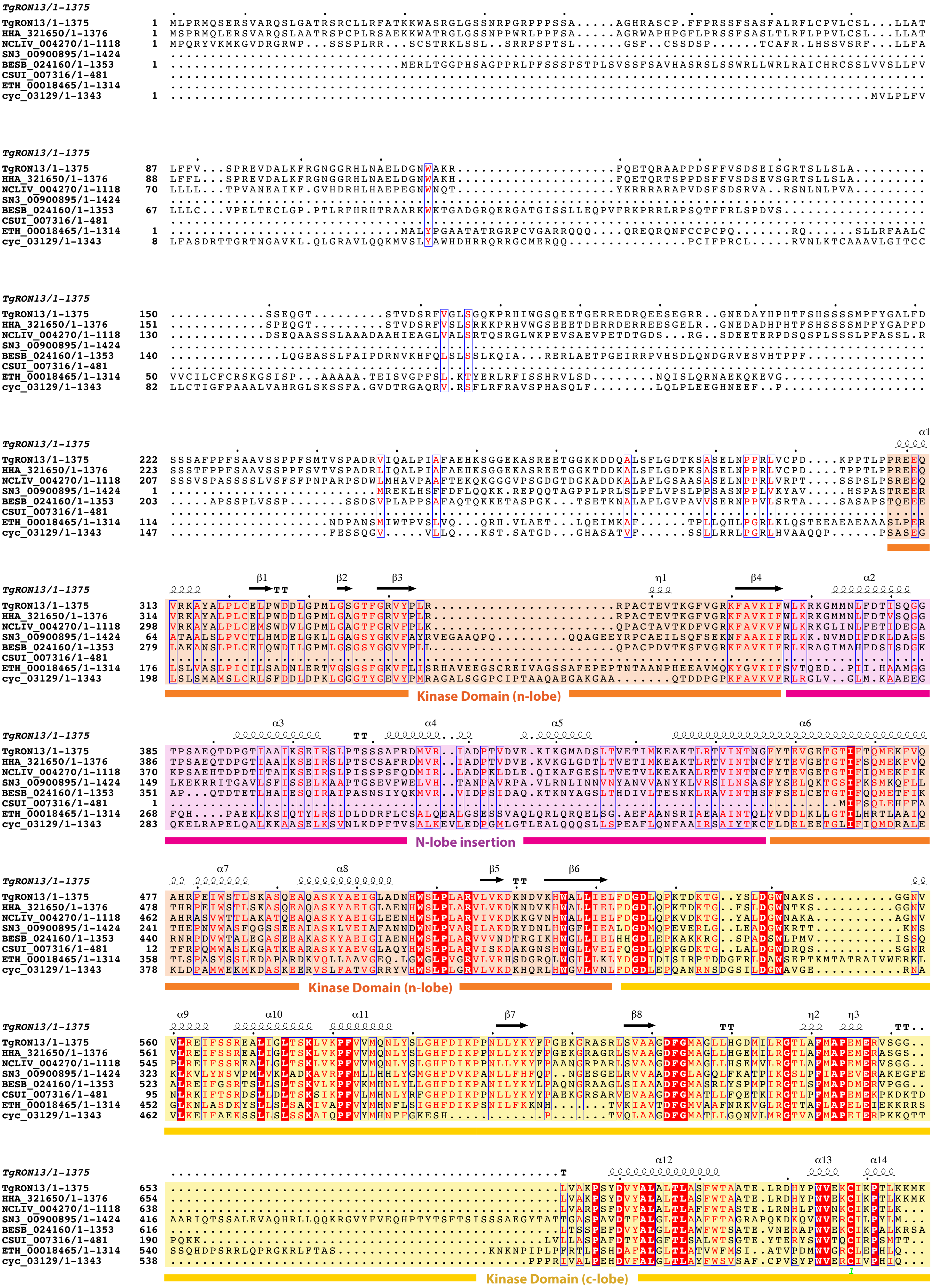

```
TgRON13/1-1375
TgRON13/1-1375         1 MLPRMQSERSVARQSLGATRSRCLLRFATKKWASRGLGSSNRPGRPPPSSA.....AGHRASCP.FFPRSSFSASFALRFLCPVLCSL...LLAT
HHA_321650/1-1376      1 MSPRMQLERSVARQSLAATRSPCPLRSAEKKWATRGLGSSNPPWRLPPFSA.....AGRWAPHPGFLPRSSFSASLTLRFLPPVLCSL...LLAT
NCLIV_004270/1-1118    1 MPQRYVKMKGVDRGRWP...SSSPLRR...SCSTRKLSSL..SRRPSPTSL......GSF..CSSDSP......TCAFR.LHSSVSRF...LLFA
SN3_00900895/1-1424      ...............................................................................................
BESB_024160/1-1353     1 .............................MERLTGGPHSAGPPRLPFSSSPSTPLSVSSFSAVHASRSLSSWRLLWRLRAICHRCSSLVVSLLFV
CSUI_007316/1-481        ...............................................................................................
ETH_00018465/1-1314      ...............................................................................................
cyc_03129/1-1343       1 ........................................................................................MVLPLFV

TgRON13/1-1375
TgRON13/1-1375        87 LFFV...SPREVDALKFRGNGGRHLNAELDGNWAKR....................FQETQRAAPPDSFFVSDSEISGRTSLLSLA.........
HHA_321650/1-1376     88 LFFL...SPREVDALKFRGNGGRHLNAELDGNWAKH....................FQETQRTSPPDSFFVSDSEVSGRTSLLSLA.........
NCLIV_004270/1-1118   70 LLLL...TPVANEAIKF.GVHDRHLHAEPEGNWNQT....................YKRRRARAPVDSFSDSRVA..RSNLNLPVA.........
SN3_00900895/1-1424      ...............................................................................................
BESB_024160/1-1353    67 LLLC...VPELTECLGP.PTLRFHRHTRAARKWKTGADGRQERGATGISSLLEQPVFRKPRRLRPSQTFFRLSPDVS..................
CSUI_007316/1-481        ...............................................................................................
ETH_00018465/1-1314    1 .............................MALYPGAATATRGRPCVGARRQQQ....QREQRQNFCCPCPQ.......RQ......SLLRFAALC
cyc_03129/1-1343       8 LFASDRTTGRTNGAVKL.QLGRAVLQQKMVSLYAWHDHRRQRRGCMERQQ...............PCIFPRCL.....RVNLKTCAAAVLGITCC

TgRON13/1-1375
TgRON13/1-1375       150 ............SSEQGT.........STVDSRFVGLSGQKPRHIWGSQEETGERREDRQEESEGRR..GNEDAYHPHTFSHSSSSMPFYGALFD
HHA_321650/1-1376    151 ............SPEQGT.........STVDSRFVSLSRKKPRHVWGSEEETDERRDERREESGELR..GNEDADHPHTFSHSSSSMPFYGAPFD
NCLIV_004270/1-1118  130 ............DSEQAASSSLAAADAAHIEAGLVALSRTQSRGLWKPEVSAEVPETDTGDS...RG..SDEETERPDSQSPLSSSLPFASSL.R
SN3_00900895/1-1424      ...............................................................................................
BESB_024160/1-1353   140 ..............LQGEASSLFAIPDRNVKHFQLSLSSLKQIA...RERLAETPGEIRRPVHSDLQNDGRVESVHTPPF...............
CSUI_007316/1-481        ...............................................................................................
ETH_00018465/1-1314   50 VVCILCFCRSKGSISP...AAAAA.TEISVGPFSL.KTYERLRFISSHRVLSD........NQISLQRNAEKQKEVG..................
cyc_03129/1-1343      82 LLCTIGFPAAALVAHRGLSKSSFA.GVDTRGAQRV.RSFLRFRAVSPHASQLF........LQLPLEEGHNEEF..P..................

TgRON13/1-1375
TgRON13/1-1375       222 SSSAFPPFSAAVSSPPFSMTVSPADRVIQALPIAFAEHKSGGEKASREETGGKKDDQALSFLGDTKSASELNPPRLVCPD....KPPTLPPREEQ
HHA_321650/1-1376    223 SSSTFPPFSAAVSSPPFSVTVSPADRLIQALPIAFAEHKSGGEKASREETGGKTDDKALSFLGDPKSASELNPPRLVCPD....TPPTLPPREEQ
NCLIV_004270/1-1118  207 SSSVSPASSSSLVSFSFPNPARPSDWLMHAVPAAFTEKQKGGGVPSGDGTDGKADDKALAFLGSAASASELNPPRLVRPT....SSPSLPSREEQ
SN3_00900895/1-1424    1 ..........................MREKLHSFFDFLQQKK.REPQQTAGPPLPRLSLPFLVPSLPPSASNPPLVKYAV.....HSPASTREER
BESB_024160/1-1353   203 .....APSSPLVSSP.......SSDSVPLAPPSAFAQTQKKETASPGK...TSETKNALAFLGVPAVVSERNPPVLSRTA....SASAPSTQEEE
CSUI_007316/1-481        ...............................................................................................
ETH_00018465/1-1314  114 ....................NDPANSMIWTPVSLVQ...QRH.VLAET...LQEIMKAF......TPLLQHLPGRLKLQSTEEAEAEAAASLPER
cyc_03129/1-1343     147 ....................FESSQGV.....VLLQ...KST.SATGD...GHASATVF......SSLLRRLPGRLHVAAQQP......PSASEG

TgRON13/1-1375
TgRON13/1-1375       313 VRKAYALPLCELPWDDLGPMLGSGTFGRVYPLR.......................RPACTEVTKGFVGRKFAVKIFWLKRKGMMNLFDTISQGG
HHA_321650/1-1376    314 VRKAYALPLCELPWDDLGPMLGAGTFGRVYPLR.......................RPACTEVTKGFVGRKFAVKIFWLKRKGMMNLFDTVSQGG
NCLIV_004270/1-1118  298 VRKAYALPLCEMSWDVLGPMLGAGTFGRVFPLK.......................QPACTAVTKDFVGRKFAVKVFWLKRKGLINLFETIDEGA
SN3_00900895/1-1424   64 ATAALSLPVCTLHMDELGKLLGAGSYGKVFAYRVEGAAQPQ.........QQAGEEYRPCAEILSQFSEKNFAAKIFRLKK.NVMDIFDKLDAGS
BESB_024160/1-1353   279 LAKANSLPLCEIQWDILGPMLGSGSYGGVYPLL.......................QPACPDVTKSFVGRKFAVKIFRLKRAGIMAHFDSISDGK
CSUI_007316/1-481        ...............................................................................................
ETH_00018465/1-1314  176 LSLVASLPICILSADNLERTVGSGSFGKVFLISRHAVEEGSCREIVAGSSAFEPEPTNTAANPHEEAVMQKYGVKIFSVTQED..PII.HAAMGG
cyc_03129/1-1343     198 LSLSMAMSLCRLSFDDLDPKLGGGTYGEVYPMRAGALSGGPCIPTAAQAEGAKGAA.......QTDDPGPKFAVKVFRLRGLV..GLM.KAAEEG

TgRON13/1-1375
TgRON13/1-1375       385 TPSAEQTDPGTIAAIKSEIRSLPTSSSAFRDMVR..IADPTVDVE.KIKGMADSLTVETIMKEAKTLRTVINTNGFYTEVGETGTIFTQMEKFVQ
HHA_321650/1-1376    386 TPSAEQTDPGTIAAIKSEIRSLPTSCSAFRDMVR..IADPTVDVE.KVKGLGDTLTVETIMKEAKTLRTVINTNCFYTEVGETGTIFSQMEKFVQ
NCLIV_004270/1-1118  370 KPSAEHTDPDTITAIKSEIRSLPISSPSFQDMIR..LADPKLDLE.QIKAFGESLTVETVLKEAKALRTVINTNCFYTEVGETGTIFIQMEKFIK
SN3_00900895/1-1424  149 LKEKRRITGAVLSFISSELKAAPTGSEVFWELVH..TANPAVRPA.VLRNLINNVNYANVVANYKLVRSILNSASFYSELQKTGSIFKSMKQFLL
BESB_024160/1-1353   351 AP...QTDTETLHAIESQIRAIPASNSIYQKMVR..VIDPSIDAQ.KTKNYAGSLTHDIVLTESNKLRAVINTHSFFSELCETGTIFQQMETFIK
CSUI_007316/1-481      1 ....................................................................................MIFSQLEHFFA
ETH_00018465/1-1314  268 FQH....PAEKLKSIQTYLRSIDLDDRFLCSALQEALGSESSVAQLQRLQRQELSG.AEFAANSRIAEAAINTQLYVDDLKLLGTILHRTLAAIQ
cyc_03129/1-1343     283 QKELRAPELQALKKAASELKSVNLKDPFTVSALKEVLEDPGMLGTLEALQQQSLLSPEAFLQNFAAIRSAIYTKCFLDELEETGLIFIQMDRALE

TgRON13/1-1375
TgRON13/1-1375       477 AHRPEIWSTLSKASQEAQASKYAEIGLADNHWSLPLARVLVKDKNDVKHWALLIELFDGDLQPKTDKTG..YSLDGWNAKS..........GGNV
HHA_321650/1-1376    478 THRPEIWSTLSKASQEAQASKYAEIGLAENHWSLPLARVLVKDKNDVKHWALLIELFDGDLQPKTDKTG..FSLDGWNTKS..........GGNV
NCLIV_004270/1-1118  462 AHRASVWTTLAKATQEAQASKYAEIGLEENHWSLPLARVIVKDKKGVNHWALLIELFDGDLQPKVDKTG..YALDGWNAKA..........AGNV
SN3_00900895/1-1424  241 THEPNVWASFQGSSEEAIASKLVEIAFANNDWNLPVARILAKDRYDNLHWGFLIEALDGDMQPEVERLG..LEADGWKRTT...........KNS
BESB_024160/1-1353   440 RNRPDVWTALEGASEEAKASKYAEIGIAENHWSLPLARVVVNDTRGIKHWGLLIELHHGDLEPKAKKRG..SPADSWLPMV..........ISSQ
CSUI_007316/1-481     12 TFRPQMWASLKGATKEARASKYAEVGLAQYHWSLPLARVISKDAKGNSHWGLLVELFQGDLQPKGDKTG..LALDGWDRQS..........SGNR
ETH_00018465/1-1314  358 TLSPASYSSLEDAPARDKVQLLAAVGEQ.LGWGLPVGRVLVRHSDGRQLWGILLKLYDGDIDISIRPTDDGFRLDAWSEPTKMTATRAIVWERKL
cyc_03129/1-1343     378 KLDPAMWEKMKDASKEERVSLFATVGRRYVHWSLPLGRVLVKDKHQRLHWGVLVNLFDGDLEPQANRNSDGSILDGWAVGE...........RNA

TgRON13/1-1375
TgRON13/1-1375       560 VLREIFSSREALIGLTSKLVKPFVVMQNLYSLGHFDIKPPNLLYKYFPGEKGRASRLSVAAGDFGMAGLLHGDMILRGTLAFMAPEMERVSGG..
HHA_321650/1-1376    561 VLREIFSSREALIGLTSKLVKPFVVMQNLYSLGHFDIKPPNLLYKYFPGEKGRAGRLSVAAGDFGMAGLLHGEMILRGTLAFMAPEMERASGS..
NCLIV_004270/1-1118  545 PLREIFSSREALLGLTSKLVKPFVVMQNLYSLGHFDIKPPNLLYKYFPAANGRPARLSVAAGDFGMAGLLHSEMVLRGTLAFMAPEMERVSGG..
SN3_00900895/1-1424  323 KLKVLYNSVPMLVKLADKAVRPFMLLHHLYGMGHFDVKPANLLFHFQP..NGESGELRVVAADFGLAGQLFKATPIKGSLPFIAPEVERAKEGFE
BESB_024160/1-1353   523 ALREIFGSRTSLLSLTSKVLKPFVKMHNLYLLGHFDIKPANILYKYLPAQNGRAAGLSIAAADFGMASRLYSPMPIRGTLSFMAPDMERVPGG..
CSUI_007316/1-481     95 NLRKIFTSRDSLLDLTSKSIKPFVLMHNLYRFGHFDIKPPNLLYKYYPAEKGRSARVEVAAGDFGMATLLFQETKIRGTLPFMAPEMEKPKDKTD
ETH_00018465/1-1314  452 GLKNLASDKYSLLSLSAKIVAPFVYMHNFLSIGHFDIKPSNILFKKNH.......TVKIAVTDFGMVAAFNRKVGLRGTTAFLAPELEIEKKRRS
cyc_03129/1-1343     462 VLKEIFAEKSSLLSLSSKAIQPFVYMHNFFGKESH............P.......TVQLAAGDFGMATLLGQNVLMRGTVAFMAPEIERPKKQTT

TgRON13/1-1375
TgRON13/1-1375       653 .................................................LVAKPSYDVYALALTLASFWTAATE.LRDHYPWVEKCIKPTLKKMK
HHA_321650/1-1376    654 .................................................LVAKPSYDVYALALTLASFWTAATE.LRDHYPWVEKCIKPTLKKMK
NCLIV_004270/1-1118  638 .................................................LVARPSFDVYALALTLAFFWTASTE.LRNHLPWVNKCIKPTLK...
SN3_00900895/1-1424  416 AARIQTSSALEVAQHRLLQQKRGVYFVEQHPTYTSFTSISSSAEGYTATTGASPAVDTFALGLTLAAFFTAGRAPQKDKQVWVEKCILPYLM...
BESB_024160/1-1353   616 .................................................LTSSPEFDVYALGLTLAWFWTSATE.VNERAPWVERCILPALKRSA
CSUI_007316/1-481    190 PQKK...........................................LVLLASPAFDTYALGFTLSALWTSGTE.YTERYSWVTQCIRPSMTT..
ETH_00018465/1-1314  540 SSQHDPSRRLQPRGKRLFTAS...................KNKNPIPLPFRTLPSHDAFALGLTLATVWFMSI..ATVPDMWVGRCLEPHLQ...
cyc_03129/1-1343     538 .............................................PPPRIVALPEHDVFALGLTLAYFWSVSAF.CPVSYPWVERCIVPHIQ...
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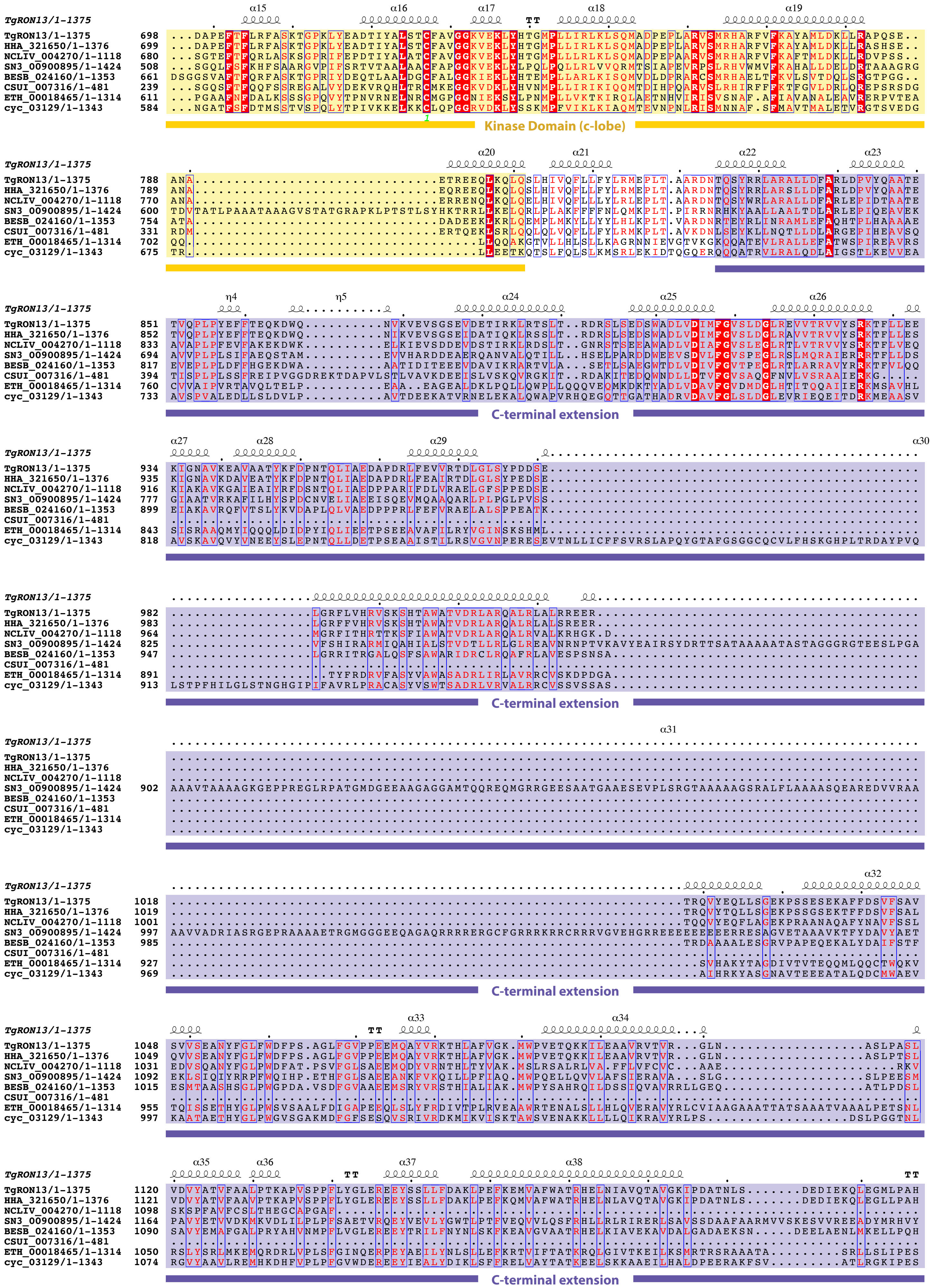

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TgRON13/1-1375        α15  α16  α17  TT  α18  α19
TgRON13/1-1375   698  ...DAPEFTFLRFASKTGPKLYEADTIYALSTCFAVGGKVEKLYHTGMPLLIRLKLSQMADPEPLARVSMRHARFVFKAYAMLDKLLRAPQSE..
HHA_321650/1-1376 699  ...DAPEFTFLRFASKTGPKLYEADTIYALSTCFAVGGKVEKLYHTGMPLLIRLKLSQMADPEPLARVSMRHARFVFKAYAMLDKLLRASHSE..
NCLIV_004270/1-1118 680  ...SGTEFTFQRLASKSGPRIFEPDTIYALATCFAVGGKVEKLYHTGMPLLLRLKLSQMADPEPAARVSMRHARFVFKAFTMLDKLLRDVPSS..
SN3_00900895/1-1424 508  ...SGQLFSFKHFSAARGVPIFSRTVTAALAACFAPGGKVEKLYLPQLPQLLRLVVQRMTSIAPEVRPSLRHVWMVFKAHALLDELDRTAAAGRG
BESB_024160/1-1353 661  DSGGSVAFTFQRFASKTGPRIYDEQTLAALDGCFALGGKIEKLYHTEMPLLARLKISQMVDLDPRARCSMRHAELTFKVLSVTDQLSRGTPGG..
CSUI_007316/1-481 239  ...SGQSFTFQQFSSREGALVYDEKVRQHLTRCMKEGGKVDKLYHVNMPLLIRIKIQQMTDIHPQARVSLRHIRFFFKTFGVLDRLQREPSRSDG
ETH_00018465/1-1314 611  ...PGAAFNFDALKSSSGPQVYTPNVRNELNRCMGPGGNIEKSYLPNMPLLVKTKIRQLAETNHVIRISVSNAF.AFIAVANALEAVRERPVTEA
cyc_03129/1-1343 584  ...NGATFSFDTMSSTVSPQLYTPIVKKELKKCLQPGGRVDKLYSSKMPFVIKLKIAQMTEVNPNLRISMNNAF.SFMAVTMALETVRGTSVEDG
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1

Kinase Domain (c-lobe)

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TgRON13/1-1375        α20  α21  α22  α23
TgRON13/1-1375   788  ANA...............................ETREEQLKQLQSLHIVQFLLFYLRMEPLT.AARDNTQSYRRLARALLDFARLDPVYQAATE
HHA_321650/1-1376 789  ANA...............................EQREEQLKQLQSLHIVQFLLFYLRMEPLT.AARDNTQSYRRLARSLLDFARLDPVYQAATE
NCLIV_004270/1-1118 770  ANA...............................ERRENQLKQLQELHIVQFLLLYLRLEPLT.AARDNTQSYWRLARALLDFARLEPIDTAATE
SN3_00900895/1-1424 600  TDVTATLPAAATAAAGVSTATGRAPKLPTSTLSYHKTRRLLKELQRLPLAKFFFFNLQMKPLT.PIRRNRHKYAALLAALTDLARLEPIQEAVEK
BESB_024160/1-1353 754  ATA...............................DADEEKLKRLQEMPLMKYLLYYLHLKPLT.VARDNRTEYRLINRAMLEFAQHTPLHAAAAE
CSUI_007316/1-481 331  RDM...............................ERTQEKLSRLQQLQLVQFLLFYLRMKPLT.AVKDNLSEYKLLNQTLLDLARGEPIHEAVSQ
ETH_00018465/1-1314 702  QQ.....................................LLQQAKGTVLLHLSLLKAGRNNIEVGTVKGKQQATEVLRALLEFATWSPIREAVRS
cyc_03129/1-1343 675  TR.....................................LLEETKQTSLFQLSLKMSRLEKIDTQGQERQQQATRVLRALQDLAIGSTLKEVVEA
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TgRON13/1-1375        η4  η5  α24  α25  α26
TgRON13/1-1375   851  TVQPLPYEFFTEQKDWQ..........NVKVEVSGSEVDETIRKLRTSLT..RDRSLSEDSWADLVDIMFGVSLDGLREVVTRVVYSRKTFLLEE
HHA_321650/1-1376 852  TVQPLPYEFFTEQKDWQ..........NIKVEVSGSEIDATIQKLRSSLT..RDRSLSEDSWADLVDIMFGVSLDGLRAVVTRVVYSRKTFLLES
NCLIV_004270/1-1118 833  AVAPLPFEVFAKEKDWK..........ELKIEVSDDEVDSTIRKLRDSLT..GNRSTSEEAWADLVDIAFGVSLEGLRTLVTRVVYSRKTFLVEQ
SN3_00900895/1-1424 694  AVVPLPLSIFAEQSTAM..........EVVHARDDEAERQANVALQTILL..HSELPARDDWEEVSDVLFGVSPEGLRSLMQRAIERRRTFLLDS
BESB_024160/1-1353 817  EVEPLPLDFFHGEKDWA..........AATIDITEEEVDAVIKRARTVLA...SETLSAEGWTDLVDIVFGVTPEGLRTLARRAVYRRKTFVLQQ
CSUI_007316/1-481 394  TISPLPLSSFREIPVGGDREKTDAPVLSTLVAVKDEEISLVSKQVRGKIT..RDAKITEDQWNDLLDTVFGVSAQGFNVLVSRAAIERKG.....
ETH_00018465/1-1314 760  CVVAIPVRTAVQLTELP..........EAA..EAGEALDKLPQLLQWPLLQQQVEQMKDKTYADLVDAVFGVDMDGLHTITQQAIIERKMSAVHL
cyc_03129/1-1343 733  AVSPVALEDLLSLDVLP..........AVTDEEKATVRNELEKALQWAPVRHQEGQTTGATHADRVDAVFGLSLDGLEVRIEQEITDRKMEAASV
```

C-terminal extension

```
TgRON13/1-1375        α27  α28  α29  α30
TgRON13/1-1375   934  KIGNAVKEAVAATYKFDPNTQLIAEDAPDRLFEVVRTDLGLSYPDDSE...............................................
HHA_321650/1-1376 935  KIGNAVKDAVEATYKFDPNTQLIAEDAPDRLFEAIRTDLGLSYPEDSE...............................................
NCLIV_004270/1-1118 916  KIAKAVKGAIEAIYRFDSNTQLIAEDPPARIFDLVRAELGFSPPEDSE...............................................
SN3_00900895/1-1424 777  GIAATVRKAFILHYSPDCNVELIAEEISQEVMQAAQARLPLPGLPVSS...............................................
BESB_024160/1-1353 899  EIAKAVRQFVTSLYKVDAPLQLVAEDPPPRLFEFVRAELALSPPEATK...............................................
CSUI_007316/1-481      ...............................................................................................
ETH_00018465/1-1314 843  SISRAAQMYIQQQLDIDPYIQLIEETPSEEAVAFILRYVGINSKSHML...............................................
cyc_03129/1-1343 818  AVSKAVQVYVNEEYSLEPNTQLLDETPSEAAISTILRSVGVNPERESEVTNLLICFFSVRSLAPQYGTAFGSGGCQCVLFHSKGHPLTRDAYPVQ
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```
TgRON13/1-1375
TgRON13/1-1375   982  ..................LGRFLVHRVSKSHTAWATVDRLARQALRLALRREER.........................................
HHA_321650/1-1376 983  ..................LGRFFVHRVSKSHTAWATVDRLARQALRLALSREER.........................................
NCLIV_004270/1-1118 964  ..................MGRFITHRTTKSFIAWATVDRLARQALRVALKRHGK.D.......................................
SN3_00900895/1-1424 825  ..................VFSHIRARMIQAHIALSTVDTLLRLGLREAVNRNPTVKAVYEAIRSYDRTTSATAAAAATASTAGGGRGTEESLPGA
BESB_024160/1-1353 947  ..................LGRRITRGALQSFSAWARIDRCLRQAFRLAVESPSNSA.......................................
CSUI_007316/1-481      ...............................................................................................
ETH_00018465/1-1314 891  ....................TYFRDRVFASYVAWASADRLIRLAVRRCVSKDPDGA.......................................
cyc_03129/1-1343 913  LSTPFHILGLSTNGHGIPIFAVRLPRACASYVSWTSADRLVRVALRRCVSSVSSAS.......................................
```

C-terminal extension

```
TgRON13/1-1375        α31
TgRON13/1-1375        ...............................................................................................
HHA_321650/1-1376      ...............................................................................................
NCLIV_004270/1-1118    ...............................................................................................
SN3_00900895/1-1424 902  AAAVTAAAAGKGEPPREGLRPATGMDGEEAAGAGGAMTQQREQMGRRGEESAATGAAESEVPLSRGTAAAAAGSRALFLAAAASQEAREDVVRAA
BESB_024160/1-1353     ...............................................................................................
CSUI_007316/1-481      ...............................................................................................
ETH_00018465/1-1314    ...............................................................................................
cyc_03129/1-1343       ...............................................................................................
```

```
TgRON13/1-1375        α32
TgRON13/1-1375  1018  .................................................................TRQVYEQLLSGEKPSSESEKAFFDSVFSAV
HHA_321650/1-1376 1019  .................................................................TRQVYTQLLSGEKPSSGSEKTFFDSVFSAL
NCLIV_004270/1-1118 1001  .................................................................TQQVYEQFLAGEKPRAANAQAFYNAVFSSL
SN3_00900895/1-1424 997  AAVVADRIASRGEPRAAAAETRGMGGGEEQAGAQRRRRERGCFGRRRKRRCRRRVGVEHGRREEEEEEEEERRESAGVETAAAVKTFYDAVYAET
BESB_024160/1-1353 985  .................................................................TRDAAAALESGRVPAPEQEKALYDAIFSTF
CSUI_007316/1-481      ...............................................................................................
ETH_00018465/1-1314 927  ...................................................................SVHAKYTAGDIVTVTEQQMLQQCTWQKV
cyc_03129/1-1343 969  ...................................................................AIHRKYASGNAVTEEEATALQDCMWAEV
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C-terminal extension

```
TgRON13/1-1375        TT  α33  α34
TgRON13/1-1375  1048  SVVSEANYFGLFWDFPS.AGLFGVPPEEMQAYVRKTHLAFVGK.MWPVETQKKILEAAVRVTVR...GLN..................ASLPASL
HHA_321650/1-1376 1049  QVVSEANYFGLFWDFPS.AGLFGVPPEEMQAYVRKTHLAFVGK.MWPVETQKKILEAAVRVTVR...GLN..................ASLPTSL
NCLIV_004270/1-1118 1031  EDVSQANYFGLPWDFAT.PSVFGLSAEEMQDYVRNTHLTYVAK.MSLRSALRLVA.FFLVFCVC...AAE......................RKV
SN3_00900895/1-1424 1092  EKLSIQIYRRPFWQIHP.ETHFGLSAEEANKFVKQILLPFIAQ.MWPQELLQVVLAFSIERAVA...SLG..................SLPEESM
BESB_024160/1-1353 1015  ESMTAASHSGLPWGPDA.VSDFGVAAEEMSRYVRSTHIALIAK.MWPYSAHRQILDSSIQVAVRRLLGEQ..................ATLPDSL
CSUI_007316/1-481      ...............................................................................................
ETH_00018465/1-1314 955  TQISSETHYGLPWSVSAALFDIGAPEEQLSLYFRDIVTPLRVEAAWRTENALSLLHLQVERAVYRLCVIAAGAAATTATSAAATVAAALPETSNL
cyc_03129/1-1343 997  KAATAETHYGLPWGVSGAKMDFGFSESQVSRIVRDKMIKVISKTAWSVENAKKLLLLQIKRAVYRLPS..................DSLPGGTNL
```

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TgRON13/1-1375        α35  α36  TT  α37  α38  TT
TgRON13/1-1375  1120  VDVYATVFAALPTKAPVSPPFLYGLEREEYSSLLFDAKLPEFKEMVAFWATRHELNIAVQTAVGKIPDATNLS.......DEDIEKQLEGMLPAH
HHA_321650/1-1376 1121  VDVYATVFAAVPTKAPVSPPFLYGLEREEYSSLLFDAKLPEFKQMVAFWATRHELNLAVQTAVGKIPDATNLS.......DEDIEKQLEGLLPAH
NCLIV_004270/1-1118 1098  SKSPFAVFCSLTHEGCAPGAF..........................................................................
SN3_00900895/1-1424 1164  PAVYETVVDKMKVDLILPLPFSAETVRQEYVEVLYGWTLPTFVEQVVLQSFRHLLRLRIRERLSAVSSDAAFAARMVVSKESVVREEADYMRHVY
BESB_024160/1-1353 1090  SAVYEMAFGALPRYAHVNMPFLVGLEREEYTRILFNYNLSKFKEAVGVAATRHELKIAVEKAVDALGADAEKSN.....DEELAENLMKELLPQH
CSUI_007316/1-481      ...............................................................................................
ETH_00018465/1-1314 1050  RSLYSRLMKEMQRDRLVPLSFGINQERPEYAEILYNLSLLEFKRTVIFTATKRQLGIVTKEILKSMRTRSRAAATA.........SRLLSLIPES
cyc_03129/1-1343 1074  RGVYAAVLREMHKDHFVPLPFGVWDEREEYIEALYDIKLSFFRELVAYTATKEELSKKAAEILHALDPEERAKFSV.........ATLRGKIPES
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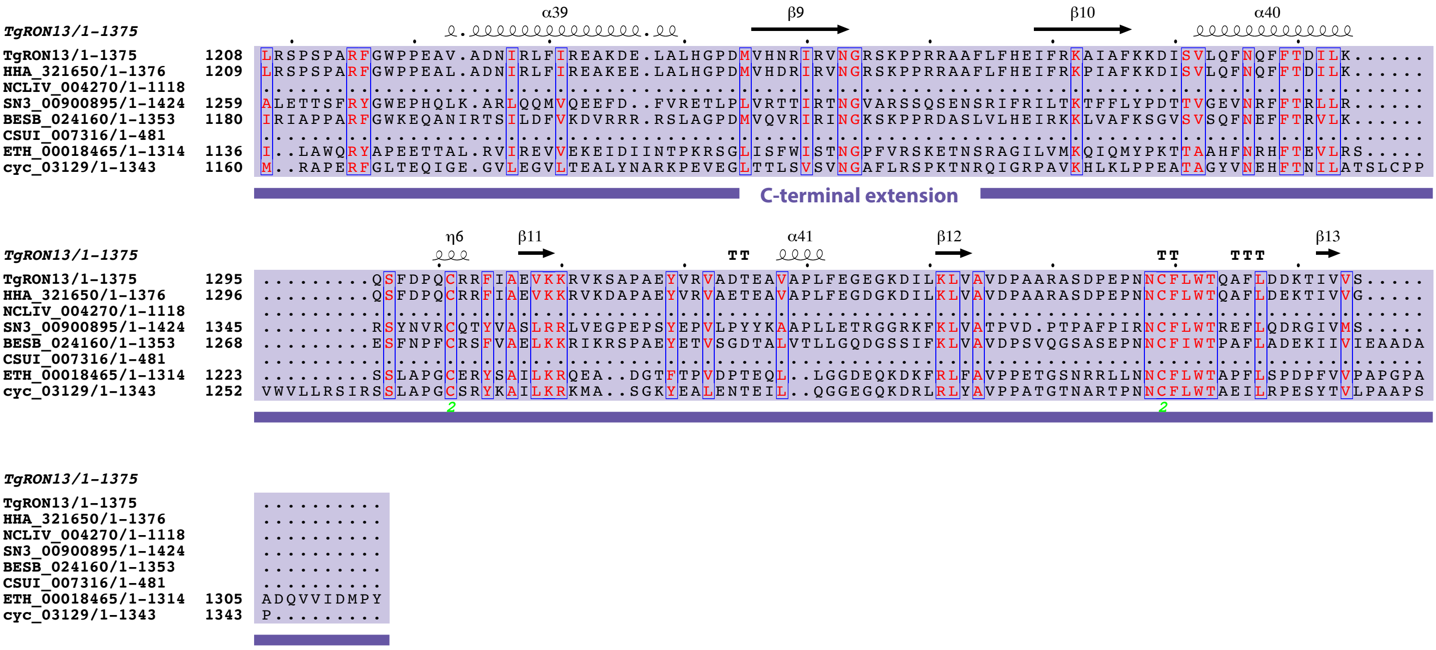
C-terminal extension



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TgRON13/1-1375

TgRON13/1-1375        1208  LRSPSPARFGWPPEAV.ADNIRLFIREAKDE.LALHGPDMVHNRIRVNGRSKPPRRAAFLFHEIFRKAIAFKKDISVLQFNQFFTDILK......
HHA_321650/1-1376     1209  LRSPSPARFGWPPEAL.ADNIRLFIREAKEE.LALHGPDMVHDRIRVNGRSKPPRRAAFLFHEIFRKPIAFKKDISVLQFNQFFTDILK......
NCLIV_004270/1-1118         ...............................................................................................
SN3_00900895/1-1424   1259  ALETTSFRYGWEPHQLK.ARLQQMVQEEFD..FVRETLPLVRTTIRTNGVARSSQSENSRIFRILTKTFFLYPDTTVGEVNRFFTRLLR......
BESB_024160/1-1353    1180  IRIAPPARFGWKEQANIRTSILDFVKDVRRR.RSLAGPDMVQVRIRINGKSKPPRDASLVLHEIRKKLVAFKSGVSVSQFNEFFTRVLK......
CSUI_007316/1-481           ...............................................................................................
ETH_00018465/1-1314   1136  I..LAWQRYAPEETTAL.RVIREVVEKEIDIINTPKRSGLISFWISTNGPFVRSKETNSRAGILVMKQIQMYPKTTAAHFNRHFTEVLRS.....
cyc_03129/1-1343      1160  M..RAPERFGLTEQIGE.GVLEGVLTEALYNARKPEVEGLTTLSVSVNGAFLRSPKTNRQIGRPAVKHLKLPPEATAGYVNEHFTNILATSLCPP

TgRON13/1-1375

TgRON13/1-1375        1295  .........QSFDPQCRRFIAEVKKRVKSAPAEYVRVADTEAVAPLFEGEGKDILKLVAVDPAARASDPEPNNCFLWTQAFLDDKTIVVS.....
HHA_321650/1-1376     1296  .........QSFDPQCRRFIAEVKKRVKDAPAEYVRVAETEAVAPLFEGDGKDILKLVAVDPAARASDPEPNNCFLWTQAFLDEKTIVVG.....
NCLIV_004270/1-1118         ...............................................................................................
SN3_00900895/1-1424   1345  .........RSYNVRCQTYVASLRRLVEGPEPSYEPVLPYYKAAPLLETRGGRKFKLVATPVD.PTPAFPIRNCFLWTREFLQDRGIVMS.....
BESB_024160/1-1353    1268  .........ESFNPFCRSFVAELKKRIKRSPAEYETVSGDTALVTLLGQDGSSIFKLVAVDPSVQGSASEPNNCFIWTPAFLADEKIIVIEAADA
CSUI_007316/1-481           ...............................................................................................
ETH_00018465/1-1314   1223  .........SSLAPGCERYSAILKRQEA..DGTFTPVDPTEQL..LGGDEQKDKFRLFAVPPETGSNRRLLNNCFLWTAPFLSPDPFVVPAPGPA
cyc_03129/1-1343      1252  VWVLLRSIRSSLAPGCSRYKAILKRKMA..SGKYEALENTEIL..QGGEGQKDRLRLYAVPPATGTNARTPNNCFLWTAEILRPESYTVLPAAPS

TgRON13/1-1375

TgRON13/1-1375              ..........
HHA_321650/1-1376           ..........
NCLIV_004270/1-1118         ..........
SN3_00900895/1-1424         ..........
BESB_024160/1-1353          ..........
CSUI_007316/1-481           ..........
ETH_00018465/1-1314   1305  ADQVVIDMPY
cyc_03129/1-1343      1343  P.........
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