

logo

T10111 QIP66200.1 MK544944:263-565MYSLVPTPTFKRDLKRLSKK.HWPMDELKTAVNLLAAGTNAELLSKKYADHALSSSSEWKG	61
T10112 QIP66198.1 MK544943:263-565MYSLVPTPTFKRDLKRLSKK.HWPMDELKTAVNLLAAGTNAELLSKKYADHALSSSSEWKG	61
T28 WP 000916169.1 NC 000915:c946611-946345VLKLNLKKSFKQDFDKLLLN.GFDDSVLNEVILTLRK...KEPLDPQFQDHALK..GKWKPF	56
T10109 QIP66204.1 MK544946:257-544MMLTINRTRTFKRQFKHLLRQ.GKDMTKLATAIDTLQRQ...DRVKLASLHDHALK..GAHSGE	58
T10110 QIP66208.1 MK544948:301-486MQRQ..GHVKLASLHDHALK..GAHSGE	24
T6139 WP 005691636.1 NC 013199:c513094-512909MQRQ..GHVKLASLHDHALK..GAHSGE	24
T6144 WP 005691636.1 NC 017491:c513270-513085MQRQ..GHVKLASLHDHALK..GAHSGE	24
T6239 WP 005691636.1 NC 017491:c513270-513085MQRQ..GHVKLASLHDHALK..GAHSGE	24
T10108 QIP66206.1 MK544947:301-486MQRQ..AHVKLASLHDHALK..GAHSGE	24
T6286 WP 014517465.1 NC 017284:30649-30924MQNKYSVTFSKRFKFKDKFKIINN.D..KKILKKIVNKLAN...DEVLEEYKDHALK..GNYIGF	57
T665 WP 002262889.1 NC 004350:850213-850491MLKIKQTRQFKKSLKVVVKQ.GKDINKLFAIVELLICQ...KSELPLALRNHEIK..GRWRGI	56
T6256 WP 012576472.1 NC 011593:c15445-15155MSGIRYTVKTTSRFRKDFKLARRR.GLDAGLFGQVVSILSE...GGTLPDRYHDHALT..GNMTGF	60
T10095 WP 002596328.1 NC 013316:c2055913-2055623MKETKYTVKYTTSFKKDYKRAIKR.GLKIELLEQVVALLAM...GEPLPKNRDHDLS..GDWAGH	60
T10070 WP 014123908.1 NC 016052:523750-524034MKNNPKYKPAFERKFKKHYKNMLKGGRYKKEDFEKVYWK.LL..YDEQLPEPRYNDHPLV..NR.KPE	61
T1038 NP 414760.1 NC 000913:c246239-245961MIQRDIEYSQGYSKDV.KLAQKRHKDMNKLKYLMTLLIN..NTLPLPAVYKDHPLQ..GSWKGY	59
T6290 WP 000615983.1 NZ CP009273:c242726-242448MIQRDIEYSQGYSKDV.KLAQKRHKDMNKLKYLMTLLIN..NTLPLPAVYKDHPLQ..GSWKGY	59
T10190 WP 176704754.1 NZ KY498026:c2572-2228	MSCSTNLKKTAAASKRASLPRAADYTKSFIKDWERLSRSGRYDMNRLKEAMLLLIA..NDAPLGAEWLHDHPLK..GDWAGH	76
consensus	* * * * *	

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T10111 QIP66200.1 MK544944:263-565	RELHVDGPRGDWLLIYKIKQDD..LILTLVRTGSHHNLLGK.	100
T10112 QIP66198.1 MK544943:263-565	RELHVDGPRGGWLLIYKIKQDD..LILTLVRTGSHHNLLGK.	100
T28 WP 000916169.1 NC 000915:c946611-946345	RECHIK...PDVLLVYLKVDDE..LIL...LRLGSHSELF...	88
T10109 QIP66204.1 MK544946:257-544	RALHVA...PDWLLVYKVDAAEA..LILMLLATGTHRDTLNIE	95
T10110 QIP66208.1 MK544948:301-486	RALRVA...PDWLLVYKVDAAEA..LILMLLATGTHRDTLNIE	61
T6139 WP 005691636.1 NC 013199:c513094-512909	RALRVA...PDWLLVYKVDAAEA..LILMLLATGTHRDTLNIE	61
T6144 WP 005691636.1 NC 017491:c513270-513085	RALRVA...PDWLLVYKVDAAEA..LILMLLATGTHRDTLNIE	61
T6239 WP 005691636.1 NC 017491:c513270-513085	RALRVA...PDWLLVYKVDAAEA..LILMLLATGTHRDTLNIE	61
T10108 QIP66206.1 MK544947:301-486	RALHIA...PDWLLVYKVDAAEA..LILKLLATGTHRDTLNIE	61
T6286 WP 014517465.1 NC 017284:30649-30924	RECHIK...PDLLLVRKNNDI..LELYLANLGNNHNNIF...	91
T665 WP 002262889.1 NC 004350:850213-850491	RELHIE...SDWLLAYQVLDDE..LVLLLIDTGSHAQMLGM.	92
T6256 WP 012576472.1 NC 011593:c15445-15155	RECYIT...PDLLLVLIEKDV..LVLTTLTRTGTHSGIFGK.	96
T10095 WP 002596328.1 NC 013316:c2055913-2055623	RECHIL...PDWLLVRIEDDV..LVLTTLARTGTHSDLFGK.	96
T10070 WP 014123908.1 NC 016052:523750-524034	RDLHIK...PDWLLIYKYDG...EFVRFIDTGTHADLFK..	94
T1038 NP 414760.1 NC 000913:c246239-245961	RDHVE...PDWLLIYKLT...KLLRFERTGTAAALFG..	92
T6290 WP 000615983.1 NZ CP009273:c242726-242448	RDHVE...PDWLLIYKLT...KLLRFERTGTAAALFG..	92
T10190 WP 176704754.1 NZ KY498026:c2572-2228	RECHVG...GDFLLAYKTDSDGKTGLIFVRTGTAAELFNE.	114
consensus	!***** * * * * * ! * * * * * * * * * * ! * * * * *	



 non conserved
 similar
 ≥ 50% conserved