AN6796.2 (1) --MAPKVLVVLTSFDKIEA-NNH---------------PTGWYLPEFAHPWEVLHSK-TELTIASPKGGA
BDBG_02344 (1) --MAPKILIVLTSQDKIPA-TGK---------------PTGWYLPELAHPYDILKGK-AELVFASPKGGL
UM00094.1 (1) --MSKKILVVFTSHTKLIG-SDH---------------PTGYYLPEIAHPYYILKDAGYTLVSASPKGGK
CCM_09248 (1) --MAPKILVVLTSADKIVK-LDK---------------PTGWYLPELAHPYDVLSPK-AELVLASPKGGV
MAC_07323 (1) --MAKKVLVVLTSADRIVK-LDK---------------PTGWYLPELAHPYDVLAPK-AEIVVASPKGGI
VDAG_09321 (1) --MASTTKPKVLVILTSVDTIPK-SGK---------------TIGWYLPELAHPWEVLRNR-AELTYASPKGGV
NCU06603 (1) ---MSAPKVLVVLTSHDKLGN-TGK---------------PTGWYLSEFSHPYDVLNSASVSLTVASPRGGL
PTT_13641 (1) ---MSKPSILFVLTSHNKLGD-TGK---------------PTGWYLPELAHPYHILRNK-ANITVASPKGGE
SNOG_04306 (1) ---MSKPSVLFVLTSHNKLGD-TGK---------------PTGWYLPELAHPYHVLRNK-VNITVASPKGGE
Rhoba1_1_64353 (1) --MAANKNILFVVSSHDQFL--DGK---------------PTGYYLPEAAHPYYVLKNAGYKIDVASPKGGK
ARB_05407 (1) --MPLPRRALIAVTSANPHFYPDGK---------------KTGLFFSEALHPFDELQSAGFHIDIASETGTF
Mucci2_157529 (1) ---MPSLPRKALIAVTSYNEPFYADGT---------------KTGLFYTEALHPYQALKKAGFEIDLASETGTY
RO3G_07202.3 (1) --MSVPRKVLLAISSYNEVFYEDGK---------------RTGLFYTEALHPYQAFVQAGFEVDVASETGTY
Phybl2_109595 (1) ---MSSLPRKALIAITSYNEVFYSDGA---------------RTGLFYTEALHPYMALVKAGFEVDLASETGTF
MGL_4192 (1) --MPASVPRRALIAVTSAHAQLYPNGG---------------ETGVFITEALHPFEGFRKAGFEVDLVSETGKY
CaO19.251 (1) ---MVKVLLALTSYNETFYSDGK---------------KTGVFVVEALHPFEVFRKKGYEIQLASETGTF
ScHsp31 (1) ---MAPKKVLLALTSYNDVFYSDGA---------------KTGVFVVEALHPFNTFRKEGFEVDFVSETGKF
YPL280W (1) ---MTPKRALISLTSYHGPFYKDGA---------------KTGVFVVEILRSFDTFEKHGFEVDFVSETGGF
YALI0C22000p (1) ---MAPPPMKALIAVTCYNDSFYPDGK---------------KTGVYFTEAYHPFMAFWAAGFDVQFVSEDGTF
YALI0F00682p (1) --MSFPKRALIAVTDYNGPFYPDGS---------------KTGLFFSEAYEPFEVFQKAGFDVQFVSEDGKY
Hsp3102 (1) --MSIAKGKNALLVASSYYGPFYPDGK---------------NTGVHFSELLIPYNVFKKAGFNVQFVSENGSY
Hsp3101 (1) ---MASEGK-VLLVASSYYGPFYPDGM---------------NTGVHFAELLIPYQVFREAGYEVQLTSETGKC
Hsp3103 (1) ---MPAKTRNVLIACSDYYGPFYKDGE---------------NTGAFFLELLHPYLVFRDACFNVDIVTESGKI
CC1G_00260 (1) ---MPSVLFVFTSTNKTL--TGA---------------QTGWYLPEAAHPYYVLAPH-VQIDFASPAGPN
Pospl1_110200 (1) ---MGRILFVYTSCSRTL--TGA---------------QTGWYLPEAAHPYYVLAAH-HEIDFASPNGPN
SERLA73DRAFT_120613 (1) --MAPNILFVFTSTDRTL--TGA---------------PTGWYLPEAAHPYYVLSPH-FNIEFAAPAGPN
SCHCODRAFT_46162 (1) --MASKILIVFTSCDKLP--NGS---------------EAGWYLPEAAHPYYVLSPS-FTIDFASPKGAN
SCHCODRAFT_49614 (1) --MSNKILFVFTSVNKTL--TGE---------------PTGWYLPEAAHPYYVLAPH-FDIDFAAPAGPN
SPPG_05672 (1) --MAGKKNIVFVLTSHSQLGN-TGK---------------KTGWYLPEVAHPYNILAPH-YNITWASPLGGE
SPPG_02734 (1) ---MAQTASKGKVLIILSGANTIHLKEGK-------------DQKTGYFLSELGHPLMKILEAGYDVVFANPTGTH
AN6810.2 (1) ---MPSKRILIVLSDANYFPLKKPAGSGEGSSSNSKIVDQPSGFFLMELAKPLQKLLDAGHEVTFASPEGRE
PTT_19431 (1) ---MAAMKVLIVLSDASSFPLYNTGSDG-------KTVSQDSGYFLMELTKPLQKVLDAGYEVTFASPEGKE
CC1G_10162 (1) ---MSKGKILIILSGADSFAVEKPDGNVS---------EEKTGFFLTELATPLEKILDAGYDVVFASPHGNK
SNOG_00505 (1) ---------------------------------------MTPEQLQTYNKASKKILIIVSDASSFPLYNTGNDG-------KTVSQDSGYFLMELAKPLQKFLDAGYEVTFASPEGKE
Pospl1_115118 (1) ---MSAGKVLIILSDADSYPVKKPDGSTT---------NQETGVFLTELAKPLQKLLDAGYEVTFASPSGRR
CCM_05507 (1) --MSNDRAPVADTAEINAWFPSPYSLTQYVPATTDFAGTSSP---RPYTGGRWKVLLIGTQERYLPMADGR-------------FFSTGNHPVELLLPLLHLDAAGFDVDVATPSGGP
VDAG_08958 (1) --MSNDRKPVADQAEDDAWFPSPYSLTQYVAPKTDFAEGDADYAATAYKGGKWKVLLIATQERYLKMADGS-------------FFSTGNHPVEMLLPMLHMDAAGFDIDIATLSGEP
MAC_05717 (1) MSNTSDRAPVADQAELNAWFPSKYSLTQYTSPKTDFDGADYP---NAYTGGKWKVLLIATQERYLRMAGGE-------------FFSTGNHPVETLLPMVHLDAAGFDIDIATLSGAP
EcHsp31 (1) MTVQTSKNPQVDIAEDNAFFPSEYSLSQYTSPVSDLDGVDYP---KPYRG-KHKILVIAADERYLPTDNGK-------------LFSTGNHPIETLLPLYHLHAAGFEFEVATISGLM
HsDJ-1 (1) ---MASKRALVILAK---------------------------GAEEMETVIPVDVMRRAGIKVTVAGLAG--

* AN6796.2 (52) APLDPSSVKMFEN---------DPVSARFLK--EQESLWKNTLKLEEVLPRA-------EKGEFDAIFYVGGHGPMFDLVTDKTSIALIQSFAKAKKPVSAVCHGP---CVFVNVTTP
BDBG_02344 (52) APLDPGSVEAFAN---------DAVAAAFVK--EKEPIWRNTVKLSEVKASD-----------FDAIFYVGGHGPLFDLYEDPDSLRLIKEFAESKKIVSAVCHAP---AVFLKATAG
UM00094.1 (53) APLDQSSVDAFKD---------DADSVKFLNDTEAQDWVNNTKRLSEFSAS--------SVSEFDAIFYPGGHGPCFDLPVDTTSQELIKTFYEAGKPTSAVCHAP---AVFADVKLS
CCM_09248 (52) APLDPSSVEAFKN---------DASSQKFL----EKKLWEKTAPLKDFVGRS---------GEFAAVFYPGGHGPMYDLVDDKDSIAIIEEFYKAGKPISAVCHGP---IVFAHVKVD MAC_07323 (52) APLDPSSIDMFKS---------DESSVNFLN--NNKSVWEKTTPLKEFIGRS---------DEFDALFYPGGHGPMYDLVTDQDSIKLIEEFHNAGKPVAAVCHGP---IVFRDAKAK VDAG_09321 (56) APLDPISVDLFSS---------DPVCKDFLD--NHKAIWENTQKLSSFAGRA---------SEFDAVFYPGGHGPMFDLAFDEDSIALIKDFDAQGKVISAVCHGP---AAFVNAKDA
NCU06603 (54) APVDPSSIEAAKD---------DQVSQNFIKSETTKPLFEQTRPLSEFVGNPS------AIAPYSAIFFPGGHGPMYDLATSSESQQLIREFWDAGKTVAAVCHGP---AALVNVKLS
PTT_13641 (53) APLDPASVEASK----------DDVSVNFLK--NDEQVWKTTQKLADFKGKA---------KDFDAIFYVGGHGPMFDLVDDATSQQLIREFWEADKIVSAVCHAP---SVFYDAKLS
SNOG_04306 (53) APLDPASVEAAK----------DDVSVNFLK--NDEQVWKNTQKLSDFSGKA---------KDFDAVFYVGGHGPMFDLADNPTSQQLIKEFWEAGKIVSAVCHAP---AVLYDVKLS
Rhoba1_1_64353 (54) APLDPSSVEAFKE---------DSDSIKFLNEDEPKQLFANTKKITDVKEAD-----------YAALALPGGHAPIFDLTTDKDSIALIESFLKAGKPVASVCHGP---TVFLNVTDP ARB_05407 (56) AFDEHSLEKKFLNK-------EDEEVLHNANDPFNKKLNSQMFKAGDLSP-----------HEYGLFFAAGGHGACYDFPHAKHLQAIASDVYNRGGVVAAVCHGP---AILAGVKN-Mucci2_157529 (57) GMDEHSTEKQFLTD-------EDEKILNDPNHPFNVLLNKHLHKASELDA-----------KQYGLFFASAGHATLYDYPHARGLQSIAEDIYKRGGIVSAVCHGP---AILPGIKG-RO3G_07202.3 (56) GLDEHSTTKDFLTD-------EDERTYNDPNHPFNVLLNKHLYKASNLDP-----------KQYGLFFASAGHATLYDYPHARGLQSIAEDIYERGGVVSAVCHGP---AILPGVKDK Phybl2_109595 (57) GLDDHSTQKMFLTD-------EDEQILKNPNHPFNVKLNKELKRASDVQQHS---------KDYGLFFASAGHATLYDYPTARGLQAIAQDIYGRGGVVSAVCHGP---AILPGIKDP MGL_4192 (58) TPDALSMTKPWITD-------EELKVYEDKNSEFRQKL-DNLKKPSDIDP-----------TKYGLFFASAGHAALIDYPDDKGLQEIASKIWEAGGIVSAVCHGG---AILPGVKD-
CaO19.251 (53) GWDDHSVVPDFLNG-------EDKEIFDNVNSEFNVAL-KILKKASDLDP-----------NDYDIFFGSAGHGTLFDYPNAKDLQKIATTVYDKGGVVSAVCHGP---AIFENLNDP
ScHsp31 (55) GWDEHSLAKDFLNG-------QDETDFKNKDSDFNKTL-AKIKTPKEVNA-----------DDYQIFFASAGHGTLFDYPKAKDLQDIASEIYANGGVVAAVCHGP---AIFDGLTDK
YPL280W (55) GWDEHYLPKSFIGG-------EDKMNFETKNSAFNKAL-ARIKTANEVNA-----------SDYKIFFASAGHGALFDYPKAKNLQDIASKIYANGGVIAAICHGP---LLFDGLIDI
YALI0C22000p (57) GYDEKSLDPINCSD-------KEMEDLRNPDSSFSKCS-AKVTTADKVNG-----------KDYGIIFFAGGHGTIHDFCDAPKLAKLASEVYFNNGILAAVCHGP---AIFNNLKG-YALI0F00682p (56) GYDAHSLDPKFATE-------EQLDAQKNPQSQYNLVL-DGILPASEIDA-----------SNYSVFFAAGGHGAIFDFVNAPVLGKIAADIYAAGGIVSAVCHGP---AIFASIKN-
Hsp3102 (58) KFDDHSIEESKLGD-------FERKVFNDKNDDFWTNL-NNMKKASDIVG-----------KDYQLLFVAGGHAAMFDLPKATNLQAVAREVFTNGGVLSAVCHGP---VLLANVKNP
Hsp3101 (56) KFDDHSIKKSALGE-------VERDAFDNKDNEFWYAL-KDIKPADKINY-----------KEFCIMFIAGGHAAMFDLPHATNLQTLAQQIYASNGVLAAVCHGP---VMLPFVDDT
Hsp3103 (57) QFDDHSVAGPAIDKGSK----AEKYVLENKDDMFWRIV-QNSKTADEVNP-----------DKYDIFFVAGGHATLFDFPKATNLQKLGTSIYENGGVVAAVCHGP---TLLPFMKRQ
CC1G_00260 (50) PPIDEGSVKAFEK---------DAESVKFLNNETVKQKLASAHKLSDINVAN-----------YDAIFYVGGHGPVIDLASDPVNGKLVSDFWNAGKIVSAVCHGPAHCSALVQGADK Pospl1_110200 (50) PPVDEGSVEMFKD---------DES-VKFLQDATVTEKLATAKKLSEVNPSQ-----------YDAVFYVGGHGPVLDLATDPTNIKVGNEFWRSGKITSAVCHGP---AALVGVTDA SERLA73DRAFT_120613 (51) PPVDPASVQMFQD---------D---VKFLEDANVQSLLAKAKKLTDVKVDD-----------YEAIFYIGGHGPVIDLAVDPANIKLASEFYRAGKLTTAVCHGP---AALVGATDA SCHCODRAFT_46162 (51) PPVSQGSVELFKE---------DAESVQFLADEIVKQKLASAKILSEVNPDD-----------YAAVFYVGGHGPCIDLPNDETNIKLANSFWRAGKIVSAVCHGP---AALVRITDA SCHCODRAFT_49614 (51) PPLDPVSKEMFQD---------E-ESQKFLTDKVPQEKLANAKKLADVNPDD-----------YAAVFYVGGHGPVIDLATDPTNVKLASKFWQQGKIVSAVCHGP---AALVGATDA SPPG_05672 (54) TPLDPSSAEAFAK---------DEECIKFLNDPVAQKGVKETVKVEDILARAN---------EFDAVFFPGGHGPMFDLFTFVPSLQLAAKVYENNGVVAAVCHGP---AAIVNIKLS SPPG_02734 (61) PVQDPISELLIWFLGNYKEREREHALIDKMKIESNFASPRPFASLTDDDLST-----------FVGVFIPGGHAPMQDLHNDKELARILGHFHRMAKPTGAICHGP---AALLSTKTE
AN6810.2 (70) PQPDPNSESLLAFAGNFYERRRENELLERMKKENGFTKPRKLNSISDDELKN-----------FAGVFIPGGHAPLADLGDNKDLGRILEYFHKENKPTAAICHGP---YALLSTKVS
PTT_19431 (63) PTPDPLSVSLAAFAGNYYEKQRELDLIERMKKENGFSRPRKFSEISDDDLKS-----------YSGVFIPGGHAPLSDLGDNPELGRILTHFHSAQKPTAALCHGP---WAFLSTKYT CC1G_10162 (61) PSIDPLSESILVYMGNYWRKKKEEELIERMRVEKSLYAPRAFSEIGDDELRG-----------FKGVFIPGGHAPLTDLGADPELGRILLHFYRNGKPTAAVCHGP---YALLSTRVA SNOG_00505 (73) PTPDPNSLSLMAFAGNFYERQRELDLIERMKKENGFSRPRKFSEISDDQLKN-----------FGGVFIPGGHAPLSDLGDNADLGRILSHFHQNAKPTAALCHGP---WAFLSTKYG Pospl1_115118 (61) PNIDPLSESLVVYFGNWLQKNRDNQLIQRMYAENNLALPRPFPSITDDELES-----------YAGVFIPGGHAPIRDLGNNPDLGRILWHFHGRGKPTAAICHGP---LALLSTKYA CCM_05507 (101) VKLEVWAFP-------------SRDEAVTQIYKKYEEKLRAPLSLEALWEGSSSNGGFDASTPYLAVFVPGGHGVLNDIPRSRLVGDVLRWAHAQDRYVVTLCHGP---AALLAAEVG VDAG_08958 (104) VKFEMWAFP-------------KEDKAVQAIYDKYRDKIRNPLNLQDVWGR-----GFTADTPYLAVFIPGGHGVLNGVPFSATVGDVLRWAHAHERFFVTLCHGP---ASMLAADVG MAC_05717 (103) VKFEVWAFP-------------KEDEAVKKIYAKYEDKLRSPLNLQDIWGKD----GFTSETPYLGIFIPGGHGALNDVPFSKLVGDIIRWAHDNQRYYLTLCHGP---ASMLAANVG EcHsp31 (102) TKFEYWAMP-------------HKDEKVMPFFEQHKSLFRNPKKLADVVAS------LNADSEYAAIFVPGGHGALIGLPESQDVAAALQWAIKNDRFVISLCHGP---AAFLALRHG
HsDJ-1 (41) --------------------------------KDPVQCSRDVVICPDASLED-----AKKEGPYDVVVLPGGNLGAQNLSESAAVKEILKEQENRKGLIAAICAGP---TALLAHEI-

* AN6796.2 (149) S---GKPLVADAEVTGFSNVEEDQVDLSKVMPFMLEDELNKKSGG---KYVKADQPWGEKVVVSQVKELGGPLITGQNPASATGVGKALLEALGA---------------------
BDBG_02344 (145) ----GKPIVADAQVTGFSNAEEDQIKMSQHLPYLLETELKKLNG----KYVKADEPWGEKVVVDKVEATGAPLITGQNPASAGGVGKEILKALGL--------------------- UM00094.1 (151) D---GSYLVNGKKITCFTNQEEEQAGLTKAIPWLVESRLIERG-----ATFEKAEPWAEKVIVD--KTGGRVLISGQNPASAAAVGRQILAALQA--------------------- CCM_09248 (145) ----GKPLVEGRTVTGFTNEEEAQVGLAEAMPFLLEDRLKAVGAK----WTQADQAWGEKVVVD------GQIITGQNPASAHAVGVALAKAIGI--------------------- MAC_07323 (147) S---GEPLLKGKNVTGFTNVEEDQVQLSAAMPFLLEDELKKVGAN----FHAADQPWGEKVVVD------GLIISGQNPASAKGVGEAIAKAIGV--------------------- VDAG_09321 (151) A---GEPLLKGKTVTAFTNEGEDMFKYTEEMNFSLEDKLNEVSGGK--FVKSEEGPMGEKVVVD------GRIITGQNPASSKGVGEEIAKALGVF-------------------- NCU06603 (154) D---GSHLLKGRKVTGFTNDEEDQVGLTKVMPFLLEDKLKEAVGTE-GAFEKAEQPWAEKVVVD----AGGRLITGQNPASAKGVGEAIVKSIKAQN------------------- PTT_13641 (147) D---GSLLIAGKEVTAFTNAEEEQAGLTKAVPFLPEDALNKASGG---KFVKAAEPWGEKVVVS------GRLITGQNPASATGVAEAIAKALGI--------------------- SNOG_04306 (147) D---GSLLVAGKEVTAFTNAEEEQVGLSKVVPFLPEDALNKASGG---KFVKAAEPWGEKVVVV------GNLITGQNPASATGVGEAIAKALKV--------------------- Rhoba1_1_64353 (149) KS--GEPFVKGKKITCFSDDEERQAGLVDSIPFLVETELRNKG----ADFQLTRKAWAEEVVVD------GQLITAGNPASASGMAKALLTVLEKA-------------------- ARB_05407 (152) --PEEEPVVKDKTVTGFTTEGELELKVIDQMRQDKVHTIEDCLAPTGAHYEAPASAFDNFEKVD------GRIVTGANPASARDTARDAIKVFDGLD------------------- Mucci2_157529 (153) --DDGKSIINGKTVTGFTNEGEVQLNILDKIKDDKVPTIEEAAASVGATYVAPPTPFADFNKTD------GRVVTGANPASAHSTAEAAIAAFEKL-------------------- RO3G_07202.3 (153) --KTGKSIIDGKTVTGFTSLGEEQMNLMQKIKGDKVLTIEEGAADAGATYVSPPTPFADFHKID------GRVVTGANPASAHSTADAAIKVFDGK-------------------- Phybl2_109595 (156) --LTGKSVVENKVVTGFTDLGEVQMKVMDKLRSDKLNTVEKWMELSHAKYIAPPEPFNCFSKID------GRIVTGANPASAKLTAENAIKVFDCQ-------------------- MGL_4192 (153) --QSGKSIISGRKITGFTDKGEEELGALAEIKNWNRPTIQESAASAGAEYVHPPGPWAPYQVTD------GRLVTGVNPQSATVTTEAAIKAFDAL-------------------- CaO19.251 (149) --KTGEPLIKGKKITGFTDIGEDILGVTDIMKKGNLLTIKQVAEKEGATYIEPEGPWDNFTVTD------GRIVTGVNPQSAVKTAEDVIAAFECN--------------------
ScHsp31 (151) --KTGRPLIEGKSITGFTDVGETILGVDSILKAKNLATVEDVAKKYGAKYLAPVGPWDDYSITD------GRLVTGVNPASAHSTAVRSIDALKN---------------------
YPL280W (151) --KTTRPLIEGKAITGFPLEGEIALGVDDILRSRKLTTVERVANKNGAKYLAPIHPWDDYSITD------GKLVTGVNANSSYSTTIRAINALYS--------------------- YALI0C22000p (152) --PDGKPLIQGKTITGFHDQGETDMGLDEILKQRSLPTIRQIAANVGANYQAPPDPWKDFSLSD------QRIVTGANPASATSTAIKAIELYNKL-------------------- YALI0F00682p (151) --EEGQPIVAGKVITGFTAEGEKEMGVSEAITKHGKKLVPEIAKEAGAEYRAPPTPFQDFSITD------DRIVTGANPASANSTAEKVVQLFDAIDAPTQSGASVLK--------
Hsp3102 (154) QSVEGKTVVYHKHVTAFNKAGEEKMGVMDELKKRGMKSLNEIFAEAGATFIDPPNPNVNFTQID------GKIVTGVNPQSAKSTAEAAVSAL-----------------------
Hsp3101 (152) KSPEGRSVVYGKKVTAFNSTGELVMGVSSALRERNMQDLNSLFREAGAEFVDPPTPMSDFTQVD------GRIVTGVNPMSAKSTAEAAIKVSQSLRKT-----------------
Hsp3103 (156) TSDGSVSIVCGKDVTAFDRVAEDKSKLMEALKKYNLEVLDDMLNDAGANFIKSPNPFGDFVIAD------GRLVTGSNPASATSTAKTALRVL-----------------------
CC1G_00260 (148) D---GKSIFAGRSFTGFSNAEEKAVDKVNDVPFLLEDKITSLGG----KYEKAAEPWGPKVVVD------GRLITGQNPASASGVGEAILKAIKGN-------------------- Pospl1_110200 (144) E---GKSIFTGKAATGFSNTEEEQVNKVKDIPFLLESRIKELGG----KYEAAAEPWGVKVVVD------GKLITGQNPASAKAIGEAIHKALA---------------------- SERLA73DRAFT_120613 (143) S---GKSIFAGKAFTGFSNVEEEQVGKVKDIPFLLEDKITSLGG----KYEKATAPWGAKVVVS------GHLITGQNPASAQPIGEAILKALKS--------------------- SCHCODRAFT_46162 (146) S---GQSIFKGRRATCFTVAEEKILGTVDAIPFQPEETLKELGA----QFENAGP-FESKVVVD------GRLLTGQNPASSRALAEEVLKALKG--------------------- SCHCODRAFT_49614 (145) S---GQSIFKGRRATCFTYDEELQVKKVDSIPFQPEHKIVELGG----KFEKTEP-WGVKVVAD------GQLYTGQNPASAGPLGQELLKALKK--------------------- SPPG_05672 (151) N---GDSLVKGKRVTSFSNSEEDAVQLSPVMPFLLENALKSAG----AKYEKAAKDWEAHVVVD------GRLITGQNPNSGAPLGEKLRELLG---------------------- SPPG_02734 (165) EGCP----YSGYKVTAYSNTEDKLNEIMWWGTLPYKLVDELEKA---GLKCEETFPMGSKVTVD------RELVSGQNPSSASAFGDAFVKKLNESVTLGGTGVHAKEI------- AN6810.2 (174) GGE---FAYKGYKITSWSNAEEKVMESMLGGEVEKVETALMNAG---AEMVEGAKEKVGQTTLH------RELLTGGNPMAADELGNRFVKMISV---------------------
PTT_19431 (167) PNKP-EFAYKGYKMTSWSDAEEKFMETIMRGQIDKVESTLREEG---ADMQEGIAKSMGSITVD------RELITGDNPMSANAIGDKFVEMMAAK-------------------- CC1G_10162 (165) PNST-GFAYKGYKLTSWSDASESLVEKLKGGHIEKVESALRDAG---ADMQTQTSKNLGSVTVD------REVVSGANPLAVAELGEKFVEMLAQKQGEEQIESLERRNRFPVQVN SNOG_00505 (177) PQK--EFAYKGYKMTSWSDAEEKMMEVYFRGEITKVEGTLREEG---ADMQEGLAKSMGSITVD------RELITGDNPMAANAIGDKFLEMLAGVK------------------- Pospl1_115118 (165) RDSP-GFAYKGYKLTSWSDAEERLVERLQGGEIPKVESTLQAEG---AEMVSTVGKKAGGITVD------REVVSGANPMAAEGLGSKLIEMLRA--------------------- CCM_05507 (203) APAGSRFLYDGYEVVAFPDALDQGTNIDIGYIPGKMQWLVGEALRK-RGVKTLNEGITGRVHRD------RLLLTGDSPLASNALGKLAAETLLEAVAKRG--------------- VDAG_08958 (201) KPAGSRYIYEGYKVDVFPDSLDEGANIDIGYIPGKMAWLVGERLRA-LGVEPINSQITGEVHRD------RLLLTGDSPLASNNLGKLAAKTLLEAVASK----------------
MAC_05717 (201) KPEGSKYIYDGYEIVVFPDSLDTGANIDMGYIPGKMPWLMGEELKK-LGVKPLNEDMTGQVHRD------RFLLTGDSPLASNALGKLAATTLLEDVAKRG---------------
EcHsp31 (198) DNP-----LNGYSICAFPDAADKQT-PEIGYMPGHLTWYFGEELKK-MGMNIINDDITGRVHKD------RKLLTGDSPFAANALGKLAAQEMLAAYAG----------------- HsDJ-1 (118) --------GFGSKVTTHPLAKDKMMNGGHYTYSENR------------------------VEKD------GLILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLVLKD------
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