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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     ....................................................................................................
cyc_03129/1-1343        ....................................................................................................
PF3D7_1321100/1-3447    MNFFLFFRNIFLLNTIIFILNQYIKRKDYGSRFFIFSLKIKSSKEEFTKNVHRKATNTKEDKSAYKNEKKEIPYRNNNKRKDKNKKGNDNKKILEKGLK


TgRON13/1-1375

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HHA_321650/1-1376       ....................................................................................................
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BESB_024160/1-1353      ....................................................................................................
CSUI_007316/1-481       ....................................................................................................
ETH_00018465/1-1314     ....................................................................................................
cyc_03129/1-1343        ....................................................................................................
PF3D7_1321100/1-3447    DTNSNIKSSTSSNTISNVSSKLSDNSNISNTFTNIKIQKLKDKHNKKNSDIKNVSTDKKKENDNNKKNNNNNKKNNKKIPIIYIPFNDIKNSPYIRGKLK


TgRON13/1-1375

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NCLIV_004270/1-1118     ....................................................................................................
SN3_00900895/1-1424     ....................................................................................................
BESB_024160/1-1353      ....................................................................................................
CSUI_007316/1-481       ....................................................................................................
ETH_00018465/1-1314     ....................................................................................................
cyc_03129/1-1343        ....................................................................................................
PF3D7_1321100/1-3447    LVYVKSFYEECQKELYEAKFQFFKNNKIYISTFAVVKNTLSENIDQTEKWVTADMKILQKNSYNISVTCNDSHEKQIQDISFTKQEKEEFELMRKSLKN


TgRON13/1-1375

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SN3_00900895/1-1424     ....................................................................................................
BESB_024160/1-1353      ....................................................................................................
CSUI_007316/1-481       ....................................................................................................
ETH_00018465/1-1314     ....................................................................................................
cyc_03129/1-1343        ....................................................................................................
PF3D7_1321100/1-3447    VVNITYDHFLYNIDTFYNAKRKYLEYINFFFRNPHIKSNMDIKKNISSNITIQKDNILLKRLGSFNKTKYILFRRMQRNNRIMCMVLTDPKRLENRFIL


TgRON13/1-1375

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CSUI_007316/1-481       ....................................................................................................
ETH_00018465/1-1314     ....................................................................................................
cyc_03129/1-1343        ....................................................................................................
PF3D7_1321100/1-3447    YNMLRDHIIEKEGFKDVIIFETDDNNIYNYDSKLSKDIRILSNKFEFEILMDEHAYINKPYEYFYLNKYIPVHFELQNKGIINYNNIFSWLCEHFINNS


TgRON13/1-1375

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SN3_00900895/1-1424     ....................................................................................................
BESB_024160/1-1353      ....................................................................................................
CSUI_007316/1-481       ....................................................................................................
ETH_00018465/1-1314     ....................................................................................................
cyc_03129/1-1343        ....................................................................................................
PF3D7_1321100/1-3447    QYKYYYPHFYLSKHSDKNDMGIRNISFYQKEDAYTFIENNKKNINKNDKCKTYDTCEKDDTYRTDKKSKLKNINRIYNTKYALSKKKNRNHKNNEINNI


TgRON13/1-1375

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CSUI_007316/1-481       ....................................................................................................
ETH_00018465/1-1314     ....................................................................................................
cyc_03129/1-1343        ....................................................................................................
PF3D7_1321100/1-3447    CSHKKEEKHMFNNYNISYNNMKYINKHNKFSFLELKEKLKSDNNEREDKKKKDESFEKNETHLMNNDDNNIGDDEFNSEVNNDNNGSYESNFFYDMINE


TgRON13/1-1375

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SN3_00900895/1-1424     ....................................................................................................
BESB_024160/1-1353      ....................................................................................................
CSUI_007316/1-481       ....................................................................................................
ETH_00018465/1-1314     ....................................................................................................
cyc_03129/1-1343        ....................................................................................................
PF3D7_1321100/1-3447    ISNKIENSDSYLNEEDIYWDDDIFFDTNEYIDDTSTITTSTNNNNIRTDQNGDNKKDDSNKDIISIQKVNDSTEVNESNKIDDTKKGESYTLNNIKGYI
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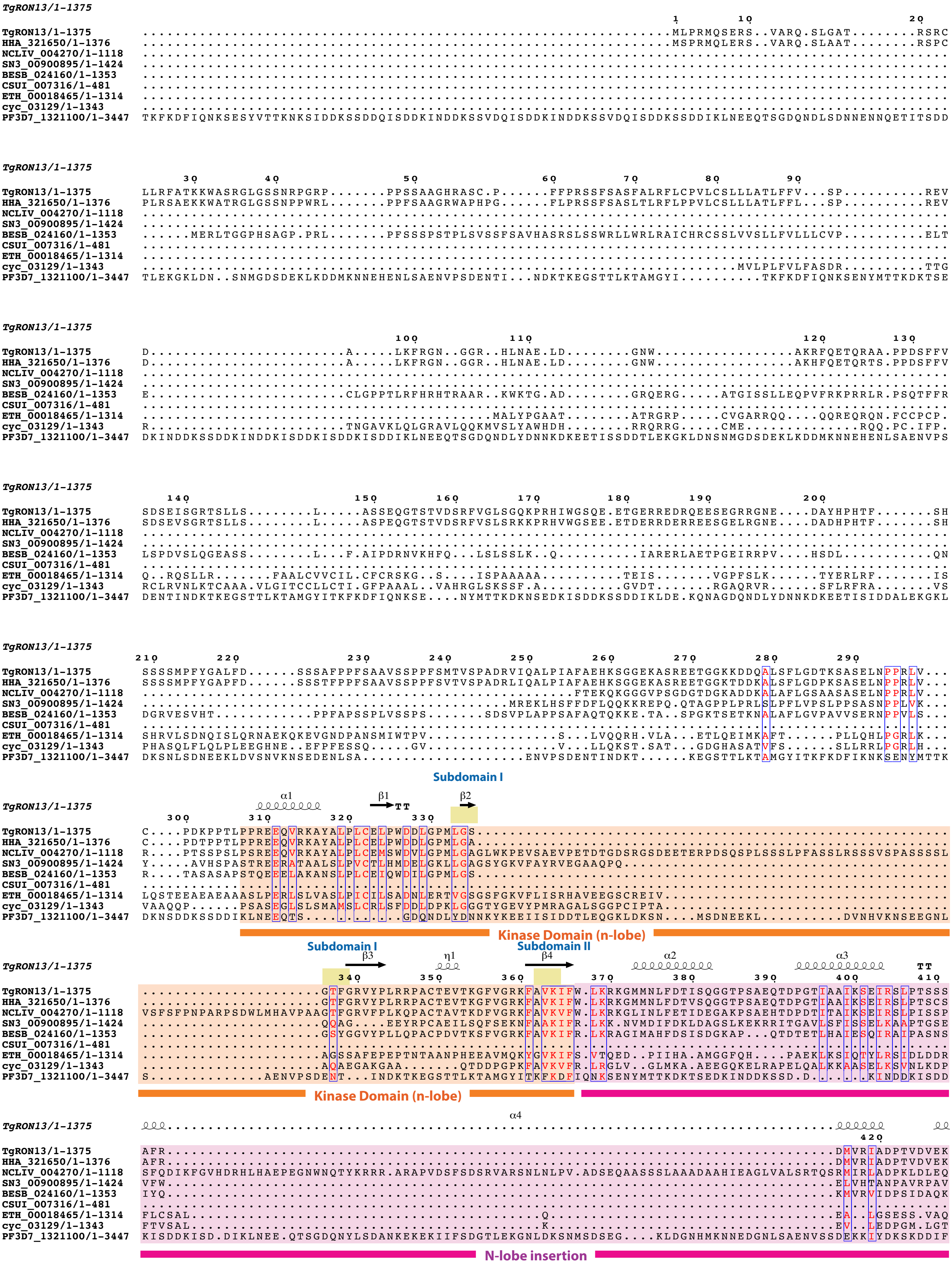
TgRON13/1-1375
TgRON13/1-1375
HHA_321650/1-1376
NCLIV_004270/1-1118
SN3_00900895/1-1424
BESB_024160/1-1353
CSUI_007316/1-481
ETH_00018465/1-1314
cyc_03129/1-1343
PF3D7_1321100/1-3447
Subdomain I
α1
β1
β2
TT
Kinase Domain (n-lobe)
Subdomain I
Subdomain II
β3
η1
β4
α2
α3
α4
N-lobe insertion
1
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
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380
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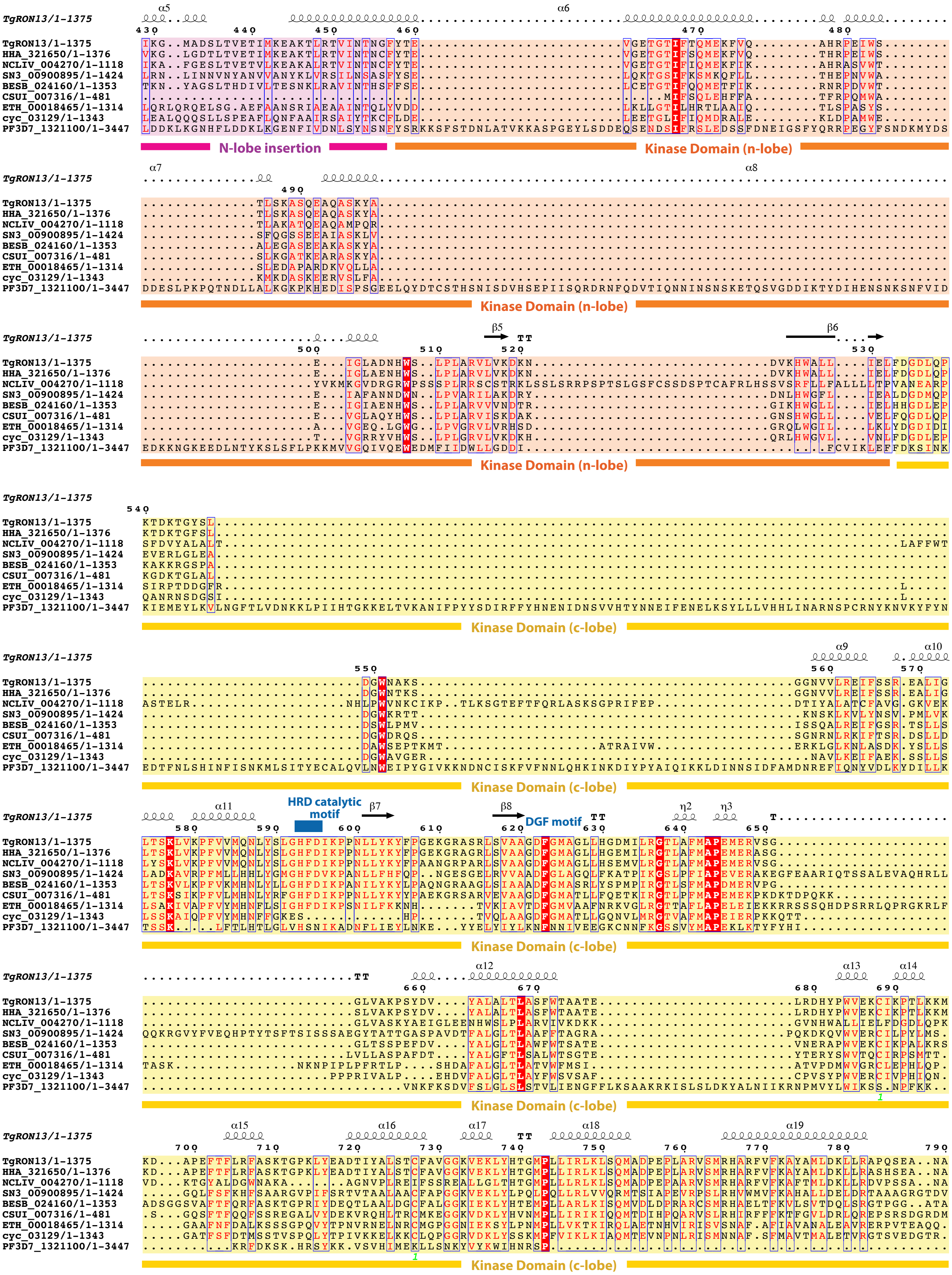
410
420


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
cyc_03129/1-1343
PF3D7_1321100/1-3447
α5
α6
α7
α8
α9
α10
α11
α12
α13
α14
α15
α16
α17
α18
α19
β5
β6
β7
β8
η2
η3
TT
N-lobe insertion
Kinase Domain (n-lobe)
Kinase Domain (c-lobe)
HRD catalytic motif
DGF motif
430
440
450
460
470
480
490
500
510
520
530
540
550
560
570
580
590
600
610
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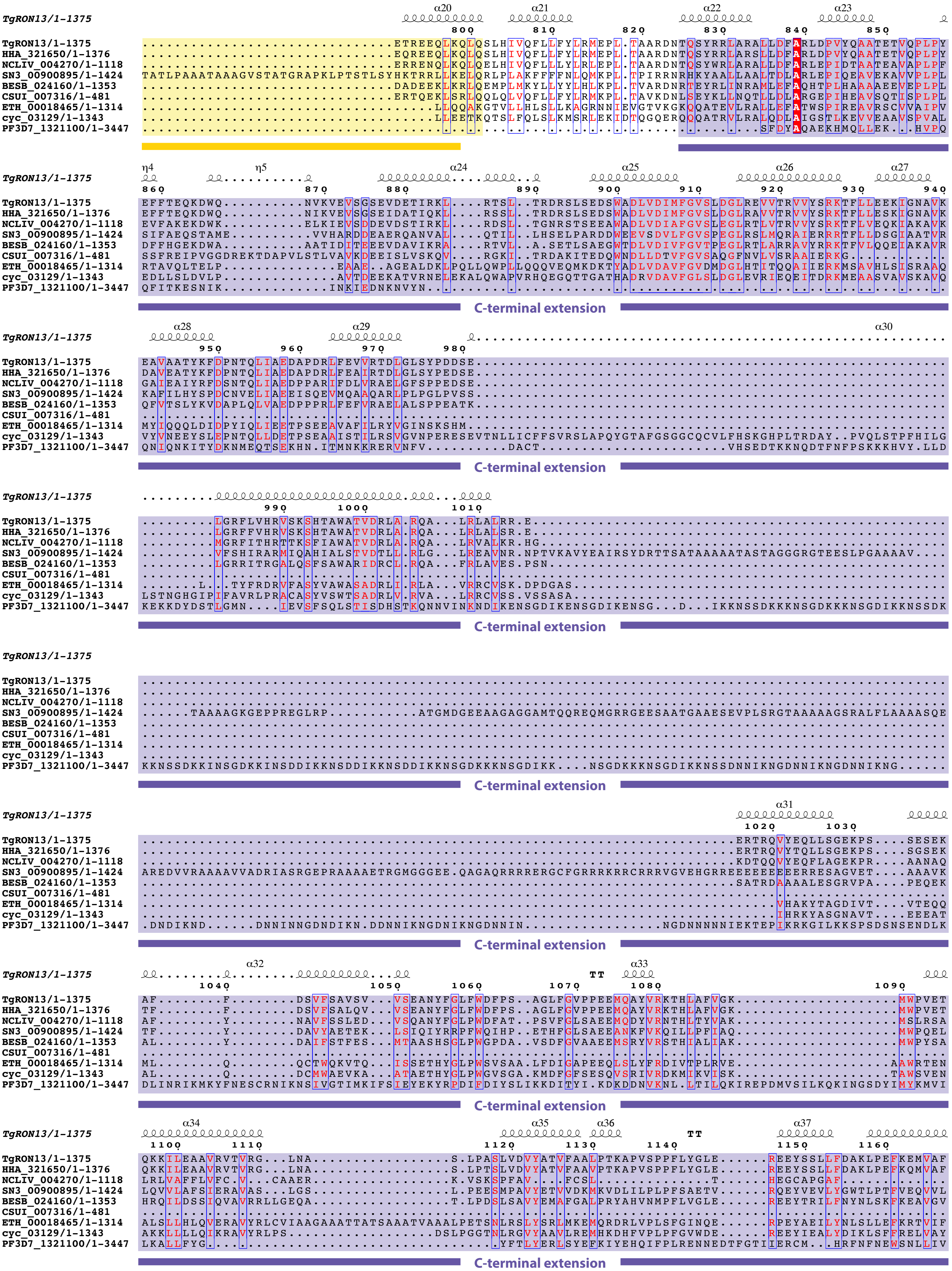
760
770
780
790
1
1



α20 α21 α22 α23
TgRON13/1-1375
800 810 820 830 840 850
TgRON13/1-1375 .................................ETREEQLKQLQSLHIVQFLLFYLRMEPL.TAARDNTQSYRRLARALLDFARLDPVYQAATETVQPLPY
HHA_321650/1-1376 .................................EQREEQLKQLQSLHIVQFLLFYLRMEPL.TAARDNTQSYRRLARSLLDFARLDPVYQAATETVQPLPY
NCLIV_004270/1-1118 .................................ERRENQLKQLQELHIVQFLLLYLRLEPL.TAARDNTQSYWRLARALLDFARLEPIDTAATEAVAPLPF
SN3_00900895/1-1424 TATLPAAATAAAGVSTATGRAPKLPTSTLSYHKTRRLLKELQRLPLAKFFFNLQMKPL.TPIRRNRHKYAALLAALTDLARLEPIQEAVEKAVVPLPL
BESB_024160/1-1353 .................................DADEEKLKRLQEMPLMKYLLYYLHLKPL.TVARDNRTEYRLINRAMLEFAQHTPLHAAAEEVEPLPL
CSUI_007316/1-481 .................................ERTQEKLSRLQQLQLVQFLLFYLRMKPL.TAVKDNLSEYKLLNQTLLDLARGEPIHEAVSQTISPLPL
ETH_00018465/1-1314 ....................................LLQQAKGTVLLHLSLLKAGRNNIEVGTVKGKQQATEVLRALLEFATWSPIREAVRSCVVAIPV
cyc_03129/1-1343 ....................................LLEETKQTSLFQLSLKMSRLEKIDTQGQERQQQATRVLRALQDLAIGSTLKEVVEAAVSPVAL
PF3D7_1321100/1-3447 ....SFDYAQAEKHMQLLEK..HVPQ

η4 η5 α24 α25 α26 α27
TgRON13/1-1375
860 870 880 890 900 910 920 930 940
TgRON13/1-1375 EFFTEQKDWQ..........NVKVEVSGSEVDETIRKL....RTSL..TRDRSLSEDSWADLVDIMFGVSLDGLREVVTRVVYSRKTFLLEEKIGNAVK
HHA_321650/1-1376 EFFTEQKDWQ..........NIKVEVSGSEIDATIQKL....RSSL..TGNRSTSEEAWADLVDIAFGVSLEGLRTLVTRVVYSRKTFLVEQKIAKAVK
NCLIV_004270/1-1118 EVFAKEKDWK..........ELKIEVSDDEVDSTIRKL....RDSL..TGNRSTSEEAWADLVDIAFGVSLEGLRTLVTRVVYSRKTFLVEQKIAKAVK
SN3_00900895/1-1424 SIFAEQSTAME.........VVHARDDEAERQANVAL....QTIL..LHSELPARDDWEEVSDVLFGVSPEGLRSLMQRAIERRTFLLDSGIAATVR
BESB_024160/1-1353 DFFHGEKDWA..........AATIDITEEVDAVIKRA....RTVL..A.SETLSAEGWTDLVDIVFGVTPEGLRTLARRAVYRRKTFVLQQEIAKAVR
CSUI_007316/1-481 SSFREIPVGGDREKTDAPVLSTLVAVKDEEISLVSKQV....RGKI..TRDAKITEDQWNDLLDTVFGVSAQGFNVLVSRAAIERKG.........
ETH_00018465/1-1314 RTAVQLTELP...............EAAE..AGEALDKLPQLLQWPLLQQQVEQMKDKTYADLVDAVFGVDMDGLHTITQQAIIERKMSAVHLSISRAAQ
cyc_03129/1-1343 EDLLSLDVLP...............AVTDEEKATVRNELEKALQWAPVRHQEGQTTGATHADRVDAVFGLSLDGLEVRIEQEITDRKMEAASVAVSKAVQ
PF3D7_1321100/1-3447 QFITKESNIK............INKIEDNKNVYN..
C-terminal extension

α28 α29 α30
TgRON13/1-1375
950 960 970 980
TgRON13/1-1375 EAVAATYKFDPNTQLIAEDAPDRLFEVVRTDLGLSYPDDSE...
HHA_321650/1-1376 DAVEATYKFDPNTQLIAEDAPDRLFEAIRTDLGLSYPEDSE...
NCLIV_004270/1-1118 GAIEAIYRFDSNTQLIAEDPPARIFDLVRAELGFSPPEDSE...
SN3_00900895/1-1424 KAFILHYSPDCNVELIAEEISQEVMQAAQARLPLPGLPVSS...
BESB_024160/1-1353 QFVTSLYKVDAPLQLVAEDPPPRLFEFVRAELALSPPEATK...
CSUI_007316/1-481 ....
ETH_00018465/1-1314 MYIQQQLDIDPYIQLIEETPSEEAVAFILRYVGINSKSHM..
cyc_03129/1-1343 VYVNEEYSLEPNTQLLDETPSEAAISTILRSVGVNPERESEVTNLLICFFSVRSLAPQYGTAFGSGGCQCVLFHSKGHPLTRDAY..PVQLSTPFHILG
PF3D7_1321100/1-3447 QNIQNKITYDKNMEQTSEKHN.ITMNKKRERVNFV..........DACT...............VHSEDTKKNQDTFNFPSKKKHVY.LLD
C-terminal extension

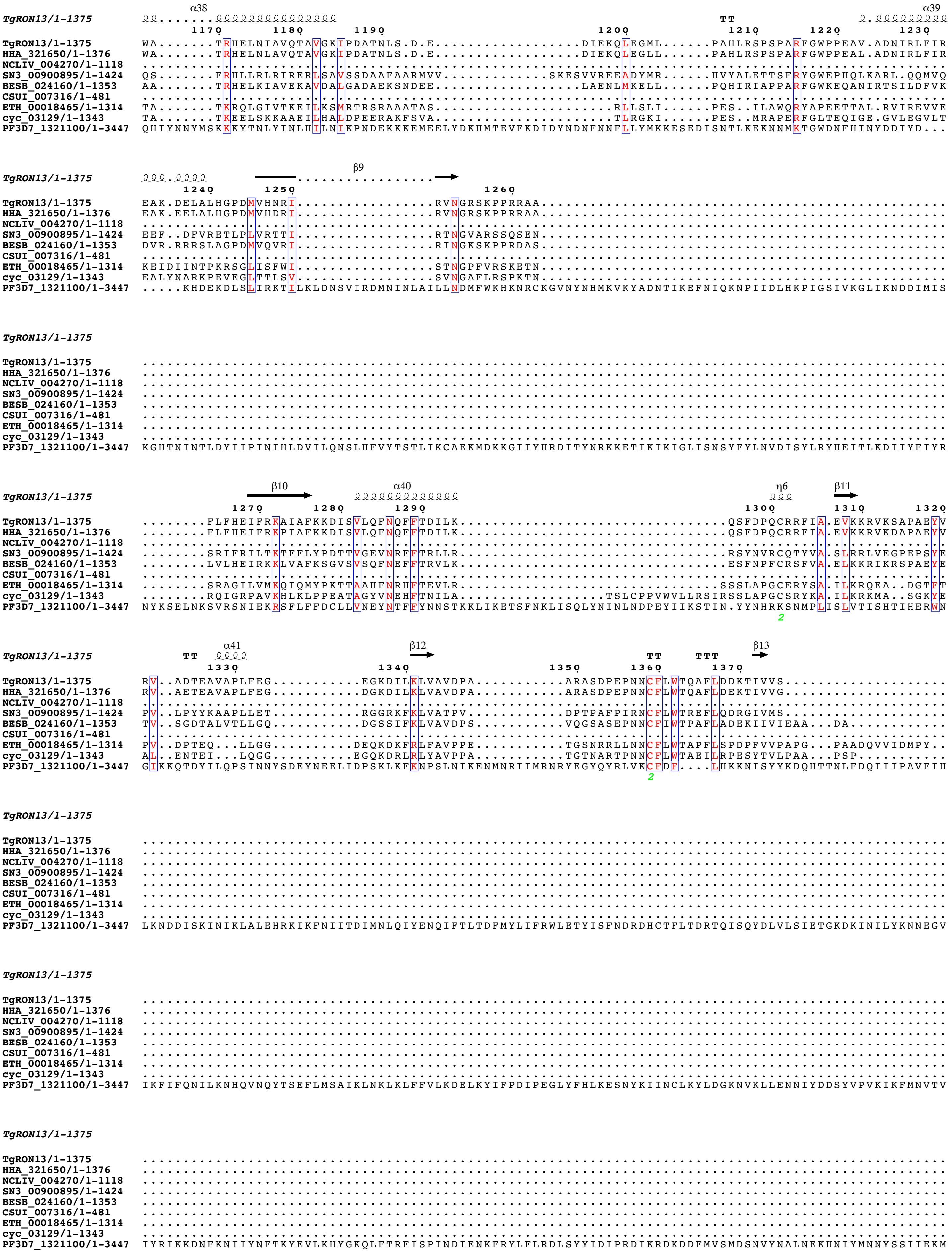
TgRON13/1-1375
990 1000 1010
TgRON13/1-1375 .........LGRFLVHRVSKSHTAWATVDRLA.RQA...LRLALRR.E..
HHA_321650/1-1376 .........LGRFFVHRVSKSHTAWATVDRLA.RQA...LRLALSR.E..
NCLIV_004270/1-1118 .........MGRFITHRTTKSFIAWATVDRLA.RQA...LRVALKR.HG...
SN3_00900895/1-1424 .........VFSHIRARMIQAHIALSTVDTLL.RLG...LREAVNR.NPTVKAVYEAIRSYDRTTSATAAAAATASTAGGGRGTEESLPGAAAAV....
BESB_024160/1-1353 .........LGRRITRGALQSFSAWARIDRCL.RQA...FRLAVES.PSN..
CSUI_007316/1-481 ....
ETH_00018465/1-1314 .......L..TYFRDRVFASYVAWASADRLI.RLA...VRRCVSK.DPDGAS..
cyc_03129/1-1343 LSTNGHGIPIFAVRLPRACASYVSWTSADRLV.RVA...LRRCVSS.VSSASA...
PF3D7_1321100/1-3447 KEKKDYDSTLGMN....IEVSFSQLSTISDHSTKQNNVINKNDIKENSGDIKENSGDIKENSG...D...IKKNSSDKKKNSGDKKKNSGDIKKNSSDK
C-terminal extension

TgRON13/1-1375
TgRON13/1-1375 ....
HHA_321650/1-1376 ....
NCLIV_004270/1-1118 ....
SN3_00900895/1-1424 .....TAAAAGKGEPPREGLRP..........ATGMDGEEAAGAGGAMTQQREQMGRRGEESAATGAAESEVPLSRGTAAAAAGSRALFLAAAASQE
BESB_024160/1-1353 ....
CSUI_007316/1-481 ....
ETH_00018465/1-1314 ....
cyc_03129/1-1343 ....
PF3D7_1321100/1-3447 KKNSSDKKINSGDKKINSDDIKKNSDDIKKNSDDIKKNSGDKKKNSGDIKK....NSGDKKKNSGDIKKNSSDNNIKNGDNNIKNGDNNIKNG.....
C-terminal extension

α31
TgRON13/1-1375
1020 1030
TgRON13/1-1375 ....ERTRQVYEQLLSGEKPS....SESEK
HHA_321650/1-1376 ....ERTRQVYTQLLSGEKPS....SGSEK
NCLIV_004270/1-1118 ....KDTQQVYEQFLAGEKPR....AANAQ
SN3_00900895/1-1424 AREDVVRAAAAVVADRIASRGEPRAAAAETRGMGGGEE.QAGAQRRRRERGCFGRRRKRRCRRVGVEHGRREEEEEEEERRESAGVET....AAAVK
BESB_024160/1-1353 ....SATRDAAAALESGRVPA....PEQEK
CSUI_007316/1-481 ....
ETH_00018465/1-1314 ....VHAKYTAGDIVT....VTEQQ
cyc_03129/1-1343 ....IHRKYASGNAVT....TEEEAT
PF3D7_1321100/1-3447 .DNDIKND......DNNINNGDNDIKN.DDNNIKNGDNIKNGDNNIN.................NGDNNNNNIEKTEPIKRKGILKKSPSDSNSENDLK
C-terminal extension

α32 TT α33
TgRON13/1-1375
1040 1050 1060 1070 1080 1090
TgRON13/1-1375 AF........F........DSVFSAVSV....VSEANYFGLFWDFPS..AGLFGVPPEEMQAYVRKTHLAFVGK...................MWPVET
HHA_321650/1-1376 TF........F........DSVFSALQV....VSEANYFGLFWDFPS..AGLFGVPPEEMQAYVRKTHLAFVGK...................MWPVET
NCLIV_004270/1-1118 AF........Y........NAVFSSLED....VSQANYFGLPWDFAT..PSVFGLSAEEMQDYVRNTHLTYVAK...................MSLRSA
SN3_00900895/1-1424 TF........Y........DAVYAETEK....LSIQIYRRPFWQIHP..ETHFGLSAEEANKFVKQILLPFIAQ...................MWPQEL
BESB_024160/1-1353 AL........Y........DAIFSTFES....MTAASHSGLPWGPDA..VSDFGVAAEEMSRYVRSTHIALIAK...................MWPYSA
CSUI_007316/1-481 ....
ETH_00018465/1-1314 ML........Q........QCTWQKVTQ....ISSETHYGLPWSVSAA.LFDIGAPEEQLSLYFRDIVTPLRVE...................AAWRTEN
cyc_03129/1-1343 AL........Q........DCMWAEVKA....ATAETHYGLPWGVSGA.KMDFGFSESQVSRIVRDKMIKVISK...................TAWSVEN
PF3D7_1321100/1-3447 DLINRIKMKYFNESCRNIKNSIVGTIMKIFSIEYEKYRPDIFDIYSLIKKDITYI.KDKDDNVKNL.LTILQKIREPDMVSILKQKINGSDYIMYKMVI
C-terminal extension

α34 α35 α36 TT α37
TgRON13/1-1375
1100 1110 1120 1130 1140 1150 1160
TgRON13/1-1375 QKKILEAAVRVTVRG...LNA......................S.LPASLVDVYATVFAALPTKAPVSPPFLYGLE......REEYSSLLFDAKLPEFKEMVAF
HHA_321650/1-1376 QKKILEAAVRVTVRG...LNA......................S.LPTSLVDVYATVFAAVPTKAPVSPPFLYGLE......REEYSSLLFDAKLPEFKQMVAF
NCLIV_004270/1-1118 LRLVAFFLVFC.V...CAAER......................K.VSKSPFAV...FCSL...............T......HEGCAPGAF..............
SN3_00900895/1-1424 LQVVLAFSIERAVAS...LGS......................L.PEESMPAVYETVVDKMKVDLILPLPFSAETV......RQEYVEVLYGWTLPTFVEQVVL
BESB_024160/1-1353 HRQILDSSIQVAVRRLLGEQA......................T.LPDSLSAVYEMAFGALPRYAHVNMPFLVGLE......REEYTRILFNYNLSKFKEAVGV
CSUI_007316/1-481 ....
ETH_00018465/1-1314 ALSLLHLQVERAVYRLCVIAAGAAATTATSAAATVAAALPETSNLRSLYSRLMKEMQRDRLVPLSFGINQE......RPEYAEILYNLSLLEFKRTVIF
cyc_03129/1-1343 AKKLLLQIKRAVYRLPS.....................DSLPGGTNLRGVYAAVLREMHKDHFVPLPFGVWDE......REEYIEALYDIKLSFFRELVAY
PF3D7_1321100/1-3447 LKALLFYG.....................................YFTLYERLSYEFKIYEHQIFPLRENNEDTFGTIIERCM...HRFNFNEWSNLLIV
C-terminal extension


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
cyc_03129/1-1343
PF3D7_1321100/1-3447
α38
α39
TT
TTT
β9
β10
β11
β12
β13
α40
α41
η6
1170
1180
1190
1200
1210
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1230
1240
1250
1260
1270
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1290
1300
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1370
2
2

TgRON13/1-1375

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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     ........................................
cyc_03129/1-1343        ........................................
PF3D7_1321100/1-3447    ITYMNVTYTEPVFIVCVVKHTVLGSKIQLLLREMKYNITS
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