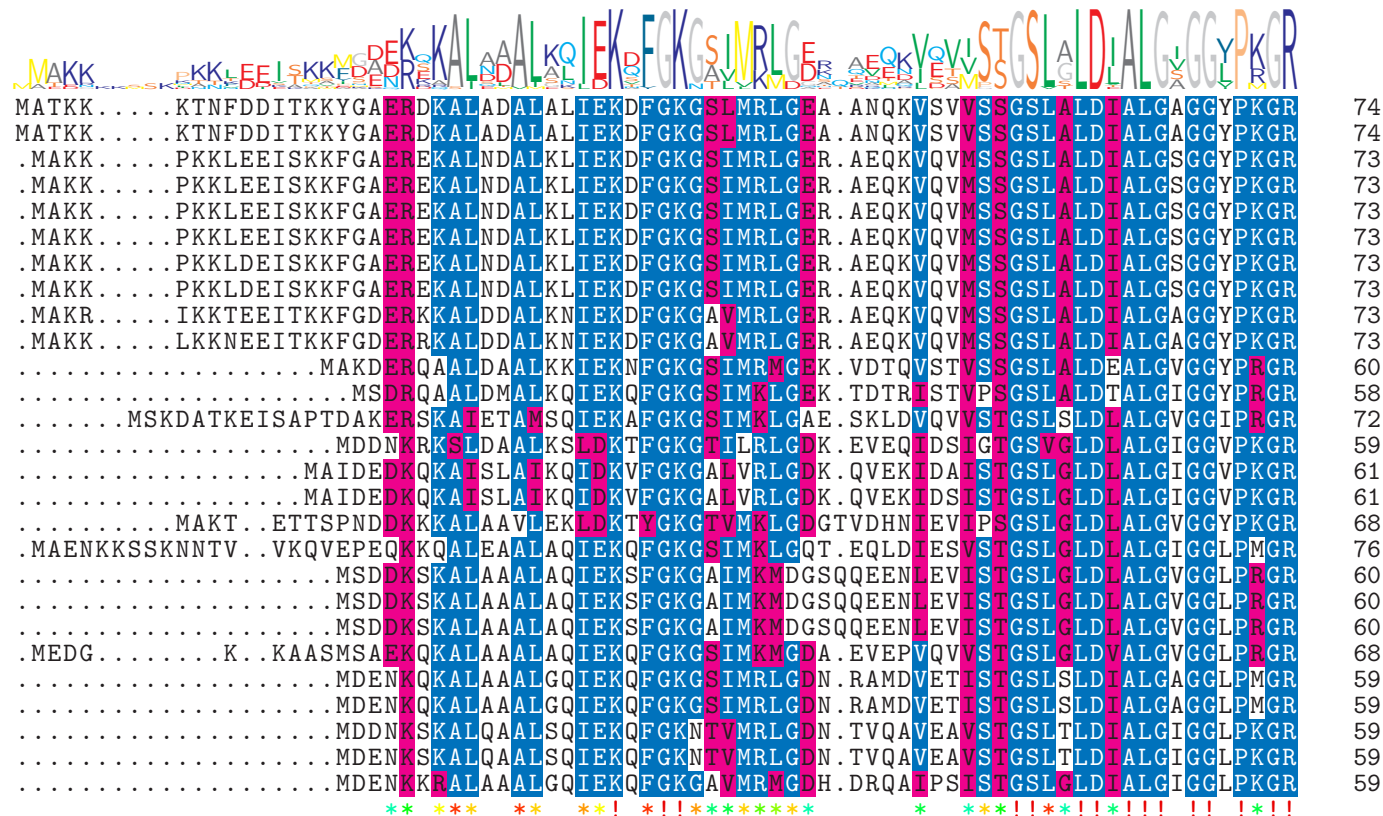


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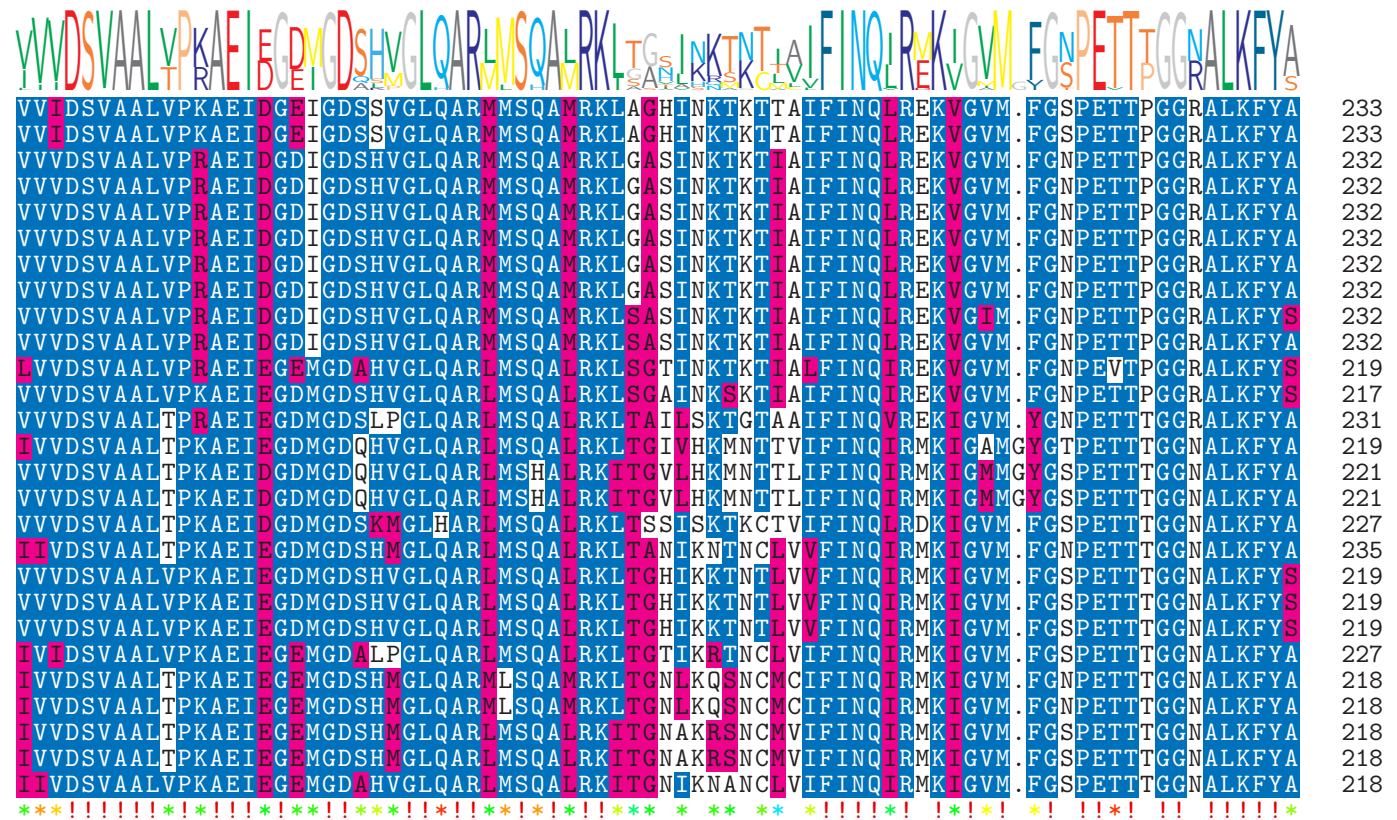
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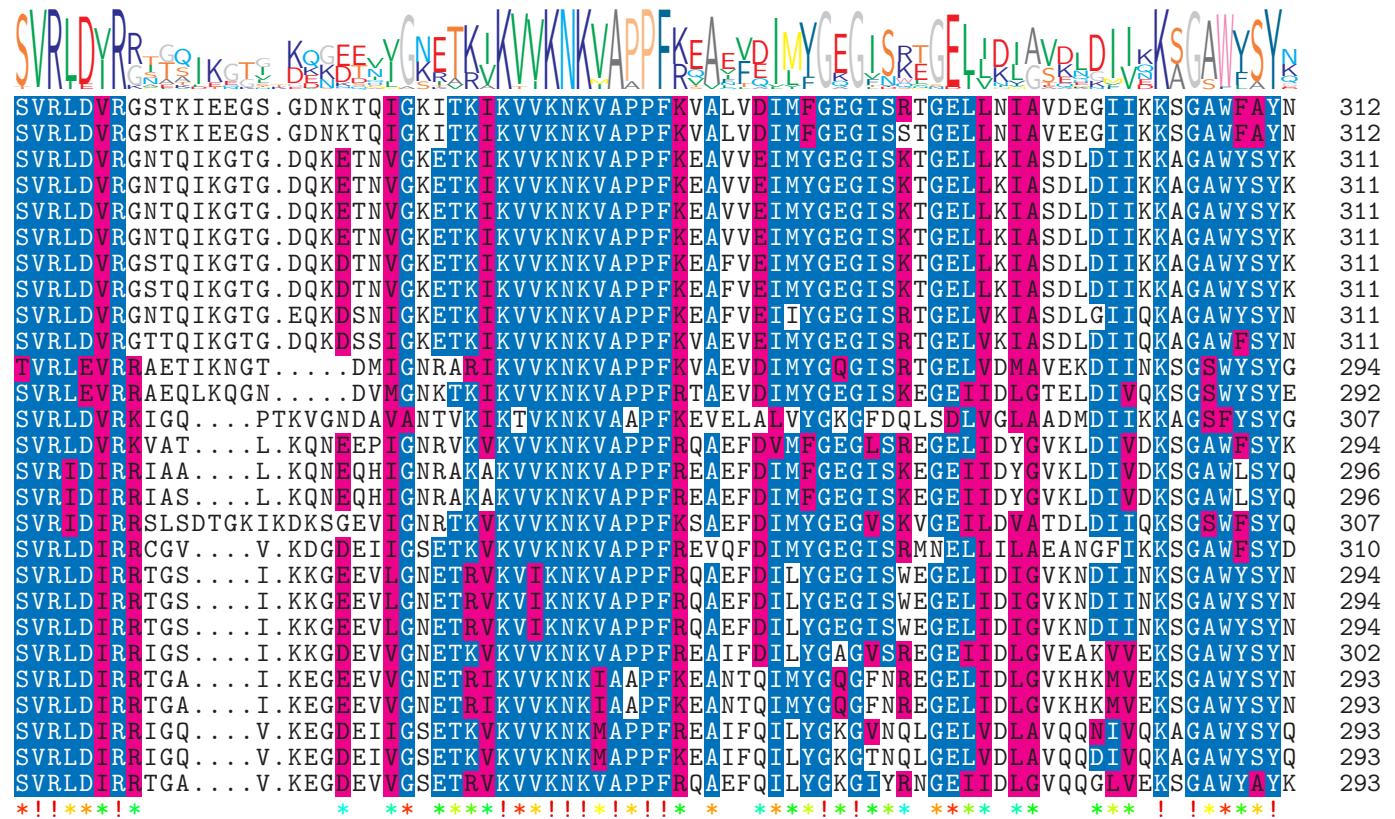
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Sequence	Score
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DEKIGQGA ⁺ EA ⁺ KA ⁺ KNYL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ EID ⁺ HKV ⁺ RAA ⁺ HGL ⁺ DDSEVAETEETETASKTKAKAKKEEKAVETE ⁺ EIELELED ⁺	387
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ EH ⁺ PEI ⁺ FD ⁺ EID ⁺ KQV ⁺ RSK ⁺ FGL ⁺ IDGEEVSEQD ⁺ TENKKDEPK ⁺ ...KEEAV ⁺ ..NEEVPLDLGDELEIE ⁺	385
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GEKIGQGS ⁺ EN ⁺ AKRYLA ⁺ DHP ⁺ QL ⁺ FD ⁺ EID ⁺ RKV ⁺ RV ⁺ KFGL ⁺ LEESEESAMAVASE ⁺ ...E.....TDD ⁺ LALDLNNGIEIE ⁺	377
SERIGQG ⁺ RENA ⁺ KNYLA ⁺ DH ⁺ DE ⁺ VE ⁺ DL ⁺ KV ⁺ RAAY ⁺ GIS ⁺ SDVPEEDLPTTEDE.QINI ⁺LPDDSTEE ⁺	355
EE ⁺ RL ⁺ GG ⁺ RENA ⁺ KQ ⁺ FL ⁺ KN ⁺ DK ⁺ IM ⁺ LM ⁺ IQE ⁺ QIREHYGL ⁺ DNNGVVQQAAETQEELEF ⁺E.E.....	348
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DK ⁺ KL ⁺ GG ⁺ RENS ⁺ KA ⁺ FL ⁺ KEN ⁺ PEI ⁺ ADEITKAIQNSMG ⁺ IEGMI ⁺ ...SGSEDD ⁺ ..EG.....EE.....	343
DK ⁺ KL ⁺ GG ⁺ RENA ⁺ KALL ⁺ KED ⁺ KALA ⁺ DEITL ⁺ KIKESIG ⁺ SNEEI ⁺ ...MPLPDE ⁺ ..PL.....EEME ⁺	347
DK ⁺ KL ⁺ GG ⁺ RENA ⁺ KALL ⁺ KED ⁺ KALA ⁺ DEITL ⁺ KIKESIG ⁺ SNEEI ⁺ ...MPLPDE ⁺ ..PL.....EEME ⁺	347
DT ⁺ KL ⁺ GG ⁺ RD ⁺ TV ⁺ KELI ⁺ DK ⁺ NP ⁺ ELAE ⁺ LEAKIREKLQAK ⁺	343
GT ⁺ KIGQ ⁺ GK ⁺ NN ⁺ AV ⁺ KL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQE ⁺ IRNTLASNPNS ⁺ ...VLKATASDSN ⁺ ...DESD ⁺ VVEEFSEEEEL ⁺ ...	372
GA ⁺ KIGQ ⁺ GK ⁺ DN ⁺ RV ⁺ WL ⁺ KEN ⁺ PEI ⁺ SDEI ⁺ DAKIRALNG ⁺ VEMHI ⁺ ...TEGTQDET ⁺ DG...ER...PEE....	348
GA ⁺ KIGQ ⁺ GK ⁺ DN ⁺ RV ⁺ WL ⁺ KEN ⁺ PEI ⁺ SDEI ⁺ DAKIRALNG ⁺ VEMHI ⁺ ...TEGTQDET ⁺ DG...ER...PEE....	348
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GN ⁺ KIGQ ⁺ GK ⁺ NN ⁺ VIRY ⁺ LEEN ⁺ PQI ⁺ STEIE ⁺ IAVIREQLLTKASD ⁺ ...QTAA ⁺ ..HDETE ⁺ ...EEDLL ⁺ ..ES.....	349
GN ⁺ KIGQ ⁺ GK ⁺ NN ⁺ VIRY ⁺ FEENN ⁺ QIA ⁺ EI ⁺ ERNIREQLLTGTN ⁺ ...GAVQ ⁺ ..I..EDE ⁺ ...EEDLL ⁺ ..LES.....	349
GS ⁺ KIGQ ⁺ GKAN ⁺ AAKYLEEN ⁺ PEI ⁺ IGQ ⁺ EIE ⁺ QQIRAKLLV ⁺ TSAN ⁺ ...TKATPVAEDL ⁺ ...ADADI ⁺	347

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consensus

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