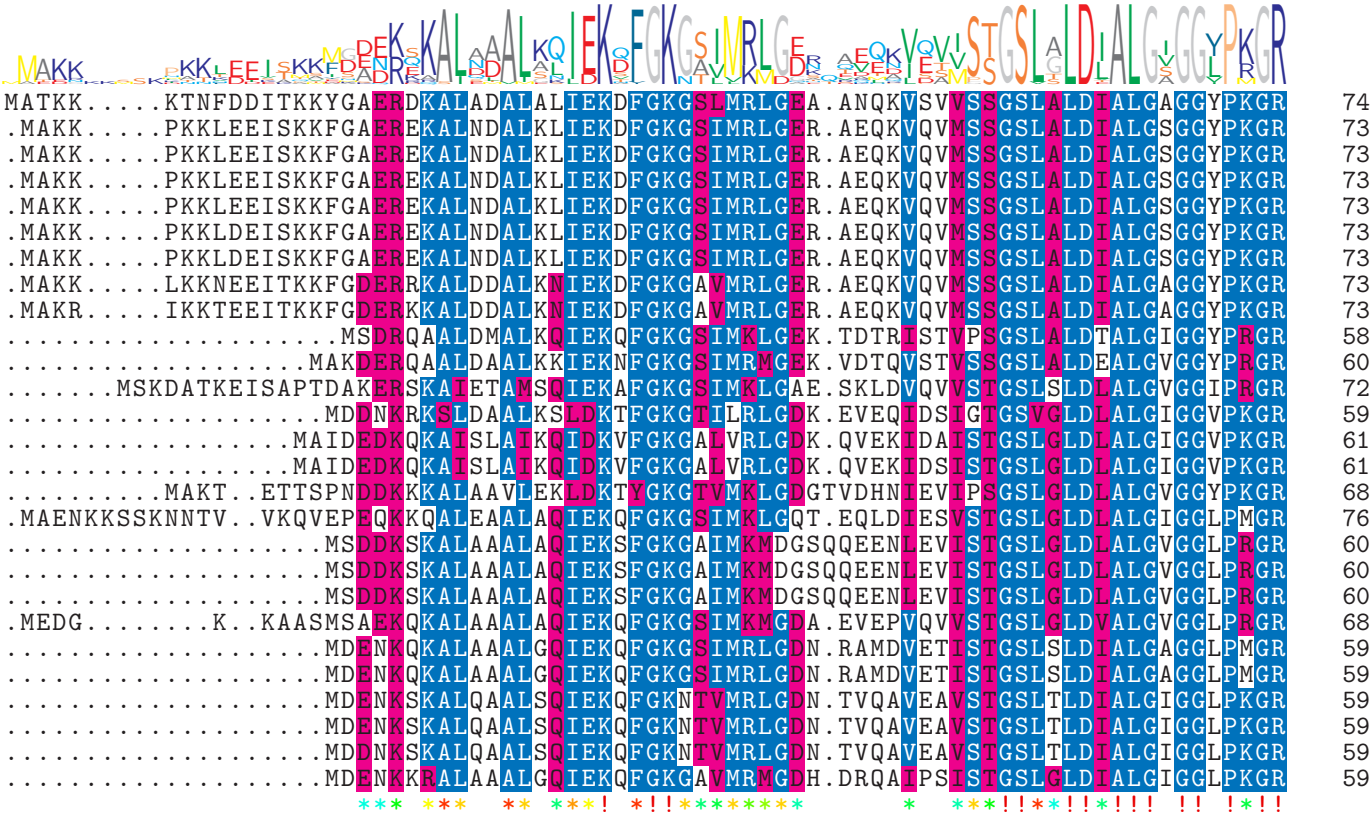


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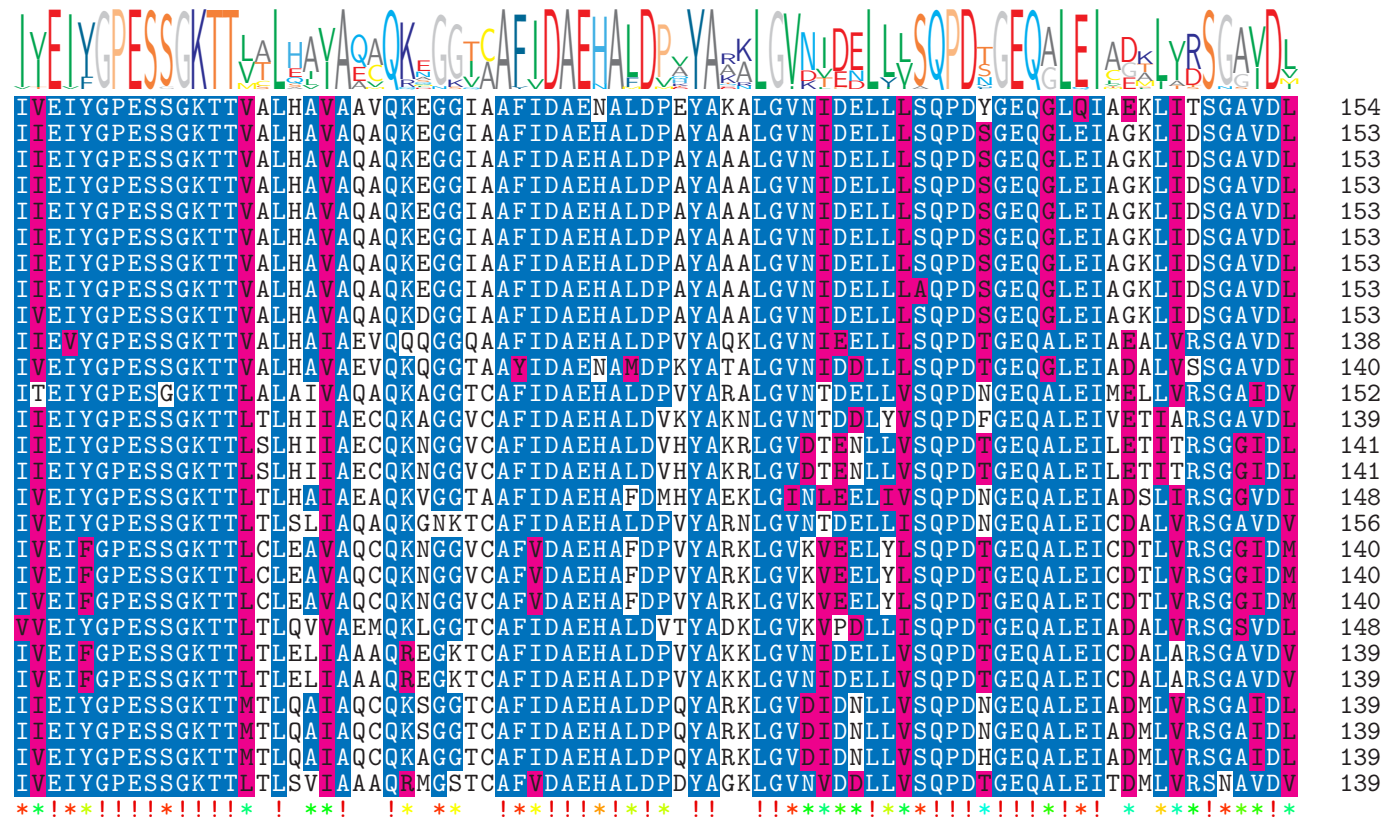
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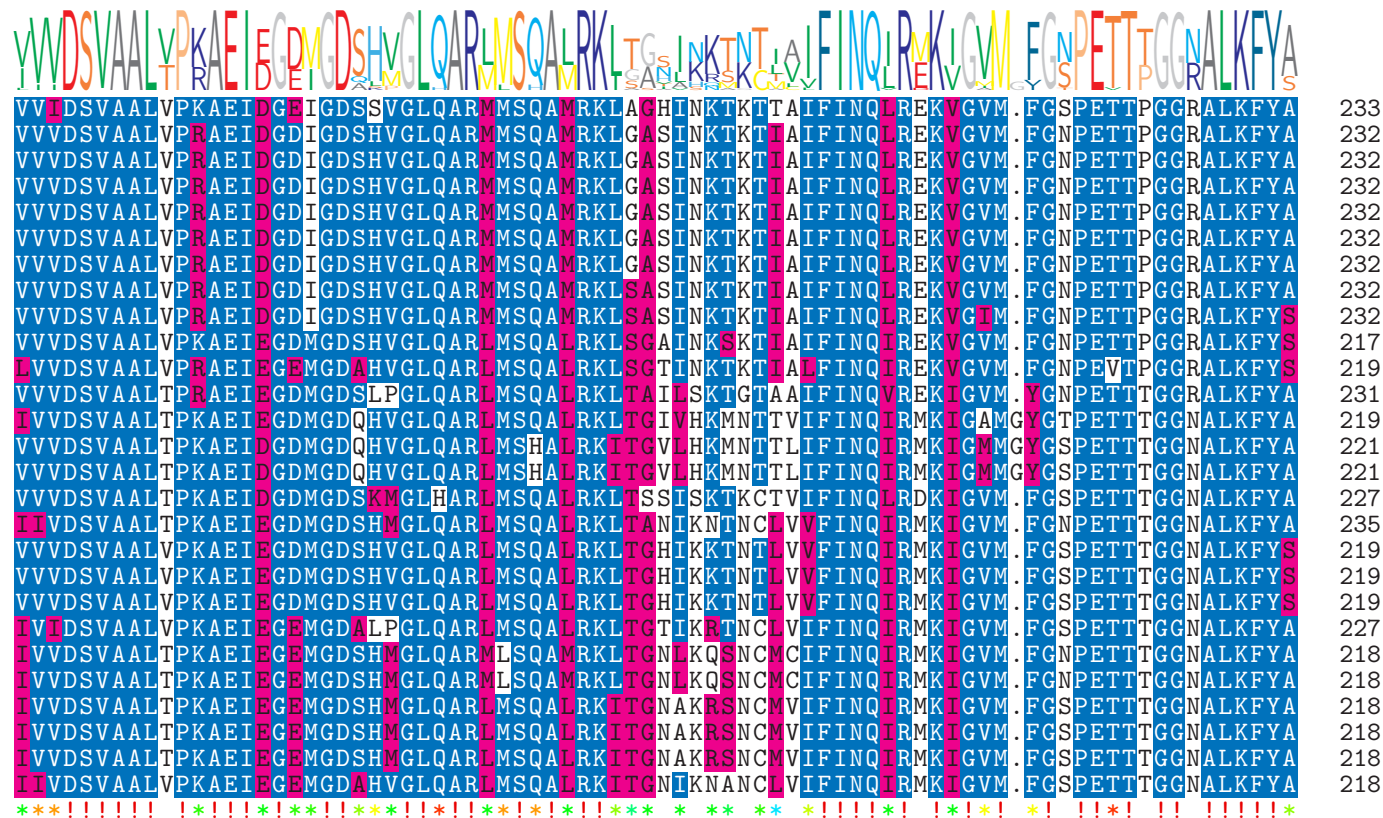
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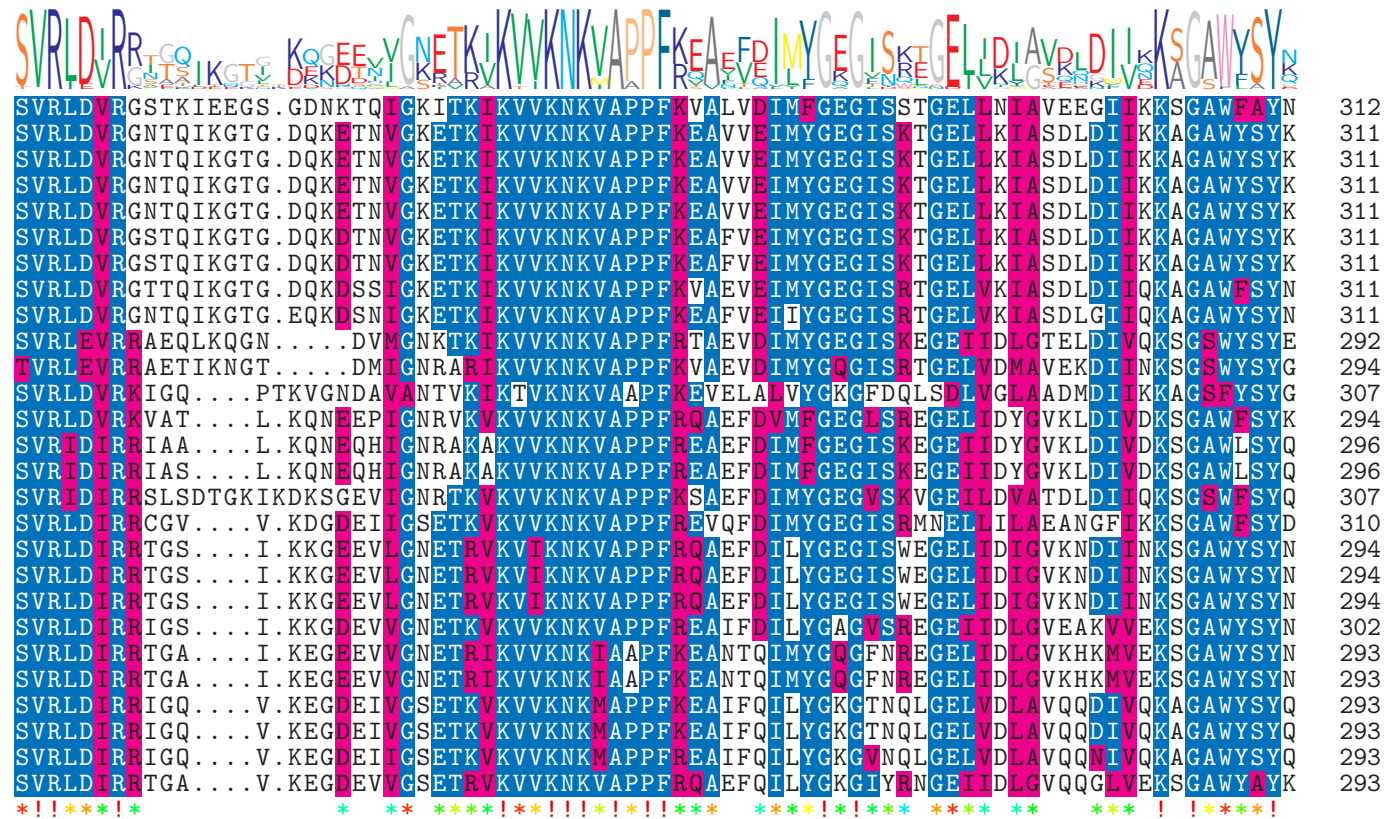
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consensus

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Sequence	Score
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DEKIGGGS E NAKKYLA E HP E IF D EIDDKVRSK F GLIDGEEVSEQDTE.NKKD EPKKEEA..VNEEVPLDLGDEL	382
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DEKIGGGS E NAKKYLA E HP E IF D EIDDKVRSK F GLIDGEEVSEQDTE.NKKD EPKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS E NAKKYLA D N P EV F AEIDHQVRVQ F GLIDGEEAAE.....SKKD EVAQVDS..VNEEVTLDLGDEL	378
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GEKIGGGS E NAKRYLADHP Q L F DEIDRKVRV K GLLEESEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGGGS E NAKKFLADN P EV F DDIDHKVRVQ Y GLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EE R LGQGG R ENAK Q FLKEN K DIM L MIQE Q IREHYGLDNNGVVQQQAEE.TQEEL.E..FE.E.....	348
SERIGQGG R ENAKNYLAD H ED V DEVR L KVRAAY G ISDVPEEDLP T TE.DE.QI.N..ILPDDST....EE.....	355
DERIGQG K EKT I AY I A E R P EME Q EIDR V MAA I RAGNAGEAPALAPAPA A PEAAEA.....	363
DKKLGGG R ENAK A FLKEN P E I AD E ITKAIQNS M G I EGMISGS..EDDEGE. E	343
DKKLGGG R ENAKALL K ED K ALAD E ITL K IKES I GSNEEIMPL..PDEPLE.. E ME.....	347
DKKLGGG R ENAKALL K ED K ALAD E ITL K IKES I GSNEEIMPL..PDEPLE.. E ME.....	347
DTKLGGG R DT V KEL I KDN P EL A E E LEAK I REKLQAK.....	343
GTKIGQG K NNAV K VLKEN P E I AD K LE Q EIRNT L ASN P NSVLK..ATASDSND E SDVEEFSE.....EEL.....	372
GAKIGGQ K DNVR V WLKEN P E I SD E IDAK I RALNG V EMH I TEG..TQDET.....GERPE.....E.....	348
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GE R IGGQ R DN C REF L REN A EL A RE I EN K VREHL G VT P MGAV...TLAEEVEED.....	352
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GNKIGGQ K NNVIR Y FE E NN Q IA E E I ERN I REQLLT T GT N GA V ..Q.I.EDEE E PD..L L LE.....S.....	349
GNKIGGQ K NNVIR Y LE E NP Q IS T E I E A V I REQLLT K AS D Q T A..A.HDETEE E PD..L L ES.....	349
GS K IGGQ K ANA A KY L EN P E I GG E IE Q Q I RA K LL V TSAN T KA..TPVAEDLAD..I.....	347

logo

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consensus								

-  non conserved
-  similar
-  ≥ 50% conserved