

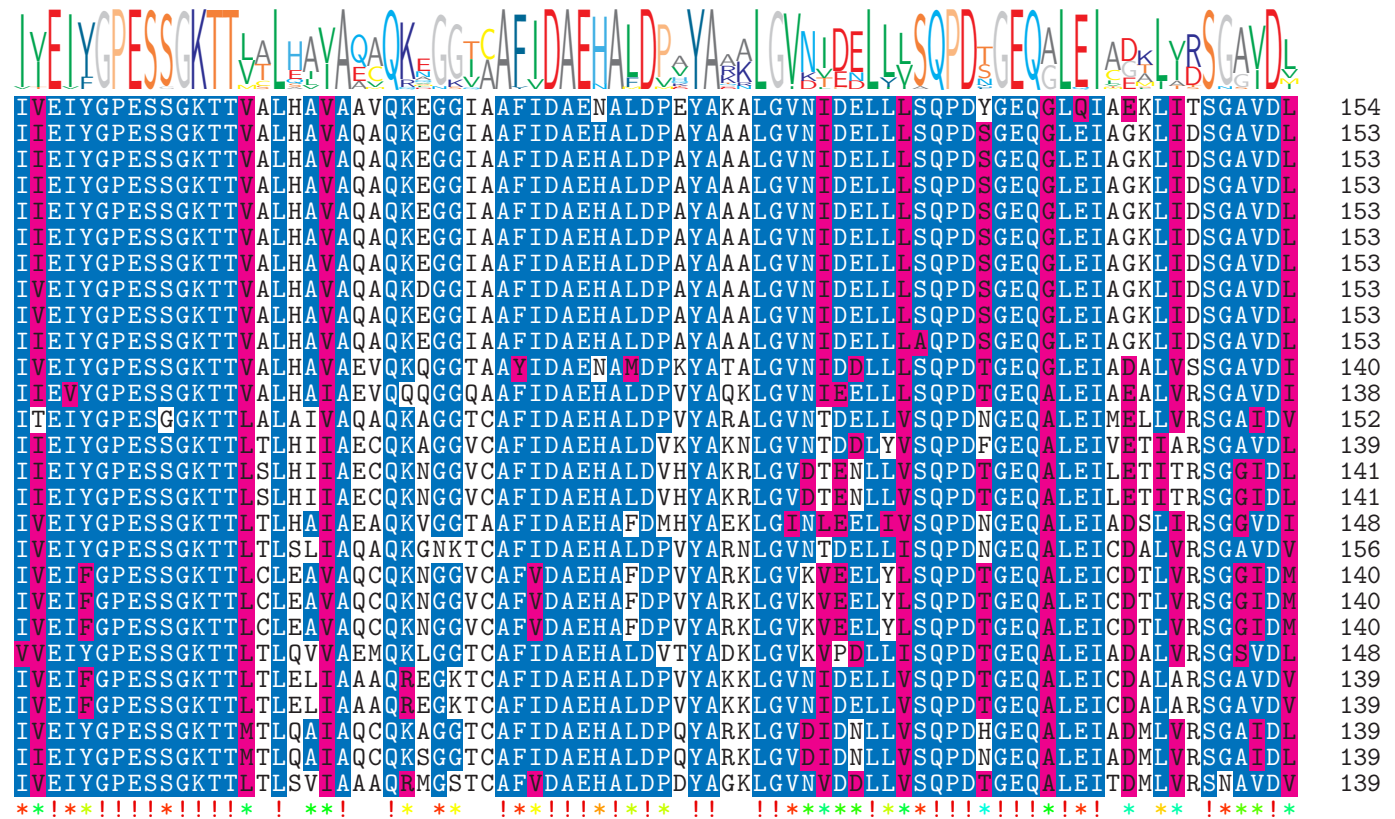
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NTDB id 600 KW2 RS01765 WP 011675413.1	MATKK....KTNFDDITKKYGAERDKALADALALIEKD FGKGSIMRLGEA.ANQKVS	74
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK....PKKLEEISKKFGAEREKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 228 SPD RS09265 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 124442 GT95 RS10570 WP 001085741.1	.MAKK....TKKAEEITKKFGDERRKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
NTDB id 453 Spy49 1753c ACI62003.1	.MAKK....LKKNEEITKKFGDERRKALDDALKNIEKD 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.QVEKIDAISTGSLGLDLALGIGGVPKGR	61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKATISLAIKQIDKVFVGKALVRLGDK.QVEKIDSISTGSLGLDLALGIGGVPKGR	61
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NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQVEPEQKKQALEAALAQIEKQFGKGSIMKLGQT.EQLDIESVSTGSLGLDLALGIGGLPMGR	76
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NTDB id 1124 NGFG RS03960 WP 003688695.1	MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQQUEENLEVISTGSLGLDLALGVGGLPRGR	60
NTDB id 1123 OK783 RS03845 WP 003688695.1	MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQQUEENLEVISTGSLGLDLALGVGGLPRGR	60
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.DRQAIPSISTGSLGLDIALGIGGLPKGR	59
consensus	*** **	

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NTDB id 600 KW2 RS01765 WP 011675413.1
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NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
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NTDB id 408 SMU RS09530 WP 002262392.1
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consensus

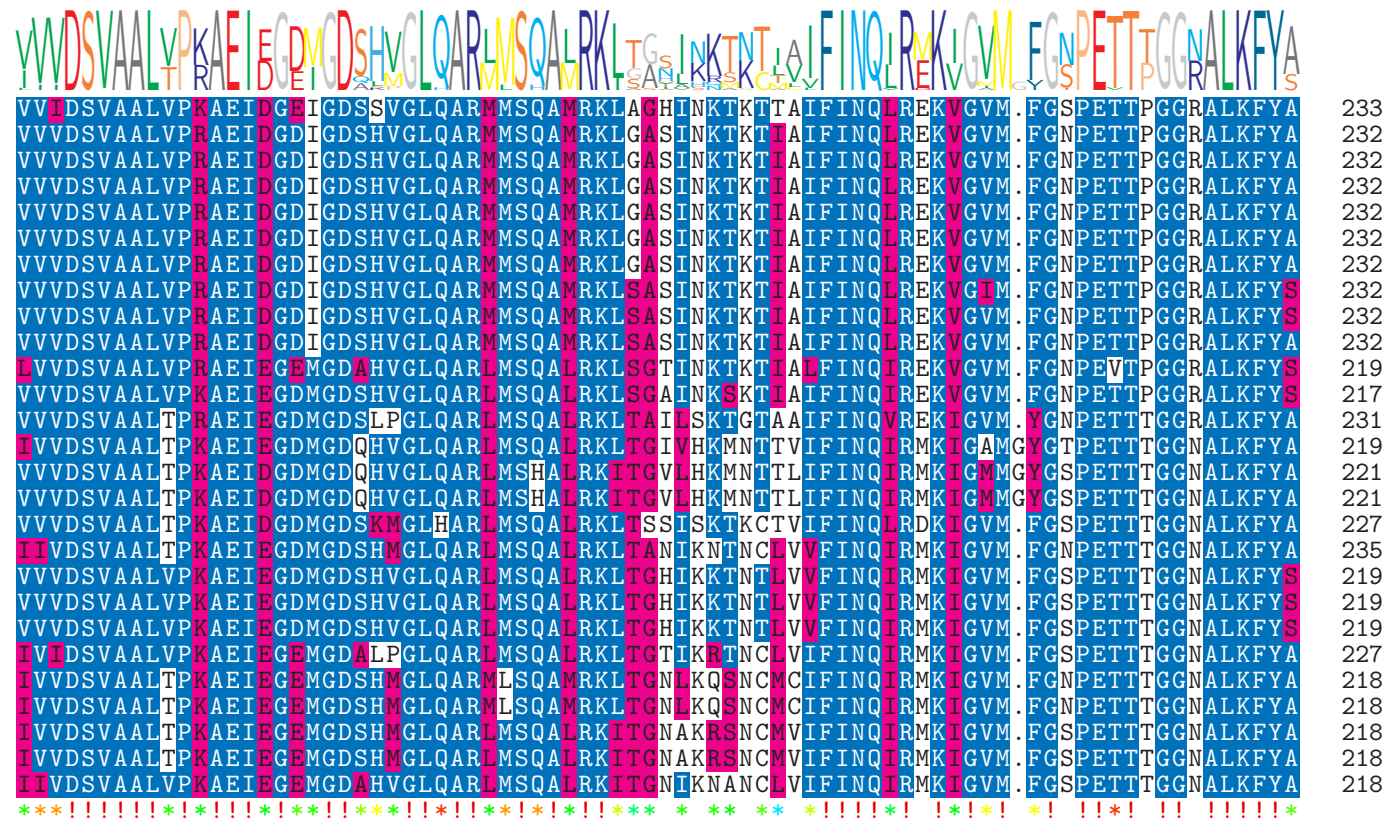
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consensus

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NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KDGDEI	IGSETKVVKNKVAPPFR	EVQFDIMYEGEGISRMNELL	ILAEANGFIKKSGAWFSYD	310
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NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETRVKNKVAPPFR	QAEFFQILYGKGIYRNGEI	IDLGVQQGLVEKSGAWAYK	293
consensus	*!!**!*~	*~	**~***!!*!!*!!*!!*~	***!!*~***~***~***~	***~!!*~***~

NTDB id 600 KW2 RS01765 WP 011675413.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKDEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ EVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKDEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ EVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKDEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ EVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ DKV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQDTENKKDEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ EVPLDLGDELEIE ⁺	385
DEKIGGGS ⁺ ENAK ⁺ KYLAD ⁺ NPEI ⁺ F ⁺ DEID ⁺ HKV ⁺ RVQF ⁺ GL ⁺ IDGEEIAES ⁺ ...KKDEAA ⁺ ...QVD ⁺ ..SVNEE ⁺ EVTLDLGDELEIE ⁺	381
DEKIGGGS ⁺ ENAK ⁺ KYLAD ⁺ NPEI ⁺ F ⁺ FAID ⁺ HQV ⁺ RVQF ⁺ GL ⁺ IDGEEAAES ⁺ ...KKDEVA ⁺ ...QVD ⁺ ..SVNEE ⁺ EVTLDLGDELEIE ⁺	381
GEKIGGGS ⁺ ENAK ⁺ KLAD ⁺ NPEI ⁺ F ⁺ DDID ⁺ HKV ⁺ RVQF ⁺ GL ⁺ IEEDNTEEKSSKEKET ⁺DE ⁺ ..KADKNLVLELDDTIELE ⁺	382
GEKIGGGS ⁺ ENAK ⁺ KYLAD ⁺ NP ⁺ AI ⁺ F ⁺ DEID ⁺ HKV ⁺ RVHF ⁺ GMTEDDSPVQSELVEE ⁺K ⁺ ..NEAD ⁺ DLVLDLDNAIEIE ⁺	378
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SERIGGGS ⁺ RENAK ⁺ NYLAD ⁺ HD ⁺ VE ⁺ DEV ⁺ RLKV ⁺ RAAY ⁺ GISDVPEEDLPTTEDE ⁺ ..QIN ⁺ILPDDSTEE ⁺ ..	355
EERLGGGRENAK ⁺ QLF ⁺ KEN ⁺ DK ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ GLDNNGVVQQQAETEELE ⁺FE ⁺ ..E ⁺	348
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DKKLGGGREN ⁺ SKA ⁺ FLKEN ⁺ PEIA ⁺ DEIT ⁺ KAI ⁺ QNSM ⁺ GT ⁺ IEGMI ⁺SGSEDD ⁺ ..E ⁺GEE ⁺	343
DKKLGGGRENAK ⁺ ALLKED ⁺ KALADEIT ⁺ LK ⁺ IKES ⁺ IGSNEEI ⁺ ...MPLPDE ⁺ ..P ⁺LEEME ⁺	347
DKKLGGGRENAK ⁺ ALLKED ⁺ KALADEIT ⁺ LK ⁺ IKES ⁺ IGSNEEI ⁺ ...MPLPDE ⁺ ..P ⁺LEEME ⁺	347
DTKLGGGRD ⁺ TVKEL ⁺ IKDN ⁺ PELA ⁺ EEL ⁺ EAK ⁺ IREKLQAK ⁺	343
GTKIGGGKNNAVK ⁺ WLKEN ⁺ PEIAD ⁺ KL ⁺ EQEI ⁺ RNTLASNPNS ⁺VLKATASDS ⁺NDES ⁺ DVEEFSEEEEL ⁺ ...	372
GAKIGGGKDNVRV ⁺ WLKEN ⁺ PEIS ⁺ DEID ⁺ AKI ⁺ RALNG ⁺ VEMHI ⁺ ...TEGTQDET ⁺GER ⁺PEE ⁺	348
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GNKIGGGKNNVIRY ⁺ FEENN ⁺ QIAE ⁺ EIERN ⁺ IREQLLT ⁺ TGTN ⁺ ...GAVQ ⁺ ..I ⁺ ED ⁺EEEPDLL ⁺ ..LES ⁺	349
GSKIGGGKANAAK ⁺ YL ⁺ ENPEI ⁺ IG ⁺ EIEQQ ⁺ IRAKLL ⁺ VT ⁺ SAN ⁺ ...TKATPVAED ⁺LADADI ⁺	347

logo

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NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
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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	
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384	
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NTDB id 408 SMU RS09530 WP 002262392.1	D..	383	
NTDB id 124442 GT95 RS10570 WP 001085741.1	E..	379	
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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved