

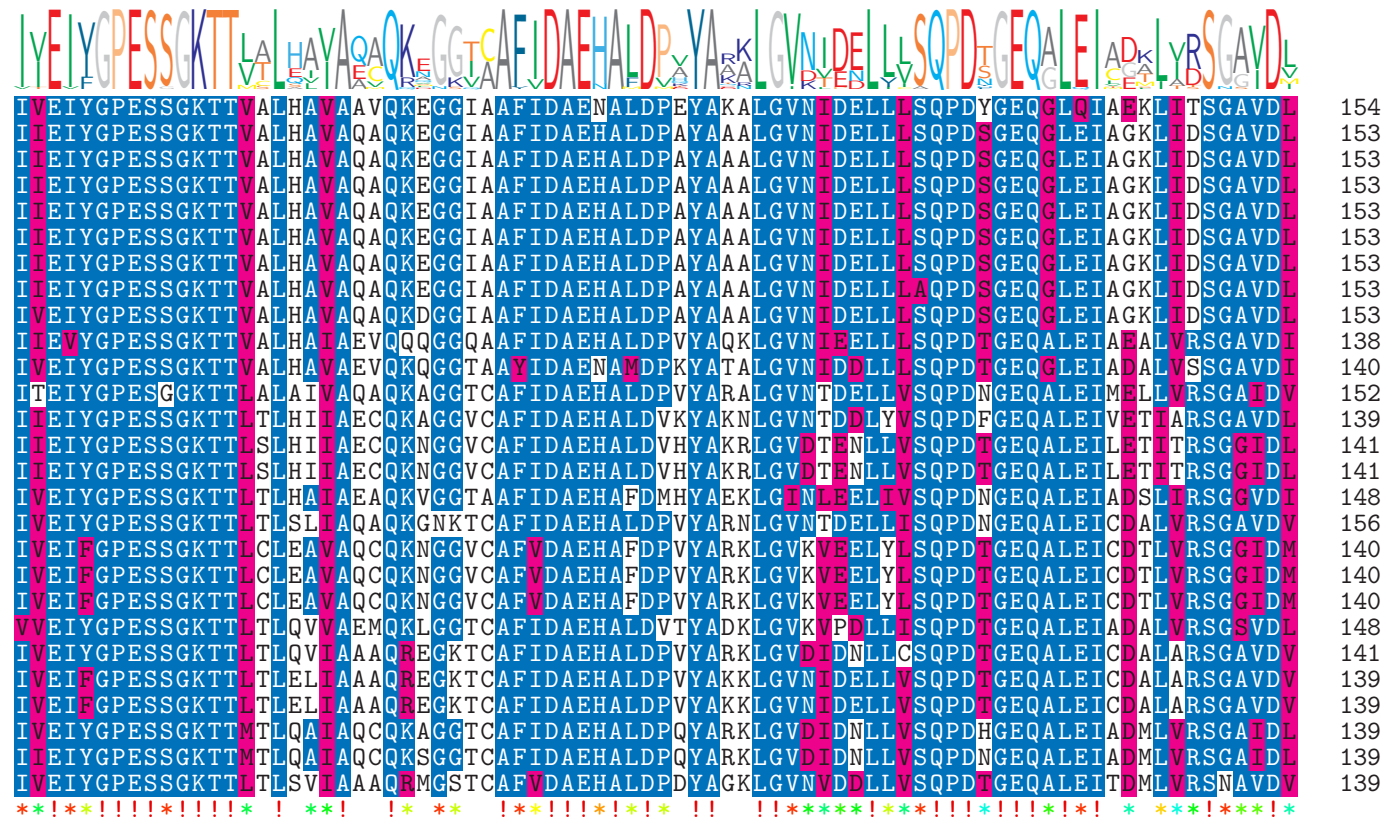
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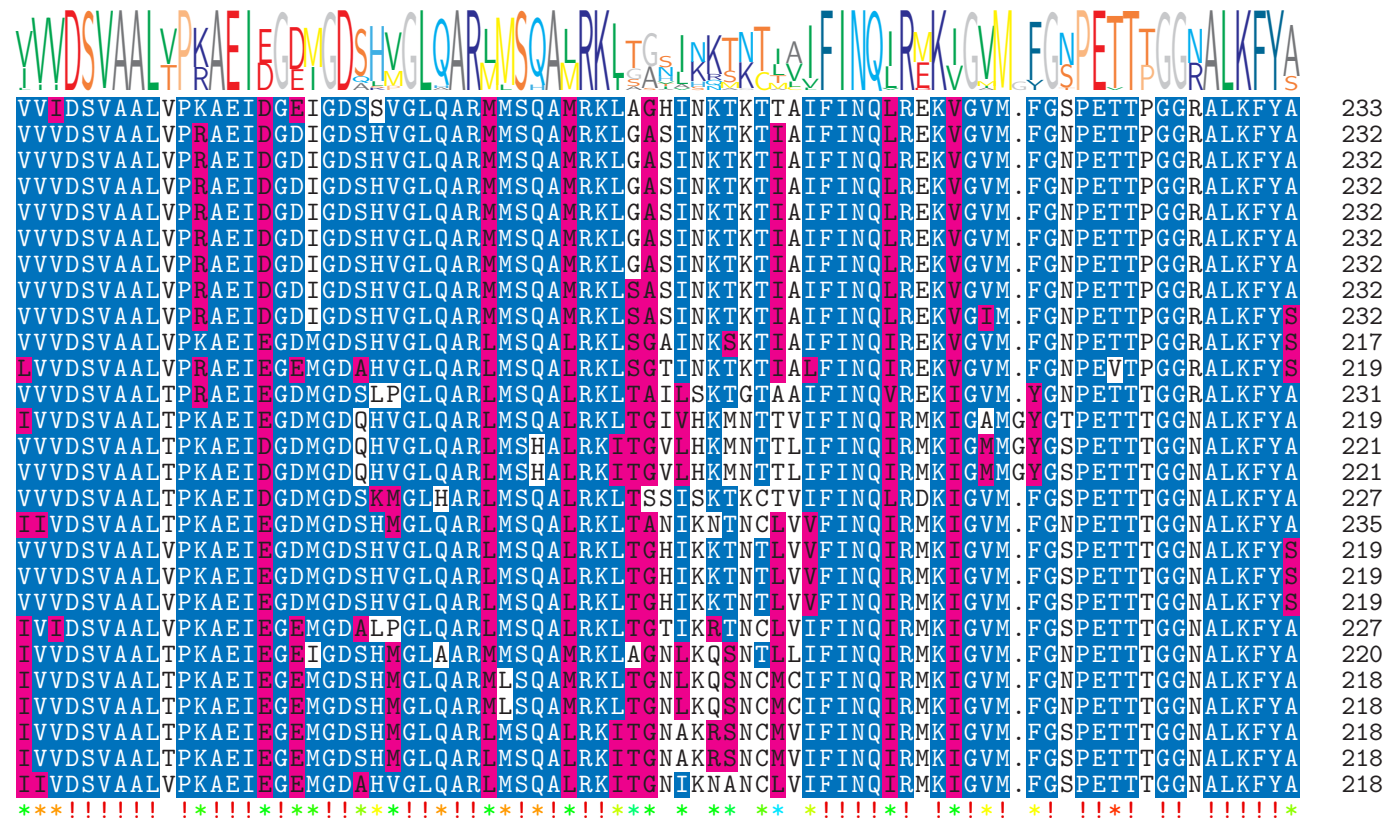
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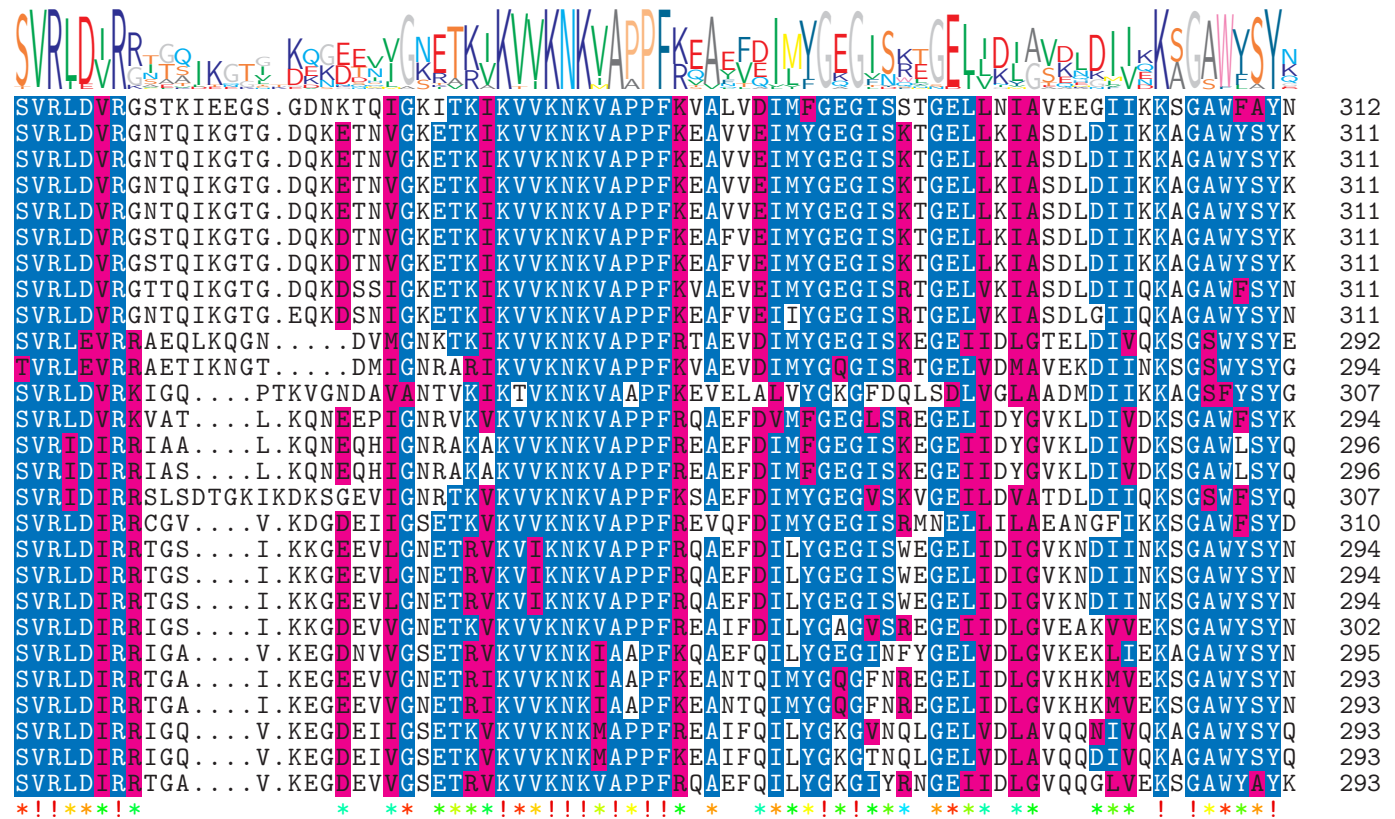
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consensus

Sequence	Score
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KY ⁺ LA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ DKQV ⁺ RSKF ⁺ CL ⁺ ID ⁺ GE ⁺ EV ⁺ SEQD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNEE ⁺ VPLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KY ⁺ LA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ DKQV ⁺ RSKF ⁺ CL ⁺ ID ⁺ GE ⁺ EV ⁺ SEQD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNEE ⁺ VPLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KY ⁺ LA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ DKQV ⁺ RSKF ⁺ CL ⁺ ID ⁺ GE ⁺ EV ⁺ SEQD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNEE ⁺ VPLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
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EER ⁺ LG ⁺ QG ⁺ RE ⁺ NA ⁺ KQ ⁺ FL ⁺ KE ⁺ NK ⁺ DI ⁺ ML ⁺ MI ⁺ QE ⁺ QI ⁺ RE ⁺ HY ⁺ CL ⁺ DN ⁺ NG ⁺ VV ⁺ QQ ⁺ AA ⁺ ET ⁺ QE ⁺ EL ⁺ .EFE ⁺ .E ⁺	348
SERIGQGR ⁺ EN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DE ⁺ ED ⁺ VL ⁺ KV ⁺ RAAY ⁺ CL ⁺ SD ⁺ VPE ⁺ ED ⁺ LP ⁺ TE ⁺ DE ⁺ .QI ⁺ .NIL ⁺ PDD ⁺ ST ⁺EE ⁺	355
DERIGQG ⁺ KE ⁺ KTI ⁺ AY ⁺ IA ⁺ ER ⁺ PE ⁺ ME ⁺ QE ⁺ ED ⁺ RD ⁺ RV ⁺ MA ⁺ AT ⁺ RAG ⁺ NAGE ⁺ AP ⁺ AL ⁺ APA ⁺ AA ⁺ PE ⁺ AA ⁺ .EA ⁺	363
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DKKL ⁺ GG ⁺ RE ⁺ NA ⁺ KALL ⁺ KE ⁺ DK ⁺ AL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ES ⁺ IG ⁺ SNE ⁺ EI ⁺MPL ⁺ PDE ⁺ PLE ⁺ ..EME ⁺	347
DKKL ⁺ GG ⁺ RE ⁺ NA ⁺ KALL ⁺ KE ⁺ DK ⁺ AL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ES ⁺ IG ⁺ SNE ⁺ EI ⁺MPL ⁺ PDE ⁺ PLE ⁺ ..EME ⁺	347
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GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RAL ⁺ NC ⁺ VE ⁺ MHI ⁺TEGT ⁺ Q ⁺ .DET ⁺DGER ⁺ PEE ⁺	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RAL ⁺ NC ⁺ VE ⁺ MHI ⁺TEGT ⁺ Q ⁺ .DET ⁺DGER ⁺ PEE ⁺	348
GERIGQGR ⁺ DNC ⁺ REF ⁺ LREN ⁺ AE ⁺ LARE ⁺ IE ⁺ EN ⁺ KV ⁺ RE ⁺ HL ⁺ CV ⁺ TPM ⁺ G....AV	

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consensus			

- non conserved
- similar
- ≥ 50% conserved