```
HsPKA/1-351

HsPKA/1-351           .....................................................................................
HsGSK3b/1-420         .....................................................................................
HsCAMK1/1-370         .....................................................................................
HsSrc/1-536         1 ...........................................................................MGSNKSKPKD
HsCK2A1/1-391         .....................................................................................
HsCDK2/1-298          .....................................................................................
TgPKAc/1-333          .....................................................................................
TgAGC/1-514         1 ...........................................................................MP......LR
TgROP5/1-461          .....................................................................................
TgROP7/1-575        1 ....................................MG.......HPTSF...GQPSCLV........WLAAAFLVLGLCLVQQ.
TgROP8/1-575        1 .........................MFS..VLRNRNMR.......HGPSI...GSSSCLI........WLAAAFFVSALGHVQQ.
TgROP16/1-707       1 ............................................................MKVTTKGLAFALALLFCTRCATA..
TgROP18/1-554         .....................................................................................
TgRON13/1-1375      1 MLPRMQSERSVARQSLGATRSRCLLRFATKKWASRGLGSSNRPGRPPPSSAAGHRASCPFFPRSSFSASFALRFLCPVLCSLLLA
TgRON13/1-1375


HsPKA/1-351

HsPKA/1-351           .....................................................................................
HsGSK3b/1-420         .....................................................................................
HsCAMK1/1-370         .....................................................................................
HsSrc/1-536        11 AS................................QR..RRS..LEPAEN.......VHGAGGGAFPASQT...............
HsCK2A1/1-391         .....................................................................................
HsCDK2/1-298          .....................................................................................
TgPKAc/1-333          .....................................................................................
TgAGC/1-514         5 T......................MSVTSGQYPVQPHQRRPLF..GRGNLFFFLNSGSSDGAAVG.....TPGVSP.SRE....QS
TgROP5/1-461          .....................................................................................
TgROP7/1-575          .....................................................................................
TgROP8/1-575          .....................................................................................
TgROP16/1-707      24 ..RYMSFEEAQ...................KASEAAK.RQIATLPSPDS.TLSNPGSKHRNRGGSPAAGQPSQSTLQPEQAAAEV
TgROP18/1-554         .....................................................................................
TgRON13/1-1375     86 TLFFVSPREVDALKFRGNGGRHLNAELDGNWAKRFQ...ETQRAAPPDSFFVSDSEISGRTSLLSLASSEQGTSTVDSR....FV
TgRON13/1-1375


HsPKA/1-351

HsPKA/1-351           .....................................................................................
HsGSK3b/1-420         .....................................................................................
HsCAMK1/1-370         .....................................................................................
HsSrc/1-536        38 .....................PSKPASADGHRGPSAAFAPAAAEPKLFGGFNSSDTVTSPQRAGPLAGGVTTFVALYDYESRTET
HsCK2A1/1-391         .....................................................................................
HsCDK2/1-298          .....................................................................................
TgPKAc/1-333          .....................................................................................
TgAGC/1-514        56 GFQMLTKRSLFGVSHPPTHS..SRTVAQ..MAPRSQAYTPQPH....................R................SSGDC
TgROP5/1-461          .....................................................................................
TgROP7/1-575       31 GAGIQRP.HQWKSSEAALSVSPA.....................G.........DIV...................DKYSHDSTE
TgROP8/1-575       40 GAGVVRP.RHWQNSEAAVSVRSP.....................G.........GAS...................PRHFHSPIE
TgROP16/1-707      86 GLGAG......GSTQGQ.....GRTGGSAGAREERRSPSPQSAY...................P................ATSSA
TgROP18/1-554       1 MFSVQRP.........PLTRTVVRMG.............................LATLLPKTAC...........LAGLNVALV
TgRON13/1-1375    164 GLSGQKPRHIWGSQEETGERREDRQEESEGRRGNEDAYHPHTF....................S................H.SSS
TgRON13/1-1375


HsPKA/1-351
                                                                                                .
HsPKA/1-351         1 .........................................................................MG...NAA....
HsGSK3b/1-420       1 ..........................MSGRPRTTSFA.....................ESCKPV....QQPSAFG...S......
HsCAMK1/1-370         .....................................................................................
HsSrc/1-536       102 DLSFKK....GERLQIVNNTEGDWWLAHSLSTGQTGY.....................I...PSNYV.............APSDS
HsCK2A1/1-391       1 ..........................MSGPVP....................................SRARVYT...D......
HsCDK2/1-298          .....................................................................................
TgPKAc/1-333          .....................................................................................
TgAGC/1-514       101 ST.......................AEK..............................ASCPTGSAAVHQATNMG...SVSAVAG
TgROP5/1-461        1 ...........................MSG............................GRVPRVPA.SSTTT......SASEGIF
TgROP7/1-575       66 GENTVS....EG..EAEGSRGGSWLEQEGV............................ELRPPLLDSQTGTS......TASPTGF
TgROP8/1-575       75 PVAFID....GE..HDEDKHEGSWLEQEAA............................EDVTPLPGSHTEAQ......TQSPSAF
TgROP16/1-707     125 SLRGYQTQLSPSHLPPRSSGPGGWFPTESIFTPWS.........................SPPQPLTQRKP.SLS...GVVVTEF
TgROP18/1-554      37 FLLFQV.....QDGTGITLGPSKLDSKPTSLD..SQQHVADKRWLATVGHYKHLAGATESTRDVSLLEERAQHRVNAQETNQRRT
TgRON13/1-1375    212 SMPFY................GALFDSSSAFPPFSAA.....................VSSPPFSMTVSPADRVI...QALPIAF
TgRON13/1-1375


HsPKA/1-351

HsPKA/1-351         6 ..................................AAK................................................
HsGSK3b/1-420      26 ....................M.............K..................................................
HsCAMK1/1-370         .....................................................................................
HsSrc/1-536       146 I.....QAEEWYFGKITRRESERLLLNAENP...RGT..............FLVRES............................
HsCK2A1/1-391      15 ....................V.............N..................................................
HsCDK2/1-298          .....................................................................................
TgPKAc/1-333          .....................................................................................
TgAGC/1-514       130 P......LGRMWGKLSSMSTM.............ATS................................................
TgROP5/1-461       24 .R.RLVRRLRR.GRGTA.................DGAGV...ADETHQEPRPPLRKRL...........................
TgROP7/1-575      111 .R.RFLRHLRFWRRGST.................RGSDD...AAEVSRRTRVPLHTRL...........................
TgROP8/1-575      120 .R.RLTRRLRFWRRGVT.................GGSDA...GEEAPQTPRPPLRTRI...........................
TgROP16/1-707     181 Q.....EPQEQYGAASSLASSPKRYVSGASSSALSGKAVPTPASLGQENPLFPVQSATLDSGIQSPAQERRGSPQRQIAMSTENP
TgROP18/1-554     115 IFQRLLNLLRRRE.........................RD..GEVSGSAADSSSRPRLS..........................
TgRON13/1-1375    257 A.....EHK.SGGEKASREET.............GGK................................................
TgRON13/1-1375
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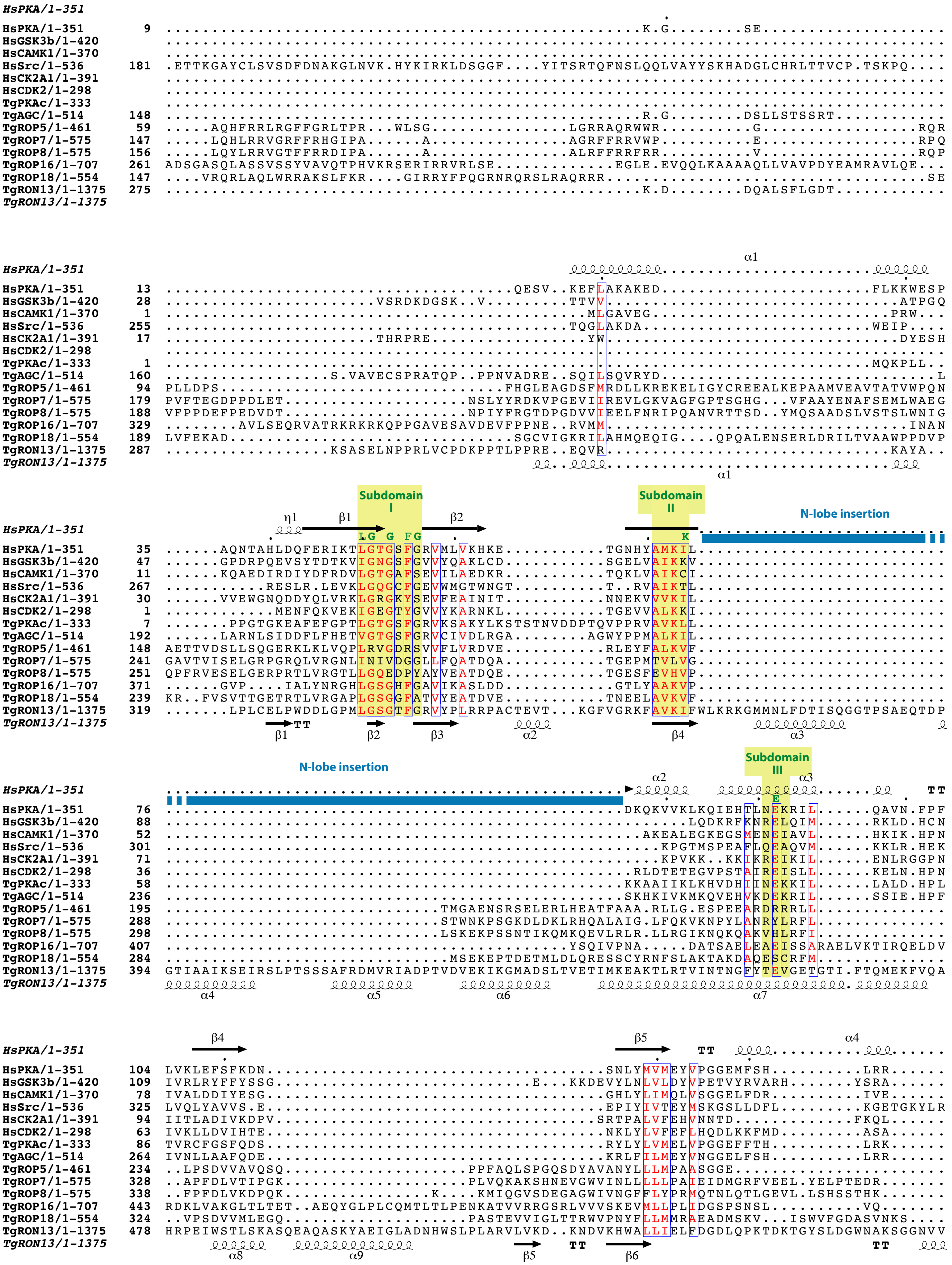

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HsPKA/1-351

HsPKA/1-351        9 ....................................................K.G........SE....................
HsGSK3b/1-420        .....................................................................................
HsCAMK1/1-370        .....................................................................................
HsSrc/1-536      181 .ETTKGAYCLSVSDFDNAKGLNVK.HYKIRKLDSGGF....YITSRTQFNSLQQLVAYYSKHADGLCHRLTTVCP.TSKPQ....
HsCK2A1/1-391        .....................................................................................
HsCDK2/1-298         .....................................................................................
TgPKAc/1-333         .....................................................................................
TgAGC/1-514      148 ....................................................R.G........DSLLSTSSRT............
TgROP5/1-461      59 .....AQHFRRLRGFFGRLTPR...WLSG...............LGRRAQRWWR..........G.................RQR
TgROP7/1-575     147 .....LQHLRRVGRFFRHGIPA......A...............AGRFFRRVWP..........E.................RPQ
TgROP8/1-575     156 .....LQYLRRVGTFFRRDIPA......A...............ALRFFRRFRR..........V.................RQP
TgROP16/1-707    261 ADSGASQLASSVSSYVAVQTPHVKRSERIRRVRLSE.............EGLE.EVQQLKAAAAQLLVAVPDYEAMRAVLQE...
TgROP18/1-554    147 ....VRQRLAQLWRRAKSLFKR....GIRRYFPQGRNRQRSLRAQRRR...................................SE
TgRON13/1-1375   275 ....................................................K.D........DQALSFLGDT............
TgRON13/1-1375

HsPKA/1-351
HsPKA/1-351       13 ......................................QESV..KEFLAKAKED.......................FLKKWESP
HsGSK3b/1-420     28 .......................VSRDKDGSK..V.........TTVV................................ATPGQ
HsCAMK1/1-370      1 ..............................................MLGAVEG..........................PRW...
HsSrc/1-536      255 ............................................TQGLAKDA.........................WEIP....
HsCK2A1/1-391     17 .......................THRPRE.................YW................................DYESH
HsCDK2/1-298         .....................................................................................
TgPKAc/1-333       1 .............................................................................MQKPLL..
TgAGC/1-514      160 ..................S.VAVECSPRATQP..PPNVADRE..SQILSQVRYD..............................L
TgROP5/1-461      94 PLLDPS...............................FHGLEAGDSFMRDLLKREKELIGYCREEALKEPAAMVEAVTATVWPQN
TgROP7/1-575     179 PVFTEGDPPDLET....................NSLYYRDKVPGEVIIREVLGKVAGFGPTSGHG...VFAAYENAFSEMLWAEG
TgROP8/1-575     188 VFPPDEFPEDVDT....................NPIYFRGTDPGDVVIEELFNRIPQANVRTTSD..YMQSAADSLVSTSLWNIG
TgROP16/1-707    329 ........AVLSEQRVATRKRKRKQPPGAVESAVDEVFPPNE..RVMM.................................INAN
TgROP18/1-554    189 LVFEKAD...............................SGCVIGKRILAHMQEQIG....QPQALENSERLDRILTVAAWPPDVP
TgRON13/1-1375   287 ..................KSASELNPPRLVCPDKPPTLPPRE..EQVR...............................KAYA..
TgRON13/1-1375

HsPKA/1-351
HsPKA/1-351       35 ......AQNTAHLDQFERIKTLGTGSFGRVMLVKHKE...........TGNHYAMKIL...........................
HsGSK3b/1-420     47 ......GPDRPQEVSYTDTKVIGNGSFGVVYQAKLCD...........SGELVAIKKV...........................
HsCAMK1/1-370     11 ......KQAEDIRDIYDFRDVLGTGAFSEVILAEDKR...........TQKLVAIKCI...........................
HsSrc/1-536      267 ...........RESLR.LEVKLGQGCFGEVWMGTWNGT..........T..RVAIKTL...........................
HsCK2A1/1-391     30 ......VVEWGNQDDYQLVRKLGRGKYSEVFEAINIT...........NNEKVVVKIL...........................
HsCDK2/1-298       1 ............MENFQKVEKIGEGTYGVVYKARNKL...........TGEVVALKKI...........................
TgPKAc/1-333       7 .......PPGTGKEAFEFGPTLGTGSFGRVKSAKYLKSTSTNVDDPTQVPPRVAVKLL...........................
TgAGC/1-514      192 ......LARNLSIDDFLFHETVGTGSFGRVCIVDLRGA........AGWYPPMALKIL...........................
TgROP5/1-461     148 AETTVDSLLSQGERKLKLVQPLRVGDRSVVFLVRDVE...........RLEYFALKVF...........................
TgROP7/1-575     241 GAVTVISELGRPGRQLVRGNLINIVDGGLLFQATDQA...........TGEPMTVLVG...........................
TgROP8/1-575     251 QPFRVESELGERPRTLVRGTLLGQEDPYAYVEATDQE...........TGESFEVHVP...........................
TgROP16/1-707    371 ......GVP....IALYNRGHLGSGHFGAVIKASLDD............GTLYAAKVP...........................
TgROP18/1-554    239 KR..FVSVTTGETRTLVRGAPLGSGGFATVYEATDVE...........TNEELAVKVF...........................
TgRON13/1-1375   319 .......LPLCELPWDDLGPMLGSGTFGRVYPLRRPACTEVT...KGFVGRKFAVKIFWLKRKGMMNLFDTISQGGTPSAEQTDP
TgRON13/1-1375

HsPKA/1-351
HsPKA/1-351       76 ..................................................DKQKVVKLKQIEHTLNEKRIL......QAVN.FPF
HsGSK3b/1-420     88 .........................................................LQDKRFKNRELQIM......RKLD.HCN
HsCAMK1/1-370     52 ....................................................AKEALEGKEGSMENEIAVL......HKIK.HPN
HsSrc/1-536      301 ......................................................KPGTMSPEAFLQEAQVM......KKLR.HEK
HsCK2A1/1-391     71 ......................................................KPVKK..KKIKREIKIL......ENLRGGPN
HsCDK2/1-298      36 ...................................................RLDTETEGVPSTAIREISLL......KELN.HPN
TgPKAc/1-333      58 ..................................................KKAAIIKLKHVDHIINEKKIL......LALD.HPL
TgAGC/1-514      236 ..................................................SKHKIVKMKQVEHVKDEKRIL......SSIE.HPF
TgROP5/1-461     195 ..............................TMGAENSRSELERLHEATFAAA.RLLG.ESPEEARDRRRLL..............
TgROP7/1-575     288 ..............................STWNKPSGKDLDKLRHQALAIG.LFQKVKNPYLANRYLRFL..............
TgROP8/1-575     298 ..............................LSKEKPSSNTIKQMKQEVLRLR.LLRGIKNQKQAKVHLRFI..............
TgROP16/1-707    407 ............................................YSQIVPNA.....DATSAELEAEISSARAELVKTIRQELDV
TgROP18/1-554    284 ...............................MSEKEPTDETMLDLQRESSCYRNFSLAKTAKDAQESCRFM..............
TgRON13/1-1375   394 GTIAAIKSEIRSLPTSSSAFRDMVRIADPTVDVEKIKGMADSLTVETIMKEAKTLRTVINTNGFYTEVGETGTI.FTQMEKFVQA
TgRON13/1-1375

HsPKA/1-351
HsPKA/1-351      104 LVKLEFSFKDN.....................................SNLYMVMEYVPGGEMFSH..........LRR......
HsGSK3b/1-420    109 IVRLRYFFYSSG............................E...KKDEVYLNLVLDYVPETVYRVARH.......YSRA......
HsCAMK1/1-370     78 IVALDDIYESG.....................................GHLYLIMQLVSGGELFDR..........IVE......
HsSrc/1-536      325 LVQLYAVVS.E.....................................EPIYIVTEYMSKGSLLDFL.........KGETGKYLR
HsCK2A1/1-391     94 IITLADIVKDPV...................................SRTPALVFEHVNNTD.............FKQL......
HsCDK2/1-298      63 IVKLLDVIHTE.....................................NKLYLVFEFLHQDLKKFMD.........ASA......
TgPKAc/1-333      86 TVRCFGSFQDS.....................................RYLYLVMELVPGGEFFTH..........LRK......
TgAGC/1-514      264 IVNLLAAFQDE.....................................KRLFILMEYVNGGELFSH..........LRR......
TgROP5/1-461     234 ..LPSDVVAVQSQ....................PPFAQLSPGQSDYAVANYLLLMPAASGGE.......................
TgROP7/1-575     328 ..APFDLVTIPGK....................PLVQKAKSHNEVGWVINLLLLLPAIEIDMGRFVEEL.YELPTEDR.......
TgROP8/1-575     338 ..FPFDLVKDPQK...............K....KMIQGVSDEGAGWIVNGFFFLYPRMQTNLQTLGEVL.LSHSSTHK.......
TgROP16/1-707    443 RDKLVAKGLTLTET..AEQYGLPLCQMTLTLPENKATVVRRGSRLVVVSKEVMLLPLIDGSPSNSL..........VQ.......
TgROP18/1-554    324 ..VPSDVVMLEGQ....................PASTEVVIGLTTRWVPNYFLLMMRAEADMSKV...ISWVFGDASVNKS....
TgRON13/1-1375   478 HRPEIWSTLSKASQEAQASKYAEIGLADNHWSLPLARVLVKD..KNDVKHWALLIELFDGDLQPKTDKTGYSLDGWNAKSGGNVV
TgRON13/1-1375
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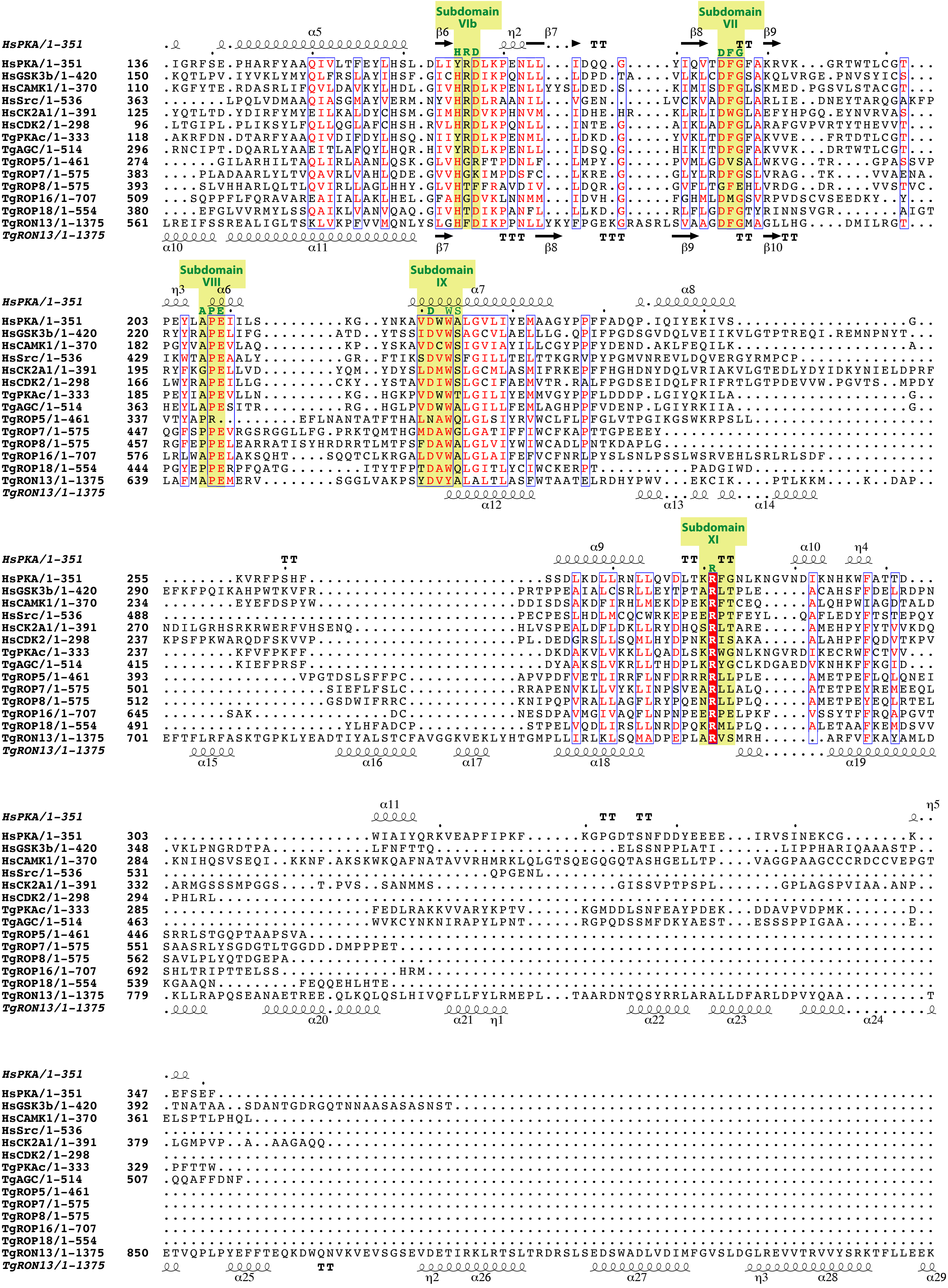
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α11 TT TT η5
α20 α21 η1 α22 α23 α24
α25 TT η2 α26 α27 η3 α28 α29
HsPKA/1-351
HsPKA/1-351 136 .IGRFSE.PHARFYAAQIVLTFEYLHSL.DLIYRDLKPENLL...IDQQ.G.....YIQVTDFGFAKRVK...GRTWTLCGT...
HsGSK3b/1-420 150 .KQTLPV.IYVKLYMYQLFRSLAYIHSF.GICHRDIKPQNLL...LDPD.TA....VLKLCDFGSAKQLVRGE.PNVSYICS...
HsCAMK1/1-370 110 .KGFYTE.RDASRLIFQVLDAVKYLHDL.GIVHRDLKPENLLYYSLDED.S.....KIMISDFGLSKMED.PGSVLSTACGT...
HsSrc/1-536 363 .......LPQLVDMAAQIASGMAYVERM.NYVHRDLRAANIL...VGEN.......LVCKVADFGLARLIE..DNEYTARQGAKFP
HsCK2A1/1-391 125 .YQTLTD.YDIRFYMYEILKALDYCHSM.GIMHRDVKPHNVM...IDHE.HR....KLRLIDWGLAEFYHPGQ.EYNVRVAS...
HsCDK2/1-298 96 .LTGIPL.PLIKSYLFQLLQGLAFCHSH.RVLHRDLKPQNLL...INTE.G.....AIKLADFGLARAFGVPVRTYTHEVVT...
TgPKAc/1-333 118 .AKRFDN.DTARFYAAQIVDIFDYLHSQ.NIIYRDLKPENML...LDKD.G.....YVKLTDFGFAKVVE...FRTDTLCGT...
TgAGC/1-514 296 .RNCIPT.DQARLYAAEITLAFQYLHQR.HIVYRDLKPENLL...IDSQ.G.....HIKITDFGFAKVVK...DRTWTLCGT...
TgROP5/1-461 274 ......GILARHILTAQLIRLAANLQSK.GLVHGRFTPDNLF...LMPY.G.....PVMLGDVSALWKVG..TR....GPASSVP
TgROP7/1-575 383 ....PLADAARLYLTVQAVRLVAHLQDE.GVVHGKIMPDSFC...LKRE.G.....GLYLRDFGSLVRAG..TK....VVAENA.
TgROP8/1-575 393 ....SLVHHARLQLTLQVIRLLAGLHHY.GLVHTFFRAVDIV...LDQR.G.....GVFLTGFEHLVRDG..DR....VVSTVC.
TgROP16/1-707 509 ...SQPPFLFQRAVAREAIIALAKLHEL.GFAHGDVKLNNMM...IDVH.G.....FGHMLDMGSVRPVDSCVSEEDKY..Y...
TgROP18/1-554 380 ....EFGLVVRMYLSSQAIKLVANVQAQ.GIVHTDIKPANFL...LLKD.G.....RLFLGDFGTYRINNSVGR.......AIGT
TgRON13/1-1375 561 LREIFSSREALIGLTSKLVKPFVVMQNLYSLGHFDIKPPNLLYKYFPGEKGRASRLSVAAGDFGMAGLLHG....DMILRGT...
TgRON13/1-1375
HsPKA/1-351
HsPKA/1-351 203 PEYLAPEIILS.........KG..YNKAVDWWALGVLIYEMAAGYPPFFADQP.IQIYEKIVS...................G..
HsGSK3b/1-420 220 RYYRAPELIFG........ATD..YTSSIDVWSAGCVLAELLLG.QPIFPGDSGVDQLVEIIKVLGTPTREQI.REMNPNYT...
HsCAMK1/1-370 182 PGYVAPEVLAQ........KP..YSKAVDCWSIGVIAYILLCGYPPFYDEND.AKLFEQILK....................A..
HsSrc/1-536 429 IKWTAPEAALY........GR..FTIKSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCP................
HsCK2A1/1-391 195 RYFKGPELLVD........YQM..YDYSLDMWSLGCMLASMIFRKEPFFHGHDNYDQLVRIAKVLGTEDLYDYIDKYNIELDPRF
HsCDK2/1-298 166 LWYRAPEILLG........CKY..YSTAVDIWSLGCIFAEMVTR.RALFPGDSEIDQLFRIFRTLGTPDEVVW.PGVTS..MPDY
TgPKAc/1-333 185 PEYIAPEVLLN........KG..HGKPVDWWTLGILIYEMMVGYPPFLDDDP.LGIYQKILA....................G..
TgAGC/1-514 363 HEYLAPESITR........RG..HGLPVDWWALGILLFEMLAGHPPFVDENP.LGIYRKIIA....................G..
TgROP5/1-461 337 VTYAPR.........EFLNANTATFTHALNAWQLGLSIYRVWCLFLPFGLVTPGIKGSWKRPSLL...................
TgROP7/1-575 447 QGFSPPEVRGSRGGLLFG.PRKTQMTHGMDAWGLGATIFFIWCFKAPTTGPEEEY..........................
TgROP8/1-575 457 RGFEPPELEARRATISYHRDRRTLMTFSFDAWALGLVIYWIWCADLPNTKDAPLG..........................
TgROP16/1-707 576 LRLWAPELAKSQHT...SQQTCLKRGALDVWALGLAIFEFVCFNRLPYSLSNLPSSLWSRVEHLSRLRLSDF..........
TgROP18/1-554 444 PGYEPPERPFQATG........ITYTFPTDAWQLGITLYCIWCKERPT..........PADGIWD.................
TgRON13/1-1375 639 LAFMAPEMERV........SGGLVAKPSYDVYALALTLASFWTAATELRDHYPWV...EKCIK....PTLKKM....K..DAP..
TgRON13/1-1375
HsPKA/1-351
HsPKA/1-351 255 ........KVRFPSHF..........................SSDLKDLLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATTD...
HsGSK3b/1-420 290 EFKFPQIKAHPWTKVFR.......................PRTPPEAIALCSRLLEYTPTARLTPLE.....ACAHSFFDELRDPN
HsCAMK1/1-370 234 ........EYEFDSPYW.......................DDISDSAKDFIRHLMEKDPEKRFTCEQ.....ALQHPWIAGDTALD
HsSrc/1-536 488 ....PECPESLHDLMCQCWRKEPEERPTFEYL...QAFLEDYFTSTEPQY
HsCK2A1/1-391 270 NDILGRHSRKRWERFVHSENQ...................HLVSPEALDFLDKLLRYDHQSRLTARE.....AMEHPYFYTVVKDQ
HsCDK2/1-298 237 KPSFPKWARQDFSKVVP.......................PL.DEDGRSLLSQMLHYDPNKRISAKA.....ALAHPFFQDVTKPV
TgPKAc/1-333 237 ........KFVFPKFF.........................DKDAKVLVKKLLQADLSKRWGNLKNGVRDIKECRWFCTVV...
TgAGC/1-514 415 ........KIEFPRSF.........................DYAAKSLVKRLLTHDPLKRYGCLKDGAEDVKNHKFFKGID...
TgROP5/1-461 393 ..............VPGTDSLSFFPC..............APVPDFVETLIRRFLNFDRRRRLLPLE.....AMETPEFLQLQNEI
TgROP7/1-575 501 ....................SIEFLFSLC............RRAPENVKLLVYKLINPSVEARLLALQ.....ATETPEYREMEEQL
TgROP8/1-575 512 ....................GSDWIFRRC............KNIPQPVRALLAGFLRYPQENRLLPLQ.....AMETPEYEQLRTEL
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TgROP18/1-554 491 ......................YLHFADCP............STPELVQDLIRSLLNRDPQKRMLPLQ.....ALETAAFKEMDSVV
TgRON13/1-1375 701 EFTFLRFASKTGPKLYEADTIYALSTCFAVGGKVEKLYHTGMPLLIRLKLSQMADPEPLARVSMRH......ARFVFKAYAMLD
TgRON13/1-1375
HsPKA/1-351
HsPKA/1-351 303 ......................WIAIYQRKVEAPFIPKF......KGPGDTSNFDDYEEEE...IRVSINEKCG.......K..
HsGSK3b/1-420 348 .VKLPNGRDTPA..........LFNFTTQ...................ELSSNPPLATI.......LIPPHARIQAAASTP..
HsCAMK1/1-370 284 .KNIHQSVSEQI..KKNF.AKSKWKQAFNATAVVRHMRKLQLGTSQEGQGQTASHGELLTP....VAGGPAAGCCCRDCCVEPGT
HsSrc/1-536 531 ....QPGENL..
HsCK2A1/1-391 332 .ARMGSSSMPGGS....T.PVS..SANMMS.................GISSVPTPSPL.......GPLAGSPVIAA.ANP..
HsCDK2/1-298 294 .PHLRL..
TgPKAc/1-333 285 ......................FEDLRAKKVVARYKPTV......KGMDDLSNFEAYPDEK...DDAVPVDPMK.......D..
TgAGC/1-514 463 ......................WVKCYNKNIRAPYLPNT......RGPQDSSMFDKYAEST...ESSSPPIGAA.......E..
TgROP5/1-461 446 SRRLSTGQPTAAPSVA..
TgROP7/1-575 551 SAASRLYSGDGTLTGGDD.DMPPPET..
TgROP8/1-575 562 SAVLPLYQTDGEPA..
TgROP16/1-707 692 SHLTRIPTTELSS............HRM..
TgROP18/1-554 539 KGAAQN..........FEQQEHLHTE..
TgRON13/1-1375 779 .KLLRAPQSEANAETREE.QLKQLQSLHIVQFLLFYLRMEPL...TAARDNTQSYRRLARALLDFARLDPVYQAA.........T
TgRON13/1-1375
HsPKA/1-351
HsPKA/1-351 347 .EFSEF..
HsGSK3b/1-420 392 .TNATAA..SDANTGDRGQTNNAASASASNST..
HsCAMK1/1-370 361 ELSPTLPHQL..
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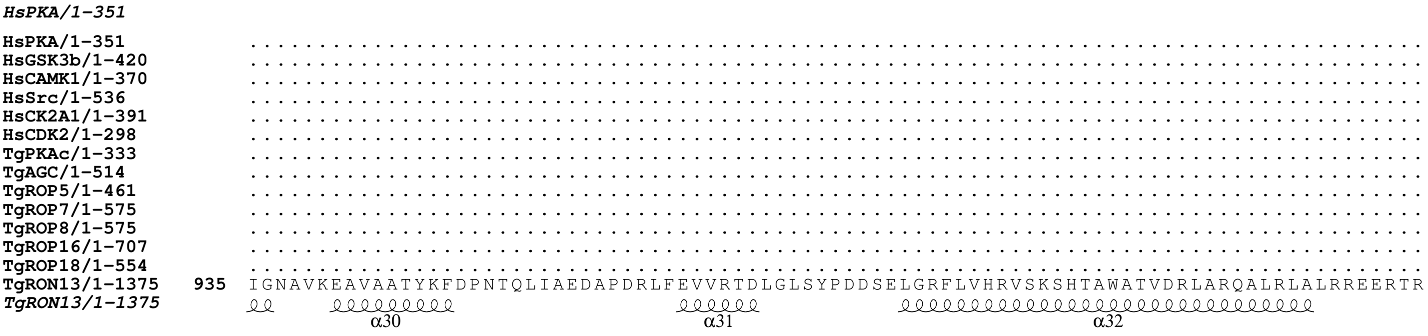
HsCK2A1/1-391 379 .LGMPVP..A..AAGAQQ..
HsCDK2/1-298 ....
TgPKAc/1-333 329 .PFTTW..
TgAGC/1-514 507 .QQAFFDNF...
TgROP5/1-461 ....
TgROP7/1-575 ....
TgROP8/1-575 ....
TgROP16/1-707 ....
TgROP18/1-554 ....
TgRON13/1-1375 850 ETVQPLPYEFFTEQKDWQNVKVEVSGSEVDETIRKLRTSLTRDRSLSEDSWADLVDIMFGVSLDGLREVVTRVVYSRKTFLLEEK
TgRON13/1-1375



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HsPKA/1-351

HsPKA/1-351              .....................................................................................
HsGSK3b/1-420            .....................................................................................
HsCAMK1/1-370            .....................................................................................
HsSrc/1-536              .....................................................................................
HsCK2A1/1-391            .....................................................................................
HsCDK2/1-298             .....................................................................................
TgPKAc/1-333             .....................................................................................
TgAGC/1-514              .....................................................................................
TgROP5/1-461             .....................................................................................
TgROP7/1-575             .....................................................................................
TgROP8/1-575             .....................................................................................
TgROP16/1-707            .....................................................................................
TgROP18/1-554            .....................................................................................
TgRON13/1-1375      935  IGNAVKEAVAATYKFDPNTQLIAEDAPDRLFEVVRTDLGLSYPDDSELGRFLVHRVSKSHTAWATVDRLARQALRLALRREERTR
TgRON13/1-1375
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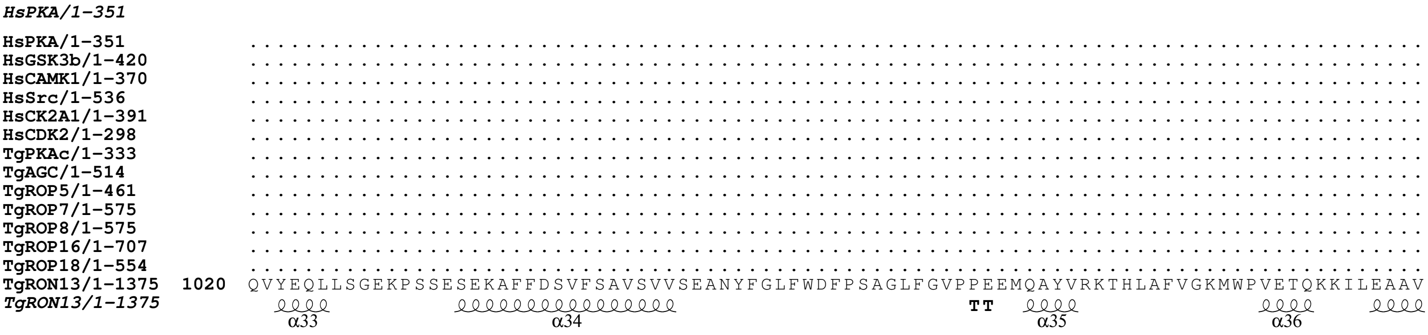

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HsPKA/1-351

HsPKA/1-351              .....................................................................................
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TgROP7/1-575             .....................................................................................
TgROP8/1-575             .....................................................................................
TgROP16/1-707            .....................................................................................
TgROP18/1-554            .....................................................................................
TgRON13/1-1375     1020  QVYEQLLSGEKPSSESEKAFFDSVFSAVSVVSEANYFGLFWDFPSAGLFGVPPEEMQAYVRKTHLAFVGKMWPVETQKKILEAAV
TgRON13/1-1375
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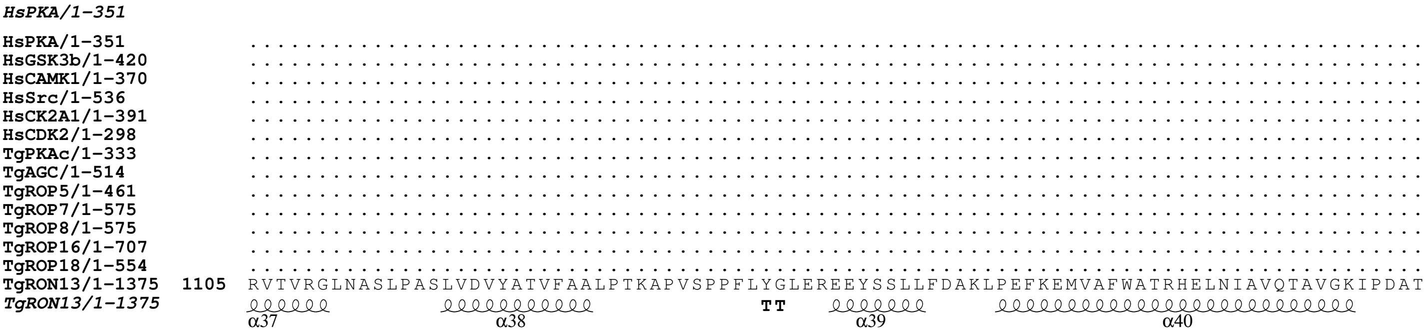

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HsPKA/1-351

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HsSrc/1-536              .....................................................................................
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TgROP5/1-461             .....................................................................................
TgROP7/1-575             .....................................................................................
TgROP8/1-575             .....................................................................................
TgROP16/1-707            .....................................................................................
TgROP18/1-554            .....................................................................................
TgRON13/1-1375     1105  RVTVRGLNASLPASLVDVYATVFAALPTKAPVSPPFLYGLEREEYSSLLFDAKLPEFKEMVAFWATRHELNIAVQTAVGKIPDAT
TgRON13/1-1375
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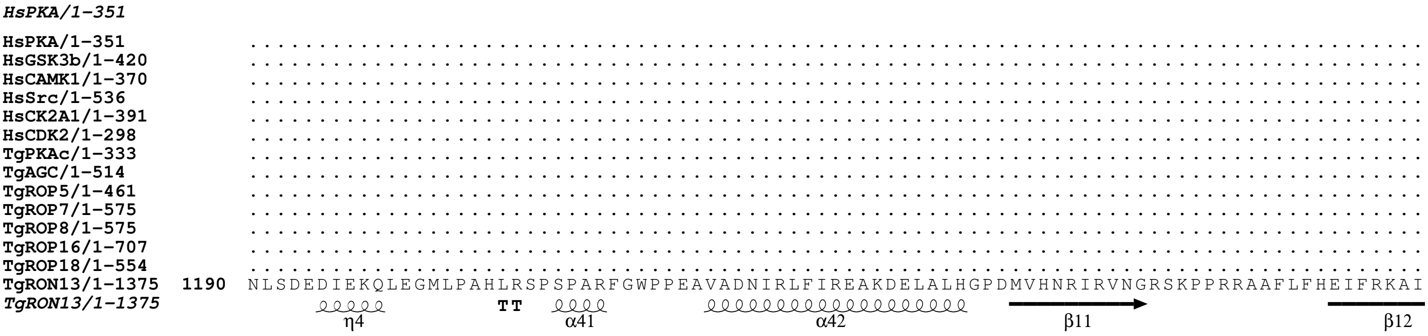

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HsPKA/1-351

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HsCAMK1/1-370            .....................................................................................
HsSrc/1-536              .....................................................................................
HsCK2A1/1-391            .....................................................................................
HsCDK2/1-298             .....................................................................................
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TgAGC/1-514              .....................................................................................
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TgROP7/1-575             .....................................................................................
TgROP8/1-575             .....................................................................................
TgROP16/1-707            .....................................................................................
TgROP18/1-554            .....................................................................................
TgRON13/1-1375     1190  NLSDEDIEKQLEGMLPAHLRSPSPARFGWPPEAVADNIRLFIREAKDELALHGPDMVHNRIRVNGRSKPPRRAAFLFHEIFRKAI
TgRON13/1-1375
```

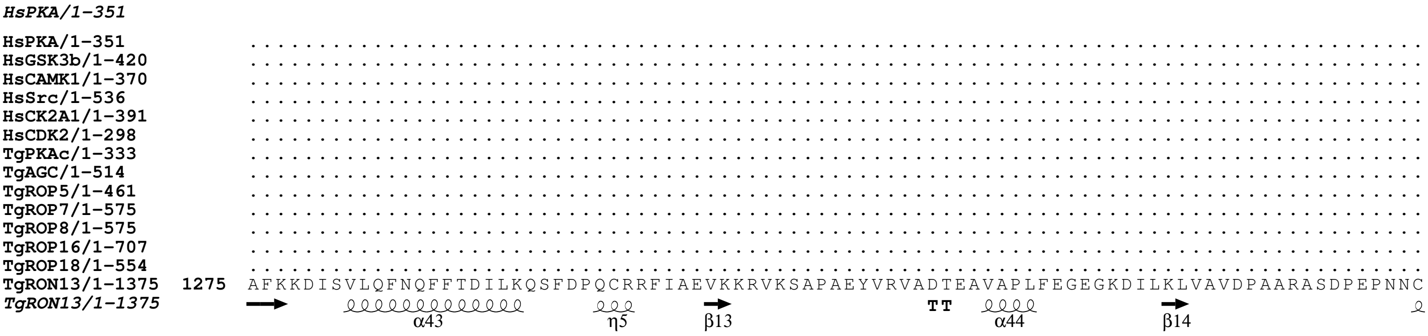

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HsPKA/1-351

HsPKA/1-351              .....................................................................................
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HsSrc/1-536              .....................................................................................
HsCK2A1/1-391            .....................................................................................
HsCDK2/1-298             .....................................................................................
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TgAGC/1-514              .....................................................................................
TgROP5/1-461             .....................................................................................
TgROP7/1-575             .....................................................................................
TgROP8/1-575             .....................................................................................
TgROP16/1-707            .....................................................................................
TgROP18/1-554            .....................................................................................
TgRON13/1-1375     1275  AFKKDISVLQFNQFFTDILKQSFDPQCRRFIAEVKKRVKSAPAEYVRVADTEAVAPLFEGEGKDILKLVAVDPAARASDPEPNNC
TgRON13/1-1375
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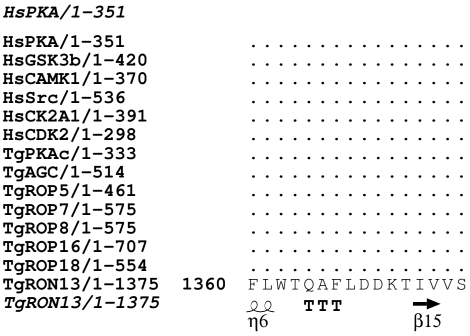

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HsPKA/1-351

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HsCAMK1/1-370             . . . . . . . . . . . . . . . .
HsSrc/1-536               . . . . . . . . . . . . . . . .
HsCK2A1/1-391             . . . . . . . . . . . . . . . .
HsCDK2/1-298              . . . . . . . . . . . . . . . .
TgPKAc/1-333              . . . . . . . . . . . . . . . .
TgAGC/1-514               . . . . . . . . . . . . . . . .
TgROP5/1-461              . . . . . . . . . . . . . . . .
TgROP7/1-575              . . . . . . . . . . . . . . . .
TgROP8/1-575              . . . . . . . . . . . . . . . .
TgROP16/1-707             . . . . . . . . . . . . . . . .
TgROP18/1-554             . . . . . . . . . . . . . . . .
TgRON13/1-1375      1360  F L W T Q A F L D D K T I V V S
TgRON13/1-1375                      T T T
                          η6                    β15
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