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logo
NTDB id 91105 SUT RS00395 WP 024532318.1   .....MDNKEFGQRVRQLREQAMITREQFCDDEMELSVRQLTRIEAGTCKPTFSKINFIADRLGMGLYELM.PDYIKLPERYSKL   79
NTDB id 458 SSUD9 RS00355 WP 002935296.1   .....MNDKEFGQRVRQLRESASMTREQFCDDELELSVRQLTRIEAGASKPTFSKIQYIATRLGMGLYELM.PDYVSLPERYSKL   79
NTDB id 455 SSU RS00330 WP 012774888.1     .....MNDKEFGQRVRQLRESASMTREQFCDDELELSVRQLTRIEAGASKPTFSKIQYIATRLGMGLYELM.PDYVSLPERYSKL   79
NTDB id 465 SSU05 0053 ABP89025.1          MEVWFMNDKEFGQRVRQLRESASMTREQFCDDELELSVRQLTRIEAGASKPTFSKIQYIATRLGMGLYELM.PDYVSLPERYSKL   84
NTDB id 451 SPYM18 RS00325 WP 002986681.1  ......MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPKRYKEL   79
NTDB id 45 SMU RS00375 WP 002263400.1      ......MLKDFGKKIKSLRLEKGLTKEAVCLDESQLSTRQLTRIESGQSTPTLNKAVYIAGRLGVTLGYLTDGENVELPSRYKEL   79
NTDB id 555 STRINF RS01865 WP 174221231.1  ................MREEKEISREEFCGDETELSVRQLARIELNQSIPNLSKASFIANRLGVKLGTLTDGDSLELPKRYKEL   68
consensus                                     *  **********!* * ***!**!*!!**!!*!!!*!!!** **!***!***!! *!******!* **** !!*!!**!

logo
NTDB id 91105 SUT RS00395 WP 024532318.1   KFDVLRTPTYGNEGLVETRNEMITEIYEEYYDDLPEEEQIAMDAFQSIIDVFETKSTQYGREILDDYFEQVYRKEKYTINDLLIL   164
NTDB id 458 SSUD9 RS00355 WP 002935296.1   KFDVLRTPTYGNEDLAEKRDAMMTEIYDDYYDELPEEEKIVVDTLCSLFDVLDTDSQEYGKEILDDYLHQSYHRSKLSINDLMIL   164
NTDB id 455 SSU RS00330 WP 012774888.1     KFDVLRTPTYGNEDLAEKRDAMMTEIYDDYYDELPEEEKIAIDAIQSRIDTLESGTAGFGKEILEDYFEQIFRKRKYELNDLLIV   164
NTDB id 465 SSU05 0053 ABP89025.1          KFDVLRTPTYGNEDLAEKRDAMMTEIYDDYYDELPEEEKIAIDAIQSRIDTLESGTAGFGKEILEDYFEQIFRKRKYELNDLLIV   169
NTDB id 451 SPYM18 RS00325 WP 002986681.1  KYLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKIIIDCLQATLDTLLSENTNFGIDLLQEYFNQIKTKVRFRQNDLILL   164
NTDB id 45 SMU RS00375 WP 002263400.1      KYLLLRTPTYGDQQRLAEKETYFDEIFSQFYDDLPEEEQLIIDGLQSKLDIHFSDNIDFGVGILNDYFDQILRKTNYQVNDLILI   164
NTDB id 555 STRINF RS01865 WP 174221231.1  KYLLLRTPTYGDQVRLDRKNDYFDEIAEVFYDVIPEEERLIIDCLQSKFDVHFSEDVNFGEGILNDYFGQVNRKKVFTINDLILI   153
consensus                                  !***!!!!!!*** ****** ***!!****!!**!!!!****!*****!******  *!***!**!**!**** ** *!!!***

logo
RLYLEHIRFEE..TSSQMFQIFLDMVKHFPNQTEAIDPGDLFIFRDIMLTSIGILGTKEQFGYIPVLFDTLDKLMMSTQDFQKKP   247
RLFIEHCQLEDLSVGTSNYALFTDLIEKLPQSIYDVHSESLFIVRDLFLAIVRILFSKELYNHIPVYIEKIENIMELSQDFQKKP   249
RLHLEYVRLSS..CDSEIFRQFLKIIEHLHEQINIINSNDLFVLRDTLLSCVNILGSKKYYEPIPKIFDSVDKIIQSTQDFQKKP   247
RLHLEYVRLSS..CDSEIFRQFLKIIEHLHEQINIINSNDLFVLRDTLLSCVNILGSKKYYEPIPKIFDSVDKIIQSTQDFQKKP   252
ELYLAYLDIEGMDGQYSDKIFYDSLLDNLSEQFEQFELDELFIVNKIIIDISSLSLKNNRLDNLEKAIEMSQKIMAKIQDWNRMP   249
DLYFSCLTVSGLDSAIFDSRKYNQLLETLLKQVDCLPLEDLFVLNNVLLNNFGLLLELKKYDFVKQLIAVSNKIMDRTHDFQKKP   249
DLYFACLSSAKKFEGIYSLDFYDDLMKRLVNQKHVSPETD.LILNNVLLNNIDLAFQFKREYYIERVITISEKIMTEIHDFQRRP   237
consensus                                  *!*** * *      *  *  *  *** *  **  *   ********** * ** *** ** ****** *****  **!****!

logo
ILNLLKWKYELRIHGNKERAREFYEEAVLFAKMIASPHLAEKLEEEWANDSQ....   299
ILNLVKWKYELKVQHNHEIAERYYNEAITFASLLNQFHLKEKLQMEWEKDTQSLKR   305
IVSVLKWKYALFVDKDRDEAEKHYLDAVLFAKLIENRELEQKIEEDWRVDNQ....   299
IVSVLKWKYALFVDKDRDEAEKHYLDAVLFAKLIENRELEQKIEEDWRVDNQ....   304
ILKLIEWKYFLIKQKDIIKAEQSFMKACLFAQMTADQYLENKLIQEWEKDVKSY..   303
IVNLLTWKHHLFVEKDYAEAKKSYDAAILFAQLTENINLRENLEKEWQKDSQNGT.   304
ILSLVEWKYYLKLKHDFALAEQSFTNATLFARLVGDTYLENKLKEEWQLDIDAVE.   292
consensus                                  !* ***!!* ! * ** * !** * *!**!!*** *  !*******!  ! *
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X non conserved

X similar

X ≥ 50% conserved