```
logo
NTDB id 144607 SAH002 RS00405 WP 000912100.1  MLKHFGSKVRNLRVTRNITREDFCGDETELSVRQLARIESGQSIPNLTKAHYIAKQLNVKLDILTGGESLELPKRYKELK   80
NTDB id 443 SPYM3 RS00325 WP 011054099.1      MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPKRYKELK   80
NTDB id 451 SPYM18 RS00325 WP 002986681.1     MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPKRYKELK   80
NTDB id 45 SMU RS00375 WP 002263400.1         MLKDFGKKIKSLRLEKGLTKEAVCLDESQLSTRQLTRIESGQSTPTLNKAVYIAGRLGVTLGYLTDGENVELPSRYKELK   80
NTDB id 555 STRINF RS01865 WP 174221231.1     ...........MREEKEISREEFCGDETELSVRQLARIELNQSIPNLSKASFIANRLGVKLGTLTDGDSLELPKRYKELK   69
consensus                                     ** *** *** *!*** ***!**!*!!**!!*!!!*!!!**!!*!*!*!***!!* !*!****!!*!* *!!!*!!!!!!

logo
NTDB id 144607 SAH002 RS00405 WP 000912100.1  YLILRIPTYADAERLKLRECQFDHIFEEFYDNLPEDECLAIDSLQAKFEVYQTGDINFGVEVLCECFDKVKYKEKYTLND  160
NTDB id 443 SPYM3 RS00325 WP 011054099.1      YLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKVAVDIIQAKFEVYQTGDINFGYSILKEFLPQLKRKSIYNLNE  160
NTDB id 451 SPYM18 RS00325 WP 002986681.1     YLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKIIIDCLQATLDTLLSENTNFGIDLLQEYFNQIKTKVRFRQND  160
NTDB id 45 SMU RS00375 WP 002263400.1         YLLLRTPTYGDQQRLAEKETYFDEIFSQFYDDLPEEEQLIIDGLQSKLDIHFSDNIDFGVGILNDYFDQILRKTNYQVND  160
NTDB id 555 STRINF RS01865 WP 174221231.1     YLLLRTPTYGDQVRLDRKNDYFDEIAEVFYDVTPEEERLIIDCLQSKFDVHFSEDVNFGEGILNDYFGQVNRKKVFTIND  149
consensus                                     !!*!!*!!!*!  *! *****!!*!******!! *!!*!****! *!*****  *****!!* *!**** ****!  * *!*

logo
NTDB id 144607 SAH002 RS00405 WP 000912100.1  LIIIDLFLTCAVVSKFNNRAFTKEVFQTICKTLISQNHKLTAEDLFWFNHVLLNCVFVGLCLNSEECLAEMLEVSRQTMV  240
NTDB id 443 SPYM3 RS00325 WP 011054099.1      LLLIDLYLIILVVSHFSDDIFDVQFYEEITESMLKQHNNLSLEDLFLLNNILLSCADTYIRLKMFGHLKETLQLSHFIMS  240
NTDB id 451 SPYM18 RS00325 WP 002986681.1     LILLELYLAYLDIEGMDGQYSDKIFYDSLLDNLSEQFEQFELDELFIVNKIIIDISSLSLKNNRLDNLEKAIEMSQKIMA  240
NTDB id 45 SMU RS00375 WP 002263400.1         LILIDLYFSCLTVSGLDSAIFDSRKYNQLLETLLKQVDCLPLEDLFVLNNVLLNNFGLLLELKKYDFVKQLIAVSNKIMD  240
NTDB id 555 STRINF RS01865 WP 174221231.1     LILIDLYFACLSSAKKFEGIYSLDFYDDLMKRLVNQKHVSPETD.LILNNVLLNNIDLAFQFKREYYIERVITISEKIMT  228
consensus                                     !****!** ** **      ***  *** ****** !   * *******!*****   * * *** * *  ** *! **!

logo
NTDB id 144607 SAH002 RS00405 WP 000912100.1  STHDFHKMPLYFMYQWKYFITIDNDIKSAENAYQQSIMFSKMIDDKHLIKKLELEWQEDITGH.   303
NTDB id 443 SPYM3 RS00325 WP 011054099.1      TIQDFQKMPMYCMYEWKLSIFYLKDINRARNYFEQSILFTQMTGDTYLVQKLRGEWNKDIHYI.   303
NTDB id 451 SPYM18 RS00325 WP 002986681.1     KIQDWNRMPILKLIEWKYFLIKQKDIIKAEQSFMKACLFAQMTADQYLENKLIQEWEKDVKSY.   303
NTDB id 45 SMU RS00375 WP 002263400.1         RTHDFQKKPIVNLLTWKHHLFVEKDYAEAKKSYDAAILFAQLTENINLRENLEKEWQKDSQNGT   304
NTDB id 555 STRINF RS01865 WP 174221231.1     EIHDFQRRPILSLVEWKYYLKLKHDFALAEQSFTNATLFARLVGDTYLENKLKEEWQLDIDAVE   292
consensus                                      **!****!** ***!!*** * *!*  !**** ****!****** *! **!  !!**!*
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X non conserved

X similar

X ≥ 50% conserved