

logo

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NTDB id 124 BSU 16930 NP 389575.2
NTDB id 226594 B9H01 RS00395 WP 012774894.1
NTDB id 462 GPW51 RS00385 WP 012774894.1
NTDB id 412 SMU RS09535 WP 002262393.1
NTDB id 170 SP RS09755 WP 000642718.1
NTDB id 280 KZH43 RS08670 WP 000642700.1
NTDB id 205 SPR RS08830 WP 000642700.1
NTDB id 239 SPD RS09270 WP 000642701.1
NTDB id 538 SMSK321 RS11060 WP 000642686.1
NTDB id 510 SM12261 RS08320 WP 000642690.1
consensus

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[illegible]

logo

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NTDB id 239 SPD RS09270 WP 000642701.1
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NTDB id 510 SM12261 RS08320 WP 000642690.1
consensus

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Sequence	Position
TKQTLAKFLGKALVFDPPQAQEKLDFFARPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVWLPGPPSE	159
TKQTLATFLGRNLVFDELAMAKLDRFFASRPGVRVTPNNERQAQIVEGSAQLQNPAGLAVGGMIEQDGVTYIVLPGPPSE	156
TKQTLATFLGRNLVFDELAMAKLDRFFASRPGVRVTPNNERQAQIVEGSAQLQNPAGLAVGGMIEQDGVTYIVLPGPPSE	156
TKQTLAKFLKRELVDKTAQERLDEFFASRPTSMRTPNNECQAQITACSQPLSNKTGLAVGGKLEADGVITYVVLPGPPSE	156
TKQTLAKFLGKALVFDPPQAQEKLDIFFTLRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE	156
TKQTLAKFLGKALVFDPPQAQEKLDIFFALRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE	156
TKQTLAKFLGKALVFDPPQAQEKLDIFFALRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE	156
TKQTLAKFLGKALVFDPPQAQEKLDIFFALRPDYARTPNNERQVQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE	156
TKQTLAKFLGKELVFDPPQAQEKLDVFFAQRPDYARTPNNERQAQIVEGATPLPNETGLAVGGKLEVDGVTYVVLPGPPSE	156
TKQTLAKFLGKELVFDPPQAQEKLDVFFAQRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE	156

logo

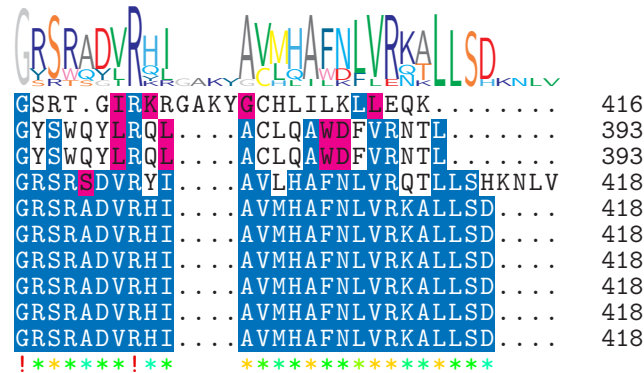
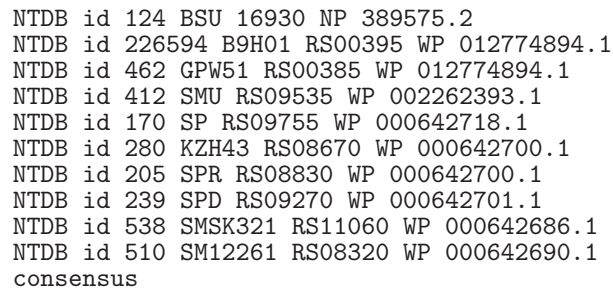
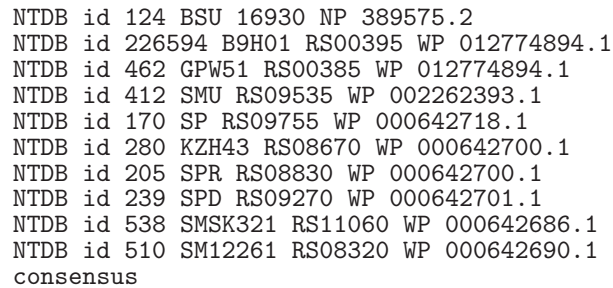
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consensus
```

Sequence	Accession
LRPMFEN ^{AK} PL ^{LL} LKKMG ^S NEK ^{IV} ST ^{VL} RFFGGIGESQ ^{LEAD} LE ^{DI} DA ^{QTN} PT ^{IA} PL ^{AD} GEVTLRL ^{IA} KHAD ^E KETERL	239
LKAMFSES ^{LL} PLLS... ^Q SSQQLYSRVLRFFGIGESQLV ^T LVAD ^{ID} KQ ^{TD} PTLAPYAK ^V GEVTLRLSTKAT ^S QEEAN ^{LR}	233
LKAMFSES ^{LL} PLLS... ^Q SSQQLYSRVLRFFGIGESQLV ^T LVAD ^{ID} KQ ^{TD} PTLAPYAK ^V GEVTLRLSTKA ^T SQEEAN ^{LR}	233
LKPMVNK ^{EL} LPYLS... ^K TSEKLYSRVLRFFGIGES ^H LV ^T L ^L HD ^{LI} AE ^Q TDPT ^{IA} PYAKTGEV ^T IRLSTKA ^H RQ ^{EAD} SK	233
LKPMVLN ^{QL} LPKLM... ^T GSKLYSRVLRFFGIGESQLV ^T ILAD ^{LI} DN ^Q IDPTLAPYAKTGEVTLRLSTKASSQEEAN ^{QA}	232
LKPMVLN ^{QL} LPKLM... ^T GSKLYSRVLRFFGIGESQLV ^T ILAD ^{LI} DN ^Q IDPTLAPYAKTGEVTLRLSTKASSQEEAN ^{QA}	232
LKPMVLN ^{QL} LPKLM... ^T GSKLYSRVLRFFGIGESQLV ^T ILAD ^{LI} DN ^Q IDPTLAPYAKTGEVTLRLSTKASSQEEAN ^{QA}	232
LKPMVLN ^{QL} LPKLM... ^T GSKLYSRVLRFFGIGESQLV ^T IL ^S DLIDNQTDP ^T LAPYAKTGEVTLRLSTKASSQEEAN ^V	232
LKPMVLN ^{QL} LPKLM... ^T GSKL ^H SRVLRFFGIGESQLV ^T IL ^S DLIDNQTDP ^T LAPYAKTGEVTLRLSTKASSQEEAN ^V	232

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consensus

```



-  non conserved
-  similar
-  > 50% conserved