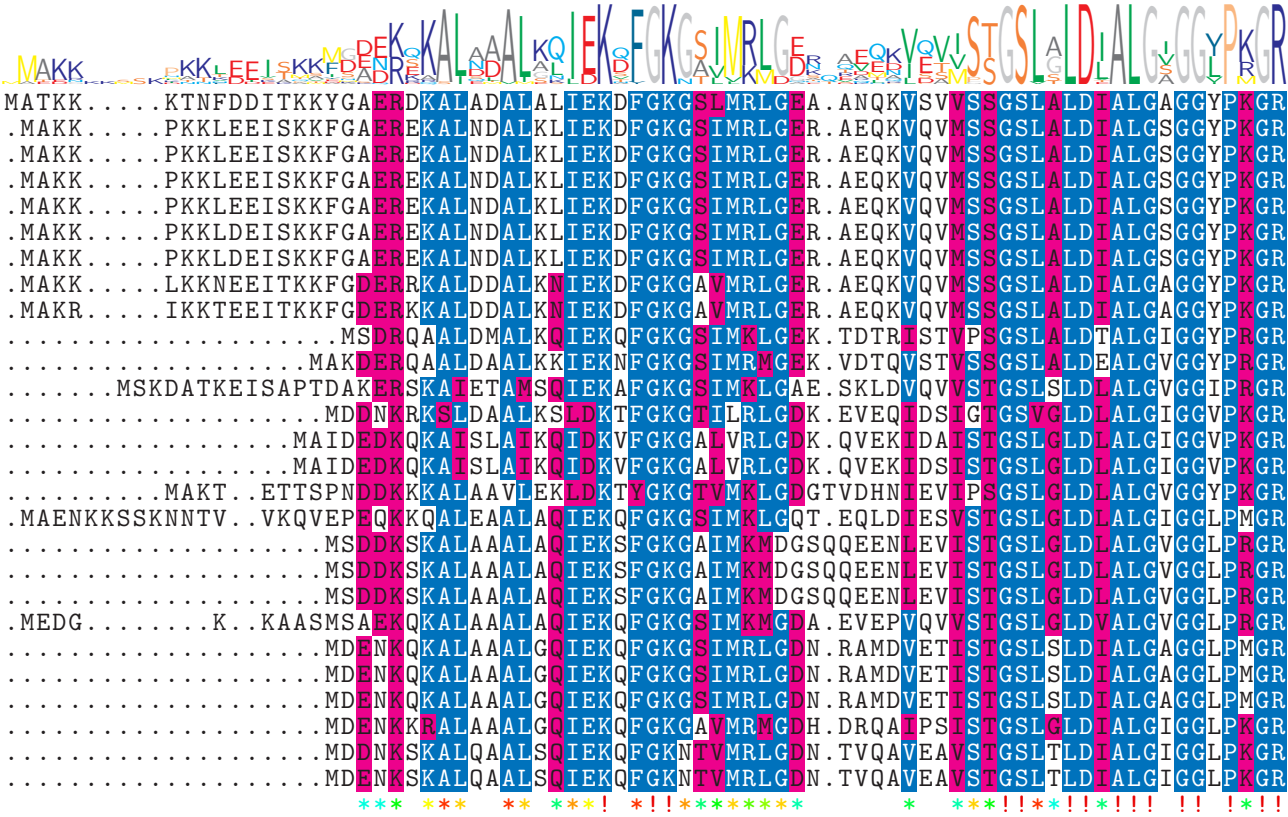


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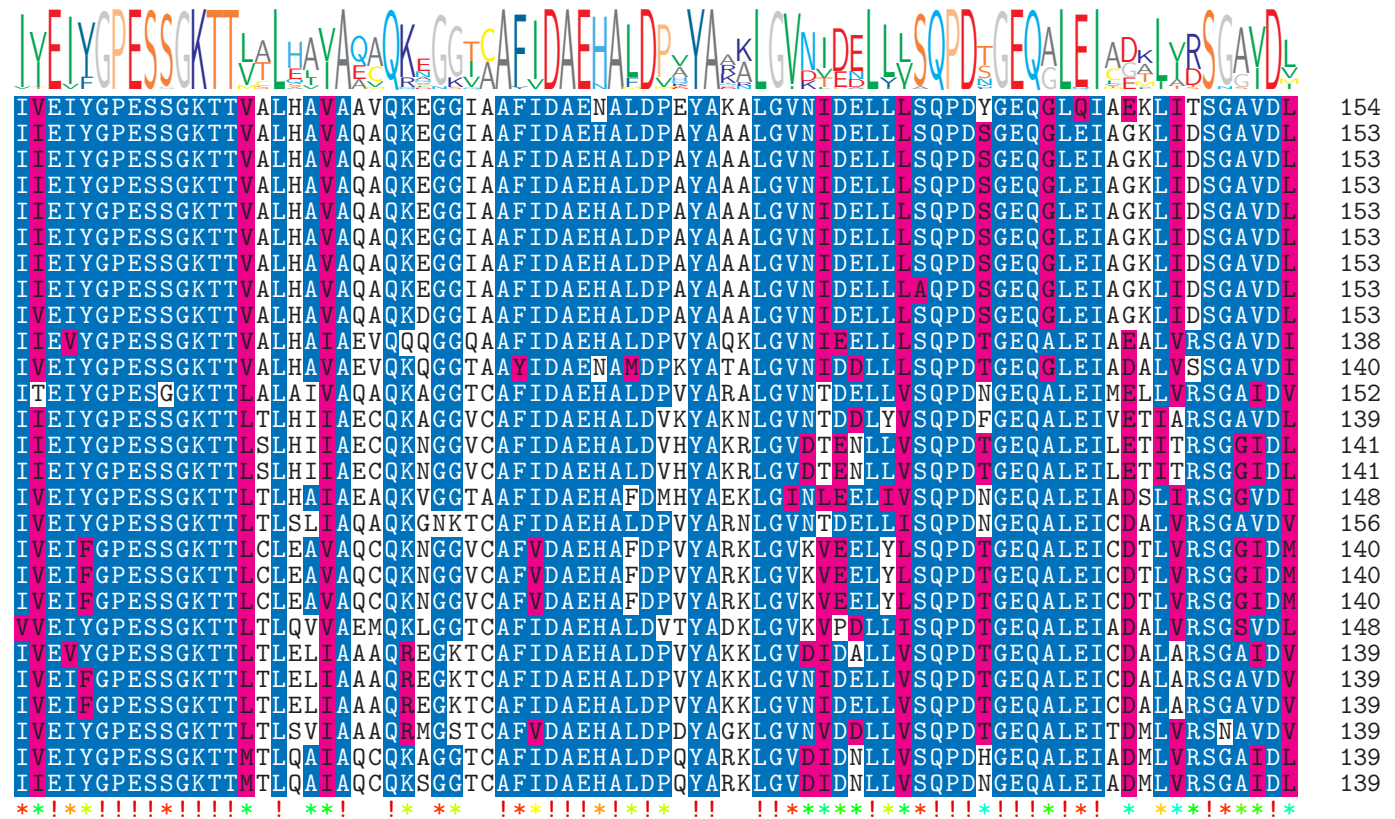


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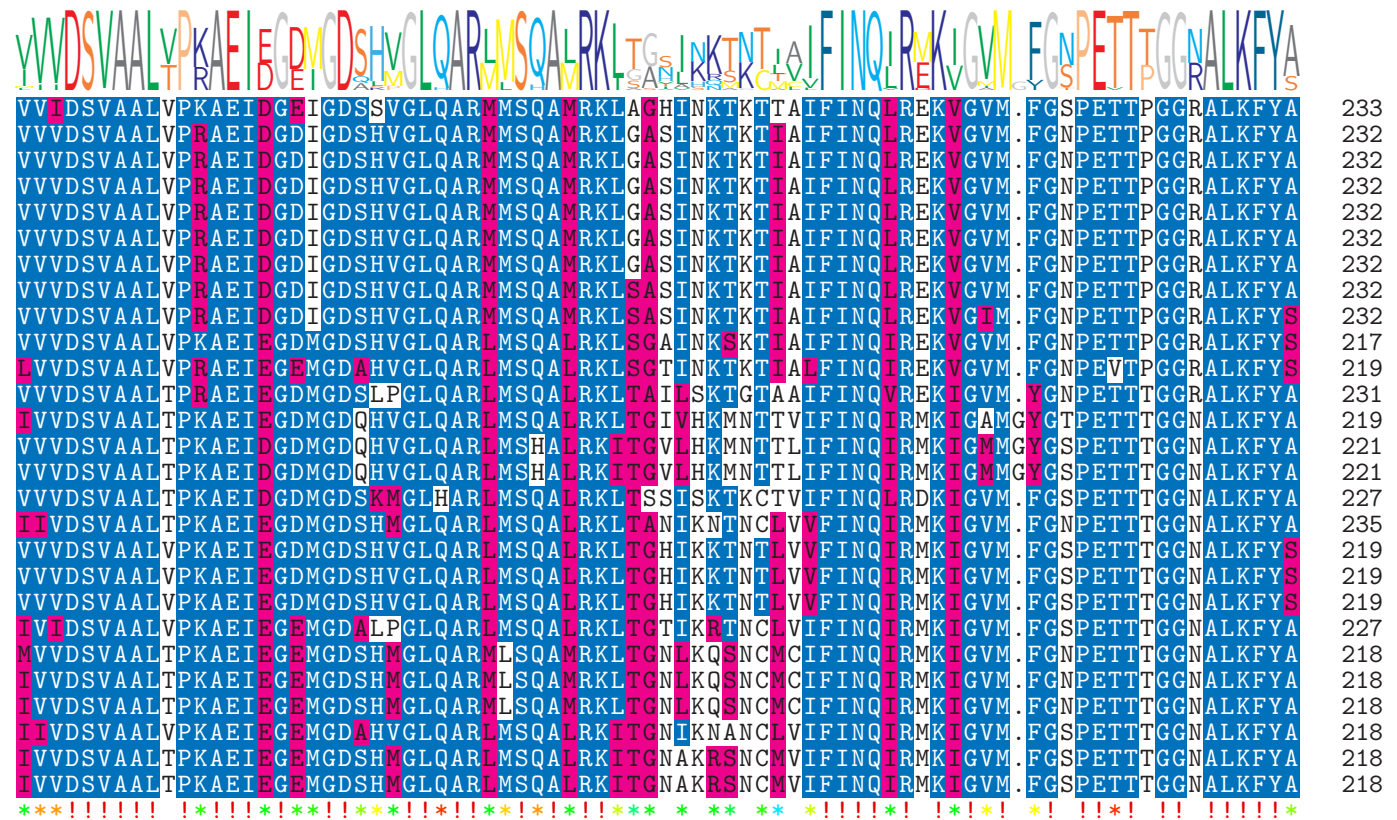
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consensus

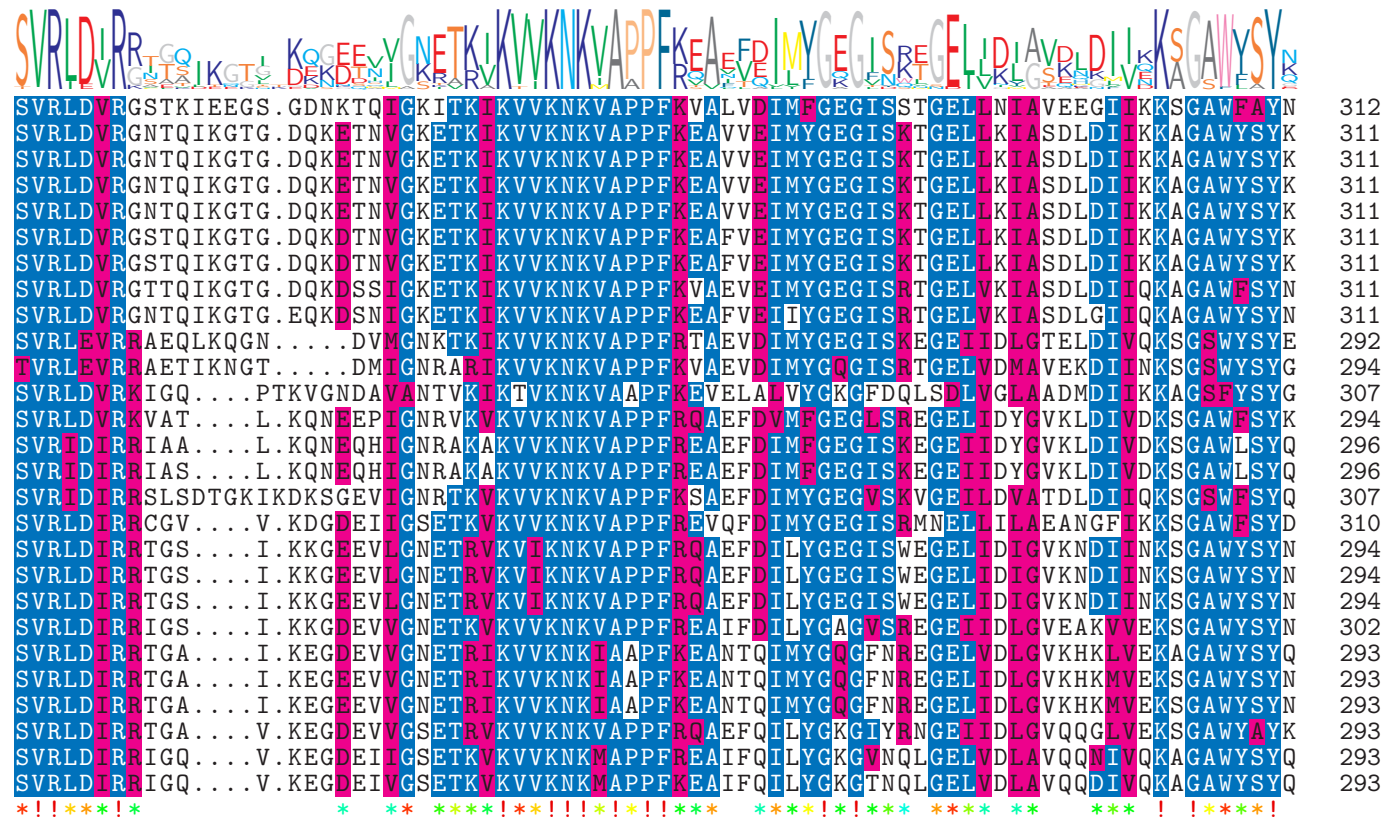
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEAAE...SKKDE...AAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGGGRENAAKQFLKENKDIMLMIQEIQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTEDE.QI.NILPDST.....EE.....	355
DERIGGQKEKTIAYIAERPEMEQETIDRVRMAAIRAGNAGEAPALAPAPAPEAAE..A.....	363
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DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..PLE..EME.....	347
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GERIGGGRDNCREFLRENAELAREIENKVRHGLVTPMG.....AVTLAE.EVEE..D.....	352
GDKIGQKANAACNYLREHPEVAKTIDTKLREMLLAPALA.....EAPAEAGEAPEQ..AEFF.....	347
GDKIGQKANAACKYLKENPEIAKTLDDKKLREMLLNPNEM.....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGQKANAACKYLKENPEIAKTLDDKKLREMLLNPNEM.....QLIAETSSAAD..DVEFGAVPEEF.....	354
GSKIGQKANAACKYLEENPEIGQEIEQQIRAKLLVTSAN.....TKATPVAEDLA..DAD..I.....	347
GDKIGQKNNVIRYLEENPEIISTEIEAVIREQLLTKASD.....QTAA.HDETEE..EPD..LLES.....	349
GNKIGQKNNVIRYFEENNQIAEIERNIQREQLLTGTN.....GAVQ.I.EDEE..EPD..LLES.....	349

logo

		IEE	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...		349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
consensus			

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