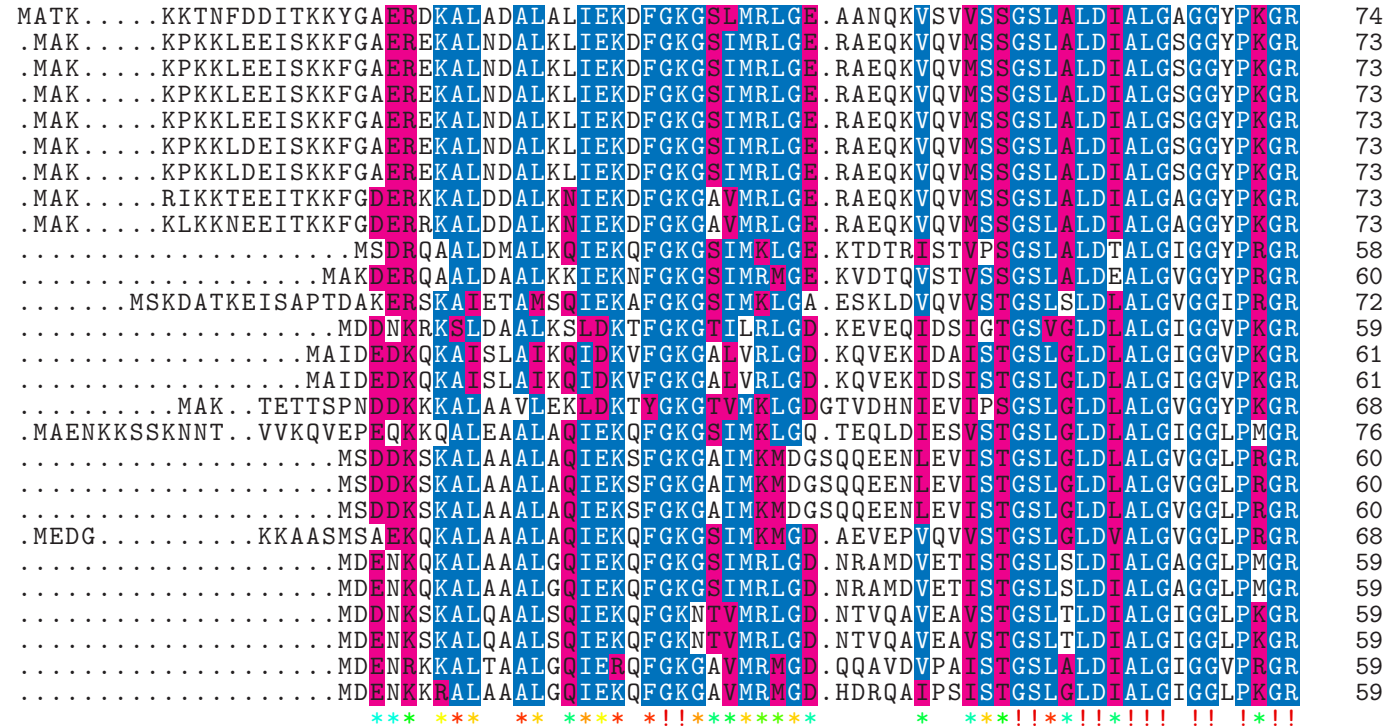


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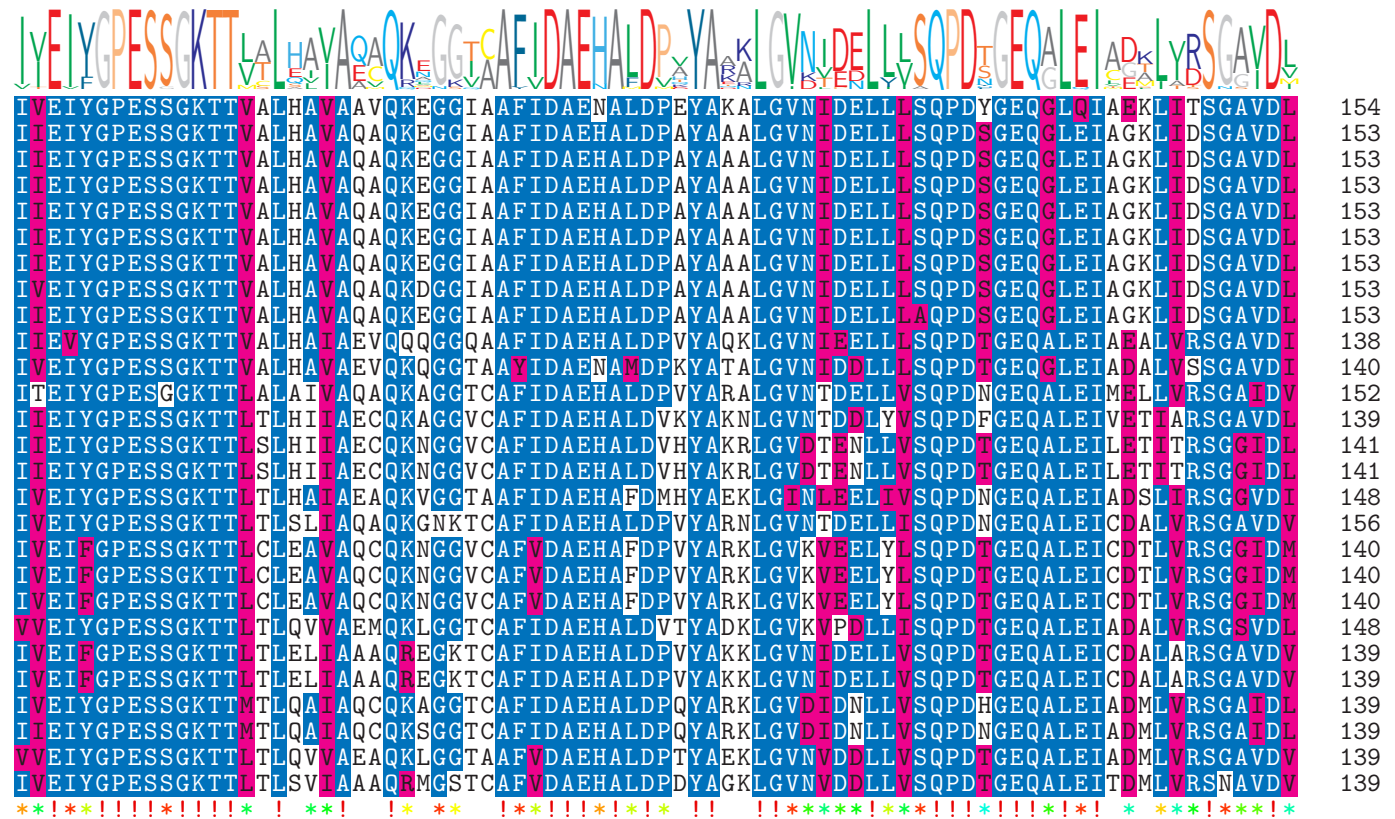
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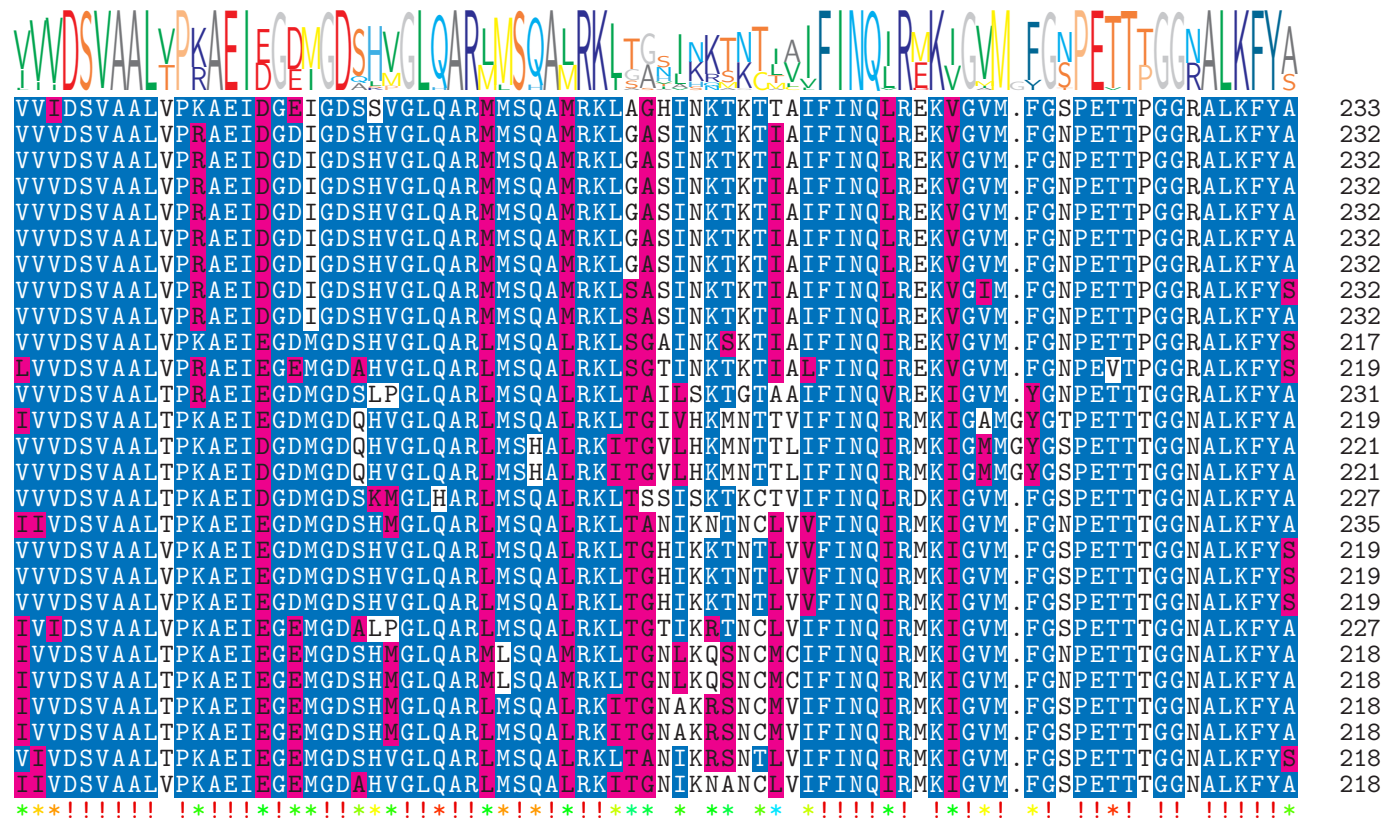
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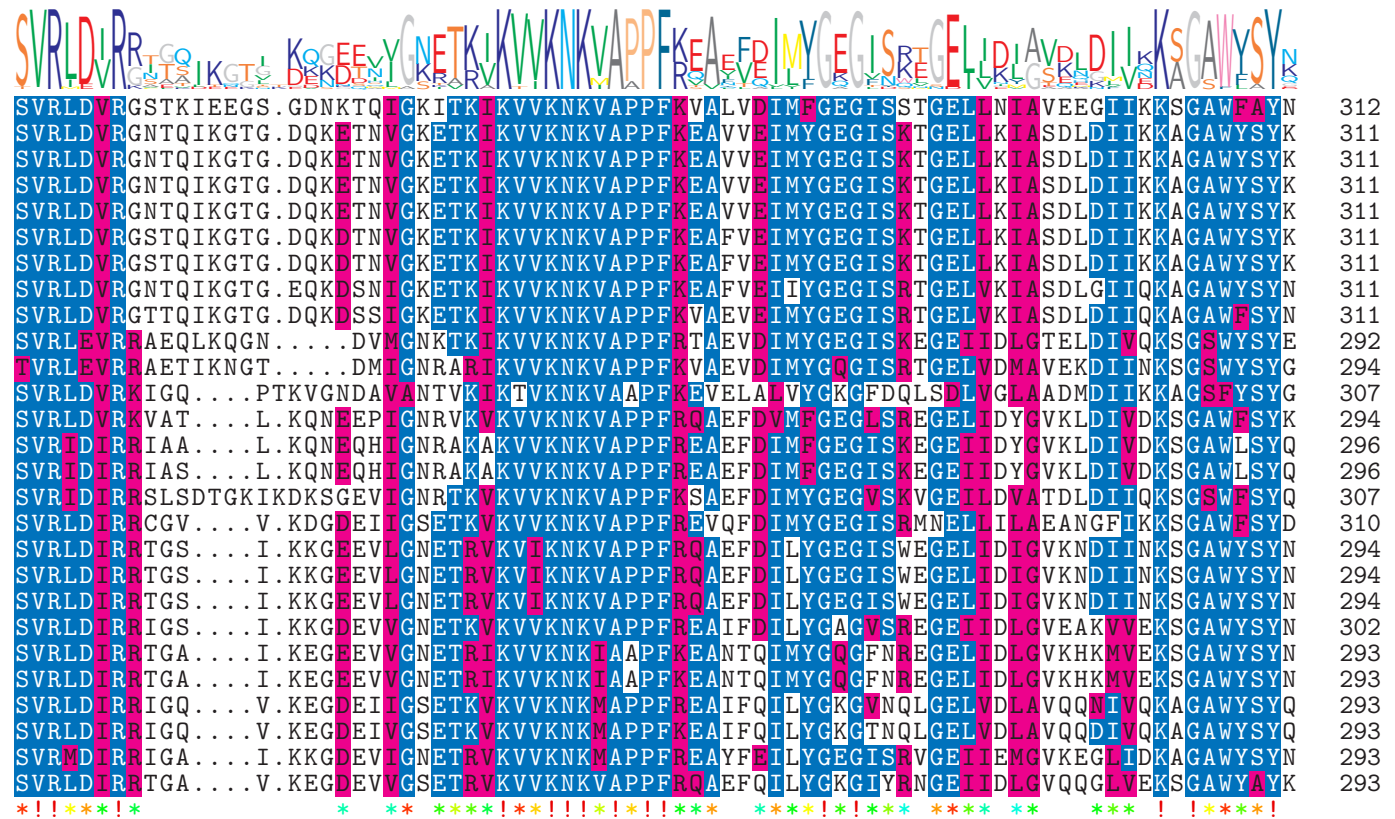
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consensus

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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 ²⁰ ...PK ²¹ KEEA ²² ..V ²³ NEEV ²⁴ PL ²⁵ DL ²⁶ GD ²⁷ ELE ²⁸ IE ²⁹	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 ²⁰ ...PK ²¹ KEEA ²² ..V ²³ NEEV ²⁴ PL ²⁵ DL ²⁶ GD ²⁷ ELE ²⁸ IE ²⁹	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 ²⁰ ...PK ²¹ KEEA ²² ..V ²³ NEEV ²⁴ PL ²⁵ DL ²⁶ GD ²⁷ ELE ²⁸ IE ²⁹	385
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GEKIGQGS ¹ EN ² AK ³ RY ⁴ LAD ⁵ HP ⁶ QL ⁷ F ⁸ DE ⁹ ID ¹⁰ DK ¹¹ VR ¹² VQ ¹³ FL ¹⁴ LEE ¹⁵ SE ¹⁶ EE ¹⁷ SA ¹⁸ MA ¹⁹ VASE ²⁰E ²¹TDD ²² LAL ²³ DL ²⁴ DN ²⁵ GI ²⁶ IE ²⁷ LE ²⁸	377
EE ¹ RL ² GQ ³ GRE ⁴ NA ⁵ KQ ⁶ FL ⁷ KE ⁸ NK ⁹ DI ¹⁰ ML ¹¹ IQ ¹² EQ ¹³ IR ¹⁴ EH ¹⁵ Y ¹⁶ GL ¹⁷ DN ¹⁸ GV ¹⁹ VQ ²⁰ QA ²¹ EET ²² QE ²³ EL ²⁴ .EFE ²⁵ .E ²⁶	348
SERIGQGRE ¹ NA ² KNY ³ LAD ⁴ HE ⁵ DVE ⁶ DEV ⁷ RL ⁸ KV ⁹ RA ¹⁰ AY ¹¹ GIS ¹² DV ¹³ PEED ¹⁴ LPT ¹⁵ TE ¹⁶ DE ¹⁷ .QI ¹⁸ .NIL ¹⁹ PDD ²⁰ ST ²¹EE ²²	355
DERIGQGRE ¹ K ² TI ³ AY ⁴ IA ⁵ ER ⁶ PE ⁷ ME ⁸ QE ⁹ IR ¹⁰ DR ¹¹ MA ¹² IR ¹³ AG ¹⁴ NAGE ¹⁵ AP ¹⁶ AL ¹⁷ AP ¹⁸ AP ¹⁹EAA ²⁰ EA ²¹	363
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DKKL ¹ GQ ² GRE ³ NA ⁴ KALL ⁵ KE ⁶ DK ⁷ AL ⁸ ADE ⁹ IT ¹⁰ LK ¹¹ IK ¹² ES ¹³ IG ¹⁴ SNEE ¹⁵ IM ¹⁶ PL ¹⁷ PDE ¹⁸ ..PLEE ¹⁹ME ²⁰	347
DKKL ¹ GQ ² GRE ³ NA ⁴ KALL ⁵ KE ⁶ DK ⁷ AL ⁸ ADE ⁹ IT ¹⁰ LK ¹¹ IK ¹² ES ¹³ IG ¹⁴ SNEE ¹⁵ IM ¹⁶ PL ¹⁷ PDE ¹⁸ ..PLEE ¹⁹ME ²⁰	347
DTKL ¹ GQ ² GR ³ DT ⁴ V ⁵ KEL ⁶ IK ⁷ DN ⁸ PE ⁹ LAE ¹⁰ ELE ¹¹ AK ¹² IRE ¹³ KL ¹⁴ QAK ¹⁵	343
GTKIGQGG ¹ KNN ² NAV ³ KL ⁴ KE ⁵ NPE ⁶ IF ⁷ AD ⁸ KL ⁹ EQ ¹⁰ IR ¹¹ NT ¹² L ¹³ ASN ¹⁴ PNS ¹⁵ VL ¹⁶ KATA ¹⁷ ..SDSN ¹⁸DESD ¹⁹ VEEF ²⁰ SE ²¹ EEL ²²	372
GAKIGQGG ¹ KDN ² VR ³ VWL ⁴ KE ⁵ NPE ⁶ IS ⁷ DE ⁸ IDA ⁹ KIR ¹⁰ AL ¹¹ NG ¹² VEM ¹³ HITE ¹⁴ GT ¹⁵ QD	

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved