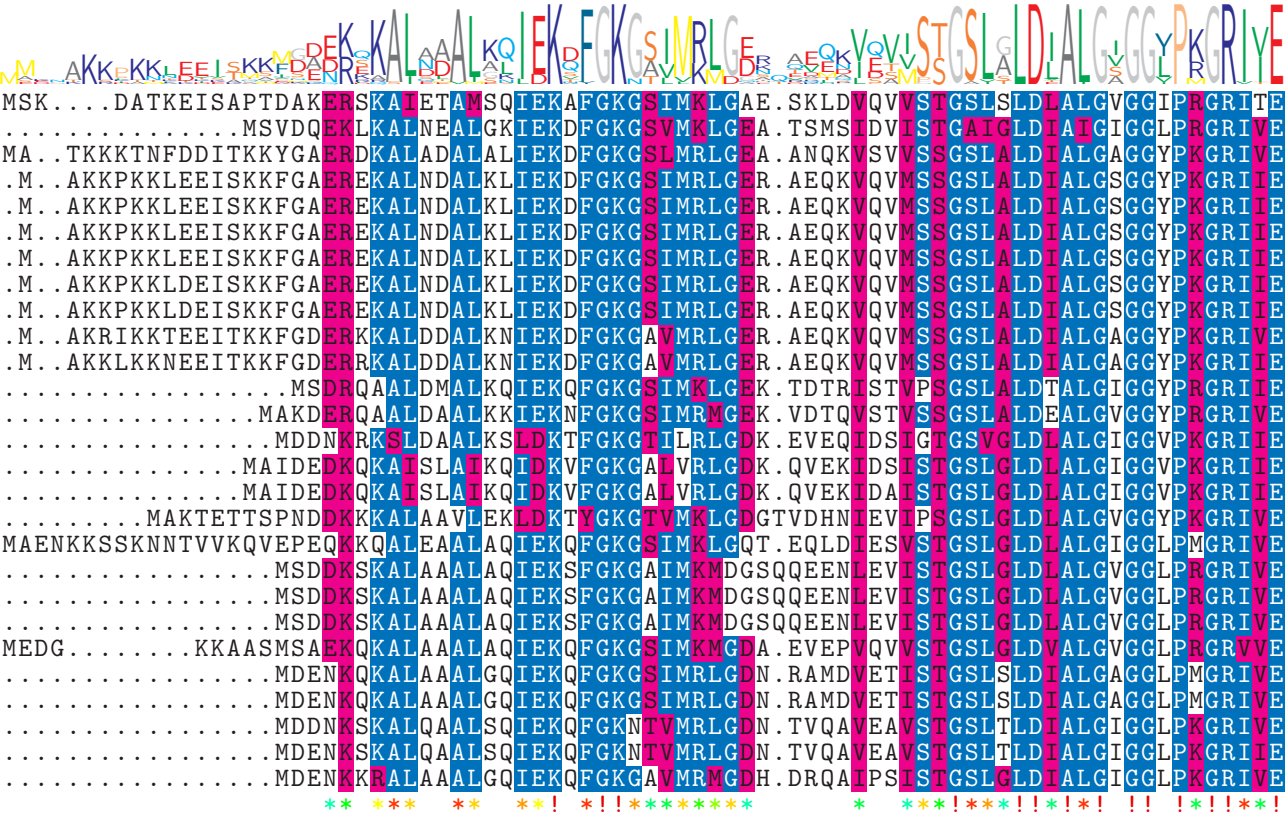


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NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
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NTDB id 159 SP RS09750 WP 001085462.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus



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logo

NTDB id 1313 DR RS12030 WP 010888966.1	IYGPESGGKTTALAI	155
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NTDB id 600 KW2 RS01765 WP 011675413.1	IYGPESGKTTVALHAVA	157
NTDB id 269 KZH43 RS08665 WP 001085462.1	IYGPESGKTTVALHAVA	156
NTDB id 228 SPD RS09265 WP 001085462.1	IYGPESGKTTVALHAVA	156
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NTDB id 1205 PSJM300 05545 AFN77183.1	IYGPESGKTTTLTSVI	142
consensus	***!!!!*!!!!* ! **! !* ** !*!!!!*!*!* !! !!*****!*****!!*!!!!*!*! * *****!*****	

logo

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consensus

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logo

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NTDB	id	185824	CDIF	29629	RS06965	WP	003428218.1	LDVRKIDT	TIKQGD	KV	IGSR	TRV	KVV	KNK	VAPP	FKQ	AEFD	IMY	GEGIS	KIGD	LLDIA	ADV	DI	VKK	SGS	WYSY	NDT	K	298																	
NTDB	id	600	KW2	RS01765	WP	011675413.1	LDVRGSTK	IEEGS	.GDN	KTK	IGKIT	IK	KVV	KNK	VAPP	FKVAL	VDIM	F	GEGIS	SST	GEL	LNIA	VEEG	IKK	SGA	WFA	YNDE	K	315																	
NTDB	id	269	KZH43	RS08665	WP	001085462.1	LDVRGNTQ	IKGTG	.DQK	ETN	VGKET	K	KVV	KNK	VAPP	FK	EA	VVEIM	Y	GEGIS	K	TGEL	LK	IAS	DL	DI	IKK	AGAW	YSY	KDE	K	314														
NTDB	id	228	SPD	RS09265	WP	001085462.1	LDVRGNTQ	IKGTG	.DQK	ETN	VGKET	K	KVV	KNK	VAPP	FK	EA	VVEIM	Y	GEGIS	K	TGEL	LK	IAS	DL	DI	IKK	AGAW	YSY	KDE	K	314														
NTDB	id	194	SPR	RS08825	WP	001085462.1	LDVRGNTQ	IKGTG	.DQK	ETN	VGKET	K	KVV	KNK	VAPP	FK	EA	VVEIM	Y	GEGIS	K	TGEL	LK	IAS	DL	DI	IKK	AGAW	YSY	KDE	K	314														
NTDB	id	159	SP	RS09750	WP	001085462.1	LDVRGNTQ	IKGTG	.DQK	ETN	VGKET	K	KVV	KNK	VAPP	FK	EA	VVEIM	Y	GEGIS	K	TGEL	LK	IAS	DL	DI	IKK	AGAW	YSY	KDE	K	314														
NTDB	id	527	SMSK321	RS11065	WP	001085454.1	LDVRGSTQ	IKGTG	.DQK	DTN	VGKET	K	KVV	KNK	VAPP	FK	EA	FVEIM	Y	GEGIS	K	TGEL	LK	IAS	DL	DI	IKK	AGAW	YSY	KDE	K	314														
NTDB	id	499	SM12261	RS08315	WP	078228268.1	LDVRGSTQ	IKGTG	.DQK	DTN	VGKET	K	KVV	KNK	VAPP	FK	EA	FVEIM	Y	GEGIS	K	TGEL	LK	IAS	DL	DI	IKK	AGAW	YSY	KDE	K	314														
NTDB	id	408	SMU	RS09530	WP	002262392.1	LDVRGNTQ	IKGTG	.EQK	DSN	IGKET	K	KVV	KNK	VAPP	FK	EA	FVEIM	Y	GEGIS	R	TGEL	VK	IAS	DL	GI	IKK	AGAW	YSY	NGEK	K	314														
NTDB	id	453	Spy49	1753c	ACI62003.1	LDVRGTTQ	IKGTG	.DQK	DSS	IGKET	K	KVV	KNK	VAPP	FK	VA	AEV	EIM	Y	GEGIS	R	TGEL	VK	IAS	DL	DI	IKK	AGAW	F	SYNGEK	K	314														
NTDB	id	115	BSU	16940	NP	389576.2	LEVRR	AEQLKQGN	DV	MGN	TKT	K	KVV	KNK	VAPP	FR	TAEV	DIM	Y	GEGIS	K	EGE	I	D	LG	TEL	DI	V	QK	SGS	WYSY	EEER	295													
NTDB	id	625	LCA	RS02525	WP	011374196.1	LEVRR	AETIKNGT	DM	IGN	RA	R	K	V	V	KNK	VAPP	FK	VA	AEV	DIM	Y	Q	GIS	R	TGEL	V	D	MA	VEK	D	I	NK	SGS	WYSY	GSER	297									
NTDB	id	1245	Cj1673c	YP	002345041.1	LDVRKVAT	L.KQN	E	E	PNR	V	K	V	V	KNK	VAPP	FR	QAEF	D	V	F	GEGIS	R	E	GEL	I	D	Y	G	V	K	L	D	I	V	D	K	SGA	W	F	SY	KD	K	297		
NTDB	id	1211	C694	RS00795	WP	000963128.1	IDIRRIA	L.KQN	E	Q	H	GN	R	A	K	V	V	KNK	VAPP	FR	AEF	D	I	F	GEGIS	K	EGE	I	D	Y	G	V	K	L	D	I	V	D	K	SGA	W	L	SY	QD	K	299
NTDB	id	1214	NCTC11637	00359	SQJ03206.1	IDIRRIA	L.KQN	E	Q	H	GN	R	A	K	V	V	KNK	VAPP	FR	AEF	D	I	F	GEGIS	K	EGE	I	D	Y	G	V	K	L	D	I	V	D	K	SGA	W	L	SY	QD	K	299	
NTDB	id	1334	RAOC	RS04870	WP	004918236.1	IDIRRLSD	TGKIKD	KS	GEV	IGN	R	T	K	V	V	KNK	VAPP	FR	QAEF	D																									

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NTDB id 1313 DR RS12030 WP 010888966.1
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NTDB id 1142 GTF74 RS11550 WP 000344154.1
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consensus

Sequence	Score
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IGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLLIDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIEIEE	388
IGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLLIDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIEIEE	388
IGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLLIDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIEIEE	388
IGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLLIDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIEIEE	388
IGQGSSENAKKYLAENPEYFAETIDHQVRVQFGLIDGEEAAE SKKDE VAQVDS . . VNEEVTLDLGDELEIEIEE	384
IGQGSSENAKKYLAENPEIFDEIDHQVRVQFGLIDGEEIAE SKKDE AAQVDS . . VNEEVTLDLGDELEIEIEE	384
IGQGSSENAKKELADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . ADKNLVLELDDTIELED . .	383
IGQGSSENAKRYLAHPQIFDEIDRKVRVKFGLLEEESEESAMAVASE E TDDLALDLNNGIEIED . .	378
LGQGRENAKQFLKNDIMLMIQEQIREHYGLDNGVQVQQAAETQFEL . E . E . E .	348
IGQGRENAKKNYLADHEDVEDEVLKVRAAAYGSDVPEEDLPTTEDE . QI . NILPDDST EE	355
LGQGRENSKAFIKENPETIADETTKAIQNSMCIEGMISGSEDD . . EGEE	343
LGQGRENAKAILKEDKALADEITLKIKESIGSNEEIMPLPDE . . PLEEM . E	347
LGQGRENAKAILKEDKALADEITLKIKESIGSNEEIMPLPDE . . PLEEM . E	347
LGQGRDITVKELIKDNPELAEELEAKIREKLQAK	343
IGQCKNNVAKVILKENPETIADKLEQEIIRNTLASNPNSVLKATASDSND . ES . DVEEF SEEEL	372
IGQCKDNVRVVLKENPEISDEIDAKIRALNGVEMHITEGTQDETDGER PEE	348
IGQCKDNVRVVLKENPEISDEIDAKIRALNGVEMHITEGTQDETDGER PEE	348
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IGQCKANACKYILKENPETIAKTLDDKKIREMLLNPNMQLIAETSSAADV . EFGAV PEEF	354
IGQCKNNVIRVYLEENPQISTEIEAVIREQLLTKASDQTAA . HDETEEE . P . DLL ES	349
IGQCKNNVIRVFEENNQIAEIERMIREQLLTTGTNGAVQ . I . EDEEE . P . DLL LES	349
IGQCKANAAKYLEENPEIQQIEQIRAKLLVTSANTKATPVAEDLADA . DI	347

- X non conserved
- X similar
- X $\geq 50\%$ conserved