

**Pyruvate kinase M knockdown induced signaling via AMP-activated protein kinase promotes mitochondrial biogenesis, autophagy, and cancer cell survival**

**Gopinath Prakasam<sup>1</sup>, Rajnish Kumar Singh<sup>1,2</sup>, Mohammad Askandar Iqbal<sup>1,3</sup>, Sunil Kumar Saini<sup>1</sup>, Ashu Bhan Tikku<sup>4</sup>, Rameshwar N.K. Bamezai<sup>1,\*</sup>**

**Author's affiliations**

1. National Center for Applied Human Genetics, School of Life Sciences, Jawaharlal Nehru University, New Delhi 110067, India. 2. Department of Microbiology and Tumor Virology Program of the Abramson Cancer Center, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania 19104. 3. Department of Biotechnology, Faculty of Natural Sciences, Jamia Millia Islamia, New Delhi 110025, India. 4. Radiation and Cancer Therapeutics Laboratory, School of Life Science, Jawaharlal Nehru University, New Delhi 110067, India.

\* Correspondence: School of Life Sciences, Jawaharlal Nehru University, New Delhi-110067, India. Fax: 0091-11-26742211. E-mail: [bamezai@hotmail.com](mailto:bamezai@hotmail.com).

**Running Title:** PKM knockdown activates AMPK to prevent cancer cell death.

**Table S1.** List of proteins identified as PKM1 interacting partners using LC/MS-MS.

<b>Accession I.D.</b>	<b>Entry</b>	<b>Description</b>	<b>Mass (Da)</b>	<b>Peptides</b>	<b>Coverage (%)</b>	<b>PLGS Score</b>
<b>P63261</b>	ACTG	Actin cytoplasmic 2	41765	13	31.4667	892.889
<b>P12814</b>	ACTN1	Alpha actinin 1	102992	32	28.5874	623.7095
<b>O43707</b>	ACTN4	Alpha actinin 4	104788	58	48.5181	1891.53
<b>P04083</b>	ANXA1	Annexin A1	38689	14	28.9017	336.3753
<b>P07355</b>	ANXA2	Annexin A2	38651	12	28.9086	850.7295
<b>P48047</b>	ATPO	ATP synthase subunit O mitochondrial	23262	7	33.8028	315.8188
<b>P33993</b>	MCM7	DNA replication licensing factor MCM7	81256	24	32.267	712.8558
<b>P68104</b>	EF1A1	Elongation factor 1 alpha 1	50109	33	47.8355	4913.585
<b>P24534</b>	EF1B	Elongation factor 1 beta	24748	3	10.6667	411.1423
<b>P04075</b>	ALDOA	Fructose biphosphate aldolase A	39395	14	48.3517	1219.534
<b>P04406</b>	G3P	Glyceraldehyde 3 phosphate dehydrogenase	36030	26	60.597	1782.219
<b>P11142</b>	HSP7C	Heat shock cognate 71 kDa protein	70827	16	22.1362	524.3831
<b>P22392-2</b>	NDKB	Isoform 3 of Nucleoside diphosphate kinase B	30117	15	36.7041	1039.605
<b>Q9H254-4</b>	SPTN4	Isoform 4 of Spectrin beta chain non erythrocytic 4	243272	20	12.0241	281.8018
<b>P14618-2</b>	KPYM	Isoform M1 of Pyruvate kinase isozymes M1 M2	58025	24	40.678	584.7386
<b>Q06830</b>	PRDX1	Peroxiredoxin 1	22096	10	38.191	1235.415
<b>Q15102</b>	PA1B3	Platelet activating factor acetylhydrolase IB subunit gamma	25718	10	37.2294	333.5217
<b>P0CG48</b>	UBC	Polyubiquitin C	85533	32	31.5374	1067.547
<b>Q5VTE0</b>	EF1A3	Putative elongation factor 1 alpha like 3	50153	26	38.961	3000.535
<b>A6NJU9</b>	NPIL5	Putative NPIP like protein LOC613037	125886	20	20.826	242.025
<b>P14618</b>	KPYM	Pyruvate kinase isozymes M1 M2	57900	29	43.5028	896.5508
<b>Q8WXA9</b>	SREK1	Splicing regulatory glutamine lysine rich protein 1	59345	32	24.2126	298.4866
<b>P17987</b>	TCPA	T complex protein 1 subunit alpha	60410	12	22.6619	496.8228
<b>P78371</b>	TCPB	T complex protein 1 subunit beta	57452	16	42.243	524.3919
<b>Q99832</b>	TCPH	T complex protein 1 subunit eta G	59328	17	21.7311	673.8492

<b>P49368</b>	TCPG	T complex protein 1 subunit gamma	60495	19	32.6605	740.262
<b>P50990</b>	TCPQ	T complex protein 1 subunit theta GN	59582	21	34.854	483.6839
<b>P40227</b>	TCPZ	T complex protein 1 subunit zeta	57987	19	34.6516	658.8874
<b>P29401</b>	TKT	Transketolase	67834	16	29.695	325.851
<b>P68363</b>	TBA1B	Tubulin alpha 1B chain	50119	35	44.1242	5546.314
<b>P07437</b>	TBB5	Tubulin beta chain	49638	39	43.6937	2897.446

**Table S2.** In silico subcellular localization prediction of PKM isoforms (PKM1 and PKM2).

Software	Localization		Basis of Prediction
	PKM1	PKM2	
CELLO v.2.5	<p>Cytoplasm</p> <p>RELIABILITY:</p> <p>Cytoplasmic 2.831</p> <p>Mitochondrial 0.958</p> <p>Nuclear 0.043</p> <p>Peroxisomal 0.116</p> <p>Cytoskeletal 0.020</p> <p>Plasma Membrane 0.009</p> <p>ER 0.007</p>	<p>Cytoplasm</p> <p>RELIABILITY:</p> <p>Cytoplasmic 2.940</p> <p>Mitochondrial 0.958</p> <p>Nuclear 0.055</p> <p>Peroxisomal 0.111</p> <p>Cytoskeletal 0.029</p> <p>Plasma Membrane 0.014</p> <p>ER 0.007</p>	Amino acid composition and its physicochemical properties (1).
HSLpred	Mitochondrial Protein.	Cytoplasmic Protein.	Support vector machine-based hybrid modules that involves amino acid composition, dipeptide compositions and evolutionary informations of protein (2)
Hum-mPLOC 2.0.	Cytoplasm and Mitochondrion	Cytoplasm and Mitochondrion	Gene ontology, functional domains and sequential evolutionary information (3)
SubLoc v1.0	<p>Mitochondrial</p> <p>Expected accuracy = 74 %</p>	<p>Mitochondrial</p> <p>Expected accuracy = 56 %</p>	Uses vector support machine Amino acid composition (4)

YLoc	<p><b>Cytoplasm</b></p> <p>Probability:</p> <p>Cytoplasm 80.2%, Nucleus 16.9%, Mitochondrion 3.0%, Secreted pathway 0.0%</p>	<p><b>Cytoplasm</b></p> <p>Probability:</p> <p>Cytoplasm 88.2%, Nucleus 7.9 %, Mitochondrion 3.8 %, Secreted pathway 0.0 %</p>	Sequence-based predictions (amino acid composition, sorting signals) (5)
BaCelLo	<p>Cytoplasm LOCALIZATION STEPS:</p> <p>Intracellular - Nucleus or Cytoplasm - Cytoplasm</p>	<p>Cytoplasm LOCALIZATION STEPS:</p> <p>Intracellular - Nucleus or Cytoplasm - Cytoplasm</p>	Support vector machine-based amino acid compositions of both the N- and C- terminal (6).

**Supplementary Table S2. In silico subcellular localization prediction of PKM isoforms.** The methods to predict subcellular Localization of PKM1 and PKM2 were acquired from Zambo et al. (7) where the amino acid sequence of PKM isoforms PKM1 (P14618-2) and PKM2 (P14618) was examined using six online computational tools that employs different algorithms to predict the subcellular localization of PKM isoforms.

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