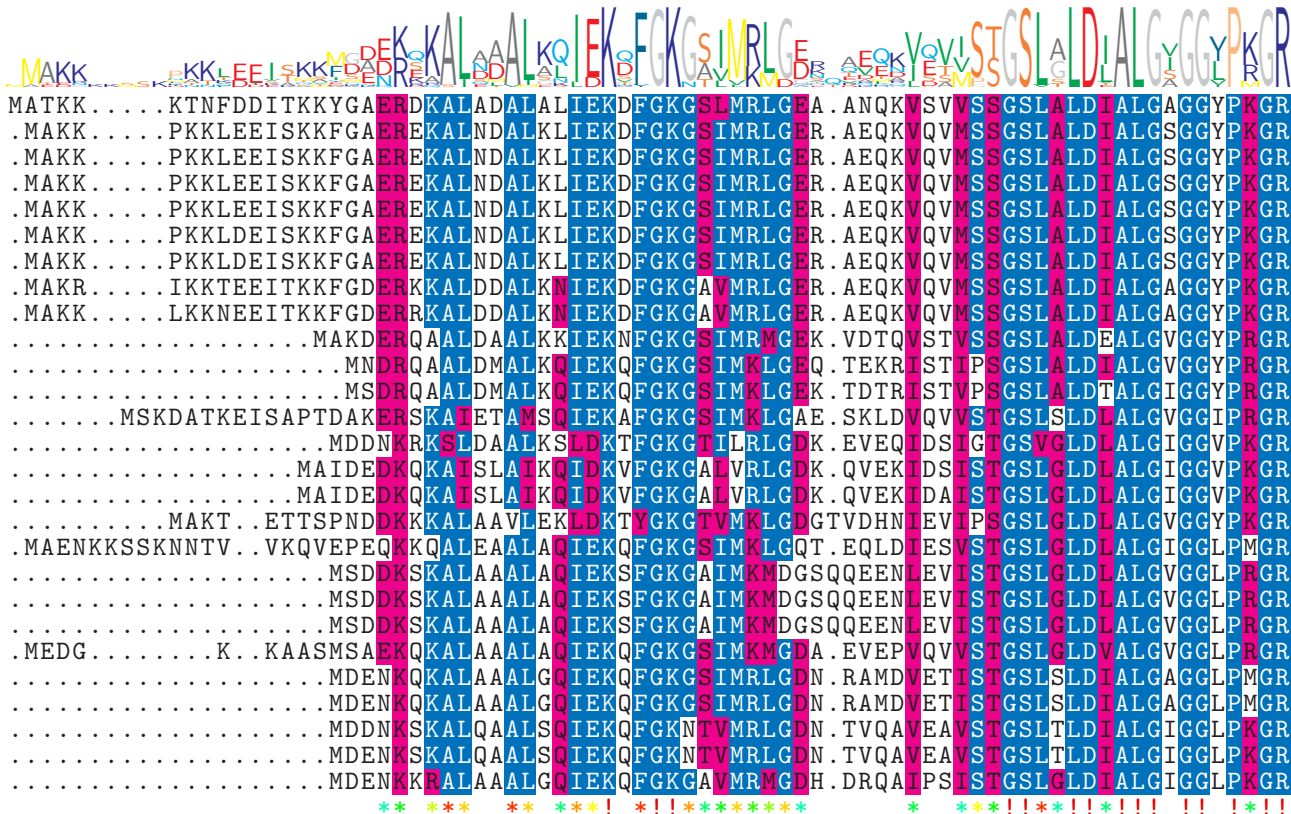


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consensus



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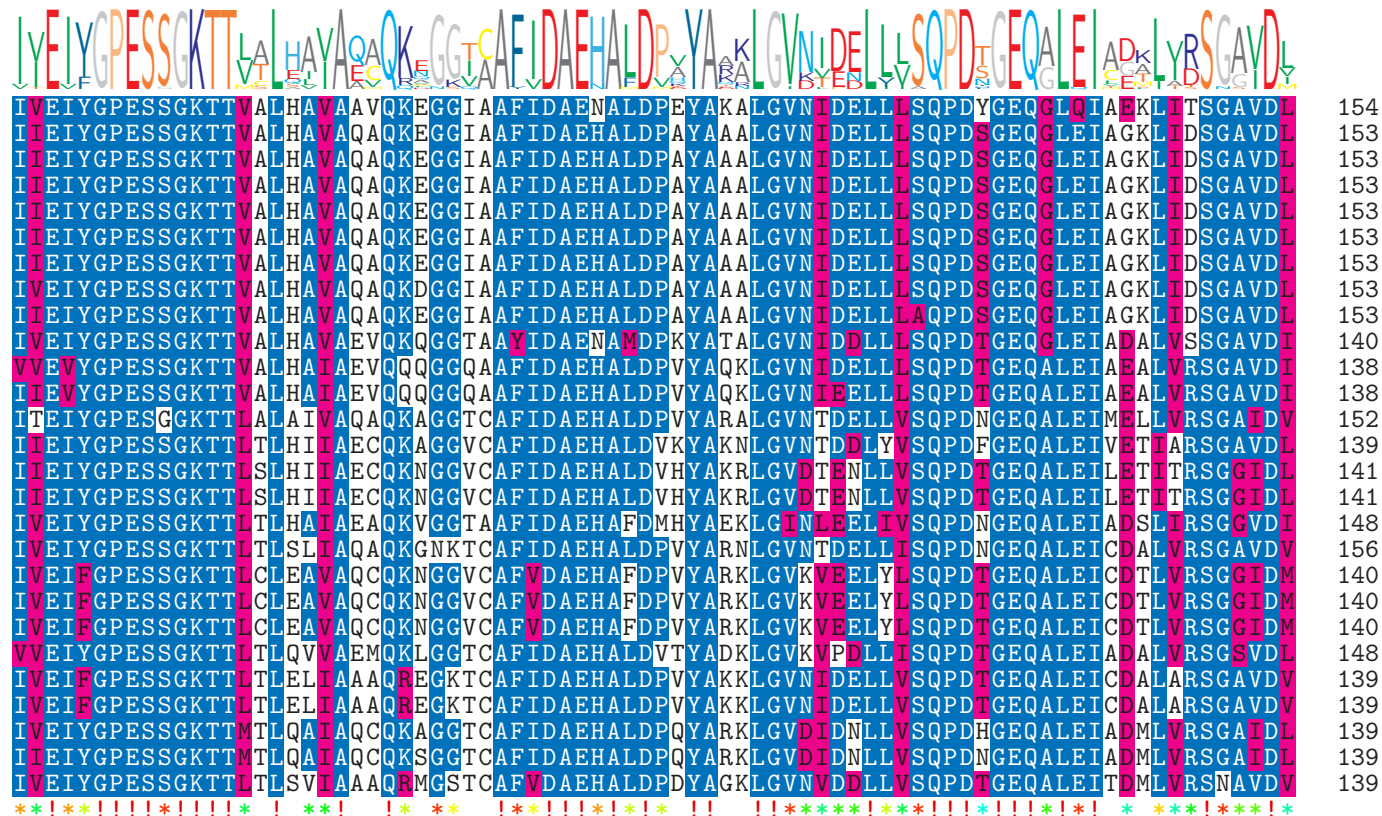
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consensus



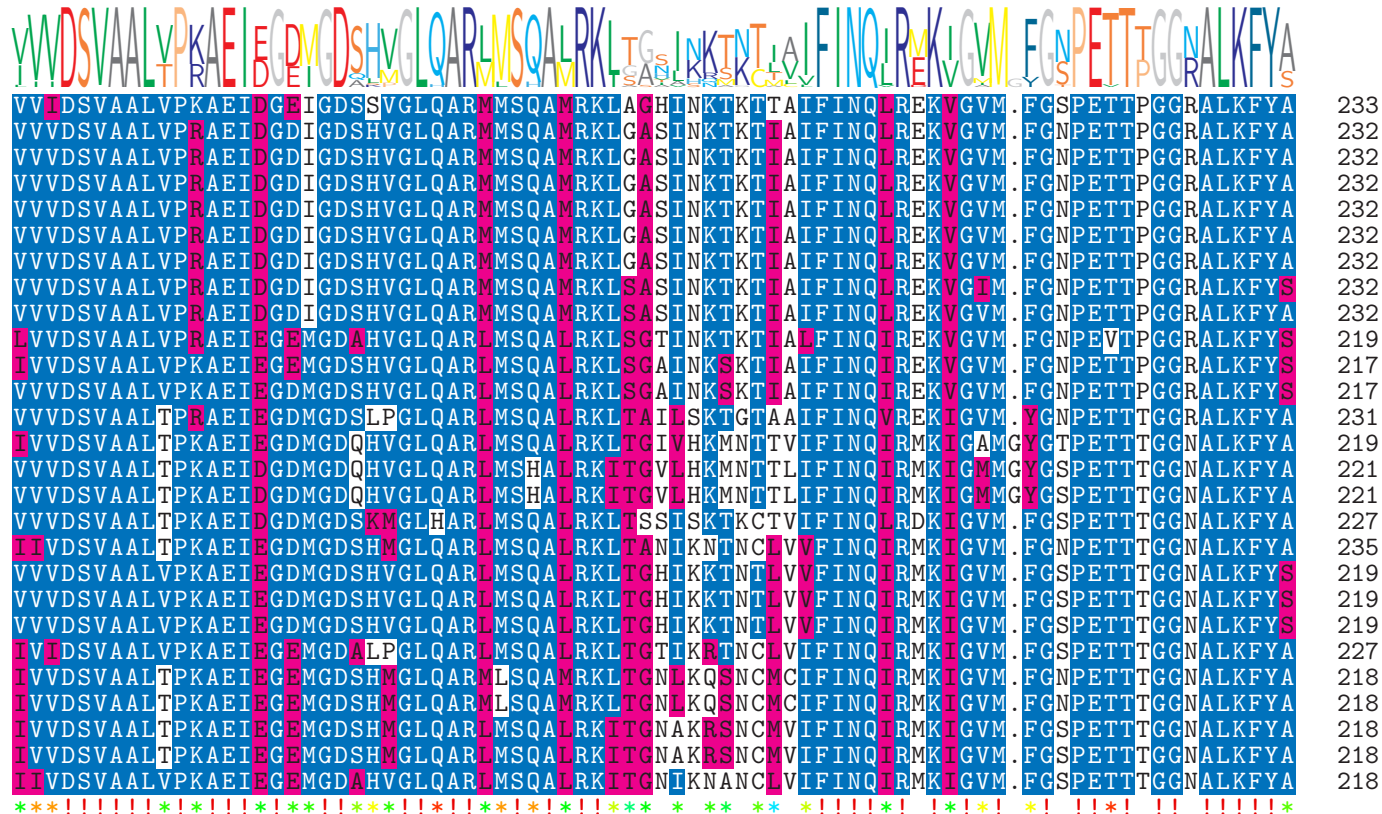
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NTDB id 1205 PSJ3M300 05545 AFN77183.1

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consensus



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NTDB id	600	KW2	RS01765	WP	011675413.1	SVRLDVRGSTKIEEGS.GDNKTQ	IGKITKI	KVVKNKVAPPFKV	ALVDIMF	GEGISSTGEL	LNI	AEEGTIKKS	GAWFAYN	312
NTDB id	269	KZH43	RS08665	WP	001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKI	KVVKNKVAPPFKAEAVV	EIMY	GEGISXTGEL	LKIASDLDI	IKKAGAWYSYK	311	
NTDB id	228	SPD	RS09265	WP	001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKI	KVVKNKVAPPFKAEAVV	EIMY	GEGISXTGEL	LKIASDLDI	IKKAGAWYSYK	311	
NTDB id	194	SPR	RS08825	WP	001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKI	KVVKNKVAPPFKAEAVV	EIMY	GEGISXTGEL	LKIASDLDI	IKKAGAWYSYK	311	
NTDB id	159	SP	RS09750	WP	001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKI	KVVKNKVAPPFKAEAVV	EIMY	GEGISXTGEL	LKIASDLDI	IKKAGAWYSYK	311	
NTDB id	527	SMSK321	RS11065	WP	001085454.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKI	KVVKNKVAPPFKAEAFV	EIMY	GEGISXTGEL	LKIASDLDI	IKKAGAWYSYK	311	
NTDB id	499	SM12261	RS08315	WP	078228268.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKI	KVVKNKVAPPFKAEAFV	EIMY	GEGISXTGEL	LKIASDLDI	IKKAGAWYSYK	311	
NTDB id	408	SMU	RS09530	WP	002262392.1	SVRLDVRGNTQIKGTG.EQKDSN	IGKETKI	KVVKNKVAPPFKAEAFV	EIIY	GEGISRRTGEL	VKIASDLGI	IQQAGAWYSYN	311	
NTDB id	453	Spy49	1753c	ACI62003.1	SVRLDVRGTTQIKGTG.DQKDSS	IGKETKI	KVVKNKVAPPFKVAEVE	EIMY	GEGISRRTGEL	VKIASDLDI	IQQAGAWFSYN	311		
NTDB id	625	LCA	RS02525	WP	011374196.1	TVRLEVRRAETIKNGT.....DI	GNRRARI	KVVKNKVAPPFKVAEVD	IMYG	QGISRTEGEL	VDMAVEKDI	INKSGSWSYG	294	
NTDB id	1007343	BACILLUS	RS22150	WP	013058804.1	SVRLEVRRAEQLKQGN.....DI	VGNKTRI	KVVKNKVAPPFRFAEVD	DIMY	GEGISKEGEIT	LDIASELDIV	QKSGSWYSYN	292	
NTDB id	115	BSU	16940	NP	389576.2	SVRLEVRRAEQLKQGN.....DV	MGNKTKI	KVVKNKVAPPFRFAEVD	DIMY	GEGISKEGEIT	IDLGTELIDIV	QKSGSWYSYE	292	
NTDB id	1313	DR	RS12030	WP	010888966.1	SVRLDVRKIGQ....PTKVGND	AVANTVKIK	TVKNKVAAPFKEVELA	LVY	GKGCFDQLSDIV	GLAADMDI	IKKAGCSFYSG	307	
NTDB id	1245	Cj1673c	YP	002345041.1	SVRLDVRKVAT....L.KQN	EEP	IGNRVKV	KVVKNKVAPPFRQA	AEFDVM	FGEGLSREGEL	IDYGVKL	DIVDKSGAWFSYK	294	
NTDB id	1211	C694	RS00795	WP	000963128.1	SVRIDIRRIAS....L.KQNEQH	IGNRAKA	KVVKNKVAPPFRFAEAFD	DMF	GEGISKEGEIT	IDYGVKL	DIVDKSGAWLSYK	296	
NTDB id	1214	NCTC11637	00359	SQJ03206.1	SVRIDIRRIAA....L.KQNEQH	IGNRAKA	KVVKNKVAPPFRFAEAFD	DMF	GEGISKEGEIT	IDYGVKL	DIVDKSGAWLSYQ	296		
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NTDB id	1389	A4U84	RS07560	WP	021112712.1	SVRLDIRRCGV....V.KDGDEI	IGSETKV	KVVKNKVAPPFRREVQFD	DIMY	GEGISMNEL	LILAEANGFI	KKSGAWFSYD	310	
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NTDB id	1427	RZ	RS02760	WP	011000510.1	SVRLDIRRIGS....I.KKGEV	VGNETKV	KVVKNKVAPPFRFAEIFD	DILY	GAGVSREGEIT	LDLGV	EAKVVEKSGAWYSYN	302	
NTDB id	1165	A1552VC	RS01565	WP	000344154.1	SVRLDIRRTGA....I.KEGEEV	VGNETRI	KVVKNKIAAPFKEANTQ	IMYG	QGFNRREGEL	IDLG	VKHKMVEKSGAWYSYN	293	
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NTDB id	1074	ABD1	RS10195	WP	000344167.1	SVRLDIRRIGQ....V.KEGDEI	IGSETKV	KVVKNKMAPPFRFAEIFQ	ILY	GKGVNLGEL	VDLAVQQN	IVQKAGAWYSYQ	293	
NTDB id	1205	PSJM300	O5545	AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETRV	KVVKNKVAPPFRQA	AEFDILY	GKGIYRN	GEITDL	GVQQGLVEK	SGAWYAYK	293	
consensus						* ! *** *	*	**	***** ** ** * *					

logo

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consensus

Sequence	Score
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DEKIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE...NKKDE...PKKEEA..VNEEVPLDLGDE	381
DEKIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE...NKKDE...PKKEEA..VNEEVPLDLGDE	381
DEKIGGQSENAKKYLAHNPEVFAEIDHQVRVQFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVPLDLGDE	377
DEKIGGQSENAKKYLAHNPEIFDEIDHQVRVQFGLIDGEEIAE...SKKDE...AAQVDS..VNEEVPLDLGDE	377
GEKIGGQSENAKKFLADNPEIFDDIDHKVRVQFGLIEEDNTEEEKQSS...KEK...ETDEK..ADKNLVLELDDT	378
GEKIGGQSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAV...ASE...E...TDDLALDLNG	373
SERIGGQRENAKNYLADHEDVEDEVRLKVRVQFGLSDVPEEDLPTTE...DEQINILPDDSTEE...DEQINILPDDSTEE	355
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EERLGGQRENAKKFLKENTDIRQETIAGQVREHHGLDQDGPEAPE.DD...D.QGDLNI	345
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DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI...MPLPDE..PLEEME	347
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GDKIGGQKANACKYLKENPEIAKTLDDKRLREMLLNPNEM...QLIAETSSAADVEFGAVPEE...F	354
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logo

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NTDB id 269 KZH43 RS08665 WP 001085462.1	LEIEIEE	388
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NTDB id 1022 ACIAD RS06390 WP 004925639.1		349
NTDB id 1074 ABD1 RS10195 WP 000344167.1		349
NTDB id 1205 PSJM300 05545 AFN77183.1		347

consensus

-  non conserved
-  similar
-  ≥ 50% conserved