Supplementary Table 5. Literature Evidence for Alternate Spatio/Functional Distribution of Glycolytic Enzymes

gene	protein name	literature location [1]	experimental function	reference [2]	Direct Antibody Detection [3]	Nuclear Protein interactions [4]
ALDOA	Fructose-bisphosphatealdolase A	N En	protection against cell senescence distribution of V-ATPase compartments	PMID: 14985089 PMID: 21307348	-	BCAT2, EGFR, MLH1, PIAS4
ALDOC	Fructose-bisphosphatealdolase C	N	maintenance of chromatin structure	PMID:9443807	-	-
ENO1	Isoform alpha-enolase of Alpha-enolase Isoform alpha-enolase of Alpha-enolase c-myc promoter binding protein 1 (MBP-1) c-myc promoter binding protein 1 (MBP-1)	P ? N N	plasminogen activation stimulation of IgM production repression of c-myc gene expression p53-p21 dependent senescence	PMID: 12666133 PMID: 1369209 PMID: 20886042 PMID: 18852884	-	ACHE, AGTPBP1, BHLHE40, EP300, GRB2, TSG101,
ENO2	Gamma-enolase	M P	Import of tRNA to mitochondria neurotrophic activity	PMID: 20348443 PMID: 21358174	-	HABP4, HSF1, SNUPN
FBP1	Fructose-1,6-bisphosphatase 1	N	S and G2 phase cell cycle	PMID: 22057438	-	ASL, BIN1
G6PD	Glucose-6-phosphate 1-dehydrogenase	P	VEGF-mediated cellular responses	PMID:19359662	S	-
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	N N N M M R/G S	Oct-1 transcription during S phase SET inhibition of cyclinB-cdk1 activity ubiquitination and degradation of N-CoR pro-apoptotic association with VDAC1 anti-apoptotic reversal of depolarization membrane trafficking switch to pentose phosphate pathway	PMID: 18682386 PMID: 16474839 PMID: 15951807 PMID: 17072346 PMID: 17540177 PMID: 19106097 PMID: 18154684	-	EGFR, KAT5, MAP3K14, MAPK1, MDM2, PRDX1, PSEN1, RPA2,SERPINB9, SGK1, TXN
GPI	Glucose-6-phosphate isomerase Autocrine motility factor	R R	Ca2+ related stress regulation regulation of ubiquitin ligase	PMID: 21252914 PMID: 19603112	N,P,S	-
HK1	Hexokinase-1	M P	binding to VDAC macrophage activation	PMID: 12756287 PMID: 8484732	N,M	MAX, SCMH1
PFKL	6-phosphofructokinase, liver type	P	Binding to vacuolar-type ATPase	PMID: 18632794	-	ATN1, COPS6, IKBKE, NFKB2, RELB, TNFRSF1A
PFKP	6-phosphofructokinase type C	-			-	EIF2C2, MAX, MCC, PRKAB1, TRAF6
PGAM1	Phosphoglyceratemutase 1	N		PMID: 22367961	-	ARL4D, XRCC6
PGD	6-phosphogluconate dehydrogenase	-			-	CDK4, IKBKE, NAA38, PRKAB1, TRAF6
PGK1	Phosphoglycerate kinase 1	N	DNA polymerase cofactor	PMID: 2324090	-	-
PKM2	Isoform M2 of Pyruvate kinase	N	Oct-4 transcription HIF1α transcription cofactor	PMID: 18191611 PMID: 21709315	P,S	ARRB1, ARRB2, LMO7, MDM2, NDRG1, PAX8, RELA
TALDO1	Transaldolase	N	nuclear transport by importin α5	PMID: 21307607	-	CHD3, EIF6, IKBKE, MCC, NAA38, TRAF6, ZHX1
TKT	Transketolase				N	FBXO11, IKBKE, MCC, VHL
TPI1	Triosephosphateisomerase				-	EFGR, SETDB1, SP1

[1] Location key: N – nucleus, M – mitochondrion, En – endosome, P – plasma membrane, R – endoplasmic reticulum, G – Golgi apparatus, S – cytoplasm/cytosol.
[2] Pubmed identifier codes.
[3] Locations measured by direct, large scale antibody screening in the Human Protein Atlas project (Barbe, L. et al. Toward a Confocal Subcellular Atlas of the Human Proteome. Molecular & Cellular Proteomics 2008. 7, 499).
[4] Proteins with GO CC annotation of nucleus with which the glycolytic protein has direct physical association in the IntAct database (Kerrien S et al, The IntAct molecular interaction database in 2012. Nucleic Acids Res. 2012, 40, D841-6.). Only human interactions are included. In all cases, the glycolytic enzyme was a prey.