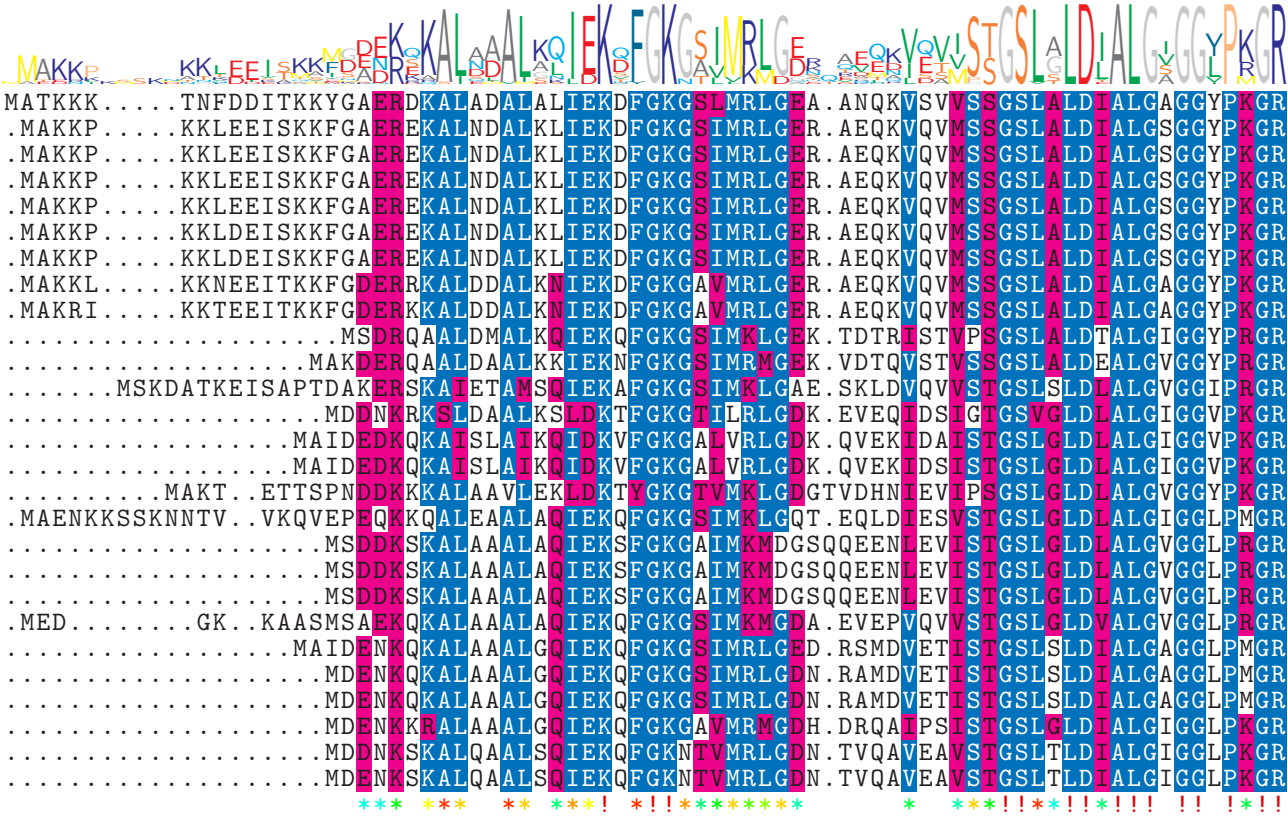


logo

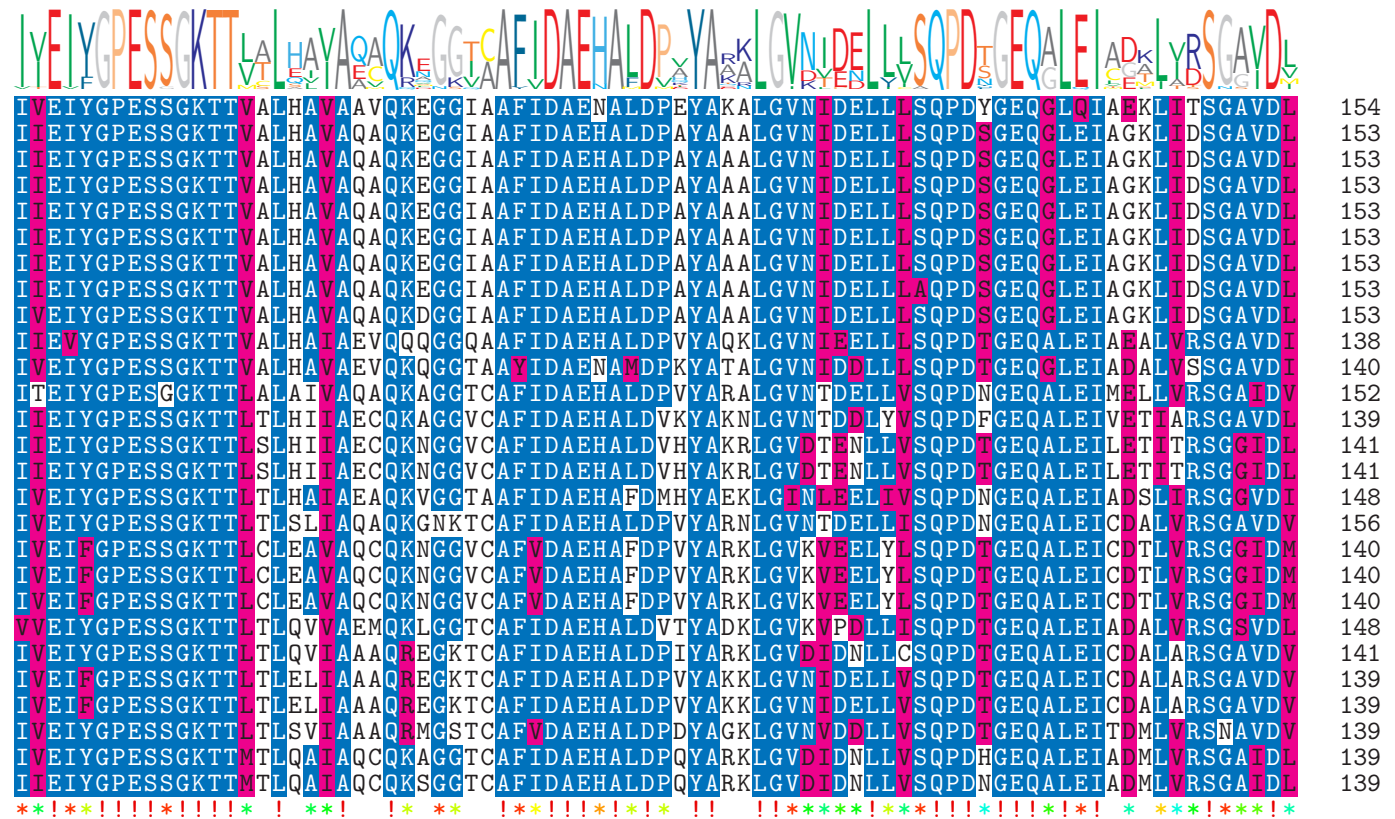
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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consensus

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consensus

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logo

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NTDB id 269 KZH43 RS08665 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311					
NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311					
NTDB id 194 SPR RS08825 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311					
NTDB id 159 SP RS09750 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311					
NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKAEAFVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311					
NTDB id 527 SMSK321 RS11065 WP 001085454.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKAEAFVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311					
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NTDB id 1313 DR RS12030 WP 010888966.1	SVRLDVRKIGQ....PTKVGND	AVANTVKIKTVKNKVAAPFKEVELALVY	GKGF	QLSDLVGL	AADMDI	IKKAGSFYSYG	307			
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NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KDGDEI	IGSETKVVKNKVAPPFR	EVQFDIMYEGEGISRMNELL	ILAEANG	FIKKSGAWFSYD	310				
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NTDB id 286251 C9E49 RS05820 WP 000963143.1	SVRLDIRRIGA....V.KEG	ENVVGS	ETRVKVVKNKIAAPFKQAEFQ	ILYGE	GINFY	GELVDL	GV	KEKLLIEKAGAWYSYK	295	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEG	DEIIG	SETKVVKNKMAPPFR	EA	IFQILYGK	GVN	QLGELVD	LAV	QQNIVQKAGAWYSYQ	293
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEG	DEIIG	SETKVVKNKMAPPFK	EA	IFQILYGK	GTN	QLGELVD	LAV	QQDIVQKAGAWYSYQ	293
consensus	*!!**!* *	*	**	*****!*****!*****!*	*	*****!*!*****	*****	***	! !*****!	

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGSENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQFGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGGGRENAAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRVQFGLSDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEKTIATIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKLGGGRENKAFLENPEIADIEITKATINSMGTIEGM.....ISGSEDDEG.....EE.....	343
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK.....	343
GTKIGQGKNNNAVKWLKENPEIADKLEQIRNTLASNPN....SVLKATASDSN...DESQVEEFSEEL	372
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GERIGGGRDNCREFLRNAAELAREIENKVRHLGVTPM.....GAVTLAEE.VE...ED.....	352
GEKIGGQKANATAWLKDNPETAKIEKKVRELLNSNP....STPDFSV...D..DSEGVATNEDF	353
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA...DDVEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA...DDVEFGAVPEEF	354
GSKIGGQKANAAKYLEENPEIGQIEEQIRAKLLVTSA....NTKATPVAEDL...ADADI.....	347
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKAS....DQTAA.HDETE...EEDPLLLES	349
GNKIGGQKNNVIRIFYENNQIAEIERNIEREQLLTGT....NGAVQ.I.EDE...EEDPLLLES	349

logo

		IEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...		387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE		388
NTDB id 228 SPD RS09265 WP 001085462.1	IEE		388
NTDB id 194 SPR RS08825 WP 001085462.1	IEE		388
NTDB id 159 SP RS09750 WP 001085462.1	IEE		388
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE		384
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE		384
NTDB id 453 Spy49 1753c ACI62003.1	D..		378
NTDB id 408 SMU RS09530 WP 002262392.1	D..		383
NTDB id 115 BSU 16940 NP 389576.2	...		348
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	...		354
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...		349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
consensus			

- X non conserved
- X similar
- X ≥ 50% conserved