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NTDB id 600 KW2 RS01765 WP 011675413.1	MATKK.....KTNFDDITKKYGAERDKALADALALIEKD FGKGSIMRLGER.A.NQKVS VSSGSLALDIALGAGGYPKGR	74
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK.....PKKLEEISKKFGEERDKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK.....PKKLEEISKKFGEERDKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 194 SPR RS08825 WP 001085462.1	.MAKK.....PKKLEEISKKFGEERDKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 159 SP RS09750 WP 001085462.1	.MAKK.....PKKLEEISKKFGEERDKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 527 SMSK321 RS11065 WP 001085454.1	.MAKK.....PKKLDEISKKFGEERDKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 499 SM12261 RS08315 WP 078228268.1	.MAKK.....PKKLDEISKKFGEERDKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 453 Spy49 1753c ACI62003.1	.MAKK.....LKKNEEITKKFGEERDKALDDALKNIEKD FGKGVAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR.....IKKTEEITKKFGEERDKALDDALKNIEKD FGKGVAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
NTDB id 115 BSU 16940 NP 389576.2	.....MSDRQAALDMALKQIEKQFGKGSIMKLG EK.TDTRISTVPSGSLALDIALGIGGYPRGR	58
NTDB id 625 LCA RS02525 WP 011374196.1	.....MAKDERQAALDAALKKIEKNFGKGSIMRMGEK.VDTQVSTVSSGSLALDEALGVGGYPRGR	60
NTDB id 1313 DR RS12030 WP 010888966.1	.....MSKDATKEISAPTD AKERSKATETAMSI EKAFGKGSIMKLGAE.SKLDVQVVSTGSLSLDLALGVGGIPRGR	72
NTDB id 1245 Cj1673c YP 002345041.1	.....MDNKRKSLDAALKS LDKT FGKGTILRLGDK.EVEQIDSIGTGSVGLDLALGIGGVPKGR	59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	.....MAIDEDKQKATISLAIKQIDKVF GK GALVRLGDK.QVEKIDAISTGSLGLDLALGIGGVPKGR	61
NTDB id 1211 C694 RS00795 WP 000963128.1	.....MAIDEDKQKATISLAIKQIDKVF GK GALVRLGDK.QVEKIDSISTGSLGLDLALGIGGVPKGR	61
NTDB id 1334 RAOC RS04870 WP 004918236.1	.....MAKT..ETTSPNDDKKKALAAVLEK LDKT YGKGTVMKLG DGTVDHNIIEVIPSGSLGLDLALGVGGYPKGR	68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKS SKNNTV.VKQVEPEQKKQALEAALAQIEKQFGKGSIMKLGQT.EQLDIESVSTGSLGLDLALGIGGLPMGR	76
NTDB id 1130 NGFG RS03960 WP 003688695.1	.....MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQREENLEVISTGSLGLDLALGVGGLPRGR	60
NTDB id 1124 NGFG RS03960 WP 003688695.1	.....MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQREENLEVISTGSLGLDLALGVGGLPRGR	60
NTDB id 1123 OK783 RS03845 WP 003688695.1	.....MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQREENLEVISTGSLGLDLALGVGGLPRGR	60
NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAASMSAEKQKALAAALAQIEKQFGKGSIMKMGDA.EVEPVQVVSTGSLGLDVALGVGGLPRGR	68
NTDB id 1165 A1552VC RS01565 WP 000344154.1	.....MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
NTDB id 1142 GTF74 RS11550 WP 000344154.1	.....MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
NTDB id 1205 PSJM300 05545 AFN77183.1	.....MDENKRRALAAALGQIEKQFGKGVAVMRLGDH.DRQAIPSIISTGSLGLDIALGIGGLPKGR	59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	.....MDDNKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDI ALGIGGLPKGR	59
NTDB id 267018 C2U64 RS09775 WP 002115680.1	.....MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDI ALGIGGLPKGR	59
NTDB id 1074 ABD1 RS10195 WP 000344167.1	.....MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDI ALGIGGLPKGR	59
consensus	*** ** * ** *! *!***** * **!*!*!*!*!*! !*! !*! !*!	







logo

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 NTDB id 194 SPR RS08825 WP 001085462.1  
 NTDB id 159 SP RS09750 WP 001085462.1  
 NTDB id 527 SMSK321 RS11065 WP 001085454.1  
 NTDB id 499 SM12261 RS08315 WP 078228268.1  
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 NTDB id 408 SMU RS09530 WP 002262392.1  
 NTDB id 115 BSU 16940 NP 389576.2  
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 NTDB id 1245 Cj1673c YP 002345041.1  
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 NTDB id 267018 C2U64 RS09775 WP 002115680.1  
 NTDB id 1074 ABD1 RS10195 WP 000344167.1



DEKIGQGA EKAKNYLKEHQDV FDEIDHKVRAAHG LLDSEVAETEEETTASKTAKAKKKEEKAVETEEIELELED . . . . . 387  
 DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFG LIDGEEVSEQD TENKKDE . . . . PKKEEA . . VNEEVPLDLGDELEIE 385  
 DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFG LIDGEEVSEQD TENKKDE . . . . PKKEEA . . VNEEVPLDLGDELEIE 385  
 DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFG LIDGEEVSEQD TENKKDE . . . . PKKEEA . . VNEEVPLDLGDELEIE 385  
 DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFG LIDGEEVSEQD TENKKDE . . . . PKKEEA . . VNEEVPLDLGDELEIE 385  
 DEKIGQGS ENAKKYLA DNPEVFAEIDHQV RVVQFGLIDGEEAAE . . . . SKKDE . . . . VAQVDS . . VNEEVTLDLGDELEIE 381  
 DEKIGQGS ENAKKYLA DNPEIFDEIDHQV RVVQFGLIDGEEIAE . . . . SKKDE . . . . AAQVDS . . VNEEVTLDLGDELEIE 381  
 GEKIGQGS ENAKRYLADHPQLFDEIDRKV RVVKFGLLEESEEEESAMAVASE . . . . . E . . . . . TDDLALDLNGIEIE 377  
 GEKIGQGS ENAKKFLADNPEIFDDIDHKV RVVQYGLIEEDNTEEKQSSKEK . . . . . ETDEK . . ADKNLVLELDDTIELE 382  
 EERLGGGREN AKQFLKENKDIMLMIQE QIREHYGLDNNGVVQQQA EETQEEL . EFE . E . . . . . 348  
 SERIGQGRENAKNYLADHEDVEDEVRLK VRAAYGISDVP EEDLPTTEDE . QI . NILPDDST . . . . . EE . . . . . 355  
 DERIGQGKEKTIAYIAERP EMEQEIRDRVMAAIRAGNAGEAPALAPAPA APEAA . . EA . . . . . 363  
 DKKLGQGRENSKAF LKENPEIAD EITKAIQNSMG IEGMIS . . . . . GSEDDEGEE . . . . . 343  
 DKKLGQGRENAKALLKEDKALADEITLKI KESIGSNEEIM . . . . . PLPDEPLEE . . ME . . . . . 347  
 DKKLGQGRENAKALLKEDKALADEITLKI KESIGSNEEIM . . . . . PLPDEPLEE . . ME . . . . . 347  
 DTKLGGGRD TVKELIKDNPELA EELAKI REKLQAK . . . . . 343  
 GTKIGQGNNAVKWLKENPEIADKLEQEIRNTL LASNPN SV . . . . . LKATASDSN . . DESDVEEFSEEL . . . . . 372  
 GAKIGQKDNV RVVWLKENPEISDEIDAKI RALNGVEMHIT . . . . . EG . . . . . T . . QDET DGERPEE . . . . . 348  
 GAKIGQKDNV RVVWLKENPEISDEIDAKI RALNGVEMHIT . . . . . EG . . . . . T . . QDET DGERPEE . . . . . 348  
 GAKIGQKDNV RVVWLKENPEISDEIDAKI RALNGVEMHIT . . . . . EG . . . . . T . . QDET DGERPEE . . . . . 348  
 GERIGQGRDNCREFLRENAELAREI ENKVREHLGVTPMGA . . . . . VTLAE . EVE . . ED . . . . . 352  
 GDKIGQKANAACKYLKENPEIAKTLDKKLREMLLN PENMQ . . . . . LIAETSSAA . . DDVEFGAVPEEF . . . . . 354  
 GDKIGQKANAACKYLKENPEIAKTLDKKLREMLLN PENMQ . . . . . LIAETSSAA . . DDVEFGAVPEEF . . . . . 354  
 GSKIGQKANAACKYLKENPEIAKTLDKKLREMLLN PENMQ . . . . . LIAETSSAA . . DDVEFGAVPEEF . . . . . 354  
 GSKIGQKANAACKYLKENPEIAKTLDKKLREMLLN PENMQ . . . . . LIAETSSAA . . DDVEFGAVPEEF . . . . . 354  
 GNKIGQKNNVIRYLEENPQISTEIEAV IREQLLTKASDQ . . . . . TAAHD . ETE . . EEP . . DLLES . . . . . 349  
 GNKIGQKNNVIRHFEENPQIMAGEIEKI IREQLLTTGTNG . . . . . AVQVE . DEE . . ED . . . . LLLES . . . . . 348  
 GNKIGQKNNVIRYFEENNQIAEIEIRN IREQLLTTGTNG . . . . . AVQIE . DEE . . EPD . . . . LLLES . . . . . 349

consensus

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logo

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NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388
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NTDB id 159 SP RS09750 WP 001085462.1	IEE	388
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384
NTDB id 453 Spy49 1753c ACI62003.1	D..	378
NTDB id 408 SMU RS09530 WP 002262392.1	D..	383
NTDB id 115 BSU 16940 NP 389576.2	...	348
NTDB id 625 LCA RS02525 WP 011374196.1	...	355
NTDB id 1313 DR RS12030 WP 010888966.1	...	363
NTDB id 1245 Cj1673c YP 002345041.1	...	343
NTDB id 1214 NCTC11637 00359 SQJ03206.1	...	347
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consensus

 non conserved  
 similar  
 ≥ 50% conserved