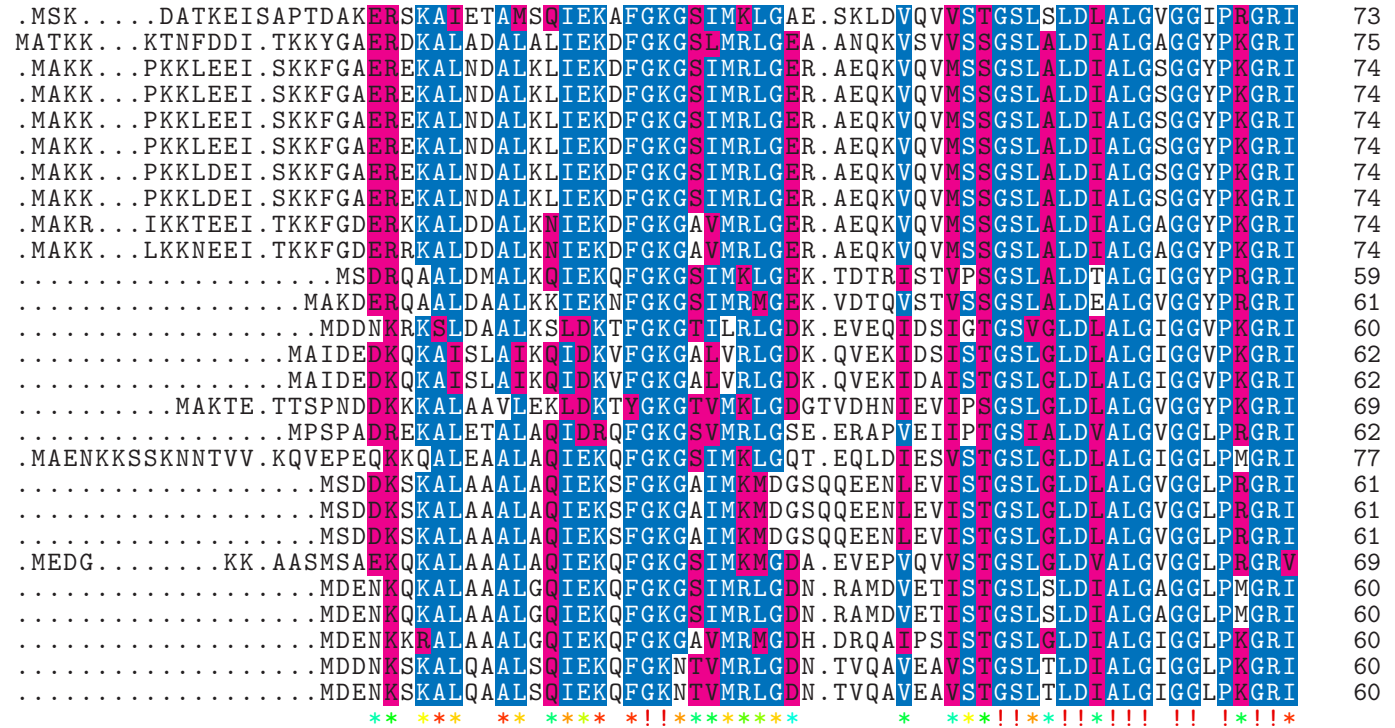


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consensus

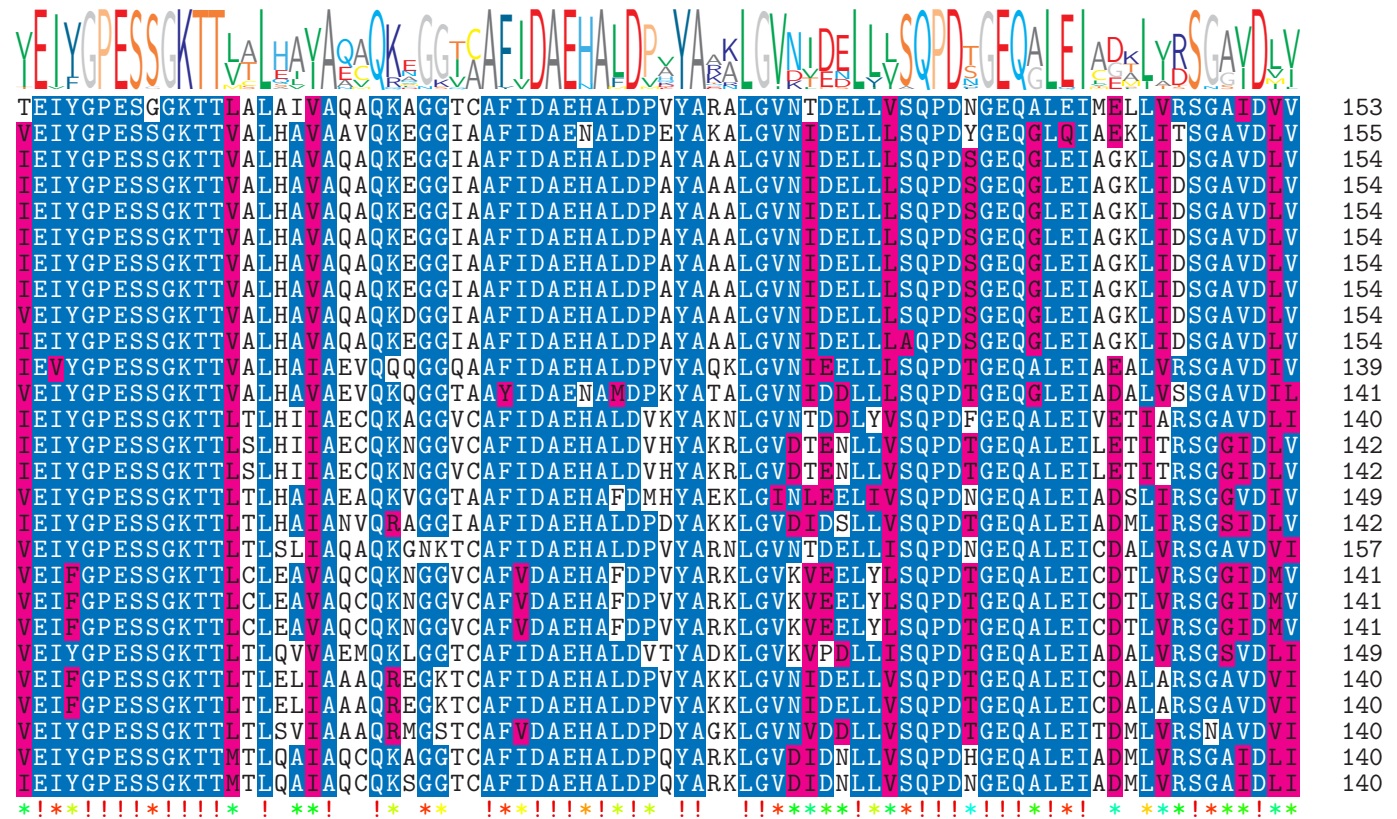
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consensus

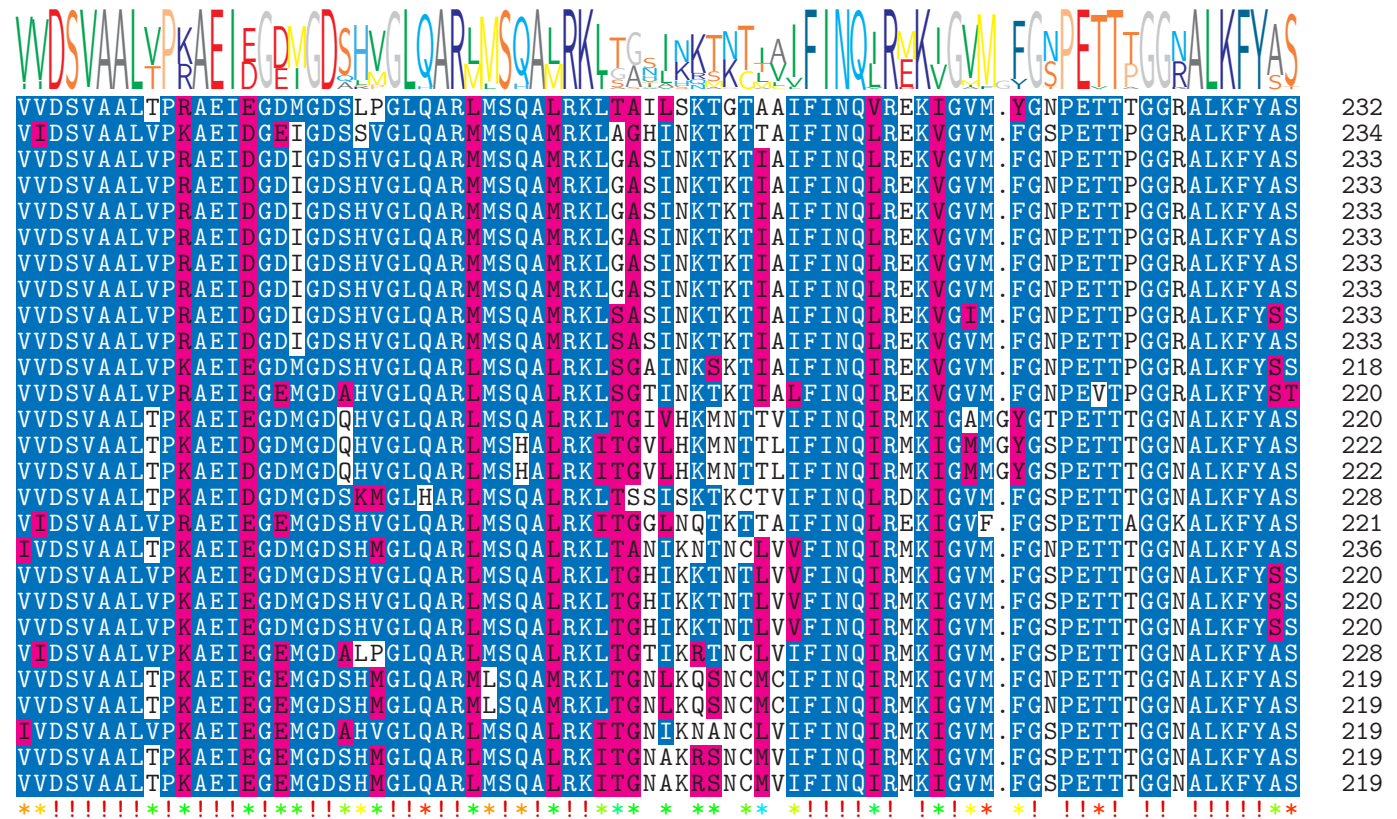
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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logo

NTDB id 1313 DR RS12030 WP 010888966.1	VRLDVRKIGQ...PTKVGND	AVANTV	KIKTVKNKV	AAPFKE	VELAL	IVYGK	GFDQLS	DLVGL	AADM	DI	TKKAGS	FFSY	SGD	308				
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NTDB id 269 KZH43 RS08665 WP 001085462.1	VRLDVRGNTQIKGTG.DQKET	NVGKET	KIKVVKNKV	VAPPFK	EAVVE	IMYG	EGIS	KTGELL	KI	ASDL	DI	TKKAGA	WYSY	KD	312			
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NTDB id 194 SPR RS08825 WP 001085462.1	VRLDVRGNTQIKGTG.DQKET	NVGKET	KIKVVKNKV	VAPPFK	EAVVE	IMYG	EGIS	KTGELL	KI	ASDL	DI	TKKAGA	WYSY	KD	312			
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NTDB id 408 SMU RS09530 WP 002262392.1	VRLDVRGNTQIKGTG.EQKDS	NIGKET	KIKVVKNKV	VAPPFK	EAFVE	IIYG	EGIS	RTGELV	KI	ASDL	GI	IQKAGA	WYSY	NG	312			
NTDB id 453 Spy49 1753c ACI62003.1	VRLDVRGTTQIKGTG.DQKDS	SIGKET	KIKVVKNKV	VAPPFK	VAEVE	IMYG	EGIS	RTGELV	KI	ASDL	DI	IQKAGA	WFSY	NG	312			
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NTDB id 625 LCA RS02525 WP 011374196.1	VRLEVRRAETIKNGT.....	DMIGN	RAIKIKVVKNKV	VAPPFK	VAEVD	IMYG	GGIS	RTGELV	DM	AVEKD	IT	NKSG	SWYS	YGS	295			
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NTDB id 1211 C694 RS00795 WP 000963128.1	VRIDIRRIAS....L.KQNE	QHIGN	RAKIKVVKNKV	VAPPFR	EAEFD	IMFG	EGIS	KEGEI	ID	YGVK	L	DIV	DKSG	AWLSY	QD	297		
NTDB id 1214 NCTC11637 00359 SQJ03206.1	VRIDIRRIAA....L.KQNE	QHIGN	RAKIKVVKNKV	VAPPFR	EAEFD	IMFG	EGIS	KEGEI	ID	YGVK	L	DIV	DKSG	AWLSY	QD	297		
NTDB id 1334 RAOC RS04870 WP 004918236.1	VRIDIRRSLSDTGKIKDKSGE	VIGN	RTKIKVVKNKV	VAPPFK	SAEFD	IMYG	EGV	SKVGE	ILD	VATD	L	DI	IQKSG	SWFSY	QD	308		
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NTDB id 1389 A4U84 RS07560 WP 021112712.1	VRLDIRRCGV....V.KDGE	DEIIG	SETKIKVVKNKV	VAPPFR	REVQF	IMYG	EGIS	RMNELL	IL	AEANG	F	IKKSG	AWFSY	DG	311			
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NTDB id 1427 RS RS02760 WP 011000510.1	VRLDIRRIGS....I.KKGE	DEVGN	ETKIKVVKNKV	VAPPFR	EAI	FDILY	GAGV	SREGE	I	IDL	G	V	EAKV	VEKSG	AWYSY	NG	303	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	VRLDIRRIGQ....V.KEGE	DEIIG	SETKIKVVKNK	MAPPFR	EAI	FQILY	GKGV	NQLG	ELVD	LAV	Q	Q	NIV	QKAG	AWYSY	Q	294	
NTDB id 1074 ABD1 RS10195 WP 000344167.1	VRLDIRRIGQ....V.KEGE	DEIIG	SETKIKVVKNK	MAPPFK	EAI	FQILY	GKGT	NQLG	ELVD	LAV	Q	Q	Q	NIV	QKAG	AWYSY	Q	294
consensus	!!****!	*	**	*****!!!!!!	!!!!!!*	*	*****!****	*****	***	***	!	!!!!!!						

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consensus

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EKIGGQSENAKKYLAEHPEIFDEIDKQVRSKFGIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIEI	386
EKIGGQSENAKKYLAEHPEIFDEIDKQVRSKFGIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIEI	386
EKIGGQSENAKKYLAEHPEIFDEIDKQVRSKFGIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIEI	386
EKIGGQSENAKKYLAEHPEIFDEIDKQVRSKFGIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIEI	386
EKIGGQSENAKKYLADNPEIFDEIDHQVRVQFGLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDLEIEI	382
EKIGGQSENAKKYLADNPEVFAEIDHQVRVQFGLIDGEEAAES....KKDE....VAQVDS..VNEEVTLDLGDLEIEI	382
EKIGGQSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELED	383
EKIGGQSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIED	378
ERLGGGRENAKQFLKENKDITMLMIQEIQREHYGLDNGGVVQQQAEETQEEL.EFE.E.....	348
ERIGGQRENAKNYLADHEDVEEDVRLKVRAYGISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
KKLGGGRENKAFLKENPEIADEITKAIQNSMGIEGMISGSEDDEGEE.....	343
KKLGGGRENAKALLKEDKALADEITLTKIKESIGSNEEIMPLPDEPLEEM..E.....	347
KKLGGGRENAKALLKEDKALADEITLTKIKESIGSNEEIMPLPDEPLEEM..E.....	347
TKLGGGRDVTVELIKDNPELAELEAKIREKLQAK.....	343
DQLGGQKENARNFLIKNPDIABEIEQKILGKLGIAGKIPMGDSVGNVESIQKGLGAKKG.....A.....	357
TKIGGQKNNAVKWLKENPEIADKLEQEIINTLASNPNSVLKATASDSND..ESDVVEEFSE.....EEL.....	372
AKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGT.....Q..DETDGERPE.....E.....	348
AKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGT.....Q..DETDGERPE.....E.....	348
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DKIGGQKANACKYLLKENPEIAKTLDDKKIREMLLNPNMQLIAETSSAAD..DVEFGAVPE.....EF.....	354
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NKIGGQKNNVIRVYLEENPQISTEIEAVIREQLLTKASDQTA..HDETEE..EPDLL..ES.....	349
NKIGGQKNNVIRVFEENNQIAEIERNIREQLLTGTNGAVQ..I..EDEE..EPDLL..LE.....S.....	349

logo

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NTDB id 1205 PSJM300 05545 AFN77183.1	..	347
NTDB id 1022 ACIAD RS06390 WP 004925639.1	..	349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	..	349

consensus

 non conserved
 similar
 ≥ 50% conserved