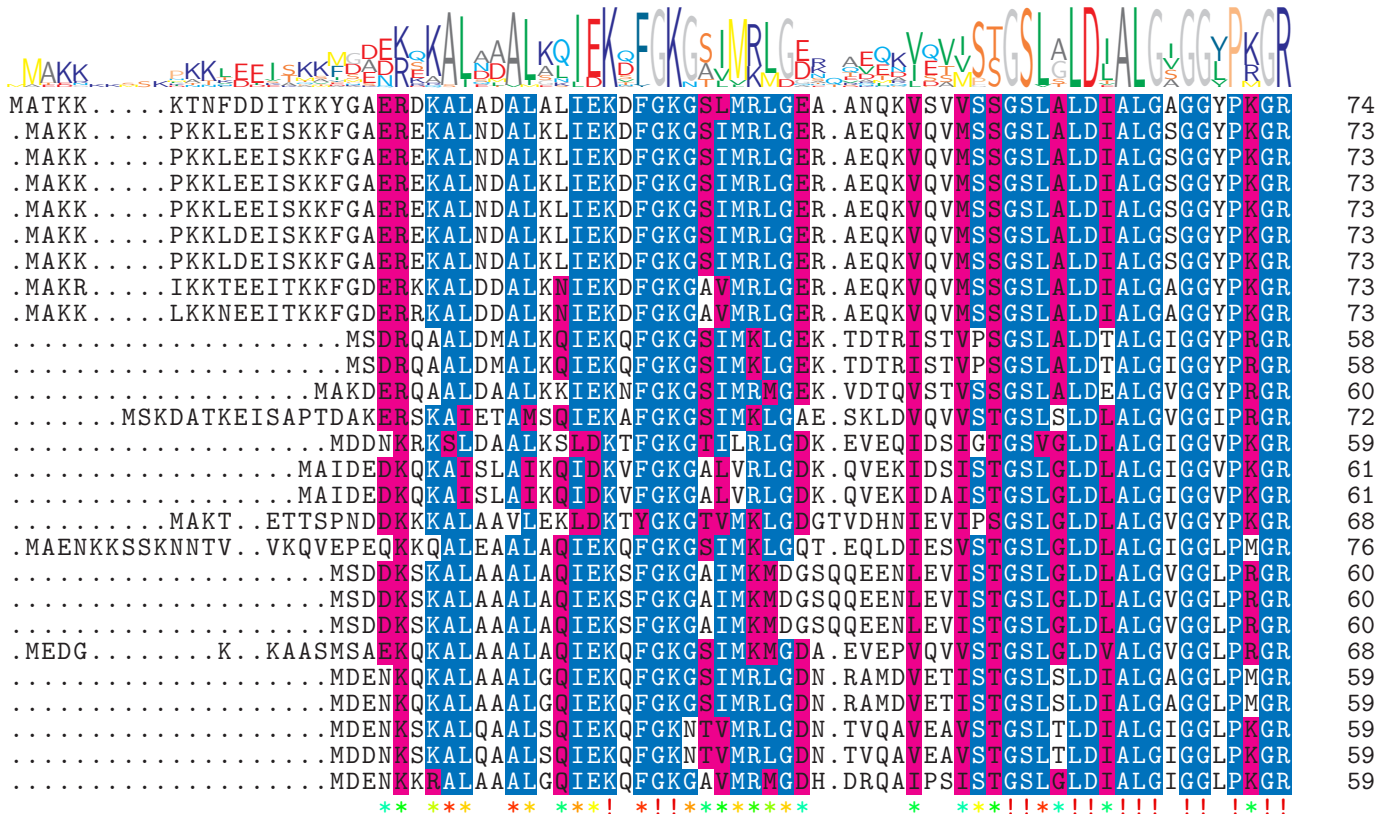


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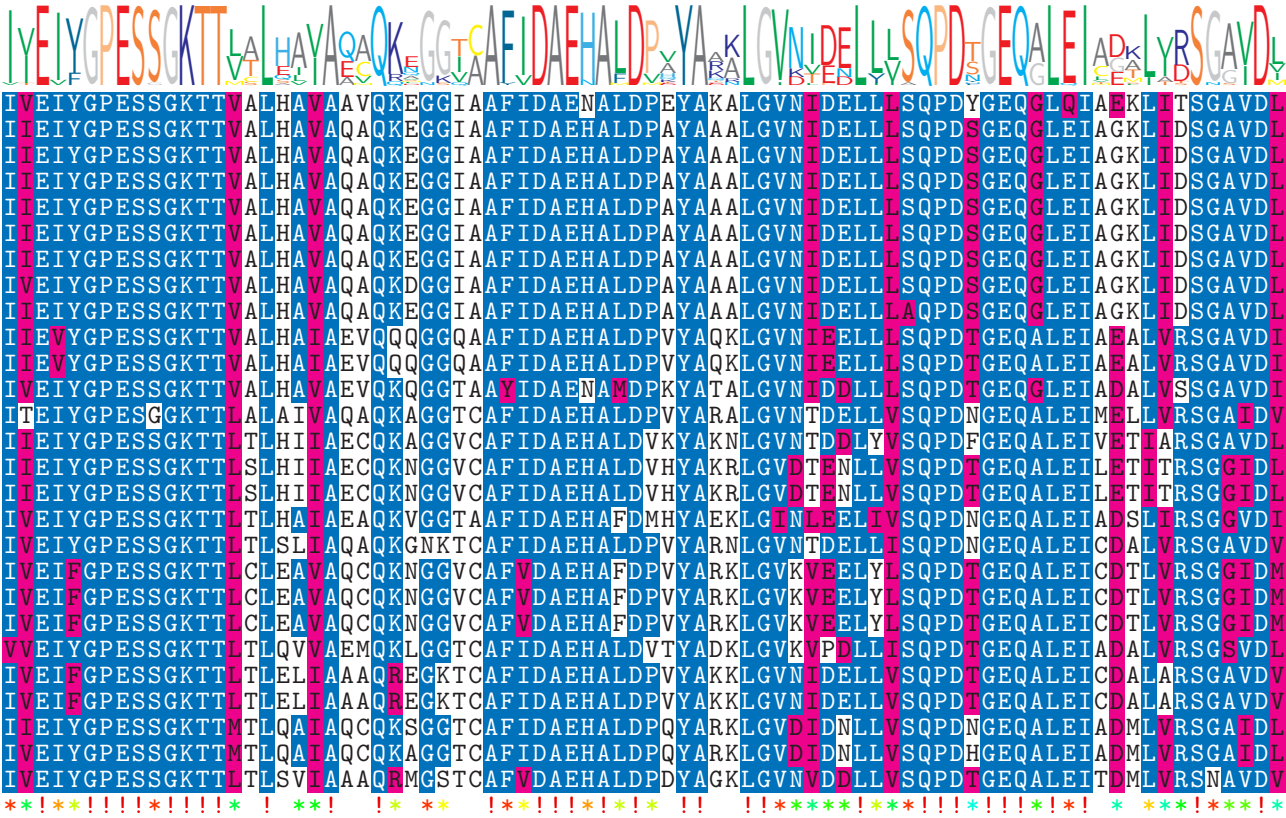
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consensus

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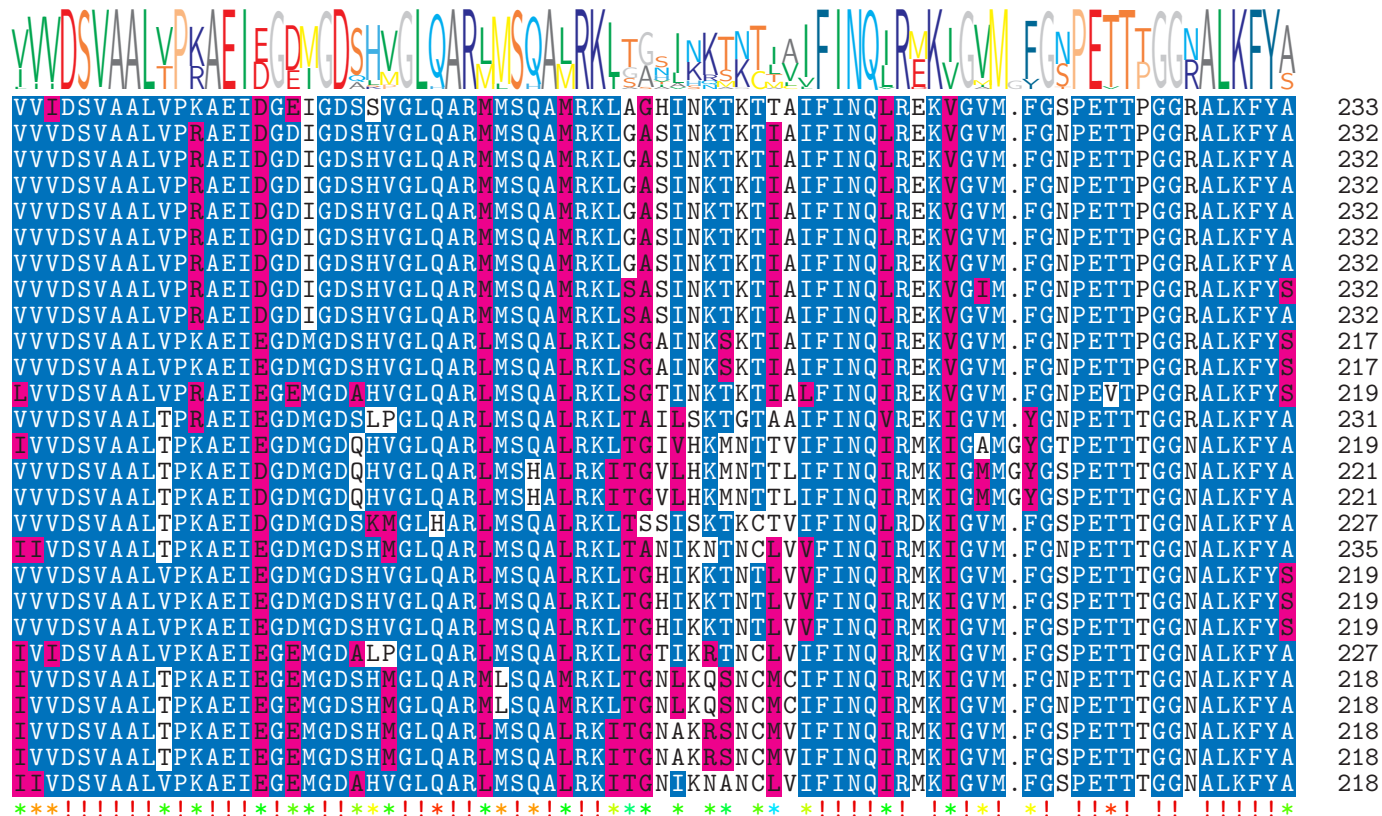


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consensus

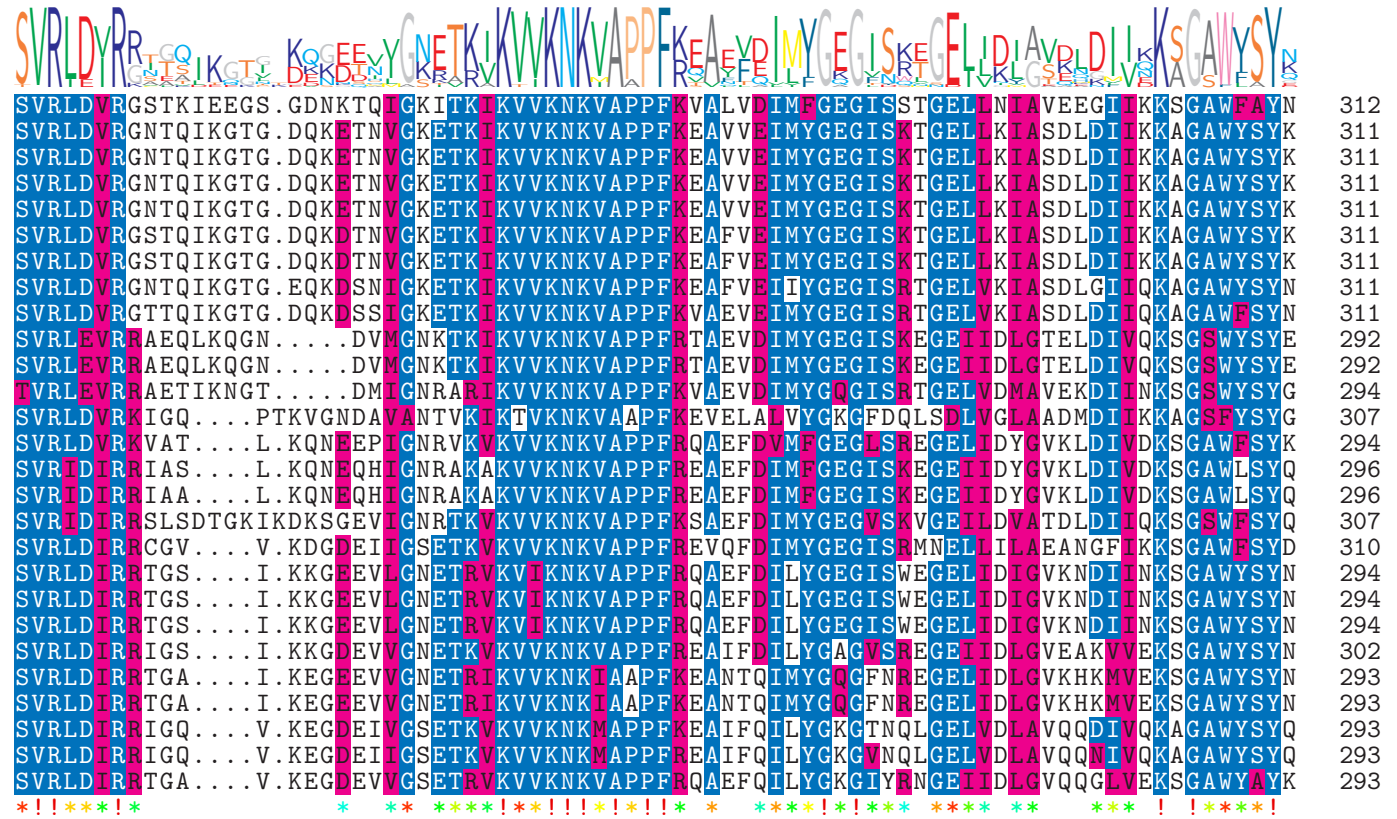
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consensus

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consensus

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Sequence	Score
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DEKIGGGS E NA K KYLAEHPEIF F DEIDKQVRSKFG L IDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS E NA K KYLAEHPEIF F DEIDKQVRSKFG L IDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS E NA K KYLAEHPEIF F DEIDKQVRSKFG L IDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS E NA K KYLAADNP E VFAEIDHQVVRVQFGLIDGEEAAE....SKKDE....VAQVDS..VNEEVTLDLGDELEIE	381
DEKIGGGS E NA K KYLAADNP E IFDEIDHQVVRVQFGLIDGEEIAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIE	381
GEKIGGGS E NA K KFLADNP E IFDDIDHKVVRVQYGLIEDNTTEEKQSSKE.....ETDEK..ADKNLVLELDDTTIEIE	382
GEKIGGGS E NA K KRYLADHPQL F DEIDRKVVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLDNNGIEIE	377
EERLGGGREN A KQFLKENKDIMLMIQE Q IREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
EERLGGGREN A KFLKENKDIMLMIQE Q IREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGGGR E NA K NFLADHED V DEVRLKVRVAAAYG I SDVPPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGGGKEKTIAYIAERP E MEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA.....	363
DKKLGGGREN S KAF L KENPEIADEITKAIQNSMG I TEGMI....SGSEDDE..GEE.....	343
DKKLGGGREN A KALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
DKKLGGGREN A KALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
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GAKIGGGKDN V RVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDETD.....GERPEE.....	348
GERIGGGRD N CREFLRENAELAREIENKVRHLGVTPMG....AV.TLAEVEED.....	352
GDKIGGGKAN A CKY L KENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GDKIGGGKAN A CKY L KENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GNKIGGGKNN V IRYFEENNQIA E EIERNIREQLLTGTN....GAVQ.I.EDEEEDPD....LLES.....	349
GNKIGGGKNN V IRYLEENPQISTEIEAVIREQLLTKASD....QTAA.HDETEEEDPD....LLES.....	349
GSKIGGGKAN A AKY L EENPEIGQEIEQQIRAKLLVTSAN....TKATPVAEDLADAD....I.....	347

logo

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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
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consensus			

- non conserved
- similar
- ≥ 50% conserved