

logo

NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1366 NTHI RS01950 WP 011271972.1		0
NTDB id 1355 HI 0298 AAC21962.1		0
NTDB id 1384 A4U84 RS08525 WP 010787006.1		0
NTDB id 1468 ASU2 RS05090 WP 014991734.1		0
NTDB id 82194 RG33 RS07555 WP 040090001.1		0
NTDB id 1436 BW25113 RS00530 WP 001025145.1		0
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

logo

NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFNLPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPPPSG	160
NTDB id 1366 NTHI RS01950 WP 011271972.1		0
NTDB id 1355 HI 0298 AAC21962.1		0
NTDB id 1384 A4U84 RS08525 WP 010787006.1		0
NTDB id 1468 ASU2 RS05090 WP 014991734.1		0
NTDB id 82194 RG33 RS07555 WP 040090001.1		0
NTDB id 1436 BW25113 RS00530 WP 001025145.1		0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1		0
consensus		

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NTDB id 1028 TT RS08215 WP 011173991.1	EGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILVRKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAALLL	240
NTDB id 1366 NTHI RS01950 WP 011271972.1		0
NTDB id 1355 HI 0298 AAC21962.1		0
NTDB id 1384 A4U84 RS08525 WP 010787006.1		0
NTDB id 1468 ASU2 RS05090 WP 014991734.1		0
NTDB id 82194 RG33 RS07555 WP 040090001.1		0
NTDB id 1436 BW25113 RS00530 WP 001025145.1		0
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
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NTDB id 1028	TT RS08215 WP 011173991.1	LRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARFYALALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSREAL	320
NTDB id 1366	NTHI RS01950 WP 011271972.1		0
NTDB id 1355	HI 0298 AAC21962.1		0
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NTDB id 1468	ASU2 RS05090 WP 014991734.1		0
NTDB id 82194	RG33 RS07555 WP 040090001.1		0
NTDB id 1436	BW25113 RS00530 WP 001025145.1		0
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
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NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
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NTDB id 1028	TT RS08215 WP 011173991.1	KEALEVQKGLPRAKPLGEIIVELGLARPEDVEEALQKQRRGGGRLEDITLVQSGKLRPEALIAQAVATQLGYPYVDPEEDPP	400
NTDB id 1366	NTHI RS01950 WP 011271972.1	MTSY....ALLHTQRVTAQNGEIFTI.....SP	24
NTDB id 1355	HI 0298 AAC21962.1	MTSY....ALLHTQRVTAQNGEIFTI.....SP	24
NTDB id 1384	A4U84 RS08525 WP 010787006.1	MSQY....T....ICEQQTERIFDI.....SP	19
NTDB id 1468	ASU2 RS05090 WP 014991734.1	MQY....S....VCDMNSQQVFDI.....SE	18
NTDB id 82194	RG33 RS07555 WP 040090001.1	MNIPQL.....	6
NTDB id 1436	BW25113 RS00530 WP 001025145.1	MNIPQL.....	6
NTDB id 1168	A1552VC RS11070 WP 000957200.1	MLTNLVAIIRQAELISATQEQAVVTQVSASGTSVPEALLLELSIFHAQELTEQLSHIFGLPETDLSRYDY	69
NTDB id 1401	DSB67 RS12665 WP 010643259.1	MLTNLSTVLRQAGILTFSQEESSLLEQVKASGISMPEALLSSGFFQSHETELHSSVFGLSCTSLNQYDY	69
NTDB id 1293	VP RS12240 WP 005479695.1	MHSNLSTILRQKGLLTFSQEESSLLEQVKASGISMPEALLSSGFFTSSELAEHLSSIFGLSQPELSQYDY	69
NTDB id 1110	NGFG RS09235 WP 003689817.1	MSVGLLRILVQNQVVTVEQAEHYY.NESQAGKEVLPMFLSDGVISPKSLAALIARVFSYSILDLRHYPR	68
NTDB id 1251	GC085 RS07725 WP 011946523.1	...MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAAQNFVPMPLDINCIDV	77
NTDB id 1018	ACIAD RS01685 WP 004920473.1	...MSAFTTPPKFSGFIRRLVEEGYVNAQNMQALEKAKKFKQDIVPYLIDNFSISPLTIAEIIISLEFGEPLLDLGVFDP	77
NTDB id 1058	ABD1 RS01615 WP 001274986.1	...MSALHTSPKFTGFFRRLVEEKHVSAAATMQTALDAKRAKQDTVAYLIEEVHLSPSLLAETISAEEFAEPYFDLDVYDT	77
consensus			

logo

NTDB id 1028	TT RS08215 WP 011173991.1	DPGAPLLLPEDLCRRYGVFPHRLEGNRLVLLMKDPRNILLALDDVRLALKRKGLNVEVAPAVATEAAITKLTIERFYGKAEL	480
NTDB id 1366	NTHI RS01950 WP 011271972.1	DLWERNQQQQSLILRYFALPLKEENNRLWLGVDLSNLSACETIAFITGK....PVEPILLESSQLKELLQQLTPHQM	99
NTDB id 1355	HI 0298 AAC21962.1	DLWERNQQQQSLILRYFALPLKEENNRLWLGVDLSNLSACETIAFITGK....PVEPILLESSQLKELLQQLTPNQ	99
NTDB id 1384	A4U84 RS08525 WP 010787006.1	SRWQKNCEEKQLLRLYLAVPVQETEHKLWLAVDDENNLTACEIFAFMTHK....QTEPVVVIASDELKYLNLALSPEQ	94
NTDB id 1468	ASU2 RS05090 WP 014991734.1	SLWQKNCEKHLILRLYLAIPIQENDDTLWLATIDDMNNLSACEIFAFIAHK....TIEPVVLISDELKYLNLALSPEQ	93
NTDB id 82194	RG33 RS07555 WP 040090001.1	TALCLRYHGVLLDASEEVVHVAVVDAPSHELLDALHFATTK....RIEITCWTRQQMEGHA.....	63
NTDB id 1436	BW25113 RS00530 WP 001025145.1	TALCLRYHGVLLDASEEVVHVAVVDAPSHELLDALHFATTK....RIEITCWTRQQMEGHA.....	63
NTDB id 1168	A1552VC RS11070 WP 000957200.1	ANLCQQLGLRELITRYDALPIAKQGNLILLAVSDPTILQAEEFEFRFATGL....QVELALADHRAALQAATIRRLYGR	144
NTDB id 1401	DSB67 RS12665 WP 010643259.1	ASLCQTLGLRLDITRHNALPLNRTSSTLILAVADPTNLQAEDDFRATGL....QVELVLADFRELTAATIRRLYGR	144
NTDB id 1293	VP RS12240 WP 005479695.1	ASLCQQLGLRELITRHNALPLHRTPTSTLLAVADPTNLQAEDDFRATGL....QVELVLADFRELSTAIRRLYGR	144
NTDB id 1110	NGFG RS09235 WP 003689817.1	HRVLMGVLTEEQMVFEHCVPVFRRGDKVFFAVSDPTQMPQIKTQVSAAGI....AVELVIVEDDQLAGLLDWVGR	143
NTDB id 1251	GC085 RS07725 WP 011946523.1	GTIPVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKETQFHTGL....NTHAIVVETDKLSALIDNLTAKES	152
NTDB id 1018	ACIAD RS01685 WP 004920473.1	ALFLKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNTEAMDAIRFNSKL....KVEPIIVEHDKLERLLSEHFVEETH	152
NTDB id 1058	ABD1 RS01615 WP 001274986.1	SQIPKDLVDQKLILKHRILPLIQRGQILYVATSNPSNIEAIDAIRFNSKL....LVEPVIVEHHKLEKVLGQHFAEES	152
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FLRQDPDIIMVGEIRDL	ETAKIATEAALTGHLVLTATLHTND	AAQATTRLDEMGVEPFNTISAALIGVLSQRLLRRVCEHCK	785
FLRQDPDIIMLGEIRDEESARIA	LRAAQTGHLVLSTLHTND	DAISATSRLLQGLTQQHEIENSL	401
FLRQDPDIIMLGEIRDEESAMIAL	RAAQTGHLVLSTLHTND	DAISATSRLLQGLTQQVEIKNSLL	401
FLRQDPDIIMLGEIRDEESAKMAL	RAAQTGHLVLSTLHTND	DAISATSRLLQGLTQQVEIKNSLL	396
FLRQDPDIIMLGEIRDQESAETIA	LRAAQTGHLVLSTLHTND	DAPSATSRLLQGLTQQVEIKNSLL	396
LLRQDPDVIMIGEIRDGETAETIA	IAKAAQTGHLVLSTLHTNSTCET	LVRLQGMGVARWMLSSATLVIAQRL	359
LLRQDPDVIMIGEIRDGETAETIA	IAKAAQTGHLVLSTLHTNSTCET	LVRLQGMGVARWMLSSATLVIAQRL	359
FLRQDPDVVMVGEIRDL	ETAEIAVKAQAQTGHLVLSTLHTNS	AAETVIRLANMGVEPFNLASSLSL	461
FLRQDPDVVMVGEIRDL	DTAEIAIKASQTGHLVLSTLHTNS	AAETVIRLANMGVEPFNLASSLSL	461
FLRQDPDVVMVGEIRDL	DTAEIAIKASQTGHLVLSTLHTNS	AAETVIRLANMGVEPFNLASSLSL	461
FLRQDPDIIMVGEIRDL	ETADIAIKAAQTGHMVFSTLHTNN	APATLSRMLNMGVAPFNIASSVSL	452
FLRQDPDIIMVGEIRDL	ETAEIAIKAAQTGHLVLSTLHTNS	AAETLNRLVMGIPTFNIASSVTL	470
FLRQDPDIIMVGEIRDL	ETAEIAIKAAQTGHLVSTLHTNS	AAETLNRLVMGVPASFNIATSVN	465
FLRQDPDIIMVGEIRDL	ETAEIAIKAAQTGHMVMSTLHTNS	APETLNRLVMGVPASFNIATSVN	465

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Sequence	Position	Score
VEV.KPDPETLRLRLGLSEAETIQ..GARLYKGMGCC..ERCGGTGYKGRYAITHETLVVDDETIRHATVAGKSATETKEIARRK	1	860
GN.....LINSCH.QGYRGRICVYQFLHWQQN.....GY.....QT	433	433
GN.....LANSCH.QGYRGRICVYQFLHWQQN.....DY.....QT	433	433
GV.....GCC..DECY.QGYRGRICVYQCLSRTAK.....KFDKQTAYL	431	431
GK.....GCC..DNCY.HGYKGRTCYQLLAKQGGK.....FFEKSTAYL	431	431
QQQGDPIHIPV.....NVWPSPLPHWQAPGCC..VHCY.HGFYGRITALFEVLPIPTVIRQLTSANTDVESLETHARQA	428	428
RQQGEPIHIPD.....NVWPSPLPHWQAPGCC..VHCY.HGFYGRITALFEVLPIPTVIRQLTSANTDVESLETHARQA	428	428
IAV.RPSALLQSQFAFPQNEIL...YEANAAGC..NECT.GGYSGRVGIYEVMAFNTELAETIQRASIHQIERLAKAN	533	533
QPQ.EPNSQLQH.IGIANTEQI...FQANPDGC..NECT.HGYSGRTCGIYEVMRFDESLEALIKGASVHELEKLAIAN	532	532
QPQ.EHTVQLQH.LGIQTTDNI...FRANPDGC..NECT.HGYSGRTCGIYEVMRFDESLEALIKGASVHELEKLAIAN	532	532
QEVERPSASALKEVCFDTEDDLAK.DWKLYRAVGC..DRCRGQGYKGRACVYEVMPISEEMQRVIMNNGTEVGILDVAYKE	529	529
AVRDDFTNQGLIELGFKEADLV..NLKLYKAVGC..EQCT.SCYRGRVCLFEVLPMTKELGQLTMSGGNSLDILKLAQSE	545	545
RPI.QVPERSLLEMCFTPEDLAQPEFQIFEPVGC..HDCR.EGYKGRVGIYEVMMKITPEISKIIMEDGNALEIAATAETL	541	541
IPA.DIPKQSLLEMCFTEQDLAHPDFRVFQPVGC..LECR.EGYKGRVGIYEVMMKVTPETISKIIMEDGNALEIAAAASEKL	541	541

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Sequence	Score
GMKTLREDGTYKALQGITTLEEV LARTIE....	889
DFENLRSEGLEKVSQGITDEKEIERVLGKNS..	464
DFKNLRASGLEKVSQGITDEKEIERVLGKNL...	464
DFSSLRESAKQKIEQQLTNETEVDRLVGYE...	461
DYDNLRSASEQKLAANITTVDEVKRVLDGD...	461
GMCTLFFENGCLAVEQCLTTFEELIRVLGMPHGE	461
GMRTLFFENGCLAVEQCLTTFEELIRVLGMPHGE	461
GMQTLQESGLEKLEEGITSFAEELQRVLYF....	562
GMQTLQMSGIEKLKQGITSFRELQRVLYF....	561
GMSTLQMSGIEKLKQGITSFSELQRVLYF....	561
GMVDLRRAGILKIMQGITSLEEV TANTND....	558
GMLTTFQSGLEKVKEGITTIIEEVNRVTVD....	574
GFNNLRRSGLKKVMQGVTSLQEINRV TSE....	570
GFNNLRRSGLKKVMQGVTSLQEVNRVTSE....	570

 non conserved
 similar
 $\geq 50\%$ conserved