cytoskeleton organization (GC:0007010) columnar/cuboidal epithelial cell development (GC:0007010) columnar/cuboidal epithelial cell development (GC:0007010) columnar/cuboidal epithelial cell development (GC:0007010) border follicle cell impiration (GC:0007286) border follicle cell impiration (GC:0007286) glycogen metabolic process (GC:00005877) maintenance of protein location in cell (GC:0002507) positive regulation of angiopenesis (GC:0005766) nucleus localization (GC:0005766) ridyceride biosynthetic process (GC:00047766) ridyceride biosynthetic process (GC:00047766) ridyceride biosynthetic process (GC:00047766) ridyceride biosynthetic process (GC:00047766) regulation of telomere maintenance via telomerase (GC:0007043) regulation of telomere maintenance via telomerase (GC:00032210) retina homeostasis (GC:0001895) regulation of telomere maintenance via telomerase (GC:0003987) microtubule polymerization (GC:0004785) positive regulation of protein export from nucleus (GC:0004785) positive regulation of protein export from nucleus (GC:00047857) regulation of historia protein export from nucleus (GC:00047857) regulation of historia protein export from nucleus (GC:00047857) regulation of protein export from nucleus (GC:00047875) vulval cell flate specification (GC:00073277) ecdysone biosynthetic process (GC:00006697) regulation of protein export from nucleus (GC:00047876) and response to sucrose stimulus (GC:00073277) ecdysone biosynthetic process (GC:00006697) regulation of myelination of protein export from nucleus (GC:00073277) ecdysone biosynthetic process (GC:00006697) regulation of myelination of protein intracellular domain protein (GC:00030538) hair follicle placede formation (GC:0006789) integrity expulsation of protein intracellular domain proteologylis (GC:0007072) regulation of verification intracellula			Significant			
columnar/cuboidal epithelial cell development (GC:000206)		0	25	50	75	100
columnar/cuboidal epithelial cell development (GC:000205)	cytoskeleton organization (GO:0	007010) -				
cell cycle phase transition (GC:0044770) border follicle cell migration (GC:000728) border follicle cell migration (GC:000758) glycogen metabolic process (GC:0005977) maintenance of protein location in cell (GC:0032567) positive regulation of angiogenesis (GC:0005767) positive regulation of angiogenesis (GC:0005767) positive regulation of angiogenesis (GC:0045768) nucleus localization (GC:0045768) nucleus localization (GC:0045768) cell-substrate junction assembly (GC:0007647) triglyceride biosynthetic process (GC:0007442) cell-substrate junction assembly (GC:0007427) response to interleukin-1 (GC:0070555) ibosomal large subunit biogenesis (GC:0042273) regulation of telomere maintenance via telomerase (GC:0032210) regulation of telomere maintenance via telomerase (GC:0032210) retina homeostasis (GC:00042873) regulation of protein export from nucleus (GC:0046875) positive regulation of protein export from nucleus (GC:0046875) positive regulation of protein export from nucleus (GC:0046887) regulation of fbroblast profiferation (GC:0046845) vulval cell fate specification (GC:0046845) regulation of myelination (GC:0032562) cellular response to sucrose stimulus (GC:00073227) cet/sysone biosynthetic process (GC:0006697) regulation of myelination (GC:0031641) secretory granule localization (GC:0031641) secretory granule localization (GC:0032562) cellular response to sucrose stimulus (GC:00071229) embryonic genitaliam morphogenesis (GC:00032562) membrane protein intracellular domain proteolysis (GC:0006087) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GC:0006082) cardiac muscle cell-acridiac muscle cell adhesion (GC:0006084) juvenile hormone mediated signaling pathway (GC:0006082) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GC:0006084) juvenile hormone mediated signaling pathway (GC:0006086) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GC:0006086) regulation of ventricular cardiac muscle cell a						
border follicle cell migration (GO:0007586)						
blood coagulation (G-0:007586) glycogen metabolic process (G0:0005977) maintenance of protein location in cell (G0:0032507) positive regulation of angiogenesis (G0:00051647) triglyceride biosynthetic process (G0:001647) triglyceride biosynthetic process (G0:0019432) cell—substrate] junction assembly (G0:0007044) response to interleukin—1 (G0:0070555) intosomal large subunit biogenesis (G0:0042273) regulation of telomere maintenance via telomerase (G0:0032210) retina homeostasis (G0:00042273) regulation of telomere maintenance via telomerase (G0:0032210) retina homeostasis (G0:00042273) regulation of protein export from nucleus (G0:00046827) regulation of forbolast proliferation (G0:0046827) regulation of forbolast proliferation (G0:0046827) regulation of fibroblast proliferation (G0:00046827) regulation of myelination (G0:00072327) regulation of myelination (G0:00072327) regulation of myelination (G0:00031641) secretory granule localization (G0:0031641) secretory granule localization (G0:0031641) secretory granule localization (G0:0031641) secretory granule localization (G0:003362) embryonic genitalia morphogenesis (G0:0006789) integrin activation (G0:003362) membrane protein intracellular domain proteolysis (G0:003638) hair follicle placede formation (G0:0033622) cardiac muscle cell—cardiac muscle cell adhesion (G0:003662) cardiac muscle cell—cardiac muscle cell adhesion (G0:003662) post-chaperonin tubulin folding pathway (G0:0007072) cardiac muscle cell—cardiac muscle cell adhesion (G0:003662) post-chaperonin tubulin folding pathway (G0:0007072) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (G0:003662) post-chaperonin tubulin folding pathway (G0:0007072) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (G0:0006648) postive regulation of imaginal disc-derived wing size (G0:00047434) histone H2A—T120 phosphorylation (G0:0006648) negative regulation of imaginal		′ =				
glycogen metabolic process (G0:000577) maintenance of protein location in cell (G0:0032507) positive regulation of angiogenesis (G0:0045766) nucleus localization (G0:0051647) triglyceride biosynthetic process (G0:0019432) cell-substrate junction assembly (G0:0007044) response to interleukin-1 (G0:0070555) integration interleukin-1 (G0:0070555) regulation of telomere maintenance via telomerase (G0:0042273) regulation of telomere maintenance via telomerase (G0:0032270) retina homeostasis (G0:0042273) regulation of protein export from nucleus (G0:0046785) positive regulation of protein export from nucleus (G0:0046875) regulation of protein export from nucleus (G0:0046877) regulation of protein export from nucleus (G0:0046877) regulation of protein export from nucleus (G0:0046877) regulation of myelination (G0:0038145) vulval cell fate specification (G0:0038145) regulation of myelination (G0:0038141) secretory granule localization (G0:0032252) cellular response to sucrose stimulus (G0:0031641) secretory granule localization (G0:00303252) rembrane protein intracellular domain proteolysis (G0:003738) hair follicle placode formation (G0:003678) membrane protein intracellular domain proteolysis (G0:0037293) vacuolar proton-transporting V-type ATPase complex assembly (G0:007072) cardiac muscle cell-cardiac muscle cell adhesion (G0:006649) juvenile hormone mediated signaling pathway (G0:00070072) cardiac muscle cell-cardiac muscle cell adhesion (G0:006649) juvenile hormone mediated signaling pathway (G0:00070072) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (G0:0006649) integrin activation (G0:003666) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (G0:0006649) integrin activation (G0:0006649) integrin ac	ũ (′ =				
maintenance of protein location in cell (GO:0035267) - positive regulation of angiogenesis (GO:0045766) nucleus localization (GO:0051647) - triglyceride biosynthetic process (GO:001442) - cell—substrate junction assembly (GO:0007044) - response to interleukin-1 (GO:007555) - regulation of telomere maintenance via telomerase (GO:0042273) - regulation of telomere maintenance via telomerase (GO:0042273) - regulation of telomere maintenance via telomerase (GO:0042273) - regulation of telomere maintenance via telomerase (GO:004878) - reina homeostasis (GO:001895) - reduce the polymerization (GO:0046785) - regulation of protein export from nucleus (GO:0046785) - positive regulation of protein export from nucleus (GO:0046785) - regulation of fibroblast profileration (GO:0046785) - regulation of fibroblast profileration (GO:0046785) - regulation of microblast profileration (GO:0046785) - regulation of myelination (GO:0036697) - regulation of myelination (GO:0036789) - regulation of myelination (GO:0036789) - regulation (GO:0036694) - regulation (GO:0036694) - cardiac muscle cell—cardiac muscle cell adhesion (GO:006694) - cardiac muscle cell—cardiac muscle cell adhesion (GO:006694) - cardiac muscle cell—cardiac muscle cell—cardiac muscle cell adhesion (GO:004689) - post—chaperonin tubulin folding pathway (GO:007025) - regulation of cell proliferation involved in imaginal disc—derived wing morphogenesis (GO:004889) - post—chaperonin tubulin folding pathway (GO:0007025) - regulation of cell proliferation involved in imaginal disc—derived wing morphogenesis (GO:004889) - regulation of sequestering activation (GO:003689) - regative regulation of maginal disc—derived wing size (GO:004689) - regative regulation of maginal		′ =				
positive regulation of angiogenesis (GC:0046766) - nucleus localization (GC:0051647) + triglyceride biosynthetic process (GC:00051647) + triglyceride biosynthetic process (GC:0007044) - cell-substrate junction assembly (GC:0007044) - response to interleukin-1 (GC:0070555) - response to interleukin-1 (GC:0070555) - regulation of telomere maintenance via telomerase (GC:0032210) - retina homeostasis (GC:00042273) - regulation of telomere maintenance via telomerase (GC:0032210) - retina homeostasis (GC:0004875) - regulation of telomere maintenance via telomerase (GC:0032210) - retina homeostasis (GC:0004887) - microtubule polymerization (GC:0046785) - positive regulation of protein export from nucleus (GC:0046887) - regulation of floroblast proliferation (GC:0048145) - vulval cell fate specification (GC:0048145) - vulval cell fate specification (GC:0048145) - vulval cell fate specification (GC:0048145) - regulation of myelination (GC:0032252) - regulation of myelination (GC:0032252) - regulation of myelination (GC:0032252) - cellular response to sucrose stimulus (GC:0071329) - embryonic genitalia morphogenesis (GC:0030358) - hair follicle placode formation (GC:0060789) - integrin activation (GC:0060789) - integrin activation (GC:0060789) - integrin activation (GC:0060789) - integrin activation (GC:0060789) - cardiac muscle cell-cardiac muscle cell adhesion (GC:0060789) - cardiac muscle cell-cardiac muscle cell cardiacion (GC:0060789) - juvenile hormone mediated signaling pathway (GC:003666) - post-chaperonin tubulin folding pathway (GC:003666) - post-chaperonin fubulin folding pathway (GC:003666) - post-chaperonin fubulin folding pathway (GC:003666) - regulation of cell proliferation involved in maginal disc-derived wing morphogenesis (GC:0004834) -						
nucleus localization (GC:0051647) triglyceride biosynthetic process (GO:0019432) cell-substrate junction assembly (GO:0007044) response to interleukin-1 (GC:0070555) fibosomal large subunit biogenesis (GC:0042273) regulation of telomere maintenance via telomerase (GC:0032210) retina homeostasis (GC:0042273) regulation of telomere maintenance via telomerase (GC:0032210) retina homeostasis (GC:0001895) endodermal cell differentiation (GC:0035987) microtubule polymerization (GC:0046785) positive regulation of protein export from nucleus (GC:0046887) regulation of fibroblast proliferation (GC:0046887) regulation of fibroblast proliferation (GC:0046887) regulation of fibroblast proliferation (GC:0047827) regulation of myelination (GC:00318416) redulation of myelination (GC:0031841) secretory granule localization (GC:0032252) cellular response to sucrose stimulus (GC:0073227) embryonic genitalia morphogenesis (GC:0036697) removation of myelination (GC:0033639) hair follicle placode formation (GC:0036679) integrin activation (GC:0036822) membrane protein intracellular domain proteolysis (GC:0031293) vacuolar proton-transporting V-type ATPase complex assembly (GC:0070772) cardiac muscle cell-cardiac muscle cell adhesion (GC:0086042) clathrin-dependent endocytosis involved in vitellogenesis (GC:0008689) juvenile hormone mediated signaling pathway (GC:0036626) positive regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GC:0090256) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GC:0090245) larval fat body development (GC:0090245) larval fat body development (GC:0090245) negative regulation of imaginal disc-derived wing size (GC:00904479) negative regulation of pre-miRNA processing (GC:0090449) negative regulation of pre-miRNA processing (GC:0090389) negative regulation of hematopoietic stem cell differentiation (GC:1990248) positive regulation of hematopoietic stem cell differ						
triglyceride biosynthetic process (G0:0019422) cell-substrate junction assembly (G0:0007044) response to interfeukin-1 (G0:0070555) fibosomal large subunit biogenesis (G0:0042273) regulation of telomere maintenance via telomerase (G0:0032210) retina homeostasis (G0:001825) reduction of telomere maintenance via telomerase (G0:0032210) retina homeostasis (G0:001895) reduction of telomere maintenance via telomerase (G0:0035987) microtubule polymerization (G0:004585) reduction of protein export from nucleus (G0:0046827) regulation of protein export from nucleus (G0:0046827) regulation of protein export from nucleus (G0:0046827) regulation of microtubule polymerization (G0:0046827) regulation of myelination (G0:003237) ecdysone biosynthetic process (G0:0006697) regulation of myelination (G0:0032252) reduction of myelination (G0:003252) reduction (G0:003608) reduction of myelination (G0:003362) reduction (G0:003608) reduction of myelination (G0:003362) reduction (G0:003608) reduction of myelination (G0:003608) reduction (G0:0						
cell-substrate junction assembly (GC:0007044) response to interleukin-1 (GC:0070555) ribosomal large subunit biogenesis (GO:0042273) regulation of telomere maintenance via telomerase (GC:0032210) regulation of telomere maintenance via telomerase (GC:0032210) retria homeostasis (GC:0001895) endodermal cell differentiation (GC:0035287) microtubule polymerization (GC:0046785) positive regulation of protein export from nucleus (GC:0046827) regulation of fibroblast proliferation (GC:0046785) positive regulation of protein export from nucleus (GC:0046827) regulation of mibroblast proliferation (GC:0008145) vulval cell late specification (GC:00073277 ecdysone biosynthetic process (GC:0006687) regulation of myelination (GC:00073277 ecdysone biosynthetic process (GC:0006687) regulation of myelination (GC:0003252) cellular response to sucrose stimulus (GC:00071329) embryonic genitalia morphogenesis (GC:0003252) cellular response to sucrose stimulus (GC:00071329) embryonic genitalia morphogenesis (GC:0003538) hair follicle placode formation (GC:0006789) integrin activation (GC:00076799) integrin activation (GC:00076799) regulation of myelination proteolysis (GC:00070072) cardiac muscle cell-cardiac muscle cell adhesion (GC:00070072) cardiac muscle cell-cardiac muscle cell adhesion (GC:0006642) clathrin-dependent endocytosis involved in vitellogenesis (GC:0006489) juvenile hormone mediated signaling pathway (GC:0007037) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GC:0000488) juvenile hormone mediated signaling pathway (GC:000703) regulation of sellular response to sucreada ving pathway (GC:0000703) larval fat body development (GC:0004780) megative regulation of epithelial to mesenchymal transition (GC:0004780) negative regulation of imaginal disc-derived wing size (GC:0004720) negative regulation of imaginal disc-derived wing size (GC:0004720) negative regulation of hematopoietic stem cell differentiation (GC:	,	/				
response to interleukin-1 (GO:0070555) ribosomal large subunit biogenesis (GO:0042273) - regulation of telomere maintenance via telomerase (GC:0032210) retina homeostasis (GO:0001895) - retina homeostasis (GO:0001895) - endodermal cell differentiation (GO:0035887) - microtubule polymerization (GO:0046785) - positive regulation of protein export from nucleus (GO:0046827) - regulation of fibroblast proliferation (GO:0046827) - regulation of fibroblast proliferation (GO:0073227) - ecdysone biosynthetic poscess (GO:0006697) - regulation of myelination (GO:0031641) - secretory granule localization (GO:0030538) - hair follice placode formation (GO:0030538) - hair follice placode formation (GO:0030538) - hair follice placode formation (GO:0036789) - integrin activation (GO:0033622) - membrane protein intracellular domain proteolysis (GO:0031293) - vacuolar proton-transporting V-type ATPase complex assembly (GO:007072) - cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:006489) - juvenile hormone mediated signaling pathway (GO:0037023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:008434) - histone H2A-T120 phosphorylation (GO:0090256) - larval fat body development (GO:0007504) - malonate atabolic process (GO:0004334) - histone H2A-T120 phosphorylation (GO:004334) - histone H2A-T120 phosphorylation (GO:0004334) - histone H2A-T120 phosphorylation (GO:0004334) - histone H2A-T120 phosphorylation (GO:0004334) - negative regulation of imaginal disc-derived wing size (GO:0004334) - negative regulation of imaginal disc-derived wing size (GO:0004040) - negative regulation of imaginal disc-derived wing size (GO:0004040) - negative regulation of hematopoietic stem cell differentiation (GO:0004040) - positive regul						
ribosomal large subunit biogenesis (GO:0042273) regulation of telomere maintenance via telomerase (GO:0032210) retina homeostasis (GO:0001895) endodermal cell differentiation (GO:0035987) microtubule polymeration (GO:0046785) positive regulation of protein export from nucleus (GO:0046785) positive regulation of protein export from nucleus (GO:0046827) regulation of fibroblast proliferation (GO:0047327) regulation of mibrobast proliferation (GO:0047327) ecdysone biosynthetic process (GO:0006697) regulation of myelination (GO:0031641) secretory granule localization (GO:0031641) secretory granule localization (GO:0031641) secretory granule localization (GO:0032522) cellular response to sucrose stimulus (GO:0071329) embryonic genitatia morphogenesis (GO:0030538) hair follicle placode formation (GO:0036058) hair follicle placode formation (GO:0036058) hair follicle placode formation (GO:0036058) regulation of collostopic place and place an						
regulation of telomere maintenance via telomerase (GO:0032210) - retina homeostasis (GO:0001895) - retina homeostasis (GO:0001895) - endodermal cell differentiation (GO:0035987) - microtubule polymerization (GO:0046785) - positive regulation of protein export from ucleus (GO:0046785) - regulation of fibroblast proliferation (GO:0046785) - regulation of fibroblast proliferation (GO:0048145) - vulval cell fate specification (GO:0048145) - vulval cell fate specification (GO:0072327) - ecdysone biosynthetic process (GO:0006697) - regulation of myelination (GO:0031641) - secretory granule localization (GO:0032252) - cellular response to sucrose stimulus (GO:0031641) - secretory granule localization (GO:003252) - embryonic genitalia morphogenesis (GO:00060789) - integria activation (GO:003688) - hair follicle placode formation (GO:003688) - integria activation (GO:0036822) - membrane protein intracellular domain proteolysis (GO:00060789) - integria activation (GO:0036622) - cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GO:0006489) - juvenile hormone mediated signaling pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0006489) - positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:0044334) - histone H2A-T120 phosphorylation (GO:0044720) - negative regulation of imaginal disc-derived wing size (GO:0006470) - negative regulation of of regulation of oseoblast proliferation (GO:003662) - negative regulation of of regulation of proliferation (GO:003663) - negative regulation of of regulation of proliferation (GO:003663) - negative regulation of hematopoietic stem cell differentiation (GO:003680) - positive regulation of hematopoietic stem cell differentiation (GO:003680) - positive regulation of hematopoietic stem cell differentiation (GO:003680) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (•	/				
retina homeostasis (GO:0001885) endodermal cell differentiation (GO:0035987) microtubule polymerization (GO:0046785) positive regulation of protein export from nucleus (GO:0046827) regulation of fibroblast proliferation (GO:0048145) vulval cell fate specification (GO:0048145) vulval cell fate specification (GO:0072327) ecdysone biosynthetic process (GO:0006697) regulation of myelination (GO:0031641) secretory granule localization (GO:0031641) secretory granule localization (GO:0032252) celluar response to sucrose stimulus (GO:0071329) embryonic genitalia morphogenesis (GO:00030538) hair follicle placode formation (GO:003789) integrin activation (GO:0033622) membrane protein intracellular domain proteolysis (GO:0037029) regulation of coloron-transporting V-type ATPase complex assembly (GO:007072) cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) clathrin-dependent endocytosis involved in vitellogenesis (GO:0066489) juvenile hormone mediated signaling pathway (GO:0036266) post-chaperonin tubulin folding pathway (GO:0007023) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:00044834) histone H2A-T12D phosphorylation (GO:1990245) larval fat body development (GO:0007504) megative regulation of epithelial to mesenchymal transition (GO:0044334) histone H2A-T12D phosphorylation (GO:1990245) larval fat body development (GO:0007504) megative regulation of imaginal disc-derived wing size (GO:0004720) negative regulation of osteoblast proliferation (GO:0044720) negative regulation of osteoblast proliferation (GO:0004720) negative regulation of osteoblast proliferation (GO:000362) negative regulation of hematopoietic stem cell differentiation (GO:003369) positive regulation of hematopoietic stem cell differentiation (GO:003369) positive regulation of hematopoietic stem cell differentiation (GO:00007504) positive regulation of maginal disc-derived wing size (GO:00007604)		/	Ī			
endodermal cell differentiation (GC:0035987) microtrubule polymerization (GC:0046785) positive regulation of protein export from nucleus (GC:0046827) regulation of protein export from nucleus (GC:0046827) regulation of fibroblast proliferation (GC:0048145) vulval cell fate specification (GC:0072327) ecdysone biosynthetic process (GC:0006697) regulation of myelination (GC:0031641) secretory granule localization (GC:0031641) secretory granule localization (GC:0031291) cellular response to sucrose stimulus (GC:0071329) embryonic genitalia morphogenesis (GC:0030538) hair follicle placode formation (GC:0033689) integrin activation (GC:0033622) membrane protein intracellular domain proteolysis (GC:0031293) vacuolar proton—transporting V—type ATPase complex assembly (GC:0070702) cardiac muscle cell—cardiac muscle cell adhesion (GC:0086042) clathrin—dependent endocytosis involved in vitellogenesis (GC:0006489) juvenile hormone mediated signaling pathway (GC:0035626) post—chaperonin tubulin folding pathway (GC:00070023) regulation of cell proliferation involved in imaginal disc—derived wing morphogenesis (GC:0090256) anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GC:0004344) histone H2A—T120 phosphorylation (GC:0007604) malonate catabolic process (GC:00004720) negative regulation of imaginal disc—derived wing morphogenesis (GC:0007604) negative regulation of involved process (GC:00004720) negative regulation of of sedeblast proliferation (GC:0007804) negative regulation of pre—miRNA processing (GC:0004720) negative regulation of hematopoietic stem cell differentiation (GC:1903946) positive regulation of hematopoietic stem cell differentiation (GC:1903946) positive regulation of hematopoietic stem cell differentiation (GC:0190380) positive regulation of hematopoietic stem cell differentiation (GC:0190390)	· · · · · · · · · · · · · · · · · · ·	/				
positive regulation of protein export from nucleus (G0:0048427) regulation of fibroblast proliferation (G0:0048145) - vulval cell fate specification (G0:0073237) ecdysone biosynthetic process (G0:0006697) regulation of myelination (G0:0031641) - secretory granule localization (G0:0031641) secretory granule localization (G0:0031641) secretory granule localization (G0:0031641) secretory granule localization (G0:0031641) secretory granule localization (G0:0031292) cellular response to sucrose stimulus (G0:0071329) embryonic genitalia morphogenesis (G0:0030538) hair follicle placode formation (G0:0060789) integrin activation (G0:0033622) membrane protein intracellular domain proteolysis (G0:0033622) wacuolar proton-transporting V-type ATPase complex assembly (G0:0070072) cardiac muscle cell-cardiac muscle cell adhesion (G0:0086042) clathrin-dependent endocytosis involved in vitellogenesis (G0:0061883) dolichyl diphosphate biosynthetic process (G0:0006489) juvenile hormone mediated signaling pathway (G0:0035626) post-chaperonin tubulin folding pathway (G0:0007023) regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (G0:0090256) anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (G0:1990245) larval fat body development (G0:0007504) malonate catabolic process (G0:0004334) histone H2A-T120 phosphorylation (G0:1990245) larval fat body development (G0:0007504) malonate catabolic process (G0:0004720) negative regulation of imaginal disc-derived wing size (G0:0004368) negative regulation of of steoblast proliferation (G0:1904878) negative regulation of pre-miRNA processing (G0:2000632) negative regulation of hematopoietic stem cell differentiation (G0:1902038) positive regulation of hematopoietic stem cell differentiation (G0:1903080)	,	/				
regulation of fibroblast proliferation (GO:0048145) - vulval cell fate specification (GO:00723277 - ecdysone biosynthetic process (GO:0006697) - regulation of myelination (GO:0031641) - secretory granule localization (GO:0032252 - cellular response to sucrose stimulus (GO:0071329) - embryonic genitalia morphogenesis (GO:0030258) - hair follicle placode formation (GO:003058) - hair follicle placode formation (GO:003622) - membrane protein intracellular domain proteolysis (GO:0031293) - vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072) - cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:0006489) - juvenile hormone mediated signaling pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0006489) - post-chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0004334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0004334) - histone H2A-T120 phosphorylation (GO:0090256) - larval fat body development (GO:0004378) - negative regulation of imaginal disc-derived wing size (GO:0003689) - negative regulation of pre-miRNA processing (GO:000632) - negative regulation of pre-miRNA processing (GO:000632) - negative regulation of pre-miRNA processing (GO:000632) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of hematopoietic stem cell differentiation (GO:190308) - positive regulation of sequestering of triglyceride (GO:0010890) -	microtubule polymerization (GO:0	046785) -				
vulval cell fate specification (GO:0072327) – ecdysone biosynthetic process (GO:0006897) – regulation of myelination (GO:0031641) – secretory granule localization (GO:0032252) – cellular response to sucrose stimulus (GO:0071329) – embryonic genitalia morphogenesis (GO:0030538) – hair follicle placode formation (GO:0030538) – hair follicle placode formation (GO:0030522) – membrane protein intracellular activation (GO:0033622) – cardiac muscle cell—cardiac muscle cell adhesion (GO:0086042) – clathrin-dependent endocytosis involved in vitellogenesis (GO:0061883) – dolichyl diphosphate biosynthetic process (GO:006489) – juvenile hormone mediated signaling pathway (GO:0035626) – post-chaperonin tubulin folding pathway (GO:0037023) – regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0090256) – anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) – histone H2A-T120 phosphorylation (GO:1090245) – larval fat body development (GO:0007504) – malonate catabolic process (GO:00090410) – negative regulation of imaginal disc-derived wing size (GO:0044720) – negative regulation of imaginal disc-derived wing size (GO:0044720) – negative regulation of imaginal disc-derived wing size (GO:0044720) – negative regulation of pre-miRNA processing (GO:2000632) – negative regulation of pre-miRNA processing (GO:2000632) – positive regulation of hematopoietic stem cell differentiation (GO:1903246) – positive regulation of sequestering of triglyceride (GO:0010890) –	positive regulation of protein export from nucleus (GO:0	046827) -				
ecdysone biosynthetic process (GC:0006697) - regulation of myelination (GC:0031641) - secretory granule localization (GC:003252) - cellular response to sucrose stimulus (GC:0071329) - embryonic genitalia morphogenesis (GC:0030538) - hair follicle placode formation (GC:0030538) - hair follicle placode formation (GC:0030638) - integrin activation (GC:0033622) - membrane protein intracellular domain proteolysis (GC:0031293) - vacuolar proton-transporting V-type ATPase complex assembly (GC:007072) - cardiac muscle cell-cardiac muscle cell adhesion (GC:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GC:00061883) - dolichyl diphosphate biosynthetic process (GC:0006489) - juvenile hormone mediated signaling pathway (GC:0035626) - post-chaperonin tubulin folding pathway (GC:0035626) - post-chaperonin tubulin folding pathway (GC:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GC:00904834) - histone H2A=T120 phosphorylation (GC:0044334) - histone H2A=T120 phosphorylation (GC:0044334) - histone H2A=T120 phosphorylation (GC:0090456) - larval fat body development (GC:0007504) - malonate catabolic process (GC:0090410) - negative regulation of imaginal disc-derived wing size (GC:00044720) - negative regulation of imaginal disc-derived wing size (GC:0004720) - negative regulation of osteoblast proliferation (GC:0033689) - negative regulation of ventricular cardiac muscle cell action potential (GC:1903946) - positive regulation of hematopoietic stem cell differentiation (GC:1903220) - positive regulation of sequestering of triglyceride (GC:0010890) -	regulation of fibroblast proliferation (GO:0	048145) -				
regulation of myelination (GO:0031641) - secretory granule localization (GO:0032252) - cellular response to sucrose stimulus (GO:0071329) - embryonic genitalia morphogenesis (GO:0030538) - hair follicle placode formation (GO:0060789) - integrin activation (GO:003622) - membrane protein intracellular domain proteolysis (GO:0031293) - vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072) - cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:006489) - juvenile hormone mediated signaling pathway (GO:0037023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:009256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0009410) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of pre-miRNA processing (GO:200632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1902038) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:190320) - positive regulation of sequestering of triglyceride (GO:0010890) -	vulval cell fate specification (GO:0	072327) -				
secretory granule localization (GO:0032252) - cellular response to sucrose stimulus (GO:0071329) - embryonic genitalia morphogenesis (GO:0030538) - hair follicle placode formation (GO:0060789) - integrin activation (GO:0033622) - membrane protein intracellular domain proteolysis (GO:0031293) - vacuolar proton-transporting V-type ATPase complex assembly (GO:007072) - cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:006489) - juvenile hormone mediated signaling pathway (GO:0035626) - post-chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0044334) - histone H2A-T120 phosphorylation (GO:0044334) - histone H2A-T120 phosphorylation (GO:0090256) - larval fat body development (GO:0090256) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0004410) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of ore-miRNA processing (GO:2000322) - negative regulation of per-miRNA processing (GO:2000322) - positive regulation of malonate cell action potential (GO:1903386) - positive regulation of malonate cell action potential (GO:1903380) - positive regulation of malonate cell action friglyceride (GO:0100380) - positive regulation of malonate cell action of triglyceride (GO:0190320)						
cellular response to sucrose stimulus (GO:0071329) - embryonic genitalia morphogenesis (GO:0030538) - hair follicle placode formation (GO:0060789) - integrin activation (GO:0063789) - integrin activation (GO:0033622) - membrane protein intracellular domain proteolysis (GO:0031293) - vacuolar proton—transporting V—type ATPase complex assembly (GO:007072) - cardiac muscle cell—cardiac muscle cell adhesion (GO:0086042) - clathrin—dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:0006489) - juvenile hormone mediated signaling pathway (GO:0035626) - post—chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc—derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:004434) - histone H2A—T120 phosphorylation (GO:090445) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of imaginal disc—derived wing size (GO:0004720) - negative regulation of imaginal disc—derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:003689) - negative regulation of pre—miRNA processing (GO:000632) - negative regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -		′ =				
embryonic genitalia morphogenesis (GO:0030538) - hair follicle placode formation (GO:0060789) - integrin activation (GO:003622) - membrane protein intracellular domain proteolysis (GO:0031293) - vacuolar proton—transporting V—type ATPase complex assembly (GO:0070072) - cardiac muscle cell—cardiac muscle cell adhesion (GO:0086042) - clathrin—dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:006489) - juvenile hormone mediated signaling pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc—derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:004434) - histone H2A—T120 phosphorylation (GO:004334) - histone H2A—T120 phosphorylation (GO:0090256) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of imaginal disc—derived wing size (GO:004720) - negative regulation of imaginal disc—derived wing size (GO:0044720) - negative regulation of opte—miRNA processing (GO:004720) - negative regulation of pre—miRNA processing (GO:004032) - positive regulation of hematopoietic stem cell differentiation (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1903200) - positive regulation of sequestering of triglyceride (GO:0010890) -		′ =				
hair follicle placode formation (GC:0060789) integrin activation (GC:0033622) membrane protein intracellular domain proteolysis (GC:0031293) vacuolar proton—transporting V—type ATPase complex assembly (GC:0070072) cardiac muscle cell—cardiac muscle cell adhesion (GC:0086042) clathrin—dependent endocytosis involved in vitellogenesis (GC:0061883) dolichyl diphosphate biosynthetic process (GC:0006489) juvenile hormone mediated signaling pathway (GC:00070023) post—chaperonin tubulin folding pathway (GC:0007023) regulation of cell proliferation involved in imaginal disc—derived wing morphogenesis (GC:0090256) anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GC:0044334) histone H2A—T120 phosphorylation (GC:1904434) histone H2A—T120 phosphorylation (GC:1903045) larval fat body development (GC:0007504) malonate catabolic process (GC:00090410) negative regulation of imaginal disc—derived wing size (GC:0044720) negative regulation of osteoblast proliferation (GC:0033689) negative regulation of pre—miRNA processing (GC:2000632) negative regulation of ventricular cardiac muscle cell action potential (GC:1903946) positive regulation of hematopoietic stem cell differentiation (GC:1903220) positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GC:1903220) positive regulation of sequestering of triglyceride (GC:0010890)	·	′ =				
membrane protein intracellular domain proteolysis (GO:0033622) - wacuolar proton-transporting V-type ATPase complex assembly (GO:0070072) - cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:0006489) - juvenile hormone mediated signaling pathway (GO:0035626) - post-chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:00090410) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of opter-miRNA processing (GO:2000632) - negative regulation of per-miRNA processing (GO:2000632) - negative regulation of hematopoietic stem cell differentiation (GO:1903246) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -		′ =				
membrane protein intracellular domain proteolysis (GO:0031293) - vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072) - cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:0006489) - juvenile hormone mediated signaling pathway (GO:0035626) - post-chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:00047023) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre-miRNA processing (GO:2000632) - negative regulation of hematopoietic stem cell differentiation (GO:1903946) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -	·	′ =				
vacuolar proton—transporting V—type ATPase complex assembly (GO:0070072) — cardiac muscle cell—cardiac muscle cell adhesion (GO:0086042) — clathrin—dependent endocytosis involved in vitellogenesis (GO:0061883) — dolichyl diphosphate biosynthetic process (GO:0006489) — juvenile hormone mediated signaling pathway (GO:0007623) — post—chaperonin tubulin folding pathway (GO:0007023) — regulation of cell proliferation involved in imaginal disc—derived wing morphogenesis (GO:0090256) — anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) — histone H2A—T120 phosphorylation (GO:0007504) — malonate catabolic process (GO:00090410) — negative regulation of calcium ion transmembrane transport via high voltage—gated calcium channel (GO:1904878) — negative regulation of imaginal disc—derived wing size (GO:0044720) — negative regulation of osteoblast proliferation (GO:0033689) — negative regulation of pre—miRNA processing (GO:2000632) — negative regulation of ventricular cardiac muscle cell action potential (GO:1903486) — positive regulation of hematopoietic stem cell differentiation (GO:1903203) — positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) — positive regulation of sequestering of triglyceride (GO:0010890) —	· · · · · · · · · · · · · · · · · · ·	/ =				
cardiac muscle cell-cardiac muscle cell adhesion (GO:0086042) - clathrin-dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:0006489) - juvenile hormone mediated signaling pathway (GO:0035626) - post-chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:003688) - negative regulation of pre-miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -						
clathrin–dependent endocytosis involved in vitellogenesis (GO:0061883) - dolichyl diphosphate biosynthetic process (GO:0006489) - juvenile hormone mediated signaling pathway (GO:0035626) - post–chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc–derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1900245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of calcium ion transmembrane transport via high voltage–gated calcium channel (GO:1904878) - negative regulation of imaginal disc–derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:033689) - negative regulation of pre–miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -						
dolichyl diphosphate biosynthetic process (GO:0006489) - juvenile hormone mediated signaling pathway (GO:0035626) - post-chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of calcium ion transmembrane transport via high voltage-gated calcium channel (GO:1904878) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:033689) - negative regulation of pre-miRNA processing (GO:000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -						
juvenile hormone mediated signaling pathway (GO:0035626) - post-chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of calcium ion transmembrane transport via high voltage-gated calcium channel (GO:1904878) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre-miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -		/				
post–chaperonin tubulin folding pathway (GO:0007023) - regulation of cell proliferation involved in imaginal disc–derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A–T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of calcium ion transmembrane transport via high voltage–gated calcium channel (GO:1904878) - negative regulation of imaginal disc–derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre–miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -						
regulation of cell proliferation involved in imaginal disc-derived wing morphogenesis (GO:0090256) - anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of calcium ion transmembrane transport via high voltage-gated calcium channel (GO:1904878) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre-miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -	,	/ I =				
anonical Wnt signaling pathway involved in positive regulation of epithelial to mesenchymal transition (GO:0044334) - histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of calcium ion transmembrane transport via high voltage-gated calcium channel (GO:1904878) - negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre-miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -	, , , , , , , , , , , , , , , , , , , ,	/ I =				
histone H2A-T120 phosphorylation (GO:1990245) - larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - malonate catabolic process (GO:0090410) - malonate catabolic process (GO:0090410) - malonate catabolic process (GO:0090470) - malonate catabolic process (GO:0090470) - malonate catabolic process (GO:0044720) - malonate regulation of imaginal disc-derived wing size (GO:0044720) - malonate regulation of osteoblast proliferation (GO:0033689) - malonate regulation of pre-miRNA processing (GO:2000632) - malonate regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -		′ 1 =				
larval fat body development (GO:0007504) - malonate catabolic process (GO:0090410) - negative regulation of calcium ion transmembrane transport via high voltage—gated calcium channel (GO:1904878) - negative regulation of imaginal disc—derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre—miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -		/ =				
malonate catabolic process (GO:0090410) - negative regulation of calcium ion transmembrane transport via high voltage—gated calcium channel (GO:1904878) - negative regulation of imaginal disc—derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre—miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -		/ =				
negative regulation of calcium ion transmembrane transport via high voltage—gated calcium channel (GO:1904878) - negative regulation of imaginal disc—derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre—miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -		/ =				
negative regulation of imaginal disc-derived wing size (GO:0044720) - negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre-miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -	1	/ :				
negative regulation of osteoblast proliferation (GO:0033689) - negative regulation of pre-miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -						
negative regulation of pre-miRNA processing (GO:2000632) - negative regulation of ventricular cardiac muscle cell action potential (GO:1903946) - positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -		/ :				
positive regulation of hematopoietic stem cell differentiation (GO:1902038) - positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -						
positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1903220) - positive regulation of sequestering of triglyceride (GO:0010890) -	negative regulation of ventricular cardiac muscle cell action potential (GO:1	903946) -				
positive regulation of sequestering of triglyceride (GO:0010890)	positive regulation of hematopoietic stem cell differentiation (GO:1	902038)				
	positive regulation of malate dehydrogenase (decarboxylating) (NADP+) activity (GO:1	903220)				
positive regulation of transforming growth factor beta3 production (GO:0032916)						
	positive regulation of transforming growth factor beta3 production (GO:0					
regulation of definitive erythrocyte differentiation (GO:0010724)						
synaptic vesicle to endosome fusion (GO:0016189)	synaptic vesicle to endosome fusion (GO:0	016189) -				