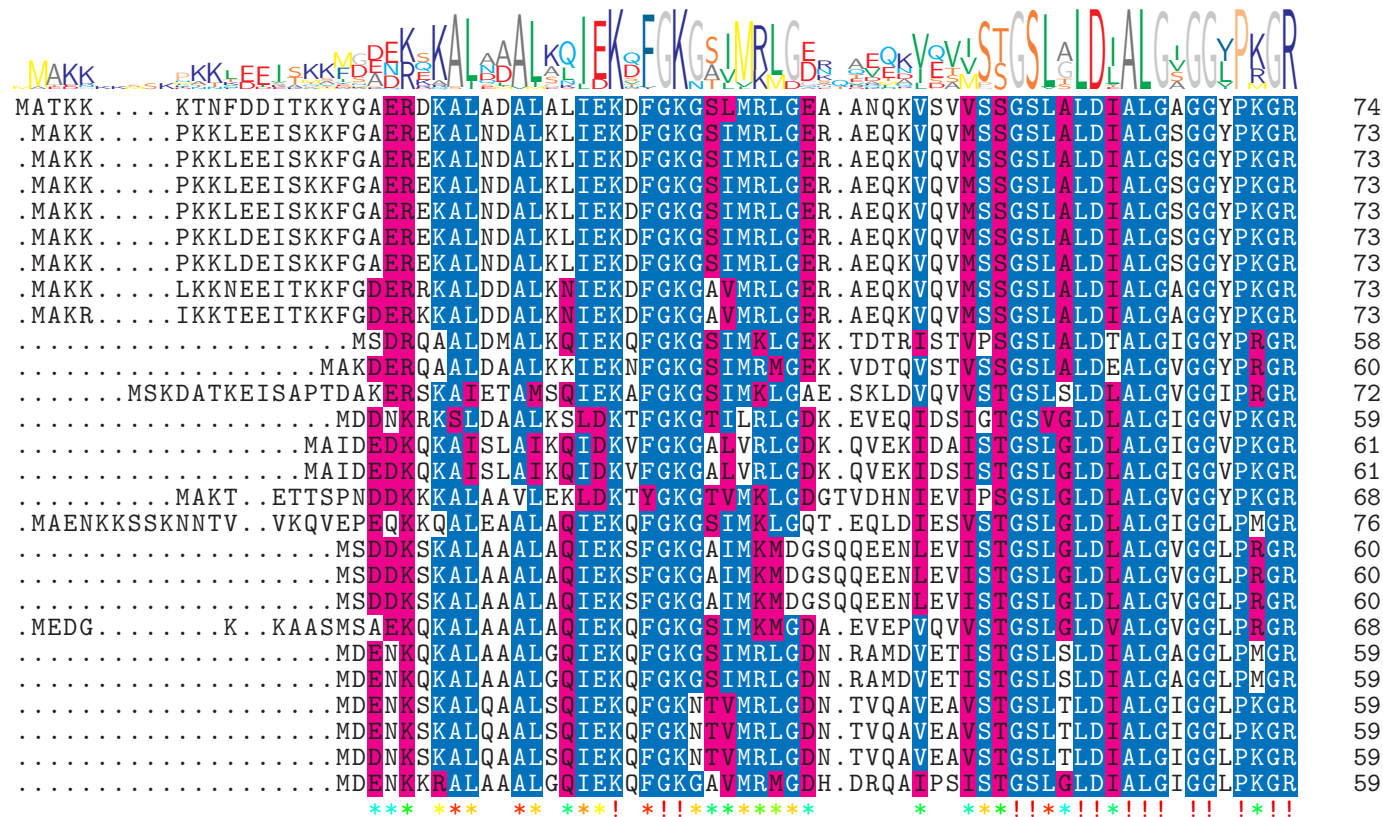


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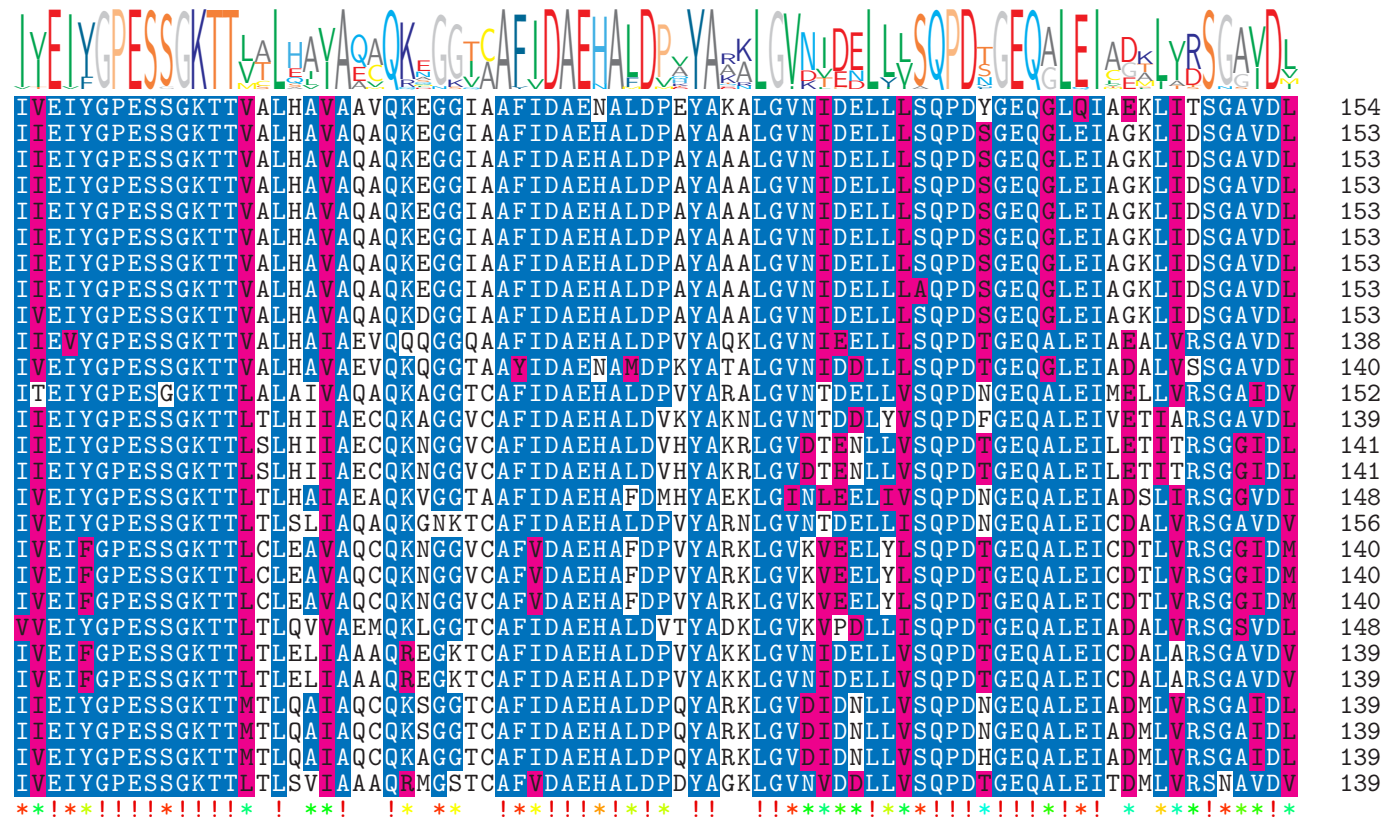
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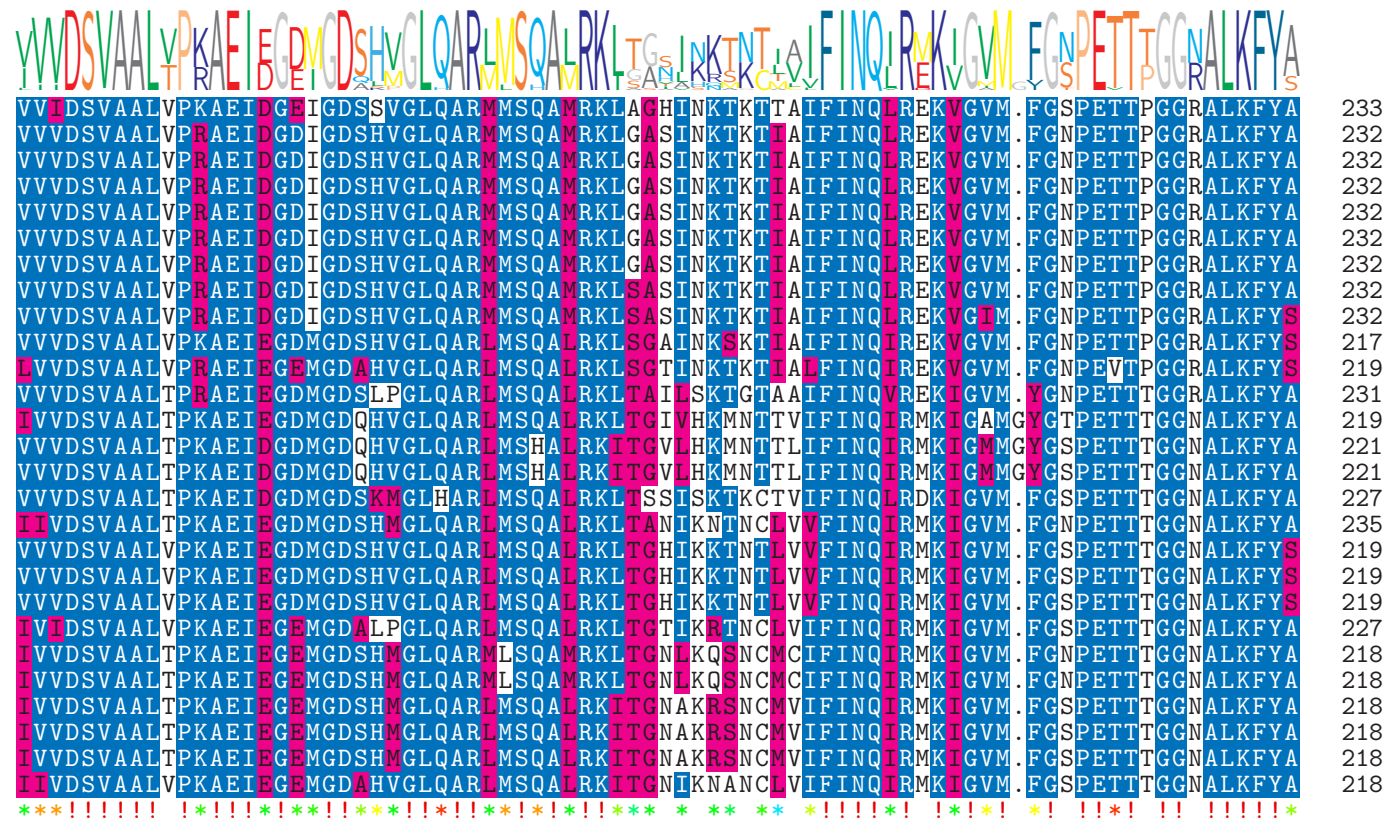
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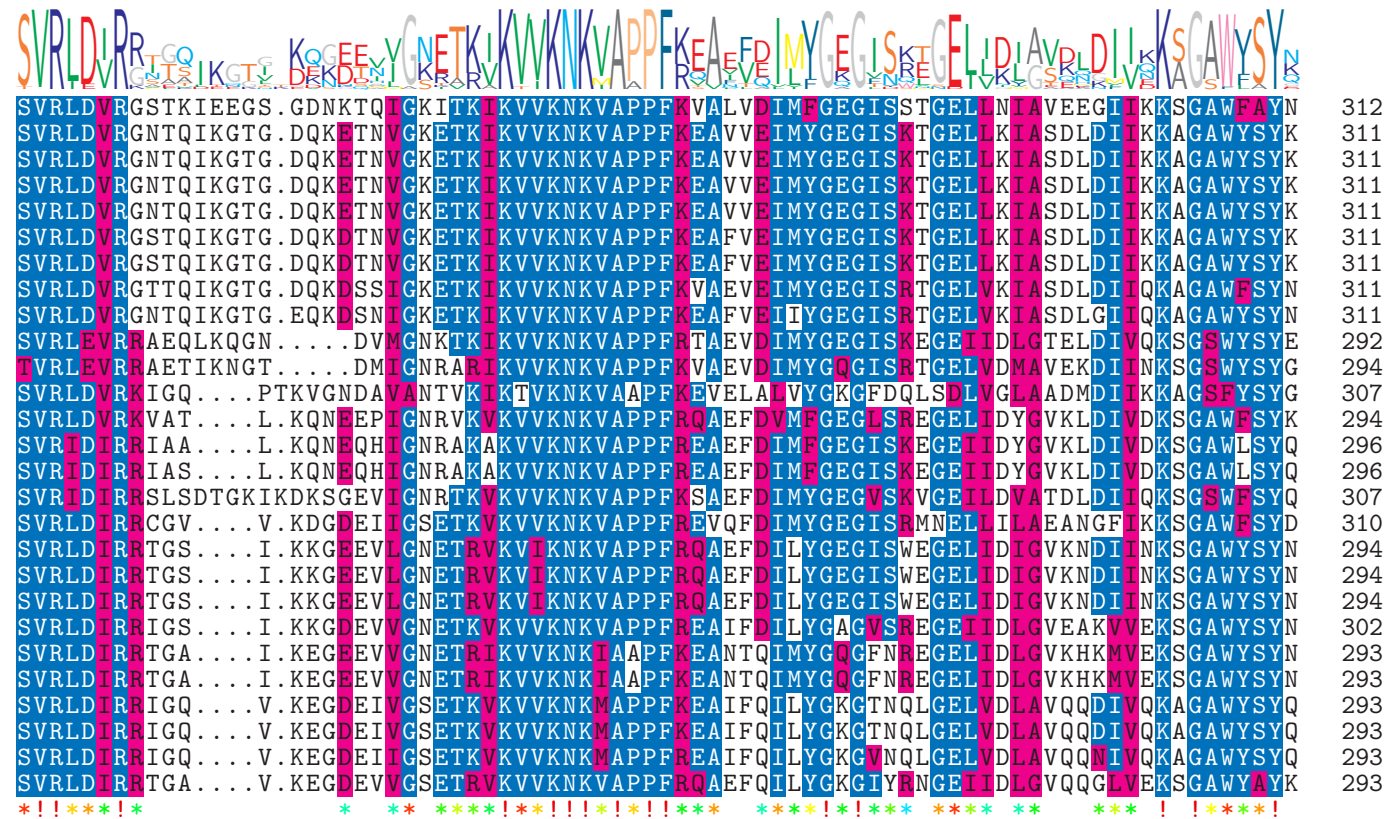
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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ VFA ⁷ EID ⁸ HQ ⁹ VR ¹⁰ VQF ¹¹ GL ¹² IDGEEAAE ¹³SKKD ¹⁴ E ¹⁵VAQVDS ¹⁶ ..VNEEVTLDLGDEL ¹⁷	378
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GEKIGQGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ FD ⁷ EID ⁸ RK ⁹ VR ¹⁰ VK ¹¹ FL ¹² LEESEESAMAV ¹³ .ASE ¹⁴E ¹⁵TDDLALDLNGI ¹⁶	374
GEKIGQGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PE ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQY ¹² GL ¹³ IEEDNTEEKQSS ¹⁴ .KEK ¹⁵ETDEK ¹⁶ ..ADKNLVLELDDTI ¹⁷	379
EE ¹ RL ² GG ³ RENA ⁴ KQ ⁵ FL ⁶ KN ⁷ KD ⁸ IM ⁹ LI ¹⁰ QE ¹¹ QI ¹² RE ¹³ HY ¹⁴ GL ¹⁵ DNNGVVQQQAEE ¹⁶ .TQEEL ¹⁷ .E ¹⁸ .FE ¹⁹ .E ²⁰	348
SERIGGG ¹ RENA ² KNYLA ³ DH ⁴ ED ⁵ VE ⁶ DE ⁷ VR ⁸ LK ⁹ VRAAY ¹⁰ GIS ¹¹ SDVPEEDLPTTE ¹² .DE ¹³ .QI ¹⁴ .N ¹⁵ ..ILPDDST ¹⁶EE ¹⁷	355
DERIGGG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ER ⁶ PE ⁷ ME ⁸ QE ⁹ IR ¹⁰ DRV ¹¹ MAA ¹² IRAGNAGEAPALAPAPAAPEAAEA ¹³	363
DKKLGGG ¹ RENS ² KA ³ FL ⁴ KN ⁵ PEIA ⁶ DEIT ⁷ KA ⁸ IQNSM ⁹ GIE ¹⁰ GMISGS ¹¹ ..EDDEGE ¹² ..E ¹³	343
DKKLGGG ¹ RENA ² KALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKES ⁸ IG ⁹ SNEEIMPL ¹⁰ ..PDEPLE ¹¹ ..EME ¹²	347
DKKLGGG ¹ RENA ² KALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKES ⁸ IG ⁹ SNEEIMPL ¹⁰ ..PDEPLE ¹¹ ..EME ¹²	347
DTKLGGGR ¹ DT ² V ³ KEL ⁴ IK ⁵ DN ⁶ PELA ⁷ E ⁸ LE ⁹ AK ¹⁰ IREKLQAK ¹¹	343
GTKIGQG ¹ KNN ² AVK ³ WL ⁴ KN ⁵ PEIA ⁶ DK ⁷ LE ⁸ QE ⁹ IR ¹⁰ NTL ¹¹ ASN ¹² PNSVLK ¹³ ..ATASDSND ¹⁴ ESD ¹⁵ VVEEFSE ¹⁶EEL ¹⁷	372
GAKIGGQ ¹ KDN ² VR ³ VL ⁴ KN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALN ⁹ GVEMHITEG ¹⁰ ..TQDET ¹¹GERPE ¹²E ¹³	348
GAKIGGQ ¹ KDN ² VR ³ VL ⁴ KN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALN ⁹ GVEMHITEG ¹⁰ ..TQDET ¹¹GERPE ¹²E ¹³	348
GAKIGGQ ¹ KDN ² VR ³ VL ⁴ KN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALN ⁹ GVEMHITEG ¹⁰ ..TQDET ¹¹GERPE ¹²E ¹³	348
GERIGGG ¹ RD ² NC ³ REFL ⁴ RENA ⁵ E ⁶ LAR ⁷ EI ⁸ EN ⁹ KV ¹⁰ REHL ¹¹ GV ¹² TPMGAV ¹³ ..TLAEEVEED ¹⁴	352
GDKIGQG ¹ KAN ² ACKYL ³ KN ⁴ PEIA ⁵ AKT ⁶ L ⁷ DKKL ⁸ REMLLN ⁹ PENMQLI ¹⁰ ..AETSSAAD ¹¹ VEFGAVPE ¹²EF ¹³	354
GDKIGGQ ¹ KAN ² ACKYL ³ KN ⁴ PEIA ⁵ AKT 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 EI ⁷ ERN ⁸ IREQLLT ⁹ TGTNGAV ¹⁰ ..Q ¹¹ .I ¹² .EDEE ¹³ EPD ¹⁴ ..LLE ¹⁵S ¹⁶	349
GNKIGQG ¹ KNN ² VIRY ³ FEENN ⁴ QIA ⁵ E ⁶ EI ⁷ ERN ⁸ IREQLLT ⁹ TGTNGAV ¹⁰ ..Q ¹¹ .I ¹² .EDEE ¹³ EPD ¹⁴ ..LLE ¹⁵S ¹⁶	349
GNKIGQG ¹ KNN ² VIRY ³ LEEN ⁴ PQIST ⁵ EI ⁶ EAV ⁷ IREQLLT ⁸ KASDQTA ⁹ ..A ¹⁰ .HDETEE	

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consensus

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