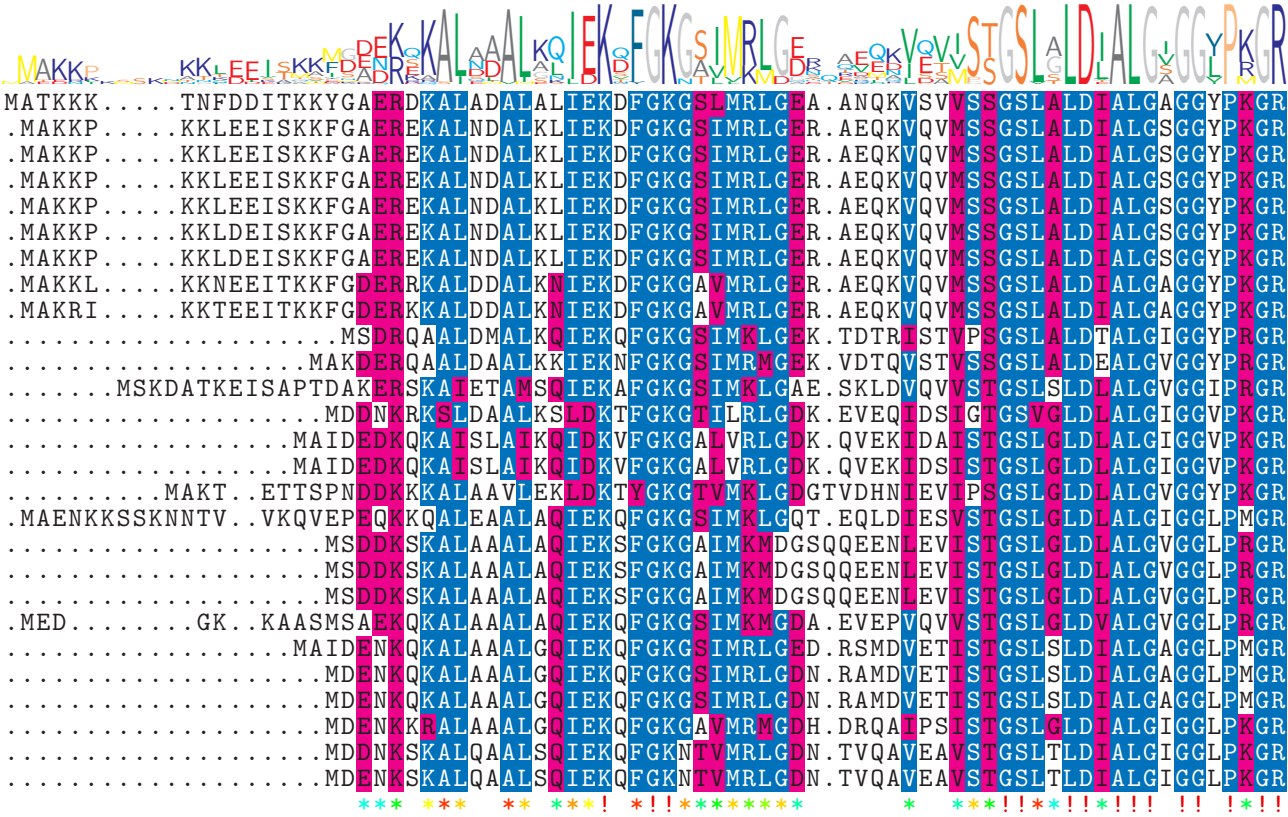


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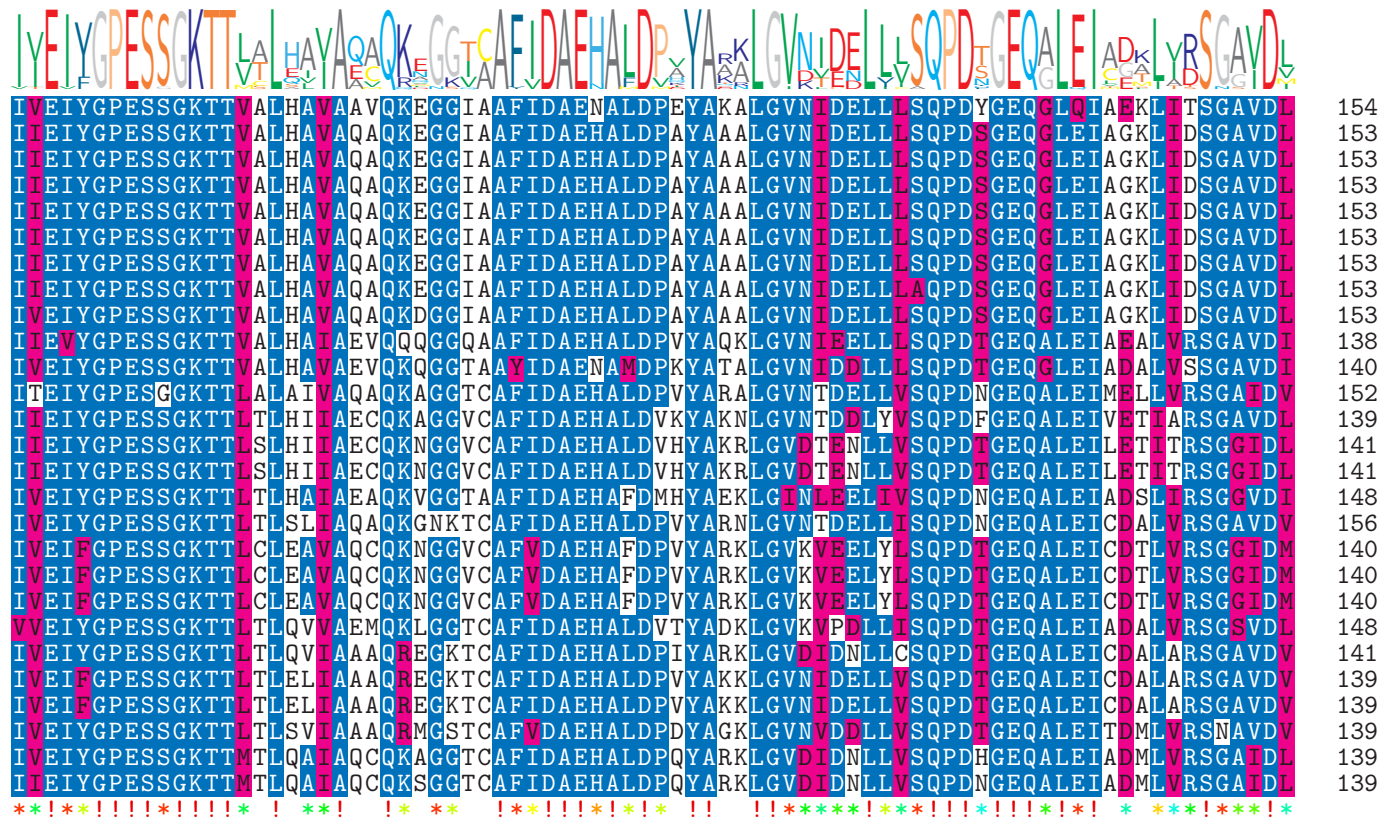


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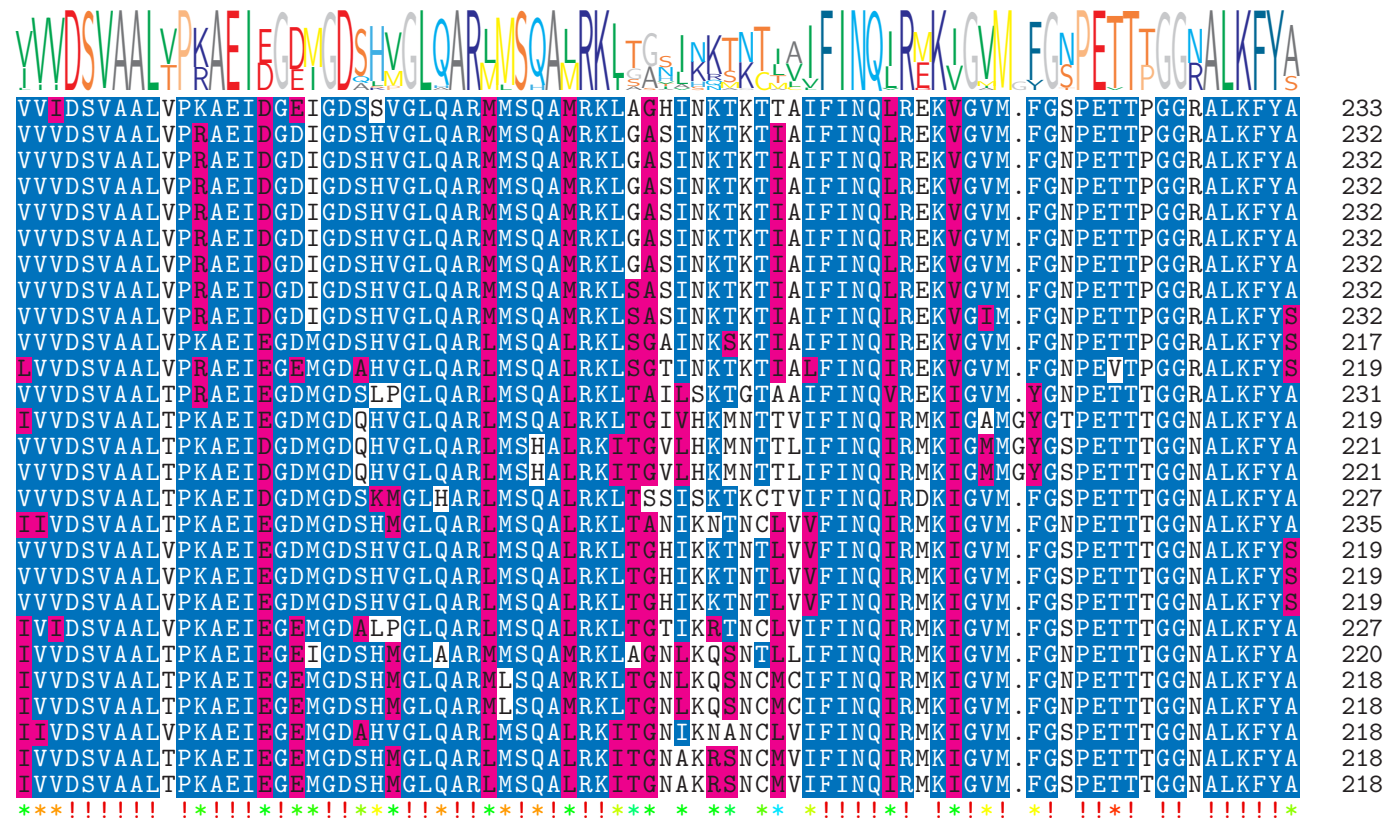
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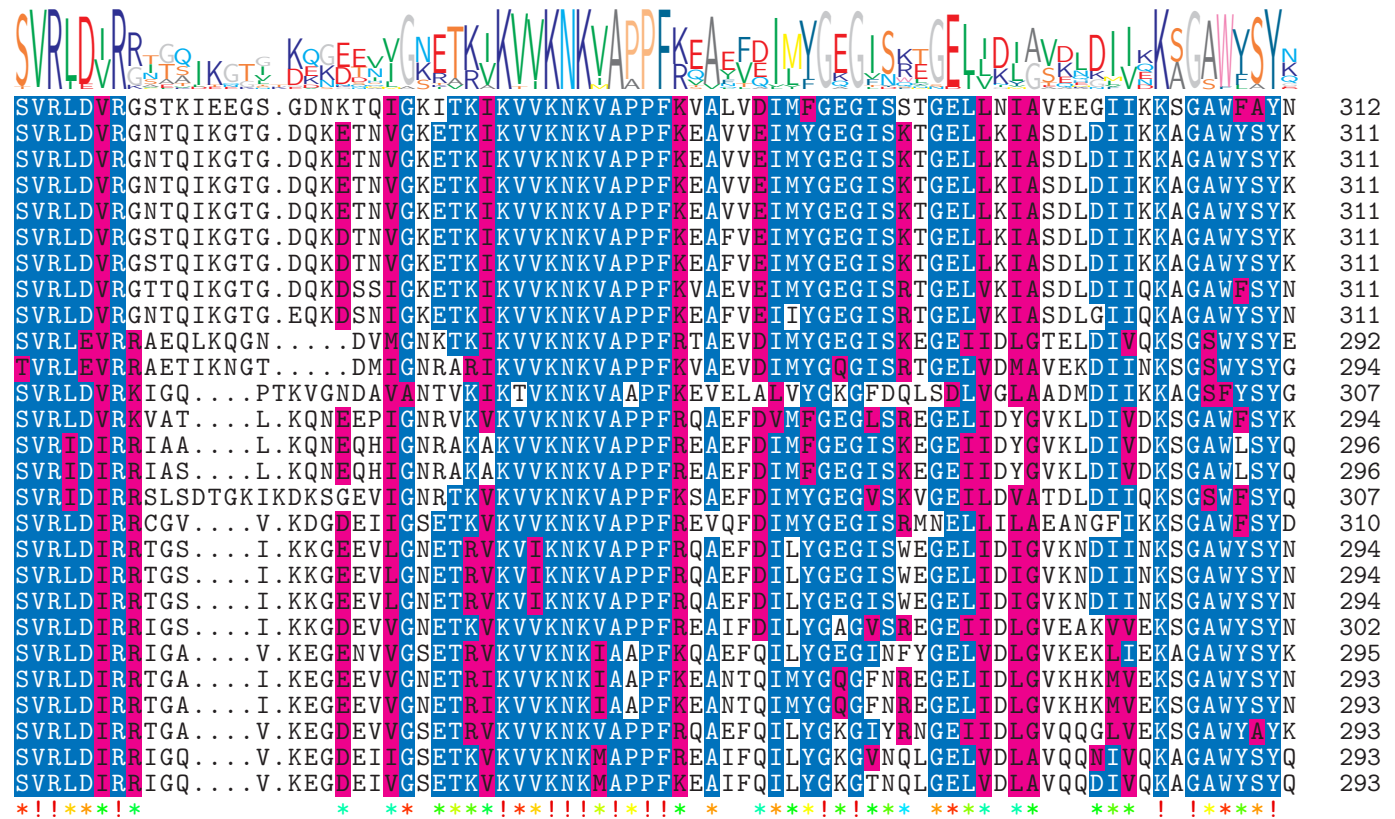
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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEI ⁶ F ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTENKKDE ¹³ ...PKKEEA ¹⁴ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEI ⁶ F ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTENKKDE ¹³ ...PKKEEA ¹⁴ ..VNEEVPLDLGDELEIE	385
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GEKIGQGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ FD ⁷ EID ⁸ DK ⁹ VR ¹⁰ VKF ¹¹ GL ¹² LEESEESAMAVASE ¹³E ¹⁴TDDLALDLNGIEIE	377
GEKIGQGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PEI ⁶ F ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQY ¹² GL ¹³ IEEDNTEEKQSSKEK ¹⁴ETDE ¹⁵ K ¹⁶ ..ADKNLVLELDDTIELE	382
EE ¹ RL ² GG ³ RENA ⁴ KQ ⁵ FL ⁶ KN ⁷ KD ⁸ IM ⁹ LM ¹⁰ IQEQ ¹¹ IREHY ¹² GL ¹³ DNNGVVQQAEETQEEL ¹⁴ .EFE ¹⁵ .E ¹⁶	348
SERIGQGS ¹ RENA ² KNYLA ³ DH ⁴ ED ⁵ VE ⁶ DE ⁷ VR ⁸ LK ⁹ VRAAY ¹⁰ GIS ¹¹ SDVPEEDLPTTEDE ¹² .QI ¹³ .NILPDDST ¹⁴EE ¹⁵	355
DERIGQG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ERP ⁶ EME ⁷ QEIR ⁸ DRV ⁹ MAAIRAGNAGEAPALAPAPAAPEAA ¹⁰ ...EA ¹¹	363
DKKLGGGREN ¹ SKA ² FL ³ IKEN ⁴ PEIA ⁵ DEIT ⁶ KA ⁷ IQNSM ⁸ GI ⁹ EGM ¹⁰ISGSEDDEG ¹¹EE ¹²	343
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DTKLGGGRD ¹ TV ² KEL ³ IK ⁴ DN ⁵ PELA ⁶ E ⁷ LE ⁸ AK ⁹ IREKLQAK ¹⁰	343
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GAKIGGQKDN ¹ VR ² VWL ³ KEN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALNG ⁸ VMH ⁹ITEG ¹⁰T ¹¹ ...QDET ¹² DGERPEE ¹³	348
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GERIGGGRD ¹ NC ² REFL ³ RENA ⁴ E ⁵ LARE ⁶ IE ⁷ ENK ⁸ VREHL ⁹ GV ¹⁰ TPM ¹¹GAVTLAEE ¹² .VE ¹³ ...ED ¹⁴	352
GEKIGGQKAN ¹ ATA ² WL ³ KN ⁴ PETA ⁵ K ⁶ IEKK ⁷ VRELLSNPN ⁸STPDFSV ⁹ ...D ¹⁰ ...DSEGVAETNEDF ¹¹	353
GDKIGGQKAN ¹ ACKYL ² KEN ³ PEIA ⁴ KT ⁵ LD ⁶ KKLREMLLNPN ⁷MQLIAETSSAA ⁸ ...DDVEFGAVPEEF ⁹	354
GDKIGGQKAN ¹ ACKYL ² KEN ³ PEIA ⁴ KT ⁵ LD ⁶ KKLREMLLNPN ⁷MQLIAETSSAA ⁸ ...DDVEFGAVPEEF ⁹	354
GSKIGGQKANA ¹ AKY ² LEEN ³ PEIG ⁴ Q ⁵ EIE ⁶ QQ ⁷ IRAKLL ⁸ VTSA ⁹NTKATPVAEDL ¹⁰ ...ADADI ¹¹	347
GNKIGGQKNN ¹ VIRY ² LEEN ³ PQIST ⁴ EIE ⁵ EAV ⁶ IREQLLTKAS ⁷DQTA ⁸ A ⁹ .HDETE ¹⁰ ...EED ¹¹ LLLES ¹²	349
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consensus

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