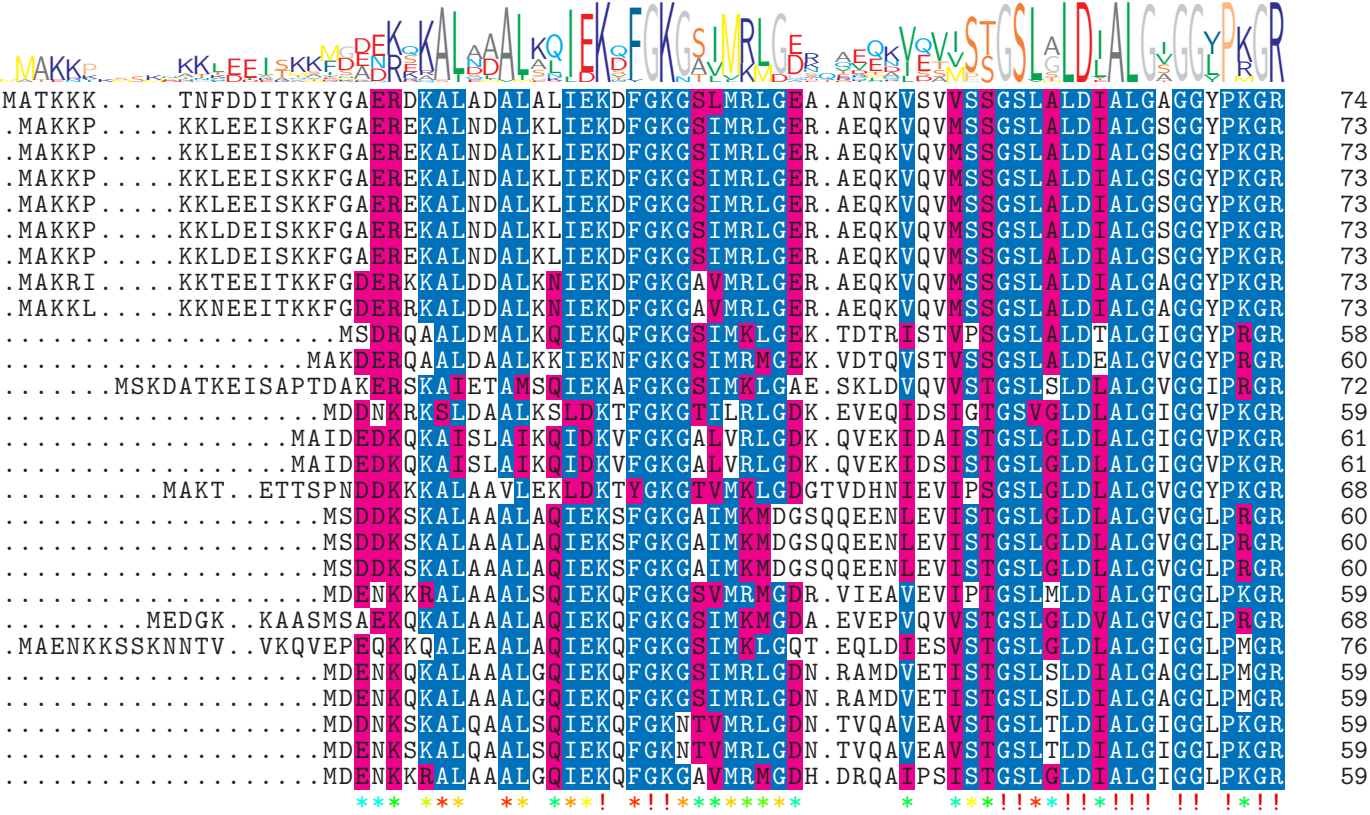


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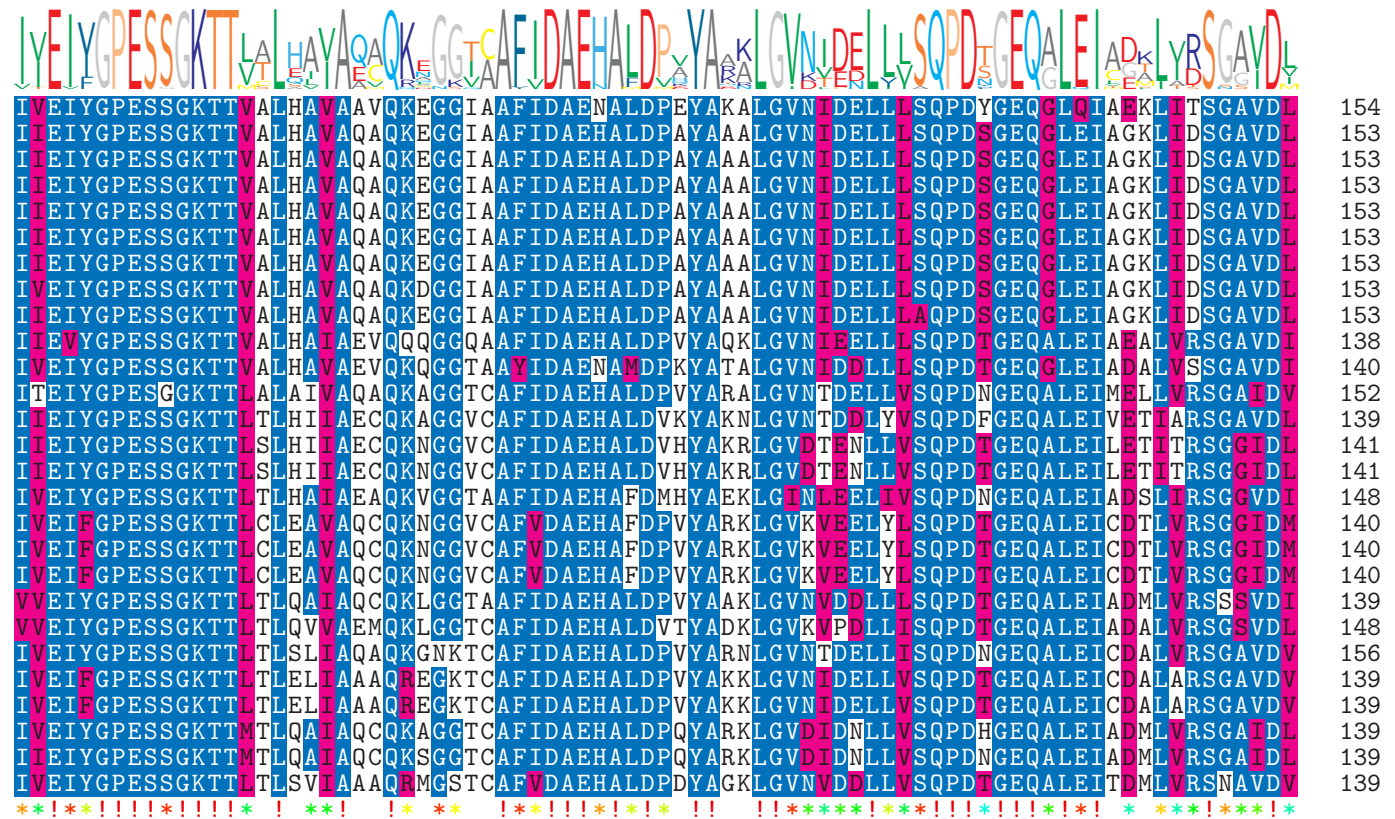
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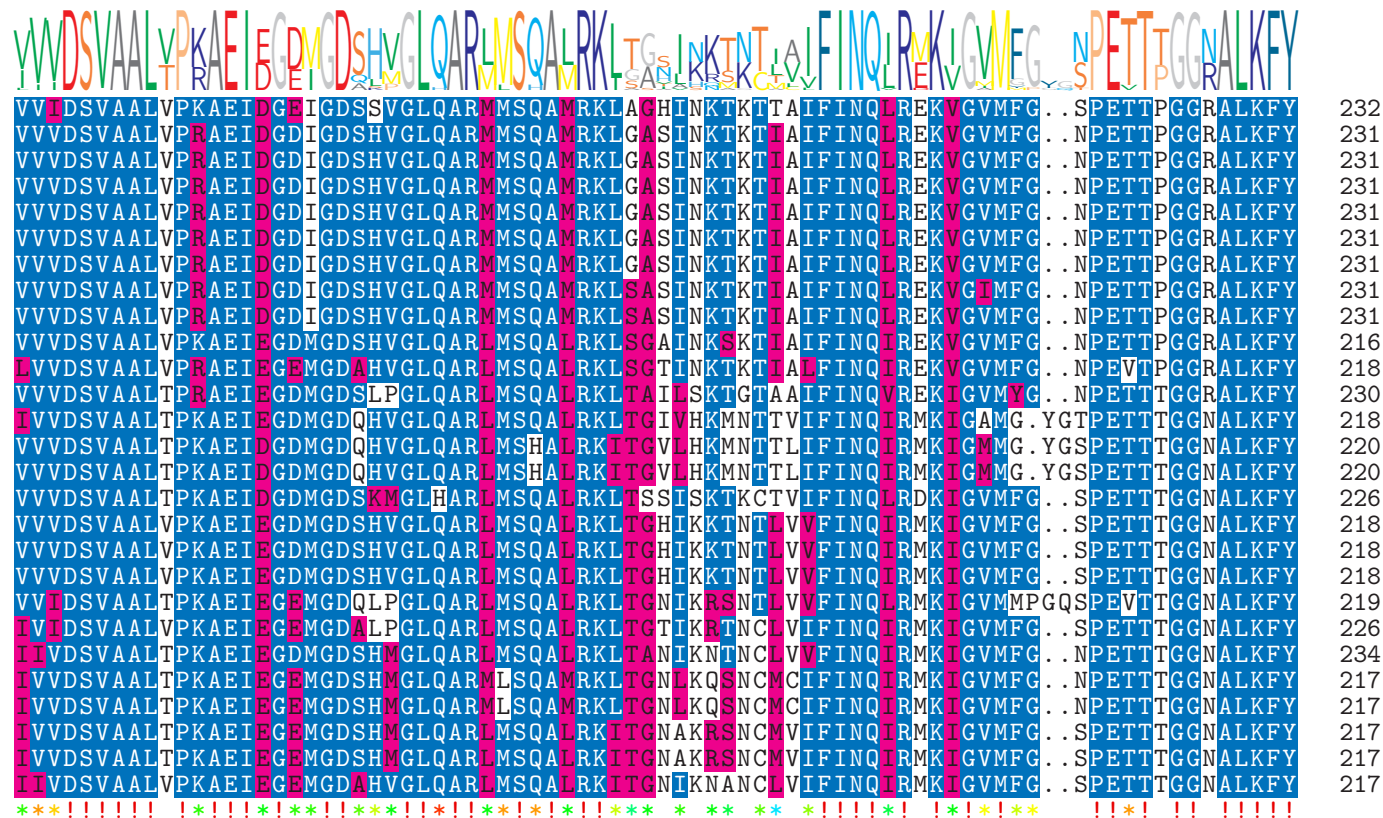
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consensus

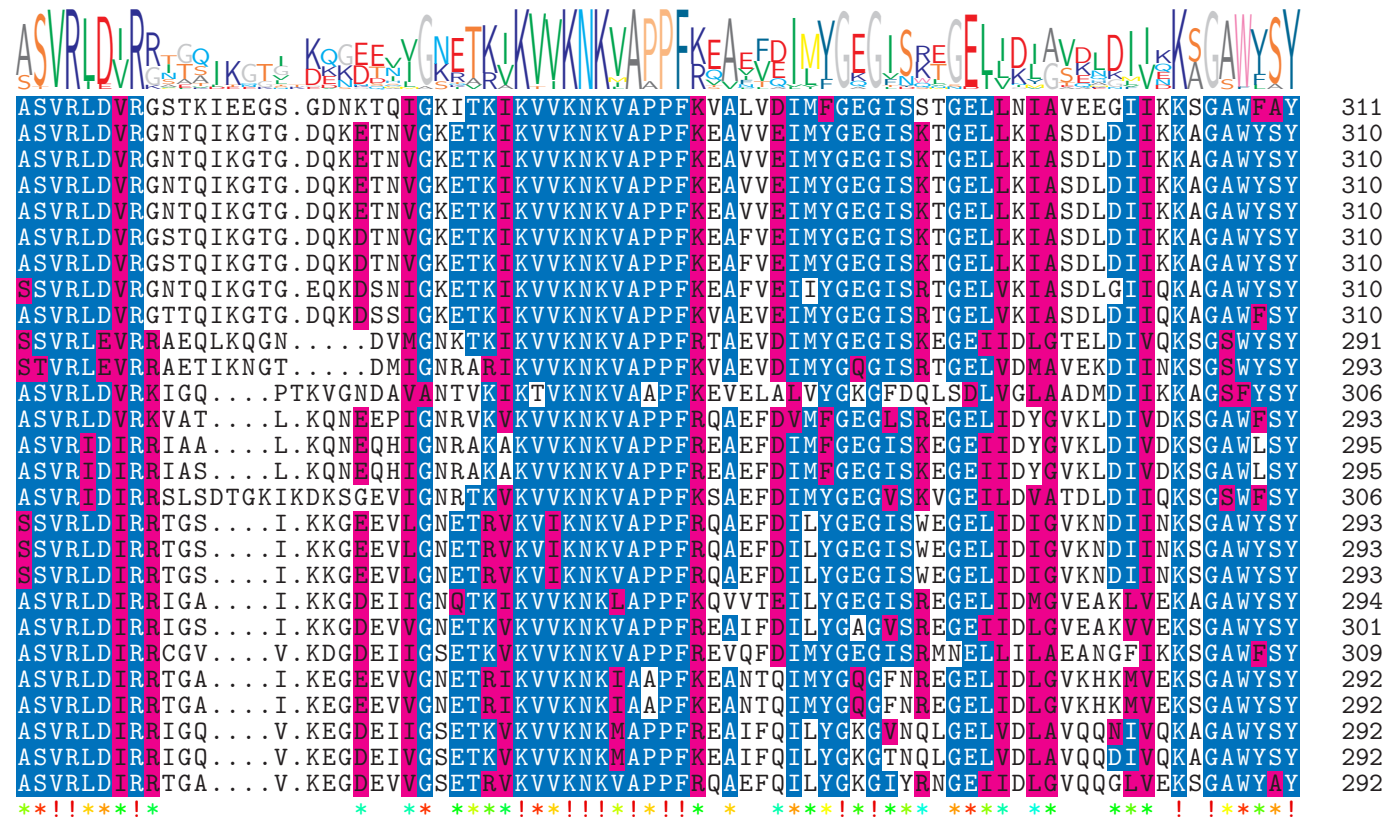
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consensus

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Iteration	Sequence	Score
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1000001	KDEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
1000002	KDEKIGQGSNAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
1000003	KDEKIGQGSNAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
1000004	KDEKIGQGSNAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
1000005	KDEKIGQGSNAKKYLADNPEVFAEIDHQVVRVQFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVPLDLGDELEI	380
1000006	KDEKIGQGSNAKKYLADNPEIFDEIDHQVVRVQFGLIDGEEIAE...SKKDE...AAQVDS..VNEEVTLDLGDELEI	380
1000007	NGEKIGQGSNAKKFLADNPEIFDDIDHKVVRVQGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDGDEITIEL	381
1000008	NGEKIGQGSNAKRYLADHPQLFDEIDRKVRVKFGLLEESEESASAMAVASE.....E.....TDDLALDLDNGIEI	376
1000009	EEEEKIGQGRNAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
1000010	GSEKIGQGRNAKNYLADHEDVEDEVRLKVRAAYGISDVPEDLPTTEDE.QI.NILPDDST.....EE.....	355
1000011	GDERIGQGKEKTIAYIAERPMEQEIETDRVMMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
1000012	KDKKILGQGRNSKAFILKENPEIADEITKATIQNSMGIEGMI.....SGSEDEGEE.....	343
1000013	QDKKILGQGRNAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDEPLEEME.....	347
1000014	QDKKILGQGRNAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDEPLEEME.....	347
1000015	QDTKILGQGRDITVKELIKDNPELAELEAKIREKLQAK.....	343
1000016	NGAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDETGERP.....EE.....	348
1000017	NGAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDETGERP.....EE.....	348
1000018	NGAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDETGERP.....EE.....	348
1000019	GDERIGQGKDNARTYLDRNPQVAVRLEAELREKFQPAEAP.....REAGDDEEKE.....	344
1000020	NGERIGQGRDNCREFLRNAAELAREIENKVRHGLVTPMG.....AVTLAEVEED.....	352
1000021	DGTKIGQGKNNAVKWLKENPEIAKLEQIEIRNTLASNPNS.....VLKATASDNDSESDVE..EFSESEL.....	372
1000022	NGDKIGQGKANACKYLKENPEIAKTLDDKLLREMLLPENM.....QLIAETSSAADDFEFG..AVPEEF.....	354
1000023	NGDKIGQGKANACKYLKENPEIAKTLDDKLLREMLLPENM.....QLIAETSSAADDFEFG..AVPEEF.....	354
1000024	QGNKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASD.....QTAA.HDETEEEPDLL...ES.....	349
1000025	QGNKIGQGKNNVIRYFEENNQIAEIEIERNIREQLLTGTN.....GAVQ.I.EDEEPPDLL...LES.....	349
1000026	KGSKIGQGKANAAKYLEENPEIQTIEEQIRAKLLVTSAN.....TKATPVAEDLADADI.....	347

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logo

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consensus

 non conserved
 similar
 ≥ 50% conserved