

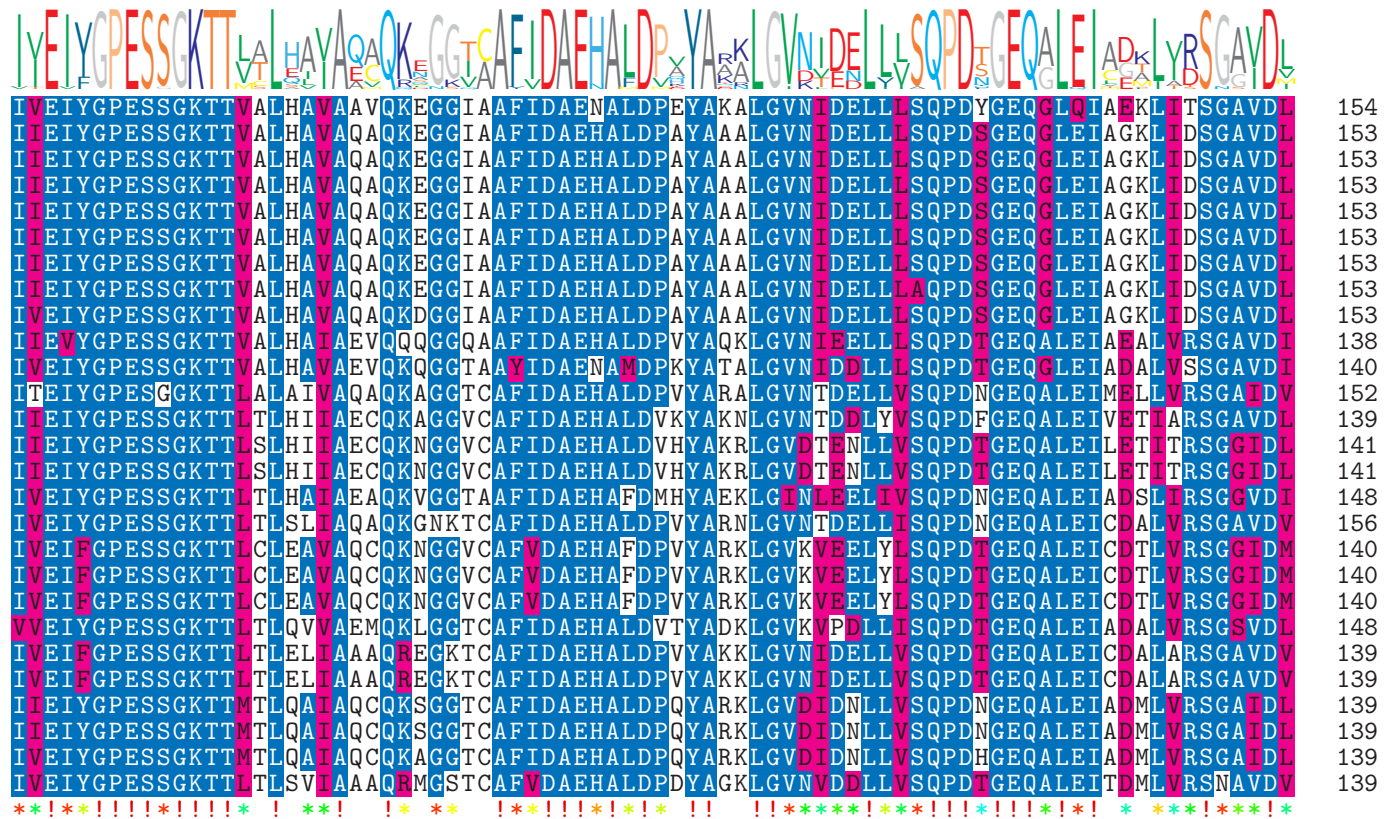
logo

NTDB id 600 KW2 RS01765 WP 011675413.1	MATKK....KTNFDDITKKYGA	ERDKALADALALIEKD	FGKGSIMRLGEA	.ANQKVS	VSSGSLALD	I	ALGAGGY	PKGR	74
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 194 SPR RS08825 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 159 SP RS09750 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 527 SMSK321 RS11065 WP 001085454.1	.MAKK....PKKLDEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 499 SM12261 RS08315 WP 078228268.1	.MAKK....PKKLDEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQ	VMSGSLALD	I	ALGSGGY	PKGR	73
NTDB id 453 Spy49 1753c ACI62003.1	.MAKK....LKKNEEITKKFG	DERRKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQ	VMSGSLALD	I	ALGAGGY	PKGR	73
NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR....IKKTEEITKKFG	DERKKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQ	VMSGSLALD	I	ALGAGGY	PKGR	73
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALK	QIEKQFGKGSIMKLGEK	.TDTR	ISTVPSGSLALD	TALGIGGY	PRGR			58
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALK	KIEKNFGKGSIMRMGEK	.VDTQVSTVSSGSLAL	DEALGVGGY	PRGR				60
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAM	QIEKAFGKGSIMKLGAE	.SKLDVQ	VSTGSLSLDL	ALGVGGI	PRGR		72
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKS	LDKTFGKGTILRLGDK	.EVEQ	IDSIGTGSVGLDL	ALGIGGV	PKGR			59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKAI	SLAIKQIDKVF	FGKGALVRLGDK	.QVEK	IDAISTGSLGLDL	ALGIGGV	PKGR		61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKAI	SLAIKQIDKVF	FGKGALVRLGDK	.QVEK	IDSISTGSLGLDL	ALGIGGV	PKGR		61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTS	PNDDKKKALA	AVLEKLDKTYGKGTVMKLG	DGTVDH	NIEVIPSGSLGLDL	ALGVGGY	PKGR		68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQ	VEPEQKKQALEA	AALQIEKQFGKGSIMKLG	QT.EQLD	IESVSTGSLGLDL	ALGIGGL	PMGR		76
NTDB id 1130 NGFG RS03960 WP 003688695.1	MSDDKSKALAA	AALQIEKSFGKGA	IMKMDGSQ	QEE	NLEVISTGSLGLDL	ALGVGGL	PRGR		60
NTDB id 1124 NGFG RS03960 WP 003688695.1	MSDDKSKALAA	AALQIEKSFGKGA	IMKMDGSQ	QEE	NLEVISTGSLGLDL	ALGVGGL	PRGR		60
NTDB id 1123 OK783 RS03845 WP 003688695.1	MSDDKSKALAA	AALQIEKSFGKGA	IMKMDGSQ	QEE	NLEVISTGSLGLDL	ALGVGGL	PRGR		60
NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAAS	MSAEKQKALAA	AALQIEKQFGKGSIMKMD	A.EVEP	VQVSTGSLGLD	VALGVGGL	PRGR		68
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAA	ALGQIEKQFGKGSIMRLG	DN.RAMD	VETISTGSLSLD	I	ALGAGGL	PMGR		59
NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAA	ALGQIEKQFGKGSIMRLG	DN.RAMD	VETISTGSLSLD	I	ALGAGGL	PMGR		59
NTDB id 155549 AN158 RS01410 WP 000344169.1	MDENKSKALQA	ALSQIEKQFGKNTVMRLG	DN.TVQ	AVEAVSTGSLTLD	I	ALGIGGL	PKGR		59
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQA	ALSQIEKQFGKNTVMRLG	DN.TVQ	AVEAVSTGSLTLD	I	ALGIGGL	PKGR		59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQA	ALSQIEKQFGKNTVMRLG	DN.TVQ	AVEAVSTGSLTLD	I	ALGIGGL	PKGR		59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAA	ALGQIEKQFGKGAVMR	MDH.DRQA	IPSISTGSLGLD	I	ALGIGGL	PKGR		59
consensus	***	***	*	***!	***!	***!	***!	***!	

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NTDB id 228 SPD RS09265 WP 001085462.1
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Sequence	Score
DEKIGGGA ⁺ E ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ EI ⁺ DH ⁺ KV ⁺ RAAH ⁺ GL ⁺ LD ⁺ DSEVAETEEE..TTASKTK..AKAKKEEKAVETEEIELELED..	387
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EI ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ ID ⁺ GEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EI ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ ID ⁺ GEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EI ⁺ FD ⁺ EI ⁺ DK ⁺ VR ⁺ SKF ⁺ GL ⁺ ID ⁺ GEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ VFA ⁺ EI ⁺ DH ⁺ QV ⁺ RVQF ⁺ GL ⁺ ID ⁺ GEEAAE.....SKKD ⁺ E.....VAQVDS..VNEEVTLDLGDEL	378
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ IF ⁺ EI ⁺ DH ⁺ QV ⁺ RVQF ⁺ GL ⁺ ID ⁺ GEEIAE.....SKKD ⁺ E.....AAQVDS..VNEEVTLDLGDEL	378
GEKIGGGS ⁺ EN ⁺ AK ⁺ RYL ⁺ AD ⁺ HP ⁺ QI ⁺ FD ⁺ EI ⁺ DR ⁺ KV ⁺ VKF ⁺ GL ⁺ LE ⁺ SEES ⁺ ESAMAV.ASE.....E.....TDDLALDLNNGI	374
GEKIGGGS ⁺ EN ⁺ AK ⁺ FL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ I ⁺ DH ⁺ KV ⁺ RVQY ⁺ GL ⁺ IE ⁺ EDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EE ⁺ RL ⁺ GGG ⁺ REN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQE ⁺ QIREHY ⁺ GL ⁺ DN ⁺ NGVV ⁺ QQQAE ⁺ E.TQEEL.E..FE.E.....	348
SERIGGG ⁺ REN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DV ⁺ RLK ⁺ VRAAY ⁺ CI ⁺ SD ⁺ VPEEDLP ⁺ TTE.DE.QI.N..ILPDDST....EE.....	355
DERIGGG ⁺ KE ⁺ KTI ⁺ AYI ⁺ AER ⁺ FEME ⁺ QE ⁺ IRDR ⁺ VMAA ⁺ IRAG ⁺ NAGEA ⁺ PALAPAA ⁺ PEAA ⁺ EAA.....	363
DKKLGGG ⁺ RENS ⁺ KA ⁺ FL ⁺ KEN ⁺ PEI ⁺ AD ⁺ EIT ⁺ KA ⁺ IQNSM ⁺ CI ⁺ EG ⁺ MISGS..EDDEGE..E.....	343
DKKLGGG ⁺ RENS ⁺ KA ⁺ LL ⁺ KED ⁺ KAL ⁺ ADEI ⁺ TL ⁺ KIK ⁺ ESIG ⁺ SNEEIMPL..PDEPLE..EME.....	347
DKKLGGG ⁺ RENS ⁺ KA ⁺ LL ⁺ KED ⁺ KAL ⁺ ADEI ⁺ TL ⁺ KIK ⁺ ESIG ⁺ SNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRD ⁺ TV ⁺ KEL ⁺ IKD ⁺ NPE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IREKLQAK.....	343
GTKIGGG ⁺ KNN ⁺ AVK ⁺ WL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQIR ⁺ NTL ⁺ ASN ⁺ PNSVLK..ATASDSND ⁺ SD ⁺ VEEFSE.....EEL.....	372
GAKIGGQK ⁺ DNVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEI ⁺ DAK ⁺ IRALN ⁺ GVEMHIT ⁺ EG..TQDET ⁺ D.....GERPE.....E.....	348
GAKIGGQK ⁺ DNVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEI ⁺ DAK ⁺ IRALN ⁺ GVEMHIT ⁺ EG..TQDET ⁺ D.....GERPE.....E.....	348
GAKIGGQK ⁺ DNVR ⁺ VWL ⁺ KEN ⁺ PEIS ⁺ DEI ⁺ DAK ⁺ IRALN ⁺ GVEMHIT ⁺ EG..TQDET ⁺ D.....GERPE.....E.....	348
GERIGGG ⁺ RD ⁺ NC ⁺ REFL ⁺ REN ⁺ AEL ⁺ AREI ⁺ ENK ⁺ VREHL ⁺ GVTPMGAV...TLAE ⁺ EEVEED.....	352
GDKIGGQK ⁺ AN ⁺ ACKYL ⁺ KEN ⁺ PEI ⁺ AK ⁺ TL ⁺ DKKL ⁺ REML ⁺ LN ⁺ PENMQLI..AETSSAAD ⁺ DVEFGAVPE.....EF.....	354
GDKIGGQK ⁺ AN ⁺ ACKYL ⁺ KEN ⁺ PEI ⁺ AK ⁺ TL ⁺ DKKL ⁺ REML ⁺ LN ⁺ PENMQLI..AETSSAAD ⁺ DVEFGAVPE.....EF.....	354
GNKIGGQK ⁺ KNN ⁺ VIRY ⁺ FEENT ⁺ QIA ⁺ EIE ⁺ ERN ⁺ IREQLLT ⁺ TGTNGAV..Q.I.EDEE ⁺ EPD..LLE.....S.....	349
GNKIGGQK ⁺ KNN ⁺ VIRY ⁺ FEENN ⁺ QIA ⁺ EIE ⁺ ERN ⁺ IREQLLT ⁺ TGTNGAV..Q.I.EDEE ⁺ EPD..LLE.....S.....	349
GNKIGGQK ⁺ KNN ⁺ VIRY ⁺ LEEN ⁺ PQISTE ⁺ IE ⁺ AVIREQLLT ⁺ TKASDQTA..A.HDETEE ⁺ EPD..LLES.....	349
GSKIGGQK ⁺ ANA ⁺ AKYLE ⁺ EN ⁺ PEI ⁺ AG ⁺ IE ⁺ QQIR ⁺ AKLL ⁺ VT ⁺ SANTKA..TPVAEDLAD ⁺ AD..I.....	347

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NTDB id 600 KW2 RS01765 WP 011675413.1		387						
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEIEE	388						
NTDB id 228 SPD RS09265 WP 001085462.1	EIEIEE	388						
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NTDB id 159 SP RS09750 WP 001085462.1	EIEIEE	388						
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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