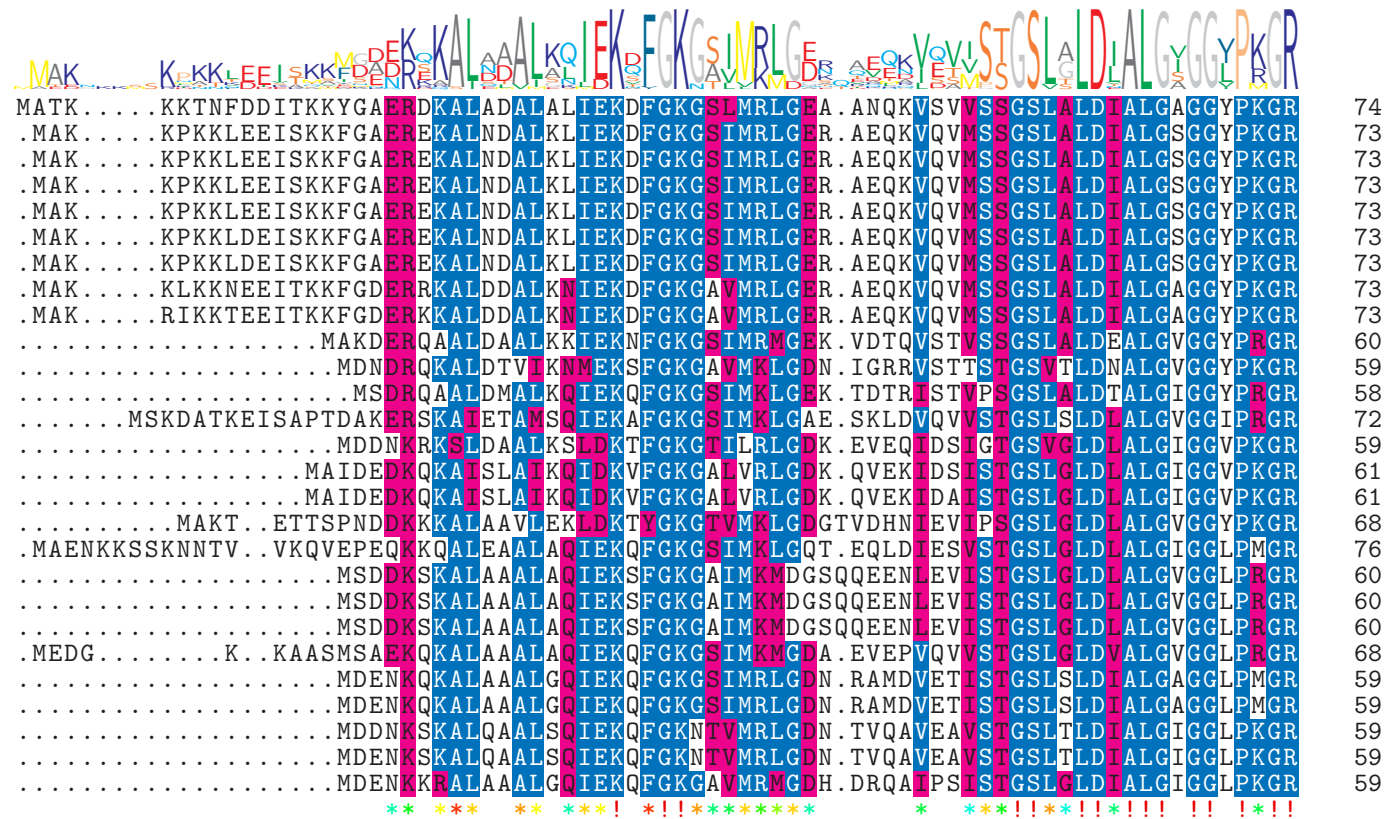


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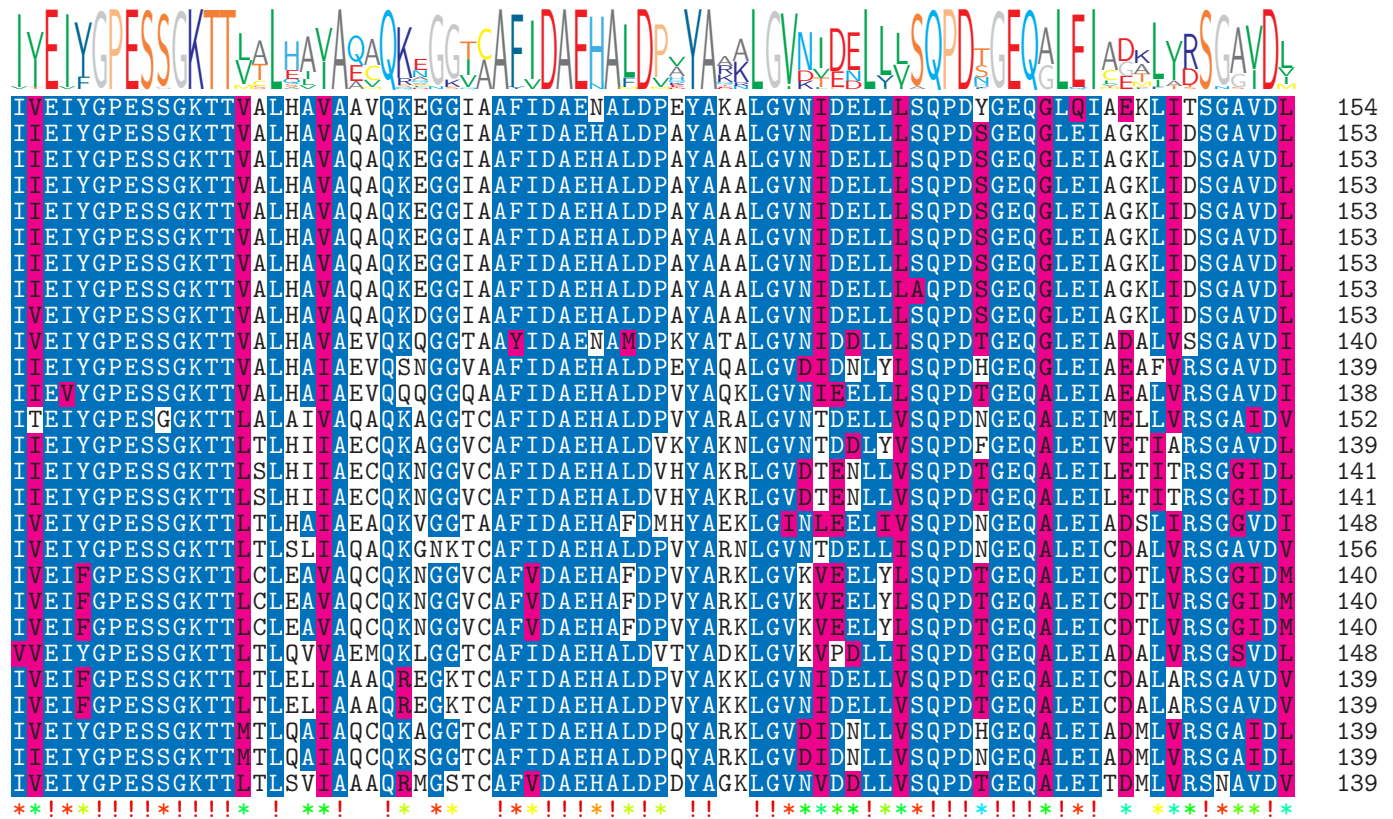
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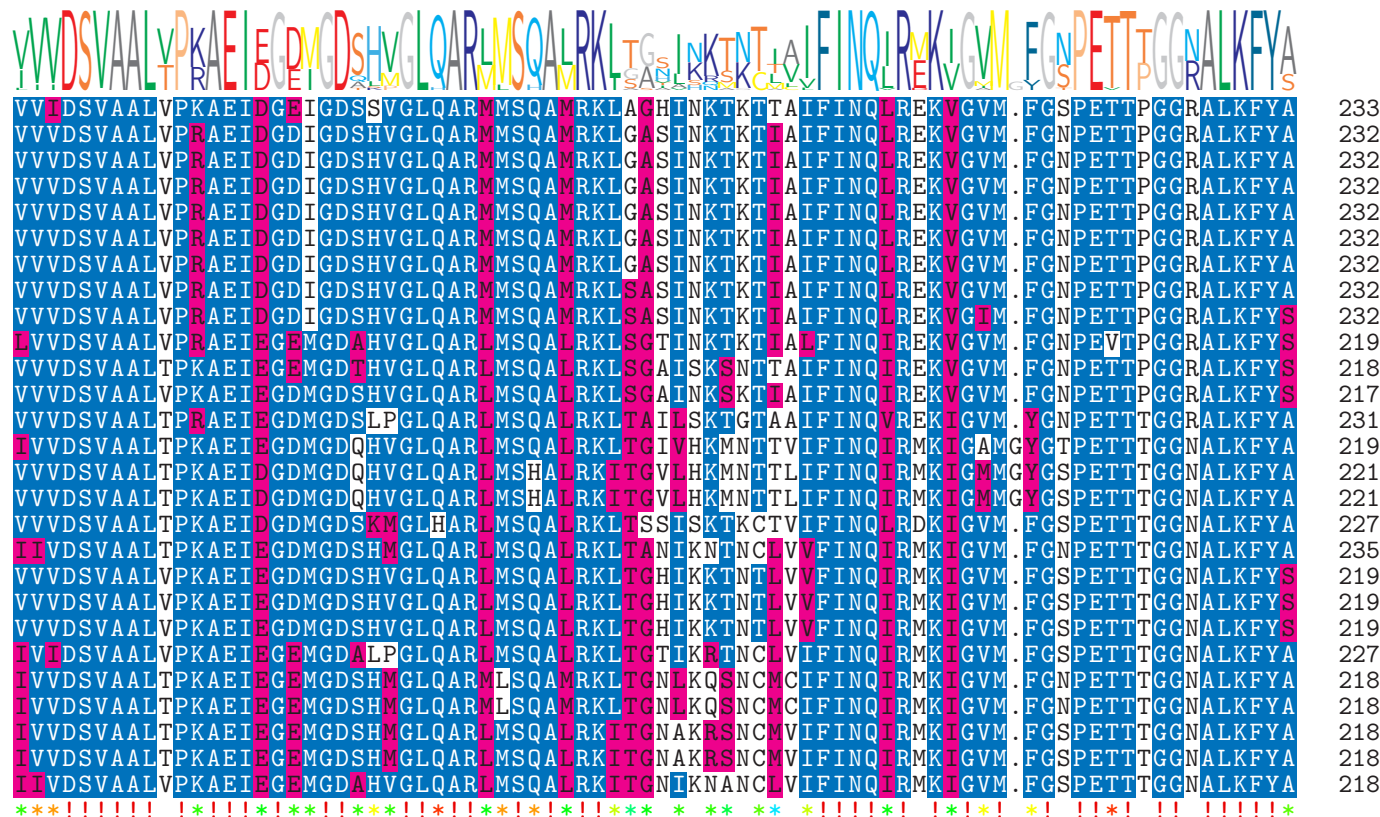
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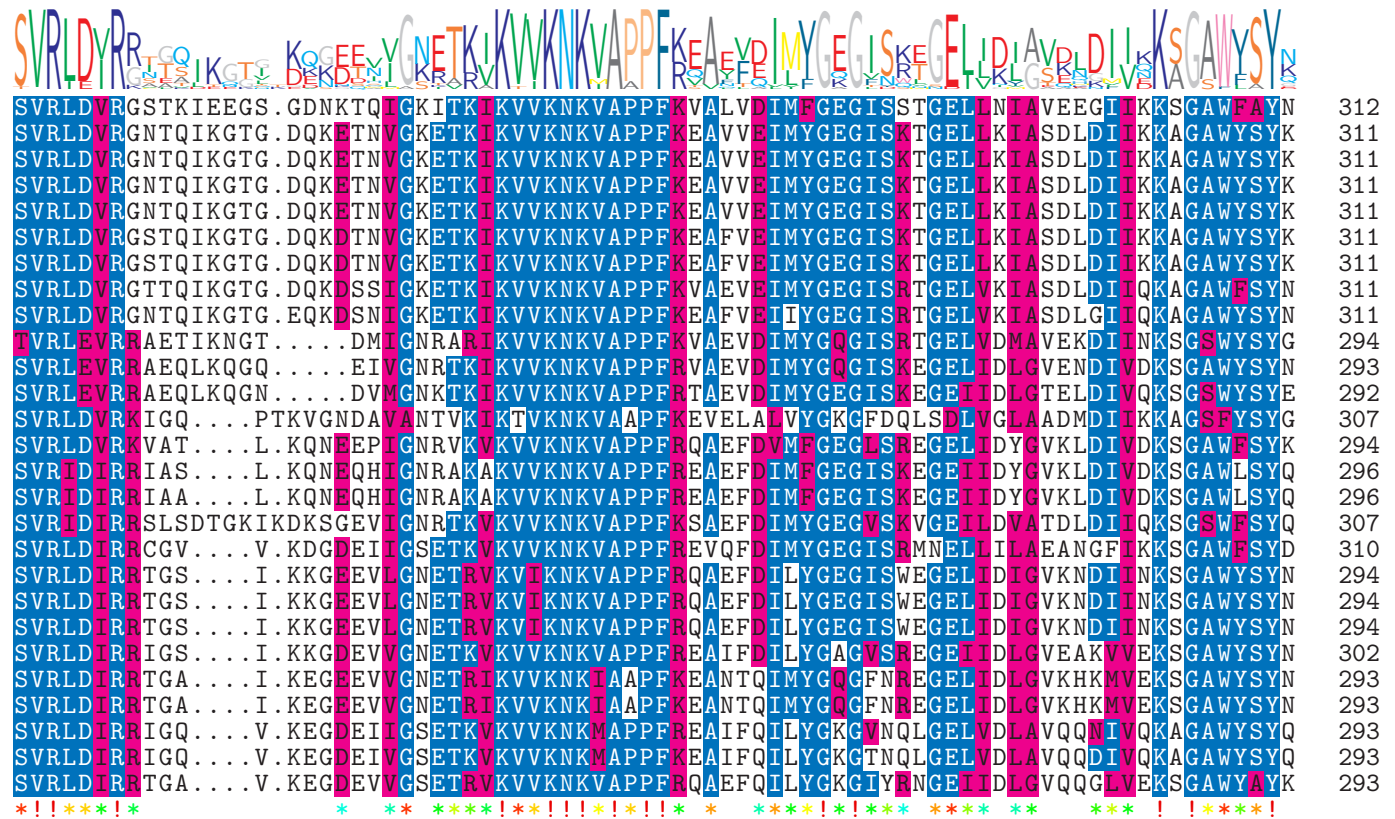
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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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 ENAKKYLAADNPEIFDEIDHQVRVQFLIDGEEIAES . . . KKDE . . . AAQVDS . VNEEVTLDLGDELEIE	381
DEKIGQGS ENAKKYLAADNPEVFAEIDHQVRVQFLIDGEEIAES . . . KKDE . . . VAQVDS . VNEEVTLDLGDELEIE	381
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGS ENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . ADKNLVLELDDTIELE	382
SERIGQGS ENAKNYLADHEDVEDEVRLKVRAAYGISDVPEEDLPTTEDEQINILPDDSTEE	355
GERMGQGS KENVKMYLKENPQIKEEIDRKLRKLGISDGDVEETEDA . . . PKSLFDEE	347
EERLGGREN AKQFLKENKDIMLMIQEIQIREHYGLDNGVQVQQAAETQEELEFEE	348
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GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GNKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASD QTAA . HDETEEEP . D . LL . ES	349
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GSKIGQGANAAKYYLENPEIQEIEEQIRAKLLVTSAN TKATPVAEDLADAD . I	347

logo

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

-  non conserved
-  similar
-  ≥ 50% conserved