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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 45 SMU RS00375 WP 002263400.1           ......MLKDFGKKIKSLRLEKGLTKEAVCLDESQLSTRQLTRIESGQSTPTLNKAVYIAGRLGVTLGYLTDGENVELPS   74
NTDB id 555 STRINF RS01865 WP 174221231.1       ..................MREEKEISREEFCGDETELSVRQLARIELNQSIPNLSKASFIANRLGVKLGTLTDGDSLELPK   63
NTDB id 1024837 ABW635 RS00395 WP 016355741.1   .......MTDFGLKIKALREEQNKTREEICGDESELSVRQLARIEQGQSIPSLAKAVYISNELGVSLSSITEDGEFDLPK   73
NTDB id 451 SPYM18 RS00325 WP 002986681.1       ......MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPK   74
NTDB id 443 SPYM3 RS00325 WP 011054099.1        ......MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPK   74
consensus                                         * *** *** *!*** ***!**!*!!**!!*!!!*!!! **!*!***!***!* *!***** ***** **!!*

logo

NTDB id 455 SSU RS00330 WP 012774888.1          RYSKLKFDVLRTPTYGNEDLAEKRDAMMTEIYDDYYDELPEEEKIAIDAIQSRIDTLESGTAGFGKEILEDYFEQIFRKR   154
NTDB id 465 SSU05 0053 ABP89025.1               RYSKLKFDVLRTPTYGNEDLAEKRDAMMTEIYDDYYDELPEEEKIAIDAIQSRIDTLESGTAGFGKEILEDYFEQIFRKR   159
NTDB id 45 SMU RS00375 WP 002263400.1           RYKELKYLLLRTPTYGDQQRLAEKETYFDEIFSQFYDDLPEEEQLIIDGLQSKLDIHFSDNIDFGVGILNDYFDQILRKT   154
NTDB id 555 STRINF RS01865 WP 174221231.1       RYKELKYLLLRTPTYGDQVRLDRKNDYFDEIAEVFYDVIPEEERLIIDCLQSKFDVHFSEDVNFGEGILNDYFGQVNRKK   143
NTDB id 1024837 ABW635 RS00395 WP 016355741.1   RYKELKHLILRTPTYKDKEKVRIREKQFDEIFINYYDNLPEEEKLVVDGLQASLDVALSKNINFGSDILNDYFEQIKVKS   153
NTDB id 451 SPYM18 RS00325 WP 002986681.1       RYKELKYLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKIIIDCLQATLDTLLSENTNFGIDLLQEYFNQIKTKV   154
NTDB id 443 SPYM3 RS00325 WP 011054099.1        RYKELKYLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKVAVDIIQAKFEVYQTGDINFGYSILKEFLPQLKRKS   154
consensus                                       !!**!!***!!!!!!*** **   **  **!!****!! *!!!!****!**!***** *  **!! **!*****!* *!

logo

KYELNDLLIVRLHLEYVRLSSCDSEIFRQ..FLKIIEHLHEQINIINSNDLFVLRDTLLSCVNILGSKKYYEPIPKIFDS   232
KYELNDLLIVRLHLEYVRLSSCDSEIFRQ..FLKIIEHLHEQINIINSNDLFVLRDTLLSCVNILGSKKYYEPIPKIFDS   237
NYQVNDLILIDLYFSCLTVSGLDSAIFDSRKYNQLLETLLKQVDCLPLEDLFVLNNVLLNNFGLLLELKKYDFVKQLIAV   234
VFTINDLILIDLYFACLSSAKKFEGIYSLDFYDDLMKRLVNQKHVSPETD.LILNNVLLNNIDLAFQFKREYYIERVITI   222
CFTRNDLIIIDLYLICVRTSKFSDAIYDAAVYKSLLKKTIAQIDCAEIDDFYVLNQVLITFYTISIQLDRPKELELIISN   233
RFRQNDLILLELYLAYLDIEGMDGQYSDKIFYDSLLDNLSEQFEQFELDELFIVNKIIIDISSLSLKNNRLDNLEKAIEM   234
IYNLNELLLIDLYLIILVVSHFSDDIFDVQFYEEITESMLKQHNNLSLEDLFLLNNILLSCADTYIRLKMFGHLKETLQL   234
consensus                                        * *!*!****!**  * **  *  ***   *  *** ** !*  * ************   * *  **** * *** *

logo

VDKIIQSTQDFQKKPIVSVLKWKYALFVDKDRDEAEKHYLDAVLFAKLIENRELEQKIEEDWRVDNQ...   299
VDKIIQSTQDFQKKPIVSVLKWKYALFVDKDRDEAEKHYLDAVLFAKLIENRELEQKIEEDWRVDNQ...   304
SNKIMDRTHDFQKKPIVNLLTWKHHLFVEKDYAEAKKSYDAAILFAQLTENINLRENLEKEWQKDSQNGT   304
SEKIMTEIHDFQRRPILSLVEWKYYLKLKHDFALAEQSFTNATLFARLVGDTYLENKLKEEWQLDIDAVE   292
CNRIMSVVNDFYRMPILYVMEWKYSIKYLDDLKKATSFYHKAKLFAQMTGDSDLANKIEKEWAMDCQ...   300
SQKIMAKIQDWNRMPILKLIEWKYFLIKQKDIIKAEQSFMKACLFAQMTADQYLENKLIQEWEKDVKSY.   303
SHFIMSTIQDFQKMPMYCMYEWKLSIFYLKDINRARNYFEQSILFTQMTGDTYLVQKLRGEWNKDIHYI.   303
consensus
* *!*  **!****!** ***!!* *** *!   !*  *  **!!******  !***** *! *! *
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X non conserved

X similar

X $\geq$ 50% conserved