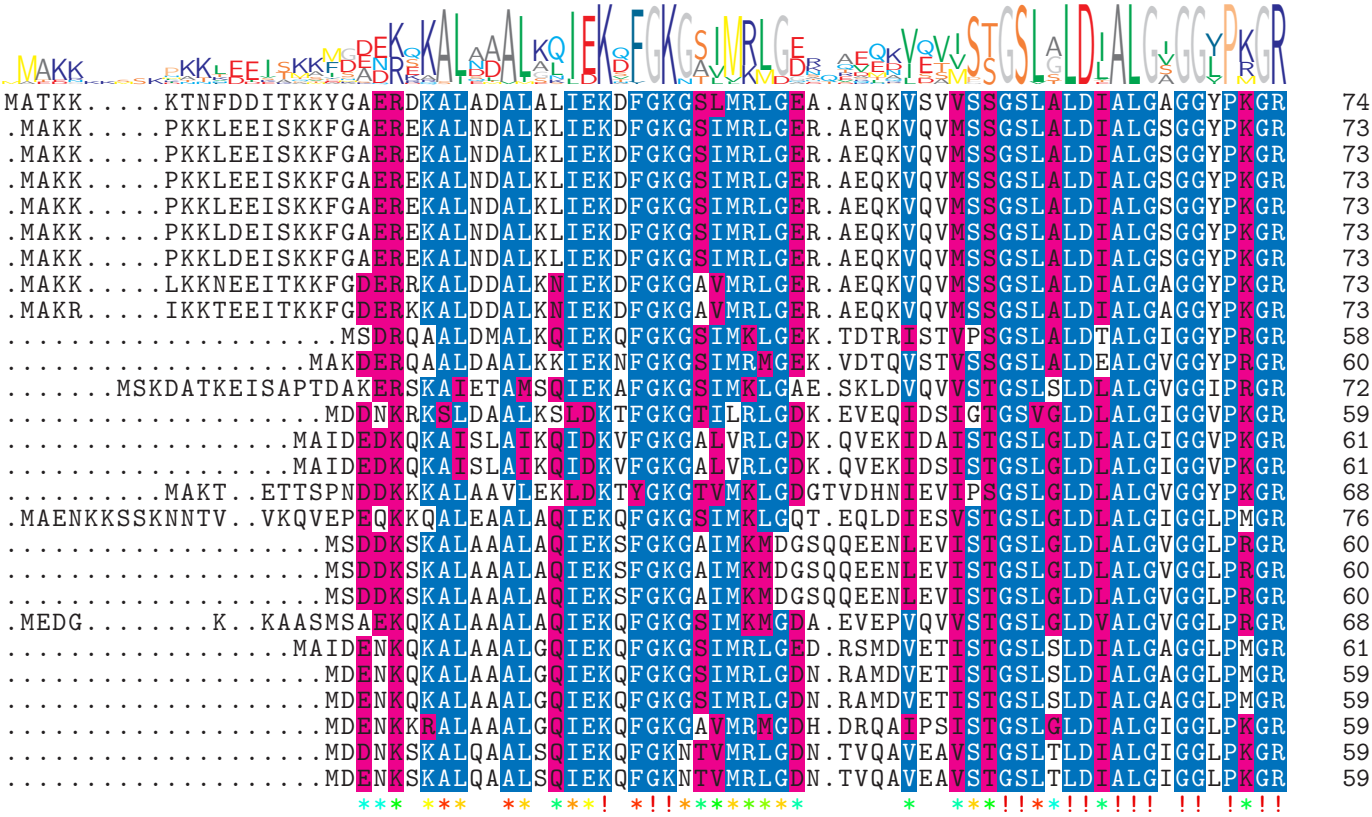


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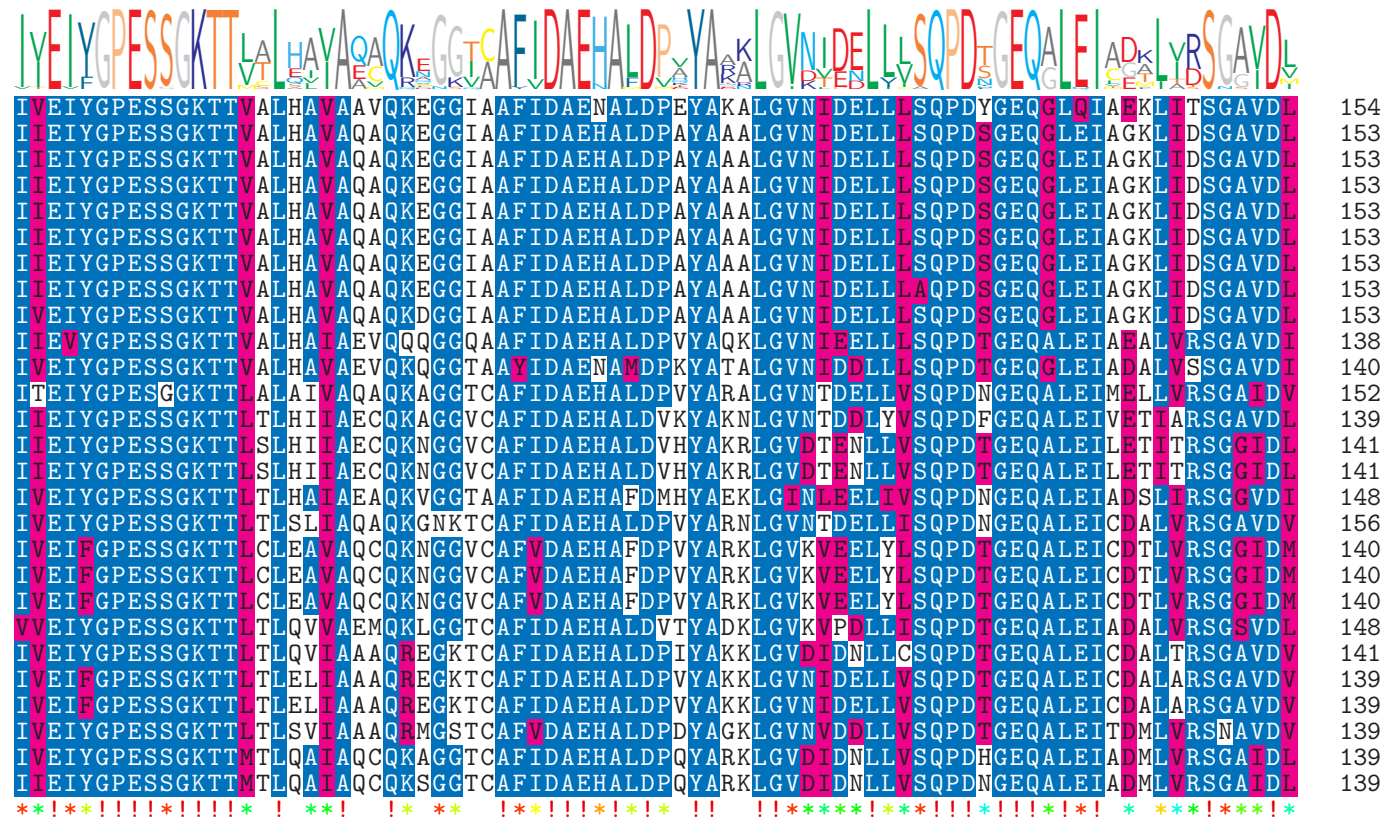
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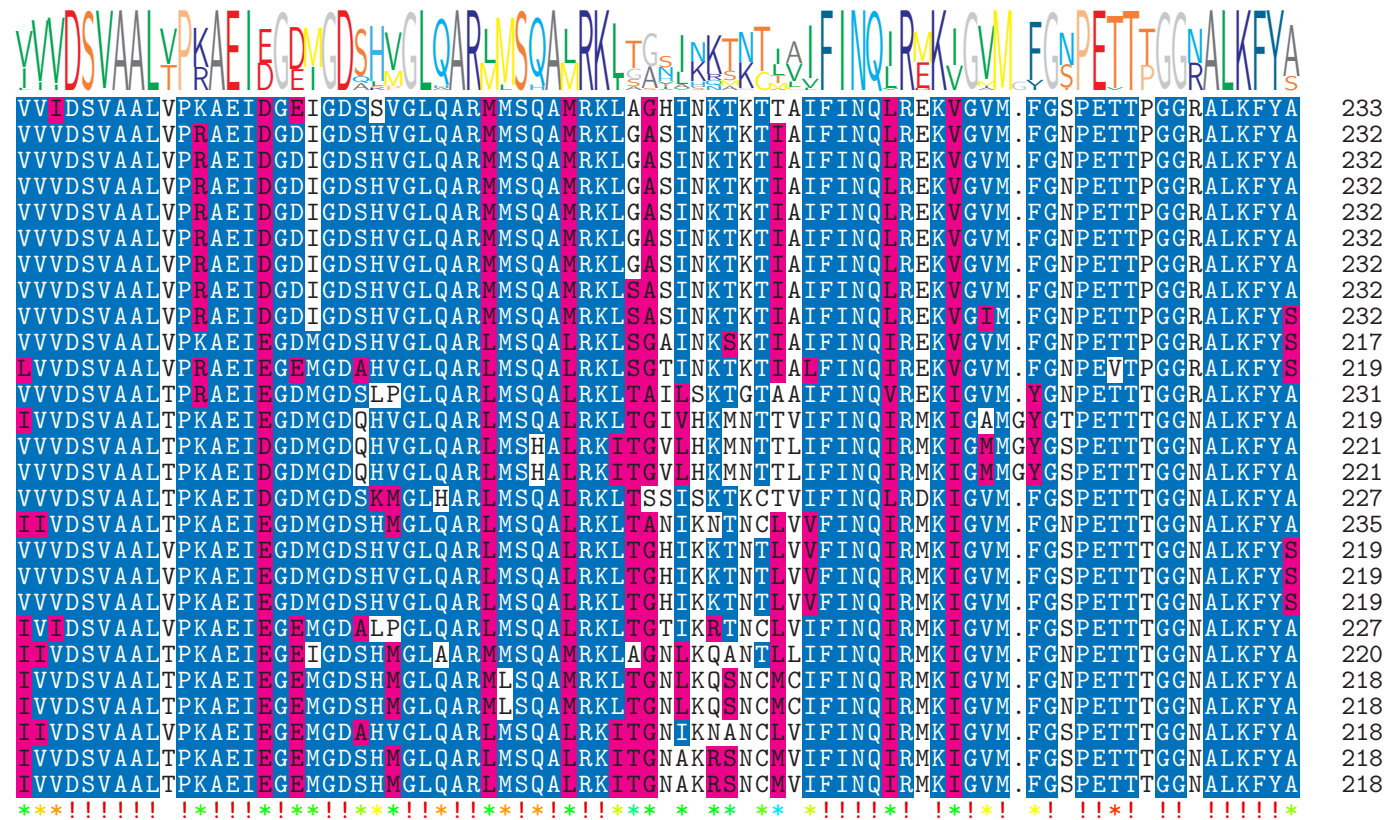
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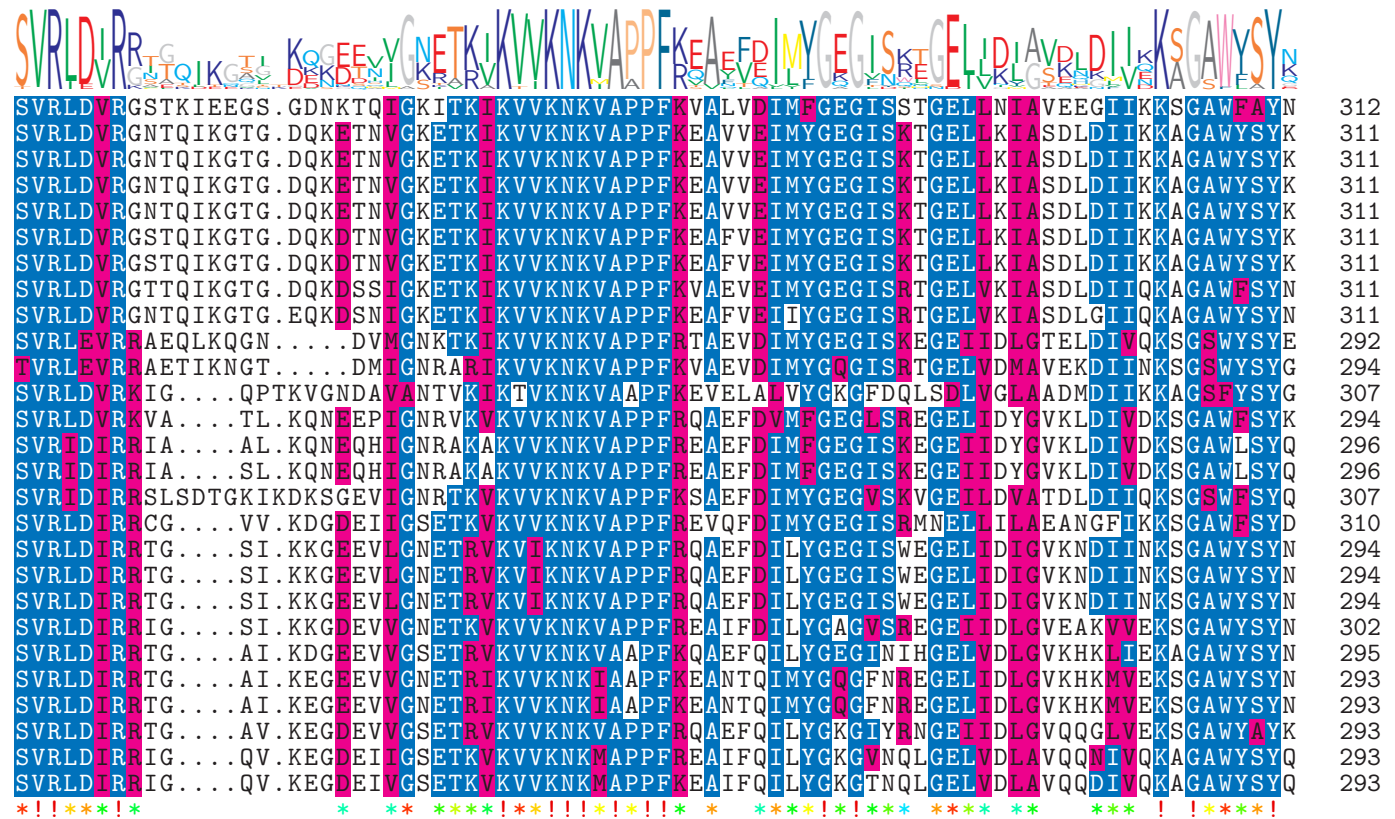
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTEN...KKDE...PKKEEA..VNEEVPLDLGDEL	382
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DEKIGQGSENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAE...S...KKDE...AAQVDS..VNEEVTLDLGDEL	378
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVA..SE.....E.....TDDLALDLNGI	374
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSK...EK.....ETDEK..ADKNLVLELDDTI	379
EERLGQGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEET...QEFL.EFE.E.....	348
SERIGQGGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTED...E.QI.NILPDDST....EE.....	355
DERIGGQKEKTIAYIAERPMEQEITDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
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DTKLGQGRDITVKELIKDNPELAELEAKIREKLQAK.....	343
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GSKIGQGGKANAAYKYLENPEIGQETIEQQIRAKLLVTSANTKA...TPVAEDLADADI.....	347
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logo

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consensus									

-  non conserved
-  similar
-  ≥ 50% conserved