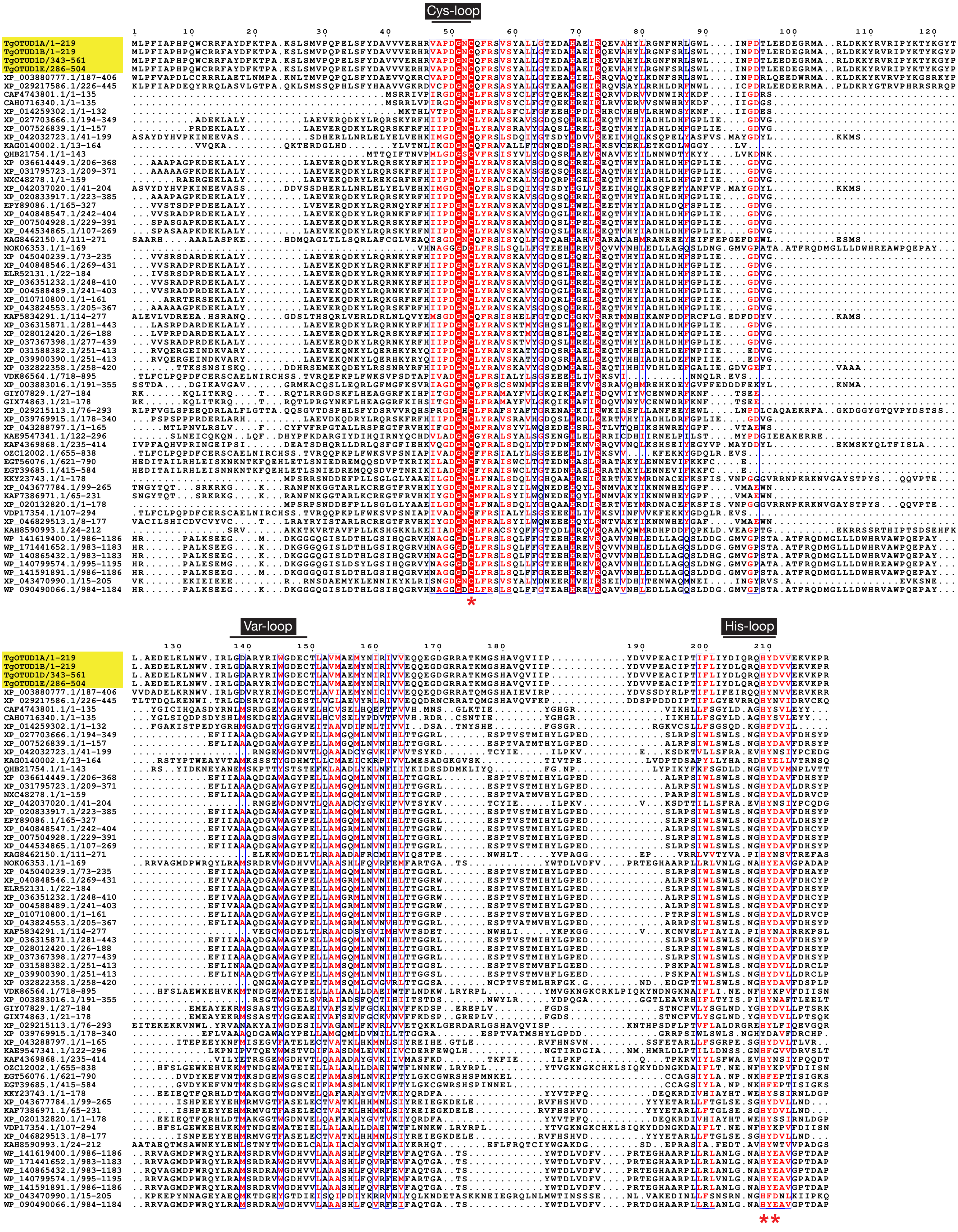
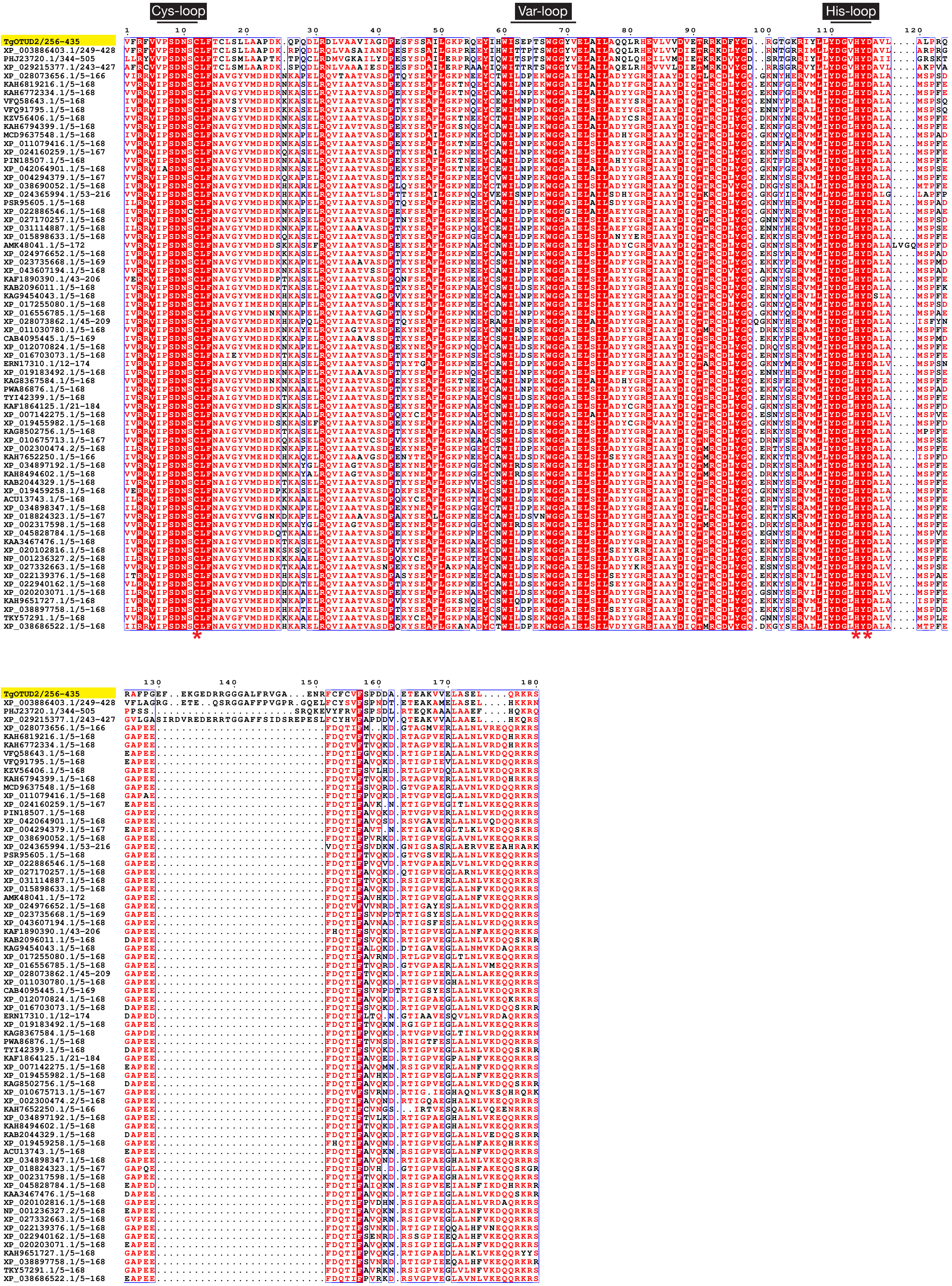
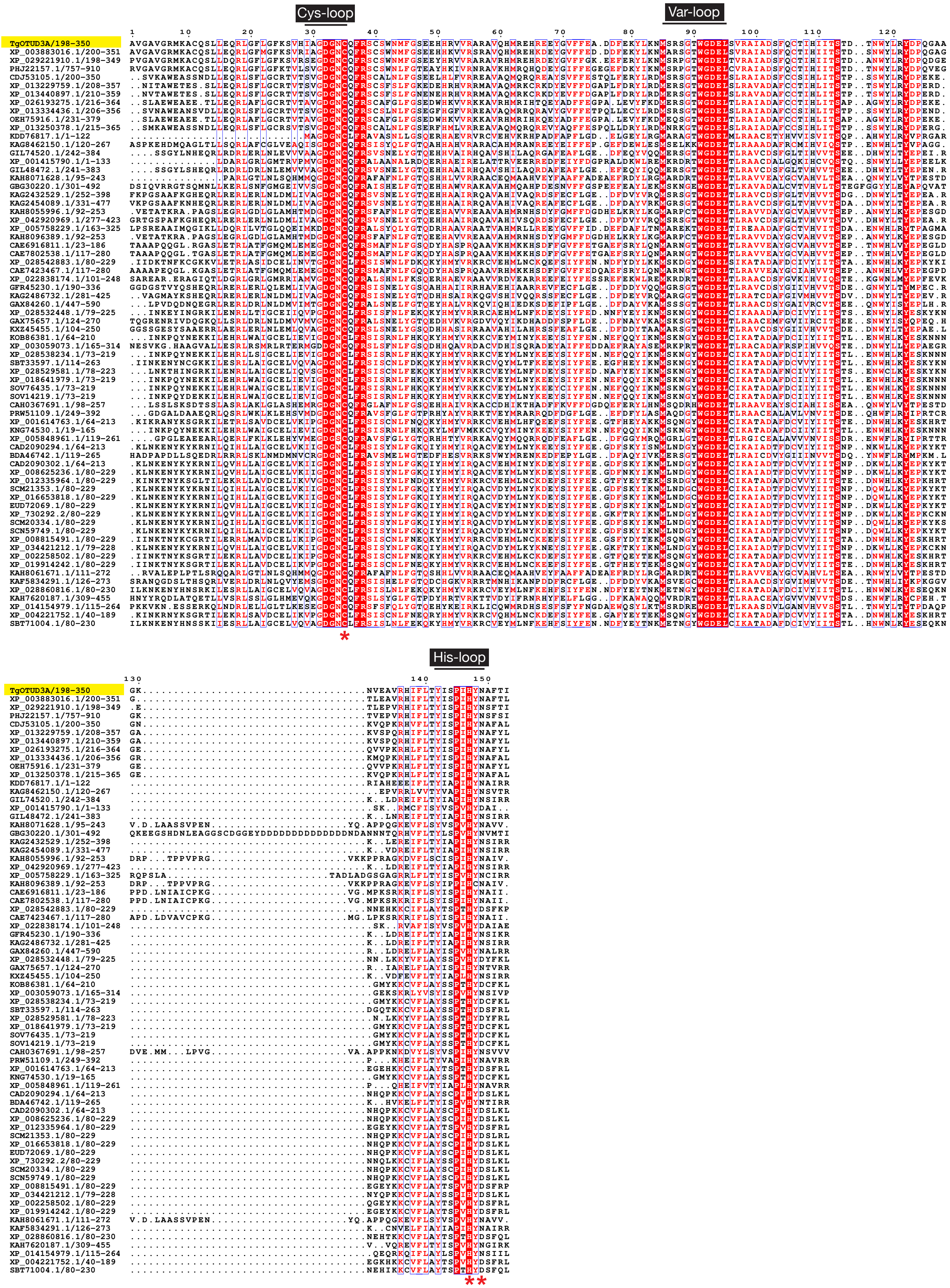
TgOTUD1


Cys-loop
Var-loop
His-loop
*
**
TgOTUD1A/1-219
TgOTUD1B/1-219
TgOTUD1D/343-561
TgOTUD1E/286-504
XP_003880777.1/187-406
XP_029217586.1/226-445
CAF4743801.1/1-135
CAH0716340.1/1-135
XP_014259302.1/1-132
XP_027703666.1/194-349
XP_007526839.1/1-157
XP_042032723.1/41-199
KAG0140002.1/13-164
QHB21754.1/1-143
XP_036614449.1/206-368
XP_031795723.1/209-371
NXC48278.1/1-159
XP_042037020.1/41-204
XP_020833917.1/223-385
EPY89086.1/165-327
XP_040848547.1/242-404
XP_007504928.1/229-391
XP_044534865.1/107-269
KAG8462150.1/111-271
NOK06353.1/1-169
XP_045040239.1/73-235
XP_040848546.1/269-431
ELR52131.1/22-184
XP_036351232.1/248-410
XP_004588489.1/241-403
XP_010710800.1/1-161
XP_043824553.1/205-367
KAF5834291.1/114-277
XP_036315871.1/281-443
XP_028012420.1/26-188
XP_037367398.1/277-439
XP_031588382.1/251-413
XP_039900390.1/251-413
XP_032822358.1/258-420
VDK86564.1/718-895
XP_003883016.1/191-355
GIY07829.1/27-184
GIX74863.1/21-178
XP_029215113.1/76-293
XP_039769915.1/178-340
XP_043288797.1/1-165
KAE9547341.1/122-296
KAF4369868.1/235-414
OZC12002.1/655-838
EGT56076.1/621-790
EGT39685.1/415-584
KKY23743.1/1-178
XP_043677784.1/99-265
KAF7386971.1/65-231
XP_020132820.1/1-178
VDP17354.1/107-294
XP_046829513.1/8-177
KAH8590993.1/24-212
WP_141619400.1/986-1186
WP_171441652.1/983-1183
WP_140865432.1/983-1183
WP_140799574.1/995-1195
WP_141591891.1/986-1186
XP_043470990.1/15-205
WP_090490066.1/984-1184

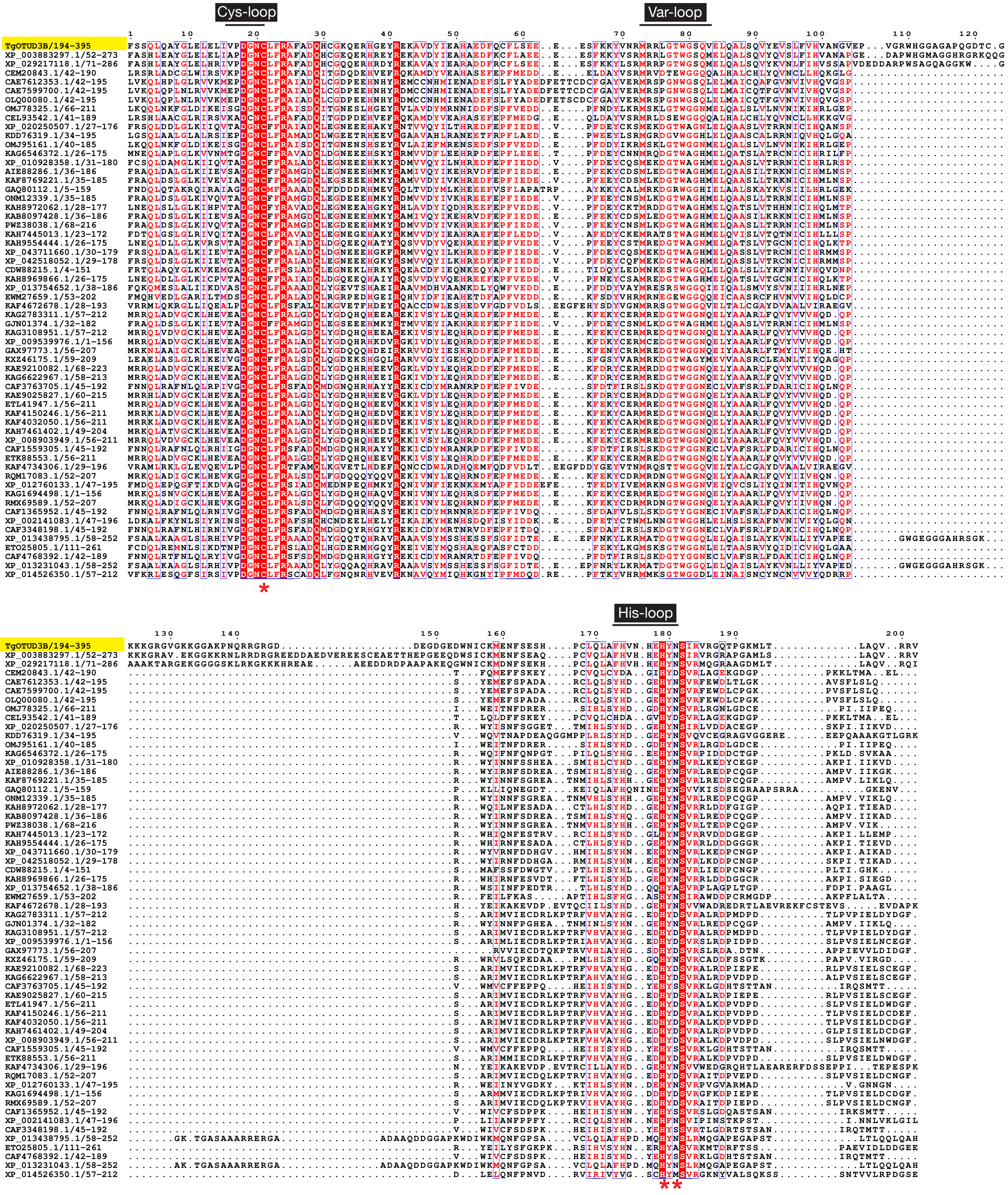
TgOTUD2


Cys-loop
Var-loop
His-loop
TgOTUD2/256-435
XP_003886403.1/249-428
PHJ23720.1/344-505
XP_029215377.1/243-427
*
**

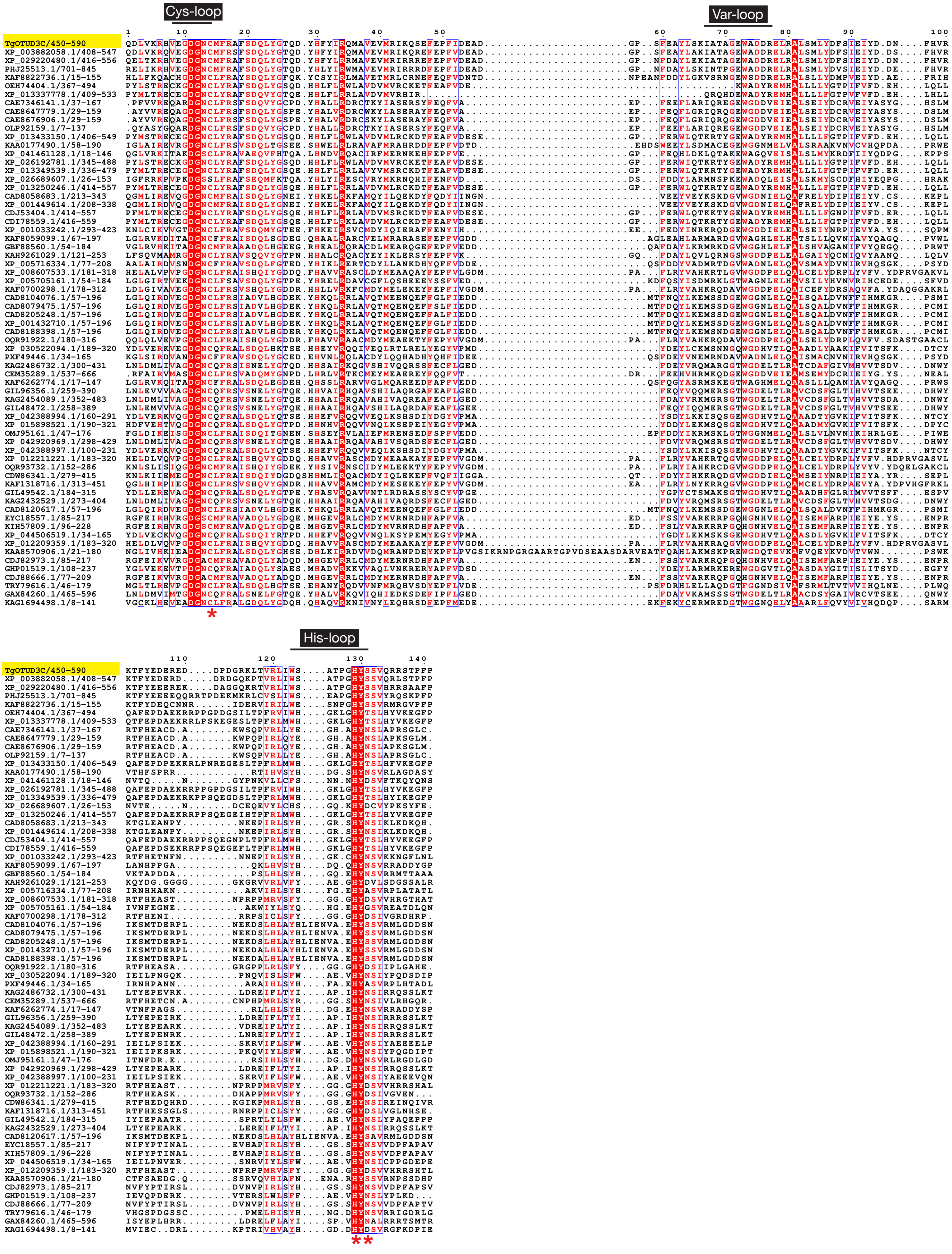
TgOTUD3A



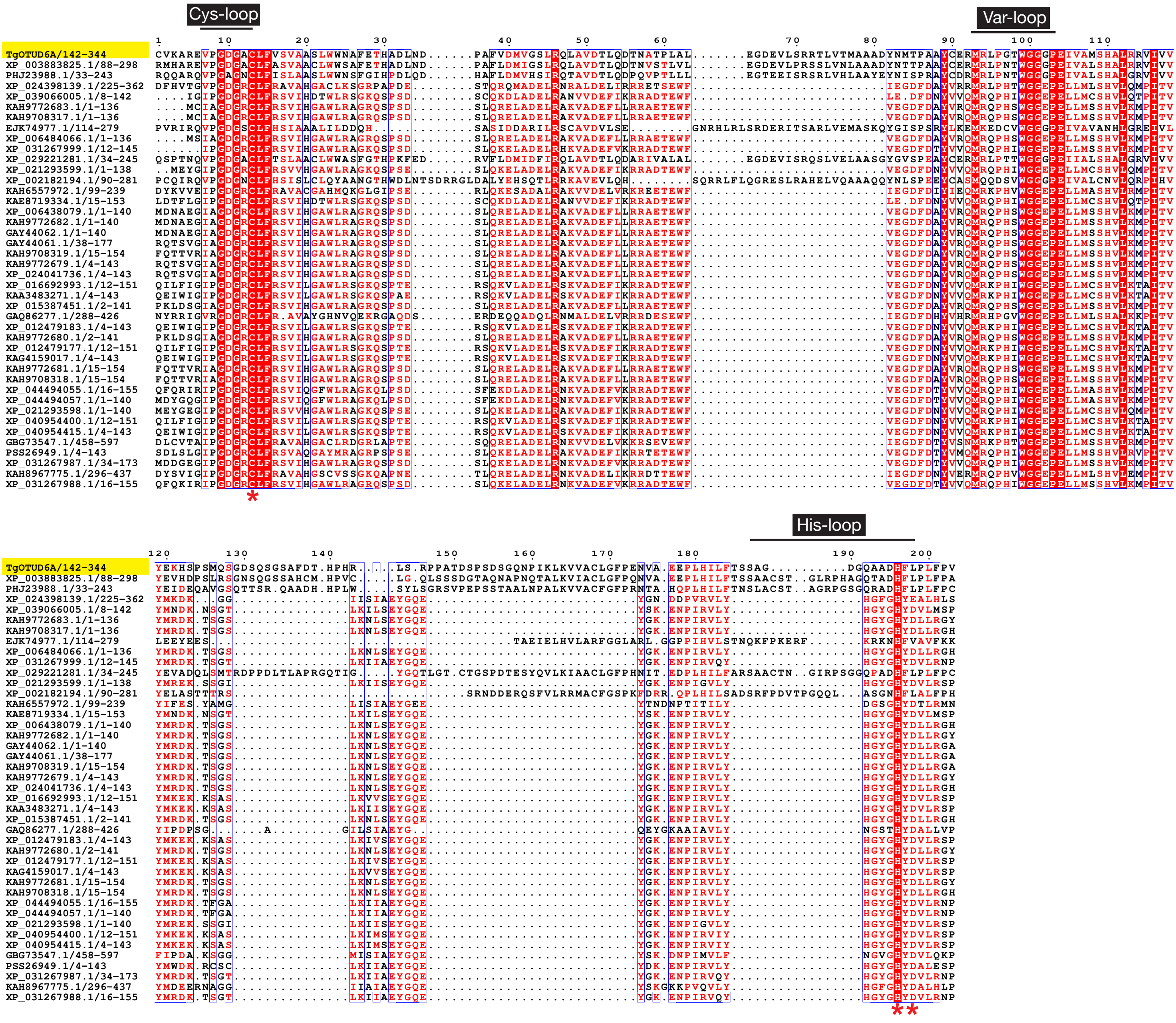
TgOTUD3B



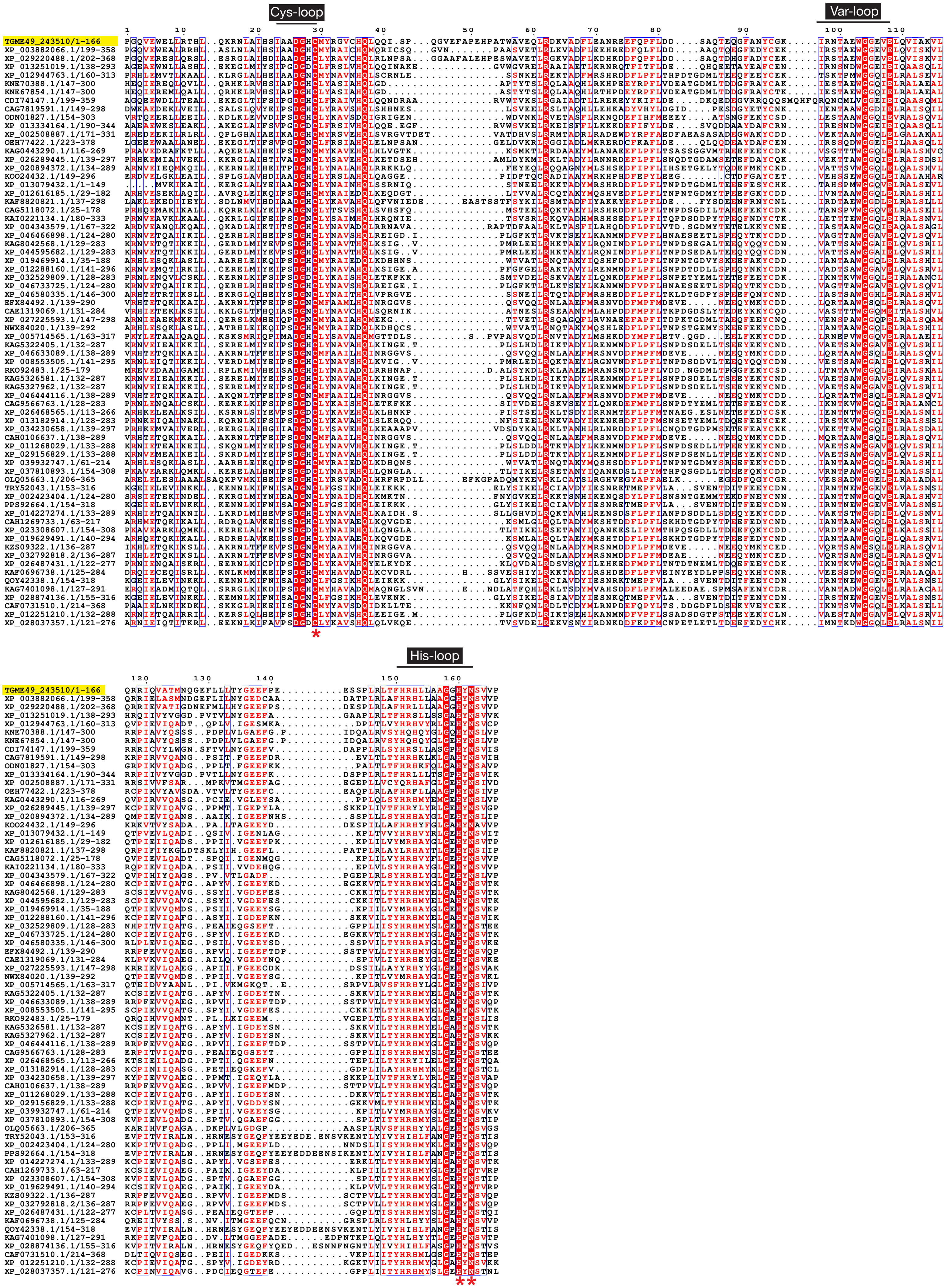
TgOTUD3C


Cys-loop
Var-loop
His-loop
TgOTUD3C/450-590
XP_003882058.1/408-547
XP_029220480.1/416-556
PHJ25513.1/701-845
KAF8822736.1/15-155
OEH74404.1/367-494
XP_013337778.1/409-533
CAE7346141.1/37-167
CAE8647779.1/29-159
CAE8676906.1/29-159
OLP92159.1/7-137
XP_013433150.1/406-549
KAA0177490.1/58-190
XP_041461128.1/18-146
XP_026192781.1/345-488
XP_013349539.1/336-479
XP_026689607.1/26-153
XP_013250246.1/414-557
CAD8058683.1/213-343
XP_001449614.1/208-338
CDJ53404.1/414-557
CDI78559.1/416-559
XP_001033242.1/293-423
KAF8059099.1/67-197
GBF88560.1/54-184
KAH9261029.1/121-253
XP_005716334.1/77-208
XP_008607533.1/181-318
XP_005705161.1/54-184
KAF0700298.1/178-312
CAD8104076.1/57-196
CAD8079475.1/57-196
CAD8205248.1/57-196
XP_001432710.1/57-196
CAD8188398.1/57-196
OQR91922.1/180-316
XP_030522094.1/189-320
PXF49446.1/34-165
KAG2486732.1/300-431
CEM35289.1/537-666
KAF6262774.1/17-147
GIL96356.1/259-390
KAG2454089.1/352-483
GIL48472.1/258-389
XP_042388994.1/160-291
XP_015898521.1/190-321
OMJ95161.1/47-176
XP_042920969.1/298-429
XP_042388997.1/100-231
XP_012211221.1/183-320
OQR93732.1/152-286
CDW86341.1/279-415
KAF1318716.1/313-451
GIL49542.1/184-315
KAG2432529.1/273-404
CAD8120617.1/57-196
EYC18557.1/85-217
KIH57809.1/96-228
XP_044506519.1/34-165
XP_012209359.1/183-320
KAA8570906.1/21-180
CDJ82973.1/85-217
GHP01519.1/108-237
CDJ88666.1/77-209
TRY79616.1/46-179
GAX84260.1/465-596
KAG1694498.1/8-141
1 10 20 30 40 50 60 70 80 90 100
110 120 130 140
*
**

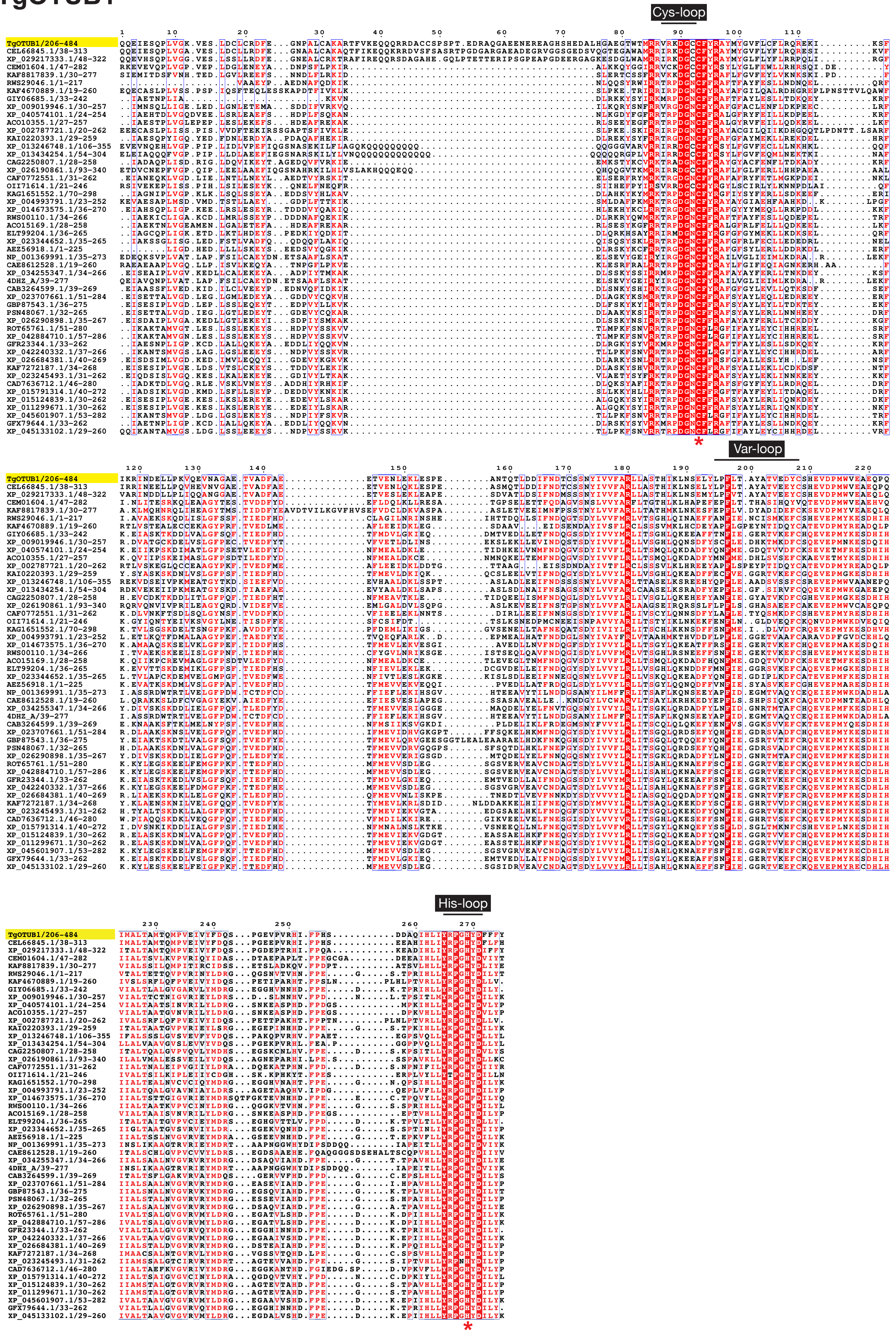
TgOTUD6A



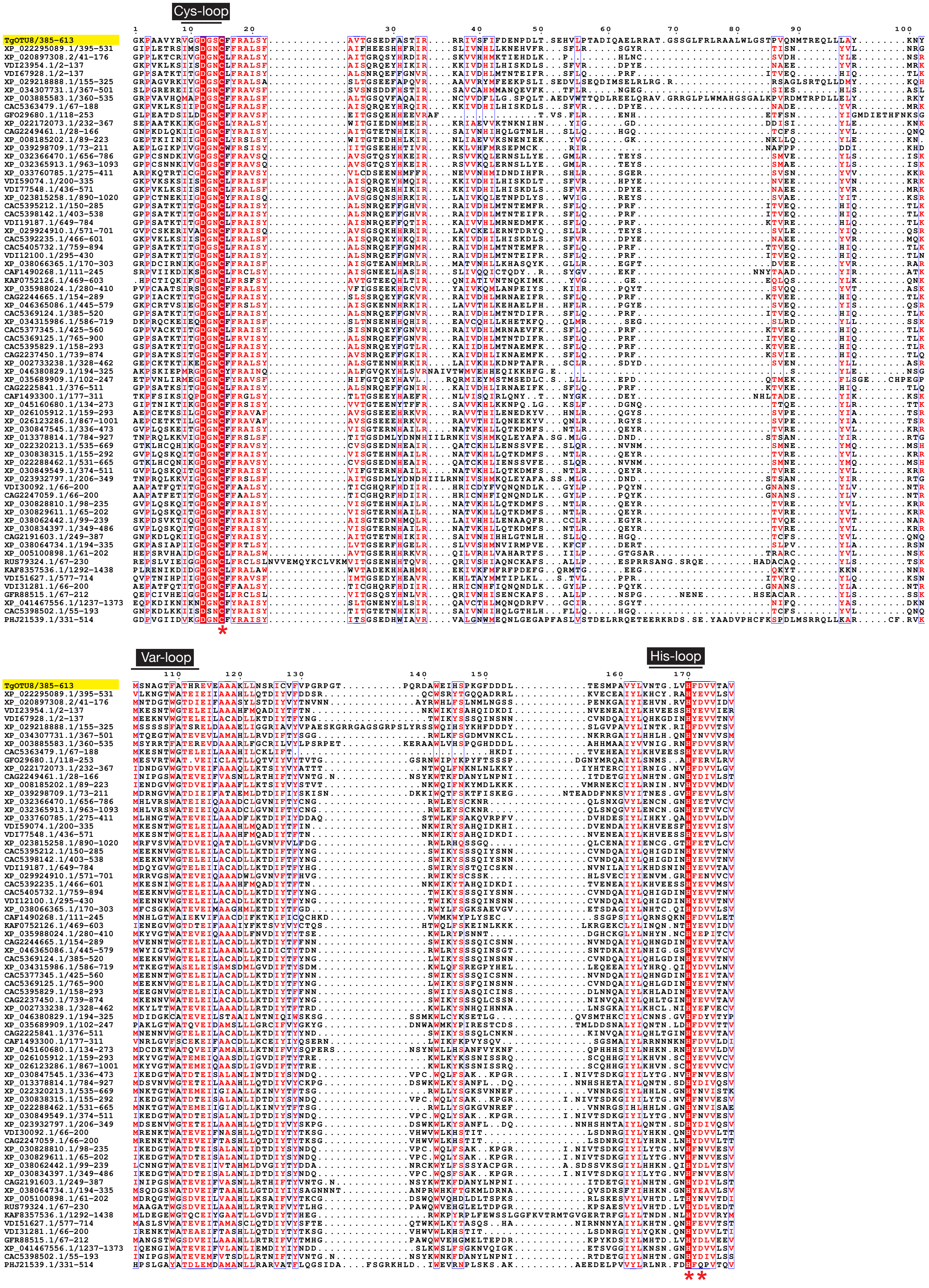
TgOTUD6B



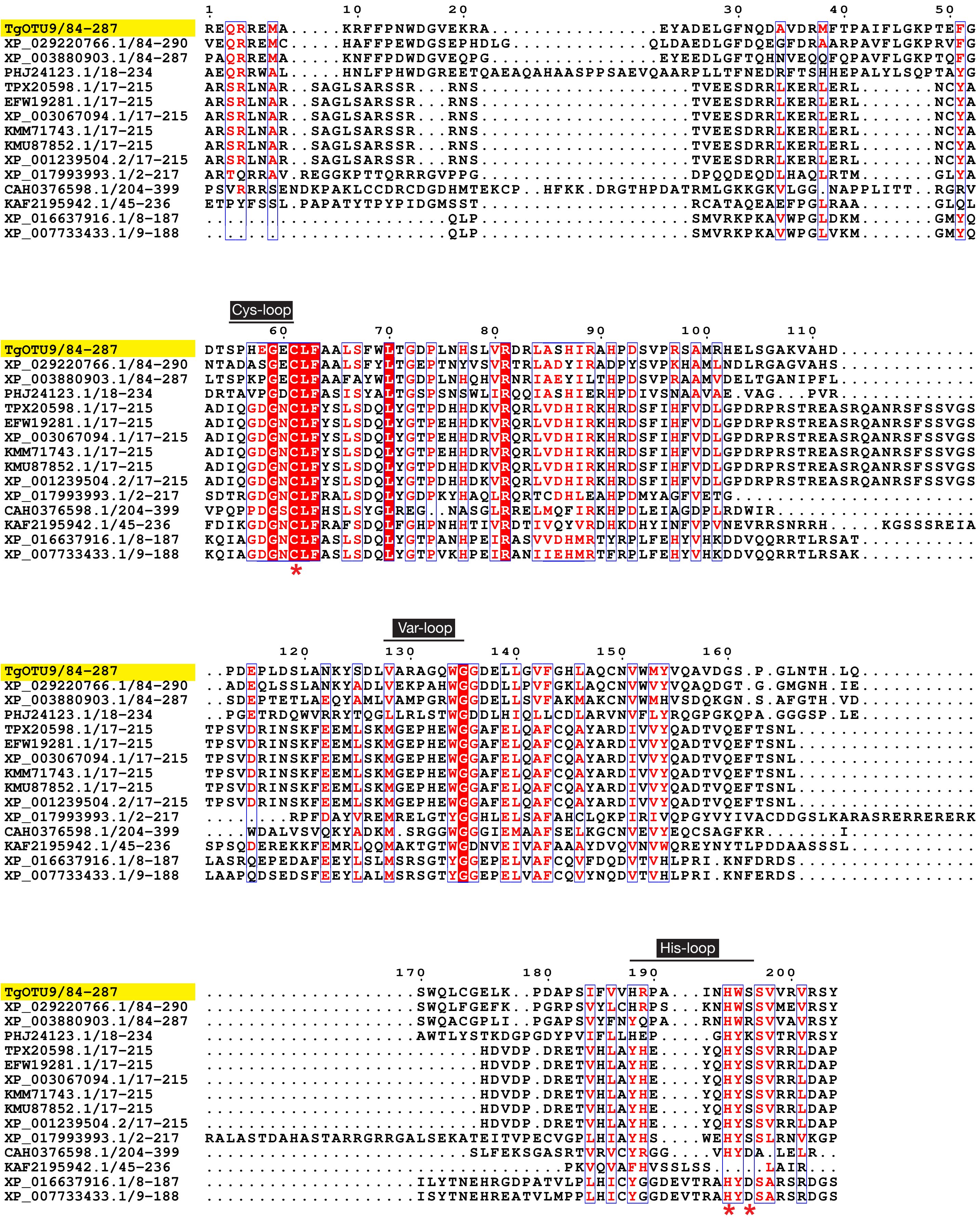
TgOTUB1



TgOTU8



TgOTU9



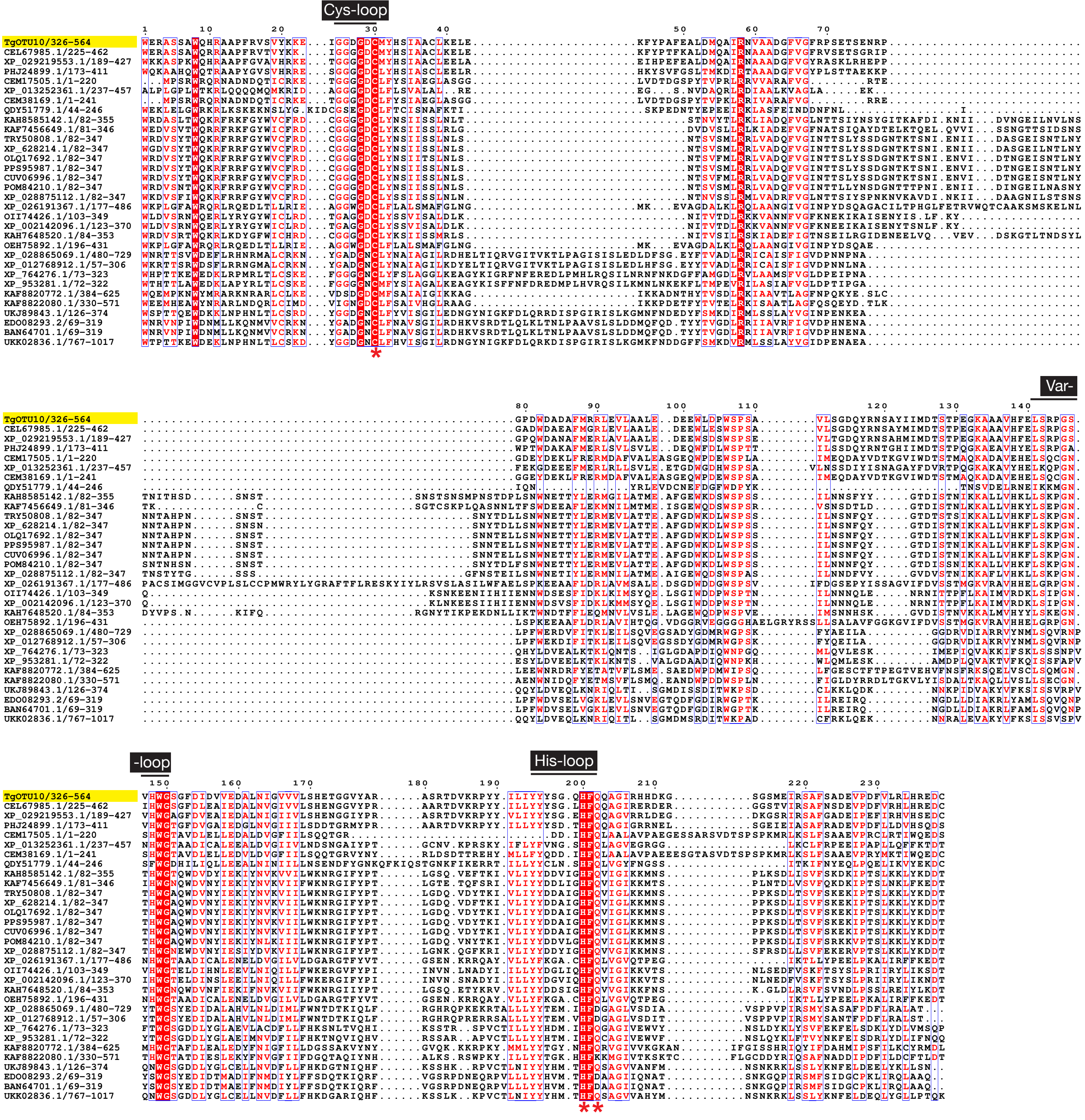
```
                       1           10        20                        30        40        50
TgOTU9/84-287          REQRREMA.....KRFFPNWDGVEKRA................EYADELGFNQDAVDRMFTPAIFLGKPTEFG
XP_029220766.1/84-290  VEQRREMC.....HAFFPEWDGSEPHDLG.............QLDAEDLGFDQEGFDRAARPAVFLGKPRVFG
XP_003880903.1/84-287  PAQRREMA.....KNFFPDWDGVEQPG................EYEEDLGFTQHNVEQQFQPAVFLGKPTQFG
PHJ24123.1/18-234      AEQRRWAL.....HNLFPHWDGREETQAEAQAHAASPPSAEVQAARPLLTFNEDRFTSHHEPALYLSQPTAYG
TPX20598.1/17-215      ARSRLNAR..SAGLSARSSR...RNS....................TVEESDRRLKERLERL.......NCYA
EFW19281.1/17-215      ARSRLNAR..SAGLSARSSR...RNS....................TVEESDRRLKERLERL.......NCYA
XP_003067094.1/17-215  ARSRLNAR..SAGLSARSSR...RNS....................TVEESDRRLKERLERL.......NCYA
KMM71743.1/17-215      ARSRLNAR..SAGLSARSSR...RNS....................TVEESDRRLKERLERL.......NCYA
KMU87852.1/17-215      ARSRLNAR..SAGLSARSSR...RNS....................TVEESDRRLKERLERL.......NCYA
XP_001239504.2/17-215  ARSRLNAR..SAGLSARSSR...RNS....................TVEESDRRLKERLERL.......NCYA
XP_017993993.1/2-217   ARTQRRAV.REGGKPTTQRRRGVPPG....................DPQQDEQDLHAQLRTM.......GLYA
CAH0376598.1/204-399   PSVRRRSENDKPAKLCCDRCDGDHMTEKCP..HFKK.DRGTHPDATRMLGKKGKVLGG.NAPPLITT..RGRV
KAF2195942.1/45-236    ETPYFSSL.PAPATYTPYPIDGMSST....................RCATAQEAEFPGLRAA.......GLQL
XP_016637916.1/8-187   .......................QLP....................SMVRKPKAVWPGLDKM.......GMYQ
XP_007733433.1/9-188   .......................QLP....................SMVRKPKAVWPGLVKM.......GMYQ

                          Cys-loop
                             60        70        80        90       100       110
TgOTU9/84-287          DTSPHEGECLFAALSFWLTGDPLNHSLVRDRLASHIRAHPDSVPRSAMRHELSGAKVAHD.............
XP_029220766.1/84-290  NTADASGECLFAALSFYLTGEPTNYVSVRTRLADYIRADPYSVPKHAMLNDLRGAGVAHS.............
XP_003880903.1/84-287  LTSPKPGECLFAAFAYWLTGDPLNHQHVRNRIAEYILTHPDSVPRAAMVDELTGANIPFL.............
PHJ24123.1/18-234      DRTAVPGDCLFASISYALTGSPSNSWLIRQQIASHIERHPDIVSNAAVAE.VAG...PVR.............
TPX20598.1/17-215      ADIQGDGNCLFYSLSDQLYGTPDHHDKVRQRLVDHIRKHRDSFIHFVDLGPDRPRSTREASRQANRSFSSVGS
EFW19281.1/17-215      ADIQGDGNCLFYSLSDQLYGTPEHHDKVRQRLVDHIRKHRDSFIHFVDLGPDRPRSTREASRQANRSFSSVGS
XP_003067094.1/17-215  ADIQGDGNCLFYSLSDQLYGTPEHHDRVRQRLVDHIRKHRDSFIHFVDLGPDRPRSTREASRQANRSFSSVGS
KMM71743.1/17-215      ADIQGDGNCLFYSLSDQLYGTPEHHDRVRQRLVDHIRKHRDSFIHFVDLGPDRPRSTREASRQANRSFSSVGS
KMU87852.1/17-215      ADIQGDGNCLFYSLSDQLYGTPDHHDKVRQRLVDHIRKHRDSFIHFVDLGPDRPRSTREASRQANRSFSSVGS
XP_001239504.2/17-215  ADIQGDGNCLFYSLSDQLYGTPDHHDKVRQRLVDHIRKHRDSFIHFVDLGPDRPRSTREASRQANRSFSSVGS
XP_017993993.1/2-217   SDTRGDGNCLFRALSDQLYGDPKYHAQLRQRTCDHLEAHPDMYAGFVETG.......................
CAH0376598.1/204-399   VPQPPDGSCLFHSLSYGLREG..NASGLRRELMQFIRKHPDLEIAGDPLRDWIR...................
KAF2195942.1/45-236    FDIKGDGNCLFRAFSDQLFGHPNHHTIVRDTIVQYVRDHKDHYINFVPVNEVRRSNRRH.....KGSSSREIA
XP_016637916.1/8-187   KQIAGDGNCLFASLSDQLYGTPANHPEIRASVVDHMRTYRPLFEHYVHKDDVQQRRTLRSAT...........
XP_007733433.1/9-188   KQIAGDGNCLFASLSDQLYGTPVKHPEIRANIIEHMRTFRPLFEHYVHKDDVQQRRTLRSAK...........
                               *

                                          Var-loop
                               120       130       140       150       160
TgOTU9/84-287          ..PDEPLDSLANKYSDLVARAGQWGGDELLGVFGHLAQCNVWMYVQAVDGS.P.GLNTH.LQ...........
XP_029220766.1/84-290  ..ADEQLSSLANKYADLVEKPAHWGGDDLLPVFGKLAQCNVWVYVQAQDGT.G.GMGNH.IE...........
XP_003880903.1/84-287  ..SDEPTETLAEQYAMLVAMPGRWGGDELLSVFAKMAKCNVWMHVSDQKGN.S.AFGTH.VD...........
PHJ24123.1/18-234      ..PGETRDQWVRRYTQGLLRLSTWGDDLHIQLLCDLARVNVFLYRQGPGKQPA.GGGSP.LE...........
TPX20598.1/17-215      TPSVDRINSKFEEMLSKMGEPHEWGGAFELQAFCQAYARDIVVYQADTVQEFTSNL.................
EFW19281.1/17-215      TPSVDRINSKFEEMLSKMGEPHEWGGAFELQAFCQAYARDIVVYQADTVQEFTSNL.................
XP_003067094.1/17-215  TPSVDRINSKFEEMLSKMGEPHEWGGAFELQAFCQAYARDIVVYQADTVQEFTSNL.................
KMM71743.1/17-215      TPSVDRINSKFEEMLSKMGEPHEWGGAFELQAFCQAYARDIVVYQADTVQEFTSNL.................
KMU87852.1/17-215      TPSVDRINSKFEEMLSKMGEPHEWGGAFELQAFCQAYARDIVVYQADTVQEFTSNL.................
XP_001239504.2/17-215  TPSVDRINSKFEEMLSKMGEPHEWGGAFELQAFCQAYARDIVVYQADTVQEFTSNL.................
XP_017993993.1/2-217   ........RPFDAYVREMRELGTYGGHLELSAFAHCLQKPIRIVQPGYVYIVACDDGSLKARASRERRERERK
CAH0376598.1/204-399   ....WDALVSVQKYADKM.SRGGWGGIEMAAFSELKGCNVEVYEQCSAGFKR.......I............
KAF2195942.1/45-236    SPSQDEREKKFEMRLQQMAKTGTWGDNVEIVAFAAAYDVQVNVWQREYNYTLPDDAASSSL............
XP_016637916.1/8-187   LASRQEPEDAFEEYLSLMSRSGTYGGEPELVAFCQVFDQDVTVHLPRI.KNFDRDS.................
XP_007733433.1/9-188   LAAPQDSEDSFEEYLALMSRSGTYGGEPELVAFCQVYNQDVTVHLPRI.KNFERDS.................

                                                                His-loop
                                          170       180        190          200
TgOTU9/84-287          ....................SWQLCGELK..PDAPSIFVVHRPA...INHWSSVVRVRSY
XP_029220766.1/84-290  ....................SWQLFGEFK..PGRPSVYLCHRPS...KNHWSSVMEVRSY
XP_003880903.1/84-287  ....................SWQACGPLI..PGAPSVYFNYQPA...RNHWRSVVAVRSY
PHJ24123.1/18-234      ....................AWTLYSTKDGPGDYPVIFLLHEP.....GHYKSVTRVRSY
TPX20598.1/17-215      ..........................HDVDP.DRETVHLAYHE....YQHYSSVRRLDAP
EFW19281.1/17-215      ..........................HDVDP.DRETVHLAYHE....YQHYSSVRRLDAP
XP_003067094.1/17-215  ..........................HDVDP.DRETVHLAYHE....YQHYSSVRRLDAP
KMM71743.1/17-215      ..........................HDVDP.DRETVHLAYHE....YQHYSSVRRLDAP
KMU87852.1/17-215      ..........................HDVDP.DRETVHLAYHE....YQHYSSVRRLDAP
XP_001239504.2/17-215  ..........................HDVDP.DRETVHLAYHE....YQHYSSVRRLDAP
XP_017993993.1/2-217   RALASTDAHASTARRGRRGALSEKATEITVPECVGPLHIAYHS....WEHYSSLRNVKGP
CAH0376598.1/204-399   .........................SLFEKSGASRTVRVCYRGG....VHYDA.LELR..
KAF2195942.1/45-236    ..................................PKVQVAFHVSSLSS.....LAIR...
XP_016637916.1/8-187   ....................ILYTNEHRGDPATVLPLHICYGGDEVTRAHYDSARSRDGS
XP_007733433.1/9-188   ....................ISYTNEHREATVLMPPLHICYGGDEVTRAHYDSARSRDGS
                                                                        * *
```

TgOTU10


Cys-loop
Var-
-loop
His-loop
1 10 20 30 40 50 60 70
80 90 100 110 120 130 140
150 160 170 180 190 200 210 220 230
TgOTU10/326-564
CEL67985.1/225-462
XP_029219553.1/189-427
PHJ24899.1/173-411
CEM17505.1/1-220
XP_013252361.1/237-457
CEM38169.1/1-241
QDY51779.1/44-246
KAH8585142.1/82-355
KAF7456649.1/81-346
TRY50808.1/82-347
XP_628214.1/82-347
OLQ17692.1/82-347
PPS95987.1/82-347
CUV06996.1/82-347
POM84210.1/82-347
XP_028875112.1/82-347
XP_026191367.1/177-486
OII74426.1/103-349
XP_002142096.1/123-370
KAH7648520.1/84-353
OEH75892.1/196-431
XP_028865069.1/480-729
XP_012768912.1/57-306
XP_764276.1/73-323
XP_953281.1/72-322
KAF8820772.1/384-625
KAF8822080.1/330-571
UKJ89843.1/126-374
EDO08293.2/69-319
BAN64701.1/69-319
UKK02836.1/767-1017
*
**