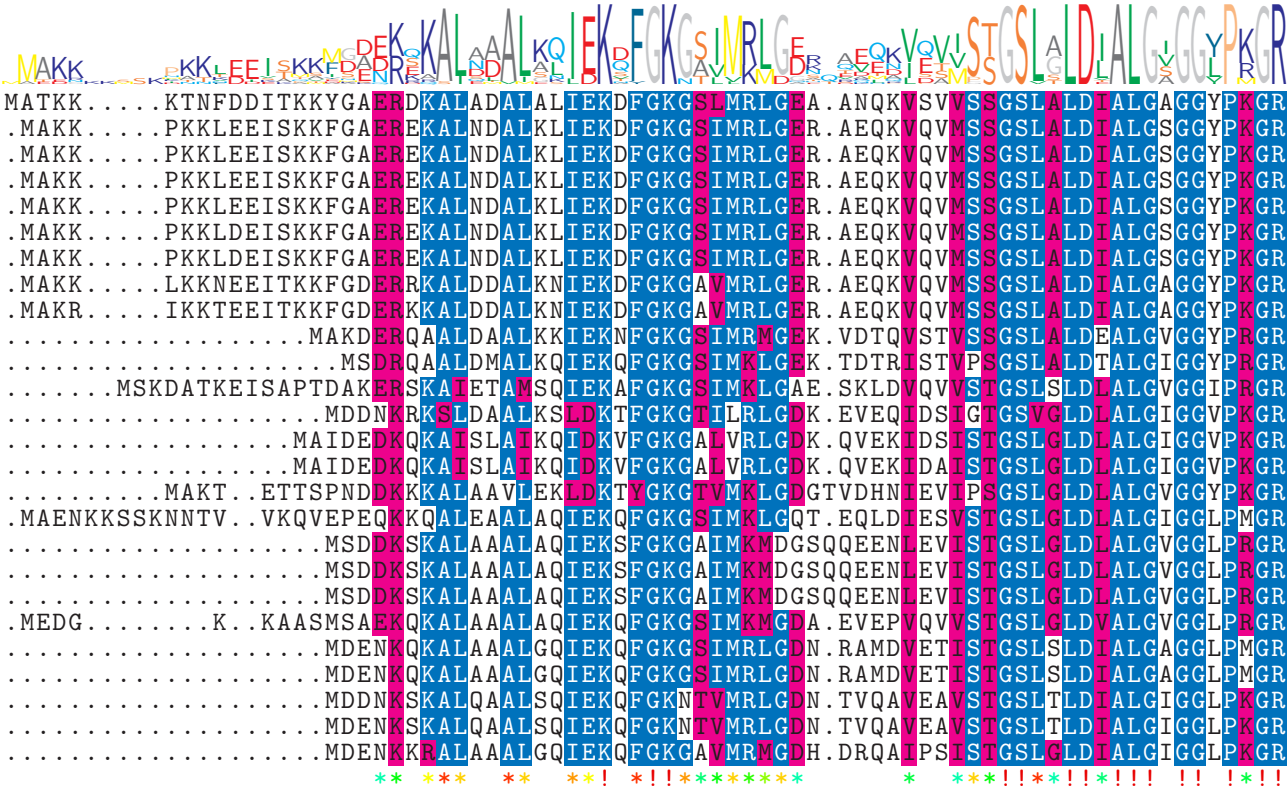


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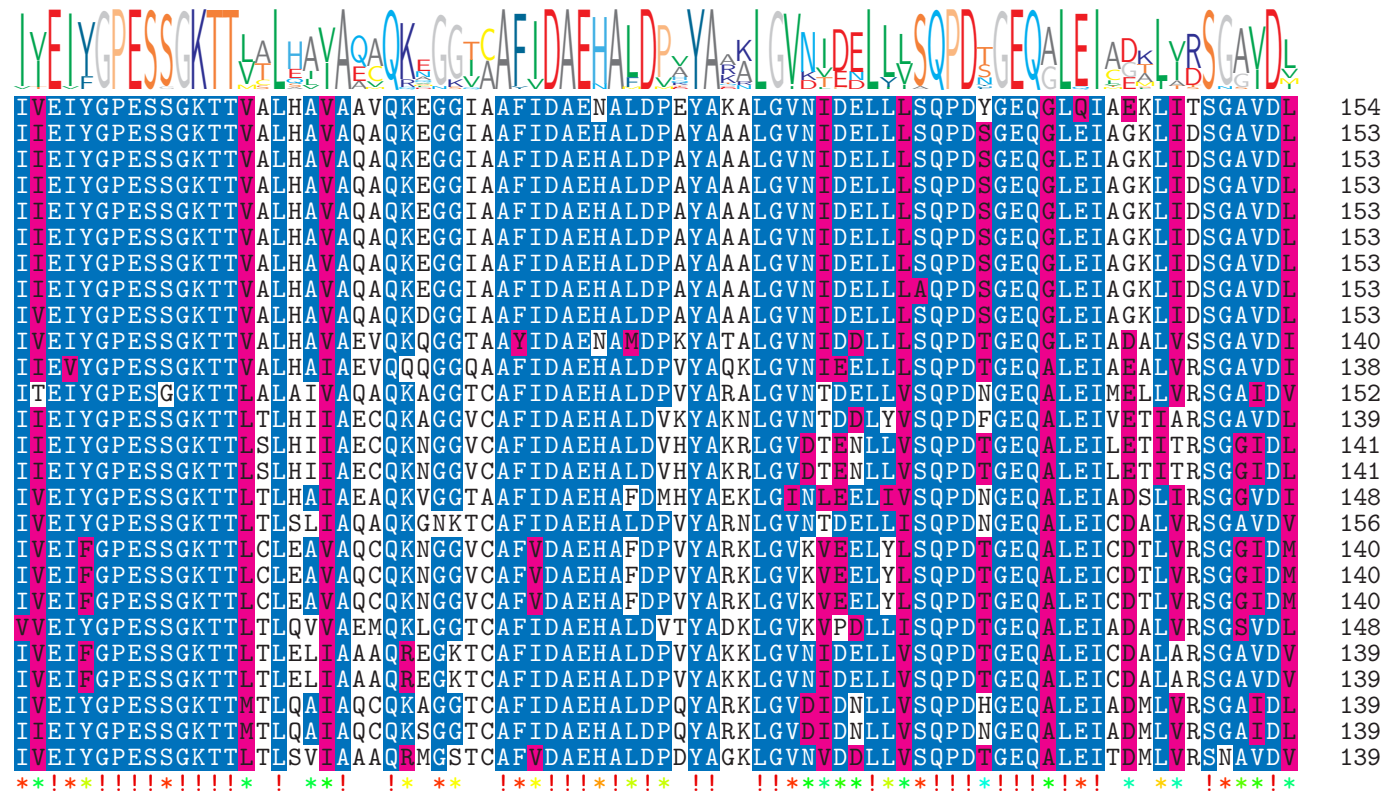


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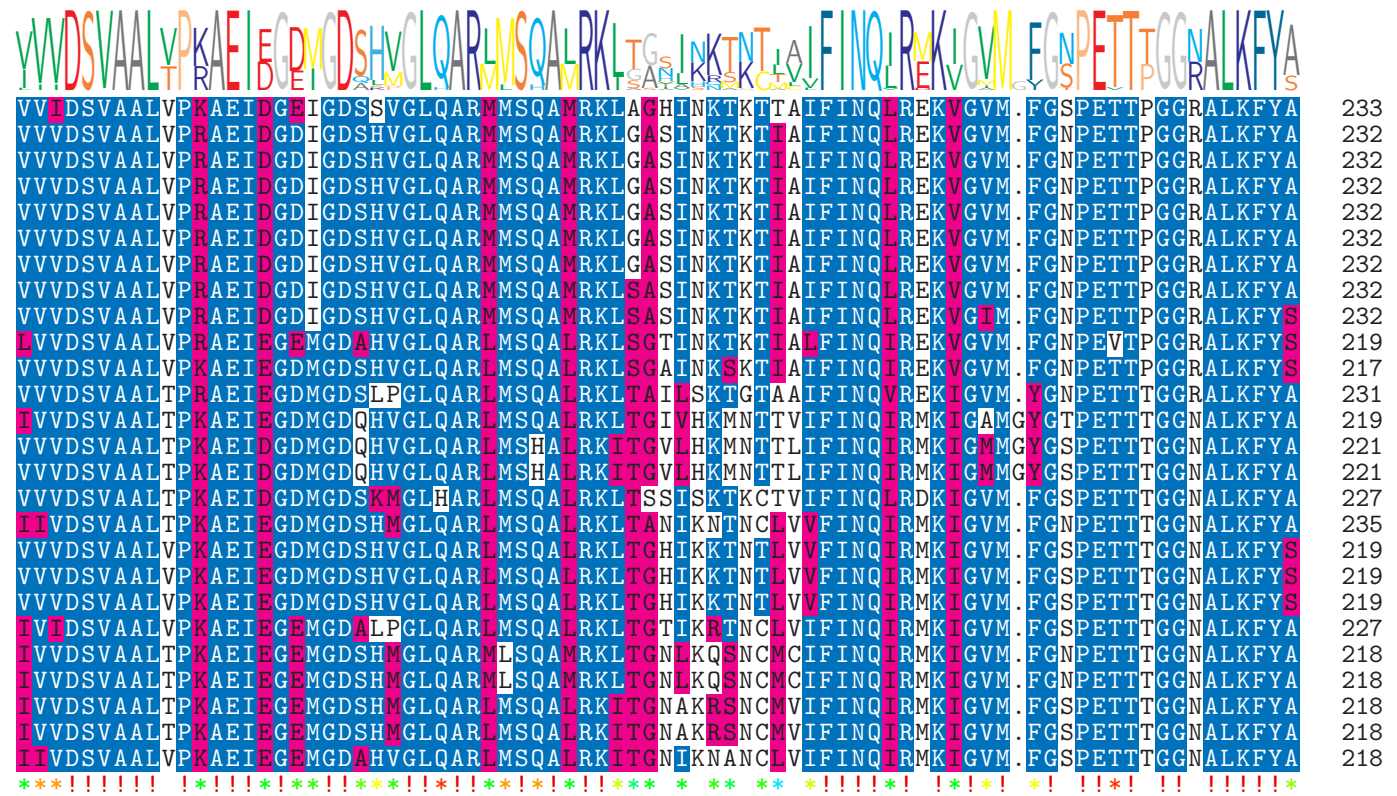
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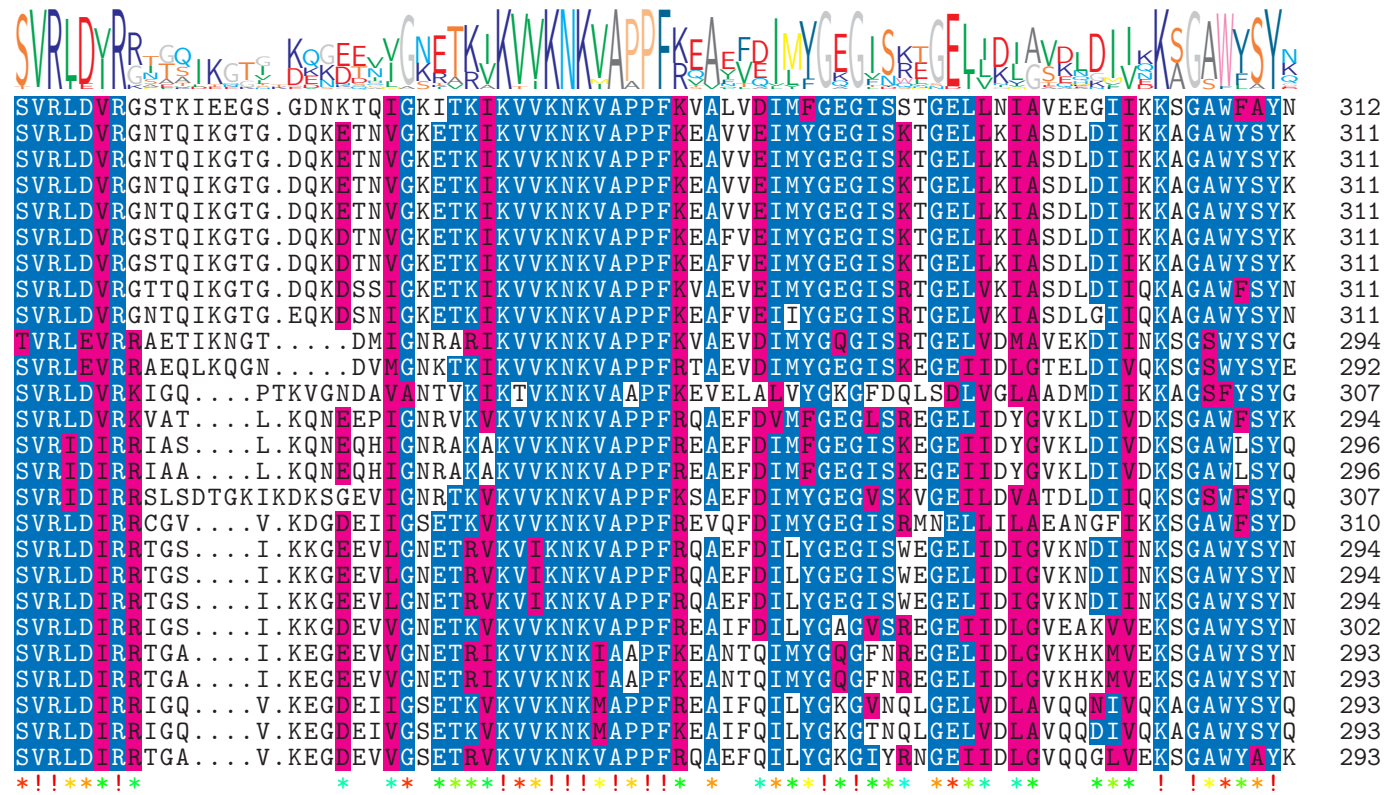
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Sequence	Score
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DEKIGQGS E NA K KYLAD N PE I F F DEID H QV R VQ F GLIDGEEIA SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGS E NA K KYLAD N PE V FA I D H QV R VQ F GLIDGEEAA SKKDE....VAQVDS..VNEEVTLDLGDELEIE	381
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GEKIGQGS E NA K KFLAD N PE I F D DI D HK V R V Q Y CLIEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
SERIGQG R ENAK N YLAD H DE V DE V RLK V RAAY G ISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
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DERIGGQ E K T IAYIA E RPE M EQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAE..A.....	363
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DKKLGGGREN A KALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..PLE..EME.....	347
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GAKIGQGK D NVRV V LKENPEIS D EIDA K IRALN G VEMHI....TEGTQDET D GE..R.....PEE.....	348
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GNKIGQGK N NVIRY L EEN P QISTEIEAVIREQLLT K ASD....QTAA.HDETEE..EPDLL..ES.....	349
GNKIGQGK N NVIRY F EEN N QIAE E IERNIREQLLT T GTN....GAVQ.I.EDEE..EPDLL..LES.....	349
GSKIGQGK A NA A KYLEENPEI G QEIE Q QIRAKLL V TSAN....TKATPVAEDLA..DADI.....	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved