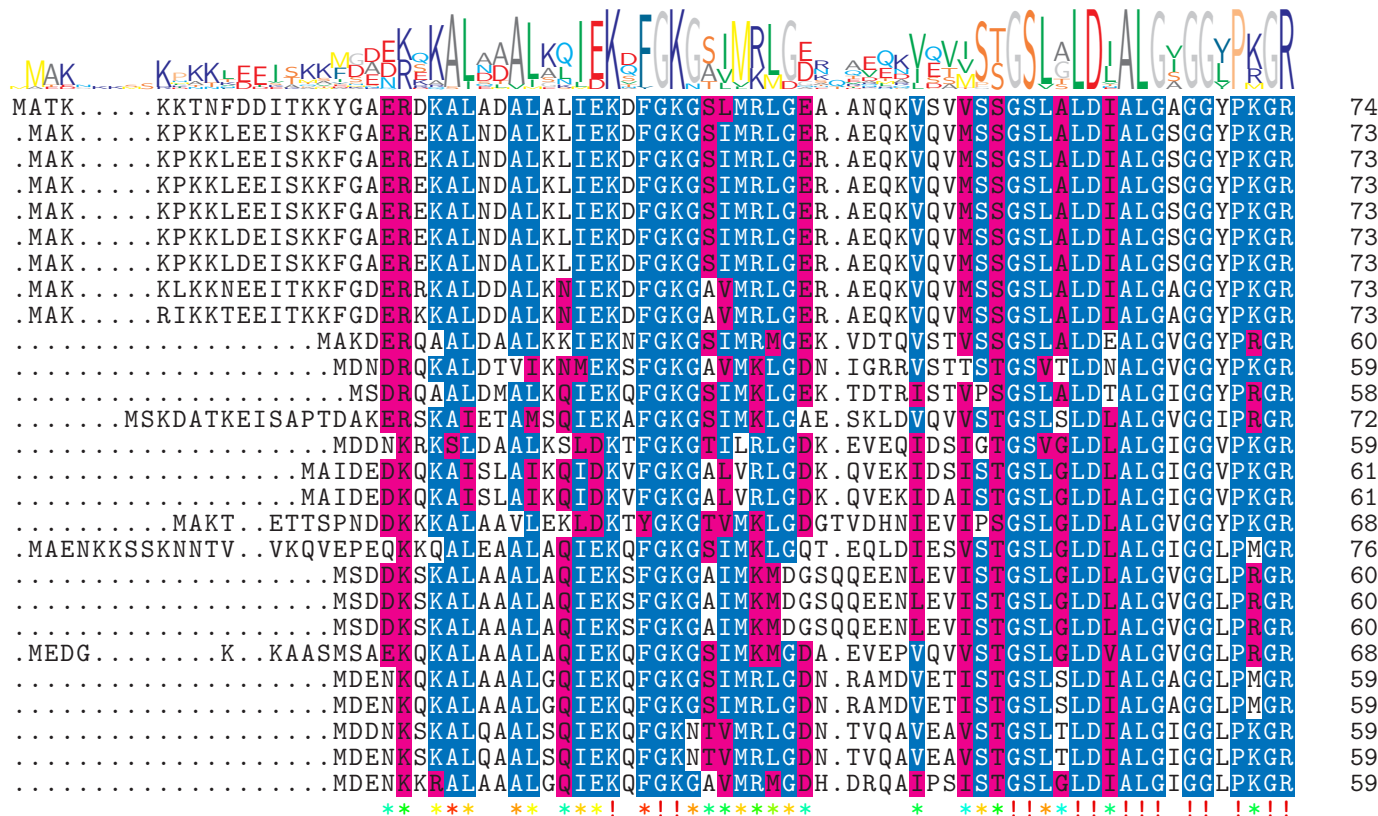


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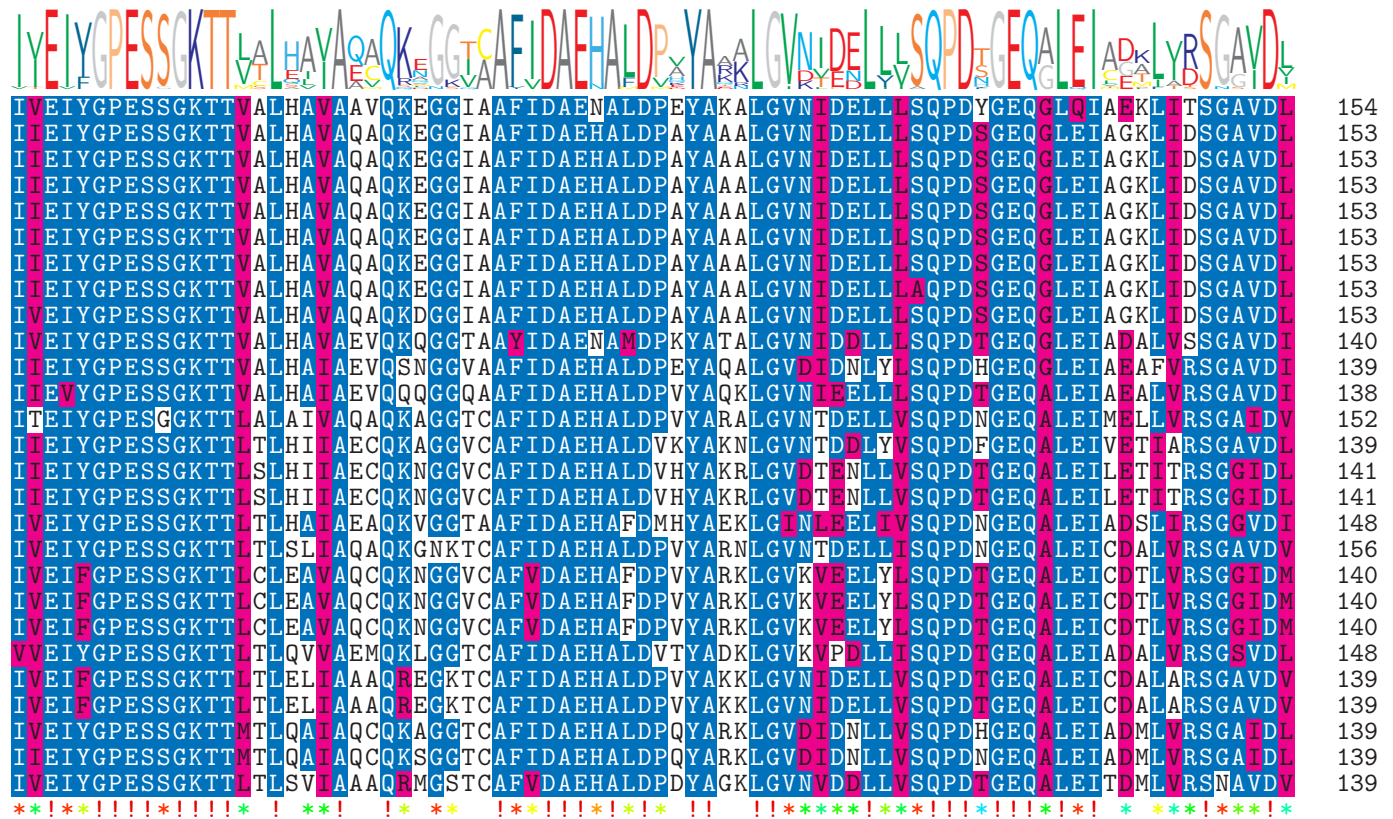
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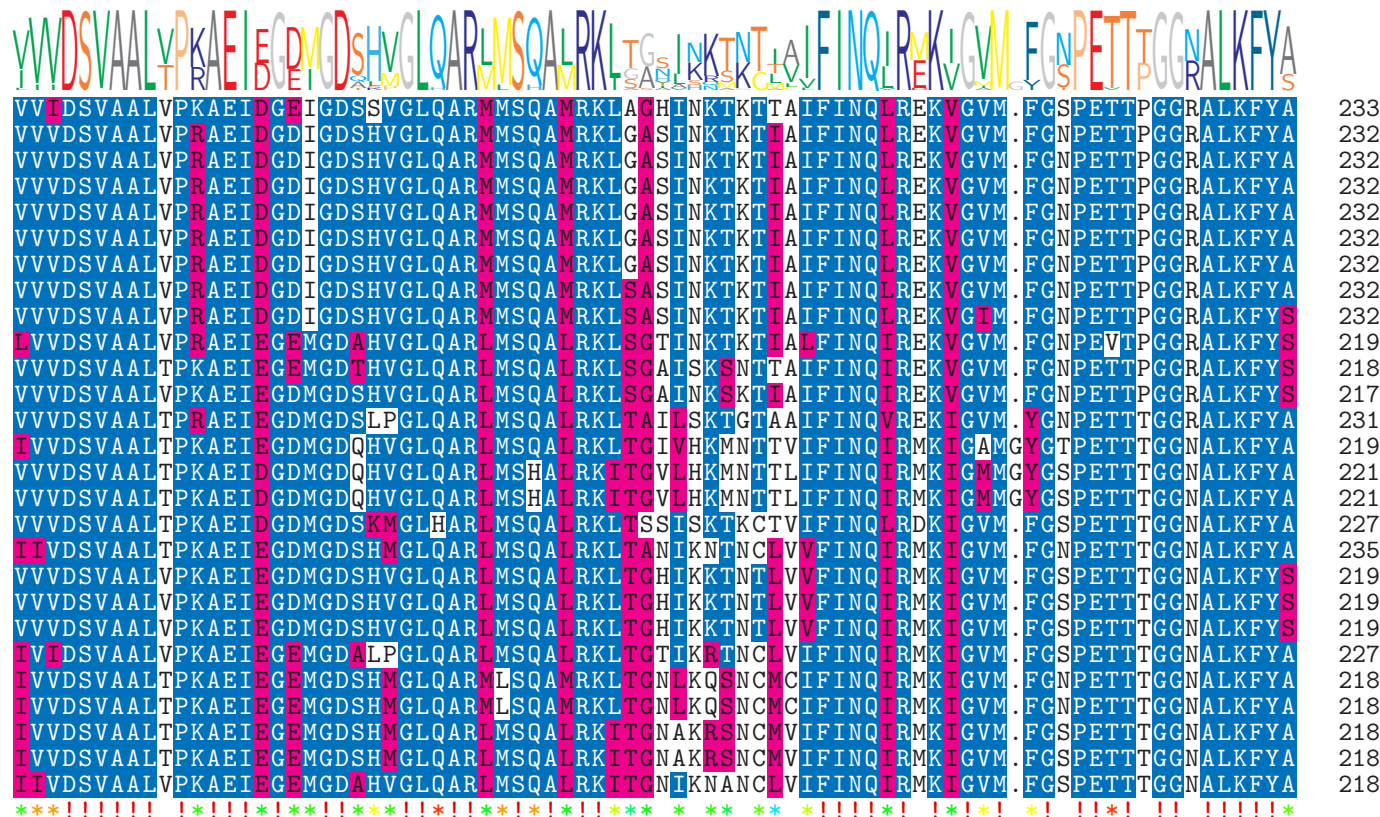
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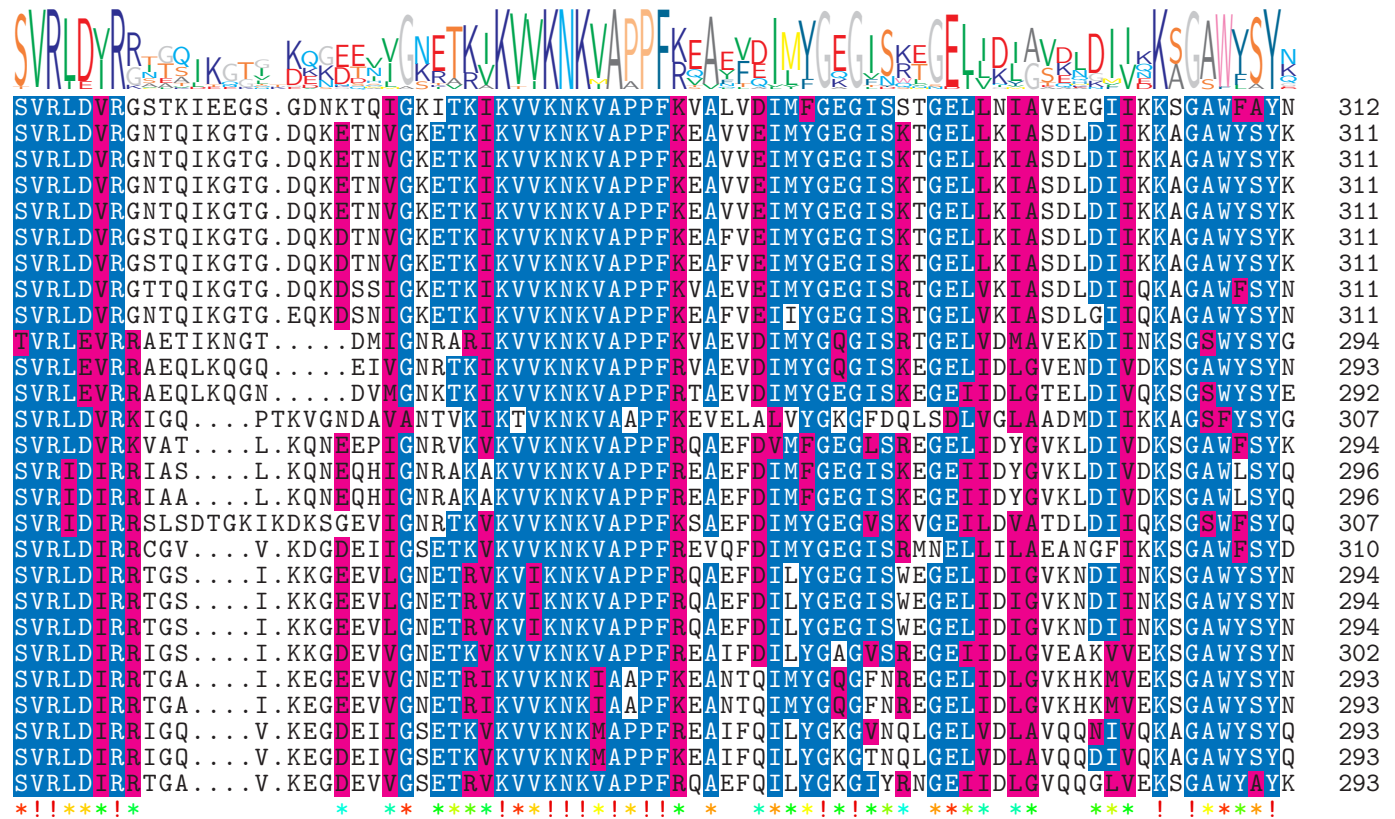
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consensus

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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
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GEKIGQGS ENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . ADKNLVLELDDTIELE	382
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EERLGGGR ENAKQFLKENKDIMLMIQEIQIREHYGLDNNGVVQQAAETQEELEFEE	348
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GSKIGQGGKANAACKYLENPEIQEIEEQIRAKLLVTSAN TKATPVAEDLADAD . I	347

logo

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved