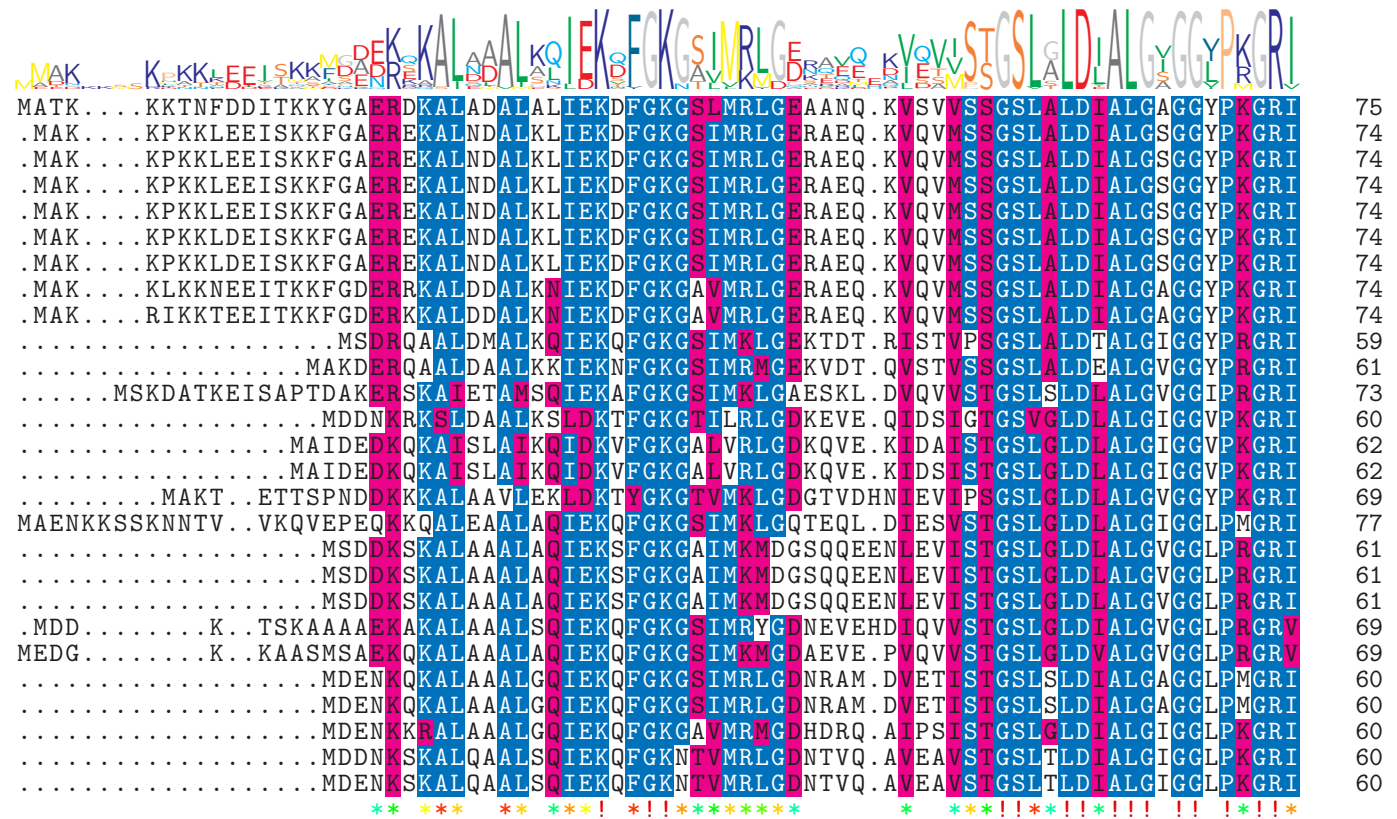


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consensus

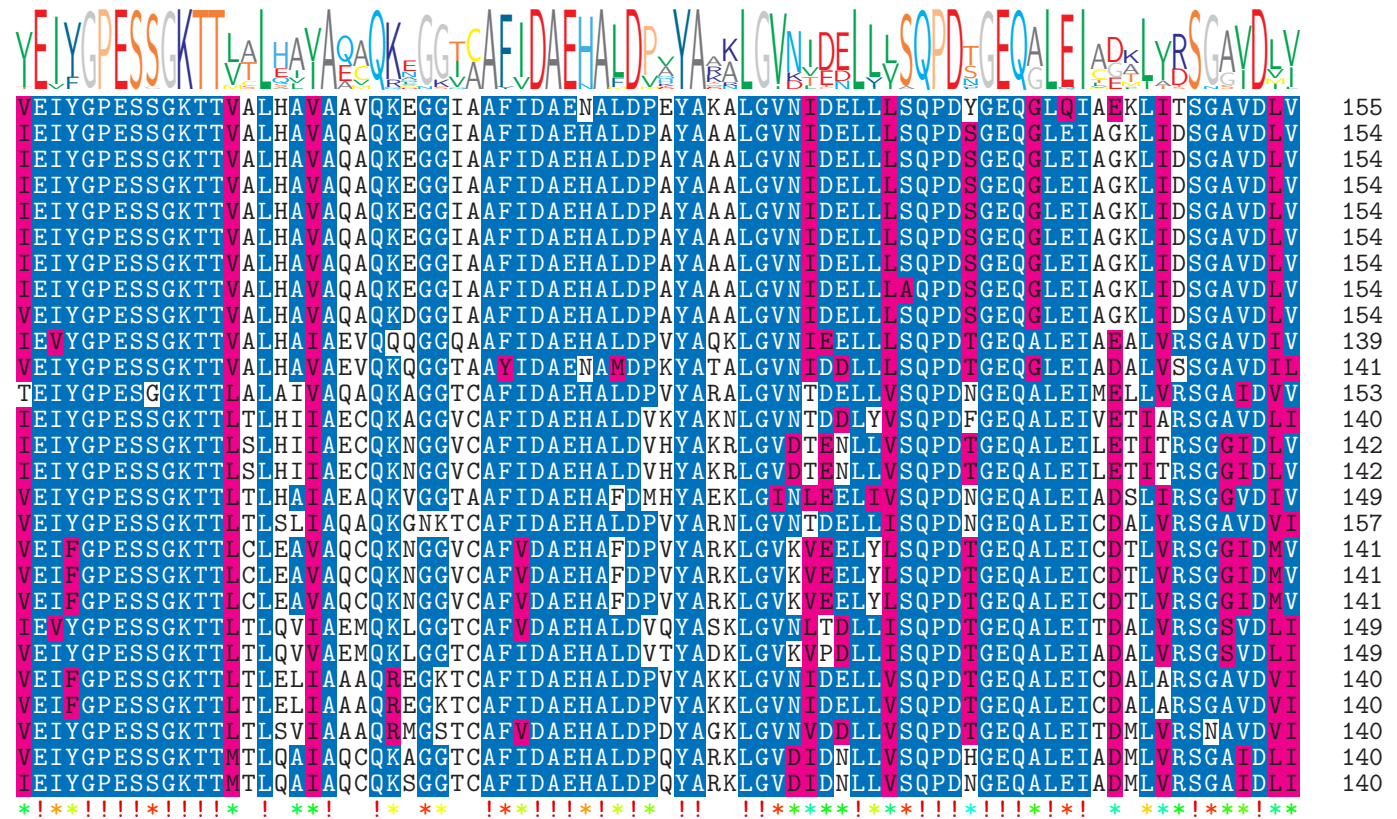
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consensus

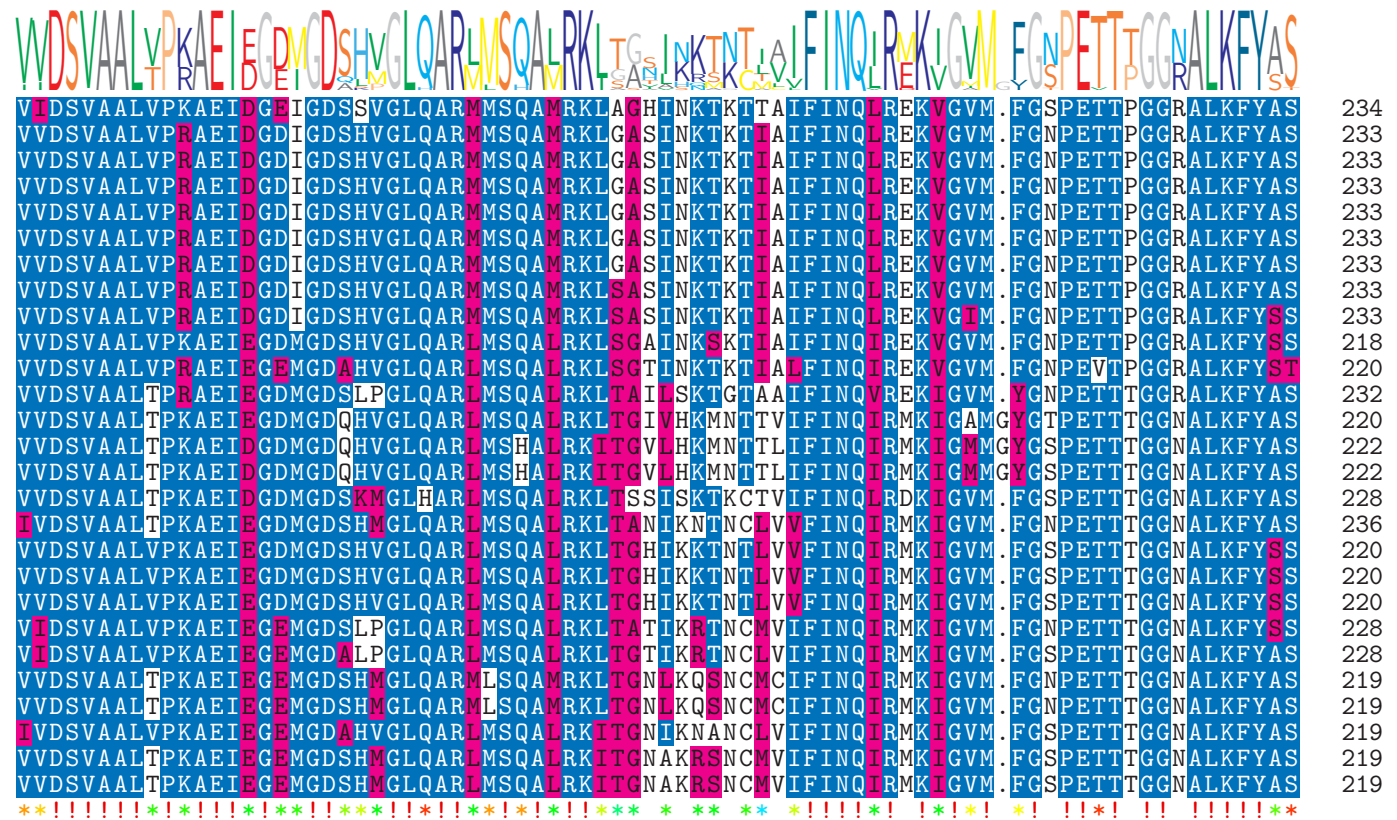
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consensus

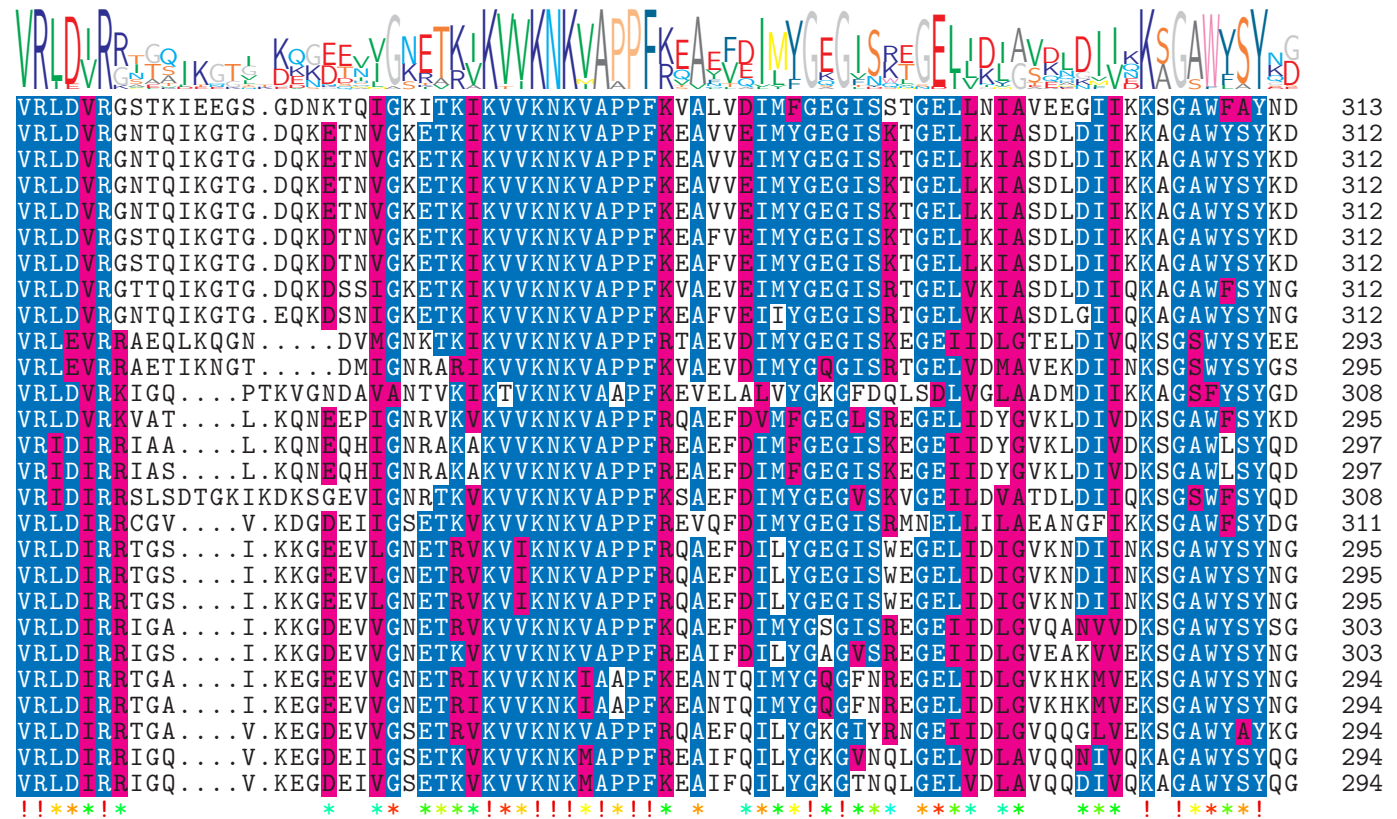
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consensus

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consensus

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Sequence	Score
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EKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLDIGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
EKIGQGSENAKKYLAHNPEVFAEIDHQVRVQFGLDIGEEAAE.....SKKDE...VAQVDS..VNEEVPLDLGDELEI	380
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EKIGQGSENAKKRYLAHPQIFDEIDRKVRVKFGLLEESEES..AMAVASE.....E.....TDDLALDLNGIEI	376
EKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEE..KQSSKEK.....ETDEK..ADKNLVLEDDTIEL	381
ERLGGGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQ..QAEETQEEL.EFE.E.....	348
ERIGGGRENAKKNYLACHEDVEDEVRLKVRAAYGISDVPEEDL..PTTEDE.QI.NILPDDST.....EE.....	355
ERIGGGKEKTIAYIAERPMEQEIRDRVMAATRAGNAGEAPALAPAPAAPEAA.EA.....	363
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KKLGGGRENAKALLKEDKALADEITLTKIKESIGSNEEIM..PLP....DEPLE.EME.....	347
TKLGGGRDRTVKELIKDNPELAELEAKIREKLQAK.....	343
TKIGQGKNNAVKWLKENPEIAKLEQEIRNTLASNPNSV..LKATASDSNDES.DVEEF.....SEEL.....	372
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ERIGGGKDNCREFLRENAELAREIENKVRHGLVTPMGA..V.TLAEVEED.....	352
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DKIGGGKANACKYILKENPEIAKTLDDKKIREMLLNPNMQ..LIAETSSAADV.EFGAV.....PEEF.....	354
SKIGGGKANAAKYILENPEIGQEIEQQIRAKLLVTSANT..KATPVAEDLADA.DI.....	347
NKIGGGKNNVIRVYLEENPQISTEIEAVIREQLLTASDQ..TAA.HDETEEEP.DLL.....ES.....	349
NKIGGGKNNVIRVFEENNQIAEIERNIREQLLTGTNG..AVQ.I.EDEEEP.DLL.....LES.....	349

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			E.IEE	
NTDB id 600 KW2 RS01765 WP 011675413.1		387		
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEE	388		
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NTDB id 1074 ABD1 RS10195 WP 000344167.1		349		
consensus				

-  non conserved
-  similar
-  ≥ 50% conserved