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logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  MALRFGLPFWIFGVLLSFALPVVPPLWVWTAVGCCAAVLFRRYRSLALLLLCLTVGAAYGVWRTEAALSQQWQTASA..A   78
NTDB id 1128 NGFG RS01490 WP 020997305.1      MFRRWFLPCWVVGVAVSFALSVVPHWPFWLAAFAVLAVLARRFA.FAGLMLCVLAGAAYGVFRTEAALSSQWRAEAVSGV   79
consensus                                     !  !* !!*!* !! *!!!!*!!!  * ! !  ** !!! !!* * ! !*!!*  !!!!!!*!!!!!!! !!      **

logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  DLTVTVDDLPQREARRVRFTAVAEDEAGRQYRLVLSDYGLRDWPVGSRWQVRARVRPPVGEVNPAGFNREAWALAKGIDG  158
NTDB id 1128 NGFG RS01490 WP 020997305.1      PLTVEVTDMPRSDGRRVQFAAKAVDSGGRTFDLLLSDYKRREWAVGSRWRITARVHPVVGELNLRGLNREAWALSNGVGG  159
consensus                                     *!!! ! !*!  **!!! ! ! ! ! *!! * !*!!!!  !*!*!!!!! * !!!*!*!!!*!* ! !!!!!!!  !* !

logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  LGTIGGERVLLAQGEAGRLLRMRDSVSRRWQQAAVVKPEFSDGQALMRALGIGEQTALDTGVWQAFRPLGLNHLVSISGL  238
NTDB id 1128 NGFG RS01490 WP 020997305.1      VGTVGADRVLLHGGSGWGIAVWRSRISRNWRQADA.DGGLSDGIGLMRALSVGEQSALRPGLWQAFRPLGLTHLVSISGL  238
consensus                                     *!!*!**!!!!* ! *  *   !  *!! ! !!  * *  !!! *!!!!! *!!!*!! *!*!!!!!!!!! !!!!!!!!

logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  HVGMVALFAGWLAKLLLACLPFSLSKPRLWMVSAGVAAGIFYAGLAGFSVPTQRSVLMLAALAWAWWCGSGVSVWRGWWQ  318
NTDB id 1128 NGFG RS01490 WP 020997305.1      HVTMVAVLFAWLAKRLLACSPRLPARPRAWVLAAGCAGALFYALLAGFSVPTQRSVLMLAAFAWAWRRG.RLSAWATWWQ  317
consensus                                     !! !!!*  *!!!! !!!! !  * *!! !** !!*!***!!! !!!!!!!!!!!!!!!!! !!!! *!* *! !  !!!

logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  ALAAVLLVQPAAVLGAGFWLSFGLVAALLWVASGRLNGLGWRAVLRGQWAVSVLSVVILGAFFASVPLISPLVNAAAIPW  398
NTDB id 1128 NGFG RS01490 WP 020997305.1      ALAAVLLFDPLAVLGVGTWLSFGLVAALIWACAGRLYEGKRQTAVRGQWAASVLSLVLLGYLFASLPLVSPLVNAVSIPW  397
consensus                                     !!!!!!!  ! !!!! ! !!!!!!!!!!*! * !!!        *!!!!! !!!!*!*!!  !!!*!!*!!!!!!  !!!

logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  FSWVLTPLALLGSILPWPRLHEFAAAAGEYTLRFLLWLAEYAPEYAVAEVPWPLVLLAVVAGGVLLLPKPTALRPWAALV  478
NTDB id 1128 NGFG RS01490 WP 020997305.1      FSWVLTPLALLGSVVPFAPLQQAGAFLAEYTLRFLVWLADVSPEFAVAAAPLPLLVLAVCAALLLLLPRGLGLRPWAVLL  477
consensus                                     !!!!!!!!!!!!!**!***!*  *!  *!!!!!!!*!!!*  !!*!!!  ! !!**!!!*!* *!!!!** *!!!!! !*

logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  LCGFVVYRKEPVQYGRVQMVVWDAGQGLSVLVRTAQRRLLFDTGTAPSAAMNILPALNAWGVRSLDALVLSHHDADHDGG  558
NTDB id 1128 NGFG RS01490 WP 020997305.1      LAGFVSYRPEAVPENEAAVTVWDAGQGLSVLVRTANRHLLFDTGTVAAAQTGIVPSLNAAGVRRLDKLVLSHHDSDHDGG  557
consensus                                     !*!!! !!*!*!*     * !!!!!!!!!!!  !!***!!!!!!! * !   !*! !!! !!! !! !!!!!!! !!!!!
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logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  FEAVARATRPKRLWAGQPQFYSGAESCDKGAWEWDGVHFEWLRPSEIVKADDNEQSCVLRVVAGGQAALVTGDLGKAGEK   638
NTDB id 1128 NGFG RS01490 WP 020997305.1      FQAVGKIP.NGGIYAGQPEFYEGARHCAEQRWQWDGVDFEFLRPSERKNIDDNGKSCVLRVVAGGAALLVTGDLDTKGEE   636
consensus                                     ! !!** ***  **!!!! !! !! *!    ! !!!!*!!*!!!!!    !!!  !!!!!!!!!! ! !!!!!!   !!

logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  SLVEQYGGGLHSNVLVLGHHGSDTSSSGVFLNAVAPEYAVASSGYANAYRHPVKAVRDRVQAHDIVLLRTDWQGALRFEL   718
NTDB id 1128 NGFG RS01490 WP 020997305.1      SLVGKYGGNLYSQVLVLGHHGSNTSSSGVFLNAVSPEYAVASSGYANAYKHPTEAVQNRVRAHGIKLLRTDLSGALQFGL   716
consensus                                     !!!  !!! !*!*!!!!!!!!! !!!!!!!!!!! !!!!!!!!!!!!!!!*!!  !!  !! !! ! !!!!!  !!! ! !

logo
NTDB id 1124130 EL309 RS09315 WP 004283556.1  GAGGEVFGGPLRQRKPYWQKKPFDNAPY   746
NTDB id 1128 NGFG RS01490 WP 020997305.1      GRGGV.KAQRLRVYKFYWQKKPFE....   739
consensus                                     ! !! * * *!!  !*!!!!!!!*****
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X non conserved

X similar

X $\geq$ 50% conserved