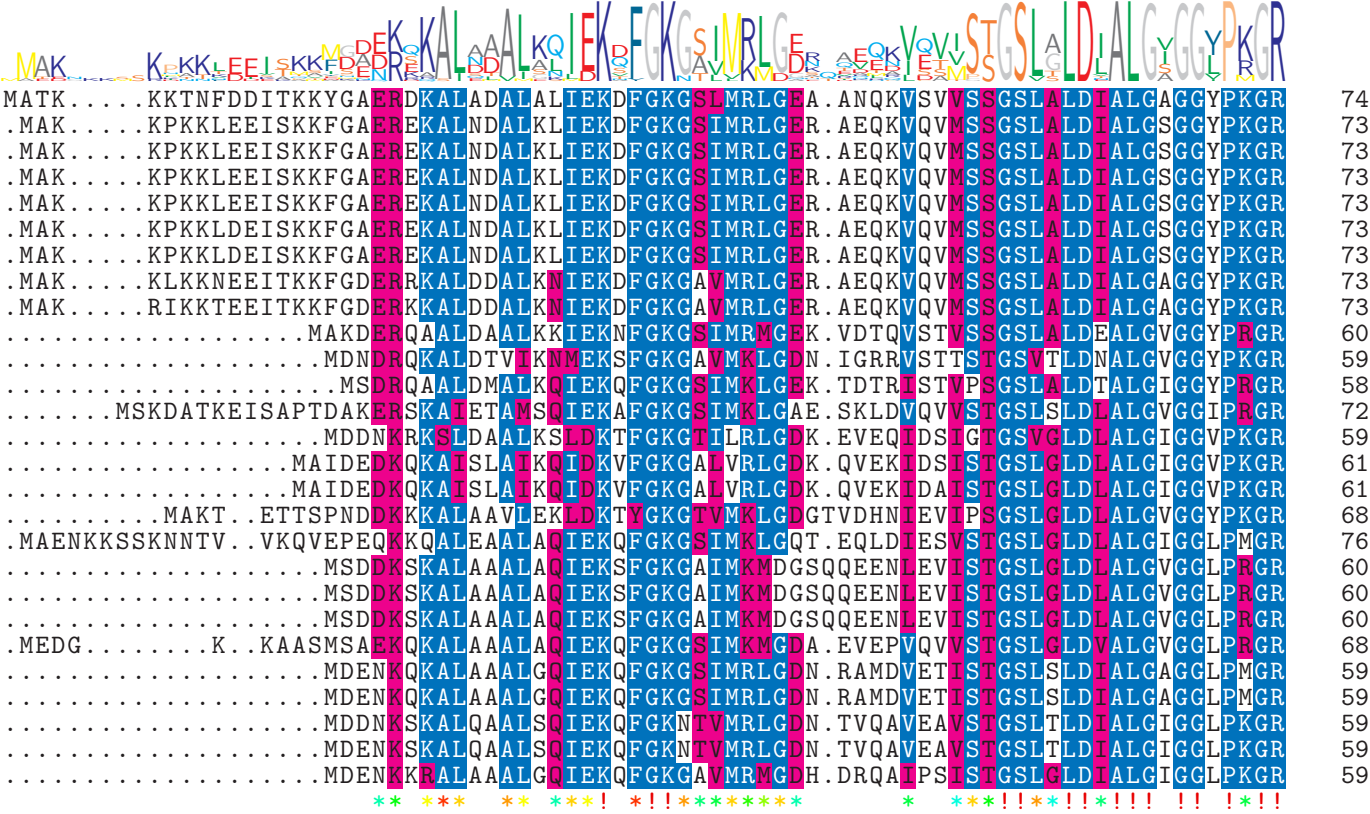


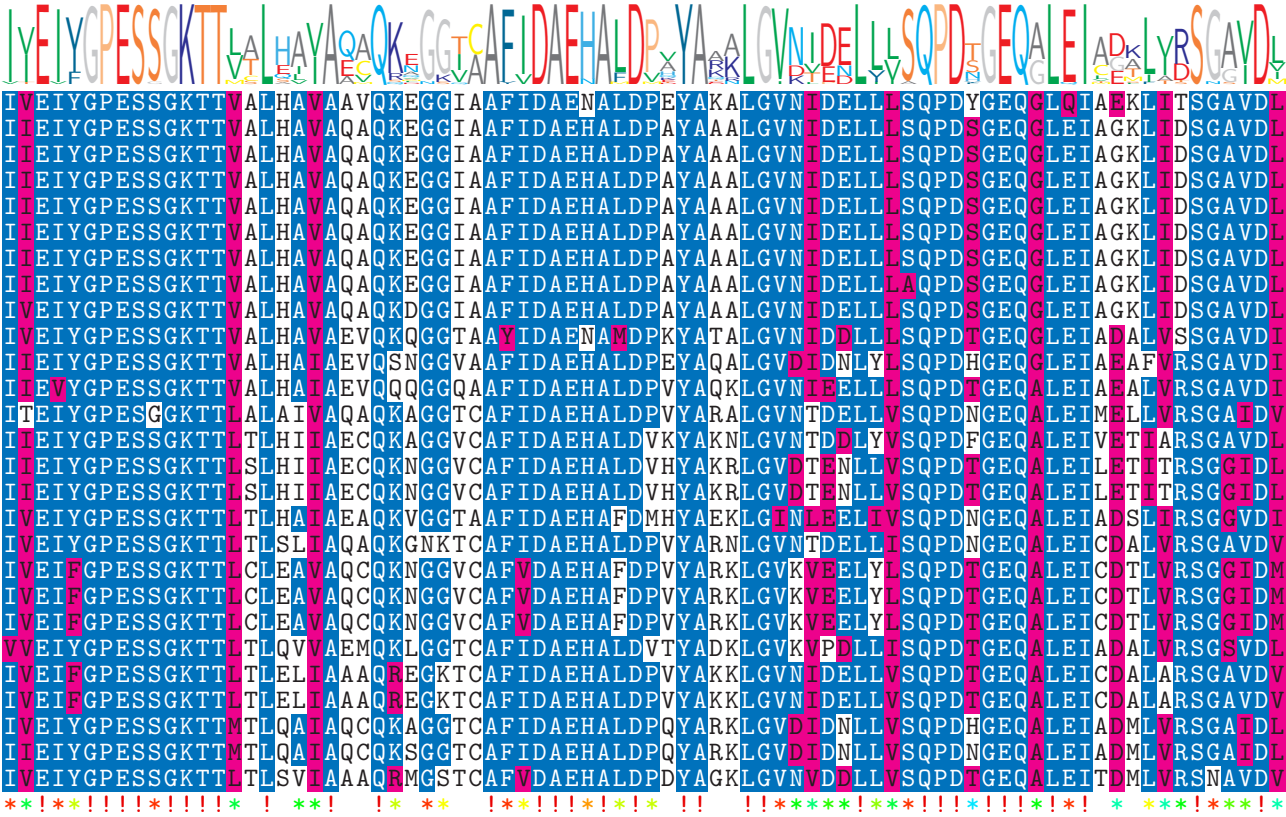
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consensus



logo

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consensus



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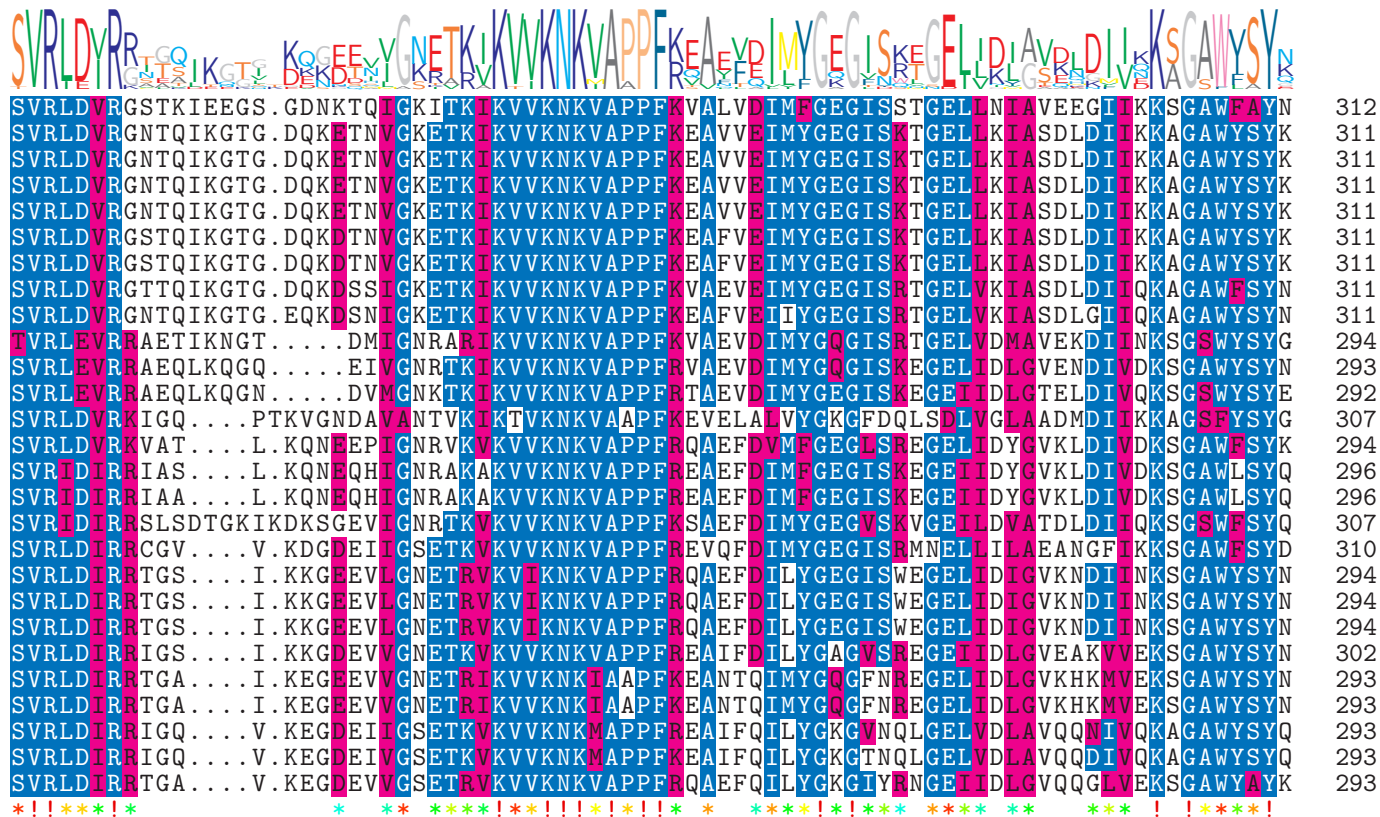
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consensus

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Sequence	Score
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DEKIGQGS E NA K KYLAEHPEIF F DEID K QVRSKFGLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLAEHPEIF F DEID K QVRSKFGLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
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SERIGQGS R ENAKNYLADHEDVEDEVRLK V RAAYG I SDVPEEDLPTTEDEQINILPDDSTEE.....	355
GERMGQG K ENV K MYLKENPQIK E EID R KLREKLG I SDGDVEETEDA...PKSLFDEE.....	347
EERLGGC R ENAKQFLKENKDIMLMIQE Q IREHYGLDNNGVVQQQAETQEELEFEE.....	348
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DKKLGGG R ENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..PLEEME.....	347
DTKLGGGRD T VKELIKDNPEIAEELAKIREKLQAK.....	343
GTKIGQG K NNAVKWLKENPEIA D KLEQIRNTLASNPNS....VLKATASDSNDESD..VEEFSEEEEL.....	372
GAKIGQG K DNVRVWLKENPEISDEIDAKIRALNCVEMHI....TEGTQDET D GER.....PEE.....	348
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GDKIGQG K ANACKYLKENPEIAKTLDKKLREMLLNPENM....QLIAETSSAADDVE..FGAVPEEF.....	354
GNKIGQG K NNVIRYLEENPQISTEIEAVIREQLLTKASD....QTAA.HDETEEEPD..LL..ES.....	349
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GSKIGQG K ANA A KYLEENPEIQGEIEQQIRAKLLVTSAN....TKATPVAEDLADAD..I.....	347

logo

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consensus			

- non conserved
- similar
- ≥ 50% conserved