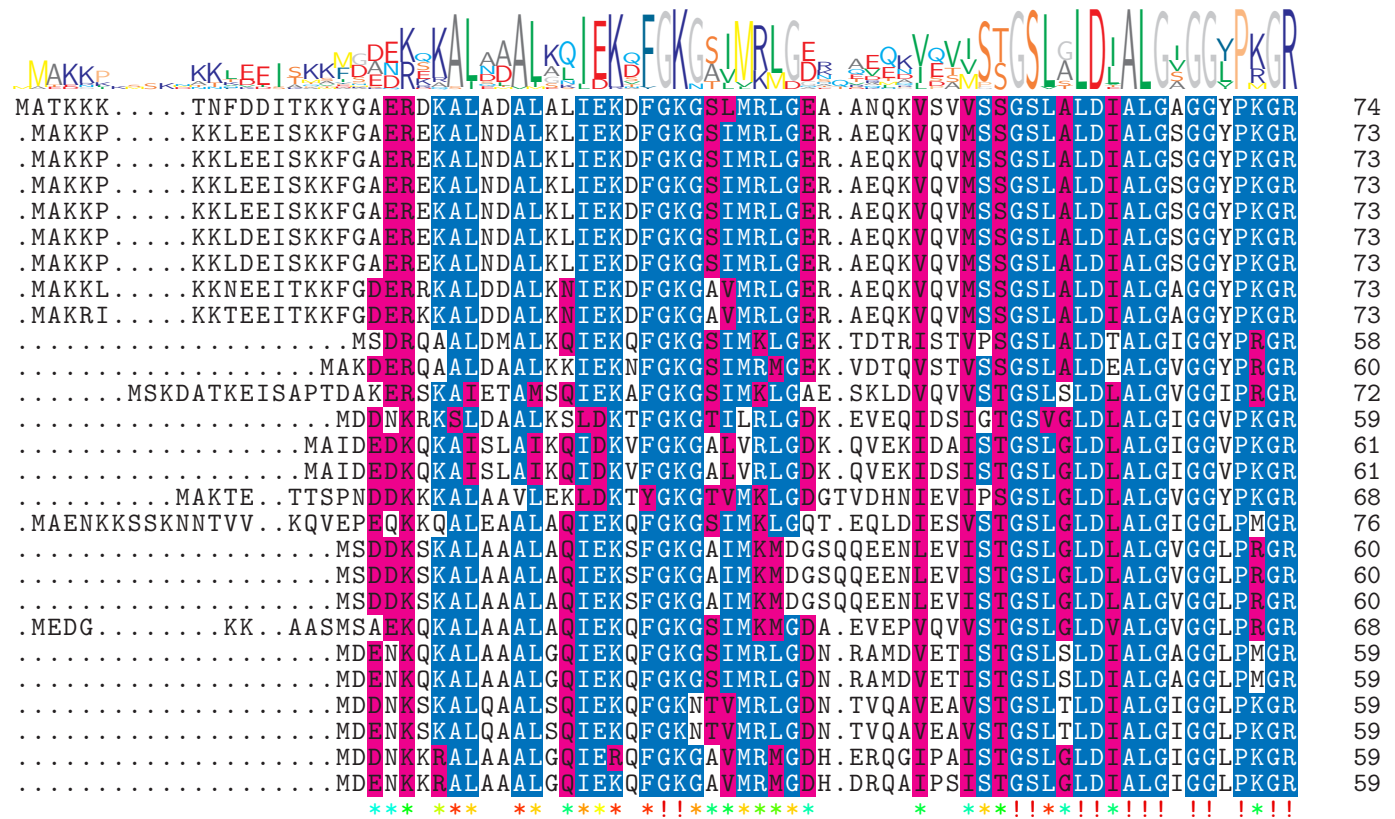


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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

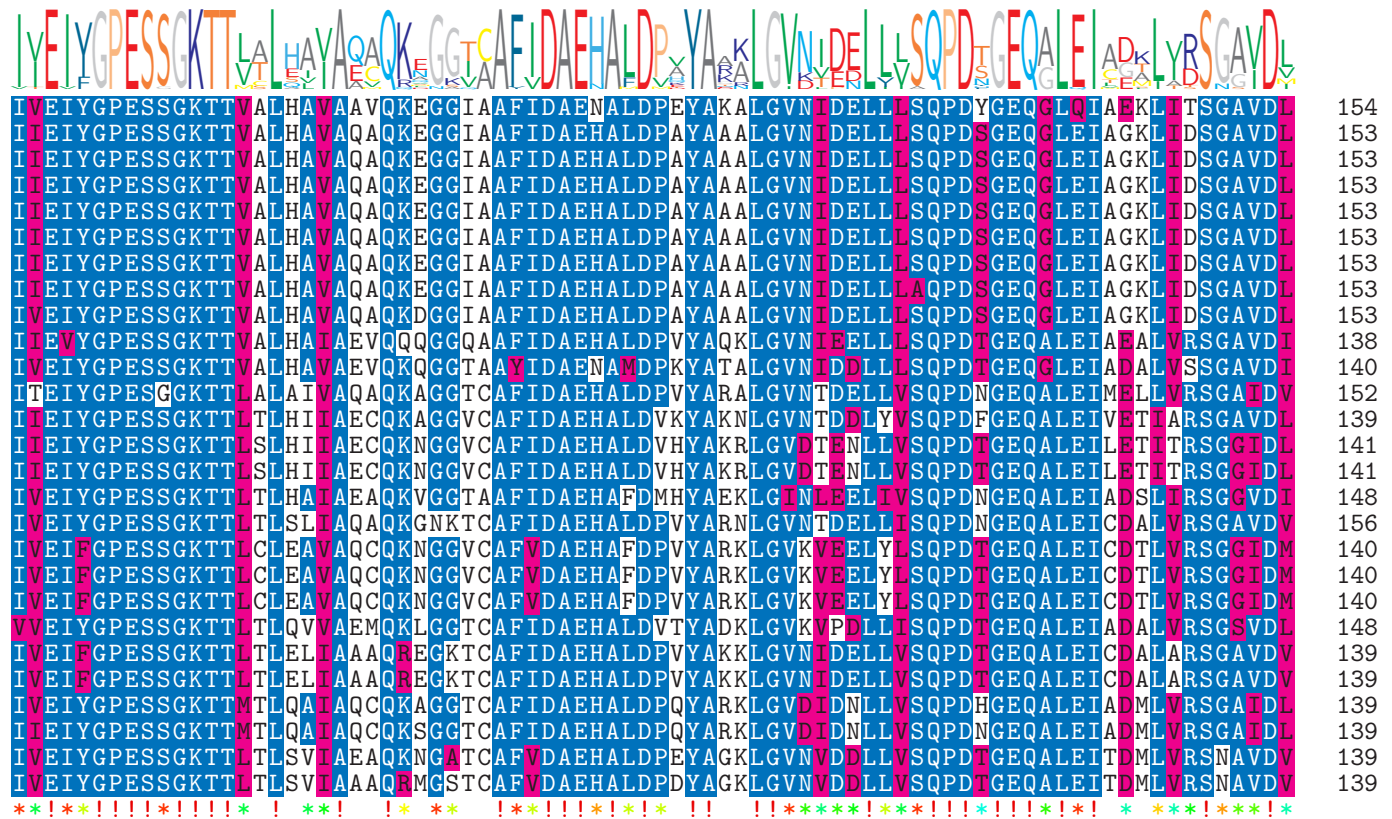
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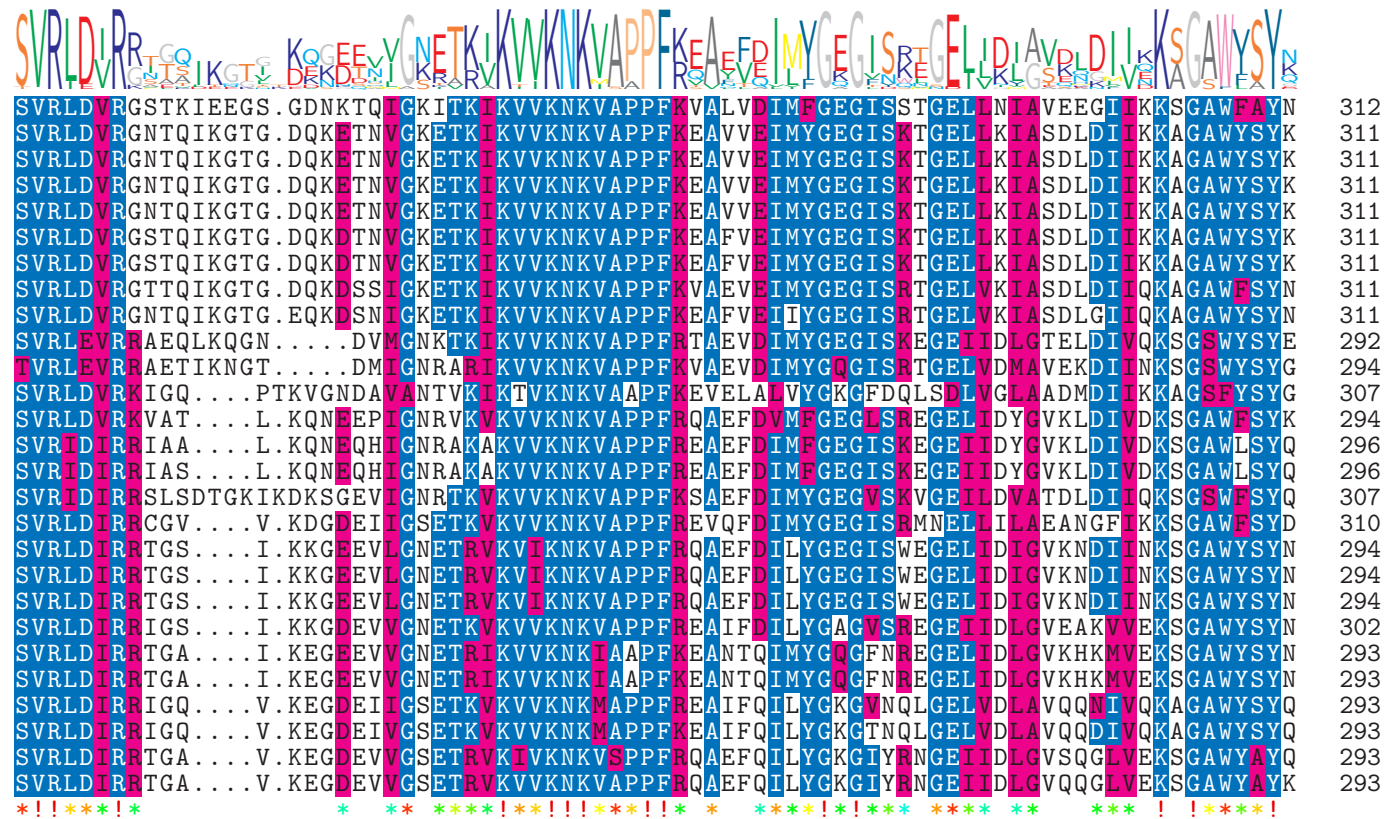
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V	V	V	D	S	V	A	A	L	V	P	R	A	E	I	D	G	D	S	H	V	L	Q	A	R	L	M	S	Q	A	R	K	L	G	A	S	I	N	K	T	K	T	I	A	F	I	N	Q	L	R	E	K	V	G	M	.	F	G	N	P	E	T	T	P	G	G	R	A	L	K	F	Y	A	232		
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V	V	V	D	S	V	A	A	L	V	P	R	A	E	I	D	G	D	S	H	V	L	Q	A	R	L	M	S	Q	A	R	K	L	G	A	S	I	N	K	T	K	T	I	A	F	I	N	Q	L	R	E	K	V	G	M	.	F	G	N	P	E	T	T	P	G	G	R	A	L	K	F	Y	A	232		
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consensus

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consensus

Sequence	Score
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DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEAAE...SKKDE...AAQVDS.VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGGRENAKNYLADHEDVEDEVRLKVRAAAGISDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQKKEKTIATYIAERPMEQEIRDRVMASAIRAGNAGEAPALAPAP...A...APE..A...AEA.....	363
DKKLGGGRENASKAFLKENPEIADEITKAIQNSMGIEMISGSEDDEGE.....E.....	343
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEPLE.....E.....ME.....	347
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEPLE.....E.....ME.....	347
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GERIGQKKRDNCREFLRENAELAREIENKVRHLGVTPM.GAVTLAAEEV...EE...D.....	352
GDKIGQKKANACKYLKENPEIAKTLKKLREMLLPENMQLIAETSSA..AD..DVE.....FGAVPEEF.....	354
GDKIGQKKANACKYLKENPEIAKTLKKLREMLLPENMQLIAETSSA..AD..DVE.....FGAVPEEF.....	354
GNKIGQKKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTAAHDETE...E...EPD..L...LES.....	349
GNKIGQKKNNVIRYFEENNQIAEIEIERNIREQLLTGTNGAVQI.EDE...E...EPD..L...LLES.....	349
GNKIGQKKANAACKYLAENPAIGAIEEKQIREKLLKAGAAAEAGKAAAA..EA...DAD...D...MADADAGY.....	355
GSKIGQKKANAACKYLENPEIQEIEQQIRAKLLVTSANTKATPVAE.....D...LADADI.....	347

logo

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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347

consensus

 non conserved
 similar
 ≥ 50% conserved