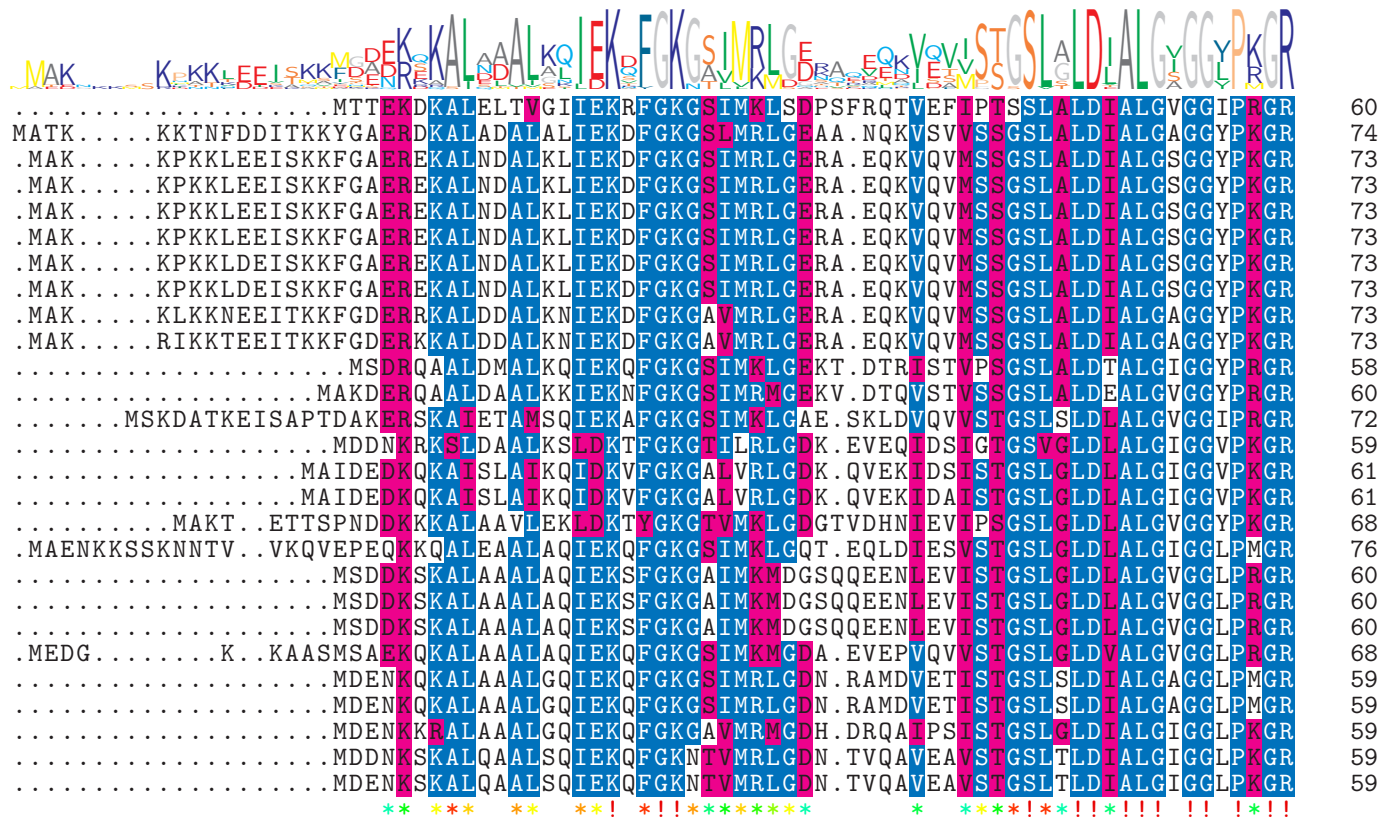


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NTDB id 527 SMSK321 RS11065 WP 001085454.1
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NTDB id 1214 NCTC11637 00359 SQJ03206.1
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consensus

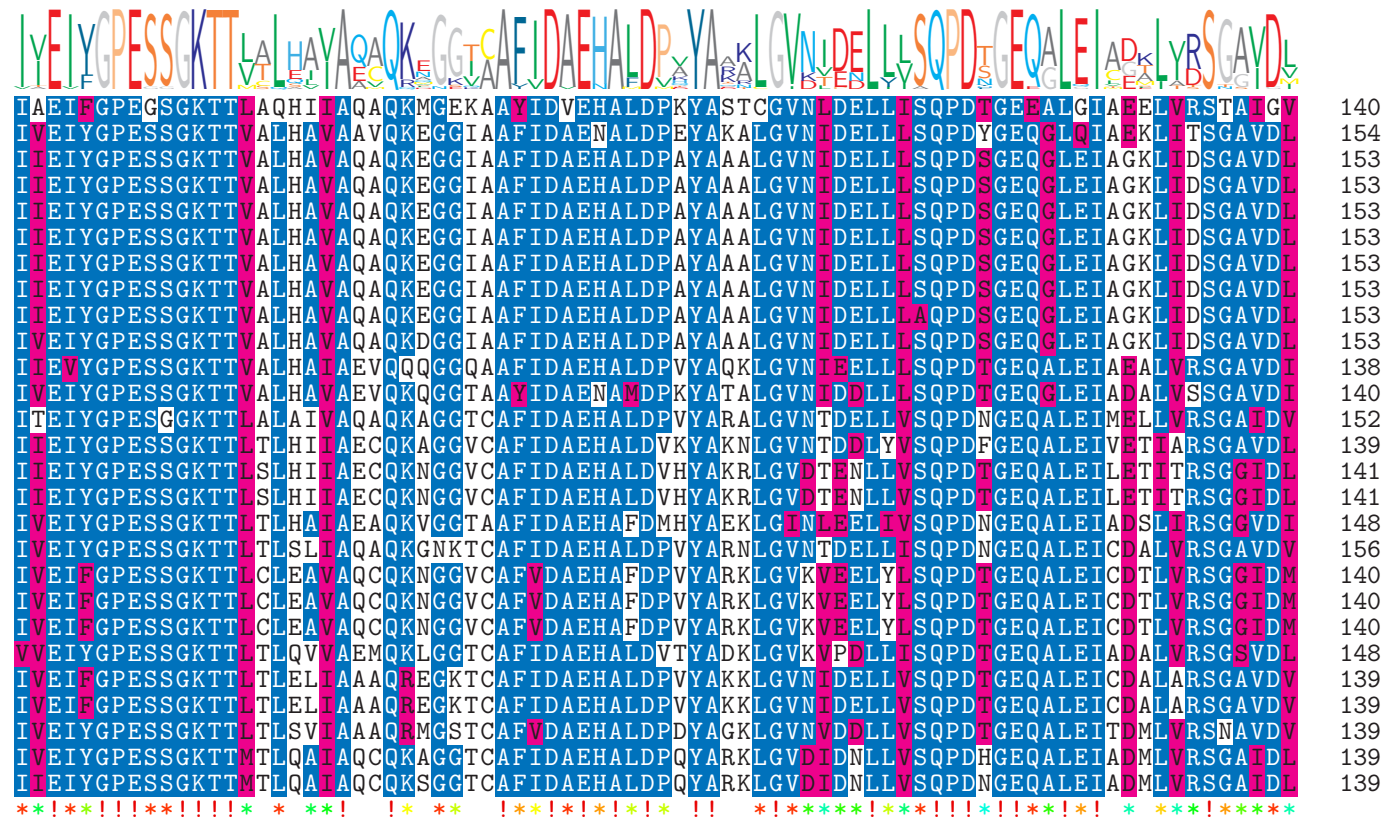
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consensus

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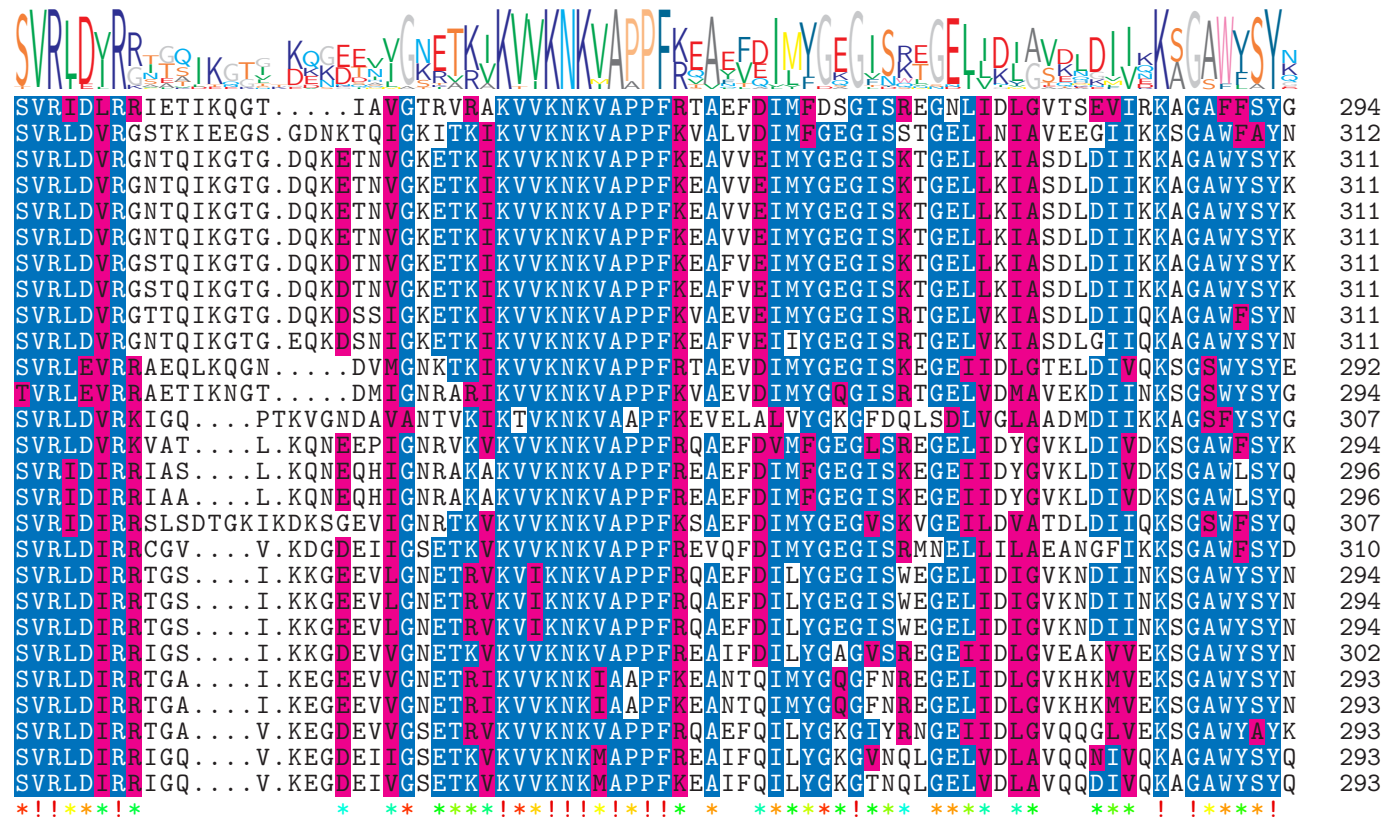




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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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| Sequence                                                                                          | Score |
|---------------------------------------------------------------------------------------------------|-------|
| DI RLGGGRESAKNYLAANPDLAQETEEKIRASAVTLCISIGDGD . . . . .                                           | 337   |
| DEKIGQGAEAKNYLKEHQDVFEIDHKVRAAHGLDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED . . . . .                 | 387   |
| DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFG LIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE            | 385   |
| DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFG LIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE            | 385   |
| DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFG LIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE            | 385   |
| DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFG LIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE            | 385   |
| DEKIGGGSSENAKKYLAENPEIFDEIDHKVRVQFGLIDGEEIAES . . . . . KKDE . . . AAQVDS . VNEEVTLDLGDLEIE       | 381   |
| DEKIGGGSSENAKKYLAENPEVFAEIDHKVRVQFGLIDGEEAAES . . . . . KKDE . . . VAQVDS . VNEEVTLDLGDLEIE       | 381   |
| GEKIGGGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE . . . . . E . . . . . TDDLALDLNGIEIE           | 377   |
| GEKIGGGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK . . . . . E . . . . . ADKNLVLELDDTIELE        | 382   |
| EERLGGGRENAAKQFLKENKDIMLMIQEIRHYGLDNNGVVQQAAETQEEL . EFE . E . . . . .                            | 348   |
| SERIGGRENAAKNYLADHEDVEVLKVRVRAAYGISDVPEEDLPTTEDE . QI . NILPDST . . . . . EE . . . . .            | 355   |
| DERIGGKEKTIAYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAAPEAAE . A . . . . .                                | 363   |
| DKKLGGGRENKAFLENPEIAD EITKAIQNSMGI EGM . . . . . SGSEDE . GE . E . . . . .                        | 343   |
| DKKLGGGRENAAKLLKEDKALADEITLKIKESIGSNEEI . . . . . MPLPDEP . LE . EME . . . . .                    | 347   |
| DKKLGGGRENAAKLLKEDKALADEITLKIKESIGSNEEI . . . . . MPLPDEP . LE . EME . . . . .                    | 347   |
| DTKLGGGRDITVKELIKDNPELADAELEAKIREKLQAK . . . . .                                                  | 343   |
| GKIGGQKNNAVKWLKENPEIADKLEQEI RNTLASNPNS . . . . . VLKATASDSND . . ESDVEEFSEEEEL . . . . .         | 372   |
| GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI . . . . . TEGT . . . . . Q . . . . . DETDGERPEE . . . . . | 348   |
| GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI . . . . . TEGT . . . . . Q . . . . . DETDGERPEE . . . . . | 348   |
| GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI . . . . . TEGT . . . . . Q . . . . . DETDGERPEE . . . . . | 348   |
| GERIGGGRDNCREFLENAAELAR E IENKVRHLGVTPMG . . . . . AV . TLAEVEE . D . . . . .                     | 352   |
| GDKIGGQKANACKYFLKENPEIAKTLDKKLREMLLNPNEM . . . . . QLIAETSSAAD . . DVEFGAVPEEF . . . . .          | 354   |
| GDKIGGQKANACKYFLKENPEIAKTLDKKLREMLLNPNEM . . . . . QLIAETSSAAD . . DVEFGAVPEEF . . . . .          | 354   |
| GSKIGGQKANAAKYLEENPEIGQEIEQQIRAKLLVTSAN . . . . . TKATPVAEDLA . . DADI . . . . .                  | 347   |
| GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASD . . . . . QTA . HDETEE . . EPDLL . ES . . . . .           | 349   |
| GNKIGGQKNNVIRIFYENNQIAEIERNIREQLLTGTN . . . . . GAVQ . I . EDEE . . EPDLL . LES . . . . .         | 349   |

logo

|                                             |     |     |  |
|---------------------------------------------|-----|-----|--|
|                                             |     | IEE |  |
| NTDB id 115141 X792 RS07740 WP 012882718.1  | ... | 337 |  |
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| NTDB id 1074 ABD1 RS10195 WP 000344167.1    | ... | 349 |  |
| consensus                                   |     |     |  |

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