

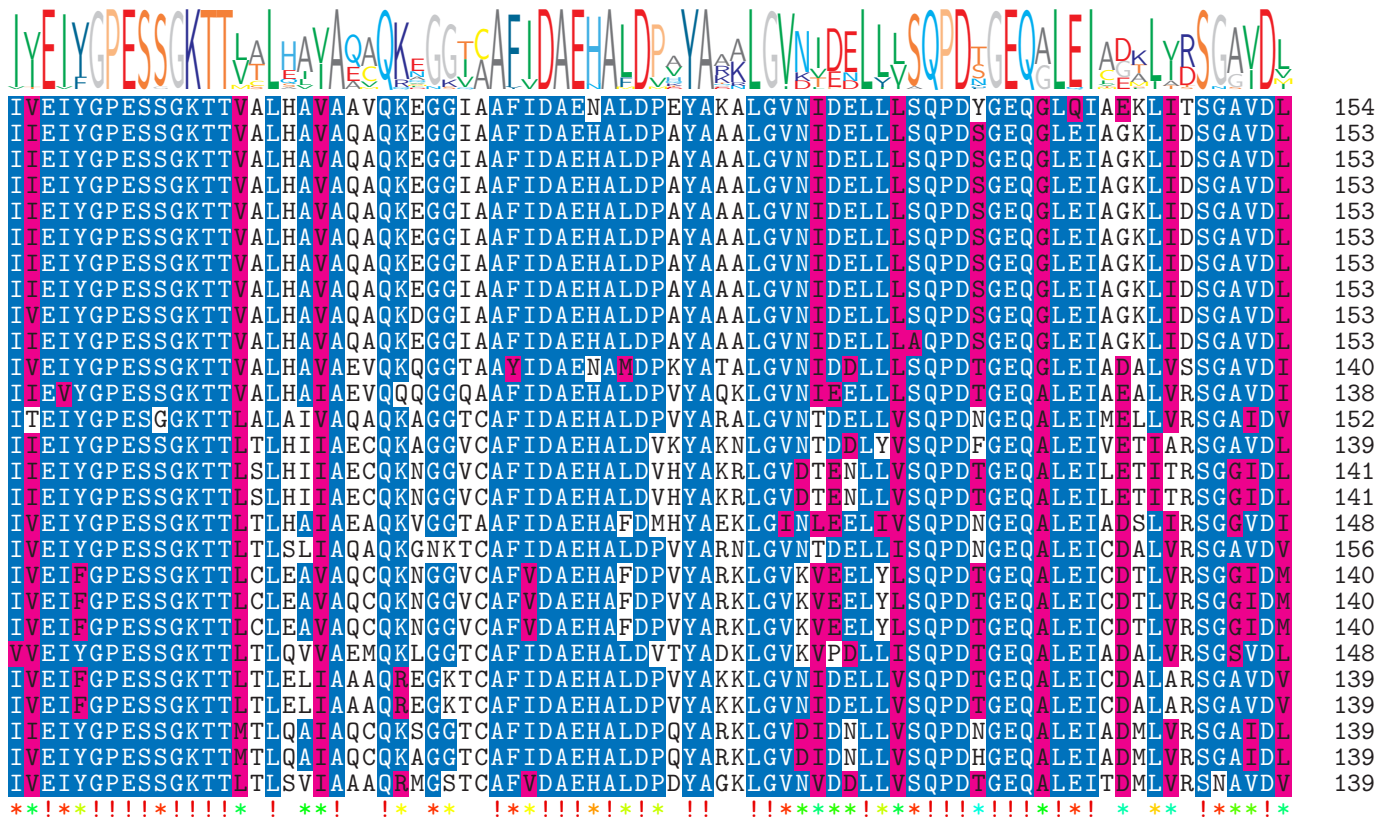
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consensus

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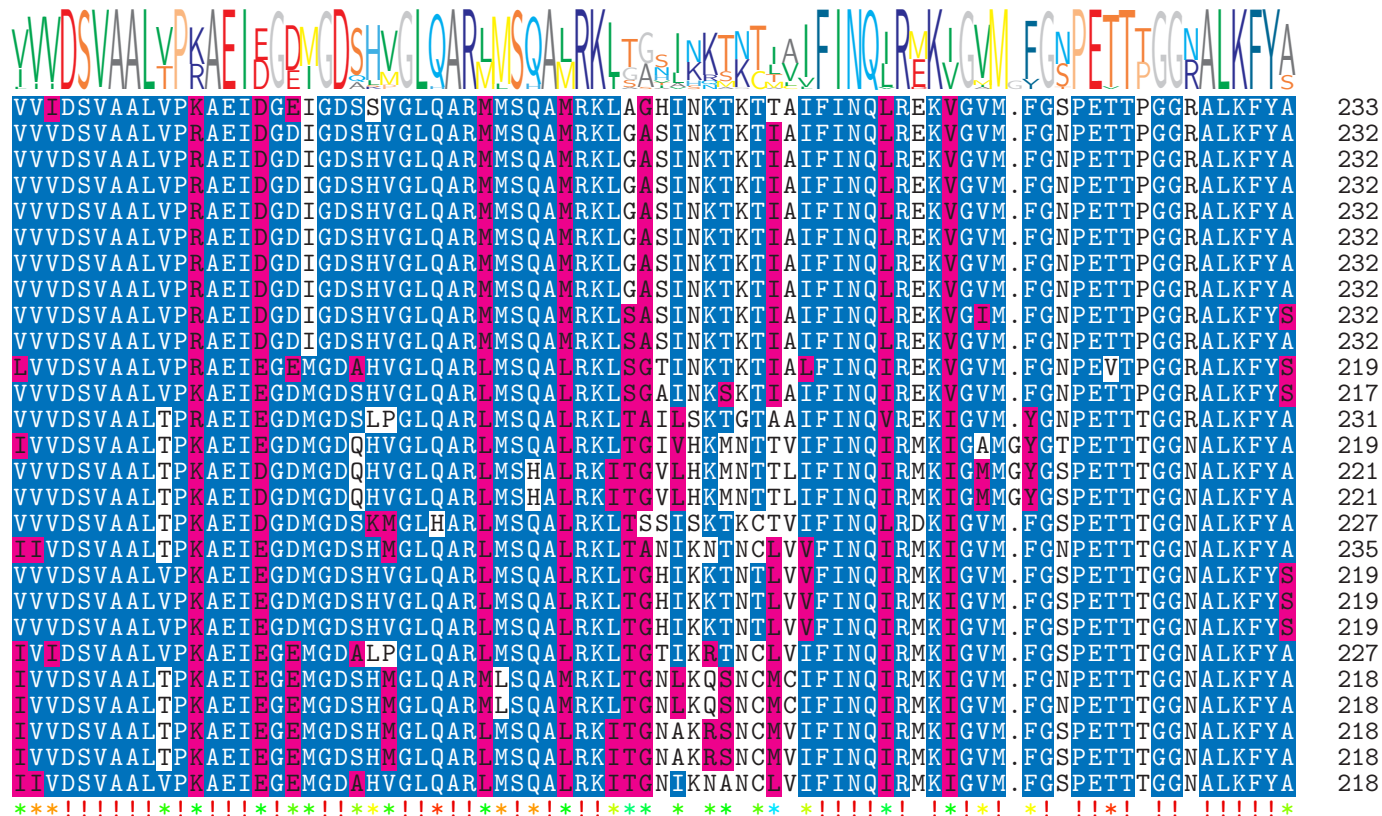
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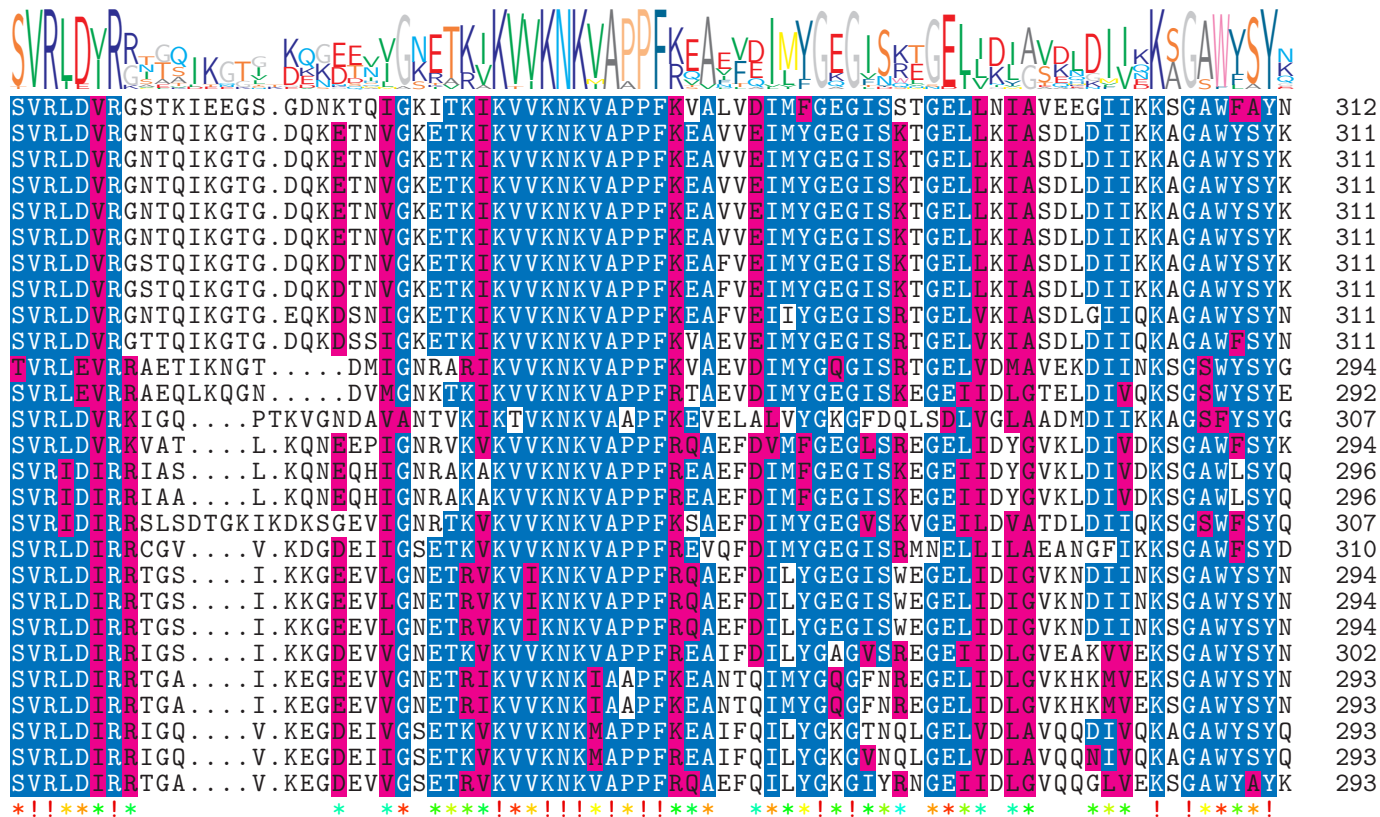
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Sequence	Score
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DEKIGGGS E NA K KYLA E HP E IF D EIDDKQVRSKF G LIDGEEVSEQDTENKKDEP...KKEEA..VNE E VPLDLGDELEIE	385
DEKIGGGS E NA K KYLA E HP E IF D EIDDKQVRSKF G LIDGEEVSEQDTENKKDEP...KKEEA..VNE E VPLDLGDELEIE	385
DEKIGGGS E NA K KYLA E HP E IF D EIDDKQVRSKF G LIDGEEVSEQDTENKKDEP...KKEEA..VNE E VPLDLGDELEIE	385
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DEKIGGGS E NA K KYLA D N P E V FA E IDHQVRSVQ F GLIDGEEAAES...KKDEV...AQVDS..VNE E VTLDLGDELEIE	381
GEKIGGGS E NA K KFL D N P E F IF D IDHKVRSVQ F GLIEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGGGS E NA K RYL D HP Q L F DEIDRKVRSVQ F GLLESEEEESAMAVASE.....E.....TD D LALDLNNGIEIE	377
SERIGGG R ENAKNYL D H D VE D EVRLKVR A AY G ISDVPEEDLPTTEDE.QIN.....ILPDDSTEE.	355
EERLGGC R ENAK F L K EN K D I ML I IQ E IR E HY G LDDNNGVVQQQA E ET Q EE LFE.E.....	348
DERIGGG K E K TI A Y I A R P E ME Q EIRDRVMAA I RAGNAGEAPALAPAPA E AA E ..A.....	363
DK K LGGG R EN K A F L K EN P E I A D E I TK A I Q NS M G I EGMI....SGSEDDE..GE..E.....	343
DK K LGGG R ENAKALL K EDKAL A D E ITL K I K ESIGS N EEI....MPLPDEP..LE..EM..... E	347
DK K LGGG R ENAKALL K EDKAL A D E ITL K I K ESIGS N EEI....MPLPDEP..LE..EM..... E	347
DTKLGGGRD T V K EL I KN P EL A E E L A K I REKL Q A.....VLKATASDSND..ES.....DVEEFSEEEEL...	372
GT K IGGG K NN A V K WL K EN P E I A D K L E I RT L AS N PN SVLKATASDSND..ES.....DVEEFSEEEEL...	372
GA K IGGG K D N VR V WL K EN P E I S D E I DA K IR A L N GV E M H I....TEGTQDETD.....GERPEE.....	348
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GE R IGGG R D N C R FL R EN A EL A R E EN K V R EHL G VP M G....AV.TLAEVEE..D.....	352
GD K IGGG K AN A CK Y L K EN P E I AK T LD K KL R E M LL N PEN MQLIAETSSAAD..DV..... E FGAVPEEF...	354
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GN K IGGG K NN V IR Y LE E NP Q I S TE I EA V IRE Q LL T K A S DQTAA.HDETEE..EP.....D..LLES.....	349
GS K IGGG K AN A AK Y L E EN P E I GE I E Q Q I RA K LL V TSAN....TKATPVAEDLA..DA.....D..I.....	347

logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved