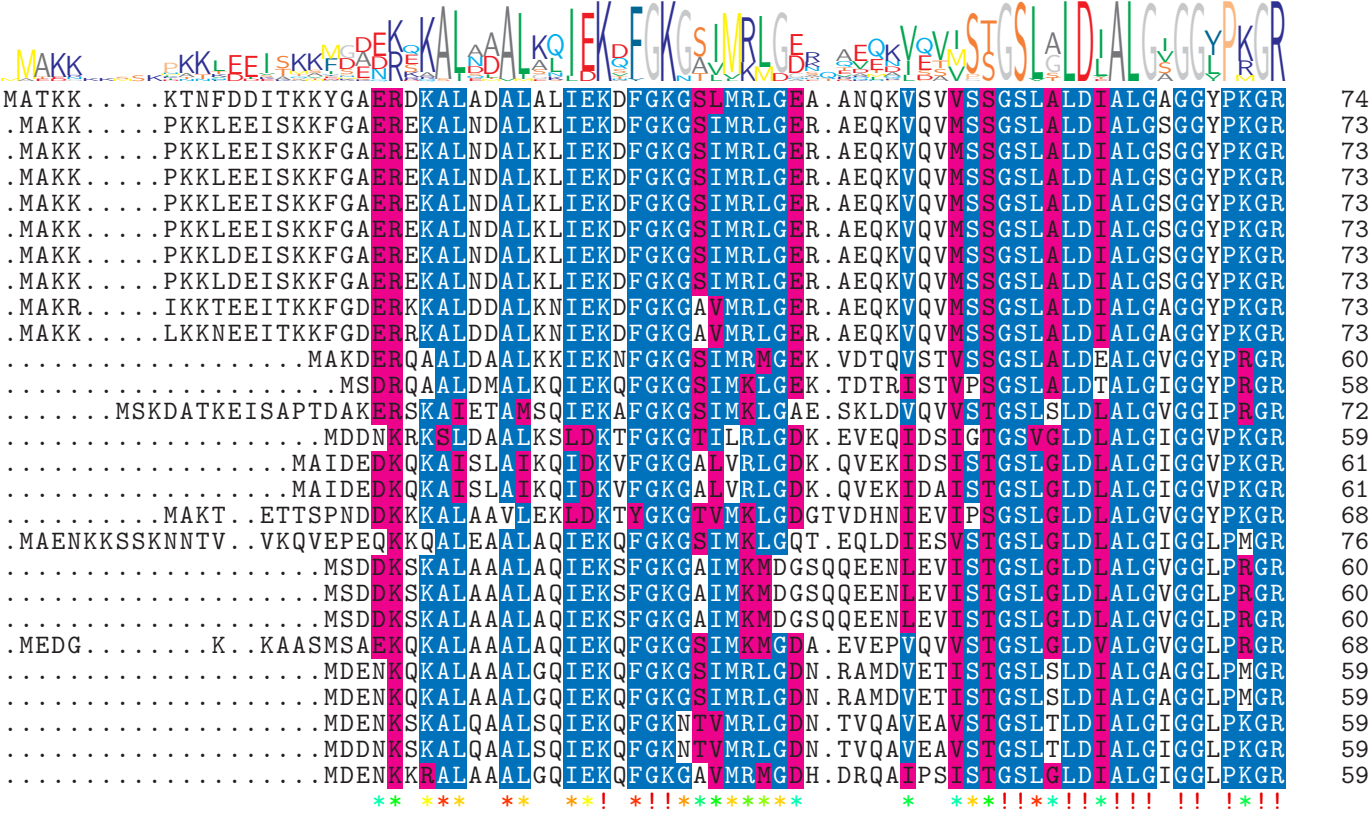


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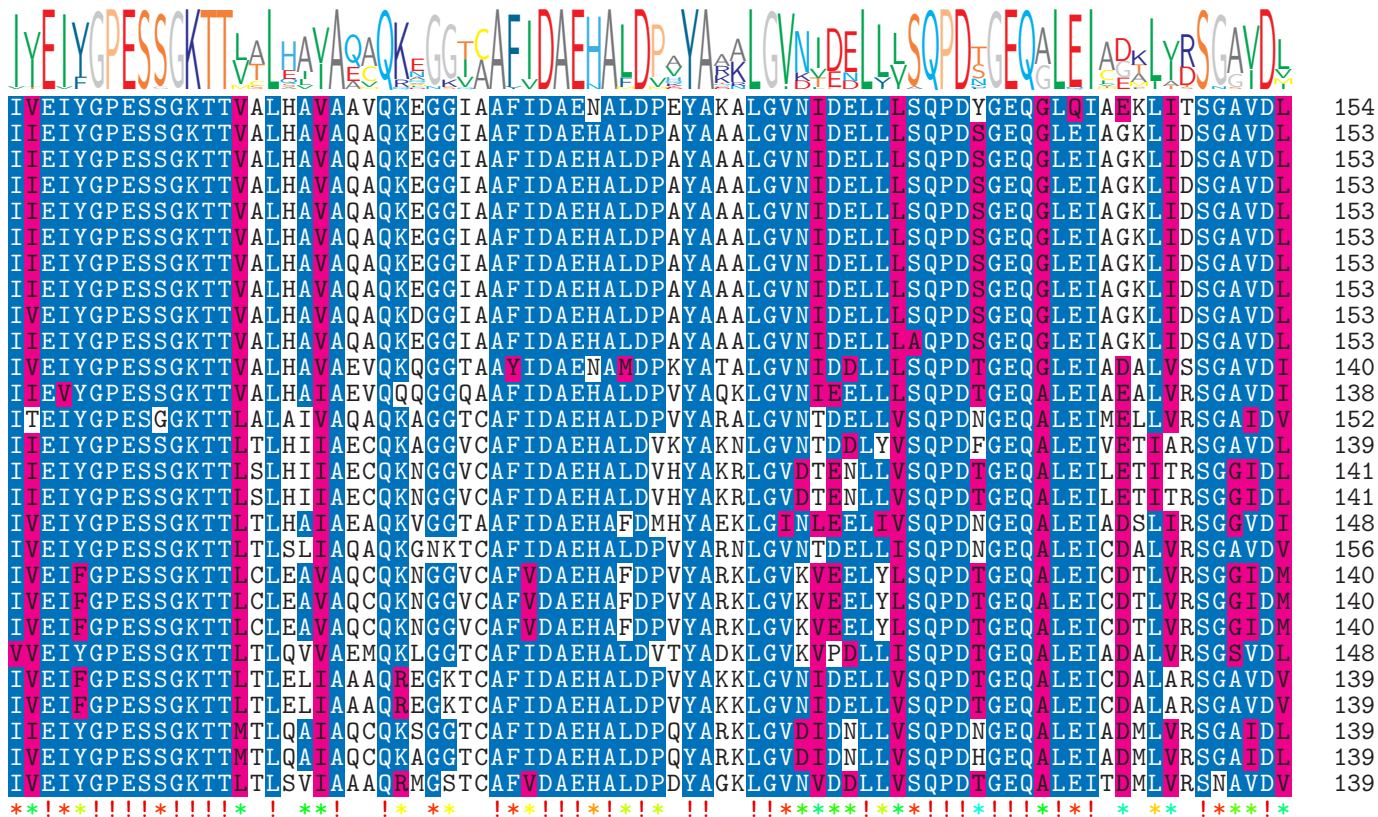
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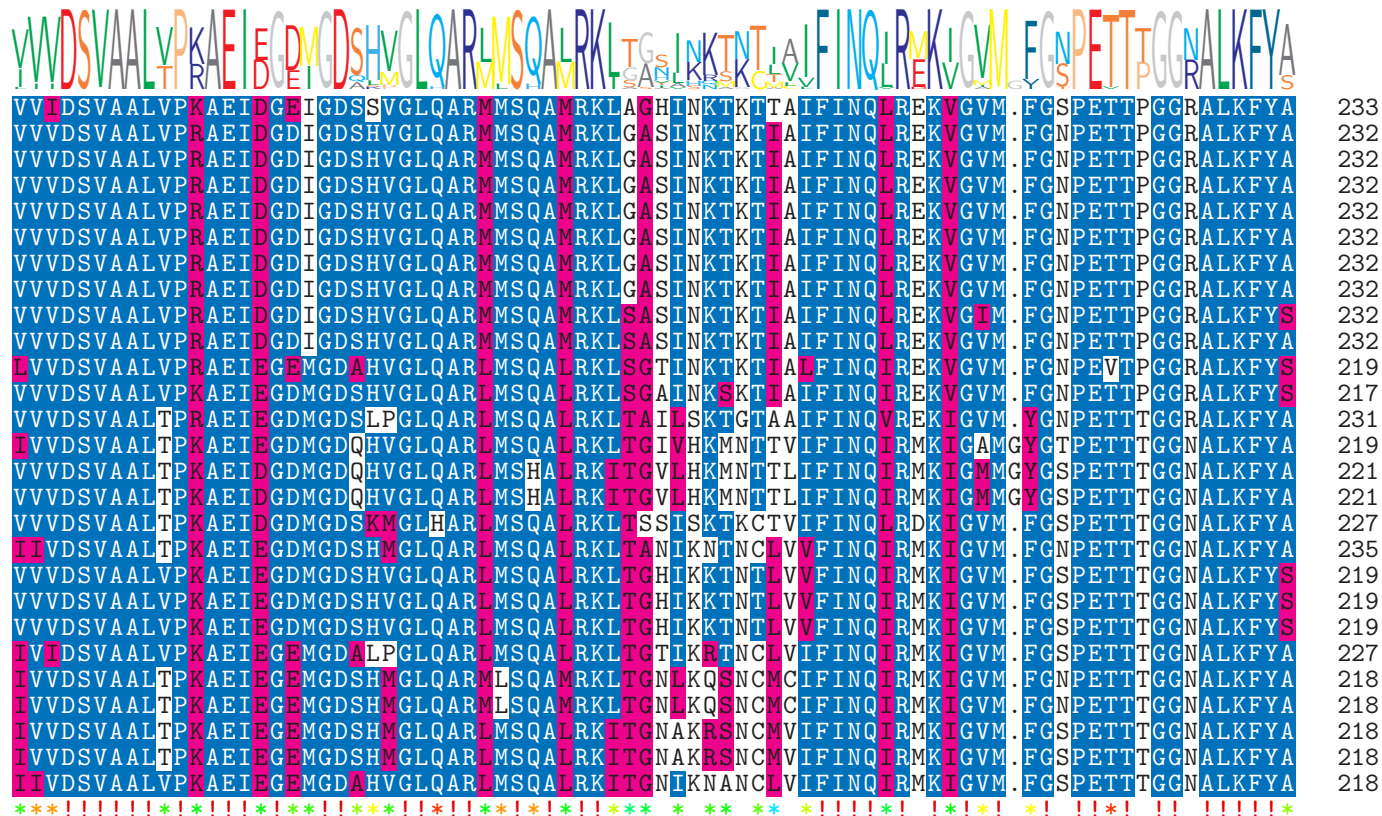
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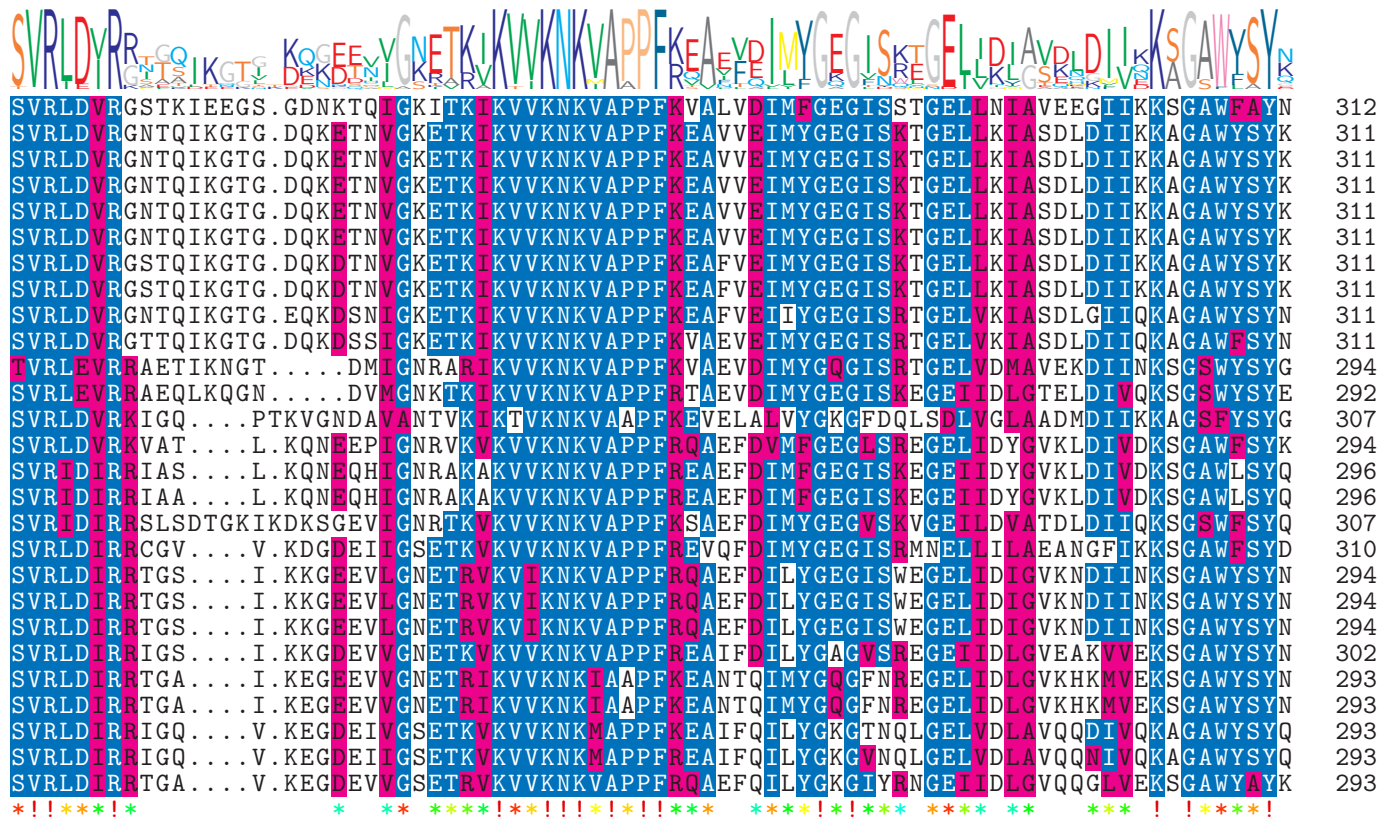
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consensus

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Sequence	Score
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SERIGGG R ENAKNYLADH D VE D EVRLKVR A AY G ISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
EE R L G GG R ENAK Q FL K EN K D I ML I Q E Q I REHY G L D NNGVVQQQA E ET Q EEL E . E . E	348
DE R IGGG K E K TI A Y I A E RP E ME Q E I RD R MA A IRAG N AGE A P A L A P A AE A EA.....	363
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DK K L G GG R ENAKALL K ED K AL A D E IT L K I KE S IG S NE E I....M P L P DE P ..L E EM E	347
DT K L G GG R DT V KE L IK D N P EL A EE L E A K I RE K L Q A K	343
G T KIGGG K NN A V K W L KE N PE I A D K L E Q E I RT N TL A SN P NS....V L K A T A SD S N D ES D ..V E EF S EE E L.....	372
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GE R IGGG R D N C R E F L N AE L ARE I EN K VR E HL G VP M G....AV.T L AE E VE E D.....	352
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GN K IGGG K NN V IR Y FE E NN Q IA E E I ERN I RE Q LL T T G T NG A V Q . I .E D EE E PD....L L ES.....	349
GN K IGGG K NN V IR Y LE E NP Q I S TE I E A VI R E Q LL T K A S DQ T AA. H DE T EE E PD....L L ES.....	349
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logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved