

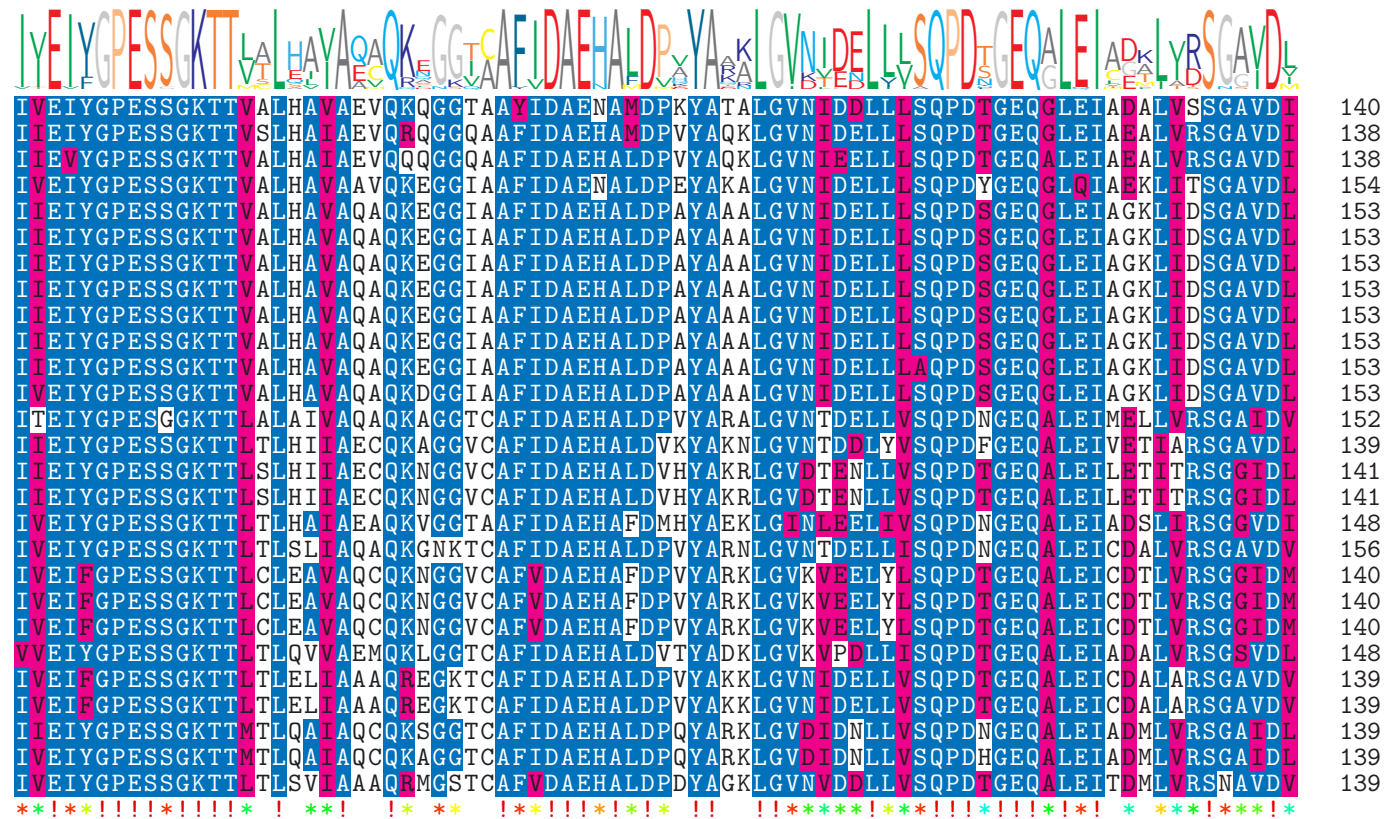
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NTDB id 527 SMSK321 RS11065 WP 001085454.1
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NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 1313 DR RS12030 WP 010888966.1
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NTDB id 1205 PSJM300 05545 AFN77183.1

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[illegible]

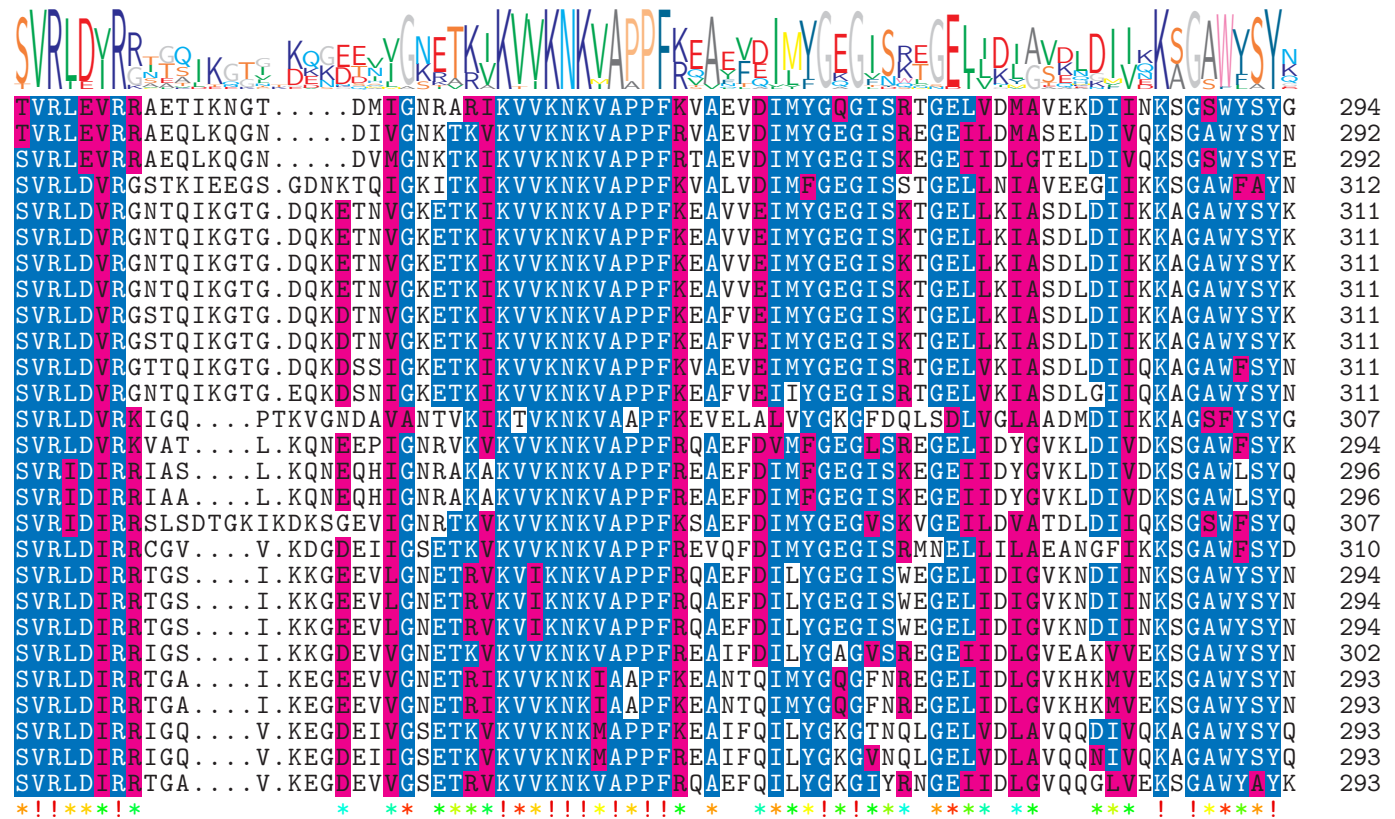
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consensus

| Sequence                                                                                         | Score |
|--------------------------------------------------------------------------------------------------|-------|
| DEKIGQGRENKYNLAHDHVEDEVRLKVR AAYGISDVPPEEDLPTTEDEQINILPDDSTEE . . . . .                          | 355   |
| EERLGGGRENKQFLKENTLREETIAFFVRDHHGIGEDSGVEDTE . . DATLQD . . . . .                                | 343   |
| EERLGGGRENKQFLKENTLREETIAFFVRDHHGIGEDSGVEDTE . . DATLQD . . . . .                                | 348   |
| DEKIGQGAEKAKNYLKEHQDVFEIDHQRVRAAHGLDDSEVAETEETETASKTKAKAKKEEKAVETEEIELELED . . . . .             | 387   |
| DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE . . . . PKKEEA . . VNEEVPLDLGDELEIE      | 385   |
| DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE . . . . PKKEEA . . VNEEVPLDLGDELEIE      | 385   |
| DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE . . . . PKKEEA . . VNEEVPLDLGDELEIE      | 385   |
| DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE . . . . PKKEEA . . VNEEVPLDLGDELEIE      | 385   |
| DEKIGQGSSENAKKYLAADNPEIFDEIDHQRVVRVQFGLIDGEEIAES . . . . KKDE . . . . AAQVDS . . VNEEVTLDLGDLEIE | 381   |
| DEKIGQGSSENAKKYLAADNPEVFAEIDHQRVVRVQFGLIDGEEIAES . . . . KKDE . . . . VAQVDS . . VNEEVTLDLGDLEIE | 381   |
| GEKIGQGSSENAKRYLADHPQLFDEIDRKRVRVKFGLLEESEESAMAVASE . . . . . E . . . . . TDDLALDLNGIEIE         | 377   |
| GEKIGQGSSENAKRYLADNPEIFDDIDHQRVVRVQGLIEEDNTEEKQSSKEK . . . . . ETDEK . . ADKNLVLELDDTIEIE        | 382   |
| DERIGGQKEKTIAYIAIERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA . . . . .                              | 363   |
| DKKLGQGRNSKAFKLENPEIAD EITKAIQNSMGTIEGMI . . . . . SGSEDDE . . GEE . . . . .                     | 343   |
| DKKLGQGRNSKAFKLENPEIAD EITKAIQNSMGTIEGMI . . . . . SGSEDDE . . GEE . . . . .                     | 347   |
| DKKLGQGRNSKAFKLENPEIAD EITKAIQNSMGTIEGMI . . . . . SGSEDDE . . GEE . . . . .                     | 347   |
| DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK . . . . .                                                  | 343   |
| GTKIGQGGKNNAVKWLKENPEIADKLEQEIRNTLASNPNS . . . . . VLKATASDSNDES DVEEF . . SEEEL . . . . .       | 372   |
| GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI . . . . . TEGTQDET D . . . . . GER . . PEE . . . . .    | 348   |
| GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI . . . . . TEGTQDET D . . . . . GER . . PEE . . . . .    | 348   |
| GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI . . . . . TEGTQDET D . . . . . GER . . PEE . . . . .    | 348   |
| GERIGQGRDNCREFLRNAAELAR E IENKVR EHLGVTPMG . . . . . AV . TLAEEVEED . . . . .                    | 352   |
| GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM . . . . . QLIAETSSAADDVEFGAV . . PEEF . . . . .         | 354   |
| GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM . . . . . QLIAETSSAADDVEFGAV . . PEEF . . . . .         | 354   |
| GNKIGQGGKNNVIRYFEENNQIAEEIERNIREQLLTGTN . . . . . GAVQ . I . EDEE EEPD . . LL . . LES . . . . .  | 349   |
| GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTQASD . . . . . QTAA . HDETEEE EEPD . . LL . . ES . . . . .   | 349   |
| GSKIGQGGKANAAKYLENPEIQEIEQQIRAKLLVTSAN . . . . . TKATPVAEDLADAD . . I . . . . .                  | 347   |

logo

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|---------------------------------------------|-----|-----|--|
|                                             |     | IEE |  |
| NTDB id 625 LCA RS02525 WP 011374196.1      | ... | 355 |  |
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| NTDB id 1205 PSJM300 05545 AFN77183.1       | ... | 347 |  |
| consensus                                   |     |     |  |

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