```
logo
NTDB id 443 SPYM3 RS00325 WP 011054099.1      MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPKRYKELK   80
NTDB id 111299 H346 RS0102790 WP 027969744.1  MLEYFGEKVRGLRHEKRISREDLCGDESELSVRQLARIELGQSIPSLAKVIFIAKALDVSVGYLTDGASLELPKRYKELK   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                                     *** ** *** *!*!!****!**!*!!**!!*!!!*!!!**!!*!*!***!!**!  !**!*!!!!* *!!!*!!!!!!
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logo
NTDB id 443 SPYM3 RS00325 WP 011054099.1      YLILRTPTYMDDGKLQVREEQFDEIFEDYYDKLPEEEKVAVDIIQAKFEVYQTGDINFGYSILKEFLPQLKRKSIYNLNE  160
NTDB id 111299 H346 RS0102790 WP 027969744.1  YLILRTPTYMDDGKLQLREEQFDEIFEDYYEQLPEEEQLIIDCLQATLDTLLSGNINFGIDLLQEYFKQIKSKSRFREND  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                                     !!*!!!!!!*!***!*****!!!!****!* *!!!!****!**!*****  *****!!* *!**** !***!* * *!*
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logo
NTDB id 443 SPYM3 RS00325 WP 011054099.1      LLLIDLYLIILVVSHFSDDIFDVQFYEEITESMLKQHNNLSLEDLFLLNNILLSCADTYIRLKMFGHLKETLQLSHFIMS  240
NTDB id 111299 H346 RS0102790 WP 027969744.1  LILIELYLAYLDIEGLNGQYSDKSFNNSLLDILLHQFESFELDELFIMNKIIIGISSLSLKNDKLDNLEKTIEMSQKIMA  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                                     !*!**!!** ! * **   ***  *** *** ** ! *   *******!****    * ** ** * *** * *!**!!
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logo
NTDB id 443 SPYM3 RS00325 WP 011054099.1      TIQDFQKMPMYCMYEWKLSIFYLKDINRARNYFEQSILFTQMTGDTYLVQKLRGEWNKDIHYI.   303
NTDB id 111299 H346 RS0102790 WP 027969744.1  KIQDWNRMPILKLIEWKYFLIKQKNKQKAKEAFVKACLFAQVTGDKYLEKQLNEEWERDINSY.   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