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logo

NTDB id 455 SSU RS00330 WP 012774888.1        .....MNDKEFGQRVRQLRESASMTREQFCDDELELSVRQLTRIEAGASKPTFSKIQYIATRLGMGLYELM.PDYVSLPE   74
NTDB id 465 SSU05 0053 ABP89025.1             MEVWFMNDKEFGQRVRQLRESASMTREQFCDDELELSVRQLTRIEAGASKPTFSKIQYIATRLGMGLYELM.PDYVSLPE   79
NTDB id 1138385 DQL29 RS00330 WP 020904818.1  ......MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPK   74
NTDB id 443 SPYM3 RS00325 WP 011054099.1      ......MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPK   74
NTDB id 451 SPYM18 RS00325 WP 002986681.1     ......MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPK   74
NTDB id 45 SMU RS00375 WP 002263400.1         ......MLKDFGKKIKSLRLEKGLTKEAVCLDESQLSTRQLTRIESGQSTPTLNKAVYIAGRLGVTLGYLTDGENVELPS   74
NTDB id 555 STRINF RS01865 WP 174221231.1     ..................MREEKEISREEFCGDETELSVRQLARIELNQSIPNLSKASFIANRLGVKLGTLTDGDSLELPK   63
consensus                                       **  ** *** *!*** ***!**!*!!**!!*!!!*!!!***!*!***!***!! *!******!**** **!!*

logo

NTDB id 455 SSU RS00330 WP 012774888.1        RYSKLKFDVLRTPTYGNEDLAEKRDAMMTEIYDDYYDELPEEEKIAIDAIQSRIDTLESGTAGFGKEILEDYFEQIFRKR   154
NTDB id 465 SSU05 0053 ABP89025.1             RYSKLKFDVLRTPTYGNEDLAEKRDAMMTEIYDDYYDELPEEEKIAIDAIQSRIDTLESGTAGFGKEILEDYFEQIFRKR   159
NTDB id 1138385 DQL29 RS00330 WP 020904818.1  RYKELKYLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKVAVDIIQAKFEVYQTGDINFGYSILKEFLPQLKRKS   154
NTDB id 443 SPYM3 RS00325 WP 011054099.1      RYKELKYLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKVAVDIIQAKFEVYQTGDINFGYSILKEFLPQLKRKS   154
NTDB id 451 SPYM18 RS00325 WP 002986681.1     RYKELKYLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKIIIDCLQATLDTLLSENTNFGIDLLQEYFNQIKTKV   154
NTDB id 45 SMU RS00375 WP 002263400.1         RYKELKYLLLRTPTYGDQQRLAEKETYFDEIFSQFYDDLPEEEQLIIDGLQSKLDIHFSDNIDFGVGILNDYFDQILRKT   154
NTDB id 555 STRINF RS01865 WP 174221231.1     RYKELKYLLLRTPTYGDQVRLDRKNDYFDEIAEVFYDVIPEEERLIIDCLQSKFDVHFSEDVNFGEGILNDYFGQVNRKK   143
consensus                                     !!**!!***!!!!!!*** **  *** **!!****!! *!!!!****! *!*****  ** **!!  *! *** !* *!

logo

KYELNDLLIVRLHLEYVRLSSCDSEIFRQ..FLKIIEHLHEQINIINSNDLFVLRDTLLSCVNILGSKKYYEPIPKIFDS   232
KYELNDLLIVRLHLEYVRLSSCDSEIFRQ..FLKIIEHLHEQINIINSNDLFVLRDTLLSCVNILGSKKYYEPIPKIFDS   237
IYNLNELLLIDLYLIILVVSHFSDDIFDAQFYEEITESMLKQHNNLSLEDLFLLNNILLSCADTYIRLKMFGRLKETLQL   234
IYNLNELLLIDLYLIILVVSHFSDDIFDVQFYEEITESMLKQHNNLSLEDLFLLNNILLSCADTYIRLKMFGHLKETLQL   234
RFRQNDLILLELYLAYLDIEGMDGQYSDKIFYDSLLDNLSEQFEQFELDELFIVNKIIIDISSLSLKNNRLDNLEKAIEM   234
NYQVNDLILIDLYFSCLTVSGLDSAIFDSRKYNQLLETLLKQVDCLPLEDLFVLNNVLLNNFGLLLELKKYDFVKQLIAV   234
VFTINDLILIDLYFACLSSAKKFEGIYSLDFYDDLMKRLVNQKHVSPETD.LILNNVLLNNIDLAFQFKREYYIERVITI   222
consensus                                  * *!*!****!**  * **  * ****  *** *** ** ! * * ************  * *  * ** * *** *

logo

VDKIIQSTQDFQKKPIVSVLKWKYALFVDKDRDEAEKHYLDAVLFAKLIENRELEQKIEEDWRVDNQ...   299
VDKIIQSTQDFQKKPIVSVLKWKYALFVDKDRDEAEKHYLDAVLFAKLIENRELEQKIEEDWRVDNQ...   304
SHFIMSTIQDFQKMPMYCMYEWKLSIFYLKDINRARNYFEQSILFTQMTGDTYLVQKLRGEWNKDIHYI.   303
SHFIMSTIQDFQKMPMYCMYEWKLSIFYLKDINRARNYFEQSILFTQMTGDTYLVQKLRGEWNKDIHYI.   303
SQKIMAKIQDWNRMPILKLIEWKYFLIKQKDIIKAEQSFMKACLFAQMTADQYLENKLIQEWEKDVKSY.   303
SNKIMDRTHDFQKKPIVNLLTWKHHLFVEKDYAEAKKSYDAAILFAQLTENINLRENLEKEWQKDSQNGT   304
SEKIMTEIHDFQRRPILSLVEWKYYLKLKHDFALAEQSFTNATLFARLVGDTYLENKLKEEWQLDIDAVE   292
consensus
* *!* ***!****!** ***!!* *** *!    !** *  **!!****** *!****  *!**!*
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X non conserved

X similar

X ≥ 50% conserved