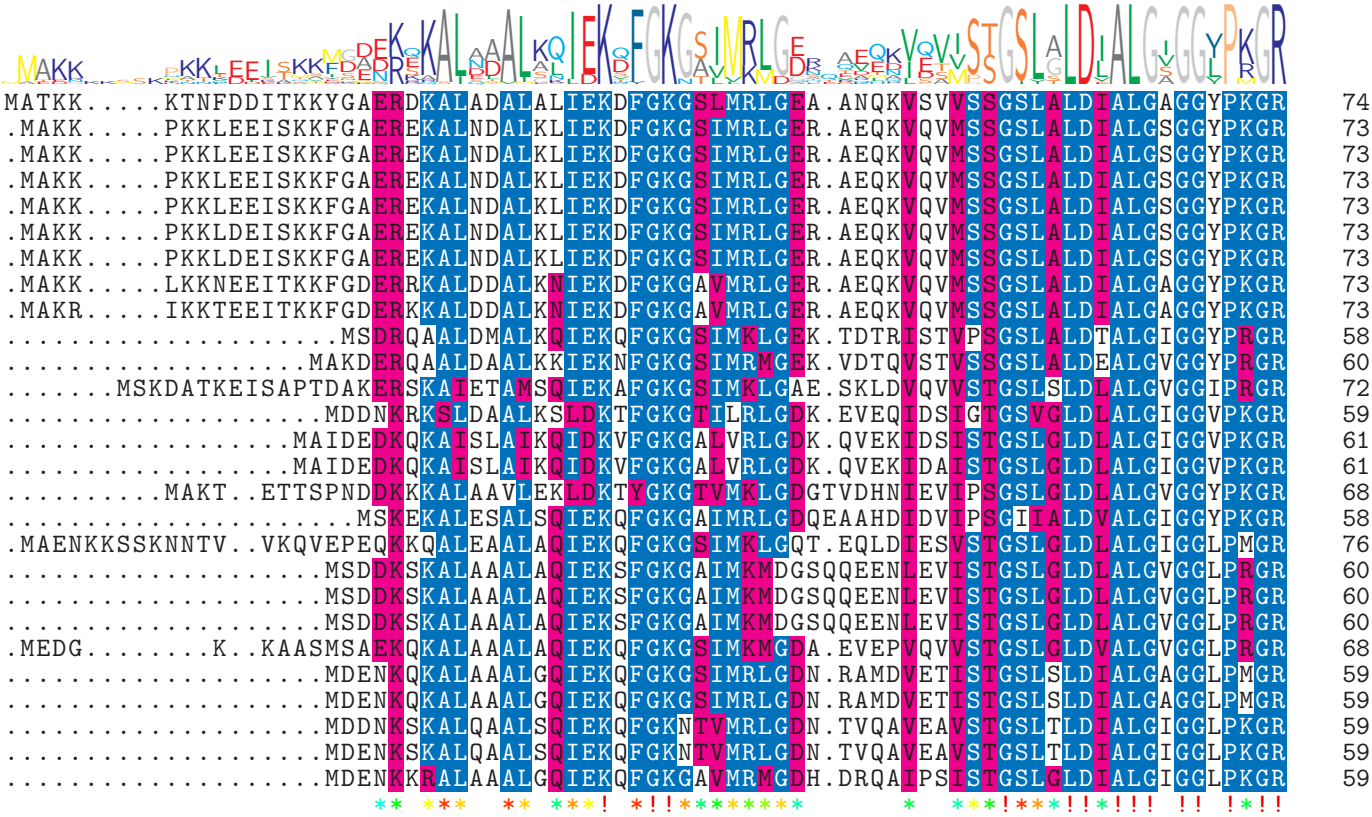


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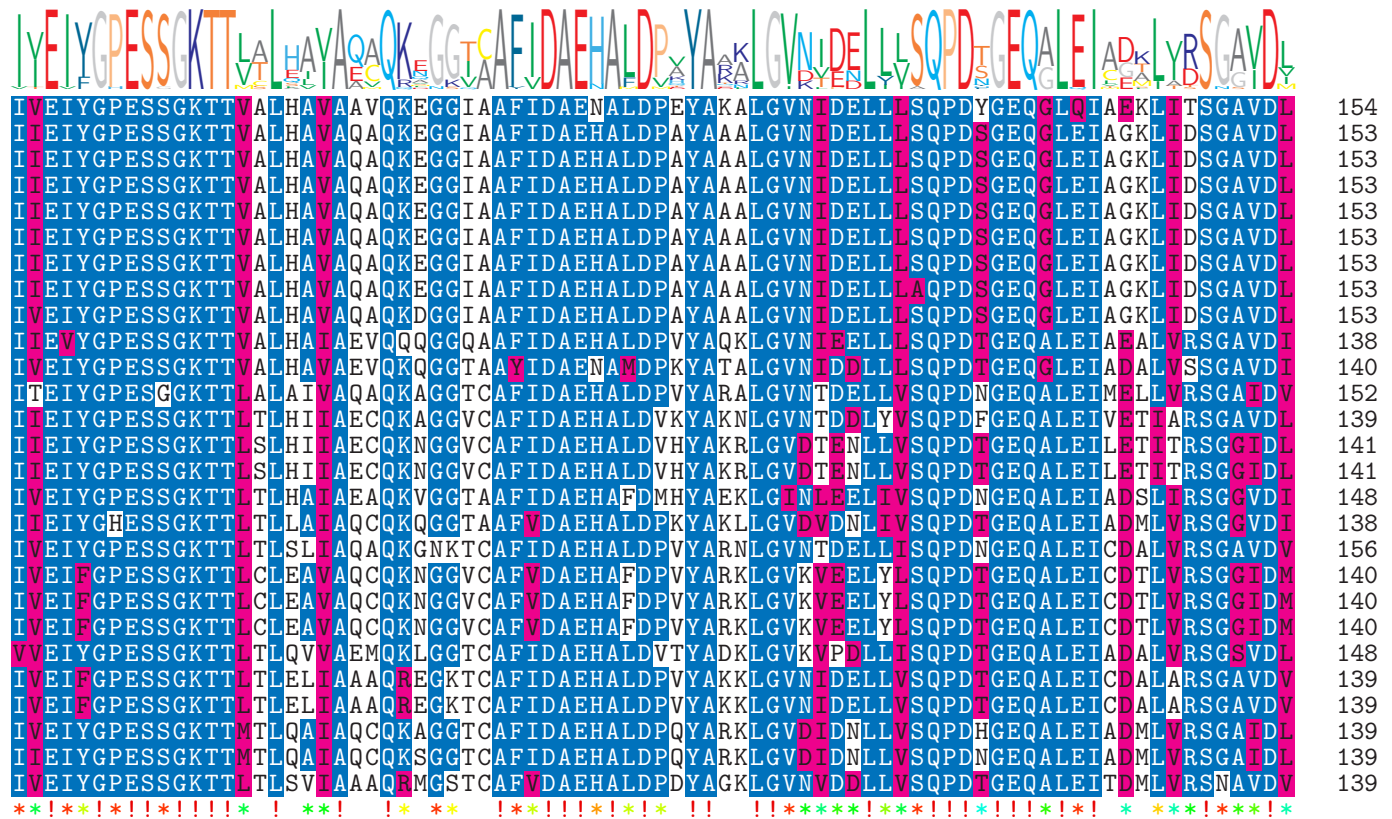
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consensus



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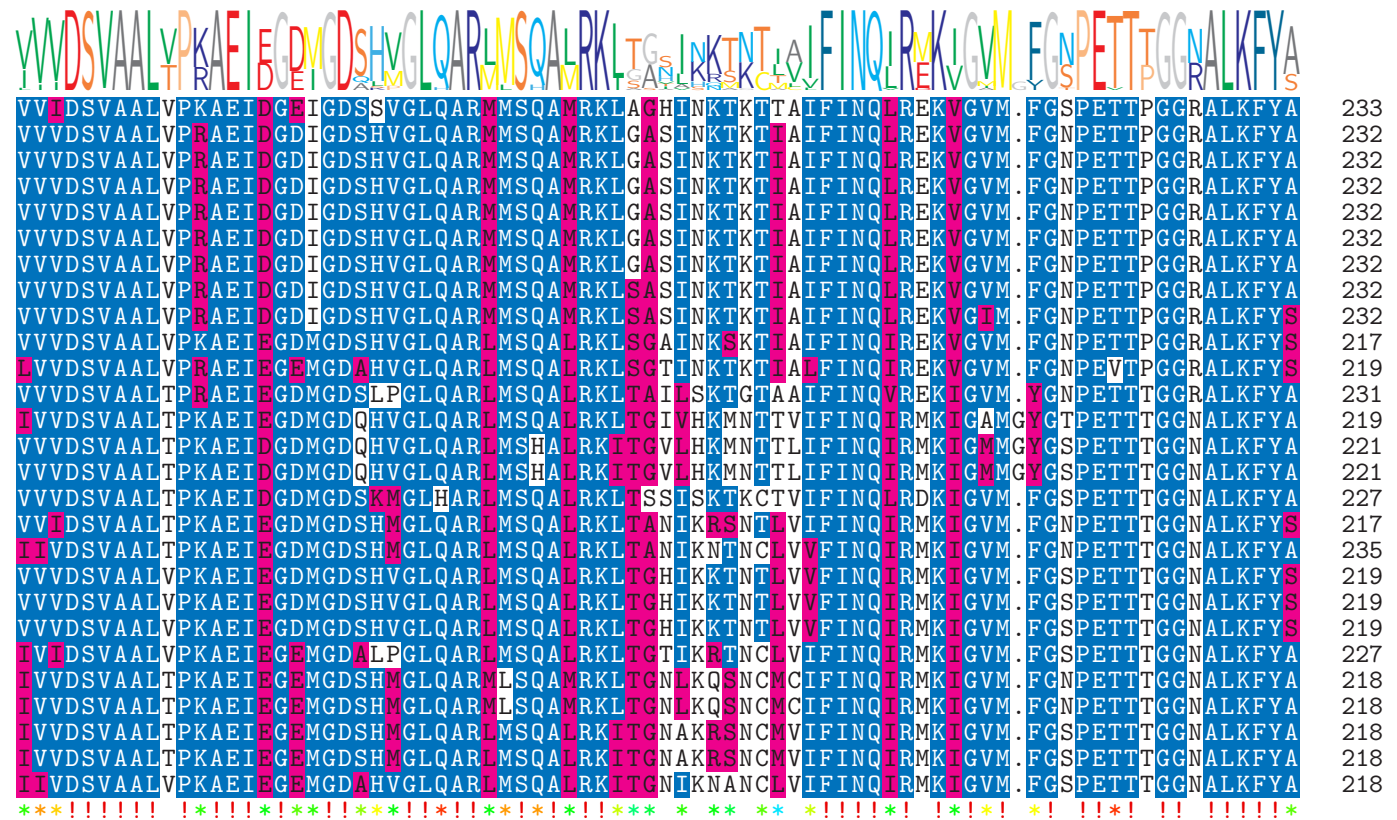
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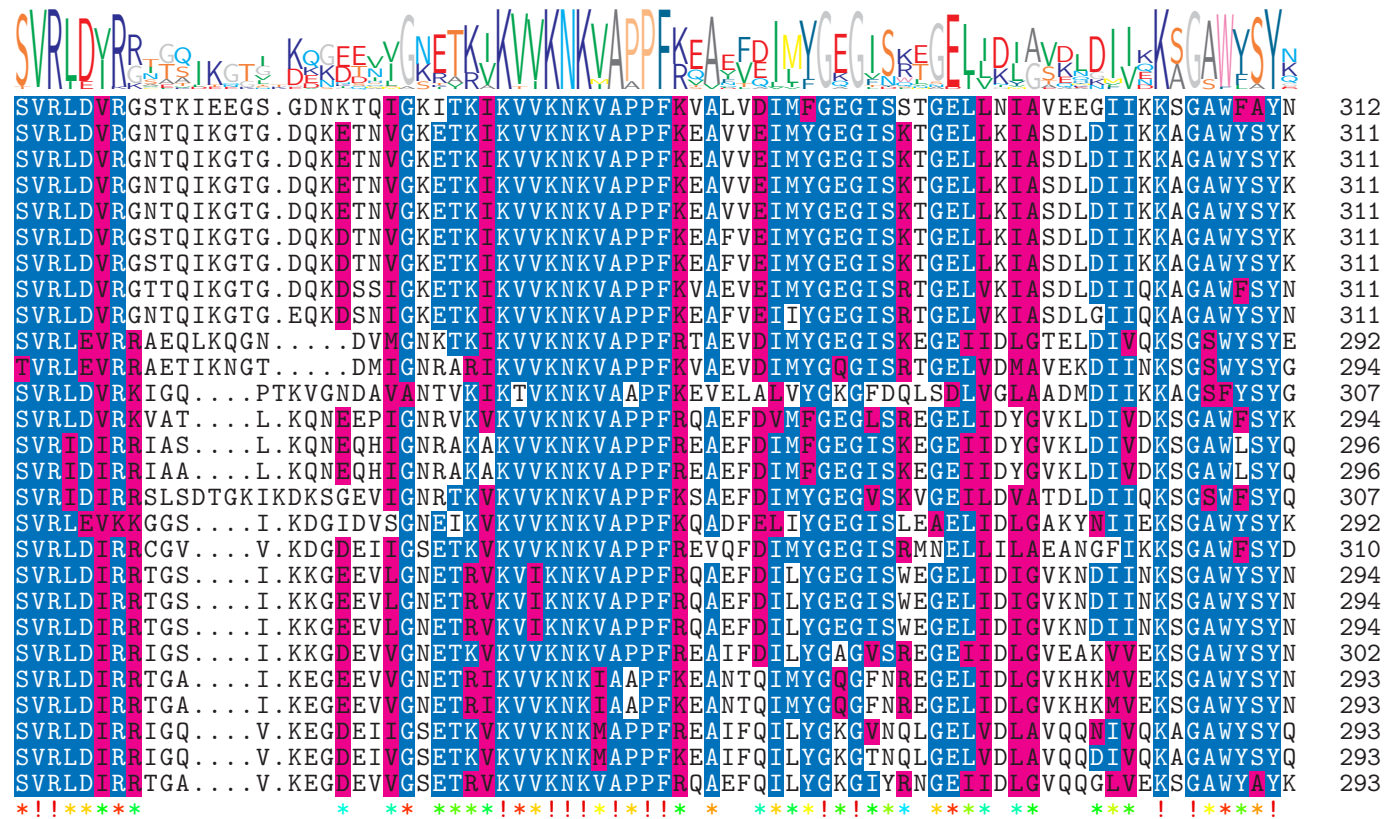
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consensus

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Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSE...QDTENKKDE...PKKEEA..VNEEVPLDLGD	380
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSE...QDTENKKDE...PKKEEA..VNEEVPLDLGD	380
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DEKIGQGSSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEAAE...S...KKDE...VAQVDS..VNEEVTLDLGD	376
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEES...AMAVASE...E...TDDLALDLN	372
GEKIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEE...KQSSKEK...ETDEK..ADKNLVLEDD	377
EERLGGQRENAAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQ...QAEETQEEL.EFE.E...	348
SERIGQGSRENAAKNYLADHEDVEDEVRLKVRRAAYGISDVPEEDL...PTTEDE.QI.NILPDDST...EE...	355
DERIGQGKEKTIAYTIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAA.EA...	363
DKKLGGQRENSKAFLKENPEIADEITKAIQNSMGI EGMIS...GSEDDEG...EE...	343
DKKLGGQRENAAKALLKEDKALADEITLKIKESIGSNEEIM...PLPDEPL...EEME...	347
DKKLGGQRENAAKALLKEDKALADEITLKIKESIGSNEEIM...PLPDEPL...EEME...	347
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GKIGQGGKNNAVKWLKENPEIADKLEQIRNTLASNPNSV...LKATASDSN.DESDVE...EFSEEL...	372
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT...EGTQDETGD.ER...PEE...	348
GERIGQGRDNCREFLRENAELARENKVRHGLVTPMGA...VTLA.EEVE.ED...	352
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GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNMQ...LIAETSSAA.DDVEFG...AVPEEF...	354
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQ...TAA.HDETE.EEPDLL...ES...	349
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GSKIGQGGKANAAYLEENPEIQEIEQQIRAKLLVTSANT...KATPVAEDL.ADADI...	347

logo

		ELELEE	
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NTDB id 269 KZH43 RS08665 WP 001085462.1	ELEIEIEE		388
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consensus			

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