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logo
NTDB id 51117 SPAF RS02785 WP 003015523.1  MKKGKVFAVAGVTLLAAGLLAACSGSNTSKASSGEDKNYGYVYSDDPQTLDYTVSSKAATHDITTNVVDGLMANDKYGNLVPSLA   85
NTDB id 475 HSISS4 RS07005 WP 021143809.1  MKKSKWLALAGVALLSVGALAACSSKSS.....TSGTTYGYVYNSDPESLDYITSNTGPTKTAVTNGVDGLMEADKYGNLVPSVA   80
NTDB id 324 STU RS16140 WP 011226306.1     MKKSKWLALAGVALLGVGVLAACSSKSN.....TSGTTYGYVYSSDPETLDYITSNTGPTKSVVTNGVDGLMEADKYGNLVPSVA   80
NTDB id 292 STER RS06940 WP 011681419.1    MKKSKWLALAGVALLGVGVLAACSSKSN.....TSGTTYGYVYSSDPETLDYITSNTGPTKSVVTNGVDGLMEADKYGNLVPSVA   80
consensus                                  !!!*!**!*!!!*!!**!*!!!!!****     ****!!!!!**!!**!!!**!***!****!**!!!!!**!!!!!!!!!*!

logo
NTDB id 51117 SPAF RS02785 WP 003015523.1  EDWSVSKDGLTYTYKIRKGVKWYDADGEEHGEVTAKDFVTGLKHAADKKSETLPLVQGSIKGLDDYVQGKITDFSQVGVKAVDDY  170
NTDB id 475 HSISS4 RS07005 WP 021143809.1  EDWSVSQDGLTYTYKIRKGVKWYTSDGEEYADVTAKDFVTGLKHAADGKAGALYLVQDSIAGLSDYLSGANKDFSNVGVKAIDDY  165
NTDB id 324 STU RS16140 WP 011226306.1     EDWSVSKDGLTYTYKIRKGIKWYTSEGEEYANVTAKDFVTGLKHAADSKAGGIYLVQDSIAGLSDYLSGTNKDFSNVGVKAIDEY  165
NTDB id 292 STER RS06940 WP 011681419.1    EDWSVSKDGLTYTYKIRKGIKWYTSEGEEYANVTAKDFVTGLKHAADSKAGGIYLVQDSIAGLSDYLSGTNKDFSNVGVKAIDDY  165
consensus                                  !!!!!!*!!!!!!!!!!!!!*!!!***!!!***!!!!!!!!!!!!!!!!*!*****!!!*!!*!!*!!**!***!!!*!!!!!*!*!

logo
NTDB id 51117 SPAF RS02785 WP 003015523.1  TLEYTLNKPETFWNSKTTNGILFPISTEFLKSKGDDFGQPNDVKSILANGPFLLKSITSKSSVVFEKNDNYWDKKNVHLKEVKLI  255
NTDB id 475 HSISS4 RS07005 WP 021143809.1  TLQYTLKKPEPYWNSKTTYGLLSPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELTKNENYWDKKNVHFDAIKLS  250
NTDB id 324 STU RS16140 WP 011226306.1     TLQYTLKQPEPYWNSKTTYSLLFPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELVKNEHYWDKKNVHFDAIKFS  250
NTDB id 292 STER RS06940 WP 011681419.1    TLQYTLKQPEPYWNSKTTYSLLFPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELVKNEHYWDKKNVHFDAIKFS  250
consensus                                  !!*!!!* !!**!!!!!!* *!*!****!!!*!!*!!!***!**!!!*!!!!!!!!*!*!!!****!!**!!!!!!!!****!  *

logo
NTDB id 51117 SPAF RS02785 WP 003015523.1  YYDGSDQDSLARGFSDGAYTVARLFPASSNFATISKKYKDNIYNTPAGSGVAVLGFNIDRQSYKHTAKKSDAEKAATKKAILNKD  340
NTDB id 475 HSISS4 RS07005 WP 021143809.1  YYDGSDQEALERGFTDGAYSLARVYPTSSNYSSVEKKYKDNIYYTAPGASTSAIGVNIDRQSYKFSAKKTDAEKTSTKKALLNKD  335
NTDB id 324 STU RS16140 WP 011226306.1     YYDGSDQDALVRGFTDGAYNFARVFPTSSNYASVEKKYKDNIYYTAPGASTSAIGINLDRQSYKYTAKKTDSEKSSTKKALLNKD  335
NTDB id 292 STER RS06940 WP 011681419.1    YYDGSDQDALVRGFTDGAYNFARVFPTSSNYASVEKKYKDNIFYTAPGASTSAIGINIDRQSYKYTAKKTDSEKSSTKKALLNKD  335
consensus                                  !!!!!!!**!*!!!*!!!!**!!**!*!!!*****!!!!!!!**!**!******!*!*!!!!!!**!!!!*! !!**!!!!*!!!!

logo
NTDB id 51117 SPAF RS02785 WP 003015523.1  FRQAITFALDRESYSAQLNSKEFAKPAIRNTYTAPAFVQVNGKDFGDVVADKLTTYGDQWKGINLADGQDGLYNKDKAKAQLEKA  425
NTDB id 475 HSISS4 RS07005 WP 021143809.1  FRQSINFAIDRTAYQSQMNGKDGAALALRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGVNFTDGQDGLYNAEKAKTEFAKA  420
NTDB id 324 STU RS16140 WP 011226306.1     FRQAINFAIDRKAYQSQINGKDGATLAVRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGVNFADSQDGLYNAEKAKTEFAKA  420
NTDB id 292 STER RS06940 WP 011681419.1    FRQAINFAIDRKAYQSQINGKDGATLGVRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGVNLADSQDGLYNAEKAKTEFAKA  420
consensus                                  !!!*!*!!*!!**!**!*!*!**!****!!******!!****!*!!!*!**!***!!!*!*!*!  *!  !!!!!!**!!!****!!

logo
NTDB id 51117 SPAF RS02785 WP 003015523.1  KAELQKDGVQFPIHIDVPVAQSSKGFVARMQSLKQTVEDTLGKDNVVLDLQMMDQDEVLNITLNVPSAADADWDLQGLVGWNPDY  510
NTDB id 475 HSISS4 RS07005 WP 021143809.1  KETLQADGVQFPIHLDLPVDQSSKINVAQAQSLKQTIEQSLGSDNVVIDVNQLSSDDIQNATLNAANAAAEDWDISNGVIWGPDY  505
NTDB id 324 STU RS16140 WP 011226306.1     KDALQADGVQFPIHLDLPVDQSSKLNVAQAQSLKQTIEKSLGSENVVIDINQLSSDDLENVTLNAANAAAEDWDISNSVAWAPDY  505
NTDB id 292 STER RS06940 WP 011681419.1    KDALQADGVQFPIHLDLPVNQSSKLNVAQVQSLKQTIEKSLGSENVVIDINQLSSDDLENATLNAANAAAEDWDISNSVGWAPDY  505
consensus                                  !**!!*!!!!!!!!!*!*!!*!!!!**!!**!!!!!!!*!**!!**!!!*!******!***!*!!!***!!**!!!****!*!*!!!
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logo
NTDB id 51117 SPAF RS02785 WP 003015523.1   DDPSTYLDTLQPSSEDQTKVYLGFAGGVDNASAKAVGLDEYAKLLADANSESLDVTKRYEKYATAQAWLSDSALVIPTMSSTGAA   595
NTDB id 475 HSISS4 RS07005 WP 021143809.1   QDPSTYLDIFKTTSSENTKTFMGYDDP.NNAAAAQVGLKDYDALLDSAASETTDLNARYDRYAQAQAWLEDSSLVIPLTVGNGAA   589
NTDB id 324 STU RS16140 WP 011226306.1      QDPSTYLDIFKTTSSENTKAFMGYDDP.NNAAAAQVGLKDYDALLNSAASETSDLNVRYDRYAQAQAWLEDSSLVIPLTVGNGAA   589
NTDB id 292 STER RS06940 WP 011681419.1     QDPSTYLDIFKTTSSENTKAFMGYDDP.NNAAAAQVGLKDYDALLNSAASETSDLNVRYDRYAQAQAWLEDSSLVIPLTVGNGAA   589
consensus                                   *!!!!!!!*****!***!!***!**** *!!*!**!!!**!**!!**!*!!**!***!!**!!*!!!!!*!!*!!!!*****!!!
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logo
NTDB id 51117 SPAF RS02785 WP 003015523.1   TVISKVVPFSGPSSQTGNKG..SSYFKYVEVQDEPVTKKQYEQAREKWQKEKAESNKKAQQDLEKHVK   661
NTDB id 475 HSISS4 RS07005 WP 021143809.1   PVISRLTPFTGASMQVGDKNS.SDYFKYVKPQEKVVTKKEYEQSREKWLKEKKASNEKAQKDLEKHVK   656
NTDB id 324 STU RS16140 WP 011226306.1      PAISRLTPFTGASLQVGDKNSSNDYIKYVKPQEKVVTKKEYEQSREKWLKEKKESNEKAQKDLEKHVK   657
NTDB id 292 STER RS06940 WP 011681419.1     PVISRLTPFTGASLQVGDKNSSNDYIKYVKPQEKVVTKKEYEQSREKWLKEKKESNEKAQKDLEKHVK   657
consensus                                   **!!***!!*!*!*!*!*!*** *! !!!**!***!!!!*!!!*!!!!*!!!**!!*!!!*!!!!!!!
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X non conserved

X similar

X $\geq$ 50% conserved