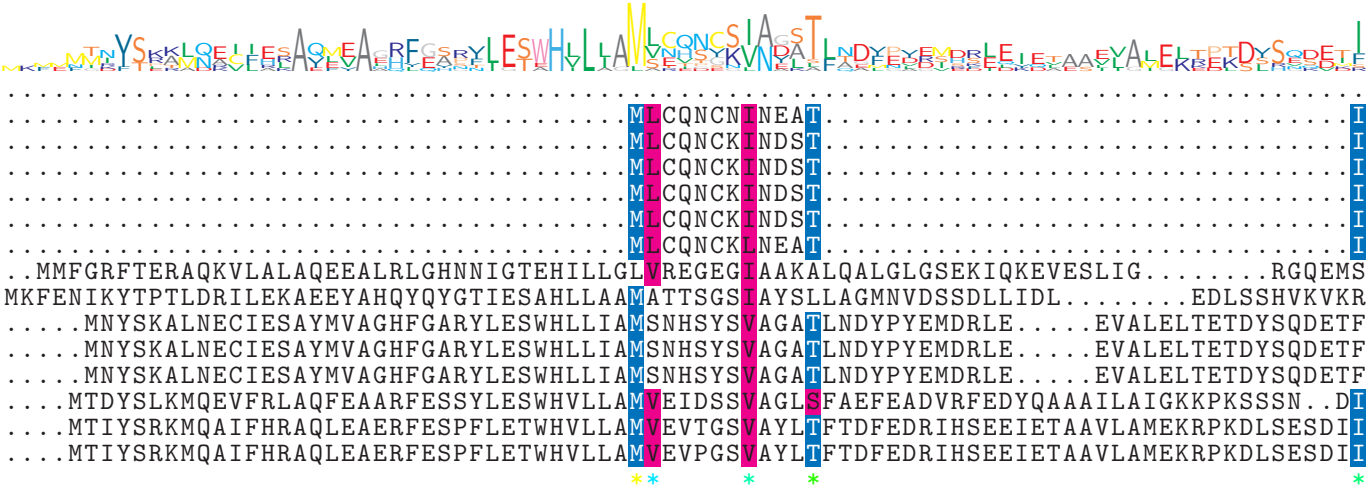


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NTDB id 243 SPR RS03635 WP 000882517.1
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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus



logo

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consensus

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Sequence	Alignment	Score
EIEPTISVVLDEILLSSKNKNNEIKIIDFLEKLIQDSRSY...SSYLLKKHNNINLNKIQELQNHENIQNIINNHTSDLTLLAQNGK	PTQSGG...SSYLLKKHNNINLNKIQELQNHENIQNIINNHTSDLTLLAQNGK	156
...QTP	PTQTG	122
...PIP	PTQSGGYGGNGGYGS	128
...PIP	PTQSGGYGGNGGYGS	128
...PIP	PTQSGGYGGNGGYGS	128
...PIP	PTQSGGYGGNGGYGS	128
...NTP	PTQAGGNGNGGN.N	129
AVTPMSK	RKMAK	178
.LRQRHR	TV.ADK	191
.LRQRHR	TV.ADK	204
.LRQRHR	TV.ADK	204
.IFEMRK	PKKVKN	208
.IHDLRK	PKKSKA	211
.IHDLRK	PKKSKA	211

logo

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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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Sequence	Position
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LDPVIGRDDEIISRMIIQLSRKTKNNPVLVGEAGVGKTALALGLAQRIASGEVPFELADMRIELELDMMSVAVAGTRFRGDFEERMNQ	296

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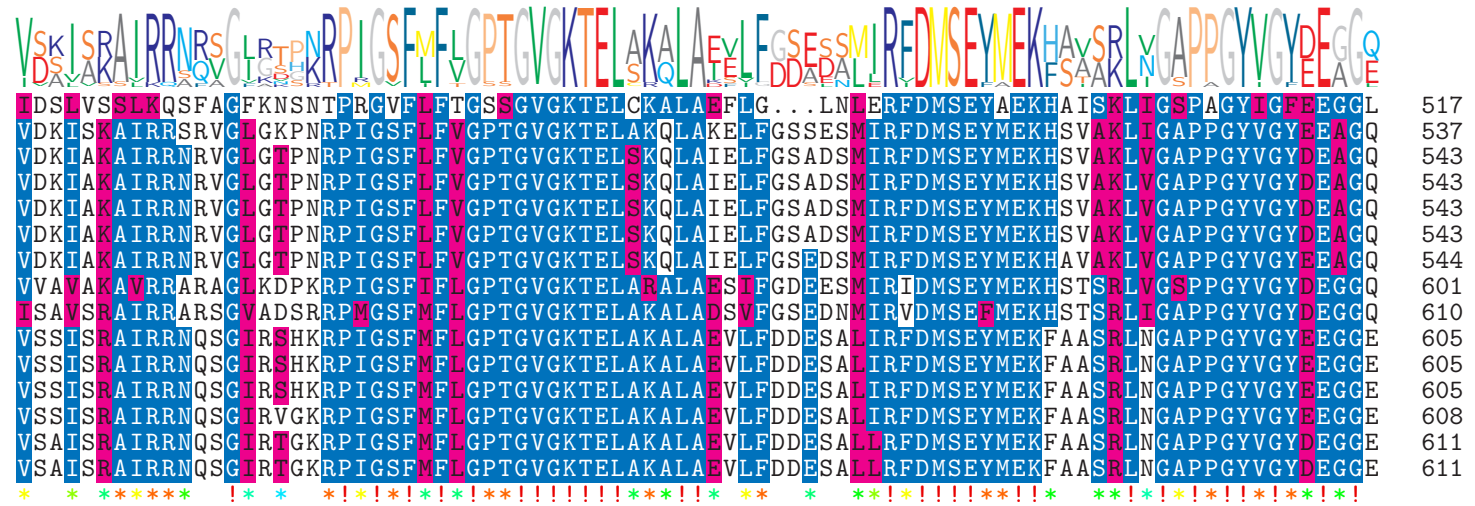


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consensus

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logo

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NTDB id 287 SP RS11210 WP 001109712.1	E V E D K L A E L L L K G D L V A G S T L K I G V K A G Q . L K F D I A	810
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NTDB id 290 KZH43 RS10025 WP 001109677.1	E V E D K L A E L L L K G D L V A G S T L K I G V K A G Q . L K F D I A	810
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NTDB id 297 STER RS00545 WP 011680614.1	Q V E D K L S E L L L G G Q V V S G Q T L K I G C S K D K . L T F T V V	816
NTDB id 329 STU RS10020 WP 011225298.1	Q V E D K L S E L L L G G Q V V S G Q T L K I G C S K D K . L T F T V V	816
consensus	* * * * * * * * * * * * *	

- non conserved
- similar
- ≥ 50% conserved