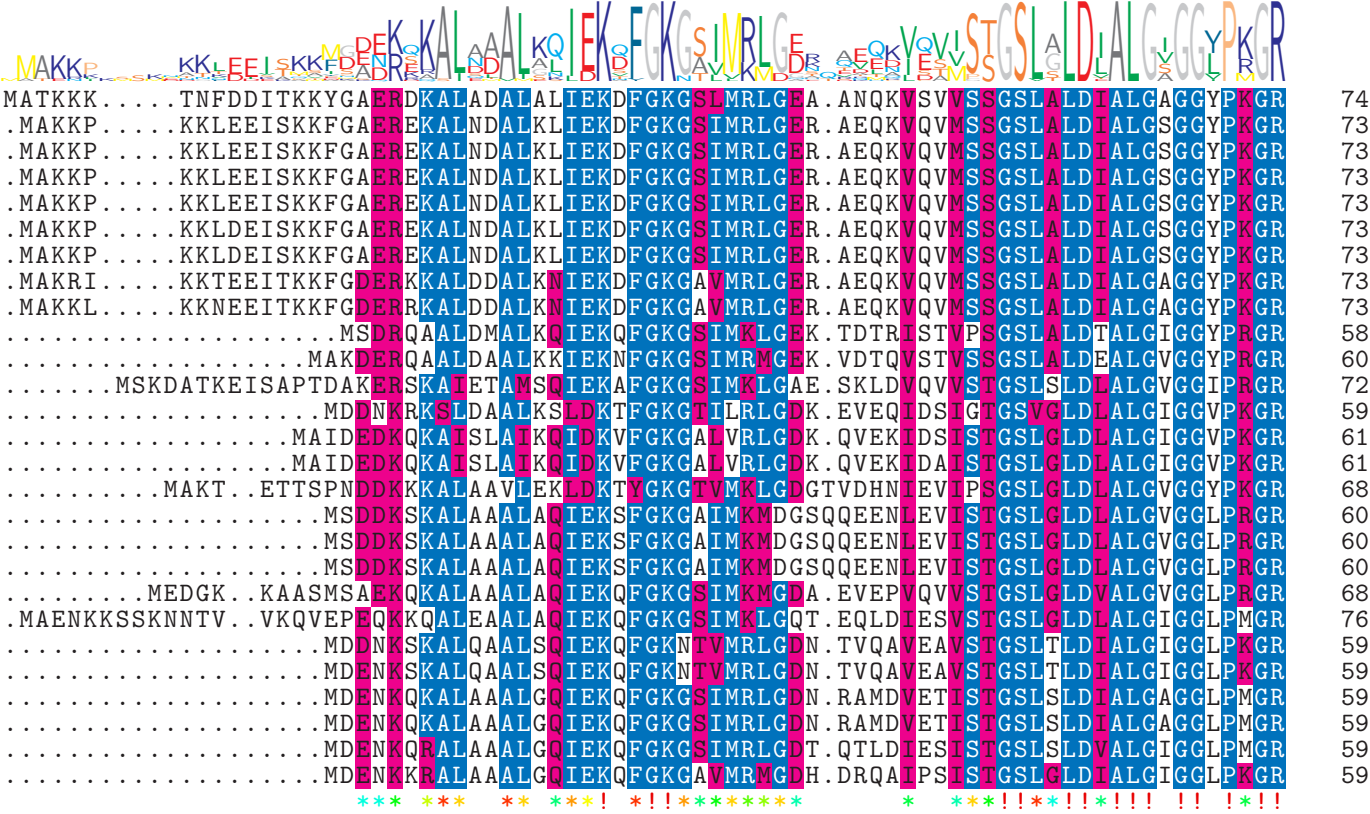


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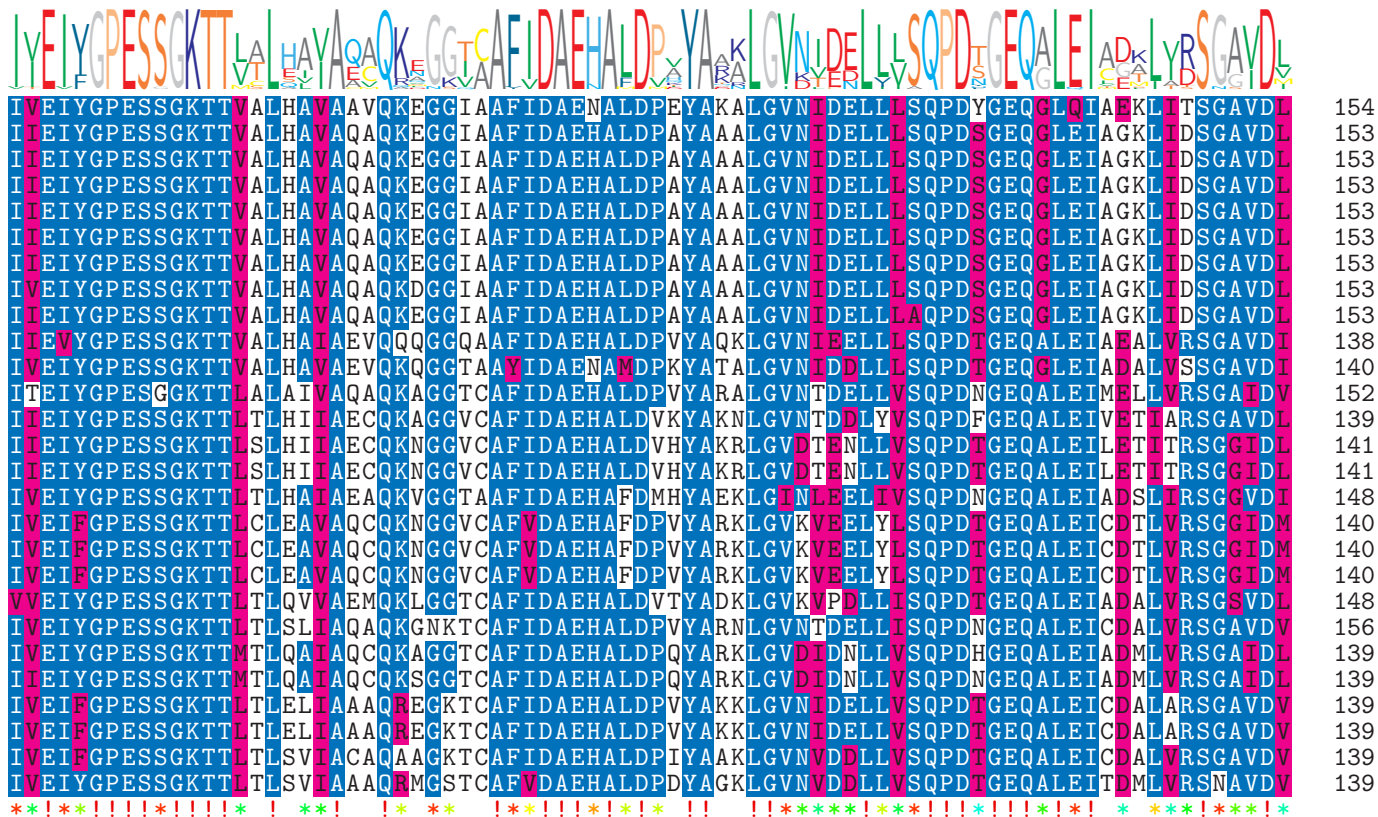
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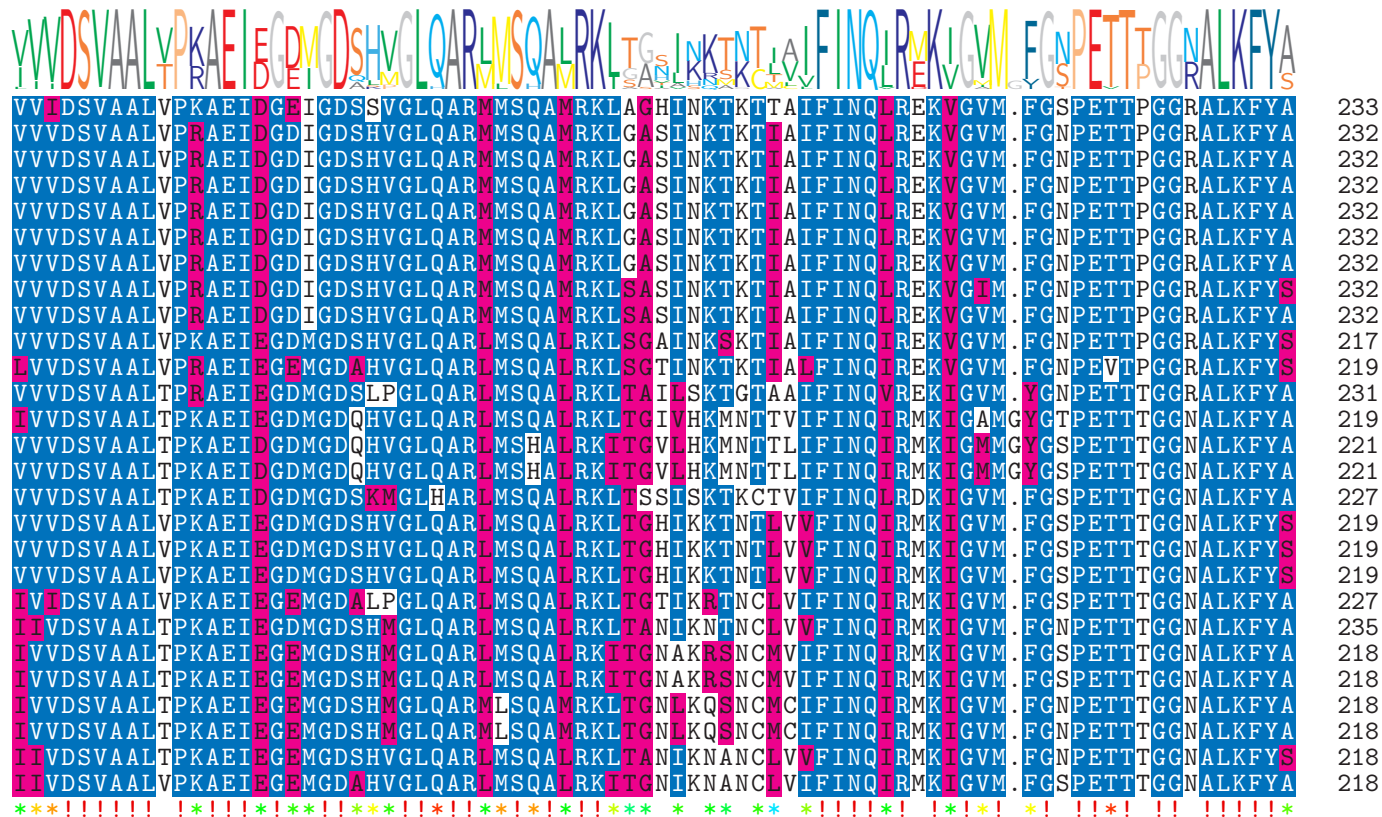
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consensus

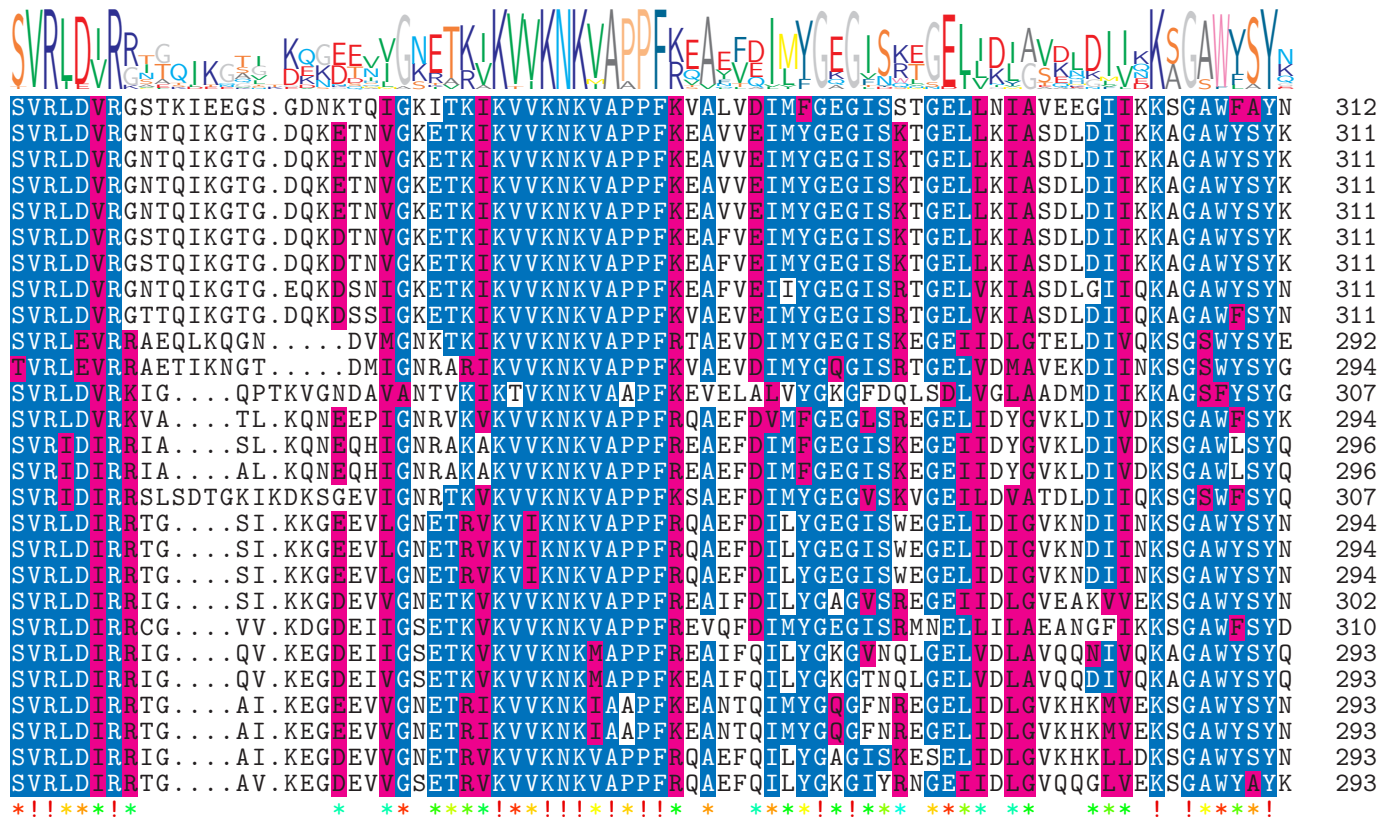
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consensus

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Sequence	Score
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SERIGGGREN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DEV ⁺ RL ⁺ KV ⁺ RA ⁺ AY ⁺ CTSDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGGQKE ⁺ KT ⁺ IAY ⁺ IA ⁺ ER ⁺ PE ⁺ ME ⁺ QE ⁺ IRDR ⁺ VMA ⁺ IRAG ⁺ NAGE ⁺ APALAPAPAAPE..A.AEA.....	363
DKKLGGGREN ⁺ SK ⁺ AF ⁺ LKEN ⁺ PE ⁺ IDE ⁺ IT ⁺ KAT ⁺ IQ ⁺ NSM ⁺ TEGMISGSEDDEGEE.....	343
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GAKIGQGKD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PE ⁺ ISDE ⁺ IDA ⁺ KIR ⁺ AL ⁺ NG ⁺ VEMHIT ⁺ EGTQ.....DET ⁺ DGER ⁺ PEE.....	348
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GAKIGQGKD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PE ⁺ ISDE ⁺ IDA ⁺ KIR ⁺ AL ⁺ NG ⁺ VEMHIT ⁺ EGTQ.....DET ⁺ DGER ⁺ PEE.....	348
GERIGGGRD ⁺ NC ⁺ REF ⁺ LIRE ⁺ NA ⁺ EL ⁺ ARE ⁺ IE ⁺ EN ⁺ KV ⁺ RE ⁺ HL ⁺ CVTPMGAVTLAAEEVEE.D.....	352
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GD ⁺ KIGQGKAN ⁺ SM ⁺ KFL ⁺ QENT ⁺ TTISAE ⁺ LEG ⁺ KLRE ⁺ LLLSHAAATDAERAGAEREDN..AAADDENF.....	353
GS ⁺ KIGQGKAN ⁺ AA ⁺ KYLE ⁺ EN ⁺ PE ⁺ IG ⁺ QE ⁺ IE ⁺ QQ ⁺ IR ⁺ AK ⁺ LV ⁺ TSANTKATPVAEDLADA..DI.....	347

logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved