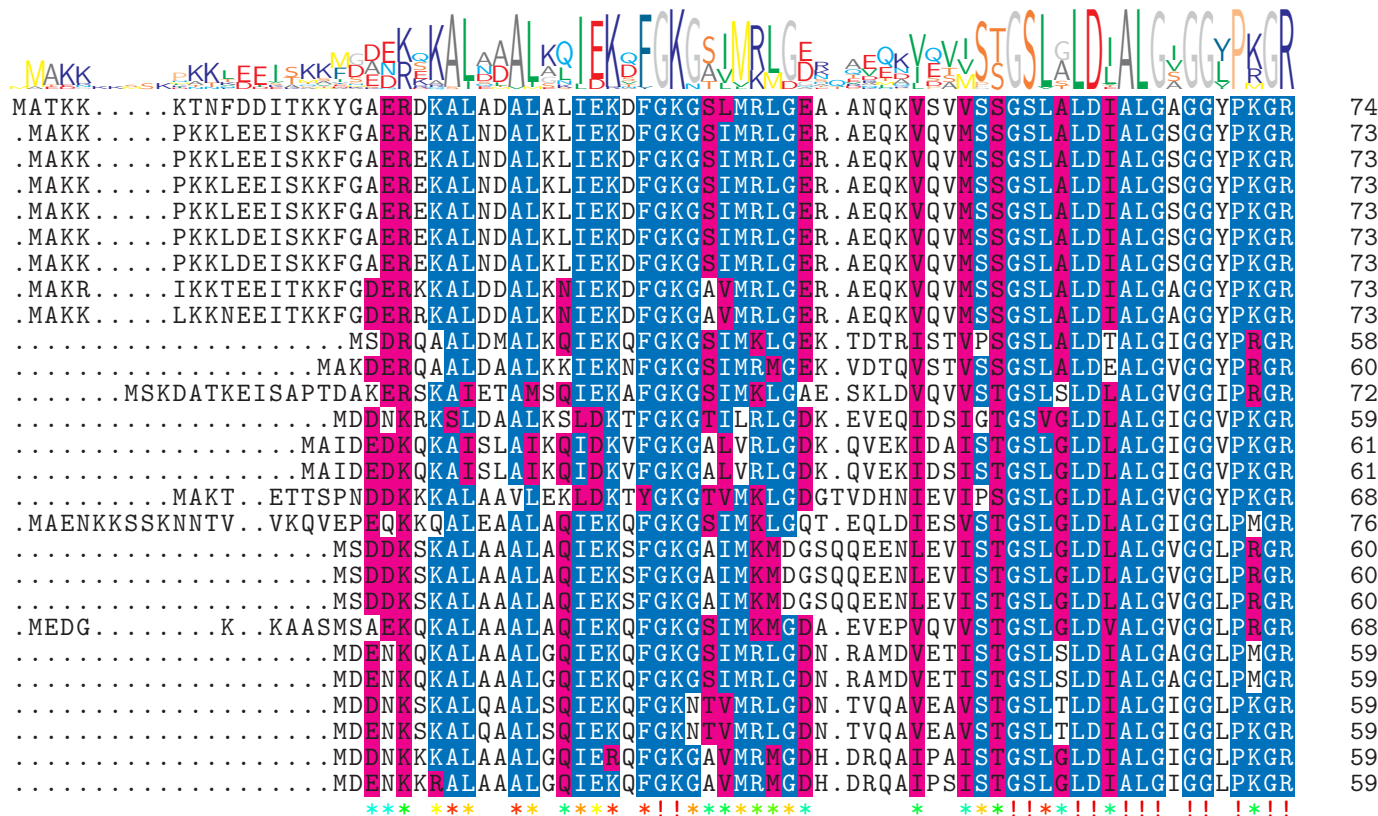


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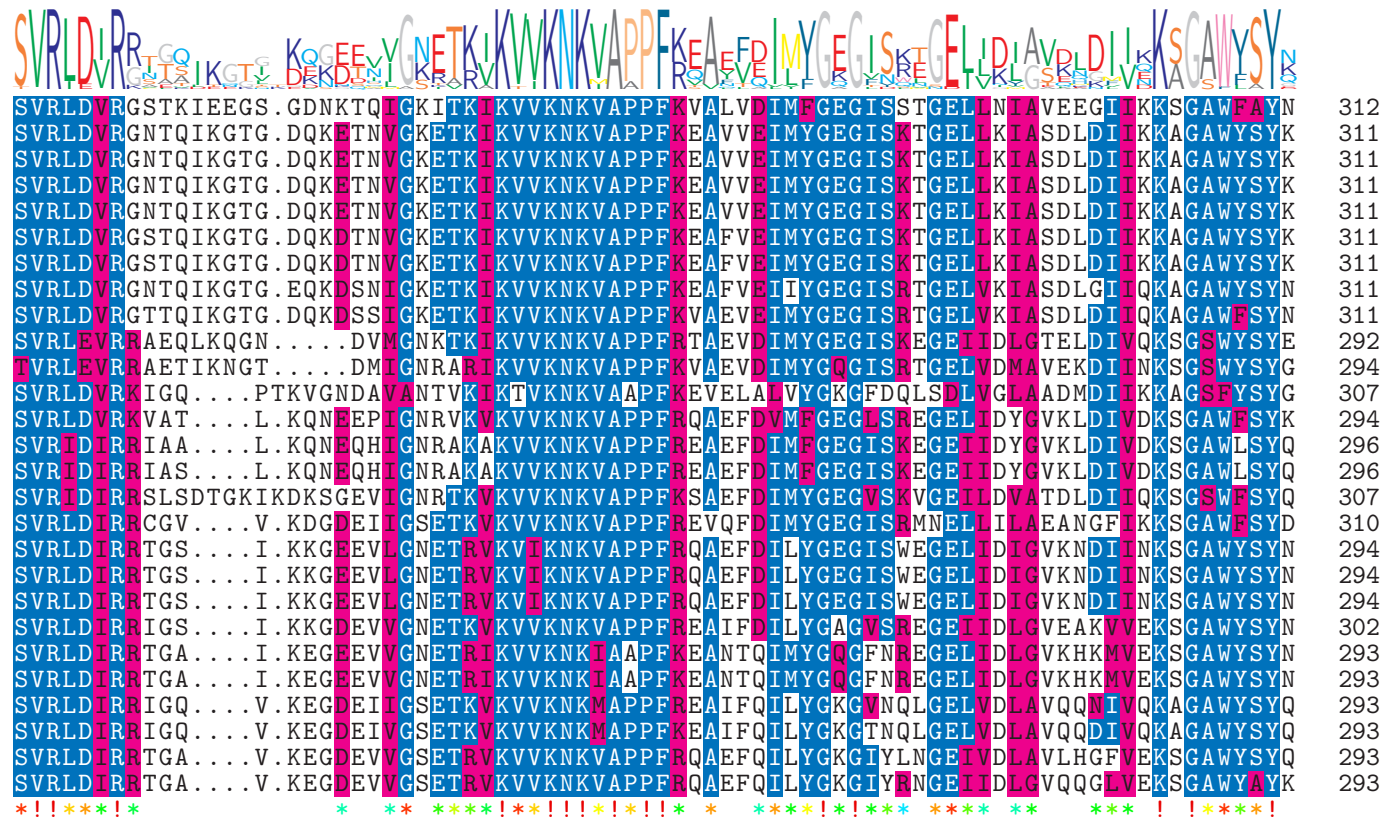
consensus




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consensus

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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPEIFDEIDHQVRVQFLIDGEEIAES . . . KKDE . . . AAQVDS . VNEEVPLDLGDELEIE	381
DEKIGQGS ENAKKYLAADNPEVFAEIDHQVRVQFLIDGEEAAES . . . KKDE . . . VAQVDS . VNEEVPLDLGDELEIE	381
GEKIGQGS ENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKQSSKEK ETDEK ADKNLVLELDDTIELE	382
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EERLGQGR ENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
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DERIGQG KEKTIAIYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAAA	363
DKKLGQGR ENSKAFLKENPEIADEITKAIQNSMGI EGM SGSEDDGE . E	343
DKKLGQGR ENAKALLKEDKALADEITLKIKESIGSNEEI MPLPDEPLE . . EME	347
DKKLGQGR ENAKALLKEDKALADEITLKIKESIGSNEEI MPLPDEPLE . . EME	347
DTKLGQGR DTVKELIKDNPELAEELEAKIREKLQAK	343
GAKIGQG KNNAVKWLKENPEIADKLEQIRNTLASPNNS VLKATASDSNDESVDVEE . FSEEL	372
GAKIGQG KDNVRVWLKENPEISDEIDAKIRALNGVEMHI TEGTQ DETDGE . . RPEE	348
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GSKIGQG KANS AKFLADNPEICKALEKQIRDKLLTPGVD TKAVGSREAVVADDVAE . . ADADS	354
GSKIGQG KANA AKYLENPEIQEIEQQIRAKLLVTSAN TKATPVAEDLADADI	347

logo

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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved