**Supplemental Table 3. Enrichment list of differentially expressed proteins on cellular component, cellular function, and biochemical process.** (cut-off valure 1.5-fold change, p value ˂ 0.05)

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| --- | --- | --- | --- | --- | --- |
| **No.** | **Gene name** | **Abbreviation** | **Cellular Component** | **Cellular Function** | **Biochemical Process (GOID)** |
| 1 | Actin, cytoplasmic 1 | Actb | extracellular exosome(GO:0070062),blood microparticle(GO:0072562),membrane(GO:0016020),focal adhesion(GO:0005925),cytosol(GO:0005829),MLL5-L complex(GO:0070688),NuA4 histone acetyltransferase complex(GO:0035267),cytoplasmic ribonucleoprotein granule(GO:0036464),myelin sheath(GO:0043209),cortical cytoskeleton(GO:0030863),nuclear chromatin(GO:0000790) | ATP binding(GO:0005524),RNA polymerase II core promoter proximal region sequence-specific DNA binding(GO:0000978),RNA polymerase II distal enhancer sequence-specific DNA binding (GO:0000980) | substantia nigra development(GO:0021762),platelet aggregation(GO:0070527),ATP-dependent chromatin remodeling(GO:0043044) |
| 2 | Adenosine deaminase | Ada | Extracellular space(GO:0005615),lysosome(GO:0005764),cytoplasm(GO:0005737),external side of plasma membrane(GO:0009897), cell junction(GO:0030054),cytoplasmic membrane-bounded vesicle lumen(GO:0060205),neuronal cell body (GO:0043025),dendrite cytoplasm (GO:0032839), | zinc ion binding (GO:0008270),purine nucleoside binding (GO:0001883), adenosine deaminase activity (GO:0004000) | Aging(GO:0007568),positive regulation of T cell differentiation in thymus(GO:0033089),liver development(GO:0001889),adenosine catabolic process(GO:0006154),negative regulation of mucus secretion (GO:0070256)，negative regulation of circadian sleep/wake cycle, non-REM sleep(GO:0042323),germinal center B cell differentiation(GO:0002314),response to hypoxia(GO:0001666),negative regulation of mature B cell apoptotic process(GO:0002906),inosine biosynthetic process(GO:0046103),dATP catabolic process(GO:0046061),positive regulation of T cell receptor signaling pathway(GO:0050862),positive regulation of germinal center formation(GO:0002636),negative regulation of leukocyte migration(GO:0002686),histamine secretion(GO:0001821),T cell activation(GO:0042110),negative regulation of thymocyte apoptotic process(GO:0070244),adenosine metabolic process(GO:0046085),negative regulation of inflammatory response(GO:0050728),positive regulation of alpha-beta T cell differentiation(GO:0046638),response to hydrogen peroxide(GO:0042542),trophectodermal cell differentiation(GO:0001829),lung alveolus development(GO:0048286),positive regulation of calcium-mediated signaling(GO:0050850),positive regulation of heart rate(GO:0010460),positive regulation of smooth muscle contraction(GO:0045987),positive regulation of B cell proliferation(GO:0030890),placenta development(GO:0001890),response to vitamin E(GO:0033197) |
| 3 | Alpha-2-HS-glycoprotein | Ahsg | extracellular space(GO:0005615),blood microparticle(GO:0072562),extracellular matrix(GO:0031012),protein complex(GO:0043234), | cysteine-type endopeptidase inhibitor activity (GO:0004869),endopeptidase inhibitor activity (GO:0004866),receptor signaling protein tyrosine kinase inhibitor activity (GO:0030294),kinase inhibitor activity (GO:0019210) | negative regulation of endopeptidase activity(GO:0010951),acute-phase response(GO:0006953),cellular response to insulin stimulus(GO:0032869),negative regulation of cell growth(GO:0030308),negative regulation of protein tyrosine kinase activity(GO:0061099),cerebral cortex development(GO:0021987),negative regulation of phosphorylation(GO:0042326),regulation of inflammatory response(GO:0050727),protein complex assembly(GO:0006461),negative regulation of insulin receptor signaling pathway(GO:0046627) |
| 4 | Fructose-bisphosphate aldolase A | Aldoa | cytoplasm(GO:0005737),mitochondrion(GO:0005739),I band(GO:0031674),M band(GO:0031430) | fructose-bisphosphate aldolase activity (GO:0004332)  | response to hypoxia(GO:0001666),glycolytic process(GO:0006096),response to estrogen(GO:0043627),protein homotetramerization(GO:0051289),response to heat(GO:0009408), |
| 5 | Protein AMBP | Ambp | extracellular space(GO:0005615)extracellular exosome(GO:0070062)blood microparticle(GO:0072562)plasma membrane(GO:0005886)cell surface (GO:0009986)intracellular membrane-bounded organelle(GO:0043231) | small molecule binding (GO:0036094), serine-type endopeptidase inhibitor activity (GO:0004867),IgA binding (GO:0019862),heme binding (GO:0020037),protein homodimerization activity (GO:0042803) | negative regulation of endopeptidase activity(GO:0010951),protein catabolic process(GO:0030163),protein-chromophore linkage(GO:0018298) |
| 6 | Annexin A1 | Anxa1 | extracellular space(GO:0005615),extracellular exosome(GO:0070062),nucleus(GO:0005634),plasma membrane(GO:0005886),cytoplasm(GO:0005737),focal adhesion(GO:0005925),apical plasma membrane(GO:0016324),lateral plasma membrane(GO:0016328),extrinsic component of external side of plasma membrane(GO:0031232),extrinsic component of endosome membrane(GO:0031313),sarcolemma(GO:0042383),protein complex(GO:0043234),basolateral plasma membrane (GO:0016323),mitochondrial membrane(GO:0031966),phagocytic cup(GO:0001891),mast cell granule(GO:0042629),cornified envelope(GO:0001533),motile cilium(GO:0031514),early endosome membrane (GO:0031901),cytoplasmic vesicle membrane (GO:0030659), | double-stranded DNA-dependent ATPase activity (GO:0033676),phospholipase A2 inhibitor activity (GO:0019834),calcium ion binding (GO:0005509), protein homodimerization activity (GO:0042803),annealing helicase activity (GO:0036310),structural molecule activity (GO:0005198),single-stranded DNA binding (GO:0003697),helicase activity (GO:0004386),phospholipid binding (GO:0005543),calcium-dependent phospholipid binding (GO:0005544) | lipase inhibitor activity (GO:0031960), regulation of lipase activity (GO:0060191), lipid transport (GO:0006869), fatty acid biosynthetic process (GO:0006633), response to glucocorticoid (GO:0051384), lipid localization (GO:0010876), Regulation of interleukin-1 production(GO:0032652),response to organic cyclic compound (GO:0014070),inflammatory response (GO:0006954),DNA rewinding(GO:0036292), cell surface receptor signaling pathway(GO:0007166),estrous cycle (GO:0044849), positive regulation of neutrophil apoptotic process (GO:0033031),negative regulation of interleukin-8 secretion (GO:2000483), response to corticosteroid (GO:0031960),positive regulation of T-helper 1 cell differentiation (GO:0045627),granulocyte chemotaxis (GO:0071621),DNA strand renaturation (GO:0000733),regulation of leukocyte migration (GO:0002685),innate immune response (GO:0045087), positive regulation of prostaglandin biosynthetic process (GO:0031394),gliogenesis (GO:0042063),negative regulation of T-helper 2 cell differentiation(GO:0045629),response to hormone (GO:0009725),response to estradiol(GO:0032355), regulation of cell shape(GO:0008360),alpha-beta T cell differentiation(GO:0046632), prolactin secretion (GO:0070459), response to glucocorticoid (GO:0051384),response to peptide hormone (GO:0043434), regulation of hormone secretion(GO:0046883),cellular response to glucocorticoid stimulus(GO:0071385),positive regulation of vesicle fusion (GO:0031340),peptide cross-linking (GO:0018149),negative regulation of protein secretion (GO:0050709), regulation of inflammatory response (GO:0050727), adaptive immune response (GO:0002250), actin cytoskeleton reorganization (GO:0031532) positive regulation of T cell proliferation (GO:0042102), arachidonic acid secretion (GO:0050482), positive regulation of interleukin-2 production (GO:0032743), keratinocyte differentiation (GO:0030216), G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (GO:0007187), DNA duplex unwinding (GO:0032508),positive regulation of G1/S transition of mitotic cell cycle (GO:1900087), response to interleukin-1 (GO:0070555),insulin secretion (GO:0030073), monocyte chemotaxis (GO:0002548) |
| 7 | ATP synthase subunit beta, mitochondrial | Atp5b | mitochondrion(GO:0005739)mitochondrial inner membrane (GO:0005743)mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)(GO:0000275)proton-transporting ATP synthase complex, catalytic core F(1) (GO:0045261)mitochondrial proton-transporting ATP synthase complex(GO:0005753) | ATP binding (GO:0005524),lipoprotein particle receptor activity (GO:0030228),calcium ion binding (GO:0005509),ATPase activity (GO:0016887),proton-transporting ATP synthase activity, rotational mechanism (GO:0046933) | ATP metabolic process(GO:0046034),receptor-mediated endocytosis(GO:0006898),ATP hydrolysis coupled proton transport(GO:0015991),ATP synthesis coupled proton transport(GO:0015986) |
| 8 | Beta-2-microglobulin | B2m | extracellular space(GO:0005615)extracellular exosome(GO:0070062)external side of plasma membrane(GO:0009897)focal adhesion(GO:0005925)Golgi apparatus(GO:0005794)MHC class I protein complex(GO:0042612) |  | protein refolding (GO:0042026),cellular response to lipopolysaccharide(GO:0071222),positive regulation of T cell cytokine production (GO:0002726),negative regulation of receptor binding(GO:1900121),regulation of membrane depolarization(GO:0003254),antigen processing and presentation of exogenous protein antigen via MHC class Ib, TAP-dependent(GO:0002481),positive regulation of T cell mediated cytotoxicity(GO:0001916),positive regulation of receptor-mediated endocytosis(GO:0048260),T cell differentiation in thymus(GO:0033077) |
| 9 | Complement C3 | C3 | extracellular space(GO:0005615) | endopeptidase inhibitor activity (GO:0004866),C5L2 anaphylatoxin chemotactic receptor binding (GO:0031715),lipid binding (GO:0008289),cofactor binding (GO:0048037) | complement activation, alternative pathway(GO:0006957),blood coagulation(GO:0007596),complement activation, classical pathway(GO:0006958),inflammatory response(GO:0006954),complement activation(GO:0006956),tolerance induction(GO:0002507),positive regulation of ERK1 and ERK2 cascade(GO:0070374),regulation of triglyceride biosynthetic process(GO:0010866),response to estradiol(GO:0032355),positive regulation of developmental growth(GO:0048639),response to glucocorticoid(GO:0051384),positive regulation of protein phosphorylation(GO:0001934),response to estrogen(GO:0043627),positive regulation of glucose transport(GO:0010828),positive regulation of lipid storage(GO:0010884),chemotaxis(GO:0006935),response to progesterone(GO:0032570),positive regulation of G-protein coupled receptor protein signaling pathway(GO:0045745),fatty acid metabolic process(GO:0006631),response to magnesium ion(GO:0032026), |
| 10 | Cathelicidin antimicrobial peptide | Camp | extracellular space(GO:0005615)cytoplasm(GO:0005737)cell projection(GO:0042995) | cysteine-type endopeptidase inhibitor activity (GO:0004869) | positive regulation of cell proliferation(GO:0008284),cellular response to lipopolysaccharide(GO:0071222),cellular response to peptidoglycan(GO:0071224),positive regulation of angiogenesis(GO:0045766),positive regulation of protein phosphorylation(GO:0001934),cellular response to tumor necrosis factor(GO:0071356),cellular response to interleukin-1(GO:0071347)cellular response to interleukin-6(GO:0071354) |
| 11 | CD44 protein | Cd44 | integral component of membrane(GO:0016021) | hyaluronic acid binding (GO:0005540) | cell adhesion(GO:0007155) |
| 12 | Cd99 protein | Cd99 | integral component of membrane(GO:0016021),focal adhesion(GO:0005925) |  |  |
| 13 | Cadherin-1 | Cdh1 | integral component of membrane(GO:0016021),extracellular exosome(GO:0070062),plasma membrane(GO:0005886),cytoplasm(GO:0005737),focal adhesion(GO:0005925),lateral plasma membrane(GO:0016328),aggresome(GO:0016235),perinuclear region of cytoplasm (GO:0048471),flotillin complex(GO:0016600),cytoplasmic side of plasma membrane(GO:0009898),catenin complex(GO:0016342),apical junction complex(GO:0043296),endosome(GO:0005768),cell-cell adherens junction(GO:0005913),trans-Golgi network(GO:0005802),lamellipodium(GO:0030027),cortical actin cytoskeleton(GO:0030864) | calcium ion binding (GO:0005509) | positive regulation of transcription, DNA-templated(GO:0045893),neuron projection development(GO:0031175),homophilic cell adhesion via plasma membrane adhesion molecules(GO:0007156),cellular response to indole-3-methanol(GO:0071681),response to organic substance(GO:0010033),single organismal cell-cell adhesion(GO:0016337),positive regulation of transcription factor import into nucleus(GO:0042993),negative regulation of cell-cell adhesion(GO:0022408),synapse assembly(GO:0007416),establishment of protein localization to plasma membrane(GO:0090002),pituitary gland development(GO:0021983) |
| 14 | Collagen alpha-1(I) chain | Col1a1 | extracellular space(GO:0005615),extracellular region(GO:0005576),collagen type I trimer(GO:0005584),Golgi apparatus(GO:0005794),endoplasmic reticulum(GO:0005783),secretory granule(GO:0030141) | metal ion binding (GO:0046872),extracellular matrix structural constituent (GO:0005201) | protein transport(GO:0015031),positive regulation of transcription, DNA-templated(GO:0045893),positive regulation of cell migration(GO:0030355),response to corticosteroid(GO:0031960),response to estradiol(GO:0032355),collagen biosynthetic process(GO:0032964),response to cAMP(GO:0051591),response to mechanical stimulus(GO:0009612),response to peptide hormone (GO:0043434),cellular response to tumor necrosis factor(GO:0071356),osteoblast differentiation(GO:0001649),bone trabecula formation(GO:0060346),cellular response to mechanical stimulus(GO:00712600),skin morphogenesis(GO:0043589),negative regulation of cell-substrate adhesion(GO:0010812),cartilage development involved in endochondral bone morphogenesis(GO:0060351),cellular response to transforming growth factor beta stimulus(GO:0071560),Ossification(GO:0001503),response to hydrogen peroxide(GO:0042542),response to steroid hormone(GO:0048545),positive regulation of canonical Wnt signaling pathway(GO:0090263),cellular response to amino acid stimulus(GO:0071230),protein heterotrimerization(GO:0070208),response to hyperoxia(GO:0055093),cellular response to fibroblast growth factor stimulus(GO:0044344),collagen fibril organization(GO:0030199),blood vessel development(GO:0001568),protein localization to nucleus(GO:0034504),cellular response to epidermal growth factor stimulus(GO:0071364),endochondral ossificationGO:0001958positive regulation of epithelial to mesenchymal transition(GO:0010718),embryonic skeletal system development(GO:0048706),face morphogenesis(GO:0060325),Response to nutrient (G0:0007584) |
| 15 | Ceruloplasmin | Cp | extracellular exosome(GO:0070062),blood microparticle(GO:0072562),lysosomal membrane(GO:0005765) | copper ion binding (GO:0005507),ferroxidase activity (GO:0004322) | copper ion transport(GO:0006825),cellular iron ion homeostasis(GO:0006879) |
| 16 | Protective protein for beta-galactosidase | Ctsa | lysosomal membrane(GO:0005765),mitochondrion(GO:0005739) | serine-type carboxypeptidase activity (GO:0004185),glycoprotein binding (GO:0001948) | Proteolysis(GO:0006508),proteolysis involved in cellular protein catabolic process(GO:0051603),regulation of protein stability(GO:0031647) |
| 17 | Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex), isoform CRA\_a | Dlst | extracellular exosome(GO:0070062),nucleus(GO:0005634),membrane(GO:0016020),mitochondrion(GO:0005739),oxoglutarate dehydrogenase complex(GO:0045252),myelin sheath(GO:0043209) | dihydrolipoyllysine-residue succinyltransferase activity (GO:0004149) | tricarboxylic acid cycle(GO:0006099) |
| 18 | Eukaryotic translation initiation factor 4A1 | Eif4a1 | extracellular exosome(GO:0070062),cytoplasm(GO:0005737),membrane(GO:0016020) | ATP binding (GO:0005524),poly(A) RNA binding (GO:0044822),ATP-dependent RNA helicase activity (GO:0004004),double-stranded RNA binding (GO:0003725),translation initiation factor activity (GO:0003743) | regulation of gene expression(GO:0010468),RNA secondary structure unwinding(GO:0010501),regulation of translational initiation(GO:0006446),translational initiation(GO:0006413) |
| 19 | Ac2-120 | F5 | extracellular region(GO:0005576),Golgi apparatus(GO:0005794),endoplasmic reticulum(GO:0005783) | serine-type endopeptidase activity (GO:0004252),copper ion binding (GO:0005507) | Proteolysis(GO:0006508),blood coagulation(GO:0007596),blood coagulation, extrinsic pathway(GO:0007598) |
| 20 | Lysosomal alpha-glucosidase | Gaa | Lysosome(GO:0005764),lysosomal membrane(GO:0005765) | maltose alpha-glucosidase activity (GO:0032450),alpha-1,4-glucosidase activity (GO:0004558),carbohydrate binding (GO:0030246) | glycogen catabolic process(GO:0005980) |
| 21 | Gamma-glutamyl hydrolase | Ggh | extracellular space(GO:0005615),extracellular exosome(GO:0070062),nucleus(GO:0005634),lysosome(GO:0005764),cytosol(GO:0005829),melanosome(GO:0042470) | gamma-glutamyl-peptidase activity (GO:0034722) | Proteolysis(GO:0006508),response to ethanol(GO:0045471),response to insulin(GO:0032868),glutamine metabolic process(GO:0006541) |
| 22 | Gamma-glutamyltranspeptidase 1 | Ggt1 | extracellular space(GO:0005615),plasma membrane(GO:0005886),integral component of plasma membrane(GO:0005887) | glutathione hydrolase activity (GO:0036374),gamma-glutamyltransferase activity (GO:0003840) | Aging(GO:0007568),peptide modification(GO:0031179),glutathione catabolic process(GO:0006751),response to lipopolysaccharide(GO:0032496),response to estradiol(GO:0032355),glutamate metabolic process(GO:0006536),glutathione biosynthetic process(GO:0006750),cellular response to oxidative stress(GO:0034599),response to tumor necrosis factor(GO:0034612) |
| 23 | Beta-galactosidase | Glb1 | extracellular exosome(GO:0070062),lysosome(GO:0005764),Golgi apparatus(GO:0005794) | galactoside binding (GO:0016936),beta-galactosidase activity (GO:0004565) | galactose catabolic process(GO:0019388),cellular carbohydrate metabolic process(GO:0044262) |
| 24 | GM2 ganglioside activator | Gm2a | extracellular exosome(GO:0070062),lysosome(GO:0005764),cytoplasm(GO:0005737),mitochondrion(GO:0005739),cytoplasmic side of plasma membrane(GO:0009898),apical cortex(GO:0045179) | beta-N-acetylhexosaminidase activity(GO:0004563),phospholipase activator activity (GO:0016004),lipid transporter activity (GO:0005319),lipid binding (GO:0008289) | positive regulation of hydrolase activity(GO:0051345),ganglioside metabolic process(GO:0001573),ganglioside catabolic process(GO:0006689),lipid transport(GO:0006869),learning or memory(GO:0007611),lipid storage(GO:0019915) |
| 25 | Heat shock 70 kDa protein 1-like | Hspa1l | blood microparticle(GO:0072562),cytosol(GO:0005829),mitochondrion(GO:0005739),zona pellucida receptor complex(GO:0002199),mitochondrial matrix(GO:0005759),COP9 signalosome(GO:0008180),cell body(GO:0044297) | ATP binding (GO:0005524) | protein refolding(GO:0042026),positive regulation of protein targeting to mitochondrion(GO:1903955) |
| 26 | Insulin-like growth factor binding protein 7, isoform CRA\_b | Igfbp7 | extracellular space(GO:0005615),extracellular exosome(GO:0070062),extracellular matrix(GO:0031012) |  | response to organic cyclic compound(GO:0014070),cell adhesion(GO:0007155),response to cortisol(GO:0051414),regulation of cell growth(GO:0001558),response to heat(GO:0009408),regulation of steroid biosynthetic process(GO:0050810),cellular response to hormonestimulus(GO:0032870), |
| 27 | Ig gamma-2B chain C region | Igh-1a | blood microparticle(GO:0072562),external side of plasma membrane(GO:0009897),immunoglobulin complex, circulating(GO:0042571) | antigen binding (GO:0003823),immunoglobulin receptor binding (GO:0034987) | complement activation, classical pathway(GO:0006958),positive regulation of B cell activation(GO:0050871),B cell receptor signaling pathway(GO:0050853),innate immune response(GO:0045087) |
| 28 | Immunoglobulin joining chain | Jchain | extracellular exosome(GO:0070062),blood microparticle(GO:0072562),secretory dimeric IgA immunoglobulin complex(GO:0071752),pentameric IgM immunoglobulin complex(GO:0071756)monomeric IgA immunoglobulin complex(GO:0071748),dimeric IgA immunoglobulin complex(GO:0071750) | immunoglobulin receptor binding (GO:0034987),peptidoglycan binding (GO:0042834),phosphatidylcholine binding (GO:0031210),single-stranded DNA binding (GO:0003697) | innate immune response(GO:0045087),positive regulation of protein oligomerization(GO:0032461),adaptive immune response(GO:0002250),glomerular filtration(GO:0003094),humoral immune response(GO:0006959) |
| 29 | Leukemia inhibitory factor receptor | Lifr | integral component of membrane(GO:0016021),extracellular exosome(GO:0070062),receptor complex(GO:0043235) | leukemia inhibitory factor receptor activity (GO:0004923),oncostatin-M receptor activity (GO:0004924) | positive regulation of cell proliferation(GO:0008284) |
| 30 | Lipoprotein lipase | Lpl | extracellular exosome(GO:0070062),plasma membrane(GO:0005886),anchored component of membrane (GO:0031225),extracellular matrix(GO:0031012),cell surface(GO:0009986),chylomicron(GO:0042627),very-low-density lipoprotein particle(GO:0034361) | triglyceride binding (GO:0017129),lipoprotein lipase activity (GO:0004465), heparin binding (GO:0008201) | positive regulation of cholesterol storage(GO:0010886),positive regulation of sequestering of triglyceride(GO:0010890),lipid catabolic process(GO:0016042),triglyceride biosynthetic process(GO:0019432)triglyceride homeostasis(GO:0070328), acyl-glycerol metabolic process (GO:0046464), neutral lipid metabolic process (GO:0046461), triglyceride metabolic process (GO:0006641), fatty acid biosynthetic process (GO:0006633) |
| 31 | Lactoperoxidase (Predicted) | Lpo | extracellular space(GO:0005615),extracellular exosome(GO:0070062),cytoplasm(GO:0005737),basolateral plasma membrane (GO:0016323) | thiocyanate peroxidase activity (GO:0036393),heme binding (GO:0020037) | response to oxidative stress(GO:0006979) |
| 32 | Protein Lrp1 | Lrp1 | integral component of membrane (GO:0016021),nucleolus(GO:0005730),focal adhesion (GO:0005925),dendrite(GO:0030425),lysosomal membrane(GO:0005765),receptor complex(GO:0043235),neuronal cell body(GO:0043025),endosome(GO:0005768),clathrin-coated vesicle(GO:0030136) | poly(A) RNA binding (GO:0044822),protease binding (GO:0002020),calcium ion binding (GO:0005509) | Aging(GO:0007568),cell proliferation(GO:0008283),lipoprotein metabolic process(GO:0042157),positive regulation of protein transport(GO:0051222),cerebral cortex development(GO:0021987),negative regulation of neuron projection development(GO:0010977),protein kinase C-activating G-protein coupled receptor signaling pathway(GO:0007205) |
| 33 | Myosin-6 | Myh6 | Nucleoplasm(GO:0005654),focal adhesion(GO:0005925),myosin complex(GO:0016459),stress fiber(GO:0001725),Z disc(GO:0030018) | ATP binding (GO:0005524),actin-dependent ATPase activity (GO:0030898),motor activity (GO:0003774) | ATP metabolic process(GO:0046034),regulation of heart rate(GO:0002027),regulation of heart growth(GO:0060420),adult heart development(GO:0007512),ventricular cardiac muscle tissue morphogenesis(GO:0055010),atrial cardiac muscle tissue morphogenesis(GO:0055009),regulation of ATPase activity(GO:0043462),cardiac muscle fiber development(GO:0048739),BMP signaling pathway(GO:0030509),canonical Wnt signaling pathway(GO:0060070),cardiac muscle contraction(GO:0060048),regulation of blood pressure(GO:0008217),actin filament-based movement(GO:0030048) |
| 34 | Niemann Pick type C2 | Npc2 | extracellular exosome(GO:0070062),lysosome(GO:0005764) | cholesterol binding (GO:0015485) | intracellular cholesterol transport(GO:0032367),cholesterol homeostasis(GO:0042632),cholesterol efflux(GO:0033344) |
| 35 | Plasminogen activator, urokinase | Plau | extracellular space(GO:0005615),extracellular exosome(GO:0070062),focal adhesion(GO:0005925),cell surface(GO:0009986) | serine-type endopeptidase activity (GO:0004252),kinase activity (GO:0016301) | response to lipopolysaccharide (GO:0032496), Fibrinolysis (GO:0042730),regulation of cell proliferation (GO:0042127),response to hypoxia (GO:0001666),regulation of receptor activity (GO:0010469),regulation of cell adhesion mediated by integrin (GO:0033628) |
| 36 | Plasminogen | Plg | plasma membrane(GO:0005886),extracellular region(GO:0005576),intracellular membrane-bounded organelle(GO:0043231),extrinsic component of plasma membrane (GO:0019897) | serine-type endopeptidase activity (GO:0004252),endopeptidase activity (GO:0004175) | Fibrinolysis(GO:0042730),tissue remodeling(GO:0048771),blood coagulation(GO:0007596),proteolysis involved in cellular protein catabolic process(GO:0051603),labyrinthine layer blood vessel development(GO:0060716),trophoblast giant cell differentiation(GO:0060707) |
| 37 | Anionic trypsin-2 | Prss2 | extracellular space(GO:0005615),extracellular region(GO:0005576) | serine-type endopeptidase activity (GO:0004252),calcium ion binding (GO:0005509) | Proteolysis(GO:0006508),response to nutrient(GO:0007584),collagen catabolic process(GO:0030574) |
| 38 | Prosaposin | Psap | extracellular exosome(GO:0070062),lysosome(GO:0005764),nucleoplasm(GO:0005654),nucleolus(GO:0005730),Golgi apparatus(GO:0005794),mitochondrion(GO:0005739) |  | negative regulation of hydrogen peroxide-induced cell death(GO:1903206),positive regulation of MAPK cascade(GO:0043410),sphingolipid metabolic process(GO:0006665),adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway(GO:0007193),cellular response to organic substance(GO:0071310),regulation of lipid metabolic process(GO:0019216) |
| 39 | Prostaglandin-H2 D-isomerase | Ptgds | extracellular space(GO:0005615),extracellular exosome(GO:0070062),extracellular region(GO:0005576),Golgi apparatus(GO:0005794),perinuclear region of cytoplasm,(GO:0048471),rough endoplasmic reticulum,(GO:0005791),nuclear envelope(GO:0005635),nuclear membrane(GO:0031965) | transporter activity (GO:0005215),prostaglandin-D synthase activity (GO:0004667),retinoid binding (GO:0005501),fatty acid binding (GO:0005504) | response to glucocorticoid(GO:0051384), response to corticosteroid (GO:0031960), fatty acid biosynthetic process (GO:0006633), prostaglandin biosynthetic process(GO:0001516) |
| 40 | Regenerating islet-derived protein 3-gamma | Reg3g | Cytoplasm(GO:0005737),extracellular region(GO:0005576) | carbohydrate binding (GO:0030246) | acute-phase response(GO:0006953),MyD88-dependent toll-like receptor signaling pathway(GO:0002755) |
| 41 | Lipase | RGD1565682 |  | hydrolase activity, acting on ester bonds (GO:0016788) | lipid catabolic process(GO:0016042) |
| 42 | Pre-eosinophil-associated ribonuclease-2 | Rnase2 |  | nucleic acid binding (GO:0003676),ribonuclease activity (GO:0004540),endonuclease activity (GO:0004519) | RNA phosphodiester bond hydrolysis(GO:0090501),nucleic acid phosphodiester bond hydrolysis(GO:0090305) |
| 43 | RCG23287, isoform CRA\_a | Rps27a | Ribosome(GO:0005840) | structural constituent of ribosome (GO:0003735) | Translation(GO:0006412) |
| 44 | Protein S100-A8 | S100a8 | extracellular space (GO:0005615),extracellular exosome (GO:0070062),nucleus (GO:0005634),plasma membrane (GO:0005886),cytoplasm (GO:0005737),cytoskeleton(GO:0005856) | zinc ion binding (GO:0008270),calcium ion binding (GO:0005509),arachidonic acid binding (GO:0050544), antioxidant activity (GO:0016209) | response to lipopolysaccharide (GO:0032496), acute inflammatory response (GO:0002526),chronic inflammatory response (GO:0002544),inflammatory response (GO:0006954),inflammatory response(GO:0006954),innate immune response(GO:0045087),positive regulation of peptide secretion(GO:0002793),peptidyl-cysteine S-nitrosylation(GO:0018119),positive regulation of inflammatory response(GO:0050729),leukocyte migration involved in inflammatory response(GO:0002523),activation of cysteine-type endopeptidase activity involved in apoptotic process(GO:0006919),neutrophil chemotaxis(GO:0030593),astrocyte development(GO:0014002) |
| 45 | Retinoid-inducible serine carboxypeptidase | Scpep1 | extracellular exosome(GO:0070062),cytosol(GO:0005829) | serine-type carboxypeptidase activity (GO:0004185) | proteolysis involved in cellular protein catabolic process(GO:0051603),positive regulation of vasodilation(GO:0045909),negative regulation of blood pressure(GO:0045776) |
| 46 | Protein Sectm1b | Sectm1b | integral component of membrane(GO:0016021) | signal transducer activity (GO:0004871) | signal transduction(GO:0007165),immune response(GO:0006955) |
| 47 | Serine protease inhibitor A3K | Serpina3k | extracellular space(GO:0005615) | serine-type endopeptidase inhibitor activity (GO:0004867) | negative regulation of endopeptidase activity(GO:0010951) |
| 48 | Corticosteroid-binding globulin | Serpina6 | extracellular space(GO:0005615),extracellular exosome(GO:0070062) | serine-type endopeptidase inhibitor activity (GO:0004867),steroid binding (GO:0005496) | negative regulation of endopeptidase activity(GO:0010951),glucocorticoid metabolic process(GO:0008211),transport(GO:0006810) |
| 49 | Protein Serpinc1 | Serpinc1 | extracellular space(GO:0005615),extracellular exosome(GO:0070062),blood microparticle(GO:0072562) | serine-type endopeptidase inhibitor activity (GO:0004867),heparin binding (GO:0008201) | response to lipopolysaccharide (GO:0032496), response to estrogen (GO:0043627), negative regulation of endopeptidase activity(GO:0010951),regulation of blood coagulation, intrinsic pathway(GO:2000266),response to nutrient(GO:0007584),negative regulation of inflammatory response(GO:0050728) |
| 50 | Protein Sh3bgrl3 | Sh3bgrl3 | extracellular exosome(GO:0070062),lamellipodium(GO:0030027) | GTPase activator activity (GO:0005096), protein disulfide oxidoreductase activity (GO:0015035),electron carrier activity (GO:0009055) | regulation of blood vessel endothelial cell migration(GO:0043535),cell redox homeostasis(GO:0045454) |
| 51 | Neutral and basic amino acid transport protein rBAT | Slc3a1 | extracellular exosome(GO:0070062),plasma membrane(GO:0005886),integral component of plasma membrane(GO:0005887),mitochondrial inner membrane(GO:0005743),vacuolar membrane(GO:0005774)brush border membrane(GO:0031526) | cation binding (GO:0043169),protein heterodimerization activity (GO:0046982),catalytic activity (GO:0003824) | carbohydrate metabolic process(GO:0005975),amino acid transport(GO:0006865) |
| 52 | Extracellular superoxide dismutase [Cu-Zn] | Sod3 | extracellular space(GO:0005615),extracellular exosome(GO:0070062),nucleus(GO:0005634),cytoplasm(GO:0005737),extracellular matrix(GO:0031012),trans-Golgi network(GO:0005802) | zinc ion binding (GO:0008270),superoxide dismutase activity (GO:0004784),copper ion binding (GO:0005507) | response to hypoxia(GO:0001666),response to superoxide(GO:0000303),response to oxidative stress(GO:0006979),removal of superoxide radicals(GO:0019430),response to copper ion(GO:0046688) |
| 53 | Trefoil factor 1 | Tff1 | extracellular space(GO:0005615),cytoplasm(GO:0005737) |  | negative regulation of cell proliferation(GO:0008285),cell differentiation(GO:0030154),response to peptide hormone(GO:0043434),response to immobilization stress(GO:0035902) |
| 54 | Protein Vnn1 | Vnn1 | extracellular exosome(GO:0070062) | pantetheine hydrolase activity (GO:0017159) | acute inflammatory response(GO:0002526),positive regulation of T cell differentiation in thymus(GO:0033089),chronic inflammatory response(GO:0002544),innate immune response(GO:0045087),single organismal cell-cell adhesion(GO:0016337),negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway(GO:1902176),central nervous system development(GO:0007417), |
| 55 | Protein Vtn | Vtn | extracellular space(GO:0005615),cytoplasm(GO:0005737),extracellular matrix(GO:0031012),basement membrane(GO:0005604),rough endoplasmic reticulum lumen(GO:0048237),Golgi lumen(GO:0005796) | polysaccharide binding (GO:0030247),heparin binding (GO:0008201),scavenger receptor activity(GO:0005044),identical protein binding (GO:0042802),collagen binding (GO:0005518) | immune responset(GO:GO:0006955),protein polymerization(GO:0051258) |