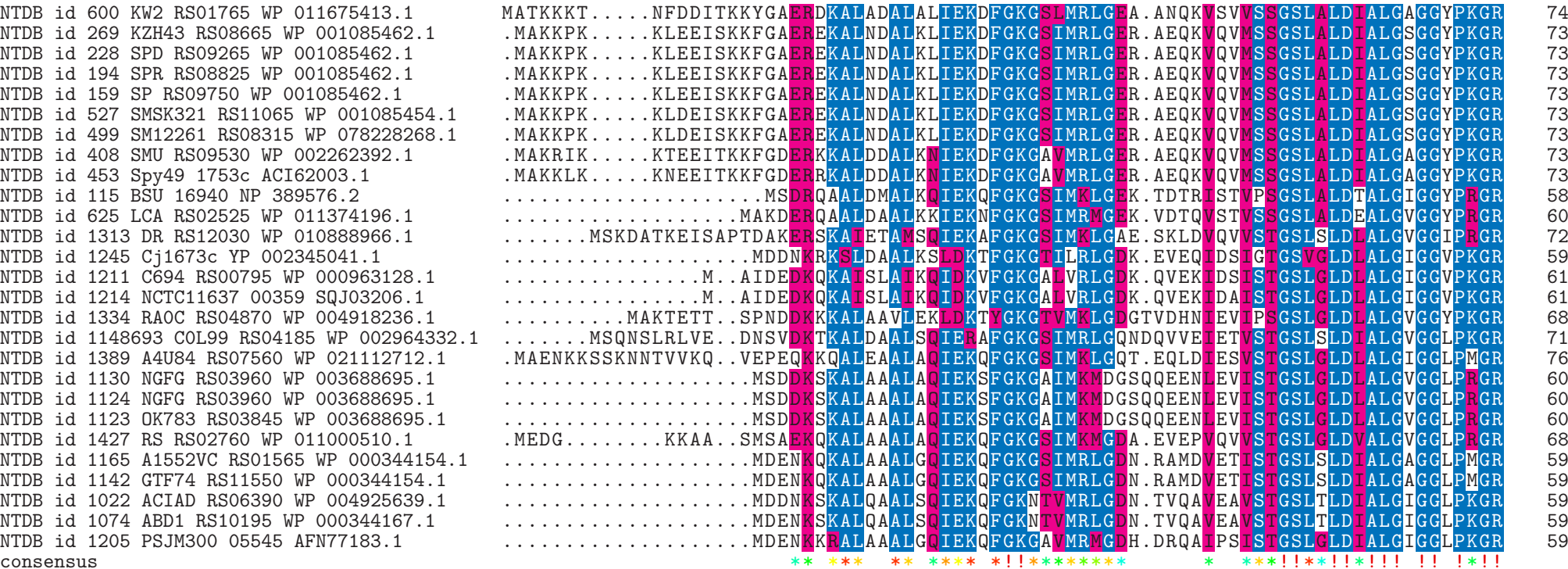


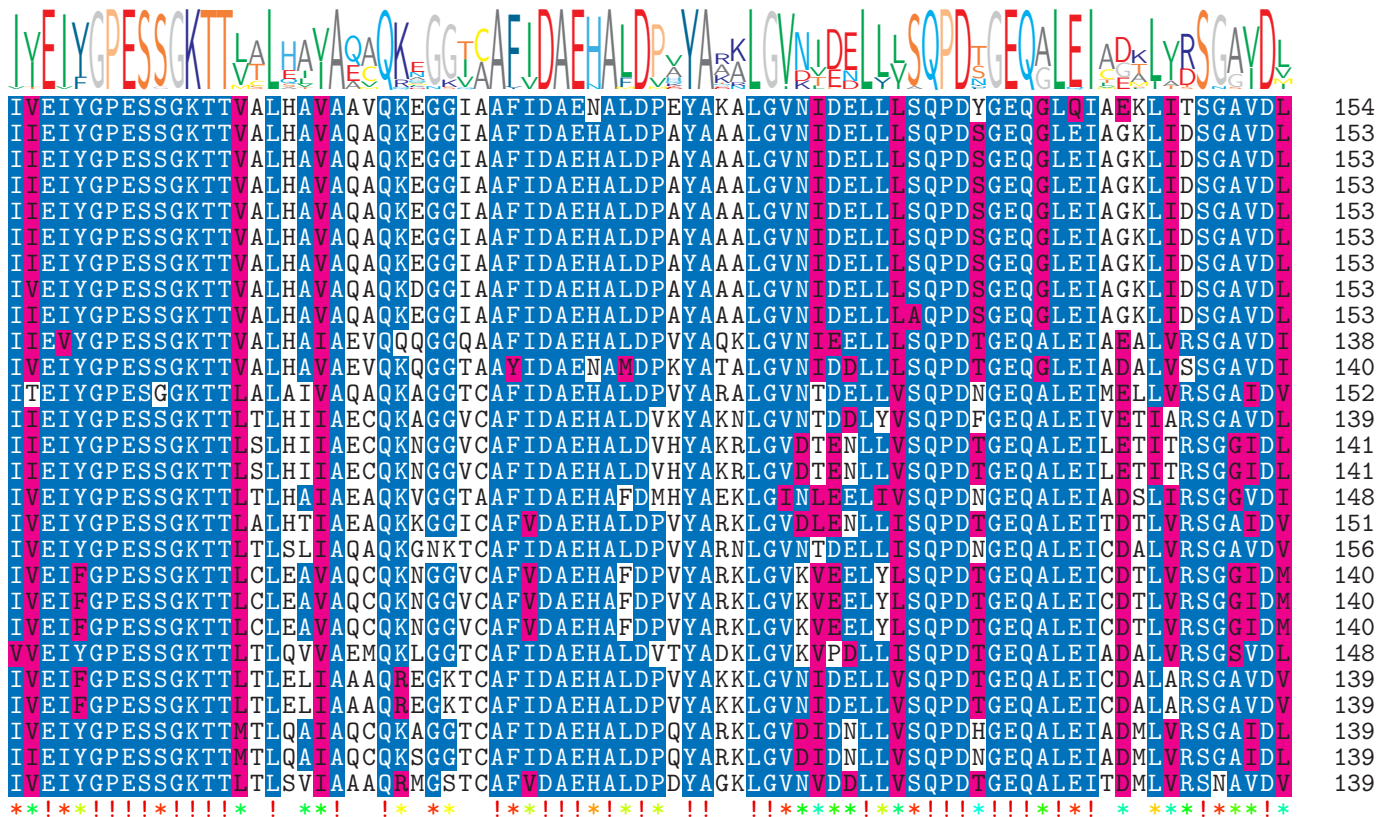
logo



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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

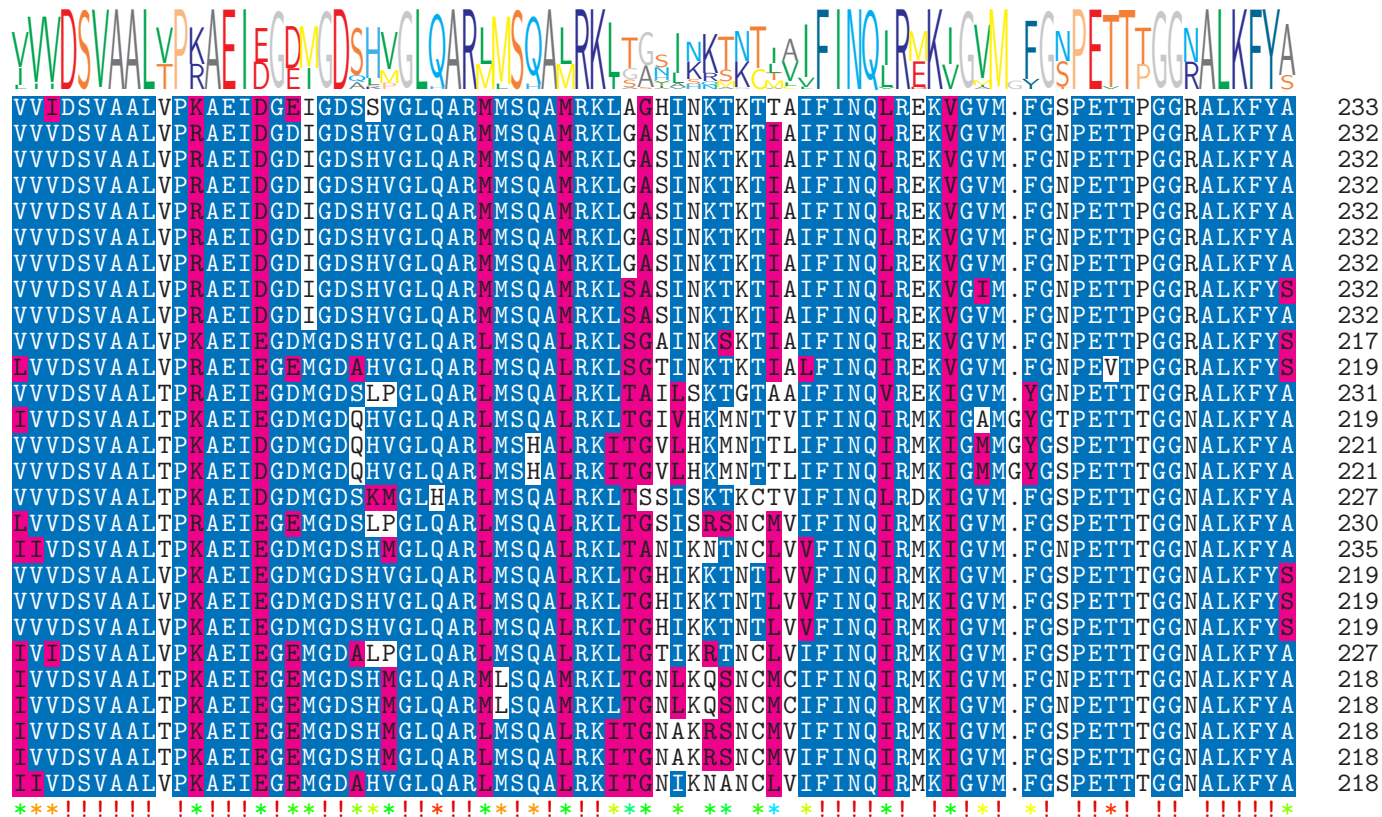
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

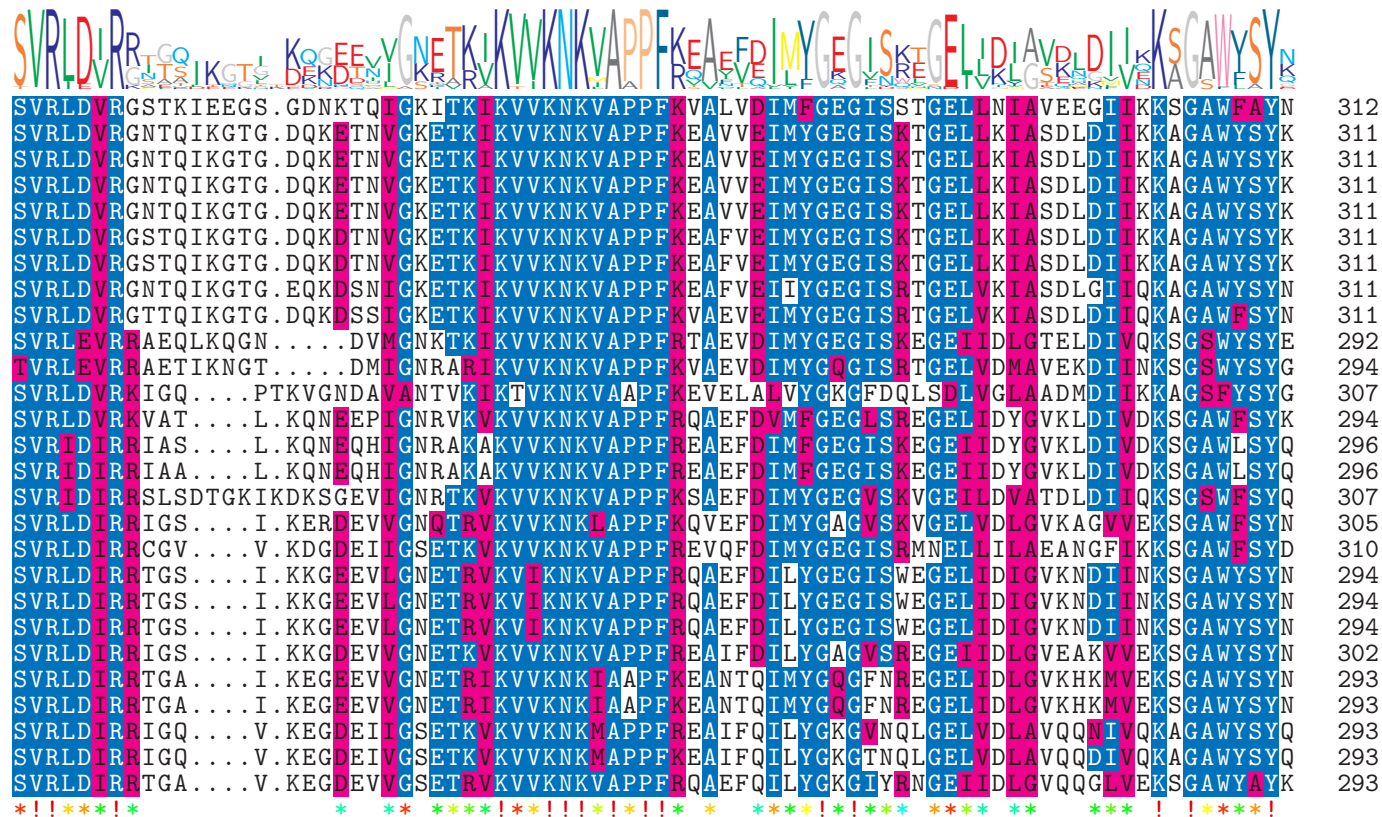
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLEDGEEVSEQDTEENK.DE...PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLEDGEEVSEQDTEENK.DE...PKKEEA..VNEEVPLDLGDELEI	384
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DEKIGQGSENAKKYLADNPVFAEIDHKVVRVQFGLIDGEEAAE...SKK.DE...VAQVDS..VNEEVTLDLGDELEI	380
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GEKIGQGSENAKKFLADNPVFEIDHQRVVRVQFGLIEDNTEEEKQSSKEK.....ETDEK..ADKNLVLELDDTIEL	381
GEKIGQGSENAKRYLADHPQLFEIDRKVRVKFGLLEESEEEESAMAVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAAKQFLKENKDIMLMIQEIQIREHYGLDNNGVVQQQAETQE.EL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRVRAAYGTSVPPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
DERIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPAAEA.....	363
DKKLGGGRENSKAFLENPEIADAITKAIQNSMTEGMISGSEDDEGEE.....	343
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DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEPLEEME.....	347
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SRLRGGGRENAKQYLKDNPEVAREIETTLRQNAGLIAEQFLDDGGPEEDAAGAAEM.....	361
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GAKIGGGKDNVRVWLKENPEISDEIDAKIRALNCVEMHITEGTQ..DETDEGER.....PEE.....	348
GAKIGGGKDNVRVWLKENPEISDEIDAKIRALNCVEMHITEGTQ..DETDEGER.....PEE.....	348
GERIGQRDNCREFLRENAELAREIENKVRHLGVTPMGAVTLA...EEVEED.....	352
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GDKIGGGKANACKYLYKENPEIAKTLDKKLREMLLNPNMQLIAE..TSSAADVEFG.....AVPEEF.....	354
GNKIGGGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTAA..HDETEEPDLL.....ES.....	349
GNKIGGGKNNVIRYFEENNQIAEEIERNIREQLLTVGTNGAVQ...I.EDEEPDLL.....LES.....	349
GSKIGGGKANAAKYLYLENPEIAGIEEQIRAKLLVTGSANTKATP..VAEDLADADI.....	347

logo

		ELEE	
NTDB id 600 KW2 RS01765 WP 011675413.1			387
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEE		388
NTDB id 228 SPD RS09265 WP 001085462.1	EIEE		388
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved