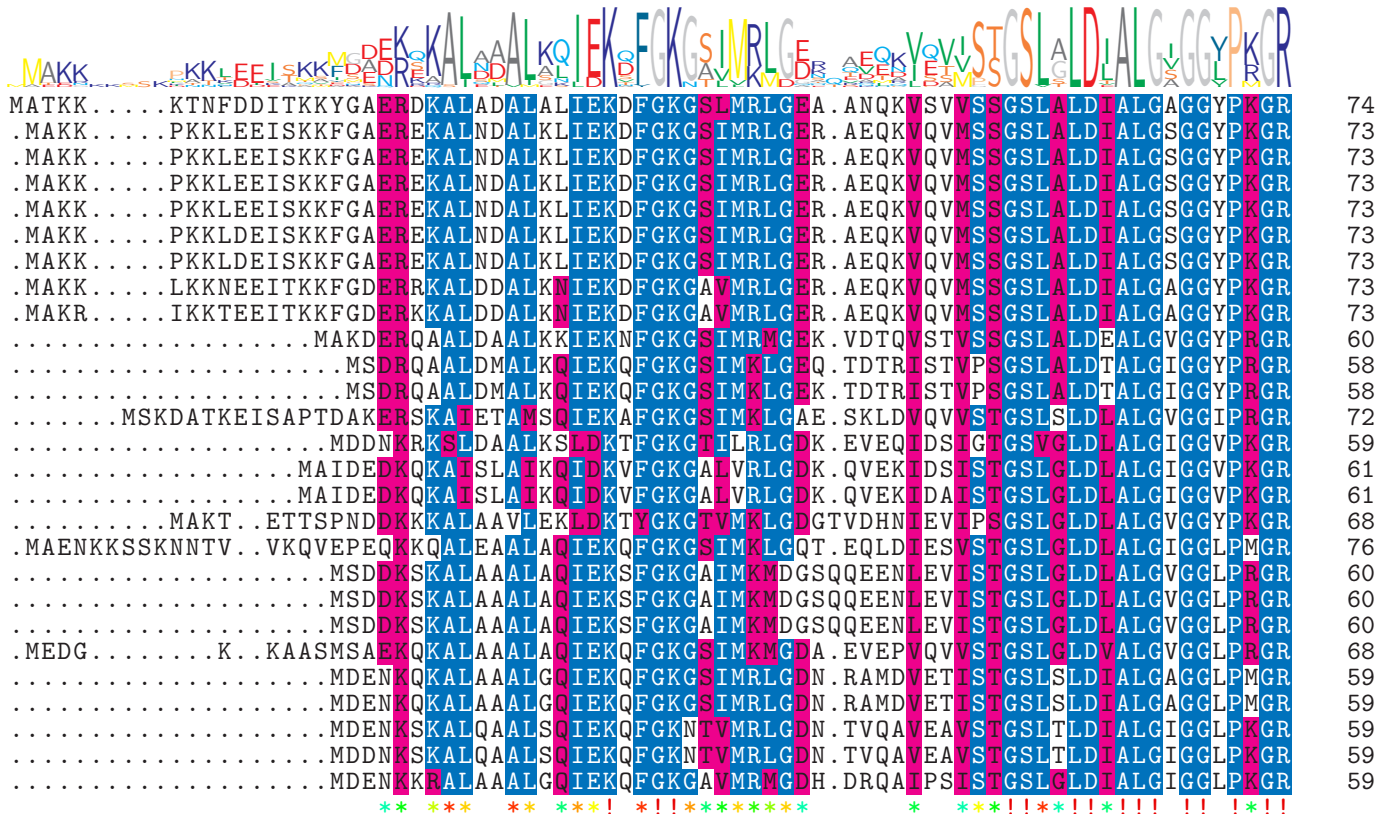


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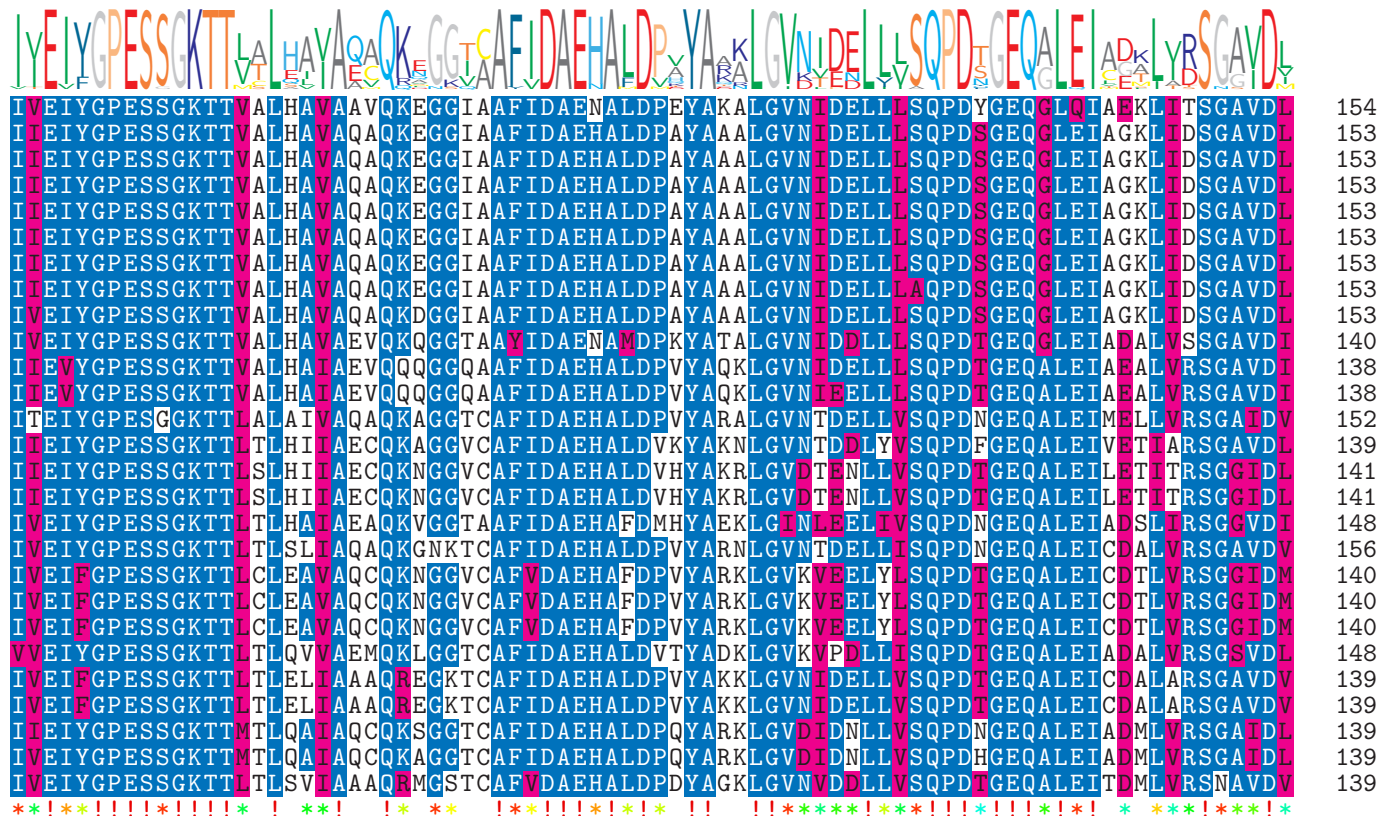
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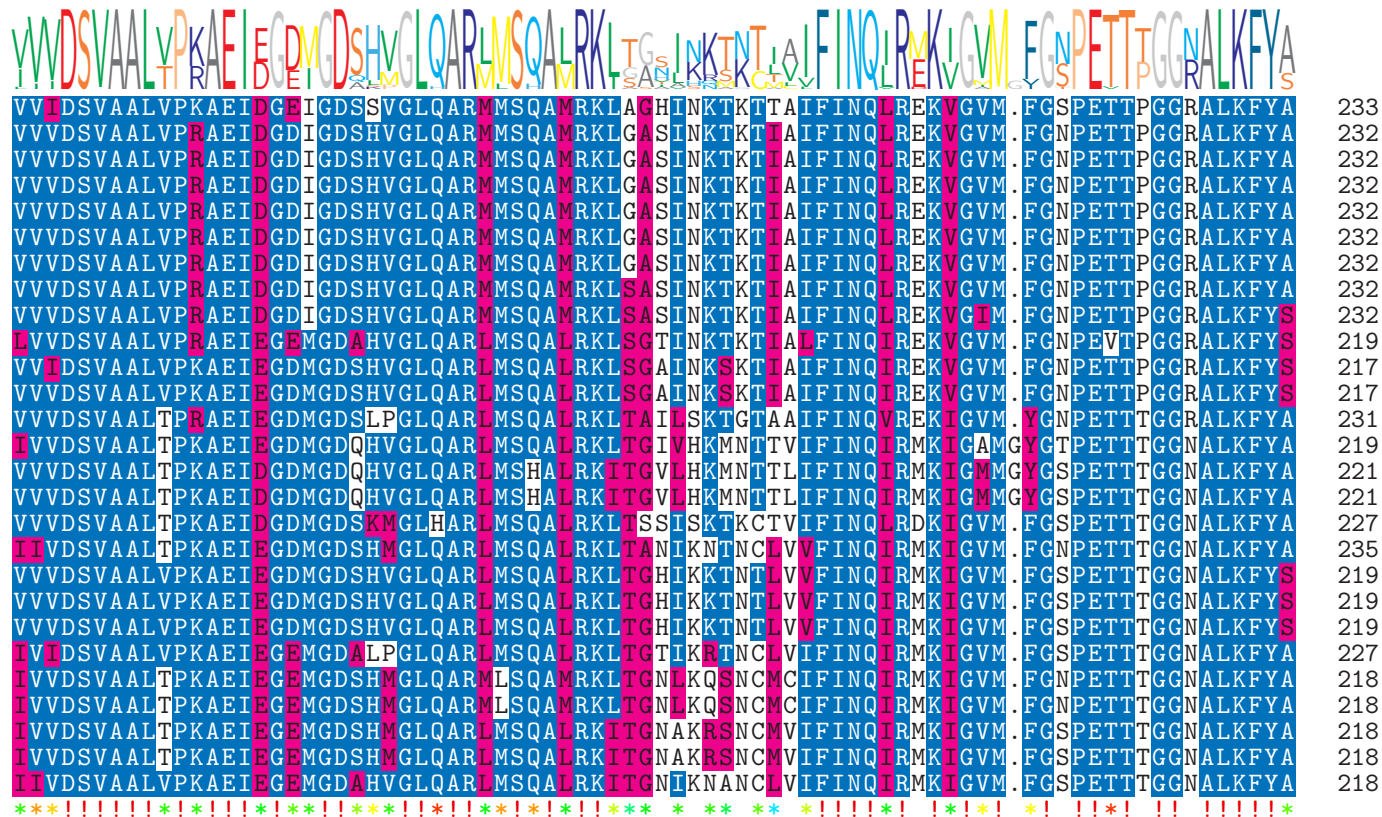
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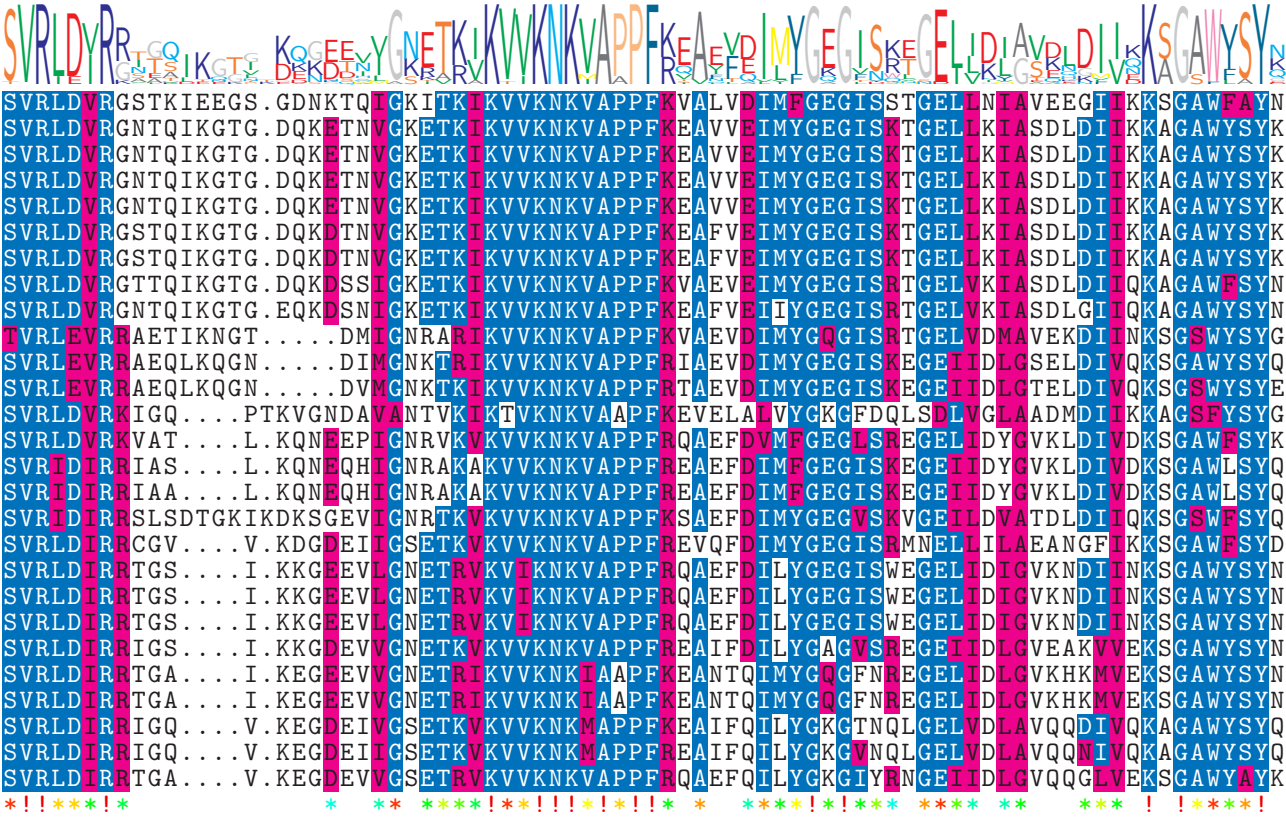
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consensus

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logo

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consensus



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consensus

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Sequence	Score
DEKIGQGA E KA K NYLKEHQ D VF E ID D HKVRAAHG L LD D SEVAETE E ET T ASKTKAKAKKEEK A VE T EEIELE D	387
DEKIGQGS E NA K KYLA A EHPEI F DEID D KQVRSKF G LID G EEVSEQD T ENKK D E....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA A EHPEI F DEID D KQVRSKF G LID G EEVSEQD T ENKK D E....PKKEEA..VNEEVPLDLGDELEIE	385
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GEKIGQGS E NA K RYLAD H PK L QF E ID D RKVRVKF G LLE E ESIESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS E NA K KFLAD N PEI F DDI D HKVRVQY G LIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
SERIGQGR E NA K NYLAD H EDVE D EVRLK V RAAY G ISD V PEEDLPTTED.EQIN.....ILPDDSTEE.	355
EERLGQGR E NA K QFLK E NKDILLMIQE Q IREHY G LDTNGVKAAEEEEEGQEELE.....I.....	346
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GAKIGQGGK D NVRV W LK E NPEIS D EIDAKIRALNGVEMHI....TEGTQDETD.....GERPEE.....	348
GAKIGQGGK D NVRV W LK E NPEIS D EIDAKIRALNGVEMHI....TEGTQDETD.....GERPEE.....	348
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logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved