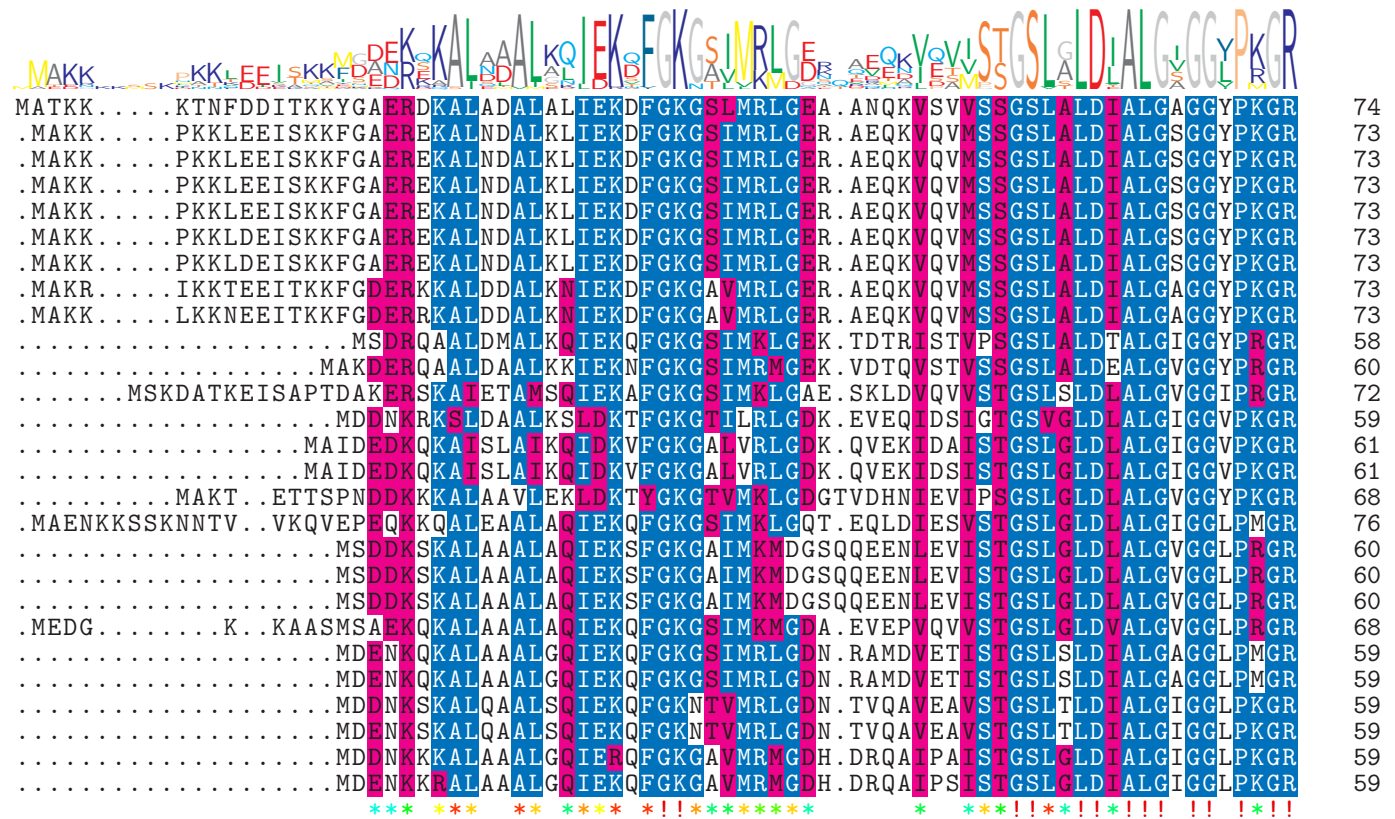


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consensus

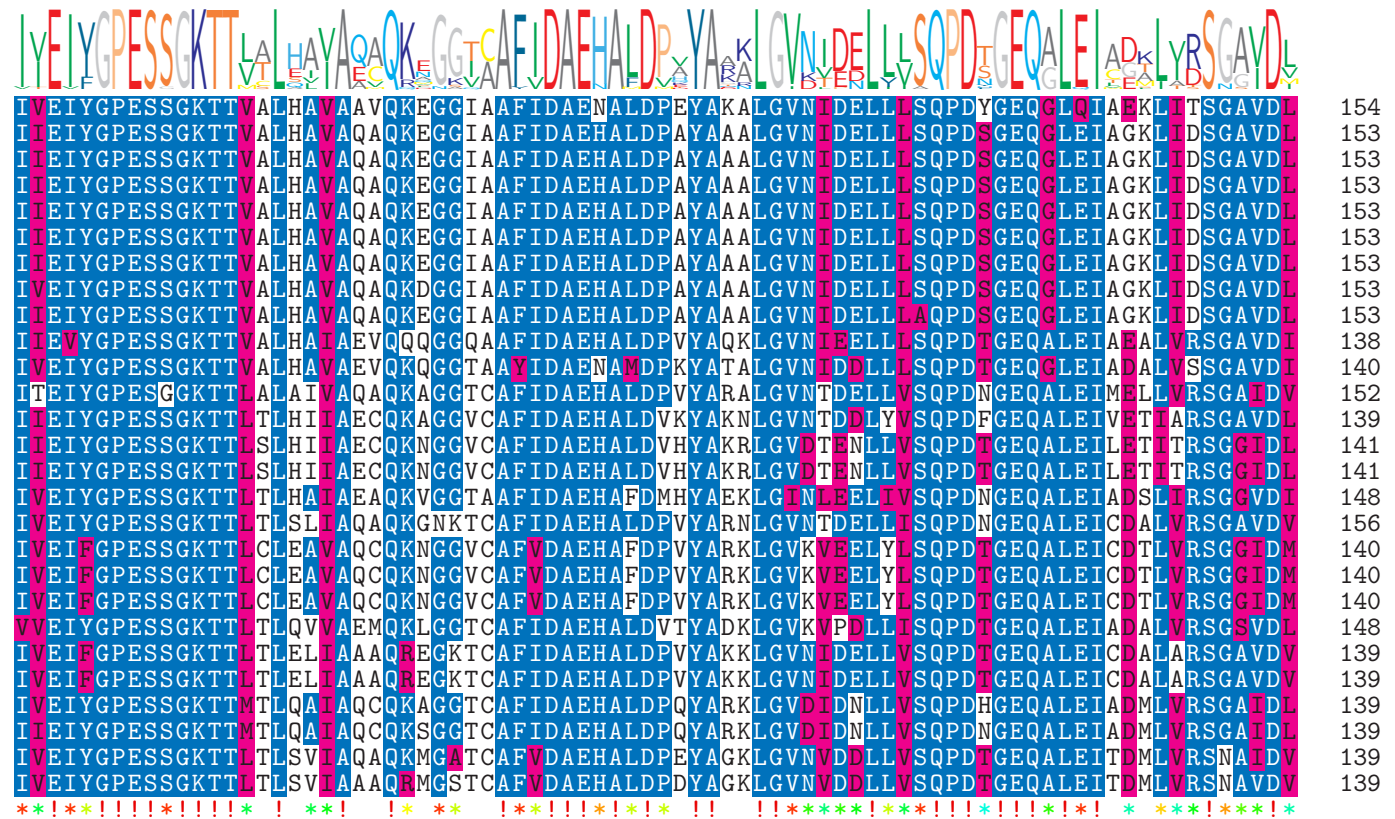
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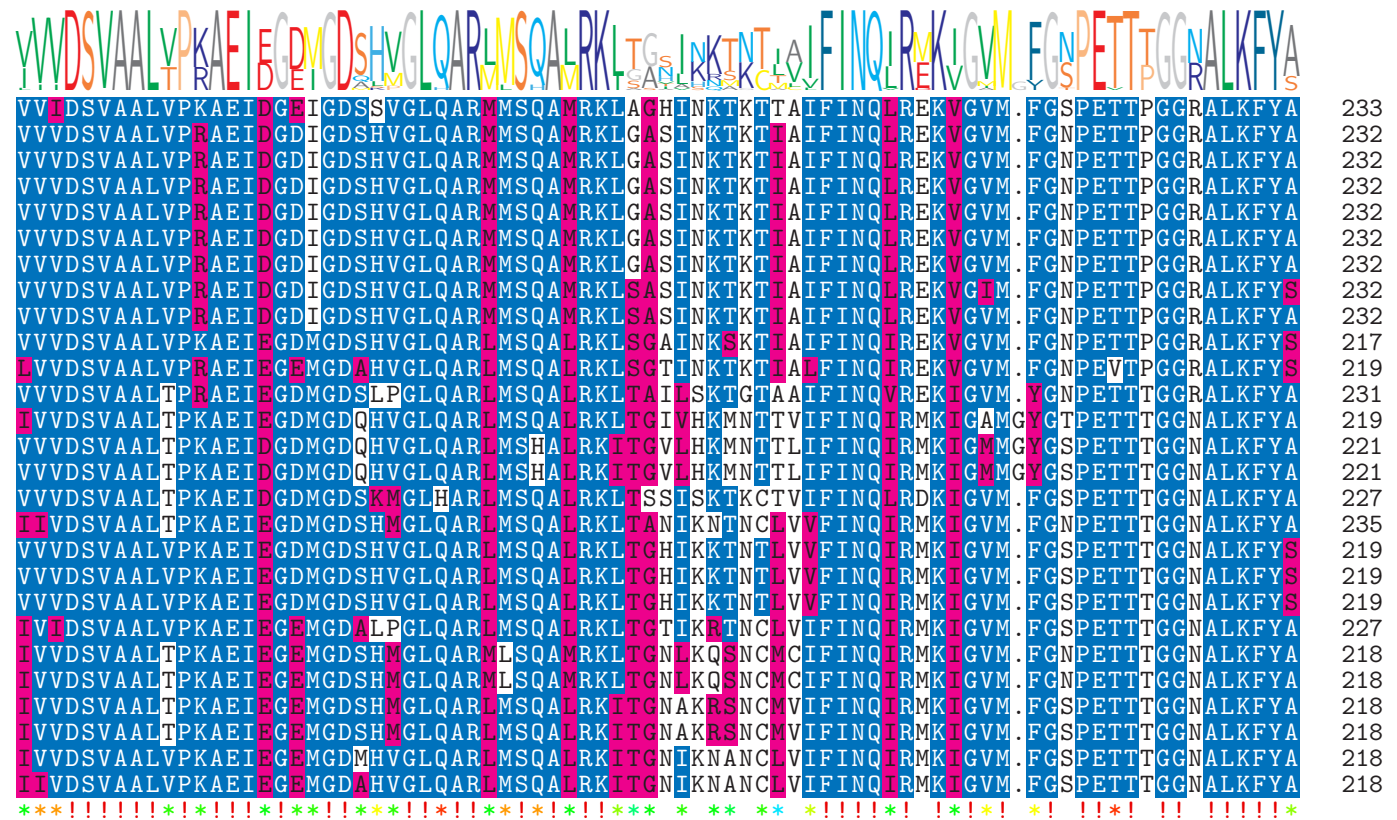
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consensus

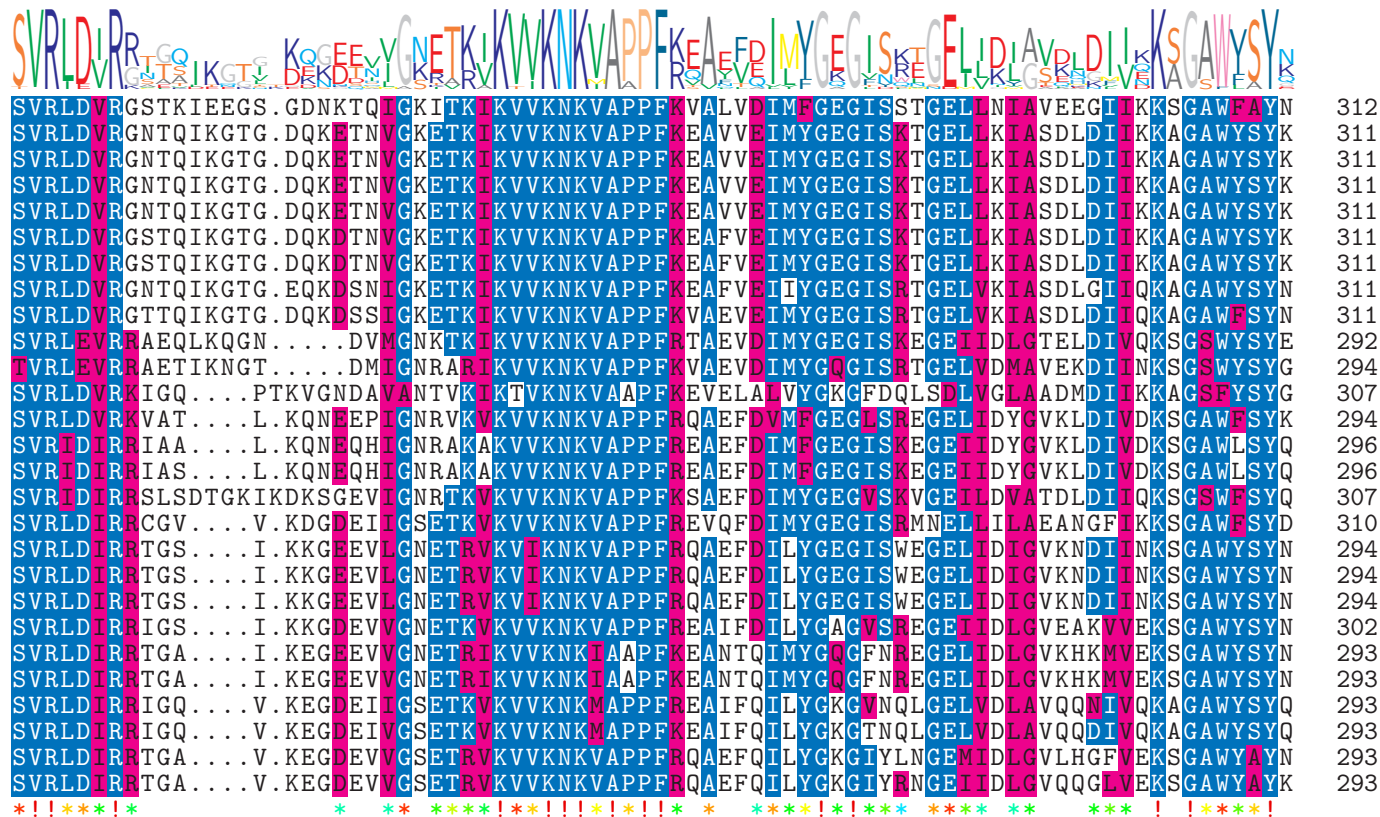
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consensus

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Sequence	Score
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DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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GEKIGGGSSENAKKFLADNPEIFDDIDHKVRVQFGLIEEDNTEEEKSSKEK...ETDEK..ADKNLVLELDDTTIELE	382
GEKIGGGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
EERLGQGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGGGSRENAKKNYLADHEDVEDEVRLKVRVQFGLSDVPEEDLPTTEDE.QI.NILPDDST...EE.....	355
DERIGGQKEKTIATYIAERPMEQEIHDRVMAAIRAGNAGEAPALAPAPAAPE.....A.AEA.....	363
DKKLGGGRENKSAFLKENPEIADEITKAIQNSMGIEGMISGSEDD...EGE...E.....	343
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DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPLPDE...PLE...EME.....	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK.....	343
GTKIGGQKNNNAVKWLKENPEIADKLEQEIRNTLASNPNSVLKATASDSNDES.....DVEEF..SEEF..	372
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GERIGGGRDNCREFLRENAELAREIENKVRHGLVTPMGA.VTLAAEEV..EE.....D.....	352
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GSKIGGQKANAAYLEENPEIQEIEQQIRAKLLVTSANTKATPVAED..LA.....D.....ADI.....	347

logo

		IEE	
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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved