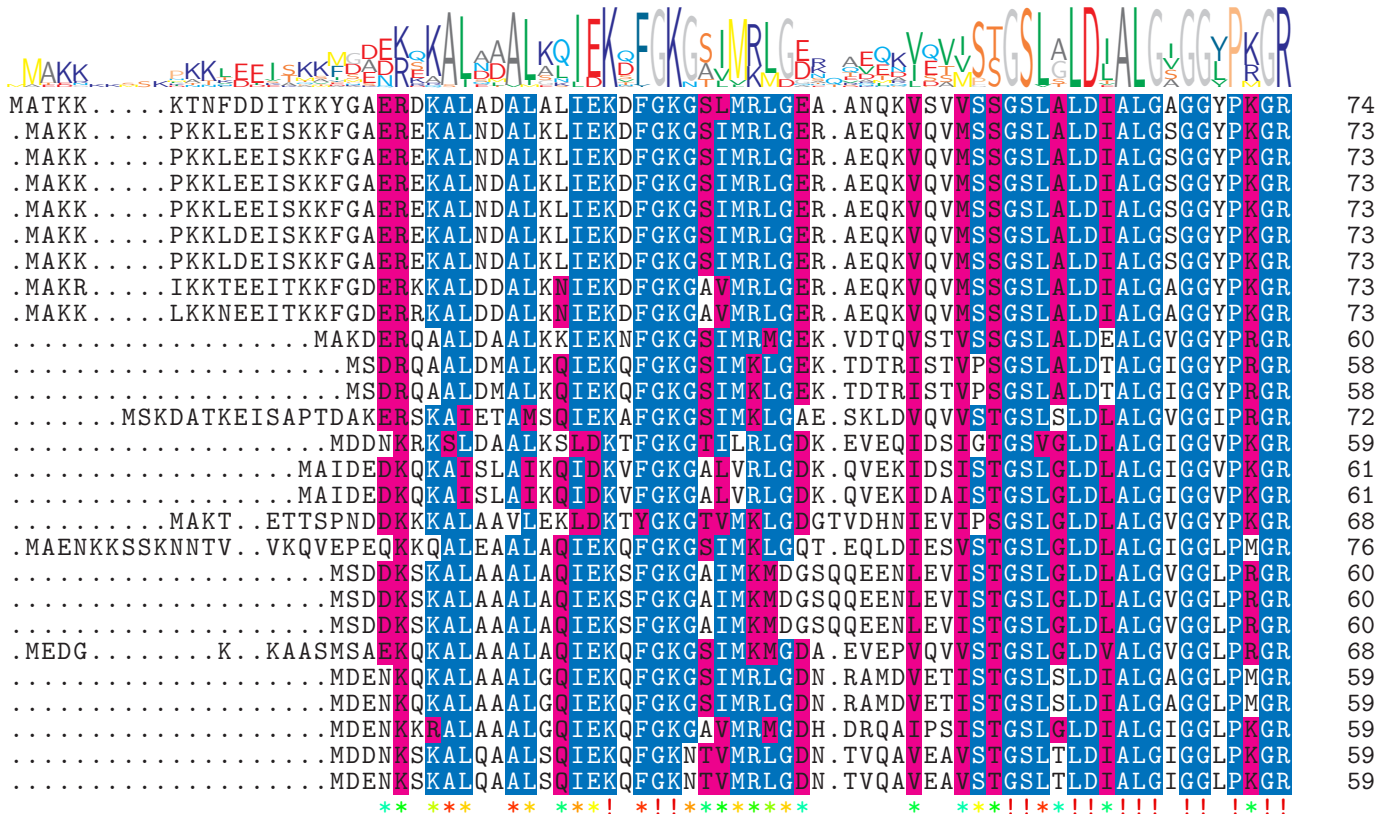


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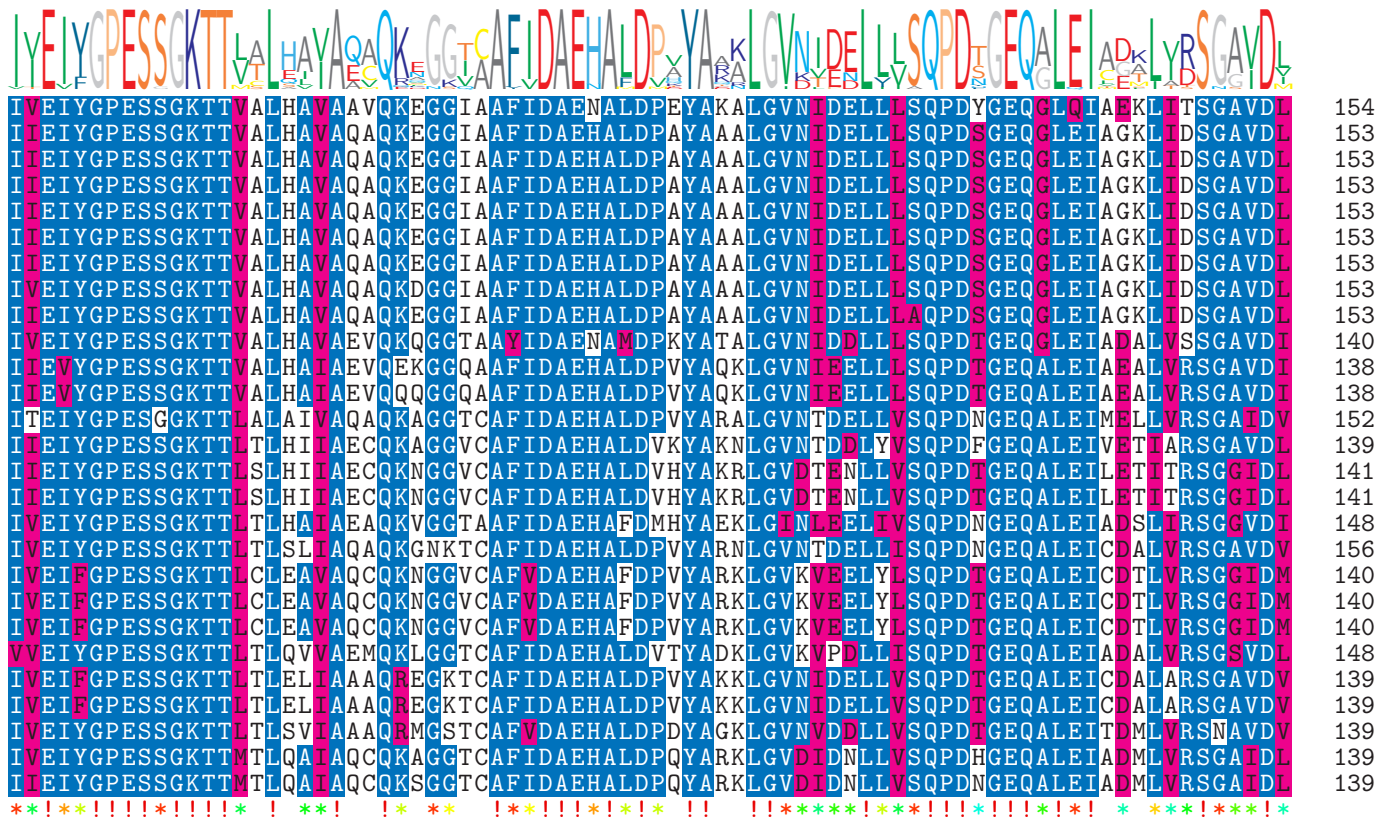
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consensus

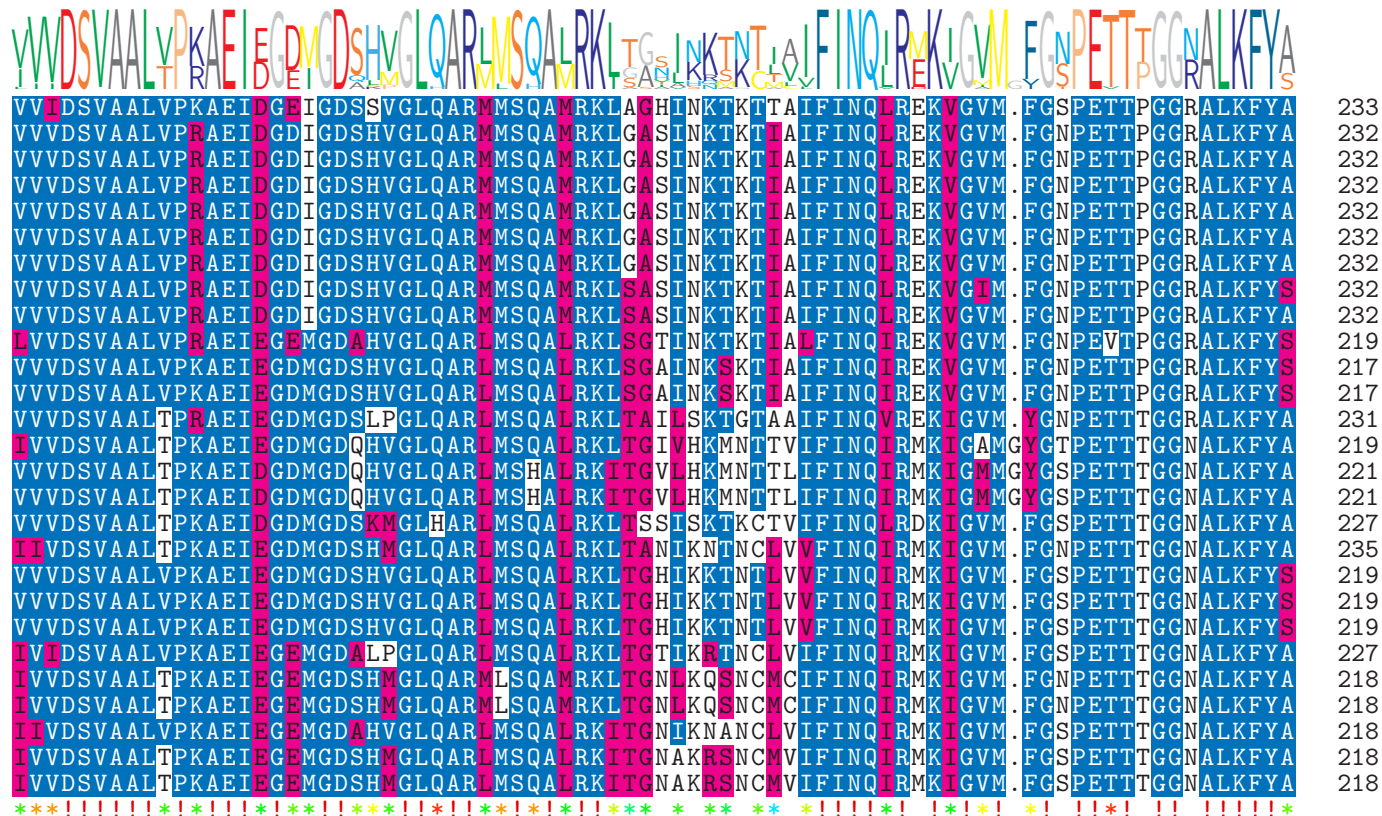
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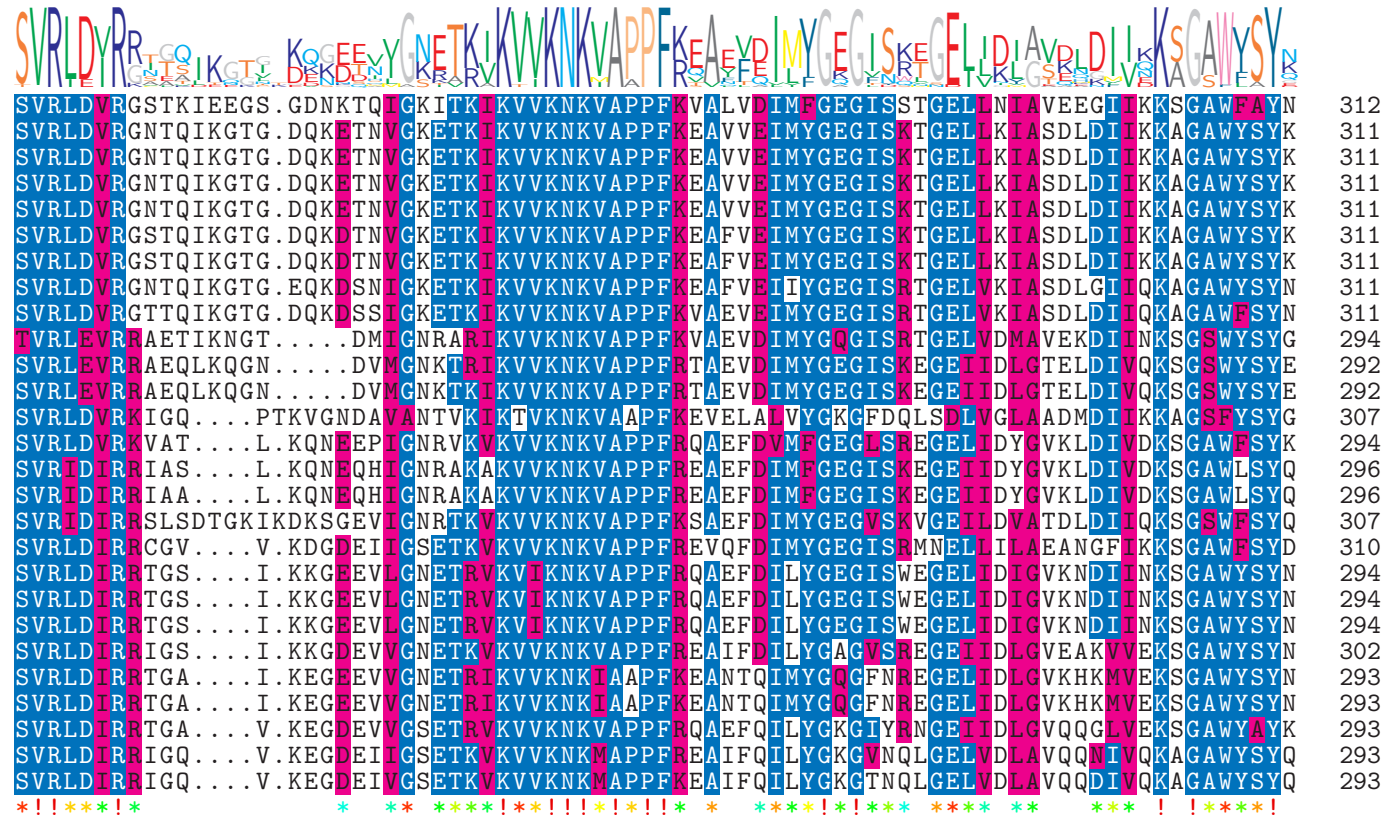
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Sequence	Score
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DEKIGQGS E NA K KYLA E HP E IF D EID K QV R SK F GLIDGEEVSEQDTE N KKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGS E NA K KYLA D N P EV F AEID H QV R V Q FGLIDGEEAAE...SKKDE...AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS E NA K KFL A D N PE I F D ID H KV R V Q YGLIEDNTEEEKQSSKE.....ETDEK..ADKNLVLELDDTIEIE	382
GEKIGQGS E NA K KRYL A D H P Q L F DEID R KV R V K FGLLEESEEEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
SE R IGQGR E NA K NYL A D H ED V ED V RL K V R AA Y GISDVPPEEDLPTTED.EQIN.....ILPDDSTEE..	355
EER L GQGR E NA K Q L F K EN K D I ML M I Q E Q IRE H Y G LDNNGVTE.KAEVQEELE.....FEE.....	347
EER L GQGR E NA K Q L F K EN K D I ML M I Q E Q IRE H Y G LDNNGVVQQQAETQEELE.....FEE.....	348
DE R IGQGG K E K TI A Y I A E R P E M E Q E I RDRV M AA I RAG N AGEAPALAPAAPEAAE..A.....	363
DK K L G QGR E NA K FL K EN P E I A D E I TK A I Q NS M G I TEGMI.....SGSEDDE..GE..E.....	343
DK K L G QGR E NA K ALL K ED K AL A D E IT L K I K E S I GS N E E I.....MPLPDEP..LE..EME.....	347
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GD K IGQGG K AN A C K YL K EN P E I AK T LD K KL R E M LL N PN E M....QLIAETSSAAD..DVEFGAVPEEF.....	354
G S KIGQGG K AN A AK Y L E EN P E I Q G E I EQ Q IR A KL L V T SA NTKATPVAEDLA..DADI....	347
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G N KIGQGG K NN V IR Y L E EN N Q I A E I E IR N I R E Q LL T TG T N....GAVQ.I.EDEE..EPDLL..LES.....	349

logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved