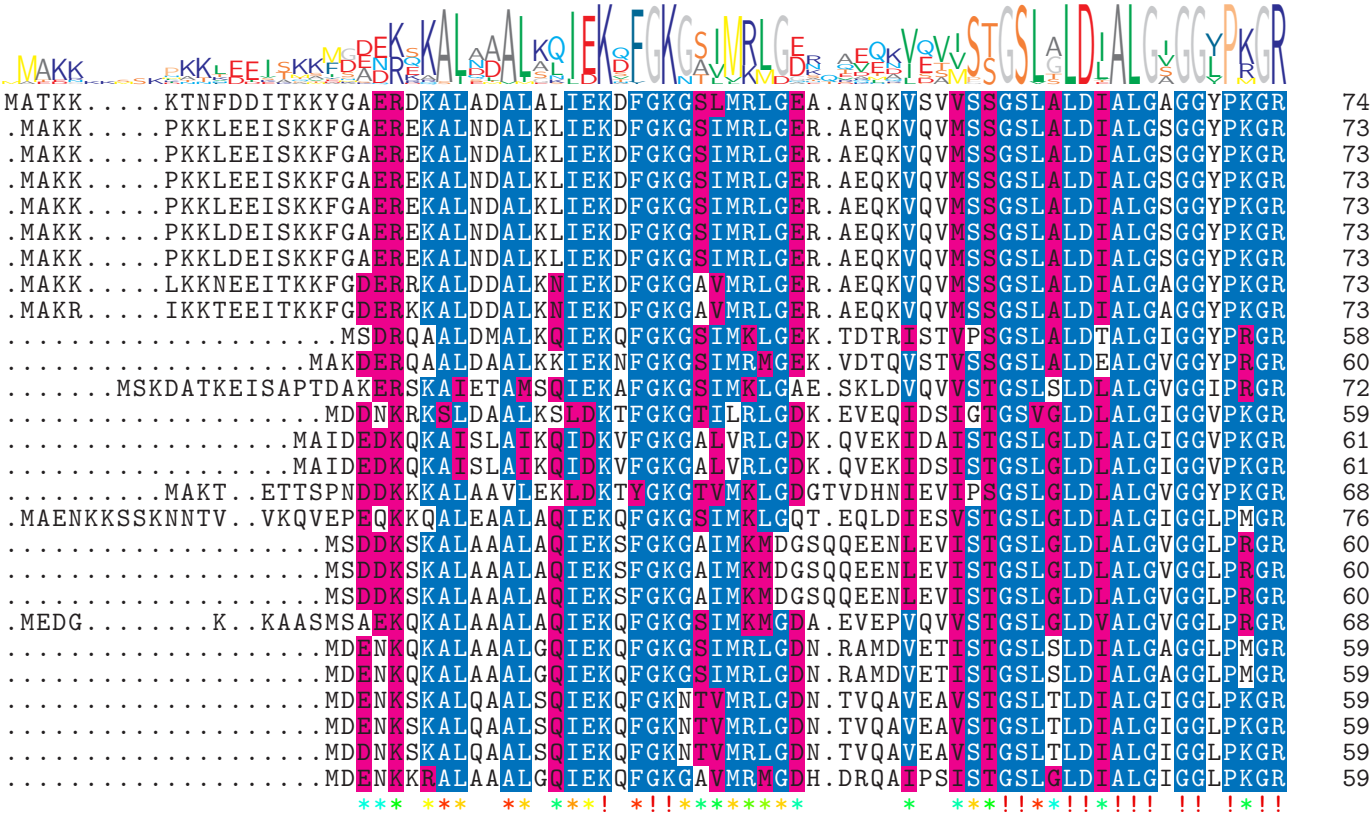


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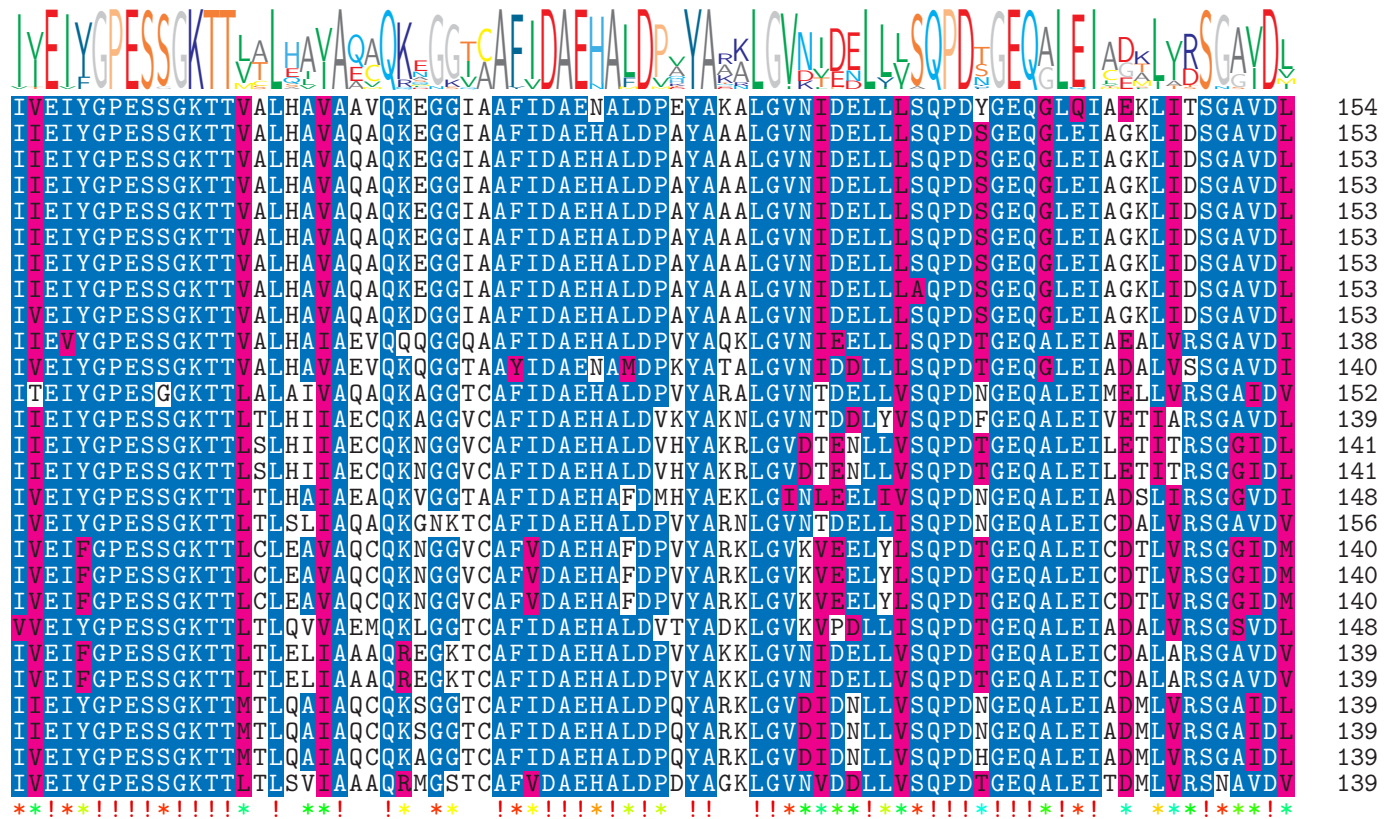
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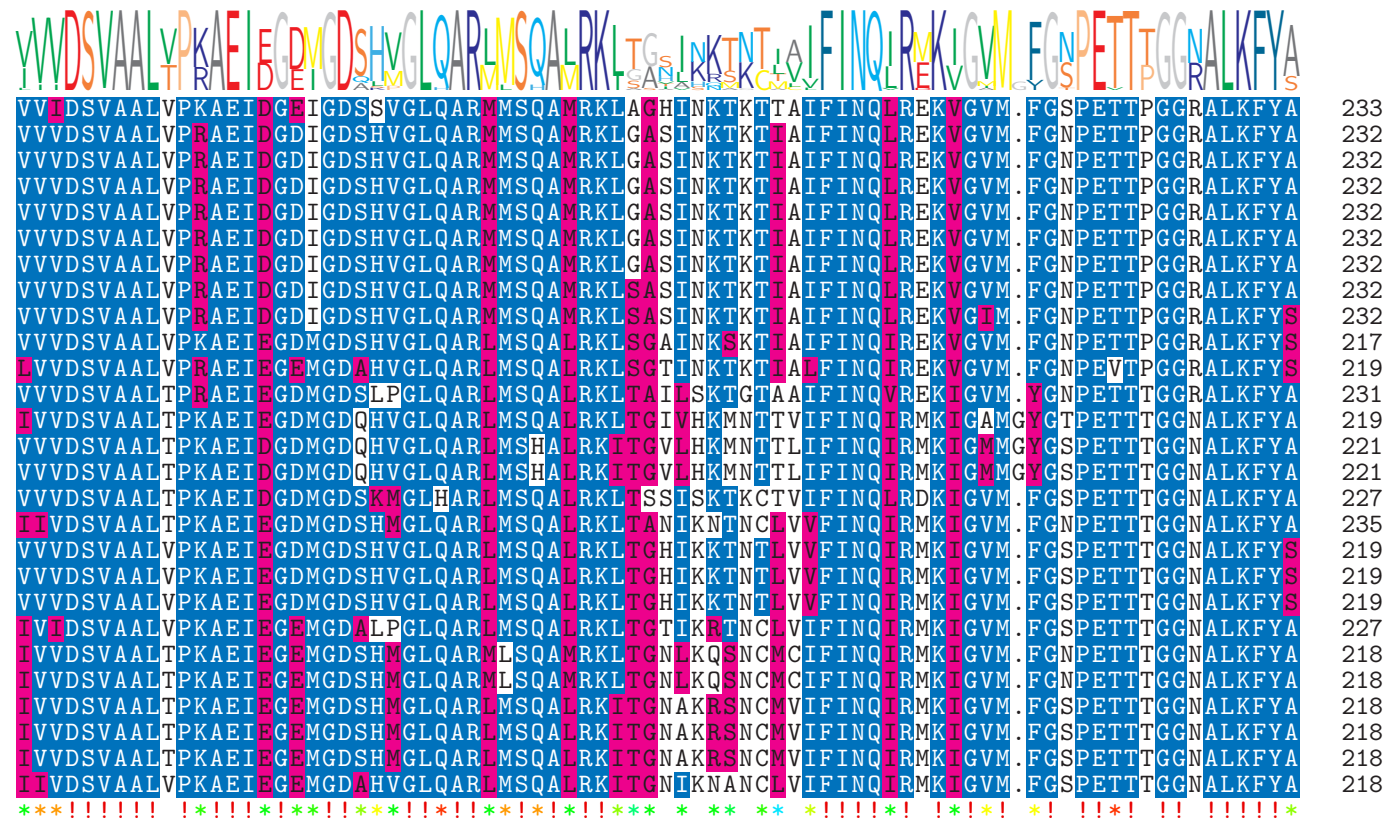
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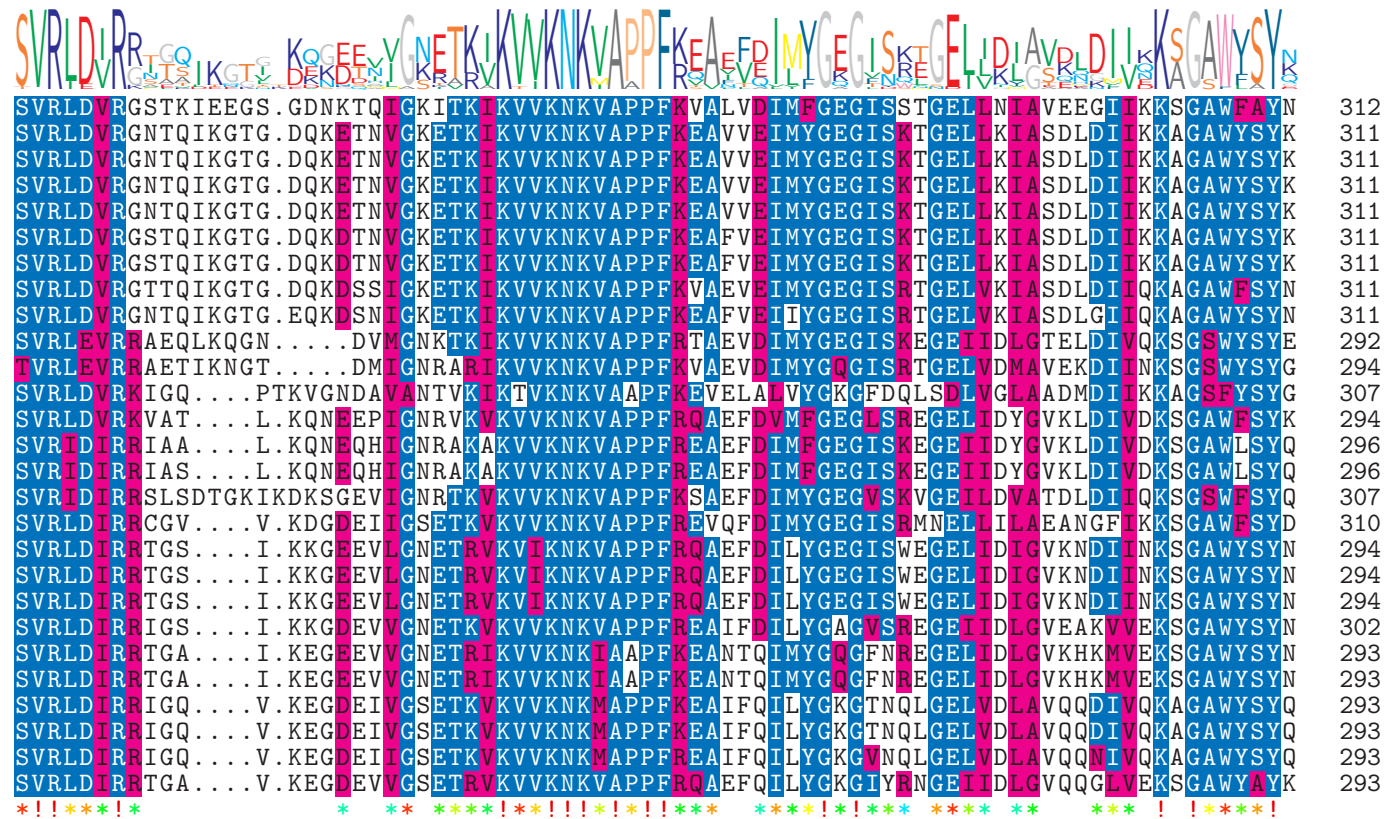
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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SK ¹¹ FG ¹² LIDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SK ¹¹ FG ¹² LIDGEEVSEQDTE 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 SK ¹¹ FG ¹² LIDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
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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 FG ¹² LLEESEESAMAV 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 VQ ¹² YGL 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 REHY ¹³ GL ¹⁴ DNNGVVQQQAEE ¹⁵ .TQEEL ¹⁶ .E ¹⁷ .FE ¹⁸ .E ¹⁹	348
SERIGGG ¹ RENA ² KNYLA ³ DH ⁴ ED ⁵ VE ⁶ DE ⁷ VR ⁸ LK ⁹ VRAAY ¹⁰ GIS ¹¹ DVPEEDLPTTE ¹² .DE ¹³ .QI ¹⁴ .N ¹⁵ ..ILPDDST ¹⁶EE ¹⁷	355
DERIGGG ¹ KE ² KTIA ³ YIA ⁴ ER ⁵ PE ⁶ ME ⁷ QE ⁸ IR ⁹ DRV ¹⁰ MAA ¹¹ IRAGNAGEAPALAPAPAAPEAAEA ¹²	363
DKKLGGG ¹ RENS ² KA ³ FL ⁴ KN ⁵ PEIA ⁶ DEIT ⁷ KA ⁸ IQNSM ⁹ GIEGMISGS ¹⁰ ..EDDEGE ¹¹ .E ¹²	343
DKKLGGG ¹ RENA ² KALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKESIG ⁸ SNEEIMPL ⁹ ..PDEPLE ¹⁰ ..EME ¹¹	347
DKKLGGG ¹ RENA ² KALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKESIG ⁸ SNEEIMPL ⁹ ..PDEPLE ¹⁰ ..EME ¹¹	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 IRNTLA ¹⁰ SNPNSVLK ¹¹ ..ATASDSND ¹² ESDVEEFSE ¹³EEL ¹⁴	372
GAKIGGQ ¹ KDN ² VR ³ VL ⁴ KN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALNG ⁹ VMHITEG ¹⁰ ..TQDET ¹¹GERPE ¹²E ¹³	348
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GERIGGG ¹ RD ² NC ³ REFL ⁴ RENA ⁵ E ⁶ LAR ⁷ EI ⁸ ENK ⁹ VREHL ¹⁰ GVTPMGAV ¹¹ ..TLAEEVEED ¹²	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 TKASDQTA ⁹ ..A ¹⁰ .HDETEE ¹¹ EPD ¹² ..LLES ¹³	349
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consensus								

-  non conserved
-  similar
-  ≥ 50% conserved