

logo

NTDB id 1284 ACE17W RS12370 WP 010946666.1	MRKIIAILII..ISASISLMAYSKDNSLISVKVLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ	78
NTDB id 1257 GC085 RS04855 WP 163621000.1	MRKIIAILIL..ISASISLAYSKDNSLISVKVLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ	78
NTDB id 1408 DSB67 RS13980 WP 010643500.1		0
NTDB id 56432 OCV30 RS14190 WP 017103612.1		0
NTDB id 1186 GTF74 RS01320 WP 000788426.1		0
NTDB id 1175 A1552VC RS12105 WP 000788426.1		0
NTDB id 1193 PA5040 NP 253727.1	MNSGLSRLGIALLAA.MFAPALLAADLEKLDVAALPGDRVELKLQFDEPVA.APRGYTIEQPARIALDLPGVQNKLG..T	76
NTDB id 1009 ACIAD RS15175 WP 004923730.1	MKQIIIRQFSIGTVAYAIMQVSAQVAITNVVPMNIPGQGTEIRVMFNGLPP.QPQAYQLEQPARLILDFDKAGQKLA..K	77
NTDB id 1052 ABD1 RS15850 WP 001017033.1	MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLILDFDKAQGGLK..Q	77
NTDB id 1039 HON27 RS01460 WP 031993779.1	MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLILDFDKAQGGLK..Q	77
consensus	* * * * * * * * * * * * * * * * * *	

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NTDB id 1284 ACE17W RS12370 WP 010946666.1	KTCTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGSTAGSIYSLVLNGKSNDLFENSKEVF.....ITNQV	145
NTDB id 1257 GC085 RS04855 WP 163621000.1	KTCTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGSTAGSVYSLVLNGKSNDLFENSKEVF.....ITNQV	145
NTDB id 1408 DSB67 RS13980 WP 010643500.1	MKMRHGLTLTPRKLTGLFSLWFSL...LLAP...FV.....A..AE	33
NTDB id 56432 OCV30 RS14190 WP 017103612.1	MIKGLS..KLINKGLQSLVSV...MLV..VSVF.....S..YA	30
NTDB id 1186 GTF74 RS01320 WP 000788426.1	MKNGLK..TYVAQTWLTLWVGL...ALCASSMVF.....S..AE	32
NTDB id 1175 A1552VC RS12105 WP 000788426.1	MKNGLK..TYVAQTWLTLWVGL...ALCASSMVF.....S..AE	32
NTDB id 1193 PA5040 NP 253727.1	KNRELISVGNTRSVTVVEAKDRTRLIINTALSSYTTTRVEGNNLFVVVGNSPAGASVASAAPVKASPAPASYAQPIKPKPY	156
NTDB id 1009 ACIAD RS15175 WP 004923730.1	SLIPVTTNEASSIDVSSDDKRARVVVNLKDAAGFTTRVEGNTFILKINNIQSTAT....PV....A..TSA.....	138
NTDB id 1052 ABD1 RS15850 WP 001017033.1	SKISVATNEASSVDVTSDDQRSRLTVNLKDAAGFTTRVEGNTFILKINSAQTSNK....PL....P..VVS.....	138
NTDB id 1039 HON27 RS01460 WP 031993779.1	SKISVATNEASSVDVTSDDQRSRLTVNLKDTGAFTTRVEGNTFILKINSAQTSNK....PL....P..VVS.....	138
consensus	* * * * * * * * * * * * * * * * * *	

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NTDB id 1284 ACE17W RS12370 WP 010946666.1	VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV	225
NTDB id 1257 GC085 RS04855 WP 163621000.1	VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV	225
NTDB id 1408 DSB67 RS13980 WP 010643500.1	EVQSNLSKSIDFRTNKDKDAVIVVELVSPAIIVDIKRVQEGLSIDLNTSVKDDQLYLVDVKDFSTVVESVEVFRDTSTT	113
NTDB id 56432 OCV30 RS14190 WP 017103612.1	ESLPNQLENIDFRVNKEKDAVITIELATSTAVVDVQRAQEGLSIELLNTQVNDKLYLLDVKDFATSVEGIEVYKETPST	110
NTDB id 1186 GTF74 RS01320 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTVDVADDKLYLLDVKDFSTPVESVEVFRKEPST	112
NTDB id 1175 A1552VC RS12105 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTVDVADDKLYLLDVKDFSTPVESVEVFRKEPST	112
NTDB id 1193 PA5040 NP 253727.1	VPAGRAIRNIDFQRGEKGEKNVVIDLSPTLSPDIQEQQGKIRLDFAKTQLPDALRVRLDVKDFATPVQFVNASDAQSDRT	236
NTDB id 1009 ACIAD RS15175 WP 004923730.1	PAPQGGIGNIGFQRGAQGEGLVVIDLQGTINTPVDVQQGSKVVRFPGIKIPHTLARRLNTTDFATPVASIDSYNDGSNG	218
NTDB id 1052 ABD1 RS15850 WP 001017033.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQGSKVVIRTIGTKIPHTLARRLNVNDFATPVSSIDAYNDKGVG	217
NTDB id 1039 HON27 RS01460 WP 031993779.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQGSKVVIRTIGTKIPHTLARRLNVNDFATPVSSIDAYNDKGVG	217
consensus	* * * * * * * * * * * * * * * * * *	

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NTDB id 1039 HON27 RS01460 WP 031993779.1
consensus

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Position	Sequence	Score
1	RMTILSKG	305
2	RMTILSKG	305
3	RLVAYIDEDY	192
4	RLLATIAG	189
5	QLVVTVDG	191
6	QLVVTVDG	191
7	SITIEPSS	316
8	VISIQSTG	297
9	VITIQSSG	296
10	VITIQSSG	296

The sequence logo above the table shows the conservation of residues. The mutation site (position 100) is highlighted with a red background. The sequence is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

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consensus

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[illegible]

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NTDB id 1039 HON27 RS01460 WP 031993779.1
consensus

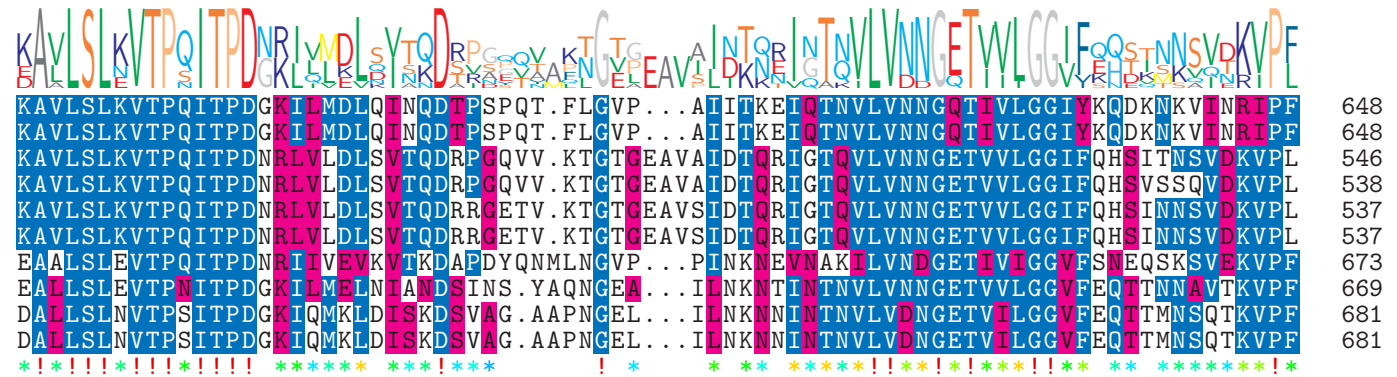
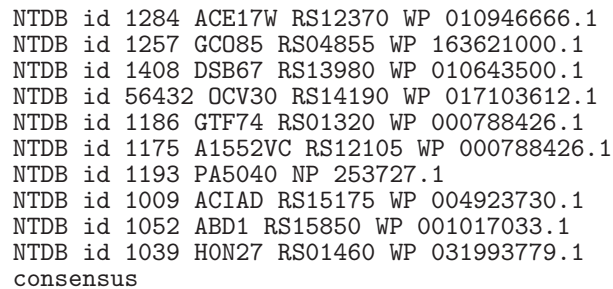
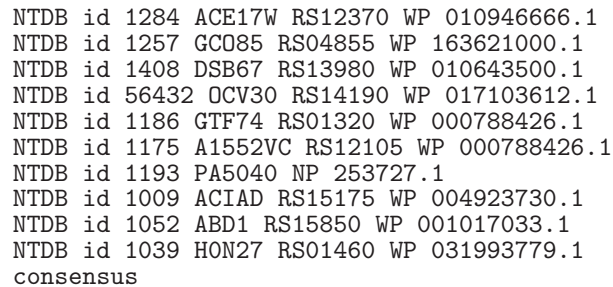
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[illegible]

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NTDB id 1257 GC085 RS04855 WP 163621000.1
NTDB id 1408 DSB67 RS13980 WP 010643500.1
NTDB id 56432 OCV30 RS14190 WP 017130612.1
NTDB id 1186 GTTF74 RS01320 WP 000788426.1
NTDB id 1175 A1552VC RS12105 WP 000788426.1
NTDB id 1193 PA5040 NP 253727.1
NTDB id 1009 ACIAD RS15175 WP 004923730.1
NTDB id 1052 ABD1 RS15850 WP 001017033.1
NTDB id 1039 HON27 RS01460 WP 031993779.1
consensus

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☐ non conserved
☒ similar
☒ ≥ 50% conserved