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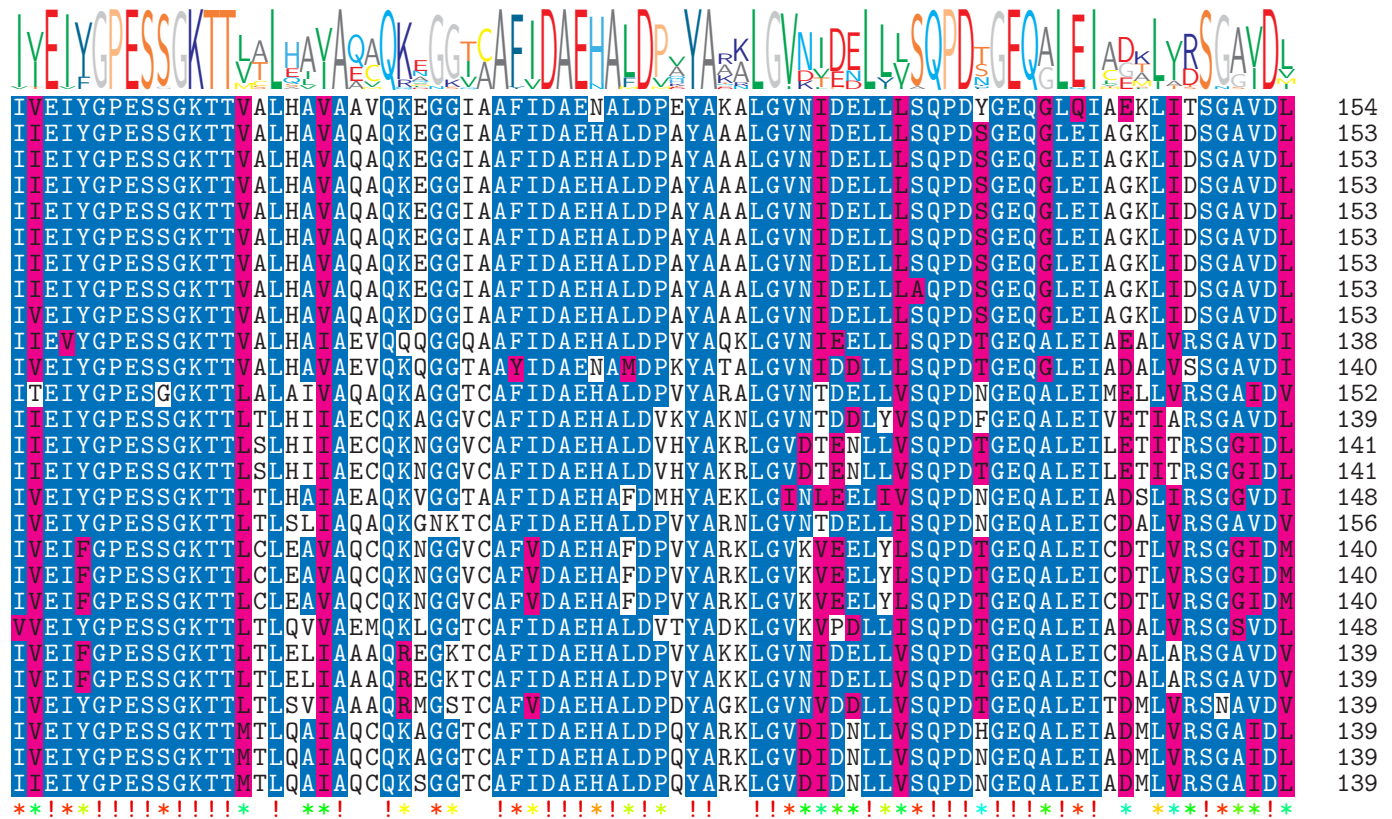
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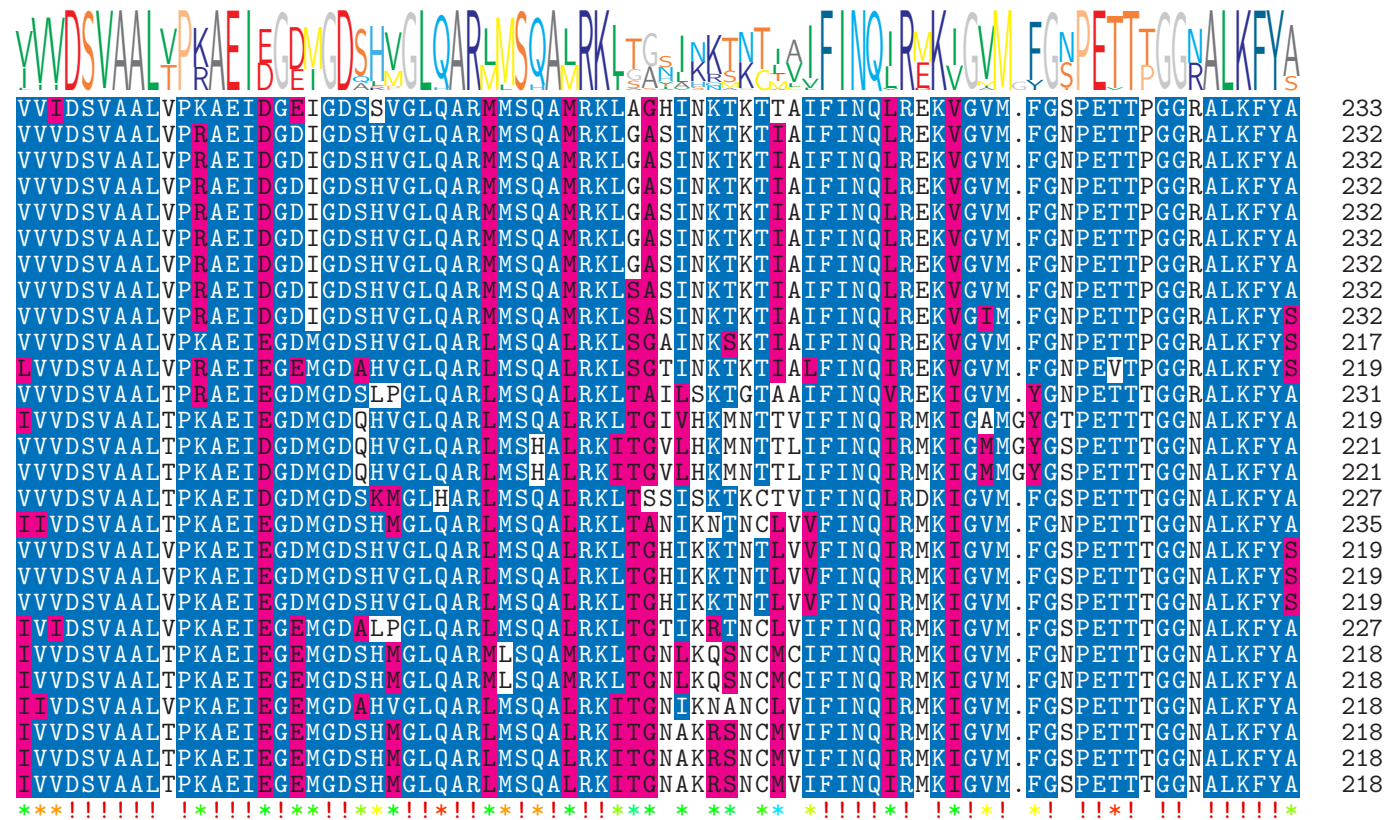
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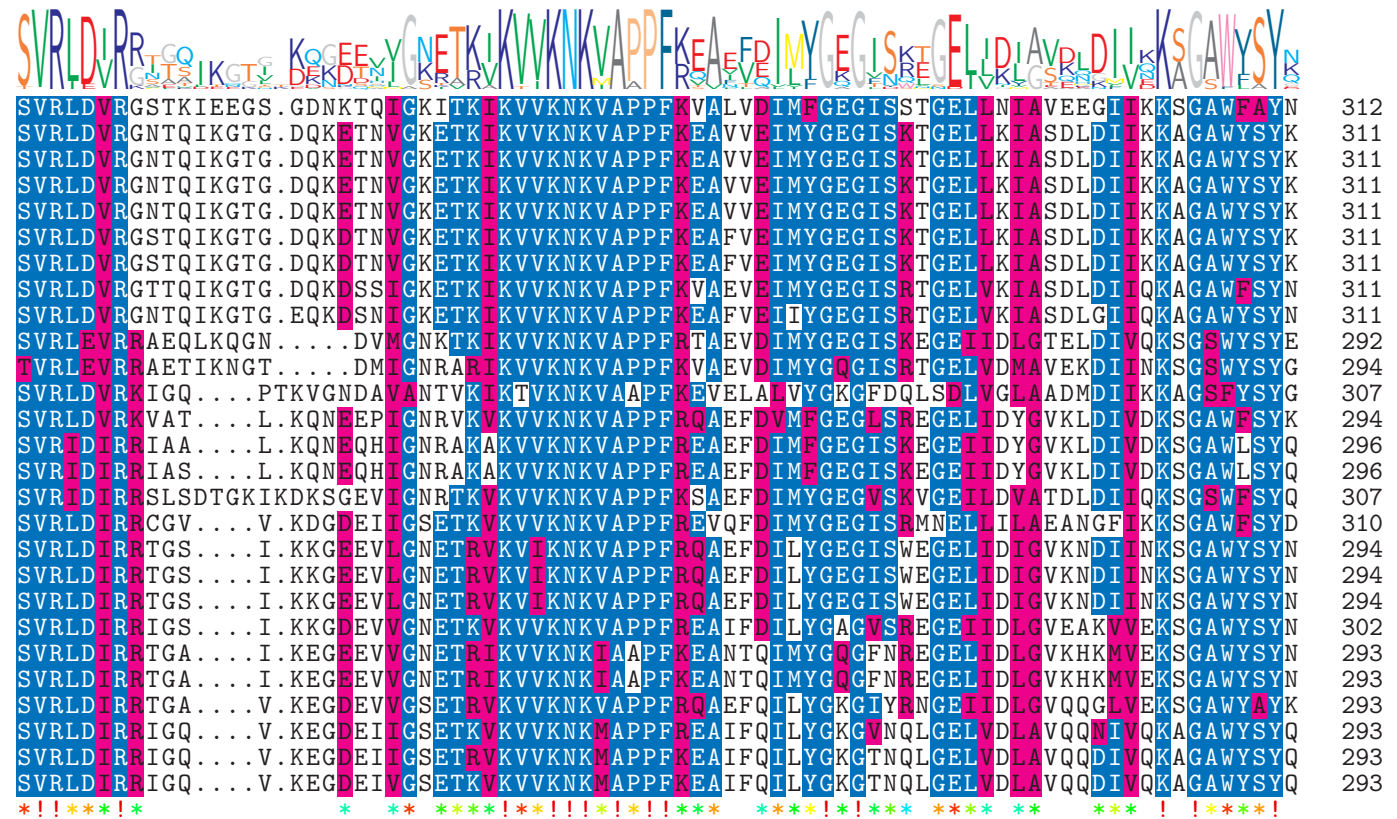
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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
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GEKIGQGSENAKKFLADNPVFAEIDHKVRSVQGLIEEDNTEEKQSSKEK ETDEK . . ADKNLVLELDDTIELE	382
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logo

		IEE	
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consensus			

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