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T6257 WP 003831807.1 NC 011593:1564802-1565095	MLKPDYTAAAFQRDIKKLKRKHT.DLRPLKEVIRLVLEDTADSKEVLRRRHRAHTLT..GDLN	59
T6289 WP 003831807.1 NC 014169:c1181695-1181402	MLKPDYTAAAFQRDIKKLKRKHT.DLRPLKEVIRLVLEDTADSKEVLRRRHRAHTLT..GDLN	59
T10070 WP 014123908.1 NC 016052:523750-524034	MKNPNPKYKPAFERKFKKKHYKNMLKGGRYKKEDFEKVYWKL....LYDEQLEPRYNDHPLV..N.RK	59
T10181 WP 005545988.1 NC 013416:c1109635-1109369	MDYVLSKEYKRDLLKLPVEIQ.SGPEYAEVLYCL.....FNQKSLPERYKDHALQ..GNWQ	53
T166 WP 000277238.1 NC 002506:c328287-328018	MYKLEYSTQFKKDFKKITKMPISDIIEVGNVISKL.....QRGEKLEPKNVDHPLT..GNWV	55
T6286 WP 014517465.1 NC 017284:30649-30924	MQNKYSVTFSKRFFKKDFKKINNN...DKKILKKIVNKL.....ANDEVLEEKYKDHALK..GNYI	55
T10088 WP 000921941.1 NC 011498:475560-475841	MLKVRTKKDFLKDFNKHILSGRITESDVTSSVVDCL.....KEQKPLQKKYCDHALS..GNLK	55
T6127 WP 000955518.1 NC 000915:c945963-945691	MLTIETSKKFDKDLKILVKNGF.DLKLLYKVVGNL.....ATEQPLAPKYKDHPK..GGLK	54
T28 WP 000916169.1 NC 000915:c946611-946345	VLKLNLLKKSFKQKDFDKILLNGF.DDSVLNEVILTTL....RKKEPLDPQEQDHALK..GKWK	54
T1038 NP 414760.1 NC 000913:c246239-245961	MIQRDIEYSGQYSKDV.KLAQKRHKDMNKLKYLMTLLINN..TL..PLPAVYKDHPLQ..GSWK	57
T6290 WP 000615983.1 NZ CP009273:c242726-242448	MIQRDIEYSGQYSKDV.KLAQKRHKDMNKLKYLMTLLINN..TL..PLPAVYKDHPLQ..GSWK	57
T10190 WP 176704754.1 NZ KY498026:c2572-2228	MSCSTNLKKTAAASKRASLPRAADYTKSFIKDWERLSRSGRYDMNRLKEAMLLLIAN..DA..PLGAELWDHPLK..GDWA	74
T10111 QIP66200.1 MK544944:263-565	MYSLVPTPTFKRDLKR.LSKKHWPMDELKTAVNLLAAG..TNAELLSKKYADHALSSSSEWK	59
T10112 QIP66198.1 MK544943:263-565	MYSLVPTPTFKRDLKR.LSKKHWPMDELKTAVNLLAAG..TNAELLSKKYADHALSSSSEWK	59
T10109 QIP66204.1 MK544946:257-544	MMLTINRTRTFKRQFKH.LLRQGGKDMTKLATAIDTLQRQ..DR..VKLASLHDHALK..GAHS	56
T665 WP 002262889.1 NC 004350:850213-850491	MLKIKQTRQFKKSLKK.VVKQGGKINKLFAIVELLCK..SE...LPLALRNHELK..GRWR	54
T6256 WP 012576472.1 NC 011593:c15445-15155	MSGIRYTVKTTSRFRKDFKL.ARRRGLDAGLFKQVVVSILSEG..GT...LPDRYHDHALT..GNMT	58
T10095 WP 002596328.1 NC 013316:c2055913-2055623	MKETKYTVKYTTTSFKKDYKR.AIKRGLKTELLEQVVALLAMG..EP...LPDKNRDHDLS..GDWA	58
consensus	* * * ***** ** * ** ** *	

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T6257 WP 003831807.1 NC 011593:1564802-1565095	GVLECHIG.NAGDWLLLLWIRDDG...TAMFMRTGSHDELLGK.	97
T6289 WP 003831807.1 NC 014169:c1181695-1181402	GVLECHIG.NAGDWLLLLWIRDDG...TAMFMRTGSHDELLGK.	97
T10070 WP 014123908.1 NC 016052:523750-524034	PERDLHIK.P..DWLLIYKYDGE...FVRFIDTGTHADLFK..	94
T10181 WP 005545988.1 NC 013416:c1109635-1109369	GFRDCHIK.N..DLILYIKTEAD...TLYFARLNSHSEVFK..	88
T166 WP 000277238.1 NC 002506:c328287-328018	GFRDCHIK.P..DLVLIYRVFND...QLQLARIGSHSDF...	89
T6286 WP 014517465.1 NC 017284:30649-30924	GFRECHIK.P..DLLLVYRKNNDI..LELYLANLGNHNNIF...	91
T10088 WP 000921941.1 NC 011498:475560-475841	GLRECHVK.P..NLLLIYEIKKQE..NELVLLRLDTHSELFKK..	93
T6127 WP 000955518.1 NC 000915:c945963-945691	DFRECHLK.P..DLLLVYQIKKQE..NTLFLVRLGSHSELF...	90
T28 WP 000916169.1 NC 000915:c946611-946345	PFRECHIK.P..DVLLVYLVKDD...ELIILLRLGSHSELF...	88
T1038 NP 414760.1 NC 000913:c246239-245961	GYRDAHVE...PDWILIYKLTID...KLLRFERTGTAAALFG..	92
T6290 WP 000615983.1 NZ CP009273:c242726-242448	GYRDAHVE...PDWILIYKLTID...KLLRFERTGTAAALFG..	92
T10190 WP 176704754.1 NZ KY498026:c2572-2228	GHRECHVG...GDFLLAYKTDDSGKTGLIIFVRTGTAAELFNE..	114
T10111 QIP66200.1 MK544944:263-565	GYRELHVDGPRGDWLLIYKIKQQD..LILTLVRTGSHHNNLLGK..	100
T10112 QIP66198.1 MK544943:263-565	GYRELHVDGPRGGWLLIYKIKQQD..LILTLVRTGSHHNNLLGK..	100
T10109 QIP66204.1 MK544946:257-544	GERALHVA...PDWLLVYKVDAEA..LILMLLATGTHRDTLNIE	95
T665 WP 002262889.1 NC 004350:850213-850491	GIRELHIE...SDWLLAYQVLDDE..LVLLLLIDTGSASHAQLGGM.	92
T6256 WP 012576472.1 NC 011593:c15445-15155	GFRECYIT...PDLLLVYLIKEDV..LVLTTLTRTGTHSGLFGK..	96
T10095 WP 002596328.1 NC 013316:c2055913-2055623	GHRECHIL...PDWLLVYRIEDDV..LVLTTLARTGTHSGLFGK..	96
consensus	***** ** ! **** * ***** ! ****	

- ☒ non conserved
- ☒ similar
- ☒ ≥ 50% conserved