

logo

NTDB id 455 SSU RS00330 WP 012774888.1	MNDKEFGQQRVRLRESASMTREQFCDELELSVRQLTRIEAGASKPTFSKIQQYIATRLGGLYELM.PDYVSLPERYSKL	79
NTDB id 465 SSU05 0053 ABP89025.1	MEVWFMNDKEFGQQRVRLRESASMTREQFCDELELSVRQLTRIEAGASKPTFSKIQQYIATRLGGLYELM.PDYVSLPERYSKL	84
NTDB id 443 SPYM3 RS00325 WP 011054099.1	MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIKAALNVSVGYLTDGADLELPKRYKEL	79
NTDB id 451 SPYM18 RS00325 WP 002986681.1	MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIKAALNVSVGYLTDGADLELPKRYKEL	79
NTDB id 45 SMU RS00375 WP 002263400.1	MLKDFGKKIKSLRLEKGLTKEAVCLDESQLSTRQLTRIESGQSTPTLNKAVYIAGRLGVTILGYLTDGENVELPSRYKEL	79
NTDB id 555 STRINF RS01865 WP 174221231.1	MREEKEISREEFCGDELELSVRQLARIELNQSIPNLSKASFIANRLGVKLGLTLDGDSLELPKRYKEL	68
consensus	*****!*!*****!!**!*!!!!!!**!*!***!***!***!***!***!	

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NTDB id 455 SSU RS00330 WP 012774888.1	KYLRLRTPTYCDQGRLOVREYDFEFEDYYDKLPEEEKKILUDLQSKIDTLESSTANFCGLLDYFQVRKYYNDLTLV	164
NTDB id 465 SSU05 0053 ABP89025.1	KEDVLRTPTYCNEDLAEKRDAMMTEIYDDYYDELPEEEKI AIDATQSRIDTLES GTAGFGKEILEDYFEQIFRKRKYELNDLLIV	169
NTDB id 443 SPYM3 RS00325 WP 011054099.1	KYLRLRTPTYMDGKQLQVREEQFDEIFEDYYDKLPEEEKKVAVDIIQAKFEVYQTDINFCGYSILKEFLPQLKRKSIYNLNEILLI	164
NTDB id 451 SPYM18 RS00325 WP 002986681.1	KYLRLRTPTYMDGKQLQVREEQFDEIFEDYYDKLPEEEKI IIDCLQATDITLLSENTNFGIDLQEYFNQIKTKVRFQRNDLILL	164
NTDB id 45 SMU RS00375 WP 002263400.1	KYLRLRTPTYGDDQLAEKETYFDEIFSQFYDDLPEEEQLIIDGLQSKLDIHFSNDIDFGVGILNDYFDQILRKTNYQVNDLILI	164
NTDB id 555 STRINF RS01865 WP 174221231.1	KYLRLRTPTYGDDQLDRKNDYFDEIAEVEYDVPEEERLIIDCLQSKLFDVHFSEDVNFCEGILNDYFGQVNRKKVETINDLILI	153
consensus	!***!!!!!!***** !***!!***!!*!!!!** **!*!**** ** !!*!***!*!***!***!	

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NTDB id 455 SSU RS00330 WP 012774888.1	RLHLEYVRLSSCDSEIFRQ...FLKILIEHLHEQINIINSNDLFVLRDTLLSCVNILGSKKYEPPIPKIFDSVDKIIQSTQDFQKKP	247
NTDB id 465 SSU05 0053 ABP89025.1	RLHLEYVRLSSCDSEIFRQ...FLKILIEHLHEQINIINSNDLFVLRDTLLSCVNILGSKKYEPPIPKIFDSVDKIIQSTQDFQKKP	252
NTDB id 443 SPYM3 RS00325 WP 011054099.1	DLYLILVVSHPFDDIFDVQFYEEITESMLKQHNNLSLEDLFLNNLILSCADTYIRLKMFGHLKETLQLSHFIMSTIQDFQKKP	249
NTDB id 451 SPYM18 RS00325 WP 002986681.1	ELYLAYLDIEGMDGQYSDKIFYDSLLDNISEQFEQFELDELFIYNKIITDISSSLKNNRNLONLEKATEMSQKIMAKIQDWNRM	249
NTDB id 45 SMU RS00375 WP 002263400.1	DLYFSCLTYSGLDSATFDSRKYNQLLETILKQVDCIPLLEDLFLVNNVLLNNFGLLELKKYDFVKQLIAVSNKIMDRTHDFQKKP	249
NTDB id 555 STRINF RS01865 WP 174221231.1	DLYFACLSSAKKFECIYSLDFYDDLKRLVNVQKHVSPETD.LLLNNVLLNNIDLAFQFKREYYIERVITISEKIMTEIHDFQRRP	237
consensus	*!*** ** ** ** * ** ** * ! * ***** ** !***!!	

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NTDB id 455 SSU RS00330 WP 012774888.1	IVSVLKWKYALFVDKDRDEAEKHVLDVLFAKLIENRELEQKTEEDWRVDNQ...	299
NTDB id 465 SSU05 0053 ABP89025.1	IVSVLKWKYALFVDKDRDEAEKHVLDVLFAKLIENRELEQKTEEDWRVDNQ...	304
NTDB id 443 SPYM3 RS00325 WP 011054099.1	MYCMYEWKLSIFYLKDINRARNYFEQSILFTQMTGDTYLVQKLRGEWNKDIHYI.	303
NTDB id 451 SPYM18 RS00325 WP 002986681.1	ILKLEIWKYFLIKQKDIKAEQSMKACLFAQMTADQYLENKLIQEWKDVKSY.	303
NTDB id 45 SMU RS00375 WP 002263400.1	IVNLLTWKHHLFVEKDYAEAKKSYDAAILFAQLTENINLRENLEKEWQKDSQNGT	304
NTDB id 555 STRINF RS01865 WP 174221231.1	ILSLVENKYVLKLEHDFALAEQSTNATLFLARLVGDTYLENKLKEEWQLDIDAVE	292
consensus	** ** !!* *** * ! ! * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * !	

- ☒ non conserved
- ☒ similar
- ☒ ≥ 50% conserved