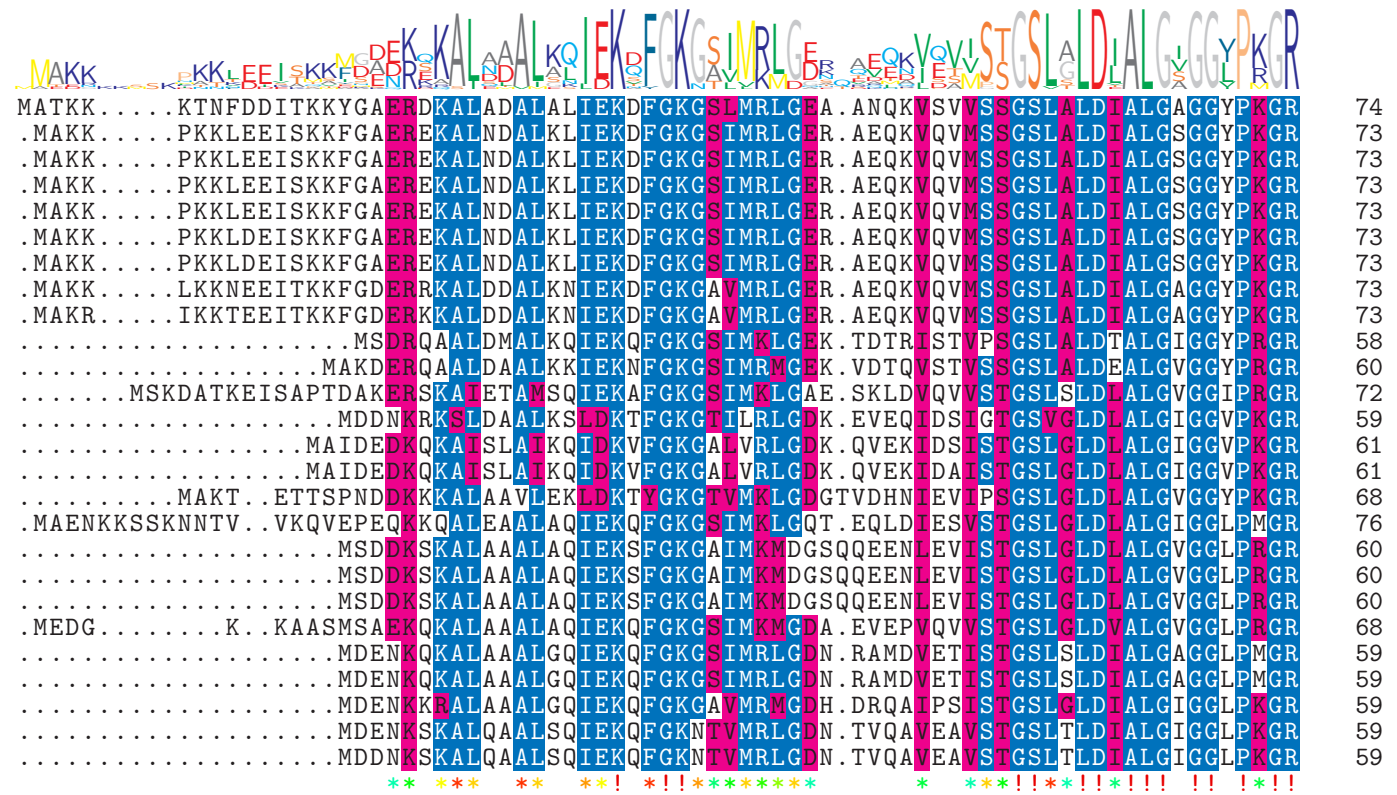


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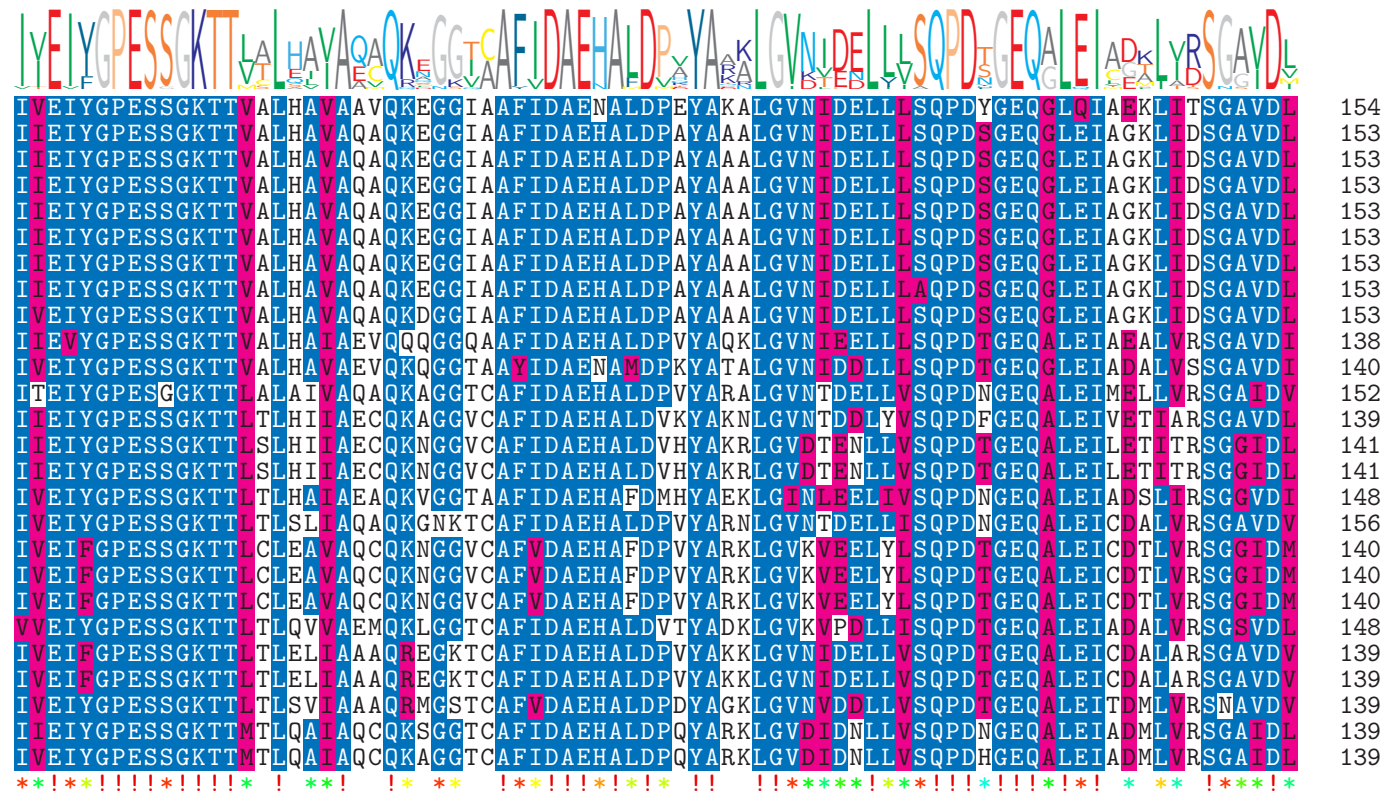
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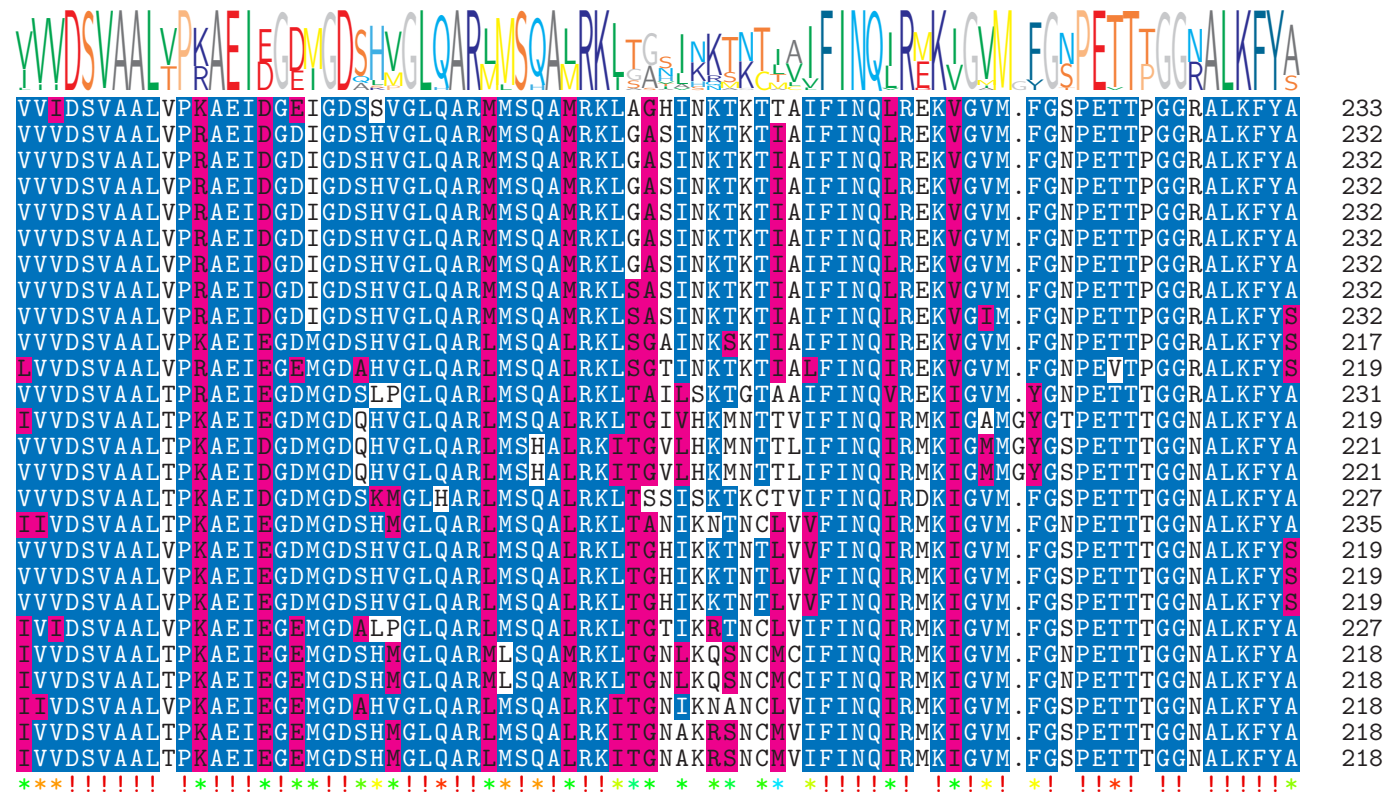
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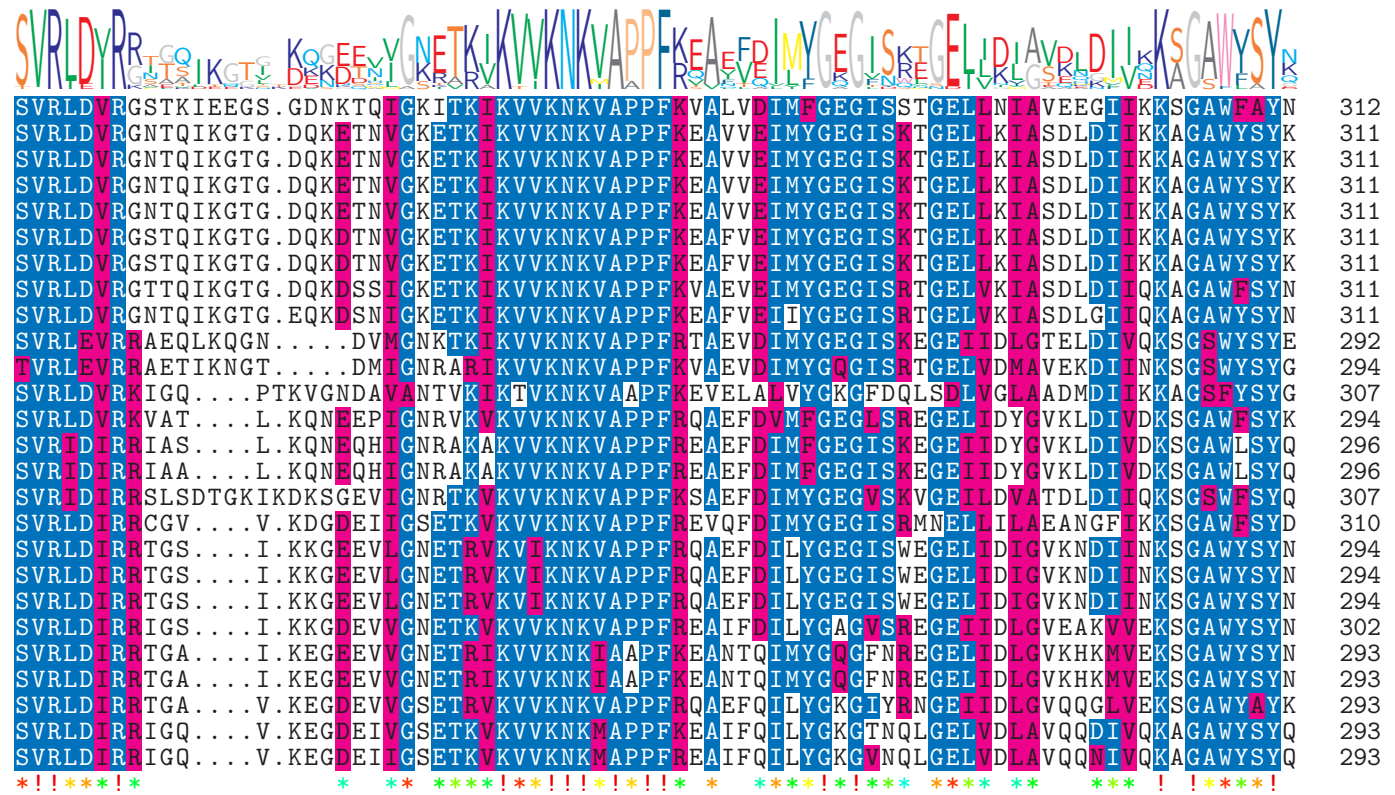
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consensus

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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FL ¹³ ID ¹⁴ GEE ¹⁵ VSE ¹⁶ QD ¹⁷ TEN ¹⁸ KK ¹⁹ DE ²⁰PK ²¹ KEEA ²² ..VNEEV ²³ PLD ²⁴ LG ²⁵ DE ²⁶ LE ²⁷ IE ²⁸	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 FL ¹³ ID ¹⁴ GEE ¹⁵ VSE ¹⁶ QD ¹⁷ TEN ¹⁸ KK ¹⁹ DE ²⁰PK ²¹ KEEA ²² ..VNEEV ²³ PLD ²⁴ LG ²⁵ DE ²⁶ LE ²⁷ IE ²⁸	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 FL ¹³ ID ¹⁴ GEE ¹⁵ VSE ¹⁶ QD ¹⁷ TEN ¹⁸ KK ¹⁹ DE ²⁰PK ²¹ KEEA ²² ..VNEEV ²³ PLD ²⁴ LG ²⁵ DE ²⁶ LE ²⁷ IE ²⁸	385
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DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AD ⁵ NPE ⁶ IF ⁷ DE ⁸ ID ⁹ HQ ¹⁰ VR ¹¹ VQ ¹² FL ¹³ ID ¹⁴ GEE ¹⁵ EIA ¹⁶ E ¹⁷SK ¹⁸ KDE ¹⁹AA ²⁰ QVDS ²¹ ..VNEEV ²² TLD ²³ LG ²⁴ DE ²⁵ LE ²⁶ IE ²⁷	381
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GEKIGQGS ¹ EN ² AK ³ KFL ⁴ AD ⁵ NPE ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQ ¹² YCL ¹³ IEED ¹⁴ NTEEK ¹⁵ QSS ¹⁶ SKEK ¹⁷ET ¹⁸ DEK ¹⁹ ..AD ²⁰ KN ²¹ LV ²² LE ²³ DD ²⁴ TIE ²⁵ LE ²⁶	382
EER ¹ L ² GG ³ GR ⁴ EN ⁵ AK ⁶ FL ⁷ KEN ⁸ KD ⁹ IM ¹⁰ LI ¹¹ Q ¹² IRE ¹³ HY ¹⁴ CL ¹⁵ DN ¹⁶ NG ¹⁷ VV ¹⁸ QQ ¹⁹ AA ²⁰ ET ²¹ QEEL ²² .EFE ²³ .E ²⁴	348
SER ¹ IG ² QGR ³ EN ⁴ AK ⁵ NYL ⁶ AD ⁷ HED ⁸ VE ⁹ LR ¹⁰ KV ¹¹ RAAY ¹² CI ¹³ SD ¹⁴ VP ¹⁵ EED ¹⁶ LP ¹⁷ TT ¹⁸ EDE ¹⁹ .QI ²⁰ .NIL ²¹ PDD ²² ST ²³EE ²⁴	355
DER ¹ IG ² QK ³ EK ⁴ TI ⁵ AY ⁶ I ⁷ AE ⁸ RP ⁹ EME ¹⁰ Q ¹¹ EIR ¹² DRV ¹³ MAA ¹⁴ IRAG ¹⁵ NAGE ¹⁶ APAL ¹⁷ APAP ¹⁸ AA ¹⁹ PEAA ²⁰ EAA ²¹ E.....	363
DKKL ¹ GG ² GR ³ EN ⁴ SKA ⁵ FL ⁶ KEN ⁷ PEI ⁸ AD ⁹ EIT ¹⁰ KAI ¹¹ QNSM ¹² CI ¹³ EGM ¹⁴IS ¹⁵ GSED ¹⁶ DE ¹⁷ ..GEE ¹⁸	343
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DTKL ¹ GG ² GR ³ AD ⁴ TV ⁵ KE ⁶ LIK ⁷ DN ⁸ PEI ⁹ AD ¹⁰ EEL ¹¹ AK ¹² IRE ¹³ KL ¹⁴ QAK ¹⁵	343
GTKIG ¹ QGG ² KNN ³ AV ⁴ KL ⁵ KEN ⁶ PEI ⁷ AD ⁸ KL ⁹ EIQ ¹⁰ EIR ¹¹ N ¹² TLAS ¹³ NP ¹⁴ N.....SVL ¹⁵ KATAS ¹⁶ DS ¹⁷ NDES ¹⁸ DV ¹⁹ ..EEF ²⁰ SEEE ²¹ L.....	372
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GAKIG ¹ QGG ² KDN ³ VR ⁴ VWL ⁵ KEN ⁶ PEI ⁷ SD ⁸ EID ⁹ AK ¹⁰ IRAL ¹¹ NG ¹² VEMH ¹³ITEGT ¹⁴ QDET ¹⁵	

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved