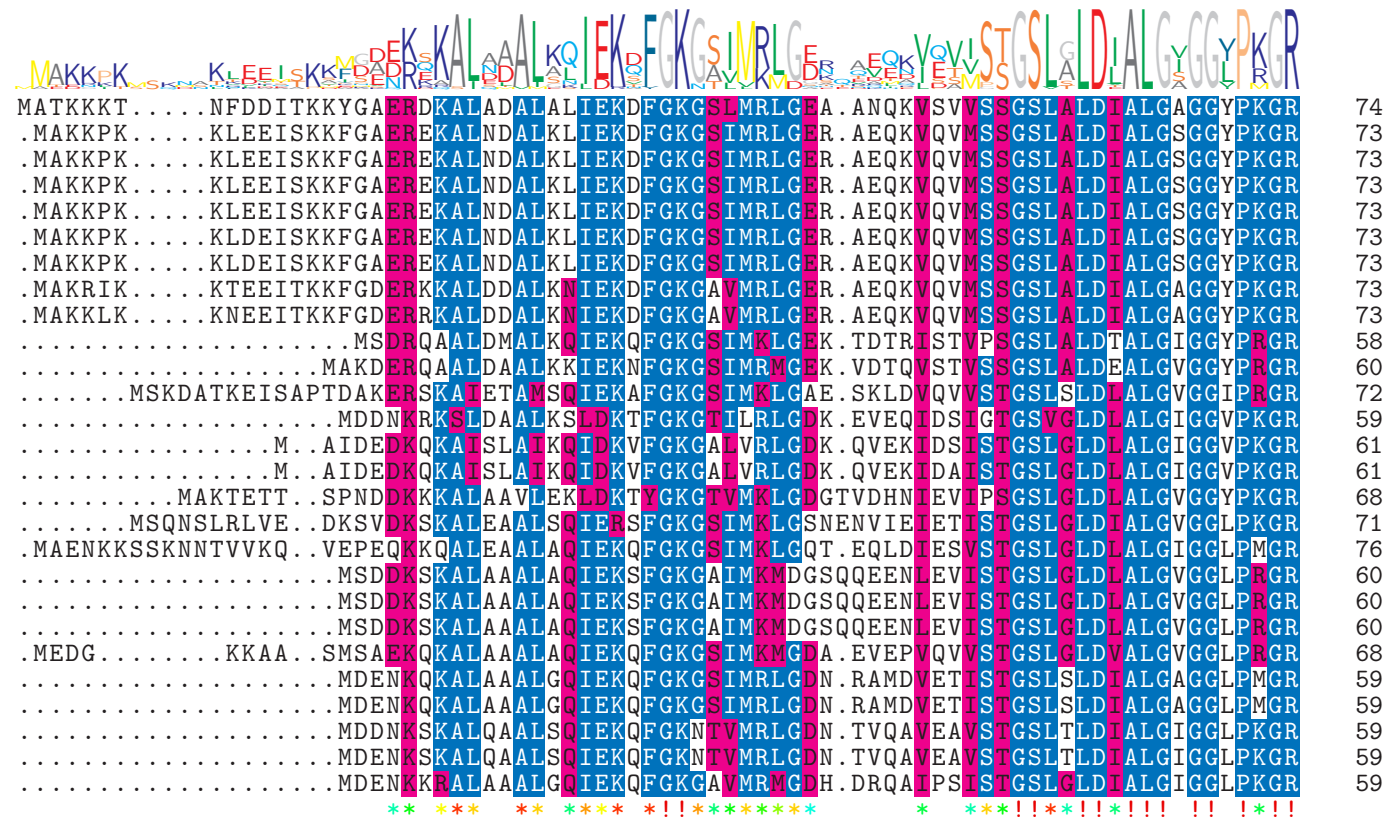


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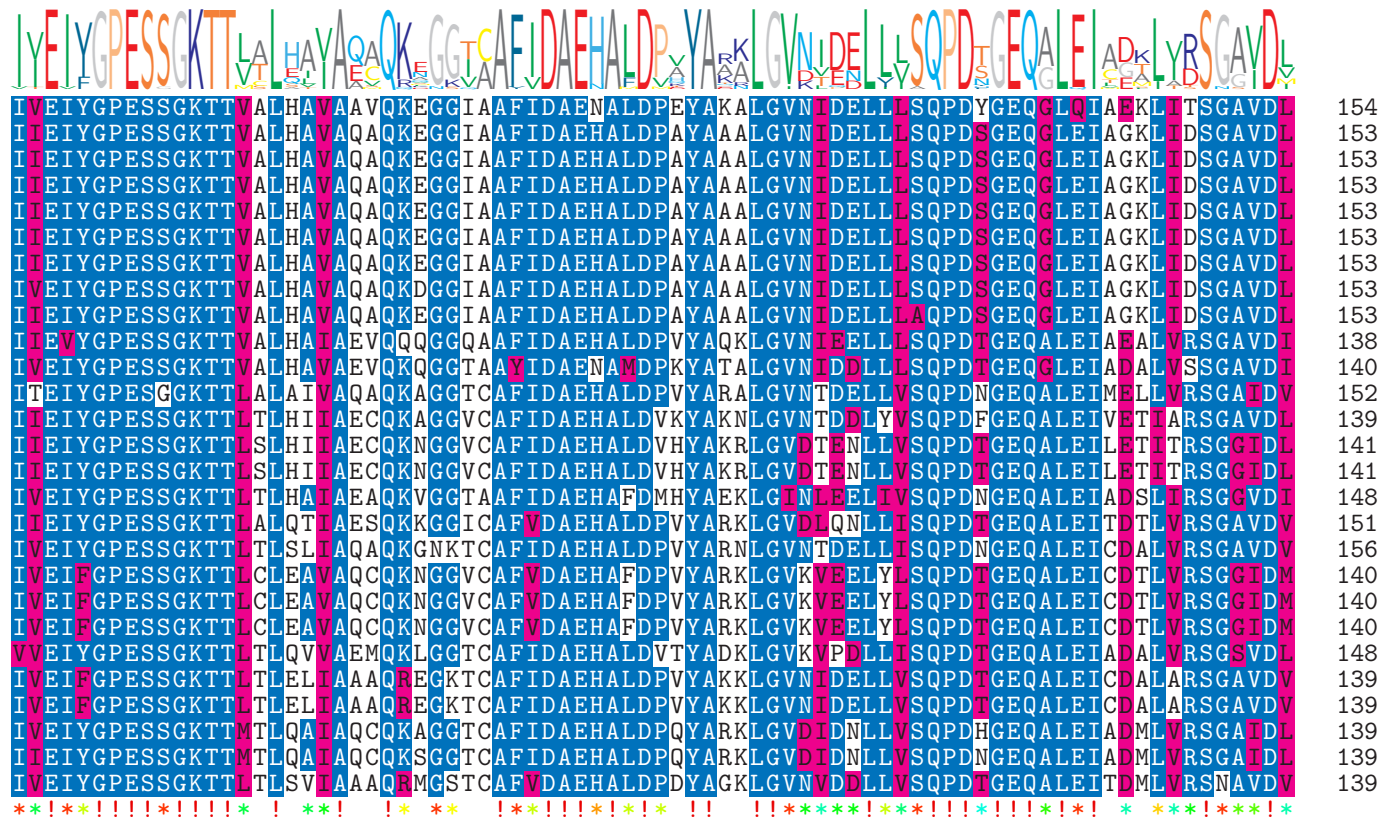
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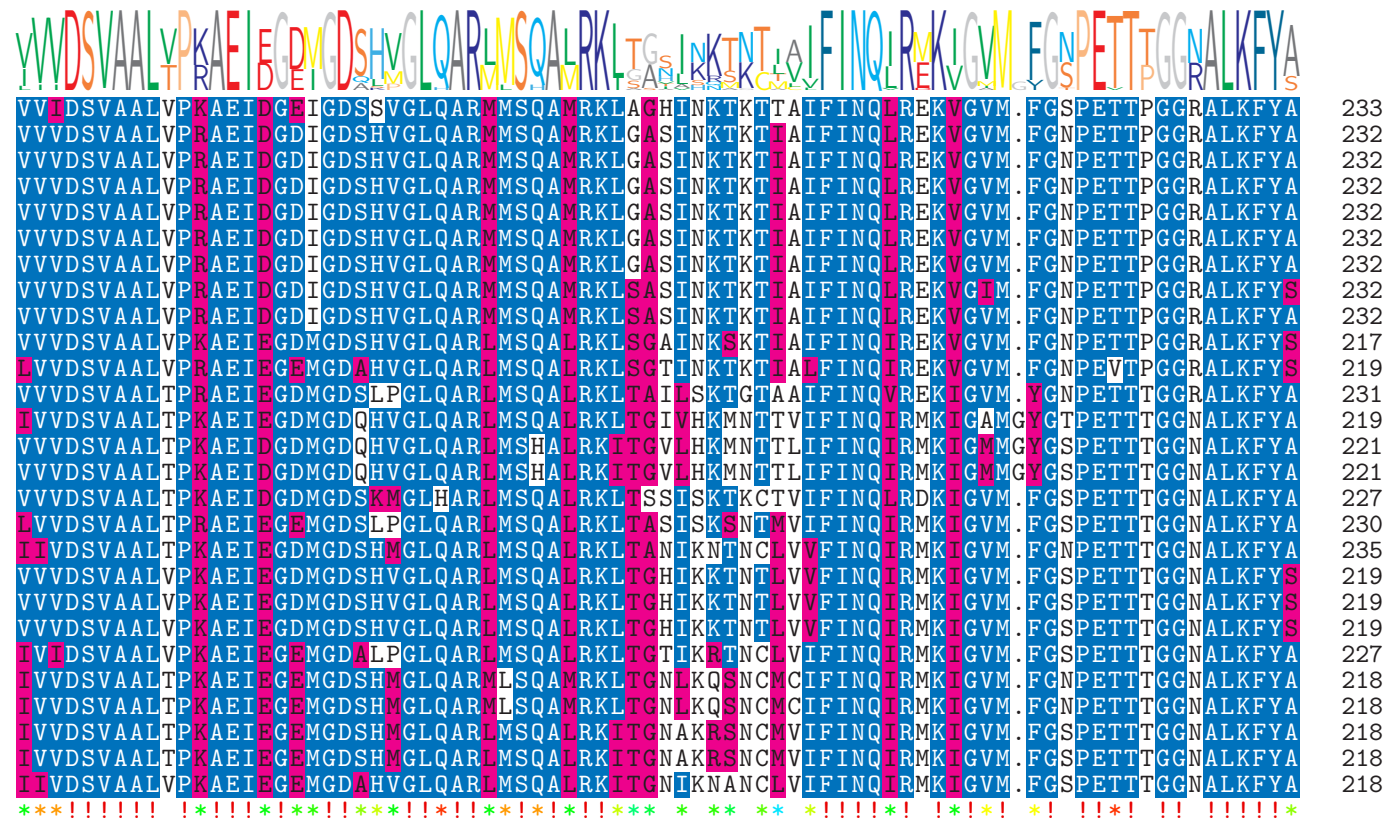
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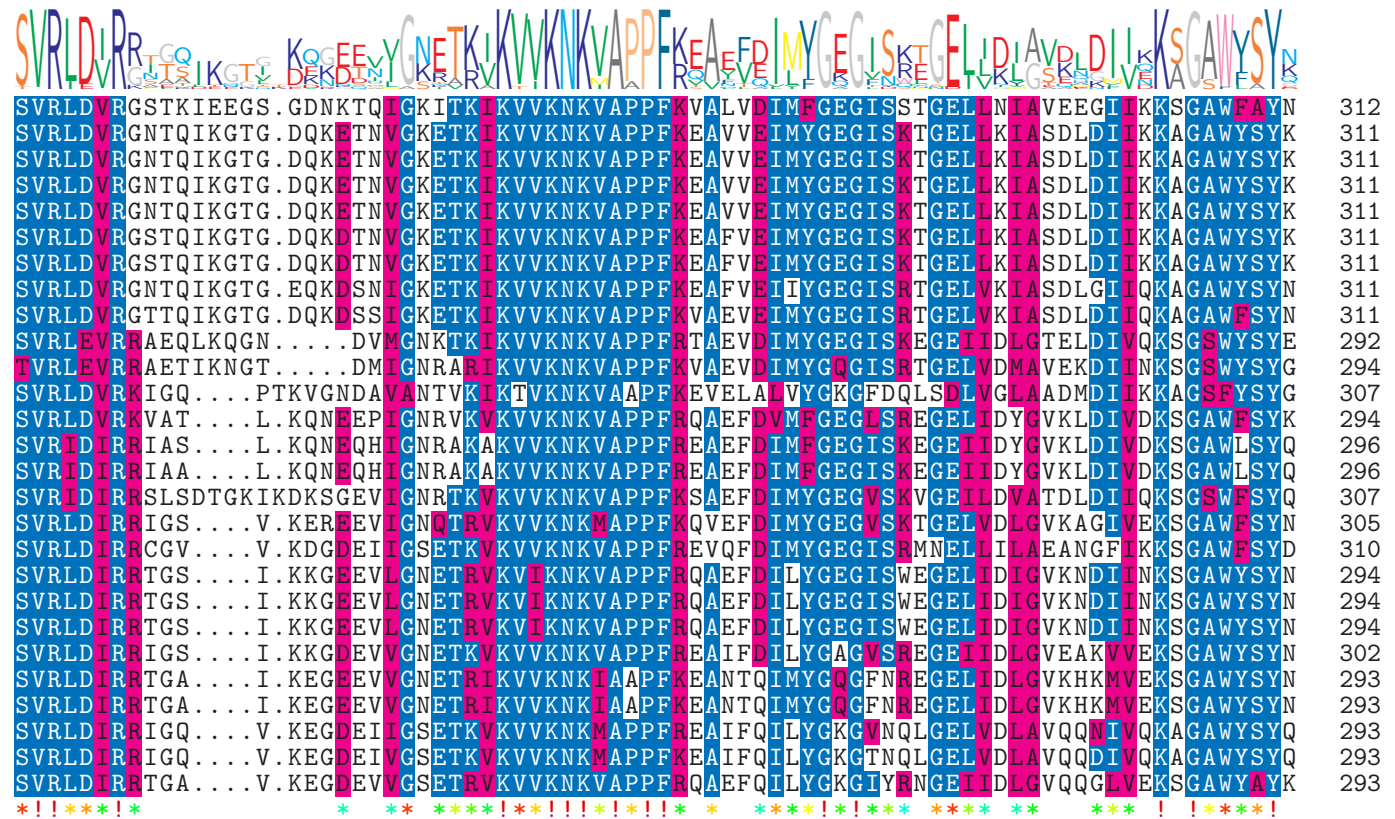
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consensus

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Sequence	Score
DEKIGQGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ FD ⁹ EID ¹⁰ HK ¹¹ VRAAH ¹² GL ¹³ LD ¹⁴ SEVAETEEETTAS ¹⁵ KT ¹⁶ KA ¹⁷ KA ¹⁸ KEEK ¹⁹ AVETEEIELE ²⁰ D.....	387
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ ID ¹² GEEVSEQD ¹³ TENK ¹⁴ DE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ ID ¹² GEEVSEQD ¹³ TENK ¹⁴ DE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ ID ¹² GEEVSEQD ¹³ TENK ¹⁴ DE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ ID ¹² GEEVSEQD ¹³ TENK ¹⁴ DE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PEIF ⁶ DEID ⁷ HQ ⁸ VR ⁹ VQF ¹⁰ GL ¹¹ ID ¹² GEEIAES....KKDE....AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PEV ⁶ FA ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQF ¹¹ GL ¹² ID ¹³ GEEAAES....KKDE....VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGS ¹ EN ² AK ³ FL ⁴ AD ⁵ NPEIF ⁶ DD ⁷ EID ⁸ HK ⁹ VR ¹⁰ VQF ¹¹ GL ¹² IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGQGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ FD ⁷ ID ⁸ RK ⁹ VR ¹⁰ VQF ¹¹ GL ¹² LEESEESAMAVASE.....E.....TDDLALDLNGLIEIE	377
EE ¹ RL ² GG ³ RE ⁴ NA ⁵ KQ ⁶ FL ⁷ KE ⁸ NK ⁹ DI ¹⁰ ML ¹¹ IQEQ ¹² IREHY ¹³ GL ¹⁴ DN ¹⁵ GVVQQAETQEEL ¹⁶ .EFE.E.....	348
SERIGQGS ¹ RE ² NA ³ KNYLA ⁴ DH ⁵ ED ⁶ VE ⁷ DE ⁸ VR ⁹ LK ¹⁰ VRAAY ¹¹ GIS ¹² DV ¹³ PEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGQG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ER ⁶ PEME ⁷ QE ⁸ IR ⁹ DRV ¹⁰ MAA ¹¹ IRAGNAGEAPALAPAPAAP ¹² .AAEA.....	363
DKKLGGG ¹ RE ² NSKA ³ FL ⁴ KEN ⁵ PEIA ⁶ EIT ⁷ KA ⁸ IQNSM ⁹ G ¹⁰ IEGMISGSEDDE...GEE.....	343
DKKLGGG ¹ RE ² NA ³ KALL ⁴ KED ⁵ KALADEIT ⁶ LK ⁷ IKESIG ⁸ SNEEIMPLPDEP...LEE...ME.....	347
DKKLGGG ¹ RE ² NA ³ KALL ⁴ KED ⁵ KALADEIT ⁶ LK ⁷ IKESIG ⁸ SNEEIMPLPDEP...LEE...ME.....	347
DTKLGGGR ¹ DT ² VKEL ³ IK ⁴ DN ⁵ PELA ⁶ EEL ⁷ EAK ⁸ IREKLQAK.....	343
SQRLGGG ¹ RE ² NA ³ KT ⁴ FL ⁵ RD ⁶ NPD ⁷ LAR ⁸ EIELAR ⁹ QNA ¹⁰ GL ¹¹ IADRFLQNGGPDADDG...AAAD..M.....	362
GTKIGQG ¹ KNN ² AVK ³ WL ⁴ KEN ⁵ PEIAD ⁶ KL ⁷ QEIR ⁸ NTLA ⁹ SNPNSVLKA..TASDSND...ESD..VEEFSEEL.....	372
GAKIGQG ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRAL ⁹ NG ¹⁰ VMHITEGT..QDET ¹¹ DGE...R.....PEE.....	348
GAKIGQG ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRAL ⁹ NG ¹⁰ VMHITEGT..QDET ¹¹ DGE...R.....PEE.....	348
GAKIGQG ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRAL ⁹ NG ¹⁰ VMHITEGT..QDET ¹¹ DGE...R.....PEE.....	348
GE ¹ RIGQGR ² DN ³ CRE ⁴ FL ⁵ RENA ⁶ EAL ⁷ EI ⁸ ENK ⁹ VREHL ¹⁰ GV ¹¹ TPMGAVTL..A.EEVEE...D.....	352
GDKIGQG ¹ KAN ² ACK ³ YL ⁴ KEN ⁵ PEIAKT ⁶ L ⁷ DKKL ⁸ REMLLN ⁹ PENMQLIA..ETSSAAD...DVE..FGAVPEEF.....	354
GDKIGQG ¹ KAN ² ACK ³ YL ⁴ KEN ⁵ PEIAKT ⁶ L ⁷ DKKL ⁸ REMLLN ⁹ PENMQLIA..ETSSAAD...DVE..FGAVPEEF.....	354
GNKIGQG ¹ KNN ² VIRY ³ LE ⁴ EN ⁵ PQISTEIE ⁶ AVIREQLLT ⁷ TKASDQTAA...HDETEE...EPD..LL..ES.....	349
GNKIGQG ¹ KNN ² VIRY ³ FE ⁴ ENN ⁵ QIA ⁶ EIEI ⁷ ERNIREQLLT ⁸ TGTNGAVQ...I.EDEE...EPD..LL..LES.....	349
GSKIGQG ¹ KANA ² AK ³ YL ⁴ EN ⁵ PEI ⁶ IG ⁷ EIEEQ ⁸ IRAKLL ⁹ VTSANTKAT..PVAEDLA...DAD..I.....	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved