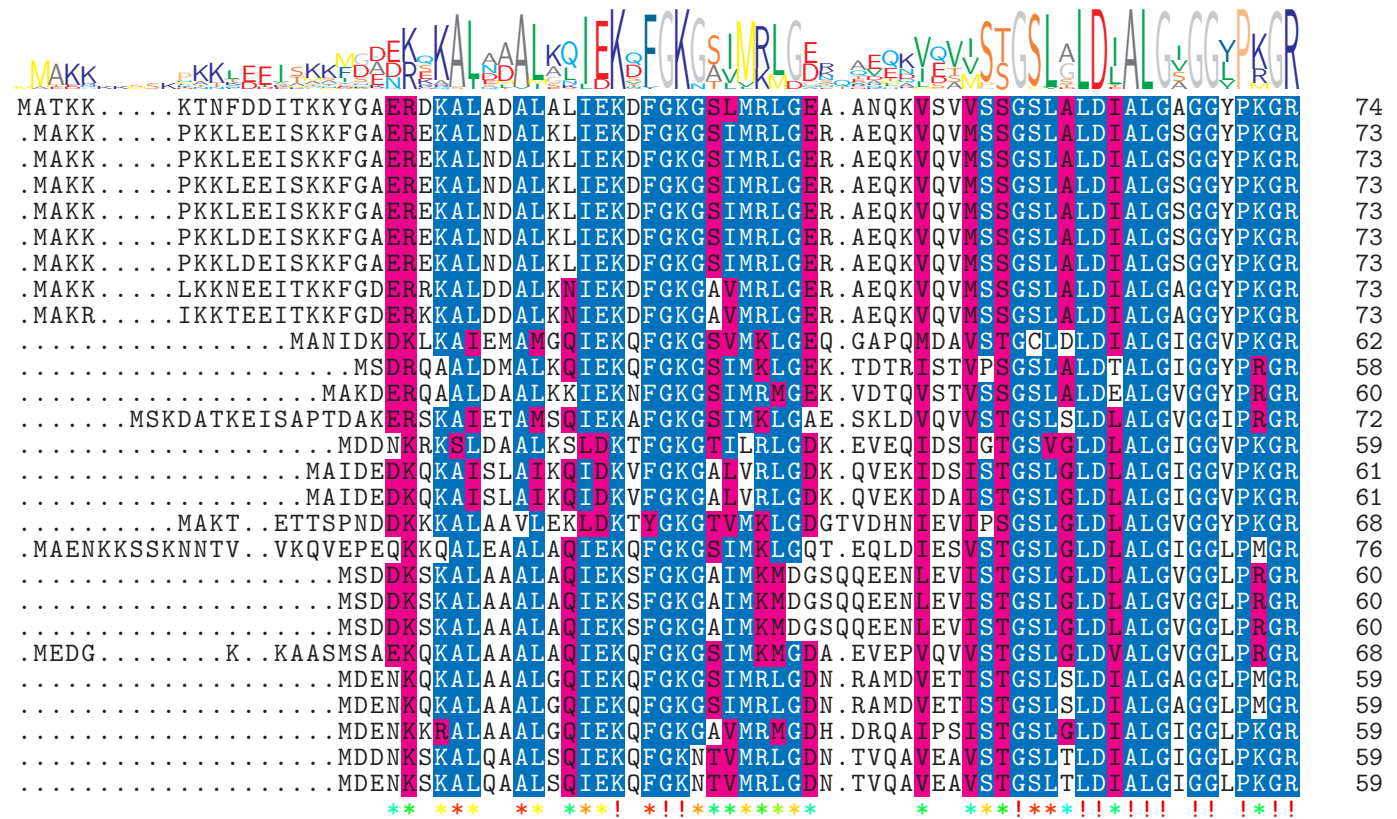


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consensus

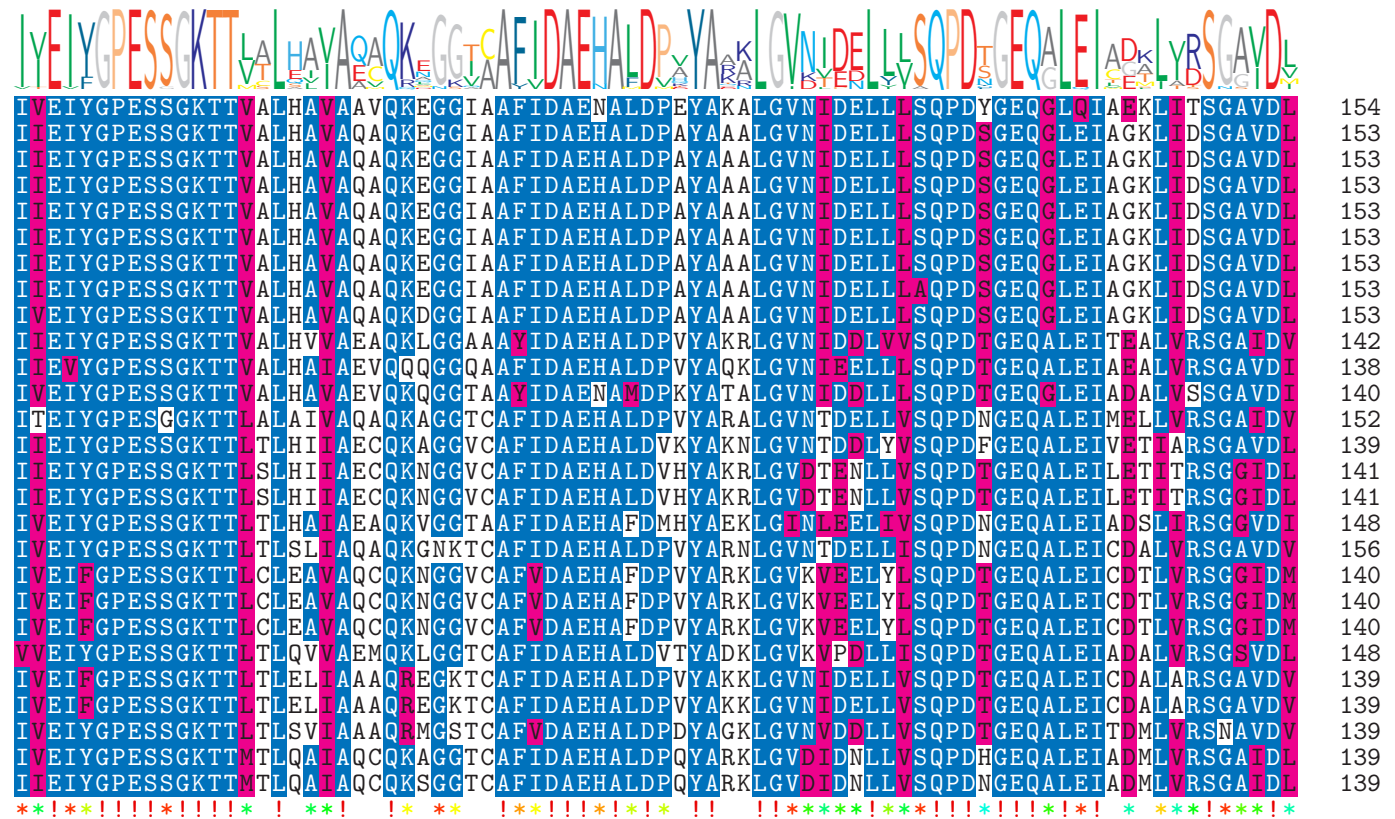
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

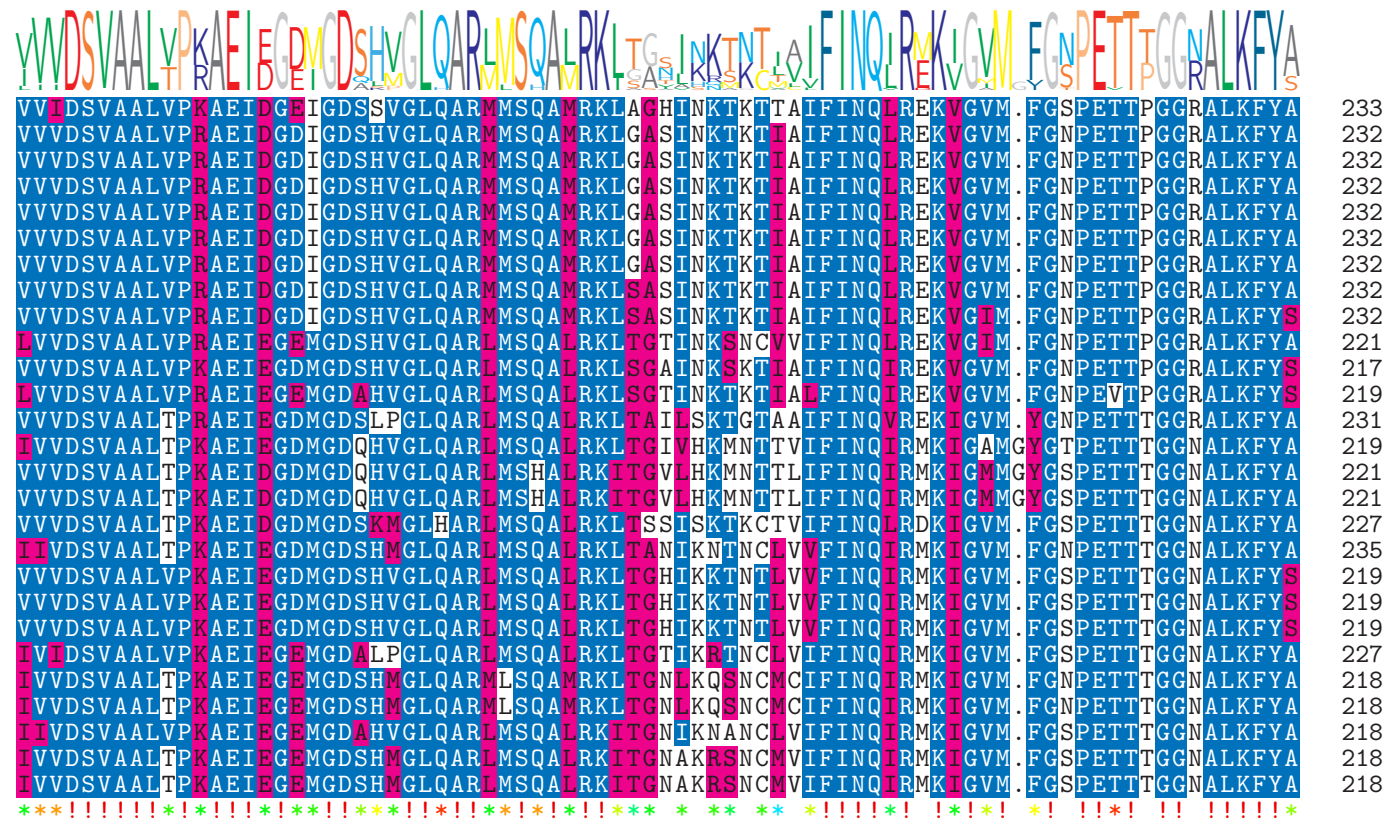
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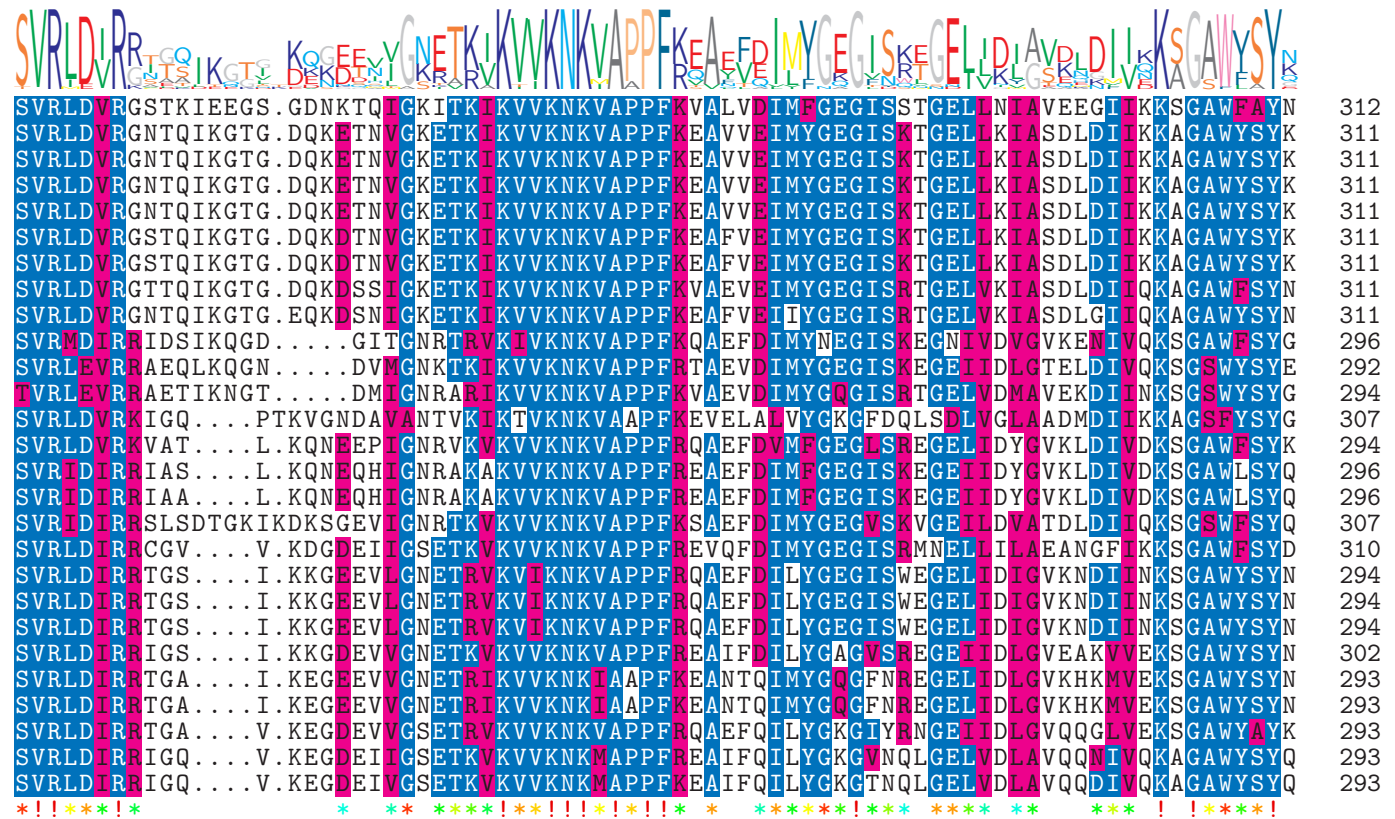
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consensus

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Sequence	Score
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DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDT...ENKKDE...PKKEEA..VNEEVPLDLG	379
DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDT...ENKKDE...PKKEEA..VNEEVPLDLG	379
DEKIGGGSSENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLG	375
DEKIGGGSSENAKKYLAHNPEIFDEIDHQVRVQFLIDGEEIAE...SKKDE...AAQVDS..VNEEVTLDLG	375
GEKIGGGSSENAKRYLADHPQLFDEIDRKVRVKFLLEESEESAMA...VASE...E...TDDLALDL	371
GEKIGGGSSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEKQS...SKEK...ETDEK..ADKNLVLELD	376
DIRLGQGRENAKQYLKENPAVALDIENQIREKYSPLAKAVESTSV...EENTEEVESV...	352
EERLGQGRENAKQFLKENKDIMLMIQEIREHYGLDNGGVVQQAAE...ETQEELEFE.E...	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAYGISDVPEEDLPTT...EDE.QINILPDDSTEE...	355
DERIGGQKEKTIAYIAERPEMEQEITRDRVMAAIRAGNAGEAPALAPAAPEAAEA...	363
DKKLGQGRNSKAFLENPEIADAITKAIQNSMGIIEGMI...SGSEDDE..GEE...	343
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI...MPLPDEP..LEEME...	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI...MPLPDEP..LEEME...	347
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GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAH.HDETEEEPDLL..ES...	349
GNKIGGQKNNVIRIYFENNQIAEIERNIREQLLTGTN...GAVQ.I.EDEEEPDLL..LE...S...	349

logo

		DELELEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	D.....		387
NTDB id 269 KZH43 RS08665 WP 001085462.1	DELEIEIEE		388
NTDB id 228 SPD RS09265 WP 001085462.1	DELEIEIEE		388
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved