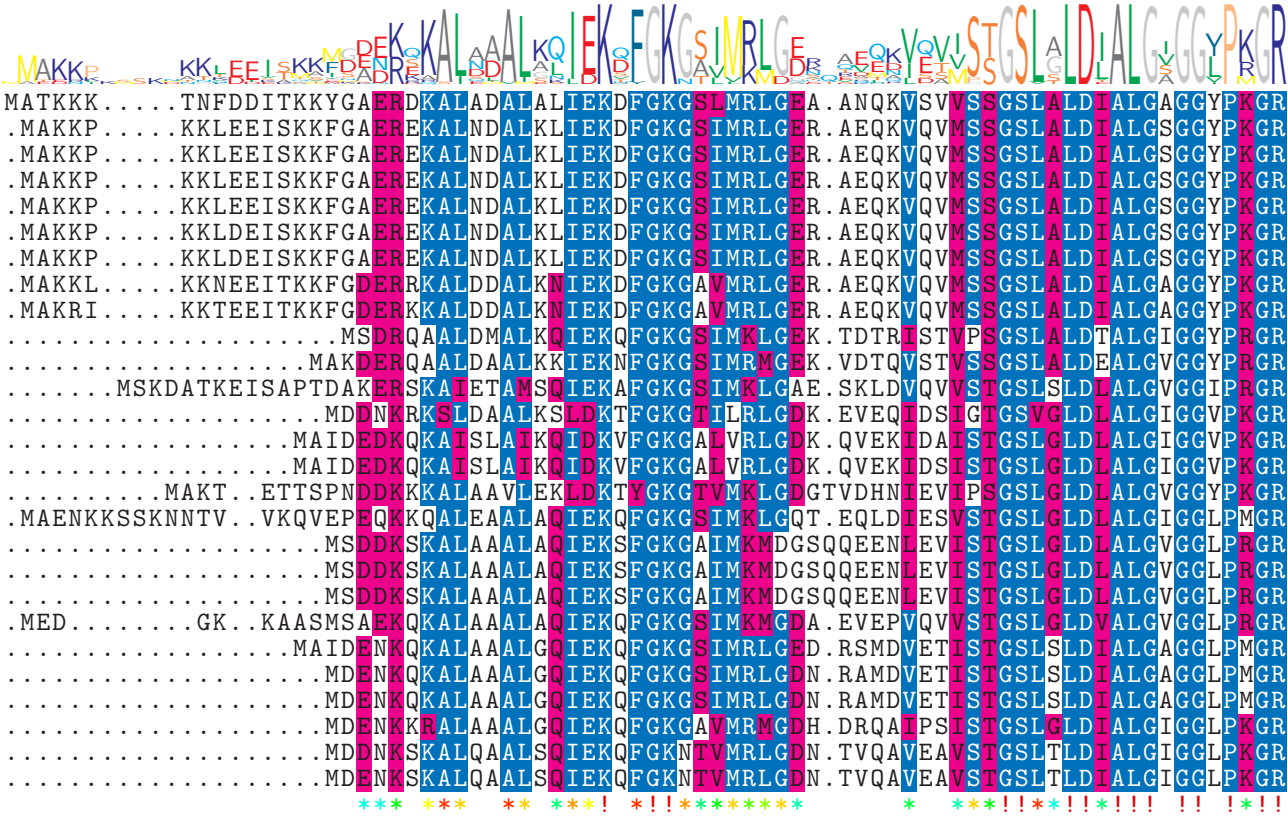


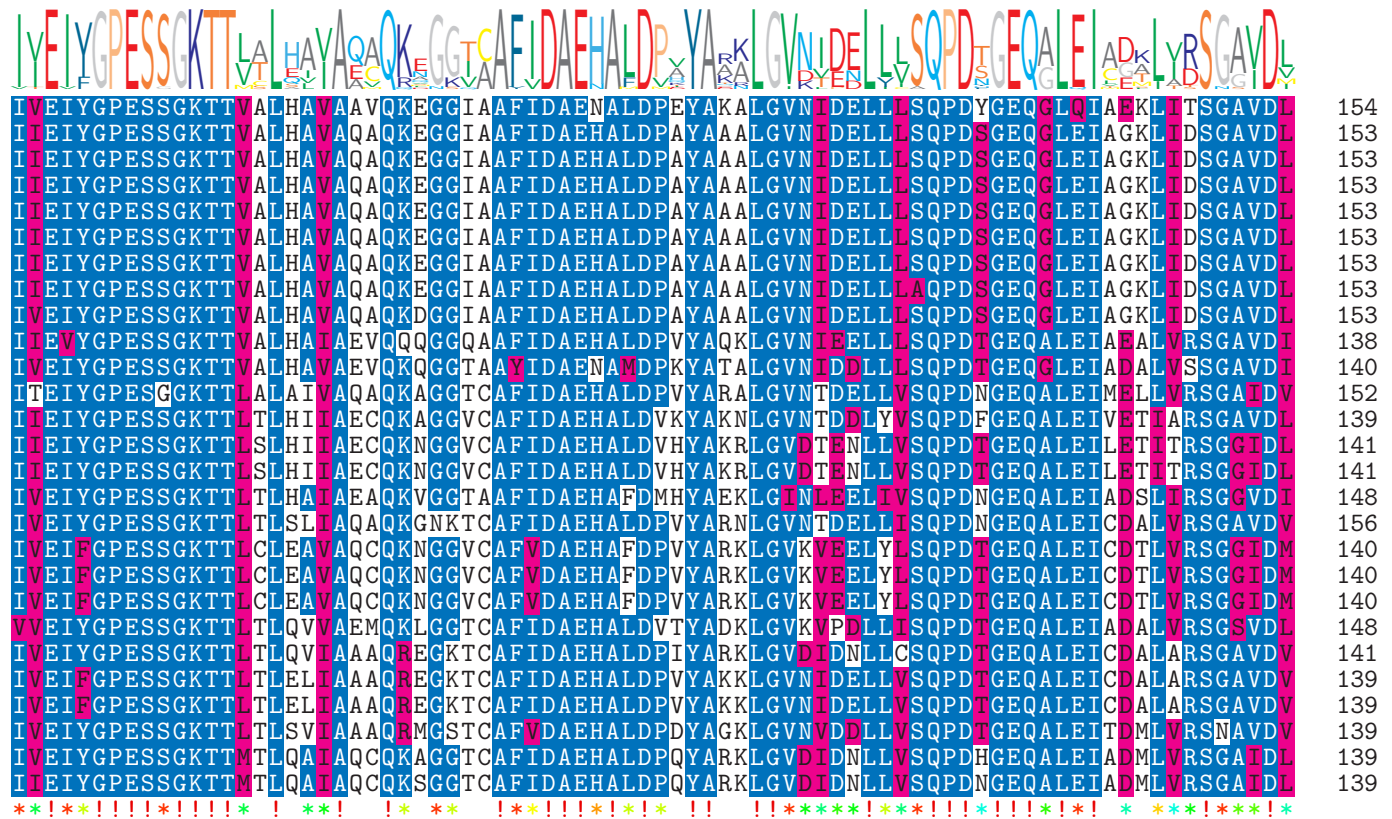
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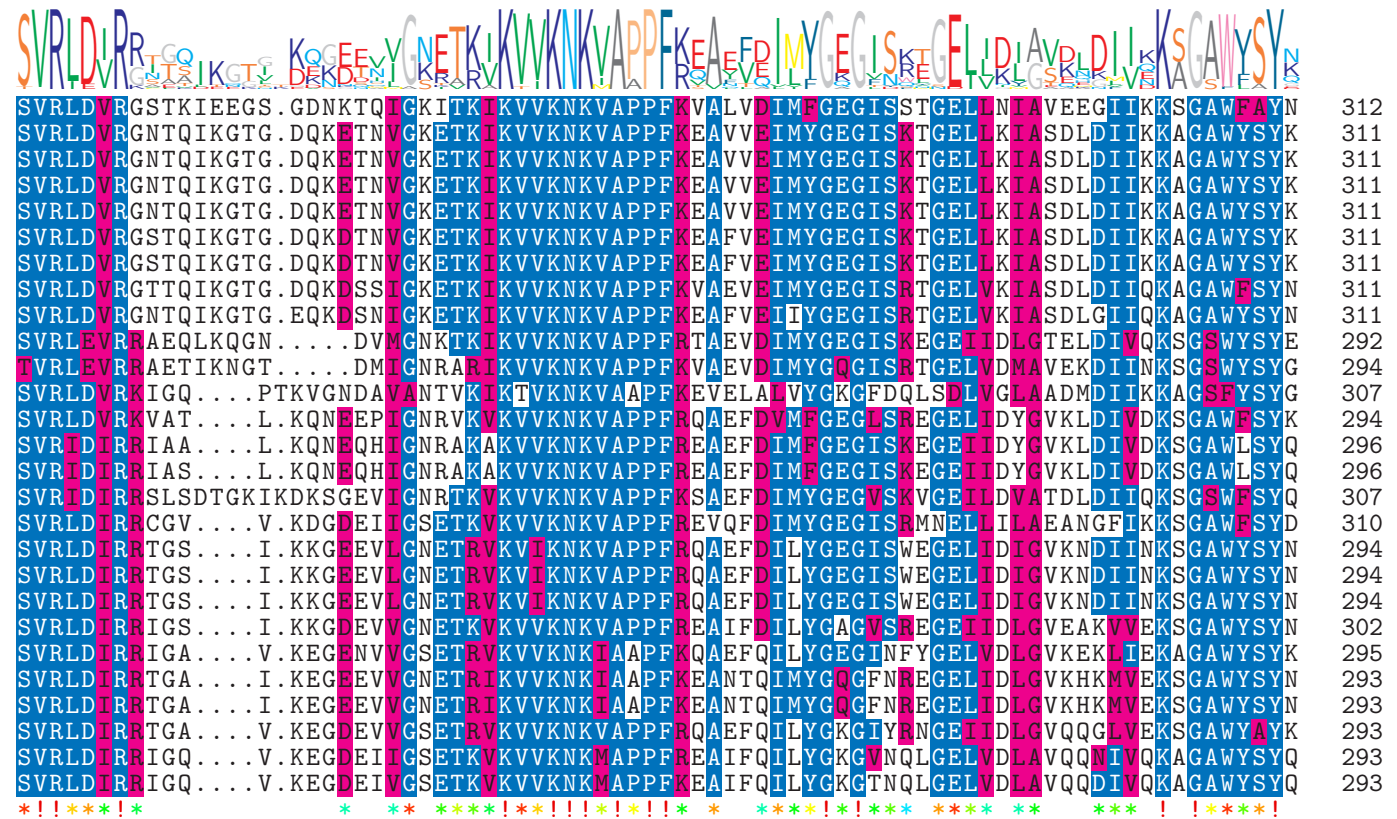
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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FG ¹³ LIDGEEVSEQD ¹⁴ TENKK ¹⁵ DEPKKEEA . .VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FG ¹³ LIDGEEVSEQD ¹⁴ TENKK ¹⁵ DEPKKEEA . .VNEEVPLDLGDELEIE	385
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DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AD ⁵ NPEIF ⁶ DE ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQ ¹¹ FG ¹² LIDGEEIAESKKDEAAQVDS . .VNEEVTLDLGDLEIE	381
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GEKIGQGS ¹ EN ² AK ³ KFL ⁴ AD ⁵ NPEIF ⁶ DD ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQ ¹¹ GLIEEDNTEEKQSSKEKETDEK . .ADKNLVLELDDTIELE	382
EE ¹ RL ² GG ³ REN ⁴ AK ⁵ QFL ⁶ KN ⁷ KDIM ⁸ LI ⁹ QEQ ¹⁰ IREHY ¹¹ GLD ¹² NNGVVQQAEETQEEL ¹³ .EFE.E	348
SERIGQGS ¹ EN ² AK ³ NYL ⁴ AD ⁵ HD ⁶ VE ⁷ DEV ⁸ RL ⁹ KV ¹⁰ RAAY ¹¹ GIS ¹² DVPEEDLPTTEDE.QI.NILPDDSTEE	355
DERIGQG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ER ⁶ PEMEQE ⁷ IRDR ⁸ VM ⁹ AAIRAGNAGEAPALAPAPAAPEAAEA	363
DKKLGGGREN ¹ SKA ² FL ³ KN ⁴ PEI ⁵ AD ⁶ EIT ⁷ KA ⁸ IQNSM ⁹ GIEGMISGSEDDEGEE	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KAL ⁵ AD ⁶ EIT ⁷ LK ⁸ IKESIG ⁹ SNEEIMPLPDEPLEEME	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KAL ⁵ AD ⁶ EIT ⁷ LK ⁸ IKESIG ⁹ SNEEIMPLPDEPLEEME	347
DTKLGGGRD ¹ TV ² KEL ³ IK ⁴ DN ⁵ PEL ⁶ AE ⁷ ELEAK ⁸ IREKLQAK	343
GTKIGQG ¹ KNN ² NAV ³ KL ⁴ KN ⁵ PEI ⁶ AD ⁷ KL ⁸ EQEIRNTL ⁹ ASNPNSVLKATASDSNDES ¹ DVEEFSEEL	372
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GNKIGGQKNN ¹ VIRY ² FEENN ³ QIA ⁴ EIE ⁵ IRN ⁶ IREQLLTGTNGAVQ.I.EDEEEDLLES	349

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consensus

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