

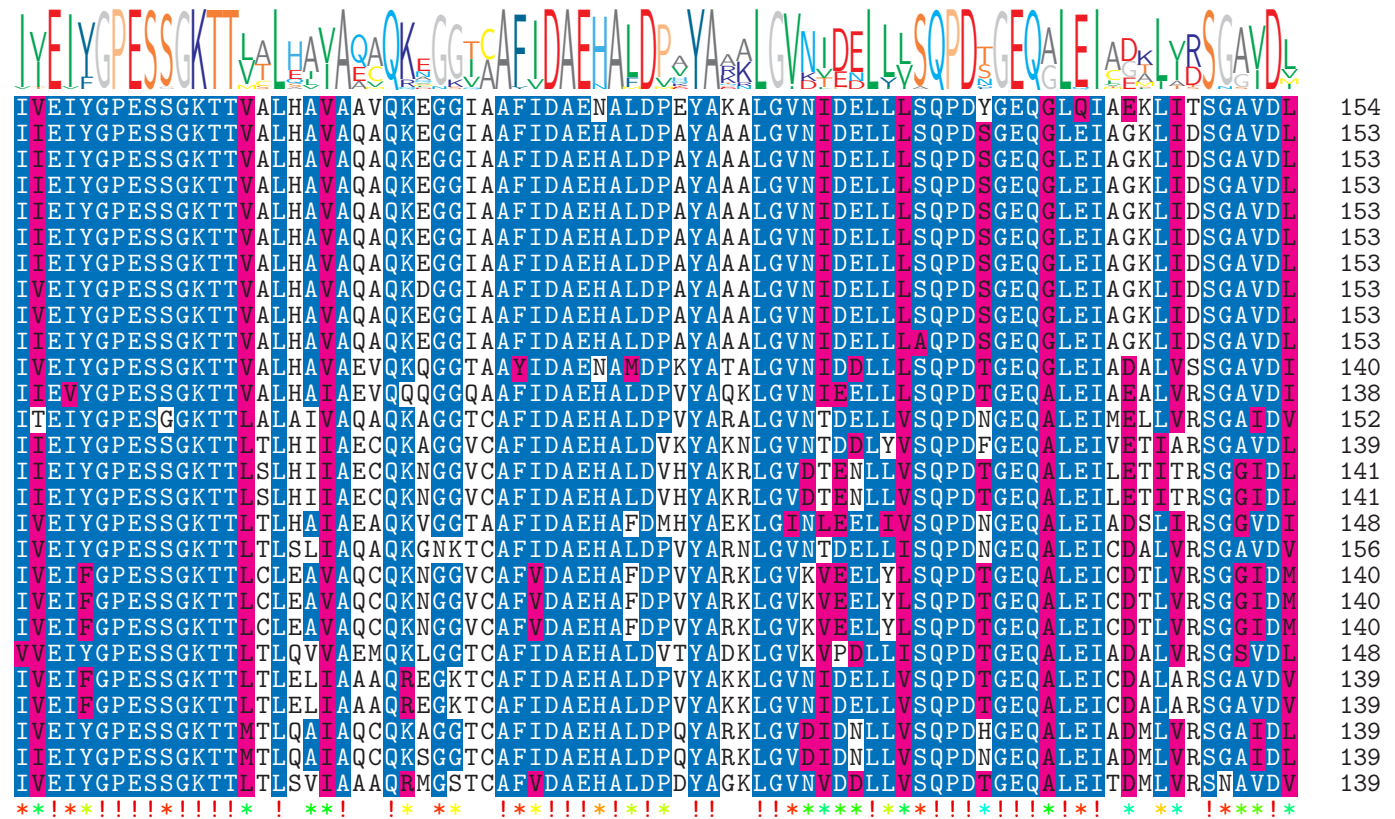
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NTDB id 600 KW2 RS01765 WP 011675413.1	MATKK....KTNFDDITKKYGAERDKALADALALIEKD FGKGSIMRLGEA.ANQKVS	74
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK....PKKLEEISKKFGAEREKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK....PKKLEEISKKFGAEREKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 194 SPR RS08825 WP 001085462.1	.MAKK....PKKLEEISKKFGAEREKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
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NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR....IKKTEEITKKFGDERKKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
NTDB id 266917 C2E46 RS10905 WP 001085741.1	.MAKK....TKKAEEITKKFGDERRKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
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NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALKQIEKQFGKGSIMKLGAE.TDTRISTVPSGSLALDTALGIGGYPRGR	58
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTDAKERSKATETAMSQIEKAFGKGSIMKLGAE.SKLDVQVVSTGSLSLDLALGVGGIPGR	72
NTDB id 1245 Cj1673c YP 002345041.1	MDNKRKSLDAALKSLDKTFGKGTILRLGDK.EVEQIDSIGTGSVGLDLALGIGGVPKGR	59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKATISLAIKQIDKVFVGKALVRLGDK.QVEKIDISTGSLGLDLALGIGGVPKGR	61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKATISLAIKQIDKVFVGKALVRLGDK.QVEKIDISTGSLGLDLALGIGGVPKGR	61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTSPNDDKKKALAAVLEKLDKTYGKGTVMKLGDTVDHNIIEVIPSGLGLDLALGVGGYPKGR	68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQVEPEQKKQALEAALAQIEKQFGKGSIMKLGQT.EQLDIESVSTGSLGLDLALGIGGLPMGR	76
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NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAASMSAEKQKALAAALAQIEKQFGKGSIMKMGDA.EVEPVQVVSTGSLGLDVALGVGGLPRGR	68
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDIALGIGGLPKGR	59
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDIALGIGGLPKGR	59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAAALGQIEKQFGKGAVMRMGDH.DRQAIPSTGSLGLDIALGIGGLPKGR	59
consensus	*** **	

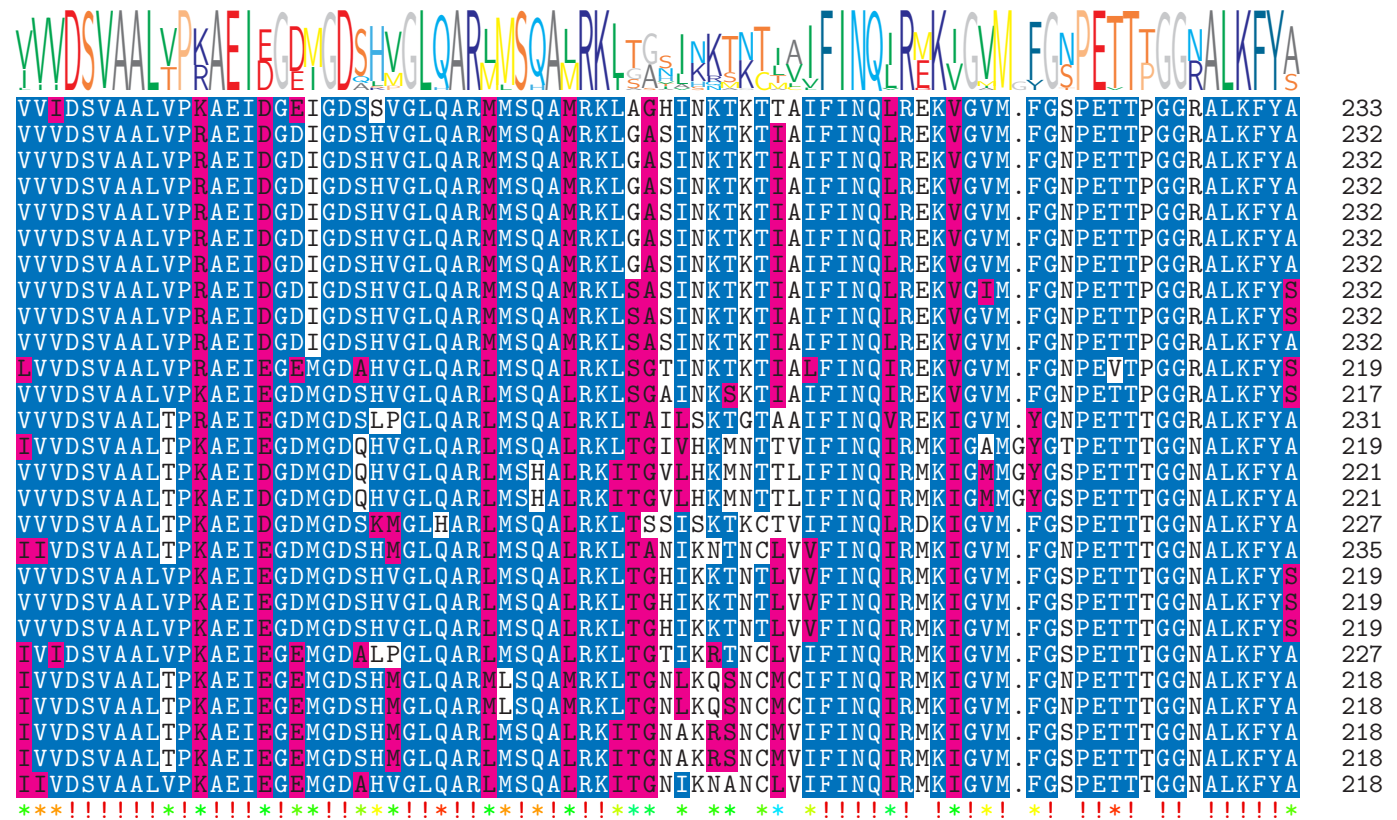
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consensus



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NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KDGDEI	IGSETKVVKNKVAPPFRQAEFDIMYEGEGISRMNELLILAEANGFIKKSGAWFSYD	310
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consensus	*!!**!*~	*~**~*****!!*!!*!!*!!*~**~*****!!*~**~*****~**~*****~**~*****!!~*****!	

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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEID ⁺ KQ ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEEV ⁺ PLDL ⁺ GDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEID ⁺ KQ ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEEV ⁺ PLDL ⁺ GDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEID ⁺ KQ ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEEV ⁺ PLDL ⁺ GDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEID ⁺ KQ ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEEV ⁺ PLDL ⁺ GDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ DNPEI ⁺ FDEID ⁺ HQ ⁺ VR ⁺ VQF ⁺ GL ⁺ IDGEEIAES...KKDEAA...QVD...SVNEE ⁺ VTLD ⁺ GDELEIE	381
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ DNPEI ⁺ FAEID ⁺ HQ ⁺ VR ⁺ VQF ⁺ GL ⁺ IDGEEAAES...KKDEVA...QVD...SVNEE ⁺ VTLD ⁺ GDELEIE	381
GEKIGQGS ⁺ ENAK ⁺ KLAD ⁺ NPEI ⁺ FD ⁺ IDHK ⁺ VR ⁺ VQY ⁺ GL ⁺ IEEDNTEEEK ⁺ QSSKEKET.....DE...KADKNL ⁺ VLELDD ⁺ TIELE	382
GEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ DNPAI ⁺ FDEID ⁺ HK ⁺ VR ⁺ VHF ⁺ GMTEDD ⁺ SPVQ ⁺ SELVEE.....K...NEAD ⁺ DLVL ⁺ DLDNAIEIE	378
GEKIGQGS ⁺ ENAK ⁺ KRYLA ⁺ DHPQL ⁺ FDEID ⁺ RK ⁺ VR ⁺ VKF ⁺ GL ⁺ LEESEE...ESAMAVA.....S...EETD ⁺ DLAL ⁺ DLNGIEIE	377
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EERLGG ⁺ RENAK ⁺ NYLAD ⁺ ENK ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ GL ⁺ DNNGVVQQA ⁺ EETQEELE.....FE.E.....	348
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DKKLGG ⁺ RENAK ⁺ ALLKED ⁺ KALADEIT ⁺ LK ⁺ IKESIG ⁺ SNEEI.....MPLPDE...P.....LEEME ⁺	347
DKKLGG ⁺ RENAK ⁺ ALLKED ⁺ KALADEIT ⁺ LK ⁺ IKESIG ⁺ SNEEI.....MPLPDE...P.....LEEME ⁺	347
DTKLGG ⁺ GRD ⁺ TVKEL ⁺ IKDN ⁺ PELA ⁺ ELE ⁺ EAK ⁺ IREKLQAK.....	343
GTKIGQG ⁺ KNN ⁺ AVK ⁺ WL ⁺ KNPEI ⁺ AD ⁺ KL ⁺ EQEIR ⁺ N ⁺ TLASNPNS.....VLKATASDS.....NDES ⁺ DVEEF ⁺ SEEEL...	372
GAKIGQG ⁺ KDN ⁺ VR ⁺ VL ⁺ KNPEI ⁺ SDEID ⁺ AK ⁺ IRAL ⁺ NGVEMHI.....TEGTQDET ⁺ D.....GER.....PEE.....	348
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G ⁺ ERIGQGR ⁺ DN ⁺ CREFL ⁺ RNAEL ⁺ AREI ⁺ ENK ⁺ VREHL ⁺ GVTPMG.....AVTLA ⁺ EEV.....EED.....	352
GDKIGQG ⁺ KANACK ⁺ YL ⁺ KNPEI ⁺ AKTLD ⁺ KKL ⁺ REMLLN ⁺ PNEM.....QLIAETSSA.....ADDV ⁺ EFGAV ⁺ PEEF.....	354
GDKIGQG ⁺ KANACK ⁺ YL ⁺ KNPEI ⁺ AKTLD ⁺ KKL ⁺ REMLLN ⁺ PNEM.....QLIAETSSA.....ADDV ⁺ EFGAV ⁺ PEEF.....	354
GNKIGQG ⁺ KNN ⁺ VIRY ⁺ LEEN ⁺ PQISTEIE ⁺ AVIRE ⁺ QLLT ⁺ TKASD.....QTAA ⁺ .HDET.....EEEP ⁺ DLL...ES.....	349
GNKIGQG ⁺ KNN ⁺ VIRY ⁺ FEENN ⁺ QIAIEI ⁺ ERNIRE ⁺ QLLT ⁺ TGTN.....GAVQ ⁺ .I.ED.....EEEP ⁺ DLL...LES.....	349
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NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388	
NTDB id 228 SPD RS09265 WP 001085462.1	IEE	388	
NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388	
NTDB id 159 SP RS09750 WP 001085462.1	IEE	388	
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NTDB id 266917 C2E46 RS10905 WP 001085741.1	E..	379	
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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