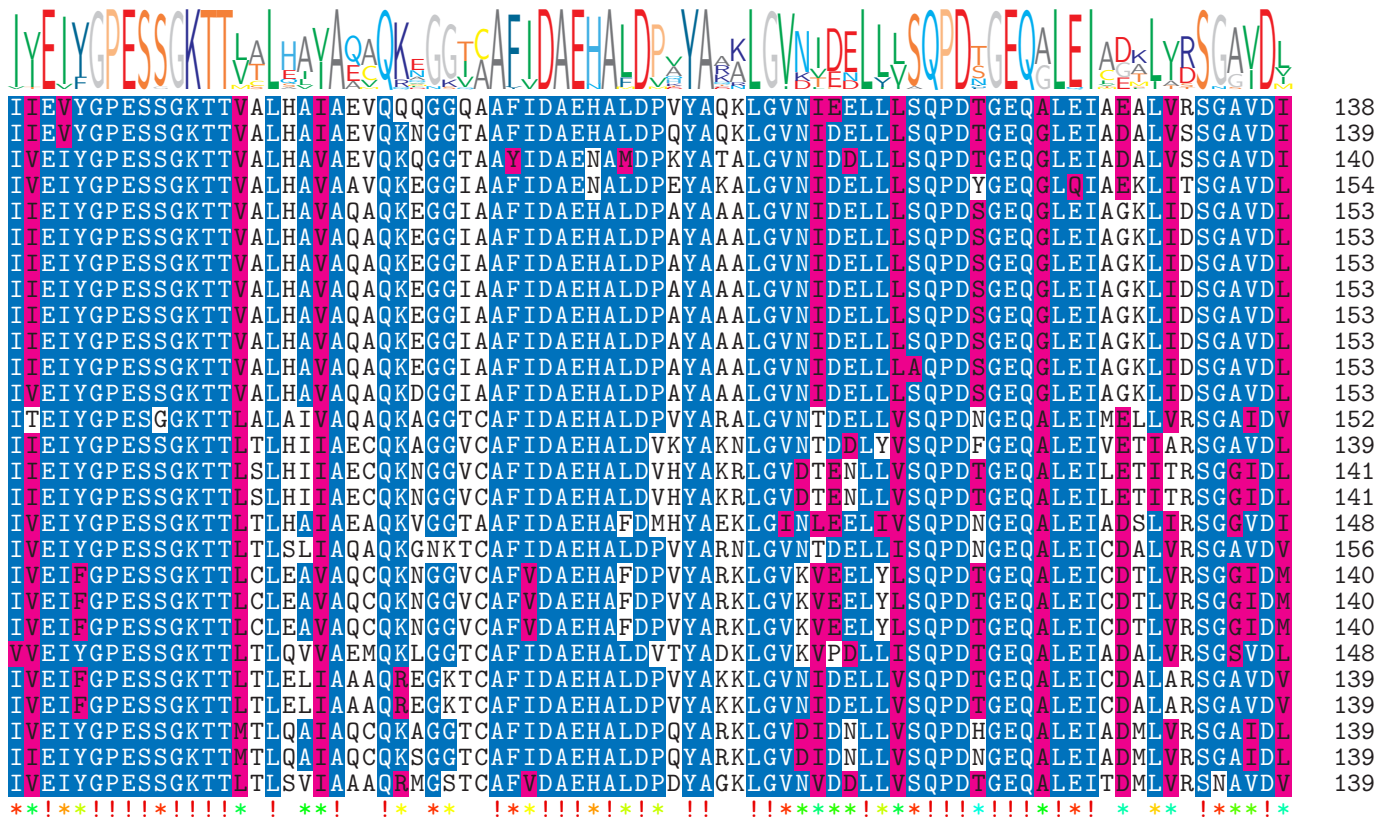


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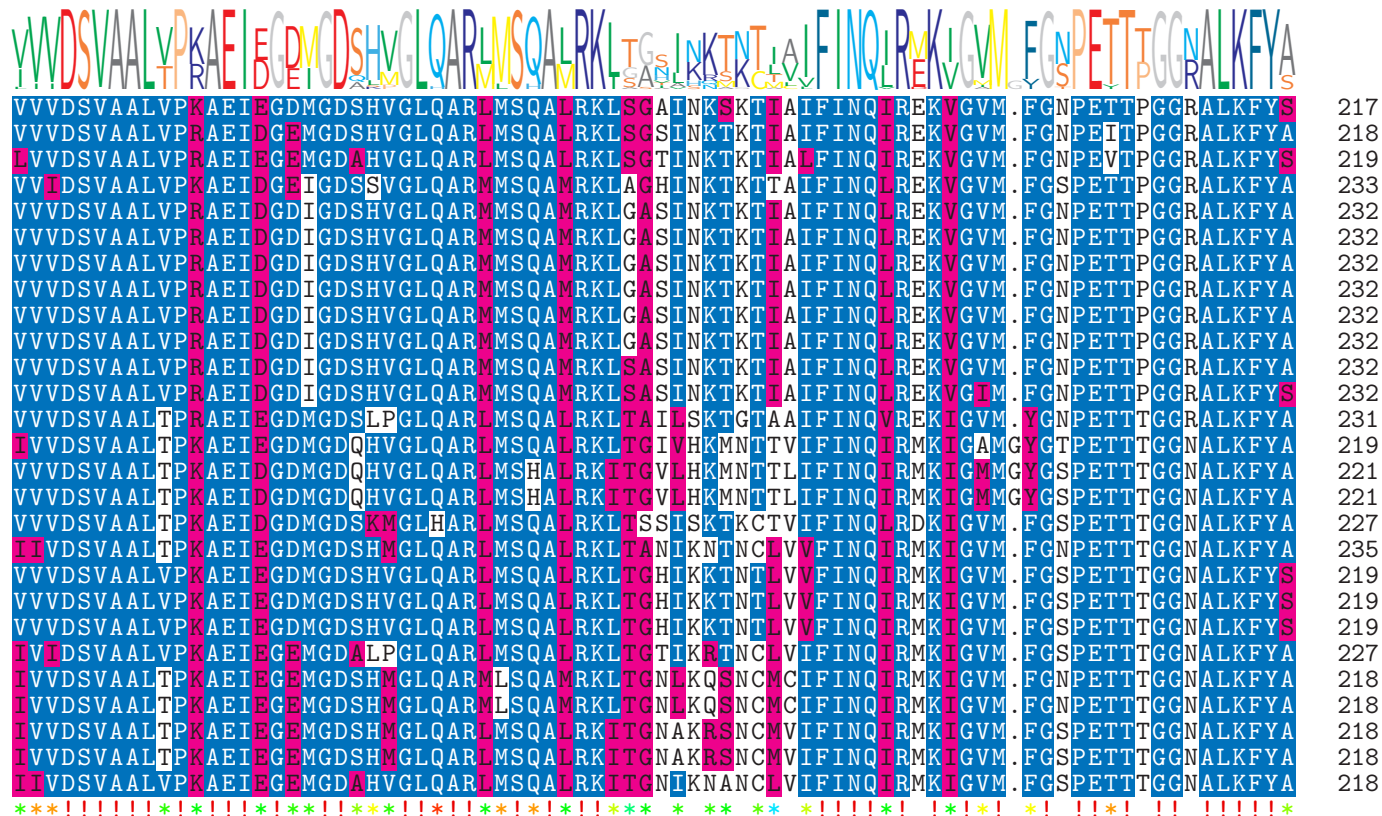
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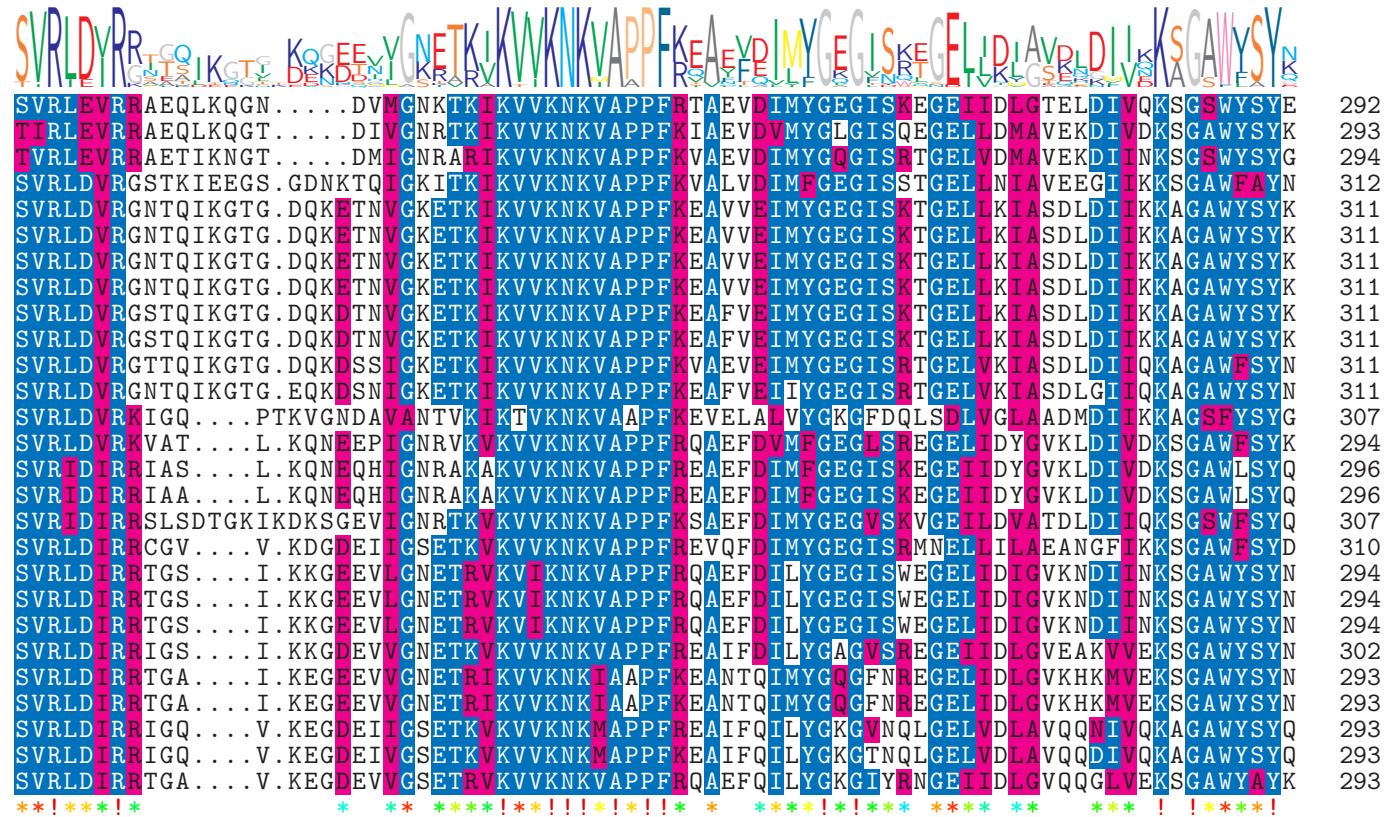
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consensus

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Sequence	Score
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SERIGQGRENAKNYLADHDVEDVRLKVRAAAYGSDVPEDELPTE.DEQI.....NILPDDSTEE..	355
DEKIGQGAEKAKNYLKEHQDVFEIDHKVRAAHGLDDSEVAETEEETTASKTAKAKKKEEKAVETEEIELELED....	387
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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consensus			

- non conserved
- similar
- ≥ 50% conserved