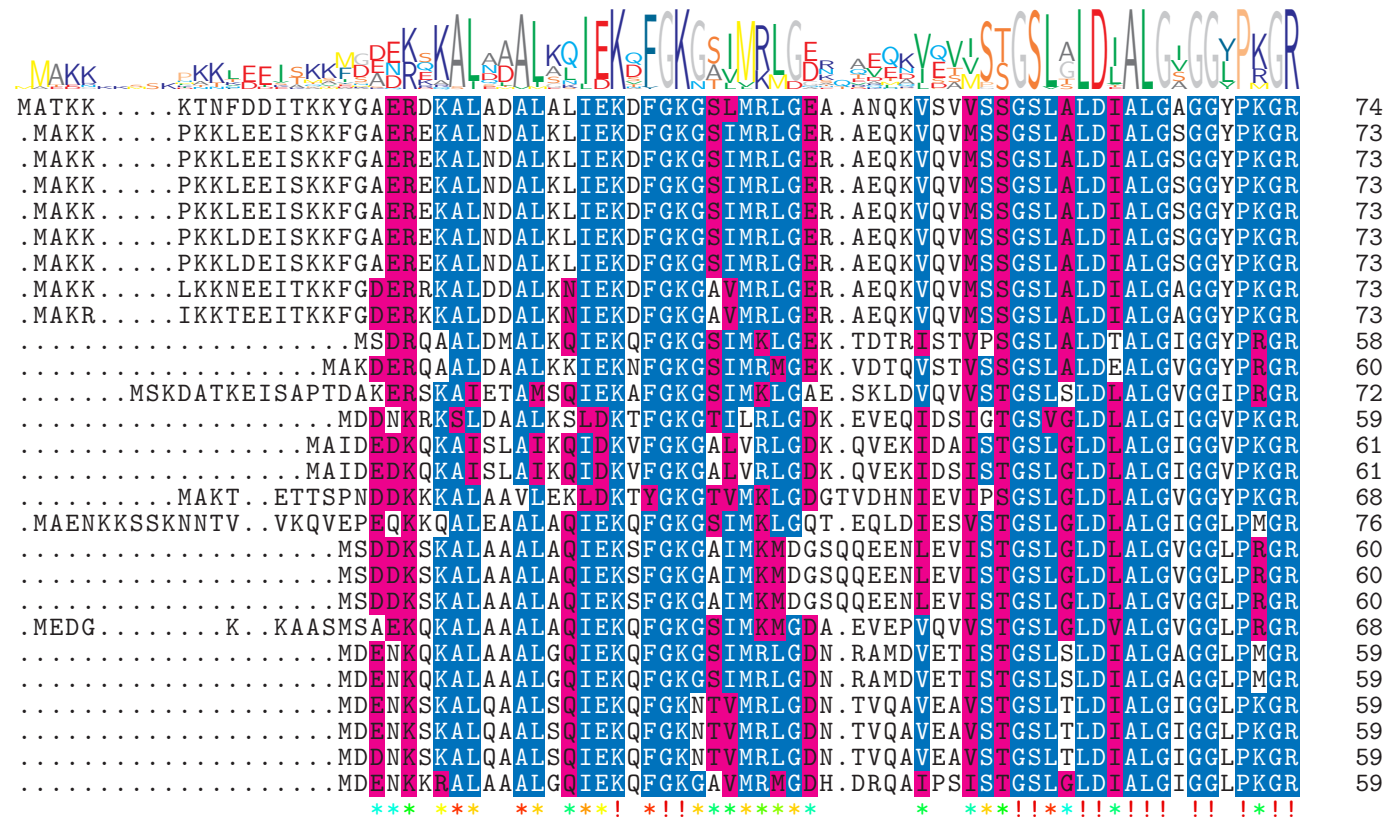


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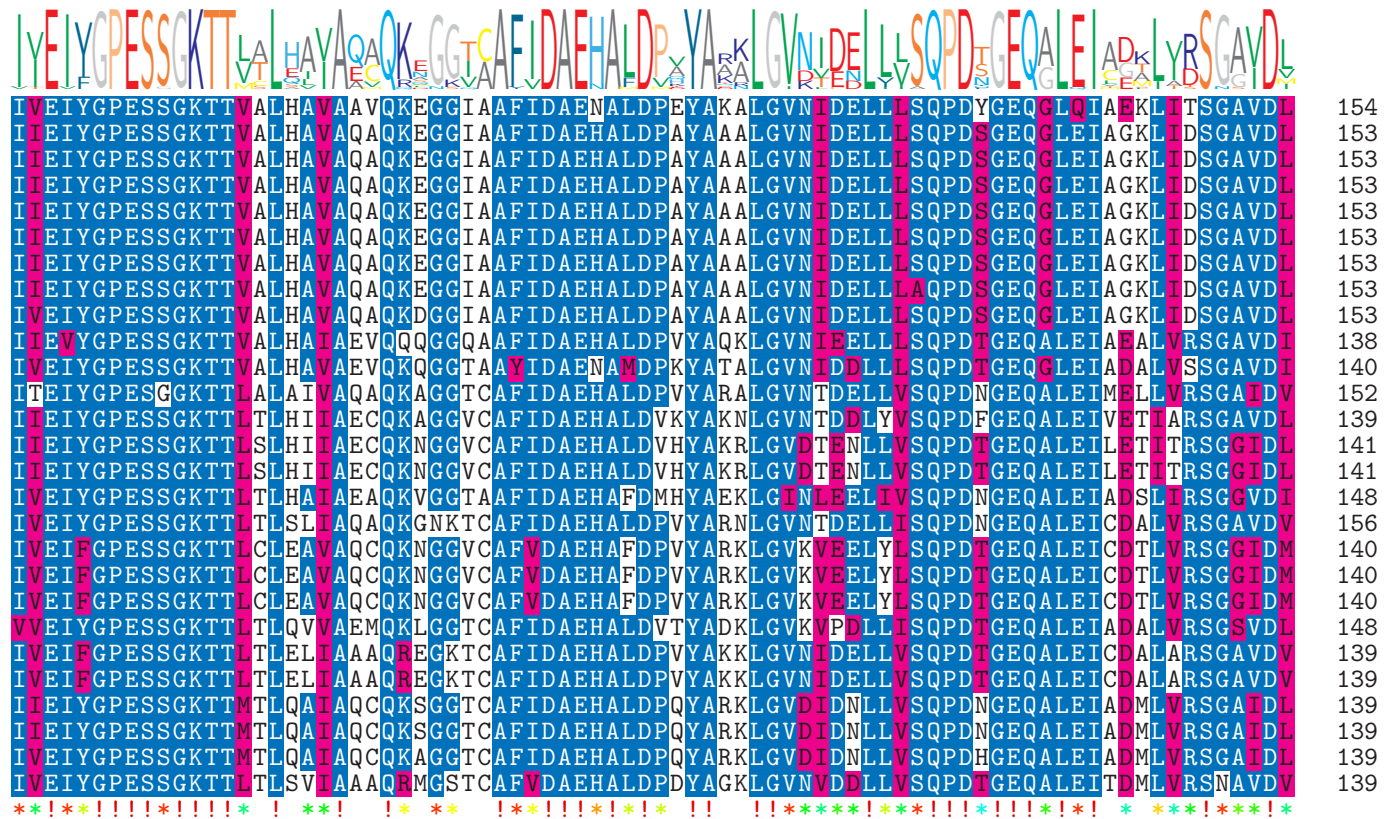
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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTE ¹³ .NKKD ¹⁴ E ¹⁵PKKEEA ¹⁶ ..VNEEVPLDLGDEL ¹⁷	382
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DEID 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
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ IF ⁷ DEID ⁸ HQ ⁹ VR ¹⁰ VQF ¹¹ GL ¹² IDGEEIAE ¹³SKKD ¹⁴ E ¹⁵AAQVDS ¹⁶ ..VNEEVTLDLGDEL ¹⁷	378
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 LM ¹⁰ IQEQ ¹¹ IREHY ¹² GL ¹³ DNNGVVQQQAEE ¹⁴ .TQEEL ¹⁵ .E ¹⁶ .FE ¹⁷ .E ¹⁸	348
SERIGQGS 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
DERIGQG ¹ KE ² KTIA ³ YIA ⁴ ERP ⁵ EME ⁶ QE ⁷ IRDRV ⁸ MAA ⁹ IRAGNAGEAPALAPAPAAPEAAEA ¹⁰	363
DKKLGGGREN ¹ SKA ² FL ³ KN ⁴ PEIA ⁵ DEIT ⁶ KA ⁷ IQNSM ⁸ GIEGMISGS ⁹ ..EDDEGE ¹⁰ ..E ¹¹	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKESIG ⁸ SNEEIMPL ⁹ ..PDEPLE ¹⁰ ..EME ¹¹	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKESIG ⁸ SNEEIMPL ⁹ ..PDEPLE ¹⁰ ..EME ¹¹	347
DTKLGGGRD ¹ TV ² KEL ³ IK ⁴ DN ⁵ PELA ⁶ E ⁷ LE ⁸ AK ⁹ IREKLQAK ¹⁰	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
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALNG ⁸ VMHITEG ⁹ ..TQDET ¹⁰GERPE ¹¹E ¹²	348
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALNG ⁸ VMHITEG ⁹ ..TQDET ¹⁰GERPE ¹¹E ¹²	348
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DEID ⁶ AK ⁷ IRALNG ⁸ VMHITEG ⁹ ..TQDET ¹⁰GERPE ¹¹E ¹²	348
GERIGGGRD ¹ NC ² REFL ³ RENA ⁴ E ⁵ LAR ⁶ EI ⁷ ENK ⁸ VREHL ⁹ GVTPMGAV ¹⁰ ..TLAEEVEED ¹¹	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
GDKIGGQKAN ¹ ACKYL ² KN ³ PEIA ⁴ AKT ⁵ L ⁶ DKKL ⁷ REMLLN ⁸ PENMQLI ⁹ ..AETSSAAD ¹⁰ VEFGAVPE ¹¹EF ¹²	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 ¹¹ EPD ¹² ..LLES ¹³	349
GSKIGGQKAN ¹ AAKY ² LEEN ³ PEI ⁴ IG ⁵ EIE ⁶ EQ ⁷ IRAKLL ⁸ VTSANTKA ⁹ ..TPVAEDLAD ¹⁰ ..I ^{11</}	

logo

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 ≥ 50% conserved