

logo



NTDB id 600 KW2 RS01765 WP 011675413.1	..MATKKKTNFDDITKKYGAERDKALADALALIEKDFGKGSIMRLGER.ANQKVSVVSSGSLALDIALGAGGYPKGRIVE	77
NTDB id 269 KZH43 RS08665 WP 001085462.1	...MAKKPKKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIE	76
NTDB id 228 SPD RS09265 WP 001085462.1	...MAKKPKKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIE	76
NTDB id 194 SPR RS08825 WP 001085462.1	...MAKKPKKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIE	76
NTDB id 159 SP RS09750 WP 001085462.1	...MAKKPKKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIE	76
NTDB id 499 SM12261 RS08315 WP 078228268.1	...MAKKPKKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIE	76
NTDB id 527 SMSK321 RS11065 WP 001085454.1	...MAKKPKKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIE	76
NTDB id 408 SMU RS09530 WP 002262392.1	...MAKRIKKTTEEITKKFGDERKALDDALKNIEKDFGKGVAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGRIVE	76
NTDB id 453 Spy49 1753c ACI62003.1	...MAKKLKKNEEITKKFGDERRKAALDDALKNIEKDFGKGVAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGRIVE	76
NTDB id 115 BSU 16940 NP 389576.2MSDRQAALDMALKQIEKQFGKGSIMKLGK.EK.TDTRISTVPSGSLALDTALGIGGYPKGRIVE	61
NTDB id 625 LCA RS02525 WP 011374196.1MAKDERQAALDAALKKIEKNFGKGSIMRMGEK.VDTQVSTVSSGSLALDEALGVGGYPKGRIVE	63
NTDB id 1313 DR RS12030 WP 010888966.1	MSK...D.ATKEISAPTDAKERSKATETAMSIIEKAFGKGSIMKLGAE.SKLDVQVVSTGSLSLDLALGVGGIPKGRITE	75
NTDB id 1245 Cj1673c YP 002345041.1MDDNKRKSLDAALKSLDKTIFGKGTILRLGDK.EVEQIDSIGTGSVGLDLALGIGGVPKGRITE	62
NTDB id 1211 C694 RS00795 WP 000963128.1MAIDEDKQKATISLAIKQIDKVFQKGAIVRLGDK.QVEKIDSISTGSLGLDLALGIGGVPKGRIVE	64
NTDB id 1214 NCTC11637 00359 SQJ03206.1MAIDEDKQKATISLAIKQIDKVFQKGAIVRLGDK.QVEKIDAISTGSLGLDLALGIGGVPKGRIVE	64
NTDB id 1334 RAOC RS04870 WP 004918236.1MAKTETTSPNDKKAALAAVLEKLDKTYGKGTVMKLGDTVDHNI.EV.IPSGSLGLDLALGVGGYPKGRIVE	71
NTDB id 1029625 AB6B37 RS09455 WP 371395527.1	...MARNSTPLTVVGKASDKNKSAALEAALGQIDRAFGKGSVMKLGDK.SAMDIASVSTGSLGLDLALGIGGLPKGRIVE	76
NTDB id 1389 A4U84 RS07560 WP 021112712.1	MAENKSSKNNTVVKQVEPEKQKQALEAALQIEKQFGKGSIMKLGQT.EQLDIESVSTGSLGLDLALGIGGLPKGRIVE	79
NTDB id 1130 NGFG RS03960 WP 003688695.1MSDDKSKALAAALQIEKSFQKGAIVMMDGSGQEEENLEVISTGSLGLDLALGVGGLPKGRIVE	63
NTDB id 1124 NGFG RS03960 WP 003688695.1MSDDKSKALAAALQIEKSFQKGAIVMMDGSGQEEENLEVISTGSLGLDLALGVGGLPKGRIVE	63
NTDB id 1123 OK783 RS03845 WP 003688695.1MSDDKSKALAAALQIEKSFQKGAIVMMDGSGQEEENLEVISTGSLGLDLALGVGGLPKGRIVE	63
NTDB id 1427 RS RS02760 WP 011000510.1	MEDG.....KKAASMSAEKQKALAAALQIEKQFGKGSIMKMGDA.EVEPVQVVSTGSLGLDVALGVGGLPKGRIVE	71
NTDB id 1165 A1552VC RS01565 WP 000344154.1MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDLALGAGGLPKGRIVE	62
NTDB id 1142 GTF74 RS11550 WP 000344154.1MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDLALGAGGLPKGRIVE	62
NTDB id 1205 PSJM300 05545 AFN77183.1MDENKQKALAAALGQIEKQFGKGAIVMMDGSDH.DRQAIPSIISTGSLGLDLALGIGGLPKGRIVE	62
NTDB id 1022 ACIAD RS06390 WP 004925639.1MDDNKSALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDIALGIGGLPKGRIVE	62
NTDB id 1074 ABD1 RS10195 WP 000344167.1MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDIALGIGGLPKGRIVE	62
consensus	*** **	

logo



NTDB id 600 KW2 RS01765 WP 011675413.1	IGQGAEKAKNYLKEHQDVFEIDHKVRAAHGLIDDSEVAETEEETTASKTAKAKKKEEKAVETEEIELELED.....	387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGIDGEEVSEQDTEENKKDE...PKKEEA..VNEEVPLDLGDELEIEIEE	388
NTDB id 228 SPD RS09265 WP 001085462.1	IGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGIDGEEVSEQDTEENKKDE...PKKEEA..VNEEVPLDLGDELEIEIEE	388
NTDB id 194 SPR RS08825 WP 001085462.1	IGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGIDGEEVSEQDTEENKKDE...PKKEEA..VNEEVPLDLGDELEIEIEE	388
NTDB id 159 SP RS09750 WP 001085462.1	IGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGIDGEEVSEQDTEENKKDE...PKKEEA..VNEEVPLDLGDELEIEIEE	388
NTDB id 499 SM12261 RS08315 WP 078228268.1	IGQGSSENAKKYLADNPEIFDEIDHQVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDELEIEIEE	384
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IGQGSSENAKKYLADNPEVFAEIDHQVVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDELEIEIEE	384
NTDB id 408 SMU RS09530 WP 002262392.1	IGQGSSENAKKFLADNPEIFDDIDHKVVRVQFGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELED..	383
NTDB id 453 Spy49 1753c ACI62003.1	IGQGSSENAKRYLADHPQLFDEIDRKRVRKFGILLESEEEESAMAVASE.....E.....TDDLALDLNGIEIED..	378
NTDB id 115 BSU 16940 NP 389576.2	LGQGRENAKQFLKENKDIMLMIQEIQIREHYGLDNNGVVQQAAEETQEEL.EFE.E.....	348
NTDB id 625 LCA RS02525 WP 011374196.1	IGQGRENAKKNYLADHEDVEDEVRLKVRVRAAYGISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
NTDB id 1313 DR RS12030 WP 010888966.1	IGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
NTDB id 1245 Cj1673c YP 002345041.1	LGQGRENSKAFLENPEIADEITKAIQNSMGTIEGM.....ISGSEDDEG..EE.....	343
NTDB id 1211 C694 RS00795 WP 000963128.1	LGQGRENAKALLKEDKALADEITLTKIKESIGSNEE.....IMPLPDEPL..EEME.....	347
NTDB id 1214 NCTC11637 00359 SQJ03206.1	LGQGRENAKALLKEDKALADEITLTKIKESIGSNEE.....IMPLPDEPL..EEME.....	347
NTDB id 1334 RAOC RS04870 WP 004918236.1	LGQGRDITVKELIKDNPEIAEELAKIREKLQAK.....	343
NTDB id 1029625 AB6B37 RS09455 WP 371395527.1	IGQGRENVRFLLIANPDIADAVELKIRQEKGLIAD.....ELLVPKE.EQND..DITD..IPAICA.....	366
NTDB id 1389 A4U84 RS07560 WP 021112712.1	IGQGNNAVKWLKENPEIADKLEQEI RNTLASNP.....SVLKATASDSNDESVDVEE..FSEEEL.....	372
NTDB id 1130 NGFG RS03960 WP 003688695.1	IGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH.....ITEGT.....QDETGE..RPEE.....	348
NTDB id 1124 NGFG RS03960 WP 003688695.1	IGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH.....ITEGT.....QDETGE..RPEE.....	348
NTDB id 1123 OK783 RS03845 WP 003688695.1	IGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH.....ITEGT.....QDETGE..RPEE.....	348
NTDB id 1427 RS RS02760 WP 011000510.1	IGQGRDNCREFLRNARELAREIENKVRHGLVTPM....GAV.TLAEVEED.....	352
NTDB id 1165 A1552VC RS01565 WP 000344154.1	IGQGANACKYLKENPEIAKTLDKKLREMLLNPN.....MQLIAETSSAADDVEFGA..VPEEF.....	354
NTDB id 1142 GTF74 RS11550 WP 000344154.1	IGQGANACKYLKENPEIAKTLDKKLREMLLNPN.....MQLIAETSSAADDVEFGA..VPEEF.....	354
NTDB id 1205 PSJM300 05545 AFN77183.1	IGQGANAAKYLEENPEIQGTEIEQQIRAKLLV TSA.....NTKATPVAEDLADADI.....	347
NTDB id 1022 ACIAD RS06390 WP 004925639.1	IGQGNNVIRYLEENPQISTEIEAVIREQLLTKAS.....DQTAA.HDETEEEPDLL...ES.....	349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	IGQGNNVIRYFENNQIAEIEIERNIREQLLTTGT.....NGAVQ.I.EDEEEPDLL...LES.....	349
consensus	*!!!***** ** ***** ***** ** **	

- non conserved
- similar
- ≥ 50% conserved