

logo

NTDB id 1257 GC085 RS04855 WP 163621000.1	MRKIIAILII..ISASISLAYSKDNSLISVKVLPLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ	78
NTDB id 1284 ACE17W RS12370 WP 010946666.1	MRKIIAILIL..ISASLSMAYSKDNSLISVKVLPLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ	78
NTDB id 1408 DSB67 RS13980 WP 010643500.1		0
NTDB id 408873 GPX94 RS05550 WP 078926717.1		0
NTDB id 1186 GTF74 RS01320 WP 000788426.1		0
NTDB id 1175 A1552VC RS12105 WP 000788426.1		0
NTDB id 1193 PAKAF RS26665 WP 003161249.1	MNSGLSRLGIALLAA.MFAPALLAADLEKLDVAALPGDRVELKLQFDEPVA.APRGYTIEQPARTIALDLPGVQNKLG..T	76
NTDB id 1009 ACIAD RS15175 WP 004923730.1	MKQIIIRQFSIGTVAYAIMQVASAQVAITNVVPMNIPGGTEIRVMFNGLPP.QPQAYQLEQPARLLIDFDKAGQKLA..K	77
NTDB id 1039 HON27 RS01460 WP 031993779.1	MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLLIDFDKAQQGLK..Q	77
NTDB id 1052 ABD1 RS15850 WP 001017033.1	MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLLIDFDKAQQGLK..Q	77
consensus	* * * * * * * * * * * * * * * * * *	

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NTDB id 1257 GC085 RS04855 WP 163621000.1	KTKTIIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGTAGSVYSLVLNGKSNDLFENSKEVF.....ITNQV	145
NTDB id 1284 ACE17W RS12370 WP 010946666.1	KTKTIIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGTAGSIYSLVLNGKSNDLFENSKEVF.....ITNQV	145
NTDB id 1408 DSB67 RS13980 WP 010643500.1	MKMRHGLTLTPRKLTGLFSLWF....SLLL...APF.....V.AAE	33
NTDB id 408873 GPX94 RS05550 WP 078926717.1	MIKGLNSV..VVRSLRYLCT....GVWTL SAVSV.....V.ASE	32
NTDB id 1186 GTF74 RS01320 WP 000788426.1	MKNGLKTY..VAQTWLTWLV....GLALCASSMV.....F.SAE	32
NTDB id 1175 A1552VC RS12105 WP 000788426.1	MKNGLKTY..VAQTWLTWLV....GLALCASSMV.....F.SAE	32
NTDB id 1193 PAKAF RS26665 WP 003161249.1	KNREL SVGNTRSVTVVEAKDRTRLIINLTTLSSYTTRVEGNLNFVVVGNSPAGASVASTAPVKASPASYAQPIKPKPY	156
NTDB id 1009 ACIAD RS15175 WP 004923730.1	SLIPVTTNEASSIDVSSDDKRARVVVNLKDAAGFTTRVEGNVFILKINNIQSTAT.....PVAT..SA.....	138
NTDB id 1039 HON27 RS01460 WP 031993779.1	SKISVATNEASSVDVTSDDQRSRLTVNLKDTGAFTTRVEGNTFILKINSAQTSNK.....PLPV..VS.....	138
NTDB id 1052 ABD1 RS15850 WP 001017033.1	SKISVATNEASSVDVTSDDQRSRLTVNLKDAAGFTTRVEGNTFILKINSAQTSNK.....PLPV..VS.....	138
consensus	* * * * * * * * * * * * * * * * *	

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NTDB id 1257 GC085 RS04855 WP 163621000.1	VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV	225
NTDB id 1284 ACE17W RS12370 WP 010946666.1	VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV	225
NTDB id 1408 DSB67 RS13980 WP 010643500.1	EVQSNLSKSIDFRTNKDKDAVIVVELVSPAIAIVDIKRVQEGLSIDLNTSVKDDQLYLVDVKDFSTVVESVEVFRDTSTT	113
NTDB id 408873 GPX94 RS05550 WP 078926717.1	LTGANQLKNIDFRLNKNKEAVLIVELASPSTVVDVQKKAQGLTIELLNTEVADDQLYLVDVKDFASAVETIEVFRQEPST	112
NTDB id 1186 GTF74 RS01320 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPST	112
NTDB id 1175 A1552VC RS12105 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPST	112
NTDB id 1193 PAKAF RS26665 WP 003161249.1	VPAGRAIRNIDFQRGEKGEKNVVIDLSDPTLSPDIEQGGKIRLDFAKTQLPDALRVRLDVKDFATPVQFVNASAQSDRT	236
NTDB id 1009 ACIAD RS15175 WP 004923730.1	PAPQGGIGNIGFQRGAQGEGLVVIDLQGTNTPVDVQQGSGKVVVRFPGIKIPHTLARRLNTTDFATPVA SIDSYNDGSNG	218
NTDB id 1039 HON27 RS01460 WP 031993779.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQGSGKVVIRTIGTKIPHTLARRLNVNDFATPVSSIDAYNDKGVG	217
NTDB id 1052 ABD1 RS15850 WP 001017033.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQGSGKVVIRTIGTKIPHTLARRLNVNDFATPVSSIDAYNDKGVG	217
consensus	* * * * * * * * * * * * * * * * *	

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consensus

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Protein	Sequence	Score
RTILSKG	RTILSKG	304
RTILSKG	RTILSKG	304
RLVAYIDEDYSHDY	RLVAYIDEDYSHDY	191
LLEVS	LLEVS	190
QLVTV	QLVTV	190
QLVTV	QLVTV	190
SITIEP	SITIEP	315
VISI	VISI	296
VITI	VITI	295
VITI	VITI	295

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consensus

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consensus

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Protein	Sequence	Length
ITKDKQ	...NSLLS ⁺ DRGK ⁺ ISV ⁺ DARTNT ⁺ IWI ⁺ QDTG ⁺ TKI ⁺ EEV ⁺ REL ⁺ IKQ ⁺ LDIPVKQ	433
IKDKQ	...NSLLS ⁺ DRGK ⁺ ISV ⁺ DARTNT ⁺ IWI ⁺ QDTG ⁺ TKI ⁺ EEV ⁺ REL ⁺ IKQ ⁺ LDIPVKQ	433
INGEGN	...IS ⁺ MLS ⁺ DRGS ⁺ MT ⁺ IDERTNS ⁺ LL ⁺ IREL ⁺ PEN ⁺ IEV ⁺ IREI ⁺ IES ⁺ LDIPVKQ	321
IGGSGT	...VN ⁺ MLS ⁺ ERGS ⁺ IS ⁺ IDERTN ⁺ ALL ⁺ IREL ⁺ PEN ⁺ IKV ⁺ IREI ⁺ IES ⁺ LDIPVKQ	320
IGGEGN	...VN ⁺ MLS ⁺ ERGS ⁺ IS ⁺ IDERTNS ⁺ LL ⁺ IREL ⁺ PONI ⁺ AV ⁺ IREI ⁺ IES ⁺ LDIPVKQ	320
IGGEGN	...VN ⁺ MLS ⁺ ERGS ⁺ IS ⁺ IDERTNS ⁺ LL ⁺ IREL ⁺ PONI ⁺ AV ⁺ IREI ⁺ IES ⁺ LDIPVKQ	320
FQSVTSDGGQEG	...KEGG ⁺ RGS ⁺ ITV ⁺ DRTNS ⁺ II ⁺ AYQP ⁺ QRL ⁺ DEL ⁺ RR ⁺ IVSQ ⁺ LDIPV ⁺ BQ	449
ITQGRNSGTSNSN	...TNGSATVEPLGDSV ⁺ G ⁺ TLLS ⁺ PRG ⁺ TIS ⁺ LD ⁺ PRTNT ⁺ LI ⁺ IND ⁺ TSQ ⁺ KI ⁺ DQ ⁺ IRK ⁺ MID ⁺ LLD ⁺ IPVKQ	447
ITQGSNNSNGLQHTSGGGTSTSTNLNTGVD ⁺ SLGNNV ⁺ G	...SLLS ⁺ PRG ⁺ TI ⁺ QDD ⁺ RTNT ⁺ LI ⁺ IND ⁺ TAQS ⁺ ID ⁺ Q ⁺ IRK ⁺ MID ⁺ LLD ⁺ VQV ⁺ KQ	455
ITQGSNNSNGLQHTSGGGTSTSTNLNTGVD ⁺ SLGNNV ⁺ G	...SLLS ⁺ PRG ⁺ TI ⁺ QDD ⁺ RTNT ⁺ LI ⁺ IND ⁺ TAQS ⁺ ID ⁺ Q ⁺ IRK ⁺ MID ⁺ LLD ⁺ VQV ⁺ KQ	455

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consensus

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NTDB id 1257 GC085 RS04855 WP 163621000.1
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NTDB id 1009 ACIAD RS15175 WP 004923730.1
NTDB id 1039 HON27 RS01460 WP 031993779.1
NTDB id 1052 ABD1 RS15850 WP 001017033.1
consensus

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NTDB id 1257 GC085 RS04855 WP 163621000.1	FFGELPVVGILFSNRQITLKNEELLIFITPRIITNALISITTIEGREKDVK	698
NTDB id 1284 ACE17W RS12370 WP 010946666.1	FFGELPVVGILFSNRQITLKNEELLIFITPRIITNALISITTIEGREKDVK	698
NTDB id 1408 DSB67 RS13980 WP 010643500.1	LLGDLPLLGALFRRSYENVGKSELLIFVTPKVVIQ.....	580
NTDB id 408873 GPX94 RS05550 WP 078926717.1	LLGDLPLLGALFRRSYQQLGKSELLIFVTPQVVIQ.....	573
NTDB id 1186 GTF74 RS01320 WP 000788426.1	LLGDLPLLGALFRRTYEQMGKSELLIFVTPKVVIQ.....	571
NTDB id 1175 A1552VC RS12105 WP 000788426.1	LLGDLPLLGALFRRTYEQMGKSELLIFVTPKVVIQ.....	571
NTDB id 1193 PAKAF RS26665 WP 003161249.1	FLGELPYLGRFLFRDRTVTDRKNELLVFLTPRIMNNQAIAIGR.....	714
NTDB id 1009 ACIAD RS15175 WP 004923730.1	FLGDLPYVGRFLFKKTAKSEAKNELLIFVTPRIVNDTIVGNH.....	709
NTDB id 1039 HON27 RS01460 WP 031993779.1	FFGDIPIVVGRFLFRKDVKSDDKQELLIFVTPRIVNDTLARNH.....	721
NTDB id 1052 ABD1 RS15850 WP 001017033.1	FFGDIPIVVGRFLFRKDVKSDDKQELLIFVTPRIVNDTLARNH.....	721
consensus	**!***!***!!!********!!!*!*!**** * *	

- ⓧ

 non conserved
- ✖

 similar
- ⓧ

 ≥ 50% conserved