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logo
NTDB id 29092 SGO RS08410 WP 012130761.1   MKPVKKLAVLGLTLASVFTLAACGNSNSGASKTYSYVYSTDPDTLDYTNTNRATTSDVIANLVDGLLENDRYGNLVPSLAEDWTV   85
NTDB id 475 HSISS4 RS07005 WP 021143809.1  MKKSKWLALAGVALLSVGALAACSSKSSTSGTTYGYVYNSDPESLDYITSNTGPTKTAVTNGVDGLMEADKYGNLVPSVAEDWSV   85
NTDB id 324 STU RS16140 WP 011226306.1     MKKSKWLALAGVALLGVGVLAACSSKSNTSGTTYGYVYSSDPETLDYITSNTGPTKSVVTNGVDGLMEADKYGNLVPSVAEDWSV   85
NTDB id 292 STER RS06940 WP 011681419.1   MKKSKWLALAGVALLGVGVLAACSSKSNTSGTTYGYVYSSDPETLDYITSNTGPTKSVVTNGVDGLMEADKYGNLVPSVAEDWSV   85
consensus                                  !!**!*!!**!**!* !**!!!!**** ****!!*!!!**!!**!!!***!***!*****!*!!!!*!*!*!!!!!!!*!!!!*!

logo
NTDB id 29092 SGO RS08410 WP 012130761.1   SKDGLTYTYKLRKGAKWYTSEGEEYAEVKAQDFVTGLKHAADSNSDALPIVQSSIKGLDAYVKGESKDFSTVGVKAIDDYTIQYT   170
NTDB id 475 HSISS4 RS07005 WP 021143809.1  SQDGLTYTYKIRKGVKWYTSDGEEYADVTAKDFVTGLKHAADGKAGALYLVQDSIAGLSDYLSGANKDFSNVGVKAIDDYTLQYT   170
NTDB id 324 STU RS16140 WP 011226306.1     SKDGLTYTYKIRKGIKWYTSEGEEYANVTAKDFVTGLKHAADSKAGGIYLVQDSIAGLSDYLSGTNKDFSNVGVKAIDEYTLQYT   170
NTDB id 292 STER RS06940 WP 011681419.1   SKDGLTYTYKIRKGIKWYTSEGEEYANVTAKDFVTGLKHAADSKAGGIYLVQDSIAGLSDYLSGTNKDFSNVGVKAIDDYTLQYT   170
consensus                                  !*!!!!!!!!*!!!*!!!!!*!!!!!*!*!*!!!!!!!!!!!!********!!*!!*!!**!**!**!!!!*!!!!!!!*!!*!!!

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NTDB id 29092 SGO RS08410 WP 012130761.1   LNQPESYWNSKTTMGILFPINEEFLKSSGKDFGTV.KPSGILYNGPYFLKSFTSKSSIEYTKNDNYWDKNNVKISDVKLTYFDGS   254
NTDB id 475 HSISS4 RS07005 WP 021143809.1  LKKPEPYWNSKTTYGLLSPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELTKNENYWDKKNVHFDAIKLSYYDGS   255
NTDB id 324 STU RS16140 WP 011226306.1     LKQPEPYWNSKTTYSLLFPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELVKNEHYWDKKNVHFDAIKFSYYDGS   255
NTDB id 292 STER RS06940 WP 011681419.1   LKQPEPYWNSKTTYSLLFPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELVKNEHYWDKKNVHFDAIKFSYYDGS   255
consensus                                  !**!!*!!!!!!!* *!*!*!!*!!!**!!!!!****!**!!!!!!**!!!*!*!!!!!* !!**!!!!*!!*****! *!*!!!

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NTDB id 29092 SGO RS08410 WP 012130761.1   DQEALVRNFKDGTYTQARLYPNSSSYASVQKQYKDNIVYSPQDATTFFYAFNYNRKAYNFTAKTTDAQKTSTTAALLNKDFRQAI   339
NTDB id 475 HSISS4 RS07005 WP 021143809.1  DQEALERGFTDGAYSLARVYPTSSNYSSVEKKYKDNIYYTAPGASTSAIGVNIDRQSYKFSAKKTDAEKTSTKKALLNKDFRQSI   340
NTDB id 324 STU RS16140 WP 011226306.1     DQDALVRGFTDGAYNFARVFPTSSNYASVEKKYKDNIYYTAPGASTSAIGINLDRQSYKYTAKKTDSEKSSTKKALLNKDFRQAI   340
NTDB id 292 STER RS06940 WP 011681419.1   DQDALVRGFTDGAYNFARVFPTSSNYASVEKKYKDNIFYTAPGASTSAIGINIDRQSYKYTAKKTDSEKSSTKKALLNKDFRQAI   340
consensus                                  !!*!!*!*!*!!*!**!!**!*!!*!*!!*!*!!!!!*!****!*!*****!**!**!***!!*!! *!*!!**!!!!!!!!!*!

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NTDB id 29092 SGO RS08410 WP 012130761.1   NFAFNRTAYGAQQNGQEGATSSLRNSLVPPTFVQIGEKNFGDIVKEDLASYGDEWKGVKLDDAQDGLFNVEKAKAEFAKAKDALQ   424
NTDB id 475 HSISS4 RS07005 WP 021143809.1  NFAIDRTAYQSQMNGKDGAALALRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGVNFTDGQDGLYNAEKAKTEFAKAKETLQ   425
NTDB id 324 STU RS16140 WP 011226306.1     NFAIDRKAYQSQINGKDGATLAVRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGVNFADSQDGLYNAEKAKTEFAKAKDALQ   425
NTDB id 292 STER RS06940 WP 011681419.1   NFAIDRKAYQSQINGKDGATLGVRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGVNLADSQDGLYNAEKAKTEFAKAKDALQ   425
consensus                                  !!!**! !!**!*!!**!!****!!**!!**!!**!*!*!!!!*!*!***!!!!!!*!!* *!*!!!!*!*!!!!*!!!!!!**!!

logo
NTDB id 29092 SGO RS08410 WP 012130761.1   AQGVEFPIHLDLPVDQTNNLLVQQANSFKQSVEEALGKDNVVIDVQQMSTENKNNVTYFAETAAQKDYDIN.IAGWGPDFQDPST   508
NTDB id 475 HSISS4 RS07005 WP 021143809.1  ADGVQFPIHLDLPVDQSSKINVAQAQSLKQTIEQSLGSDNVVIDVNQLSSDDIQNATLNAANAAAEDWDISNGVIWGPDYQDPST   510
NTDB id 324 STU RS16140 WP 011226306.1     ADGVQFPIHLDLPVDQSSKLNVAQAQSLKQTIEKSLGSENVVIDINQLSSDDLENVTLNAANAAAEDWDISNSVAWAPDYQDPST   510
NTDB id 292 STER RS06940 WP 011681419.1   ADGVQFPIHLDLPVNQSSKLNVAQVQSLKQTIEKSLGSENVVIDINQLSSDDLENATLNAANAAAEDWDISNSVGWAPDYQDPST   510
consensus                                  !*!!*!!!!!!!!!!*!*****!*!**!*!!**!**!!**!!!!!!**!*!*****! !**!**!!**!*!!*****!*!!*!!!!!
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logo
NTDB id 29092 SGO RS08410 WP 012130761.1   YLNIFDPDKGDMLQNIGLEKGQNADLADKLGLNEFKKLNEEADSEKQDTTARYTKYAAAQAWLTDSSLVIPIQSN.GGTPLVMKA   592
NTDB id 475 HSISS4 RS07005 WP 021143809.1  YLDIFKTTSSENTKTFMGYDDPNNAAAAQVGLKDYDALLDSAASETTDLNARYDRYAQAQAWLEDSSLVIPLTVGNGAAPVISRL   595
NTDB id 324 STU RS16140 WP 011226306.1     YLDIFKTTSSENTKAFMGYDDPNNAAAAQVGLKDYDALLNSAASETSDLNVRYDRYAQAQAWLEDSSLVIPLTVGNGAAPAISRL   595
NTDB id 292 STER RS06940 WP 011681419.1   YLDIFKTTSSENTKAFMGYDDPNNAAAAQVGLKDYDALLNSAASETSDLNVRYDRYAQAQAWLEDSSLVIPLTVGNGAAPVISRL   595
consensus                                  !!*!!*****************!***!***!!*****!***!*!!**!** !!**!!*!!!!!*!!!!!!!*****!**!*****

logo
NTDB id 29092 SGO RS08410 WP 012130761.1   VPFTKPYSLVGIKGD.AYVFKYREVQNDIVTAKDYKAAEKKWKKEKEKTNAKAQEELADHVK   653
NTDB id 475 HSISS4 RS07005 WP 021143809.1  TPFTGASMQVGDKNS.SDYFKYVKPQEKVVTKKEYEQSREKWLKEKKASNEKAQKDLEKHVK   656
NTDB id 324 STU RS16140 WP 011226306.1     TPFTGASLQVGDKNSSNDYIKYVKPQEKVVTKKEYEQSREKWLKEKKESNEKAQKDLEKHVK   657
NTDB id 292 STER RS06940 WP 011681419.1   TPFTGASLQVGDKNSSNDYIKYVKPQEKVVTKKEYEQSREKWLKEKKESNEKAQKDLEKHVK   657
consensus                                  *!!!*****!!*!****** !!***!***!!*!*!*****!!*!!!***!*!!!**!**!!!
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X non conserved

X similar

X $\geq$ 50% conserved