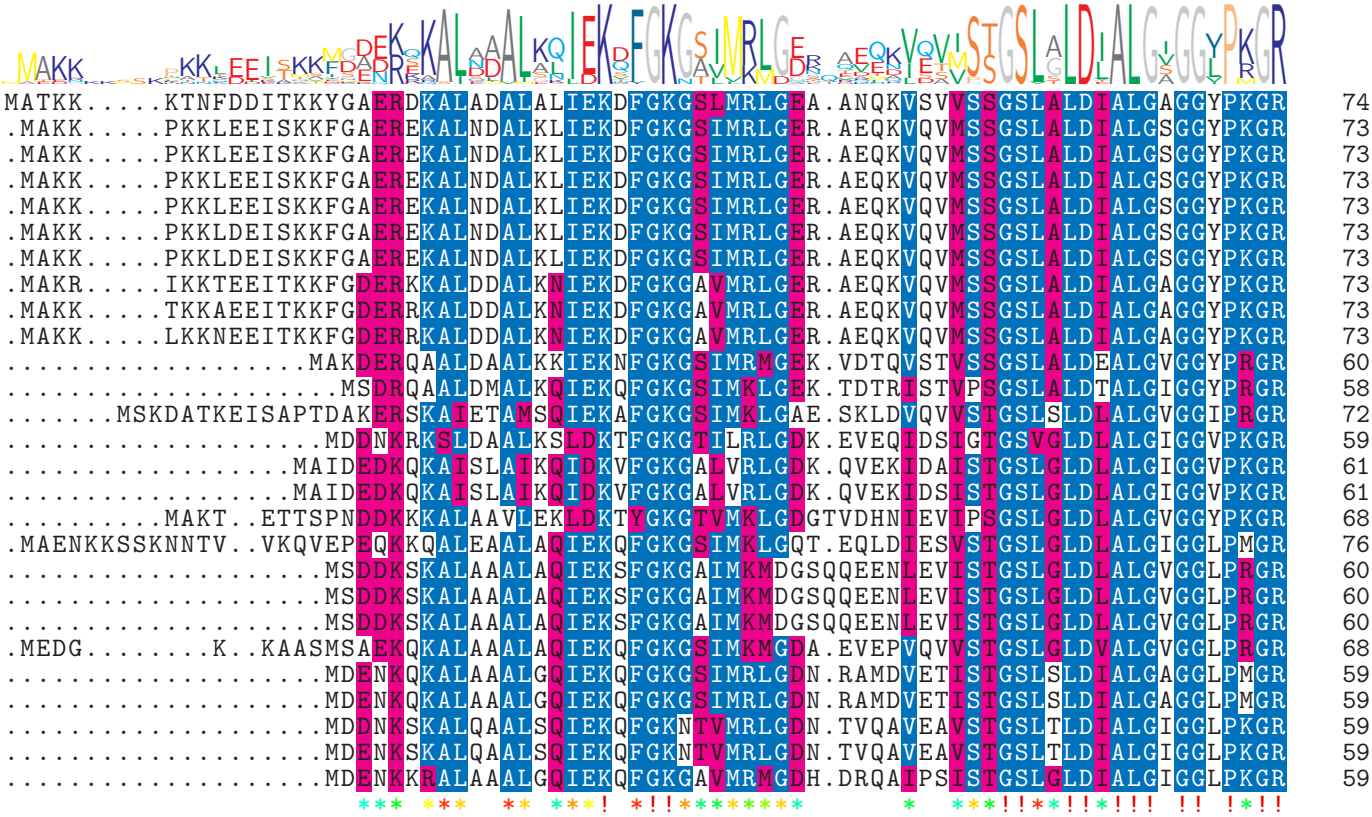


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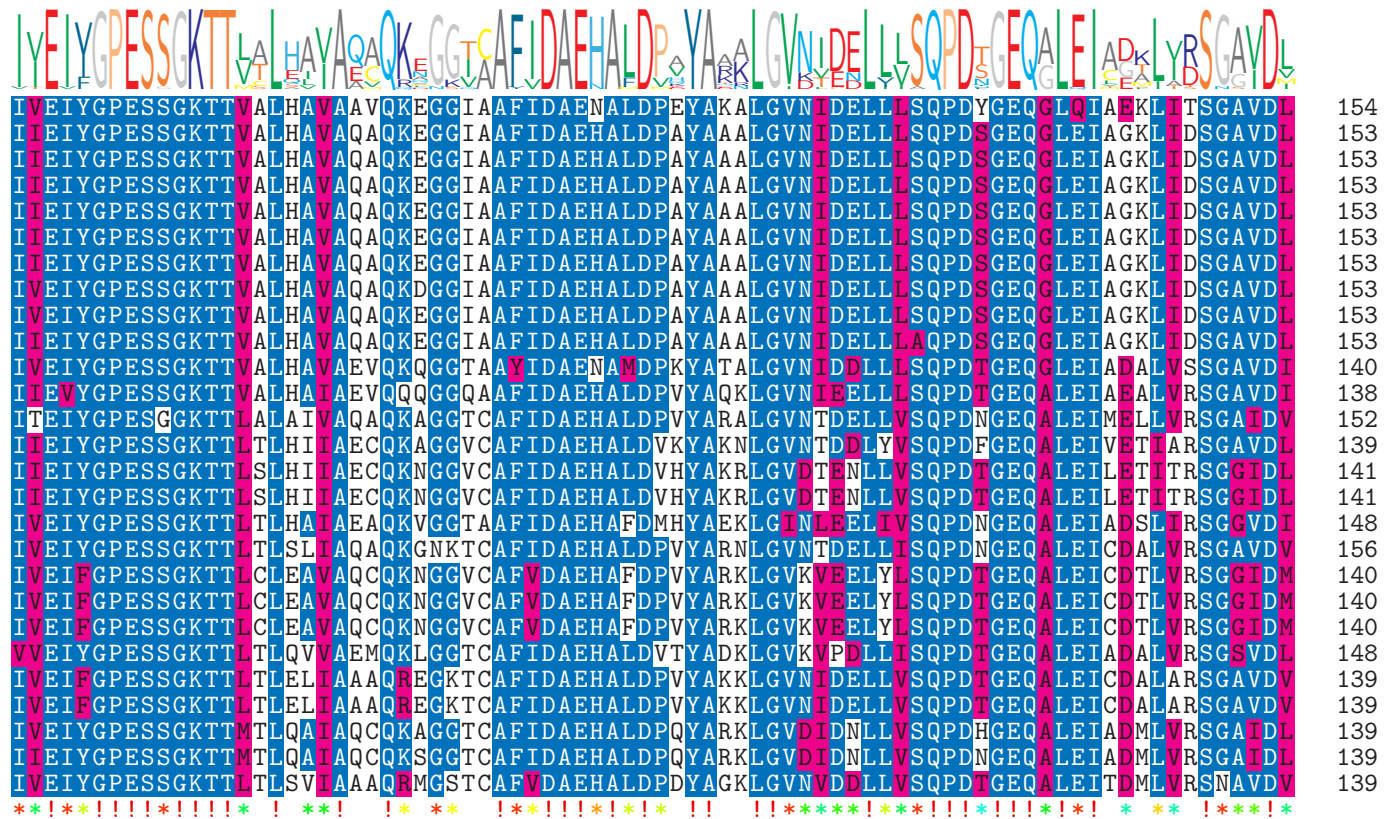
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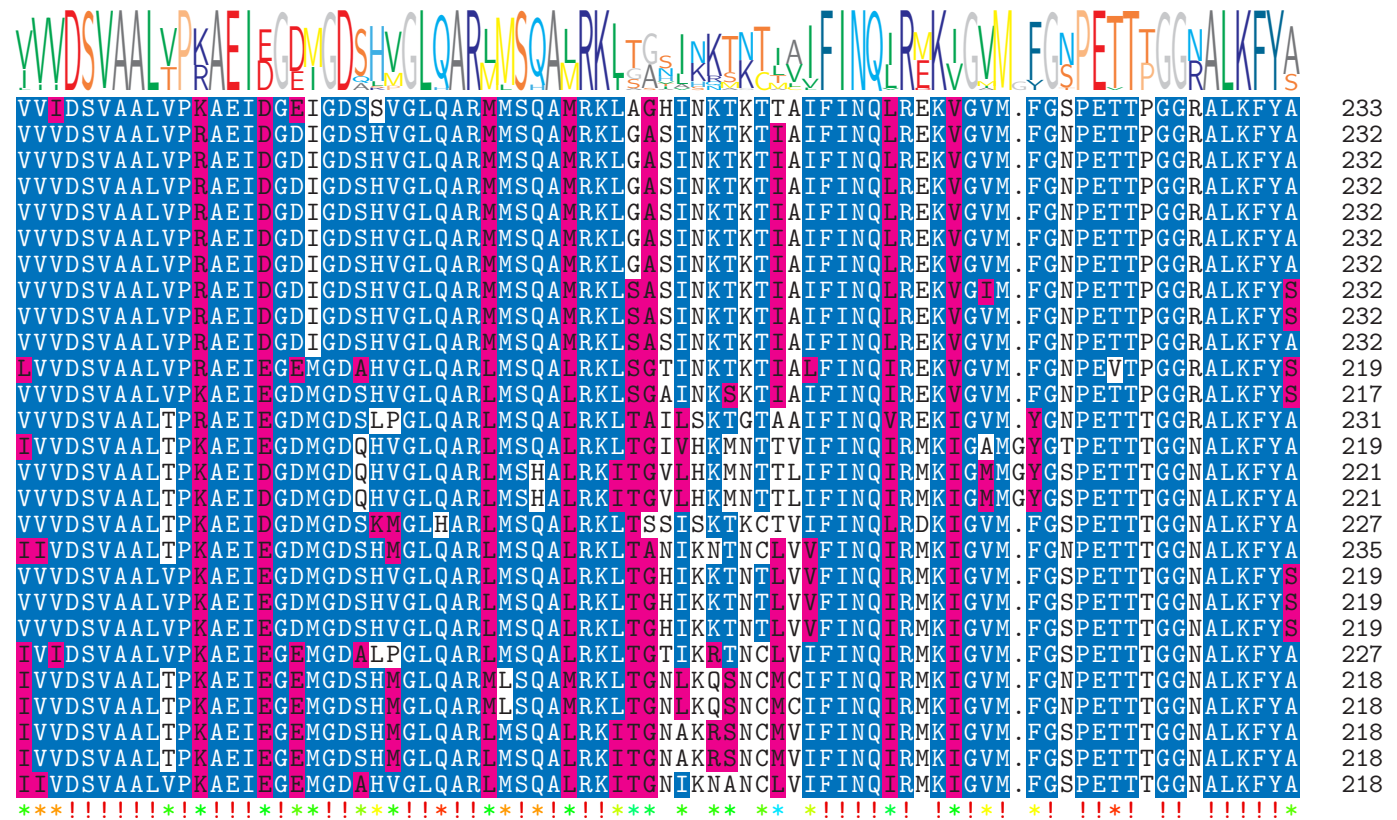
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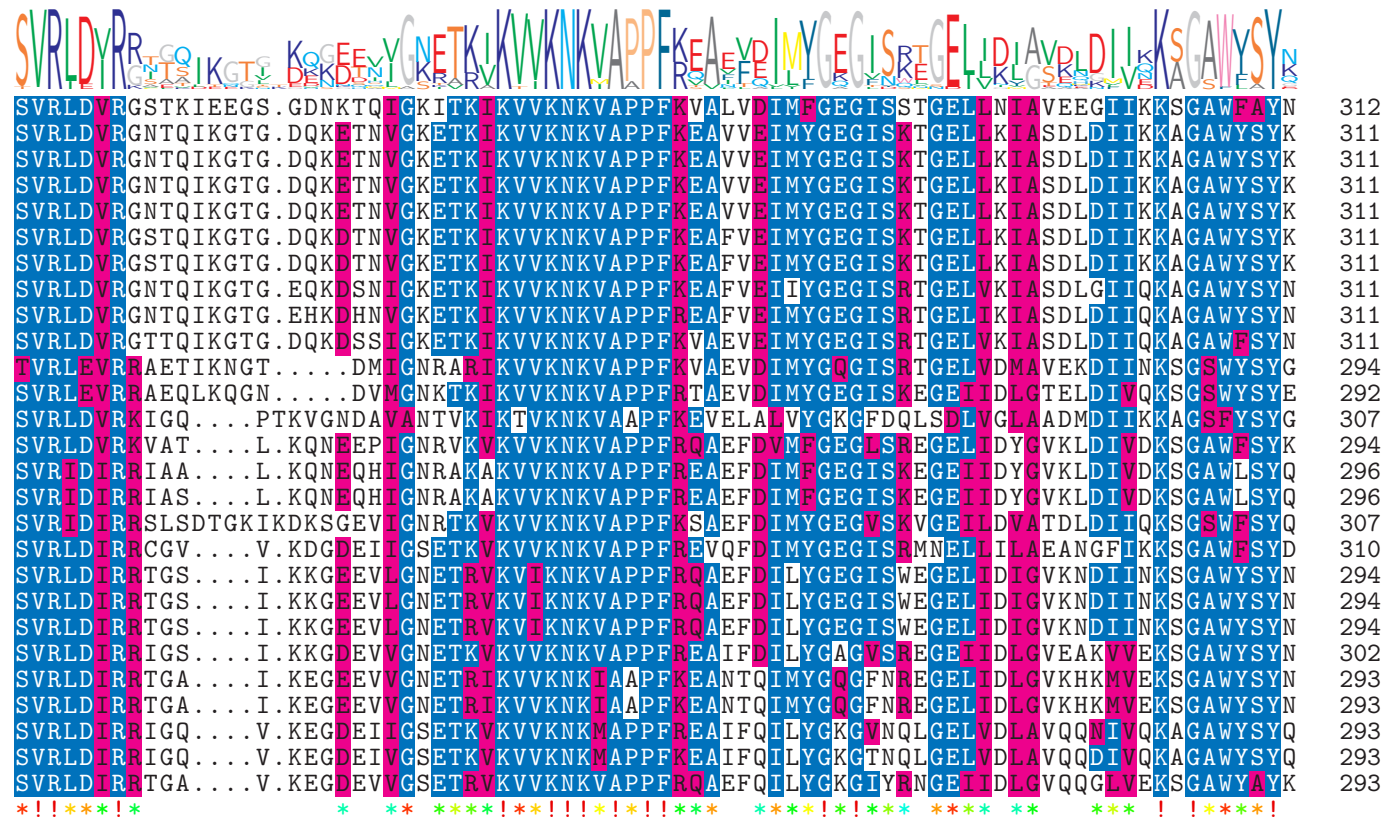
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consensus

Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ VPLDL ⁺ GDELE ⁺ IE ⁺	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ VPLDL ⁺ GDELE ⁺ IE ⁺	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ VPLDL ⁺ GDELE ⁺ IE ⁺	385
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GEKIGQGS ⁺ ENAK ⁺ KLAD ⁺ NPEI ⁺ F ⁺ DDID ⁺ HKV ⁺ RVQF ⁺ GL ⁺ IEEDNT ⁺ EKK ⁺ SSKEK ⁺ E ⁺DE ⁺ ..KADKNL ⁺ VLED ⁺ DDT ⁺ IE ⁺ LE ⁺	382
GEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NP ⁺ AI ⁺ F ⁺ DEID ⁺ HKV ⁺ RVHF ⁺ GMT ⁺ EDDSPV ⁺ QSELVEE ⁺K ⁺ ..NEAD ⁺ DLVL ⁺ DLDNA ⁺ IE ⁺ IE ⁺	378
GEKIGQGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ QL ⁺ F ⁺ DEID ⁺ RKV ⁺ RVKF ⁺ GL ⁺ LEESE ⁺ E ⁺ ESAMAVA ⁺S ⁺ ..EETD ⁺ DLAL ⁺ DLN ⁺ GIE ⁺ IE ⁺	377
SERIGQGS ⁺ RENAK ⁺ NYLAD ⁺ HE ⁺ DVE ⁺ DEV ⁺ RLK ⁺ VRAAY ⁺ GIS ⁺ DVPEED ⁺ LPTTE ⁺ DE ⁺ .QIN ⁺ILPDD ⁺ STEE ⁺ ..	355
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DERIGQGS ⁺ EKKT ⁺ IAYIA ⁺ IER ⁺ PEME ⁺ Q ⁺ EIRDR ⁺ VM ⁺ AIRAG ⁺ NAEAPALAPAPA ⁺ AEPA ⁺AEA ⁺	363
DKKL ⁺ GQGS ⁺ RENSK ⁺ AF ⁺ LKEN ⁺ PEI ⁺ AD ⁺ EITK ⁺ AIQNSM ⁺ GI ⁺ EGMI ⁺SGSEDD ⁺ ..E ⁺GEE ⁺	343
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DKKL ⁺ GQGS ⁺ RENAK ⁺ ALL ⁺ KED ⁺ KAL ⁺ AD ⁺ EITL ⁺ KIKES ⁺ IG ⁺ SNEEI ⁺ ...MPLPDE ⁺ ..P ⁺LEEME ⁺	347
DTKL ⁺ GQGRD ⁺ TVKEL ⁺ IK ⁺ DNPE ⁺ LAE ⁺ LEAK ⁺ IREKL ⁺ QAK ⁺	343
GTKIGQGS ⁺ KNN ⁺ AVK ⁺ WLKEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQE ⁺ IRNTL ⁺ ASNPNS ⁺VLKATASDS ⁺NDES ⁺ DVEEF ⁺ SEEE ⁺ EL ⁺ ...	372
GAKIGQGS ⁺ KDN ⁺ VRV ⁺ WLKEN ⁺ PEIS ⁺ DEI ⁺ DAK ⁺ IRALN ⁺ GVEMHI ⁺ ...TEGTQDET ⁺GER ⁺PEE ⁺	348
GAKIGQGS ⁺ KDN ⁺ VRV ⁺ WLKEN ⁺ PEIS ⁺ DEI ⁺ DAK ⁺ IRALN ⁺ GVEMHI ⁺ ...TEGTQDET ⁺GER ⁺PEE ⁺	348
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GDKIGQGS ⁺ KANACK ⁺ YLKEN ⁺ PEIAKT ⁺ LDKK ⁺ LREMLLN ⁺ PNEM ⁺ ...QLIAETSSA ⁺ADDV ⁺ EFGAV ⁺ PEEF ⁺	354
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GNKIGQGS ⁺ KNN ⁺ VIRY ⁺ LEEN ⁺ PQIST ⁺ EIEAV ⁺ IREQLLT ⁺ TKASD ⁺ ...QTAA ⁺ .HDET ⁺EEEP ⁺ DLL ⁺ ..ES ⁺	349
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GSKIGQGS ⁺ KANAAK ⁺ YL ⁺ ENPEI ⁺ IG ⁺ EIEQQ ⁺ IRAKLL ⁺ VTSAN ⁺ ...TKATPVAED ⁺LADADI ⁺	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved