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Sequence	Alignment	End
NTDB id 320 STU RS10340 WP 002949220.1	MEQEVFVKAYEKVRPIVLKAFRQYFIQLWDQ	31
NTDB id 47 STER RS00925 WP 002949220.1	MEQEVFVKAYEKVRPIVLKAFRQYFIQLWDQ	31
NTDB id 50 STRSA0001 RS07545 WP 002885610.1	MEQEVFVHAYEVVRPIVLKASRQYFIQLWDL	31
NTDB id 468 HSISS4 RS00725 WP 021143466.1	MEQEVFVHAYEVVRPIVLKASRQYFIQLWDQ	31
NTDB id 457 SSUD9 RS00080 WP 002936602.1	MEFEKVYASVKGIVNKAREFYIKLWDR	28
NTDB id 461 GPW51 RS00080 WP 011921639.1	MEFEKVYASVKGIVNKAREFYIKLWDR	28
NTDB id 454 SSU RS00080 WP 011921639.1	MEFEKVYASVKGIVNKAREFYIKLWDR	28
NTDB id 44 SMU RS09085 WP 002263585.1	MEEDFEIVFNKVKPIVWKLSRYYFIKMWTR	30
NTDB id 252 KZH43 RS09050 WP 000588897.1	MIKELYEEVQGTVYKCRNEYYLHLWEL	27
NTDB id 251 KZH43 RS09050 WP 000588897.1	MIKELYEEVQGTVYKCRNEYYLHLWEL	27
NTDB id 211 SPD RS09675 WP 000588897.1	MIKELYEEVQGTVYKCRNEYYLHLWEL	27
NTDB id 210 SPD RS00065 WP 000588897.1	MIKELYEEVQGTVYKCRNEYYLHLWEL	27
NTDB id 177 SPR RS09210 WP 000588897.1	MIKELYEEVQGTVYKCRNEYYLHLWEL	27
NTDB id 176 SPR RS00065 WP 000588897.1	MIKELYEEVQGTVYKCRNEYYLHLWEL	27
NTDB id 141 SP RS10155 WP 000588925.1	MIKELYEEVQGTVYKCRNEYYLHLWEL	27
NTDB id 140 SP RS00070 WP 000588925.1	MIKELYEEVQGTVYKCRNEYYLHLWEL	27
NTDB id 489 SM12261 RS01070 WP 000471940.1	MFKELYEEVQGIVYKCRNEYYLHLWEL	27
NTDB id 488 SM12261 RS00065 WP 000471939.1	MFKELYEEVQGIVYKCRNEYHLHLWEL	27
NTDB id 517 SMSK321 RS10700 WP 000471945.1	MFKELYKEVQGIVYKSRNEYYLHLWEL	27
NTDB id 516 SMSK321 RS09125 WP 000471944.1	MFKELYKEVQGIVYKSRNEYYLHLWEL	27
NTDB id 1081732 ACK2I7 RS07005 WP 003026301.1	MEFKELYGKVRGIVLKCRREYYVHLWEL	28
NTDB id 424 SGO RS10430 WP 012130755.1	MKFEDVYKQVEGIVKRCYKDYYLHLWEY	28
NTDB id 423 SGO RS08370 WP 012130755.1	MKFEDVYKQVEGIVKRCYKDYYLHLWEY	28
NTDB id 582 DLJ51 RS00505 WP 002962720.1	MDKEKLKEIFNKHSALPEEVEEFDDGMVKEVITAGLLFCLKEVL....DMDDSSFVSARSRVEKTVSKLAKDYYIKLWTY	76
NTDB id 450 SPYM18 RS08475 WP 011018214.1	MS..CCFFVVLFILGIVKKKRRLKMSIETRAAFEKVKPIILKLRHYYIQLWDR	52
NTDB id 449 SPYM18 RS01395 WP 011018214.1	MS..CCFFVVLFILGIVKKKRRLKMSIETRAAFEKVKPIILKLRHYYIQLWDR	52
NTDB id 442 SPYM3 RS08515 WP 011106595.1	MS..CCFFVVLFILGIVKKKRRLKMSIETRAVFEKVKPIILKLRHYYIQLWDR	52
NTDB id 441 SPYM3 RS01385 WP 011106595.1	MS..CCFFVVLFILGIVKKKRRLKMSIETRAVFEKVKPIILKLRHYYIQLWDR	52
NTDB id 448 SpyM6JRS4 RS07800 WP 010921894.1	MS..CCFFVVLFILGIVKKKRRLKMSIETRAAFEKVKPIILKLRHYYIQLWDR	52
NTDB id 447 SpyM6JRS4 RS01370 WP 010921894.1	MS..CCFFVVLFILGIVKKKRRLKMSIETRAAFEKVKPIILKLRHYYIQLWDR	52
NTDB id 554 STRINF RS00370 WP 115283725.1	MDFERYFQTVKPIILKLRRHYFVKLWDY	28

consensus   ** *** ! * *** * ****** *!*

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NTDB id 320 STU RS10340 WP 002949220.1        ADMEQEAMMTLYQLLKKFPDLEKDDDKLRRYFKTKFRNRLNDEVRRQESVKRQANRQCYVEISDIAFCIPNKELD.MVDR    110
NTDB id 47 STER RS00925 WP 002949220.1         ADMEQEAMMTLYQLLKKFPDLEKDDDKLRRYFKTKFRNRLNDEVRRQESVKRQANRQCYVEISDIAFCIPNKELD.MVDR    110
NTDB id 50 STRSA0001 RS07545 WP 002885610.1    ADMEQEAMMTLYQLLEKFPELKSDDDKLRRYFKTKFRNRLNDEVRRQESVKRQANRQCYIEISDIAFCLPNKELD.AVDR    110
NTDB id 468 HSISS4 RS00725 WP 021143466.1      ADMEQEAMMTLYQLLEKFPELKSDDDKLRRYFKTKFRNRLNDEVRRQESVKRQANRQCYIEISDIAFCLPNKELD.AVDR    110
NTDB id 457 SSUD9 RS00080 WP 002936602.1       DDWEQEGMMTLFELLEAQPWLVDEQVQLYCYFKVKFRNRIKDRIRKQESQKRKFDRMPHEDIHELSHAIQSPGLI.NDEL    107
NTDB id 461 GPW51 RS00080 WP 011921639.1       DDWEQEGMMTLFELLEAQPWLVDEQVQLYCYFKVKFRNRIKDRIRKQESQKRKFDRMPHEDIYELSHAIQSPGLI.NDEL    107
NTDB id 454 SSU RS00080 WP 011921639.1         DDWEQEGMMTLFELLEAQPWLVDEQVQLYCYFKVKFRNRIKDRIRKQESQKRKFDRMPHEDIYELSHAIQSPGLI.NDEL    107
NTDB id 44 SMU RS09085 WP 002263585.1          EDWQQEGMLILHQLLREHPELEEDDTKLYIYFKTRFSNYIKDVLRQQESQKRRFNRMSYEEVGEIEHCLSSGMQ.LDEY    109
NTDB id 252 KZH43 RS09050 WP 000588897.1       SDWDQEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGLW.LDDY    106
NTDB id 251 KZH43 RS09050 WP 000588897.1       SDWDQEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGLW.LDDY    106
NTDB id 211 SPD RS09675 WP 000588897.1         SDWDQEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGLW.LDDY    106
NTDB id 210 SPD RS00065 WP 000588897.1         SDWDQEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGLW.LDDY    106
NTDB id 177 SPR RS09210 WP 000588897.1         SDWDQEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGLW.LDDY    106
NTDB id 176 SPR RS00065 WP 000588897.1         SDWDQEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGLW.LDDY    106
NTDB id 141 SP RS10155 WP 000588925.1          SDWEQEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGLW.LDDY    106
NTDB id 140 SP RS00070 WP 000588925.1          SDWEQEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGLW.LDDY    106
NTDB id 489 SM12261 RS01070 WP 000471940.1     SDWDQEGMICLHELISREEELVEDIPRLRKYFKTKFRNRILDHIRKQESQKRRYDKEPYEEVGEISHRISEGGMW.LDEY    106
NTDB id 488 SM12261 RS00065 WP 000471939.1     SDWDQEGMICLHELISREEGIVEDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEPYEEVGEISHRISEGGMW.LDEY    106
NTDB id 517 SMSK321 RS10700 WP 000471945.1     SDWDQEGMICLHELISREEELVEDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKEAYEEVGEISHRIGEGGLW.LDDY    106
NTDB id 516 SMSK321 RS09125 WP 000471944.1     SDWDQEGMICLHELISKEEELAEDIPRLRKYFKTKFRNRILDYIRKQESQKRRYDKESYEEVGEISHRIGEGGLW.LDEY    106
NTDB id 1081732 ACK2I7 RS07005 WP 003026301.1  SDWDQEGMLVLYQLVSQYPQLVEEDHQLYVYYKTKFRNHILDILRKQESQKRKLDRQAYEEVSEIGHKLSLKELY.LDEL    107
NTDB id 424 SGO RS10430 WP 012130755.1         ADWRQEGMLVLYELLKSHPNLLEDQPRLYRYFKTKFRNRIHDLIRRQESQKRKLDRQPYEEVSEIGHRLRMKELY.LDEL    107
NTDB id 423 SGO RS08370 WP 012130755.1         ADWRQEGMLVLYELLKSHPNLLEDQPRLYRYFKTKFRNRIHDLIRRQESQKRKLDRQPYEEVSEIGHRLRMKELY.LDEL    107
NTDB id 582 DLJ51 RS00505 WP 002962720.1       DDWRQEARIILYQLLERFPDLANDEEKLRIYFKTKFRSYVLDNIRKQESQKRAFDRMIYEEISELGHMIPSQQMD.TADY    155
NTDB id 450 SPYM18 RS08475 WP 011018214.1      DDWLQEGHIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGLW.LDDY    131
NTDB id 449 SPYM18 RS01395 WP 011018214.1      DDWLQEGHIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGLW.LDDY    131
NTDB id 442 SPYM3 RS08515 WP 011106595.1       DDWLQEGHIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGLW.LDDY    131
NTDB id 441 SPYM3 RS01385 WP 011106595.1       DDWLQEGHIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGLW.LDDY    131
NTDB id 448 SpyM6JRS4 RS07800 WP 010921894.1   DDWLQEGHIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGLW.LDDY    131
NTDB id 447 SpyM6JRS4 RS01370 WP 010921894.1   DDWLQEGHIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEIGEVAHAIPSRGLW.LDDY    131
NTDB id 554 STRINF RS00370 WP 115283725.1      EDWIQEGRIVFFQLLEEHPDLLNNEGKCYSYFKTKFSNHVKDIIRHQESFKRKFNRMPYEEISDISHCVPQVFFFEVEDY    108
consensus                                      !*!!!*!!**!!!*!**!**!!****!**!**!!*!*****!*!**!!!!!*!!*****!!!!!**!*!!!**!!!!*!!****
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NTDB id 320 STU RS10340 WP 002949220.1        LAYDEQLNAFREQLSSEDSLKLDRLLGGECFRGRKKMIRELRFWMVDFDPCNEED      165
NTDB id 47 STER RS00925 WP 002949220.1        LAYDEQLNAFREQLSSEDSLKLDRLLGGECFRGRKKMIRELRFWMVDFDPCNEED      165
NTDB id 50 STRSA0001 RS07545 WP 002885610.1   LVYDEQLNAFRNQLSSEDATKLDRLLAGECFRGRKKMIRELKFWMVDFDPYNEDD      165
NTDB id 468 HSISS4 RS00725 WP 021143466.1     LVYDEQLNAFRNQLSSEDATKLDRLLAGECFRGRKKMIRELKFWMVDFDPYNEDD      165
NTDB id 457 SSUD9 RS00080 WP 002936602.1      LMLRGALRDYRKNLSNDQLDKYEKLISGQCFNGRREMIRDLQIHLKDFR......      156
NTDB id 461 GPW51 RS00080 WP 011921639.1      LMLRGALRDYRKNLSNDQLDKYEKLISGQCFNGRREMIRDLQIHLKDFR......      156
NTDB id 454 SSU RS00080 WP 011921639.1        LMLRGALRDYRKNLSNDQLDKYEKLISGQCFNGRREMIRDLQIHLKDFR......      156
NTDB id 44 SMU RS09085 WP 002263585.1         ILFRDSLLAYKQGLSTEKQELFERLVAGEHFLGRQSMLKDLRKKLSDFKEK....      160
NTDB id 252 KZH43 RS09050 WP 000588897.1      YLFHETLRDYRNKQSKEKQEELERVLSNERFRGRQRVLRDLRIVFKEFTIRTH..      159
NTDB id 251 KZH43 RS09050 WP 000588897.1      YLFHETLRDYRNKQSKEKQEELERVLSNERFRGRQRVLRDLRIVFKEFTIRTH..      159
NTDB id 211 SPD RS09675 WP 000588897.1        YLFHETLRDYRNKQSKEKQEELERVLSNERFRGRQRVLRDLRIVFKEFTIRTH..      159
NTDB id 210 SPD RS00065 WP 000588897.1        YLFHETLRDYRNKQSKEKQEELERVLSNERFRGRQRVLRDLRIVFKEFTIRTH..      159
NTDB id 177 SPR RS09210 WP 000588897.1        YLFHETLRDYRNKQSKEKQEELERVLSNERFRGRQRVLRDLRIVFKEFTIRTH..      159
NTDB id 176 SPR RS00065 WP 000588897.1        YLFHETLRDYRNKQSKEKQEELERVLSNERFRGRQRVLRDLRIVFKEFTIRTH..      159
NTDB id 141 SP RS10155 WP 000588925.1         YLFHETLRDYRNKQSKEKQEELERVLSNERFRGRQRVLRDLRIVFKEFTIRTH..      159
NTDB id 140 SP RS00070 WP 000588925.1         YLFHETLRDYRNKQSKEKQEELERVLSNERFRGRQRVLRDLRIVFKEFTIRTH..      159
NTDB id 489 SM12261 RS01070 WP 000471940.1    YLFHETLRDYRNKQSKDKQEELERVLRHERFRGRQRVLRDLRIVFKEFDIRTH..      159
NTDB id 488 SM12261 RS00065 WP 000471939.1    YLFHETLRDYRNKQSKDKQEELERVLRHERFRGRQRVLRDLRIVFKEFDIRTH..      159
NTDB id 517 SMSK321 RS10700 WP 000471945.1    YLFHETLRDYRSKQSKDKQEELERVLRHERFRGRQRVLRDLRIVFKEFDIRTQ..      159
NTDB id 516 SMSK321 RS09125 WP 000471944.1    YLFHETLRDYRSKQSKDKQEELERVLRHERFRGRQRVLRDLRIVFKEFDIRTR..      159
NTDB id 1081732 ACK2I7 RS07005 WP 003026301.1 VILRDQLKSYQAQLSPEKQEQYERLLADERFKGRQAMIRELRAYLKDYSD.....      157
NTDB id 424 SGO RS10430 WP 012130755.1        VAFRSAMSEYRSRLSPEEAKQYERLMADERFKGRKAMLKDLSYHLRDFNPRLD..      160
NTDB id 423 SGO RS08370 WP 012130755.1        VAFRSAMSEYRSRLSPEEAKQYERLMADERFKGRKAMLKDLSYHLRDFNPRLD..      160
NTDB id 582 DLJ51 RS00505 WP 002962720.1      CALKEKLKELKQKLAPEDYAKILLLMRGGAFKGRSAFIKDIKVEFEDFDEDN...      207
NTDB id 450 SPYM18 RS08475 WP 011018214.1     VAYQEVIASLENQLNSQERMQFKALIRGERFKGRRALLRKISPYFKEFAQQL...      183
NTDB id 449 SPYM18 RS01395 WP 011018214.1     VAYQEVIASLENQLNSQERMQFKALIRGERFKGRRALLRKISPYFKEFAQQL...      183
NTDB id 442 SPYM3 RS08515 WP 011106595.1      VAYQEVIASLENQLNSQERMQFQALIRGERFKGRRALLRKISPYFKEFAQQL...      183
NTDB id 441 SPYM3 RS01385 WP 011106595.1      VAYQEVIASLENQLNSQERMQFQALIRGERFKGRRALLRKISPYFKEFAQQL...      183
NTDB id 448 SpyM6JRS4 RS07800 WP 010921894.1  VAYQEVIASLENQLNSQERMQFQALIRGERFKGRRALLRKISPYFKEFAQQL...      183
NTDB id 447 SpyM6JRS4 RS01370 WP 010921894.1  VAYQEVIASLENQLNSQERMQFQALIRGERFKGRRALLRKISPYFKEFAQQL...      183
NTDB id 554 STRINF RS00370 WP 115283725.1     VAYQDSLACLRRTLGREDRLKLEKVIRGERFEGKKAFLKSIELYFSDFRP.....      158
consensus                                     *** * * ****** ** * * ***** **!*!* ******* ****
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	Legend
X (white)	non conserved
X (pink)	similar
X (blue)	≥ 50% conserved