

Muscle-specific age-related GO terms in Cluster 1 (Upregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0019731 antibacterial humoral response	CG10363	FBgn0041180	Thiolester containing protein IV	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG10794	FBgn0034407	Diptericin B	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG10810	FBgn0010381	Drosomycin	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG10816	FBgn0010388	Drosocin	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG12763	FBgn0004240	Diptericin	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG1365	FBgn0000276	Cecropin A1	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG1367	FBgn0000277	Cecropin A2	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG15066	FBgn0034328	Immune induced molecule 23	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG16844	FBgn0040736	Immune induced molecule 3	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG18279	FBgn0033835	Immune induced molecule 10	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG18372	FBgn0041581	Attacin-B	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG4740	FBgn0041579	Attacin-C	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG7052	FBgn0041182	Thiolester containing protein II	1.42E-14	37	15	40.5%
GO:0019731 antibacterial humoral response	CG8175	FBgn0014865	Metchnikowin	1.42E-14	37	15	40.5%
GO:0009617 response to bacteria	CG10363	FBgn0041180	Thiolester containing protein IV	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG10794	FBgn0034407	Diptericin B	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG10810	FBgn0010381	Drosomycin	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG10816	FBgn0010388	Drosocin	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG12763	FBgn0004240	Diptericin	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG13422	FBgn0034511		1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG1365	FBgn0000276	Cecropin A1	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG1367	FBgn0000277	Cecropin A2	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG15066	FBgn0034328	Immune induced molecule 23	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG16844	FBgn0040736	Immune induced molecule 3	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG18279	FBgn0033835	Immune induced molecule 10	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG18372	FBgn0041581	Attacin-B	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG4740	FBgn0041579	Attacin-C	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG7052	FBgn0041182	Thiolester containing protein II	1.30E-12	66	17	25.8%

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GO:0009617 response to bacteria	CG8175	FBgn0014865	Metchnikowin	1.30E-12	66	17	25.8%
GO:0009617 response to bacteria	CG8577	FBgn0033327		1.30E-12	66	17	25.8%
GO:0019730 antimicrobial humoral response	CG10363	FBgn0041180	Thiolester containing protein IV	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG10794	FBgn0034407	Diptericin B	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG10810	FBgn0010381	Drosomycin	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG10816	FBgn0010388	Drosocin	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG12763	FBgn0004240	Diptericin	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG1365	FBgn0000276	Cecropin A1	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG1367	FBgn0000277	Cecropin A2	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG15066	FBgn0034328	Immune induced molecule 23	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG16844	FBgn0040736	Immune induced molecule 3	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG18279	FBgn0033835	Immune induced molecule 10	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG18372	FBgn0041581	Attacin-B	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG4740	FBgn0041579	Attacin-C	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG6819	FBgn0026207	members only	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG7052	FBgn0041182	Thiolester containing protein II	2.57E-12	59	16	27.1%
GO:0019730 antimicrobial humoral response	CG8175	FBgn0014865	Metchnikowin	2.57E-12	59	16	27.1%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG10363	FBgn0041180	Thiolester containing protein IV	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG10794	FBgn0034407	Diptericin B	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG10810	FBgn0010381	Drosomycin	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG10816	FBgn0010388	Drosocin	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG12763	FBgn0004240	Diptericin	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG1365	FBgn0000276	Cecropin A1	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG1367	FBgn0000277	Cecropin A2	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG18372	FBgn0041581	Attacin-B	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG4740	FBgn0041579	Attacin-C	3.07E-12	22	11	50.0%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG7052	FBgn0041182	Thiolester containing protein II	3.07E-12	22	11	50.0%

GO:0006961 antibacterial humoral response (sensu Protostomia)	CG8175	FBgn0014865	Metchnikowin	3.07E-12	22	11	50.0%
GO:0042742 defense response to bacteria	CG10363	FBgn0041180	Thiolester containing protein IV	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG10794	FBgn0034407	Diptericin B	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG10810	FBgn0010381	Drosomycin	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG10816	FBgn0010388	Drosocin	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG12763	FBgn0004240	Diptericin	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG13422	FBgn0034511		4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG1365	FBgn0000276	Cecropin A1	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG1367	FBgn0000277	Cecropin A2	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG15066	FBgn0034328	Immune induced molecule 23	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG16844	FBgn0040736	Immune induced molecule 3	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG18279	FBgn0033835	Immune induced molecule 10	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG18372	FBgn0041581	Attacin-B	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG4740	FBgn0041579	Attacin-C	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG7052	FBgn0041182	Thiolester containing protein II	4.52E-12	61	16	26.2%
GO:0042742 defense response to bacteria	CG8175	FBgn0014865	Metchnikowin	4.52E-12	61	16	26.2%
GO:0006955 immune response	CG10363	FBgn0041180	Thiolester containing protein IV	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG10794	FBgn0034407	Diptericin B	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG10810	FBgn0010381	Drosomycin	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG10816	FBgn0010388	Drosocin	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG12763	FBgn0004240	Diptericin	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG1365	FBgn0000276	Cecropin A1	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG1367	FBgn0000277	Cecropin A2	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG15066	FBgn0034328	Immune induced molecule 23	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG16844	FBgn0040736	Immune induced molecule 3	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG18279	FBgn0033835	Immune induced molecule 10	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG18372	FBgn0041581	Attacin-B	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG4740	FBgn0041579	Attacin-C	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG6819	FBgn0026207	members only	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG7052	FBgn0041182	Thiolester containing protein II	6.66E-12	106	20	18.9%

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GO:0006955 immune response	CG7496	FBgn0035806		6.66E-12	106	20	18.9%
GO:0006955 immune response	CG8175	FBgn0014865	Metchnikowin	6.66E-12	106	20	18.9%
GO:0006955 immune response	CG8577	FBgn0033327		6.66E-12	106	20	18.9%
GO:0006955 immune response	CG8902	FBgn0031886		6.66E-12	106	20	18.9%
GO:0006955 immune response	CG9681	FBgn0043578		6.66E-12	106	20	18.9%
GO:0006959 humoral immune response	CG10363	FBgn0041180	Thiolester containing protein IV	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG10794	FBgn0034407	Diptericin B	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG10810	FBgn0010381	Drosomycin	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG10816	FBgn0010388	Drosocin	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG12763	FBgn0004240	Diptericin	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG1365	FBgn0000276	Cecropin A1	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG1367	FBgn0000277	Cecropin A2	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG15066	FBgn0034328	Immune induced molecule 23	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG16844	FBgn0040736	Immune induced molecule 3	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG18279	FBgn0033835	Immune induced molecule 10	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG18372	FBgn0041581	Attacin-B	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG4740	FBgn0041579	Attacin-C	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG6819	FBgn0026207	members only	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG7052	FBgn0041182	Thiolester containing protein II	2.17E-11	67	16	23.9%
GO:0006959 humoral immune response	CG8175	FBgn0014865	Metchnikowin	2.17E-11	67	16	23.9%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG10363	FBgn0041180	Thiolester containing protein IV	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG10794	FBgn0034407	Diptericin B	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG10810	FBgn0010381	Drosomycin	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG10816	FBgn0010388	Drosocin	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG12763	FBgn0004240	Diptericin	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG1365	FBgn0000276	Cecropin A1	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG1367	FBgn0000277	Cecropin A2	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG18372	FBgn0041581	Attacin-B	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG4740	FBgn0041579	Attacin-C	5.81E-10	41	12	29.3%

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GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG6819	FBgn0026207	members only	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG7052	FBgn0041182	Thiolester containing protein II	5.81E-10	41	12	29.3%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG8175	FBgn0014865	Metchnikowin	5.81E-10	41	12	29.3%
GO:0043207 response to external biotic stimulus	CG10363	FBgn0041180	Thiolester containing protein IV	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG10794	FBgn0034407	Diptericin B	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG10810	FBgn0010381	Drosomycin	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG10816	FBgn0010388	Drosocin	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG12763	FBgn0004240	Diptericin	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG13422	FBgn0034511		9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG1365	FBgn0000276	Cecropin A1	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG1367	FBgn0000277	Cecropin A2	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG15066	FBgn0034328	Immune induced molecule 23	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG16844	FBgn0040736	Immune induced molecule 3	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG18279	FBgn0033835	Immune induced molecule 10	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG18372	FBgn0041581	Attacin-B	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG4740	FBgn0041579	Attacin-C	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG6819	FBgn0026207	members only	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG7052	FBgn0041182	Thiolester containing protein II	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG8175	FBgn0014865	Metchnikowin	9.23E-10	110	18	16.4%
GO:0043207 response to external biotic stimulus	CG8577	FBgn0033327		9.23E-10	110	18	16.4%
GO:0009613 response to pest pathogen or parasite	CG10363	FBgn0041180	Thiolester containing protein IV	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG10794	FBgn0034407	Diptericin B	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG10810	FBgn0010381	Drosomycin	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG10816	FBgn0010388	Drosocin	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG12763	FBgn0004240	Diptericin	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG1365	FBgn0000276	Cecropin A1	9.78E-10	85	16	18.8%

GO:0009613 response to pest pathogen or parasite	CG1367	FBgn0000277	Cecropin A2	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG15066	FBgn0034328	Immune induced molecule 23	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG16844	FBgn0040736	Immune induced molecule 3	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG18279	FBgn0033835	Immune induced molecule 10	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG18372	FBgn0041581	Attacin-B	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG4740	FBgn0041579	Attacin-C	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG6819	FBgn0026207	members only	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG7052	FBgn0041182	Thiolester containing protein II	9.78E-10	85	16	18.8%
GO:0009613 response to pest pathogen or parasite	CG8175	FBgn0014865	Metchnikowin	9.78E-10	85	16	18.8%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG10363	FBgn0041180	Thiolester containing protein IV	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG10794	FBgn0034407	Diptericin B	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG10810	FBgn0010381	Drosomycin	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG10816	FBgn0010388	Drosocin	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG12763	FBgn0004240	Diptericin	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG1365	FBgn0000276	Cecropin A1	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG1367	FBgn0000277	Cecropin A2	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG18372	FBgn0041581	Attacin-B	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG4740	FBgn0041579	Attacin-C	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG6819	FBgn0026207	members only	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG7052	FBgn0041182	Thiolester containing protein II	1.44E-09	44	12	27.3%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG8175	FBgn0014865	Metchnikowin	1.44E-09	44	12	27.3%
GO:0006510 ATP-dependent proteolysis	CG10938	FBgn0016697	Proteasome alpha subunit	4.33E-07	19	7	36.8%
GO:0006510 ATP-dependent proteolysis	CG11981	FBgn0026380		4.33E-07	19	7	36.8%

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GO:0006510 ATP-dependent proteolysis	CG12000	FBgn0037314		4.33E-07	19	7	36.8%
GO:0006510 ATP-dependent proteolysis	CG1489	FBgn0020369		4.33E-07	19	7	36.8%
GO:0006510 ATP-dependent proteolysis	CG3422	FBgn0004066	Proteasome 28kD subunit 1	4.33E-07	19	7	36.8%
GO:0006510 ATP-dependent proteolysis	CG4097	FBgn0002284	Proteasome 26kD subunit	4.33E-07	19	7	36.8%
GO:0006510 ATP-dependent proteolysis	CG6512	FBgn0036702		4.33E-07	19	7	36.8%
GO:0050829 defense response to Gram-negative bacteria	CG10810	FBgn0010381	Drosomycin	1.72E-06	15	6	40.0%
GO:0050829 defense response to Gram-negative bacteria	CG10816	FBgn0010388	Drosocin	1.72E-06	15	6	40.0%
GO:0050829 defense response to Gram-negative bacteria	CG12763	FBgn0004240	Diptericin	1.72E-06	15	6	40.0%
GO:0050829 defense response to Gram-negative bacteria	CG13422	FBgn0034511		1.72E-06	15	6	40.0%
GO:0050829 defense response to Gram-negative bacteria	CG1365	FBgn0000276	Cecropin A1	1.72E-06	15	6	40.0%
GO:0050829 defense response to Gram-negative bacteria	CG1367	FBgn0000277	Cecropin A2	1.72E-06	15	6	40.0%
GO:0050830 defense response to Gram-positive bacteria	CG10816	FBgn0010388	Drosocin	1.06E-05	12	5	41.7%
GO:0050830 defense response to Gram-positive bacteria	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	1.06E-05	12	5	41.7%
GO:0050830 defense response to Gram-positive bacteria	CG1365	FBgn0000276	Cecropin A1	1.06E-05	12	5	41.7%
GO:0050830 defense response to Gram-positive bacteria	CG1367	FBgn0000277	Cecropin A2	1.06E-05	12	5	41.7%
GO:0050830 defense response to Gram-positive bacteria	CG8175	FBgn0014865	Metchnikowin	1.06E-05	12	5	41.7%
GO:0019941 modification-dependent protein catabolism	CG10938	FBgn0016697	Proteasome alpha subunit	4.17E-05	76	10	13.2%
GO:0019941 modification-dependent protein catabolism	CG11981	FBgn0026380		4.17E-05	76	10	13.2%
GO:0019941 modification-dependent protein catabolism	CG12000	FBgn0037314		4.17E-05	76	10	13.2%
GO:0019941 modification-dependent protein catabolism	CG12276	FBgn0029512		4.17E-05	76	10	13.2%
GO:0019941 modification-dependent protein catabolism	CG12323	FBgn0029134		4.17E-05	76	10	13.2%
GO:0019941 modification-dependent protein catabolism	CG1489	FBgn0020369		4.17E-05	76	10	13.2%
GO:0019941 modification-dependent protein catabolism	CG18495	FBgn0026781	Proteasome alpha6 subunit	4.17E-05	76	10	13.2%
GO:0019941 modification-dependent protein catabolism	CG3422	FBgn0004066	Proteasome 28kD subunit 1	4.17E-05	76	10	13.2%

Muscle-specific age-related GO terms in Cluster 1

GO:0019941 modification-dependent protein catabolism	CG4097	FBgn0002284	Proteasome 26kD subunit	4.17E-05	76	10	13.2%
GO:0019941 modification-dependent protein catabolism	CG8392	FBgn0010590		4.17E-05	76	10	13.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG10938	FBgn0016697	Proteasome alpha subunit	1.89E-04	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG11981	FBgn0026380		1.89E-04	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG12000	FBgn0037314		1.89E-04	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG12323	FBgn0029134		1.89E-04	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG1489	FBgn0020369		1.89E-04	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG18495	FBgn0026781	Proteasome alpha6 subunit	1.89E-04	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG3422	FBgn0004066	Proteasome 28kD subunit 1	1.89E-04	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG4097	FBgn0002284	Proteasome 26kD subunit	1.89E-04	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG8392	FBgn0010590		1.89E-04	74	9	12.2%
GO:0000270 peptidoglycan metabolism	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	2.39E-04	12	4	33.3%
GO:0000270 peptidoglycan metabolism	CG7496	FBgn0035806		2.39E-04	12	4	33.3%
GO:0000270 peptidoglycan metabolism	CG8577	FBgn0033327		2.39E-04	12	4	33.3%
GO:0000270 peptidoglycan metabolism	CG9681	FBgn0043578		2.39E-04	12	4	33.3%
GO:0009253 peptidoglycan catabolism	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	2.39E-04	12	4	33.3%
GO:0009253 peptidoglycan catabolism	CG7496	FBgn0035806		2.39E-04	12	4	33.3%
GO:0009253 peptidoglycan catabolism	CG8577	FBgn0033327		2.39E-04	12	4	33.3%
GO:0009253 peptidoglycan catabolism	CG9681	FBgn0043578		2.39E-04	12	4	33.3%
GO:0050832 defense response to fungi	CG10810	FBgn0010381	Drosomycin	1.30E-03	18	4	22.2%
GO:0050832 defense response to fungi	CG1365	FBgn0000276	Cecropin A1	1.30E-03	18	4	22.2%
GO:0050832 defense response to fungi	CG1367	FBgn0000277	Cecropin A2	1.30E-03	18	4	22.2%
GO:0050832 defense response to fungi	CG8175	FBgn0014865	Metchnikowin	1.30E-03	18	4	22.2%
GO:0009620 response to fungi	CG10810	FBgn0010381	Drosomycin	1.61E-03	19	4	21.1%
GO:0009620 response to fungi	CG1365	FBgn0000276	Cecropin A1	1.61E-03	19	4	21.1%
GO:0009620 response to fungi	CG1367	FBgn0000277	Cecropin A2	1.61E-03	19	4	21.1%
GO:0009620 response to fungi	CG8175	FBgn0014865	Metchnikowin	1.61E-03	19	4	21.1%
GO:0006457 protein folding	CG2852	FBgn0034753		1.66E-03	119	10	8.4%
GO:0006457 protein folding	CG3315	FBgn0029752	Thioredoxin T	1.66E-03	119	10	8.4%
GO:0006457 protein folding	CG5374	FBgn0003676	Tcp1-like	1.66E-03	119	10	8.4%
GO:0006457 protein folding	CG6988	FBgn0014002	Protein disulfide isomerase	1.66E-03	119	10	8.4%

Muscle-specific age-related GO terms in Cluster 1

GO:0006457 protein folding	CG7048	FBgn0038976		1.66E-03	119	10	8.4%
GO:0006457 protein folding	CG8258	FBgn0033342		1.66E-03	119	10	8.4%
GO:0006457 protein folding	CG8531	FBgn0033918		1.66E-03	119	10	8.4%
GO:0006457 protein folding	CG8542	FBgn0001220	Heat shock protein cognate 5	1.66E-03	119	10	8.4%
GO:0006457 protein folding	CG8669	FBgn0000370	cryptocephal	1.66E-03	119	10	8.4%
GO:0006457 protein folding	CG9916	FBgn0004432	Cyclophilin 1	1.66E-03	119	10	8.4%
GO:0008063 Toll signaling pathway	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	6.99E-03	28	4	14.3%
GO:0008063 Toll signaling pathway	CG15066	FBgn0034328	Immune induced molecule 23	6.99E-03	28	4	14.3%
GO:0008063 Toll signaling pathway	CG16844	FBgn0040736	Immune induced molecule 3	6.99E-03	28	4	14.3%
GO:0008063 Toll signaling pathway	CG18279	FBgn0033835	Immune induced molecule 10	6.99E-03	28	4	14.3%
GO:0048193 Golgi vesicle transport	CG14813	FBgn0028969	delta-coatomer protein	1.13E-02	32	4	12.5%
GO:0048193 Golgi vesicle transport	CG1528	FBgn0028968	gamma-coatomer protein	1.13E-02	32	4	12.5%
GO:0048193 Golgi vesicle transport	CG8487	FBgn0033714	gartenzweig	1.13E-02	32	4	12.5%
GO:0048193 Golgi vesicle transport	CG9931	NA	NA	1.13E-02	32	4	12.5%
GO:0045087 innate immune response	CG11709	FBgn0030310	Peptidoglycan recognition protein SA	3.58E-02	11	2	18.2%
GO:0045087 innate immune response	CG8577	FBgn0033327		3.58E-02	11	2	18.2%
GO:0006725 aromatic compound metabolism	CG10484	FBgn0000486	Diphenol oxidase A2	4.67E-02	144	8	5.6%
GO:0006725 aromatic compound metabolism	CG11089	FBgn0039241		4.67E-02	144	8	5.6%
GO:0006725 aromatic compound metabolism	CG2674	FBgn0005278	Minute (2) 21AB	4.67E-02	144	8	5.6%
GO:0006725 aromatic compound metabolism	CG3989	FBgn0020513		4.67E-02	144	8	5.6%
GO:0006725 aromatic compound metabolism	CG4067	FBgn0020385	pugilist	4.67E-02	144	8	5.6%
GO:0006725 aromatic compound metabolism	CG4798	FBgn0022029		4.67E-02	144	8	5.6%
GO:0006725 aromatic compound metabolism	CG6330	FBgn0039464		4.67E-02	144	8	5.6%
GO:0006725 aromatic compound metabolism	CG9441	FBgn0003162	Punch	4.67E-02	144	8	5.6%
GO:0035070 salivary gland histolysis	CG1365	FBgn0000276	Cecropin A1	4.67E-02	71	5	7.0%
GO:0035070 salivary gland histolysis	CG1643	FBgn0029943	Autophagy-specific gene 5	4.67E-02	71	5	7.0%
GO:0035070 salivary gland histolysis	CG3186	FBgn0034967		4.67E-02	71	5	7.0%
GO:0035070 salivary gland histolysis	CG3845	FBgn0010488		4.67E-02	71	5	7.0%
GO:0035070 salivary gland histolysis	CG9916	FBgn0004432	Cyclophilin 1	4.67E-02	71	5	7.0%
GO:0035071 salivary gland cell death	CG1365	FBgn0000276	Cecropin A1	4.67E-02	71	5	7.0%
GO:0035071 salivary gland cell death	CG1643	FBgn0029943	Autophagy-specific gene 5	4.67E-02	71	5	7.0%
GO:0035071 salivary gland cell death	CG3186	FBgn0034967		4.67E-02	71	5	7.0%
GO:0035071 salivary gland cell death	CG3845	FBgn0010488		4.67E-02	71	5	7.0%
GO:0035071 salivary gland cell death	CG9916	FBgn0004432	Cyclophilin 1	4.67E-02	71	5	7.0%
GO:0048102 autophagic cell death	CG1365	FBgn0000276	Cecropin A1	4.67E-02	71	5	7.0%

GO:0048102 autophagic cell death	CG1643	FBgn0029943	Autophagy-specific gene 5	4.67E-02	71	5	7.0%
GO:0048102 autophagic cell death	CG3186	FBgn0034967		4.67E-02	71	5	7.0%
GO:0048102 autophagic cell death	CG3845	FBgn0010488		4.67E-02	71	5	7.0%
GO:0048102 autophagic cell death	CG9916	FBgn0004432	Cyclophilin 1	4.67E-02	71	5	7.0%
GO:0006891 intra-Golgi transport	CG8487	FBgn0033714	gartenzwerg	4.89E-02	13	2	15.4%
GO:0006891 intra-Golgi transport	CG9931	NA	NA	4.89E-02	13	2	15.4%
GO:0007032 endosome organization and biogenesis	CG11027	FBgn0013749	ADP ribosylation factor 102F	4.89E-02	13	2	15.4%
GO:0007032 endosome organization and biogenesis	CG8385	FBgn0010348	ADP ribosylation factor 79F	4.89E-02	13	2	15.4%
GO:0016197 endosome transport	CG11027	FBgn0013749	ADP ribosylation factor 102F	4.89E-02	13	2	15.4%
GO:0016197 endosome transport	CG8385	FBgn0010348	ADP ribosylation factor 79F	4.89E-02	13	2	15.4%
GO:0007559 histolysis	CG1365	FBgn0000276	Cecropin A1	4.91E-02	72	5	6.9%
GO:0007559 histolysis	CG1643	FBgn0029943	Autophagy-specific gene 5	4.91E-02	72	5	6.9%
GO:0007559 histolysis	CG3186	FBgn0034967		4.91E-02	72	5	6.9%
GO:0007559 histolysis	CG3845	FBgn0010488		4.91E-02	72	5	6.9%
GO:0007559 histolysis	CG9916	FBgn0004432	Cyclophilin 1	4.91E-02	72	5	6.9%
GO:0016271 tissue death	CG1365	FBgn0000276	Cecropin A1	4.91E-02	72	5	6.9%
GO:0016271 tissue death	CG1643	FBgn0029943	Autophagy-specific gene 5	4.91E-02	72	5	6.9%
GO:0016271 tissue death	CG3186	FBgn0034967		4.91E-02	72	5	6.9%
GO:0016271 tissue death	CG3845	FBgn0010488		4.91E-02	72	5	6.9%
GO:0016271 tissue death	CG9916	FBgn0004432	Cyclophilin 1	4.91E-02	72	5	6.9%

Muscle-specific age-related GO terms in Cluster 2 (Upregulated)							
GO term	CG_ID	FB_ID	Full name	P-value	Total gene	Changed gene	% of change
GO:0051189 prosthetic group metabolism	CG10026	FBgn0032785		5.67E-03	55	5	9.1%
GO:0051189 prosthetic group metabolism	CG10546	FBgn0035636	Cellular retinaldehyde binding protein	5.67E-03	55	5	9.1%
GO:0051189 prosthetic group metabolism	CG2663	FBgn0037323		5.67E-03	55	5	9.1%
GO:0051189 prosthetic group metabolism	CG5973	FBgn0031914		5.67E-03	55	5	9.1%
GO:0051189 prosthetic group metabolism	CG6646	FBgn0033885		5.67E-03	55	5	9.1%
GO:0006458 'de novo' protein folding	CG12101	FBgn0015245	Heat shock protein 60	2.12E-02	11	2	18.2%
GO:0006458 'de novo' protein folding	CG9920	FBgn0038200		2.12E-02	11	2	18.2%
GO:0009084 glutamine family amino acid biosynthesis	CG4233	FBgn0001125	Glutamate oxaloacetate transaminase 2	2.51E-02	12	2	16.7%
GO:0009084 glutamine family amino acid biosynthesis	CG5840	FBgn0038516		2.51E-02	12	2	16.7%
GO:0007560 imaginal disc morphogenesis	CG8347	FBgn0000546	Ecdysone receptor	3.83E-02	15	2	13.3%
GO:0007560 imaginal disc morphogenesis	CG2248	FBgn0010333		3.83E-02	15	2	13.3%
GO:0009636 response to toxin	CG12013	FBgn0035438		4.56E-02	124	6	4.8%
GO:0009636 response to toxin	CG16936	FBgn0027590		4.56E-02	124	6	4.8%
GO:0009636 response to toxin	CG17534	FBgn0063491	Glutathione S transferase E9	4.56E-02	124	6	4.8%
GO:0009636 response to toxin	CG4421	FBgn0010044	Glutathione S transferase D8	4.56E-02	124	6	4.8%
GO:0009636 response to toxin	CG4688	FBgn0033817		4.56E-02	124	6	4.8%
GO:0009636 response to toxin	CG8453	FBgn0025454		4.56E-02	124	6	4.8%
GO:0050793 regulation of development	CG1081	FBgn0041191		4.88E-02	95	5	5.3%
GO:0050793 regulation of development	CG8347	FBgn0000546	Ecdysone receptor	4.88E-02	95	5	5.3%
GO:0050793 regulation of development	CG2248	FBgn0010333		4.88E-02	95	5	5.3%
GO:0050793 regulation of development	CG4207	FBgn0026261		4.88E-02	95	5	5.3%
GO:0050793 regulation of development	CG9786	FBgn0001180	hunchback	4.88E-02	95	5	5.3%

Muscle-specific age-related GO terms in Cluster 3 (Upregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG10130	FBgn0010638		1.08E-03	17	3	17.6%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG11642	FBgn0040340		1.08E-03	17	3	17.6%
GO:0006614 SRP-dependent cotranslational protein-membrane targeting	CG5064	FBgn0035947		1.08E-03	17	3	17.6%
GO:0006613 cotranslational protein-membrane targeting	CG10130	FBgn0010638		1.28E-03	18	3	16.7%
GO:0006613 cotranslational protein-membrane targeting	CG11642	FBgn0040340		1.28E-03	18	3	16.7%
GO:0006613 cotranslational protein-membrane targeting	CG5064	FBgn0035947		1.28E-03	18	3	16.7%
GO:0045047 protein-ER targeting	CG10130	FBgn0010638		1.28E-03	18	3	16.7%
GO:0045047 protein-ER targeting	CG11642	FBgn0040340		1.28E-03	18	3	16.7%
GO:0045047 protein-ER targeting	CG5064	FBgn0035947		1.28E-03	18	3	16.7%
GO:0006612 protein-membrane targeting	CG10130	FBgn0010638		1.76E-03	20	3	15.0%
GO:0006612 protein-membrane targeting	CG11642	FBgn0040340		1.76E-03	20	3	15.0%
GO:0006612 protein-membrane targeting	CG5064	FBgn0035947		1.76E-03	20	3	15.0%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG18158	NA	NA	6.87E-03	32	3	9.4%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG12212	FBgn0003053	pebbled	6.87E-03	32	3	9.4%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG8056	FBgn0052177		6.87E-03	32	3	9.4%
GO:0048193 Golgi vesicle transport	CG17884	NA	NA	6.87E-03	32	3	9.4%
GO:0048193 Golgi vesicle transport	CG3529	FBgn0035995		6.87E-03	32	3	9.4%
GO:0048193 Golgi vesicle transport	CG7961	FBgn0025725	alpha-coatomer protein	6.87E-03	32	3	9.4%
GO:0006968 cellular defense response	CG11992	FBgn0014018	Relish	7.64E-03	11	2	18.2%
GO:0006968 cellular defense response	CG17367	FBgn0028717		7.64E-03	11	2	18.2%
GO:0007163 establishment and or maintenance of cell polarity	CG18158	NA	NA	1.00E-02	69	4	5.8%
GO:0007163 establishment and or maintenance of cell polarity	CG12212	FBgn0003053	pebbled	1.00E-02	69	4	5.8%
GO:0007163 establishment and or maintenance of cell polarity	CG5700	FBgn0028573	pericardin	1.00E-02	69	4	5.8%
GO:0007163 establishment and or maintenance of cell polarity	CG8056	FBgn0052177		1.00E-02	69	4	5.8%
GO:0035295 tube development	CG1004	FBgn0004635	rhomboid	1.16E-02	72	4	5.6%
GO:0035295 tube development	CG18158	NA	NA	1.16E-02	72	4	5.6%
GO:0035295 tube development	CG3375	NA	NA	1.16E-02	72	4	5.6%
GO:0035295 tube development	CG7260	FBgn0011723	brachyenteron	1.16E-02	72	4	5.6%

GO:0048522 positive regulation of cellular process	CG1004	FBgn0004635	rhomboid	1.17E-02	155	6	3.9%
GO:0048522 positive regulation of cellular process	CG10473	FBgn0032745		1.17E-02	155	6	3.9%
GO:0048522 positive regulation of cellular process	CG11992	FBgn0014018	Relish	1.17E-02	155	6	3.9%
GO:0048522 positive regulation of cellular process	CG12876	FBgn0039541		1.17E-02	155	6	3.9%
GO:0048522 positive regulation of cellular process	CG3848	FBgn0023518	trithorax-related	1.17E-02	155	6	3.9%
GO:0048522 positive regulation of cellular process	CG8056	FBgn0052177		1.17E-02	155	6	3.9%
GO:0016477 cell migration	CG10446	FBgn0032741	similar to Deadpan	1.25E-02	157	6	3.8%
GO:0016477 cell migration	CG3375	NA	NA	1.25E-02	157	6	3.8%
GO:0016477 cell migration	CG4383	FBgn0034125		1.25E-02	157	6	3.8%
GO:0016477 cell migration	CG5700	FBgn0028573	pericardin	1.25E-02	157	6	3.8%
GO:0016477 cell migration	CG6963	FBgn0011253	gilgamesh	1.25E-02	157	6	3.8%
GO:0016477 cell migration	CG7260	FBgn0011723	brachyenteron	1.25E-02	157	6	3.8%
GO:0001736 establishment of planar polarity	CG18158	NA	NA	1.28E-02	40	3	7.5%
GO:0001736 establishment of planar polarity	CG12212	FBgn0003053	pebbled	1.28E-02	40	3	7.5%
GO:0001736 establishment of planar polarity	CG8056	FBgn0052177		1.28E-02	40	3	7.5%
GO:0007164 establishment of tissue polarity	CG18158	NA	NA	1.28E-02	40	3	7.5%
GO:0007164 establishment of tissue polarity	CG12212	FBgn0003053	pebbled	1.28E-02	40	3	7.5%
GO:0007164 establishment of tissue polarity	CG8056	FBgn0052177		1.28E-02	40	3	7.5%
GO:0045045 secretory pathway	CG10130	FBgn0010638		1.44E-02	210	7	3.3%
GO:0045045 secretory pathway	CG11642	FBgn0040340		1.44E-02	210	7	3.3%
GO:0045045 secretory pathway	CG12473	NA	NA	1.44E-02	210	7	3.3%
GO:0045045 secretory pathway	CG17884	NA	NA	1.44E-02	210	7	3.3%
GO:0045045 secretory pathway	CG3529	FBgn0035995		1.44E-02	210	7	3.3%
GO:0045045 secretory pathway	CG5064	FBgn0035947		1.44E-02	210	7	3.3%
GO:0045045 secretory pathway	CG7961	FBgn0025725	alpha-coatomer protein	1.44E-02	210	7	3.3%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG1004	FBgn0004635	rhomboid	1.52E-02	119	5	4.2%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG17367	FBgn0028717		1.52E-02	119	5	4.2%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG3375	NA	NA	1.52E-02	119	5	4.2%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG12212	FBgn0003053	pebbled	1.52E-02	119	5	4.2%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG8056	FBgn0052177		1.52E-02	119	5	4.2%
GO:0009967 positive regulation of signal transduction	CG1004	FBgn0004635	rhomboid	1.60E-02	16	2	12.5%
GO:0009967 positive regulation of signal transduction	CG8056	FBgn0052177		1.60E-02	16	2	12.5%

GO:0002009 morphogenesis of an epithelium	CG18158	NA	NA	1.68E-02	122	5	4.1%
GO:0002009 morphogenesis of an epithelium	CG12212	FBgn0003053	pebbled	1.68E-02	122	5	4.1%
GO:0002009 morphogenesis of an epithelium	CG5588	FBgn0039532	Mig-2-like	1.68E-02	122	5	4.1%
GO:0002009 morphogenesis of an epithelium	CG5700	FBgn0028573	pericardin	1.68E-02	122	5	4.1%
GO:0002009 morphogenesis of an epithelium	CG8056	FBgn0052177		1.68E-02	122	5	4.1%
GO:0046903 secretion	CG10130	FBgn0010638		1.94E-02	223	7	3.1%
GO:0046903 secretion	CG11642	FBgn0040340		1.94E-02	223	7	3.1%
GO:0046903 secretion	CG12473	NA	NA	1.94E-02	223	7	3.1%
GO:0046903 secretion	CG17884	NA	NA	1.94E-02	223	7	3.1%
GO:0046903 secretion	CG3529	FBgn0035995		1.94E-02	223	7	3.1%
GO:0046903 secretion	CG5064	FBgn0035947		1.94E-02	223	7	3.1%
GO:0046903 secretion	CG7961	FBgn0025725	alpha-coatomer protein	1.94E-02	223	7	3.1%
GO:0048518 positive regulation of biological process	CG1004	FBgn0004635	rhomboid	1.98E-02	174	6	3.4%
GO:0048518 positive regulation of biological process	CG10473	FBgn0032745		1.98E-02	174	6	3.4%
GO:0048518 positive regulation of biological process	CG11992	FBgn0014018	Relish	1.98E-02	174	6	3.4%
GO:0048518 positive regulation of biological process	CG12876	FBgn0039541		1.98E-02	174	6	3.4%
GO:0048518 positive regulation of biological process	CG3848	FBgn0023518	trithorax-related	1.98E-02	174	6	3.4%
GO:0048518 positive regulation of biological process	CG8056	FBgn0052177		1.98E-02	174	6	3.4%
GO:0001738 morphogenesis of a polarized epithelium	CG18158	NA	NA	2.08E-02	48	3	6.3%
GO:0001738 morphogenesis of a polarized epithelium	CG12212	FBgn0003053	pebbled	2.08E-02	48	3	6.3%
GO:0001738 morphogenesis of a polarized epithelium	CG8056	FBgn0052177		2.08E-02	48	3	6.3%
GO:0006928 cell motility	CG10446	FBgn0032741	similar to Deadpan	2.45E-02	234	7	3.0%
GO:0006928 cell motility	CG3375	NA	NA	2.45E-02	234	7	3.0%
GO:0006928 cell motility	CG4383	FBgn0034125		2.45E-02	234	7	3.0%
GO:0006928 cell motility	CG5700	FBgn0028573	pericardin	2.45E-02	234	7	3.0%
GO:0006928 cell motility	CG6963	FBgn0011253	gilgamesh	2.45E-02	234	7	3.0%
GO:0006928 cell motility	CG7260	FBgn0011723	brachyenteron	2.45E-02	234	7	3.0%
GO:0006928 cell motility	CG9073	FBgn0010423	Troponin C at 47D	2.45E-02	234	7	3.0%
GO:0006730 one-carbon compound metabolism	CG18672	FBgn0040628		2.46E-02	20	2	10.0%
GO:0006730 one-carbon compound metabolism	CG7820	FBgn0027844	Carbonic anhydrase 1	2.46E-02	20	2	10.0%
GO:0016318 ommatidial rotation	CG12212	FBgn0003053	pebbled	2.46E-02	20	2	10.0%
GO:0016318 ommatidial rotation	CG8056	FBgn0052177		2.46E-02	20	2	10.0%
GO:0040011 locomotion	CG10446	FBgn0032741	similar to Deadpan	2.71E-02	239	7	2.9%
GO:0040011 locomotion	CG3375	NA	NA	2.71E-02	239	7	2.9%
GO:0040011 locomotion	CG4383	FBgn0034125		2.71E-02	239	7	2.9%
GO:0040011 locomotion	CG5700	FBgn0028573	pericardin	2.71E-02	239	7	2.9%

GO:0040011 locomotion	CG6963	FBgn0011253	gilgamesh	2.71E-02	239	7	2.9%
GO:0040011 locomotion	CG7260	FBgn0011723	brachyenteron	2.71E-02	239	7	2.9%
GO:0040011 locomotion	CG9073	FBgn0010423	Troponin C at 47D	2.71E-02	239	7	2.9%
GO:0001707 mesoderm formation	CG3375	NA	NA	3.20E-02	23	2	8.7%
GO:0001707 mesoderm formation	CG7260	FBgn0011723	brachyenteron	3.20E-02	23	2	8.7%
GO:0048332 mesoderm morphogenesis	CG3375	NA	NA	3.20E-02	23	2	8.7%
GO:0048332 mesoderm morphogenesis	CG7260	FBgn0011723	brachyenteron	3.20E-02	23	2	8.7%
GO:0007507 heart development	CG18158	NA	NA	3.26E-02	57	3	5.3%
GO:0007507 heart development	CG3375	NA	NA	3.26E-02	57	3	5.3%
GO:0007507 heart development	CG5700	FBgn0028573	pericardin	3.26E-02	57	3	5.3%
GO:0001704 formation of primary germ layer	CG3375	NA	NA	3.73E-02	25	2	8.0%
GO:0001704 formation of primary germ layer	CG7260	FBgn0011723	brachyenteron	3.73E-02	25	2	8.0%
GO:0001700 embryonic development (sensu Insecta)	CG18158	NA	NA	4.35E-02	108	4	3.7%
GO:0001700 embryonic development (sensu Insecta)	CG12212	FBgn0003053	pebbled	4.35E-02	108	4	3.7%
GO:0001700 embryonic development (sensu Insecta)	CG5588	FBgn0039532	Mig-2-like	4.35E-02	108	4	3.7%
GO:0001700 embryonic development (sensu Insecta)	CG7260	FBgn0011723	brachyenteron	4.35E-02	108	4	3.7%
GO:0035239 tube morphogenesis	CG1004	FBgn0004635	rhomboid	4.37E-02	64	3	4.7%
GO:0035239 tube morphogenesis	CG3375	NA	NA	4.37E-02	64	3	4.7%
GO:0035239 tube morphogenesis	CG7260	FBgn0011723	brachyenteron	4.37E-02	64	3	4.7%
GO:0009792 embryonic development (sensu Metazoa)	CG18158	NA	NA	4.55E-02	159	5	3.1%
GO:0009792 embryonic development (sensu Metazoa)	CG3375	NA	NA	4.55E-02	159	5	3.1%
GO:0009792 embryonic development (sensu Metazoa)	CG12212	FBgn0003053	pebbled	4.55E-02	159	5	3.1%
GO:0009792 embryonic development (sensu Metazoa)	CG5588	FBgn0039532	Mig-2-like	4.55E-02	159	5	3.1%
GO:0009792 embryonic development (sensu Metazoa)	CG7260	FBgn0011723	brachyenteron	4.55E-02	159	5	3.1%
GO:0009611 response to wounding	CG11992	FBgn0014018	Relish	4.59E-02	28	2	7.1%
GO:0009611 response to wounding	CG17367	FBgn0028717		4.59E-02	28	2	7.1%
GO:0001709 cell fate determination	CG1004	FBgn0004635	rhomboid	4.73E-02	111	4	3.6%
GO:0001709 cell fate determination	CG18158	NA	NA	4.73E-02	111	4	3.6%
GO:0001709 cell fate determination	CG12212	FBgn0003053	pebbled	4.73E-02	111	4	3.6%
GO:0001709 cell fate determination	CG7260	FBgn0011723	brachyenteron	4.73E-02	111	4	3.6%
GO:0007167 enzyme linked receptor protein signaling pathway	CG1004	FBgn0004635	rhomboid	4.76E-02	161	5	3.1%
GO:0007167 enzyme linked receptor protein signaling pathway	CG17367	FBgn0028717		4.76E-02	161	5	3.1%
GO:0007167 enzyme linked receptor protein signaling pathway	CG3375	NA	NA	4.76E-02	161	5	3.1%

Muscle-specific age-related GO terms in Cluster 3

GO:0007167 enzyme linked receptor protein signaling pathway	CG12212	FBgn0003053	pebbled	4.76E-02	161	5	3.1%
GO:0007167 enzyme linked receptor protein signaling pathway	CG8056	FBgn0052177		4.76E-02	161	5	3.1%

Muscle-specific age-related GO terms in Cluster 4 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0015980 energy derivation by oxidation of organic compounds	CG10924	FBgn0034356		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG11661	FBgn0010352	Neural conserved at 73EF	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG11876	FBgn0039635		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG12233	FBgn0027291		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG17654	FBgn0000579	Enolase	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG3001	FBgn0001186	Hexokinase A	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG3127	FBgn0003075	Phosphoglycerate kinase	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG3283	FBgn0014028	Succinate dehydrogenase B	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG3861	FBgn0026708		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG4023	NA	NA	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG4094	FBgn0028336		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG5177	FBgn0031908		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG5214	FBgn0037891		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG5320	FBgn0001098	Glutamate dehydrogenase	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG6904	FBgn0038293		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG7010	FBgn0028325		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG7070	FBgn0003178	Pyruvate kinase	8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG7430	FBgn0036762		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG7766	FBgn0030087		8.73E-13	114	22	19.3%

GO:0015980 energy derivation by oxidation of organic compounds	CG7998	FBgn0038587		8.73E-13	114	22	19.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG9244	FBgn0010100	Aconitase	8.73E-13	114	22	19.3%
GO:0006119 oxidative phosphorylation	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG10897	FBgn0033636	toutatis	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG12203	FBgn0031021		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG12859	FBgn0033961		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG14235	FBgn0031066		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG14724	FBgn0019624	Cytochrome c oxidase subunit Va	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG15434	FBgn0040705		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG15328	NA	NA	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG3192	FBgn0029888		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG3321	FBgn0038224		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG3683	FBgn0035046		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG3731	FBgn0038271		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG4412	FBgn0016119	ATPase coupling factor 6	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG4624	FBgn0039058		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG4985	NA	NA	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG5548	FBgn0030605		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG6030	FBgn0016120	ATP synthase, subunit d	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG7361	FBgn0021906	Rieske iron-sulfur protein	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG8764	FBgn0011227	oxen	6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG9140	FBgn0031771		6.34E-11	140	22	15.7%
GO:0006119 oxidative phosphorylation	CG9160	FBgn0011361	mitochondrial acyl carrier protein 1	6.34E-11	140	22	15.7%
GO:0006092 main pathways of carbohydrate metabolism	CG10924	FBgn0034356		3.86E-10	100	18	18.0%
	CG11661	FBgn0010352	Neural conserved at 73EF	3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG11876	FBgn0039635		3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG12233	FBgn0027291		3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG17654	FBgn0000579	Enolase	3.86E-10	100	18	18.0%

GO:0006092 main pathways of carbohydrate metabolism	CG3001	FBgn0001186	Hexokinase A	3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG3283	FBgn0014028	Succinate dehydrogenase B	3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG3861	FBgn0026708		3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG4094	FBgn0028336		3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG5214	FBgn0037891		3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG5320	FBgn0001098	Glutamate dehydrogenase	3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG7010	FBgn0028325		3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG7070	FBgn0003178	Pyruvate kinase	3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG7430	FBgn0036762		3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG7998	FBgn0038587		3.86E-10	100	18	18.0%
GO:0006092 main pathways of carbohydrate metabolism	CG9244	FBgn0010100	Aconitase	3.86E-10	100	18	18.0%
GO:0006084 acetyl-CoA metabolism	CG11661	FBgn0010352	Neural conserved at 73EF	4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG11876	FBgn0039635		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG12233	FBgn0027291		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG3283	FBgn0014028	Succinate dehydrogenase B	4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG3861	FBgn0026708		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG4094	FBgn0028336		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG5214	FBgn0037891		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG7010	FBgn0028325		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG7430	FBgn0036762		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG7920	FBgn0039737		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG7998	FBgn0038587		4.23E-10	47	13	27.7%
GO:0006084 acetyl-CoA metabolism	CG9244	FBgn0010100	Aconitase	4.23E-10	47	13	27.7%
GO:0006099 tricarboxylic acid cycle	CG11661	FBgn0010352	Neural conserved at 73EF	4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG11876	FBgn0039635		4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG12233	FBgn0027291		4.28E-09	46	12	26.1%

Muscle-specific age-related GO terms in Cluster 4

GO:0006099 tricarboxylic acid cycle	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG3283	FBgn0014028	Succinate dehydrogenase B	4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG3861	FBgn0026708		4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG4094	FBgn0028336		4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG5214	FBgn0037891		4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG7010	FBgn0028325		4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG7430	FBgn0036762		4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG7998	FBgn0038587		4.28E-09	46	12	26.1%
GO:0006099 tricarboxylic acid cycle	CG9244	FBgn0010100	Aconitase	4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG11661	FBgn0010352	Neural conserved at 73EF	4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG11876	FBgn0039635		4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG12233	FBgn0027291		4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG3283	FBgn0014028	Succinate dehydrogenase B	4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG3861	FBgn0026708		4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG4094	FBgn0028336		4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG5214	FBgn0037891		4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG7010	FBgn0028325		4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG7430	FBgn0036762		4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG7998	FBgn0038587		4.28E-09	46	12	26.1%
GO:0009060 aerobic respiration	CG9244	FBgn0010100	Aconitase	4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG11661	FBgn0010352	Neural conserved at 73EF	4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG11876	FBgn0039635		4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG12233	FBgn0027291		4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG3283	FBgn0014028	Succinate dehydrogenase B	4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG3861	FBgn0026708		4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG4094	FBgn0028336		4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG5214	FBgn0037891		4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG7010	FBgn0028325		4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG7430	FBgn0036762		4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG7998	FBgn0038587		4.28E-09	46	12	26.1%
GO:0045333 cellular respiration	CG9244	FBgn0010100	Aconitase	4.28E-09	46	12	26.1%

GO:0046356 acetyl-CoA catabolism	CG11661	FBgn0010352	Neural conserved at 73EF	4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG11876	FBgn0039635		4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG12233	FBgn0027291		4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG3283	FBgn0014028	Succinate dehydrogenase B	4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG3861	FBgn0026708		4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG4094	FBgn0028336		4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG5214	FBgn0037891		4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG7010	FBgn0028325		4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG7430	FBgn0036762		4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG7998	FBgn0038587		4.28E-09	46	12	26.1%
GO:0046356 acetyl-CoA catabolism	CG9244	FBgn0010100	Aconitase	4.28E-09	46	12	26.1%
GO:0009109 coenzyme catabolism	CG11661	FBgn0010352	Neural conserved at 73EF	5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG11876	FBgn0039635		5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG12233	FBgn0027291		5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG3283	FBgn0014028	Succinate dehydrogenase B	5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG3861	FBgn0026708		5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG4094	FBgn0028336		5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG5214	FBgn0037891		5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG7010	FBgn0028325		5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG7430	FBgn0036762		5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG7998	FBgn0038587		5.60E-09	47	12	25.5%
GO:0009109 coenzyme catabolism	CG9244	FBgn0010100	Aconitase	5.60E-09	47	12	25.5%
GO:0051187 cofactor catabolism	CG11661	FBgn0010352	Neural conserved at 73EF	7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG11876	FBgn0039635		7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG12233	FBgn0027291		7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG3283	FBgn0014028	Succinate dehydrogenase B	7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG3861	FBgn0026708		7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG4094	FBgn0028336		7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG5214	FBgn0037891		7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG7010	FBgn0028325		7.28E-09	48	12	25.0%

GO:0051187 cofactor catabolism	CG7430	FBgn0036762		7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG7998	FBgn0038587		7.28E-09	48	12	25.0%
GO:0051187 cofactor catabolism	CG9244	FBgn0010100	Aconitase	7.28E-09	48	12	25.0%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG12203	FBgn0031021		2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG12859	FBgn0033961		2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG14724	FBgn0019624	Cytochrome c oxidase subunit Va	2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG15434	FBgn0040705		2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG15328	NA	NA	2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG3192	FBgn0029888		2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG3683	FBgn0035046		2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG3731	FBgn0038271		2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG5548	FBgn0030605		2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG7361	FBgn0021906	Rieske iron-sulfur protein	2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG8764	FBgn0011227	oxen	2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG9140	FBgn0031771		2.09E-08	63	13	20.6%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG9160	FBgn0011361	mitochondrial acyl carrier protein 1	2.09E-08	63	13	20.6%
GO:0051186 cofactor metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG10897	FBgn0033636	toutatis	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG11661	FBgn0010352	Neural conserved at 73EF	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG11876	FBgn0039635		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG12233	FBgn0027291		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG12727	NA	NA	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG3017	FBgn0020764	Aminolevulinate synthase	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG3283	FBgn0014028	Succinate dehydrogenase B	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG3321	FBgn0038224		2.15E-08	240	25	10.4%

Muscle-specific age-related GO terms in Cluster 4

GO:0051186 cofactor metabolism	CG3861	FBgn0026708		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG4094	FBgn0028336		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG4624	FBgn0039058		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG4985	NA	NA	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG5037	FBgn0032222		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG5214	FBgn0037891		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG5231	FBgn0029158	Lipoic acid synthase	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG7010	FBgn0028325		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG7430	FBgn0036762		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG7920	FBgn0039737		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG7998	FBgn0038587		2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG9244	FBgn0010100	Aconitase	2.15E-08	240	25	10.4%
GO:0051186 cofactor metabolism	CG9589	FBgn0038361		2.15E-08	240	25	10.4%
GO:0042773 ATP synthesis coupled electron transport	CG12203	FBgn0031021		3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG12859	FBgn0033961		3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG14724	FBgn0019624	Cytochrome c oxidase subunit Va	3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG15434	FBgn0040705		3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG15328	NA	NA	3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG3192	FBgn0029888		3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG3683	FBgn0035046		3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG3731	FBgn0038271		3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG5548	FBgn0030605		3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG7361	FBgn0021906	Rieske iron-sulfur protein	3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG8764	FBgn0011227	oxen	3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG9140	FBgn0031771		3.11E-08	65	13	20.0%
GO:0042773 ATP synthesis coupled electron transport	CG9160	FBgn0011361	mitochondrial acyl carrier protein 1	3.11E-08	65	13	20.0%
GO:0006732 coenzyme metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG10897	FBgn0033636	toutatis	1.27E-07	226	23	10.2%

Muscle-specific age-related GO terms in Cluster 4

GO:0006732 coenzyme metabolism	CG11661	FBgn0010352	Neural conserved at 73EF	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG11876	FBgn0039635		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG12233	FBgn0027291		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG12727	NA	NA	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG17246	FBgn0017539	Succinyl coenzyme A synthetase flavoprotein subunit	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG3283	FBgn0014028	Succinate dehydrogenase B	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG3321	FBgn0038224		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG3861	FBgn0026708		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG4094	FBgn0028336		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG4624	FBgn0039058		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG4985	NA	NA	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG5037	FBgn0032222		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG5214	FBgn0037891		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG5231	FBgn0029158	Lipoic acid synthase	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG7010	FBgn0028325		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG7430	FBgn0036762		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG7920	FBgn0039737		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG7998	FBgn0038587		1.27E-07	226	23	10.2%
GO:0006732 coenzyme metabolism	CG9244	FBgn0010100	Aconitase	1.27E-07	226	23	10.2%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG12203	FBgn0031021		1.55E-06	40	9	22.5%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG12859	FBgn0033961		1.55E-06	40	9	22.5%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG15434	FBgn0040705		1.55E-06	40	9	22.5%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG15328	NA	NA	1.55E-06	40	9	22.5%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG3192	FBgn0029888		1.55E-06	40	9	22.5%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG3683	FBgn0035046		1.55E-06	40	9	22.5%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG5548	FBgn0030605		1.55E-06	40	9	22.5%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG9140	FBgn0031771		1.55E-06	40	9	22.5%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	CG9160	FBgn0011361	mitochondrial acyl carrier protein 1	1.55E-06	40	9	22.5%
GO:0006936 muscle contraction	CG12969	NA	NA	4.29E-05	88	11	12.5%

Muscle-specific age-related GO terms in Cluster 4

GO:0006936 muscle contraction	CG1776	FBgn0033441		4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG2981	FBgn0013348	Troponin C at 41C	4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG3849	FBgn0063485		4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG5023	FBgn0038774		4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG5596	FBgn0002772	Myosin alkali light chain 1	4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG6117	FBgn0000489	cAMP-dependent protein kinase	4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG13413	NA	NA	4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG7178	FBgn0004028	wings up A	4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG8109	NA	NA	4.29E-05	88	11	12.5%
GO:0006936 muscle contraction	CG8604	FBgn0027356	Amphiphysin	4.29E-05	88	11	12.5%
GO:0051188 cofactor biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG10897	FBgn0033636	toutatis	1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG3017	FBgn0020764	Aminolevulinate synthase	1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG3321	FBgn0038224		1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG4624	FBgn0039058		1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG4985	NA	NA	1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG5037	FBgn0032222		1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG5231	FBgn0029158	Lipoic acid synthase	1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	1.40E-04	100	11	11.0%
GO:0051188 cofactor biosynthesis	CG9589	FBgn0038361		1.40E-04	100	11	11.0%
GO:0006112 energy reserve metabolism	CG4023	NA	NA	5.51E-04	14	4	28.6%
GO:0006112 energy reserve metabolism	CG5177	FBgn0031908		5.51E-04	14	4	28.6%
GO:0006112 energy reserve metabolism	CG6904	FBgn0038293		5.51E-04	14	4	28.6%
GO:0006112 energy reserve metabolism	CG7766	FBgn0030087		5.51E-04	14	4	28.6%
GO:0006818 hydrogen transport	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.29E-03	74	8	10.8%
GO:0006818 hydrogen transport	CG10897	FBgn0033636	toutatis	1.29E-03	74	8	10.8%
GO:0006818 hydrogen transport	CG3321	FBgn0038224		1.29E-03	74	8	10.8%
GO:0006818 hydrogen transport	CG4412	FBgn0016119	ATPase coupling factor 6	1.29E-03	74	8	10.8%
GO:0006818 hydrogen transport	CG4624	FBgn0039058		1.29E-03	74	8	10.8%
GO:0006818 hydrogen transport	CG4985	NA	NA	1.29E-03	74	8	10.8%
GO:0006818 hydrogen transport	CG6030	FBgn0016120	ATP synthase, subunit d	1.29E-03	74	8	10.8%
GO:0006818 hydrogen transport	CG6213	FBgn0026753	Vacuolar H ⁺ ATPase G-subunit	1.29E-03	74	8	10.8%
GO:0015992 proton transport	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.29E-03	74	8	10.8%
GO:0015992 proton transport	CG10897	FBgn0033636	toutatis	1.29E-03	74	8	10.8%
GO:0015992 proton transport	CG3321	FBgn0038224		1.29E-03	74	8	10.8%

Muscle-specific age-related GO terms in Cluster 4

GO:0015992 proton transport	CG4412	FBgn0016119	ATPase coupling factor 6	1.29E-03	74	8	10.8%
GO:0015992 proton transport	CG4624	FBgn0039058		1.29E-03	74	8	10.8%
GO:0015992 proton transport	CG4985	NA	NA	1.29E-03	74	8	10.8%
GO:0015992 proton transport	CG6030	FBgn0016120	ATP synthase, subunit d	1.29E-03	74	8	10.8%
GO:0015992 proton transport	CG6213	FBgn0026753	Vacuolar H ⁺ ATPase G-subunit	1.29E-03	74	8	10.8%
GO:0007498 mesoderm development	CG11186	FBgn0019650	twin of eyeless	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG11916	NA	NA	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG18255	FBgn0013988	Stretchin-Mlck	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG3090	FBgn0005612	Sox box protein 14	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG4945	FBgn0034137		1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG5596	FBgn0002772	Myosin alkali light chain 1	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG5656	FBgn0037083		1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG5939	FBgn0003149	Paramyosin	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG6416	FBgn0035917		1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG6500	FBgn0000242	Beadex	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG7107	FBgn0004169	upheld	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG7238	FBgn0024191	septin interacting protein 1	1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG8806	FBgn0033413		1.34E-03	192	14	7.3%
GO:0007498 mesoderm development	CG9480	FBgn0034603	Glycogenin	1.34E-03	192	14	7.3%
GO:0006753 nucleoside phosphate metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.82E-03	61	7	11.5%
GO:0006753 nucleoside phosphate metabolism	CG10897	FBgn0033636	toutatis	1.82E-03	61	7	11.5%
GO:0006753 nucleoside phosphate metabolism	CG3321	FBgn0038224		1.82E-03	61	7	11.5%
GO:0006753 nucleoside phosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	1.82E-03	61	7	11.5%
GO:0006753 nucleoside phosphate metabolism	CG4624	FBgn0039058		1.82E-03	61	7	11.5%
GO:0006753 nucleoside phosphate metabolism	CG4985	NA	NA	1.82E-03	61	7	11.5%
GO:0006753 nucleoside phosphate metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	1.82E-03	61	7	11.5%
GO:0006754 ATP biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.82E-03	61	7	11.5%
GO:0006754 ATP biosynthesis	CG10897	FBgn0033636	toutatis	1.82E-03	61	7	11.5%
GO:0006754 ATP biosynthesis	CG3321	FBgn0038224		1.82E-03	61	7	11.5%
GO:0006754 ATP biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.82E-03	61	7	11.5%
GO:0006754 ATP biosynthesis	CG4624	FBgn0039058		1.82E-03	61	7	11.5%
GO:0006754 ATP biosynthesis	CG4985	NA	NA	1.82E-03	61	7	11.5%
GO:0006754 ATP biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	1.82E-03	61	7	11.5%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.82E-03	61	7	11.5%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG10897	FBgn0033636	toutatis	1.82E-03	61	7	11.5%

GO:0015985 energy coupled proton transport down electrochemical gradient	CG3321	FBgn0038224		1.82E-03	61	7	11.5%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG4412	FBgn0016119	ATPase coupling factor 6	1.82E-03	61	7	11.5%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG4624	FBgn0039058		1.82E-03	61	7	11.5%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG4985	NA	NA	1.82E-03	61	7	11.5%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG6030	FBgn0016120	ATP synthase, subunit d	1.82E-03	61	7	11.5%
GO:0015986 ATP synthesis coupled proton transport	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.82E-03	61	7	11.5%
GO:0015986 ATP synthesis coupled proton transport	CG10897	FBgn0033636	toutatis	1.82E-03	61	7	11.5%
GO:0015986 ATP synthesis coupled proton transport	CG3321	FBgn0038224		1.82E-03	61	7	11.5%
GO:0015986 ATP synthesis coupled proton transport	CG4412	FBgn0016119	ATPase coupling factor 6	1.82E-03	61	7	11.5%
GO:0015986 ATP synthesis coupled proton transport	CG4624	FBgn0039058		1.82E-03	61	7	11.5%
GO:0015986 ATP synthesis coupled proton transport	CG4985	NA	NA	1.82E-03	61	7	11.5%
GO:0015986 ATP synthesis coupled proton transport	CG6030	FBgn0016120	ATP synthase, subunit d	1.82E-03	61	7	11.5%
GO:0046034 ATP metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.00E-03	62	7	11.3%
GO:0046034 ATP metabolism	CG10897	FBgn0033636	toutatis	2.00E-03	62	7	11.3%
GO:0046034 ATP metabolism	CG3321	FBgn0038224		2.00E-03	62	7	11.3%
GO:0046034 ATP metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.00E-03	62	7	11.3%
GO:0046034 ATP metabolism	CG4624	FBgn0039058		2.00E-03	62	7	11.3%
GO:0046034 ATP metabolism	CG4985	NA	NA	2.00E-03	62	7	11.3%
GO:0046034 ATP metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	2.00E-03	62	7	11.3%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.63E-03	65	7	10.8%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG10897	FBgn0033636	toutatis	2.63E-03	65	7	10.8%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG3321	FBgn0038224		2.63E-03	65	7	10.8%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.63E-03	65	7	10.8%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG4624	FBgn0039058		2.63E-03	65	7	10.8%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG4985	NA	NA	2.63E-03	65	7	10.8%

Muscle-specific age-related GO terms in Cluster 4

GO:0009145 purine nucleoside triphosphate biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	2.63E-03	65	7	10.8%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.63E-03	65	7	10.8%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG10897	FBgn0033636	toutatis	2.63E-03	65	7	10.8%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG3321	FBgn0038224		2.63E-03	65	7	10.8%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.63E-03	65	7	10.8%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG4624	FBgn0039058		2.63E-03	65	7	10.8%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG4985	NA	NA	2.63E-03	65	7	10.8%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	2.63E-03	65	7	10.8%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.63E-03	65	7	10.8%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG10897	FBgn0033636	toutatis	2.63E-03	65	7	10.8%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG3321	FBgn0038224		2.63E-03	65	7	10.8%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.63E-03	65	7	10.8%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG4624	FBgn0039058		2.63E-03	65	7	10.8%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG4985	NA	NA	2.63E-03	65	7	10.8%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	2.63E-03	65	7	10.8%
GO:0009142 nucleoside triphosphate biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.88E-03	66	7	10.6%
GO:0009142 nucleoside triphosphate biosynthesis	CG10897	FBgn0033636	toutatis	2.88E-03	66	7	10.6%
GO:0009142 nucleoside triphosphate biosynthesis	CG3321	FBgn0038224		2.88E-03	66	7	10.6%
GO:0009142 nucleoside triphosphate biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.88E-03	66	7	10.6%
GO:0009142 nucleoside triphosphate biosynthesis	CG4624	FBgn0039058		2.88E-03	66	7	10.6%
GO:0009142 nucleoside triphosphate biosynthesis	CG4985	NA	NA	2.88E-03	66	7	10.6%
GO:0009142 nucleoside triphosphate biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	2.88E-03	66	7	10.6%

GO:0009144 purine nucleoside triphosphate metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.88E-03	66	7	10.6%
GO:0009144 purine nucleoside triphosphate metabolism	CG10897	FBgn0033636	toutatis	2.88E-03	66	7	10.6%
GO:0009144 purine nucleoside triphosphate metabolism	CG3321	FBgn0038224		2.88E-03	66	7	10.6%
GO:0009144 purine nucleoside triphosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.88E-03	66	7	10.6%
GO:0009144 purine nucleoside triphosphate metabolism	CG4624	FBgn0039058		2.88E-03	66	7	10.6%
GO:0009144 purine nucleoside triphosphate metabolism	CG4985	NA	NA	2.88E-03	66	7	10.6%
GO:0009144 purine nucleoside triphosphate metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	2.88E-03	66	7	10.6%
GO:0009199 ribonucleoside triphosphate metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.88E-03	66	7	10.6%
GO:0009199 ribonucleoside triphosphate metabolism	CG10897	FBgn0033636	toutatis	2.88E-03	66	7	10.6%
GO:0009199 ribonucleoside triphosphate metabolism	CG3321	FBgn0038224		2.88E-03	66	7	10.6%
GO:0009199 ribonucleoside triphosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.88E-03	66	7	10.6%
GO:0009199 ribonucleoside triphosphate metabolism	CG4624	FBgn0039058		2.88E-03	66	7	10.6%
GO:0009199 ribonucleoside triphosphate metabolism	CG4985	NA	NA	2.88E-03	66	7	10.6%
GO:0009199 ribonucleoside triphosphate metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	2.88E-03	66	7	10.6%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	2.88E-03	66	7	10.6%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG10897	FBgn0033636	toutatis	2.88E-03	66	7	10.6%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG3321	FBgn0038224		2.88E-03	66	7	10.6%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.88E-03	66	7	10.6%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG4624	FBgn0039058		2.88E-03	66	7	10.6%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG4985	NA	NA	2.88E-03	66	7	10.6%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	2.88E-03	66	7	10.6%
GO:0006779 porphyrin biosynthesis	CG3017	FBgn0020764	Aminolevulinate synthase	3.36E-03	11	3	27.3%
GO:0006779 porphyrin biosynthesis	CG5037	FBgn0032222		3.36E-03	11	3	27.3%

Muscle-specific age-related GO terms in Cluster 4

GO:0006779 porphyrin biosynthesis	CG9589	FBgn0038361		3.36E-03	11	3	27.3%
GO:0042168 heme metabolism	CG3017	FBgn0020764	Aminolevulinate synthase	3.36E-03	11	3	27.3%
GO:0042168 heme metabolism	CG5037	FBgn0032222		3.36E-03	11	3	27.3%
GO:0042168 heme metabolism	CG9589	FBgn0038361		3.36E-03	11	3	27.3%
GO:0009141 nucleoside triphosphate metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	3.41E-03	68	7	10.3%
GO:0009141 nucleoside triphosphate metabolism	CG10897	FBgn0033636	toutatis	3.41E-03	68	7	10.3%
GO:0009141 nucleoside triphosphate metabolism	CG3321	FBgn0038224		3.41E-03	68	7	10.3%
GO:0009141 nucleoside triphosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	3.41E-03	68	7	10.3%
GO:0009141 nucleoside triphosphate metabolism	CG4624	FBgn0039058		3.41E-03	68	7	10.3%
GO:0009141 nucleoside triphosphate metabolism	CG4985	NA	NA	3.41E-03	68	7	10.3%
GO:0009141 nucleoside triphosphate metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	3.41E-03	68	7	10.3%
GO:0006752 group transfer coenzyme metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	3.70E-03	69	7	10.1%
GO:0006752 group transfer coenzyme metabolism	CG10897	FBgn0033636	toutatis	3.70E-03	69	7	10.1%
GO:0006752 group transfer coenzyme metabolism	CG3321	FBgn0038224		3.70E-03	69	7	10.1%
GO:0006752 group transfer coenzyme metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	3.70E-03	69	7	10.1%
GO:0006752 group transfer coenzyme metabolism	CG4624	FBgn0039058		3.70E-03	69	7	10.1%
GO:0006752 group transfer coenzyme metabolism	CG4985	NA	NA	3.70E-03	69	7	10.1%
GO:0006752 group transfer coenzyme metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	3.70E-03	69	7	10.1%
GO:0006096 glycolysis	CG17654	FBgn0000579	Enolase	4.03E-03	37	5	13.5%
GO:0006096 glycolysis	CG3001	FBgn0001186	Hexokinase A	4.03E-03	37	5	13.5%
GO:0006096 glycolysis	CG3127	FBgn0003075	Phosphoglycerate kinase	4.03E-03	37	5	13.5%
GO:0006096 glycolysis	CG7070	FBgn0003178	Pyruvate kinase	4.03E-03	37	5	13.5%
GO:0006096 glycolysis	CG7430	FBgn0036762		4.03E-03	37	5	13.5%
GO:0009108 coenzyme biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	4.17E-03	89	8	9.0%
GO:0009108 coenzyme biosynthesis	CG10897	FBgn0033636	toutatis	4.17E-03	89	8	9.0%
GO:0009108 coenzyme biosynthesis	CG3321	FBgn0038224		4.17E-03	89	8	9.0%
GO:0009108 coenzyme biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	4.17E-03	89	8	9.0%
GO:0009108 coenzyme biosynthesis	CG4624	FBgn0039058		4.17E-03	89	8	9.0%
GO:0009108 coenzyme biosynthesis	CG4985	NA	NA	4.17E-03	89	8	9.0%
GO:0009108 coenzyme biosynthesis	CG5231	FBgn0029158	Lipoic acid synthase	4.17E-03	89	8	9.0%
GO:0009108 coenzyme biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	4.17E-03	89	8	9.0%

GO:0006778 porphyrin metabolism	CG3017	FBgn0020764	Aminolevulinate synthase	5.58E-03	13	3	23.1%
GO:0006778 porphyrin metabolism	CG5037	FBgn0032222		5.58E-03	13	3	23.1%
GO:0006778 porphyrin metabolism	CG9589	FBgn0038361		5.58E-03	13	3	23.1%
GO:0006006 glucose metabolism	CG10924	FBgn0034356		5.91E-03	57	6	10.5%
GO:0006006 glucose metabolism	CG17654	FBgn0000579	Enolase	5.91E-03	57	6	10.5%
GO:0006006 glucose metabolism	CG3001	FBgn0001186	Hexokinase A	5.91E-03	57	6	10.5%
GO:0006006 glucose metabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	5.91E-03	57	6	10.5%
GO:0006006 glucose metabolism	CG7070	FBgn0003178	Pyruvate kinase	5.91E-03	57	6	10.5%
GO:0006006 glucose metabolism	CG7430	FBgn0036762		5.91E-03	57	6	10.5%
GO:0015672 monovalent inorganic cation transport	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG10897	FBgn0033636	toutatis	9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG12904	FBgn0033510		9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG2287	NA	NA	9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG3321	FBgn0038224		9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG4412	FBgn0016119	ATPase coupling factor 6	9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG4624	FBgn0039058		9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG4985	NA	NA	9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG5670	FBgn0002921	Na pump alpha subunit	9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG6030	FBgn0016120	ATP synthase, subunit d	9.59E-03	168	11	6.5%
GO:0015672 monovalent inorganic cation transport	CG6213	FBgn0026753	Vacuolar H ⁺ ATPase G- subunit	9.59E-03	168	11	6.5%
GO:0009152 purine ribonucleotide biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.22E-02	86	7	8.1%
GO:0009152 purine ribonucleotide biosynthesis	CG10897	FBgn0033636	toutatis	1.22E-02	86	7	8.1%
GO:0009152 purine ribonucleotide biosynthesis	CG3321	FBgn0038224		1.22E-02	86	7	8.1%
GO:0009152 purine ribonucleotide biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.22E-02	86	7	8.1%
GO:0009152 purine ribonucleotide biosynthesis	CG4624	FBgn0039058		1.22E-02	86	7	8.1%
GO:0009152 purine ribonucleotide biosynthesis	CG4985	NA	NA	1.22E-02	86	7	8.1%
GO:0009152 purine ribonucleotide biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	1.22E-02	86	7	8.1%
GO:0006007 glucose catabolism	CG17654	FBgn0000579	Enolase	1.23E-02	48	5	10.4%
GO:0006007 glucose catabolism	CG3001	FBgn0001186	Hexokinase A	1.23E-02	48	5	10.4%

GO:0006007 glucose catabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	1.23E-02	48	5	10.4%
GO:0006007 glucose catabolism	CG7070	FBgn0003178	Pyruvate kinase	1.23E-02	48	5	10.4%
GO:0006007 glucose catabolism	CG7430	FBgn0036762		1.23E-02	48	5	10.4%
GO:0019320 hexose catabolism	CG17654	FBgn0000579	Enolase	1.23E-02	48	5	10.4%
GO:0019320 hexose catabolism	CG3001	FBgn0001186	Hexokinase A	1.23E-02	48	5	10.4%
GO:0019320 hexose catabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	1.23E-02	48	5	10.4%
GO:0019320 hexose catabolism	CG7070	FBgn0003178	Pyruvate kinase	1.23E-02	48	5	10.4%
GO:0019320 hexose catabolism	CG7430	FBgn0036762		1.23E-02	48	5	10.4%
GO:0046164 alcohol catabolism	CG17654	FBgn0000579	Enolase	1.23E-02	48	5	10.4%
GO:0046164 alcohol catabolism	CG3001	FBgn0001186	Hexokinase A	1.23E-02	48	5	10.4%
GO:0046164 alcohol catabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	1.23E-02	48	5	10.4%
GO:0046164 alcohol catabolism	CG7070	FBgn0003178	Pyruvate kinase	1.23E-02	48	5	10.4%
GO:0046164 alcohol catabolism	CG7430	FBgn0036762		1.23E-02	48	5	10.4%
GO:0046365 monosaccharide catabolism	CG17654	FBgn0000579	Enolase	1.23E-02	48	5	10.4%
GO:0046365 monosaccharide catabolism	CG3001	FBgn0001186	Hexokinase A	1.23E-02	48	5	10.4%
GO:0046365 monosaccharide catabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	1.23E-02	48	5	10.4%
GO:0046365 monosaccharide catabolism	CG7070	FBgn0003178	Pyruvate kinase	1.23E-02	48	5	10.4%
GO:0046365 monosaccharide catabolism	CG7430	FBgn0036762		1.23E-02	48	5	10.4%
GO:0009150 purine ribonucleotide metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.30E-02	87	7	8.0%
GO:0009150 purine ribonucleotide metabolism	CG10897	FBgn0033636	toutatis	1.30E-02	87	7	8.0%
GO:0009150 purine ribonucleotide metabolism	CG3321	FBgn0038224		1.30E-02	87	7	8.0%
GO:0009150 purine ribonucleotide metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	1.30E-02	87	7	8.0%
GO:0009150 purine ribonucleotide metabolism	CG4624	FBgn0039058		1.30E-02	87	7	8.0%
GO:0009150 purine ribonucleotide metabolism	CG4985	NA	NA	1.30E-02	87	7	8.0%
GO:0009150 purine ribonucleotide metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	1.30E-02	87	7	8.0%
GO:0006164 purine nucleotide biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.37E-02	88	7	8.0%
GO:0006164 purine nucleotide biosynthesis	CG10897	FBgn0033636	toutatis	1.37E-02	88	7	8.0%
GO:0006164 purine nucleotide biosynthesis	CG3321	FBgn0038224		1.37E-02	88	7	8.0%
GO:0006164 purine nucleotide biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.37E-02	88	7	8.0%
GO:0006164 purine nucleotide biosynthesis	CG4624	FBgn0039058		1.37E-02	88	7	8.0%
GO:0006164 purine nucleotide biosynthesis	CG4985	NA	NA	1.37E-02	88	7	8.0%
GO:0006164 purine nucleotide biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	1.37E-02	88	7	8.0%
GO:0009260 ribonucleotide biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.37E-02	88	7	8.0%
GO:0009260 ribonucleotide biosynthesis	CG10897	FBgn0033636	toutatis	1.37E-02	88	7	8.0%
GO:0009260 ribonucleotide biosynthesis	CG3321	FBgn0038224		1.37E-02	88	7	8.0%

GO:0009260 ribonucleotide biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.37E-02	88	7	8.0%
GO:0009260 ribonucleotide biosynthesis	CG4624	FBgn0039058		1.37E-02	88	7	8.0%
GO:0009260 ribonucleotide biosynthesis	CG4985	NA	NA	1.37E-02	88	7	8.0%
GO:0009260 ribonucleotide biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	1.37E-02	88	7	8.0%
GO:0006163 purine nucleotide metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.46E-02	89	7	7.9%
GO:0006163 purine nucleotide metabolism	CG10897	FBgn0033636	toutatis	1.46E-02	89	7	7.9%
GO:0006163 purine nucleotide metabolism	CG3321	FBgn0038224		1.46E-02	89	7	7.9%
GO:0006163 purine nucleotide metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	1.46E-02	89	7	7.9%
GO:0006163 purine nucleotide metabolism	CG4624	FBgn0039058		1.46E-02	89	7	7.9%
GO:0006163 purine nucleotide metabolism	CG4985	NA	NA	1.46E-02	89	7	7.9%
GO:0006163 purine nucleotide metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	1.46E-02	89	7	7.9%
GO:0009259 ribonucleotide metabolism	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	1.46E-02	89	7	7.9%
GO:0009259 ribonucleotide metabolism	CG10897	FBgn0033636	toutatis	1.46E-02	89	7	7.9%
GO:0009259 ribonucleotide metabolism	CG3321	FBgn0038224		1.46E-02	89	7	7.9%
GO:0009259 ribonucleotide metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	1.46E-02	89	7	7.9%
GO:0009259 ribonucleotide metabolism	CG4624	FBgn0039058		1.46E-02	89	7	7.9%
GO:0009259 ribonucleotide metabolism	CG4985	NA	NA	1.46E-02	89	7	7.9%
GO:0009259 ribonucleotide metabolism	CG6030	FBgn0016120	ATP synthase, subunit d	1.46E-02	89	7	7.9%
GO:0009309 amine biosynthesis	CG12233	FBgn0027291		2.01E-02	74	6	8.1%
GO:0009309 amine biosynthesis	CG1417	FBgn0003423	sluggish A	2.01E-02	74	6	8.1%
GO:0009309 amine biosynthesis	CG4300	FBgn0036272		2.01E-02	74	6	8.1%
GO:0009309 amine biosynthesis	CG6950	FBgn0037955		2.01E-02	74	6	8.1%
GO:0009309 amine biosynthesis	CG7811	FBgn0000153	black	2.01E-02	74	6	8.1%
GO:0009309 amine biosynthesis	CG9244	FBgn0010100	Aconitase	2.01E-02	74	6	8.1%
GO:0006100 tricarboxylic acid cycle intermediate metabolism	CG4094	FBgn0028336		2.19E-02	21	3	14.3%
GO:0006100 tricarboxylic acid cycle intermediate metabolism	CG5320	FBgn0001098	Glutamate dehydrogenase	2.19E-02	21	3	14.3%
GO:0006100 tricarboxylic acid cycle intermediate metabolism	CG7998	FBgn0038587		2.19E-02	21	3	14.3%
GO:0019318 hexose metabolism	CG10924	FBgn0034356		2.27E-02	76	6	7.9%
GO:0019318 hexose metabolism	CG17654	FBgn0000579	Enolase	2.27E-02	76	6	7.9%
GO:0019318 hexose metabolism	CG3001	FBgn0001186	Hexokinase A	2.27E-02	76	6	7.9%
GO:0019318 hexose metabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	2.27E-02	76	6	7.9%
GO:0019318 hexose metabolism	CG7070	FBgn0003178	Pyruvate kinase	2.27E-02	76	6	7.9%
GO:0019318 hexose metabolism	CG7430	FBgn0036762		2.27E-02	76	6	7.9%
GO:0009165 nucleotide biosynthesis	CG1088	FBgn0015324	Vacuolar H ⁺ -ATPase 26kD E subunit	3.27E-02	105	7	6.7%
GO:0009165 nucleotide biosynthesis	CG10897	FBgn0033636	toutatis	3.27E-02	105	7	6.7%

Muscle-specific age-related GO terms in Cluster 4

GO:0009165 nucleotide biosynthesis	CG3321	FBgn0038224		3.27E-02	105	7	6.7%
GO:0009165 nucleotide biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	3.27E-02	105	7	6.7%
GO:0009165 nucleotide biosynthesis	CG4624	FBgn0039058		3.27E-02	105	7	6.7%
GO:0009165 nucleotide biosynthesis	CG4985	NA	NA	3.27E-02	105	7	6.7%
GO:0009165 nucleotide biosynthesis	CG6030	FBgn0016120	ATP synthase, subunit d	3.27E-02	105	7	6.7%
GO:0008652 amino acid biosynthesis	CG12233	FBgn0027291		3.35E-02	62	5	8.1%
GO:0008652 amino acid biosynthesis	CG1417	FBgn0003423	sluggish A	3.35E-02	62	5	8.1%
GO:0008652 amino acid biosynthesis	CG6950	FBgn0037955		3.35E-02	62	5	8.1%
GO:0008652 amino acid biosynthesis	CG7811	FBgn0000153	black	3.35E-02	62	5	8.1%
GO:0008652 amino acid biosynthesis	CG9244	FBgn0010100	Aconitase	3.35E-02	62	5	8.1%
GO:0006473 protein amino acid acetylation	CG11412	FBgn0024362		3.89E-02	11	2	18.2%
GO:0006473 protein amino acid acetylation	CG1894	FBgn0039585		3.89E-02	11	2	18.2%
GO:0006874 calcium ion homeostasis	CG3725	FBgn0004551	Calcium ATPase at 60A	3.89E-02	11	2	18.2%
GO:0006874 calcium ion homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	3.89E-02	11	2	18.2%
GO:0007616 long-term memory	CG10901	FBgn0003015	oskar	3.89E-02	11	2	18.2%
GO:0007616 long-term memory	CG6103	FBgn0014467	Cyclic-AMP response element binding protein B at 17A	3.89E-02	11	2	18.2%
GO:0016052 carbohydrate catabolism	CG17654	FBgn0000579	Enolase	4.22E-02	66	5	7.6%
GO:0016052 carbohydrate catabolism	CG3001	FBgn0001186	Hexokinase A	4.22E-02	66	5	7.6%
GO:0016052 carbohydrate catabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	4.22E-02	66	5	7.6%
GO:0016052 carbohydrate catabolism	CG7070	FBgn0003178	Pyruvate kinase	4.22E-02	66	5	7.6%
GO:0016052 carbohydrate catabolism	CG7430	FBgn0036762		4.22E-02	66	5	7.6%
GO:0044275 cellular carbohydrate catabolism	CG17654	FBgn0000579	Enolase	4.22E-02	66	5	7.6%
GO:0044275 cellular carbohydrate catabolism	CG3001	FBgn0001186	Hexokinase A	4.22E-02	66	5	7.6%
GO:0044275 cellular carbohydrate catabolism	CG3127	FBgn0003075	Phosphoglycerate kinase	4.22E-02	66	5	7.6%
GO:0044275 cellular carbohydrate catabolism	CG7070	FBgn0003178	Pyruvate kinase	4.22E-02	66	5	7.6%
GO:0044275 cellular carbohydrate catabolism	CG7430	FBgn0036762		4.22E-02	66	5	7.6%
GO:0016051 carbohydrate biosynthesis	CG10924	FBgn0034356		4.37E-02	46	4	8.7%
GO:0016051 carbohydrate biosynthesis	CG5177	FBgn0031908		4.37E-02	46	4	8.7%
GO:0016051 carbohydrate biosynthesis	CG6904	FBgn0038293		4.37E-02	46	4	8.7%
GO:0016051 carbohydrate biosynthesis	CG9480	FBgn0034603	Glycogenin	4.37E-02	46	4	8.7%
GO:0044264 cellular polysaccharide metabolism	CG4023	NA	NA	4.70E-02	68	5	7.4%
GO:0044264 cellular polysaccharide metabolism	CG4090	FBgn0038492		4.70E-02	68	5	7.4%
GO:0044264 cellular polysaccharide metabolism	CG6904	FBgn0038293		4.70E-02	68	5	7.4%
GO:0044264 cellular polysaccharide metabolism	CG7766	FBgn0030087		4.70E-02	68	5	7.4%
GO:0044264 cellular polysaccharide metabolism	CG9558	NA	NA	4.70E-02	68	5	7.4%

Muscle-specific age-related GO terms in Cluster 5 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0007519 myogenesis	CG1019	FBgn0014863	Muscle LIM protein at 84B	7.72E-05	41	5	12.2%
GO:0007519 myogenesis	CG17155	NA	NA	7.72E-05	41	5	12.2%
GO:0007519 myogenesis	CG13754	NA	NA	7.72E-05	41	5	12.2%
GO:0007519 myogenesis	CG14026	FBgn0003716	thickveins	7.72E-05	41	5	12.2%
GO:0007519 myogenesis	CG6803	FBgn0038294		7.72E-05	41	5	12.2%
GO:0007517 muscle development	CG1019	FBgn0014863	Muscle LIM protein at 84B	9.70E-05	99	7	7.1%
GO:0007517 muscle development	CG10293	FBgn0017397	held out wings	9.70E-05	99	7	7.1%
GO:0007517 muscle development	CG17155	NA	NA	9.70E-05	99	7	7.1%
GO:0007517 muscle development	CG13754	NA	NA	9.70E-05	99	7	7.1%
GO:0007517 muscle development	CG14026	FBgn0003716	thickveins	9.70E-05	99	7	7.1%
GO:0007517 muscle development	CG1539	FBgn0082582	tropomodulin	9.70E-05	99	7	7.1%
GO:0007517 muscle development	CG6803	FBgn0038294		9.70E-05	99	7	7.1%
GO:0006874 calcium ion homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	6.15E-03	11	2	18.2%
GO:0006874 calcium ion homeostasis	CG6702	FBgn0004580	Calbindin 53E	6.15E-03	11	2	18.2%
GO:0007520 myoblast fusion	CG17155	NA	NA	9.96E-03	14	2	14.3%
GO:0007520 myoblast fusion	CG13754	NA	NA	9.96E-03	14	2	14.3%
GO:0007243 protein kinase cascade	CG14217	FBgn0031030		1.11E-02	123	5	4.1%
GO:0007243 protein kinase cascade	CG2252	FBgn0004656	female sterile (1) homoeotic	1.11E-02	123	5	4.1%
GO:0007243 protein kinase cascade	CG2275	FBgn0001291	Jun-related antigen	1.11E-02	123	5	4.1%
GO:0007243 protein kinase cascade	CG5848	FBgn0000250	cactus	1.11E-02	123	5	4.1%
GO:0007243 protein kinase cascade	CG7393	FBgn0024846		1.11E-02	123	5	4.1%
GO:0007432 salivary gland determination	CG10334	FBgn0005672	spitz	1.14E-02	15	2	13.3%
GO:0007432 salivary gland determination	CG14026	FBgn0003716	thickveins	1.14E-02	15	2	13.3%
GO:0007254 JNK cascade	CG14217	FBgn0031030		1.30E-02	45	3	6.7%
GO:0007254 JNK cascade	CG2275	FBgn0001291	Jun-related antigen	1.30E-02	45	3	6.7%
GO:0007254 JNK cascade	CG7393	FBgn0024846		1.30E-02	45	3	6.7%
GO:0031098 stress-activated protein kinase signaling pathway	CG14217	FBgn0031030		1.30E-02	45	3	6.7%
GO:0031098 stress-activated protein kinase signaling pathway	CG2275	FBgn0001291	Jun-related antigen	1.30E-02	45	3	6.7%
GO:0031098 stress-activated protein kinase signaling pathway	CG7393	FBgn0024846		1.30E-02	45	3	6.7%
GO:0046843 dorsal appendage formation	CG2275	FBgn0001291	Jun-related antigen	1.46E-02	17	2	11.8%
GO:0046843 dorsal appendage formation	CG5848	FBgn0000250	cactus	1.46E-02	17	2	11.8%
GO:0030005 di- tri-valent inorganic cation homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	1.63E-02	18	2	11.1%
GO:0030005 di- tri-valent inorganic cation homeostasis	CG6702	FBgn0004580	Calbindin 53E	1.63E-02	18	2	11.1%
GO:0006875 metal ion homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	1.99E-02	20	2	10.0%

GO:0006875 metal ion homeostasis	CG6702	FBgn0004580	Calbindin 53E	1.99E-02	20	2	10.0%
GO:0000165 MAPKKK cascade	CG14217	FBgn0031030		2.39E-02	100	4	4.0%
GO:0000165 MAPKKK cascade	CG2252	FBgn0004656	female sterile (1) homoeotic	2.39E-02	100	4	4.0%
GO:0000165 MAPKKK cascade	CG2275	FBgn0001291	Jun-related antigen	2.39E-02	100	4	4.0%
GO:0000165 MAPKKK cascade	CG7393	FBgn0024846		2.39E-02	100	4	4.0%
GO:0007424 tracheal system development (sensu Insecta)	CG10334	FBgn0005672	spitz	2.39E-02	100	4	4.0%
GO:0007424 tracheal system development (sensu Insecta)	CG14026	FBgn0003716	thickveins	2.39E-02	100	4	4.0%
GO:0007424 tracheal system development (sensu Insecta)	CG4220	FBgn0004858	elbow B	2.39E-02	100	4	4.0%
GO:0007424 tracheal system development (sensu Insecta)	CG5670	FBgn0002921	Na pump alpha subunit	2.39E-02	100	4	4.0%
GO:0007179 transforming growth factor beta receptor signaling pathway	CG14026	FBgn0003716	thickveins	2.81E-02	24	2	8.3%
GO:0007179 transforming growth factor beta receptor signaling pathway	CG7393	FBgn0024846		2.81E-02	24	2	8.3%
GO:0030162 regulation of proteolysis and peptidolysis	CG1903	FBgn0005410	strawberry notch	2.81E-02	24	2	8.3%
GO:0030162 regulation of proteolysis and peptidolysis	CG2028	FBgn0015024	Casein kinase Ialpha	2.81E-02	24	2	8.3%
GO:0006040 amino sugar metabolism	CG17065	FBgn0031099		3.04E-02	62	3	4.8%
GO:0006040 amino sugar metabolism	CG7306	FBgn0036947		3.04E-02	62	3	4.8%
GO:0006040 amino sugar metabolism	CG9558	NA	NA	3.04E-02	62	3	4.8%
GO:0006041 glucosamine metabolism	CG17065	FBgn0031099		3.04E-02	62	3	4.8%
GO:0006041 glucosamine metabolism	CG7306	FBgn0036947		3.04E-02	62	3	4.8%
GO:0006041 glucosamine metabolism	CG9558	NA	NA	3.04E-02	62	3	4.8%
GO:0006044 N-acetylglucosamine metabolism	CG17065	FBgn0031099		3.04E-02	62	3	4.8%
GO:0006044 N-acetylglucosamine metabolism	CG7306	FBgn0036947		3.04E-02	62	3	4.8%
GO:0006044 N-acetylglucosamine metabolism	CG9558	NA	NA	3.04E-02	62	3	4.8%
GO:0006873 cell ion homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	3.04E-02	25	2	8.0%
GO:0006873 cell ion homeostasis	CG6702	FBgn0004580	Calbindin 53E	3.04E-02	25	2	8.0%
GO:0030003 cation homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	3.04E-02	25	2	8.0%
GO:0030003 cation homeostasis	CG6702	FBgn0004580	Calbindin 53E	3.04E-02	25	2	8.0%
GO:0050801 ion homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	3.04E-02	25	2	8.0%
GO:0050801 ion homeostasis	CG6702	FBgn0004580	Calbindin 53E	3.04E-02	25	2	8.0%
GO:0007167 enzyme linked receptor protein signaling pathway	CG10334	FBgn0005672	spitz	3.16E-02	161	5	3.1%
GO:0007167 enzyme linked receptor protein signaling pathway	CG11622	FBgn0026056		3.16E-02	161	5	3.1%
GO:0007167 enzyme linked receptor protein signaling pathway	CG14026	FBgn0003716	thickveins	3.16E-02	161	5	3.1%
GO:0007167 enzyme linked receptor protein signaling pathway	CG1903	FBgn0005410	strawberry notch	3.16E-02	161	5	3.1%

GO:0007167 enzyme linked receptor protein signaling pathway	CG7393	FBgn0024846		3.16E-02	161	5	3.1%
GO:0009894 regulation of catabolism	CG1903	FBgn0005410	strawberry notch	3.50E-02	27	2	7.4%
GO:0009894 regulation of catabolism	CG2028	FBgn0015024	Casein kinase Ialpha	3.50E-02	27	2	7.4%
GO:0019725 cell homeostasis	CG5398	FBgn0034882		3.98E-02	69	3	4.3%
GO:0019725 cell homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	3.98E-02	69	3	4.3%
GO:0019725 cell homeostasis	CG6702	FBgn0004580	Calbindin 53E	3.98E-02	69	3	4.3%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG10334	FBgn0005672	spitz	4.04E-02	118	4	3.4%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG14026	FBgn0003716	thickveins	4.04E-02	118	4	3.4%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG1903	FBgn0005410	strawberry notch	4.04E-02	118	4	3.4%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG2275	FBgn0001291	Jun-related antigen	4.04E-02	118	4	3.4%
GO:0042592 homeostasis	CG5398	FBgn0034882		4.59E-02	73	3	4.1%
GO:0042592 homeostasis	CG5670	FBgn0002921	Na pump alpha subunit	4.59E-02	73	3	4.1%
GO:0042592 homeostasis	CG6702	FBgn0004580	Calbindin 53E	4.59E-02	73	3	4.1%

Muscle-specific age-related GO terms in Cluster 6 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0016042 lipid catabolism	CG14507	FBgn0039655		3.50E-04	17	3	17.6%
GO:0016042 lipid catabolism	CG15102	FBgn0034405	Juvenile hormone epoxide hydrolase 2	3.50E-04	17	3	17.6%
GO:0016042 lipid catabolism	CG1583	FBgn0030013		3.50E-04	17	3	17.6%
GO:0006305 DNA alkylation	CG15635	FBgn0031617		7.69E-03	16	2	12.5%
GO:0006305 DNA alkylation	CG15723	FBgn0052647		7.69E-03	16	2	12.5%
GO:0006306 DNA methylation	CG15635	FBgn0031617		7.69E-03	16	2	12.5%
GO:0006306 DNA methylation	CG15723	FBgn0052647		7.69E-03	16	2	12.5%
GO:0006304 DNA modification	CG15635	FBgn0031617		1.31E-02	21	2	9.5%
GO:0006304 DNA modification	CG15723	FBgn0052647		1.31E-02	21	2	9.5%
GO:0007446 imaginal disc growth	CG14228	FBgn0013951	Merlin	1.43E-02	22	2	9.1%
GO:0007446 imaginal disc growth	CG2048	FBgn0002413	discs overgrown	1.43E-02	22	2	9.1%
GO:0019725 cell homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	1.98E-02	69	3	4.3%
GO:0019725 cell homeostasis	CG4019	FBgn0034885		1.98E-02	69	3	4.3%
GO:0019725 cell homeostasis	CG8627	FBgn0010387	Diazepam-binding inhibitor	1.98E-02	69	3	4.3%
GO:0007600 sensory perception	CG15872	NA	NA	2.18E-02	192	5	2.6%
GO:0007600 sensory perception	CG5279	FBgn0014019	Rhodopsin 5	2.18E-02	192	5	2.6%
GO:0007600 sensory perception	CG7189	FBgn0035870	Gustatory receptor 66a	2.18E-02	192	5	2.6%
GO:0007600 sensory perception	CG8532	FBgn0028582	liquid facets	2.18E-02	192	5	2.6%
GO:0007600 sensory perception	CG9358	FBgn0035089	Pherokine 3	2.18E-02	192	5	2.6%
GO:0006644 phospholipid metabolism	CG1583	FBgn0030013		2.22E-02	72	3	4.2%
GO:0006644 phospholipid metabolism	CG5162	FBgn0030828		2.22E-02	72	3	4.2%
GO:0006644 phospholipid metabolism	CG8962	FBgn0025809	Platelet-activating factor acetylhydrolase alpha	2.22E-02	72	3	4.2%
GO:0042592 homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	2.30E-02	73	3	4.1%
GO:0042592 homeostasis	CG4019	FBgn0034885		2.30E-02	73	3	4.1%
GO:0042592 homeostasis	CG8627	FBgn0010387	Diazepam-binding inhibitor	2.30E-02	73	3	4.1%
GO:0007218 neuropeptide signaling pathway	CG11051	FBgn0040813	Neuropeptide-like precursor 2	2.75E-02	31	2	6.5%
GO:0007218 neuropeptide signaling pathway	CG14919	FBgn0032336	Allatostatin C	2.75E-02	31	2	6.5%
GO:0009581 detection of external stimulus	CG15872	NA	NA	2.80E-02	205	5	2.4%
GO:0009581 detection of external stimulus	CG5279	FBgn0014019	Rhodopsin 5	2.80E-02	205	5	2.4%
GO:0009581 detection of external stimulus	CG7189	FBgn0035870	Gustatory receptor 66a	2.80E-02	205	5	2.4%
GO:0009581 detection of external stimulus	CG8532	FBgn0028582	liquid facets	2.80E-02	205	5	2.4%
GO:0009581 detection of external stimulus	CG9358	FBgn0035089	Pherokine 3	2.80E-02	205	5	2.4%
GO:0030001 metal ion transport	CG15872	NA	NA	2.94E-02	140	4	2.9%
GO:0030001 metal ion transport	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	2.94E-02	140	4	2.9%

GO:0030001 metal ion transport	CG3979	FBgn0036816	I'm not dead yet	2.94E-02	140	4	2.9%
GO:0030001 metal ion transport	CG9065	FBgn0030610		2.94E-02	140	4	2.9%
GO:0006643 membrane lipid metabolism	CG1583	FBgn0030013		3.01E-02	81	3	3.7%
GO:0006643 membrane lipid metabolism	CG5162	FBgn0030828		3.01E-02	81	3	3.7%
GO:0006643 membrane lipid metabolism	CG8962	FBgn0025809	Platelet-activating factor acetylhydrolase alpha	3.01E-02	81	3	3.7%
GO:0015674 di- tri-valent inorganic cation transport	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	4.01E-02	38	2	5.3%
GO:0015674 di- tri-valent inorganic cation transport	CG9065	FBgn0030610		4.01E-02	38	2	5.3%
GO:0050909 perception of taste	CG15872	NA	NA	4.01E-02	38	2	5.3%
GO:0050909 perception of taste	CG7189	FBgn0035870	Gustatory receptor 66a	4.01E-02	38	2	5.3%
GO:0006814 sodium ion transport	CG15872	NA	NA	4.80E-02	42	2	4.8%
GO:0006814 sodium ion transport	CG3979	FBgn0036816	I'm not dead yet	4.80E-02	42	2	4.8%