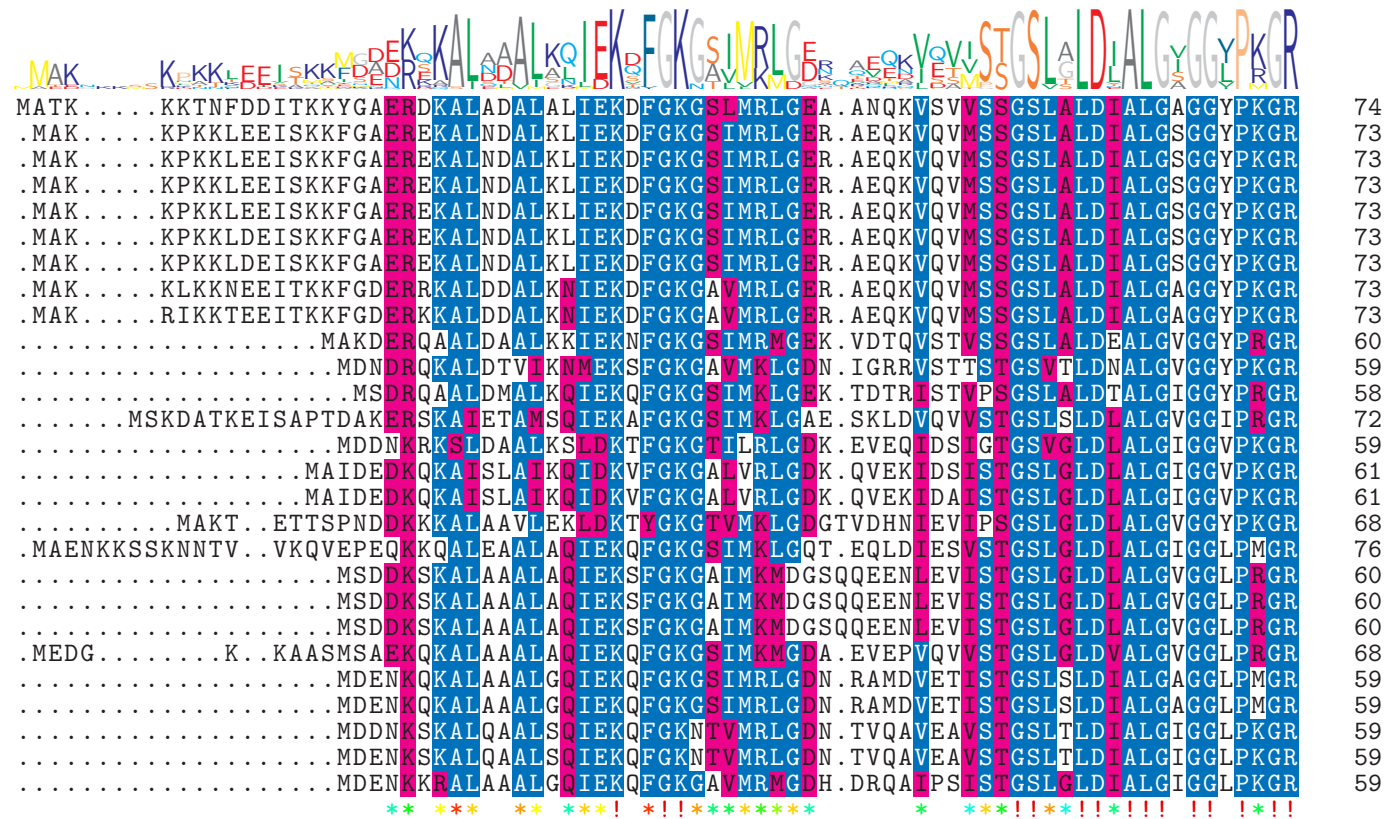


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NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 453 Spy49 1753c ACI62003.1
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consensus

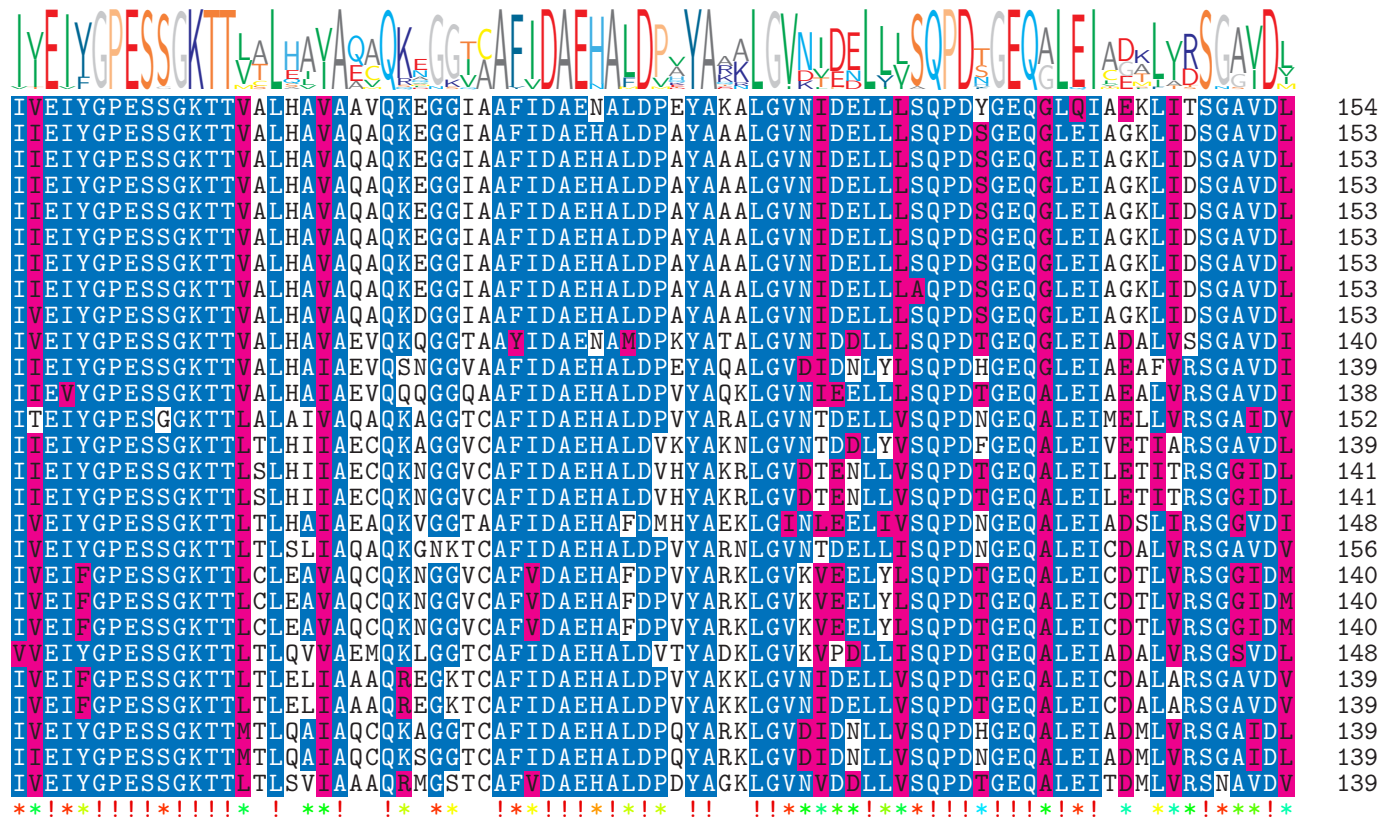
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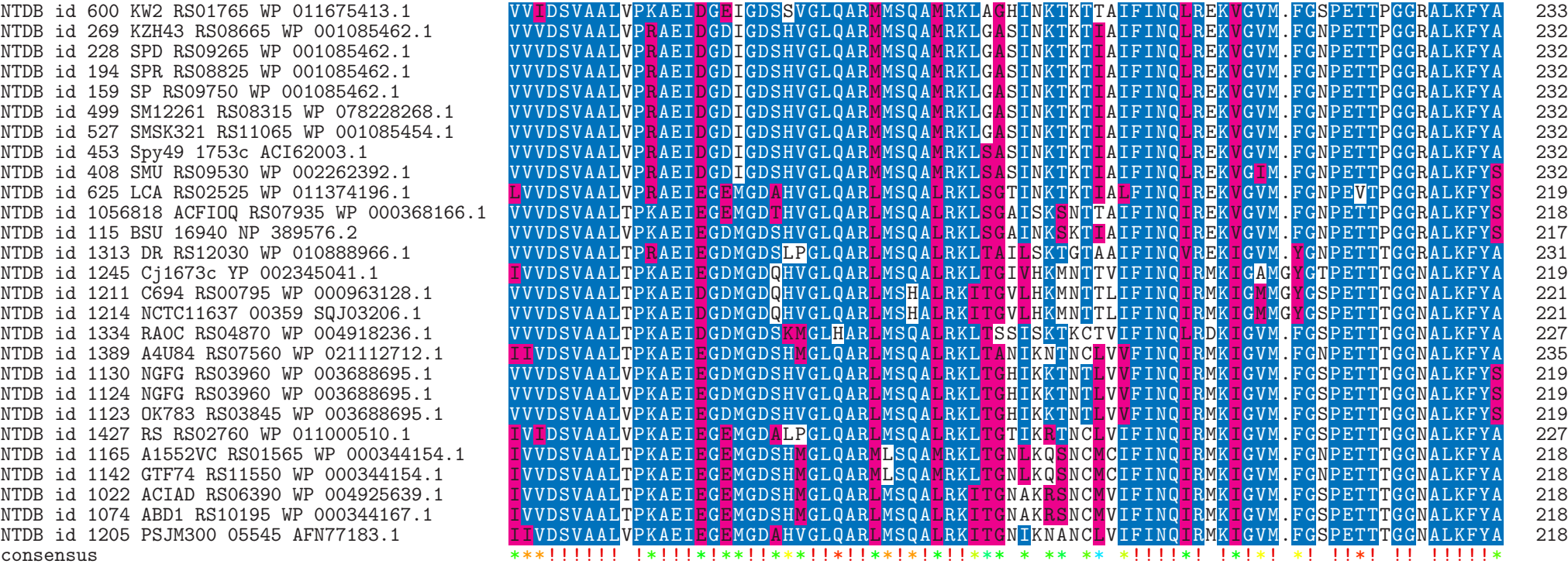
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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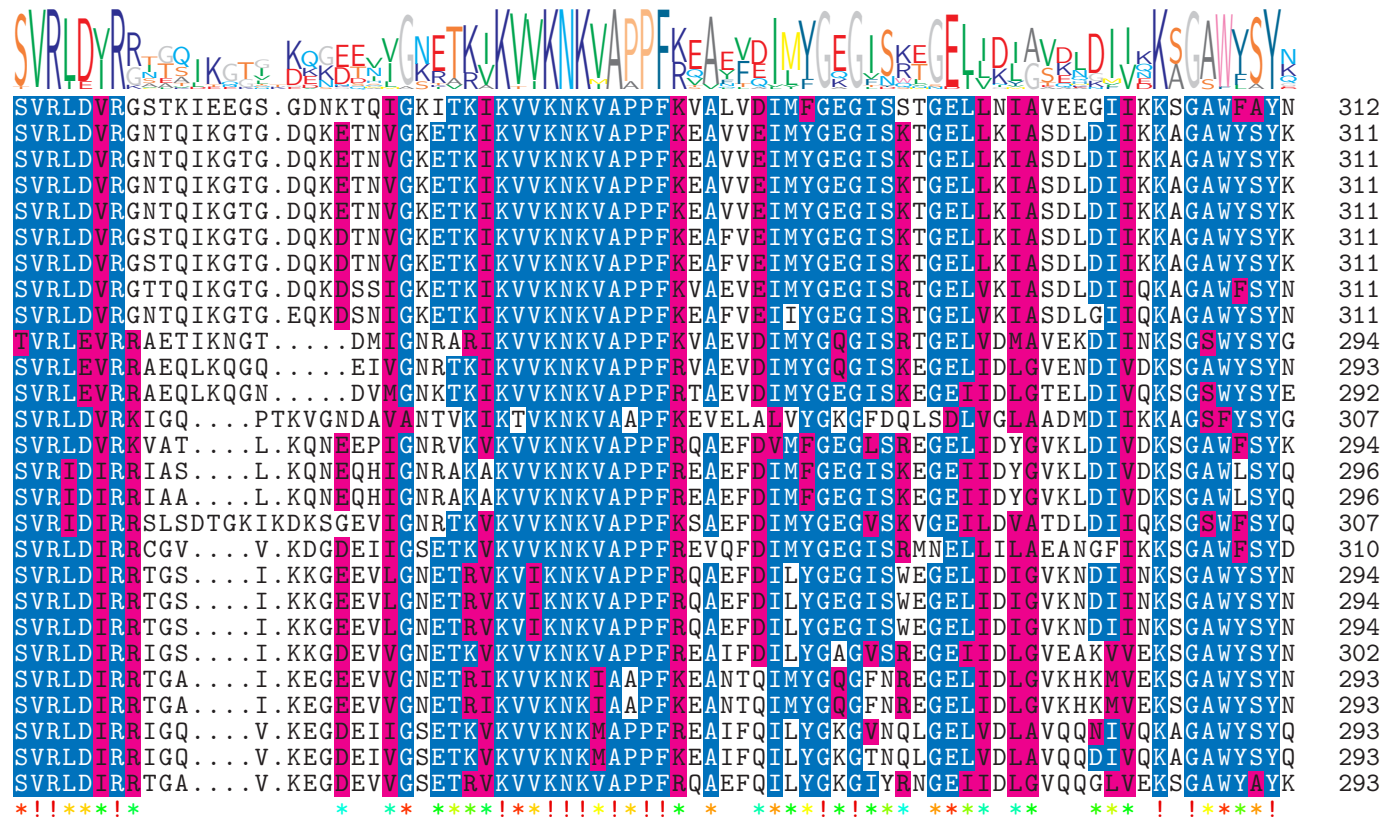
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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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 ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPEIFDEIDHQVRVQFLIDGEEIAES . . . KKDE . . . AAQVDS . VNEEVTLDLGDELEIE	381
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EERLGGGR ENAKQFLKENKDIMLMIQEIQIREHYGLDNGVQVQQAAETQEELEFEE	348
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GSKIGQGGKANAACKYLENPEI GQIEEQIRAKLLVTSAN TKATPVAEDLADAD . I	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	... 387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE 388
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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved