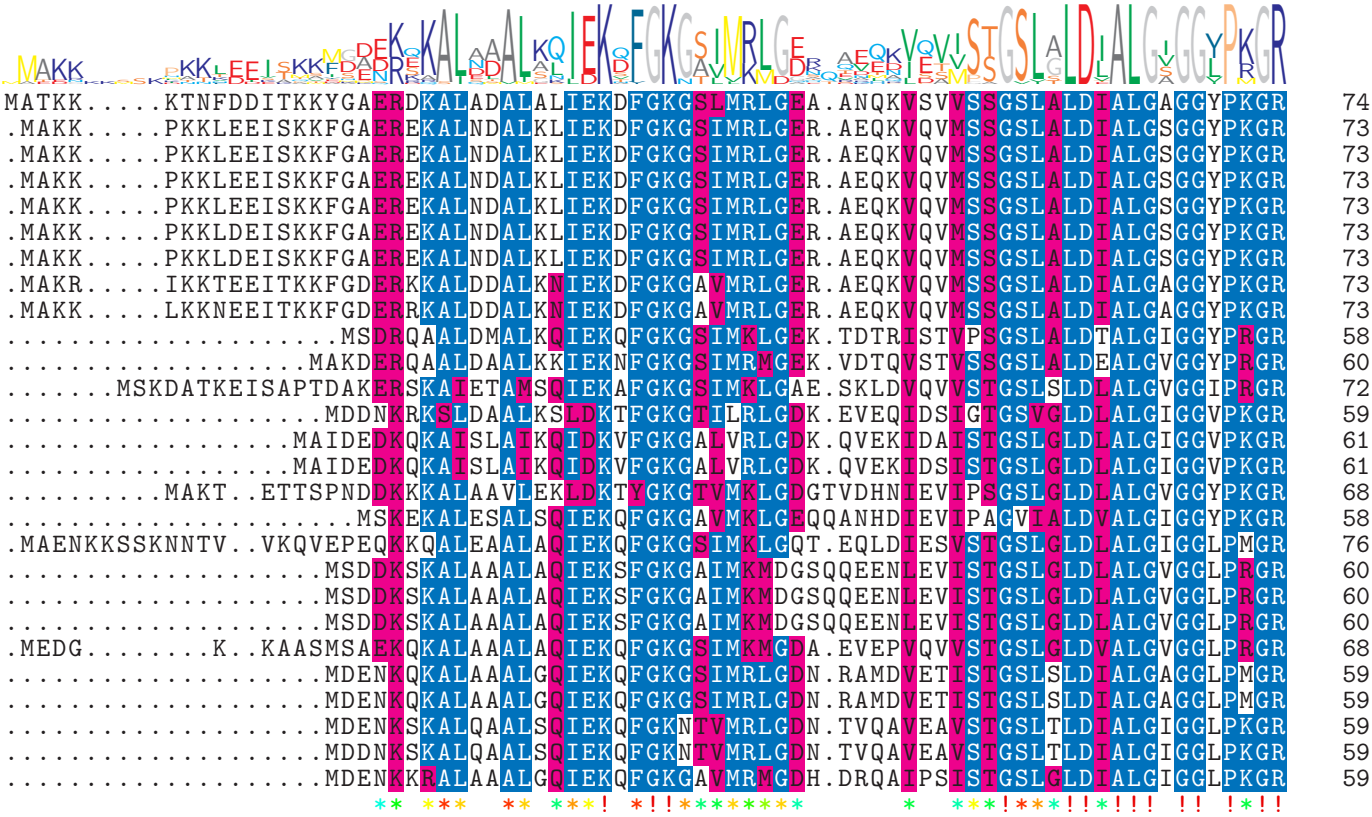


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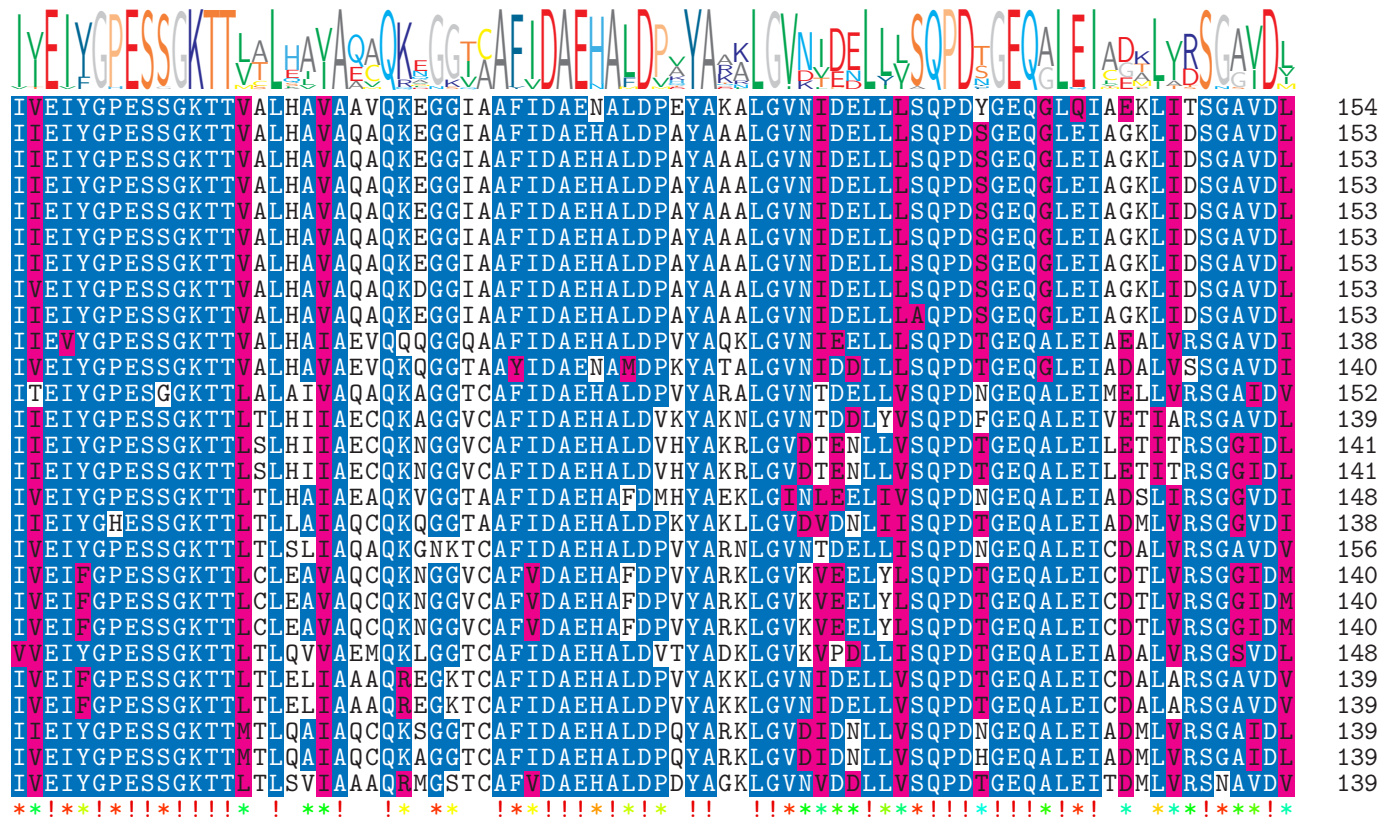
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consensus

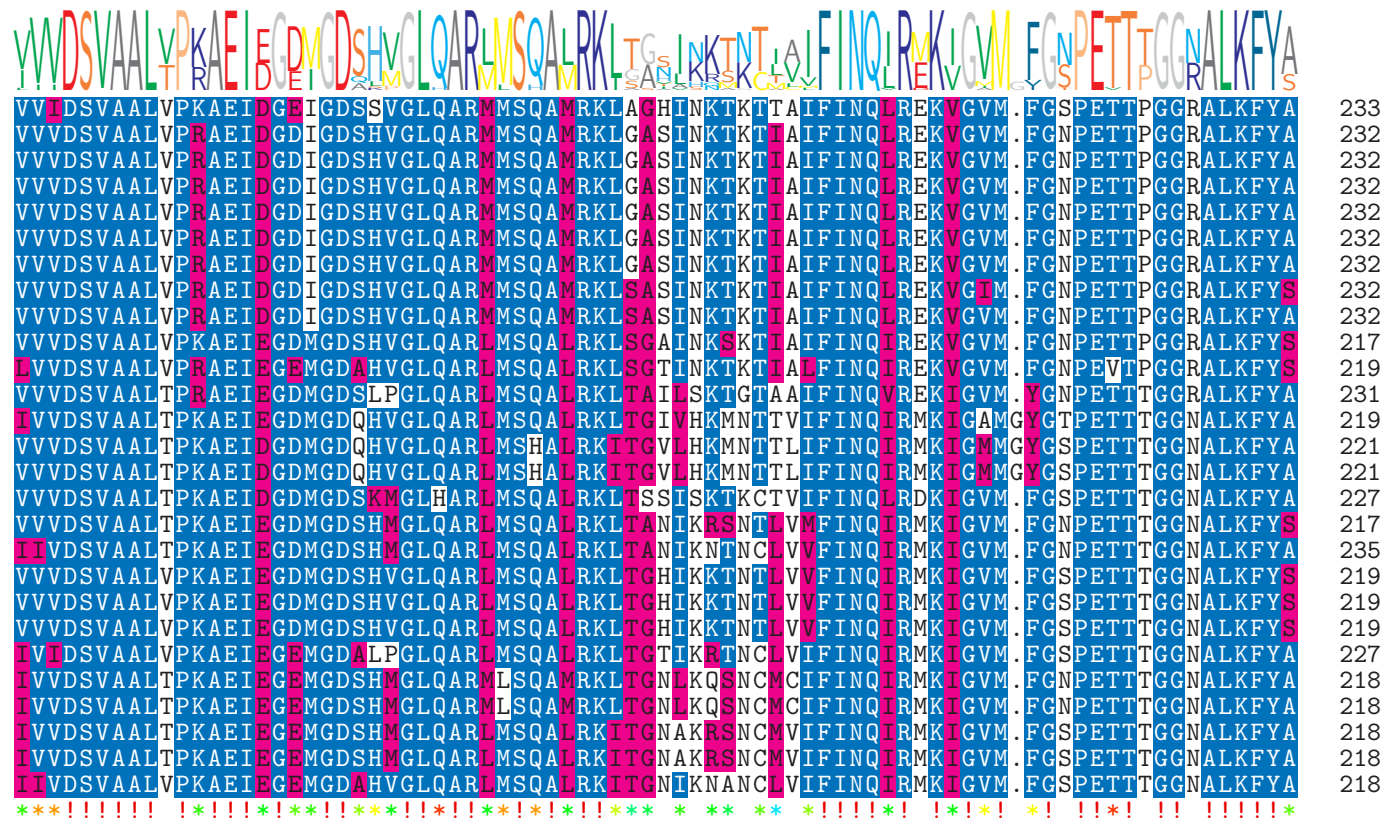
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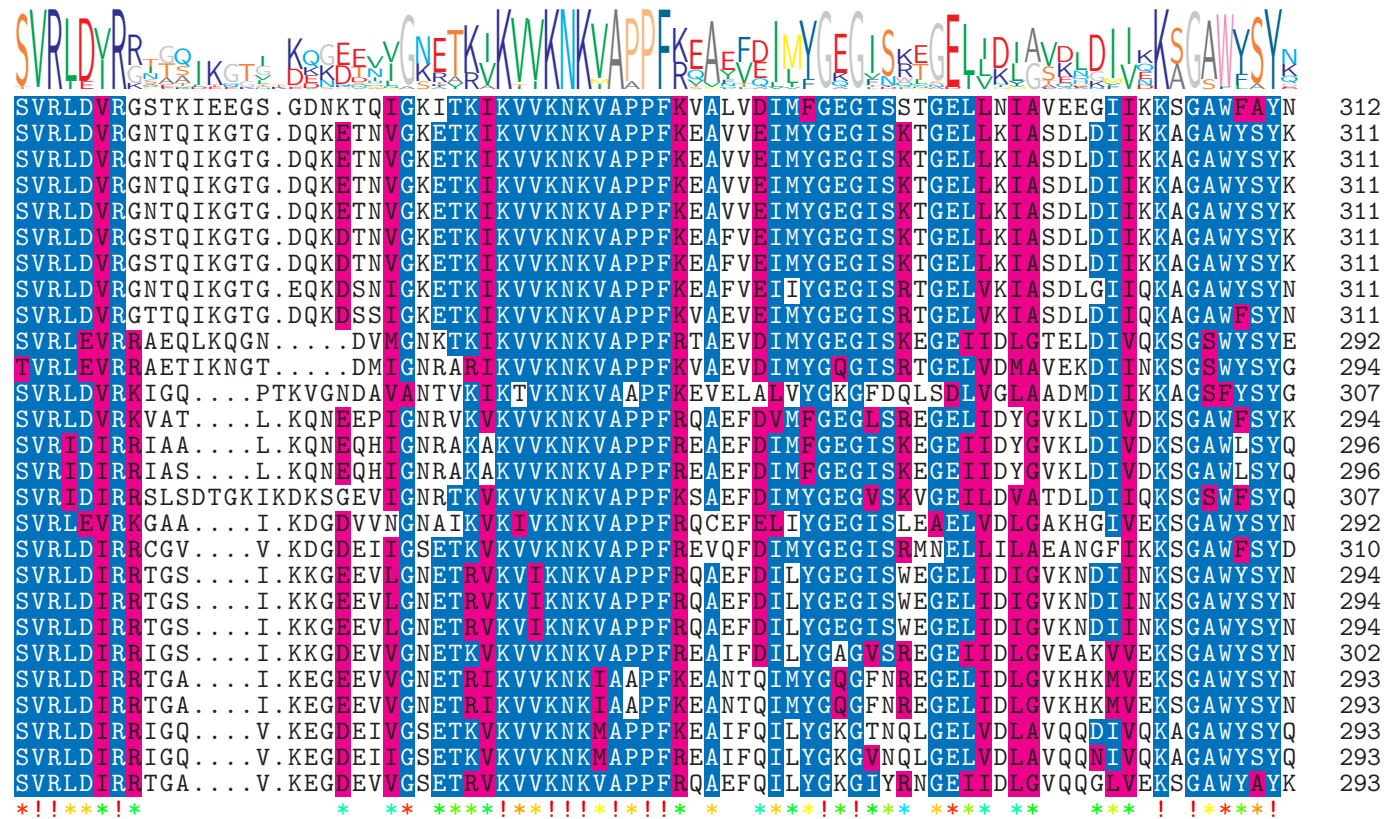
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consensus

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Sequence	Score
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DEKIGGGS E NA K KYLA E HP E IF D EID K Q V RS K FG L IDGEEVSEQDT...EN K KDE...PKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS E NA K KYLA E HP E IF D EID K Q V RS K FG L IDGEEVSEQDT...EN K KDE...PKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS E NA K KYLA D N P E I F D EID H Q V RV Q FG L IDGEEIAES...KKDE...AAQVDS..VNEEVPLDLGDEL	378
DEKIGGGS E NA K KYLA D N P E F A I D H Q V RV Q FG L IDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDEL	378
GEKIGGGS E NA K KFL A D N P E IF D DI D H K V R V Q GLIEEDNTEEKQS...SKEK...ETDEK..ADKNLVLELDDTI	379
GEKIGGGS E NA K RYL A D H P Q L F DEID R K V RV K FLLEESEESAMA...VASE...E.....TDDLALDLNGI	374
EER L G G GR E NA K Q F L K EN K D I M L M I Q E Q I REHY G L D NN G V V Q Q Q A E...ETQEEL.EFE.E.....	348
SERIGGGR E NA K NYL A D H D E VE D E V RL K V R A A Y G IS D V P EED L P T T...EDE.QI.NILPDDST....EE.....	355
DERIGG G KE K TI A Y I A E R P E M E Q E I RD R V M A A I R AG N A G E A P A L A P A P A E A E A E A A.....	363
DKKLGGGR E NS K A F L K EN P E I DE I TK A I Q NS M G I E G MIS G SEDD...EGEE.....	343
DKKLGGGR E NA K ALL K ED K AL A DE I TL K I K ES I GS N EE I ML P DE...PLEEME.....	347
DKKLGGGR E NA K ALL K ED K AL A DE I TL K I K ES I GS N EE I ML P DE...PLEEME.....	347
DTKLGGGR D TV K EL I K D N P EL A E E LE A K I RE K L Q A K	343
GS K IG G Q K ES K D Y L K EN T E I R D E I ER K L L EM L PH K Y A K E T Q EP K AP V K S ET K K S K V K.....ANTQDELI.....	359
G T KIGG G K N NA V K L EN K EN P E I AK D K L E I Q E I R NT L AS N P N S V L K A...TASDSNDESDVE.....EFSEEEEL.....	372
GAKIGG G K D N V RV L EN K EN P E I S D EID A K I R A L N G V EM H IT E G T ...QDET.....G.....ERPEE.....	348
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GAKIGG G K D N V RV L EN K EN P E I S D EID A K I R A L N G V EM H IT E G T ...QDET.....G.....ERPEE.....	348
RIGG G R D N C REF L EN A EL A R E I N K V RE H L G VT P M G A V .T...LAEVEEED.....	352
GDKIGG G K A NA C K Y L K EN P E I AK T LD K KL R EM L LN P EN M Q L IA...ETSSAADDVEFG.....AVPEEF.....	354
GDKIGG G K A NA C K Y L K EN P E I AK T LD K KL R EM L LN P EN M Q L IA...ETSSAADDVEFG.....AVPEEF.....	354
GNKIGG G K N N V IR Y FE E NN Q IA E E I ER N I R E Q LL T T G T N G A V QI.EDEE E PD.....L L ES.....	349
GNKIGG G K N N V IR Y LE E NP Q I S TE I E A V I RE Q LL T K A S D Q T A AHDETEE E PD.....L L ES.....	349
GS K IGG G K A NA A K Y LE E NP E I G Q E IE Q IR A KL L Y T S A N T K A T...PVAEDLADAD.....I.....	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved