

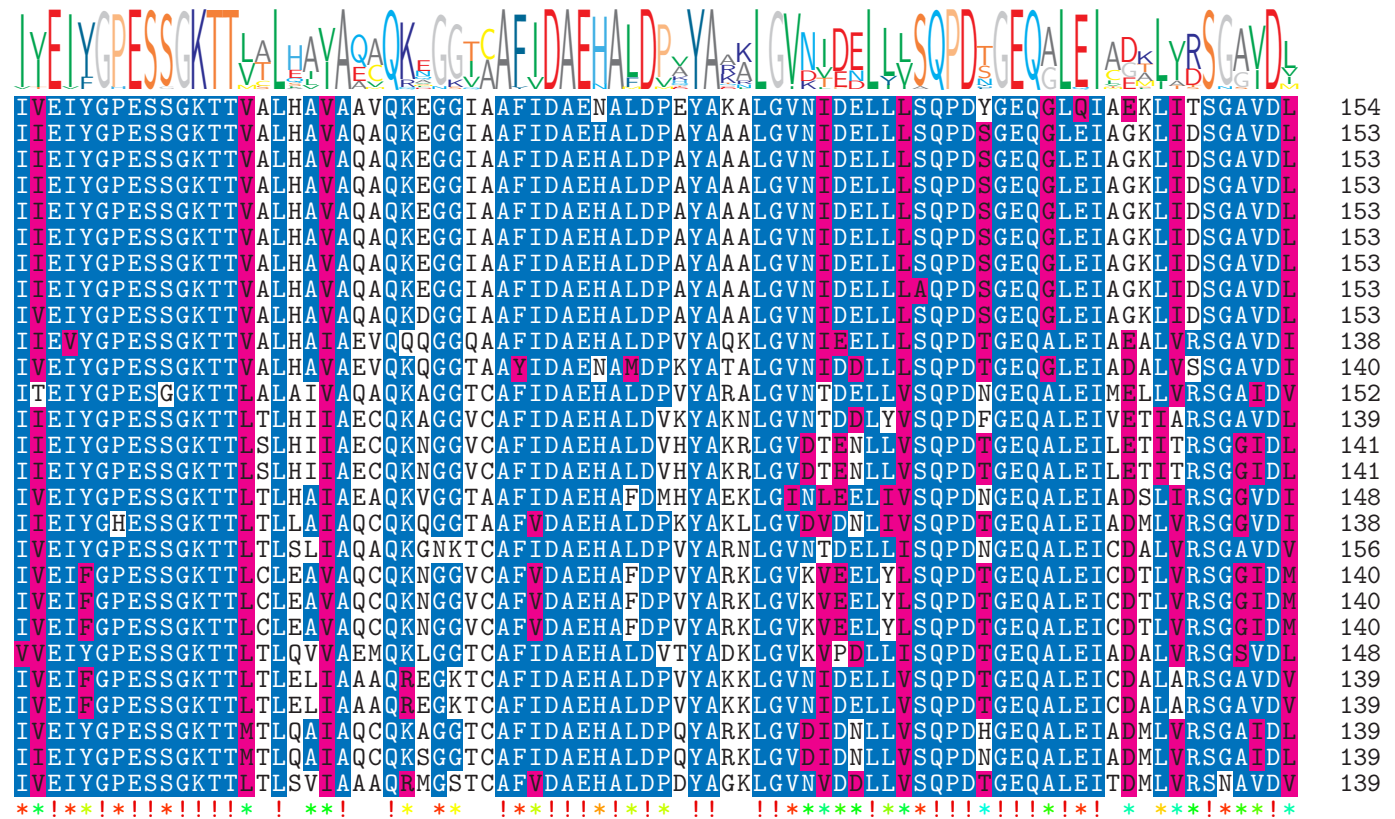
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NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQVM	SSGSLALD	I	ALGSGGY	PKGR	73
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NTDB id 115 BSU 16940 NP 389576.2	MS	DRQAALDMALKQIEKQ	FGKGSIMKLGEK	.TDTRISTV	PSGSLALD	T	ALGIGGY	PRGR	58
NTDB id 625 LCA RS02525 WP 011374196.1	MAKD	ERQAALDAALKKIEKN	FGKGSIMRMGEK	.VDTQVSTV	SSGSLALD	E	ALGVGGY	PRGR	60
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAM	QIEKAFGKGSIMKLGA	E.SKLDVQV	VSTGSLSLD	L	ALGVGGI	PRGR	72
NTDB id 1245 Cj1673c YP 002345041.1	MDDN	KRKSLSDAALKS	LDKTFGKGTILRLG	DK.EVEQID	ISTGTSVGLD	L	ALGIGGV	PKGR	59
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NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDE	DKQKALISLAIKQID	KVFGKGALVRLG	DK.QVEKID	ISTGSLGLD	L	ALGIGGV	PKGR	61
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NTDB id 44086 FTU RS09775 WP 003013734.1	MSKEKALES	ALSQIEKQFGKGA	IMRLGDQEA	AHDIDVIPS	GIIT	ALD	VALGIGGY	PKGR	58
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQVEPEQ	KKQALEAALAQIEKQ	FGKGSIMKLQGT	.EQLDIES	VSTGSLGLD	L	ALGIGGL	PMGR	76
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDN	KSKALQAALSQIEKQ	FGKNTVMRLGDN	.TVQAVEA	VSTGSLTLD	I	ALGIGGL	PKGR	59
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NTDB id 1205 PSJM300 05545 AFN77183.1	MDEN	KKRALAAALGQIEKQ	FGKGAVMRMGDH	.DRQAIPS	ISTGSLGLD	I	ALGIGGL	PKGR	59
consensus		* * *	* * *	* * *	* * *	!	* * * !	* * * !	

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NTDB id 1124 NGFG RS03960 WP 003688695.1
NTDB id 1123 OK783 RS03845 WP 003688695.1
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consensus

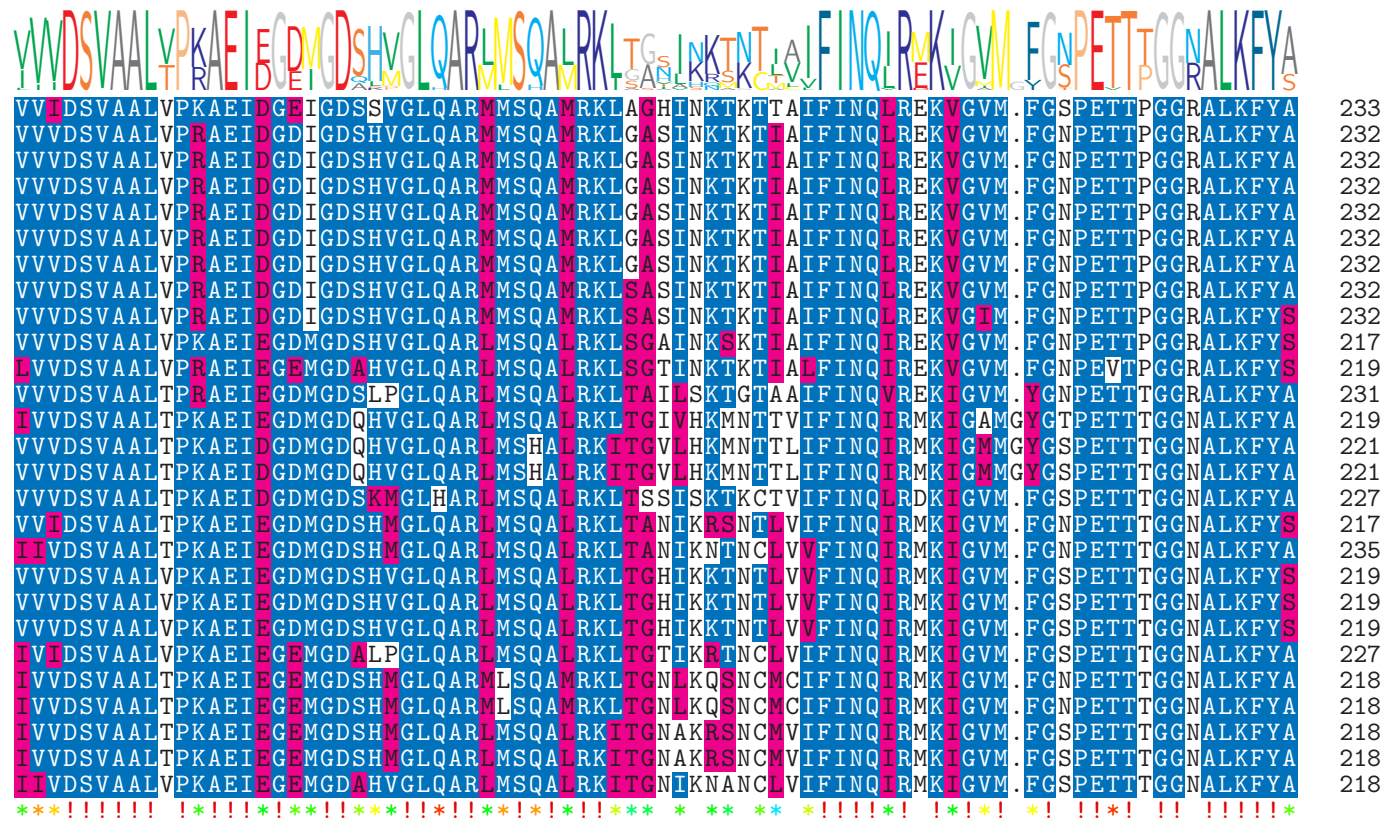
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consensus

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NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEI	IGSETK	VKKVVKNKMAPPFREAIFQ	ILYGKGVNQLGELVDLAVQQ	NIVQKAGAWYSYQ	293			
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEI	IGSETK	VKKVVKNKMAPPFKEAIFQ	ILYGKGTNQLGELVDLAVQQ	DIVQKAGAWYSYQ	293			
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETR	VKKVVKNKVAPPFRQAEFQ	ILYGKGIYRNGEIIDLG	VQQGLVEKSGAWAYK	293			
consensus	*!!*****	*	**	*****!!*!!*!!*!!*!!*	*	*****!!*!!*!!*!!*!!*	*****	***	!!*****!

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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

Sequence	Score
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DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ ID ⁺ DK ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSE QDTENKK ⁺ DE PKKEEA ⁺ .VN ⁺ EEV ⁺ PLDL ⁺ GD	380
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ ID ⁺ DK ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSE QDTENKK ⁺ DE PKKEEA ⁺ .VN ⁺ EEV ⁺ PLDL ⁺ GD	380
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ ID ⁺ DK ⁺ VR ⁺ SKF ⁺ CL ⁺ IDGEEVSE QDTENKK ⁺ DE PKKEEA ⁺ .VN ⁺ EEV ⁺ PLDL ⁺ GD	380
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GEKIGGGS ⁺ EN ⁺ AK ⁺ FL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ DK ⁺ VR ⁺ VQY ⁺ CL ⁺ IEEDNTEE KQSSKEK ETDEK ADKNLVLELDD	377
EE ⁺ RL ⁺ GGGREN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CL ⁺ DNNGVVQQ QAEETQE ⁺ FL ⁺ .EFE ⁺ .E	348
SERIGGGREN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DEV ⁺ RLK ⁺ VR ⁺ AA ⁺ YCI ⁺ SDVPEEDL PTEDE ⁺ .QI ⁺ .NILPDDST EE	355
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DKKLGGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEIA ⁺ DEIT ⁺ KA ⁺ IQNSM ⁺ CI ⁺ EGMIS GSEDEG EE	343
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DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITL ⁺ KIK ⁺ ESIG ⁺ SNEEIM PLPDEPL EEME	347
DTKLGGGRD ⁺ TVKEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IREKLQAK	343
GKKIGGGRD ⁺ SK ⁺ EYL ⁺ KEN ⁺ TAER ⁺ DEI ⁺ ERAIL ⁺ ELL ⁺ LPNKYSN KDSNDSPK EGSKI ⁺ KT ⁺ KN ⁺ .PAVTQDELI	359
GTKIGGQKNN ⁺ AVK ⁺ VL ⁺ KEN ⁺ PEIA ⁺ AD ⁺ KL ⁺ BE ⁺ QIRNTL ⁺ ASNPNSV LKATASDSN ⁺ .DESDVE EFSEEEEL	372
GAKIGGQKDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AK ⁺ IRAL ⁺ NG ⁺ VEMHIT EGTQDET ⁺ DG ⁺ .ER PEE	348
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GDKIGGQKAN ⁺ ACKYL ⁺ KEN ⁺ PEIA ⁺ AK ⁺ TL ⁺ DKK ⁺ IREMLLN ⁺ PENMQ LIAETSSAA ⁺ .DDVEFG AVPEEF	354
GDKIGGQKAN ⁺ ACKYL ⁺ KEN ⁺ PEIA ⁺ AK ⁺ TL ⁺ DKK ⁺ IREMLLN ⁺ PENMQ LIAETSSAA ⁺ .DDVEFG AVPEEF	354
GNKIGGQKNN ⁺ VIRY ⁺ LEEN ⁺ PQIST ⁺ EIE ⁺ AVI ⁺ REQLL ⁺ TKASDQ TAA ⁺ .HDETE ⁺ .E ⁺ EPDLL ES	349
GNKIGGQKNN ⁺ VIRY ⁺ FEEN ⁺ NQIA ⁺ EIE ⁺ ERN ⁺ IREQL ⁺ LTGTNG AVQ ⁺ .I ⁺ .EDE ⁺ .E ⁺ EPDLL LES	349
GSKIGGQKANA ⁺ AKYL ⁺ LEEN ⁺ PIG ⁺ IEEQ ⁺ IRAKLL ⁺ VTSANT KATPVAEDL ⁺ .ADADI	347

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NTDB id 600 KW2 RS01765 WP 011675413.1			387
NTDB id 269 KZH43 RS08665 WP 001085462.1	ELEIEIEE		388
NTDB id 228 SPD RS09265 WP 001085462.1	ELEIEIEE		388
NTDB id 194 SPR RS08825 WP 001085462.1	ELEIEIEE		388
NTDB id 159 SP RS09750 WP 001085462.1	ELEIEIEE		388
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NTDB id 527 SMSK321 RS11065 WP 001085454.1	ELEIEIEE		384
NTDB id 453 Spy49 1753c ACI62003.1	GIEIED..		378
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NTDB id 1074 ABD1 RS10195 WP 000344167.1			349
NTDB id 1205 PSJM300 05545 AFN77183.1			347
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved