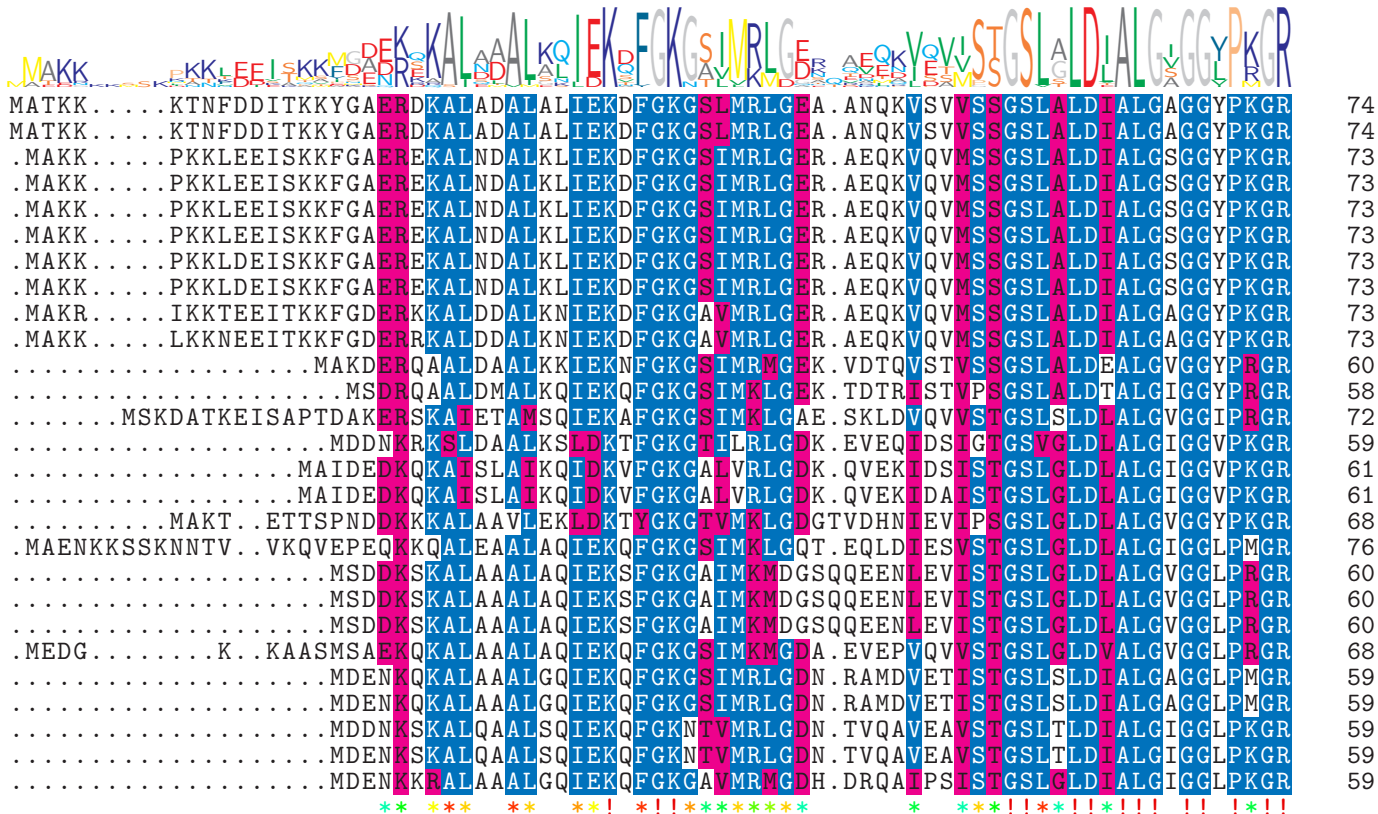


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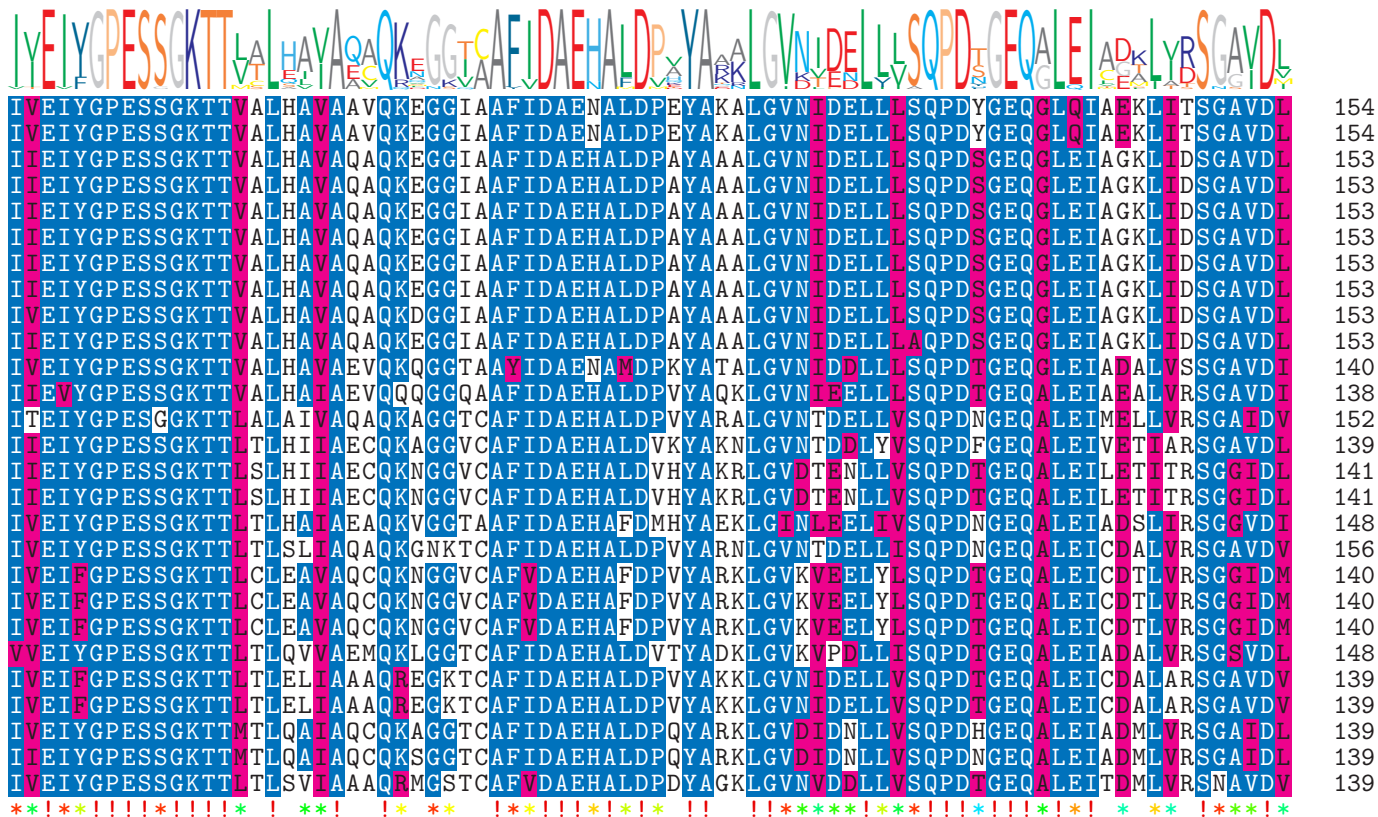
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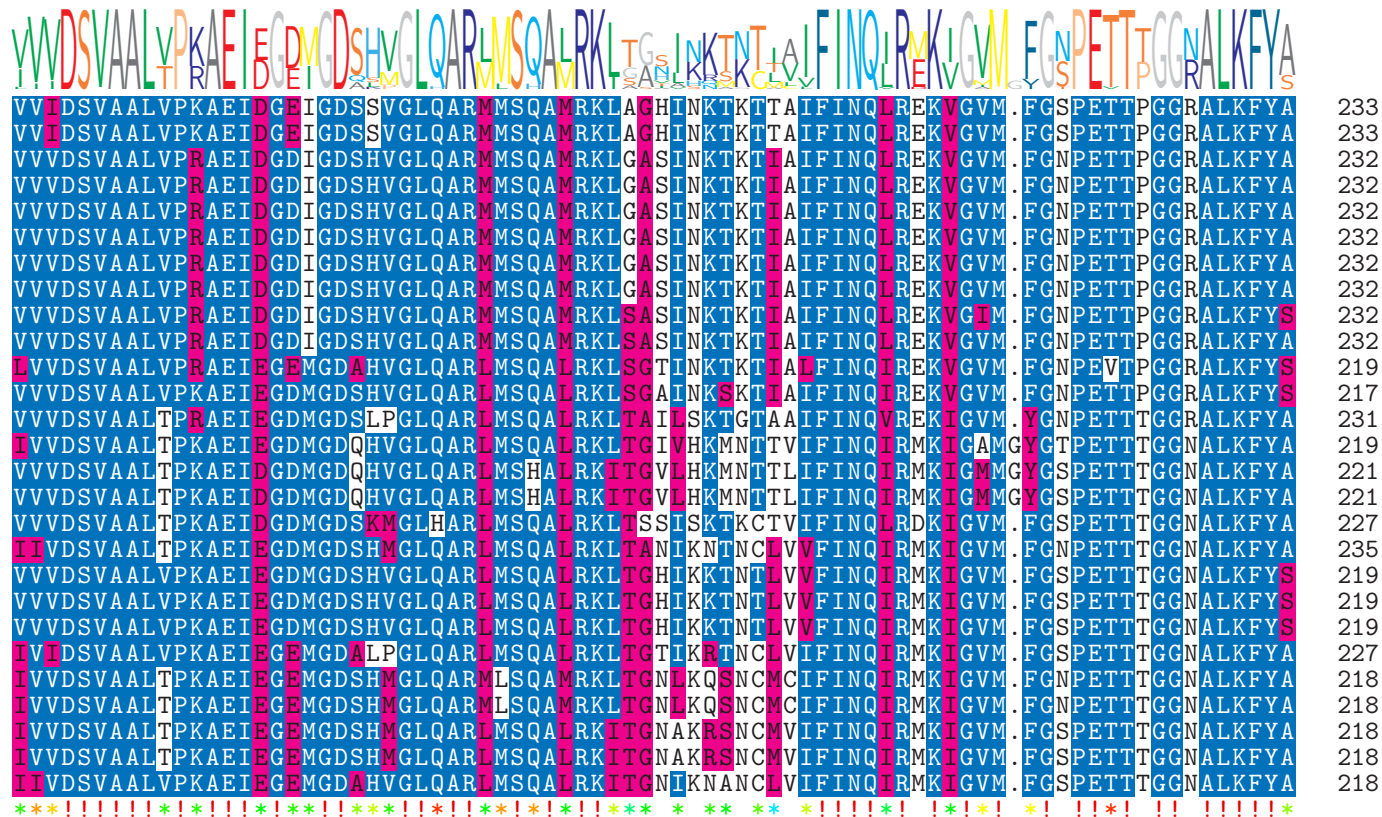
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consensus

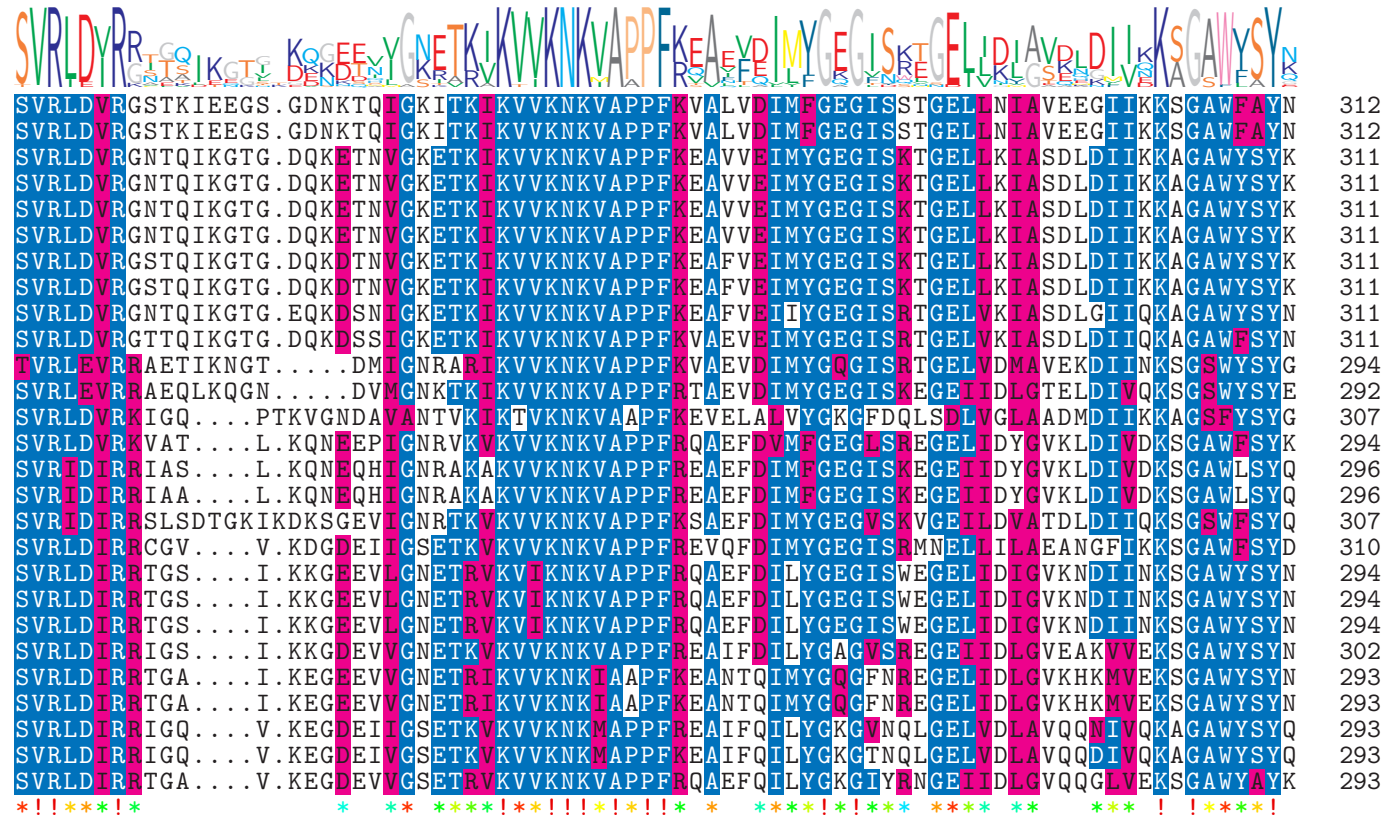
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consensus

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Sequence	Score
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DEKIGGGS E NA K KYLA E HP E IF D EID K QVRSK F GLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGGGS E NA K KYLA D N P E V FA E ID H QVVRV Q GLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDELEIE	381
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GEKIGGGS E NA K RYL A D H P Q L F DEID R KVVRV K GLLEESEEEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
SERIGGG R EN A KNYL A D H DE V EL R LKVRA E Y G ISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
EERLGGC R EN A K Q FL K EN K D I ML I Q E IR E HY L DNNGVVQQAEETQEEL.EFE.E.....	348
DERIGGG K E K TI A Y I A E R P E M E Q E I R D RV M AA I R A G N A E AP A L A P A PA E AA E ..A.....	363
DK K LGGG R EN A K F L K EN P E I A D E I T K A I Q N S M G I EGMI....SGSEDD..EGE..E.....	343
DK K LGGG R EN A K A L L K E D K A L A D E I T L K I K E S I G S NEEI....MPLPDE..PLE..EME.....	347
DK K LGGG R EN A K A L L K E D K A L A D E I T L K I K E S I G S NEEI....MPLPDE..PLE..EME.....	347
DT K LGGG R D T V K E L I K D N PE L A E E L E A K I RE K L Q A.....	343
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GA K IGGG K D N VR V W L EN P E I S D E I D A K I R A L N G V EM H I....TEGTQDET D GE..R.....PEE.....	348
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GD K IGGG K AN A C K Y L EN P E I A K T L D K K L RE M LL N PN E M....QLIAETSSAAD..DVEFGAVPEEF....	354
GN K IGGG K NN V IR Y LE E NP Q I S TE I E A V I RE Q LL T K A S DQTAA.HDETEE..EPDLL..ES.....	349
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logo

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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved