Gu: Deconvoluting AMPK adenine nucleotide binding and sensing

Supplemental Table 1: Complete Δ HDX-MS peptide list for the γ 1-subunit. Resolved peptides are listed in the first column and % changes in HDX are indicated by numbers and heat map color.

Sequence	Charge	Start	END -	w	α1β2γ1 AMPK with	out added nucleotid	es versus	CBS4 only	CBS3 only	CBS1 only
	Gilaige		END -	2.5 mM AMP	2.5 mM ATP	Non-stress AXP	Stress AXP		+ 2.5 mM AMP	
NEHPQETPESNNSVY	2	15	29	N/A	N/A	N/A	N/A	6 (3)	5 (4)*	N/A
MKSHRCYDLIPTSSKL	2	33	48	1 (3)*	2 (1)*	1 (1)	0 (1)*	2 (1)*	1 (1)	1 (1)
VFDTSL	1	49	55	-1 (2)*	0 (1)*	0 (1)*	0 (0)*	0 (0)*	0 (0)	0 (0)*
OTSLQVKKAFF	2	52	62	N/A	1 (2)*	N/A	-3 (2)	0 (2)*	0 (2)*	0 (1)
QVKKAF	2	56	61	N/A	0 (1)*	N/A	-1 (1)	-1 (2)*	0 (1)*	N/A
QVKKAFF	2	56	62	0 (1)*	-1 (1)*	0 (1)	0 (1)	-1 (0)*	0 (0)	0 (0)*
TITD	1	86	90	N/A	-1(1) N/A	N/A	N/A	20 (3)	16 (4)	N/A
		86								
LTITDF	1		91	-9 (4)	4 (5)*	-13 (2)	-15 (2)	12 (2)	10 (2)	-3 (2)
FINILHRYYKSAL	2	91	103	N/A	N/A	N/A	N/A	-12 (4)	-4 (3)	N/A
FINILHRYYKSAL	3	91	103	N/A	-14 (2)	-7 (3)	-10 (2)	-13 (3)	-5 (3)	-7 (2)
NILHRYYKSAL	2	92	103	-1 (2)	-14 (2)	-8 (2)	-10 (2)	-14 (2)	-4 (3)	-7 (2)
NILHRYYKSAL	3	92	103	-2 (3)	-14 (2)	-8 (2)	-10 (2)	-14 (2)	-5 (3)	-7 (2)
VQIYE	1	104	108	3 (3)	12 (3)	8 (2)	9 (3)	8 (3)	5 (3)*	10 (2)
/QIYEL	1	104	109	N/A	6 (3)	5 (3)	5 (4)	2 (3)*	3 (3)	7 (2)
EEHKIET	1	109	116	N/A	-13 (4)	-10 (2)	-11 (2)	-16 (3)	-6 (3)	-6 (1)
EEHKIET	2	109	116	-7 (3)	-12 (4)	-10 (2)	-11 (2)	-16 (3)	-7 (3)	-6 (1)
EEHKIETWRE	2	109	119	N/A	-13 (4)	N/A	N/A	-15 (4)	-7 (3)	N/A
	1									
VREVYLQD	1	117	124	N/A	-6 (4)	-4 (3)	-6 (3)	-2 (5)*	2 (3)	-7 (3)
VREVYLQD	2	117	124	-10 (3)	-7 (3)	-7 (2)	-7 (2)	-3 (2)*	1 (3)	-5 (2)
FKPLVC	2	125	131	-6 (3)	0 (3)*	-3 (3)	-4 (4)	N/A	N/A	-2 (2)
DAVSSL	1	139	145	0 (1)*	0 (1)*	0 (1)*	0 (1)*	N/A	0 (0)	0 (0)
/ILTHKRILKF	2	165	175	-1 (1)	1 (0)*	-1 (0)	-1 (0)	N/A	1 (0)	0 (0)
/ILTHKRILKF	3	165	175	-1 (1)*	0 (0)*	-1 (0)	-1 (0)	N/A	1 (0)	0 (0)
LTHKRILKF	3	166	175	-1 (2)*	0 (1)*	-1 (1)	-1 (1)*	N/A	1 (1)*	0 (1)
TITEFPKPEF	1	179	188	-1 (4)*	2 (3)*	0 (3)	-2 (3)	N/A	5 (4)	-2 (3)
TITEFPKPEF	2	179	188	-1 (3)*	2 (3)*	-1 (3)	-2 (3) -2 (3)	N/A	4 (4)	-2 (3) -3 (3)
MSKSLEE	1	189	195		2 (3)* N/A			N/A N/A	-13 (4)	
	1			-4 (2)		-6 (1)	-6 (1)			N/A
ISKSLEE	2	189	195	-2 (2)	N/A	-7 (1)	-7 (1)	N/A	-12 (3)	-23 (2)
QIGT	1	196	200	-4 (2)	N/A	-8 (2)	-7 (1)	-27 (3)	-16 (3)	-26 (2)
QIGTY	1	196	201	-8 (3)	N/A	-10 (1)	-8 (1)	-31 (4)	-15 (2)	-24 (3)
ANIAM	1	201	206	-7 (4)	-14 (4)	-9 (2)	-10 (2)	-19 (3)	-4 (3)	-10 (3)
NIAM	1	202	206	N/A	-19 (3)	-12 (4)	-11 (3)	-22 (3)	N/A	-14 (3)
IVRTTTPVY	2	206	214	-3 (3)*	-14 (5)	-4 (3)	-5 (3)	-19 (3)	-8 (4)	-19 (3)
RTTTPVY	1	207	214	-6 (3)	-17 (4)	-6 (2)	-6 (2)	-24 (3)	-10 (3)	-22 (3)
RTTTPVY	2	207	214	-3 (3)	-17 (4)	-6 (2)		-24 (3)	-10 (3)	-20 (2)
	2	218	228				-6 (2)			
GIFVQHRVSAL	2			N/A	-25 (3)	N/A	N/A	N/A	-6 (3)	N/A
/QHRVSAL	1	221	228	-13 (4)	-34 (3)	-14 (2)	-16 (2)	-29 (3)	-6 (3)	-15 (3)
/QHRVSAL	2	221	228	-10 (4)	-33 (4)	-14 (3)	-16 (2)	-29 (3)	-6 (4)	-15 (3)
PVVDEKGRVVD	3	229	239	N/A	-16 (4)	-7 (2)	-9 (1)	-20 (3)	-12 (4)	N/A
VVDEKGRVVDI	3	229	240	-9 (4)*	-17 (4)	-9 (1)	-9 (1)	-21 (3)	-12 (3)	-20 (2)
PVVDEKGRVVDIYSKF	2	229	244	-7 (2)	-17 (3)	-11 (1)	-11 (1)	-21 (2)	-11 (2)	-19 (2)
GRVVDIYSKF	3	234	244	N/A	N/A	N/A	N/A	-20 (3)	N/A	-16 (2)
YSKF	2	240	244	N/A	-18 (4)	N/A	N/A	-15 (3)	-9 (4)	N/A
OVINL	1	245	249		-16 (2)		-7 (1)			
	1			-2 (2)*		-6 (1)		-18 (1)	-7 (3)	-13 (1)
AEKTYNNL	2	250	258	0 (4)*	-8 (3)	-6 (3)	-10 (3)	-19 (4)	0 (4)	-2 (4)
MEKTYNNLD	2	250	259	N/A	-11 (5)	N/A	N/A	-22 (4)	-3 (4)	N/A
OVSVTKALQHRSHY	3	259	272	N/A	N/A	N/A	N/A	-24 (3)	N/A	N/A
VSVTKALQHRSHYFEGGGKC	2	259	279	N/A	N/A	N/A	N/A	-20 (4)	N/A	-17 (3)
CYLHETLET	2	278	287	N/A	-3 (2)*	-4 (2)	-3 (2)	N/A	-3 (2)*	N/A
LHETL	1	280	285	-4 (3)	-5 (2)	-4 (2)	-5 (2)	N/A	-4 (2)	N/A
LHETLET	2	280	287	-1 (1)	-3 (1)*	-2 (1)	-2 (1)	-12 (2)	-3 (1)	-14 (2)
ETLET	1	282	287	N/A	-3 (1)*	-3 (1)	-2 (1) -2 (1)	-10 (1)	-2 (1)	-11 (1)
	2	286	294							
TIINRLVE	2	286		-2 (1)	0 (4)*	-1 (0)	-1 (0)	-2 (1)*	-1 (0)	-1 (1)
INRLVE	2		294	-3 (1)	-2 (1)*	-2 (1)	-2 (1)	-2 (1)*	0 (1)	-1 (1)
NRLVEA	2	288	295	N/A	-5 (2)*	-5 (1)	-5 (1)	4 (2)*	1 (1)	3 (2)
EVHRLVV	2	295	302	-6 (3)	-9 (2)	-7 (1)	-9 (1)	2 (3)*	-1 (2)	1 (3)
EVHRLVVVDEND	2	295	307	-4 (2)	-6 (2)	-5 (2)	-6 (1)	-1 (2)*	-3 (2)	-6 (1)
EVHRLVVVDEND	3	295	307	N/A	-6 (2)	-5 (2)	-5 (1)	-1 (2)*	-2 (3)	-5 (2)
DENDVVKGDVSL	2	303	315	N/A	N/A	N/A	N/A	N/A	-6 (2)	N/A
DENDVVKGIVSL	2	303	315	-3 (2)	-8 (2)	-4 (1)	-3 (1)	-9 (2)	N/A	N/A
DVVKG	1	306	311	N/A	-12 (5)	N/A	-7 (4)	-8 (3)	-9 (4)	-8 (3)
	2									
DVVKGDVSL	2	306	315	N/A	N/A	N/A	N/A	N/A	-9 (2)	-19 (1)
VVKGDVSL	2	307	315	N/A	N/A	N/A	N/A	N/A	-5 (3)	-13 (3)
VKGIVSL	2	308	315	-3 (1)	-10 (2)	-5 (1)	-4 (1)	-12 (1)	N/A	N/A
VKGDVSL	2	308	315	N/A	N/A	N/A	N/A	N/A	-9 (3)	-20 (2)
DILQA	1	316	321	1 (1)*	-1 (0)*	0 (1)*	0 (0)*	-1 (0)*	-1 (0)	-2 (0)
QALVLTGGEKKP	2	320	331	N/A	2 (4)*	2 (3)	0 (3)	1 (4)*	4 (3)	-2 (3)
ALVLTGGEKKP	2	321	331	N/A	2 (5)*	N/A	N/A	2 (3)*	3 (4)	-1 (3)
LVLTGGEKKP	2	322	331		2 (4)*	3 (4)	1 (3)			
	_			0 (4)*				3 (3)*	4 (4)	-1 (4)
LVLTGGEKKP	3	322	331	1 (4)	3 (4)*	2 (4)	-1 (3)*	4 (3)*	4 (4)	0 (4)