

logo

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NTDB id 124 BSU 16930 NP 389575.2
NTDB id 334790 EQI29 RS12475 WP 002293079.1
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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MEFPK SELL SELL LVAALSTKQALL ELYHQLVLAEEVRYEEQSYCA A

MEFPK MKAETIAVGSSELLLGQIAANTNAQFLISKQLAEIGVNVFYHTAVGDNPERLKQVIRIAEERSDFIIFS GGLGPTKDDL 80

.... MKAETIAVGTETLLGQIVVNTNATFLSEQLADLGIEVYVQTAVGDNQRLLEELIALAETRSELLILCGGLGPTEDDL 76

.... MKAELIAVGTETLLGQIVNTNAQFLSEKCAELGIDVYFHTAVGDNERRLLSTLEVASKRSNMVVL CGGLGPTEDDL 76

.... MKSEIIAVGTETLLGQIVNTNSQFLSEKFAELGIDVYFHTAVGDNERRLLSVLKIAKERSDLIVLCGGLGPTEDDL 76

.... MKAETIAVGTETLLGQIVNTNAQFLSEKLAELIGVDVYFHTAVGDNERRLLSLELIASQRSSLVILTGGLGPTEDDL 76

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.... MKAETIAVGTETLLGQIVNTNAQFLSEKLAELIGVDVYFHTAVGDNERRLLSLELIASQRSSLVILTGGLGATEDDL 76

.... MKAETIAVGTETLLGQIVNTNAQFLSEKLAELIGVDVYFHTAVGDNERRLLSLELIASQRSSLVILTGGLGPTEDDL 76

.... MKAETIAVGTETLLGQIVNTNAQFLSEKLAELIGVDVYFHTAVGDNERRLLSLELIASQRSSLVILTGGLGPTEDDL 76

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NTDB id 510 SM12261 RS08320 WP 000642690.1
consensus
```

[illegible]

logo

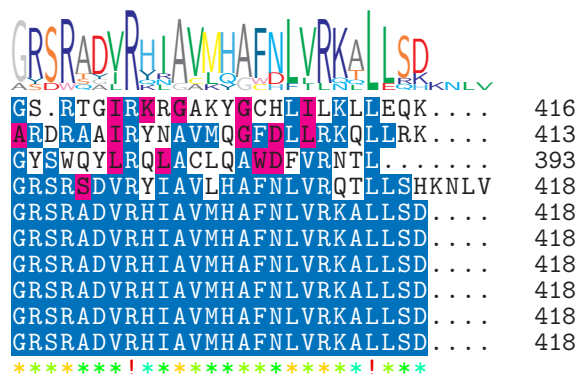
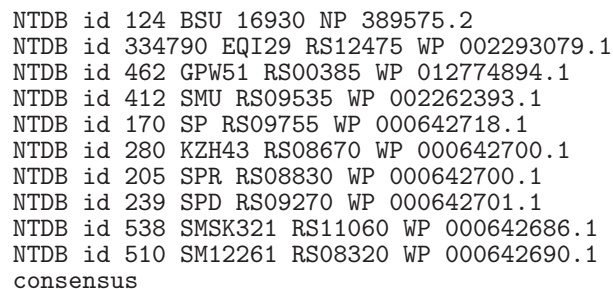
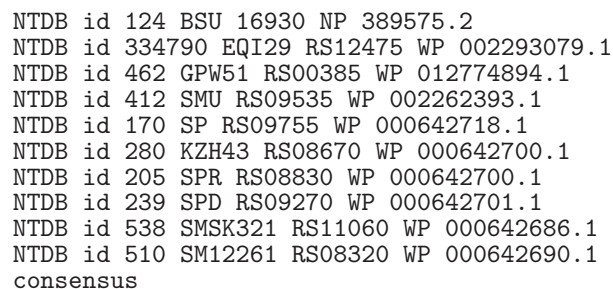
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consensus
```

Sequence	Accession
LRPMFNEAKPLLLKKMGSNKIVSTVLRFFGGIGESQLEADLEIDAQTNPITAPLAADGEVTLRLTAKHAEKETERL	239
LKPMFVEQVRPLLEERFPESEKLISKVLRVYFGIGESRLVTEKDLIEQTINPTIAPYAKPNEVTLRLTVKTKDVQAGNQA	235
LKAMFSESLPLLS...SSQQQLKSVLRVFFGIGESQLVTILADVIDKQTDPTLAPYAKVGEVTLRLSTKASSQEEANLR	233
LKPMVNKEBLLPYLS...KTSEKLYSRVLRVFFGIGESHVLTLLHDLIAEQTDPTIAPYAKTGEVTIRLSTKAHRQKEADSK	233
LKPMVLNQLLPKML...TGSKLYSRVLRVFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA	232
LKPMVLNQLLPKML...TGSKLYSRVLRVFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA	232
LKPMVLNQLLPKML...TGSKLYSRVLRVFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA	232
LKPMVLNQLLPKML...TGSKLYSRVLRVFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA	232
LKPMVLNQLLPKML...TGSKLYSRVLRVFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV	232
LKPMVLNQLLPKML...TGSKLHRSRVLRVFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV	232

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consensus

```



-  non conserved
-  similar
-  > 50% conserved