

logo

NTDB id	Accession	Length	Sequence	Score
NTDB id 1193	PAKAF RS26665 WP 003161249.1	100	MNSGLSRLGIALLAAMFAPALLAADLEKLDVAALPGDRVELKLQFDEPVAAPRGYTIEQPARIALDLPGVQNKLGTKN	78
NTDB id 1186	GTKF74 RS01320 WP 000788426.1	100		0
NTDB id 1175	A1552VC RS12105 WP 000788426.1	100		0
NTDB id 1408	DSB67 RS13980 WP 010643500.1	100		0
NTDB id 1257	GCO85 RS04855 WP 163621000.1	100	MRKIAAILILISASLSL..AYSKDNSLISVKVLPLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ	78
NTDB id 1284	ACE17W RS12370 WP 010946666.1	100	MRKIAAILILISASLSM..AYSKDNSLISVKVLPLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ	78
NTDB id 145270	AAX07 RS02890 WP 080946075.1	100		0
NTDB id 1009	ACTAD RS15175 WP 004923730.1	100	MKQIRQFSIGTVAYAIMQVASAQVAITNVVPMNIPGQGTEIRVMF.NGLPPQPQAYQLEQPARLILDFDKAGQKLAQSL	79
NTDB id 1039	HON27 RS01460 WP 031993779.1	100	MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMF.NGLPPQPQAYQLENPSRLILDFDKAQGGLKQSK	79
NTDB id 1052	ABD1 RS15850 WP 001017033.1	100	MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMF.NGLPPQPQAYQLENPSRLILDFDKAQGGLKQSK	79
consensus			* * * * * * * * * * * * * * * *	

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NTDB id	Accession	Length	Sequence	Score
NTDB id 1193	PAKAF RS26665 WP 003161249.1	156	..RE[L]SVGNTR[S]VT[V]VEAKD[R]TR[L]I[N]LTTLSS[Y]TTRVEGN[N]LFV[V]VGNSPAGASVASTAPVKASPAPASYAQPIKPKPY	156
NTDB id 1186	GTF74 RS01320 WP 000788426.1	32	[M]K[N]GLKT..YVAQTWL[T]LW[V]GLAL.....CASSM.....VF.SAE	32
NTDB id 1175	A1552VC RS12105 WP 000788426.1	32	[M]K[N]GLKT..YVAQTWL[T]LW[V]GLAL.....CASSM.....VF.SAE	32
NTDB id 1408	DSB67 RS13980 WP 010643500.1	33	[M]K[M]RHGL[T]L[T]P[R]KL[T]GL[F]SL[W]FSL[L].....AP.....FV.AAE	33
NTDB id 1257	GC085 RS04855 WP 163621000.1	145	KTKT[I]QLGSLH[S]YNTIVAVGD[R]VRAILEL[L]DRSV[S]SGTAG[S]V[S]SLV[L]NGKSNDLFENSKEV.....FITNQV	145
NTDB id 1284	ACE17W RS12370 WP 010946666.1	145	KTKT[I]QLGSLH[S]YNTIVAVGD[R]VRAILEL[L]DRSV[S]SGTAG[S]I[S]SLV[L]NGKSNDLFENSKEV.....FITNQV	145
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NTDB id 1039	HON27 RS01460 WP 031993779.1	138	IS..[V]ATNEAS[S]VDV[T]SDDQ[R]SL[T]VN[L]KDTGAF[T]TTRVEGN[T]FILK[I]NSAQTSN...KP...[L]PVVS	138
NTDB id 1052	ABD1 RS15850 WP 001017033.1	138	IS..[V]ATNEAS[S]VDV[T]SDDQ[R]SL[T]VN[L]KDAGAF[T]TTRVEGN[T]FILK[I]NSAQTSN...KP...[L]PVVS	138
consensus			* * * * *	

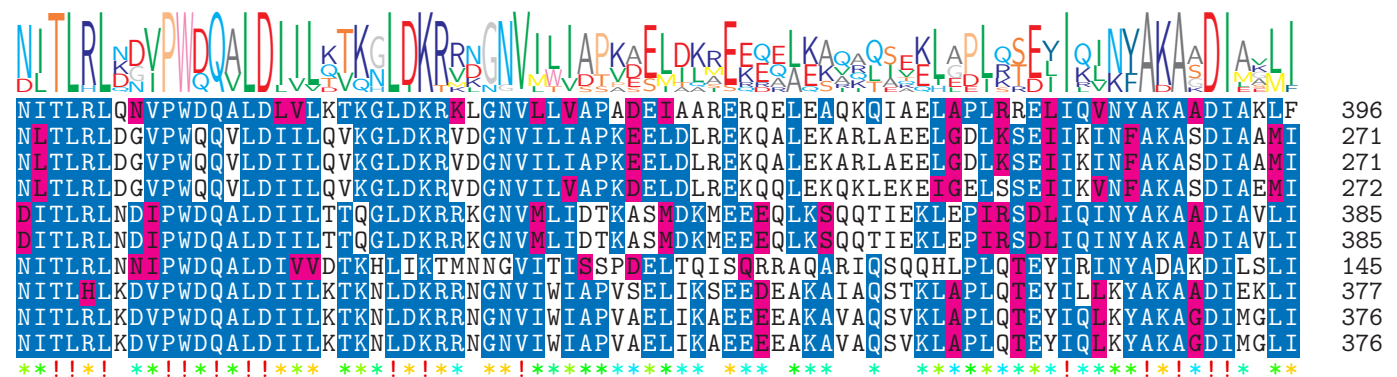
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NTDB id	1193	PAKAF	RS26665	WP	003161249.1	VPAAGRAIRNIDFRGQEKGEGNVVILDSPTLSPDIQEQGGKIRLDFAKTQLPDA	LRVRRLDVKDFA	TPVQFVNASAQSDRT	236
NTDB id	1186	GTF74	RS01320	WP	000788426.1	SATANQLENIDFRVNKEKA A VLIVELASPSAVVDVQKVQEGLSIELLKTDVADDDKLYLLDVKDFSTPVESVEVFRKEPST			112
NTDB id	1175	A1552VC	RS12105	WP	000788426.1	SATANQLENIDFRVNKEKA A VLIVELASPSAVVDVQKVQEGLSIELLKTDVADDDKLYLLDVKDFSTPVESVEVFRKEPST			112
NTDB id	1408	DSB67	RS13980	WP	010643500.1	EVQSNSLKSIDFRTNKDKDAVIIVVELVSPA I VIDIKRVQEGLSIDLNLTSVKDDQLYLLDVKDFSTVVESVEVFRDTSTT			113
NTDB id	1257	GCO85	RS04855	WP	163621000.1	VNAKHETKRIDFRGIEKQGGRVLIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVDHFSVPVQIITMQQEGKKV			225
NTDB id	1284	ACE17W	RS12370	WP	010946666.1	VNAKHETKRIDFRGIEKQGGRVLIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVDHFSVPVQIITMQQEGKKV			225
NTDB id	145270	AAX07	RS02890	WP	080946075.1	.	.	0	
NTDB id	1009	ACIAD	RS15175	WP	004923730.1	PAPQQGTIGNIGFQRGAQGEGLVVILDLQGTINTPVDVQQQGSKVVFRRFGIKIPHTHLARRLNITTDFATPVA	SIDSYN	DGSGNG	218
NTDB id	1039	HON27	RS01460	WP	031993779.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQQGSKVVRTIGTKIPHTHLARRLNVDNFATPVS	SIDAYND	KGVG	217
NTDB id	1052	ABD1	RS15850	WP	001017033.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQQGSKVVRTIGTKIPHTHLARRLNVDNFATPVS	SIDAYND	KGVG	217
consensus									
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NTDB id 1193 PAKAF RS26665 WP 003161249.1
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NTDB id 1175 A1552VC RS12105 WP 000788426.1
NTDB id 1408 DSB67 RS13980 WP 010643500.1
NTDB id 1257 GC085 RS04855 WP 163621000.1
NTDB id 1284 ACE17W RS12370 WP 010946666.1
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NTDB id 1009 ACIAD RS15175 WP 004923730.1
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consensus

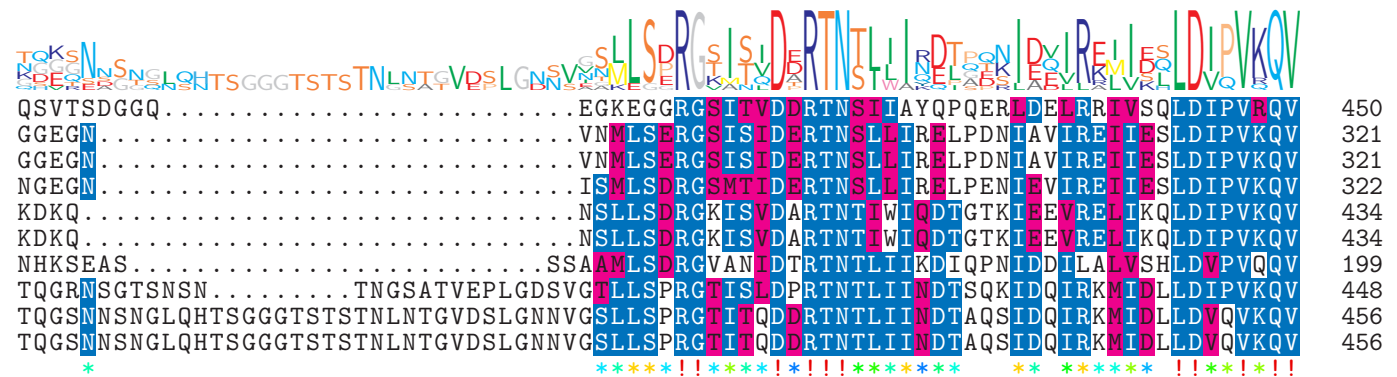
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consensus

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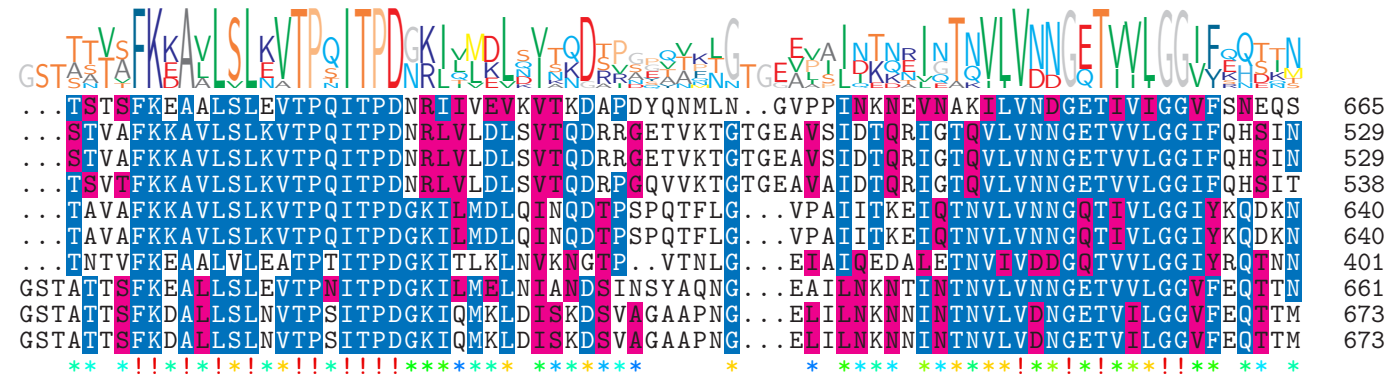
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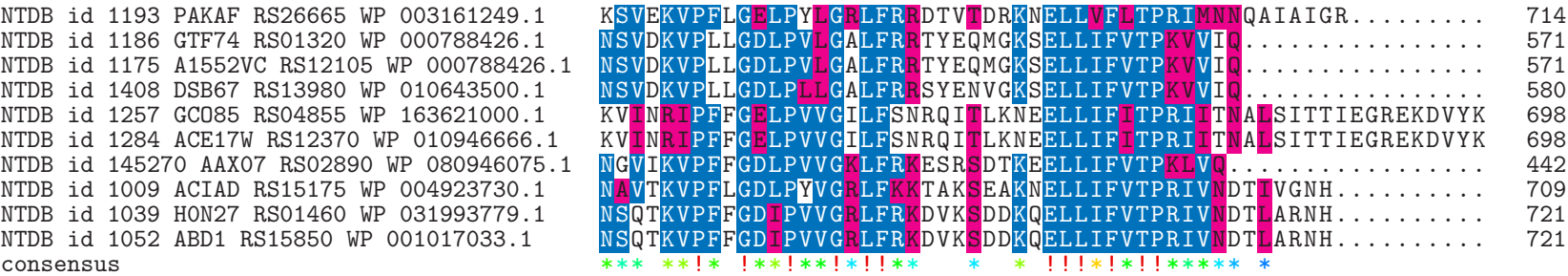
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NTDB id 1175 A1552VC RS12105 WP 000788426.1
NTDB id 1408 DSB67 RS13980 WP 010643500.1
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NTDB id 1039 HON27 RS01460 WP 031993779.1
NTDB id 1052 ABD1 RS15850 WP 001017033.1
consensus
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logo



☐ non conserved
☒ similar
☒ ≥ 50% conserved