

logo

NTDB id 1257 GC085 RS04855 WP 163621000.1	MRKIIAILII..ISASISLAYSKDNSIISVKVLP	78
NTDB id 1284 ACE17W RS12370 WP 010946666.1	MRKIIAILIL..ISASISLAYSKDNSIISVKVLP	78
NTDB id 1408 DSB67 RS13980 WP 010643500.1		0
NTDB id 343604 ET951 RS06855 WP 187377498.1		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.MFAPALLAADLEKLDVAALPGDRVELK	76
NTDB id 1009 ACIAD RS15175 WP 004923730.1	MKQIIRQFSIGTVAYAIMQVSAQVAITNVVPMNIPGQGTEIRVMF	77
NTDB id 1052 ABD1 RS15850 WP 001017033.1	MNHVFRQFSMGAVAIAIMQAAQAQVSMTNIVPMQIAGQGTEIRVMF	77
NTDB id 1039 HON27 RS01460 WP 031993779.1	MNHVFRQFSMGAVAIAIMQAAQAQVSMTNIVPMQIAGQGTEIRVMF	77
consensus	* * * * *	

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NTDB id 1257 GC085 RS04855 WP 163621000.1	KTCTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGTAGSVYSLVL	145
NTDB id 1284 ACE17W RS12370 WP 010946666.1	KTCTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGTAGSVYSLVL	145
NTDB id 1408 DSB67 RS13980 WP 010643500.1	MKMRHGLTLTPRKLTGLFSLWFS.....LLLIAP.....	33
NTDB id 343604 ET951 RS06855 WP 187377498.1	MRNGLKTY..VAQTWLTWAG.....LALCAS.....	32
NTDB id 1186 GTF74 RS01320 WP 000788426.1	MKNGLKTY..VAQTWLTWVG.....LALCAS.....	32
NTDB id 1175 A1552VC RS12105 WP 000788426.1	MKNGLKTY..VAQTWLTWVG.....LALCAS.....	32
NTDB id 1193 PAKAF RS26665 WP 003161249.1	KNRELISVGNTRSVTVVEAKDRTRLINLTTLSYYTTRVEGNLNFVV	156
NTDB id 1009 ACIAD RS15175 WP 004923730.1	SLIPVTTNEASSIDVSSDDKRARVVNLKDGAFITTRVEGNVFILKIN	138
NTDB id 1052 ABD1 RS15850 WP 001017033.1	SKISVATNEASSVDVTSDDQRSRLTVNLKDGAFITTRVEGNVFILKIN	138
NTDB id 1039 HON27 RS01460 WP 031993779.1	SKISVATNEASSVDVTSDDQRSRLTVNLKDGAFITTRVEGNVFILKIN	138
consensus	* * * * *	

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NTDB id 1257 GC085 RS04855 WP 163621000.1	VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVN	225
NTDB id 1284 ACE17W RS12370 WP 010946666.1	VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVN	225
NTDB id 1408 DSB67 RS13980 WP 010643500.1	EVQSNLSKSIDFRTNKDKDAVIVVELVSPAIIVDIKRVQEGLSIDL	113
NTDB id 343604 ET951 RS06855 WP 187377498.1	SASANQLENIDFRVNKDKA AVLIVELASPSAVVDVQKVQEGLSIEL	112
NTDB id 1186 GTF74 RS01320 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIEL	112
NTDB id 1175 A1552VC RS12105 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIEL	112
NTDB id 1193 PAKAF RS26665 WP 003161249.1	VPAGRAIRNIDFQRGEKGENVIDLSPTLSPDIQEQQGKIRLDFAKT	236
NTDB id 1009 ACIAD RS15175 WP 004923730.1	PAPQGGIGNIGFQRGAQGEGLVVIDLQGTNTPVDVQQGSKVVVRF	218
NTDB id 1052 ABD1 RS15850 WP 001017033.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQGSKVVIRT	217
NTDB id 1039 HON27 RS01460 WP 031993779.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQGSKVVIRT	217
consensus	* * * * *	

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consensus

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Position	Residue	Conservation
1	R	High
2	M	High
3	T	High
4	I	High
5	L	High
6	S	High
7	K	High
8	G	High
9	D	High
10	H	High
11	Y	High
12	K	High
13	K	High
14	Y	High
15	K	High
16	L	High
17	V	High
18	F	High
19	P	High
20	P	High
21	D	High
22	N	High
23	S	High
24	L	High
25	K	High
26	K	High
27	A	High
28	E	High
29	K	High
30	E	High
31	K	High
32	S	High
33	L	High
34	N	High
35	T	High
36	G	High
37	K	High
38	L	High
39	S	High
40	N	High
41	F	High
42	Q	High
43	D	High
44	I	High
45	V	High
46	R	High
47	V	High
48	L	High
49	Q	High
50	L	High
51	A	High
52	D	High
53	E	High
54	T	High
55	G	High
56	I	High
57	N	High
58	V	High
59	S	High
60	D	High
61	S	High
62	V	High
63	S	High
64	V	High
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89	S	High
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91	S	High
92	V	High
93	S	High
94	V	High
95	S	High
96	V	High
97	S	High
98	V	High
99	S	High
100	V	High

logo

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consensus

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[illegible]

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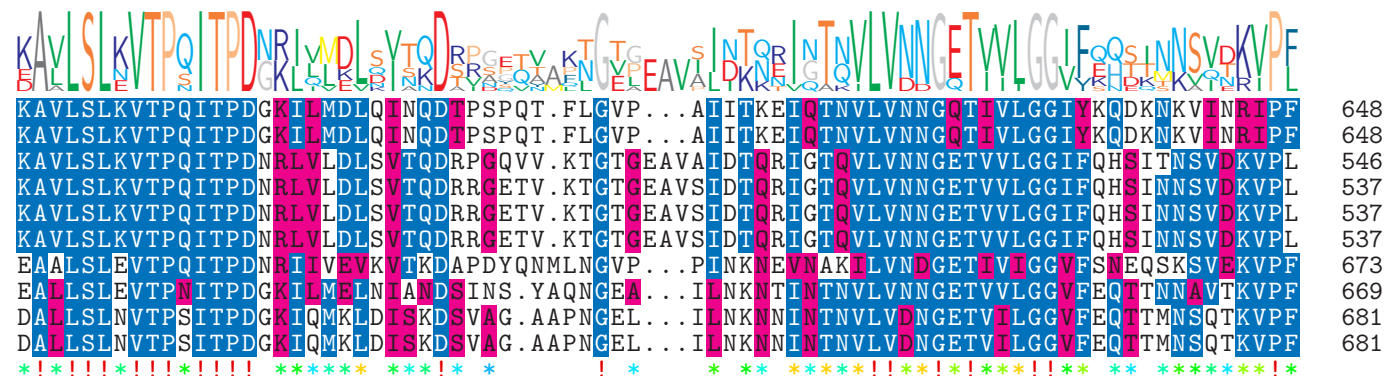
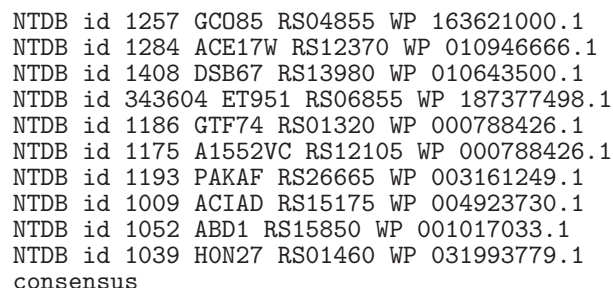
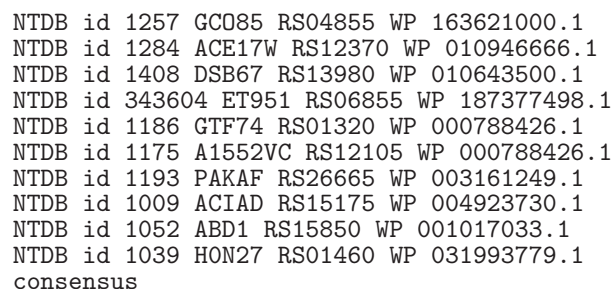
Sequence	Position
KDKQ.N	434
KDKQ.N	434
NGEG.NI	322
GGEENV	321
GGEENV	321
GGEENV	321
QSVTSDGGQEG	450
TQGRNSGTSNSN	448
TQGSNNSNGLQHTSGGGTSTSTNLNTGVDSLGNVVG	456
TQGSNNSNGLQHTSGGGTSTSTNLNTGVDSLGNVVG	456

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NTDB id 1052 ABD1 RS15850 WP 001017033.1
NTDB id 1039 HON27 RS01460 WP 031993779.1
consensus

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X non conserved
X similar
X ≥ 50% conserved