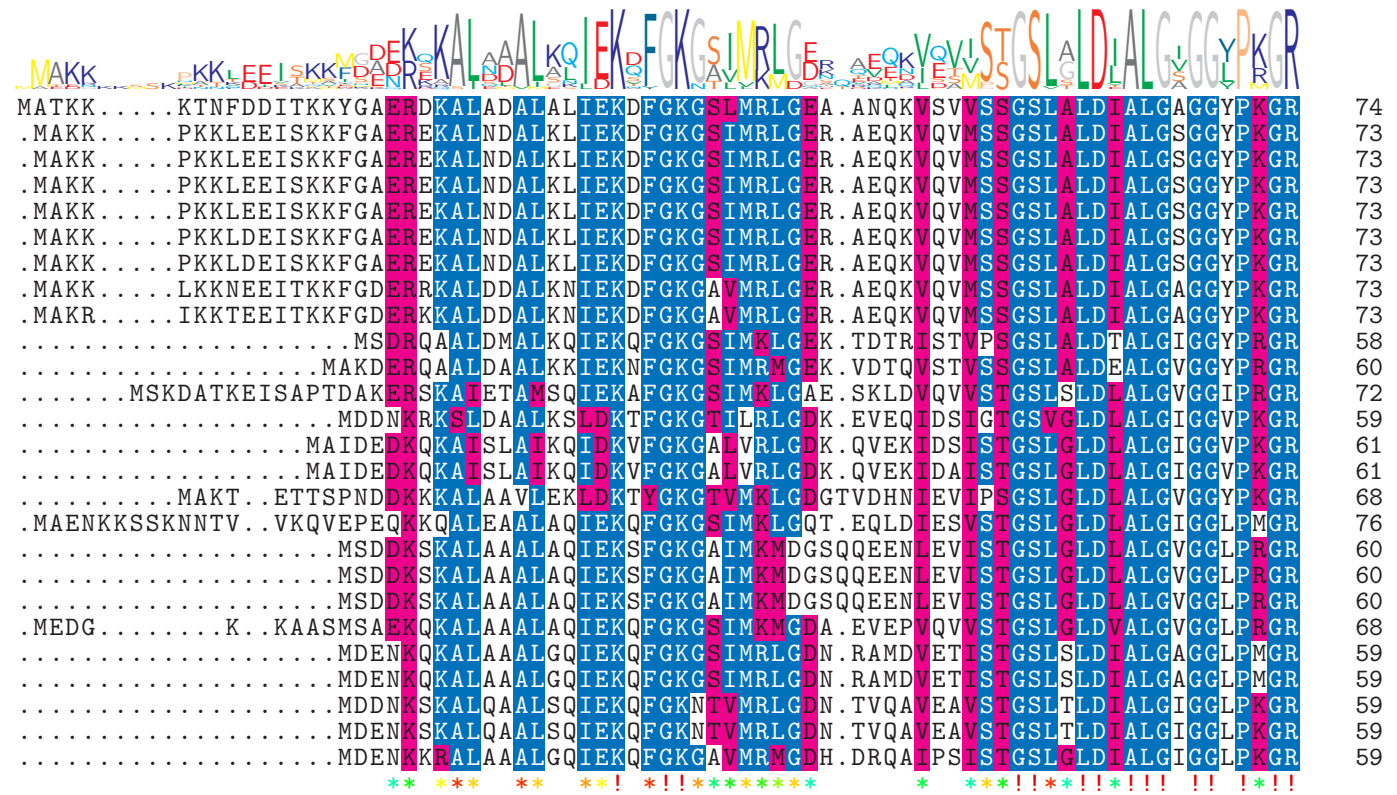


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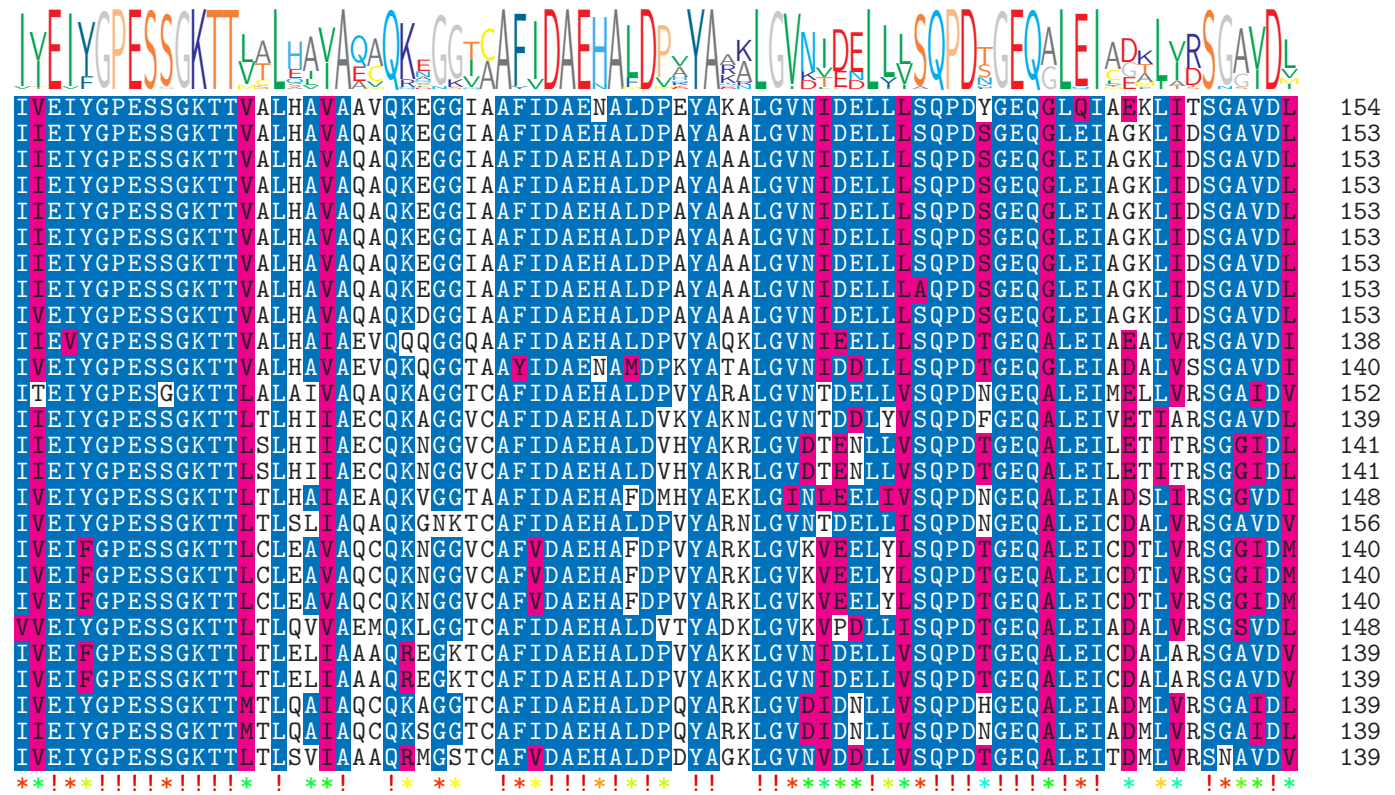
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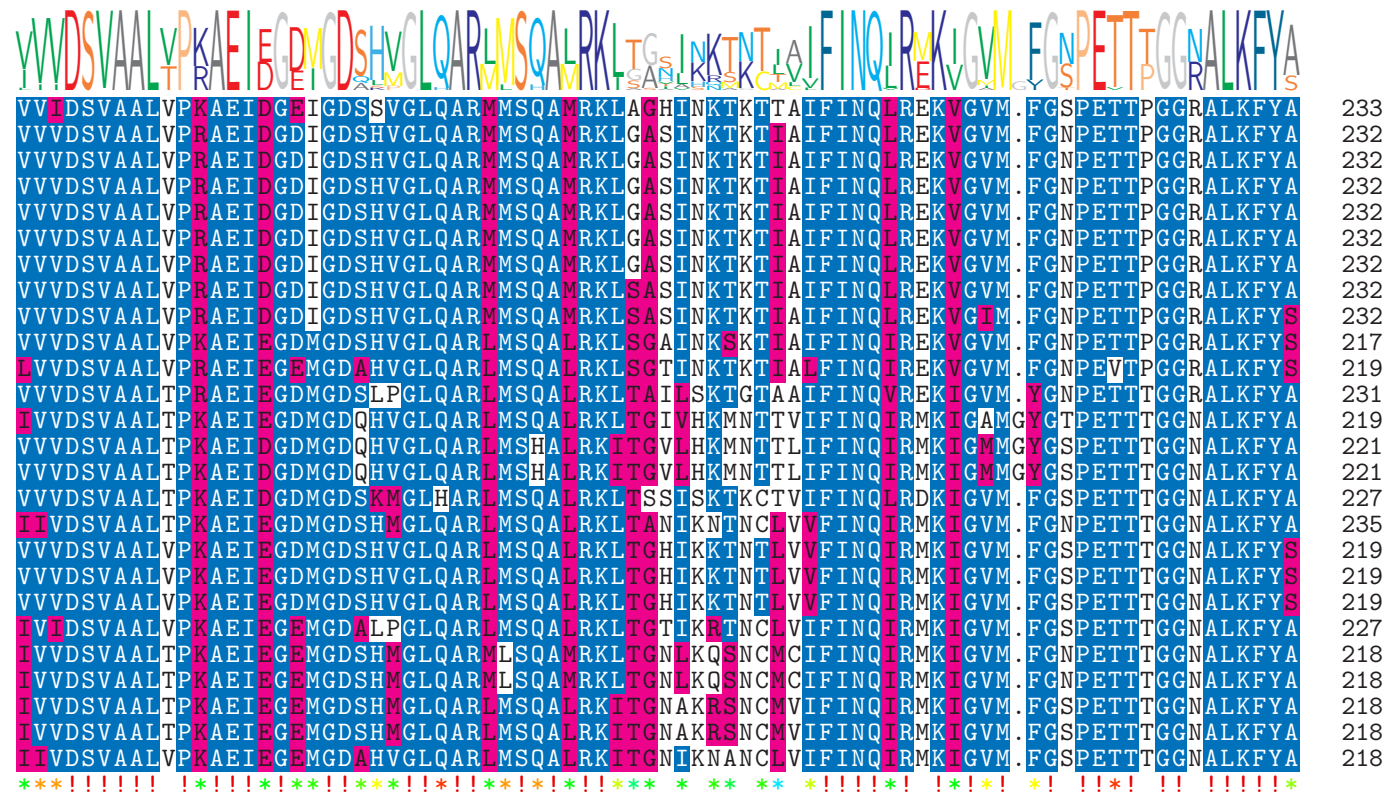
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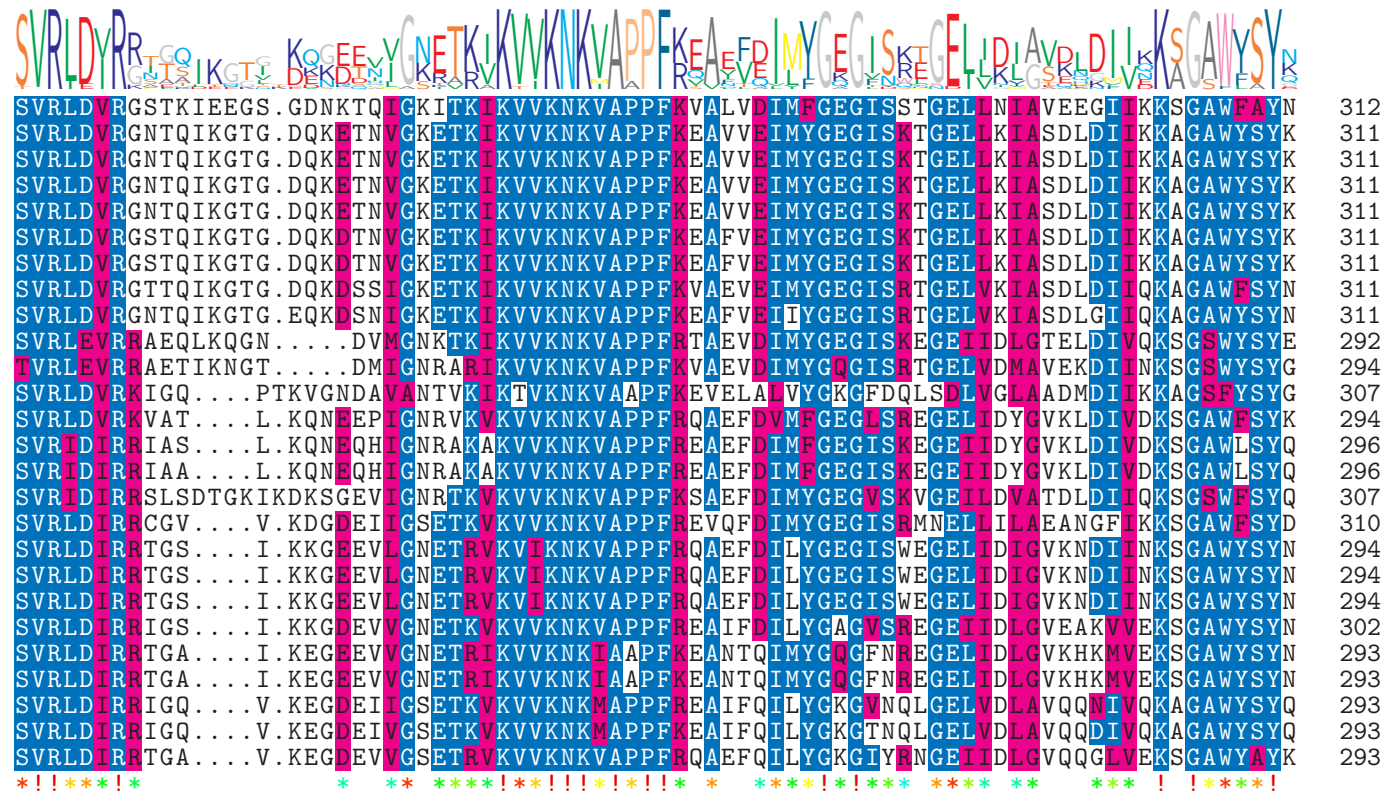
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consensus

Sequence	Score
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ ID ⁺ QK ⁺ VR ⁺ SK ⁺ FC ⁺ LID ⁺ GEE ⁺ VSE ⁺ QD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNEE ⁺ VPLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ ID ⁺ QK ⁺ VR ⁺ SK ⁺ FC ⁺ LID ⁺ GEE ⁺ VSE ⁺ QD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNEE ⁺ VPLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved