

logo

NTDB id 114 BSU 16110 NP 389493.1  
 NTDB id 626 LCA RS04960 WP 011374694.1  
 NTDB id 1314 DR RS00625 WP 010886768.1  
 NTDB id 1043 HON27 RS16615 WP 168727007.1  
 NTDB id 1073 ABD1 RS00865 WP 015451369.1  
 NTDB id 1021 ACIAD RS00975 WP 004930462.1  
 NTDB id 1037 TT RS09535 WP 011174226.1  
 NTDB id 1388 A4U84 RS04945 WP 062924099.1  
 NTDB id 1361 HI 0985 AAC22646.1  
 NTDB id 599 KW2 RS05940 WP 021037268.1  
 NTDB id 407 SMU RS04605 WP 002262865.1  
 NTDB id 525 SMSK321 RS06295 WP 000705298.1  
 NTDB id 267 KZH43 RS05590 WP 000705306.1  
 NTDB id 226 SPD RS05990 WP 000705306.1  
 NTDB id 192 SPR RS05715 WP 000705306.1  
 NTDB id 157 SP RS06205 WP 000705306.1  
 NTDB id 497 SM12261 RS05565 WP 000705318.1  
 NTDB id 1094 KZH42 RS01320 WP 002224767.1  
 NTDB id 1089 NMB RS00600 WP 002224767.1  
 NTDB id 1120 NGFG RS10355 WP 020997408.1  
 NTDB id 1122 OK783 RS09595 WP 003705341.1  
 NTDB id 1399 DSB67 RS15600 WP 010645755.1  
 NTDB id 1152 A1552VC RS00200 WP 000654772.1  
 NTDB id 299032 DPM16 RS08150 WP 112236933.1  
 NTDB id 1250 GC085 RS13065 WP 027219989.1  
 consensus

M K M L E D E L F A W K S S F L P Q I G N S I L K L L E Y F C N Y D A L S L D I A Q I S C L L P A F L E R W C L R H I E N Y L A Y E N A D P K L L  
 .....MDQAAVCLTTCRINQLL..SPSLLKWKADPSMSLTSPVLQTVTRDQTKA.AALKNEIEQFY.....  
 ....ML....TKNQLLKVVHLAAGFGTISELRRLAALWSTSHNWALSA.....LEIAQIAR...LPER...YWPTFQASFQ  
 MTLPSPAAAHAELILALLTLRFPTPLGPRRTIENLRRHFGSAE.AALAA.....PLTELRRVEGLDSRSVAATGGAKA...  
 ....MLTQLSSHQYHTLKVWYLVQHSLSVSFKKIIDYFGNCE.KATQP.....DGLAKWSS.LGLHANHLKRVNEFQTPQG  
 ....MLTQLSSHQYHTLKVWYLVQHSLSVSFKKIIDYFGNCE.KATQP.....DGLAKWSS.LGLHANHLKRVNEFQTTQG  
 ....MITILSSHQYHTIKVWYVLQHSLSGFKKLIHYFGDCE.TALQP.....QRLSDWQK.LGLHANHLKRLKEEVHTLQG  
 .....MDPLALALLPGIGPKRLLLEVLKAEDPLG.F.....LRRERFPEAWRHLPEAEA  
 .....MTHLTKLLALLQVPQLGAQRIGRLLSEVDF...GEFCQ....YDKTALKQ.MGWNERQIQRFNPEHK..  
 .....MNDITYTLLRRLMQVPKLGGVGTIDKILSNITL...NELLN....YDDVAFRQ.MGWGAIQIRRFKPEAK..  
 .....MITNFDLFRWKKAGMT....NLGVNKKLKFRRKYD.RKISL....RQMGQVAQ.VKSIPNFIQYKNQDVKKL  
 .....MDNFQLFKLKKAGLT....NLNILNIDYEERTQ.KSLSL....RDMAVVSK.NKKPLIFMEHYKNLDSKAL  
 .....MKITNYEIYKLLKKSGLT....NQQILKVLEYGENVD.QELLL....GDIADISG.CRNPAVFMERYFQIDDAHL  
 .....MKITNYEIYKLLKKSGLT....NQQILKVLEYGENVD.QELLL....GDIADISG.CRNPAVFMERYFQIDDAHL  
 .....MKITNYEIYKLLKKSGLT....NQQILKVLEYGENVD.QELLL....GDIADISG.CRNPAVFMERYFQIDDAHL  
 .....MKITNYEIYKLLKKSGLT....NQQILKVLEYGENVD.QELLL....GDIADISG.CRNPAVFMERYFQIDDAHL  
 .....MKITNYEIYKLLKKSGLT....NQQVLAVLEYGENVD.QELLL....GDIADISG.CRNPAVFMERYFQIDDAHL  
 .....MTEDERFAWLQLAFTPYIGAESFLLLRRFGSAQ.NALS....APAEQVAA.LIRHKQALEAWRNAEKRAL  
 .....MTEDERFAWLQLAFTPYIGAESFLLLRRFGSAQ.NALS....APAEQVAA.LIRHKQALEAWRNAEKRAL  
 .....MTEDERFAWLQLAFTPYIGAESFLLLRRSFGSAQ.NALS....APAEQVAP.AVRHKHALEAWRNAEKRAL  
 .....MTEDERFAWLQLAFTPYIGAESFLLLRRSFGSAQ.NALS....APAEQVAP.AVRHKHALEAWRNAEKRAL  
 ....MTPQNDIDLAAWLKLISCLPGIGGVKMNKLLSKDTPSN.I.VQ.....YSTEQLQL.LGLTAKQLQAW.SQVDK..  
 .....MKDQDLAAWLALCFTPKLGSKTISHLLATRLPAQ.L.QS.....FTPKQWLA.CGLKPEQLVFLTTQAAK..  
 .....MNNLQPLLALINRMKRIGPRTVLKILQK.RWPD.L.N.LM.....F...QLSS.VDLEEAGLPSWLAQTIKFN  
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 consensus

FEF LQW FASSY SINK GIPEK RITAVQTASDQLSLPEGKMPSEKTENRPVGG SILD RMG FDPVHP DV LAGQLAMPAAD  
 CPGLLQNTGASSYSINKGIPEK RITAVQTASDQLSLPEGKMPSEKTENRPVGG SILD RMG FDPVHP DV LAGQLAMPAAD  
 CPGLLQNTGASSYSINKDTPDTGRRTVQTAY..APPPAAKMPSEGAAGGTAVGG ILDKMG.FDPIHP DV LAGQLAMPAAD  
 CPGLLQNTGASSYSINKDTPDTGRRVQTAY..APPPAAKMPSEGAAGGTAVGG ILDKMG.FDPVHP DV LAGQLAMPAAD  
 IQSLLDW.....SINQSL.....DLFSAPIDE.....EELFPFQLLANVG.NEATPVDI L ASRTNIPVQE  
 LKNALTW.....SLSEQVPYQA.....TLFSAVQSD.....EELFPPELLANVG.IEATPIDI L ASRTQIPVQD  
 LIY.....  
 LKIEHHQ.....F.....TSNK.....PIFSLASGK.....ENLVKFIG.FETTTIDQ I IDRSYGMEQ

I PERNVQYTEP.....F..... 297  
 LRYFD..... 288  
 LNWGLAPAPAVP.....DLP...PEQARVLRAL..QTPATLDDI AATTGLSIPE 347  
 LALPTQWQSQQQNQT.....EET.....NTNT....PEIPEHLIDLYQSLD....WVGQNI DQLV VVHNI PVSE 350  
 LALPTQWQSQQQNQT.....EEA.....NTNT....PEIREHLIDLYQSLD....WVGQNI DQLV VVHNI PVSE 350  
 LALPTHWHSQSTASGEANADDSG.....KTDD....ADLPDDLPLYQLLD....WQGQDL DQLA QHYQGSTAE 355  
 LGMSARPKPLPG.....LSPEEE...ALYALLQEKKEALP EALAMALGIPPER 309  
 IAWQRQSVHI.....QPSL.FDTKP.....KQAVKSEPKFAKNLPELTACQQQLFEQIS.LEPISVDD LAKATDMAVET 351  
 LYQHS..IHS.....QTEIDFDQIAV....PNYTPPPDPR...RL.VEAPSHPKLYSRIG.YTPVSI DDLAE EEFNLSVDV 349  
 YLYN..... 282  
 FNF..... 280  
 FEF..... 282  
 FEF..... 282  
 FEF..... 282  
 FEF..... 282  
 FEF..... 282  
 FEF..... 282  
 CPGLLQNTGASSYSINKGIPEK RITAVQTASDQLSLPEGKMPSEKTENRPVGG SILD RMG.FDPVHP DV LAGQLAMPAAD 370  
 CPGLLQNTGASSYSINKGIPEK RITAVQTASDQLSLPEGKMPSEKTENRPVGG SILD RMG.FDPVHP DV LAGQLAMPAAD 370  
 CPGLLQNTGASSYSINKDTPDTGRRTVQTAY..APPPAAKMPSEGAAGGTAVGG ILDKMG.FDPIHP DV LAGQLAMPAAD 368  
 CPGLLQNTGASSYSINKDTPDTGRRVQTAY..APPPAAKMPSEGAAGGTAVGG ILDKMG.FDPVHP DV LAGQLAMPAAD 368  
 IQSLLDW.....SINQSL.....DLFSAPIDE.....EELFPFQLLANVG.NEATPVDI L ASRTNIPVQE 342  
 LKNALTW.....SLSEQVPYQA.....TLFSAVQSD.....EELFPPELLANVG.IEATPIDI L ASRTQIPVQD 344  
 LIY..... 222  
 LKIEHHQ.....F.....TSNK.....PIFSLASGK.....ENLVKFIG.FETTTIDQ I IDRSYGMEQ 333  
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NTDB id 1314 DR RS00625 WP 010886768.1	.....	370
NTDB id 1043 HON27 RS16615 WP 168727007.1	LQTAIVMLQLQGLAYEVGGRWSR.....	376
NTDB id 1073 ABD1 RS00865 WP 015451369.1	LTSSLMELELLGLCMQQSGLYLRCRS..	376
NTDB id 1021 ACIAD RS00975 WP 004930462.1	LTSSLMELELLGLCMQQSGLYLRCRS..	383
NTDB id 1037 TT RS09535 WP 011174226.1	LTAQLMELELLGVCIQQSGRYLRCRSPY	334
NTDB id 1388 A4U84 RS04945 WP 062924099.1	VLSLLTLELKLGLARALPGGRYGGPG...	375
NTDB id 1361 HI 0985 AAC22646.1	ALIELLNLELLGVVKQVRGGYVIT....	373
NTDB id 599 KW2 RS05940 WP 021037268.1	ILVQLLDLELQDLIISENGLYKRV....	282
NTDB id 407 SMU RS04605 WP 002262865.1	.....	280
NTDB id 525 SMSK321 RS06295 WP 000705298.1	.....	282
NTDB id 267 KZH43 RS05590 WP 000705306.1	.....	282
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NTDB id 157 SP RS06205 WP 000705306.1	.....	282
NTDB id 497 SM12261 RS05565 WP 000705318.1	.....	282
NTDB id 1094 KZH42 RS01320 WP 002224767.1	LYAALLELELDGSVAAMPGGRYQRIRT.	397
NTDB id 1089 NMB RS00600 WP 002224767.1	LYAALLELELDGSVAAMPGGRYQRIRT.	397
NTDB id 1120 NGFG RS10355 WP 020997408.1	LYAALLELELDGSVAAMPGGRYQRIRT.	395
NTDB id 1122 OK783 RS09595 WP 003705341.1	LYAALLELELDGSVAAMPGGRYQRIRT.	395
NTDB id 1399 DSB67 RS15600 WP 010645755.1	VMMQLLELELSGHVVAVSGGYIRKGRG.	369
NTDB id 1152 A1552VC RS00200 WP 000654772.1	IMMQLLELELLGHVVAVPGGYIRKGRG.	371
NTDB id 299032 DPM16 RS08150 WP 112236933.1	.....	222
NTDB id 1250 GC085 RS13065 WP 027219989.1	VTSGLAELELKGAVIAVPGGYIRCEYER	361
consensus	* * *** *	

- X non conserved
- X similar
- X ≥ 50% conserved