

**Supplementary Table 1.** List of genes in categories in this study

Molecular antioxidant activity function (GO:0016209)	glutathione dehydrogenase (ascorbate) activity (GO:0045174)		quaternary ammonium group binding (GO:0050997)
	glutathione-disulfide reductase activity (GO:0004362)		ribonucleoprotein complex binding (GO:0043021)
	peroxidase activity (GO:0004601)		S-nitrosoglutathione binding (GO:0035730)
	sulfiredoxin activity (GO:0032542)		selenium binding (GO:0008430)
	superoxide dismutase activity (GO:0004784)		small molecule binding (GO:0036094)
	superoxide reductase activity (GO:0050605)		sulfur compound binding (GO:1901681)
	thioredoxin-disulfide reductase activity (GO:0004791)		toxic substance binding (GO:0015643)
binding (GO:0005488)	2-aminoethylphosphonate binding (GO:0033226)	catalytic activity (GO:0003824)	virion binding (GO:0046790)
	acyl binding (GO:0000035)		water binding (GO:0050824)
	alkene binding (GO:0072328)		catalysis of free radical formation (GO:0043364)
	amide binding (GO:0033218)		cyclase activity (GO:0009975)
	amine binding (GO:0043176)		deaminase activity (GO:0019239)
	antigen binding (GO:0003823)		demethylase activity (GO:0032451)
	binding, bridging (GO:0060090)		first spliceosomal transesterification activity (GO:0000384)
	calcium oxalate binding (GO:0046904)		glycogen debranching enzyme activity (GO:0004133)
	carbohydrate binding (GO:0030246)		glyoxalase III activity (GO:0019172)
	carbohydrate derivative binding (GO:0097367)		hydrolase activity (GO:0016787)
	chromatin binding (GO:0003682)		integrase activity (GO:0008907)
	cofactor binding (GO:0048037)		isomerase activity (GO:0016853)
	dinitrosyl-iron complex binding (GO:0035731)		ligase activity (GO:0016874)
	drug binding (GO:0008144)		lyase activity (GO:0016829)
	extracellular matrix binding (GO:0050840)		Mo-molybdopterin cofactor sulfurase activity (GO:0008265)
	fatty acid derivative binding (GO:1901567)		Mo-molybdopterin synthase activity (GO:0030366)
	flavonoid binding (GO:0097243)		N-ethylmeline chlorohydrolase activity (GO:0016217)
	flurbiprofen binding (GO:0035923)		oxidoreductase activity (GO:0016491)
	heterocyclic compound binding (GO:1901363)		phenylacetaldehyde synthase activity (GO:1990055)
	hormone binding (GO:0042562)		phytoene synthase activity (GO:0046905)
	host cell surface binding (GO:0046812)		quinolate synthetase A activity (GO:0008987)
	hydroxyapatite binding (GO:0046848)		radical SAM enzyme activity (GO:0070283)
	ion binding (GO:0043167)		recombinase activity (GO:0000150)
	kinetochore binding (GO:0043515)		second spliceosomal transesterification activity (GO:0000386)
	lipid binding (GO:0008289)		site-specific recombinase activity (GO:0009009)
	lipoteichoic acid binding (GO:0070891)		site-specific telomere resolvase activity (GO:0043336)
	metal cluster binding (GO:0051540)		small protein activating enzyme activity (GO:0008641)
	microfibril binding (GO:0050436)		transferase activity (GO:0016740)
	neurotransmitter binding (GO:0042165)		transposase activity (GO:0004803)
	nitric oxide binding (GO:0070026)		UDP-L-rhamnose synthase activity (GO:0010280)
	odorant binding (GO:0005549)		versicolorin B synthase activity (GO:0046572)
	organic cyclic compound binding (GO:0097159)		
	oxygen binding (GO:0019825)	channel regulator activity (GO:0016247)	calcium channel regulator activity (GO:0005246)
	pattern binding (GO:0001871)		channel inhibitor activity (GO:0016248)
	pigment binding (GO:0031409)		
	poly(3-hydroxyalkanoate) binding (GO:0043287)		
	polyamine binding (GO:0019808)		
	protein binding (GO:0005515)		
	protein-lipid complex binding (GO:0071814)		

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	chloride channel regulator activity (GO:0017081)		ligase regulator activity (GO:0055103)
	potassium channel regulator activity (GO:0015459)		metalloenzyme regulator activity (GO:0010576)
	sodium channel regulator activity (GO:0017080)		methionine adenosyltransferase regulator activity (GO:0048270)
chemoattractant activity (GO:0042056)	chemoattractant activity		nitric-oxide synthase regulator activity (GO:0030235)
chemorepellent activity (GO:0045499)	chemorepellent activity		nucleoside-triphosphatase regulator activity (GO:0060589)
D-alanyl carrier activity (GO:0036370)	D-alanyl carrier activity		ornithine decarboxylase regulator activity (GO:0042979)
electron carrier activity (GO:0009055)	electron transporter, transferring electrons from CoQH2-cytochrome c reductase complex and cytochrome c oxidase complex activity (GO:0045155)		peptidase regulator activity (GO:0061134)
	electron transporter, transferring electrons from cytochrome b6/f complex of photosystem II activity (GO:0046028)	metallochaperone activity (GO:0016530)	phosphatase regulator activity (GO:0019208)
	electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activity (GO:0045153)	molecular transducer activity (GO:0060089)	UTP:glucose-1-phosphate uridylyltransferase regulator activity (GO:0043763)
	electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity (GO:0045158)	morphogen activity (GO:0016015)	copper chaperone activity (GO:0016531)
	electron transporter, transferring electrons within cytochrome c oxidase complex activity (GO:0045154)	nucleic acid binding transcription factor activity (GO:0001071)	iron chaperone activity (GO:0034986)
	electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity (GO:0045156)	nutrient reservoir activity (GO:0045735)	energy transducer activity (GO:0031992)
	electron transporter, transferring electrons within the noncyclic electron transport pathway of photosynthesis activity (GO:0045157)	protein binding transcription factor activity (GO:0000988)	signal transducer activity (GO:0004871)
enzyme regulator activity (GO:0030234)	cyclase regulator activity (GO:0010851)	protein tag (GO:0031386)	morphogen activity
	cyclin-dependent protein kinase 5 activator regulator activity (GO:0016536)	receptor activity (GO:0004872)	RNA binding transcription factor activity (GO:0001070)
	cysteine-type endopeptidase regulator activity involved in apoptotic process (GO:0043028)		sequence-specific DNA binding transcription factor activity (GO:0003700)
	DNA polymerase processivity factor activity (GO:0030337)		nutrient reservoir activity
	enzyme activator activity (GO:0008047)		
	enzyme inhibitor activity (GO:0004857)		core RNA polymerase binding transcription factor activity (GO:0000990)
	GTP cyclohydrolase I regulator activity (GO:0060308)		transcription factor binding transcription factor activity (GO:0000989)
	guiding stereospecific synthesis activity (GO:0042349)		protein tag
	histone acetyltransferase regulator activity (GO:0035034)		apolipoprotein receptor activity (GO:0030226)
	histone deacetylase regulator activity (GO:0035033)		cargo receptor activity (GO:0038024)
	inositol phosphoceramide synthase regulator activity (GO:0070917)		decoy death receptor activity (GO:0005040)
	kinase regulator activity (GO:0019207)		laminin receptor activity (GO:0005055)
			pattern recognition receptor activity (GO:0038187)
			signaling receptor activity (GO:0038023)
			virus receptor activity (GO:0001618)
			acetylcholine receptor regulator activity (GO:0030548)
			receptor activator activity (GO:0030546)
			receptor inhibitor activity (GO:0030547)
			extracellular matrix structural constituent (GO:0005201)
			protein complex scaffold (GO:0032947)
			structural constituent of albumen (GO:0097099)
			structural constituent of bone (GO:0008147)

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	structural constituent of carboxysome (GO:0043886)		
	structural constituent of cell wall (GO:0005199)		
	structural constituent of chorion (GO:0005213)		
	structural constituent of chromatin (GO:0030527)		
	structural constituent of cuticle (GO:0042302)		
	structural constituent of cytoskeleton (GO:0005200)		
	structural constituent of egg coat (GO:0035804)		
	structural constituent of epidermis (GO:0030280)		
	structural constituent of eye lens (GO:0005212)		
	structural constituent of muscle (GO:0008307)		
	structural constituent of myelin sheath (GO:0019911)		
	structural constituent of nuclear pore (GO:0017056)		
	structural constituent of peritrophic membrane (GO:0016490)		
	structural constituent of ribosome (GO:0003735)		
translation regulator activity (GO:0045182)	translation factor activity, non-nucleic acid binding (GO:0045183)		
	translation regulator activity, nucleic acid binding (GO:0090079)		
	translation repressor activity (GO:0030371)		
transporter activity (GO:0005215)	alkane transporter activity (GO:0015567)		
	carbohydrate derivative transporter activity (GO:1901505)		
	carbohydrate transporter activity (GO:1901476)		
	cofactor transporter activity (GO:0051184)		
	drug transporter activity (GO:0090484)		
	fatty-acyl-CoA transporter activity (GO:0015607)		
	neurotransmitter transporter activity (GO:0005326)		
	nucleocytoplasmic transporter activity (GO:0005487)		
	odorant transporter activity (GO:0043563)		
	siderophore transporter activity (GO:0042927)		
	substrate-specific transporter activity (GO:0022892)		
	toxin transporter activity (GO:0019534)		
	transmembrane transporter activity (GO:0022857)		
	vitamin transporter activity (GO:0051183)		
	xenobiotic transporter activity (GO:0042910)		
Cellular component	cell (GO:0005623)	cell part (GO:0044464)	
	cell junction (GO:0030054)	Dxr protein complex (GO:1990065)	
		anchoring junction (GO:0070161)	
		cell-cell junction (GO:0005911)	
		cell-substrate junction (GO:0030055)	
		plasma membrane part of cell junction (GO:0061466)	
	cell part (GO:0044464)	3-phenylpropionate dioxygenase complex (GO:0009334)	
		annulate lamellae (GO:0005642)	
		apical complex (GO:0020007)	
		apical part of cell (GO:0045177)	
		ascus epiplasm (GO:0072324)	
		aspartate carbamoyltransferase complex (GO:0009347)	
		basal labyrinth (GO:0033774)	
		basal part of cell (GO:0045178)	
		basal ring of apical complex (GO:0020032)	
		CD20-Lck-Fyn complex (GO:0070331)	
		CD20-Lck-Lyn-Fyn complex (GO:0070332)	
		cell body (GO:0044297)	
		cell division site (GO:0032153)	
		cell division site part (GO:0032155)	
		cell envelope Sec protein transport complex (GO:0031522)	
		cell leading edge (GO:0031252)	
		cell periphery (GO:0071944)	
		cell pole (GO:0060187)	
		cell projection (GO:0042995)	
		cell projection part (GO:0044463)	
		cell septum (GO:0030428)	
		cell septum part (GO:0044457)	
		cell surface (GO:0009986)	
		cellular bud (GO:0005933)	
		coated pit (GO:0005905)	
		compact myelin (GO:0043218)	
		contractile ring (GO:0070938)	
		cyclic-nucleotide phosphodiesterase complex (GO:0005966)	
		cytoophidium (GO:0097268)	
		dimethyl sulfoxide reductase complex (GO:0009390)	
		Dxr protein complex (GO:1990065)	
		eisosome (GO:0032126)	
		endomembrane system (GO:0012505)	
		ensheathing process (GO:1990015)	
		envelope (GO:0031975)	
		external encapsulating structure (GO:0030312)	
		external encapsulating structure part (GO:0044462)	
		Flemming body (GO:0090543)	
		formate dehydrogenase complex (GO:0009326)	
		germ tube (GO:0032179)	
		HICS complex (GO:0044697)	

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inner membrane complex (GO:0070258)	site of polarized growth (GO:0030427)
intracellular (GO:0005622)	sperm individualization complex (GO:0070864)
intracellular immature spore (GO:0042763)	sperm part (GO:0097223)
intracellular part (GO:0044424)	spitzenkorper (GO:0031521)
Kibra-Ex-Mer complex (GO:0036375)	stereocilia ankle link complex (GO:0002142)
lateral loop (GO:0043219)	stereocilia coupling link (GO:0002139)
lateral part of motile cell (GO:0031255)	tail portion of tanyocyte (GO:1990018)
longitudinal side of cell surface (GO:0009930)	trailing edge (GO:0031254)
methane monooxygenase complex (GO:0015050)	trimethylamine-N-oxide reductase complex (GO:0009322)
midbody (GO:0030496)	tripartite ATP-independent periplasmic transporter complex (GO:0031317)
molybdopterin synthase complex (GO:0019008)	type I protein secretion system complex (GO:0030256)
myelin sheath (GO:0043209)	type II protein secretion system complex (GO:0015627)
myelin sheath abaxonal region (GO:0035748)	type III protein secretion system complex (GO:0030257)
myelin sheath adaxonal region (GO:0035749)	type IV secretion system complex (GO:0043684)
neck portion of tanyocyte (GO:1990016)	type V protein secretion system complex (GO:0098046)
neuron part (GO:0097458)	type VI protein secretion system complex (GO:0033104)
NHE3/E3KARP/ACTN4 complex (GO:0032766)	vesicle membrane (GO:0012506)
nitrate reductase complex (GO:0009325)	extracellular matrix (GO:0031012)
nitrite reductase complex [NAD(P)H] (GO:0009344)	biofilm matrix (GO:0097311)
nuclear outer membrane-endoplasmic reticulum membrane network (GO:0042175)	extracellular matrix part (GO:0044420)
pellicle (GO:0020039)	plant extracellular matrix (GO:0048196)
periplasmic space (GO:0042597)	proteinaceous extracellular matrix (GO:0005578)
plant extracellular matrix (GO:0048196)	extracellular matrix part (GO:0044420)
plasma membrane (GO:0005886)	apical lamina of hyaline layer (GO:0032579)
plasma membrane part (GO:0044459)	basal lamina (GO:0005605)
polar ring of apical complex (GO:0020031)	basement membrane (GO:0005604)
polar tube (GO:0044099)	biofilm matrix part (GO:0097312)
polyphosphate kinase complex (GO:0009358)	collagen (GO:0005581)
prospore membrane (GO:0005628)	collagen and cuticulin-based cuticle extracellular matrix part (GO:0060103)
prospore membrane leading edge (GO:0070056)	columella (GO:0043674)
prospore membrane spindle pole body attachment site (GO:0070057)	ectexine (GO:0043669)
protein serine/threonine phosphatase complex (GO:0008287)	elastic fiber (GO:0071953)
retromer complex (GO:0030904)	endexine (GO:0043671)
retromer complex, inner shell (GO:0030906)	exine (GO:0043668)
retromer complex, outer shell (GO:0030905)	fibril (GO:0043205)
rhoptry (GO:0020008)	foot layer (GO:0043670)
rhoptry lumen (GO:0034591)	germination pore (GO:0043677)
rhoptry membrane (GO:0033016)	intine (GO:0043678)
riboflavin synthase complex (GO:0009349)	lamina densa (GO:0008003)
Schmidt-Lanterman incisure (GO:0043220)	lamina lucida (GO:0008002)
	lamina reticularis (GO:0008004)
	laminin complex (GO:0043256)
	middle lamella (GO:0009519)
	nexine (GO:0043672)
	perineuronal net (GO:0072534)
	pollen coat (GO:0070505)
	pollen wall (GO:0043667)

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	sculpture element (GO:0043675)		lamina reticularis (GO:0008004)
	sexine (GO:0043673)		laminin complex (GO:0043256)
	synaptic cleft (GO:0043083)		larval serum protein complex (GO:0005616)
	tectum (GO:0043676)		mucus layer (GO:0070701)
	Ubisch body (GO:0070645)		other organism part (GO:0044217)
extracellular region (GO:0005576)	apoplast (GO:0048046)		plasma lipoprotein particle (GO:0034358)
extracellular region part (GO:0044421)	extracellular region part (GO:0044421)		proteinaceous extracellular matrix (GO:0005578)
	activin complex (GO:0048180)	macromolecular complex (GO:0032991)	dosage compensation complex (GO:0046536)
	angiogenin-PR1 complex (GO:0032311)		protein complex (GO:0043234)
	apical lamina of hyaline layer (GO:0032579)		protein-carbohydrate complex (GO:0032992)
	apoptotic body (GO:0097189)		protein-DNA complex (GO:0032993)
	basal lamina (GO:0005605)		protein-DNA-RNA complex (GO:0001114)
	basement membrane (GO:0005604)		protein-lipid complex (GO:0032994)
	blood microparticle (GO:0072562)		ribonucleoprotein complex (GO:0030529)
	bursicon neuropeptide hormone complex (GO:0031395)		sperm individualization complex (GO:0070864)
	classical-complement-pathway C3/C5 convertase complex (GO:0005601)		subapical complex (GO:0035003)
	CNTFR-CLCF1 complex (GO:0097059)	membrane (GO:0016020)	ascus membrane (GO:0036362)
	collagen (GO:0005581)		coated membrane (GO:0048475)
	collagen and cuticulin-based cuticle extracellular matrix part (GO:0060103)		membrane part (GO:0044425)
	complement component C1 complex (GO:0005602)		nuclear outer membrane-endoplasmic reticulum membrane network (GO:0042175)
	CRLF-CLCF1 complex (GO:0097058)		organelle membrane (GO:0031090)
	extra-invasive hyphal space (GO:0085040)		outer membrane (GO:0019867)
	extracellular ferritin complex (GO:0070289)		photoreceptor inner segment membrane (GO:0060342)
	extracellular isoamylase complex (GO:0010367)		photosynthetic membrane (GO:0034357)
	extracellular organelle (GO:0043230)		plasma membrane (GO:0005886)
	extracellular space (GO:0005615)		pre-autophagosomal structure membrane (GO:0034045)
	extracellular space of host (GO:0043655)		prospore membrane (GO:0005628)
	extrahaustorial matrix (GO:0085036)		synaptic membrane (GO:0097060)
	extraorganismal space (GO:0043245)		virion membrane (GO:0055036)
	female germline ring canal inner rim (GO:0035183)	membrane part (GO:0044425)	annulate lamellae (GO:0005642)
	female germline ring canal outer rim (GO:0035182)		AP-type membrane coat adaptor complex (GO:0030119)
	fibril (GO:0043205)		ATP-binding cassette (ABC) transporter complex (GO:0043190)
	fibrinogen complex (GO:0005577)		Bam protein complex (GO:1990063)
	follicle-stimulating hormone complex (GO:0016914)		cation-transporting ATPase complex (GO:0090533)
	hyaluronan cable (GO:0036117)		Cdc48p-Npl4p-Ufd1p AAA ATPase complex (GO:0034098)
	immunoglobulin complex, circulating (GO:0042571)		chloroplast ATP synthase complex (GO:0009544)
	inhibin complex (GO:0043511)		chloroplast outer membrane translocon (GO:0010278)
	insulin-like growth factor binding protein complex (GO:0016942)		chromosome segregation-directing complex (GO:0043913)
	intercellular bridge (GO:0045171)		clathrin complex (GO:0071439)
	interleukin-12 complex (GO:0043514)		coated pit (GO:0005905)
	interleukin-23 complex (GO:0070743)		
	interleukin-27 complex (GO:0070744)		
	interleukin-35 complex (GO:0070745)		
	lamina densa (GO:0008003)		
	lamina lucida (GO:0008002)		

**Supplementary Table 1. Continued**

cytochrome o ubiquinol oxidase complex (GO:0009319)	nuclear membrane part (GO:0044453)
dolichyl-phosphate-mannose-protein mannosyltransferase complex (GO:0031502)	nuclear outer membrane (GO:0005640)
Dsc E3 ubiquitin ligase complex (GO:0044695)	nuclear outer membrane-endoplasmic reticulum membrane network (GO:0042175)
EGO complex (GO:0034448)	nuclear pore central transport channel (GO:0044613)
endoplasmic reticulum membrane (GO:0005789)	nuclear pore cytoplasmic filaments (GO:0044614)
endoplasmic reticulum palmitoyltransferase complex (GO:0031211)	nuclear pore inner ring (GO:0044611)
endoplasmic reticulum Sec complex (GO:0031205)	nuclear pore linkers (GO:0044612)
endosomal scaffold complex (GO:0032969)	nuclear pore nuclear basket (GO:0044615)
ER membrane protein complex (GO:0072546)	nuclear pore outer ring (GO:0031080)
ER ubiquitin ligase complex (GO:0000835)	nuclear pore transmembrane ring (GO:0070762)
ESCRT I complex (GO:0000813)	oligosaccharyltransferase complex (GO:0008250)
ESCRT II complex (GO:0000814)	organelle membrane contact site (GO:0044232)
ESCRT III complex (GO:0000815)	outer acrosomal membrane (GO:0002081)
external side of cell outer membrane (GO:0031240)	oxygen evolving complex (GO:0009654)
external side of endosome membrane (GO:0010009)	PAS complex (GO:0070772)
extrinsic to membrane (GO:0019898)	photosystem (GO:0009521)
fatty acid elongase complex (GO:0009923)	photosystem I antenna complex (GO:0009782)
fully spanning plasma membrane (GO:0044214)	photosystem I reaction center (GO:0009538)
fumarate reductase complex (GO:0045283)	photosystem II antenna complex (GO:0009783)
GPI-anchor transamidase complex (GO:0042765)	photosystem II reaction center (GO:0009539)
HOPS complex (GO:0030897)	phycobilisome (GO:0030089)
inner acrosomal membrane (GO:0002079)	plasma membrane part (GO:0044459)
internal side of cell outer membrane (GO:0031241)	pore complex (GO:0046930)
intrinsic to membrane (GO:0031224)	pre-B cell receptor complex (GO:0035369)
ion channel complex (GO:0034702)	prospore membrane leading edge (GO:0070056)
leaflet of membrane bilayer (GO:0097478)	prospore membrane spindle pole body attachment site (GO:0070057)
lipopolysaccharide receptor complex (GO:0046696)	protein C inhibitor-acrosin complex (GO:0033282)
membrane coat (GO:0030117)	proton-transporting ATP synthase, catalytic core (GO:0045267)
membrane raft (GO:0045121)	proton-transporting ATP synthase, central stalk (GO:0045269)
mepripin A complex (GO:0017090)	proton-transporting ATP synthase, stator stalk (GO:0045265)
MHC class I peptide loading complex (GO:0042824)	proton-transporting two-sector ATPase complex (GO:0016469)
mitochondrial membrane part (GO:0044455)	proton-transporting two-sector ATPase complex, catalytic domain (GO:0033178)
NAD(P)H dehydrogenase complex (plastoquinone) (GO:0010598)	proton-transporting two-sector ATPase complex, proton-transporting domain (GO:0033177)
NADH dehydrogenase complex (GO:0030964)	PSII associated light-harvesting complex II, core complex (GO:0009655)
Nem1-Spo7 phosphatase complex (GO:0071595)	

Supplementary Table 1. Continued

	PSII associated light-harvesting complex II, peripheral complex (GO:0009656)		non-membrane-bounded organelle (GO:0043228)
	PSII associated light-harvesting complex II, peripheral complex, LHCIIb subcomplex (GO:0030085)		organelle part (GO:0044422)
	Ragulator complex (GO:0071986)	organelle part (GO:0044422)	vesicle (GO:0031982)
	respiratory chain (GO:0070469)		axoneme (GO:0005930)
	respiratory chain complex II (GO:0045273)		axoneme part (GO:0044447)
	respiratory chain complex III (GO:0045275)		bacterial-type flagellum part (GO:0044461)
	respiratory chain complex IV (GO:0045277)		contractile fiber part (GO:0044449)
	retromer complex (GO:0030904)		Dsc E3 ubiquitin ligase complex (GO:0044695)
	retromer complex, inner shell (GO:0030906)		intracellular organelle part (GO:0044446)
	retromer complex, outer shell (GO:0030905)		kinocilium (GO:0060091)
	Sec62/Sec63 complex (GO:0031207)		organellar ribosome (GO:0000313)
	signal peptidase complex (GO:0005787)		organelle lumen (GO:0043233)
	signal recognition particle receptor complex (GO:0005785)		organelle membrane (GO:0031090)
	SNARE complex (GO:0031201)		organelle membrane contact site (GO:0044232)
	sodium ion-transporting two-sector ATPase complex (GO:0016472)		plasma membrane-derived photosystem I (GO:0030094)
	SREBP-SCAP complex (GO:0032936)		plasma membrane-derived thylakoid membrane (GO:0031676)
	SREBP-SCAP-Insig complex (GO:0032937)		plasma membrane-derived thylakoid photosystem II (GO:0030096)
	starch utilization system complex (GO:0044570)		plasma membrane-derived thylakoid ribulose biphosphate carboxylase complex (GO:0048493)
	succinate dehydrogenase complex (GO:0045281)		stereocilium (GO:0032420)
	TAP complex (GO:0042825)		stereocilium membrane (GO:0060171)
	thylakoid light-harvesting complex (GO:0009503)		symbiont-containing vacuolar membrane network (GO:0020006)
	Tic complex (GO:0031897)		symbiont-containing vacuolar space (GO:0020004)
	Toc complex (GO:0010006)		symbiont-containing vacuole membrane (GO:0020005)
	translocon complex (GO:0071256)	symplast (GO:0055044)	TRAPPI protein complex (GO:1990070)
	UDP-N-acetylglucosamine transferase complex (GO:0043541)	synapse (GO:0045202)	plasmodesma (GO:0009506)
	Vps55/Vps68 complex (GO:0034424)		asymmetric synapse (GO:0032279)
membrane-enclosed lumen (GO:0031974)	organelle envelope lumen (GO:0031970)		excitatory synapse (GO:0060076)
	organelle lumen (GO:0043233)		inhibitory synapse (GO:0060077)
mitochondrion-associated adherens complex (GO:0097423)	mitochondrion-associated adherens complex		mossy fiber rosette (GO:0097471)
nucleoid (GO:0009295)	bacterial nucleoid (GO:0043590)		neuromuscular junction (GO:0031594)
	mitochondrial nucleoid (GO:0042645)		ribbon synapse (GO:0097470)
	plastid nucleoid (GO:0042646)		symmetric synapse (GO:0032280)
	single-stranded DNA-binding protein complex (GO:0044777)	synapse part (GO:0044456)	synapse part (GO:0044456)
	virion nucleoid (GO:0039642)		clathrin coat of synaptic vesicle (GO:0030129)
organelle (GO:0043226)	extracellular organelle (GO:0043230)		integral to synaptic vesicle membrane (GO:0030285)
	intracellular organelle (GO:0043229)		postsynaptic density (GO:0014069)
	membrane-bounded organelle (GO:0043227)		presynaptic active zone (GO:0048786)
			presynaptic active zone dense projection (GO:0097445)
			presynaptic cytoskeletal matrix assembled at active zones (GO:0048788)
			presynaptic grid (GO:1990013)

Supplementary Table 1. Continued

	presynaptic periaxonal zone (GO:0036062)		
	subsynaptic reticulum (GO:0071212)		
	synaptic cleft (GO:0043083)		
	synaptic membrane (GO:0097060)		
	synaptic vesicle (GO:0008021)		
	synaptic vesicle lumen (GO:0034592)		
	synaptic vesicle membrane (GO:0030672)		
	terminal bouton (GO:0043195)		
virion (GO:0019012)	virion part (GO:0044423)		
virion part (GO:0044423)	capsomere (GO:0046727)		
	icosahedral viral capsid, collar (GO:0098031)		
	icosahedral viral capsid, collar fiber (GO:0098032)		
	icosahedral viral capsid, neck (GO:0098030)		
	icosahedral viral capsid, neck fiber (GO:0098033)		
	icosahedral viral capsid, spike (GO:0098029)		
	viral capsid (GO:0019028)		
	viral capsid, decoration (GO:0098021)		
	viral capsid, internal space (GO:0098061)		
	viral genome (GO:0019015)		
	viral inner capsid (GO:0039625)		
	viral intermediate capsid (GO:0039626)		
	viral membrane (GO:0036338)		
	viral nucleocapsid (GO:0019013)		
	viral outer capsid (GO:0039624)		
	viral portal complex (GO:0046798)		
	viral procapsid (GO:0046729)		
	viral scaffold (GO:0046806)		
	viral tegument (GO:0019033)		
	viral terminase complex (GO:0043493)		
	virion membrane (GO:0055036)		
	virion nucleoid (GO:0039642)		
	virus tail (GO:0098015)		
	virus tail, baseplate (GO:0098025)		
	virus tail, fiber (GO:0098024)		
	virus tail, major subunit (GO:0098019)		
	virus tail, minor subunit (GO:0098020)		
	virus tail, shaft (GO:0098028)		
	virus tail, sheath (GO:0098027)		
	virus tail, tip (GO:0098023)		
	virus tail, tube (GO:0098026)		
	virus terminase, large subunit (GO:0098009)		
Biological process (GO:0022610)	adhesion to other organism involved in symbiotic interaction (GO:0051825)		
	cell adhesion (GO:0007155)		
	multicellular organism adhesion (GO:0022608)		
		biological regulation (GO:0065007)	regulation of biological process (GO:0050789)
			regulation of biological quality (GO:0065008)
			regulation of molecular function (GO:0065009)
		cell killing (GO:0001906)	complement-dependent cytotoxicity (GO:0097278)
			killing of cells of other organism (GO:0031640)
			leukocyte mediated cytotoxicity (GO:0001909)
			negative regulation of cell killing (GO:0031342)
			positive regulation of cell killing (GO:0031343)
			regulation of cell killing (GO:0031341)
		cellular component organization or biogenesis (GO:0071840)	cell wall organization or biogenesis (GO:0071554)
			cellular component biogenesis (GO:0044085)
			cellular component organization (GO:0016043)
		cellular process (GO:0009987)	cellular metabolic process (GO:0044237)
			cellular process involved in reproduction (GO:0048610)
			multi-organism cellular process (GO:0044764)
			negative regulation of cellular process (GO:0048523)
			phenotypic switching (GO:0036166)
			positive regulation of cellular process (GO:0048522)
			regulation of cellular process (GO:0050794)
			single-organism cellular process (GO:0044763)
		developmental process (GO:0032502)	abscission (GO:0009838)
			age-dependent behavioral decline (GO:0035982)
			anatomical structure development (GO:0048856)
			anatomical structure formation involved in morphogenesis (GO:0048646)
			anatomical structure morphogenesis (GO:0009653)
			cellular developmental process (GO:0048869)
			development involved in symbiotic interaction (GO:0044111)
			developmental pigmentation (GO:0048066)
			developmental process involved in reproduction (GO:0003006)
			dormancy process (GO:0022611)
			innervation (GO:0060384)
			keratinization (GO:0031424)
			megagametogenesis (GO:0009561)
			meristem determinacy (GO:0010022)



Supplementary Table 1. Continued

	meristem maintenance (GO:0010073)		immune system process (GO:0002376)	activation of immune response (GO:0002253)
	microgametogenesis (GO:0055046)			antigen processing and presentation (GO:0019882)
	midbrain-hindbrain boundary maturation during brain development (GO:0022004)			antigen sampling in mucosal-associated lymphoid tissue (GO:0002404)
	midbrain-hindbrain boundary maturation during neural plate development (GO:0022005)			B cell selection (GO:0002339)
	multicellular organismal development (GO:0007275)			hemocyte differentiation (GO:0042386)
	muscle attachment (GO:0016203)			hemocyte proliferation (GO:0035172)
	negative regulation of developmental process (GO:0051093)			immune effector process (GO:0002252)
	organism emergence from protective structure (GO:0071684)			immune response (GO:0006955)
	otolith tethering (GO:0035889)			immune system development (GO:0002520)
	pattern specification process (GO:0007389)			leukocyte activation (GO:0045321)
	polyphenic determination (GO:0048647)			leukocyte homeostasis (GO:0001776)
	positive regulation of developmental process (GO:0051094)			leukocyte migration (GO:0050900)
	post-embryonic development (GO:0009791)			lymphocyte costimulation (GO:0031294)
	pseudocleavage (GO:0030588)			myeloid cell homeostasis (GO:0002262)
	pupariation (GO:0035073)			negative regulation of immune system process (GO:0002683)
	pupation (GO:0035074)			positive regulation of immune system process (GO:0002684)
	regulation of developmental process (GO:0050793)			production of molecular mediator of immune response (GO:0002440)
	single-organism developmental process (GO:0044767)			regulation of immune system process (GO:0002682)
	spore germination (GO:0009847)			somatic diversification of immune receptors (GO:0002200)
	stem cell maintenance (GO:0019827)			T cell selection (GO:0045058)
establishment of localization (GO:0051234)	establishment of localization in cell (GO:0051649)		localization (GO:0051179)	tolerance induction (GO:0002507)
	establishment of organelle localization (GO:0051656)			cellular localization (GO:0051641)
	establishment of protein localization (GO:0045184)			establishment of localization (GO:0051234)
	establishment of RNA localization (GO:0051236)			localization of cell (GO:0051674)
	transport (GO:0006810)			macromolecule localization (GO:0033036)
growth (GO:0040007)	budding cell bud growth (GO:0007117)			maintenance of location (GO:0051235)
	cardiac muscle tissue growth (GO:0055017)			nitric oxide storage (GO:0035732)
	cell growth (GO:0016049)			regulation of localization (GO:0032879)
	developmental growth (GO:0048589)		locomotion (GO:0040011)	cell motility (GO:0048870)
	filamentous growth (GO:0030447)			directional locomotion (GO:0033058)
	growth involved in symbiotic interaction (GO:0044110)			dissemination or transmission of organism from other organism involved in symbiotic interaction (GO:0051821)
	lateral growth (GO:0080190)			flight (GO:0060361)
	multicellular organism growth (GO:0035264)			locomotion involved in locomotory behavior (GO:0031987)
	negative regulation of growth (GO:0045926)			movement in environment of other organism involved in symbiotic interaction (GO:0052192)
	organ growth (GO:0035265)			negative regulation of locomotion (GO:0040013)
	positive regulation of growth (GO:0045927)			positive regulation of locomotion (GO:0040017)
	primary growth (GO:0080189)			regulation of locomotion (GO:0040012)
	regulation of growth (GO:0040008)			swimming (GO:0036268)
				taxis (GO:0042330)
			metabolic process (GO:0008152)	biosynthetic process (GO:0009058)
				catabolic process (GO:0009056)

Supplementary Table 1. Continued

	cellular metabolic process (GO:0044237)		negative regulation of border follicle cell delamination (GO:0030712)
	hormone metabolic process (GO:0042445)		negative regulation of cell cycle checkpoint (GO:1901977)
	methylation (GO:0032259)		negative regulation of cell killing (GO:0031342)
	multi-organism metabolic process (GO:0044033)		negative regulation of cellular component organization (GO:0051129)
	negative regulation of metabolic process (GO:0009892)		negative regulation of cellular process (GO:0048523)
	nitrogen compound metabolic process (GO:0006807)		negative regulation of circadian rhythm (GO:0042754)
	organic substance metabolic process (GO:0071704)		negative regulation of defecation rhythm (GO:2000747)
	positive regulation of metabolic process (GO:0009893)		negative regulation of developmental process (GO:0051093)
	primary metabolic process (GO:0044238)		negative regulation of dosage compensation by inactivation of X chromosome (GO:1900096)
	regulation of metabolic process (GO:0019222)		negative regulation of fibrinolysis (GO:0051918)
	single-organism metabolic process (GO:0044710)		negative regulation of growth (GO:0045926)
	tyrocidine metabolic process (GO:1901902)		negative regulation of homeostatic process (GO:0032845)
	wax metabolic process (GO:0010166)		negative regulation of immune system process (GO:0002683)
multi-organism process (GO:0051704)	adhesion to other organism involved in symbiotic interaction (GO:0051825)		negative regulation of lipid storage (GO:0010888)
	development involved in symbiotic interaction (GO:0044111)		negative regulation of locomotion (GO:0040013)
	growth involved in symbiotic interaction (GO:0044110)		negative regulation of long term synaptic depression (GO:1900453)
	interspecies interaction between organisms (GO:0044419)		negative regulation of long-term synaptic potentiation (GO:1900272)
	intraspecies interaction between organisms (GO:0051703)		negative regulation of metabolic process (GO:0009892)
	mating (GO:0007618)		negative regulation of multi-organism process (GO:0043901)
	modification of morphology or physiology of other organism (GO:0035821)		negative regulation of multicellular organismal process (GO:0051241)
	multi-multicellular organism process (GO:0044706)		negative regulation of nitrogen utilization (GO:0045847)
	multi-organism behavior (GO:0051705)		negative regulation of ovarian follicle development (GO:2000355)
	multi-organism cellular process (GO:0044764)		negative regulation of phosphorus utilization (GO:0045942)
	multi-organism metabolic process (GO:0044033)		negative regulation of Ran GTPase activity (GO:1902264)
	multi-organism signaling (GO:0035636)		negative regulation of reproductive process (GO:2000242)
	multi-organism transport (GO:0044766)		negative regulation of response to stimulus (GO:0048585)
	negative regulation of multi-organism process (GO:0043901)		negative regulation of sequestering of calcium ion (GO:0051283)
	pathogenesis (GO:0009405)		negative regulation of sequestering of zinc ion (GO:0061089)
	positive regulation of multi-organism process (GO:0043902)		negative regulation of signaling (GO:0023057)
	regulation of multi-organism process (GO:0043900)		
	response to other organism (GO:0051707)		
multicellular organismal process (GO:0032501)	multi-multicellular organism process (GO:0044706)		
	multicellular organism reproduction (GO:0032504)		
	single-multicellular organism process (GO:0044707)		

Supplementary Table 1. Continued

	negative regulation of sulfur utilization (GO:0045882)		positive regulation of response to stimulus (GO:0048584)
	negative regulation of transport (GO:0051051)		positive regulation of sequestering of calcium ion (GO:0051284)
	negative regulation of viral protein levels in host cell (GO:0046725)		positive regulation of sequestering of zinc ion (GO:0061090)
positive regulation of biological process (GO:0048518)	positive regulation of border follicle cell delamination (GO:0030711)		positive regulation of signaling (GO:0023056)
	positive regulation of cell cycle checkpoint (GO:1901978)		positive regulation of sulfur utilization (GO:0045883)
	positive regulation of cell killing (GO:0031343)		positive regulation of transport (GO:0051050)
	positive regulation of cellular component biogenesis (GO:0044089)		positive regulation of viral protein levels in host cell (GO:0046726)
	positive regulation of cellular component organization (GO:0051130)	regulation of biological process (GO:0050789)	negative regulation of biological process (GO:0048519)
	positive regulation of cellular process (GO:0048522)		positive regulation of biological process (GO:0048518)
	positive regulation of circadian rhythm (GO:0042753)		regulation of carbohydrate utilization (GO:0043610)
	positive regulation of defecation rhythm (GO:2000748)		regulation of carbon utilization (GO:0043609)
	positive regulation of developmental process (GO:0051094)		regulation of cell killing (GO:0031341)
	positive regulation of dosage compensation by inactivation of X chromosome (GO:1900097)		regulation of cellular component biogenesis (GO:0044087)
	positive regulation of fibrinolysis (GO:0051919)		regulation of cellular component organization (GO:0051128)
	positive regulation of growth (GO:0045927)		regulation of cellular process (GO:0050794)
	positive regulation of homeostatic process (GO:0032846)		regulation of circadian rhythm (GO:0042752)
	positive regulation of immune system process (GO:0002684)		regulation of developmental process (GO:0050793)
	positive regulation of induction of conjugation with cellular fusion (GO:1900237)		regulation of dosage compensation by inactivation of X chromosome (GO:1900095)
	positive regulation of lipid storage (GO:0010884)		regulation of estrogen receptor binding (GO:0071898)
	positive regulation of locomotion (GO:0040017)		regulation of fibrinolysis (GO:0051917)
	positive regulation of long term synaptic depression (GO:1900454)		regulation of growth (GO:0040008)
	positive regulation of long-term synaptic potentiation (GO:1900273)		regulation of homeostatic process (GO:0032844)
	positive regulation of metabolic process (GO:0009893)		regulation of immune system process (GO:0002682)
	positive regulation of multi-organism process (GO:0043902)		regulation of localization (GO:0032879)
	positive regulation of multicellular organismal process (GO:0051240)		regulation of locomotion (GO:0040012)
	positive regulation of nitrogen utilization (GO:0045848)		regulation of long term synaptic depression (GO:1900452)
	positive regulation of ovarian follicle development (GO:2000386)		regulation of long-term synaptic potentiation (GO:1900271)
	positive regulation of phosphorus utilization (GO:0045949)		regulation of metabolic process (GO:0019222)
	positive regulation of reproductive process (GO:2000243)		regulation of multi-organism process (GO:0043900)
			regulation of multicellular organismal process (GO:0051239)
			regulation of nitrogen utilization (GO:0006808)
			regulation of phosphorus utilization (GO:0006795)

Supplementary Table 1. Continued

	regulation of plasma lipoprotein particle levels (GO:0097006)		response to dietary excess (GO:0002021)
	regulation of reproductive process (GO:2000241)		response to endogenous stimulus (GO:0009719)
	regulation of response to stimulus (GO:0048583)		response to external stimulus (GO:0009605)
	regulation of Rho guanyl-nucleotide exchange factor activity (GO:2001106)		response to inactivity (GO:0014854)
	regulation of signaling (GO:0023051)		response to redox state (GO:0051775)
	regulation of sulfur utilization (GO:0006792)		response to stimulus involved in regulation of muscle adaptation (GO:0014874)
reproduction (GO:0000003)	asexual reproduction (GO:0019954)	rhythmic process (GO:0048511)	response to stress (GO:0006950)
	cellular process involved in reproduction (GO:0048610)		circadian rhythm (GO:0007623)
	multicellular organism reproduction (GO:0032504)		ovulation cycle (GO:0042698)
	reproduction of a single-celled organism (GO:0032505)		ovulation cycle process (GO:0022602)
	reproductive process (GO:0022414)	signaling (GO:0023052)	rhythmic behavior (GO:0007622)
	sexual reproduction (GO:0019953)	single-organism process (GO:0044699)	ultradian rhythm (GO:0007624)
reproductive process (GO:0022414)	developmental process involved in reproduction (GO:0003006)		multi-organism signaling (GO:0035636)
	multi-organism reproductive process (GO:0044703)		single organism signaling (GO:0044700)
	multicellular organismal reproductive process (GO:0048609)		antibody-dependent cellular cytotoxicity (GO:0001788)
	negative regulation of reproductive process (GO:2000242)		carbohydrate utilization (GO:0009758)
	positive regulation of reproductive process (GO:2000243)		carbon utilization (GO:0015976)
	regulation of reproductive process (GO:2000241)		cell proliferation (GO:0008283)
	reproductive behavior (GO:0019098)		complement-dependent cytotoxicity (GO:0097278)
	single organism reproductive process (GO:0044702)		death (GO:0016265)
response to stimulus (GO:0050896)	behavior (GO:0007610)		eclosion rhythm (GO:0008062)
	cellular response to stimulus (GO:0051716)		establishment of pole plasm mRNA localization (GO:0046595)
	detection of stimulus (GO:0051606)		establishment of protein localization to extracellular region (GO:0035592)
	immune response (GO:0006955)		filamentous growth (GO:0030447)
	muscle adaptation (GO:0043500)		lateral growth (GO:0080190)
	negative regulation of response to stimulus (GO:0048585)		locomotor rhythm (GO:0045475)
	positive regulation of response to stimulus (GO:0048584)		natural killer cell mediated cytotoxicity (GO:0042267)
	protein activation cascade (GO:0072376)		nitrogen utilization (GO:0019740)
	regulation of response to stimulus (GO:0048583)		ovulation cycle process (GO:0022602)
	response to abiotic stimulus (GO:0009628)		phosphorus utilization (GO:0006794)
	response to activity (GO:0014823)		pigmentation (GO:0043473)
	response to biotic stimulus (GO:0009607)		protein activation cascade (GO:0072376)
	response to chemical stimulus (GO:0042221)		single organism reproductive process (GO:0044702)
			single organism signaling (GO:0044700)
			single-multicellular organism process (GO:0044707)
			single-organism cellular process (GO:0044763)
			single-organism developmental process (GO:0044767)
			single-organism transport (GO:0044765)
			sulfur utilization (GO:0006791)
			T cell mediated cytotoxicity (GO:0001913)
			ultradian rhythm (GO:0007624)