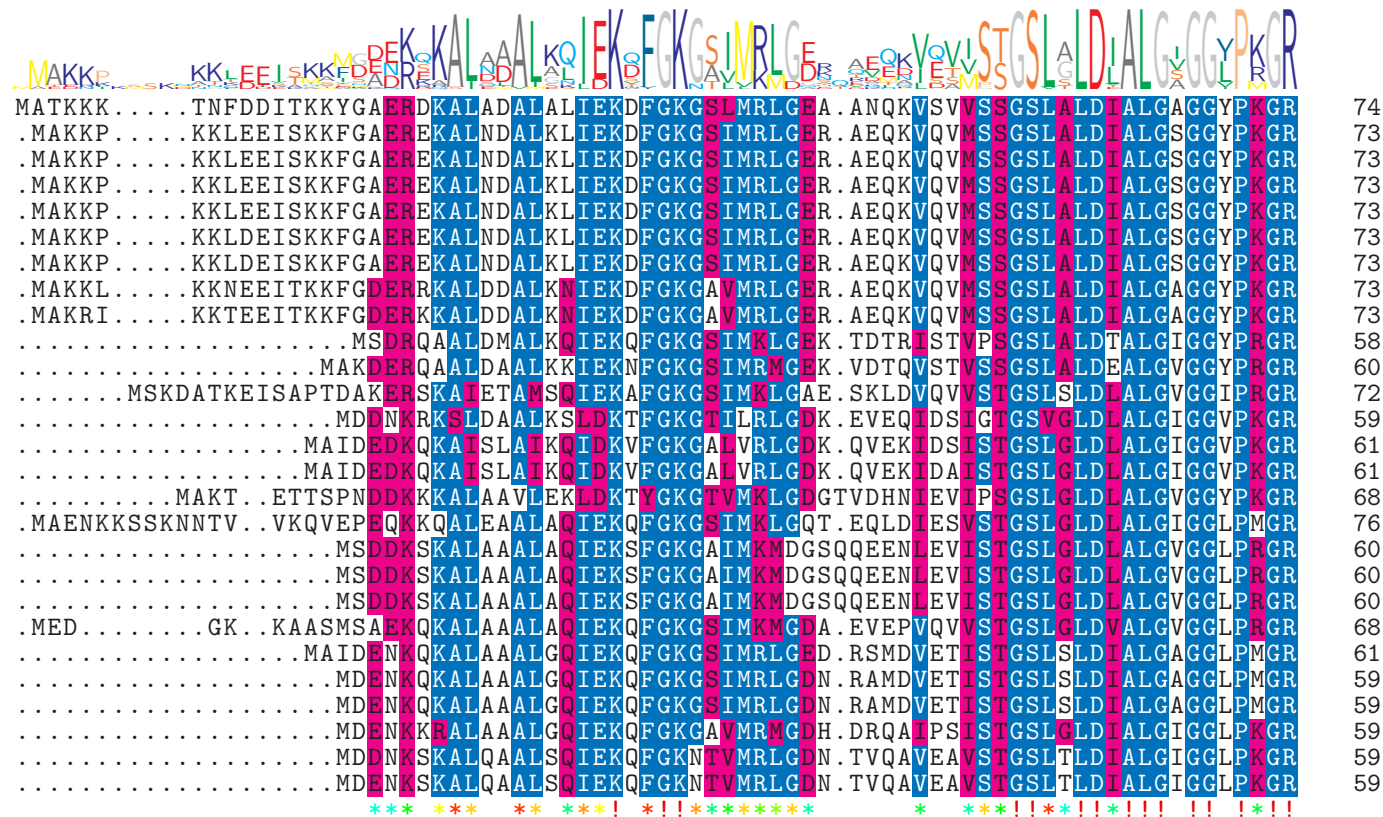


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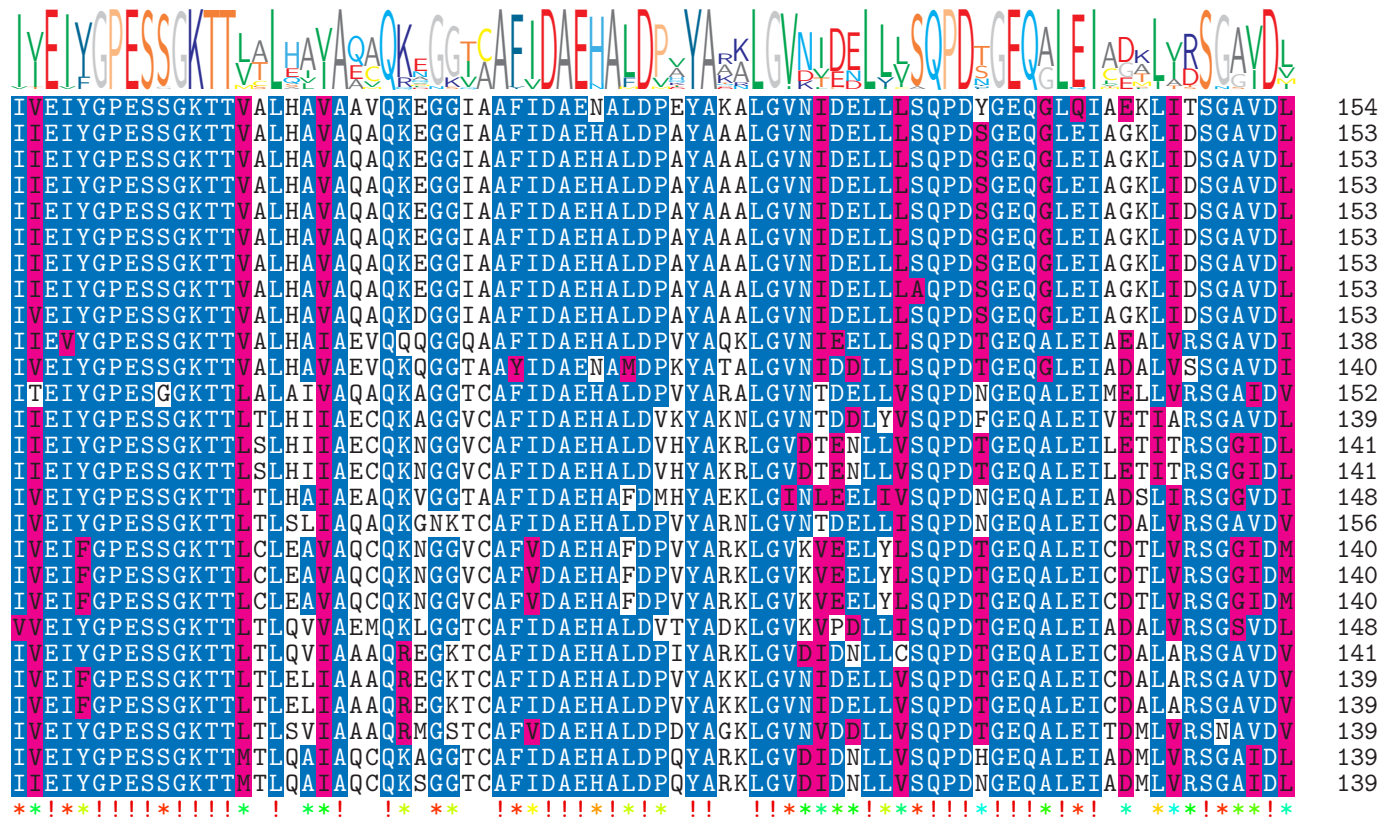
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consensus

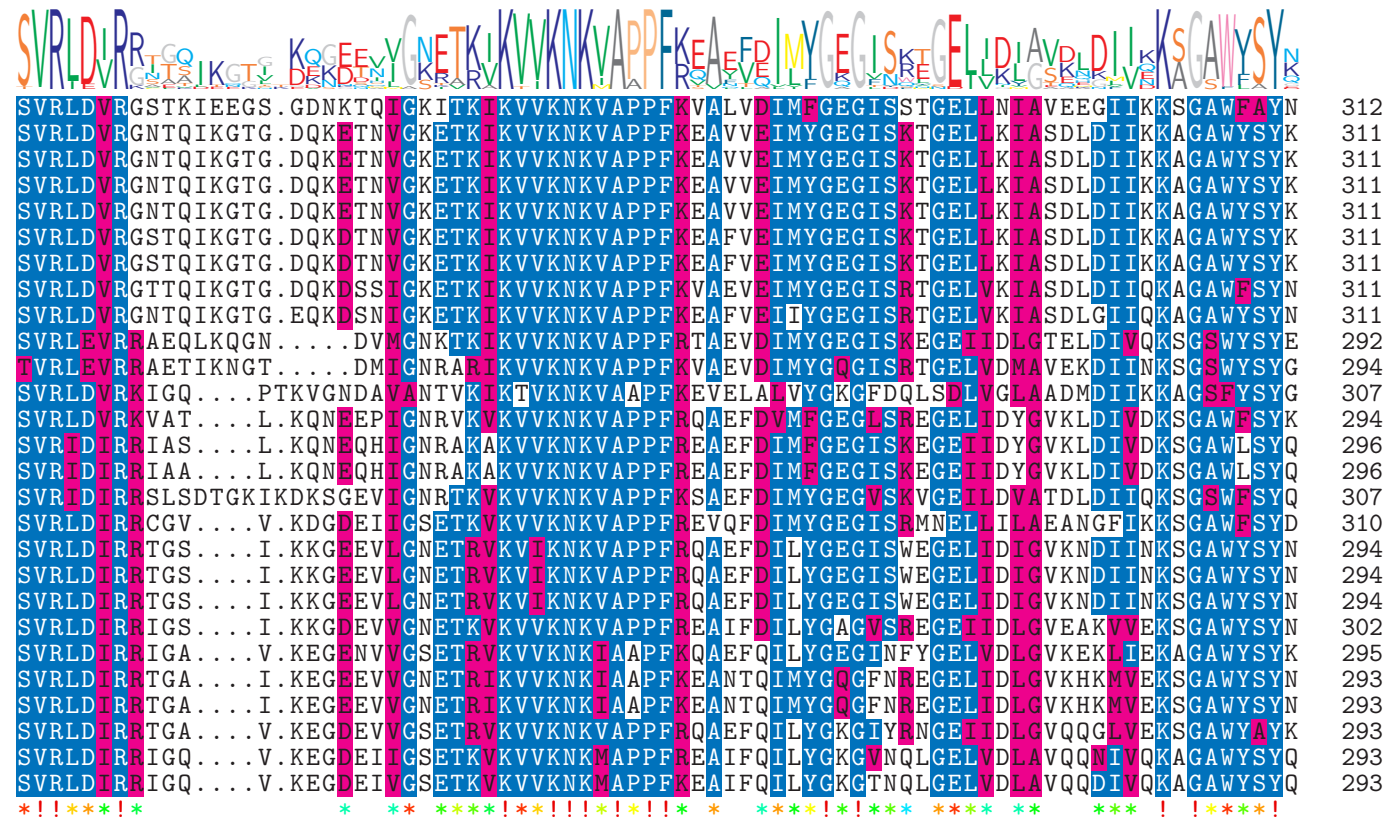
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consensus

Sequence	Score
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DEKIGQGS E NA K KYLA E HP E IF D EID K QV R SKF G LIDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGS E NA K KYLA E HP E IF D EID K QV R SKF G LIDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIE	385
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DEKIGQGS E NA K KYLA D NPE V FA I ED H QV R VQF G LIDGEEAAS KKDE VAQVDS . . VNEEVTLDLGDLEIE	381
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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved