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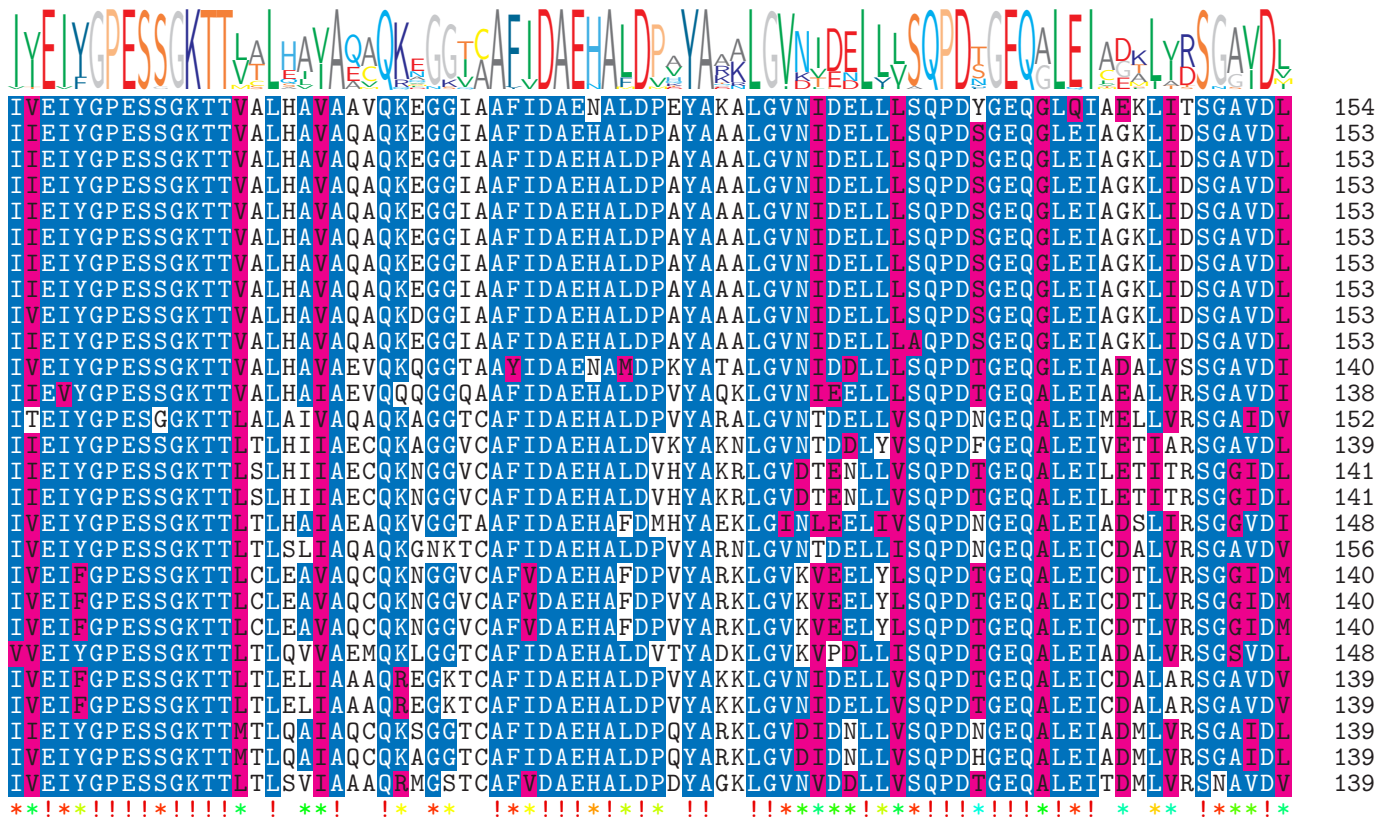
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consensus

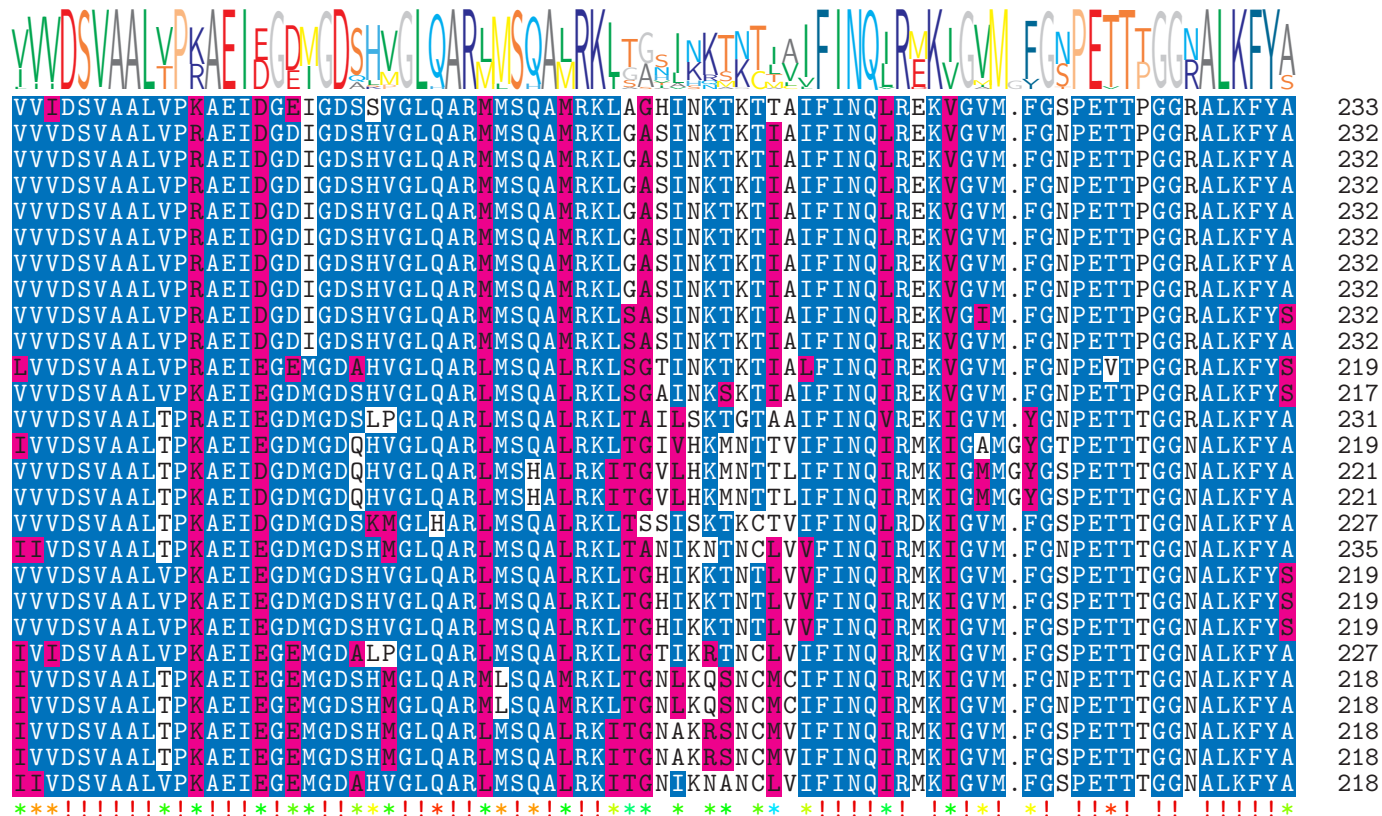
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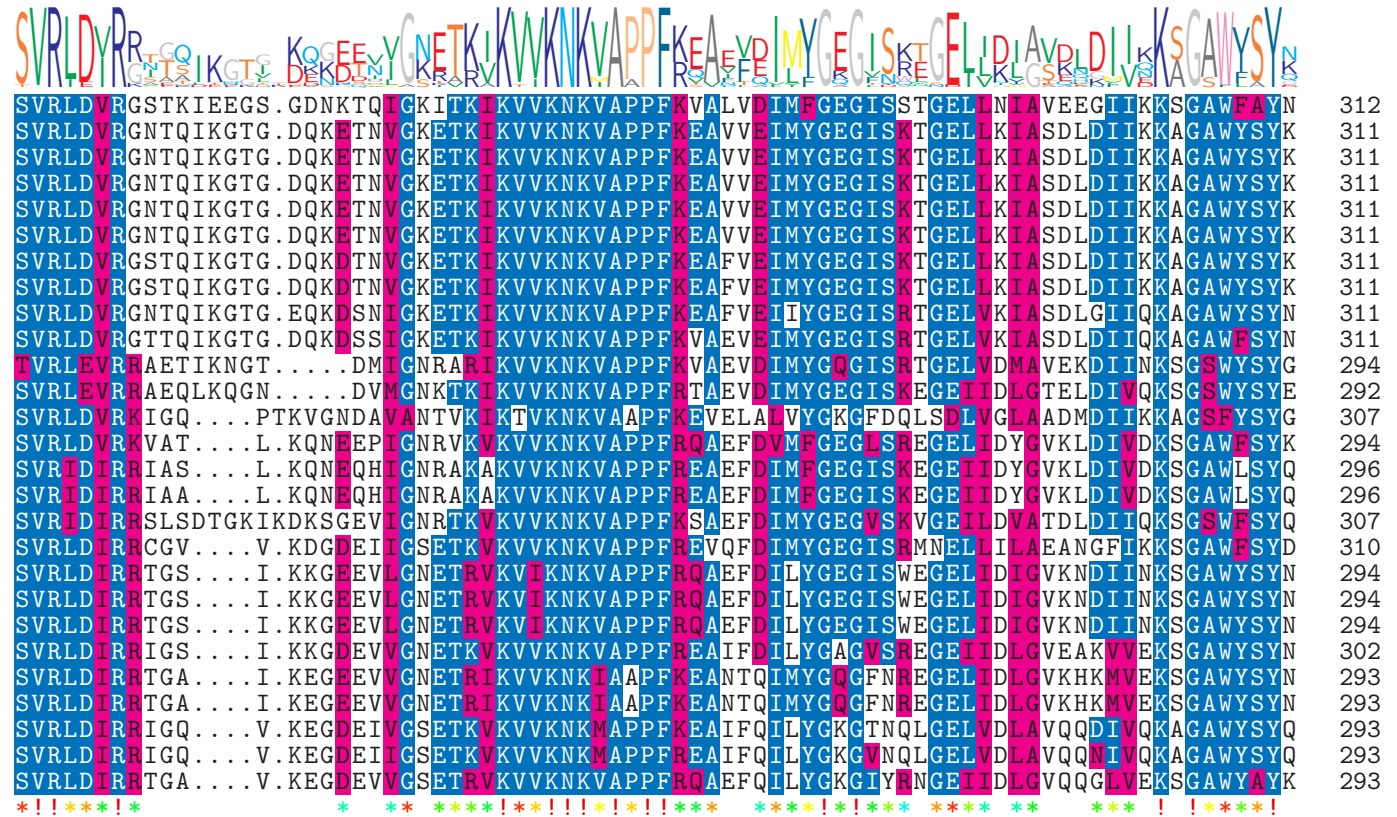
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consensus

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Sequence	Score
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DEKIGGGS E NA K KYLA E HP E IF D EIDDKQVRSKF G LIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS E NA K KYLA E HP E IF D EIDDKQVRSKF G LIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS E NA K KYLA E HP E IF D EIDDKQVRSKF G LIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS E NA K KYLA D N P E I F D EIDHQVVRVQ F GLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGGGS E NA K KYLA D N P E V FA E IDHQVVRVQ F GLIDGEEAAES....KKDE....VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGGGS E NA K KFL D N P E I F D IDHKVVRVQ F GLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGGGS E NA K RYL D HP Q L F DEIDRKVVRV K FLLEESEEEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
SERIGGG R EN A KNYL D H E D V E V RLKVR A E G ISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
EERLGGC R EN A K Q FL K EN K D I ML I Q E IR E HY L DNNGVVQQ A E T Q E EL.EFE.E.....	348
DERIGGG E K T I A Y I A R P E M E Q E IR D RV M A I R A G N A E P A L A P A P A E A E A	363
DK K LGG R EN S K A FL K EN P E I A D E I TK A I Q NS M G I EGMI....SGSEDDE..GEE.....	343
DK K LGG R EN A K A LL K ED K AL A D E IT L K I K E S I GS N E E I....MPLPDEP..LEEME.....	347
DK K LGG R EN A K A LL K ED K AL A D E IT L K I K E S I GS N E E I....MPLPDEP..LEEME.....	347
DT K LGG R DT V K E L I KN P E L A E E L E A K I RE K L Q A.....	343
GT K IGGG K NN A V K W L EN P E I A D K L E I Q E IR T N L A S N P NS....VLKATASDSNDESD..VEEFSEEL.....	372
GA K IGGG K DN V RV W L K EN P E I S D E I DA K I R AL N GV E M H I....TEGTQDET.....GERPEE.....	348
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GE R IGGG R DN C REF L RE N A E L A RE I EN K VR E HL G VP M G....AV.TLAEVEED.....	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 P E N MQLIAETSSAADDVE..FGAVPEEF.....	354
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logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved