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Analysis Summary: Please report in publication [?](#)

Analysis Type: PANTHER Overrepresentation Test (release 20160321)

Annotation Version and Release Date: GO Ontology database Released 2016-04-23

Analyzed List: upload\_1 (Drosophila melanogaster) [Change](#)

Reference List: Drosophila melanogaster (all genes in database) [Change](#)

Annotation Data Set: 

GO biological process complete

☒ Use the Bonferroni correction for multiple testing [?](#)

Results [?](#)

	Reference list	upload_1
Mapped IDs:	<a href="#">13690</a>	<a href="#">1639</a>
Unmapped IDs:	<a href="#">0</a>	<a href="#">67</a>

[Export results](#)

Displaying only results with P<0.05; [click here to display all results](#)

- [GO biological process complete](#)
- [regulation of vascular permeability](#)
- [↳vascular process in circulatory system](#)

[↳circulatory system process](#)

[↳blood circulation](#)
- [fusion of virus membrane with host plasma membrane](#)
- [↳membrane fusion involved in viral entry into host cell](#)

[↳viral entry into host cell](#)

[↳viral life cycle](#)

[↳viral process](#)

<a href="#">Drosophila melanogaster</a> (REF)		<a href="#">upload_1</a> ( <a href="#">Hierarchy</a> <a href="#">NEW!</a> <a href="#">?</a> )			
	#	#	<a href="#">expected</a>	<a href="#">Fold Enrichment</a>	<a href="#">+/-</a> <a href="#">P value</a>
	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+ 1.42E-27
	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+ 1.42E-27
	<a href="#">19</a>	<a href="#">17</a>	2.27	7.47	+ 1.04E-06
	<a href="#">8</a>	<a href="#">17</a>	.96	17.75	+ 1.46E-12
	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+ 1.42E-27
	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+ 1.42E-27
	<a href="#">3</a>	<a href="#">18</a>	.36	50.12	+ 2.88E-21
	<a href="#">10</a>	<a href="#">18</a>	1.20	15.03	+ 3.40E-12
	<a href="#">12</a>	<a href="#">19</a>	1.44	13.23	+ 5.40E-12

<a href="#">↳symbiosis, encompassing mutualism through parasitism</a>	<a href="#">19</a>	<a href="#">20</a>	2.27	8.79	+	1.71E-09
<a href="#">↳interspecies interaction between organisms</a>	<a href="#">19</a>	<a href="#">20</a>	2.27	8.79	+	1.71E-09
<a href="#">↳multi-organism cellular process</a>	<a href="#">15</a>	<a href="#">19</a>	1.80	10.58	+	2.67E-10
<a href="#">↳cellular process</a>	<a href="#">6505</a>	<a href="#">875</a>	778.79	1.12	+	3.22E-03
<a href="#">↳entry into host cell</a>	<a href="#">4</a>	<a href="#">18</a>	.48	37.59	+	4.57E-19
<a href="#">↳entry into host</a>	<a href="#">4</a>	<a href="#">18</a>	.48	37.59	+	4.57E-19
<a href="#">↳entry into other organism involved in symbiotic interaction</a>	<a href="#">4</a>	<a href="#">18</a>	.48	37.59	+	4.57E-19
<a href="#">↳movement in environment of other organism involved in symbiotic interaction</a>	<a href="#">4</a>	<a href="#">18</a>	.48	37.59	+	4.57E-19
<a href="#">↳movement in host environment</a>	<a href="#">4</a>	<a href="#">18</a>	.48	37.59	+	4.57E-19
<a href="#">↳interaction with host</a>	<a href="#">10</a>	<a href="#">20</a>	1.20	16.71	+	1.25E-14
<a href="#">↳entry into cell of other organism involved in symbiotic interaction</a>	<a href="#">4</a>	<a href="#">18</a>	.48	37.59	+	4.57E-19
<a href="#">↳multi-organism membrane fusion</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳membrane fusion</a>	<a href="#">34</a>	<a href="#">21</a>	4.07	5.16	+	6.85E-06
<a href="#">↳cellular component organization</a>	<a href="#">2517</a>	<a href="#">439</a>	301.34	1.46	+	1.20E-13
<a href="#">↳cellular component organization or biogenesis</a>	<a href="#">2578</a>	<a href="#">445</a>	308.64	1.44	+	3.84E-13
<a href="#">↳multi-organism membrane organization</a>	<a href="#">2</a>	<a href="#">17</a>	.24	71.00	+	1.66E-22
<a href="#">viral attachment to host cell</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳adhesion of symbiont to host cell</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳adhesion of symbiont to host</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">fusion of virus membrane with host endosome membrane</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">clathrin-mediated endocytosis of virus by host cell</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳clathrin-mediated endocytosis</a>	<a href="#">50</a>	<a href="#">28</a>	5.99	4.68	+	1.48E-07
<a href="#">↳receptor-mediated endocytosis</a>	<a href="#">61</a>	<a href="#">29</a>	7.30	3.97	+	2.76E-06
<a href="#">↳receptor-mediated endocytosis of virus by host cell</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳endocytosis involved in viral entry into host cell</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳transport of virus</a>	<a href="#">2</a>	<a href="#">17</a>	.24	71.00	+	1.66E-22
<a href="#">↳multi-organism transport</a>	<a href="#">2</a>	<a href="#">17</a>	.24	71.00	+	1.66E-22
<a href="#">↳multi-organism localization</a>	<a href="#">2</a>	<a href="#">17</a>	.24	71.00	+	1.66E-22
<a href="#">positive regulation of vasoconstriction</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳positive regulation of blood circulation</a>	<a href="#">8</a>	<a href="#">18</a>	.96	18.79	+	7.66E-14
<a href="#">↳regulation of blood circulation</a>	<a href="#">31</a>	<a href="#">20</a>	3.71	5.39	+	7.96E-06
<a href="#">↳regulation of system process</a>	<a href="#">51</a>	<a href="#">24</a>	6.11	3.93	+	8.92E-05
<a href="#">↳regulation of vasoconstriction</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27

<a href="#">↳regulation of blood vessel size</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳regulation of tube size</a>	<a href="#">54</a>	<a href="#">26</a>	6.47	4.02	+	1.54E-05
<a href="#">eosinophil chemotaxis</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳eosinophil migration</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳granulocyte migration</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳myeloid leukocyte migration</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳leukocyte migration</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳granulocyte chemotaxis</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳leukocyte chemotaxis</a>	<a href="#">1</a>	<a href="#">17</a>	.12	> 100	+	1.42E-27
<a href="#">↳cell chemotaxis</a>	<a href="#">9</a>	<a href="#">18</a>	1.08	16.71	+	5.71E-13
<a href="#">antigen processing and presentation of peptide antigen via MHC class I</a>	<a href="#">3</a>	<a href="#">17</a>	.36	47.33	+	1.46E-19
<a href="#">↳antigen processing and presentation of peptide antigen</a>	<a href="#">3</a>	<a href="#">17</a>	.36	47.33	+	1.46E-19
<a href="#">↳antigen processing and presentation</a>	<a href="#">5</a>	<a href="#">18</a>	.60	30.07	+	2.27E-17
<a href="#">negative regulation of histone modification</a>	<a href="#">6</a>	<a href="#">19</a>	.72	26.45	+	2.02E-17
<a href="#">↳negative regulation of chromatin modification</a>	<a href="#">16</a>	<a href="#">21</a>	1.92	10.96	+	6.90E-12
<a href="#">↳negative regulation of chromosome organization</a>	<a href="#">32</a>	<a href="#">25</a>	3.83	6.53	+	1.58E-09
<a href="#">↳regulation of chromosome organization</a>	<a href="#">117</a>	<a href="#">37</a>	14.01	2.64	+	5.99E-04
<a href="#">↳regulation of chromatin modification</a>	<a href="#">75</a>	<a href="#">33</a>	8.98	3.68	+	1.36E-06
<a href="#">↳regulation of chromatin organization</a>	<a href="#">79</a>	<a href="#">34</a>	9.46	3.59	+	1.30E-06
<a href="#">↳regulation of histone modification</a>	<a href="#">27</a>	<a href="#">20</a>	3.23	6.19	+	7.85E-07
<a href="#">nucleosome assembly</a>	<a href="#">91</a>	<a href="#">114</a>	10.89	10.46	+	1.48E-71
<a href="#">↳protein complex assembly</a>	<a href="#">342</a>	<a href="#">150</a>	40.95	3.66	+	1.75E-37
<a href="#">↳protein complex subunit organization</a>	<a href="#">657</a>	<a href="#">200</a>	78.66	2.54	+	4.64E-29
<a href="#">↳macromolecular complex subunit organization</a>	<a href="#">980</a>	<a href="#">247</a>	117.33	2.11	+	1.36E-24
<a href="#">↳protein complex biogenesis</a>	<a href="#">344</a>	<a href="#">150</a>	41.18	3.64	+	3.35E-37
<a href="#">↳cellular component biogenesis</a>	<a href="#">917</a>	<a href="#">228</a>	109.79	2.08	+	1.26E-21
<a href="#">↳macromolecular complex assembly</a>	<a href="#">424</a>	<a href="#">159</a>	50.76	3.13	+	4.55E-32
<a href="#">↳cellular component assembly</a>	<a href="#">841</a>	<a href="#">221</a>	100.69	2.19	+	7.09E-24
<a href="#">↳chromatin assembly</a>	<a href="#">99</a>	<a href="#">115</a>	11.85	9.70	+	8.73E-69
<a href="#">↳chromatin assembly or disassembly</a>	<a href="#">130</a>	<a href="#">116</a>	15.56	7.45	+	1.41E-57
<a href="#">↳chromatin organization</a>	<a href="#">388</a>	<a href="#">161</a>	46.45	3.47	+	1.30E-37
<a href="#">↳chromosome organization</a>	<a href="#">627</a>	<a href="#">181</a>	75.07	2.41	+	2.47E-23
<a href="#">↳organelle organization</a>	<a href="#">1656</a>	<a href="#">321</a>	198.26	1.62	+	1.00E-14

<a href="#">↳DNA packaging</a>	<a href="#">149</a>	<a href="#">121</a>	17.84	6.78	+	6.93E-56
<a href="#">↳DNA conformation change</a>	<a href="#">163</a>	<a href="#">123</a>	19.51	6.30	+	1.70E-53
<a href="#">↳nucleosome organization</a>	<a href="#">119</a>	<a href="#">119</a>	14.25	8.35	+	2.43E-64
<a href="#">↳protein-DNA complex subunit organization</a>	<a href="#">148</a>	<a href="#">122</a>	17.72	6.89	+	4.66E-57
<a href="#">↳protein-DNA complex assembly</a>	<a href="#">113</a>	<a href="#">116</a>	13.53	8.57	+	8.12E-64
<a href="#">↳cellular macromolecular complex assembly</a>	<a href="#">280</a>	<a href="#">139</a>	33.52	4.15	+	3.37E-40
<a href="#">peptidyl-tyrosine dephosphorylation</a>	<a href="#">15</a>	<a href="#">17</a>	1.80	9.47	+	2.92E-08
<a href="#">larval somatic muscle development</a>	<a href="#">30</a>	<a href="#">22</a>	3.59	6.13	+	1.24E-07
<a href="#">↳somatic muscle development</a>	<a href="#">83</a>	<a href="#">28</a>	9.94	2.82	+	5.22E-03
<a href="#">female meiosis chromosome segregation</a>	<a href="#">35</a>	<a href="#">23</a>	4.19	5.49	+	3.75E-07
<a href="#">↳female meiotic division</a>	<a href="#">74</a>	<a href="#">26</a>	8.86	2.93	+	5.87E-03
<a href="#">↳cell cycle</a>	<a href="#">751</a>	<a href="#">136</a>	89.91	1.51	+	5.17E-03
<a href="#">↳cell cycle process</a>	<a href="#">695</a>	<a href="#">131</a>	83.21	1.57	+	1.08E-03
<a href="#">↳single-organism organelle organization</a>	<a href="#">1163</a>	<a href="#">205</a>	139.24	1.47	+	7.26E-05
<a href="#">↳meiotic chromosome segregation</a>	<a href="#">69</a>	<a href="#">27</a>	8.26	3.27	+	4.98E-04
<a href="#">centrosome duplication</a>	<a href="#">84</a>	<a href="#">43</a>	10.06	4.28	+	2.42E-11
<a href="#">↳centrosome organization</a>	<a href="#">128</a>	<a href="#">48</a>	15.32	3.13	+	4.24E-08
<a href="#">↳microtubule organizing center organization</a>	<a href="#">133</a>	<a href="#">49</a>	15.92	3.08	+	4.76E-08
<a href="#">↳microtubule cytoskeleton organization</a>	<a href="#">415</a>	<a href="#">83</a>	49.68	1.67	+	1.98E-02
<a href="#">↳cytoskeleton organization</a>	<a href="#">640</a>	<a href="#">122</a>	76.62	1.59	+	1.59E-03
<a href="#">↳centrosome cycle</a>	<a href="#">98</a>	<a href="#">44</a>	11.73	3.75	+	9.65E-10
<a href="#">chromatin silencing</a>	<a href="#">56</a>	<a href="#">28</a>	6.70	4.18	+	1.80E-06
<a href="#">↳negative regulation of gene expression, epigenetic</a>	<a href="#">57</a>	<a href="#">28</a>	6.82	4.10	+	2.63E-06
<a href="#">↳regulation of gene expression, epigenetic</a>	<a href="#">121</a>	<a href="#">43</a>	14.49	2.97	+	2.35E-06
<a href="#">↳negative regulation of transcription, DNA-templated</a>	<a href="#">288</a>	<a href="#">67</a>	34.48	1.94	+	1.25E-03
<a href="#">↳negative regulation of cellular macromolecule biosynthetic process</a>	<a href="#">353</a>	<a href="#">77</a>	42.26	1.82	+	2.02E-03
<a href="#">↳negative regulation of cellular biosynthetic process</a>	<a href="#">364</a>	<a href="#">78</a>	43.58	1.79	+	3.31E-03
<a href="#">↳negative regulation of biosynthetic process</a>	<a href="#">364</a>	<a href="#">78</a>	43.58	1.79	+	3.31E-03
<a href="#">↳negative regulation of macromolecule biosynthetic process</a>	<a href="#">353</a>	<a href="#">77</a>	42.26	1.82	+	2.02E-03
<a href="#">↳negative regulation of nucleic acid-templated transcription</a>	<a href="#">288</a>	<a href="#">67</a>	34.48	1.94	+	1.25E-03
<a href="#">↳negative regulation of RNA biosynthetic process</a>	<a href="#">288</a>	<a href="#">67</a>	34.48	1.94	+	1.25E-03
<a href="#">↳negative regulation of RNA metabolic process</a>	<a href="#">302</a>	<a href="#">68</a>	36.16	1.88	+	3.12E-03
<a href="#">↳negative regulation of nucleobase-containing compound metabolic process</a>	<a href="#">323</a>	<a href="#">70</a>	38.67	1.81	+	7.96E-03

<a href="#">negative regulation of nitrogen compound metabolic process</a>	<a href="#">385</a>	<a href="#">78</a>	46.09	1.69	+	2.40E-02
<a href="#">gene silencing</a>	<a href="#">108</a>	<a href="#">36</a>	12.93	2.78	+	2.53E-04
<a href="#">chromosome condensation</a>	<a href="#">47</a>	<a href="#">22</a>	5.63	3.91	+	3.59E-04
<a href="#">DNA-templated transcription, initiation</a>	<a href="#">76</a>	<a href="#">30</a>	9.10	3.30	+	8.80E-05
<a href="#">DNA damage checkpoint</a>	<a href="#">87</a>	<a href="#">27</a>	10.42	2.59	+	3.44E-02
<a href="#">DNA repair</a>	<a href="#">148</a>	<a href="#">38</a>	17.72	2.14	+	4.86E-02
Unclassified	<a href="#">2662</a>	<a href="#">275</a>	318.70	.86	-	0.00E00