	1	10	20	30	40	50	60	70	80	90	100	110	120		130	140	150	160	170	180	190	200
Unc51 ULK1 ULK2 ULK4	1	MEPGR	GGTETVGKEE	ESRKDI TGHO	AFAIYYRGRYY Afayyfkgrhr Afayyfrgrhr Sktyyykgrrk	EKHDI EVAVI	CTNKKNI AK	SOTI I GKETK	I KEIKI	HENTVALYDI	FOFMANSVYL	VHEYCNGGD	ADYL HANRI	TLNED TLSED			TIQHF	I DOTAGAMRI	LHSKGTTHR	I KPONTLES	NPAG-RRANP	NSTRVK
Atg1 ULK3		MAG	NHNLMASAGN Pghgpprldg	YTAEKEIGKG Filterlgsg	isfatyyrghlt Ityatyykayak	SDKSQH <mark>vai</mark> Kdtrev <mark>vai</mark>	EYSRAKLKN Cya <mark>kk</mark> slnki	KKLLENL <mark>et</mark> e: RSYenllti	AI-LKKIK IEILKGIR	HPHIYGLID HPHIYQLKDI	CERTSTDFYL Fqhdsdniyl	INEYCALGO	TFLLKRRKE SRFIHTRRJ	elmenhpli Ilpek	LRTYFEKYF	PPSENHNG	lhrafyls <mark>y</mark> yaryf	'LQQLASALKF 'Hqqlasalqf	LRSKNLYHRD	IKPQNLLLS	TPLIGYHDSK Slekphlk 	SFHELGFY
Consensus	201	210	220	230	i.fa.¥%kgr 240	250	260	270	280	290	300	310	320	0 :	330	340	350	360	370	JIKPqniLLs 380	 390	400
	-LADF	GFARFLND	6		ISPHYHAPEVIN ISPHYHAPEVIN	sho <mark>y</mark> daka <mark>dl</mark>	ASIGTILFQ	CLT <mark>gkapf</mark> ya	otpp <mark>ol</mark> kay	YEKTRELRP	NIPEHO	SPHERDLE	RLLKRNAKDE	RISFEDFF	NHPFLT	SPLL	PS <mark>PSKRIL</mark> E	SARSPLLAN	RIITPOSSLP			
ULK2 ULK4 Atg1	NLEEF	FALVAAEE	GGDNGENYL	KKSMKSRYK	ISPHYHAPEVIN ISPYYTAPEVYR ISPLYHAPEILN	GADFSISSDL	HSLGCLLYE	HFSGKPPFFS	SISELTEK	ILCEDPLPP:	EPKDSSRPKF	SSDFINLLD	LLORDPOK	RLTHTRLL	QHSFAKKA-	FAGAD	QESSYEDLS	LSRNTHECSG	PODSKELLON	ISQSRQAKGH	ksgq <mark>p</mark> lghsf	RLENPTEF
ULK3 Consensus	-LADF	GFAQHMSP	4	DEKHYLRG	ISPLYHAPENYC	QRQ <mark>Y</mark> DARY <mark>DL</mark>	HSHGYTLYE	ALFGQPPFASI	RSFSELEEK	IRSNRVIEL-	PLRPLL	SRDCRDLLQ	RLLERDPSRF	RISFQDFF	AHPWYD	LE	HMPSGESLG	RATALYYQAY	'KKDQEGD <mark>s</mark> aa	ALSLYCKAL	DFFY <mark>palhy</mark> e	Ydaqrkea
	1				440			470	480	490		510		+		540	550	560	570	580	590	600 1
	66S	KDSSCDTD	DFYHYPAQ	FPGDLVAEA	SAKPPPDSLHC	SGSSLYASAG	LESHGRTPS	PSPPCSSSPS	SGRAGPES	SSRCGASYP:	EPYPTQYQNY	QRIE-RNLQ	SPTQFQT	PRSSA	IRRSGSTSF	LGFARASP	SPPA	HAEHG-GYLA	RKHSLGGGRP	YTPSPQYGT	IPERPGHSGT	PSPQGAEN
ULK4 Atg1 ULK3	TAPAY	KTDHTQAY	DKKASNNKYH	NSLYSDRSFE	'gedhthcspqk :Reyyyyekksy irdllremardk	EYNSLADEYF	QAGENPNPI	KHPTSTQNQN	/LLNEQFSPI	NNQQYFQNQI	Genprllrat	SSSSGGSDG	SRRPS	-LYDRRLS	IS <mark>slnps</mark> nf	ILSRALGIA	STRLFGGAN	HQEVATRLLH Iqqqqqqqtts	ISPLFQLLIQH Ssppysqtlln	ILRIAPNHDI I-sqlfhelt	RAKŸAHŸIGL ENIILRIDHL	lashtael Qhpetlkl
Consensus	•••••	•••••	••••• <mark>P</mark> •••	••••• P	••••••			s		•••••P		el.	•••••	···· ^r ····	ss.	ls.a	•••••			pt		•••P•••••
Unc51	601 ERMTM	+ P	620 NPTFVV	630 CGSSTKPSPN	640 INA-NRYRRS	TITSPAD	+	670	680 +	690 TQDM	/AADOMLSNL	710 + 	-IPKSATTA	HINIOGI	730 +	740	750 +	760	-PRGARDRSY	/80 /TSP	/90	1 POPTI
ULK1 ULK2 ULK4 Atg1	RSRNS Qentp	SGSPV- VVEAIVLL	PQAQSPQSLL Telirenfrn	SGARLQSAPT Sklkqcllpt	ILSDL-HYVRPK Iltdi-Yqnkqk Ilgeliylyntq .sttlkgmanfe	lrkqhsdpv(Eekkknpre(PSHTGAGYS Wayplaayt	YSPOPSRPGSI VLMRCLREGEI	.GTSPTKHL	GSSPRSSDNI Kiienvctti	FKTPLPTII	GSPTKTTAP	KIPKTQASS FRHSTADSL	SNLLALYTI LRITAYSA	RHGPAEEQS	KDGNEP	RECAHCLLY	QGSERQRAEQ Islasaickyq	iqskavfgrsv Iqymltlfaam	'STGKLSDQQ Ilscgihlqr	GKTPICR Liqekgfyst	HQGSTDSL IIRLLDSP
ULK3 Consensus	•••••	•••••		P.		•••••		•••••		•••••			•••P•••••	•••••	•••••		•••••					
	801 I	+	820	830	840	850	860	870	880	890	900	+		+	930	940	950	960	970	980	990	1000
Unc51 ULK1 ULK2 ULK4 Atg1 ULK3	Q-EKP NTERP Stcir	MEIAPSAG HDIAPAGA Akaflyll	FGGSLHPGAR CGGVLAPPA- YILIYNREML	AGGTSSPSPY -GTAASSKAY Llscoarlyh	PFIIKNQTTCS VFTVGSPPSGS VLFTVGSPPHSA VIERDSRKTTP IELKGENLYNCE	TPPQGP Raptcthmfl Gkeqosgney	RTRMFSAGP RTRTTSYGP LSKCLDLLT	TGSASSS SNSGGSLCANS CHIYOELPRI	SARHLYI Sgrycygspi _gdtln-sli	PGP-CSEAPI PGPGFGSSPI ANYSGRKHPS	APELPAPGHO PGAEAAPSLR STYOYKOLKL	CSFADPIAA YVPYGASPP CLPLMPYYL	ILEGAVTFEF Sleglitfef Ilvtsøvfrf	APDLPEETI Apelpeeti Poyyteefi	LMEQEH-TE LMEREH-TO	ILRGLRFT TLRHLNVH	LLFVQHVLE Lhftecvlo	IAALKGSASE	AAGGPEYQ	LQESYVADQ IQESYVADQ	ISLLSRENGF ISQLSKDNGN	AEQLYLYL Veqlylyn
Consensus			1020	 1030		<mark>s</mark> 1050		P 1070	1080									1160	1170	1180		lv 1200
ULK1 ULK2	i Ralhm Kyael Kaaql	lssglqsa Laaslhla	QTNYANRY IDQIRAGK KAQIKSGK	LHPSVAVQQV LCLSSTVKQV LSPSTAVKQV	LINGUNDKYHQC VRRLNELYKAS VKNLNERYKFC	LYRSQELA-S Vyscqglslf Thckklte	LGLPGQDPA LQRFFLDKQ LNRFFSDKQ	HAVISI RLLDRIHSITI RFIDEINSYTI	ERIMYRHA Perlifsha Pekliynca	IELCOAAALI Vohvosaali Vehvosaali	DEMFQHREGO Demfqqted1	SQRYQTAYN Ypryhkall Yyryhkall	ILHTLAEQYN Leglohmls Leglsrilo	+ NCDQDKTYI SDQADIEN' QDPADIEN'	+ LTRYKYAYE YTKCKLCIE YHKYKCSIE	RRLSALLT	GICA Staty	·+	+	+	+	1
ULK4 Atg1 ULK3					DSDSNLLALIR	•									•							SUSUEDPŲ
Consensus		1 1210	 1220	v 1230	1240	1250	1260	1270							330333	1	•••••	•••••	•••••	••••	•••••	•••••
Unc51 ULK1 ULK2 ULK4 Atg1 ULK3 Consensus	I	LLLNRPLT	DLISLLIPLL	PNEDPEIFDV	YSSKCLSILVQL	YGGENPDSLS	PENVEIFAH	LLTSKEDPKE	QKLLLRILR	RMITSNEKHI	LESLKNAGSL	LRALERLAP	isgsfadsa\	+	+1 LQAYGH							

Supplemental Figure 1. Alignment of the amino acid sequences of Atg1 homologues from yeast, C. elegans, and homo sapiens (ULK1, ULK2, ULK3 and ULK4). The software Multalin (F. Corpet (1988). Nucl. Acids Res., 16 (22), 10881-10890) was used.