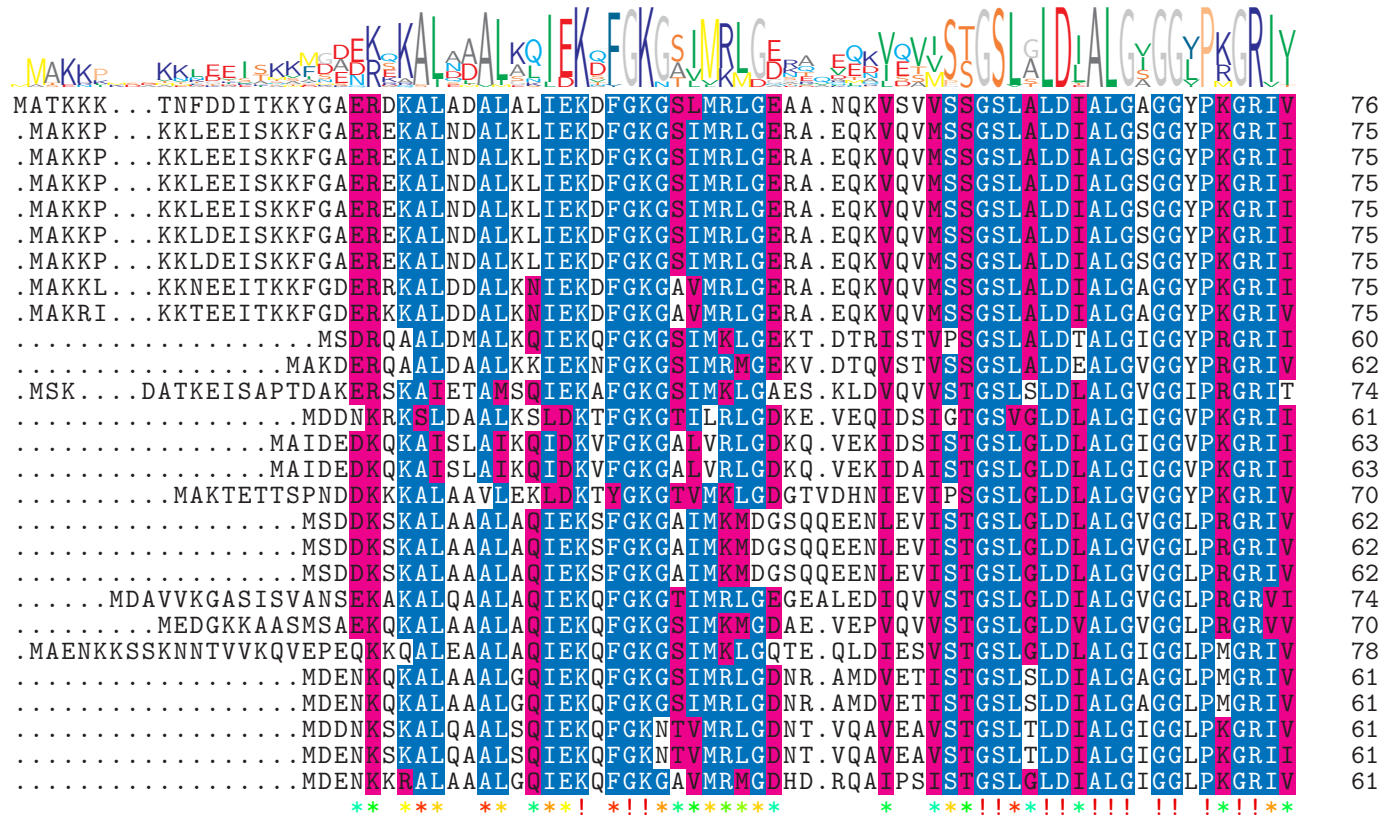


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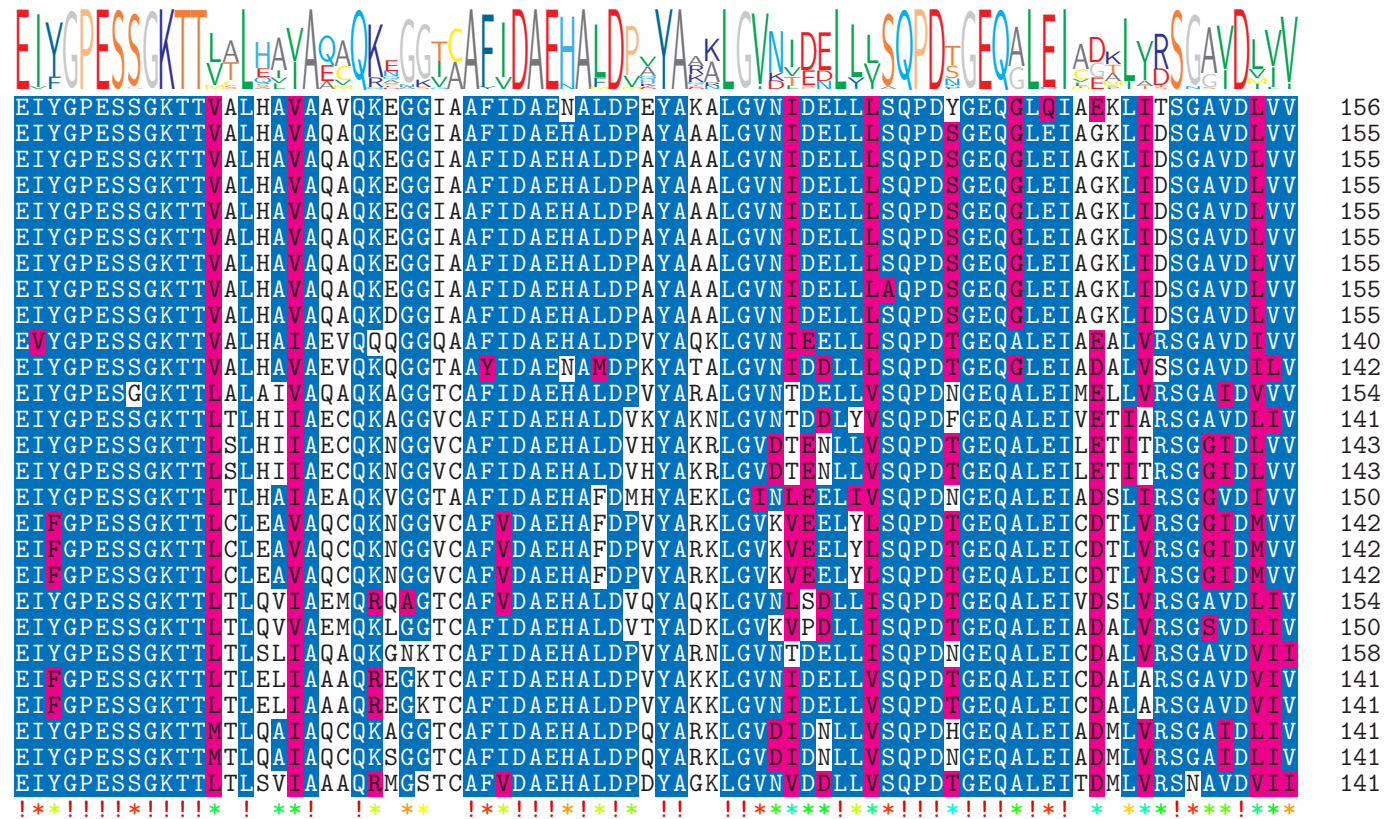
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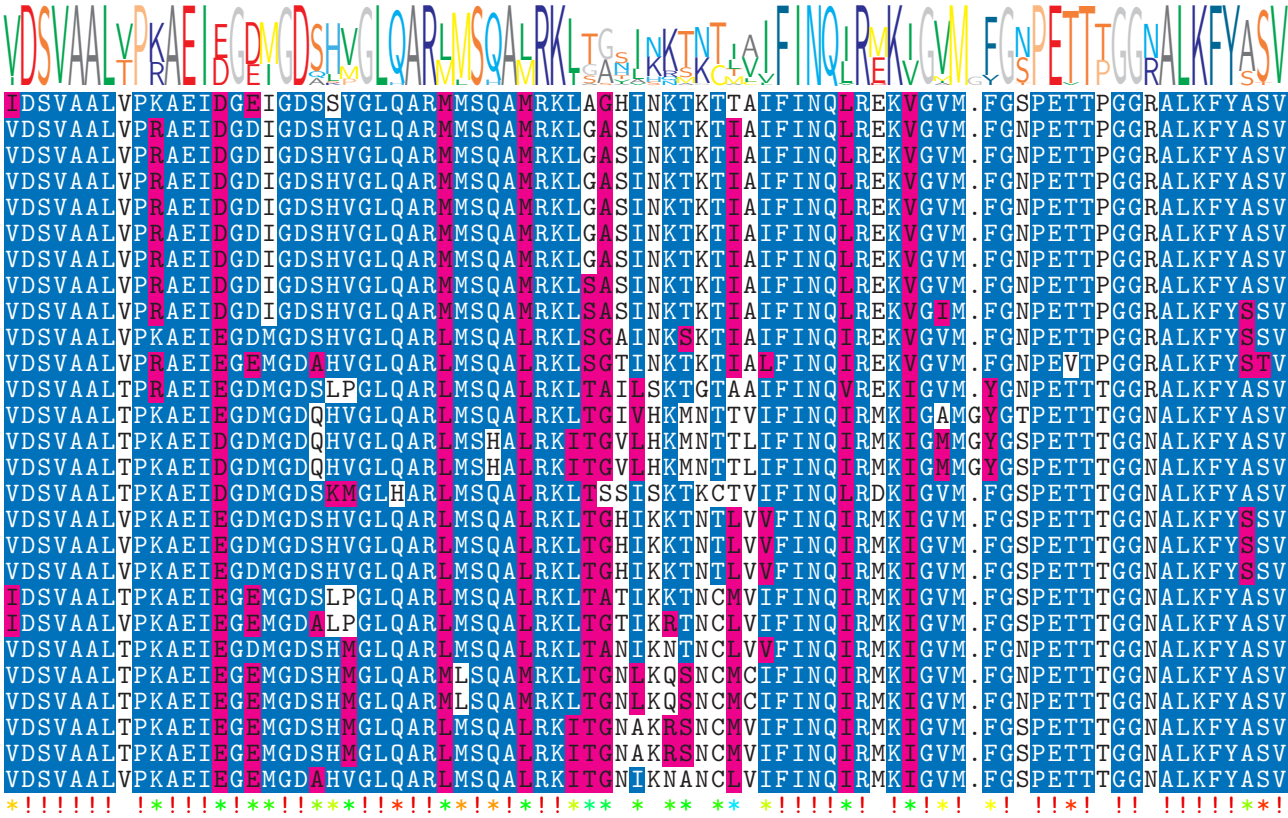
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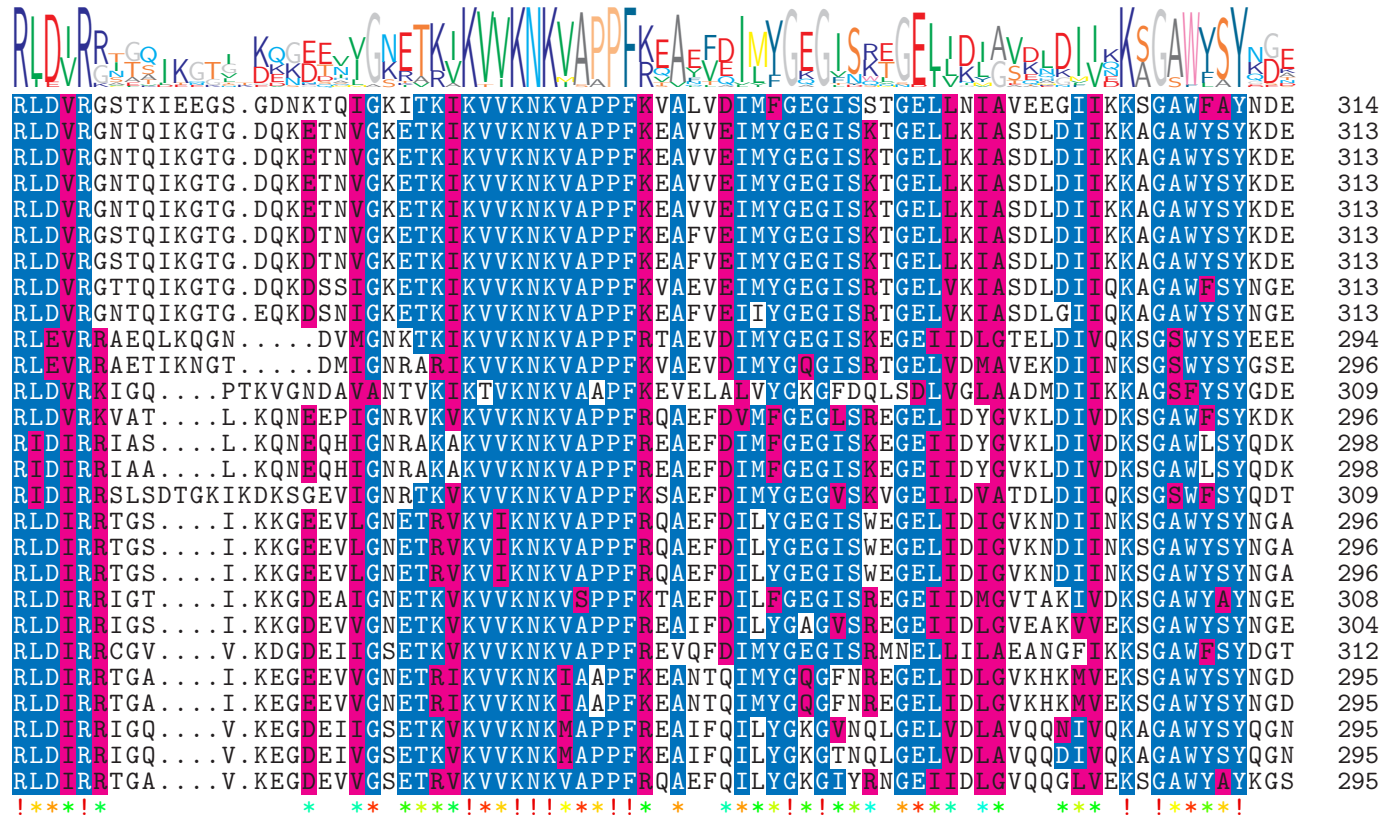


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consensus

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Sequence	Score
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KIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ ED ⁺ DH ⁺ KV ⁺ RS ⁺ KFG ⁺ LIDGEEVSEQD ⁺ TENKK ⁺ .DE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELE ⁺ IEI ⁺	386
KIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ ED ⁺ DH ⁺ KV ⁺ RS ⁺ KFG ⁺ LIDGEEVSEQD ⁺ TENKK ⁺ .DE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELE ⁺ IEI ⁺	386
KIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ ED ⁺ DH ⁺ KV ⁺ RS ⁺ KFG ⁺ LIDGEEVSEQD ⁺ TENKK ⁺ .DE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELE ⁺ IEI ⁺	386
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KIGGGS ⁺ EN ⁺ AK ⁺ FL ⁺ AD ⁺ NP ⁺ EI ⁺ FD ⁺ DD ⁺ ID ⁺ HK ⁺ RV ⁺ VQY ⁺ GLIEEDNTEEKQSSKEK ⁺ETDEK ⁺ ..ADKNLVLELDD ⁺ TIELED ⁺	383
RLGQGR ⁺ EN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IM ⁺ LI ⁺ QE ⁺ QIRE ⁺ HY ⁺ GLDNNGVVQQQAETQE ⁺ .EL ⁺ .EFE ⁺ .E ⁺	348
RIGQGR ⁺ EN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DEV ⁺ RL ⁺ KV ⁺ RA ⁺ AY ⁺ GT ⁺ ISDVPEEDLPTTEDE ⁺ ..QI ⁺ .NILPDDST ⁺EE ⁺	355
RIGQG ⁺ KE ⁺ KTI ⁺ AY ⁺ IA ⁺ ER ⁺ PE ⁺ ME ⁺ QE ⁺ IR ⁺ DRV ⁺ MA ⁺ AIRAGNAGEAPALAPAPAAP ⁺ .AAAA ⁺	363
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KLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ AD ⁺ EIT ⁺ LK ⁺ IK ⁺ ES ⁺ IGSNEEIMP ⁺ ..LPDEPLE ⁺ ..EME ⁺	347
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KIGGQKNN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PQ ⁺ ISTE ⁺ IE ⁺ AV ⁺ IREQLLT ⁺ TKASDQT ⁺ ..AA ⁺ .HDETE ⁺ EPDLL ⁺ES ⁺	349
KIGGQKNN ⁺ VIR ⁺ YFE ⁺ EN ⁺ NQ ⁺ IAE ⁺ EI ⁺ ERN ⁺ IREQLLT ⁺ TGTNGA ⁺ ..VQ ⁺ .I ⁺ .EDE ⁺ EPDLL ⁺LES ⁺	349
KIGGQKANA ⁺ AK ⁺ YLE ⁺ EN ⁺ PEI ⁺ GQE ⁺ EIQ ⁺ IRAKLL ⁺ VTSANTK ⁺ ..ATPVAEDLADADI ⁺	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved