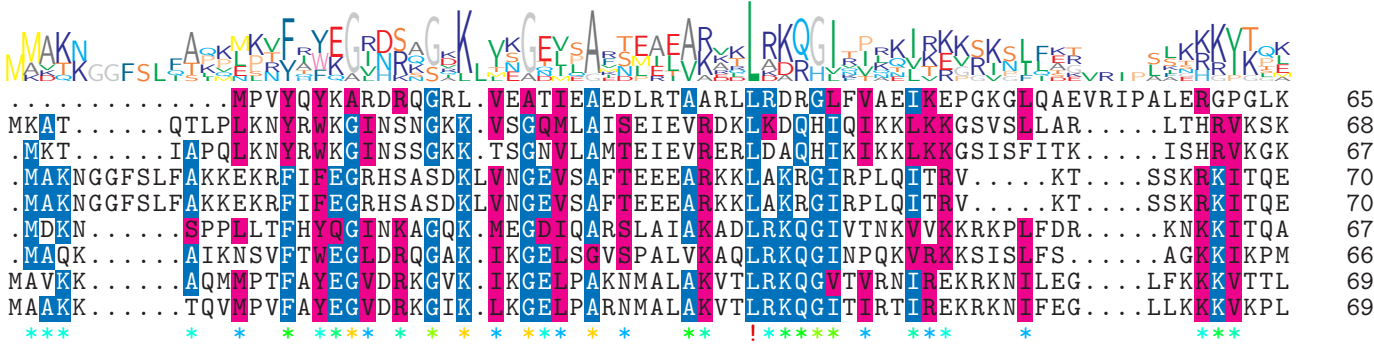


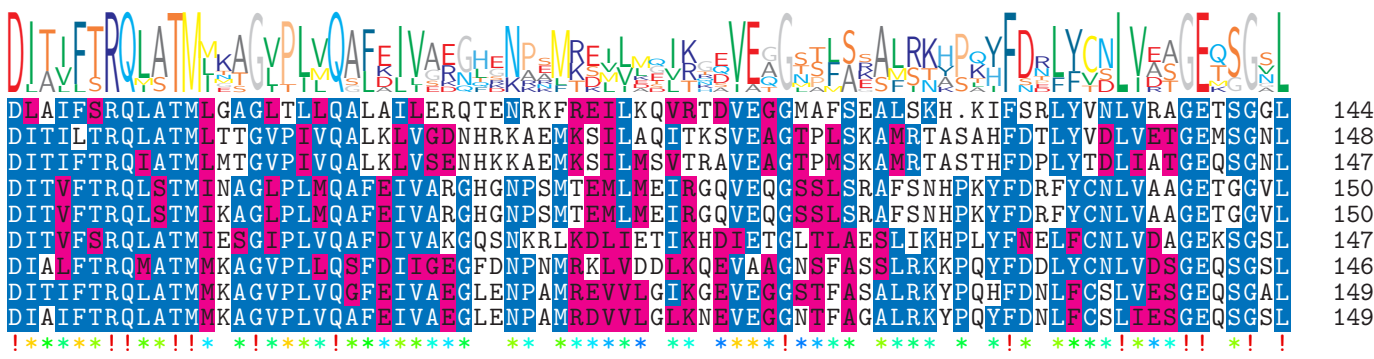
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consensus



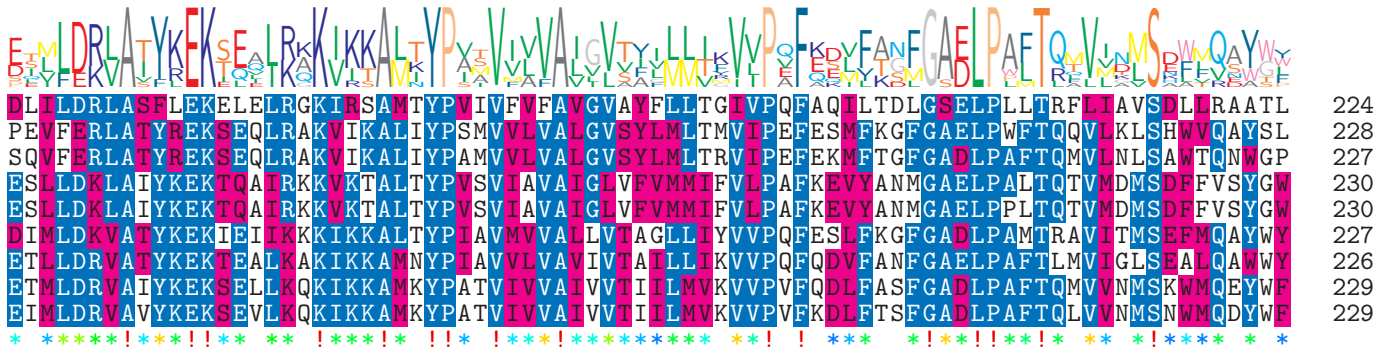
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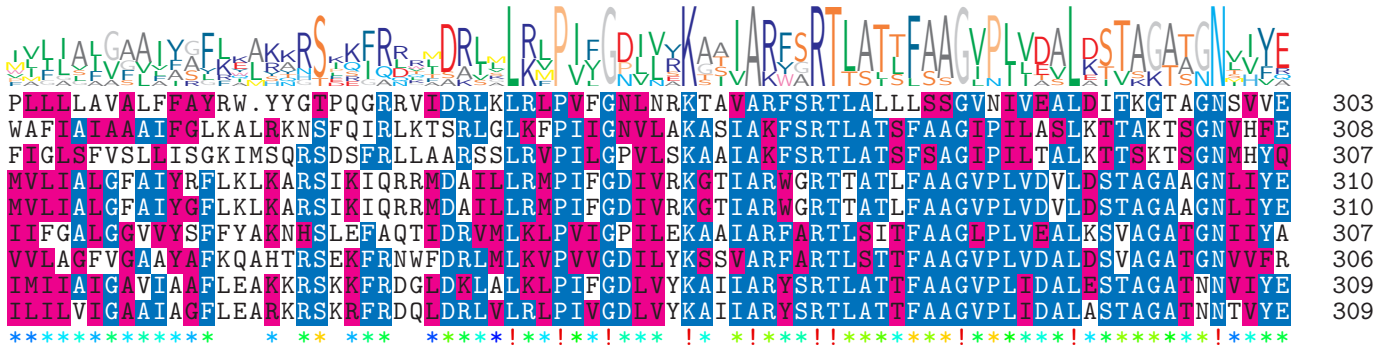
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consensus
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consensus
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Sequence	Position
IVGMIVAGMFLPLFKITIGTLISVQ	406
VVGGLVIVAMFLPIFNLMISVLG..	408
VVGGLVITAMFLPIFNLMISVLG..	407
VIGTLLVAMFLPIFNLGNVVA..	410
VIGTLLVAMFLPIFNLGNVVA..	410
LVGGLVIVAMFLPIFKLGSAV...	406
LVGGLITIAMFLPIFQMGSVV...	405
LVGGLVIAMFLPIFQMGSVV...	408
LVGGLVITAMFLPIFQMGSVV...	408

-  non conserved
-  similar
-  $\geq 50\%$ conserved