUMAN (75) PIRLQVPVEAVNMSLGLSLAATTSPPOQLLACGPTVHQTCSENTYVKGICFLFGSNLRQQPQKFPEALRGCPQEDS
ITAL_HUMAN (82) PVTLR-GSNYTSKYLGMTLATDPTDGSILACDPGLSRTCQNTYLSGLCYLFRQNLQGPMLOGRPGFQECIKGNV
ITA2_HUMAN (100) STSIPNVTEKTNMSLGLILTRNMGTTGGFLTCGPLWAQQCGNQYTTTGVCSDISPDF-QLSASFSPATQPCP-SLI

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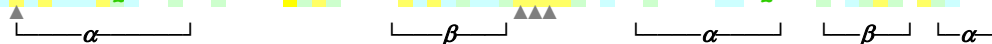
MIDA_HUMAN (5384) QICLAIIDSSSMVDNHTKQLAFESLAVIGNALTLLLEVGOIAVCSFGESVKLLHPFHEQFSDYSGSQILRLCKFQQ
MIDA_YEAST (4704) QIMIALDDSKSMSESKCVKLAFDSLCLVSKTLTQLEAGGLSIVKFGENIKEVHSFDQQFSNESGARAFQWFGFQE
MIDA_GIARD (4629) QVLLAVDDSSSMAP--IAKYALQAITLLFNACKFLEVGOQSVFSGQKFELLIPITDQYNDASLAYAIGSFTFAQ
BCHD_RHOCA (379) VLIFAVDASGSAAVARLSEAKGAVELLGRAYAARDH--VSLITFRGTAAQVLLQPSRSLTQTKRQLQGLPGGG-
BCHD_CHLFL (442) LFCFLVDASGSMALHRMRQAKGAVNALLQQAYVHRDQ--VALLAFRGERADLLPPSQSVELAKRALDVLPETGG-
CHLD_ARATH (574) LVIFVVDASGSMALNRMQNAKGAALKLLAESYTSRDQ--VSIIPFRGDAAEVLLPPSRSIAMARNRLERLPCGG-
ITAM_HUMAN (150) DIAFLIDGSGSIIIPHDFRMKEFVSTVMEQLK--KSKTLFSLMQYSEEFRIHFTTFKEFQNNPNPNRSLVKPITQLL
ITAL_HUMAN (156) DLVFLFDGSMQLQDEFQKILDFMKDVMKKLS--NTSYQFAAVQFSTSYKTEFFDFSDYVKRKDPDALLKHVKHML
ITA2_HUMAN (174) DVVVVCDESNSIYP--WDAVKNFLEKEFVQGLDIGPTKTQVGLIQYANNPRVVFNLNTYKTEEMIVATSQTSQYG

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MIDA_HUMAN (5459) K-KTKIAQFL SVANMFAAAQQLSQNISSSETAQLLLVSDGRGLFLEGKERVLAAVQAARNANIFVIFVV---L
MIDA_YEAST (4779) T-KTDVKKLVAESTKIFERARAMVHN---DQWQLEIVISDG---ICEDHETIQKLVRRARENKIMLVFVI---I
MIDA_GIARD (4702) N-ETRVSDAISIASDYLDVSRFFKG--SDSALQLLLMISDGR--LKEKGGVAREIRKCMGRGQLPVLIV---L
BCHD_RHOCA (451) --GTPLASGMEMAMVTAQQRSR-----GMPPTIALLTGDRG-NIALDGTANREL-----AGEQ TK-----
BCHD_CHLFL (514) --GTPLAAALLAAYQISEQRSRG-----IFRTTIVLITDGRP-NVPLKADPTMDK-----ARRLEQAR-----Q
CHLD_ARATH (648) --GSPLAHGLTTAVRVGLNAEKSGD-----VGRIMIVAITDGRA-NITLKRSTDPEISIAPDAPRPTSKELK-----D
ITAM_HUMAN (223) G-RTHTATGIRKVVRELFNITNGARK--NAFKILVITDGEKFGDPLGYEDVIPEADREGVIRYVIGV-----G
ITAL_HUMAN (229) L-LTNTFGAINYVATEVFREELGARP--DATKVLIIITDGEATDS--GNIDAAKD-----IIRYIIGI-----G
ITA2_HUMAN (247) GDLTNTFGAIQYARKYAYSAASGGRR--SATKVMVVVTDGESHDGSM-LKAVIDQCNDNILRFGLIAVLGYLNR

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MIDA_HUMAN (5529) DNPSSRDSILDIKVPIFKGPGEMPEIR---SYMEFFPPPYIILRDVNALPETLSDALRQWFELVTASDHP*
MIDA_YEAST (4843) DGITSNESILDMSQVNIYPDQYGNPQLKITKYLDTFPFEFYVVVHDISELPEMLSLILRQYFTDLASS*
MIDA_GIARD (4767) D--TDKKSIMDIKSVSFITDSSGKRVRQTSMYLDDFPFQCYALLRHIEDLPETLVAVIKRWIESVSVYNAV*
BCHD_RHOCA (505) ----VARAIRASGMPAVIIDTAMRPNP-----ALVDLARTMDAHYIALPRATAHKMADVLGAALEA*
BCHD_CHLFL (571) EVQQLAGRLRAAGVGAVVIDTQRSFVSR----GEAQQLAAWLGCRYVYLPENGRGDQIANAVIAASEEG*
CHLD_ARATH (712) EILEVAGKIYKAGMSLLVIDTENKFVST----GFAKEIARVAQGKYRYLPNASDAVISATTRDALSDLKNS*
ITAM_HUMAN (289) DAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSN
ITAL_HUMAN (288) KHFTKESQETLHKFASKPASEFVKILDTFEKLKDLFTELQKKIYVIEGTSKQDLTSFNMELSSSGISADLSRGH
ITA2_HUMAN (318) NALDTKNLIKEIKAIASIPTEYFFNVSDAALLEKAGTLGEQIFSIIEGTV-QGGDNFQMEMSQVGFSA DYSSQN

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