

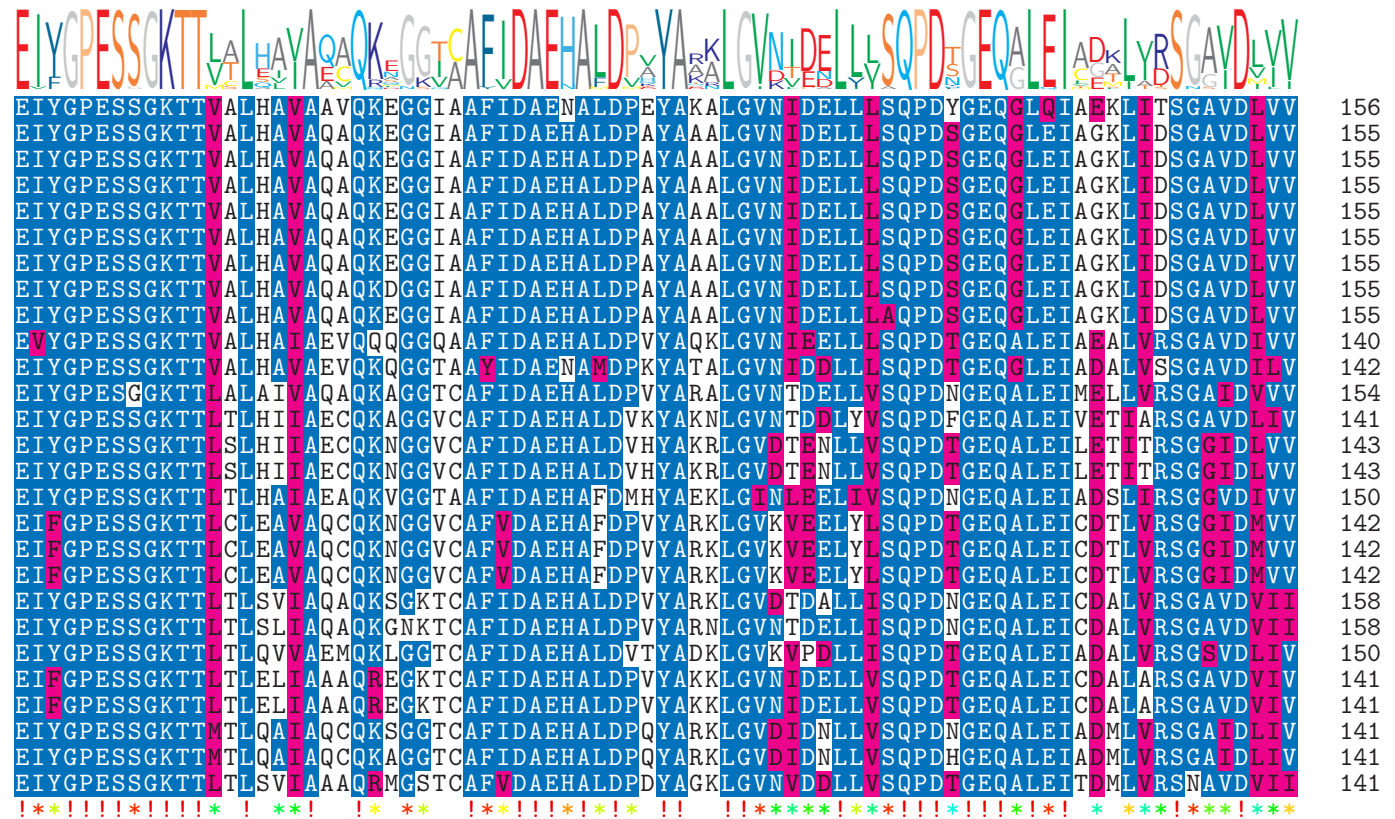
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NTDB id 600 KW2 RS01765 WP 011675413.1	MATKKK...TNFDDITKKYGAERDKALADALALIEKD FGKGSIMRLGEA.ANQKVSVVSSGSLALDIALGAGGYPKGRIV	76
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKKP...KKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIT	75
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKKP...KKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIT	75
NTDB id 194 SPR RS08825 WP 001085462.1	.MAKKP...KKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIT	75
NTDB id 159 SP RS09750 WP 001085462.1	.MAKKP...KKLEEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIT	75
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NTDB id 499 SM12261 RS08315 WP 078228268.1	.MAKKP...KKLDEISKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGRIT	75
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NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALKKIEKNFGKGSIMRMGEK.VDTQVSTVSSGSLALDEALGVGGYPRGRIV	62
NTDB id 1313 DR RS12030 WP 010888966.1	.MSKD....ATKEISAPTDAKERSKATETAMSQIEKAFGKGSIMKLGAE.SKLDVQVVSTGSLSLDLALGVGGIPRGRIT	74
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKSLDKTFGKGTILRLGDK.EVEQIDSIGTGSVGLDLALGIGGVPKGRIT	61
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKAIISLAIKQIDKVFVGKGAIVRLGDK.QVEKIDAISTGSLGLDLALGIGGVPKGRIT	63
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKAIISLAIKQIDKVFVGKGAIVRLGDK.QVEKIDSISTGSLGLDLALGIGGVPKGRIT	63
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKTETTSPNDDKKKALAAVLEKLDKTYGKGTVMKLGDDGTVDHNIIEVIPSGSLGLDLALGVGGYPKGRIV	70
NTDB id 1130 NGFG RS03960 WP 003688695.1	MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQQUEENLEVISTGSLGLDLALGVGGLPRGRIV	62
NTDB id 1124 NGFG RS03960 WP 003688695.1	MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQQUEENLEVISTGSLGLDLALGVGGLPRGRIV	62
NTDB id 1123 OK783 RS03845 WP 003688695.1	MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQQUEENLEVISTGSLGLDLALGVGGLPRGRIV	62
NTDB id 27620 APL RS05985 WP 005598042.1	.MAADNKKKAQKNTVTKQIDPEQKEKALAAALAQIEKQFGKGSIMRLGDT.QALDIEAVSTGSLGLDAALGIGGLPMGRIV	78
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTVVVKQVEPEQKKQALEAALAQIEKQFGKGSIMKLQQT.EQLDIESVSTGSLGLDLALGIGGLPMGRIV	78
NTDB id 1427 RS RS02760 WP 011000510.1	.ME.....DGKKAASMSAEKQKALAAALAQIEKQFGKGSIMKMGDA.EVEPVQVVSTGSLGLDVALGVGGLPRGRVV	70
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGRIV	61
NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGRIV	61
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDLALGIGGLPKGRIT	61
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDLALGIGGLPKGRIV	61
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAAALGQIEKQFGKGAVMRMGDH.DRQAIPSISTGSLGLDIALGIGGLPKGRIV	61
consensus	*** **	

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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 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA RS02525 WP 011374196.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

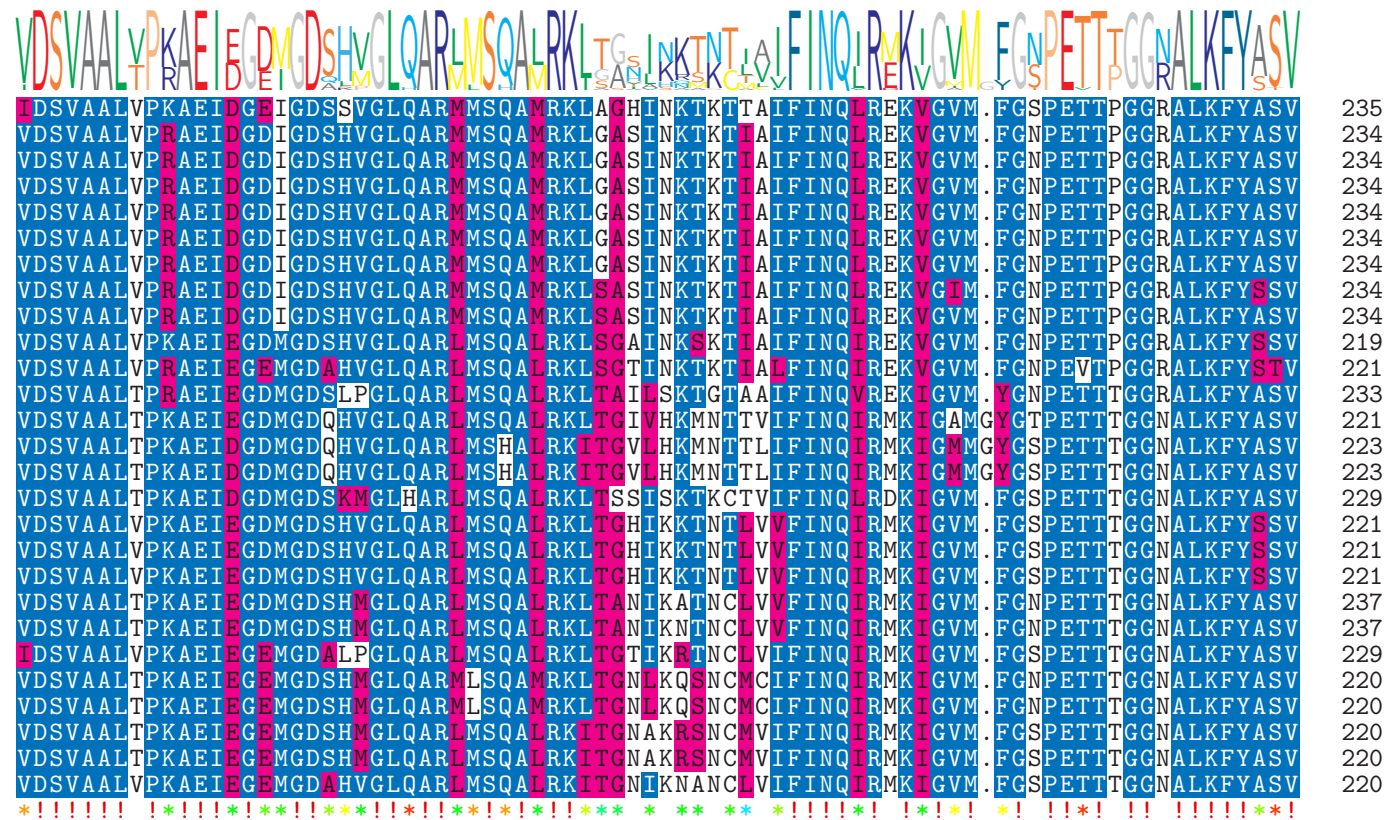
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consensus

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logo

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NTDB id 194 SPR RS08825 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVV	VKNKVAPPF	KEAVV	EIMY	GEGIS	KTGEL	LKIAS	DLDII	KK	KAGAW	YSYK	DE	313		
NTDB id 159 SP RS09750 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVV	VKNKVAPPF	KEAVV	EIMY	GEGIS	KTGEL	LKIAS	DLDII	KK	KAGAW	YSYK	DE	313		
NTDB id 527 SMSK321 RS11065 WP 001085454.1	RLDVRG	STQIKGTG	.DQKDTN	VGKETK	IKVV	VKNKVAPPF	KEAFV	EIMY	GEGIS	KTGEL	LKIAS	DLDII	KK	KAGAW	YSYK	DE	313		
NTDB id 499 SM12261 RS08315 WP 078228268.1	RLDVRG	STQIKGTG	.DQKDTN	VGKETK	IKVV	VKNKVAPPF	KEAFV	EIMY	GEGIS	KTGEL	LKIAS	DLDII	KK	KAGAW	YSYK	DE	313		
NTDB id 408 SMU RS09530 WP 002262392.1	RLDVRG	NTQIKGTG	.EQKDSN	IGKETK	IKVV	VKNKVAPPF	KEAFV	EIIY	GEGIS	RGTGEL	VKIAS	DLGII	QK	KAGAW	YSYNGE		313		
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NTDB id 1214 NCTC11637 00359 SQJ03206.1	RIDIRRI	AA....	L.KQNE	QHIGN	RAKAKV	VKNKVAPPF	REAEF	DIMF	GEGIS	KEGE	IIDYGV	KLDI	VDK	SGAW	LSYQ	DK			298
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NTDB id 1389 A4U84 RS07560 WP 021112712.1	RLDIRR	RCGV....	V.KDGE	DEIIG	SETKV	VKNKVAPPF	REVQ	FDIM	YGEGIS	RMNELL	ILAE	ANGFI	QK	KAGAW	FSYDGT				312
NTDB id 1427 RS RS02760 WP 011000510.1	RLDIRR	IGS....	I.KKGE	DEVV	NETKV	VKNKVAPPF	REAI	FDILY	GAGV	SREGE	IIDL	GV	EAKV	VVEK	SGAW	SYNGE			304
NTDB id 1165 A1552VC RS01565 WP 000344154.1	RLDIRR	TGA....	I.KEGE	EEVVG	NETRIK	VKNK	IAAPF	KEANT	QIMY	GGFN	REGEL	IDL	GV	KKH	MVEK	SGAW	SYNGD		295
NTDB id 1142 GTF74 RS11550 WP 000344154.1	RLDIRR	TGA....	I.KEGE	EEVVG	NETRIK	VKNK	IAAPF	KEANT	QIMY	GGFN	REGEL	IDL	GV	KKH	MVEK	SGAW	SYNGD		295
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consensus	!***!*		*	*	*	*****!***!!*!!*!!*	*	*****!*	*****	*****	*	***	!	!*****!					

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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE.....PKKEEA..VNEEVPLDLGDELE	383
KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE.....PKKEEA..VNEEVPLDLGDELE	383
KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE.....PKKEEA..VNEEVPLDLGDELE	383
KIGQGSSENAKKYLADNPEVFAEIDHQVRVQFGLIDGEEAAE...SKKDE.....VAQVDS..VNEEVTLDLGDELE	379
KIGQGSSENAKKYLADNPEIFDEIDHQVRVQFGLIDGEEIAE...SKKDE.....AAQVDS..VNEEVTLDLGDELE	379
KIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEDNTEEEKQSSKEK.....ETDEK..ADKNLVLELDDTTIE	380
KIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIE	375
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KLGGGRENKALLKEDKALADEITLKI KESIGSNEEI...MPLPDE..PLEEME.....	347
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KLGGGRD TVKELIKDNPELAELEAKIREKLQAK.....	343
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logo

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NTDB id 1022 ACIAD RS06390 WP 004925639.1		349
NTDB id 1205 PSJM300 05545 AFN77183.1		347

consensus

 non conserved
 similar
 ≥ 50% conserved