

## Early 1<sup>st</sup> instar larvae: 2-fold downregulated

<b>Biological Processes GO Term</b>	<b>Fold Enrichment</b>	<b>p-value</b>
GO:0032367~intracellular cholesterol transport	18.7565032	8.88E-04
GO:0015918~sterol transport	14.58839138	0.0020
GO:0006013~mannose metabolic process	14.58839138	0.0020
GO:0006020~inositol metabolic process	14.0673774	0.0174
GO:0006807~nitrogen compound metabolic process	12.30895522	8.32E-05
GO:0046855~inositol phosphate dephosphorylation	10.94129353	0.0288
GO:0006517~protein deglycosylation	9.378251599	0.0079
GO:0043171~peptide catabolic process	9.054863613	1.96E-05
GO:0006261~DNA-dependent DNA replication	8.205970149	0.0116
GO:0006400~tRNA modification	8.205970149	0.0497
GO:0006270~DNA replication initiation	7.459972863	0.0040
GO:0046701~insecticide catabolic process	7.135626217	0.0047
GO:0042023~DNA endoreduplication	6.910290652	0.0188
GO:0046680~response to DDT	5.861407249	0.0096
GO:0070050~neuron cellular homeostasis	5.251820896	0.0390
GO:0006260~DNA replication	5.148844015	8.21E-04
GO:0016311~dephosphorylation	4.304771226	0.0024
GO:0005975~carbohydrate metabolic process	3.40625176	0.0014
GO:0040003~chitin-based cuticle development	3.30303201	9.78E-05
GO:0006508~proteolysis	3.1787337	7.57E-12
GO:0055114~oxidation-reduction process	3.027445298	2.88E-09
GO:0055085~transmembrane transport	2.829644879	8.22E-06
GO:0008152~metabolic process	2.248211	0.0340

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<b>Biological Processes GO Term</b>	<b>Fold Enrichment</b>	<b>p-value</b>
GO:0030259~lipid glycosylation	43.12156863	0.0457
GO:0043487~regulation of RNA stability	43.12156863	0.0457
GO:0022404~molting cycle process	30.80112045	9.21E-06
GO:0003383~apical constriction	27.44099822	6.01E-08
GO:0032053~ciliary basal body organization	25.87294118	0.0051
GO:0016476~regulation of embryonic cell shape	15.09254902	4.23E-06
GO:0042335~cuticle development	14.37385621	3.10E-04
GO:0061723~glycophagy	11.76042781	0.0255
GO:0007160~cell-matrix adhesion	10.78039216	0.0055
GO:0016236~macroautophagy	9.240336134	0.0402
GO:0007472~wing disc morphogenesis	8.624313725	0.0104
GO:0044719~regulation of imaginal disc-derived wing size	7.186928105	0.0172
GO:0035096~larval midgut cell programmed cell death	6.634087481	0.0214
GO:0045214~sarcomere organization	5.749542484	0.0312
GO:0010506~regulation of autophagy	5.673890609	0.0111
GO:0008063~Toll signaling pathway	4.928179272	0.0463
GO:0050830~defense response to Gram-positive bacterium	4.620168067	0.0093
GO:0006914~autophagy	4.068072512	0.0337
GO:0007608~sensory perception of smell	3.544238517	0.0266
GO:0007015~actin filament organization	3.080112045	0.0447
GO:0005975~carbohydrate metabolic process	2.847650758	0.0360
GO:0055114~oxidation-reduction process	2.09328003	0.0033
GO:0006508~proteolysis	1.906427245	0.0071

**Late 1<sup>st</sup> instar larvae: 2-fold downregulated**

<b>Biological Processes GO Term</b>	<b>Fold Enrichment</b>	<b>p-value</b>
GO:0051923~sulfation	16.86503067	0.0111
GO:0009913~epidermal cell differentiation	14.99113838	0.0016
GO:0006805~xenobiotic metabolic process	13.49202454	0.0180
GO:0003383~apical constriction	12.26547685	6.24E-05
GO:0010171~body morphogenesis	11.77875158	6.14E-09
GO:0006035~cuticle chitin biosynthetic process	11.24335378	0.0262
GO:0006031~chitin biosynthetic process	11.24335378	0.0262
GO:0008299~isoprenoid biosynthetic process	10.22123071	9.85E-04
GO:0006032~chitin catabolic process	9.894151329	4.85E-08
GO:0010025~wax biosynthetic process	9.83793456	4.05E-05
GO:0035336~long-chain fatty-acyl-CoA metabolic process	9.83793456	4.05E-05
GO:0030497~fatty acid elongation	9.199107641	2.62E-06
GO:0042759~long-chain fatty acid biosynthetic process	8.432515337	0.0461
GO:0045455~ecdysteroid metabolic process	8.17698457	0.0110
GO:0040003~chitin-based cuticle development	8.061272524	4.88E-36
GO:0006807~nitrogen compound metabolic process	7.027096115	0.0046
GO:0046701~insecticide catabolic process	6.843780564	3.92E-04
GO:0016476~regulation of embryonic cell shape	6.74601227	0.0015
GO:0006030~chitin metabolic process	5.905599967	7.04E-13
GO:0046680~response to DDT	5.621676892	0.0012
GO:0035025~positive regulation of Rho protein signal transduction	5.621676892	0.0316
GO:0007160~cell-matrix adhesion	5.621676892	0.0316
GO:0018990~ecdysis, chitin-based cuticle	5.353977992	0.0126
GO:0035017~cuticle pattern formation	5.290990016	0.0372
GO:0051017~actin filament bundle assembly	5.290990016	0.0372
GO:0007158~neuron cell-cell adhesion	4.91896728	0.0025
GO:0005975~carbohydrate metabolic process	4.667052514	6.04E-09
GO:0050804~modulation of synaptic transmission	4.036075717	0.0069
GO:0016042~lipid catabolic process	3.818497511	0.0022
GO:0007416~synapse assembly	3.818497511	0.0022
GO:0006749~glutathione metabolic process	3.349084106	0.0170
GO:0016311~dephosphorylation	3.317710952	0.0053
GO:0006810~transport	2.984961181	4.62E-04
GO:0055114~oxidation-reduction process	2.674389978	6.69E-10
GO:0007480~imaginal disc-derived leg morphogenesis	2.623449216	0.0492
GO:0006629~lipid metabolic process	2.529754601	0.0251
GO:0006508~proteolysis	2.130319664	2.68E-06

### Late 1<sup>st</sup> instar larvae: 2-fold upregulated

<b>Biological Processes GO Term</b>	<b>Fold Enrichment</b>	<b>p-value</b>
GO:0007202~activation of phospholipase C activity	43.984	0.045
GO:0051290~protein heterotetramerization	43.984	0.045
GO:0048791~calcium ion-regulated exocytosis of neurotransmitter	16.494	0.0131
GO:0009790~embryo development	9.425142857	0.0389
GO:0010171~body morphogenesis	8.377904762	0.0113
GO:0006749~glutathione metabolic process	7.486638298	8.14E-05
GO:0006959~humoral immune response	7.330666667	0.0163
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	7.03744	0.0183
GO:0070050~neuron cellular homeostasis	7.03744	0.0183
GO:0050830~defense response to Gram-positive bacterium	5.498	0.0016
GO:0007474~imaginal disc-derived wing vein specification	4.149433962	0.0316
GO:0007606~sensory perception of chemical stimulus	3.824695652	0.0048
GO:0040003~chitin-based cuticle development	3.596176101	2.62E-04
GO:0050829~defense response to Gram-negative bacterium	2.850814815	0.0359
GO:0055085~transmembrane transport	2.426703448	0.00250
GO:0007165~signal transduction	2.328564706	0.0395

## Early 2<sup>nd</sup> instar larvae: 2-fold downregulated

<b>Biological Processes GO Term</b>	<b>Fold Enrichment</b>	<b>p-value</b>
GO:0008608~attachment of spindle microtubules to kinetochore	9.140482128	0.0048
GO:0035561~regulation of chromatin binding	9.140482128	0.0332
GO:0055129~L-proline biosynthetic process	9.140482128	0.0332
GO:0006567~threonine catabolic process	9.140482128	0.0332
GO:0006551~leucine metabolic process	9.140482128	0.0332
GO:0006613~cotranslational protein targeting to membrane	9.140482128	0.0332
GO:0032367~intracellular cholesterol transport	7.834698967	2.69E-04
GO:0009913~epidermal cell differentiation	7.61706844	0.0018
GO:0010884~positive regulation of lipid storage	7.312385702	0.0110
GO:0015918~sterol transport	7.109263877	1.06E-04
GO:0022404~molting cycle process	6.528915806	0.0038
GO:0033539~fatty acid beta-oxidation using acyl-CoA dehydrogenase	6.093654752	5.87E-06
GO:0006013~mannose metabolic process	6.093654752	0.0013
GO:0003383~apical constriction	5.816670445	4.79E-04
GO:0006807~nitrogen compound metabolic process	5.71280133	1.21E-05
GO:0006270~DNA replication initiation	5.401193985	6.27E-07
GO:0006517~protein deglycosylation	5.223132645	3.14E-04
GO:0002027~regulation of heart rate	5.223132645	0.0325
GO:0000086~G2/M transition of mitotic cell cycle	5.078045627	0.0114
GO:0006635~fatty acid beta-oxidation	5.043024622	6.13E-08
GO:0009813~flavonoid biosynthetic process	4.839078774	1.55E-08
GO:0052696~flavonoid glucuronidation	4.839078774	1.55E-08
GO:0046701~insecticide catabolic process	4.768947197	9.89E-06
GO:0006631~fatty acid metabolic process	4.570241064	0.0174
GO:0045455~ecdysteroid metabolic process	4.154764604	0.0250
GO:0043171~peptide catabolic process	4.097457506	2.42E-05
GO:0035336~long-chain fatty-acyl-CoA metabolic process	3.998960931	0.0051
GO:0006261~DNA-dependent DNA replication	3.998960931	0.0051
GO:0010025~wax biosynthetic process	3.998960931	0.0051
GO:0046680~response to DDT	3.917349483	9.37E-05
GO:0055088~lipid homeostasis	3.833105409	5.35E-05
GO:0042381~hemolymph coagulation	3.80853422	0.0343
GO:0048800~antennal morphogenesis	3.656192851	0.0182
GO:0042335~cuticle development	3.656192851	0.0182
GO:0006820~anion transport	3.590903693	4.84E-04
GO:0008363~larval chitin-based cuticle development	3.427680798	0.0242
GO:0035017~cuticle pattern formation	3.226052516	0.0312
GO:0007031~peroxisome organization	3.226052516	0.0312
GO:0016476~regulation of embryonic cell shape	3.199168745	0.0170
GO:0008152~metabolic process	2.879877931	4.40E-11

GO:0007158~neuron cell-cell adhesion	2.856400665	0.0059
GO:0016042~lipid catabolic process	2.759390831	3.92E-04
GO:0016311~dephosphorylation	2.697191448	2.01E-04
GO:0055114~oxidation-reduction process	2.684461984	2.26E-25
GO:0005975~carbohydrate metabolic process	2.673159868	6.08E-07
GO:0035317~imaginal disc-derived wing hair organization	2.665973954	0.0404
GO:0050804~modulation of synaptic transmission	2.578084703	0.0077
GO:0006626~protein targeting to mitochondrion	2.521512311	0.0332
GO:0006260~DNA replication	2.509151957	0.0027
GO:0030261~chromosome condensation	2.437461901	0.0393
GO:0006508~proteolysis	2.386146913	3.98E-21
GO:0009306~protein secretion	2.223360518	0.0432
GO:0055085~transmembrane transport	2.206323272	2.10E-10
GO:0000278~mitotic cell cycle	2.160477594	0.0141
GO:0006749~glutathione metabolic process	2.139261775	0.0282
GO:0006810~transport	2.022230559	0.0010
GO:0040003~chitin-based cuticle development	1.954568505	2.00E-04
GO:0006030~chitin metabolic process	1.938890148	0.0047

## Early 2<sup>nd</sup> instar larvae: 2-fold upregulated

<b>Biological Processes GO Term</b>	<b>Fold Enrichment</b>	<b>p-value</b>
GO:0048499~synaptic vesicle membrane organization	10.65503876	0.0031
GO:0042256~mature ribosome assembly	10.65503876	0.0247
GO:0044246~regulation of multicellular organismal metabolic process	10.65503876	0.0247
GO:1990834~response to odorant	10.65503876	0.0247
GO:0007212~dopamine receptor signaling pathway	10.65503876	0.0247
GO:0097090~presynaptic membrane organization	10.65503876	0.0247
GO:0099509~regulation of presynaptic cytosolic calcium ion concentration	10.65503876	0.0247
GO:0016056~rhodopsin mediated signaling pathway	9.323158915	1.59E-05
GO:0007004~telomere maintenance via telomerase	7.99127907	0.0464
GO:0034097~response to cytokine	7.99127907	0.0464
GO:0040012~regulation of locomotion	7.99127907	0.0464
GO:0048133~male germ-line stem cell asymmetric division	7.99127907	0.0464
GO:0001941~postsynaptic membrane organization	7.99127907	0.0464
GO:0007296~vitellogenesis	7.99127907	0.0464
GO:0006895~Golgi to endosome transport	7.99127907	0.0464
GO:0048172~regulation of short-term neuronal synaptic plasticity	7.610741971	0.0021
GO:0048790~maintenance of presynaptic active zone structure	7.103359173	6.55E-04
GO:0055065~metal ion homeostasis	7.103359173	0.0132
GO:0016200~synaptic target attraction	7.103359173	0.0132
GO:0014067~negative regulation of phosphatidylinositol 3-kinase signaling	7.103359173	0.0132
GO:0048791~calcium ion-regulated exocytosis of neurotransmitter	6.659399225	0.0040
GO:0046928~regulation of neurotransmitter secretion	6.556946929	6.45E-05
GO:0048489~synaptic vesicle transport	6.088593577	1.19E-04
GO:0048526~imaginal disc-derived wing expansion	6.088593577	0.0216
GO:0003012~muscle system process	6.088593577	0.0216
GO:0048789~cytoskeletal matrix organization at active zone	6.088593577	0.0216
GO:0016079~synaptic vesicle exocytosis	5.771479328	4.03E-07
GO:0007271~synaptic transmission, cholinergic	5.682687339	2.04E-04
GO:0050803~regulation of synapse structure or activity	5.32751938	3.34E-04
GO:0019722~calcium-mediated signaling	5.32751938	0.0010
GO:0050774~negative regulation of dendrite morphogenesis	5.32751938	0.0102
GO:0010038~response to metal ion	5.32751938	0.0321
GO:0007415~defasciculation of motor neuron axon	5.32751938	0.0321
GO:0016059~deactivation of rhodopsin mediated signaling	4.972351421	0.0016
GO:0035094~response to nicotine	4.917710197	0.0049
GO:0007615~anesthesia-resistant memory	4.843199436	0.0148
GO:1901215~negative regulation of neuron death	4.843199436	0.0148
GO:0061723~glycophagy	4.843199436	0.0148
GO:1900073~regulation of neuromuscular synaptic transmission	4.843199436	0.0148
GO:0043162~ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	4.843199436	0.0148

GO:0042058~regulation of epidermal growth factor receptor signaling pathway	4.843199436	0.0148
GO:0044130~negative regulation of growth of symbiont in host	4.735572782	0.0449
GO:0043153~entrainment of circadian clock by photoperiod	4.735572782	0.0449
GO:0090328~regulation of olfactory learning	4.735572782	0.0449
GO:0007418~ventral midline development	4.735572782	0.0449
GO:0001963~synaptic transmission, dopaminergic	4.735572782	0.0449
GO:0032509~endosome transport via multivesicular body sorting pathway	4.661579457	0.0024
GO:0019731~antibacterial humoral response	4.632625548	1.31E-04
GO:0006963~positive regulation of antibacterial peptide biosynthetic process	4.439599483	0.0206
GO:0007218~neuropeptide signaling pathway	4.408981556	6.39E-10
GO:0061057~peptidoglycan recognition protein signaling pathway	4.143626184	0.0046
GO:0048082~regulation of adult chitin-containing cuticle pigmentation	4.098091831	0.0276
GO:0008343~adult feeding behavior	4.098091831	0.0276
GO:0009612~response to mechanical stimulus	4.059062385	0.0022
GO:0008345~larval locomotory behavior	3.805370986	7.22E-04
GO:0007465~R7 cell fate commitment	3.805370986	0.0358
GO:0051124~synaptic growth at neuromuscular junction	3.729263566	4.34E-05
GO:0050808~synapse organization	3.674151296	6.80E-07
GO:0018990~ecdysis, chitin-based cuticle	3.551679587	0.0106
GO:0032008~positive regulation of TOR signaling	3.551679587	0.0218
GO:0045197~establishment or maintenance of epithelial cell apical/basal polarity	3.551679587	0.0218
GO:0043052~thermotaxis	3.551679587	0.0218
GO:0016082~synaptic vesicle priming	3.551679587	0.0218
GO:0034605~cellular response to heat	3.551679587	0.0453
GO:0007413~axonal fasciculation	3.551679587	0.0453
GO:0007412~axon target recognition	3.551679587	0.0453
GO:0008355~olfactory learning	3.442397138	1.08E-06
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	3.409612403	0.0066
GO:0000045~autophagosome assembly	3.409612403	0.0066
GO:2000331~regulation of terminal button organization	3.409612403	0.0066
GO:0007274~neuromuscular synaptic transmission	3.390239605	1.41E-06
GO:0000723~telomere maintenance	3.390239605	0.0135
GO:0048814~regulation of dendrite morphogenesis	3.364749082	0.0274
GO:0061024~membrane organization	3.364749082	0.0274
GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	3.306736167	0.0042
GO:0050965~detection of temperature stimulus involved in sensory perception of pain	3.278473465	6.66E-04
GO:0007614~short-term memory	3.278473465	0.0083
GO:0035096~larval midgut cell programmed cell death	3.278473465	0.0084
GO:0007611~learning or memory	3.242837883	2.16E-04
GO:0006302~double-strand break repair	3.242837883	0.0168
GO:0007268~chemical synaptic transmission	3.228799624	6.00E-06



GO:0006446~regulation of translational initiation	3.196511628	0.0338
GO:0051607~defense response to virus	3.157048521	0.0104
GO:0019730~antimicrobial humoral response	3.157048521	0.0104
GO:0001666~response to hypoxia	3.133834929	0.0033
GO:0016322~neuron remodeling	3.107719638	3.43E-04
GO:0006959~humoral immune response	3.107719638	0.0207
GO:0001731~formation of translation preinitiation complex	3.107719638	0.0207
GO:0007528~neuromuscular junction development	3.078122308	6.71E-04
GO:0000422~mitophagy	3.044296788	0.0410
GO:0006914~autophagy	3.015577007	2.73E-04
GO:0009617~response to bacterium	3.011206606	8.31E-04
GO:0042059~negative regulation of epidermal growth factor receptor signaling pathway	3.005267342	0.0026
GO:0070050~neuron cellular homeostasis	2.983410853	0.0251
GO:0007426~tracheal outgrowth, open tracheal system	2.983410853	0.0251
GO:0048675~axon extension	2.939321037	0.0155
GO:0030536~larval feeding behavior	2.905919662	0.0492
GO:0030431~sleep	2.882100648	5.05E-08
GO:0007269~neurotransmitter secretion	2.873268879	4.98E-06
GO:0007602~phototransduction	2.868664281	7.93E-04
GO:0007601~visual perception	2.854028239	5.04E-04
GO:0045887~positive regulation of synaptic growth at neuromuscular junction	2.841343669	0.0186
GO:0006952~defense response	2.820451436	0.0116
GO:0007616~long-term memory	2.811746339	8.38E-05
GO:0007173~epidermal growth factor receptor signaling pathway	2.762417456	0.0357
GO:0045475~locomotor rhythm	2.66375969	6.75E-04
GO:0045793~positive regulation of cell size	2.66375969	0.0261
GO:0007623~circadian rhythm	2.577831958	0.0015
GO:0048102~autophagic cell death	2.577831958	0.0015
GO:0016197~endosomal transport	2.571905908	0.0490
GO:0016318~ommatidial rotation	2.571905908	0.0490
GO:0007606~sensory perception of chemical stimulus	2.547944051	9.33E-05
GO:0032482~Rab protein signal transduction	2.507067943	0.0355
GO:0048488~synaptic vesicle endocytosis	2.507067943	0.0355
GO:0007166~cell surface receptor signaling pathway	2.458855098	0.0024
GO:0008063~Toll signaling pathway	2.435437431	0.0410
GO:0048149~behavioral response to ethanol	2.430096559	0.0058
GO:0007155~cell adhesion	2.380381	3.70E-04
GO:0042594~response to starvation	2.367786391	0.0050
GO:0045886~negative regulation of synaptic growth at neuromuscular junction	2.367786391	0.0219
GO:0045087~innate immune response	2.356402803	2.10E-04
GO:0035071~salivary gland cell autophagic cell death	2.322252037	0.0021
GO:0050830~defense response to Gram-positive bacterium	2.283222591	0.0136

GO:0008593~regulation of Notch signaling pathway	2.283222591	0.0388
GO:0042127~regulation of cell proliferation	2.283222591	0.0388
GO:0043547~positive regulation of GTPase activity	2.283222591	0.0388
GO:0008045~motor neuron axon guidance	2.260159737	0.0075
GO:0006811~ion transport	2.230124392	0.0440
GO:0035556~intracellular signal transduction	2.215404099	9.74E-04
GO:0008344~adult locomotory behavior	2.204490778	0.0175
GO:0006897~endocytosis	2.198658792	0.0130
GO:0007264~small GTPase mediated signal transduction	2.193684451	0.0096
GO:0007409~axonogenesis	2.131007752	0.0222
GO:0042060~wound healing	2.131007752	0.0222
GO:0040018~positive regulation of multicellular organism growth	2.131007752	0.0301
GO:0043087~regulation of GTPase activity	2.131007752	0.0407
GO:0007186~G-protein coupled receptor signaling pathway	2.086301296	3.12E-04
GO:0009408~response to heat	2.036992704	0.0230
GO:0040003~chitin-based cuticle development	1.943371849	7.85E-04
GO:0050829~defense response to Gram-negative bacterium	1.87449756	0.0113
GO:0016192~vesicle-mediated transport	1.864631783	0.0078
GO:0006979~response to oxidative stress	1.853050219	0.0235
GO:0006915~apoptotic process	1.846873385	0.0454
GO:0008360~regulation of cell shape	1.826578073	0.0177
GO:0009267~cellular response to starvation	1.794532844	0.0305
GO:0010906~regulation of glucose metabolic process	1.685542855	0.0077
GO:0006357~regulation of transcription from RNA polymerase II promoter	1.601335305	0.0191
GO:0008340~determination of adult lifespan	1.566917465	0.0274
GO:0055085~transmembrane transport	1.432919006	0.0212

**Overlapping: 2-fold downregulated**

<b>Biological Processes GO Term</b>	<b>Fold Enrichment</b>	<b>p-value</b>
GO:0006807~nitrogen compound metabolic process	30.20879	2.75E-04
GO:0005975~carbohydrate metabolic process	9.119635	2.46E-05
GO:0016311~dephosphorylation	7.923617	0.013558
GO:0055114~oxidation-reduction process	3.81276	1.27E-04
GO:0006508~proteolysis	2.543898	0.015464

**Overlapping: 2-fold upregulated**

<b>Biological Processes GO Term</b>	<b>Fold Enrichment</b>	<b>p-value</b>
GO:0006959~humoral immune response	42.95313	0.002043
GO:0050830~defense response to Gram-positive bacterium	24.54464	5.08E-04
GO:0050829~defense response to Gram-negative bacterium	9.545139	0.036938
GO:0055085~transmembrane transport	4.739655	0.047388