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logo
NTDB id 1142062 DQL01 RS07470 WP 111702615.1  MKKSKSKYLTLAGLVL.GTGVLLSACGNSSTASKTYNYVYSSDPSSLNYLAENRAATSDIVANLVDGLLENDQYGNIIPS   79
NTDB id 475 HSISS4 RS07005 WP 021143809.1     ..MKKSKWLALAGVALLSVGALAACSSKSSTSGTTYGYVYNSDPESLDYITSNTGPTKTAVTNGVDGLMEADKYGNLVPS   78
NTDB id 324 STU RS16140 WP 011226306.1        ..MKKSKWLALAGVALLGVGVLAACSSKSNTSGTTYGYVYSSDPETLDYITSNTGPTKSVVTNGVDGLMEADKYGNLVPS   78
NTDB id 292 STER RS06940 WP 011681419.1       ..MKKSKWLALAGVALLGVGVLAACSSKSNTSGTTYGYVYSSDPETLDYITSNTGPTKSVVTNGVDGLMEADKYGNLVPS   78
consensus                                       **!!!*!*!!!**!***!*!******!  !***!!*!!!*!!!**!*!***!***!***!*!*!!!!*!*!*!!!**!!

logo
NTDB id 1142062 DQL01 RS07470 WP 111702615.1  LAEDWTVSQDGLTYTYKLRKDAKWFTSEGEEYAPVTAQDFVTGLQYAADKKSEALYLVQDSVAGLDDYITGKTSDFSTVG  159
NTDB id 475 HSISS4 RS07005 WP 021143809.1     VAEDWSVSQDGLTYTYKIRKGVKWYTSDGEEYADVTAKDFVTGLKHAADGKAGALYLVQDSIAGLSDYLSGANKDFSNVG  158
NTDB id 324 STU RS16140 WP 011226306.1        VAEDWSVSKDGLTYTYKIRKGIKWYTSEGEEYANVTAKDFVTGLKHAADSKAGGIYLVQDSIAGLSDYLSGTNKDFSNVG  158
NTDB id 292 STER RS06940 WP 011681419.1       VAEDWSVSKDGLTYTYKIRKGIKWYTSEGEEYANVTAKDFVTGLKHAADSKAGGIYLVQDSIAGLSDYLSGTNKDFSNVG  158
consensus                                     *!!!!*!!  !!!!!!!!*!!**!!*!!*!!!!!*!!!*!!!!!!**!!!*!****!!!!!!*!!!*!!**!***!!!*!!

logo
NTDB id 1142062 DQL01 RS07470 WP 111702615.1  VKALDDQTVQYTLVKPELYWNSKTLATILFPVNADFLKSKGDDFGKA.DPSSILYNGPFLMKALVSKSAIEYKKNPNYWD  238
NTDB id 475 HSISS4 RS07005 WP 021143809.1     VKAIDDYTLQYTLKKPEPYWNSKTTYGLLSPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELTKNENYWD  238
NTDB id 324 STU RS16140 WP 011226306.1        VKAIDEYTLQYTLKQPEPYWNSKTTYSLLFPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELVKNEHYWD  238
NTDB id 292 STER RS06940 WP 011681419.1       VKAIDDYTLQYTLKQPEPYWNSKTTYSLLFPVNEDFLKNKGKDFGKSTDPTSILYNGPFLLKSLTAKSSIELVKNEHYWD  238
consensus                                     !!!*!**!*!!!!* !!*!!!!!!****!*!!!*!!!!*!!*!!!!**!!*!!!!!!!!!*!*!**!!*!!**!!**!!!

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NTDB id 1142062 DQL01 RS07470 WP 111702615.1  AKNVFVDDVKLTYYDGSDQESLERNFTAGAYTTARLFPNSSSYEGIKEKYKNNIIYSMQNSTSYFFNFNLDRKSYNYTSK  318
NTDB id 475 HSISS4 RS07005 WP 021143809.1     KKNVHFDAIKLSYYDGSDQEALERGFTDGAYSLARVYPTSSNYSSVEKKYKDNIYYTAPGASTSAIGVNIDRQSYKFSAK  318
NTDB id 324 STU RS16140 WP 011226306.1        KKNVHFDAIKFSYYDGSDQDALVRGFTDGAYNFARVFPTSSNYASVEKKYKDNIYYTAPGASTSAIGINLDRQSYKYTAK  318
NTDB id 292 STER RS06940 WP 011681419.1       KKNVHFDAIKFSYYDGSDQDALVRGFTDGAYNFARVFPTSSNYASVEKKYKDNIFYTAPGASTSAIGINIDRQSYKYTAK  318
consensus                                     *!!!**!**!  *!!!!!!!**!  !*!!*!!!**!!**!*!!*!*****!!!*!!*!*************!*!!*!!****!

logo
NTDB id 1142062 DQL01 RS07470 WP 111702615.1  TSDIEKKSTQEAVLNKNFRQAINFAFDRTSYGAQSEGKEGATKILRNLVVPPNFVSIKGKDFGEVVASKMVNYGKEWQGI  398
NTDB id 475 HSISS4 RS07005 WP 021143809.1     KTDAEKTSTKKALLNKDFRQSINFAIDRTAYQSQMNGKDGAALALRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGV  398
NTDB id 324 STU RS16140 WP 011226306.1        KTDSEKSSTKKALLNKDFRQAINFAIDRKAYQSQINGKDGATLAVRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGV  398
NTDB id 292 STER RS06940 WP 011681419.1       KTDSEKSSTKKALLNKDFRQAINFAIDRKAYQSQINGKDGATLGVRNLFVPSDFVSAGDKTFGDLVTEKMSSYGDEWSGV  398
consensus                                     **!*!!*!!**!*!!!*!!!*!!!!*!!  *!**!**!!*!!****!!!*!!**!!!***!*!!**!**!!**!!*!!*!*

logo
NTDB id 1142062 DQL01 RS07470 WP 111702615.1  NFVDGQDPYYNPEKAKAKFAEAKKELEAKGVQFPIHLDKTVEVTDKVGIQGVSSIKQSIESVLGSDNVVIDIQQLTSDEF  478
NTDB id 475 HSISS4 RS07005 WP 021143809.1     NFTDGQDGLYNAEKAKTEFAKAKETLQADGVQFPIHLDLPVDQSSKINVAQAQSLKQTIEQSLGSDNVVIDVNQLSSDDI  478
NTDB id 324 STU RS16140 WP 011226306.1        NFADSQDGLYNAEKAKTEFAKAKDALQADGVQFPIHLDLPVDQSSKLNVAQAQSLKQTIEKSLGSENVVIDINQLSSDDL  478
NTDB id 292 STER RS06940 WP 011681419.1       NLADSQDGLYNAEKAKTEFAKAKDALQADGVQFPIHLDLPVNQSSKLNVAQVQSLKQTIEKSLGSENVVIDINQLSSDDL  478
consensus                                     !**!  !!**!!*!!!!**!!*!!**!*!*!!!!!!!!!!**!****!***** *!*!!*!!**!!!*!!!!!**!!*!!**
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logo

NTDB id 1142062 DQL01 RS07470 WP 111702615.1  DSSGYFAQTAAQKDYDLYHG.GWGPDYQDPSTYLDILSVKSGGMLQNFGLEPGEVNEKAKAVGLDTYTQMLEEANK.EQD   556
NTDB id 475 HSISS4 RS07005 WP 021143809.1     QNATLNAANAAAEDWDISNGVIWGPDYQDPSTYLDIFKTTSSENTKTFMGYDDPNNAAAAQVGLKDYDALLDSAASETTD   558
NTDB id 324 STU RS16140 WP 011226306.1        ENVTLNAANAAAEDWDISNSVAWAPDYQDPSTYLDIFKTTSSENTKAFMGYDDPNNAAAAQVGLKDYDALLNSAASETSD   558
NTDB id 292 STER RS06940 WP 011681419.1       ENATLNAANAAAEDWDISNSVGWAPDYQDPSTYLDIFKTTSSENTKAFMGYDDPNNAAAAQVGLKDYDALLNSAASETSD   558
consensus                                     ******!**!!**!*!*** **!*!!!!!!!!!!!!****!******!*******!**!**!!!**!***!**!*****!

logo

NTDB id 1142062 DQL01 RS07470 WP 111702615.1  PAKRYEKYADIQAWLIDSSLVLPSV.SRGGTPSLRRTVPFAAAYGLTGTKG..VESYKYLKVQDKIVTTDEYAKAREKWL   633
NTDB id 475 HSISS4 RS07005 WP 021143809.1     LNARYDRYAQAQAWLEDSSLVIPLTVGNGAAPVISRLTPFTGASMQVGDKNS.SDYFKYVKPQEKVVTKKEYEQSREKWL   637
NTDB id 324 STU RS16140 WP 011226306.1        LNVRYDRYAQAQAWLEDSSLVIPLTVGNGAAPAISRLTPFTGASLQVGDKNSSNDYIKYVKPQEKVVTKKEYEQSREKWL   638
NTDB id 292 STER RS06940 WP 011681419.1       LNVRYDRYAQAQAWLEDSSLVIPLTVGNGAAPVISRLTPFTGASLQVGDKNSSNDYIKYVKPQEKVVTKKEYEQSREKWL   638
consensus                                     ***!!**!!**!!!!*!!!!!*!*****!**!***!**!!**!****!*!*******!!*!*!*!*!!**!!***!!!!!

logo

NTDB id 1142062 DQL01 RS07470 WP 111702615.1  KEKEESNKKAQEELVKHVK   652
NTDB id 475 HSISS4 RS07005 WP 021143809.1     KEKKASNEKAQKDLEKHVK   656
NTDB id 324 STU RS16140 WP 011226306.1        KEKKESNEKAQKDLEKHVK   657
NTDB id 292 STER RS06940 WP 011681419.1       KEKKESNEKAQKDLEKHVK   657
consensus                                     !!!**!!*!!!**!*!!!!
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X non conserved

X similar

X $\geq$ 50% conserved