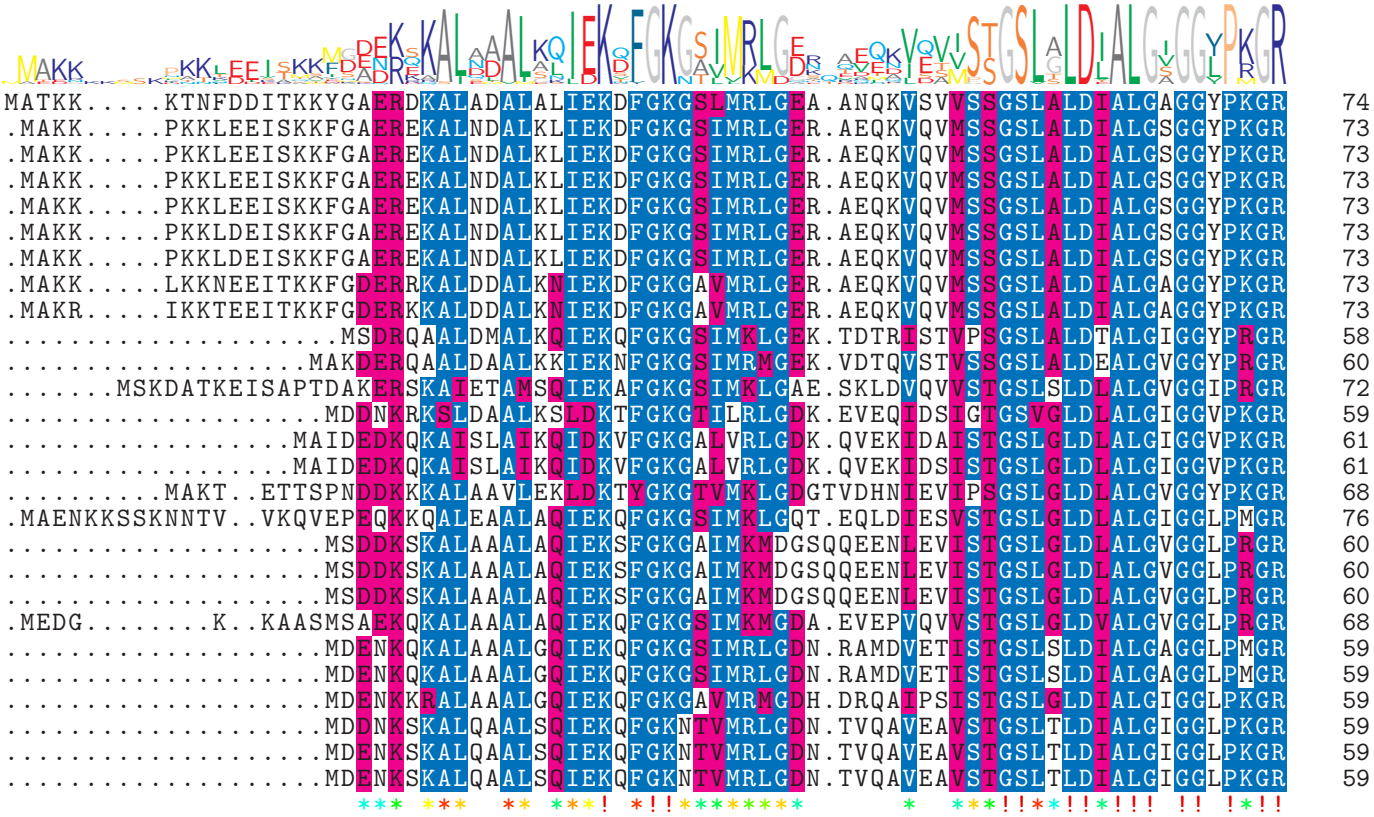


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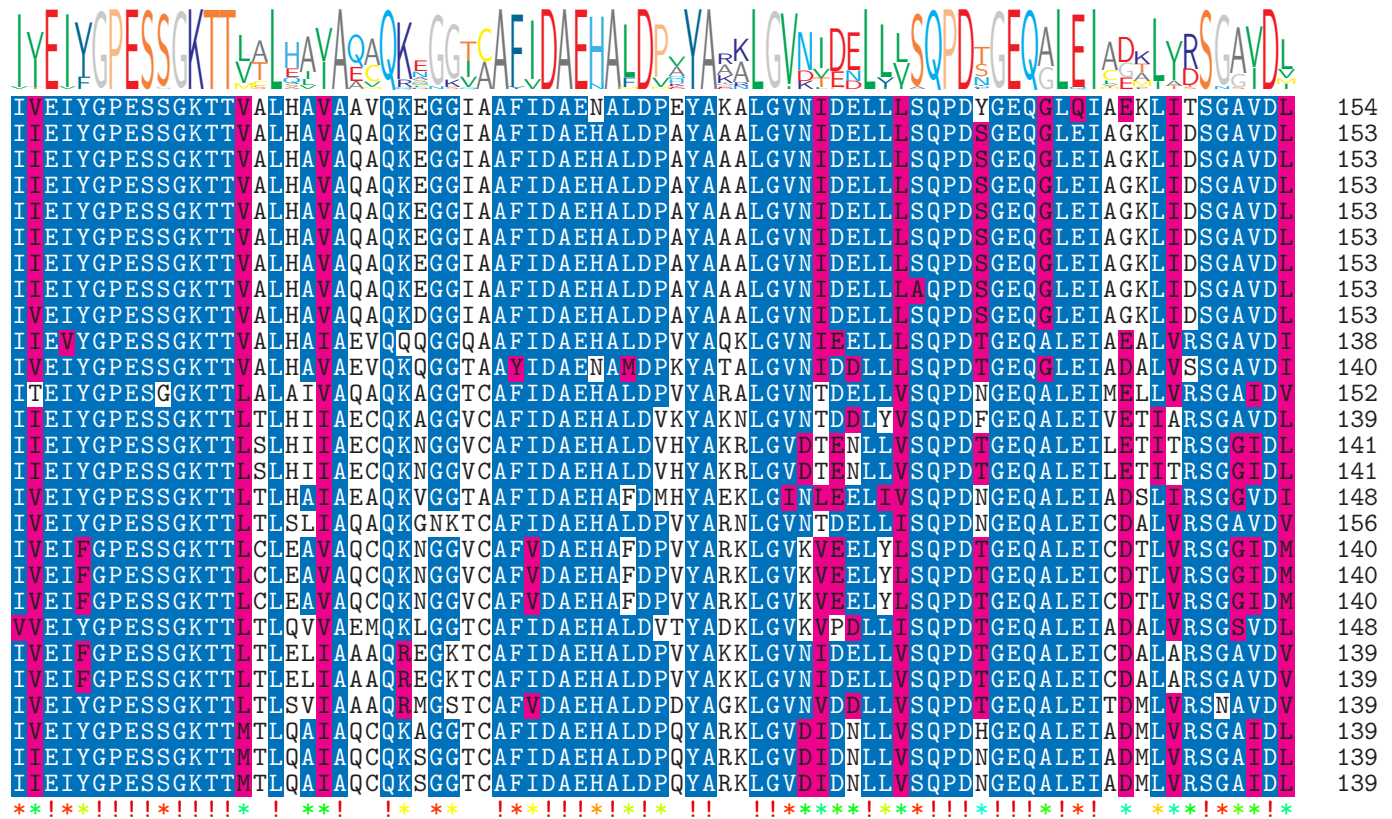
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consensus



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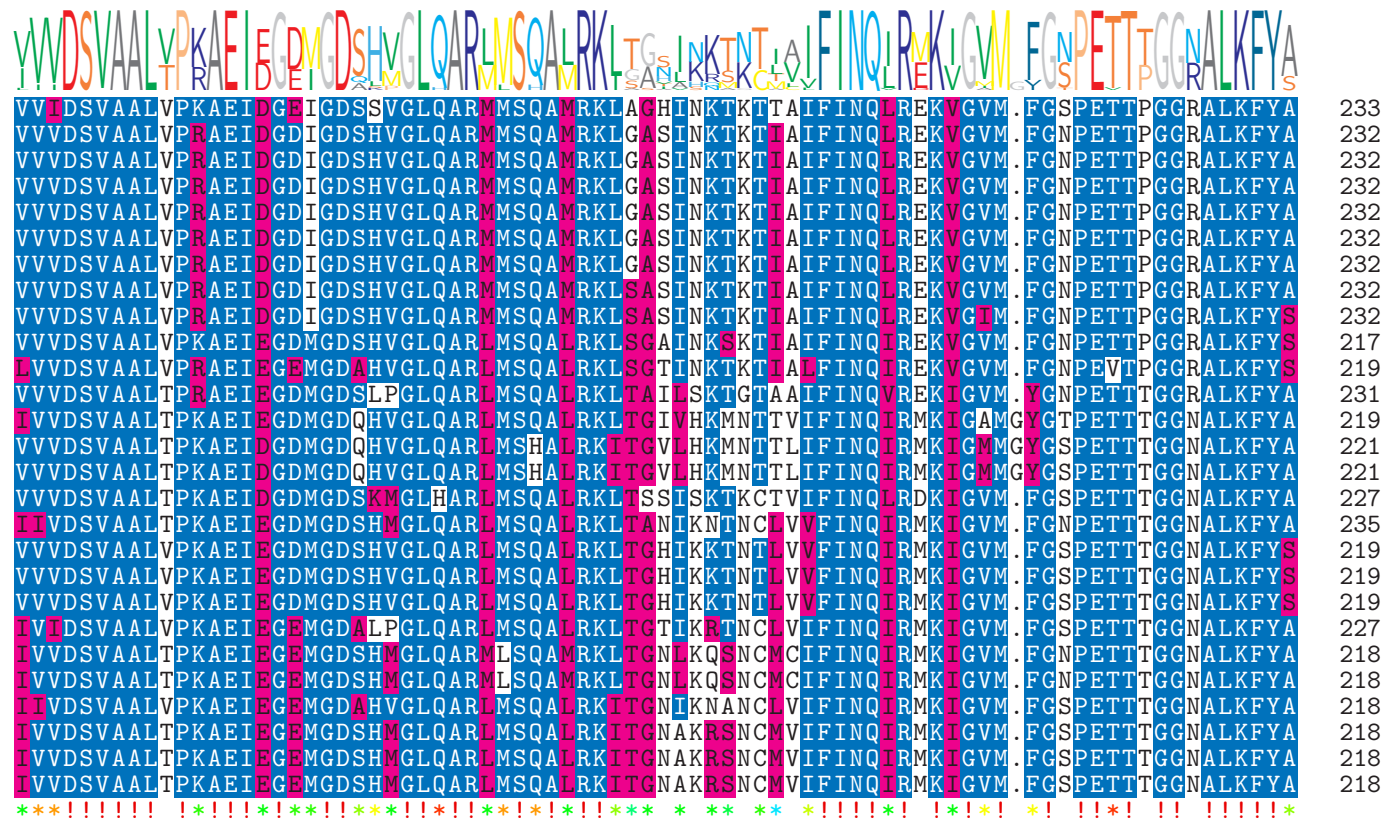
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consensus

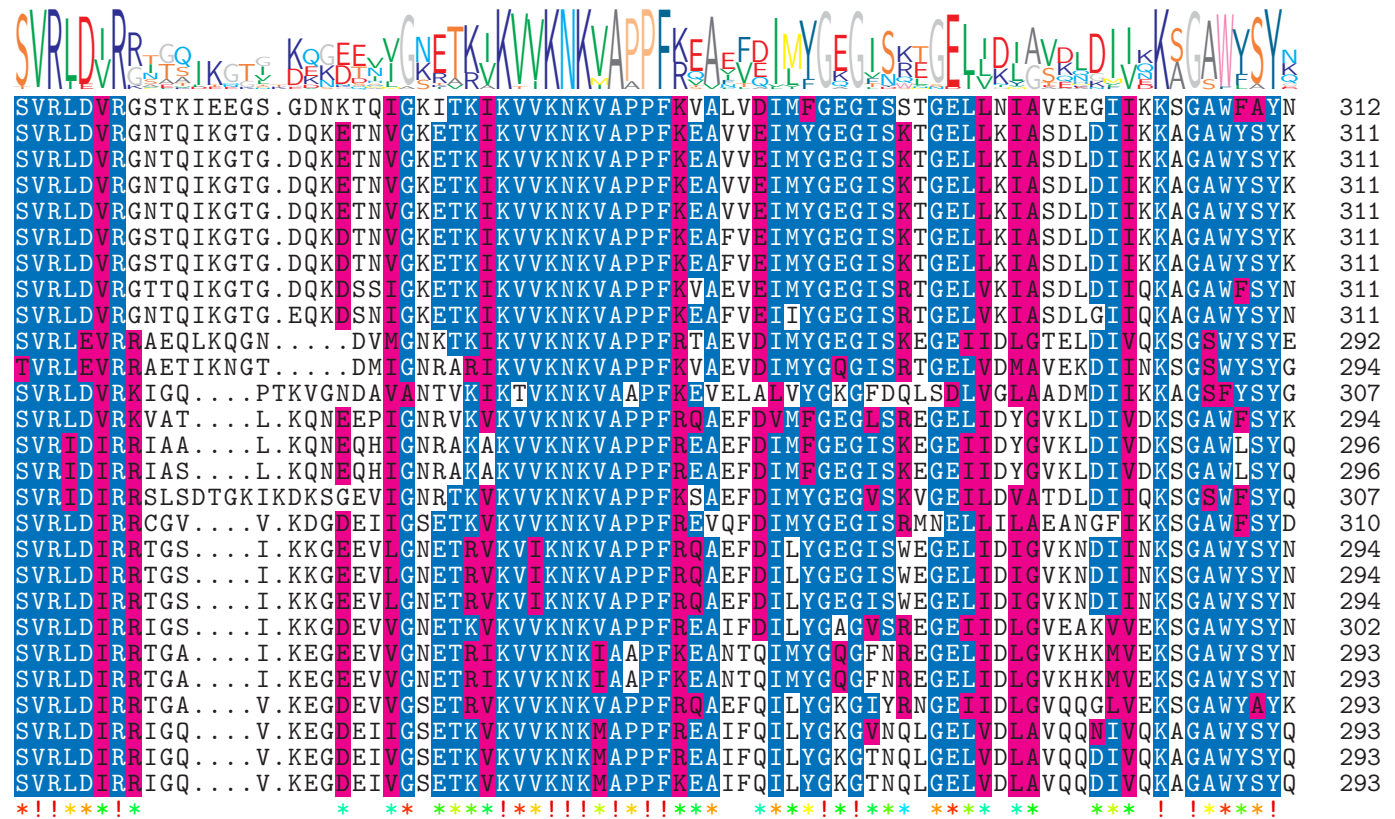
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consensus

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consensus

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| Sequence                                                                                   | Score |
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| DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE     | 385   |
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| DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEIAES . . . KKDE . . . VAQVDS . . VNEEVTLDLGDLEIE    | 381   |
| GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE . . . . . E . . . . . TDDLALDLNGIEIE     | 377   |
| GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK . . . . . ETDEK . . ADKNLVLELDDTIELE    | 382   |
| EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E . . . . .                   | 348   |
| SERIGQGRENAKNYLADHEDVEDEVRLKVRVQYGLSDVPEEDLPTTEDE . QI . NILPDDST . . . . . EE . . . . .   | 355   |
| DERIGQGEKTIATYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPE . . . . . AAAA . . . . .                | 363   |
| DKKLGGGRENKSAFLKENPEIADEITKAIQNSMGTIEGMISGSEDDEGEE . . . . .                               | 343   |
| DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEPLEEME . . . . .                              | 347   |
| DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEPLEEME . . . . .                              | 347   |
| DTKLGGGRDTPVKELIKDNPELAELEAKIREKLQAK . . . . .                                             | 343   |
| GTKIGQGGKNNAVKWLKENPEIADKLEQEIRNTLASNPNSVLKATASDSNDE . . . . . SDVEE . FSEEE . . . . .     | 372   |
| GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDET . . D . . . . . GERPEE . . . . .           | 348   |
| GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDET . . D . . . . . GERPEE . . . . .           | 348   |
| GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDET . . D . . . . . GERPEE . . . . .           | 348   |
| GERIGQGRDNCREFLRENAELAREIENKVRHLGVTPMGAVTLAAEEVEED . . . . .                               | 352   |
| GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNMQL . . IAETSSAA . . . . . DDVEFGAVPPEEF . . . . .   | 354   |
| GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNMQL . . IAETSSAA . . . . . DDVEFGAVPPEEF . . . . .   | 354   |
| GSKIGQGGKANAACKYLEENPEIGQETIEQQIRAKLLVTSANTK . . ATPVAEDLA . . . . . DADI . . . . .        | 347   |
| GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQT . . AA . HDETEE . . . . . EPDLLS . . . . .      | 349   |
| GNKIGQGGKNNVIRYFEENKHIAEIEIERNIREQLLTTGTNGA . . VQ . IEDDEE . . . . . EPDLLLES . . . . .   | 350   |
| GNKIGQGGKNNVIRYFEENQIAEIEIERNIREQLLTTGTNGA . . VQ . IEDEE . E . . . . . EPDLLLES . . . . . | 349   |

logo

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| consensus                                   |     |     |  |

- X non conserved
- X similar
- X ≥ 50% conserved