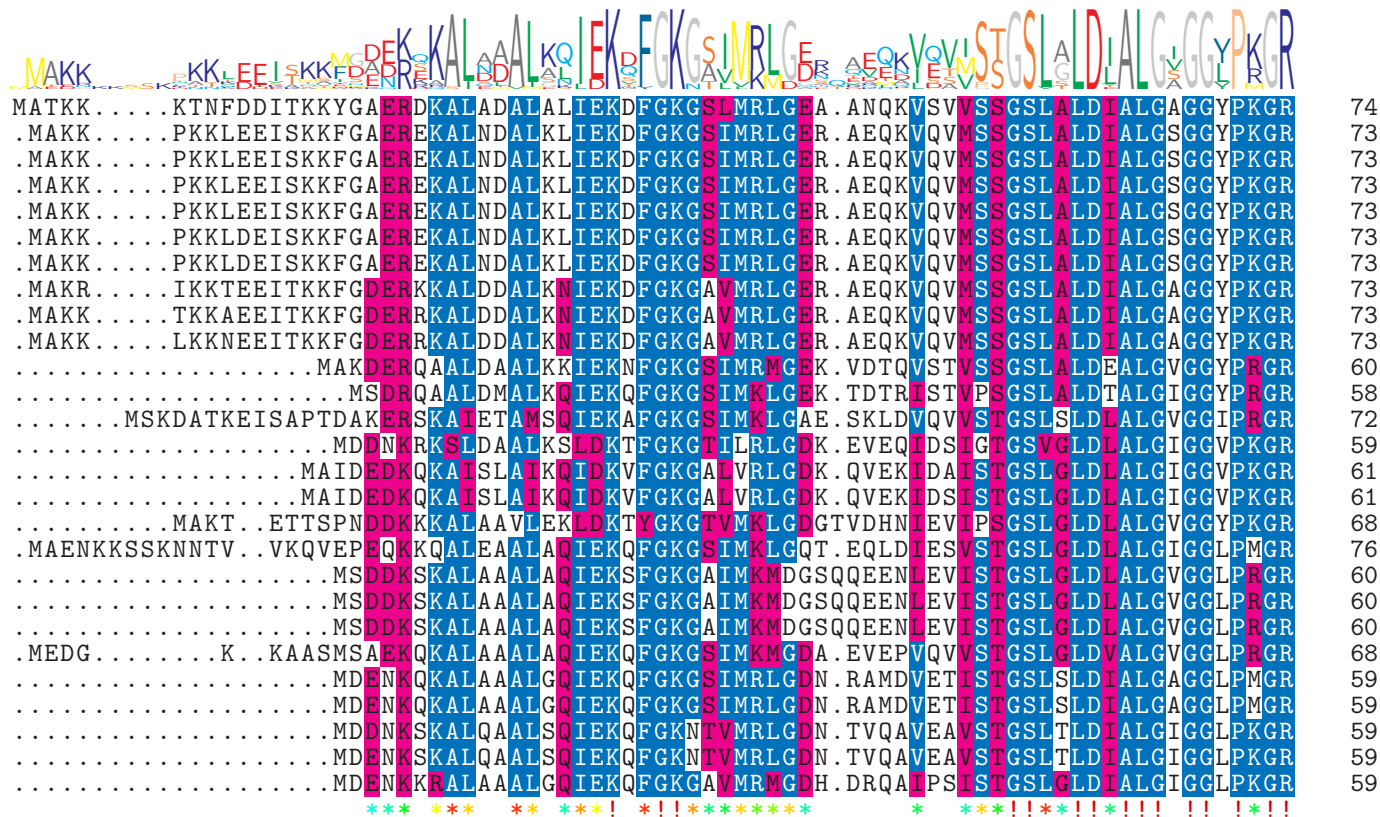


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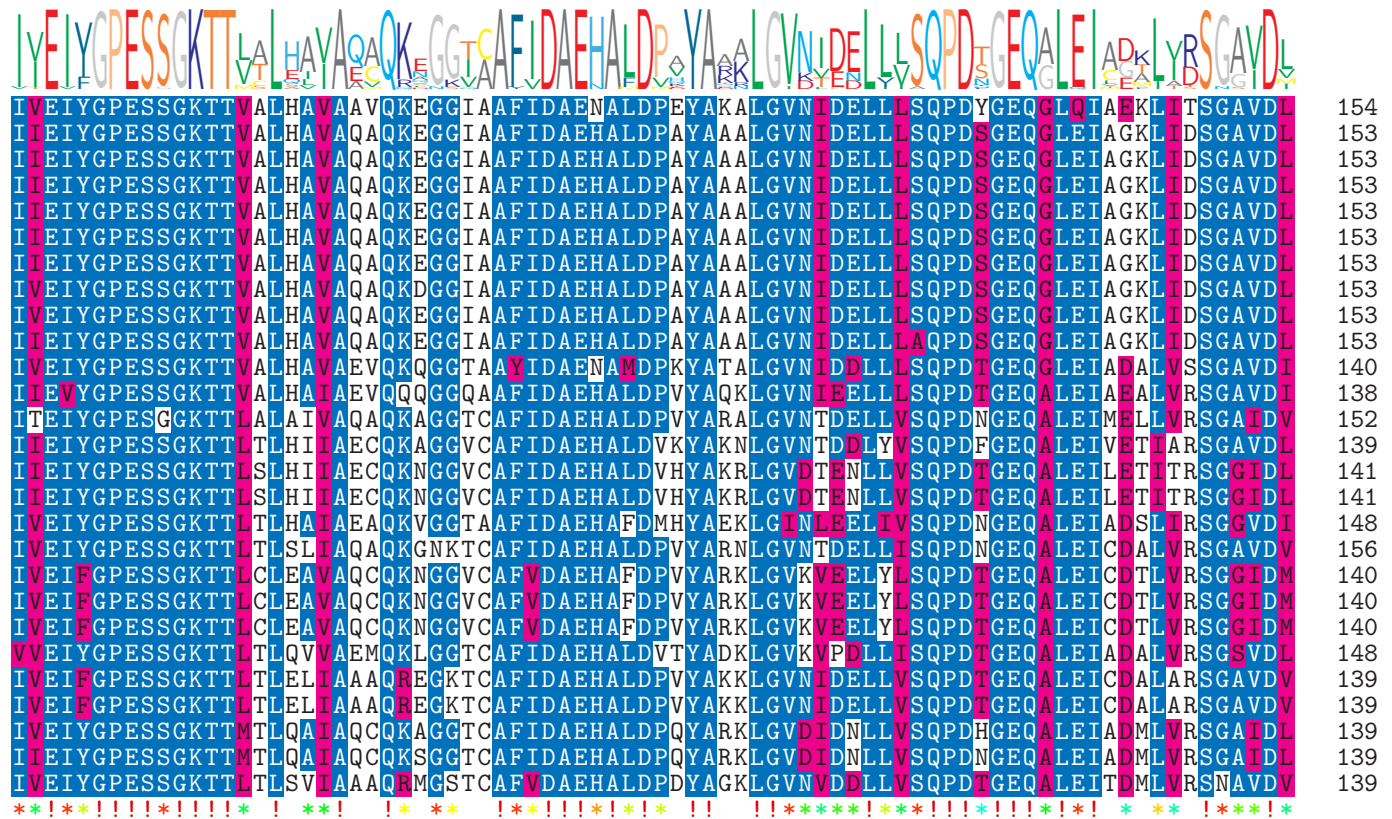
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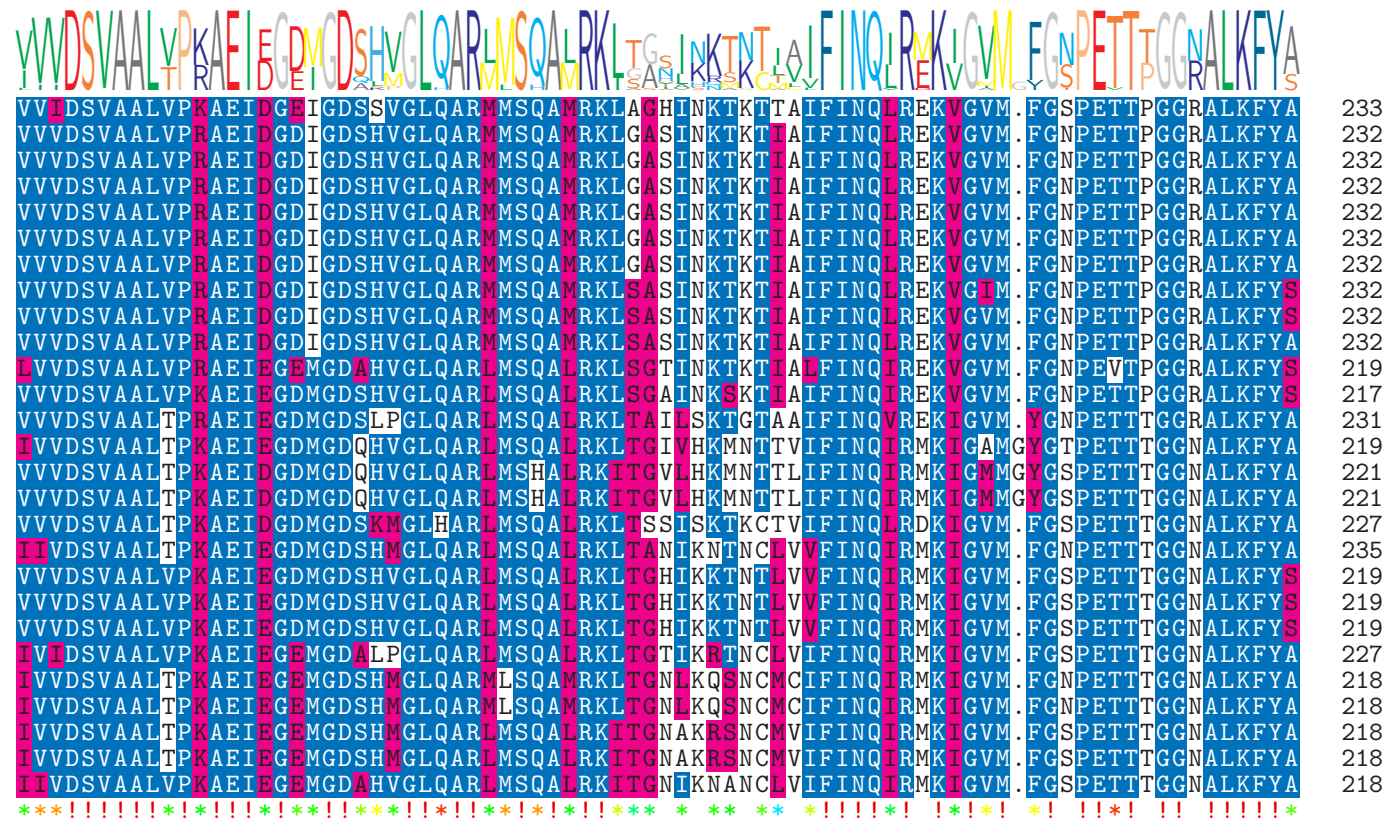
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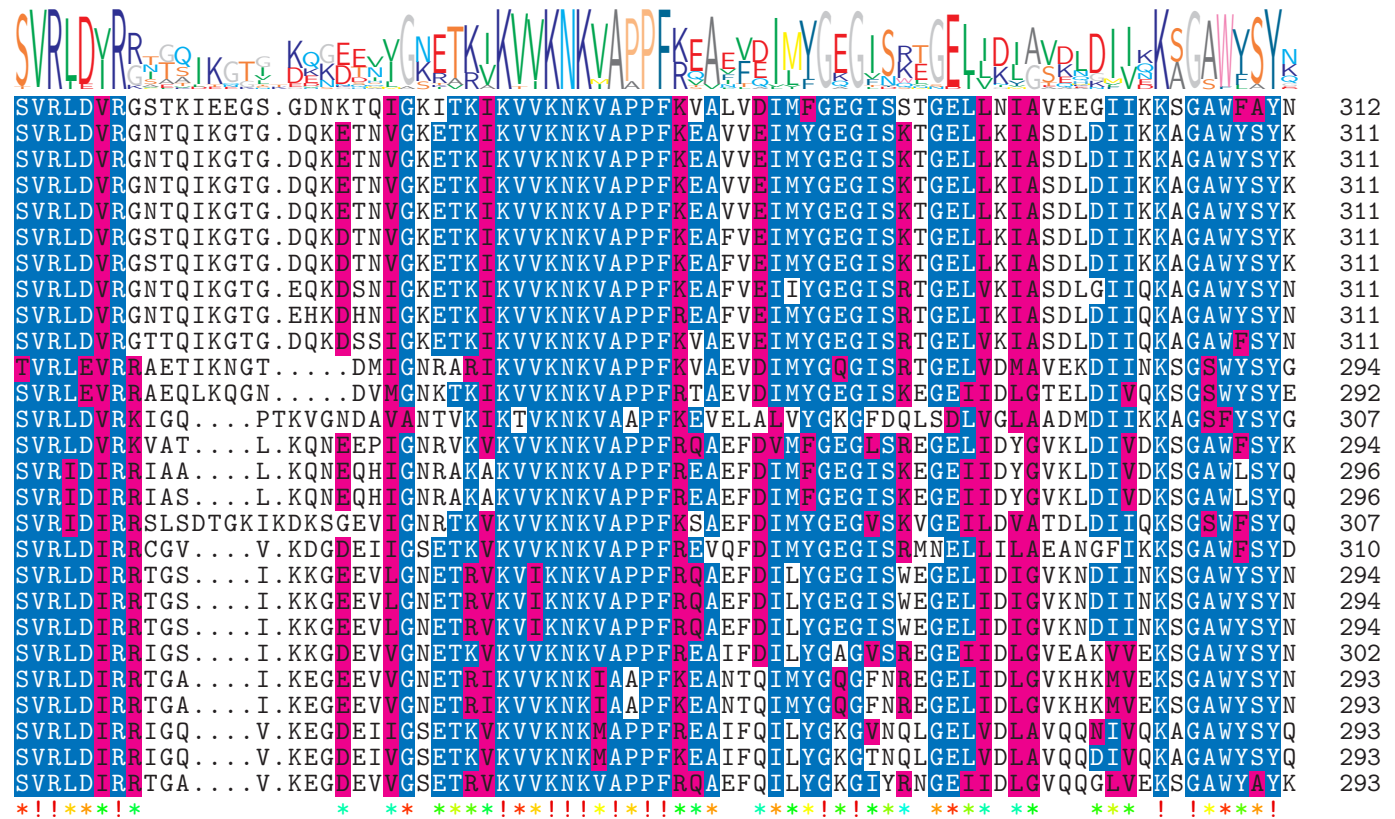
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consensus

Sequence	Score
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DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKDEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ EVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKDEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ EVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKDEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ EVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKDEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ EVPLDLGDELEIE ⁺	385
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GEKIGGGS ⁺ ENAK ⁺ KYLAD ⁺ NP ⁺ AI ⁺ F ⁺ DEID ⁺ HKV ⁺ RVHF ⁺ GMTEDDSPVQSELVEE ⁺K ⁺ ..NEAD ⁺ DLVL ⁺ DLDNAIEIE ⁺	378
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SERIGGGS ⁺ RENAK ⁺ NYLAD ⁺ HD ⁺ VE ⁺ DEV ⁺ RLK ⁺ VRAAY ⁺ GISDVPEEDLPTTEDE ⁺ ..QIN ⁺ILPDDSTEE ⁺ ..	355
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DKKLGGGREN ⁺ SKA ⁺ FLKEN ⁺ PEIA ⁺ DEIT ⁺ KA ⁺ IQNSM ⁺ GTIEGMI ⁺SGSEDD ⁺ ..E ⁺GEE ⁺	343
DKKLGGGRENAK ⁺ ALLKED ⁺ KALADEIT ⁺ LK ⁺ IKESIG ⁺ SNEEI ⁺ ...MPLPDE ⁺ ..P ⁺LEEME ⁺	347
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DTKLGGGRD ⁺ TVKEL ⁺ IKDN ⁺ PELA ⁺ EEL ⁺ EAK ⁺ IREKLQAK ⁺	343
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logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved