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logo
T10136 WP 015060653.1 NC 019265:c23853-23533      ..MAKKPARPANLKRAPLPKRTAYTPEFKKSWKRHNDAGRQPMTEARDVMRMLWEG...DTLPAQYLDHELQ..GEWAGN   73
T1038 NP 414760.1 NC 000913:c246239-245961        ................MIQRDIEYSGQYSKDV.KLAQKRHKDMNKLKYLMTLLINN..TLPLPAVYKDHPLQ..GSWKGY   59
T6290 WP 000615983.1 NZ CP009273:c242726-242448   ................MIQRDIEYSGQYSKDV.KLAQKRHKDMNKLKYLMTLLINN..TLPLPAVYKDHPLQ..GSWKGY   59
T10190 WP 176704754.1 NZ KY498026:c2572-2228      MSCSTNLKKTAASKRASLPRAADYTKSFIKDWERLSRSGRYDMNRLKEAMLLLIAN..DAPLGAEWLDHPLK..GDWAGH   76
T10070 WP 014123908.1 NC 016052:523750-524034     .............MKNNPKYKPAFERKFKKHYKNMLKGGRYKKEDFEKVYWKLLYD...EQLEPRYNDHPLV...NRKPE   61
T10111 QIP66200.1 MK544944:263-565                ..................MYSLVPTPTFKRDLKRLSKKHW.PMDELKTAVNLLAAGTNAELLSKKYADHALSSSSEWKGY   61
T10112 QIP66198.1 MK544943:263-565                ..................MYSLVPTPTFKRDLKRLSKKHW.PMDELKTAVNLLAAGTNAELLSKKYADHALSSSSEWKGY   61
T10088 WP 000921941.1 NC 011498:475560-475841     ..................MLKVRTKKDFLKDFNKHILSGRITESDVTSVVDCLKEQ...KPLQQKYCDHALS..GNLKGL   57
T166 WP 000277238.1 NC 002506:c328287-328018      ..................MYKLEYSTQFKKDFKKITKMPISDIIEVGNVISKLQRG...EKLEPKNVDHPLT..GNWVGF   57
T665 WP 002262889.1 NC 004350:850213-850491       ..................MLKIKQTRQFKKSLKKVVKQGK.DINKLFAIVELLCQK...SELPLALRNHELK..GRWRGI   56
T6256 WP 012576472.1 NC 011593:c15445-15155       .............MSGIRYTVKTTSRFRKDFKLARRRGL.DAGLFKQVVSILSEG...GTLPDRYHDHALT..GNMTGF   60
T10095 WP 002596328.1 NC 013316:c2055913-2055623  .............MKETKYTVKYTTSFKKDYKRAIKRGL.KIELLEQVVALLAMG...EPLPDKNRDHDLS..GDWAGH   60
consensus                                                        * **  ******** * *   *  ** ** *!        !  ** *! !   * ***

logo

T10136 WP 015060653.1 NC 019265:c23853-23533      RECHIR...GDFLLVYQVTK....TDVIFVDIGTHAELFK.   106
T1038 NP 414760.1 NC 000913:c246239-245961        RDAHVE...PDWILIYKLTD....KLLRFERTGTHAALFG.    92
T6290 WP 000615983.1 NZ CP009273:c242726-242448   RDAHVE...PDWILIYKLTD....KLLRFERTGTHAALFG.    92
T10190 WP 176704754.1 NZ KY498026:c2572-2228      RECHVG...GDFLLAYKTDDSGKTGLIIFVRTGTHAELFNE   114
T10070 WP 014123908.1 NC 016052:523750-524034     RDLHIK...PDWLLIYKYDGE..F..VRFIDTGTHADLFK.    94
T10111 QIP66200.1 MK544944:263-565                RELHVDGPRGDWLLIYKIKQQ..DLILTLVRTGSHHNLLGK   100
T10112 QIP66198.1 MK544943:263-565                RELHVDGPRGGWLLIYKIKQQ..DLILTLVRTGSHHNLLGK   100
T10088 WP 000921941.1 NC 011498:475560-475841     RECHVK...PNLLLIYEIKKQ..ENELVLLRLDTHSELFKK    93
T166 WP 000277238.1 NC 002506:c328287-328018      RDCHIK...PDLVLIYRVFND..QLQ..LARIGSHSDLF..    89
T665 WP 002262889.1 NC 004350:850213-850491       RELHIE...SDWLLAYQVLDD..ELVLLLIDTGSHAQMLGM    92
T6256 WP 012576472.1 NC 011593:c15445-15155       RECYIT...PDLLLVYLIEKD..VLVLTLTRTGTHSGLFGK    96
T10095 WP 002596328.1 NC 013316:c2055913-2055623  RECHIL...PDWLLVYRIEDD..VLVLTLARTGTHSDLFGK    96
consensus                                         !* **    ****!*!**        ** ******!  ***
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X non conserved

X similar

X $\geq$ 50% conserved