

logo



NTDB id 600 KW2 RS01765 WP 011675413.1	MATKK...KTNFDDITKKYGAERDKALADALALIEKD	FGKGSIMRLGERAAEQ.KVSVVSSGSLALDIALGAGGYPKGRI	75
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK...PKKLEEISKKFGEREKALNDALKLEKD	FGKGSIMRLGERAEQ.KVQVMSSGSLALDIALGSGGYPKGRI	74
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK...PKKLEEISKKFGEREKALNDALKLEKD	FGKGSIMRLGERAEQ.KVQVMSSGSLALDIALGSGGYPKGRI	74
NTDB id 194 SPR RS08825 WP 001085462.1	.MAKK...PKKLEEISKKFGEREKALNDALKLEKD	FGKGSIMRLGERAEQ.KVQVMSSGSLALDIALGSGGYPKGRI	74
NTDB id 159 SP RS09750 WP 001085462.1	.MAKK...PKKLEEISKKFGEREKALNDALKLEKD	FGKGSIMRLGERAEQ.KVQVMSSGSLALDIALGSGGYPKGRI	74
NTDB id 499 SM12261 RS08315 WP 078228268.1	.MAKK...PKKLDEISKKFGEREKALNDALKLEKD	FGKGSIMRLGERAEQ.KVQVMSSGSLALDIALGSGGYPKGRI	74
NTDB id 527 SMSK321 RS11065 WP 001085454.1	.MAKK...PKKLDEISKKFGEREKALNDALKLEKD	FGKGSIMRLGERAEQ.KVQVMSSGSLALDIALGSGGYPKGRI	74
NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR...IKKTEEITKKFGDERKKALDDALKNIEKD	FGKGVMLRGERAEQ.KVQVMSSGSLALDIALGAGGYPKGRI	74
NTDB id 453 Spy49 1753c ACI62003.1	.MAKK...LKKNEEITKKFGDERKKALDDALKNIEKD	FGKGVMLRGERAEQ.KVQVMSSGSLALDIALGAGGYPKGRI	74
NTDB id 115 BSU 16940 NP 389576.2	.....MSDRQAALDMALKQIEKQFGKGSIMKLG	EKTDT.RISTVPSGSLALDIALGIGGYPRGRI	59
NTDB id 625 LCA RS02525 WP 011374196.1	.....MAKDERQAALDAALKKIEKNFGKGSIMRM	GKEVDT.QVSTVSSGSLALDEALGVGGYPRGRI	61
NTDB id 1313 DR RS12030 WP 010888966.1	.....MSKDATKEISAPTDAKERSKATETAMSQIEKA	FGKGSIMKLGAEKSL.DVQVVSTGSLSLDLALGVGGIPRGRI	73
NTDB id 1245 Cj1673c YP 002345041.1	.....MDDNKRKSLDAALKSLDKTFGKGTILRLGD	KEVE.QIDSIGTGSVGLDLALGIGGVPKGRI	60
NTDB id 1211 C694 RS00795 WP 000963128.1	.....MAIDEDKQKATSLAIKQIDKVFGKGALVRLGD	KQVE.KIDSISTGSLGLDLALGIGGVPKGRI	62
NTDB id 1214 NCTC11637 00359 SQJ03206.1	.....MAIDEDKQKATSLAIKQIDKVFGKGALVRLGD	KQVE.KIDAISTGSLGLDLALGIGGVPKGRI	62
NTDB id 1334 RAOC RS04870 WP 004918236.1	.....MAKT..ETTSPNDKSKKALAAVLEKLDKT	YGKGTVMKLGDTVDHNIIEVIPSGSLGLDLALGVGGYPKGRI	69
NTDB id 1130 NGFG RS03960 WP 003688695.1	.....MSDDKSKALAAALAQIEKSF	FGKGAIMKMDGSQEQEENLEVISTGSLGLDLALGVGGIPRGRI	61
NTDB id 1124 NGFG RS03960 WP 003688695.1	.....MSDDKSKALAAALAQIEKSF	FGKGAIMKMDGSQEQEENLEVISTGSLGLDLALGVGGIPRGRI	61
NTDB id 1123 OK783 RS03845 WP 003688695.1	.....MSDDKSKALAAALAQIEKSF	FGKGAIMKMDGSQEQEENLEVISTGSLGLDLALGVGGIPRGRI	61
NTDB id 413144 PI93 RS07015 WP 039370955.1	MEESK.....K..GSANLSAEKGKALAAALAQIEKQ	FGKGSIMRLGDSEVEADIQVVSTGSLGLDIALGVGGIPRGRI	71
NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAASMSAEKQKALAAALAQIEKQ	FGKGSIMKMGDAEVEP.VQVVSTGSLGLDVALGVGGIPRGRI	69
NTDB id 1389 A4U84 RS07560 WP 021112712.1	MAENKKSSKNNTV..VKQVEPEQKKQALEAALAQIEKQ	FGKGSIMKLGQTEQL.DIESVSTGSLGLDIALGIGGLPMGRI	77
NTDB id 1165 A1552VC RS01565 WP 000344154.1	.....MDENKQKALAAALGQIEKQFGKGSIMRLGD	NRAM.DVETISTGSLSLDIALGAGGLPMGRI	60
NTDB id 1142 GTF74 RS11550 WP 000344154.1	.....MDENKQKALAAALGQIEKQFGKGSIMRLGD	NRAM.DVETISTGSLSLDIALGAGGLPMGRI	60
NTDB id 1022 ACIAD RS06390 WP 004925639.1	.....MDDNKSKALQAALSQIEKQFGKNTVMRLGD	NNTVQ.AVEAVSTGSLTLDIALGIGGLPKGRI	60
NTDB id 1074 ABD1 RS10195 WP 000344167.1	.....MDENKSKALQAALSQIEKQFGKNTVMRLGD	NNTVQ.AVEAVSTGSLTLDIALGIGGLPKGRI	60
NTDB id 1205 PSJM300 05545 AFN77183.1	.....MDENKKRALAAALGQIEKQFGKGVMLRMD	HDRQ.AIPSIISTGSLGLDIALGIGGLPKGRI	60
consensus	*** **	***! *!*****	* **!!!*!!*!!*!!*!!*!!*!!*!!*







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 NTDB id 1123 OK783 RS03845 WP 003688695.1  
 NTDB id 413144 PI93 RS07015 WP 039370955.1  
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 consensus

E K I G Q G K E N A K K Y L K E N P E I A D E I D K Y R E K G L P L E Y E D F E R E K D E E E A A V N E E Y L D L G D E L E I E I  
 S R L S R V L P E F A D I S K L A F E L E K Q K S T L P L E Y E D F E R E K D E E E A A V N E E Y L D L G D E L E I E I  
 EKIGQGA EKAKNYLKEHQDVFD EIDHKVRAAHG LDDSEVAETEEETTASKTAKAKKKEEKAVETEEIELELED..... 387  
 EKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFG LIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIEI 386  
 EKIGQGS ENAKKYLADNPEIFDEIDHQVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDELEIEI 382  
 EKIGQGS ENAKKYLADNPEVFAEIDHQVVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDELEIEI 382  
 EKIGQGS ENAKKFLADNPEIFDDIDHKVVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELED 383  
 EKIGQGS ENAKRYLADHPQLFDEIDRKVVRVKFGLLEESEEEESAMAVASE.....E.....TDDLALDLDNNGIEIED 378  
 ERLGQGR ENAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQQAEETQEEL.EFE.E..... 348  
 ERIGQGR ENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE.QI.NILPDDST.....EE..... 355  
 ERIGQGKEKTIA YTAERP EMEQEIRDRVMAAIRAGNAGEAPALAP.APAAP.....EAA..EA..... 363  
 KKLGGGR ENSKAFLKENPEIADEITKAIQNSMGTIEGMISGSEDDEGEE..... 343  
 KKLGGGR ENAKALLKEDKALADEITLKI KESIGSNEEIMPLPDEPLEEME..... 347  
 KKLGGGR ENAKALLKEDKALADEITLKI KESIGSNEEIMPLPDEPLEEME..... 347  
 TKLGGGRD TVKELIKDNPELAEELEAKIREKLQAK..... 343  
 AKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDET DGERP.....EE..... 348  
 AKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDET DGERP.....EE..... 348  
 AKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDET DGERP.....EE..... 348  
 EKIGQGD NAREFLRENPEIAHDIENKVRASLGVTAINETGEIEEED EA..... 354  
 ERIGQGRDNCREFLRENAELAREIENKVRHLGVTPMGAVTLAAEEVEED..... 352  
 TKIGQGD KNNAVKWLKENPEIADKLEQEI RNTLASNPNSVLKATASDSNDES....DVE..EFSEEEL..... 372  
 DKIGQGD KANACKY LKENPEIAKTLDKKLREMLLN PENMQLIAETSSAADDV....EFG..AVPEEF..... 354  
 DKIGQGD KANACKY LKENPEIAKTLDKKLREMLLN PENMQLIAETSSAADDV....EFG..AVPEEF..... 354  
 NKIGQGD KNNVIRYFEENPQISTEIEAVIREQLLTKASDQTA A.HDETEEEP....DLL...ES..... 349  
 NKIGQGD KNNVIRYFEENPQIAEEIERNIREQLLTTGTNGAVQ.I.EDEEEP....DLL...LES..... 349  
 SKIGQGD KANA AKYLEENPEIGQEIEQQIRAKLLVTSANTKATPVAEDLADA.....DI..... 347  
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consensus

 non conserved  
 similar  
 ≥ 50% conserved