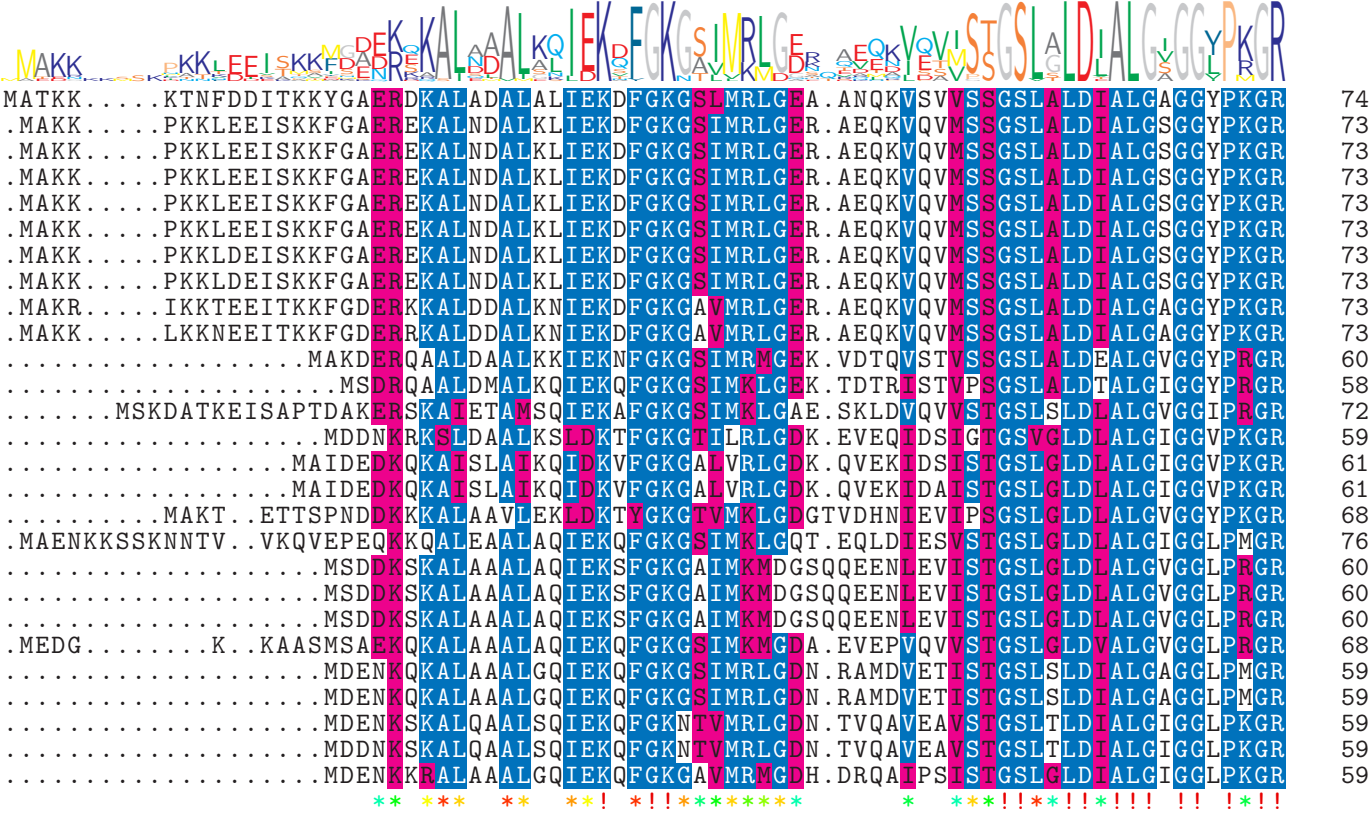


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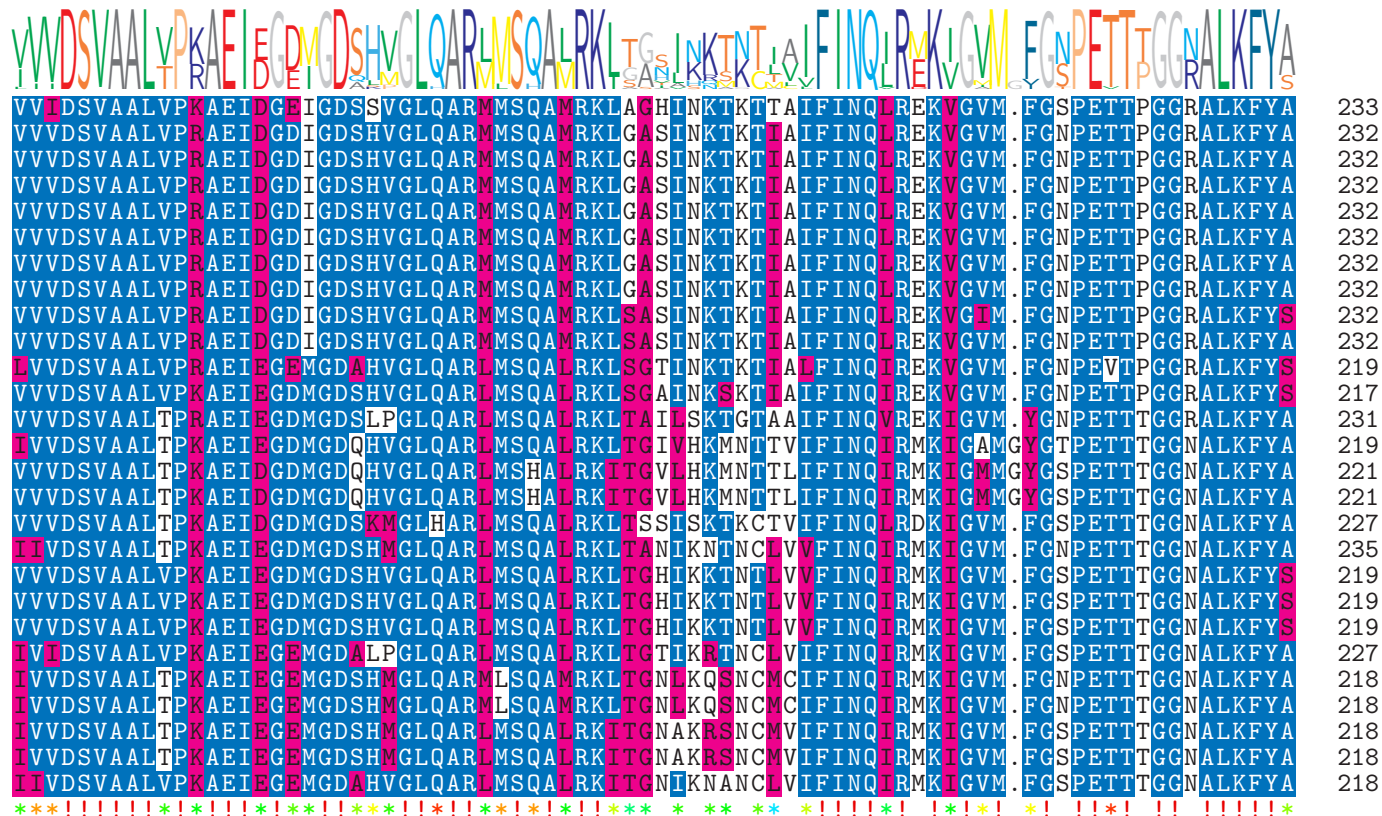
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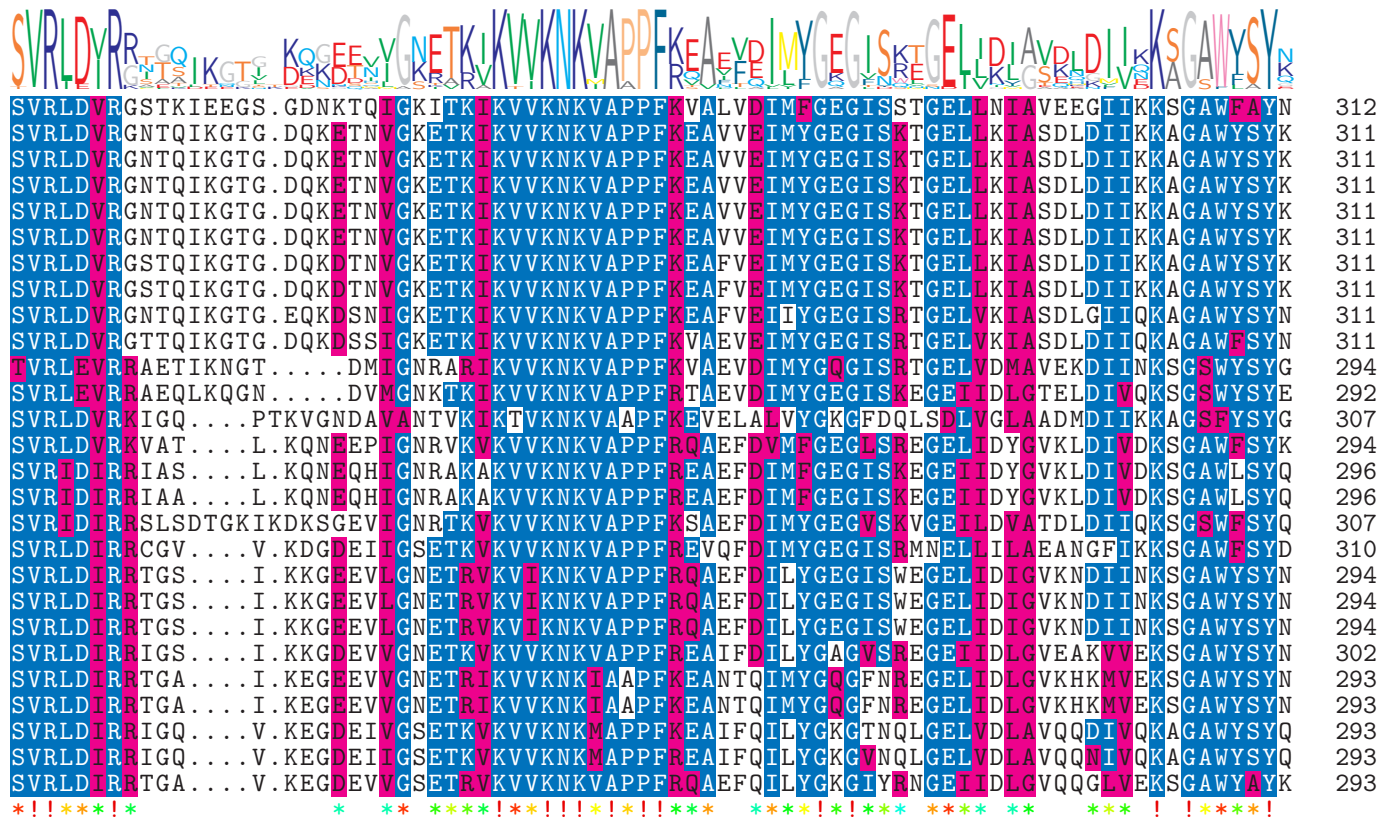
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consensus

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Sequence	Score
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DEKIGGGS E NA K KYLA E HP E IFDEIDKQVRSKFGLIDGEEVSEQDTENKKDEP....KKEEA..VNEEVVTLDLGDELEIE	385
DEKIGGGS E NA K KYLA E HP E IFDEIDKQVRSKFGLIDGEEVSEQDTENKKDEP....KKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS E NA K KYLA E HP E IFDEIDKQVRSKFGLIDGEEVSEQDTENKKDEP....KKEEA..VNEEVPLDLGDELEIE	385
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DEKIGGGS E NA K KYLA D N P EF F AEIDHQVVRVQFGLIDGEEVSEQDTENKKDEP....KKEEA..VNEEVPLDLGDELEIE	381
GEKIGGGS E NA K KFL D N P EF D IDHQVVRVQFGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGGGS E NA K RYL D HP Q LFDEIDRKVVRVKFGLLEESEEEESAMAVASE.....E.....T D LALDLNNGIEIE	377
SERIGGG R ENAKNYL D H D VEDEVRQKVRVQFGLISDVPEEDLPTTEDE.QIN.....ILPDDSTEE.	355
EERLGGC R ENAK Q FL K EN K D I ML I QLKQVIREHYGLDNNGVVQQQAETQEELE.....FE.E.....	348
DERIGGG K EKT I AY I A R PE M E Q EIRDRVMAAIRAGNAGEAPALAPAPAPEAAE..A.....	363
DK K LGGG R EN K AF L KE N PE I AD E IT K AIQNSM G TEGMI....SGSEDDE..GE..E.....	343
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DT K LGGG R DT V KE L IK D N P EL A EE L EAK I REKLQAK.....	343
GT K IGGG K NN A V K WL K EN P E I AD K LE I RT L AS N PN SVLKATASDSND..ES..... D VEEFSEEEEL...	372
GA K IGGG K D N VR V WL K EN P E I S D E I DA K IR A LN G VE M HI....TEGTQDET.....GERPEE....	348
GA K IGGG K D N VR V WL K EN P E I S D E I DA K IR A LN G VE M HI....TEGTQDET.....GERPEE....	348
GA K IGGG K D N VR V WL K EN P E I S D E I DA K IR A LN G VE M HI....TEGTQDET.....GERPEE....	348
GE R IGGG R DN C REF L RE N AE L ARE I EN K VR E HL G VT P MG....AV.TLAEVEE..D.....	352
GD K IGGG K AN A CK Y L K EN P E I AK T LD K KLREMLLN P EN MQLIAETSSAAD..DV..... E FGAVPEEF....	354
GD K IGGG K AN A CK Y L K EN P E I AK T LD K KLREMLLN P EN MQLIAETSSAAD..DV..... E FGAVPEEF....	354
GN K IGGG K NN V IR Y FE E NN Q IA E FE I ERN I REQLLT T GT NGAVQ.I.EDEE..EP..... D ..LLES.....	349
GN K IGGG K NN V IR Y LE E NN P Q I STE I E A V I REQLLT K AS DQTAA.HDETEE..EP..... D ..LLES.....	349
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logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved