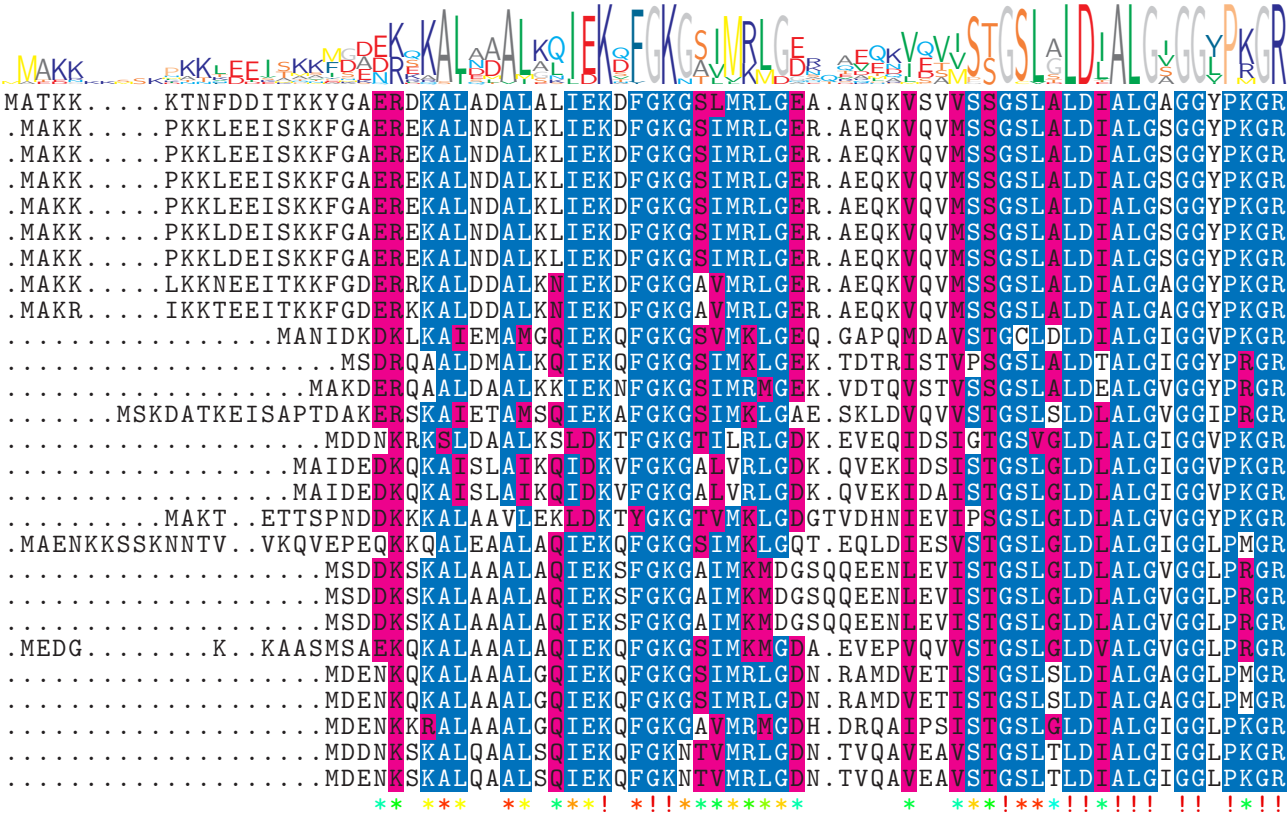


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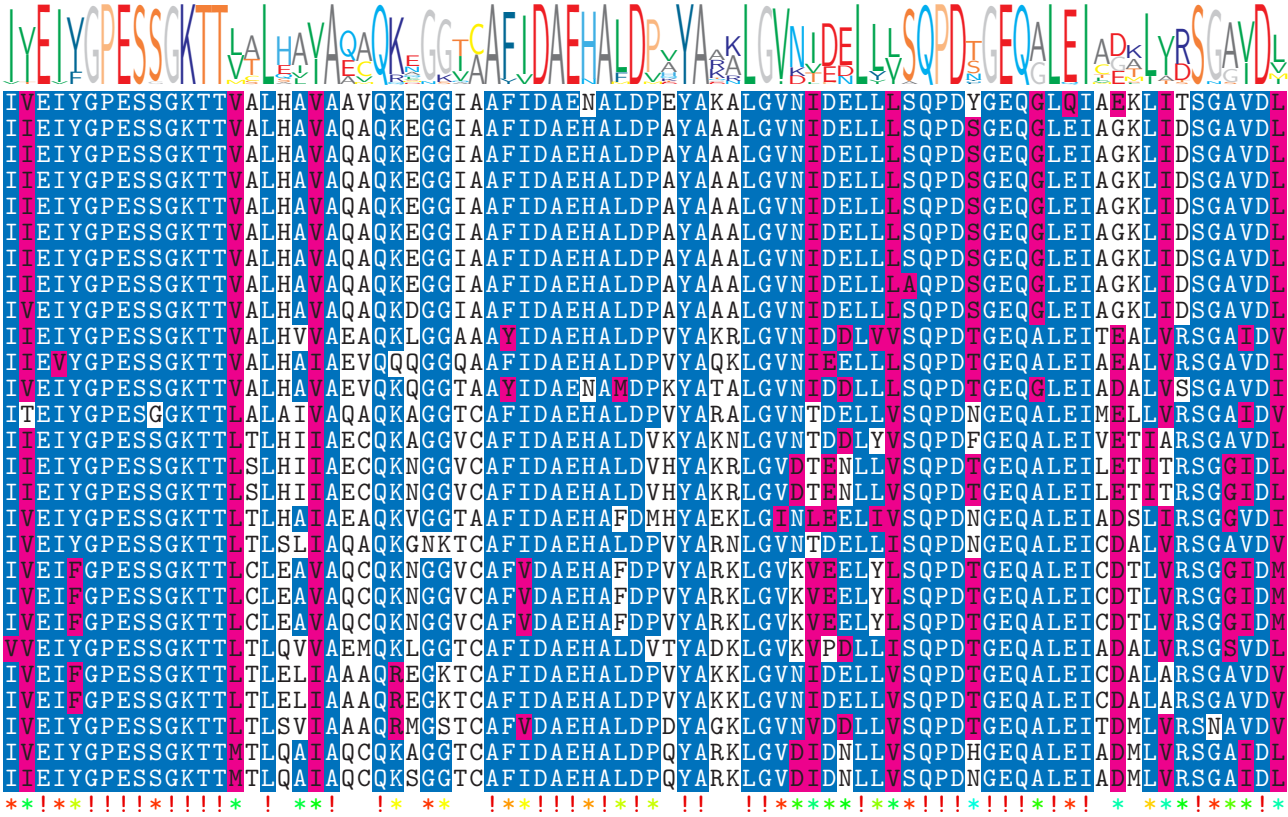
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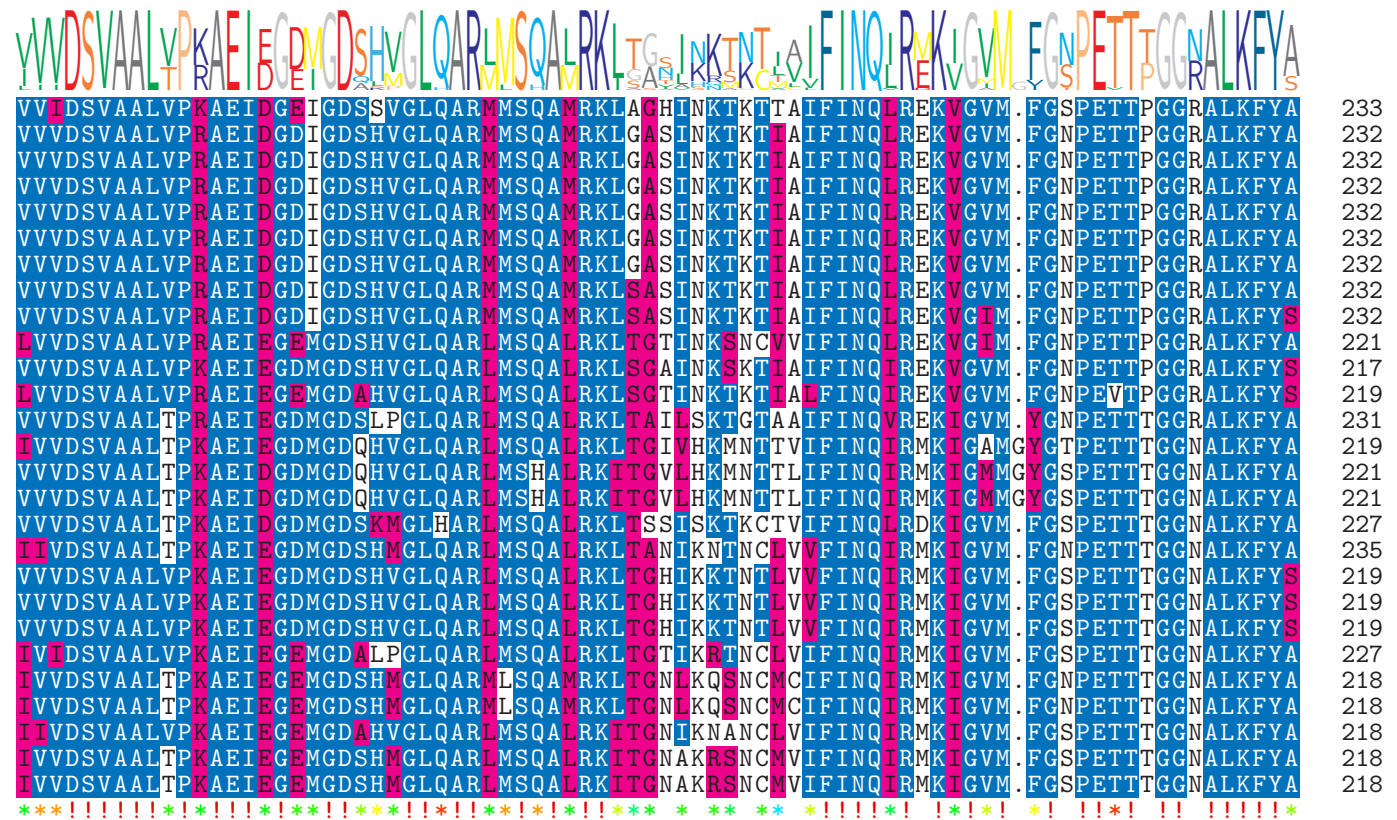


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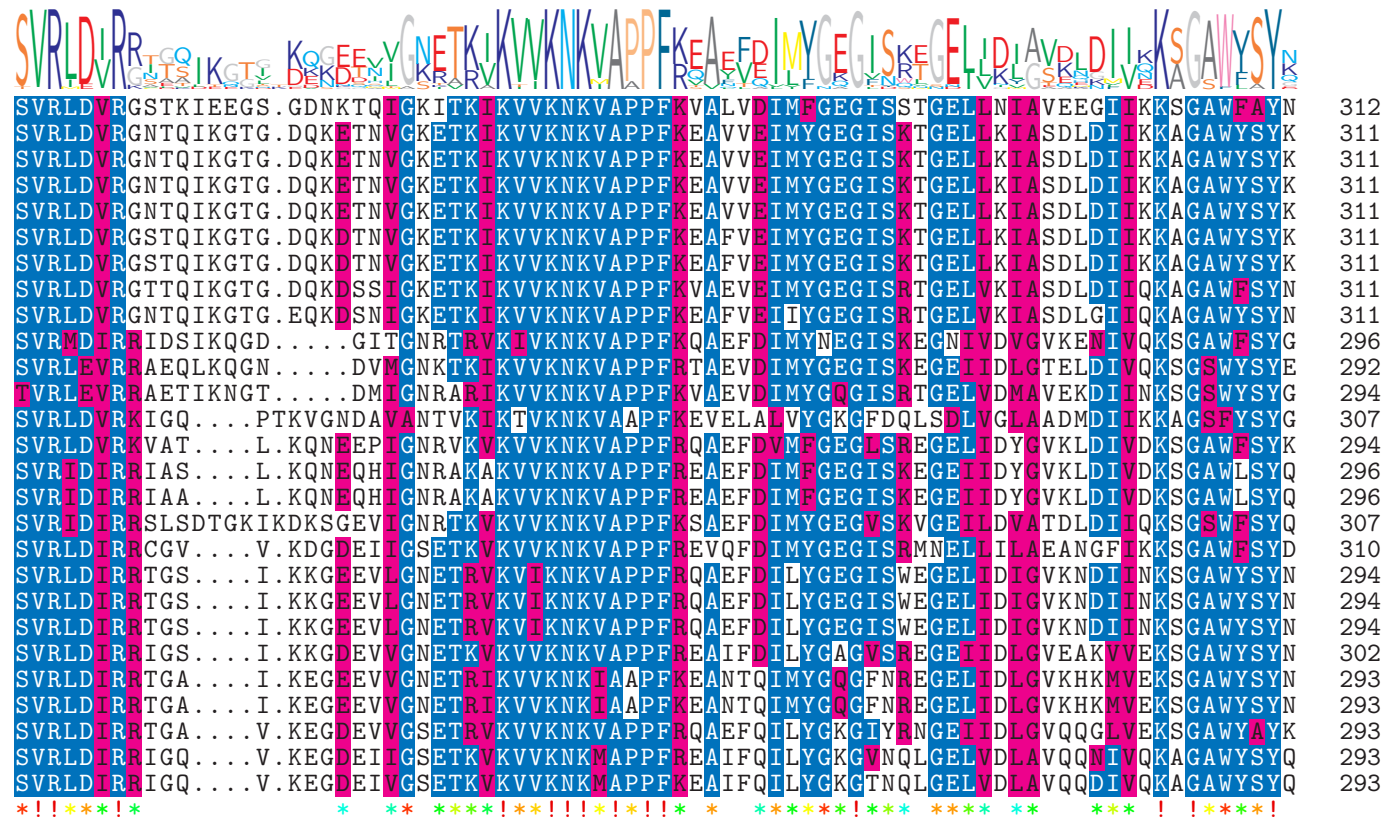
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Sequence	Score
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DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EID ⁺ DKV ⁺ RSKF ⁺ CL ⁺ IDGEEVSEQDT ENKK ⁺ DE PKKEEA . VNEEVPLDLG	379
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EID ⁺ DKV ⁺ RSKF ⁺ CL ⁺ IDGEEVSEQDT ENKK ⁺ DE PKKEEA . VNEEVPLDLG	379
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ VFA ⁺ EID ⁺ HQV ⁺ RVQF ⁺ CL ⁺ IDGEEAAE SKK ⁺ DE VAQVDS . VNEEVTLDLG	375
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GEKIGGGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DDI ⁺ DHK ⁺ V ⁺ RVQY ⁺ CL ⁺ IEEDNTEEEKQS SKEK ETDEK . . ADKNLVLELD	376
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EER ⁺ LGQGR ⁺ EN ⁺ AK ⁺ FL ⁺ KEN ⁺ KDI ⁺ MLM ⁺ IQE ⁺ QI ⁺ REHY ⁺ CL ⁺ DNNGVVQQQAE ETQE ⁺ LEFE . E	348
SERIGGG ⁺ REN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DV ⁺ IRLKV ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPTT EDE . QINILPDDSTEE	355
DERIGGG ⁺ EK ⁺ TIAY ⁺ IA ⁺ ERP ⁺ EME ⁺ QI ⁺ IRDRV ⁺ MAAIRAGNAGEAPALAPAPAAPEAAEA	363
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DKK ⁺ LGQGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ AD ⁺ EIT ⁺ TLK ⁺ IKES ⁺ GSNEEI MPLPDEP . . LE ⁺ ME	347
DKK ⁺ LGQGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ AD ⁺ EIT ⁺ TLK ⁺ IKES ⁺ GSNEEI MPLPDEP . . LE ⁺ ME	347
DTKL ⁺ GQGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ EL ⁺ AKI ⁺ REKLQAK	343
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GAKIGGQ ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDEI ⁺ DAK ⁺ IRALN ⁺ GVEMHI TEGT QDET ⁺ DGERPE E	348
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GNKIGGQ ⁺ KNNV ⁺ IRY ⁺ LE ⁺ EN ⁺ PQI ⁺ STE ⁺ IE ⁺ AVI ⁺ REQLLT ⁺ TKASD QTAA . HDETEE ⁺ PDLL . . ES	349
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consensus			

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-  ≥ 50% conserved