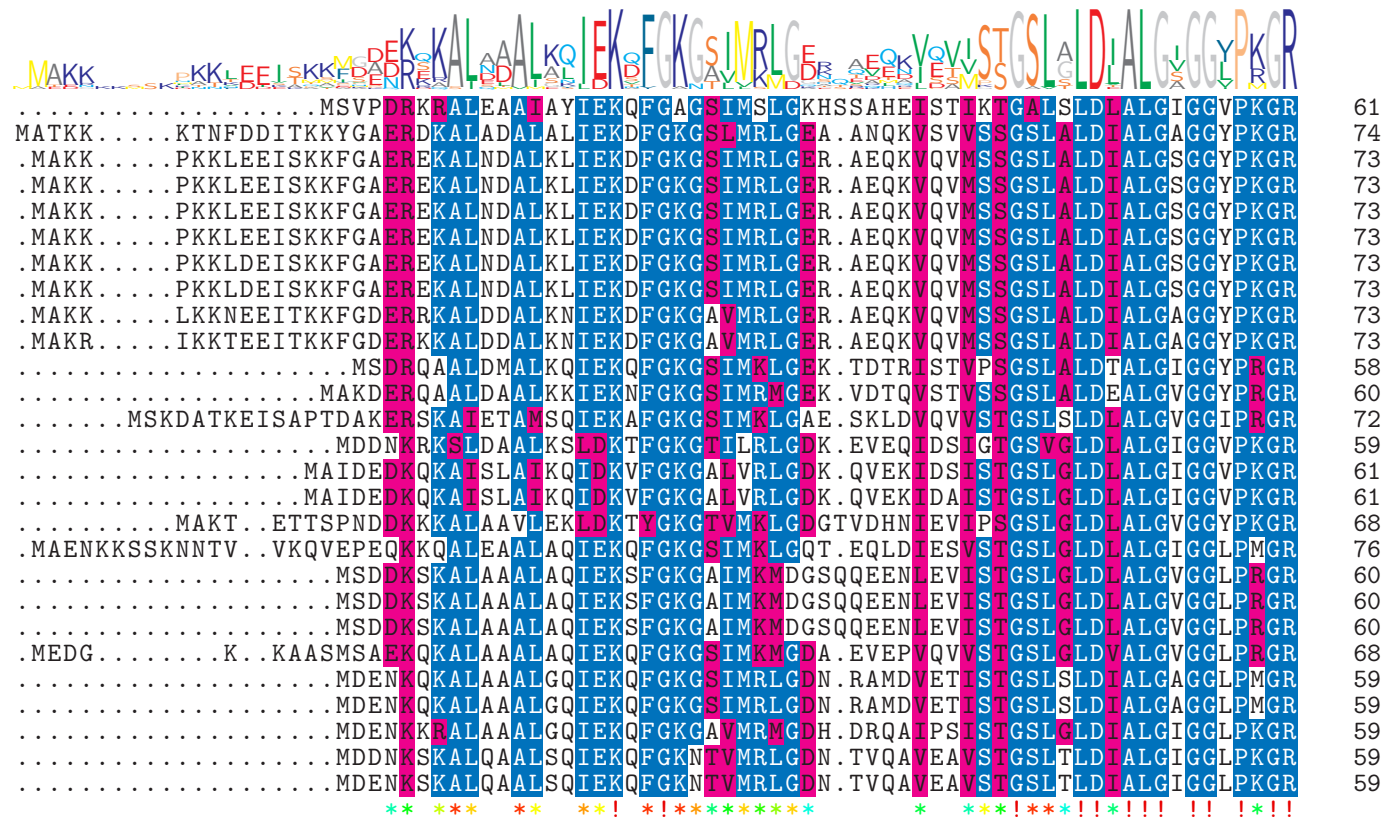


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consensus

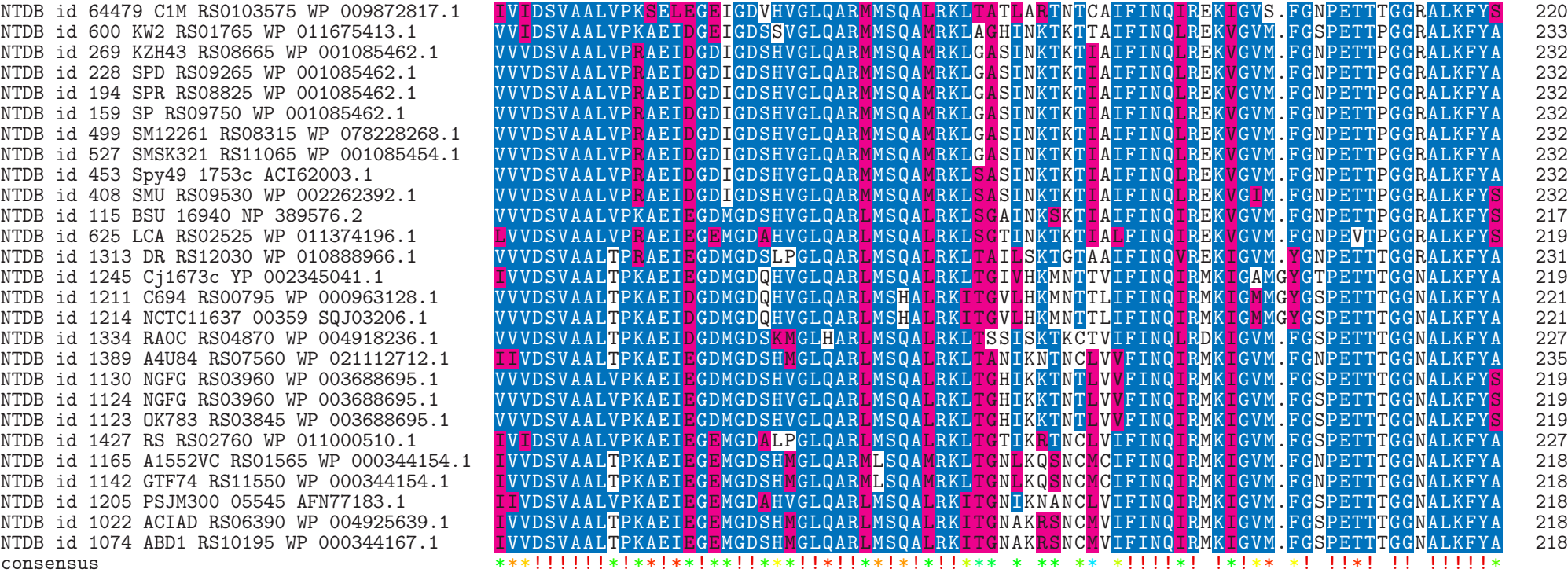
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consensus	*	*	!	*	*	!	!	!	!	!	!	!	!	*	*	*	*	!	!	*	*	*	!	!	*	*	!	!	*	*	*	!	!	*	*	!	!	*	*	*	!	!	*	*	*	!																																				

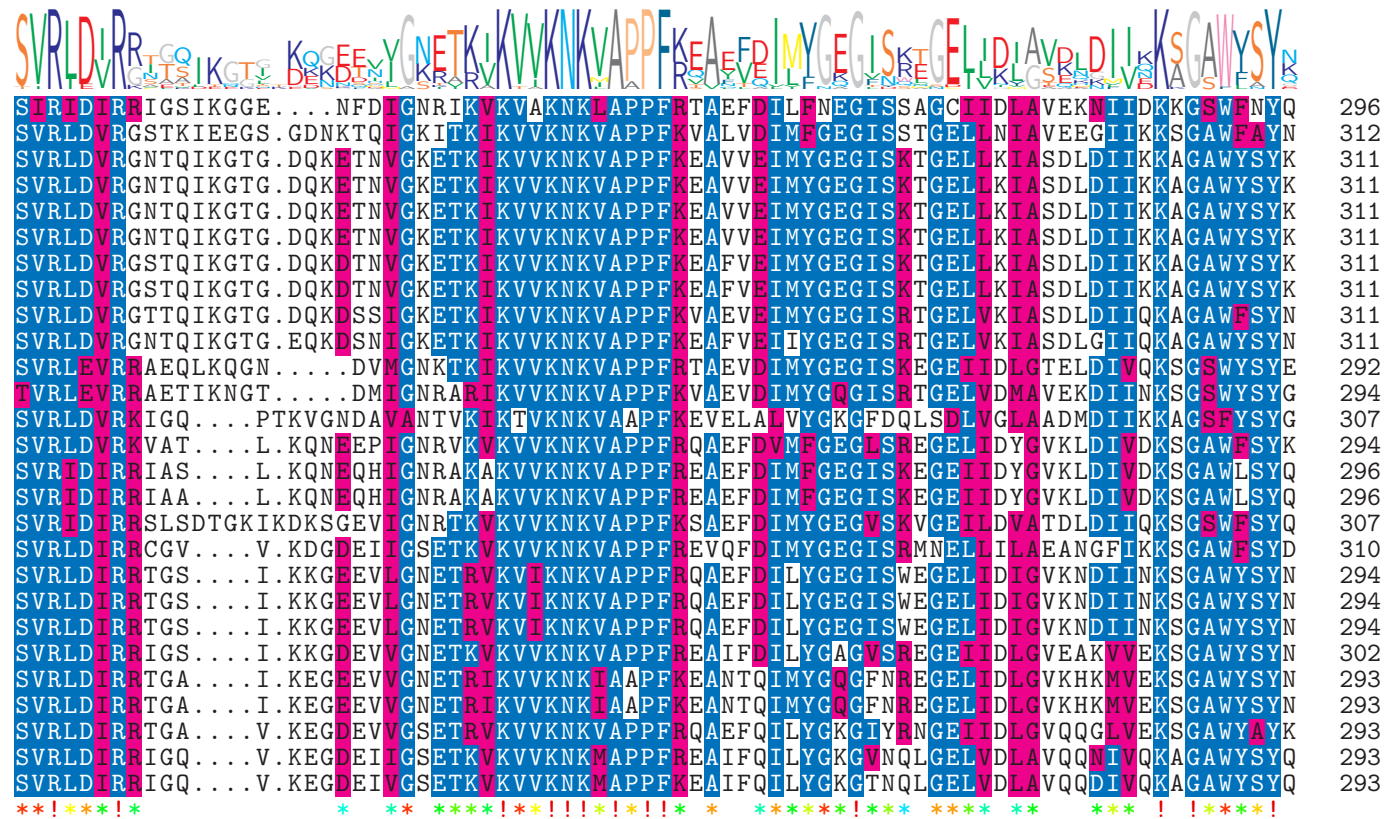
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consensus

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Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTEENKKDE... PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTEENKKDE... PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTEENKKDE... PKKEEA..VNEEVPLDLGDELEIE	385
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GEKIGQGSSENAKKFLADNPEIFDDIDHKVVRVQYGLIEEDNTEEKQSSKEK... ETDEK..ADKNLVLELDDTIELE	382
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GKIGQGKNNNAVKWLKENPEIADKLEQEIRNTLASNPNS...VLKATASDSND..ESDVVEEFSEEL	372
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logo

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consensus

 non conserved
 similar
 ≥ 50% conserved