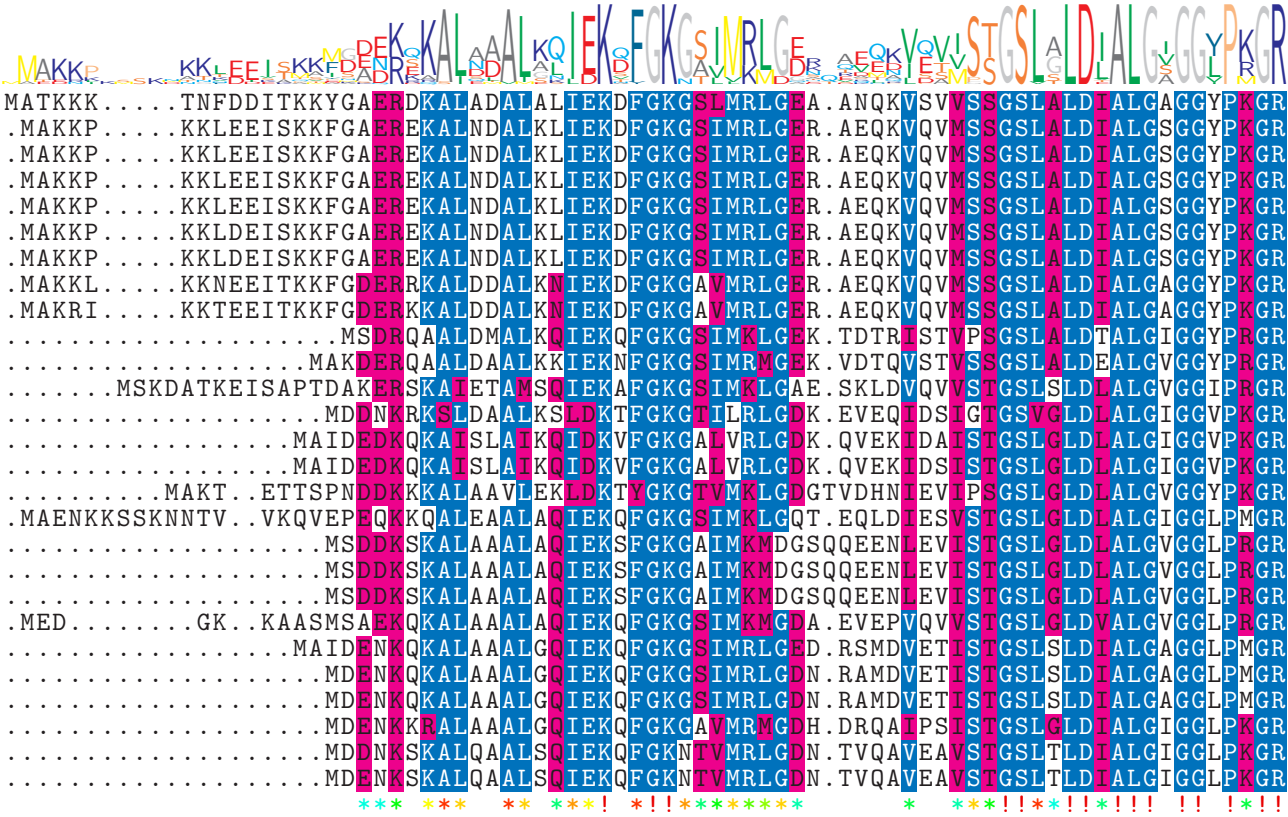


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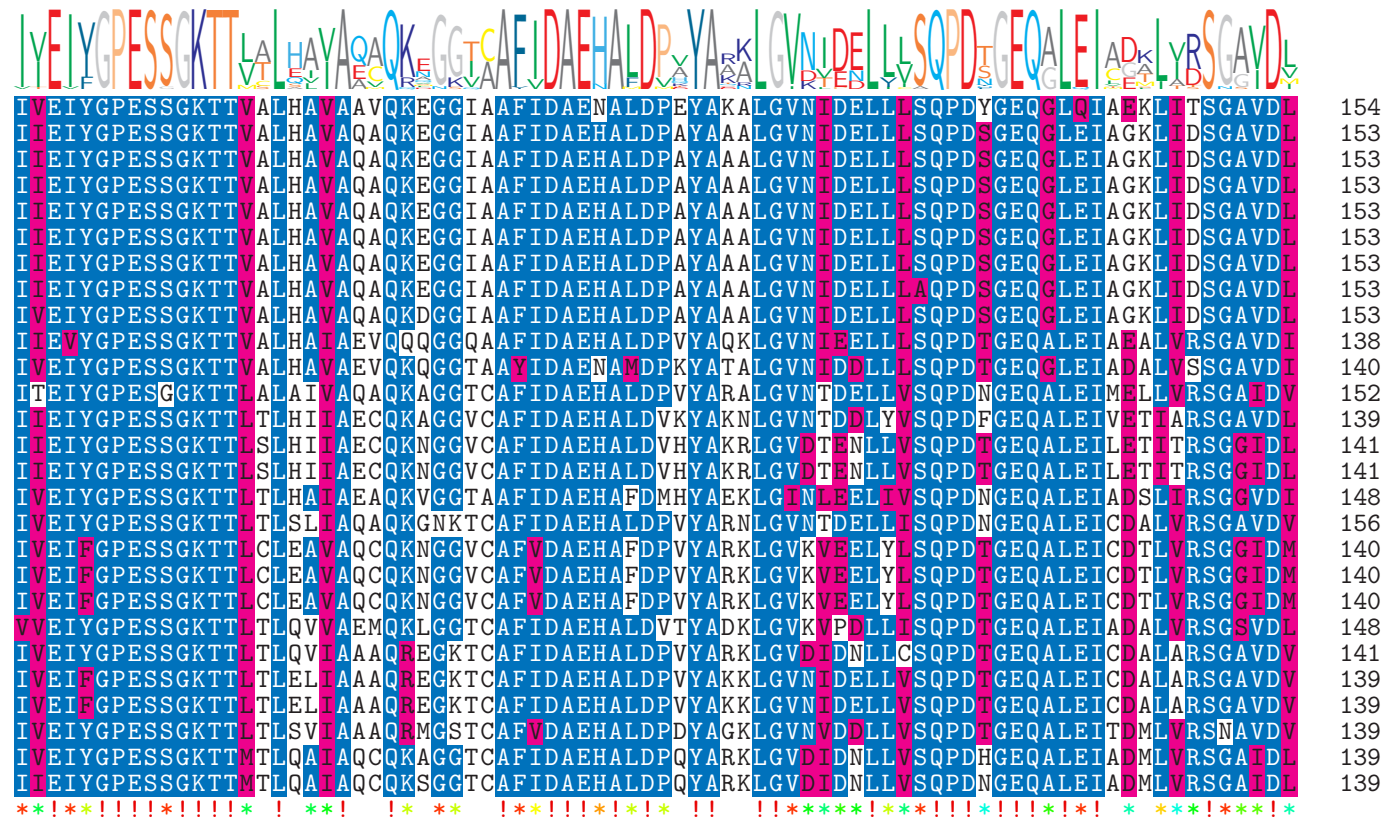


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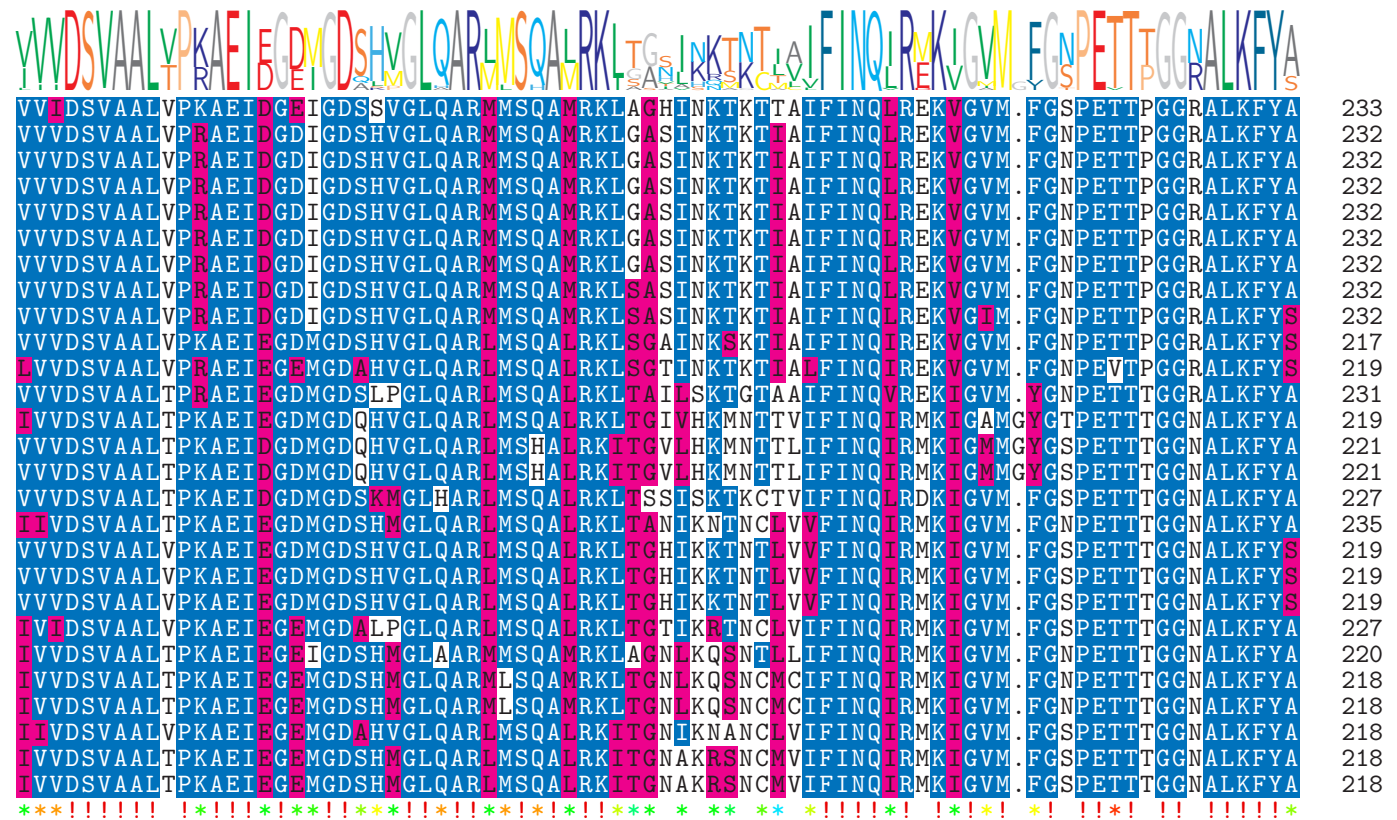
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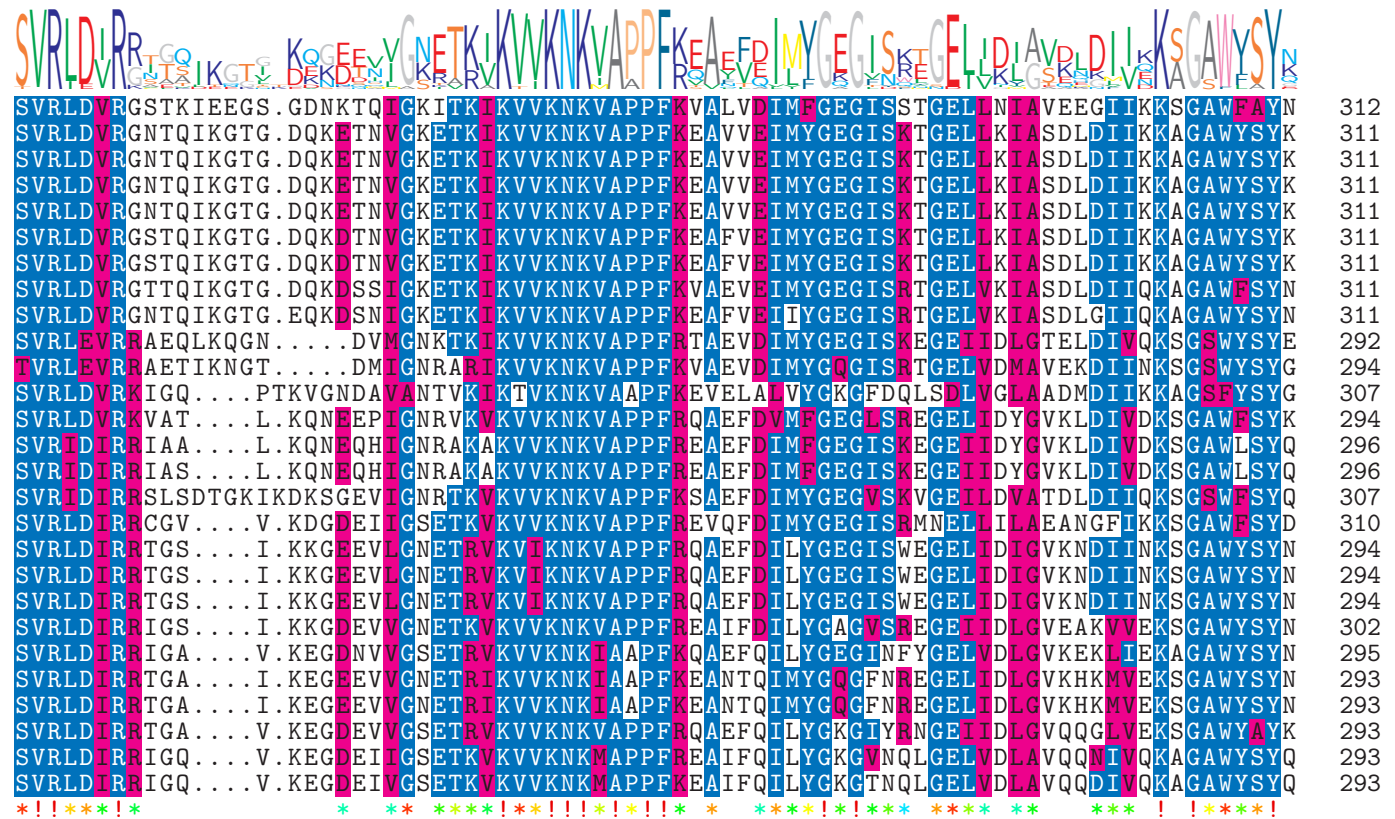
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consensus

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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EI ⁷ F ⁸ DE ⁹ ID ¹⁰ KQ ¹¹ V ¹² RS ¹³ KF ¹⁴ GLIDGEEVSEQD ¹⁵ TEN ¹⁶ KK ¹⁷ DE PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EI ⁷ F ⁸ DE ⁹ ID ¹⁰ KQ ¹¹ V ¹² RS ¹³ KF ¹⁴ GLIDGEEVSEQD ¹⁵ TEN ¹⁶ KK ¹⁷ DE PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EI ⁷ F ⁸ DE ⁹ ID ¹⁰ KQ ¹¹ V ¹² RS ¹³ KF ¹⁴ GLIDGEEVSEQD ¹⁵ TEN ¹⁶ KK ¹⁷ DE PKKEEA . . VNEEVPLDLGDELEIE	385
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GEKIGQGS ¹ EN ² AK ³ RYL ⁴ AD ⁵ HP ⁶ QL ⁷ F ⁸ DE ⁹ ID ¹⁰ DR ¹¹ KV ¹² RV ¹³ KF ¹⁴ GLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGS ¹ EN ² AK ³ KFL ⁴ AD ⁵ N ⁶ PEI ⁷ F ⁸ DD ⁹ ID ¹⁰ HK ¹¹ VR ¹² VQ ¹³ GLIEEDNTEEKQSSKEK ETDEK ADKNLVLELDDTIELE	382
EE ¹ RL ² GG ³ REN ⁴ AK ⁵ QFL ⁶ KEN ⁷ KDIM ⁸ LM ⁹ I ¹⁰ QEQ ¹¹ IRE ¹² HY ¹³ GLD ¹⁴ NNGV ¹⁵ VQ ¹⁶ QAE ¹⁷ ET ¹⁸ QEEL ¹⁹ .EFE.E	348
SERIGQGS ¹ EN ² AK ³ NYL ⁴ AD ⁵ HE ⁶ DVE ⁷ DEV ⁸ RL ⁹ KV ¹⁰ RA ¹¹ AY ¹² GISD ¹³ VPEEDLPTTEDE.QI.NILPDDST EE	355
DERIGQG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ERP ⁶ ME ⁷ QE ⁸ IR ⁹ DR ¹⁰ VMA ¹¹ IRAG ¹² NAGEAPALAPAPAAPEAA EA	363
DKKLGGG ¹ REN ² SKA ³ FL ⁴ KN ⁵ PEI ⁶ AD ⁷ EIT ⁸ KA ⁹ IQNSM ¹⁰ GIEGM ISGSEDDG EE	343
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GNKIGGQ ¹ KNN ² VIR ³ YLEEN ⁴ PQ ⁵ ISTE ⁶ IEAV ⁷ IREQLL ⁸ TKAS DQTA HDETE EEPDLLS	349

logo

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- X similar
- X ≥ 50% conserved