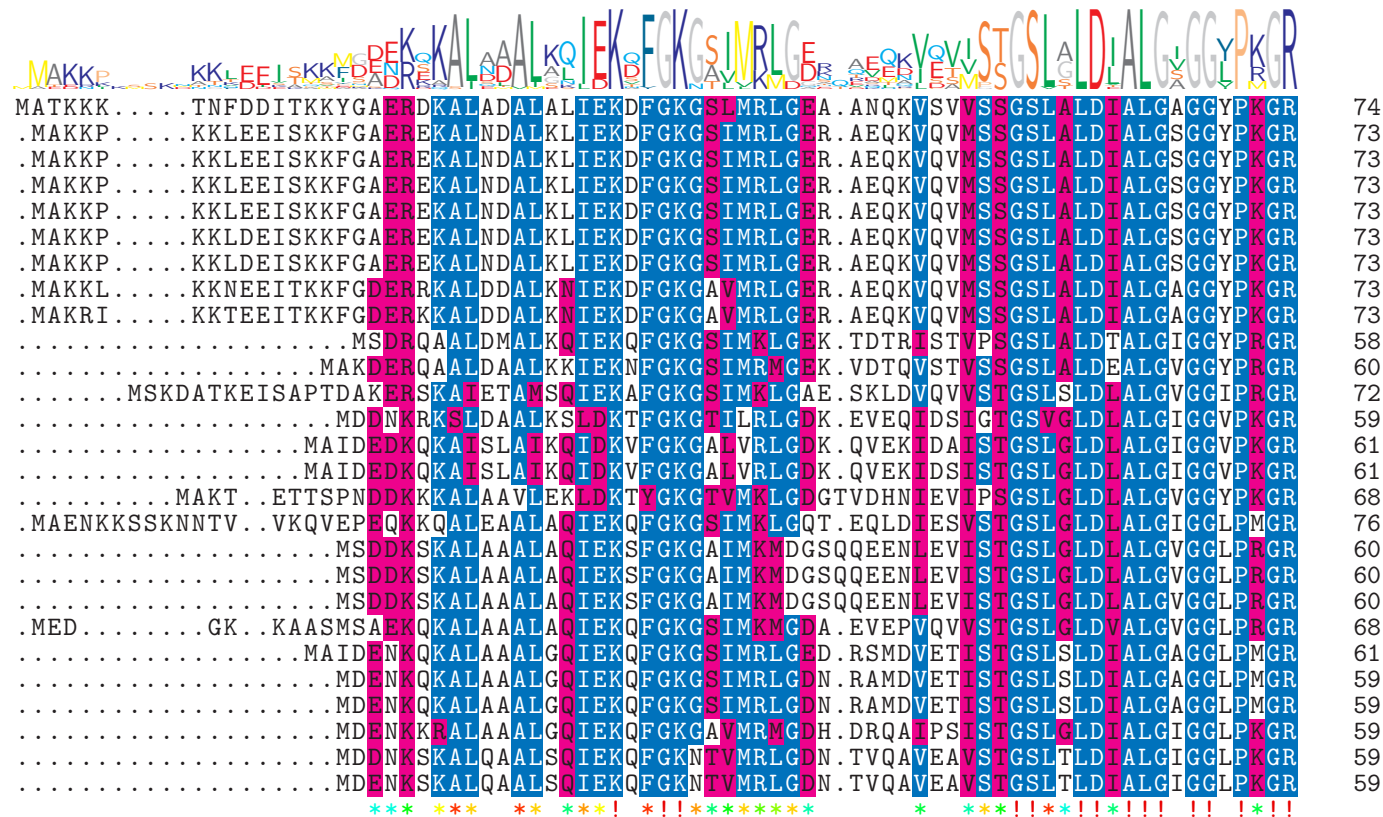


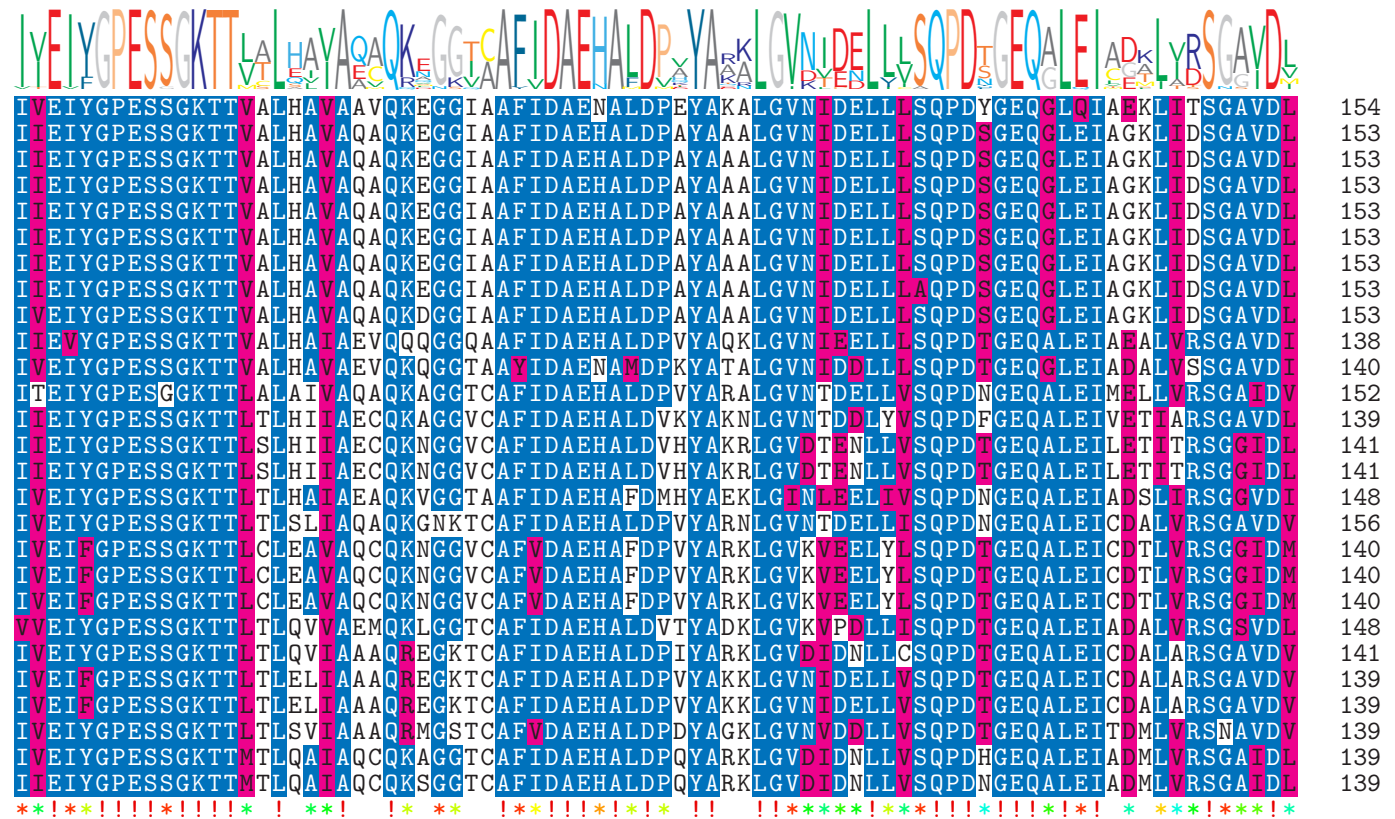
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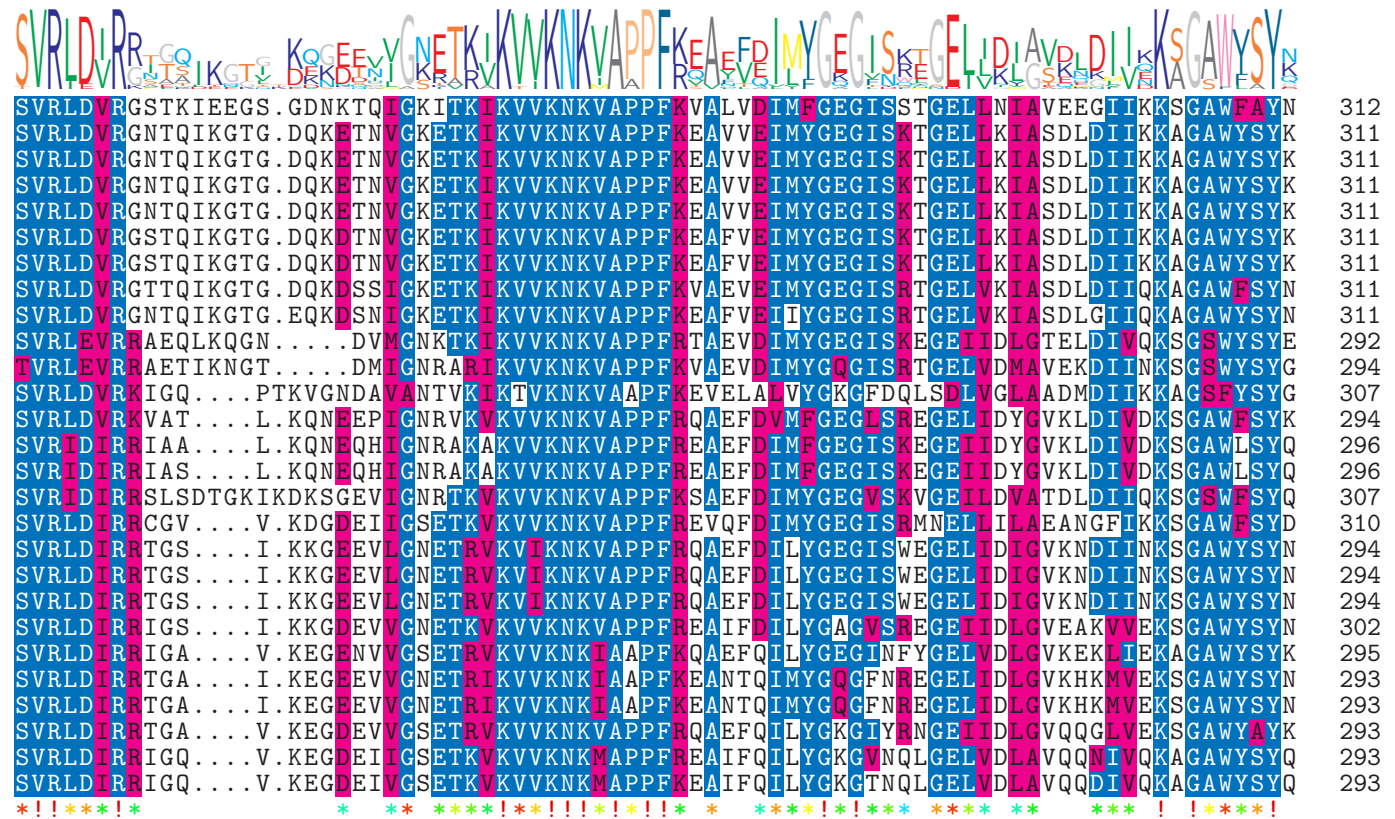
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEIAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGGGRENAAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRVAAAYGISDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEKTIATYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKLGGGRENKAFLENPEIADIEITKATINSMGTIEGM.....ISGSEDDEG.....EE.....	343
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GERIGGGRDNCREFLRNAAELAREIENKVRHGLVTPM.....GAVTLAEE.VE...ED.....	352
GEKIGGQKANATAWLKDNPETAKIEKKVRELLNSNP....STPDFSV...D..DSEGVATNEDF	353
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA...DDVEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA...DDVEFGAVPEEF	354
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GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKAS....DQTAA.HDETE...EEDPLLLES	349
GNKIGGQKNNVIRIFYEENQIAEIEIRNIEREQLLTGT....NGAVQ.I.EDE...EEDPLLLES	349

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	...	387
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consensus

 non conserved
 similar
 ≥ 50% conserved