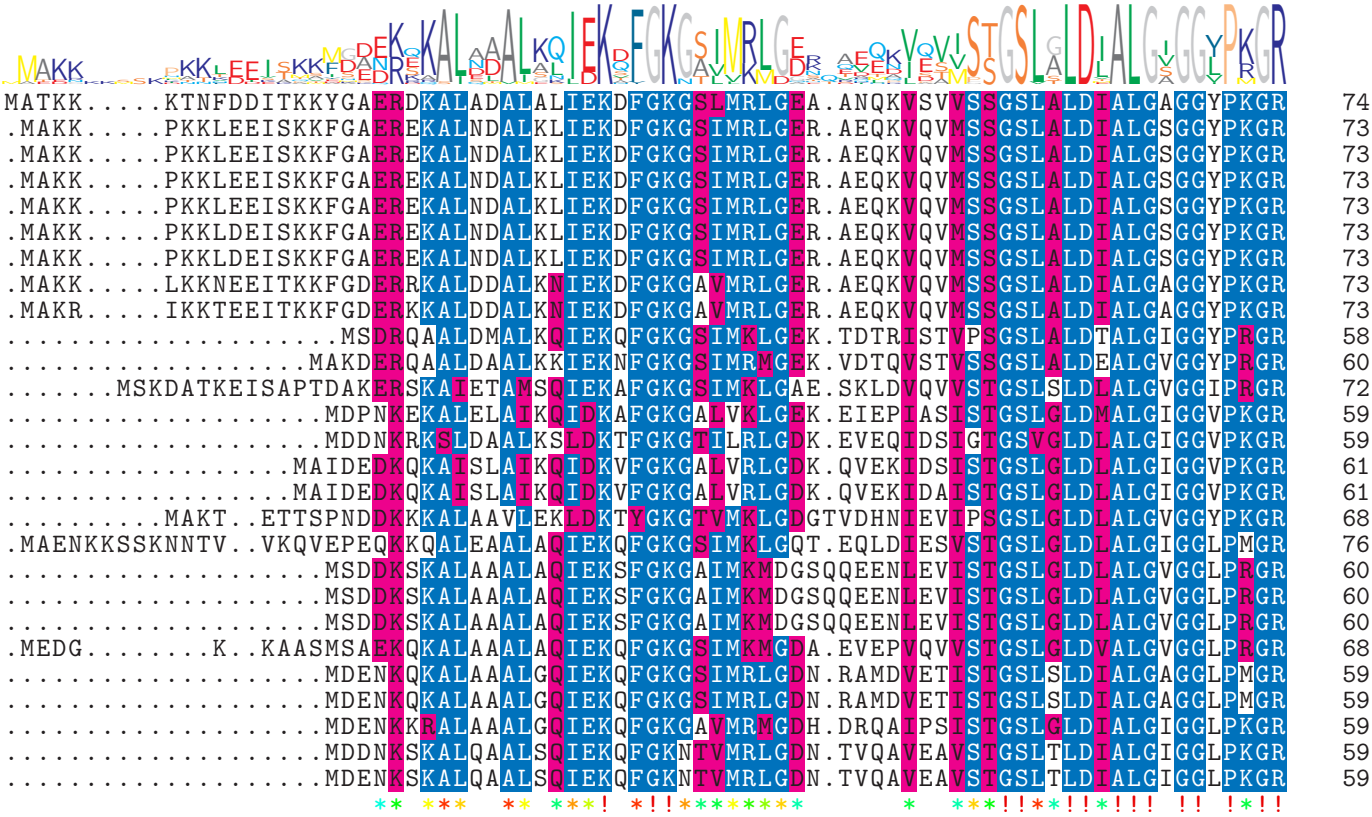


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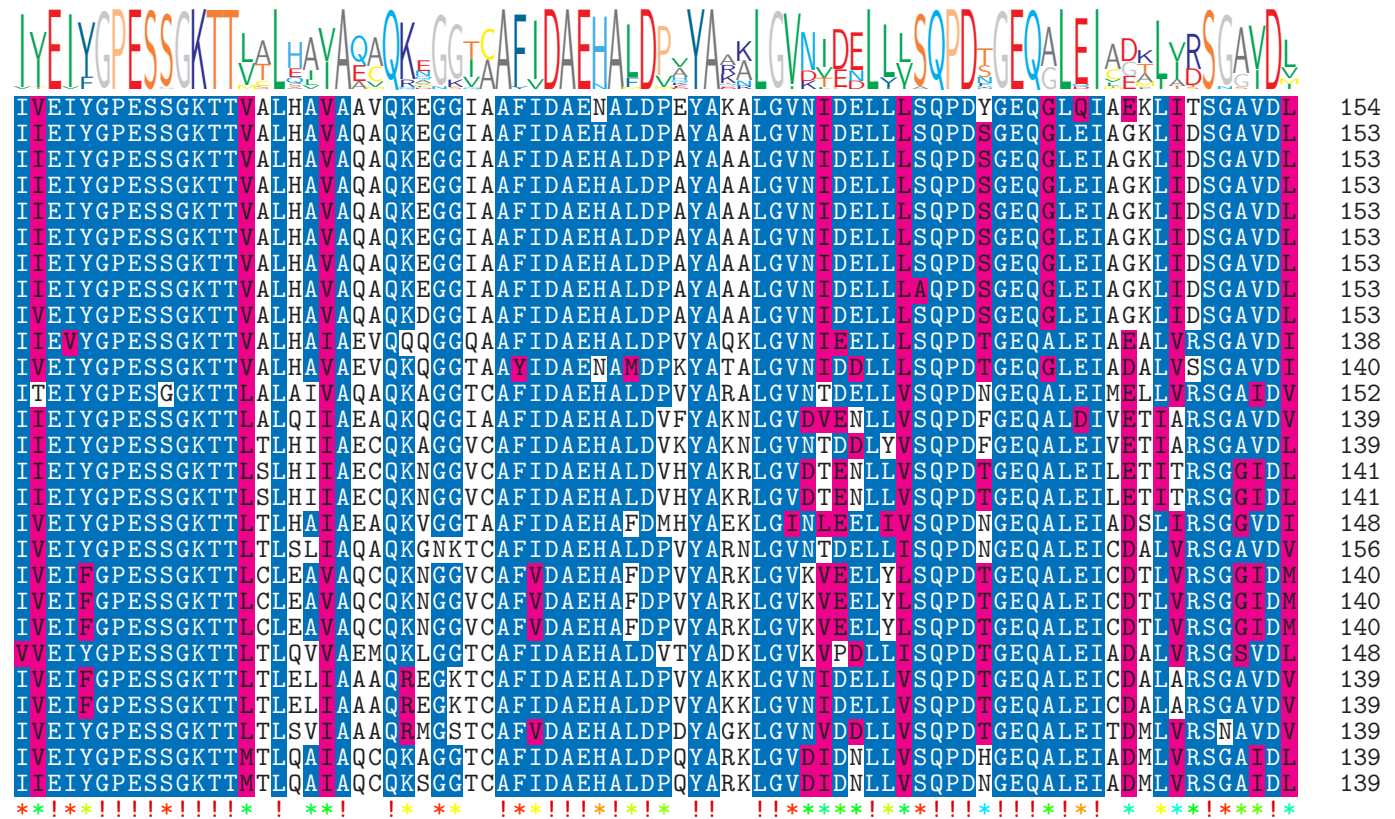
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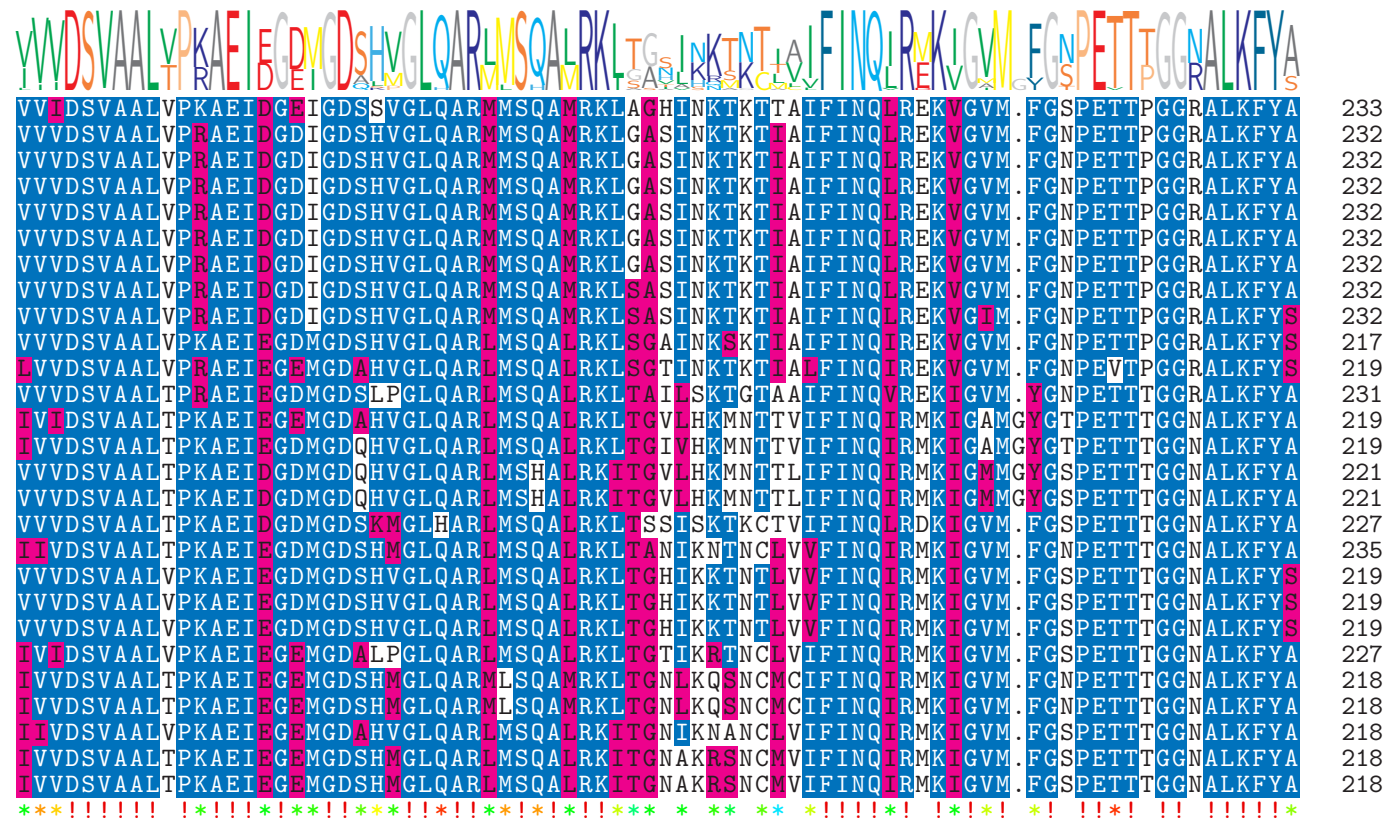
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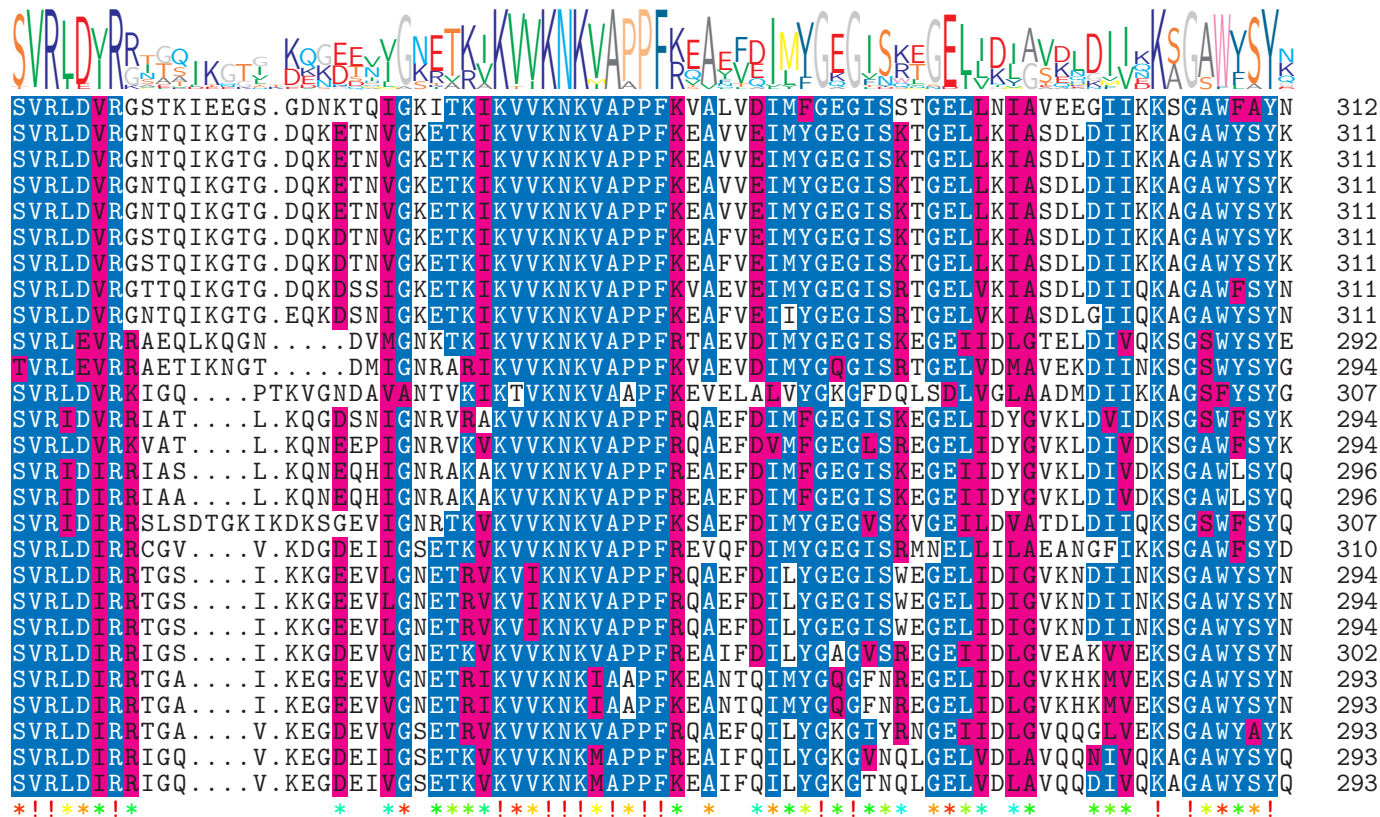
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consensus

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Sequence	Score
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DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DKQ ⁺ V ⁺ RSKF ⁺ GL ⁺ ID ⁺ GEEVSEQD ⁺ TENKKDE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DKQ ⁺ V ⁺ RSKF ⁺ GL ⁺ ID ⁺ GEEVSEQD ⁺ TENKKDE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
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SERIGGG ⁺ RE ⁺ NA ⁺ KN ⁺ YL ⁺ AD ⁺ HED ⁺ VED ⁺ EV ⁺ RL ⁺ KV ⁺ RAAY ⁺ CT ⁺ SD ⁺ VPEEDLPTTEDE ⁺ .QI ⁺ .NILPDDST ⁺EE ⁺	355
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DTKL ⁺ GG ⁺ RD ⁺ TV ⁺ KE ⁺ LK ⁺ DN ⁺ PE ⁺ LA ⁺ EEL ⁺ EAK ⁺ IREKLQAK ⁺	343
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GD ⁺ KIG ⁺ GQ ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ KT ⁺ LD ⁺ KK ⁺ LREMLLN ⁺ PNEMQ ⁺LIAETSSAADDVEFG ⁺ ..AVPEEF ⁺	354
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logo

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consensus			

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