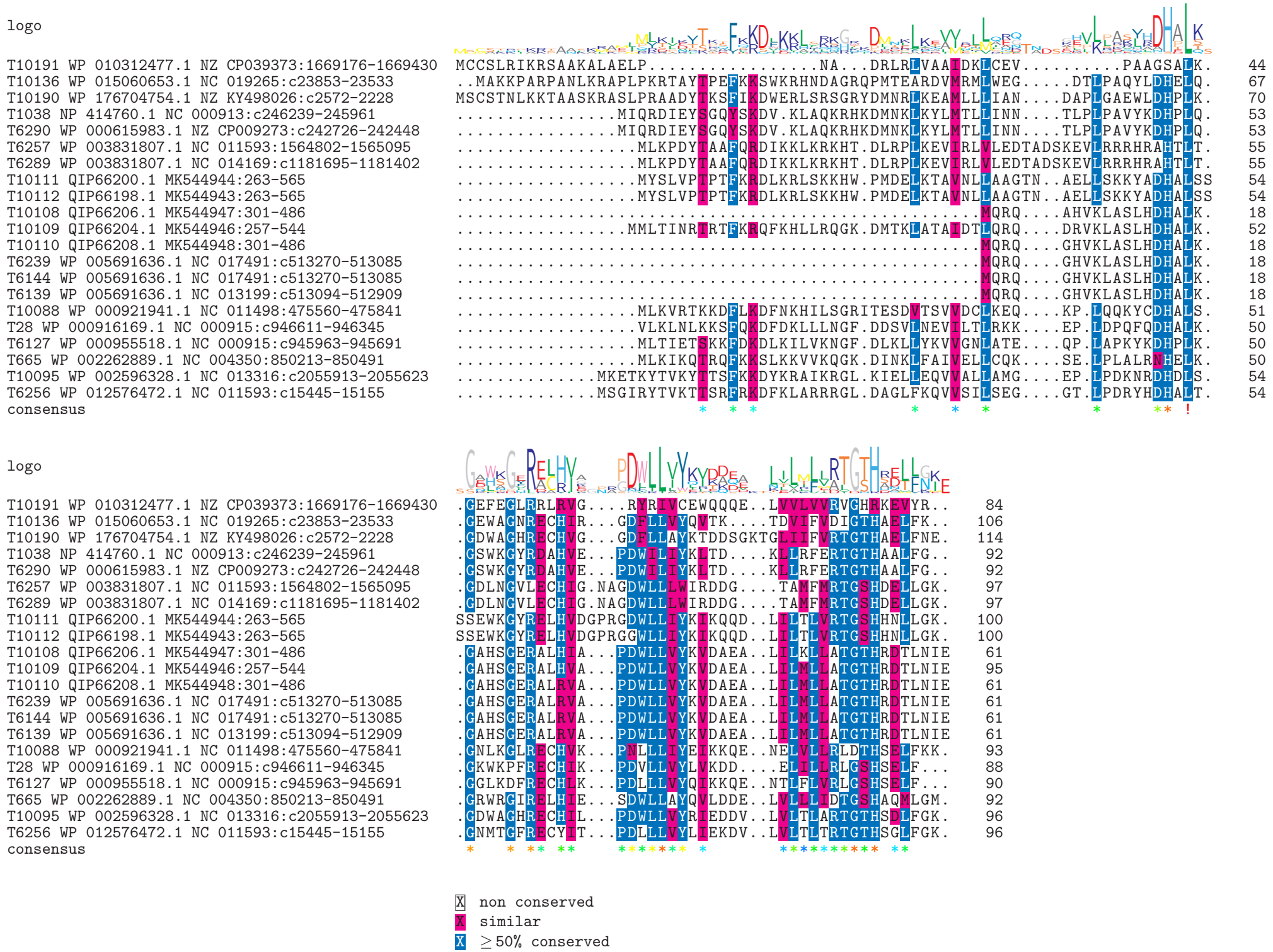
logo
T10191 WP 010312477.1 NZ CP039373:1669176-1669430 MCCSLRIKRSAAKALAELP.....NA...DRLRLVAAIDKLCEV.....PAAGSALK. 44
T10136 WP 015060653.1 NC 019265:c23853-23533 ..MAKKPARPANLKRAPLPKRTAYTPEFKKSWKRHNDAGRQPMTEARDVMRMLWEG.....DTLPAQYLDHELQ. 67
T10190 WP 176704754.1 NZ KY498026:c2572-2228 MSCSTNLKKTAASKRASLPRAADYTKSFIKDWERLSRSGRYDMNRLKEAMLLLIAN....DAPLGAEWLDHPLK. 70
T1038 NP 414760.1 NC 000913:c246239-245961 .....MIQRDIEYSGQYSKDV.KLAQKRHKDMNKLKYLMTLLINN....TLPLPAVYKDHPLQ. 53
T6290 WP 000615983.1 NZ CP009273:c242726-242448 .....MIQRDIEYSGQYSKDV.KLAQKRHKDMNKLKYLMTLLINN....TLPLPAVYKDHPLQ. 53
T6257 WP 003831807.1 NC 011593:1564802-1565095 .....MLKPDYTAAFQRDIKKLKRKHT.DLRPLKEVIRLVLEDTADSKEVLRRRHRAHTLT. 55
T6289 WP 003831807.1 NC 014169:c1181695-1181402 .....MLKPDYTAAFQRDIKKLKRKHT.DLRPLKEVIRLVLEDTADSKEVLRRRHRAHTLT. 55
T10111 QIP66200.1 MK544944:263-565 .....MYSLVPTPTFKRDLKRLSKKHW.PMDELKTAVNLLAAGTN..AELLSKKYADHALSS 54
T10112 QIP66198.1 MK544943:263-565 .....MYSLVPTPTFKRDLKRLSKKHW.PMDELKTAVNLLAAGTN..AELLSKKYADHALSS 54
T10108 QIP66206.1 MK544947:301-486 .....MQRQ....AHVKLASLHDHALK. 18
T10109 QIP66204.1 MK544946:257-544 .....MMLTINRIRTFKRQFKHLLRQGK.DMTKLATAIDTLQRQ....DRVKLASLHDHALK. 52
T10110 QIP66208.1 MK544948:301-486 .....MQRQ....GHVKLASLHDHALK. 18
T6239 WP 005691636.1 NC 017491:c513270-513085 .....MQRQ....GHVKLASLHDHALK. 18
T6144 WP 005691636.1 NC 017491:c513270-513085 .....MQRQ....GHVKLASLHDHALK. 18
T6139 WP 005691636.1 NC 013199:c513094-512909 .....MQRQ....GHVKLASLHDHALK. 18
T10088 WP 000921941.1 NC 011498:475560-475841 .....MLKVRTKKDFLKDFNKHILSGRITESDVTSVVDCLKEQ....KP.LQQKYCDHALS. 51
T28 WP 000916169.1 NC 000915:c946611-946345 .....VLKLNLKKSFQKDFDKLLLNGF.DDSVLNEVILTLRKK....EP.LDPQFQDHALK. 50
T6127 WP 000955518.1 NC 000915:c945963-945691 .....MLTIETSKKFDKDLKILVKNGF.DLKLLYKVVGNLATE....QP.LAPKYKDHPLK. 50
T665 WP 002262889.1 NC 004350:850213-850491 .....MLKIKQTRQFKKSLKKVVKQGK.DINKLFAIVELLCQK....SE.LPLALRNHELK. 50
T10095 WP 002596328.1 NC 013316:c2055913-2055623 .....MKETKYTVKYTTSFKKDYKRAIKRGL.KIELLEQVVALLAMG....EP.LPDKNRDHDLS. 54
T6256 WP 012576472.1 NC 011593:c15445-15155 .....MSGIRYTVKTTSRFRKDFKLARRRGL.DAGLFKQVVSILSEG....GT.LPDRYHDHALT. 54
consensus
logo
T10191 WP 010312477.1 NZ CP039373:1669176-1669430 .GEFEGLRRLRVG....RYRIVCEWQQQE..LVVLVVRVGHRKEVYR.. 84
T10136 WP 015060653.1 NC 019265:c23853-23533 .GEWAGNRECHIR...GDFLLVYQVTK....TDVIFVDIGTHAELFK.. 106
T10190 WP 176704754.1 NZ KY498026:c2572-2228 .GDWAGHRECHVG...GDFLLAYKTDDSGKTGLIIFVRTGTHAELFNE. 114
T1038 NP 414760.1 NC 000913:c246239-245961 .GSWKGYRDAHVE...PDWILIYKLTD....KLLRFERTGTHAALFG.. 92
T6290 WP 000615983.1 NZ CP009273:c242726-242448 .GSWKGYRDAHVE...PDWILIYKLTD....KLLRFERTGTHAALFG.. 92
T6257 WP 003831807.1 NC 011593:1564802-1565095 .GDLNGVLECHIG.NAGDWLLLWIRDDG....TAMFMRTGSHDELLGK. 97
T6289 WP 003831807.1 NC 014169:c1181695-1181402 .GDLNGVLECHIG.NAGDWLLLWIRDDG....TAMFMRTGSHDELLGK. 97
T10111 QIP66200.1 MK544944:263-565 SSEWKGYRELHVDGPRGDWLLIYKIKQQD..LILTLVRTGSHHNLLGK. 100
T10112 QIP66198.1 MK544943:263-565 SSEWKGYRELHVDGPRGGWLLIYKIKQQD..LILTLVRTGSHHNLLGK. 100
T10108 QIP66206.1 MK544947:301-486 .GAHSGERALHIA...PDWLLVYKVDAEA..LILKLLATGTHRDTLNIE 61
T10109 QIP66204.1 MK544946:257-544 .GAHSGERALHVA...PDWLLVYKVDAEA..LILMLLATGTHRDTLNIE 95
T10110 QIP66208.1 MK544948:301-486 .GAHSGERALRVA...PDWLLVYKVDAEA..LILMLLATGTHRDTLNIE 61
T6239 WP 005691636.1 NC 017491:c513270-513085 .GAHSGERALRVA...PDWLLVYKVDAEA..LILMLLATGTHRDTLNIE 61
T6144 WP 005691636.1 NC 017491:c513270-513085 .GAHSGERALRVA...PDWLLVYKVDAEA..LILMLLATGTHRDTLNIE 61
T6139 WP 005691636.1 NC 013199:c513094-512909 .GAHSGERALRVA...PDWLLVYKVDAEA..LILMLLATGTHRDTLNIE 61
T10088 WP 000921941.1 NC 011498:475560-475841 .GNLKGLRECHVK...PNLLLIYEIKKQE..NELVLLRLDTHSELFKK. 93
T28 WP 000916169.1 NC 000915:c946611-946345 .GKWKPFRECHIK...PDVLLVYLVKDD....ELILLRLGSHSELF... 88
T6127 WP 000955518.1 NC 000915:c945963-945691 .GGLKDFRECHLK...PDLLLVYQIKKQE..NTLFLVRLGSHSELF... 90
T665 WP 002262889.1 NC 004350:850213-850491 .GRWRGIRELHIE...SDWLLAYQVLDDE..LVLLLIDTGSHAQMLGM. 92
T10095 WP 002596328.1 NC 013316:c2055913-2055623 .GDWAGHRECHIL...PDWLLVYRIEDDV..LVLTLARTGTHSDLFGK. 96
T6256 WP 012576472.1 NC 011593:c15445-15155 .GNMTGFRECYIT...PDLLLVYLIEKDV..LVLTLTRTGTHSGLFGK. 96
consensus
X non conserved
X similar
X ≥50% conserved