

Table S1 Primer sequences used in qRT-PCR

Gene name	Reference ID	Sequence (5' → 3')	Product size (bp)
<i>GAPDH</i>	NM_001034034.2	F: TTGTCTCCTGCGACTTCAACA R: TCGTACCAGGAAATGAGCTTGAC	103
<i>UXT</i>	NM_001037471.2	F: TGTGGCCCTTGGATATGGTT R: GGTTGTCGCTGAGCTCTGTG	101
<i>RPS9</i>	NM_001101152.2	F: CCTCGACCAAGAGCTGAAG R: CCTCCAGACCTCACGTTTGTTTC	64
<i>SLC1A1</i>	NM_174599.2	F: GGCTTGCAATCCACTCCATT R: CAGAAGAGCTGGGCCATT	101
<i>SLC1A5</i>	NM_174601.2	F: CTGGTGAAGGTGCCCACTG R: GAAGAAGCGAATGAGCAGCTC	129
<i>SLC3A2</i>	NM_001024488.2	F: GTGTGGACGGGTTTCAGGTC R: CCGATCCTCACTGACGCTCT	101
<i>SLC7A1</i>	NM_001135792.1	F: CTTGACCTGAAGGACCTGG R: GCTCGGGCTGGTATCGTAAG	101
<i>SLC7A5</i>	NM_174613.2	F: GGGTGACGTAGCCAATCTGG R: ATCCCCATAGGCAAAGAGG	107
<i>SLC38A2</i>	NM_001082424	F: TGAAAAGCCATTATGCCGATGT R: CCCACAATCGCATTGCTCAG	148
<i>SLC38A9</i>	NM_001102163	F: GGGCATAAAACAGGCTGGGT R: CTTGACCACTGCCAAAGGA	183
<i>CASTOR1</i>	NM_001081514.1	F: CTGCACATCCTAGAGCACCG R: AAGAACTTGCACCGGCTTCG	119
<i>MIOS</i>	NM_001192318.1	F: CTTCCGAGGCCGAGATGAG R: TCAGAGAGTCCAGTTAGGTCCA	140
<i>DEPDC5</i>	XM_005218191.4	F: GACTCTGGGGGCGTAGGAG R: TCATCTTGCCTCCCCGCA	118
<i>RRAGA</i>	NM_001035499.1	F: CTTGCGCTTCCCAGCTGTA R: CTGTATTTGGCATCACCCGC	147
<i>WDR24</i>	NM_001045973.2	F: TGGATACAGCCGAGCGTTAC R: CGTCTGAGCCACCTGGTTAC	107
<i>TAS1R3</i>	XM_015466888.1	F: AATGTGGACCTTGCTTATG R: AGATCATGCTGGAGAACT	115
<i>PIK3C3</i>	NM_001099067.1	F: GCCAAGCATTGTTGAAGGGT R: GCACCAGCCGATCTACAAAAG	87
<i>SIRT1</i>	NM_001192980.3	F: TCATGGTTCCTTTGCAACAGC R: AGGACATCGAGGAACCACCTG	103
<i>NAMPT</i>	NM_001244141.1	F: TTCTGGTGGAGCCTTGCTAC R: GAAGACGTTAATCCCAAGGCCA	100
<i>STK11</i>	DN517838	F: GCCCCTCTTTTGAAGCTT R: TTATCCGCAAGATGTCTGCG	151

Table S2 RT-PCR performance

Gene	Median Ct	Median Δ Ct	Slope	R ²	Efficiency
<i>GAPDH</i>	17.945		-3.29	0.999	2.012
<i>UTX</i>	23.081		-3.30	0.997	2.009
<i>RPS9</i>	18.782		-3.23	0.999	2.038
<i>SLC1A1</i>	22.911	3.088	-3.36	0.999	1.986
<i>SLC1A5</i>	21.738	1.940	-3.24	0.996	2.036
<i>SLC3A2</i>	22.356	2.482	-3.32	0.995	2.000
<i>SLC7A1</i>	23.452	3.648	-3.26	0.994	2.026
<i>SLC7A5</i>	23.053	3.261	-3.28	0.994	2.016
<i>SLC38A2</i>	19.990	0.146	-3.25	0.999	2.030
<i>SLC38A9</i>	23.957	4.106	-3.24	0.998	2.035
<i>CASTOR1</i>	32.786	13.032	-3.38	0.997	1.977
<i>MIOS</i>	27.968	8.191	-3.46	0.992	1.945
<i>DEPDC5</i>	26.975	7.164	-3.19	0.999	2.058
<i>RRAGA</i>	22.129	2.328	-3.32	0.996	2.001
<i>WDR24</i>	25.060	5.292	-3.28	0.999	2.018
<i>TAS1R3</i>	31.379	11.514	-3.11	0.997	2.097
<i>PIK3C3</i>	24.788	4.952	-3.17	0.992	2.070
<i>SIRT1</i>	25.510	5.711	-3.22	0.996	2.046
<i>NAMPT</i>	23.749	3.913	-3.05	0.998	2.128
<i>STK11</i>	24.616	4.809	-3.22	0.992	2.043

Table S3 Antibodies used for western blotting

Antibody	Cat. No.	Source	Molecular Weight (kDa)	Dilution
CASTOR1	ARP70446_P050	Avivasysbio.	36	1:125
MIOS	ab202274	Abcam	99	1:1000
NPRL3	ab229735	Abcam	64	1:500
RRAGA	ab91062	Abcam	35	1:250
PIK3C3	ab227861	Abcam	120	1:500
α s1-casein	ab166596	Abcam	22	1:200
ERK	OASE00362	Aviva Syst. Biol.	44, 42	1:1000
p-ERK(Thr ²⁰² /Tyr ²⁰⁴)	4370T	Cell Signaling Technol.	44, 42	1:1000
Akt	9272S	Cell Signaling Technol.	60	1:1000
p-Akt(Ser ⁴⁷³)	9271S	Cell Signaling Technol.	60	1:250
AMPK	5831S	Cell Signaling Technol.	62	1:1000
p-AMPK(Thr ¹⁷²)	2535	Cell Signaling Technol.	62	1:250
TSC2	4308	Cell Signaling Technol.	200	1:500
p-TSC2(Thr ¹⁴⁶²)	3617S	Cell Signaling Technol.	200	1:250
mTOR	2972S	Cell Signaling Technol.	289	1:1000
p-mTOR(Ser ²⁴⁴⁸)	2971S	Cell Signaling Technol.	289	1:1000
CLOCK	ARP33730_P050	Aviva Syst. Biol.	95	1:500
ARNT1	ab93806	Abcam	69	1:250
CRY1	ab229631	Abcam	66	1:250
PER1	SC398890	Santa Cruz Biotechnol.	136	1:200
PER2	20359-1-AP	Proteintech	136	1:100
GAPDH	2118S	Cell Signaling Technol.	37	1:1000
Anti-rabbit IgG	7074	Cell Signaling Technol.		1:1500
m-IgGk BP-HRP	SC516102	Santa Cruz Biotechnol.		1:1500

Table S4 Description of amino acid transporters evaluated

AA transporter	Name	Function
<i>SCL1A1 (EAAT3)</i>	solute carrier family 1 member 1	Glutamate transporter
<i>SLC1A5 (ASCT2)</i>	solute carrier family 1 member 5	Neutral amino acid transporter
<i>SCL3A2 (4F2hc)</i>	solute carrier family 3 member 2	Heavy-chain amino acid transporter
<i>SLC7A1 (CAT1)</i>	solute carrier family 7 member 1	High affinity cationic amino acid transporter
<i>SCL7A5 (LAT1)</i>	solute carrier family 7 member 5	Branched-chain and aromatic amino acid transporter
<i>SCL38A2</i>	solute carrier family 38 member 2	Na ⁺ -coupled neutral amino acid transporter
<i>SCL38A9</i>	solute carrier family 38 member 9	Na ⁺ -coupled neutral amino acid transporter

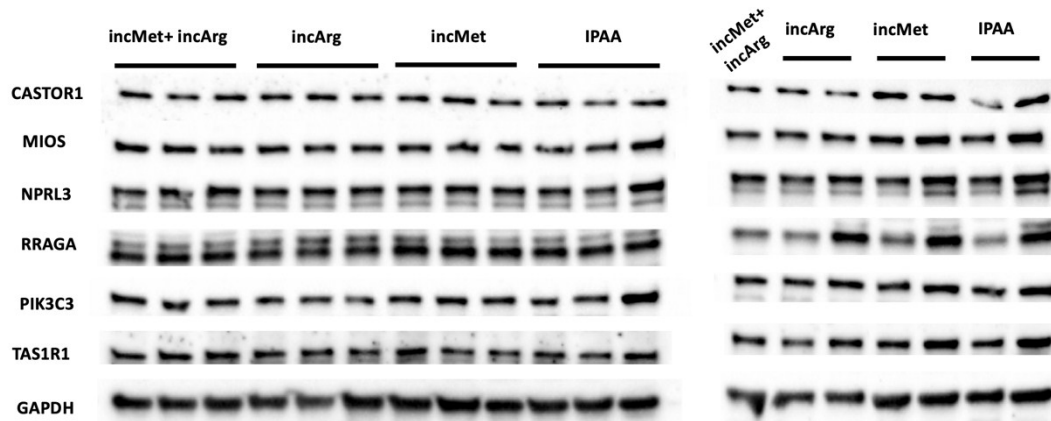


Figure S1 Representative western blots¹ of regulators of the mTORC1 pathway

¹ Five replicates per treatment were subjected to two 10% SDS/PAGE gels.

The intensity of GAPDH was used to normalize target protein abundance.

IPAA = ideal profile of AA, Lys:Met 2.9:1, Lys:Arg 2:1; incArg = increased supply of Arg, Lys:Met 2.9:1, Lys:Arg 1:1; incMet = increased supply of Met, Lys:Met 2.5:1, Lys:Arg 2:1; incMet+ incArg = increased supply both of Met and Arg, Lys:Met 2.5:1, Lys:Arg 1:1.

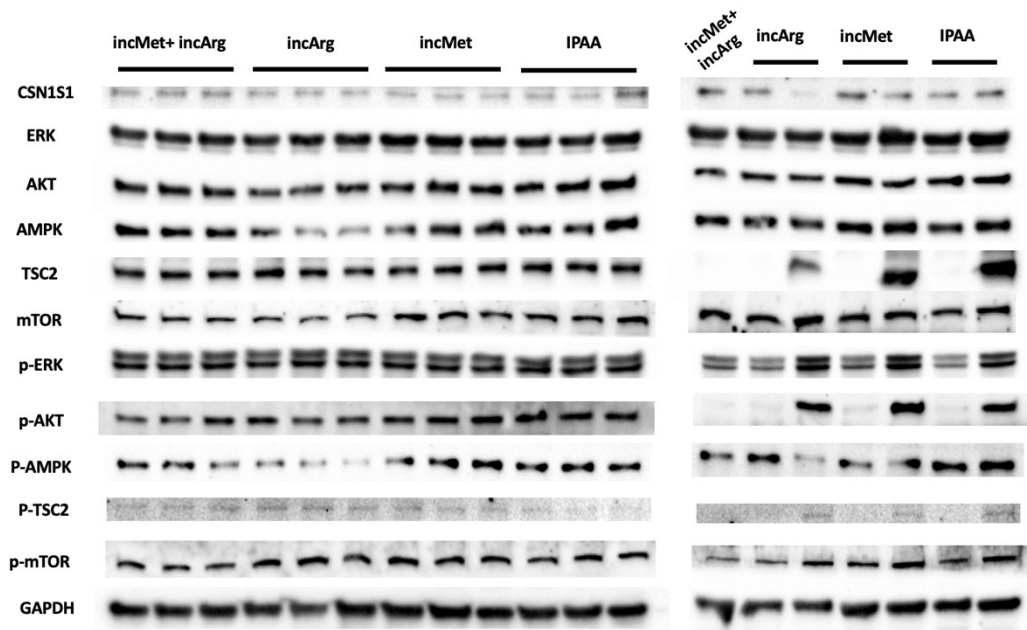


Figure S2 Representative western blot¹ of α -s1-casein and components in mTORC1 related pathways

¹ Five replicates per treatment were subjected to two 10% SDS/PAGE gels.

The intensity of GAPDH was used to normalize target protein abundance.

IPAA = ideal profile of AA, Lys:Met 2.9:1, Lys:Arg 2:1; incArg = increased supply of Arg, Lys:Met 2.9:1, Lys:Arg 1:1; incMet = increased supply of Met, Lys:Met 2.5:1, Lys:Arg 2:1; incMet+ incArg = increased supply both of Met and Arg,

Lys:Met
2.5:1,
Lys:Arg
1:1.

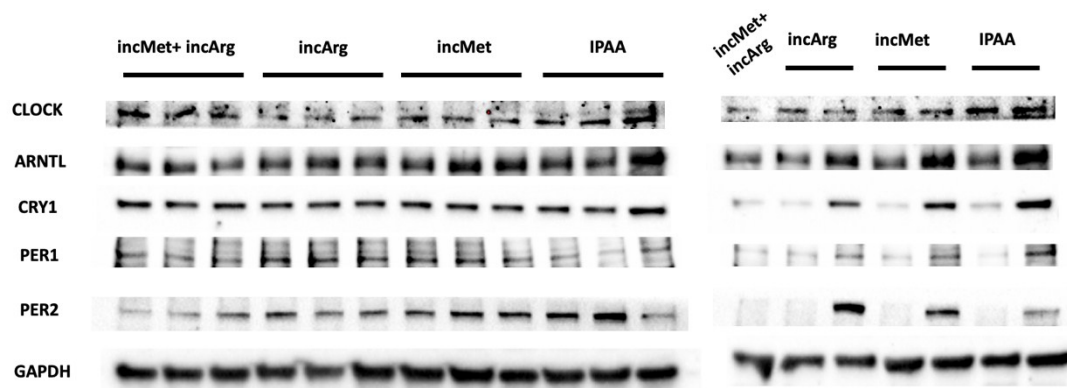


Figure S3 Representative western blot of circadian clock proteins

¹Five replicates per treatment were subjected to two 10% SDS/PAGE gels.

The intensity of GAPDH was used to normalize target protein abundance.

IPAA = ideal profile of AA, Lys:Met 2.9:1, Lys:Arg 2:1; incArg = increased supply of Arg, Lys:Met 2.9:1, Lys:Arg 1:1; incMet = increased supply of Met, Lys:Met 2.5:1, Lys:Arg 2:1; incMet+ incArg = increased supply both of Met and Arg, Lys:Met 2.5:1, Lys:Arg 1:1.