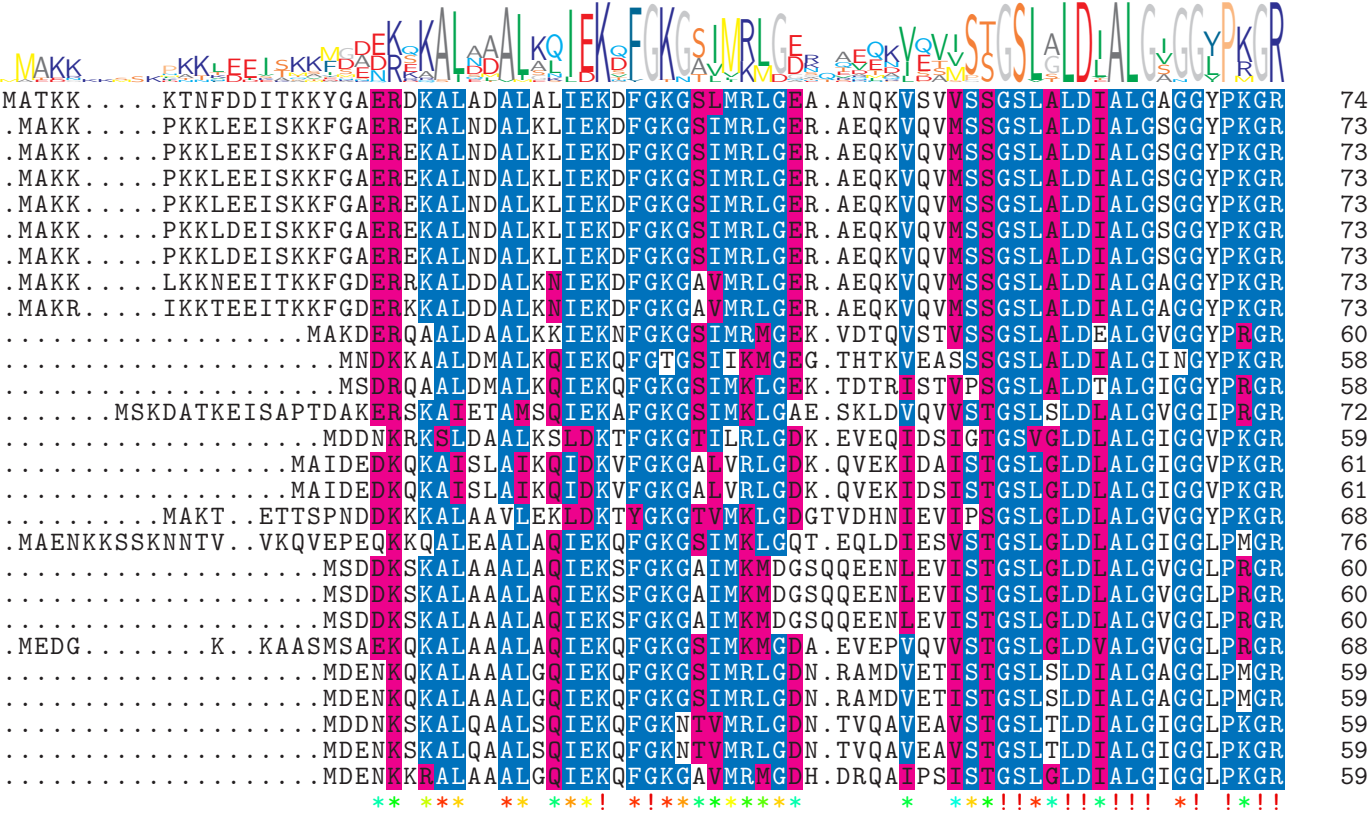


logo

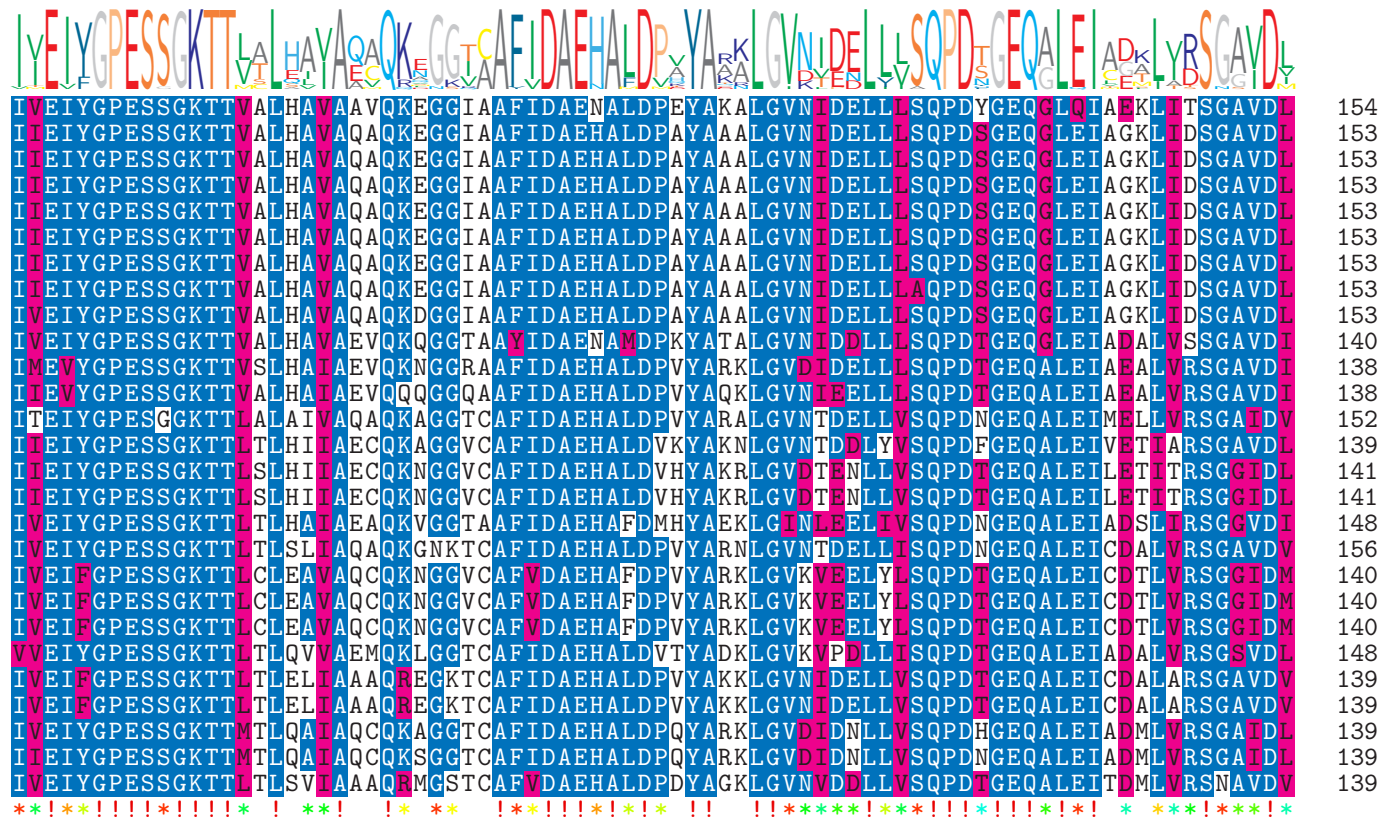
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consensus



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logo

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NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DVMGNKTKIKVVKNKVAPPFRTAEVDIMYEGEGISKEGEIIDLGTELDIVQKSGSWYSYE	292
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
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DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTEN... KKDE... PKKEEA..VNEEVPLDLGDE	381
DEKIGGGSSENAKKYLAHNPEIFDEIDHQVRVQFLIDGEEIAES... KKDE... AAQVDS..VNEEVTLDLGDE	377
DEKIGGGSSENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAES... KKDE... VAQVDS..VNEEVTLDLGDE	377
GEKIGGGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVA... SE... E... TDDLALDLNG	373
GEKIGGGSSENAKKFLADNPFIIDDHQRVQVGLIEEDNTEEKQSSK... EK... ETDEK..ADKNLVLELDDT	378
SERIGGGRNENAKNYLADHEDVEVRLKVRVAAAGISDVPEEDLPTTED... EQINILPDDSTEE	355
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EERLGGGRENAKIFLKENKIDMLMIQEIQIREHYGLDNGVVQQAAET... QEELEFEE	348
DERIGGQKEKTIAYIAIERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA	363
DKKLGQGRNSKAFLENPEIADBITKAIQNSMGIEGMI... SGSEDD..EGEE	343
DKKLGQGRNENAKALLKEDKALADEITLKIKESIGSNEEI... MPLPDE..PLEEME	347
DKKLGQGRNENAKALLKEDKALADEITLKIKESIGSNEEI... MPLPDE..PLEEME	347
DTKLGGGRDITVKELIKDNPELAEELEAKIREKLQAK	343
GTKIGGQKNNNAVKWLKENPEIADKLEQEIINTLASNPNS... VLKATASDSNDESDFVEEFSEE... EL	372
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI... TEGTQDETGDGER... PEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI... TEGTQDETGDGER... PEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI... TEGTQDETGDGER... PEE	348
GERIGGGRDNCREFLENARLEIENKVRHLGVTPMG... AVTLA.EEEVEE	352
GDKIGGQKANACKYLKENPEIAKTLDDKLREMLLNPNEM... QLIAETSSAADDFVEFGAVPEE... F	354
GDKIGGQKANACKYLKENPEIAKTLDDKLREMLLNPNEM... QLIAETSSAADDFVEFGAVPEE... F	354
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASD... QTAA.HDETEEEPDLL..ES	349
GNKIGGQKNNVIRYFEENNQIAEIEIERNIREQLLTTGTN... GAVQ.I.EDEEPEEPLL..LES	349
GSKIGGQKANAAKYLEENPEIQEIEQQIRAKLLVTSAN... TKATPVAEDLADADI	347

logo

		LEIELEE	
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NTDB id 269 KZH43 RS08665 WP 001085462.1	LEIEIEE		388
NTDB id 228 SPD RS09265 WP 001085462.1	LEIEIEE		388
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved