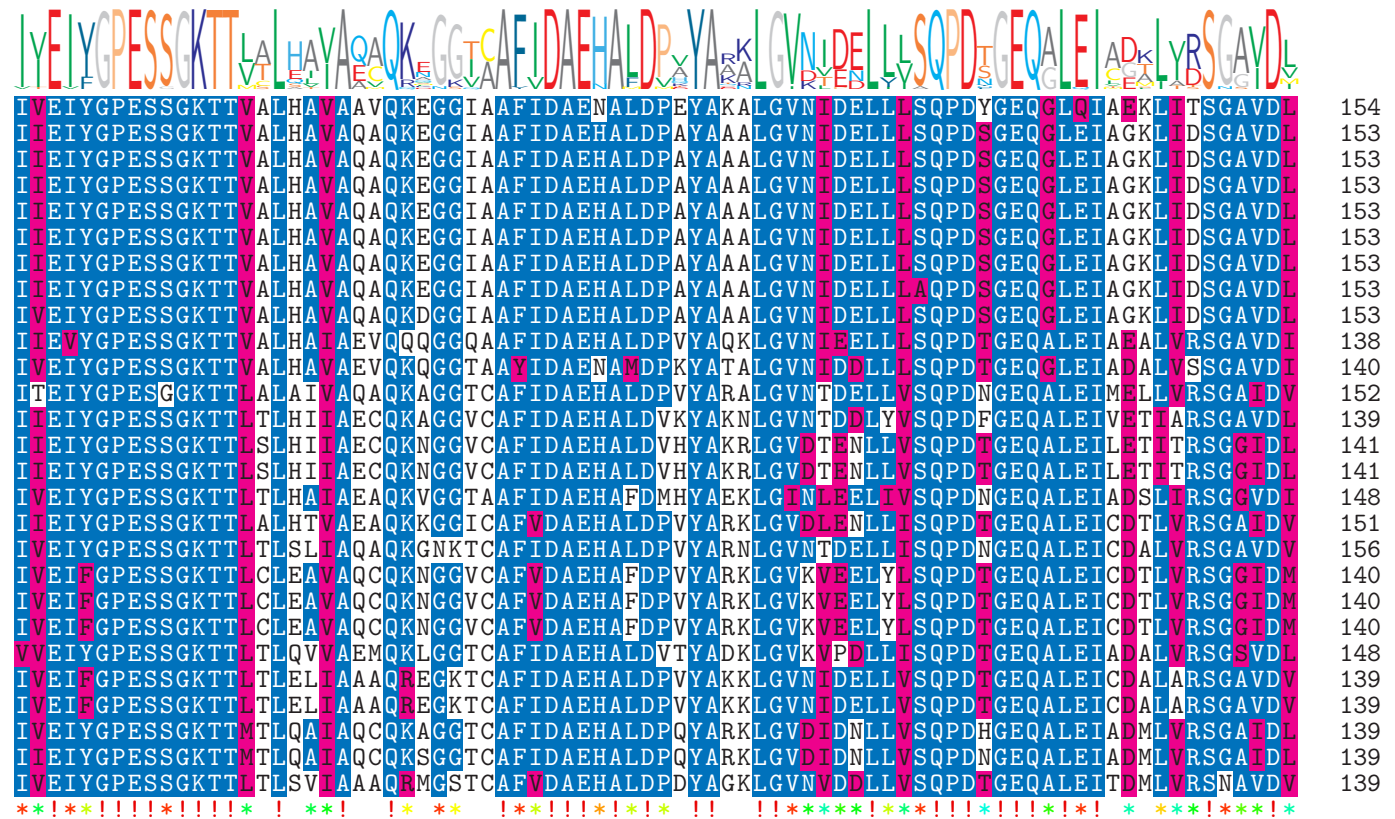


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NTDB	id	269	KZH43	RS08665	WP	001085462.1	MAKKPKKLEEISKKFGA	EREKALND	ALKL	IEKDFGKG	SIMRLGER	.AEQKV	QVM	MSSGSL	ALD	IALGS	GGYP	PKGR	73					
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NTDB	id	194	SPR	RS08825	WP	001085462.1	MAKKPKKLEEISKKFGA	EREKALND	ALKL	IEKDFGKG	SIMRLGER	.AEQKV	QVM	MSSGSL	ALD	IALGS	GGYP	PKGR	73					
NTDB	id	159	SP	RS09750	WP	001085462.1	MAKKPKKLEEISKKFGA	EREKALND	ALKL	IEKDFGKG	SIMRLGER	.AEQKV	QVM	MSSGSL	ALD	IALGS	GGYP	PKGR	73					
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NTDB	id	499	SM12261	RS08315	WP	078228268.1	MAKKPKKLDEISKKFGA	EREKALND	ALKL	IEKDFGKG	SIMRLGER	.AEQKV	QVM	MSSGSL	ALD	IALGS	GGYP	PKGR	73					
NTDB	id	453	Spy49	1753c	ACI62003.1		MAKKLKKNEEITKKFGD	ERRKALDD	ALKN	IEKDFGKG	AVMRLGER	.AEQKV	QVM	MSSGSL	ALD	IALG	AGGY	PKGR	73					
NTDB	id	408	SMU	RS09530	WP	002263292.1	MAKRIKKTTEEITKKFGD	ERRKALDD	ALKN	IEKDFGKG	AVMRLGER	.AEQKV	QVM	MSSGSL	ALD	IALG	AGGY	PKGR	73					
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NTDB	id	1214	NCTC11637	00359	SQJ03206.1				M..AIDE	DKQKAT	ISLAIKQID	KVFGKGA	LVRL	GDK	.QVEK	IDA	ISTGSL	GLDL	ALGI	GGVPKGR		61		
NTDB	id	1334	RAOC	RS04870	WP	004918236.1			MA...K.TETT	.SPND	DKKKALAA	AVLEK	LDKTYGKT	TVMK	LGDTVDHN	IEV	IP	SGSL	GLDL	ALGV	GGYPKGR		68	
NTDB	id	322989	EB815	RS24240	WP	013895892.1			MAQNSL	.RLVE..DKAV	DKSKALDA	ALSQIERA	FGKGSIMRL	GA	NEQVVE	IET	VPT	SGSL	GLDL	IALGV	GGLPRGR		71	
NTDB	id	1389	A4U84	RS07560	WP	021112712.1			MAENKKSSKNNT	.VVKQ..VEPEQ	KKQALEA	ALAQIEKQ	FGKGSIMKL	GQT	.EQLD	IES	V	STGSL	GLDL	ALGI	GGLPMGR		76	
NTDB	id	1130	NGFG	RS03960	WP	003688695.1				MSD	DKSKALAA	ALAQIEKS	FGKGA	IMKMD	GSQ	QEEN	LEV	IST	SGSL	GLDL	ALGV	GGLPRGR		60
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NTDB	id	1427	RS	RS02760	WP	011000510.1			MEDG.....KKA	.SMSA	EKQKALAA	ALAQIEKQ	FGKGSIMK	MGDA	.EVEP	VQV	V	STGSL	GLD	VALGV	GGLPRGR		68	
NTDB	id	1165	A1552VC	RS01565	WP	000344154.1				MDEN	KQKALAA	ALGQIEKQ	FGKGSIMRL	GDN	.RAMD	VET								

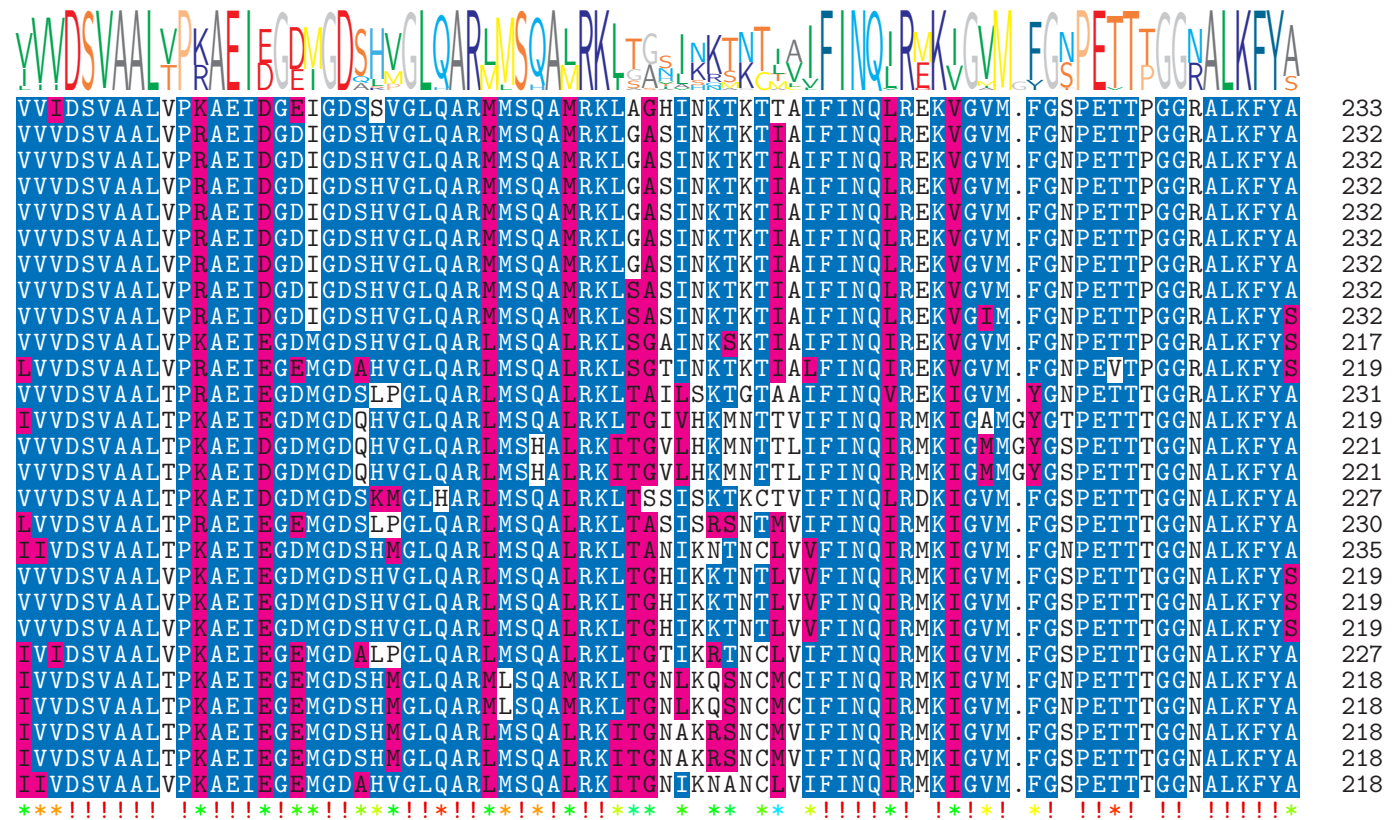
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NTDB id 499 SM12261 RS08315 WP 078228268.1
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NTDB id 625 LCA RS02525 WP 011374196.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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consensus



logo

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NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTNVGKETKIKVVKNKVAPPFKAEAFVEIMYEGEGISKTGELLKIASDLDIKKAGAWYSYK	311
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consensus

 non conserved
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 ≥ 50% conserved