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NTDB id 587 KW2 RS10850 WP 042211510.1	MQT	DILRLILRPKGGKKLALIKQAKLIQLMGNLNNMGFNLGCVTNFLALSKLVEKEFVFKMHQGLSSGKSLSEIL	ESL	76
NTDB id 1127717 FGL14 RS00695 WP 138084099.1	.MTFLQR	DISVRSKQGLKKLSSKEQYKLIQLLANLLL	TGFNLAEITAFLLKSHLIPPEPYVLRMEEALLKGRGLADMLAGI	79
NTDB id 395 FSA28 RS09400 WP 257638827.1	.MTFLQQ	DISLKEKHKQKKLKIKKQKQKVIQLFNNLFTSGFNLTEIDFLERSHLLAEIYTKKMRQGLNLGLHLAEIMSSL		79
NTDB id 386 SMU RS09030 WP 255262721.1	.MTFLQQ	DISLKEKHKQKKLKIKKQKQKVIQLFNNLFTSGFNLTEIDFLERSHLLAEIYTKKMRQGLNLGLHLAEIMSSL		79
NTDB id 430 SGO RS09415 WP 012130941.1	MISFLQQ	DISILSKQKQKKLGTSGKQKQVIELFNNLFSSSGFHLAETVDFLGRSALLEKNYVQQMRQGLANGQAFSEIMASL		80
NTDB id 271 KZH43 RS09260 WP 074196785.1		MDISQVFRLRRKKLATAKQKNIITLFNNLFSSSGFHLVETISFLDRSALLDKQCVTQMRVGLSQGKSFSEMMESL		74
NTDB id 230 SPD RS09890 WP 074196785.1		MDISQVFRLRRKKLATAKQKNIITLFNNLFSSSGFHLVETISFLDRSALLDKQCVTQMRVGLSQGKSFSEMMESL		74
NTDB id 196 SPR RS09425 WP 074196785.1		MDISQVFRLRRKKLATAKQKNIITLFNNLFSSSGFHLVETISFLDRSALLDKQCVTQMRVGLSQGKSFSEMMESL		74
NTDB id 161 SP RS10375 WP 074196785.1		MDISQVFRLRRKKLATAKQKNIITLFNNLFSSSGFHLVETISFLDRSALLDKQCVTQMRVGLSQGKSFSEMMESL		74
NTDB id 529 SMSK321 RS09235 WP 080550783.1		MDISQVFRLRRKKLATAKQKNIITLFNNLFSSSGFHLVETISFLDRSALLDKQCVTQMRDLSQGKSFSEMMESL		74
NTDB id 501 SM12261 RS00950 WP 004238896.1		MDISQVFRLRRKKLATAKQKNIITLFNNLFSSSGFHLVETISFLDRSALLDKQCVTQMRAGLSQGKSFSEMMESL		74
consensus		*****		

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NTDB id 587 KW2 RS10850 WP 042211510.1	SFSKNVVTQLALVEVHGNI	VGTMQLVELHKKQLKVKKKLIEVATYPVLLVFLGIMWGLKNYLLPQLDKGNMFATLLI		156
NTDB id 1127717 FGL14 RS00695 WP 138084099.1	GFSDAILTQISLADGHGNI	ETTLVNIQGYLNQMAKIKKKTIEVVTYPIILLVFLFVIMILGLRHYVMPQLEAQ	NQITIFI	158
NTDB id 395 FSA28 RS09400 WP 257638827.1	GFSDDDVTQLALSEVHGNT	TQKSLKIESYLNLLILVKKKLIEVITYPIILLIFLVLVIMLGLKNYLLPQLDKG	NFATRLI	158
NTDB id 386 SMU RS09030 WP 255262721.1	GFSDDDVTQLALSEVHGNT	TQKSLKIESYLNLLILVKKKLIEVITYPIILLIFLVLVIMLGLKNYLLPQLDKG	NFATRLI	158
NTDB id 430 SGO RS09415 WP 012130941.1	GFSDAVVTQLSLAEIHGNI	SLALLKIEEYLDNLAKVKKKLIEVATYPMLLGFLVLMIGLRNYLLPQLSSQ	NFATQII	159
NTDB id 271 KZH43 RS09260 WP 074196785.1	GCSSAIVTQLSLAEVHGNI	LHLSLKGIEEYLDNLAKVKKKLIEVATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIAATQII	153
NTDB id 230 SPD RS09890 WP 074196785.1	GCSSAIVTQLSLAEVHGNI	LHLSLKGIEEYLDNLAKVKKKLIEVATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIAATQII	153
NTDB id 196 SPR RS09425 WP 074196785.1	GCSSAIVTQLSLAEVHGNI	LHLSLKGIEEYLDNLAKVKKKLIEVATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIAATQII	153
NTDB id 161 SP RS10375 WP 074196785.1	GCSSAIVTQLSLAEVHGNI	LHLSLKGIEEYLDNLAKVKKKLIEVATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIAATQII	153
NTDB id 529 SMSK321 RS09235 WP 080550783.1	GFSSAIVTQLSLAEVHGNI	LHLSLKGIEEYLDNLAKVKKKLIEVATYPLILLGFLLSIMLGLRNYLLPQLDSS	NIAATQII	153
NTDB id 501 SM12261 RS00950 WP 004238896.1	GFSSAIVTQLSLAEVHGNI	LHLSLKGIEEYLDNLAKVKKKLIEVATYPLILLGFLLLIMLGLRNYLLPQLDSS	NIAATQII	153
consensus		*****		

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NTDB id 587 KW2 RS10850 WP 042211510.1	NHLPPLVFFSVGALIVLLTS	LSTIIFKHISALTNFTFLVKVPLVSSFIRLYLTAYFSREWGNLIAQGVELRQIIEIMKKQK		236
NTDB id 1127717 FGL14 RS00695 WP 138084099.1	THFPATIFFGILFLIGVLLGGIWLH	WRSQSRLKLFTHFSAYPVLCKLLQQYLTAYYAREWGTLIGGQLELPVILDIMAMEK		238
NTDB id 395 FSA28 RS09400 WP 257638827.1	SNFPILFILLGCCFFILLVGI	FTFFSRKISRHLHIGFCSHLPFVCKYLQLYLTAYYAREWGNLIGQGVEMAQIVRIMQDQK		238
NTDB id 386 SMU RS09030 WP 255262721.1	SNFPILFILLGCCFFILLVGI	FTFFSRKISRHLHIGFCSHLPFVCKYLQLYLTAYYAREWGNLIGQGVEMAQIVRIMQDQK		238
NTDB id 430 SGO RS09415 WP 012130941.1	GHLPTIFLLTLVLMLLGLT	GAIIYLVFKGQKHIPVVSFLARLPFGSFVRIYLTAYYAREWGNMIGQGLELSQIFQIMQEQR		239
NTDB id 271 KZH43 RS09260 WP 074196785.1	GNLPQIFLGMVGLVSVLALL	ALTIFYKRSKMSVFSILARLPFGIFVQTYLTAYYAREWGNMISQGMELTQIFQIMQEQQ		233
NTDB id 230 SPD RS09890 WP 074196785.1	GNLPQIFLGMVGLVSVLALL	ALTIFYKRSKMSVFSILARLPFGIFVQTYLTAYYAREWGNMISQGMELTQIFQIMQEQQ		233
NTDB id 196 SPR RS09425 WP 074196785.1	GNLPQIFLGMVGLVSVLALL	ALTIFYKRSKMSVFSILARLPFGIFVQTYLTAYYAREWGNMISQGMELTQIFQIMQEQQ		233
NTDB id 161 SP RS10375 WP 074196785.1	GNLPQIFLGMVGLVSVLALL	ALTIFYKRSKMSVFSILARLPFGIFVQTYLTAYYAREWGNMISQGMELTQIFQIMQEQQ		233
NTDB id 529 SMSK321 RS09235 WP 080550783.1	GNLPQIFLGMVGLVSLTLL	ALTIFYKRSKMRVFSILARLPFGIFVQTYLTAYYAREWGNMISQGMELTQIFQIMQEQQ		233
NTDB id 501 SM12261 RS00950 WP 004238896.1	GNLPQIFLGMVGFVSVGV	LLALTIFYKRSKMRVFSILARLPFGIFVQTYLTAYYAREWGNMISQGMELTQIFQIMQEQQ		233
consensus		*****		

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consensus

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- X non conserved
- X similar
- X $\geq 50\%$ conserved