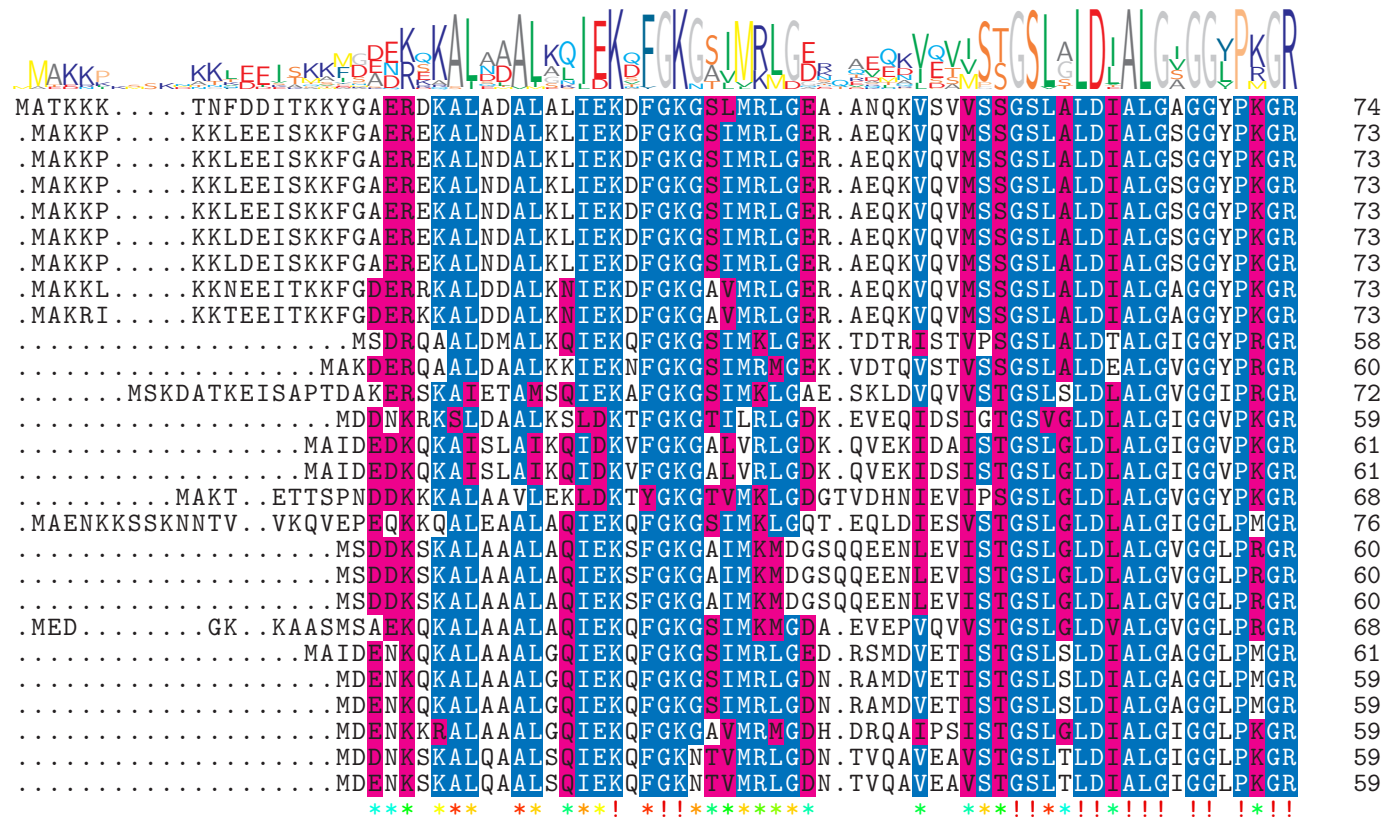


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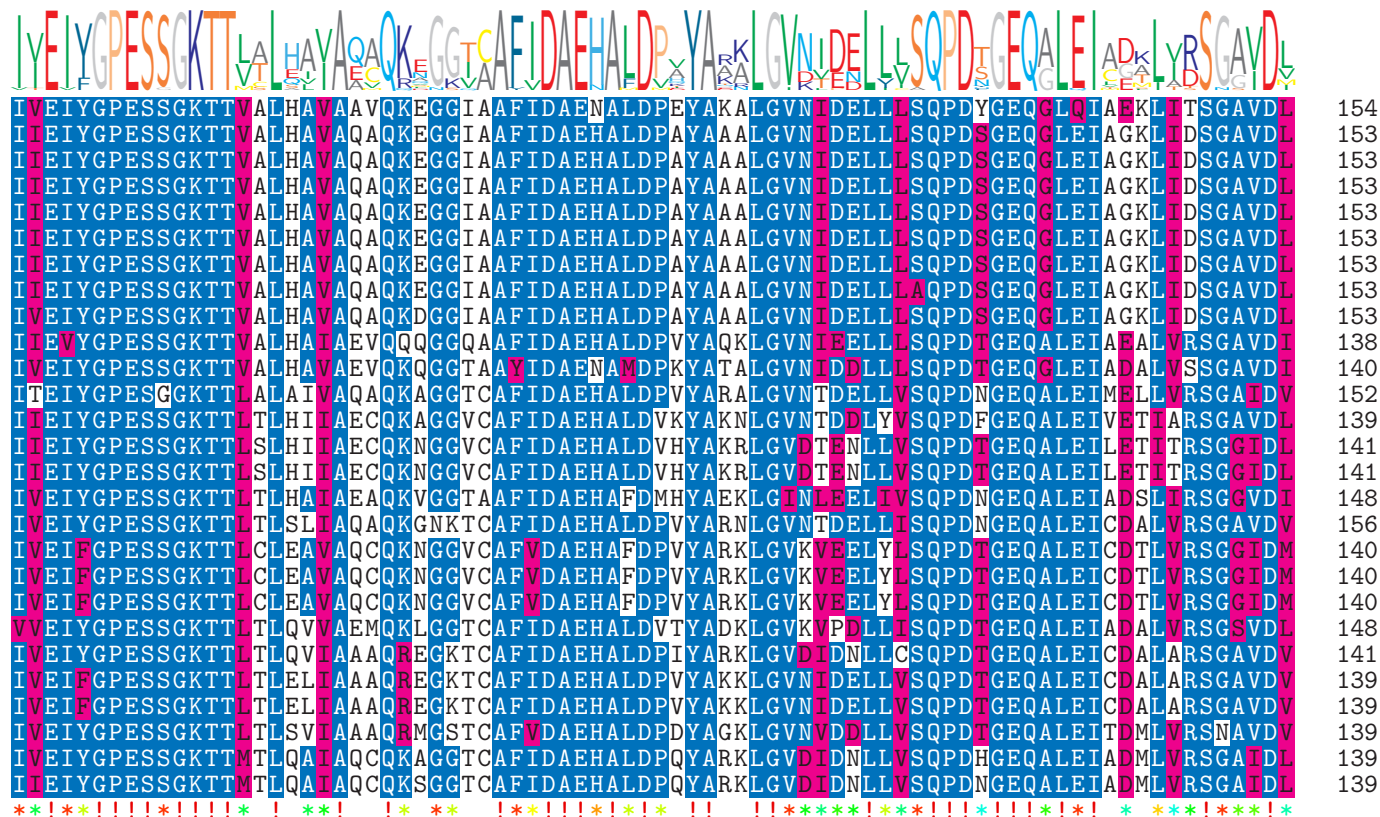
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consensus

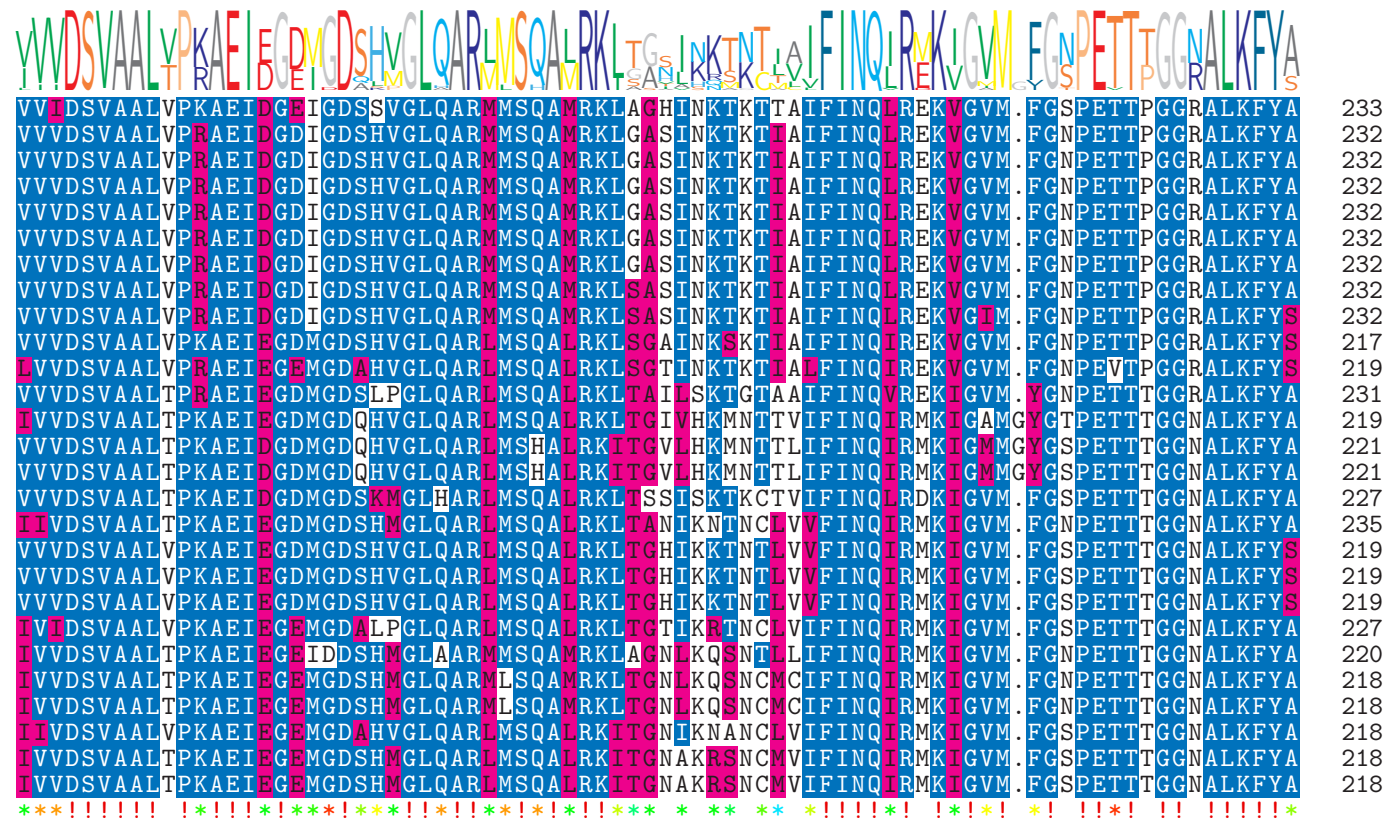
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Sequence	Score
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DEKIGQGS E NA K KYLA E HP E IF D EID K QV R SK F GLIDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA D N P E I F D EID H Q V RV Q FLIDGEEIAES KKDE AAQVDS . . VNEEVTLDLGDLEIE	381
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SERIGGGREN A KNYLA D H E D V DE V RLK V RAAYGISDVPEEDLPTTEDE . QI . NILPDDST EE	355
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consensus

 non conserved
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 ≥ 50% conserved