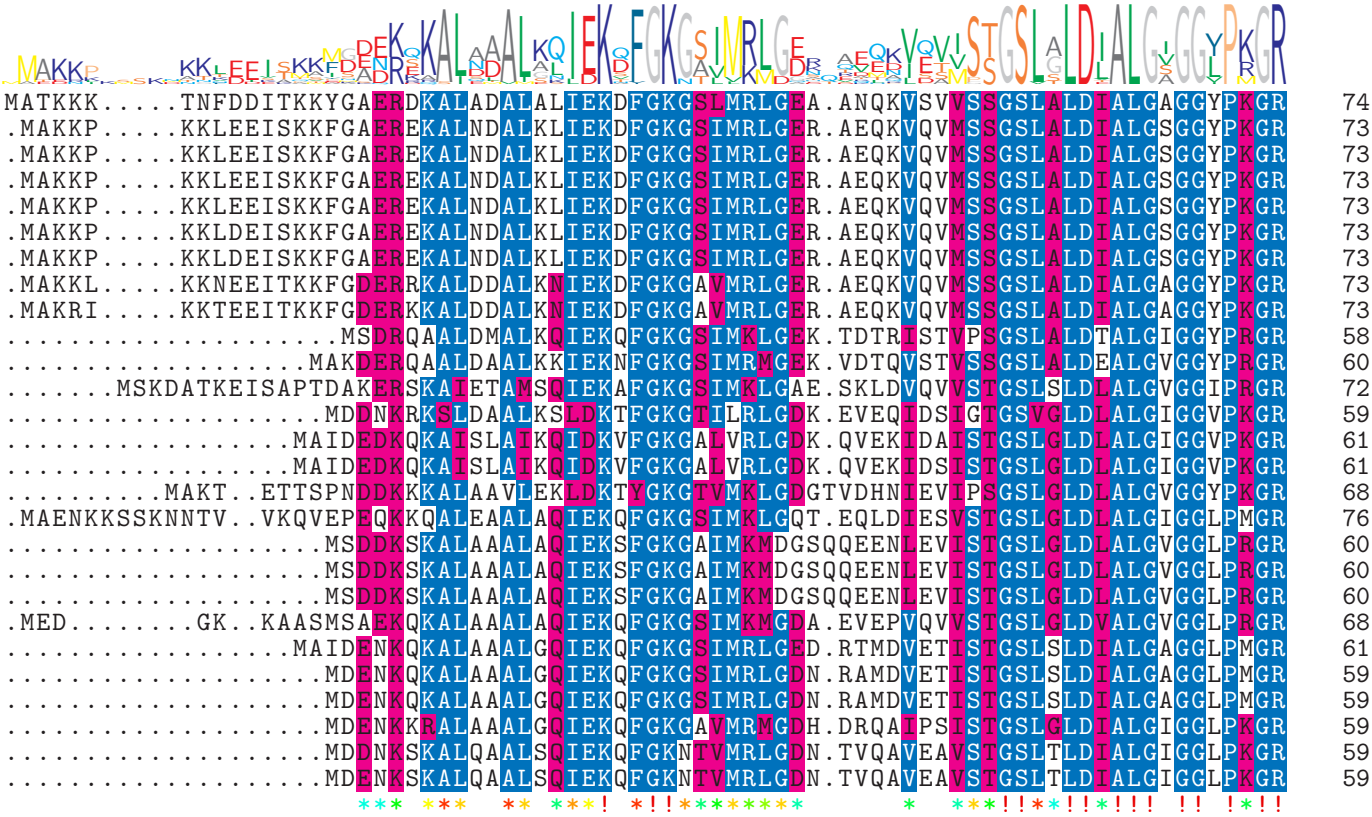


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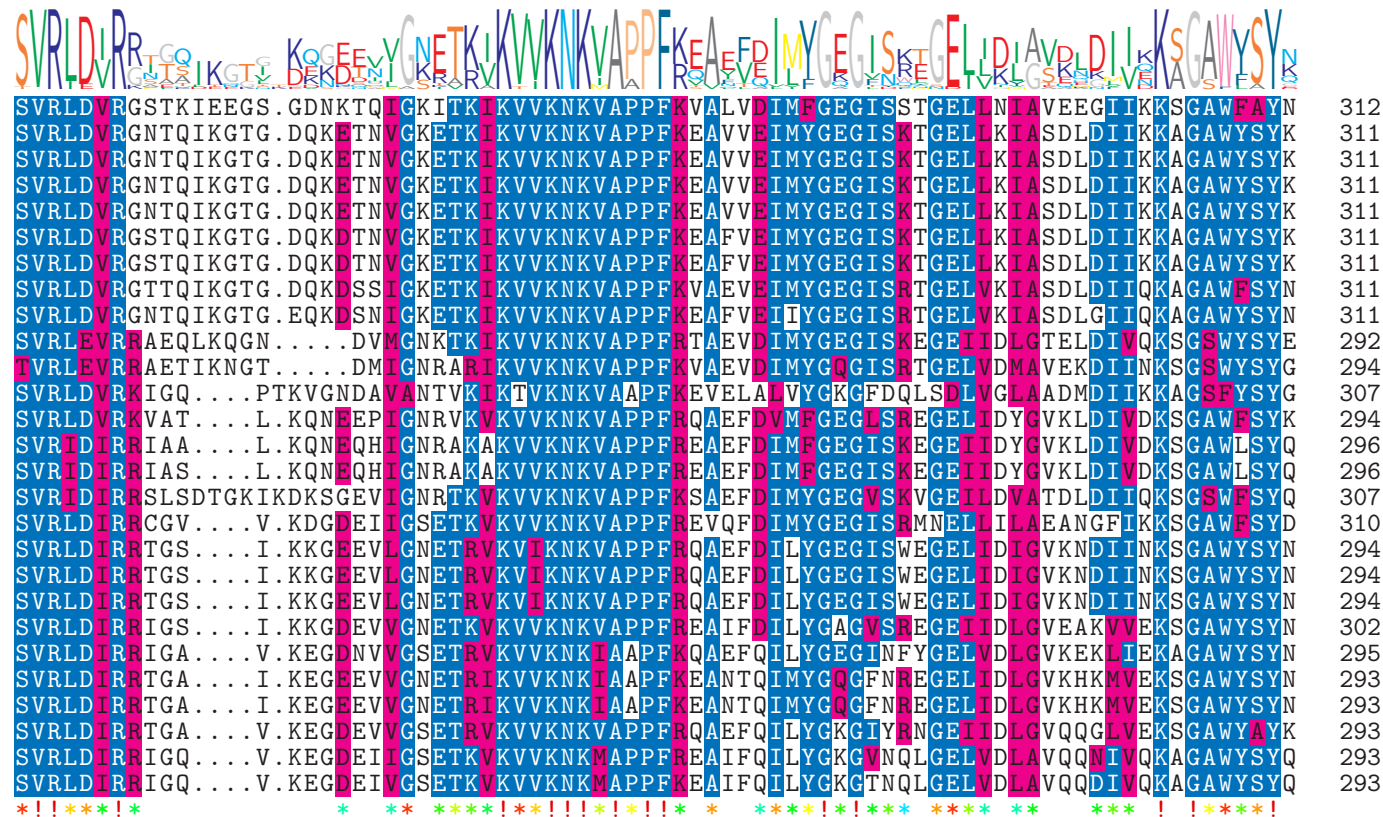
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Sequence	Score
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ DK ⁺ QV ⁺ RSK ⁺ FL ⁺ ID ⁺ GEE ⁺ VSE ⁺ QD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNEE ⁺ VPLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ DK ⁺ QV ⁺ RSK ⁺ FL ⁺ ID ⁺ GEE ⁺ VSE ⁺ QD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNEE ⁺ VPLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
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GEKIGQGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ HK ⁺ VR ⁺ VQ ⁺ YGL ⁺ IE ⁺ ED ⁺ NT ⁺ EEK ⁺ Q ⁺ SS ⁺ SEK ⁺ET ⁺ DEK ⁺ ..AD ⁺ KN ⁺ LV ⁺ LE ⁺ DD ⁺ TIE ⁺ LE ⁺	382
EE ⁺ RL ⁺ GG ⁺ GR ⁺ EN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IM ⁺ LI ⁺ QE ⁺ QI ⁺ RE ⁺ HY ⁺ GL ⁺ DN ⁺ NG ⁺ VV ⁺ QQ ⁺ AA ⁺ ET ⁺ QE ⁺ EL ⁺ .EFE ⁺ .E ⁺	348
SERIGQGR ⁺ EN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DV ⁺ RL ⁺ KV ⁺ RAAY ⁺ CT ⁺ SD ⁺ VP ⁺ EED ⁺ LP ⁺ TT ⁺ ED ⁺ E.QI ⁺ .NIL ⁺ PDD ⁺ ST ⁺EE ⁺	355
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DKKLGGGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ES ⁺ IG ⁺ SNEE ⁺ IM ⁺ PL ⁺ PDE ⁺ P..LE ⁺ .EME ⁺	347
DKKLGGGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ES ⁺ IG ⁺ SNEE ⁺ IM ⁺ PL ⁺ PDE ⁺ P..LE ⁺ .EME ⁺	347
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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved