

Supplementary Tables 6+7. Functional constraint of human sperm proteins used for evolutionary analyses as assessed by gene ontology annotations and numbers of protein-protein interaction partners

Supplementary Table 6. Sperm phosphoproteins with (with) and without Y phosphorylation (without) in human probands: gene ontology (GO) annotations and number of protein-protein interaction partners (nPPI)

Protein	Y phos- phorylation	GO annotation	nPPI
ACADS	without	energy production ¹	5
ACRBP	with	cell recognition ²	0
ACTA2	with	cytoskeleton, flagella and cell movement ³	144
AK8	without	Metabolism ⁴	0
ANXA1	with	cell cycle, apoptosis and oxidative stress ⁵	111
APEH	without	transcription, protein synthesis, transport, folding and turnover ⁶	7
CAPZA1	with	cytoskeleton, flagella and cell movement ⁷	43
CAPZB	without	cytoskeleton, flagella and cell movement ⁷	31
CRISP1	without	cell recognition ⁸	0
DNAJB11	with	transcription, protein synthesis, transport, folding and turnover ⁹	32
ECI1	with	energy production ¹⁰	5
ENO1	without	energy production ¹¹	55
GDI2	without	transcription, protein synthesis, transport, folding and turnover ¹²	48
GK2	without	energy production ¹³	6

Protein	Y phos-phorylation	GO annotation	nPPI
GLUL	without	metabolism ¹⁴	18
GOT1	without	transcription, protein synthesis, transport, folding and turnover ¹⁵	8
GSTM3	with	cell cycle, apoptosis and oxidative stress ¹⁶	14
HIBADH	with	Metabolism ¹⁷	0
HSPA1L	with	transcription, protein synthesis, transport, folding and turnover ¹⁸	138
HSPA9	without	transcription, protein synthesis, transport, folding and turnover ¹⁹	59
HSPD1	without	transcription, protein synthesis, transport, folding and turnover ²⁰	263
IDH3A	without	energy production ²¹	23
LAP3	without	transcription, protein synthesis, transport, folding and turnover ²²	5
LZTFL1	without	signal transduction ²³	5
MPST	with	transcription, protein synthesis, transport, folding and turnover ²⁴	3
NME5	without	cell cycle, apoptosis and oxidative stress ²⁵	4
NME7	without	cytoskeleton, flagella and cell movement ²⁶	11
ODF1	without	cytoskeleton, flagella and cell movement ²⁷	4
PARK7	with	cell cycle, apoptosis and oxidative stress ²⁸	30
PCYT2	without	cell cycle, apoptosis and oxidative stress ²⁹	6

Protein	Y phos- phorylation	GO annotation	nPPI
PDHB	without	energy production ³⁰	24
PHB	without	energy production ³¹	268
PPP1CB	without	transcription, protein synthesis, transport, folding and turnover ³²	93
PRDX4	without	cell cycle, apoptosis and oxidative stress ³³	41
PSMA1	without	transcription, protein synthesis, transport, folding and turnover ³⁴	106
PSMA6	without	transcription, protein synthesis, transport, folding and turnover ³⁴	88
PSMB2	without	transcription, protein synthesis, transport, folding and turnover ³⁴	33
PSMB3	without	transcription, protein synthesis, transport, folding and turnover ³⁴	96
PSMC2	without	transcription, protein synthesis, transport, folding and turnover ³⁵	79
PSMD11	with	transcription, protein synthesis, transport, folding and turnover ³⁶	79
PSMD13	without	transcription, protein synthesis, transport, folding and turnover ³⁷	46
PSMD14	with	transcription, protein synthesis, transport, folding and turnover ³⁸	29
ROPN1	with	energy production ³⁹	2

Protein	Y phos- phorylation	GO annotation	nPPI
SDHA	with	energy production ⁴⁰	16
SPAG6	without	cytoskeleton, flagella and cell movement ⁴¹	1
TEKT1	with	cytoskeleton, flagella and cell movement ⁴²	0
TUBA1A	without	cytoskeleton, flagella and cell movement ⁴³	153
TUBB2A	without	cytoskeleton, flagella and cell movement ⁴³	62
TUBB2C	with	cytoskeleton, flagella and cell movement ⁴³	58
UQCRC1	with	energy production ⁴⁴	19
YWHAZ	without	signal transduction ⁴⁵	121
See below for references.			

Supplementary Table 7. Sperm proteins that were non-phosphorylated in human probands: gene ontology (GO) annotations and number of protein-protein interaction partners (nPPI)

Protein	GO annotation	nPPI
ALDH9A1	Metabolism ⁴⁶	5
CRISP2	cell recognition ⁴⁷	0
DLD	cell recognition ⁴⁸	15
DNAJB8	transcription, protein synthesis, transport, folding and turnover ⁴⁹	0
ECHS1	energy production ⁵⁰	41
PRDX2	cell cycle, apoptosis and oxidative stress ⁵¹	36
SPESP1	cell recognition ⁵²	0
TEKT2	cytoskeleton, flagella and cell movement ⁴²	0
See below for references.		

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