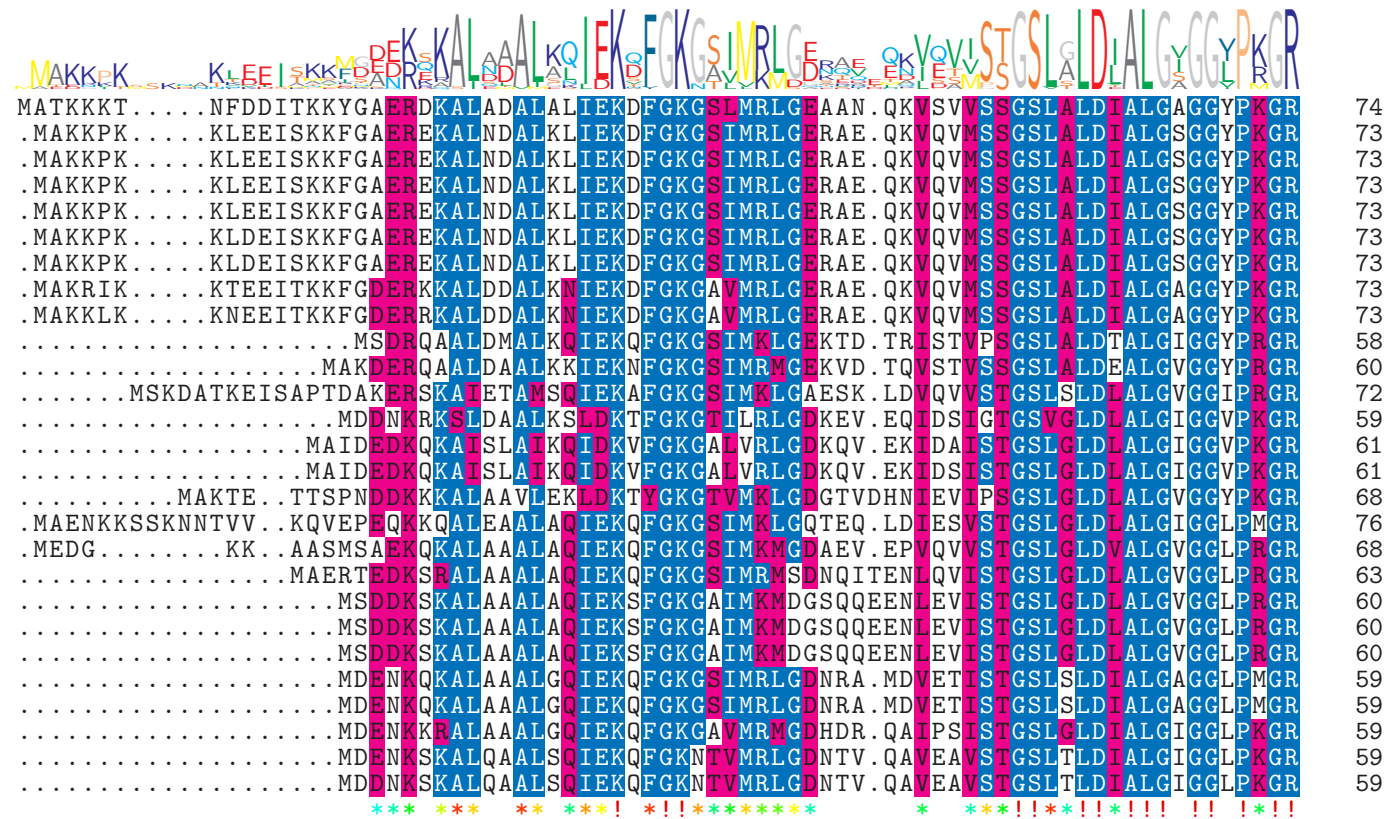


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consensus

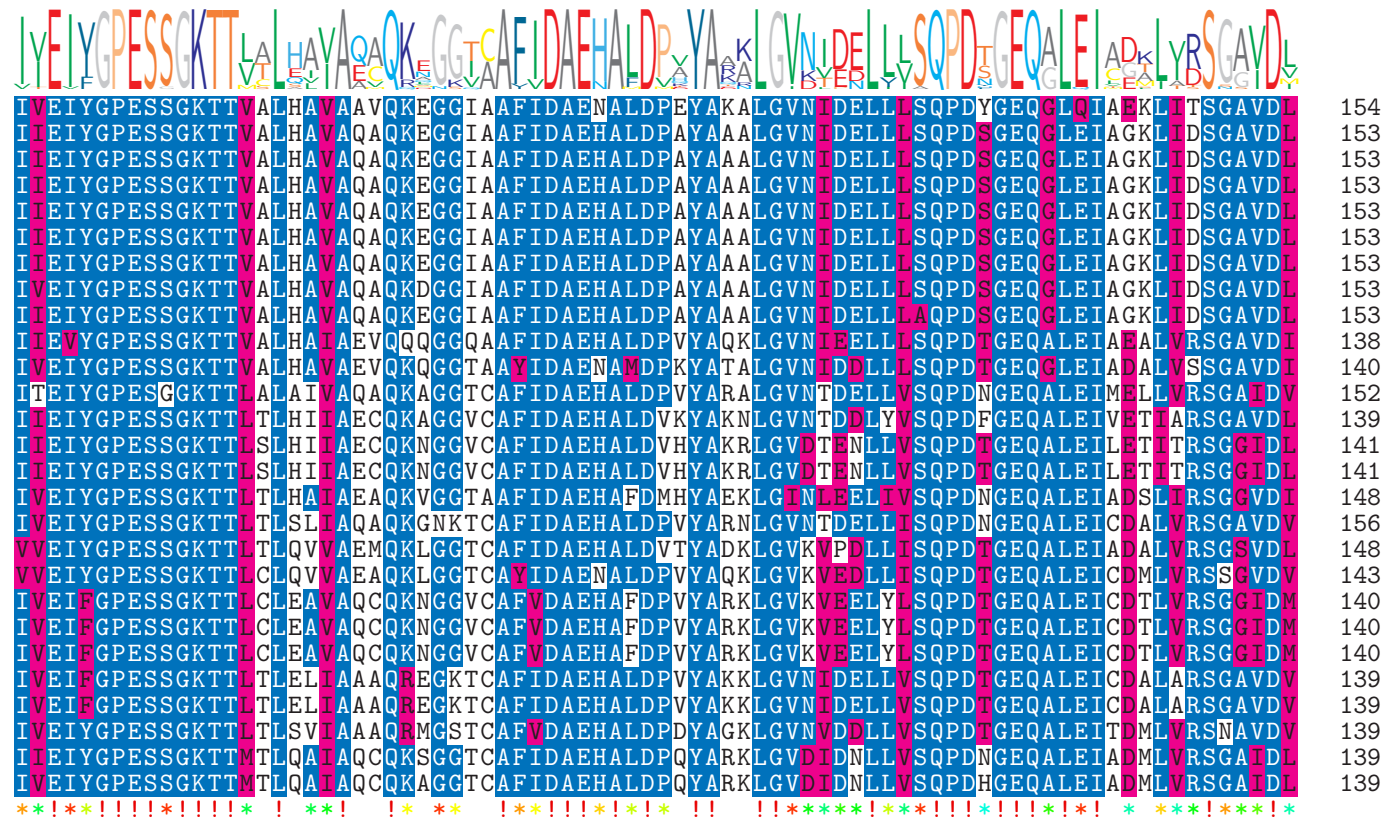
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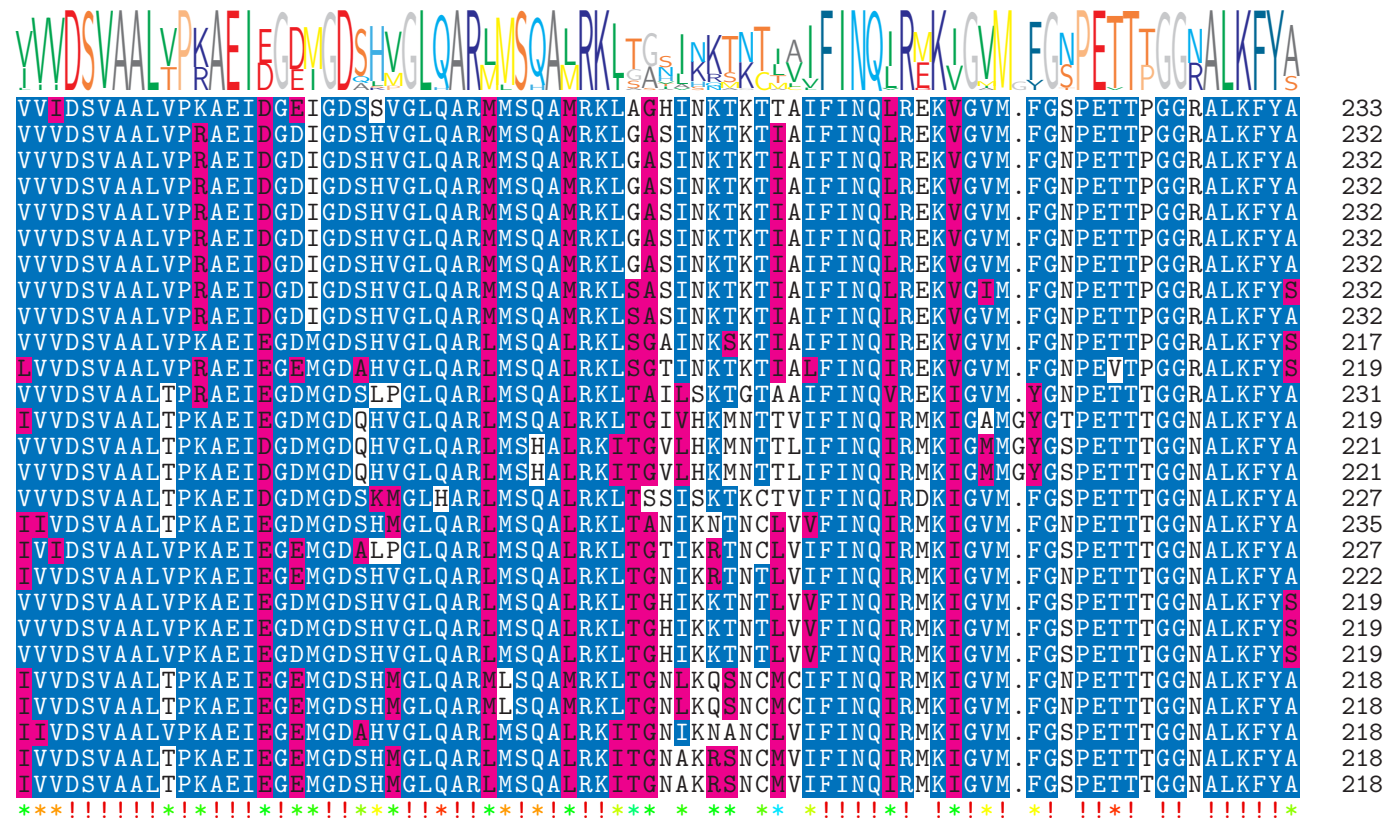
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consensus

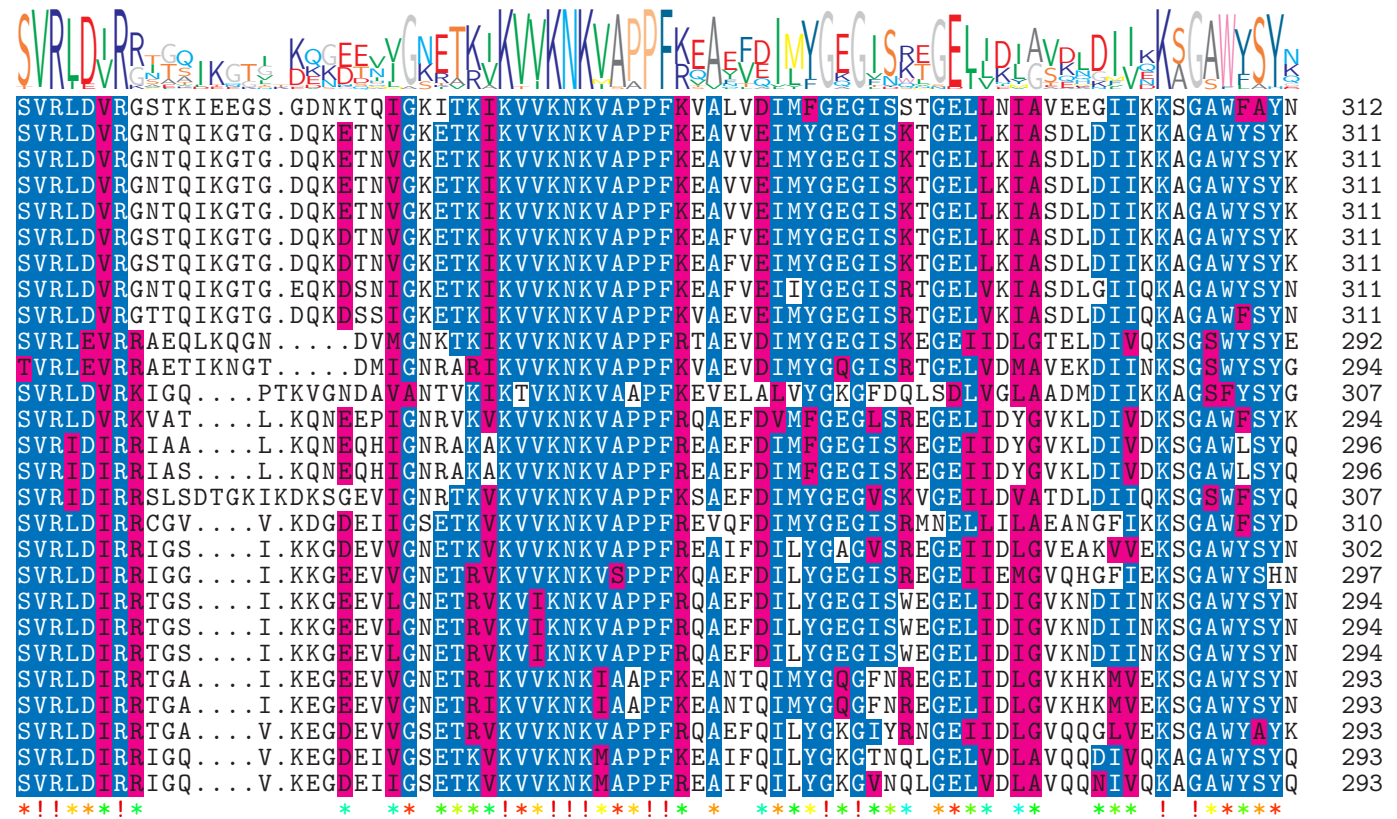
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIE	385
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DEKIGQGSENAKKYLAADNPVFDEIDHQVRVQFLIDGEEIAES KKDE VAQVDS . . VNEEVTLDLGDLEIE	381
GEKIGQGSENAKKFLADNPVFDDIDHKVRVQGLIEEDNTEEEKSSKEK ETDEK . . ADKNLVLELDDTTIELE	382
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE E TDDLALDLNNGIEIE	377
EERLGGGRENAAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
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logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved