

logo

NTDB id 1020 ACIAD RS04210 WP 011182164.1		MDITELLAFSVQNRASDLHLSAGIPPMIRVDGEVRRINLPAMDHSEVHNLIYDIMNDKQRRDYEEKLE	68
NTDB id 1283 ACE17W RS02630 WP 010947729.1		MDIAELLAFSVKNKSSDLHISAGMPPMIRVDGDLRKINLPPLLEHKDVIKIYDIMNDRQRKEYEEFFFE	68
NTDB id 1259 GC085 RS10305 WP 010947729.1		MDIAELLAFSVKNKSSDLHISAGMPPMIRVDGDLRKINLPPLLEHKDVIKIYDIMNDRQRKEYEEFFFE	68
NTDB id 1177 A1552VC RS01165 WP 000422572.1		MELNQYLDGMLTHKASDLYITVGAPILYRVDGELRAQGEALSVAD.VTALLHAMMDARQAEFKQTRE	67
NTDB id 391531 GBN67 RS07920 WP 234964034.1	MYSAEELLEEAR	MMF.HMLSKVVEYGGSDLFISADFPPIKHKGLMKPLGQQNLPSDQTKLFAYSIMNEKQRLFEFETELE	79
NTDB id 1203 PSJM300 01605 AFN76401.1		MEFEKLLRLMVEKGGSDLFITAGVPPSMKVNGKILPVNKTTPMSPEMTRETVHGVMNEQQRRREFTENHE	68
NTDB id 1019 ACIAD RS04205 WP 004922051.1		MDFNDLLNLMAKHKASDLFITAGVEPSLKINGEITPVSKTKLDGDMIAQLIDSITTQKQRQEFIEETHE	68
consensus		! ** * * ! * * * * ! ! * * * * * * * * * * ! * * * * * * * * * * !	

logo

NTDB id 1020 ACIAD RS04210 WP 011182164.1		TDFSFEPN.LARFRVNVFNQNRGAGAVFRTIPSQVLTLEELGLGKIFRDTICDYPRGLVLVTGPTGSGKSTTLAAMDYI	147
NTDB id 1283 ACE17W RS02630 WP 010947729.1		TDFSFETIAN.LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYI	147
NTDB id 1259 GC085 RS10305 WP 010947729.1		TDFSFETIAN.LARFRVNAFNQSRGAAAVFRTIPSEILSMEDLGLPPIFKEMASFSRGLVLVTGPTGSGKSTTLAAVIDYI	147
NTDB id 1177 A1552VC RS01165 WP 000422572.1		ANFAVVRD..SGRFRVSFAFFQRELPGAVIRRIETRIPTFEELKLPEVLQNLATAKRGVLVLVVGATGSGKSTTMAAMTGyr	145
NTDB id 391531 GBN67 RS07920 WP 234964034.1	CNFAISVPN.VSRFRVNVFQQQLHVGVMVIRITITAEIPNFTKLQLPTSCLKDVIMEKRGVLVLVVGATGSGKSTSLAAMIDHR		158
NTDB id 1203 PSJM300 01605 AFN76401.1	CNFAISARG.IGRFRVSFAFYQRNLAGMVLRRITETNIPTIEDLKLDPVLKKLALTKRGVLVLVVGATGTGKSTSLAAMIGYR		147
NTDB id 1019 ACIAD RS04205 WP 004922051.1	CNFAILNREKNERFRVSFAFQQRDMPGMVIIRRIETKIPSPDDLHLPPILKELAMSKRGITTFSGATGTGKSTSLASMIQHR		148
consensus		* ! * * * * * * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * !	

logo

NTDB id 1020 ACIAD RS04210 WP 011182164.1		NNHRYDHILTVEDPIEFVHEPKKCLINQREVHRDTLGFNEALRSALREDPDIILVGEMRDLETIRLALTAAETGHLVFGT	227
NTDB id 1283 ACE17W RS02630 WP 010947729.1		NSSRYEHILTVEDPIEFVHQSKKCLVNQREVHKDTLSFNAALRSALREDPDIILVGELRDLETIRLAMTAAETGHLVFGT	227
NTDB id 1259 GC085 RS10305 WP 010947729.1		NSSRYEHILTVEDPIEFVHQSKKCLVNQREVHKDTLSFNAALRSALREDPDIILVGELRDLETIRLAMTAAETGHLVFGT	227
NTDB id 1177 A1552VC RS01165 WP 000422572.1		NQHRTGHILTVEDPIEFVHEHKRCIVTQREVGLDTESYEVALKNSLRQAPDMILIGEIRSRRETMEYAMTFAETGHLCLMAT	225
NTDB id 391531 GBN67 RS07920 WP 234964034.1	NENSAGHIITVEDPVEYVHKHKKSMITHREVGVDCSHWNALKNLTRQAPDVLIGEIRDTEHAIATAETGHLCLGT		238
NTDB id 1203 PSJM300 01605 AFN76401.1	NKNSSGHIISIEDPIEFIHQHQCIVTQREVGITDTSFEVALKNTLRQAPDVLIGEVRTRETMDHAVATAETGHLCLAT		227
NTDB id 1019 ACIAD RS04205 WP 004922051.1	NQHSKGHIITIEDPIEFIEHAGCIITQREVGITDTSFEIALKNLTRQAPDVLIGEIRSRREVMYALATAETGHLVFAT		228
consensus		! * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * !	

logo

NTDB id 1020 ACIAD RS04210 WP 011182164.1		LHTTSAAKTIDRIIDVFPAEEKDMVRTMLSESLSQAVISQTLLKK.EGGGRVAAHEIMTIGIPAIRNLIREGKVAQMYSSIQ	306
NTDB id 1283 ACE17W RS02630 WP 010947729.1		LHTNSATKTINRIIDVFPAEEKSMVRSMLSESLSQAVVAQSLLKK.NKGGRVAALEIMMCTGAIRNLIREDKIAQMYSSIQ	306
NTDB id 1259 GC085 RS10305 WP 010947729.1		LHTNSATKTINRIIDVFPAEEKSMVRSMLSESLSQAVVAQSLLKK.NKGGRVAALEIMMCTGAIRNLIREDKIAQMYSSIQ	306
NTDB id 1177 A1552VC RS01165 WP 000422572.1		LHANNANQALERILHLPKEQREQFLDLSLNLKGVIQAQLLRDKNGKGRHGVFEVLLNSPRIADLIRRGELHELKATMA	305
NTDB id 391531 GBN67 RS07920 WP 234964034.1	LHANNANQALDRIINFFPDERRLNLDLSSNMKATISQRLVRTEGRCRRAAVEIMLNTPLMDLILKGNFHELKEVMS		318
NTDB id 1203 PSJM300 01605 AFN76401.1	LHANNANQALDRIINFFPADRQNVQVMDLSLNLKAIQAQLVPTPDGKRRRAVIEVLINTPLAADLIRKGEVHELKGLMK		307
NTDB id 1019 ACIAD RS04205 WP 004922051.1	LHANNANQTLERIIHFFDADRHQQIFMDLSLNLKAVISQQLIPTHDQGSRRAAVEVLINTPLLSDYIRQGEIYKIKELMA		308
consensus		! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * ! * * * * * !	

logo



X non conserved
X similar
X ≥ 50% conserved