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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 1362 HI 1008 AAC22669.1
NTDB id 1382 A4U84 RS07375 WP 062924234.1
NTDB id 595 KW2 RS08725 WP 021037687.1
NTDB id 521 SMSK321 RS04960 WP 000443804.1
NTDB id 493 SM12261 RS04300 WP 000387351.1
NTDB id 263 KZH43 RS04195 WP 000387330.1
NTDB id 222 SPD RS04535 WP 000387330.1
NTDB id 188 SPR RS04295 WP 000387330.1
NTDB id 153 SP RS04730 WP 000387344.1
NTDB id 1069 ABD1 RS03060 WP 043960841.1
NTDB id 1041 HON27 RS14740 WP 005124713.1
NTDB id 36 MW RS08230 WP 001793467.1
NTDB id 20 SA RS08005 WP 001802022.1
NTDB id 105 BSU 25590 NP 390437.1
NTDB id 1014 ACIAD RS13855 WP 004924483.1
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 27325 CJJ81176 RS00055 WP 002855574.1
NTDB id 1242 Cj0011c YP 002343483.1
consensus

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[illegible]

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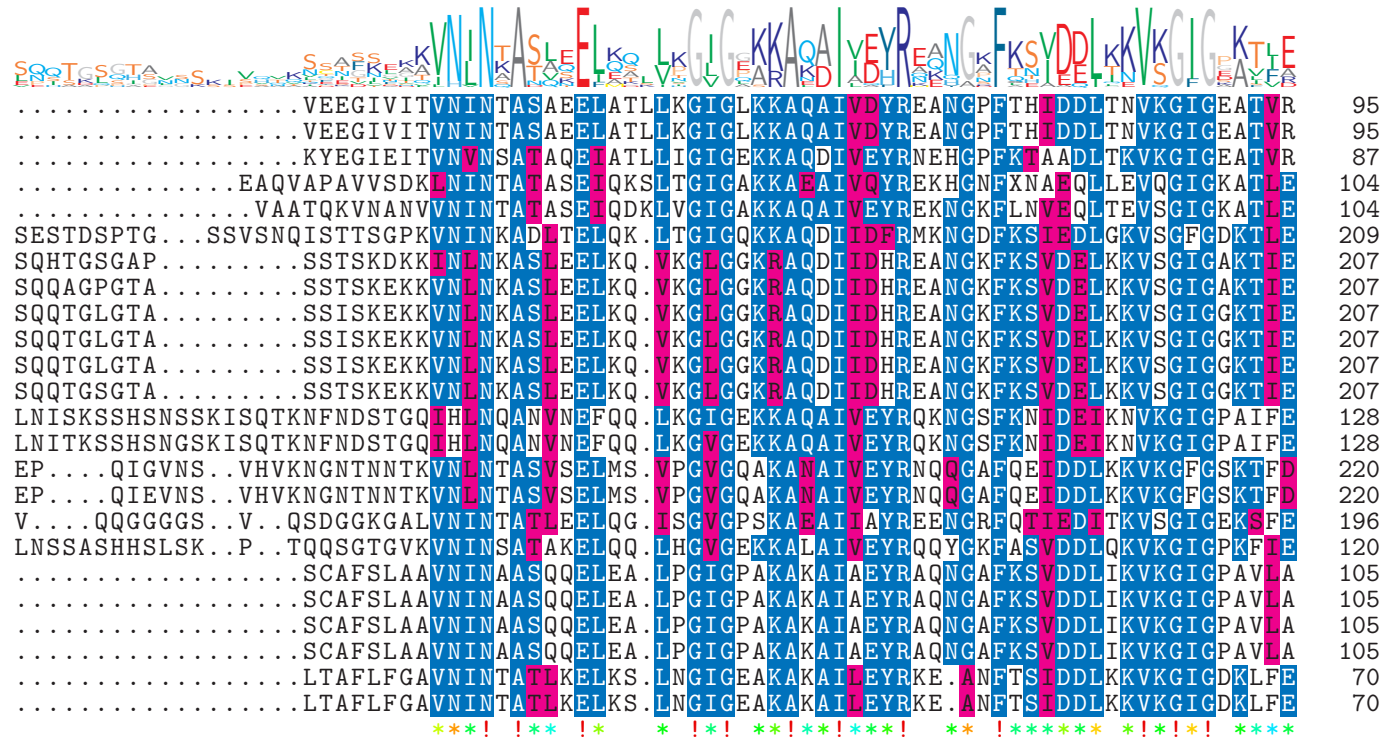
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.....MQIKT.KIVT ⁺ LFSLCLPTLP ⁺ LLAN ⁺ AEETAPAA ⁺ Q	33
.....MQIKT.KIVT ⁺ LFSLCLPTLP ⁺ LLAN ⁺ AEETAPAA ⁺ Q	33
.....MKWMLTLC ⁺ LLILAPMSW ⁺ AE.TKTKAD	25
.....MKT.L.FTSVVL ⁺ CGALVVSS ⁺ FAEEKATXQ ⁺ TAQSVV.....TTQA.....	38
.....MKK.LSRYTFS ⁺ LLFG.LFSATT ⁺ FAEEKVTT ⁺ STEHTPV.....VMQQ.....	39
NKNEIMVD ⁺ LKGA ⁺ VAKPN ⁺ VYQISSDER ⁺ LVDLI.....RQAGGFTDQ ⁺ ADQKSINLSAKLKDEEVIYVPKVGESS ⁺ S	133
EQDLITVD ⁺ VKGA ⁺ VKSPG ⁺ IYDLSV ⁺ GSRVND ⁺ AV.....QKAGGLTEQ ⁺ ADSKSLNLAQKVSDEALVYVPTKGEESA ⁺	137
EQDLITVD ⁺ VKGA ⁺ VKSPG ⁺ IYDLPV ⁺ GSRVND ⁺ AV.....QKAGGLTEQ ⁺ ADSKSLNLAQKVSDEALVYVPTKGEESA ⁺	137
EQDLITVD ⁺ VKGA ⁺ VKSPG ⁺ IYDLPV ⁺ GSRVND ⁺ AV.....QKAGGLTEQ ⁺ ADSKSLNLAQKVSDEALVYVPTKGEESA ⁺	137
EQDLITVD ⁺ VKGA ⁺ VKSPG ⁺ IYDLPV ⁺ GSRVND ⁺ AV.....QKAGGLTEQ ⁺ ADSKSLNLAQKVSDEALVYVPTKGEESA ⁺	137
EQDLITVD ⁺ VKGA ⁺ VKSPG ⁺ IYDLPV ⁺ GSRVND ⁺ AV.....QKAGGLTEQ ⁺ ADSKSLNLAQKVSDEALVYVPTKGEESA ⁺	137
EQDLITVD ⁺ VKGA ⁺ VKSPG ⁺ IYDLPV ⁺ GSRVND ⁺ AV.....QKAGGLTEQ ⁺ ADSKSLNLAQKVSDEALVYVPTKGEESA ⁺	137
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.....MQYSMR ⁺ FWKN.....K.YFVLIMLC ⁺ LGVISPSVCAQSF ⁺ DQNFQEWKVKQ ⁺ QM..YDQK.....	49
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NKGPVYVD ⁺ VKGA ⁺ VKHPN ⁺ VYKMTSKD ⁺ RVVD.LL.....DKAQLLED ⁺ ADV ⁺ SQLNLSEK ⁺ LT ⁺ DQK ⁺ MIFIPHK ⁺ GQKNV	147
SNETIVID ⁺ IKGA ⁺ VQH ⁺ PGVYEM.RTGDRVS.....QAI...EKAGGTSE ⁺ QA ⁺ DEAQNLA ⁺ EILQDGT ⁺ VVYIPKKGE ⁺ ETA	125
.....MSIRHFFT...FFWAT.....LLTLFSMQI...VFAQG ⁺ FDQ ⁺ QYDAW.....KTQQAHD ⁺ TR	45
ATPYRFL ⁺ LI ⁺ RHIVARCGL ⁺ LFAT ⁺ LK ⁺ GXTM ⁺ KKMFVLFC ⁺ MLF.....	44
ATPYRFL ⁺ LI ⁺ RHIVARCGL ⁺ LFAT ⁺ LK ⁺ GXTM ⁺ KKMFVLFC ⁺ MLF.....	44
ATPYRFL ⁺ LI ⁺ RHIVARCGL ⁺ LFAT ⁺ LK ⁺ GXTM ⁺ KKMFVLFC ⁺ MLF.....	44
ATPYRFL ⁺ LI ⁺ RHIVARCGL ⁺ LFAT ⁺ LK ⁺ GXTM ⁺ KKMFVLFC ⁺ MLF.....	44
.....MKKLLFLF..FA.....	10
.....MKKLLFLF..FA.....	10

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consensus

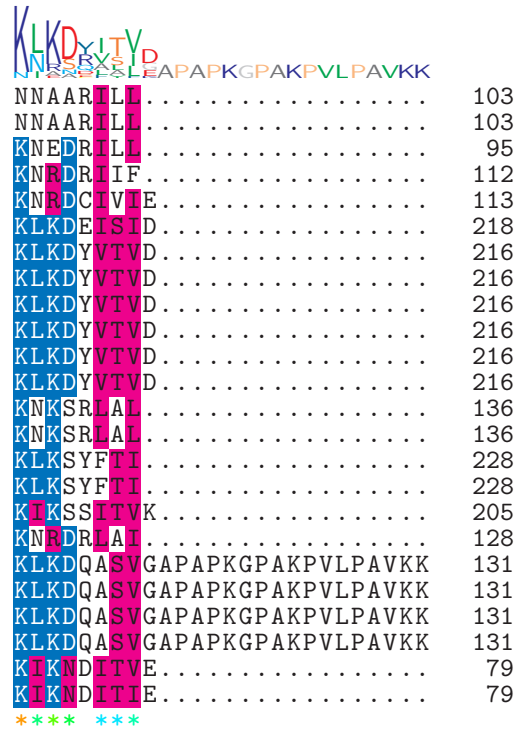
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consensus

```



 non conserved
 similar
 $\geq 50\%$ conserved