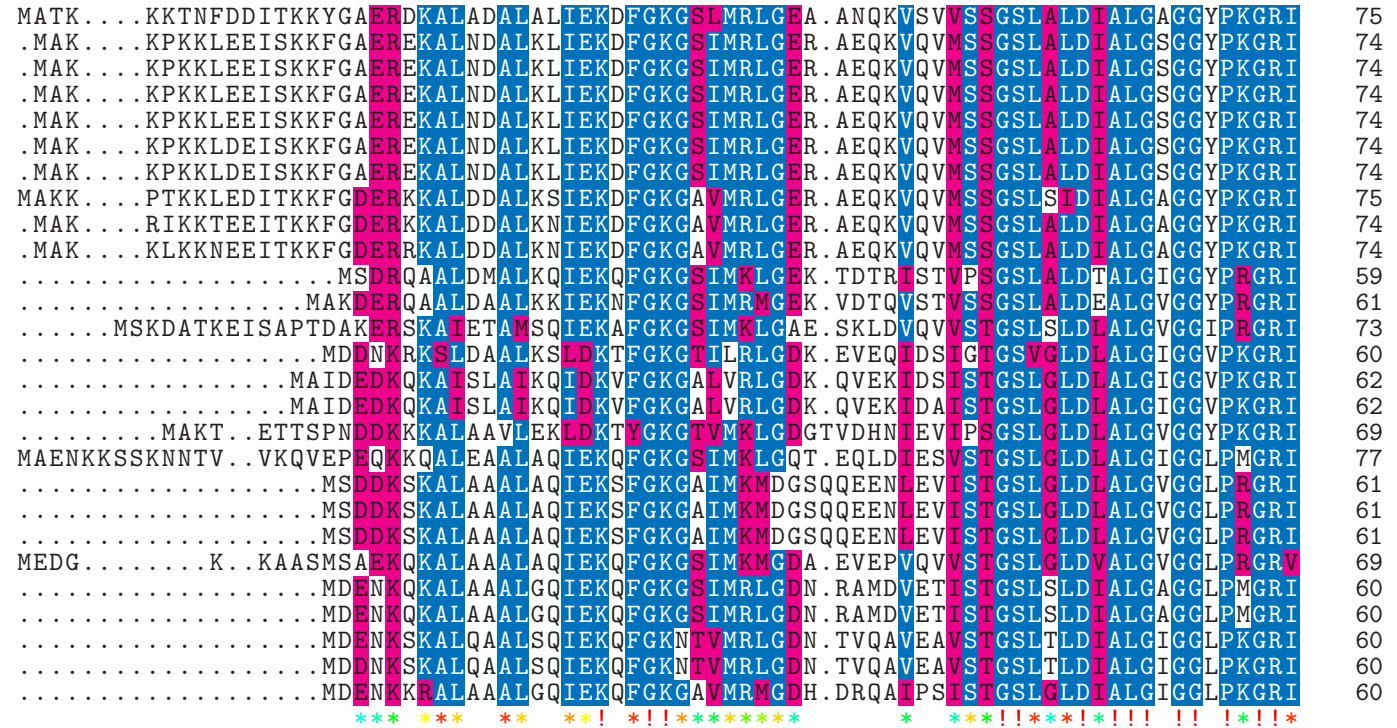


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consensus

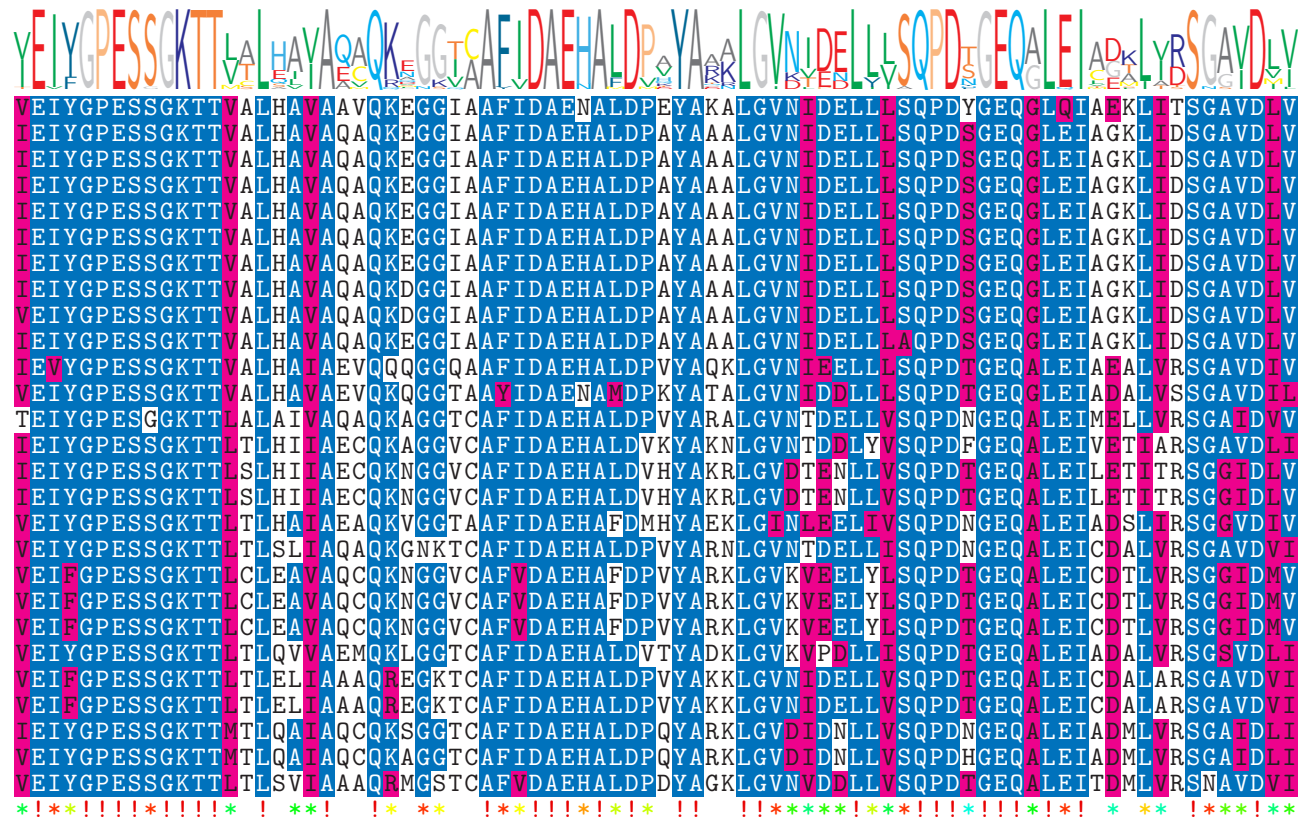
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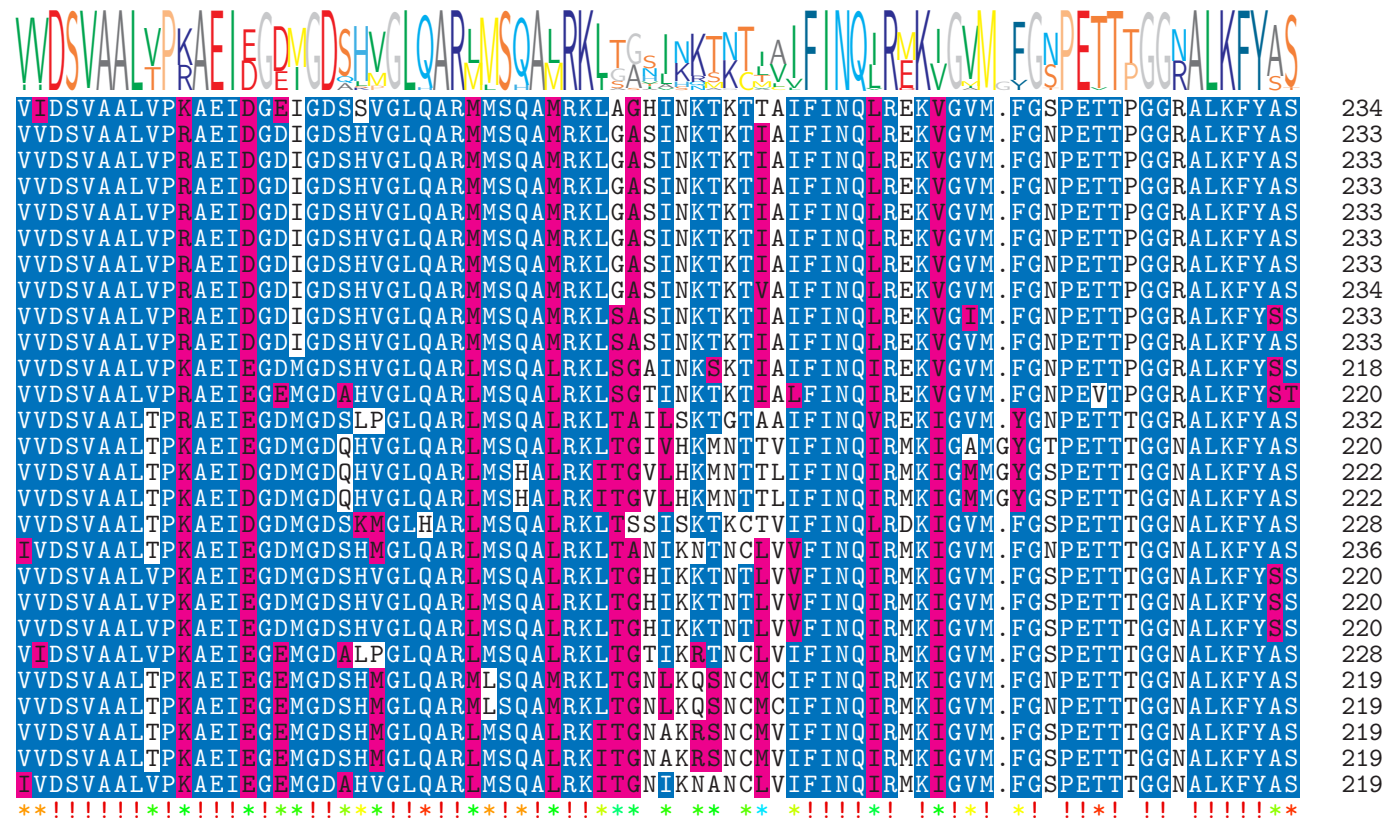


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consensus

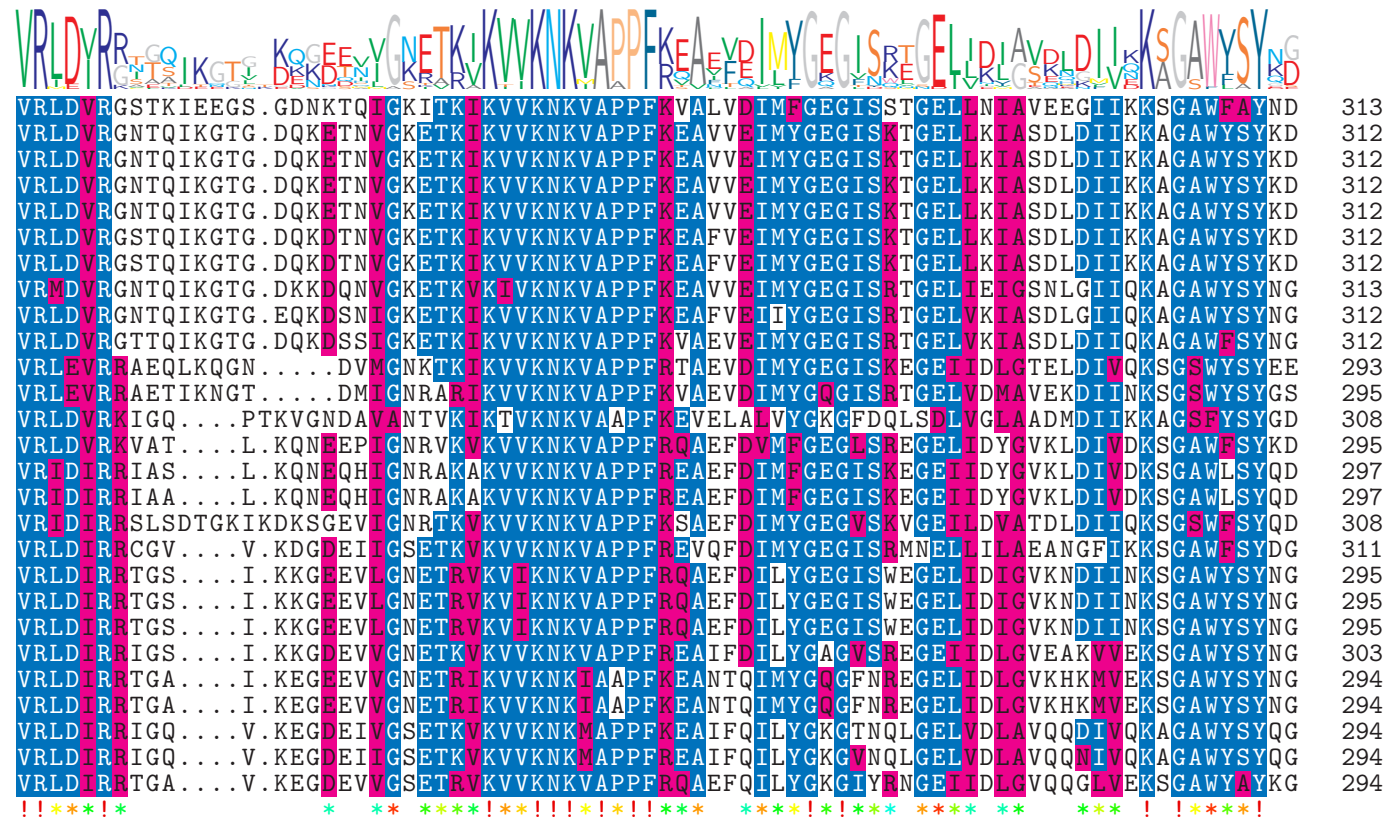
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consensus

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consensus

Sequence	Score
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EKIGQGSENAKKYLAEHPFIDEIDKQVRSKFGLDIGEEVSEQDT...ENKKDEP...KKEEA..VNEEVPLDLGDE	381
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EKIGQGSENAKKYLADNPEIFDEIDHQVRVQFGLDIGEEIAES...KKDEA...AQVDS..VNEEVPLDLGDE	377
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EKIGQGSENAKKFLADNPATFDEIDRKIRVHYGLIEADGVEEVAT...EEA.PVV...AE..EIQDVILDLDGG	378
EKIGQGSENAKKFLADNPEIFDIDHKVRVQYGLIEEDNTEEEKQS...SKEKETD...EK..ADKNLVLELDDT	378
EKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESASAMA...VASEE...TDDLALDLNG	373
ERIGGGRENAKQFLKENKDIIMLMIQEQIREHYGLDNGGVVQQQAE...ETQEELFE.E	348
ERIGGGRENAKNYLADHEDVEVRLKVRAAAGISDVPPEEDLPTT...EDE.QINILPDDSTEE	355
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KKLGGGRENSKAFLEKENPEIADEITKAIQNSMGTGMI...SGSEDDE..GEE	343
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SKIGGGKANAAKYLEENPEIGQEIEQIRAKLIVTSAN...TKATPVAEDLAD..I	347

logo

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved