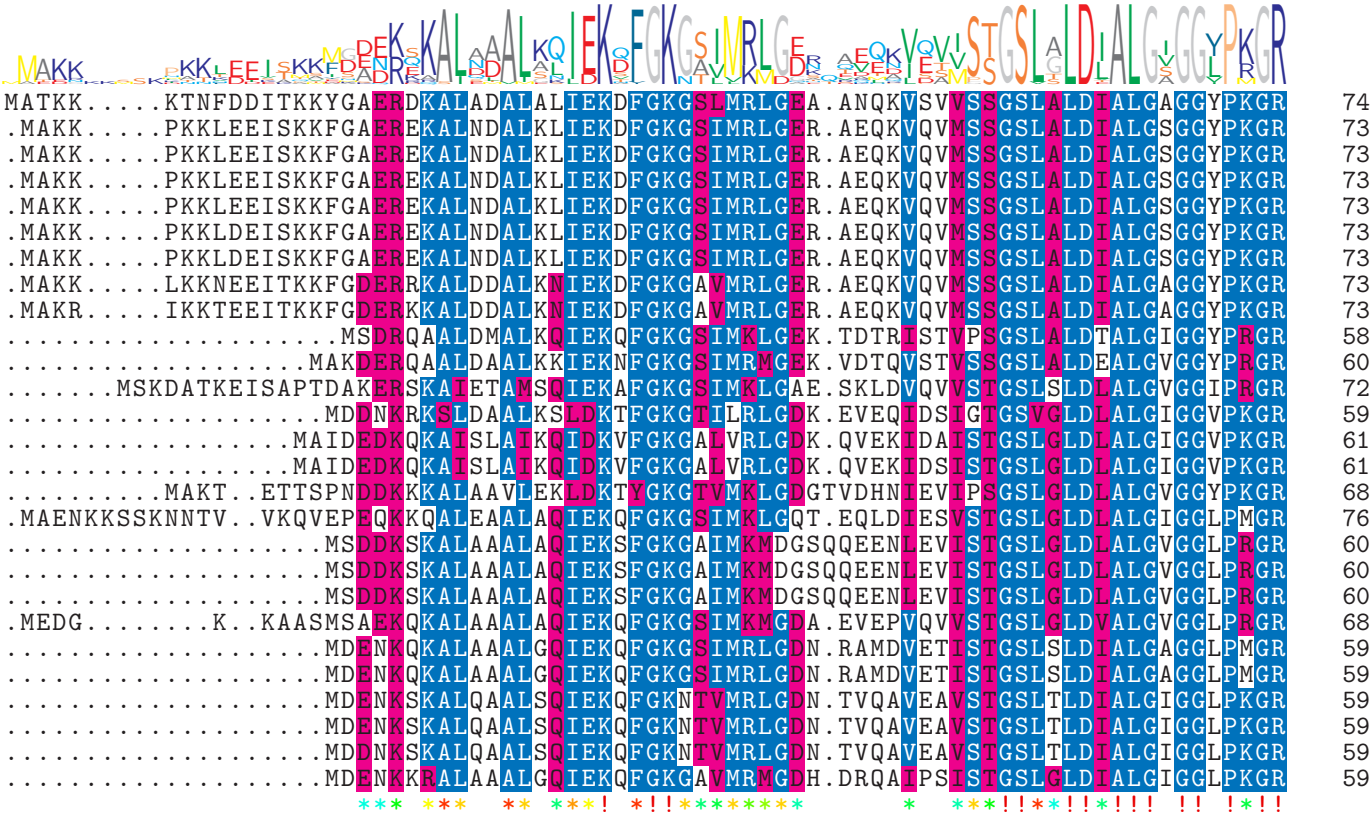


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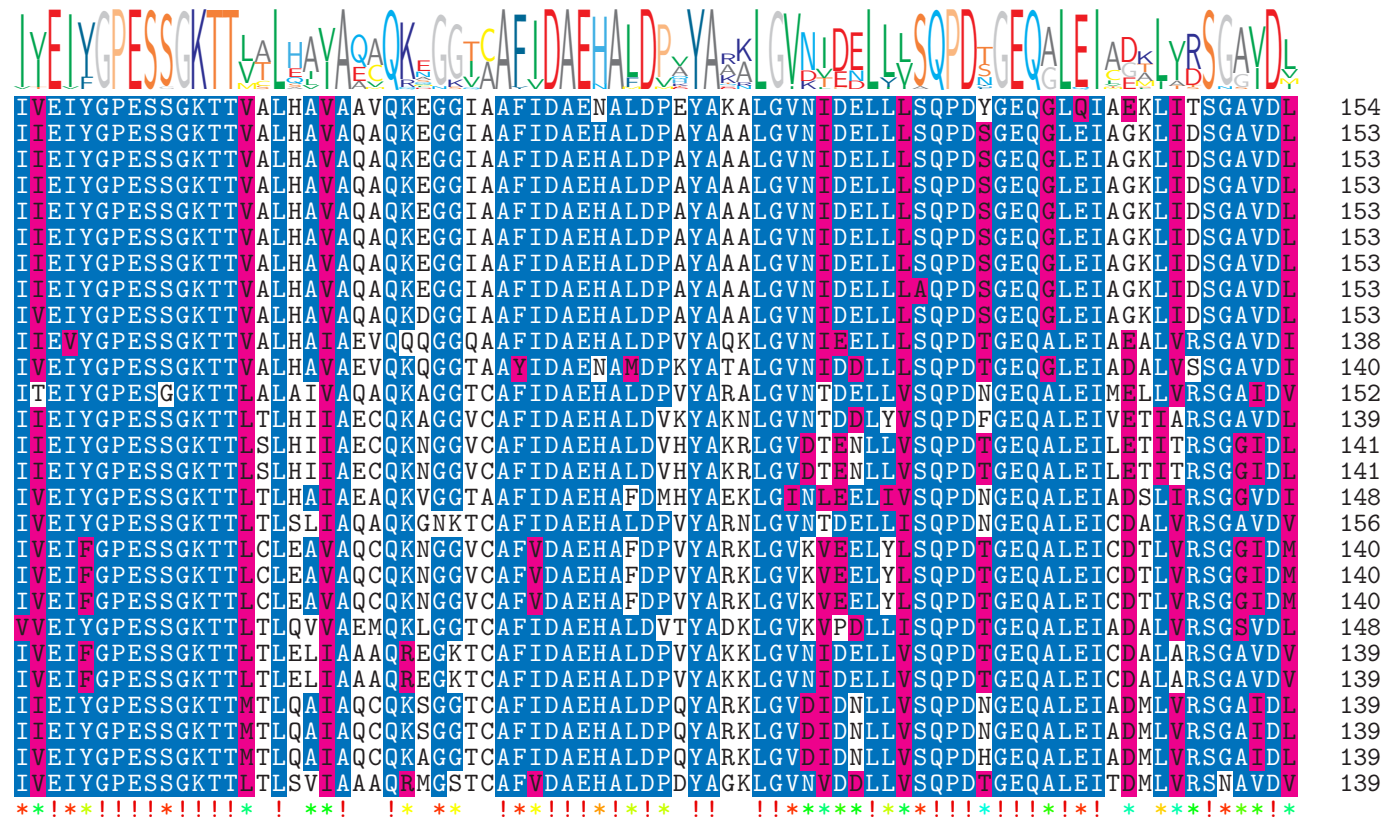
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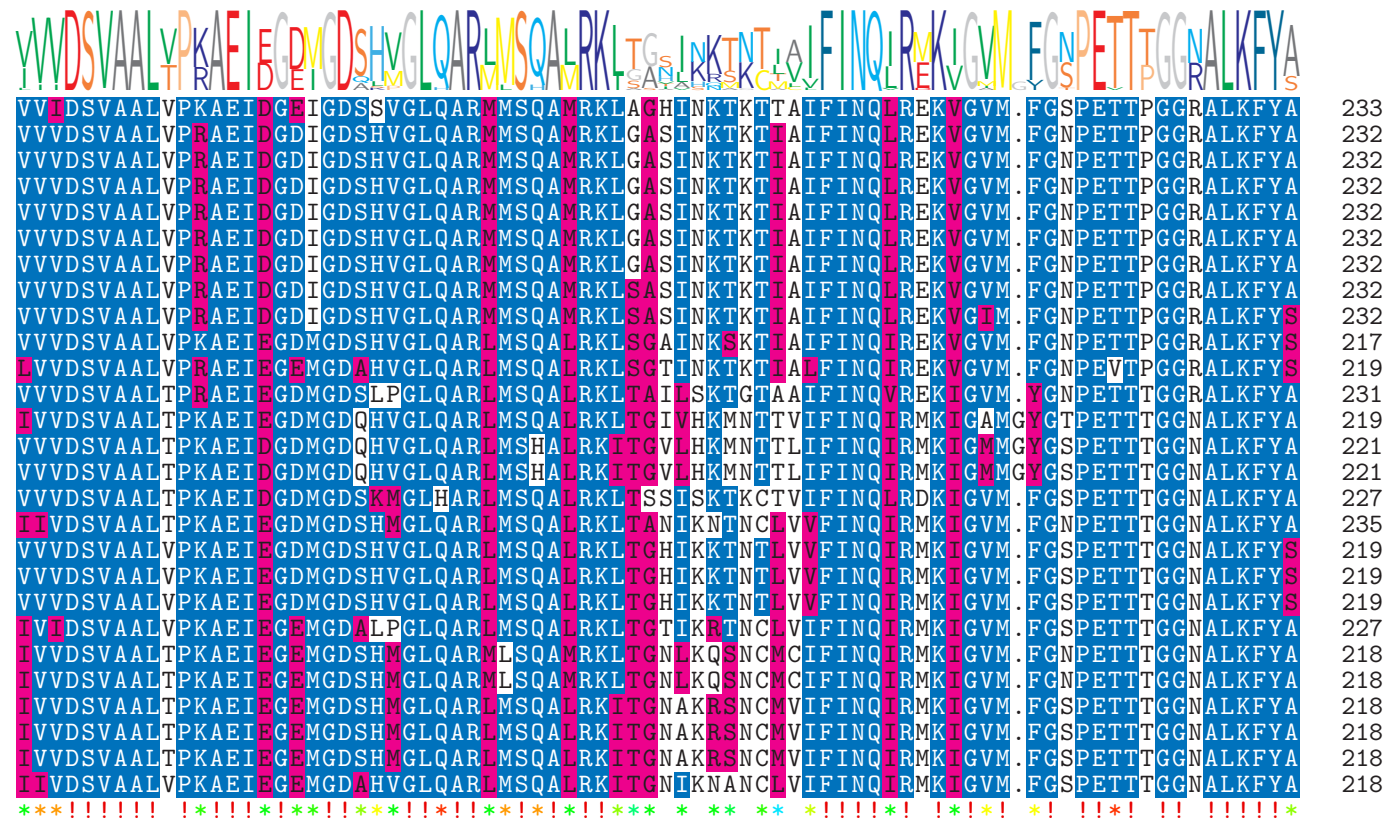
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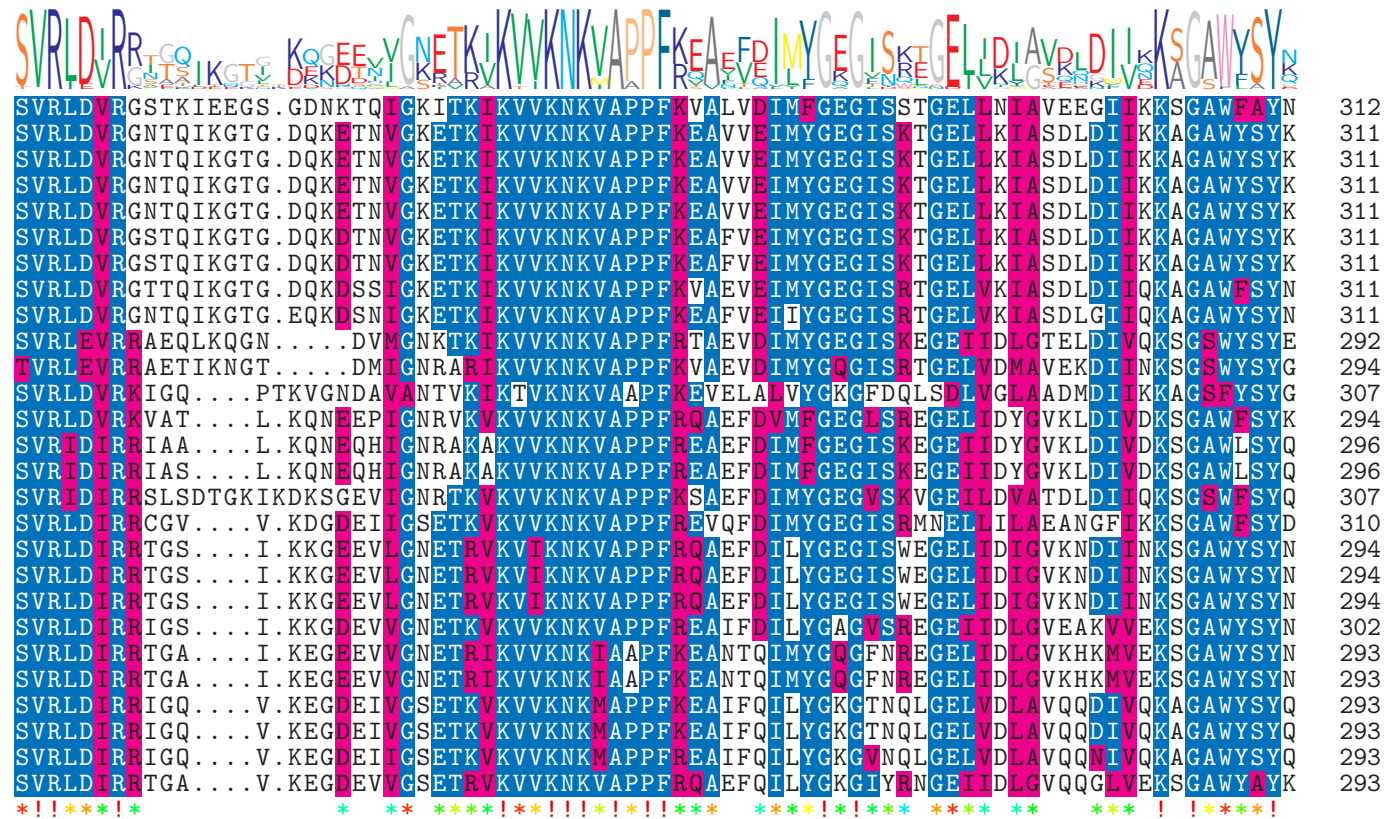
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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FG ¹³ LIDGEEVSEQDTE ¹⁴ .NKKD ¹⁵ E ¹⁶PKKEEA ¹⁷ ..VNEEVPLDLGDEL ¹⁸	382
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GEKIGQGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PE ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQ ¹² YGL ¹³ IEEDNTEEKQSS ¹⁴ .KEK ¹⁵ETDEK ¹⁶ ..ADKNLVLELDDTI ¹⁷	379
EE ¹ RL ² GG ³ RE ⁴ NA ⁵ KQ ⁶ FL ⁷ KN ⁸ KD ⁹ IM ¹⁰ LI ¹¹ QE ¹² QI ¹³ RE ¹⁴ HY ¹⁵ GL ¹⁶ DNNGVVQQQAEE ¹⁷ .TQEEL ¹⁸ .E ¹⁹ .FE ²⁰ .E ²¹	348
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DKKLGGGREN ¹ SKA ² FL ³ KN ⁴ PE ⁵ IA ⁶ DE ⁷ IT ⁸ KA ⁹ IQ ¹⁰ NSM ¹¹ GI ¹² EGMISGS ¹³ ..EDDEGE ¹⁴ ..E ¹⁵	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DE ⁶ IT ⁷ LK ⁸ IKES ⁹ IG ¹⁰ SNEEIMPL ¹¹ ..PDEPLE ¹² ..EME ¹³	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DE ⁶ IT ⁷ LK ⁸ IKES ⁹ IG ¹⁰ SNEEIMPL ¹¹ ..PDEPLE ¹² ..EME ¹³	347
DTKLGGGRD ¹ TV ² KEL ³ IK ⁴ DN ⁵ PE ⁶ LA ⁷ E ⁸ LE ⁹ AK ¹⁰ IREKLQAK ¹¹	343
GTKIGQG ¹ KNN ² AVK ³ WL ⁴ KN ⁵ PE ⁶ IA ⁷ DK ⁸ LE ⁹ QE ¹⁰ IR ¹¹ NTL ¹² ASN ¹³ PNSVLK ¹⁴ ..ATASDSND ¹⁵ ESDVEEFSE ¹⁶EEL ¹⁷	372
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GERIGQGRD ¹ NC ² REFL ³ RENA ⁴ E ⁵ LAR ⁶ E ⁷ IEN ⁸ KV ⁹ REHL ¹⁰ GV ¹¹ TPMGAV ¹² ..TLAEEVEED ¹³	352
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GDKIGQG ¹ KAN ² ACKYL ³ KN ⁴ PE ⁵ IAKT ⁶ L ⁷ DKKL ⁸ REMLLN ⁹ PENMQLI ¹⁰ ..AETSSAAD ¹¹ VEFGAVPE ¹²EF ¹³	354
GNKIGQG ¹ KNN ² VIRY ³ FEENT ⁴ QIA ⁵ E ⁶ E ⁷ IE ⁸ RN ⁹ IREQLLT ¹⁰ TGTNGAV ¹¹ ..Q ¹² .I ¹³ .EDEE ¹⁴ EPD ¹⁵ ..LLE ¹⁶S ¹⁷	349
GNKIGQG ¹ KNN ² VIRY ³ FEENN ⁴ QIA ⁵ E ⁶ E ⁷ IE ⁸ RN ⁹ IREQLLT ¹⁰ TGTNGAV ¹¹ ..Q ¹² .I ¹³ .EDEE ¹⁴ EPD ¹⁵ ..LLE ¹⁶	

logo

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consensus									

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-  similar
-  ≥ 50% conserved