

Accession	Protein	Length	Score	Identity	Positives	Negatives	Gaps
NTDB id 47	STER RS00925 WP 002949220.1	24	MEQEVFVKAYEKVRPIVLKAFRQY	24	24	0	0
NTDB id 320	STU RS10340 WP 002949220.1	24	MEQEVFVKAYEKVRPIVLKAFRQY	24	24	0	0
NTDB id 50	STRSA0001 RS07545 WP 002885610.1	24	MEQEVFVHAYEVVRPIVLKASRQY	24	24	0	0
NTDB id 468	HSISS4 RS00725 WP 021143466.1	24	MEQEVFVHAYEVVRPIVLKASRQY	24	24	0	0
NTDB id 44	SMU RS09085 WP 002263585.1	23	MEEDFEIVFNKVKPIVWKLRY	23	23	0	0
NTDB id 423	SGO RS08370 WP 012130755.1	21	MKFEDVYKQVEGIVKRCYKDY	21	21	0	0
NTDB id 424	SGO RS10430 WP 012130755.1	21	MKFEDVYKQVEGIVKRCYKDY	21	21	0	0
NTDB id 454	SSU RS00080 WP 011921639.1	21	MEFEKVYASVKGIVNKARKEF	21	21	0	0
NTDB id 461	GPW51 RS00080 WP 011921639.1	21	MEFEKVYASVKGIVNKARKEF	21	21	0	0
NTDB id 457	SSUD9 RS00080 WP 002936602.1	21	MEFEKVYASVKGIVNKARKEF	21	21	0	0
NTDB id 582	DLJ51 RS00505 WP 002962720.1	69	MDKEKLKEIFNKHSA LPEEVEEFDDGMVKEVITAGLLFCLKEVL...D...MDDSSFVSASF SRVEKTVSKLAKDY	69	69	0	0
NTDB id 554	STRINF RS00370 WP 115283725.1	21	MDFERYFCTVKPIILKLRHY	21	21	0	0
NTDB id 449	SPYM18 RS01395 WP 011018214.1	45	MSCCFVVLFILGIVKKKRLKMSIETRAAFEKVKPIILKLRHY	45	45	0	0
NTDB id 450	SPYM18 RS08475 WP 011018214.1	45	MSCCFVVLFILGIVKKKRLKMSIETRAAFEKVKPIILKLRHY	45	45	0	0
NTDB id 441	SPYM3 RS01385 WP 011106595.1	45	MSCCFVVLFILGIVKKKRLKMSIETRAVFEKVKPIILKLRHY	45	45	0	0
NTDB id 442	SPYM3 RS08515 WP 011106595.1	45	MSCCFVVLFILGIVKKKRLKMSIETRAVFEKVKPIILKLRHY	45	45	0	0
NTDB id 447	SpyM6JRS4 RS01370 WP 010921894.1	45	MSCCFVVLFILGIVKKKRLKMSIETRAAFEKVKPIILKLRHY	45	45	0	0
NTDB id 448	SpyM6JRS4 RS07800 WP 010921894.1	45	MSCCFVVLFILGIVKKKRLKMSIETRAAFEKVKPIILKLRHY	45	45	0	0
consensus			*** **				

NTDB	id	47	STER RS00925 WP 002949220.1	FIQLWDQADMEQEAMMTLYQLLKKFPDLEKDDDKLRRYFKTKFRNRLNDEVRRQESVKRQANRQCYVEISDI AF CIP NKE	104
NTDB	id	320	STU RS10340 WP 002949220.1	FIQLWDQADMEQEAMMTLYQLLKKFPDLEKDDDKLRRYFKTKFRNRLNDEVRRQESVKRQANRQCYVEISDI AF CIP NKE	104
NTDB	id	50	STRSA0001 RS07545 WP 002885610.1	FIQLWDLADMEQEAMMTLYQLLEKFPELKSDDDKL RRYFKTKFRNRLNDEVRRQESVKRQANRQC YIETS DI AF CLPN KE	104
NTDB	id	468	HSISSA RS00725 WP 021143466.1	FIQLWDQADMEQEAMMTLYQLLEKFPELKSDDDKL RRYFKTKFRNRLNDEVRRQESVKRQANRQC Y IETSDIAFCLPNKE	104
NTDB	id	44	SMU RS09085 WP 002263585.1	FIKMWTREDDMQEGMLIHQLHREHPLEEDDTKLYIFYKTRFSNY TKDVLRQQESQKRKRFNRMSYE EVGEIEHC LSSGG	103
NTDB	id	423	SGO RS08370 WP 012130755.1	YLHLWEYADWRQEGMLVLVELLKSHPNLLEDQPRLYRYFKTKFRNIHD LR RR QESQKR KLD RPQPYEEVSEIGH RL RMKE	101
NTDB	id	424	SGO RS10430 WP 012130755.1	YLHLWEYADWRQEGMLVLVELLKSHPNLLEDQPRLYRYFKTKFRNIHD LR RR QESQKR KLD RPQPYEEVSEIGH RL RMKE	101
NTDB	id	454	SSU RS00080 WP 011921639.1	YIKLWDRDDWEQEGMMTLFELLEAQPWLVDEQVQLCYCFKV KFRNRIKDRI RKQESQKR KF DRMPHE D IYELSHA IQSPG	101
NTDB	id	461	GPW51 RS00080 WP 011921639.1	YIKLWDRDDWEQEGMMTLFELLEAQPWLVDEQVQLCYCFKV KFRNRIKDRI RKQESQKR KF DRMPHE D IYELSHA IQSPG	101
NTDB	id	457	SSUD9 RS00080 WP 002936602.1	YIKLWDRDDWEQEGMMTLFELLEAQPWLVDEQVQLCYCFKV KFRNRIKDRI RKQESQKR KF DRMPHE D IHLSHA IQSPG	101
NTDB	id	582	DLJ51 RS00505 WP 002962720.1	YIKLWTYDDWRQEARIILYQLLERFFPDLANDEEKLRIYFKTKFRSYVDNIRKQESQKRAFDRMIYEEI SELGH MIP SQ	149
NTDB	id	554	STRINF RS00370 WP 115283725.1	FVKLWIDYEDWIQEGRIVFEGLLEEHPDLINNEGKCYSFYKTGFNSHWKDJRHQS F KRKF NR MP YE ETS DIS HC VPQVF	101
NTDB	id	449	SPYM18 RS01395 WP 011018214.1	YIQLWDRDDWL QECHII LL QL LERY PEL IE EEER LYRY FKTK F SSYL KD LL RR QESQKR QFH KLAYEEIGEV AHA IPSRG	125
NTDB	id	450	SPYM18 RS08475 WP 011018214.1	YIQLWDRDDWL QECHII LL QL LERY PEL IE EEER LYRY FKTK F SSYL KD LL RR QESQKR QFH KLAYEEIGEV AHA IPSRG	125
NTDB	id	441	SPYM3 RS01385 WP 011106595.1	YIQLWDRDDWL QECHII LL QL LERY PEL IE EEER LYRY FKTK F SSYL KD LL RR QESQKR QFH KLAYEEIGEV AHA IPSRG	125
NTDB	id	442	SPYM3 RS08515 WP 011106595.1	YIQLWDRDDWL QECHII LL QL LERY PEL IE EEER LYRY FKTK F SSYL KD LL RR QESQKR QFH KLAYEEIGEV AHA IPSRG	125
NTDB	id	447	SpyM6JRS4 RS01370 WP 010921894.1	YIQLWDRDDWL QECHII LL QL LERY PEL IE EEER LYRY FKTK F SSYL KD LL RR QESQKR QFH KLAYEEIGEV AHA IPSRG	125
NTDB	id	448	SpyM6JRS4 RS07800 WP 010921894.1	YIQLWDRDDWL QECHII LL QL LERY PEL IE EEER LYRY FKTK F SSYL KD LL RR QESQKR QFH KLAYEEIGEV AHA IPSRG	125
consensus				* ** * * * *	125

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NTDB id 47 STER RS00925 WP 002949220.1	LD.MVDRLAYDEQLNAFREQLSSESLKLDRLIGGECFRGRKKMIRELRFWMVDFDPCNEED	165
NTDB id 320 STU RS10340 WP 002949220.1	LD.MVDRLAYDEQLNAFREQLSSESLKLDRLIGGECFRGRKKMIRELRFWMVDFDPCNEED	165
NTDB id 50 STRSA0001 RS07545 WP 002885610.1	LD.AVDRLVYDEQLNAFRNQLSSEDA TKLDRLLAGECFRGRKKMIRELKFWMVDFDPYNEDD	165
NTDB id 468 HSISS4 RS00725 WP 021143466.1	LD.AVDRLVYDEQLNAFRNQLSSEDA TKLDRLLAGECFRGRKKMIRELKFWMVDFDPYNEDD	165
NTDB id 44 SMU RS09085 WP 002263585.1	MQ.LDEYILFRDSL LAYKQGLSTEKQELFERLVAGEHFLGRQSM LKDLRKKLSDFKEK....	160
NTDB id 423 SGO RS08370 WP 012130755.1	LY.LDELVAFRSAMSEYRSRLSPEEAKQYERLMADERFKGRKAMLKDLSYHLRDFNPRLD..	160
NTDB id 424 SGO RS10430 WP 012130755.1	LY.LDELVAFRSAMSEYRSRLSPEEAKQYERLMADERFKGRKAMLKDLSYHLRDFNPRLD..	160
NTDB id 454 SSU RS00080 WP 011921639.1	LI.NDELLMLRGALRDYRK NLSNDQLDKYEKLISGQCFNGRREMIRDLQIHLKDFR.....	156
NTDB id 461 GPW51 RS00080 WP 011921639.1	LI.NDELLMLRGALRDYRK NLSNDQLDKYEKLISGQCFNGRREMIRDLQIHLKDFR.....	156
NTDB id 457 SSUD9 RS00080 WP 002936602.1	LI.NDELLMLRGALRDYRK NLSNDQLDKYEKLISGQCFNGRREMIRDLQIHLKDFR.....	156
NTDB id 582 DLJ51 RS00505 WP 002962720.1	MD.TADYCALKEK LKELKQKLAPEDYAKILLMRGAFKGRSAFIKDIKVEFEDFDEDN...	207
NTDB id 554 STRINF RS00370 WP 115283725.1	FFEVEDYVAYQQLSLACLRR TLGREDRLKLEKVIRGERFECKKAFIKSTIELYFSDFRP.....	158
NTDB id 449 SPYM18 RS01395 WP 011018214.1	LW.LDDYVAYQEVIASLENQLNSQERMQFKALIRGERFKGRRALLRKISPYFKEFAQQL...	183
NTDB id 450 SPYM18 RS08475 WP 011018214.1	LW.LDDYVAYQEVIASLENQLNSQERMQFKALIRGERFKGRRALLRKISPYFKEFAQQL...	183
NTDB id 441 SPYM3 RS01385 WP 011106595.1	LW.LDDYVAYQEVIASLENQLNSQERMQFQALIRGERFKGRRALLRKISPYFKEFAQQL...	183
NTDB id 442 SPYM3 RS08515 WP 011106595.1	LW.LDDYVAYQEVIASLENQLNSQERMQFQALIRGERFKGRRALLRKISPYFKEFAQQL...	183
NTDB id 447 SpyM6JRS4 RS01370 WP 010921894.1	LW.LDDYVAYQEVIASLENQLNSQERMQFQALIRGERFKGRRALLRKISPYFKEFAQQL...	183
NTDB id 448 SpyM6JRS4 RS07800 WP 010921894.1	LW.LDDYVAYQEVIASLENQLNSQERMQFQALIRGERFKGRRALLRKISPYFKEFAQQL...	183
consensus	* *** ** * * *****!***** ***** * * !*!***** * * *!*	

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