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NTDB id 1127 NGFG RS10560 WP 003703428.1
NTDB id 1126 NGFG RS09375 WP 003703428.1
NTDB id 1125 NGFG RS07215 WP 003703428.1
NTDB id 1108 NGFG RS06525 WP 003703428.1
NTDB id 153 SP RS04730 WP 000387344.1
NTDB id 1272 LPP RS04360 WP 010946546.1
NTDB id 1249 GC085 RS04230 WP 010946546.1
NTDB id 1159 ABDM36 RS04765 WP 001166105.1
NTDB id 1150 A1552VC RS08580 WP 001166105.1
NTDB id 1395 DSB67 RS04445 WP 010649155.1
NTDB id 167751 AL537 RS09330 WP 031780151.1
NTDB id 1294 VP RS04495 WP 021449594.1
NTDB id 1362 HI 1008 AAC22669.1
NTDB id 1382 A4U84 RS07375 WP 062924234.1
consensus

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[illegible]

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NTDB id 1127 NGFG RS10560 WP 003703428.1
NTDB id 1126 NGFG RS09375 WP 003703428.1
NTDB id 1125 NGFG RS07215 WP 003703428.1
NTDB id 1108 NGFG RS06525 WP 003703428.1
NTDB id 153 SP RS04730 WP 000387344.1
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NTDB id 167751 AL537 RS09330 WP 031780151.1
NTDB id 1294 VP RS04495 WP 021449594.1
NTDB id 1362 HI 1008 AAC22669.1
NTDB id 1382 A4U84 RS07375 WP 062924234.1
consensus

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	YKELRLRLIVLALCGLLFAPLSAEEKKTEA	ESCEGI				
AVKSPGIIYDLPVGSRVNDAVQRA	MSRGGATP	YRFLLRHIVARCGLLFATLKGKTMKKMF	VLFC	MLFSCAFS		
.....	MSRGGATP	YRFLLRHIVARCGLLFATLKGKTMKKMF	VLFC	MLFSCAFS	49	
.....	MSRGGATP	YRFLLRHIVARCGLLFATLKGKTMKKMF	VLFC	MLFSCAFS	49	
.....	MSRGGATP	YRFLLRHIVARCGLLFATLKGKTMKKMF	VLFC	MLFSCAFS	49	
.....	MSRGGATP	YRFLLRHIVARCGLLFATLKGKTMKKMF	VLFC	MLFSCAFS	49	
AVKSPGIIYDLPVGSRVNDAVQKAGGLTEQADSK	SLNLAQKV	SDEALVYVPTK	GEEAVSQQT		GSGTASSTSK	151
.....	MKAR	LIATLLSFIVIPFSSQAENEPQK		TPAKQVL	V	35
.....	MKAR	LIATLLSFIVIPFSSQAENEPQK		TPAKQVL	V	35
.....	MQIKTKIV	TLFSLCLPTLPLLANAEETAPAA		QVEEGI		38
.....	MQIKTKIV	TLFSLCLPTLPLLANAEETAPAA		QVEEGI		38
.....	MKWMITLCLL	LAPMSWAE	TKTKA		DKYEGI	30
.....	MKWILTLC	LVFVAPFMSAA	DSAT		DKYEGI	29
.....	MKWILTLC	LVFVAPFMSAA	DTKA		DKYEGI	29
.....	MKTL	FTSVVLCGALVVSSSF	EEKATXQTAQSVVTTQAE	QVAPAV	V	47
.....	MKKLSRYTFS	LVFG	LSATTFA	EEKVTTSTEHTPVVMQ	Q	47
	*	*	**	**	*	*

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NTDB id 1362 HI 1008 AAC22669.1
NTDB id 1382 A4U84 RS07375 WP 062924234.1
consensus

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Sequence	Score
LAAVNINAAASQQELE. ALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAPKPVLP	128
LAAVNINAAASQQELE. ALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAPKPVLP	128
LAAVNINAAASQQELE. ALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAPKPVLP	128
LAAVNINAAASQQELE. ALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAPKPVLP	128
EKKVNLNKASLEELK. QVKGLGGKRAQDIIDHREANGKFKSVDELKKVSGIGGKTIKLDKYTVTD.....	216
KGKINLNTADVSLTGSFKGIGKKRAEAI IAYRENHQGFKSLEELAEVKGIGQRFVDKNREKLKEIFVIN.....	105
KGKINLNTADVSLTGSFKGIGKKRAEAI IAYRENHQGFKSLEELAEVKGIGQRFVDKNREKLKEIFVIN.....	105
VITVNINTASAEELATLLKGIGLKKQAIVDYREANGPFTHIDDLTNVKGIGEATVRNNAARILL.....	103
VITVNINTASAEELATLLKGIGLKKQAIVDYREANGPFTHIDDLTNVKGIGEATVRNNAARILL.....	103
EITVNVNSATAQEIIATLLIGIGEKKAQDIVEYRNEHPGFKTAADLTNKGIGEATVRKNEDRILL.....	95
EITVNINTASAEIIATMLKGIGEKKAQSIDYREEHGPFKTAADLKS VKGIGEATVKKNEDRILL.....	94
EITVNINTASAEIIATMLKGIGEKKAQSIDYRTEHGPFKTAADLTNKGIGEATIKKNEDRILL.....	94
SDKLNINTATASEIQKSLTVGIGAKKAIAIVQYREKHGKFNFXNAEQLELVQGIGKATLEKNRDRIIF.....	112
ANVNVNINTATASEIQDKLVGIGAKKAIAIVQYREKHGKFLNVEQLTEVSGIGKATLEKNRDCIVIE.....	113

logo

NTDB id 1127 NGFG RS10560 WP 003703428.1	VKK	131
NTDB id 1126 NGFG RS09375 WP 003703428.1	VKK	131
NTDB id 1125 NGFG RS07215 WP 003703428.1	VKK	131
NTDB id 1108 NGFG RS06525 WP 003703428.1	VKK	131
NTDB id 153 SP RS04730 WP 000387344.1	...	216
NTDB id 1272 LPP RS04360 WP 010946546.1	...	105
NTDB id 1249 GC085 RS04230 WP 010946546.1	...	105
NTDB id 1159 ABDM36 RS04765 WP 001166105.1	...	103
NTDB id 1150 A1552VC RS08580 WP 001166105.1	...	103
NTDB id 1395 DSB67 RS04445 WP 010649155.1	...	95
NTDB id 167751 AL537 RS09330 WP 031780151.1	...	94
NTDB id 1294 VP RS04495 WP 021449594.1	...	94
NTDB id 1362 HI 1008 AAC22669.1	...	112
NTDB id 1382 A4U84 RS07375 WP 062924234.1	...	113
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved