**Supporting information**

Table S1 Proteins identified in sperm derived factors after mass spectrometric analysis by MS fit from NCBI data base

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene symbol | Accession no. | MOWSE score | Protein name | Functions in sperm | Gene/protein function | Pathways involved | |
| Enzymes | | | | | | | |
| Pgk2 | 582444 | 239 | phosphoglycerate kinase 2 (phosphoglycerate kinase, testis specific) | * sperm fertility (Liu *et al.*, 2016), motility and ATP levels (Danshina *et al.*, 2010) | * ATP binding * kinase activity * nucleotide binding * phosphoglycerate kinase activity * transferase activity | * glycolytic process * mitophagy in response to mitochondrial depolarization * phosphorylation * sperm motility | |
| Fer | 6636121 | 119 | tyrosine-protein kinase Fe | * present | * ATP binding * Rab GTPase binding * actin binding * cadherin binding * cell adhesion molecule binding * cytoskeletal protein binding * epidermal growth factor receptor binding * gamma-catenin binding * kinase activity * lipid binding * non-membrane spanning protein tyrosine kinase activity * non-membrane spanning protein tyrosine kinase activity * nucleotide binding * protein binding * protein kinase activity protein kinase binding * protein phosphatase 1 binding * protein tyrosine kinase activity * receptor binding * transferase activity | * Fc-epsilon receptor signalling pathway * Kit signalling pathway * actin cytoskeleton reorganization * cell adhesion and proliferation * cell-cell adhesion mediated by cadherin * cellular response to insulin stimulus * cellular response to macrophage colony-stimulating factor stimulus * cellular response to reactive oxygen species * chemotaxis * cytokine-mediated signalling pathway * diapedesis * epidermal growth factor receptor signalling pathway * extracellular matrix-cell signalling * innate immune response * insulin receptor signalling pathway via phosphatidylinositol 3-kinase * interleukin-6-mediated signalling pathway * microtubule cytoskeleton organization * mitotic cell cycle * negative regulation of mast cell activation involved in immune response * peptidyl-tyrosine autophosphorylation * peptidyl-tyrosine phosphorylation * phosphorylation * platelet-derived growth factor receptor signalling pathway * positive regulation of NF-kappaB transcription factor activity * positive regulation of actin filament polymerization * positive regulation of cell migration * positive regulation of cell proliferation * protein autophosphorylation * regulation of epidermal growth factor receptor signalling pathway * regulation of fibroblast migration * regulation of lamellipodium assembly * regulation of mast cell degranulation * regulation of protein phosphorylation * response to lipopolysaccharide * response to platelet-derived growth factor * signal transduction * substrate adhesion-dependent cell spreading * tyrosine phosphorylation of Stat3 protein | |
| Psmb10 | 15963453 | 122 | proteasome (prosome, macropain) subunit, beta type 10 (prosomeMecl1, partial ) | * sperm aster formation and pronuclear development/apposition in bovine and human zygotes (Rawe *et al.*, 2008) | * endopeptidase activity * hydrolase activity * peptidase activity * threonine-type endopeptidase activity | * T cell proliferation * cell morphogenesis * proteolysis * proteolysis involved in cellular protein catabolic process | |
| Tshb | 192216 | 1593 | thyroid stimulating hormone, beta subunit (thyrotropin beta-subunit, partial) | * Not present | * hormone activity |  | |
| Syk | 2780404 | 4957 | tyrosine-protein kinase SYK | * Present in Strongylocentrotus purpuratus] –Sea urchin | * ATP binding * integrin binding * kinase activity * non-membrane spanning protein tyrosine kinase activity * nucleotide binding * protein binding * protein domain specific binding * protein kinase activity * protein kinase binding * protein serine/threonine kinase activity * protein tyrosine kinase activity * receptor binding * receptor signaling protein tyrosine kinase activity * transferase activity | * B cell receptor signaling pathway * G-protein coupled receptor signaling pathway * activation of JUN kinase and MAPK activity * adaptive immune response * angiogenesis * beta selection * blood vessel morphogenesis * cell surface receptor signaling pathway * cellular response to low-density lipoprotein particle stimulus , molecule of fungal origin * defence response to bacterium * enzyme linked receptor protein signaling pathway * immune system process * innate immune response * integrin-mediated signaling pathway * intracellular signal transduction * leukocyte activation involved in immune response * leukocyte cell-cell adhesion * leukotriene biosynthetic process * lymph vessel development * neutrophil and macrophage activation involved in immune response * neutrophil chemotaxis * peptidyl-serine phosphorylation * peptidyl-tyrosine autophosphorylation * positive regulation of B cell differentiation and alpha-beta T cell differentiation * positive regulation of bone resorption, calcium-mediated signalling, cell adhesion mediated by integrin, cytokine secretion, gamma-delta T cell differentiation, granulocyte macrophage colony-stimulating factor biosynthetic process, interleukin-3 biosynthetic process, mast cell degranulation, peptidyl-tyrosine phosphorylation, receptor internalization, type I interferon production * receptor internalization * regulation of ERK1 and ERK2 cascade, arachidonic acid secretion, immune response, neutrophil degranulation, phagocytosis, platelet activation, platelet aggregation, sequence-specific DNA binding transcription factor activity, superoxide anion generation, tumour necrosis factor-mediated signaling pathway * serotonin secretion by platelet * transcription factor import into nucleus * transmembrane receptor protein tyrosine kinase signaling pathway | |
| Channels | | | | | | | |
| Slc2a1 | 3582350 | 1757 | solute carrier family 2 (facilitated glucose transporter), member 1 (type 1 glucose transporter protein) | * Sperm quality (Kim & Moley, 2008) | * D-glucose transmembrane transporter activity * dehydroascorbic acid transporter activity * glucose transmembrane transporter activity * identical protein binding * kinase binding * protein binding * protein self-association * substrate-specific transmembrane transporter activity * transmembrane transporter activity * transporter activity * xenobiotic transporter activity | * carbohydrate transport * cellular response to glucose starvation * dehydroascorbic acid transport * glucose transport * protein complex assembly * transmembrane transport * transport * xenobiotic transport | |
| Slc4a2 | 2707264 | 1155 | solute carrier family 4 (anion exchanger), member 2 (anion exchanger ) | * Sperm capacitation ( Chemn *et al.*, 2009) | * anion transmembrane transporter activity * anion:anion antiporter activity * antiporter activity * chloride transmembrane transporter activity * enzyme binding * inorganic anion exchanger activity * transporter activity | * anion transport * chloride transport * ion transport * regulation of intracellular pH * transport | |
| Dpf1 | 6649548 | 808 | D4, zinc and double PHD fingers family 1 (zinc finger protein neuro-d4 ) | * Present in sperm whale and Drosophila | * metal ion binding * nucleic acid binding * zinc ion binding | * nervous system development * nervous system development * regulation of transcription, DNA-templated * transcription, DNA-templated | |
| Aebp1 | 25137551 | 888 | AE binding protein 1 (aor­­­­­­­tic carboxypeptidase-like protein ACLP) | * spermatogonial stem cell | * DNA binding * RNA polymerase II regulatory region sequence-specific DNA binding * calmodulin binding * carboxypeptidase activity * metallocarboxypeptidase activity * serine-type carboxypeptidase activity * transcription corepressor activity * transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding * zinc ion binding | * negative regulation of transcription from RNA polymerase II promoter * peptide metabolic process * protein processing * proteolysis * regulation of transcription, DNA-templated * transcription, DNA-templated | |
| Slc8a1 | 9757634 | 121 | solute carrier family 8 (sodium/calcium exchanger), member 1 (Na/Ca exchanger) | * No report | * ankyrin binding * antiporter activity * calcium:sodium antiporter activity involved in regulation of cardiac muscle cell membrane potential * calmodulin binding * cytoskeletal protein binding * ion channel binding * metal ion binding * protein binding | * calcium ion export, homeostasis, import, transmembrane transport, transport into cytosol * cardiac muscle cell development, contraction * cell communication by electrical coupling involved in cardiac conduction * cellular calcium ion homeostasis * cellular response to cAMP * cellular response to caffeine * cellular sodium ion homeostasis * embryonic heart tube development * embryonic placenta development * heart morphogenesis * ion transport * muscle fiber development * negative regulation of cytosolic calcium ion concentration * positive regulation of bone mineralization * positive regulation of cytosolic calcium ion concentration , fibroblast migration, the force of heart contraction * post-embryonic development * regulation of calcium ion transport * regulation of cardiac muscle cell membrane potential * regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion * regulation of heart rate * regulation of sodium ion transport * regulation of the force of heart contraction * relaxation of smooth muscle * response to ATP * response to hypoxia * response to muscle stretch * sodium ion export * sodium ion import * sodium ion transmembrane transport * sodium ion transport * transmembrane transport * transport * vascular smooth muscle contraction | |
| Cacna1s | 1524149 | 544 | calcium channel, voltage-dependent, L type, alpha 1S subunit (skeletal muscle specific calcium channel ) | * No report | * calcium channel activity * high voltage-gated calcium channel activity * ion channel activity * metal ion binding * voltage-gated calcium channel activity * voltage-gated calcium channel activity * voltage-gated ion channel activity | * calcium ion transmembrane transport * calcium ion transport * endoplasmic reticulum organization * extraocular skeletal muscle development * ion transport * membrane depolarization during action potential * muscle cell development * muscle contraction * myoblast fusion * neuromuscular junction development * regulation of ion transmembrane transport * skeletal muscle adaptation * skeletal muscle fiber development * skeletal muscle tissue development * skeletal system development * striated muscle contraction * transmembrane transport * transport | |
| Transcription factor | | | | | | | |
| Pou2f1 | 13445262 | 376 | POU domain, class 2, transcription factor 1 (Oct-1L ) | * Present | * DNA binding * chromatin binding * chromatin binding * protein binding * receptor binding * sequence-specific DNA binding * transcription factor activity, * transcription regulatory region sequence-specific DNA binding | * lens induction in camera-type eye * negative regulation of transcription, DNA-templated * olfactory placode formation * positive regulation of transcription from RNA polymerase II promoter * positive regulation of transcription from RNA polymerase II promoter * regulation of transcription, DNA-templated * transcription, DNA-templated | |
| Extracellular exosome | | | | | | | |
| Ganab | 5452938 | 61.6 | alpha glucosidase 2 alpha neutral subunit | * Present | * carbohydrate binding * catalytic activity * glucan 1,3-alpha-glucosidase activity * glucosidase activity * hydrolase activity * hydrolase activity, acting on glycosyl bonds * hydrolase activity, hydrolyzing O-glycosyl compounds * poly(A) RNA binding * protein binding | * N-glycan processing * carbohydrate metabolic process * metabolic process | |
| Runx1 | 2213483 | 424 | runt related transcription factor 1 (AML1) | * Present (Jeong *et al.*, 2008) | * ATP binding * DNA binding * RNA polymerase II regulatory region sequence-specific DNA binding * RNA polymerase II transcription factor activity, sequence-specific DNA binding * core promoter binding * promoter-specific chromatin binding * protein binding * regulatory region DNA binding * repressing transcription factor binding * sequence-specific double-stranded DNA binding * transcription factor activity, sequence-specific DNA binding * transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding | * behavioural response to pain * cellular response to transforming growth factor beta stimulus * central nervous system development * chondrocyte differentiation * definitive haemopoiesis * embryonic haemopoiesis * hair follicle morphogenesis * haemopoiesis * *in utero* embryonic development * liver development * myeloid progenitor cell differentiation * negative regulation of cell proliferation * negative regulation of transcription, DNA-templated * neuron development, differentiation and fate commitment * ossification * positive regulation of angiogenesis, cell maturation, granulocyte differentiation, interferon-gamma production, interleukin-2 production, transcription from RNA polymerase II promoter, transcription, DNA-templated * progesterone secretion * regulation of T cell anergy, hair follicle cell proliferation, signal transduction, transcription, DNA-templated * response to retinoic acid * skeletal system development * transcription, DNA-templated | |
| AGALS | 59011863 | 147 | insulin-like growth factor-binding protein complex acid labile subunit | * Present (Yuri Sano *et al.*, 2001) | * insulin-like growth factor binding * insulin-like growth factor binding * protein C-terminus binding * protein binding | * cell adhesion | |
| Cell membrane receptors | | | | | | | |
| Oprm1 | 217330399 | 1129 | opioid receptor, mu 1 | * Present | * G-protein alpha-subunit binding * G-protein beta-subunit binding * G-protein coupled receptor activity * beta-endorphin receptor activity * filamin binding * morphine receptor activity * neuropeptide binding * opioid receptor activity * protein C-terminus binding * protein binding * protein domain specific binding * signal transducer activity * voltage-gated calcium channel activity | * G-protein coupled receptor signaling pathway * adenylate cyclase-activating dopamine receptor signaling pathway * adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway * adenylate cyclase-inhibiting opioid receptor signaling pathway * behavioural response to ethanol * cellular response to morphine, stress * chemical synaptic transmission * eating behaviour * excitatory postsynaptic potential * locomotory behaviour * negative regulation of WNT protein secretion, adenylate cyclase activity, cAMP biosynthetic process * opioid receptor signaling pathway * phospholipase C-activating G-protein coupled receptor signaling pathway * positive regulation of ERK1 and ERK2 cascade, appetite, neurogenesis * regulation of N-methyl-D-aspartate selective glutamate receptor activity, sensory perception of pain * response to ethanol * sensory perception of pain * signal transduction | |
| Clec2i | 6166463 | 86.6 | C-type lectin domain family 2, member i | * Not reported | * carbohydrate binding * natural killer cell lectin-like receptor binding * protein binding * transmembrane signaling receptor activity | * T cell receptor signaling pathway * membrane raft assembly * negative regulation of osteoclast differentiation * positive regulation of immunological synapse formation * receptor clustering * regulation of T cell proliferation * regulation of actin filament polymerization * regulation of interleukin-2 biosynthetic process | |
| Msr1 | 192740 | 1335 | macrophage scavenger receptor types I and II | * Not reported | * low-density lipoprotein particle binding * scavenger receptor activity | * cholesterol transport * endocytosis * lipoprotein transport * plasma lipoprotein particle clearance * positive regulation of cholesterol storage * positive regulation of macrophage derived foam cell differentiation * receptor-mediated endocytosis | |
| Ifnar1 | 755810 | 50 | interferon (alpha and beta) receptor 1 | * Reported | * interferon receptor activity * phosphoribosylamine-glycine ligase activity * type I interferon binding * type I interferon receptor activity | * T cell activation * cellular response to interferon-alpha * cytokine-mediated signaling pathway * defence response to virus * positive regulation of interferon-beta production, interferon-gamma production, interleukin-1 beta secretion, transcription, DNA-templated * regulation of peptidyl-tyrosine phosphorylation * response to lipopolysaccharide * type I interferon biosynthetic process * type I interferon signaling pathway | |
| H2-L | 2137547 | 1759 | MHC H2-L antigen | * Not reported | * peptide antigen binding * receptor binding | * antigen processing and presentation * antigen processing and presentation of peptide antigen via MHC class I * defence response * immune response * immune system process | |
| TCRα | 31874365  31874299 | 5188 | T cell receptor alpha chain |  | * carbohydrate binding * molecular function | * biological process * protein transport * transport | |
| TCRβ | 3986239 | 1793 | T cell receptor (TCR) beta chain |  |  |  | |
| Igh | 224492146  224492328 | 128  1569 | immunoglobulin heavy chain variable DJH region (immunoglobulin heavy chain complex) |  |  |  | |
| Spag16 | 54042993 | 5318 | sperm associated antigen 16 (Pf20) | * human sperm axoneme , motility (Zhang *et al.*, 2006, 2007) | * protein binding | * axoneme assembly * cell motility in response to calcium ion * cell projection organization * cilium assembly * cilium movement involved in cell motility * microtubule sliding * sperm axoneme assembly | |
| Components of cell junctions | | | | | | | |
| Lcp1 | 1813738 | 210 | lymphocyte cytosolic protein 1  (L-plastin) | * Present (Pilatz *et al.*, 2014) | * GTPase binding * actin binding * actin filament binding * actin filament binding * calcium ion binding * identical protein binding * metal ion binding * protein binding | * T cell activation involved in immune response * actin filament bundle assembly * cell migration * extracellular matrix disassembly * positive regulation of podosome assembly * protein kinase A signaling * regulation of intracellular protein transport * response to wounding | |
| Dsg3 | 2290198 | 1054 | desmoglein 3 | * Present in Physeter catodon | * calcium ion binding * metal ion binding | * cell adhesion * homophilic cell adhesion via plasma membrane adhesion molecules | |
| Hcfc1 | 27902532 | 885 | host cell factor C1 (HCFC1 protein) | * Present in Physeter catodon | * chromatin binding * contributes to histone acetyltransferase activity (H4-K16, K5,K8 specific) * identical protein binding * transcription coactivator activity * transcriptional activator activity, RNA polymerase II distal enhancer sequence-specific binding | * cell cycle * chromatin modification * histone H4-K16, H4-K5, H4-K8 acetylation * negative regulation of transcription from RNA polymerase II promoter * positive regulation of gene expression * protein stabilization * regulation of protein complex assembly * regulation of transcription, DNA-templated * release from viral latency | |
| Nuclear factor | | | | | | |
| Eif5a | 58041005  33383434 | 550 | eukaryotic translation initiation factor 5A (Uorf1) | * Sperm fertility (Bonache *et al.*, 2012) | |  | | --- | | * RNA binding | | * U6 snRNA binding | | * poly(A) RNA binding | | * protein N-terminus binding | | * ribosome binding | | * translation elongation factor activity | | * apoptotic process * mRNA export from nucleus * mRNA transport * negative regulation of apoptotic process * positive regulation of apoptotic process * and cardiac muscle cell apoptotic process * positive regulation of cell proliferation and cytosolic calcium ion concentration, muscle cell differentiation, reactive oxygen species metabolic process, translational elongation and termination * protein export from nucleus * protein transport * translation * translational elongation * translational frameshifting * transport | |
| Tbp | 2511436 | 6858 | TATA binding protein | * not reported | * DNA binding * DNA binding * RNA polymerase II core promoter proximal region sequence-specific DNA binding * RNA polymerase II core promoter sequence-specific DNA binding * RNA polymerase II repressing transcription factor binding * enzyme binding * protein binding * repressing transcription factor binding * contributes to transcription factor activity, sequence-specific DNA binding * transcription factor binding * transcription regulatory region DNA binding | * DNA-templated transcription, initiation * positive regulation of transcription, DNA-templated * regulation of transcription, DNA-templated * transcription from RNA polymerase II promoter * transcription from RNA polymerase II promoter * transcription from RNA polymerase III promoter * transcription from RNA polymerase III promoter * transcription, DNA-templated | |
| Eif4ebp1 | 13540382 | 1159 | eukaryotic initiation factor 4E |  | * eukaryotic initiation factor 4E binding * protein phosphatase 2A binding * translation initiation factor binding * translation repressor activity | * G1/S transition of mitotic cell cycle * IRES-dependent translational initiation * TOR signaling * cellular response to dexamethasone stimulus * cellular response to hypoxia * insulin receptor signaling pathway * lung development * negative regulation of protein complex assembly and translational initiation * positive regulation of mitotic cell cycle * response to amino acid starvation * response to ethanol * response to ischemia | |
| Eif4a2 | 581985 | 3833 | initiation factor 4A (eukaryotic translation initiation factor 4A2) |  | * ATP binding * ATP-dependent RNA helicase activity * ATPase activity * RNA binding * helicase activity * hydrolase activity * nucleic acid binding * nucleotide binding * poly(A) RNA binding * translation initiation factor activity | * RNA secondary structure unwinding * negative regulation of RNA-directed RNA polymerase activity * regulation of gene expression * regulation of translational initiation * translation * translational initiation | |
| Adat1 | 13345381 | 1246 | adenosine deaminase tRNA specific 1, partial |  | * RNA binding * adenosine deaminase activity * hydrolase activity * metal ion binding * tRNA-specific adenosine deaminase activity | * RNA processing * tRNA processing | |
| Rps18 | 2980874 | 215 | Ribosomal protein S18 |  | * RNA binding * nucleic acid binding * poly(A) RNA binding * protein binding * protein kinase binding * rRNA binding * structural constituent of ribosome | * ribosome biogenesis * translation | |
| Sf1 | 5102741 | 774 | splicing factor 1 (CW17) | * Present | * RNA binding * metal ion binding * nucleic acid binding * pre-mRNA branch point binding * zinc ion binding | * Leydig cell differentiation * RNA splicing * mRNA processing * mRNA splicing, via spliceosome * male sex determination * negative regulation of smooth muscle cell proliferation * regulation of steroid biosynthetic process * regulation of transcription, DNA-templated * transcription, DNA-templated | |
| FLI1 | 1000864 | 1756 | Fli-1 proto-oncogene, ETS transcription factor (Friend leukemia virus integration 1) |  | * DNA binding * RNA polymerase II core promoter proximal region sequence-specific DNA binding * RNA polymerase II distal enhancer sequence-specific DNA binding * RNA polymerase II transcription factor activity, sequence-specific DNA binding * chromatin binding * protein binding * transcription factor activity, sequence-specific DNA binding * transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding | * blood circulation * cell differentiation * haemostasis * megakaryocyte development * organ morphogenesis * positive regulation of transcription from RNA polymerase II promoter * regulation of transcription from RNA polymerase II promoter * transcription from RNA polymerase II promoter | |
| Isozyme/Co-factor | | | | | | | |
| ADH1A | 178094 | 1115 | alcohol dehydrogenase | * Not reported | * alcohol dehydrogenase (NAD) activity * alcohol dehydrogenase activity, zinc-dependent * alcohol dehydrogenase activity, zinc-dependent * protein binding * retinol dehydrogenase activity * zinc ion binding | * alcohol metabolic process * drug metabolic process * ethanol oxidation | |
| * Growth factor | | | | | | | |
| Pgf | 9837316 | 50.9 | placental growth factor | * Not reported | * growth factor activity * protein heterodimerization activity | * angiogenesis * branching involved in ureteric bud morphogenesis * cell differentiation * multicellular organism development * positive regulation of angiogenesis, cell division, cell proliferation, endothelial cell proliferation * regulation of morphogenesis of a branching structure * sprouting angiogenesis | |
| * cytoplasmic vesicle | | | | | | | |
| Zg16 | 1334245 | 550 | zymogen (zymogen granule membrane protein 16) | * Not reported | * carbohydrate binding * molecular function | * biological process * protein transport * transport | |
| Plasma membrane component | | | | | | | |
| Apoa2 | 642826 | 1582 | apolipoprotein A-II | * Not reported | * apolipoprotein receptor binding * cholesterol binding * contributes to cholesterol transporter activity * cholesterol transporter activity * high-density lipoprotein particle binding * high-density lipoprotein particle receptor binding * lipase inhibitor activity * lipid binding * lipid transporter activity * phosphatidylcholine binding * phosphatidylcholine-sterol O-acyltransferase activator activity * phospholipid binding * protein heterodimerization activity | * beta-glucoside transport * cholesterol efflux * cholesterol homeostasis * cholesterol homeostasis * cholesterol homeostasis * cholesterol homeostasis * cholesterol metabolic process * cholesterol metabolic process * cholesterol transport * diacylglycerol catabolic process * fatty acid metabolic process * high-density lipoprotein particle assembly * high-density lipoprotein particle assembly * high-density lipoprotein particle clearance * high-density lipoprotein particle remodeling * lipid transport * lipoprotein metabolic process * low-density lipoprotein particle remodeling * negative regulation of cholesterol import * negative regulation of cholesterol transport * negative regulation of cholesterol transporter activity * negative regulation of cytokine secretion involved in immune response * negative regulation of lipase activity * negative regulation of lipid catabolic process * negative regulation of very-low-density lipoprotein particle remodeling * organ regeneration * peptidyl-methionine modification * phosphatidylcholine biosynthetic process * phospholipid catabolic process * phospholipid efflux * positive regulation of cholesterol esterification * positive regulation of interleukin-8 biosynthetic process * positive regulation of lipid catabolic process * protein oxidation * regulation of intestinal cholesterol absorption * regulation of protein stability * response to glucose * reverse cholesterol transport * transport * triglyceride-rich lipoprotein particle remodeling | |
|  | | | | | | | |
|  |  |  | mCG3700, isoform CRA\_b | * Not present |  |  | |