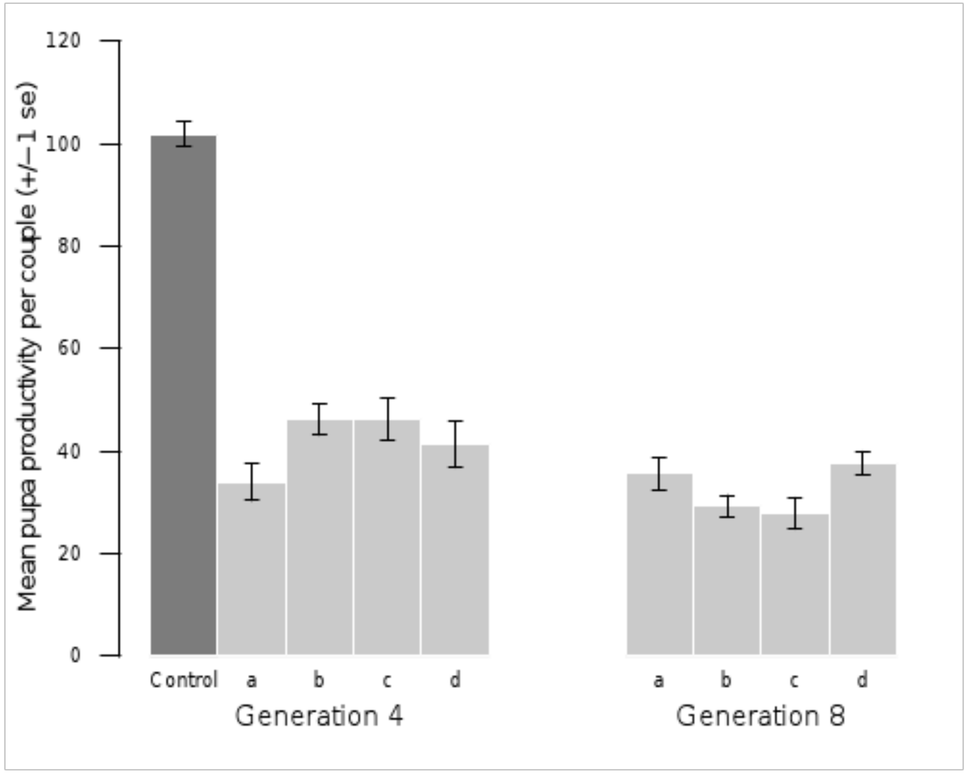

Figure S1 Mean pupa productivity for the four inbred lines and the outbred control at generations 4 and 8. At generation 4, the rate of inbreeding depression was 1.14, 1.02, 0.97 and 1.12% per 1% increased in inbreeding for lines *a*, *b*, *c* and *d*, respectively.

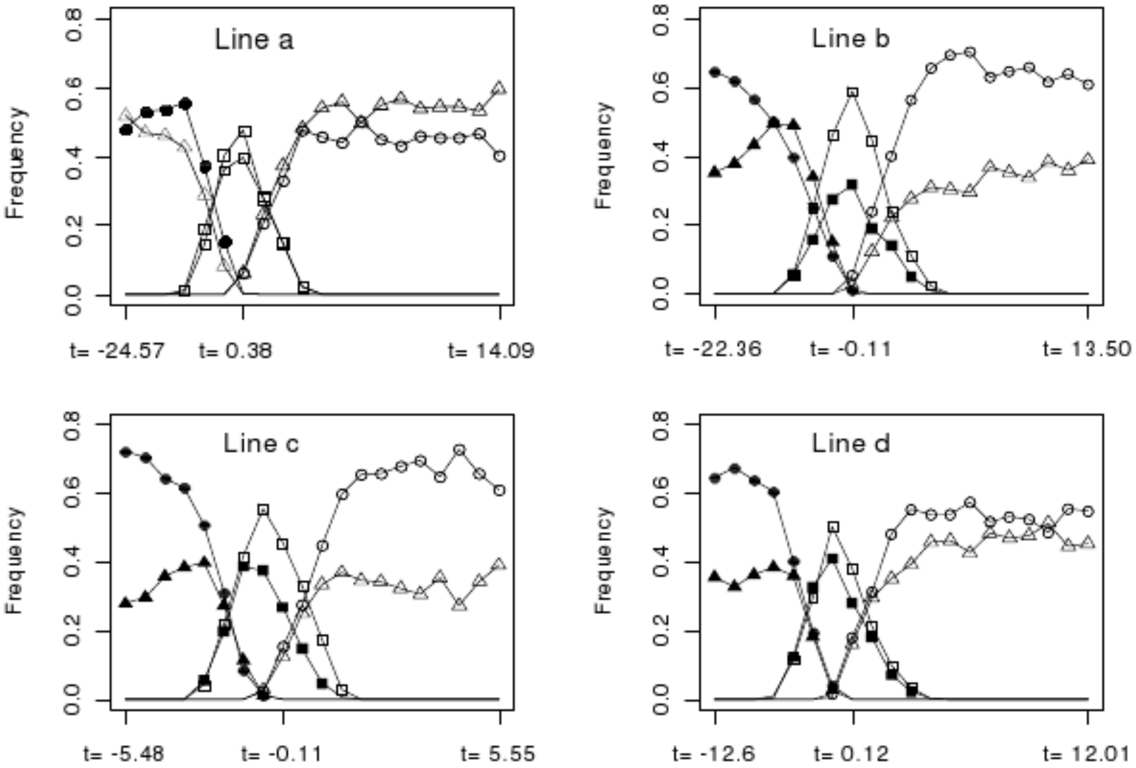

Figure S2 Relative frequencies of probe sets in each of the gene expression profiles shown in Figure 5 of the main text for each inbred line. We ranked the 9133 expressed probe sets according to their Student's *t* value in the inbreds *vs.* control test, and divided the rank in 20 tiers of size 456 (except the last one, of size 469). Thus, the right-hand part of the figure includes probes up-regulated with inbreeding, and those in the left-hand side are probes down-regulated with inbreeding.

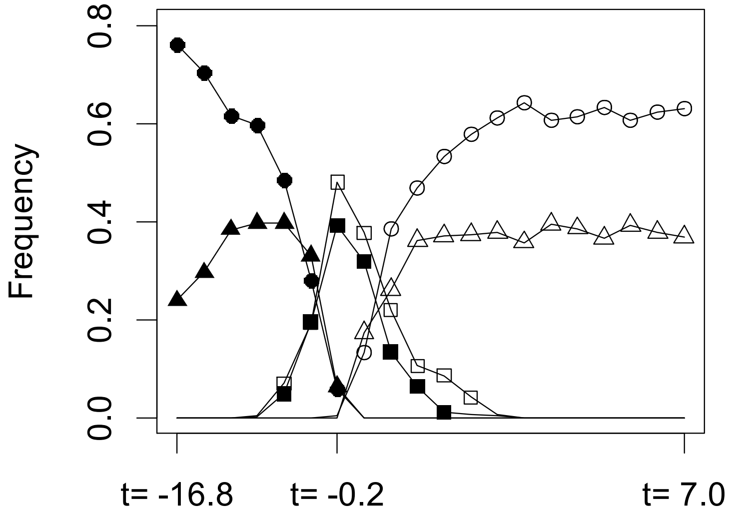

Figure S3 Relative frequencies of probe sets in each of the gene expression profiles shown in Figure 5 of the main text for each inbred line. Profiles in this figure correspond to raw gene expressions, i.e., the average of the perfect match probes in each probe set. We ranked the 9133 expressed probe sets according to their Student's *t* value in the inbreds *vs.* control test, and divided the rank in 20 tiers of size 456 (except the last one, of size 469). Thus, the right-hand part of the figure includes probes up-regulated with inbreeding, and those in the left-hand side are probes down-regulated with inbreeding.

Table S1

Category	Cluster	Classification	Term's name	Number of genes
Inbreds up-regulated, protective configuration	Cluster 1, ES: 2.25	GOTERM_BP_FAT	RNA processing	60
		KEGG_PATHWAY	Spliceosome	40
		GOTERM_CC_FAT	Small nuclear ribonucleoprotein complex	22
	Cluster 2: ES: 2.04	GOTERM_BP_FAT	RNA localization	20
		GOTERM_BP_FAT	Nucleocytoplasmic transport	19
		GOTERM_BP_FAT	mRNA export from nucleus	11
	Cluster 3: ES: 1.76	GOTERM_CC_FAT	Extracellular region	46
		UP_SEQ_FEATURE	Signal peptide	44
		SP_PIR_KEYWORDS	Glycoprotein	25
	Cluster 4, ES: 1.44	GOTERM_BP_FAT	Cell surface receptor linked signal transduction	24
		GOTERM_MF_FAT	Hormone activity	16
		GOTERM_BP_FAT	G-protein coupled receptor protein signaling pathway	11
Inbreds down-regulated, protective configuration	Cluster 1, ES: 2.36	GOTERM_BP_FAT	Phosphate metabolic process	121
		GOTERM_CC_FAT	Mitochondrion	116
		GOTERM_BP_FAT	Energy derivation by oxidation of organic compounds	55
	Cluster 2, ES: 2.03	GOTERM_MF_FAT	Nucleotide binding	149
		GOTERM_MF_FAT	ATP binding	101
		INTERPRO	Protein kinase, ATP binding site	40
	Cluster 3, ES: 1.44	GOTERM_BP_FAT	Protein amino acid phosphorylation	50
		INTERPRO	Serine/threonine protein kinase-related	35
		UP_SEQ_FEATURE	Active site:Proton acceptor	25

Table S1 (cont.)

Inbreds up-regulated, non-protective configuration	Cluster 1, ES: 1.35	SMART	JHBP	5
		INTERPRO	Hormone binding	5
		INTERPRO	Odorant binding protein	5

Cluster annotation analysis of the probe sets showing the most extreme Student’s *t* values in the test of inbreds’ *vs.* controls’ expression (1846 and 1860 probes for the positive and negative *t* values respectively), using as background all probes in the same expression pattern. The lists of functional terms shown are not exhaustive, we chose three informative and less redundant terms in each cluster. No significant clusters were found in the analysis of down-regulated probes having non-protective configurations. ES: Enrichment Score.

Table S2 Comparison with Kristensen et al gene lists

	Number of probe sets in the Kristensen et al. list	Correspon-dences in our platform	Expressed in this experiment	*Inb* effects OBS	*Inb* effects EXP	*Inb* same dir. OBS	*Inb* same dir. EXP	*Dep* effects OBS	*Dep* effects EXP	*Dep* same dir. OBS	*Dep* same dir. EXP
Fast+	60	38	35	14	14.70	13	9.8	4	5.60	2	2.80
Fast-	13	15	11	4	4.62	3	1.2	4	1.76	2	1.20
Slow+	113	76	69	42	28.98	32	29.4	12	11.4	5	8.40
Slow-	41	20	19	7	7.98	4	2.1	4	3.04	3	1.20
Joint+	9	9	8	5	3.36	4	3.5	3	1.28	2	2.10
Joint-	12	12	12	9	5.04	8	2.7	2	1.92	1	0.60
25º+	5	5	5	3	2.10	2	2.1	2	0.80	1	1.40
25º-	7	7	7	5	2.94	1	1.5	1	1.12	0	0.3
Total	**260**	**182**	**166**	**89**	**69.72**	**67**	**52.3**	**32**	**26.92**	**16**	**18**
χ^2 (7 d.f.)				5.09, P = 0.649		9.53, P = 0.217		5.73, P = 0.572		5.96, P = 0.544	

Inb and *Dep* effects for the probe sets listed as SAM-selected in the Fast and Slow inbreeding treatments and the Joint analysis in Kristensen et al. [2005] and in the 25ºC treatment in Kristensen et al. [2006]. Plus and minus signs indicate over and down regulated probe sets in the inbred samples, respectively. Because their results correspond to the older Affymetrix Drosophila Genome Array Version 1, we show the number of equivalent probe sets in our Version 2 Array (note that the equivalences were not one to one); of these, the number expressed in the current experiment; the number of *Inb* or *Dep* significant, and the number showing these effects in the same direction. The expected numbers of probe sets showing *Inb* and *Dep* effects were calculated as: number of Kristensen et al.'s SAM-selected probe sets expressed in our experiment × our overall proportion of probe sets showing *Inb* or *Dep* effects (0.42 and 0.16). The expected counts in the same direction were calculated as: number of expressed probe sets showing *Inb* or *Dep* effects x overall proportion of up or down regulated genes in our experiment (0.7 and 03 for *Inb* and 0.41 and 0.59 for *Dep*).

Table S3 Comparison with Sorensen et al. gene lists

Selected line	In Sorensen's list	Expressed in this experiment	*Inb* effects OBS	*Inb* effects EXP	*Inb* same dir. OBS	*Inb* same dir. EXP	*Dep* effects OBS	*Dep* effects EXP	*Dep* same dir. OBS	*Dep* same dir. EXP
Heat survival	94	78	28	33.12	6	-	12	12.76	5	
Starvation	230	176	74	74.73	19	22.20	20	28.80	12	11.80
Longevity	64	54	27	22.92	8	8.10	9	8.83	2	5.31
Heat knock down	21	16	4	6.79	3	2.80	8	2.62	8	3.28
Dessication	262	154	53	65.39	20	15.9	21	25.20	11	12.39
Constant 30º C	12	10	4	4.25	2	3.00	0	1.64	0	-
Combined	262	245	108	104.03	51	75.6	46	40.08	24	18.86
Goodness-of-fit χ^2			4.82, $P = 0.566$, 6 d.f.		6.35, $P = 0.273$, 5 d.f.		17.44, $P = 0.008$, 6 d.f.		8.93, $P = 0.063$, 4 d.f.	

Numbers of genes differentially expressed in the Sorensen et al. (2003) stress selection lines; number of these genes expressed in our experiment (only the counts in the *Inb* analysis lists are shown; the counts difference with the *Dep* analysis lists was never greater than two); of these, numbers showing *Inb* or *Dep* effects ($P < 0.05$ in *t* test and ANOVA respectively); of these, numbers with expression changed in the same direction as in the Sorensen's et al experiment. The expected numbers of *Inb* and *Dep* effects genes were calculated as: number of Sorensen's et al. significant genes expressed in this experiment × our overall proportion of genes showing *Inb* or *Dep* effects (0.42 and 0.16). The expected counts in the same direction were calculated using the number of expressed genes with *Inb* or *Dep* effects × overall proportion of up- or down-regulated genes in our experiment (0.7 and 0.3 for *Inb* and 0.41 and 0.59 for *Dep*). All genes in each selected line list showed changes in the same direction, with the exception of Heat survival, for which we calculated no expected direction changes. Combined: genes differentially expressed in a joint analysis of all selected lines versus controls in Sorensen's et al. experiment.

File S1

Lists of probe sets showing (FDR<0.1) ***Inb***, ***Lin***, ***Dep*** **and** ***Lin*** **x** ***Dep*** **effects**

****

Inb Effects UP regulated FDR < 0.1

1635494_at
1633048_at
1627088_at
1631523_at
1623935_at
1638090_at
1624914_at
1633844_at
1629050_at
1637290_at
1628639_at
1640956_at
1635008_at
1630761_at
1627529_at
1627419_at
1625828_at
1636885_at
1638742_at
1640979_at
1634935_a_at
1640144_at
1629014_s_at
1623018_at
1640157_at
1623900_a_at
1630516_at
1623521_at
1626266_at
1627312_at
1627667_at
1634243_a_at
1629101_a_at
1639914_at
1637390_at
1638827_at
1639262_at
1628020_at
1628657_at
1633586_at
1641502_a_at
1636764_at
1631246_at
1632259_at
1638887_a_at
1636856_at
1639108_at
1626605_at
1633357_at
1624079_a_at
1641434_at
1623327_at
1640221_at
1632908_s_at
1633005_at
1623866_at
1631290_at
1634529_at
1633363_at
1635251_at
1623355_at
1637567_at
1629061_s_at
1629771_at
1623191_at
1626789_at
1631099_at
1639528_at
1634551_at
1627631_s_at
1628006_at
1635088_at
1626699_at
1628814_s_at
1638166_at
1629205_at
1640230_at
1632298_s_at
1623335_a_at
1636660_at
1628376_x_at
1633410_at
1631173_at
1635848_at
1625125_at
1633613_at
1635318_at
1639188_at
1625503_at
1634207_at
1631876_at
1634687_at
1625367_at
1628599_at
1639932_at
1636108_at

1625315_at
1637063_at
1636888_a_at
1637754_at
1630795_at
1629977_at
1628831_at
1636482_at
1639981_at
1638585_at
1637160_at
1635935_at
1626051_at
1628719_at
1632007_at
1627489_a_at
1638654_at
1637367_at
1623675_at
1628969_s_at
1640520_at
1625763_at
1636526_at
1630975_at
1628338_at
1641491_at
1630831_at
1632452_at
1639563_at
1640950_at
1637667_at
1639401_at
1628271_at
1635183_at
1635030_at
1633283_at
1630299_at
1640158_at
1641567_at
1641718_at
1627119_at
1640424_at
1638193_at
1623659_at
1623250_at
1629220_at
1638164_at
1632274_at
1630574_at
1634384_at
1639048_a_at
1641123_at
1624130_at
1632396_at
1625410_at
1623599_at
1640356_a_at
1636343_at
1636950_at
1630049_at
1627124_at
1636804_at
1624354_at
1628884_at
1631813_at
1636842_at
1627773_a_at
1631837_at
1628505_at
1631816_at
1634180_s_at
1637462_at
1630808_at
1641259_at
1629222_at
1636705_at
1641513_at
1638161_at
1634854_at
1633549_s_at
1624986_at
1634664_at
1632917_at
1640689_a_at
1638167_at
1632067_at
1639397_at
1634731_at
1638630_at
1630845_at
1634157_at
1627595_at
1629662_at
1627062_s_at
1637432_at
1629942_at
1631775_at
1627590_at
1639850_at
1628567_at
1623194_at
1633639_at
1636929_at
1638256_at
1632689_at
1627117_a_at
1637291_at
1638481_at
1640400_at
1635649_at
1623298_at
1636220_at
1627380_at
1635945_at
1625634_at
1637940_s_at
1624057_at
1627327_at
1626263_at
1641234_at
1627664_a_at
1634817_at
1623989_at
1631719_at
1636131_at
1623076_at

1641552_at
1627634_at
1641584_at
1635744_at
1631381_at
1632490_at
1623105_at
1625962_at
1631729_at
1623430_at
1631674_at
1627330_at
1628446_at
1628560_at
1626785_at
1636912_at
1641454_at
1627897_at
1631212_at
1641201_at
1634591_at
1635137_a_at
1630557_at
1637300_at
1627465_at
1640161_at
1628514_at
1636420_at
1640249_at
1635506_at
1632752_at
1635086_at
1631390_at
1640103_s_at
1637799_at
1628883_at
1624074_at
1641371_at
1631493_at
1634436_at
1635542_at
1635283_at
1625260_at
1638038_at
1632721_at
1638516_s_at
1623481_at
1639052_a_at
1635530_at
1627027_at
1624090_at
1625430_at
1627609_at
1628572_s_at
1636129_s_at
1629518_at
1640056_at
1641137_at
1634542_at
1641373_at
1627002_at
1624263_at
1633812_at
1634849_at
1631660_at
1632958_a_at
1632515_a_at
1638342_at
1627817_at
1628611_at
1638455_at
1632391_at
1627399_at
1628610_at
1623906_at
1630797_at
1639273_s_at
1627939_a_at
1636174_at
1636486_at
1630528_at
1624186_at
1632540_at
1625231_at
1637224_at
1626203_at
1635098_a_at
1624152_at
1630214_a_at
1625840_at
1631351_s_at
1634055_at
1631787_at
1640194_a_at
1627782_at
1625963_at
1623384_at
1638233_at
1632828_at
1630640_at
1626909_at
1628806_at
1625477_a_at
1632551_at
1631541_at
1633961_s_at
1623453_at
1633861_at
1638774_at
1631827_at
1637717_at
1625058_at
1634569_at
1637571_at
1641108_at
1624468_a_at
1626557_at
1626350_at
1639046_at
1634449_at
1624935_at
1640748_at
1635608_at
1625512_s_at
1626366_at
1637797_at

1625338_at
1626240_s_at
1635151_at
1624180_at
1636255_s_at
1636694_at
1640246_at
1634552_at
1625466_at
1641479_at
1634077_at
1629578_at
1631479_at
1631472_at
1630006_at
1636491_at
1623793_at
1638724_at
1640440_at
1625680_a_at
1640963_at
1630375_at
1636407_at
1640906_at
1633730_at
1637485_at
1634940_at
1641084_at
1627822_at
1630170_at
1626173_at
1632212_at
1633951_at
1632683_s_at
1630503_at
1631971_at
1625764_at
1629375_at
1634107_at
1641071_at
1625837_at
1631017_at
1626831_at
1630750_at
1627087_at
1630057_at
1634507_s_at
1627495_at
1640066_at
1629620_s_at
1637262_at
1626724_at
1624032_at
1638576_at
1638468_at
1634779_at
1634208_a_at
1636488_at
1632565_at
1623045_at
1623244_at
1628103_at
1636246_a_at
1640977_at
1634583_s_at
1634647_at
1637084_at
1640746_at
1641160_s_at
1623239_at
1633292_a_at
1631817_a_at
1640653_at
1631127_at
1628986_at
1634909_at
1632630_at
1628272_a_at
1626568_at
1635712_at
1635637_at
1626653_a_at
1636153_at
1639857_at
1630763_at
1635356_at
1636217_at
1628714_at
1635365_at
1629756_at
1635875_at
1625147_at
1638884_at
1629309_at
1633958_at
1630619_at
1629432_at
1628041_a_at
1637249_at
1641428_at
1631749_at
1623702_at
1638248_at
1630208_at
1628682_at
1638036_at
1633381_at
1631228_a_at
1629209_at
1639170_at
1641168_s_at
1625002_a_at
1634575_at
1632142_at
1640884_at
1640458_at
1640399_at
1641654_a_at
1627068_at
1627464_at
1636508_at
1632343_at
1634257_at
1637164_at
1635968_at
1640006_at

1635892_at
1628161_at
1626180_at
1638070_at
1638179_at
1640101_at
1638970_at
1628175_at
1628818_at
1632984_s_at
1639357_at
1641420_s_at
1635981_a_at
1635931_at
1641529_s_at
1635028_s_at
1637265_at
1628088_at
1628785_at
1638763_at
1632222_a_at
1623643_s_at
1639415_at
1637470_at
1626783_at
1638830_at
1632089_at
1632438_at
1630467_a_at
1631684_at
1623546_at
1633857_at
1633675_at
1639731_at
1632772_at
1633915_at
1638120_at
1632389_at
1628784_at
1623852_at
1638305_at
1626883_at
1634070_at
1635130_a_at
1624150_at
1623268_a_at
1629733_at
1624668_s_at
1625169_at
1641357_at
1625589_at
1635343_a_at
1626414_at
1627377_at
1636611_at
1626499_at
1639359_at
1630398_at
1626345_at
1624292_a_at
1640315_at
1641714_at
1626929_at
1635049_at
1634594_at
1626986_at
1632370_at
1637776_at
1635450_a_at
1635344_at
1638414_a_at
1641288_at
1624113_at
1631533_at
1629270_at
1625792_s_at
1641430_at
1635437_at
1628924_a_at
1625573_at
1631604_at
1635223_at
1637955_a_at
1640329_s_at
1633382_s_at
1641116_at
1640480_at
1639153_at
1627060_s_at
1638297_at
1623425_at
1632504_at
1626328_at
1635593_at
1634412_at
1626811_at
1629158_at
1637053_at
1640700_at
1641498_at
1625426_at
1623733_at
1629036_at
1641268_at
1628483_at
1626401_at
1628264_a_at
1625565_at
1630805_at
1638680_at
1625276_a_at
1636273_at
1625257_s_at
1631171_at
1641455_at
1623704_at
1633023_at
1635796_a_at
1638938_at
1633054_at
1630410_at
1633523_at
1638157_at
1624484_a_at
1640138_at
1641280_at

1622965_s_at
1638237_at
1629718_at
1638265_s_at
1632813_at
1638889_at
1632923_at
1631766_at
1636773_a_at
1627845_at
1634193_at
1629868_s_at
1624364_at
1636606_at
1623154_a_at
1636740_at
1624482_at
1641699_at
1640289_a_at
1641623_at
1639632_at
1632111_at
1641196_at
1638981_at
1638238_at
1632263_at
1625849_at
1640666_at
1637332_at
1624260_at
1635603_at
1627031_at
1631115_at
1640346_at
1638549_at
1623478_at
1638312_at
1625598_at
1636769_at
1639205_s_at
1629241_at
1625444_at
1631149_s_at
1625268_at
1632087_at
1625387_s_at
1637226_at
1637727_at
1636451_a_at
1635836_at
1635299_at
1631821_at
1632711_at
1635203_at
1639349_at
1640147_at
1640263_at
1641741_a_at
1634697_at
1629759_at
1637752_a_at
1641359_at
1636884_s_at
1629136_at
1631227_at
1629221_at
1637773_s_at
1636550_at
1634560_at
1635840_s_at
1631509_a_at
1633247_at
1638765_at
1624423_at
1637605_s_at
1631191_at
1634563_at
1637444_s_at
1637299_s_at
1625165_at
1641369_at
1626552_at
1623166_at
1639075_a_at
1630344_at
1626324_at
1624656_s_at
1630754_at
1622935_at
1623564_at
1633566_at
1633031_at
1632433_at
1633743_at
1625833_at
1635915_at
1633430_at
1630820_at
1640944_at
1624390_a_at
1629777_at
1633822_at
1622948_at
1629406_at
1630729_at
1640078_at
1627449_at
1631784_at
1632954_at
1633082_at
1625363_at
1635342_at
1630993_at
1625480_at
1627666_at
1627393_at
1635126_a_at
1624271_at
1640069_at
1629537_s_at
1640236_at
1632313_at
1625244_at
1636806_at
1639019_s_at
1636722_at

1622907_at
1639337_at
1631369_at
1632383_at
1638339_at
1624836_at
1637520_at
1639313_at
1633215_at
1627982_at
1632517_at
1641193_s_at
1637993_at
1629109_at
1640793_at
1641541_a_at
1635704_at
1634541_a_at
1629525_at
1633584_at
1624782_a_at
1631581_at
1636693_at
1634300_at
1631723_at
1636353_s_at
1630351_at
1629834_at
1637015_s_at
1635031_s_at
1638496_at
1634427_at
1637852_at
1634177_a_at
1640191_a_at
1638146_at
1634518_at
1629466_at
1627015_at
1626204_at
1641372_at
1624193_s_at
1629055_a_at
1624195_at
1634442_at
1626949_at
1638453_at
1630519_at
1630746_at
1624635_at
1626371_at
1630781_at
1634217_s_at
1634029_at
1633322_at
1626769_s_at
1640826_at
1639440_at
1637402_at
1629124_at
1631671_at
1624510_at
1630527_at
1634437_at
1638750_at
1633609_at
1636732_at
1625934_at
1627577_at
1640633_s_at
1627794_a_at
1640239_at
1623824_at
1632931_at
1636256_s_at
1635645_at
1630565_at
1630949_s_at
1624795_at
1634048_a_at
1623449_at
1631446_at
1624357_at
1629655_at
1623838_s_at
1626392_s_at
1625806_at
1640660_at
1639367_a_at
1626586_at
1641157_at
1637125_at
1627961_a_at
1634324_at
1638862_at
1638343_at
1634143_at
1639818_s_at
1625129_at
1636505_at
1633349_at
1633760_at
1625624_at
1632392_s_at
1627676_at
1630861_at
1630550_a_at
1628745_at
1638101_at
1639302_at
1624372_at
1630881_at
1626918_at
1636291_at
1626222_at
1636788_a_at
1633646_at
1625032_s_at
1637632_at
1638354_at
1633060_at
1634240_at
1623902_at
1636600_a_at
1625996_s_at
1631948_s_at

1627824_at
1624145_a_at
1636243_at
1634289_at
1636358_a_at
1641187_at
1633716_at
1636632_at
1641062_at
1637309_a_at
1627850_at
1630661_at
1638078_at
1630844_at
1635218_at
1630144_at
1624742_a_at
1625688_at
1624571_s_at
1637997_at
1633617_at
1640121_a_at
1630917_at
1637715_a_at
1630743_at
1627403_s_at
1625845_s_at
1623456_at
1639845_at
1636919_at
1633059_at
1627546_at
1639398_at
1634012_at
1627116_at
1623090_at
1636958_s_at
1639430_at
1633700_at
1623673_at
1634750_at
1630672_at
1631194_at
1638562_a_at
1634957_at
1628552_at
1632420_at
1626435_at
1636175_a_at
1635740_at
1637982_at
1623650_a_at
1640957_at
1627662_at
1634164_at
1623809_s_at
1636051_at
1629367_at
1625531_at
1627505_at
1637716_a_at
1640351_s_at
1623985_at
1625212_at
1641429_at
1624485_at
1623491_at
1635280_at
1639544_at
1636089_at
1637946_at
1633346_at
1630309_s_at
1636967_a_at
1633980_at
1625571_at
1641120_at
1630991_at
1625773_at
1636249_at
1629930_s_at
1627934_at
1624156_at
1635492_at
1627073_a_at
1625134_at
1632545_s_at
1637608_at
1625490_at
1639646_at
1627938_at
1641340_s_at
1639067_at
1632491_at
1623306_at
1639972_at
1628637_at
1632180_at
1639264_at
1638844_s_at
1632810_at
1633503_at
1631546_at
1624555_at
1636021_at
1630745_at
1624159_at
1630216_at
1630987_at
1637298_at
1636777_at
1638415_at
1629960_s_at
1624950_a_at
1623934_at
1631370_at
1630568_at
1640178_at
1632728_at
1627990_at
1631226_at
1629762_at
1628299_at
1632548_a_at
1623487_at
1628723_at

1626028_at
1639966_a_at
1625295_at
1634577_s_at
1633261_a_at
1626300_at
1629541_at
1635389_s_at
1633380_at
1638216_at
1634429_at
1623794_at
1627349_at
1624028_at
1622930_a_at
1635878_s_at
1631520_at
1629598_at
1634383_a_at
1639867_at
1636533_at
1630318_at
1625266_at
1640691_at
1635394_at
1624550_at
1627827_a_at
1640298_at
1627405_at
1623641_at
1626309_at
1629716_a_at
1627620_at
1626844_at
1634311_at
1640698_at
1640683_at
1632233_at
1637956_s_at
1626313_at
1627562_at
1624700_a_at
1625733_at
1627516_at
1623609_at
1625000_a_at
1638147_at
1638804_a_at
1637825_at
1625474_s_at
1638385_at
1625345_at
1638808_at
1637676_at
1638236_at
1628632_at
1632393_at
1630997_at
1624614_at
1638869_at
1636211_at
1626846_s_at
1632410_at
1638974_at
1630131_at
1623553_a_at
1628167_s_at
1626382_s_at
1639553_at
1626117_at
1639324_at
1633830_at
1640202_at
1636287_at
1625017_at
1629472_s_at
1628389_at
1634264_at
1632254_a_at
1638272_at
1626579_at
1636607_at
1628490_at
1623404_at
1639180_at
1634072_s_at
1628468_at
1625700_a_at
1635654_at
1626055_at
1638677_at
1637422_at
1634848_at
1631045_a_at
1634527_s_at
1634625_at
1639354_at
1628798_at
1638326_at
1638675_at
1626075_at
1635581_at
1633492_at
1641317_at
1635670_at
1622962_a_at
1639272_at
1641494_at
1625436_at
1636883_s_at
1624788_at
1641336_at
1624008_at
1641105_at
1634558_s_at
1627959_a_at
1633139_at
1635135_at
1630438_at
1626880_at
1636644_at
1637269_at
1629610_at
1638001_a_at
1640511_at
1639087_at

1635636_at
1623875_at
1633536_at
1625112_at
1632663_at
1638849_a_at
1627646_at
1635468_a_at
1626823_a_at
1633540_at
1638735_at
1629053_at
1625242_at
1630635_s_at
1624670_at
1625393_s_at
1624204_at
1640974_a_at
1625185_at
1628187_s_at
1625006_at
1631873_at
1638857_at
1633210_at
1623009_at
1641023_at
1627165_a_at
1632808_at
1628630_at
1635230_at
1640540_at
1634966_a_at
1631652_at
1634101_at
1626373_at
1628828_s_at
1638528_at
1628779_a_at
1635470_at
1636354_at
1625522_at
1626606_at
1626718_at
1630080_at
1624798_s_at
1623363_at
1634408_at
1624080_s_at
1626835_at
1628057_at
1640577_a_at
1634713_at
1628615_at
1625905_at
1623387_at
1633260_at
1632322_at
1633765_at
1628424_at
1635016_at
1631637_a_at
1626325_a_at
1630325_at
1638104_a_at
1628494_a_at
1633163_at
1630623_a_at
1628309_at
1631842_at
1639599_at
1638669_at
1634253_at
1641704_at
1638927_at
1628450_at
1629563_at
1627623_s_at
1641401_s_at
1641606_s_at
1632472_s_at
1632245_a_at
1641669_a_at
1639424_at
1638464_a_at
1640509_s_at
1626110_a_at
1639016_at
1638208_at
1624489_a_at
1626678_at
1623722_at
1631897_s_at
1634809_s_at
1629420_at
1633091_at
1627423_at
1625193_at
1638821_a_at
1640566_at
1640744_a_at
1636781_at
1625646_at
1635831_at
1641244_at
1638247_at
1626738_at
1634696_at
1639604_at
1632642_a_at
1628418_at
1623955_at
1635983_a_at
1628539_at
1627713_at
1624572_a_at
1634970_at
1626886_at
1635207_at
1636541_at
1639230_at
1638257_at
1627738_a_at
1625217_at
1623847_at
1631192_at
1623046_at

1623629_at
1632471_at
1629952_at
1640657_at
1639809_at
1624503_at
1623716_at
1632654_at
1636990_at
1637578_at
1636996_at
1635165_a_at
1639485_at
1632875_at
1637742_at
1634943_at
1641664_at
1634299_at
1632342_a_at
1628133_at
1627415_at
1623027_s_at
1623318_s_at
1635111_s_at
1640738_a_at
1639388_a_at
1631636_at
1626439_at
1626981_s_at
1633789_at
1625876_at
1639600_at
1636980_s_at
1623820_at
1627138_at
1638819_at
1631627_at
1637429_at
1634176_a_at
1632400_at
1636298_at
1640768_at
1626360_at
1634641_a_at
1628648_at
1624996_at
1626524_at
1631696_s_at
1628456_at
1632743_a_at
1627699_at
1627448_at
1633266_at
1623020_at
1629520_at
1631029_at
1623108_at
1639853_at
1633664_at
1635580_at
1626649_s_at
1628731_s_at
1625744_at
1627674_at
1628869_s_at
1637085_at
1636197_at
1630011_at
1635683_at
1631776_at
1623331_at
1639626_at
1626818_at
1625756_at
1630289_at
1628213_s_at
1629623_at
1624222_s_at
1633338_at
1627655_at
1637002_at
1624318_at
1637403_at
1633364_at
1635527_at
1629161_at
1632487_at
1632336_at
1634320_at
1641000_a_at
1624983_s_at
1627343_a_at
1632292_at
1633003_at
1639691_at
1632928_at
1641659_s_at
1640052_at
1624474_at
1627958_at
1640489_at
1631223_at
1632956_at
1641232_s_at
1627171_at
1635198_at
1637282_at
1635301_at
1629279_at
1625027_a_at
1626577_at
1634604_at
1630112_at
1633399_at
1624337_at
1628249_at
1638270_at
1627184_at
1639212_a_at
1625892_a_at
1633448_at
1623635_at
1640644_at
1627325_at
1634130_a_at
1629088_at

1636206_at
1626049_at
1624037_s_at
1626788_a_at
1630800_s_at
1639520_at
1625414_at
1640005_at
1632024_at
1639286_s_at
1635768_at
1635799_at
1623688_at
1625166_at
1640669_at
1640695_at
1626436_at
1626458_at
1640452_at
1641424_at
1633826_at
1638919_at
1637325_at
1637660_at
1640058_at
1637423_at
1640943_at
1641342_at
1627627_at
1632161_at
1632696_at
1638196_at
1627900_at
1637576_s_at
1627739_at
1640487_at
1634000_a_at
1638310_at
1627323_at
1630900_at
1628486_a_at
1637497_at
1635250_at
1640418_at
1626817_at
1636887_s_at
1625549_at
1633284_at
1637494_at
1626209_a_at
1623508_at
1640429_a_at
1624738_at
1636628_at
1630073_at
1628960_s_at
1631158_at
1623428_at
1623569_at
1639178_s_at
1625464_at
1626068_at
1639060_at
1623797_at
1640549_at
1638522_at
1638030_at
1629180_at
1629008_at
1635185_at
1636797_at
1631278_a_at
1631266_a_at
1635314_at
1639094_at
1639625_at
1639389_at
1630405_at
1629444_at
1636574_s_at
1622944_at
1628279_s_at
1635442_a_at
1636623_at
1624386_at
1631116_at
1631675_a_at
1638126_at
1635668_at
1633791_at
1640535_s_at
1628173_at
1632103_at
1629480_at
1638501_at
1632652_s_at
1629039_at
1638509_at
1630514_at
1628040_at
1626514_at
1639256_at
1635821_at
1634953_at
1625344_at
1624198_at
1641419_at
1638822_at
1638321_s_at
1626507_at
1639761_s_at
1625375_at
1627861_s_at
1631618_s_at
1626169_at
1631137_at
1627007_at
1634528_at
1632586_at
1622924_at
1626476_at
1629941_a_at
1628351_at
1626739_s_at
1633565_at
1631973_at

1629821_at
1624801_at
1628882_at
1623724_at
1624840_at
1641493_at
1634481_at
1629428_at
1634593_at
1630543_at
1641508_s_at
1631595_at
1639102_at
1624285_at
1640898_at
1629106_at
1633602_at
1630778_at
1631822_at
1629967_s_at
1630177_at
1633308_at
1634553_at
1641146_at
1634002_at
1637747_s_at
1635588_at
1640251_s_at
1633568_s_at
1636925_at
1629426_s_at
1635723_s_at
1627526_at
1638714_at
1640504_at
1640243_at
1630877_a_at
1640118_at
1625026_at
1637205_at
1622920_at
1640845_at
1630916_at
1639895_at
1641488_at
1632078_at
1631561_s_at
1640227_at
1636986_at
1632533_at
1625947_at
1640421_at
1633129_at
1634121_at
1631648_at
1636738_at
1627155_s_at
1628972_at
1630422_at
1639328_at
1632731_at
1628123_at
1641650_at
1625891_at
1639025_at
1629896_at
1640781_a_at
1624883_at
1629176_at
1639890_at
1625458_a_at
1628201_at
1641212_a_at
1638847_s_at
1633076_at
1624345_a_at
1631362_at
1629159_at
1627183_at
1635336_at
1628976_at
1624297_at
1625078_at
1629350_at
1635751_at
1633047_at
1631224_at
1625657_at
1623256_at
1624179_at
1625530_at
1629903_at
1624395_at
1627080_at
1637260_at
1624101_at
1624888_at
1627742_at
1640803_at
1637027_s_at
1636459_s_at
1639480_at
1628345_at
1634942_at
1637203_at
1630115_at
1632846_at
1635978_at
1637489_at
1638511_at
1628937_s_at
1636770_at
1638678_at
1630645_at
1630162_at
1629778_s_at
1635294_at
1630792_at
1623111_at
1633383_at
1624141_at
1641285_at
1632703_at
1632341_at
1636040_at
1634839_at

1641223_at
1623272_at
1623605_a_at
1638020_at
1635271_at
1627768_at
1628292_s_at
1624170_at
1633819_at
1624515_at
1623956_at
1641318_at
1632198_at
1630637_s_at
1624514_at
1623817_at
1639265_at
1638292_at
1635870_at
1641381_s_at
1627048_at
1636210_at
1633418_at
1632701_at
1641624_at
1635084_at
1632272_a_at
1641469_at
1634977_at
1634980_s_at
1633050_at
1640244_at
1635076_at
1629251_at
1638853_at
1639374_s_at
1623806_at
1626022_at
1637501_a_at
1624975_at
1626304_at
1630437_s_at
1626680_at
1636379_a_at
1632435_at
1629084_at
1634377_at
1628834_a_at
1624993_at
1627206_at
1632184_at
1637316_at
1639694_s_at
1627249_a_at
1628558_at
1623271_a_at
1637274_at
1622983_a_at
1623281_s_at
1638580_at
1638007_at
1641689_at
1624496_at
1635972_at
1640846_at
1640053_at
1633224_at
1630915_at
1626230_s_at
1624815_at
1640544_a_at
1627759_at
1638645_at
1624777_at
1637547_at
1626170_at
1635200_at
1631513_at
1626942_at
1623940_at
1628131_at
1637992_at
1634419_at
1640997_at
1624239_at
1641017_at
1631251_at
1641720_at
1641012_at
1629295_at
1636793_at
1639908_a_at
1635761_at
1633749_at
1639159_at
1631466_at
1627499_at
1630268_at
1639727_at
1637928_at
1625839_at
1622941_at
1624543_s_at
1630242_at
1628290_s_at
1640855_at
1637319_at
1625755_at
1624257_at
1629955_at
1636767_at
1623030_at
1634919_at
1625974_at
1638367_at
1625829_a_at
1628764_at
1626023_at
1624246_s_at
1633751_at
1637032_at
1623471_s_at
1632759_at
1637475_at
1630952_at
1623796_at

1630403_s_at
1627401_at
1635687_at
1634194_at
1636141_s_at
1629430_s_at
1626039_at
1628061_at
1631954_at
1626720_at
1635939_a_at
1635060_at
1631200_at
1630530_at
1637559_at
1627669_at
1627314_s_at
1631455_at
1623088_at
1640699_at
1623247_at
1634464_at
1639663_at
1635548_s_at
1628521_at
1624406_at
1623645_a_at
1635040_a_at
1638658_at
1634278_at
1632878_at
1632303_a_at
1625989_at
1624092_at
1630206_at
1641626_at
1639406_at
1630882_s_at
1640177_at
1638313_at
1632710_s_at
1641655_at
1633926_at
1636002_at
1628241_at
1625783_at
1625948_at
1639654_at
1632271_a_at
1623551_at
1629809_at
1635079_at
1624894_s_at
1624763_at
1637121_at
1639530_at
1629449_at
1623440_at
1625233_at
1625978_at
1639211_at
1622998_a_at
1637926_s_at
1632207_a_at
1639579_s_at
1632415_s_at
1631512_at
1627642_at
1636314_at
1631214_at
1639641_at
1624253_at
1633576_s_at
1623826_at
1632350_at
1626987_at
1633560_at
1624736_a_at
1635666_at
1633012_at
1632513_at
1637479_at
1632140_at
1627453_s_at
1634808_at
1637959_at
1623015_at
1637275_a_at
1637240_a_at
1639882_at
1633053_at
1634601_at
1625632_at
1638392_at
1636774_at
1640915_at
1636653_at
1641178_s_at
1627709_at
1625835_at
1631267_at
1635463_at
1623102_at
1631268_at
1638173_s_at
1637564_a_at
1634159_s_at
1628634_at
1640145_at
1623495_at
1641370_s_at
1624010_a_at
1640184_at
1626600_at
1628792_at
1629470_at
1632611_at
1629149_at
1638319_at
1630141_at
1637735_at
1636829_at
1631208_at
1634146_at
1626853_a_at
1628658_at

1638591_at
1638690_at
1626217_at
1627545_at
1639442_a_at
1632374_at
1628930_at
1636858_at
1641605_at
1641298_at
1629285_at
1629698_at
1623747_at
1627154_at
1628353_at
1637581_at
1636005_at
1630363_at
1629918_at
1624699_s_at
1634158_at
1626702_at
1634245_at
1630492_at
1629476_at
1635512_at
1640848_at
1634258_at
1636708_at
1640446_s_at
1633106_at
1633592_a_at
1637320_at
1625872_at
1641025_at
1640984_s_at
1632873_at
1629607_at
1641568_a_at
1638469_s_at
1631088_at
1631139_a_at
1636245_at
1630440_at
1640335_at
1638670_a_at
1622980_at
1626580_at
1635989_at
1626011_at
1631122_at
1640920_at
1640762_at
1629949_at
1623540_at
1631180_at
1638485_s_at
1625252_s_at
1624194_a_at
1629954_at
1640610_at
1626801_at
1624858_at
1641734_at
1639638_a_at
1636336_at
1629474_at
1636735_s_at
1636036_at
1624697_at
1636190_at
1630823_at
1622933_at
1628804_at
1637617_at
1641214_at
1629440_at
1629089_a_at
1624596_at
1631712_at
1627581_at
1634531_at
1629879_at
1637101_at
1634298_at
1628547_at
1629939_a_at
1638153_at
1632026_at
1641252_at
1634700_at
1637466_at
1640333_at
1626112_at
1626486_at
1636615_at
1637798_at
1633256_at
1641671_at
1624693_at
1635925_at
1635517_at
1634390_s_at
1629405_s_at
1624848_at
1626988_at
1624518_at
1641124_at
1632364_at
1633810_at
1627831_at
1638317_at
1634124_at
1630233_at
1640656_a_at
1623479_at
1639509_at
1637941_at
1630932_at
1631640_a_at
1625836_at
1632503_at
1640411_at
1628826_at
1630981_at
1638609_s_at

1634798_at
1625044_at
1631861_at
1638614_at
1640981_at
1637618_at
1635221_at
1637554_a_at
1640080_at
1635187_s_at
1640009_at
1629391_at
1627685_a_at
1639527_at
1630989_a_at
1638942_at
1640794_at
1625748_s_at
1633709_at
1640339_at
1629787_at
1625995_a_at
1629602_at
1633253_s_at
1639769_at
1635370_at
1627788_at
1626475_at
1634117_at
1640887_at
1639071_a_at
1630958_at
1632318_at
1637313_at
1627132_at
1633008_at
1635330_at
1625728_at
1624718_a_at
1628928_s_at
1629208_at
1624050_at
1627837_at
1627977_at
1624887_at
1631739_at
1630982_at
1636122_at
1636631_at
1629853_at
1631919_at
1636073_at
1626733_at
1638997_at
1624603_at
1625679_at
1636809_at
1634879_at
1636173_s_at
1628593_at
1637056_s_at
1634740_at
1628963_at
1629673_at
1628887_a_at
1633649_s_at
1633209_s_at
1633856_at
1623816_s_at
1639228_at
1631196_at
1623844_at
1638564_at
1639588_at
1638841_at
1635278_at
1636163_at
1626164_at
1628044_at
1626787_s_at
1632197_at
1630498_at
1628874_at
1640824_at
1630431_s_at
1631258_at
1638476_s_at
1633554_at
1636657_at
1625860_s_at
1623235_at
1633019_a_at
1637192_at
1627770_at
1638995_at
1627527_s_at
1632894_at
1632771_at
1630732_at
1626092_at
1631690_a_at
1625572_s_at
1628620_at
1635621_at
1635524_at
1623861_at
1633277_at
1637682_at
1636231_at
1633596_at
1624690_at
1634196_at
1636442_at
1640198_at
1624692_at
1634858_s_at
1627437_at
1627996_a_at
1627657_at
1628922_s_at
1640127_at
1633761_at
1624599_at
1623312_s_at
1630547_at
1623329_at

1636935_at
1629552_at
1639013_at
1634074_a_at
1635987_at
1625855_at
1637829_at
1636583_at
1628700_at
1627868_at
1630817_s_at
1630912_at
1631907_at
1639539_at
1630740_at
1637648_at
1631751_at
1628278_at
1637775_at
1634430_at
1633000_a_at
1623706_at
1637923_at
1624137_at
1629906_s_at
1629811_at
1629288_s_at
1638600_at
1639901_a_at
1623612_at
1633117_at
1624613_at
1626412_at
1629692_at
1641721_a_at
1633191_at
1641648_at
1635487_at
1637893_at
1641629_at
1631677_at
1635862_at
1627144_at
1640961_at
1641481_at
1629349_at
1625817_at
1633134_at
1639665_at
1628925_at
1624797_at
1633755_at
1633731_at
1632519_at
1629820_at
1636351_at
1630241_at
1623109_at
1628559_at
1633650_at
1630940_at
1634630_at
1629606_at
1627307_at
1625856_at
1641549_at
1631392_at
1638801_at
1634304_a_at
1632200_s_at
1629195_at
1624684_at
1632189_at
1633213_at
1634769_at
1633964_at
1634262_s_at
1632847_at
1628529_a_at
1628920_at
1635513_at
1633886_at
1629705_at
1625725_at
1629144_at
1630086_at
1638431_at
1630051_at
1636014_at
1636587_at
1626563_at
1641294_a_at
1631030_at
1634714_at
1634720_at
1628216_at
1623128_at
1638571_at
1632816_at
1627661_at
1626156_at
1632510_at
1639288_at
1635428_at
1627640_at
1625177_at
1639688_at
1633911_a_at
1633439_at
1633940_at
1623759_at
1624669_at
1636709_at
1639198_at
1635447_at
1623754_s_at
1626251_at
1632138_at
1637216_at
1636498_at
1628148_at
1631645_at
1632182_at
1637511_at
1632955_at
1631058_s_at

1635659_at
1627142_at
1640150_s_at
1625109_at
1626701_at
1626651_at
1640638_at
1629928_a_at
1633254_at
1636198_at
1631829_at
1638403_at
1641335_at
1628578_at
1636470_at
1630992_at
1633908_at
1629369_at
1631105_at
1640862_a_at
1625814_at
1624549_at
1629509_s_at
1629799_at
1640357_at
1630468_at
1633379_s_at
1626213_a_at
1627123_at
1628561_at
1623147_at
1623839_at
1635907_at
1624153_at
1637807_at
1633634_at
1638192_a_at
1632962_at
1641203_at
1623202_at
1627246_at
1630118_s_at
1632876_a_at
1638697_at
1625702_s_at
1635502_at
1631465_at
1632269_at
1637597_a_at
1638171_s_at
1630600_at
1628485_at
1640010_at
1631464_at
1630167_at
1626808_s_at
1637209_at
1634874_at
1625583_at
1639653_at
1639107_at
1634883_at
1625853_at
1633274_at
1641519_at
1628603_at
1624978_at
1640051_s_at
1627293_at
1632384_at
1641601_at
1624592_at
1632430_at
1638544_at
1633691_at
1624226_at
1626224_s_at
1634579_at
1630132_at
1627013_at
1629530_at
1638796_at
1636645_at
1624201_at
1623974_at
1637689_at
1634949_at
1634094_a_at
1633020_at
1624714_at
1626696_at
1638088_at
1638988_at
1636258_at
1635213_at
1624694_at
1627216_s_at
1631819_s_at
1632762_s_at
1630355_a_at
1633782_at
1633454_s_at
1640031_at
1628866_at
1628179_at
1630202_a_at
1626478_at
1637960_at
1627514_at
1627308_s_at
1641263_at
1636861_at
1632114_at
1632600_at
1626993_at
1625651_at
1636271_a_at
1639931_at
1622952_at
1623291_at
1639240_a_at
1623085_at
1625062_a_at
1631335_a_at
1628683_at
1639421_at

1626469_at
1636501_at
1629507_a_at
1635279_at
1635125_a_at
1622903_s_at
1638410_at
1623998_at
1629355_at
1630246_at
1639392_at
1634296_s_at
1641597_a_at
1640316_at
1638087_at
1634407_at
1624945_a_at
1640601_at
1626957_at
1633078_at
1624860_at

1634045_at
1636596_at
1634982_at
1636910_at
1624570_a_at
1634868_at
1623040_at
1627331_at
1626667_at
1629489_at
1625280_at
1638793_at
1641520_at
1637346_at
1638499_s_at
1630419_a_at
1626155_at
1623475_s_at
1629625_at
1640642_at
1638811_at

1637628_at
1633736_at
1636564_at
1636949_s_at
1637469_at
1640174_at
1630016_at
1629302_at
1630813_at
1635439_at
1628382_at
1631130_at
1634382_at
1637919_at
1641326_at
1627511_at
1624404_a_at
1638661_at
1640905_at
1640343_at
1637369_at

1627725_at
1631198_at
1626698_at
1632623_at
1635247_at
1639307_at
1633259_a_at
1635564_at
1629363_at
1632665_a_at
1638797_a_at
1629644_s_at
1632277_a_at
1632251_s_at
1627985_a_at
1629374_at
1640619_at
1632098_at
1638651_a_at
1640425_at
1632593_at

1634862_at
1625334_at
1633517_at
1639444_a_at
1624070_at
1630803_at
1637962_at
1631182_at
1641306_at
1624913_s_at
1634795_a_at
1641327_at
1623745_at
1632250_at
1626572_at
1639768_at
1639112_s_at
1636320_at
1633642_at
1636630_s_at
1634212_at

1639640_at
1623737_a_at
1627613_at
1641681_s_at
1633055_at
1633606_s_at
1625377_at
1623606_at
1624807_at
1640323_at
1630332_at
1639478_at
1635121_a_at
1636327_at
1625172_s_at
1635887_at
1635379_at
1639312_at
1641350_at
1633703_s_at
1625120_at

1627993_at
1625665_at
1635067_at
1636268_at
1624099_at
1633294_at
1630187_a_at
1625639_at
1637881_at
1640088_at
1631853_at
1639715_at
1631862_at
1627141_at
1639503_at
1627153_at
1623426_at
1631588_at
1638870_at
1626850_s_at
1628917_at
1625746_at
1624854_s_at
1640821_at
1625945_a_at
1640477_at
1639413_at
1641126_at
1636020_s_at
1626432_at
1638074_at
1627842_at
1625658_at
1636923_a_at
1634116_at
1629155_at
1634446_at
1635115_at
1634238_a_at
1624725_at
1631849_at
1625085_at
1624509_at
1624214_at
1634504_a_at
1628342_s_at
1630815_at
1624173_at
1626201_at
1634209_at
1636154_at
1632567_at
1638834_a_at
1633804_at
1625481_a_at
1628101_s_at
1625096_at
1631984_at
1629780_at
1624841_s_at
1626658_at
1628297_a_at
1637098_at
1627774_a_at
1633001_at
1633100_a_at
1637329_a_at
1633949_at
1624064_at
1631048_at
1636323_at
1640064_at
1626369_at
1626236_at
1630008_at
1631619_a_at
1634767_at
1641347_s_at
1626289_at
1631800_at
1627459_at
1628677_at
1632266_at
1632368_at
1639891_at
1639648_at
1640134_a_at
1632577_a_at
1639483_s_at
1634600_at
1626719_a_at
1627100_s_at
1632262_at
1627538_at
1635774_at
1635801_at
1638958_at
1625055_at
1624014_at
1633957_s_at
1634241_at
1639499_at
1624973_at
1633797_at
1623502_at
1633394_a_at
1641687_at
1635410_at
1626007_at
1625844_s_at
1638634_at
1629619_at
1638158_at
1638224_at
1637144_a_at
1635813_at
1623646_at
1623258_at
1637264_at
1640034_at
1631296_at
1637845_at
1637317_at
1632777_at
1638671_at
1623342_at

1635035_at
1631998_at
1624019_s_at
1633034_s_at
1626620_at
1641069_at
1637827_at
1628809_at
1637100_at
1636293_at
1629194_s_at
1628503_at
1637626_at
1629246_at
1628617_at
1623203_at
1639645_at
1634334_at
1624168_at
1640799_at
1635073_at
1637972_at
1624414_at
1641451_at
1626931_a_at
1627460_at
1637665_at
1629046_a_at
1638349_s_at
1631527_at
1638923_at
1635186_at
1636382_at
1636571_at
1633615_at
1624450_at
1635911_s_at
1628767_s_at
1633835_s_at
1641096_s_at
1634616_at
1626108_at
1626734_at
1632557_s_at
1627888_at
1634172_at
1633442_at
1623297_at
1641478_s_at
1635792_a_at
1637142_at
1638218_at
1639807_s_at
1635917_at
1626984_at
1628393_at
1638712_at
1628028_s_at
1640870_s_at
1626272_s_at
1636270_at
1623879_at
1636971_at
1626508_at
1627469_at
1634655_at
1630934_at
1633661_at
1623375_at
1623663_a_at
1641038_at
1635811_at
1630213_at
1637023_at
1629041_at
1636652_a_at
1637314_at
1635355_a_at
1639276_at
1640084_a_at
1632256_at
1627665_at
1626125_at
1634856_at
1641309_s_at
1640068_at
1630542_at
1623376_s_at
1634076_at
1625528_at
1635650_at
1623936_at
1640995_at
1630276_at
1623086_at
1624984_at
1628947_s_at
1634811_at
1640980_at
1628605_at
1641614_at
1632394_s_at
1629920_at
1624779_at
1639495_at
1640927_at
1624343_at
1630841_at
1636847_s_at
1631777_a_at
1636140_at
1627023_at
1625343_at
1638277_at
1640173_at
1634261_at
1627081_at
1637871_at
1624405_a_at
1639111_at
1625048_at
1639346_at
1627898_at
1623482_at
1631293_at
1635897_at

1634922_s_at
1629746_at
1632594_at
1641522_at
1635854_s_at
1630679_at
1623789_at
1625041_at
1638374_at
1628448_at
1638548_at
1631621_s_at
1631383_at
1626786_at
1632135_a_at
1635830_at
1628186_at
1631263_at
1636192_at
1623972_a_at
1635627_at
1633593_s_at
1634757_a_at
1630756_at
1631006_a_at
1634764_at
1623904_a_at
1632575_at
1632483_at
1634168_s_at
1624475_at
1632580_at
1640073_at
1634859_at
1633558_s_at
1636932_at
1631098_at
1639951_at
1624213_at
1624939_at
1640992_at
1628387_s_at
1632606_a_at
1636544_at
1629001_at
1639954_at
1625031_at
1633011_at
1634095_at
1641068_a_at
1627743_at
1627245_s_at
1639251_at
1625918_a_at
1637399_at
1631264_at
1627589_s_at
1632188_at
1634463_at
1639744_at
1636988_at
1629795_at
1625878_at
1631633_a_at
1631525_at
1623901_s_at
1628240_at
1628565_at
1640185_at
1641148_a_at
1640584_at
1641449_at
1635616_a_at
1623448_at
1632897_at
1640240_s_at
1627218_a_at
1638325_at
1632590_at
1628959_at
1628399_s_at
1636147_at
1624750_at
1625633_a_at
1639678_at
1633778_at
1635063_at
1626947_s_at
1626003_s_at
1633545_at
1639197_at
1640852_at
1630529_at
1635881_at
1638840_at
1631688_at
1640309_s_at
1633652_at
1639070_a_at
1627337_at
1629726_at
1622949_at
1629316_at
1627812_s_at
1631935_at
1627778_a_at
1625422_at
1633491_s_at
1640211_at
1634301_at
1627844_at
1627235_at
1631745_at
1640719_at
1624280_at
1638526_a_at
1639115_s_at
1636003_at
1624529_at
1638178_at
1639195_a_at
1639993_at
1626854_at
1638387_at
1632640_at
1628277_at

1638973_s_at
1624905_at
1623339_at
1623584_at
1641117_a_at
1633559_at
1630199_at
1637866_at
1639500_at
1623193_at
1634722_s_at
1623698_s_at
1641362_at
1631603_at
1624409_a_at
1623408_s_at
1624663_a_at
1626506_at
1641579_at
1637549_at
1626911_at
1632583_at
1628340_s_at
1626693_at
1632803_at
1625893_a_at
1627239_s_at
1632282_s_at
1622895_at
1631591_at
1633858_at
1631313_at
1629433_at
1641143_s_at
1635794_a_at
1637521_at
1625863_at
1631994_a_at
1630669_at
1625081_at
1625722_at
1626888_at
1631015_s_at
1637322_at
1639193_a_at
1630067_a_at
1625051_at
1623485_at
1636942_at
1641645_at
1635027_at
1627472_at
1625354_at
1640552_at
1637990_s_at
1623231_at
1638615_s_at
1623766_at
1625337_s_at
1631515_at
1638795_at
1640190_at
1637951_at
1634265_at
1633625_s_at
1630735_at
1628670_at
1628681_at
1633389_at
1626898_at
1631218_at
1635953_at
1628117_at
1638350_at
1623591_a_at
1636599_at
1638259_s_at
1622975_at
1628612_at
1638782_at
1632427_at
1631304_a_at
1636812_at
1634126_at
1634881_at
1639243_at
1631347_at
1633498_at
1632106_at
1636795_at
1635361_at
1641399_at
1635934_at
1623744_at
1629395_at
1624765_at
1629867_a_at
1634224_at
1622971_at
1636341_at
1637220_s_at
1626924_a_at
1640460_at
1624229_at
1624499_s_at
1629303_at
1629018_a_at
1634197_at
1636019_at
1624587_at
1639202_a_at
1634057_at
1625339_at
1632335_at
1625144_at
1630636_s_at
1639680_at
1635857_at
1623117_at
1629838_at
1632226_at
1623044_at
1634651_at
1638739_at
1635448_at
1629358_s_at

1634644_at
1631106_s_at
1623241_s_at
1624419_a_at
1631820_at
1623862_at
1635826_s_at
1624617_at
1640618_at
1627473_at
1633767_at
1631308_at
1628000_s_at
1639101_at
1634281_at
1630396_at
1640565_at
1623214_at
1640755_at
1640529_at
1641459_at
1632581_at
1629685_at
1626710_at
1638448_at
1626326_at
1638110_at
1631034_at
1627056_a_at
1639322_at
1641003_at
1637368_at
1626531_at
1636170_at
1630130_at
1635469_at
1629862_at
1639064_s_at
1631114_a_at
1640368_at
1627673_at
1630340_at
1624458_at
1624808_at
1633168_at
1623992_at
1637623_at
1641489_at
1630278_s_at
1635547_a_at
1636484_at
1625190_at
1623943_at
1640151_at
1637740_at
1627605_at
1633237_at
1637193_at
1636476_a_at
1639848_at
1637060_a_at
1639955_at
1623819_at
1624456_at
1628839_at
1624639_at
1634167_a_at
1630050_at
1623595_at
1623190_at
1625486_a_at
1638527_a_at
1628248_at
1639629_at
1639295_at
1635521_at
1628479_at
1641313_at
1632636_at
1625859_at
1636227_at
1625141_at
1628995_at
1629252_at
1634178_at
1640317_at
1634239_at
1625898_s_at
1631469_at
1634019_at
1631047_at
1625521_at
1628114_s_at
1635128_a_at
1628829_at
1624427_at
1625450_at
1631828_s_at
1635996_at
1631204_at
1627746_at
1629614_at
1636094_at
1637394_s_at
1640122_at
1636357_at
1624775_at
1626873_a_at
1631610_at
1625136_s_at
1637277_at
1629984_s_at
1641426_at
1626864_at
1634271_at
1627111_at
1631572_at
1637738_at
1640825_a_at
1634015_s_at
1624415_s_at
1636237_s_at
1637191_at
1631486_at
1623887_at
1638438_a_at

1639976_at
1635160_at
1633883_at
1639737_at
1635421_at
1627659_at
1625966_at
1635824_at
1629792_at
1626933_s_at
1636614_a_at
1623903_at
1638130_at
1639391_at
1635951_at
1634003_at
1629558_at
1627682_at
1626231_at
1631915_at
1624792_at
1640599_at
1640560_at
1641444_a_at
1624678_at
1640170_at
1629027_at
1640233_at
1625772_at
1628667_at
1626768_at
1633361_at
1628759_a_at
1627638_s_at
1639633_at
1624118_at
1631168_at
1630264_at
1641101_at
1641532_at
1633490_at
1627680_at
1627180_at
1637068_at
1625566_a_at
1636512_s_at
1639968_at
1624380_at
1629021_at
1638637_at
1640818_at
1626133_s_at
1632176_at
1640187_a_at
1639662_at
1640999_at
1629603_at
1636602_at
1634898_a_at
1641534_at
1625631_at
1627832_at
1627910_s_at
1628427_a_at
1635607_at
1623377_at
1626717_at
1637809_at
1631672_at
1639698_at
1641476_a_at
1641031_s_at
1640782_at
1630753_at
1631148_at
1632971_at
1629409_s_at
1631330_at
1628649_at
1635051_a_at
1628312_at
1623439_at
1625824_at
1627099_at
1639034_at
1635454_a_at
1626766_s_at
1630366_at
1623463_at
1636894_s_at
1636193_at
1636837_at
1623770_at
1630388_at
1629943_at
1634988_a_at
1639898_at
1639642_a_at
1625714_a_at
1633080_at
1625608_at
1629327_at
1624483_at
1635629_at
1627055_at
1634636_at
1635714_s_at
1634331_at
1635446_at
1630395_at
1638183_at
1634784_at
1623353_at
1640109_at
1623138_at
1630723_a_at
1622928_at
1630851_s_at
1626964_at
1632139_at
1627781_at
1627894_s_at
1625879_at
1629462_at
1631848_at
1639403_s_at

1625590_a_at
1623587_at
1627078_at
1627643_at
1636242_at
1624073_at
1623539_at
1627967_a_at
1635552_s_at
1624877_at
1631288_at
1636852_at
1626810_at
1623926_at
1636816_s_at
1637601_at
1627492_at
1627433_at
1637050_at
1627829_at
1634204_at
1631009_at
1622921_at
1635725_a_at
1638229_at
1633754_at
1636098_at
1629473_at
1628663_s_at
1627729_s_at
1624435_at
1629401_s_at
1634174_at
1641685_at
1630003_at
1640655_s_at
1634615_at
1640215_at
1639057_at
1625340_at
1630798_at
1633923_at
1631602_at
1636743_s_at
1640774_a_at
1639950_at
1627364_s_at
1634230_s_at
1641737_a_at
1638217_at
1627660_a_at
1640454_at
1635550_at
1629921_a_at
1629629_at
1632179_at
1634619_at
1632422_s_at
1638427_at
1628204_at
1639957_s_at
1639567_at
1640998_at
1625016_at
1636009_at
1631767_at
1627873_at
1626332_s_at
1639519_at
1627865_a_at
1622940_at
1636717_at
1631368_s_at
1633998_s_at
1633912_at
1638162_s_at
1625540_at
1626781_at
1631077_at
1633074_a_at
1628459_at
1640126_at
1633967_at
1636262_at
1623746_a_at
1631740_at
1634492_s_at
1631931_s_at
1638748_at
1624581_at
1639152_at
1628601_at
1624919_at
1625674_at
1637383_at
1624192_at
1630630_at
1624628_at
1628673_at
1640336_at
1638693_s_at
1640548_at
1623206_a_at
1632855_at
1640492_at
1632688_s_at
1627271_at
1641366_at
1632247_at
1640765_at
1633335_at
1634979_at
1623699_a_at
1639598_at
1636412_at
1623134_at
1628011_a_at
1627733_at
1639712_at
1637963_at
1623094_at
1640954_at
1632171_a_at
1635903_at
1629189_at
1629468_at

1635528_s_at
1634081_at
1628035_at
1641610_at
1629784_a_at
1636525_at
1633079_at
1632702_at
1630001_at
1634068_at
1623320_at
1634692_at
1625317_at
1633784_at
1626123_at
1640349_at
1630988_at
1635239_at
1639309_at
1632521_at
1626215_at
1628981_at
1632465_s_at
1623573_s_at
1624906_at
1640382_at
1640881_at
1638839_at
1628352_a_at
1627779_at
1627009_at
1625585_at
1629956_at
1628574_at
1637589_at
1631815_at
1627575_at
1628788_a_at
1628608_at
1637621_at
1637954_at
1639168_at
1628997_at
1632800_at
1636589_s_at
1628364_at
1636851_at
1627447_at
1624027_at
1632194_at
1640020_at
1640574_at
1641462_at
1634128_at
1624991_at
1624208_s_at
1634801_at
1631877_a_at
1629096_at
1630539_at
1630794_at
1628775_s_at
1634992_s_at
1640269_at
1627916_s_at
1640867_s_at
1628901_at
1634100_at
1633004_at
1630673_at
1632381_at
1627983_at
1633113_at
1627925_at
1628627_at
1641142_at
1629663_at
1639817_at
1636130_at
1641530_s_at
1629870_at
1625095_at
1627813_at
1628260_at
1624332_s_at
1628968_at
1629151_at
1637546_at
1638618_a_at
1635281_at
1636896_a_at
1627945_at
1633771_s_at
1630024_at
1625960_at
1631447_at
1632714_at
1631244_a_at
1624938_at
1638882_at
1623115_at
1639554_at
1627458_at
1636807_at
1637620_s_at
1625137_at
1631179_s_at
1631653_at
1636356_at
1625923_s_at
1636087_at
1639903_at
1640602_s_at
1636109_at
1632882_at
1627863_at
1628295_at
1624060_at
1628557_at
1631282_at
1627431_at
1628832_s_at
1623644_s_at
1623286_at
1633212_s_at
1641553_at

1622939_at
1628243_at
1637526_s_at
1624595_a_at
1626798_a_at
1637138_at
1632850_at
1632261_at
1629751_at
1634983_s_at
1629319_at
1625683_at
1632338_a_at
1636160_at
1638980_at
1625220_at
1626425_at
1627292_at
1636286_at
1631062_at
1625502_at
1631363_at
1635201_at
1623686_at
1626073_a_at
1628686_a_at
1636269_at
1636900_at
1641600_at
1633061_at
1636322_at
1639189_at
1628111_at
1638204_s_at
1640716_at
1628729_at
1632999_at
1636426_at
1632019_s_at
1637625_s_at
1640532_at
1633704_at
1640278_at
1630737_at
1627240_at
1628507_at
1627796_s_at
1636446_at
1639375_a_at
1630093_at
1640108_at
1637980_at
1639622_at
1633194_at
1623888_at
1640485_at
1624653_at
1626344_at
1623873_at
1628092_at
1630950_at
1638351_s_at
1623465_at
1640967_at
1631270_at
1634316_at
1640076_at
1629365_at
1625439_at
1634738_s_at
1631757_at
1623590_s_at
1633906_at
1631174_at
1635118_at
1641386_at
1640801_at
1626010_at
1627340_at
1641702_at
1633362_at
1626689_at
1625047_at
1630149_at
1624831_at
1630699_at
1636119_at
1638603_at
1631578_s_at
1625533_at
1626175_at
1627677_s_at
1638456_at
1624583_at
1624504_s_at
1626148_at
1639762_at
1640086_at
1639779_at
1638397_at
1632662_at
1628180_at
1623792_a_at
1638659_at
1638582_at
1629239_s_at
1624719_at
1630258_at
1632589_at
1635157_at
1635435_at
1635874_at
1628422_s_at
1634359_a_at
1628428_at
1639607_at
1623346_at
1638334_at
1636711_at
1636330_at
1637007_s_at
1639015_s_at
1640455_a_at
1637795_at
1623248_s_at
1637267_at

1633776_s_at
1632730_at
1623997_s_at
1629884_at
1626747_at
1623993_at
1639037_at
1630172_at
1628016_s_at
1626503_at
1636515_at
1631763_at
1634402_at
1624338_at
1638699_at
1625822_at
1629923_at
1627973_s_at
1640525_a_at
1640067_at
1641102_at
1636080_a_at
1625626_at
1641745_a_at
1636468_a_at
1637124_at
1627003_at
1630675_at
1635927_at
1629148_a_at
1626468_a_at
1631869_at
1635773_at
1624744_a_at
1635944_a_at
1626438_at
1640401_at
1634127_a_at
1639952_at
1628275_at
1623557_at
1629217_at
1635969_at
1629431_at
1637284_at
1630999_at
1627539_at
1634629_at
1632462_at
1632621_at
1635631_a_at
1634969_at
1641485_at
1625469_at
1633680_at
1630263_at
1625567_a_at
1639191_at
1629888_at
1635549_at
1630768_s_at
1623407_at
1625348_s_at
1632761_at
1638640_at
1631326_at
1623118_s_at
1640679_at
1628987_at
1638053_at
1627597_at
1627168_at
1626257_at
1637453_at
1625004_at
1630312_s_at
1625145_a_at
1626561_at
1627890_at
1639344_at
1634845_at
1627004_at
1633916_at
1626858_a_at
1627254_at
1635155_a_at
1639471_s_at
1635303_at
1633287_at
1625990_at
1628706_at
1637662_at
1635382_at
1623670_at
1640123_at
1625425_a_at
1626307_at
1635671_at
1624363_at
1631172_at
1624902_at
1624296_at
1640930_at
1624134_a_at
1637447_at
1629479_a_at
1636401_a_at
1623856_at
1627716_at
1635482_at
1631756_at
1625595_a_at
1636016_at
1631631_at
1630227_a_at
1630555_at
1634302_s_at
1633651_at
1623554_at
1628017_a_at
1625022_a_at
1638282_at
1628435_at
1631321_s_at
1635508_at
1626613_at

1641006_s_at
1625514_s_at
1637994_at
1631067_at
1635632_at
1626906_at
1627439_at
1640201_at
1639748_at
1624287_at
1634882_at
1630469_a_at
1623438_at
1638652_at
1641384_a_at
1629023_s_at
1631867_at
1641471_at
1636920_s_at
1629400_at
1627564_s_at
1625114_at
1635923_at
1641632_at
1633574_at
1635572_at
1630076_at
1628991_at
1625465_a_at
1629886_s_at
1632458_at
1635269_at
1626482_a_at
1633962_a_at
1638235_at
1625263_at
1635305_s_at
1623122_at
1627551_s_at
1628957_at
1639372_s_at
1636556_at
1624638_a_at
1628669_at
1630270_s_at
1632264_at
1627339_at
1632332_at
1635248_at
1628694_a_at
1628109_at
1639147_s_at
1631083_at
1636523_at
1631393_at
1632756_at
1625850_at
1629848_s_at
1637048_at
1636866_at
1626096_at
1634927_at
1627697_at
1628281_at
1641348_at
1629752_at
1628604_at
1641170_a_at
1637713_at
1625869_at
1627566_a_at
1638846_at
1632584_at
1629122_at
1638311_at
1626197_at
1626522_at
1641465_at
1638140_at
1633128_at
1635293_s_at
1623535_at
1626444_at
1631593_at
1631286_at
1623501_at
1627028_at
1640281_s_at
1640426_at
1633301_at
1628998_at
1641516_at
1637198_at
1623175_at
1631344_at
1624139_at
1630370_at
1630487_s_at
1627209_at
1625126_at
1639677_at
1634008_at
1636368_at
1626829_s_at
1629569_at
1635240_at
1627022_at
1633805_a_at
1628476_at
1633369_s_at
1634362_a_at
1629546_at
1641722_at
1637847_at
1628258_at
1633466_at
1624378_at
1630327_at
1624389_at
1635335_at
1632484_at
1640751_at
1633170_at
1623119_at
1633282_at
1637110_at

1633821_at
1626418_a_at
1638092_a_at
1627435_at
1633102_at
1640897_at
1632912_s_at
1629690_at
1623689_a_at
1640495_at
1635523_a_at
1624007_at
1628871_at
1626602_at
1624236_at
1626845_at
1623853_at
1632655_at
1624890_s_at
1638119_at
1640044_at
1633823_at
1628438_at
1630907_at
1641262_at
1628072_at
1641103_at
1641456_at
1639552_s_at
1627133_at
1629153_s_at
1625609_at
1640673_at
1640082_at
1624559_a_at
1638201_at
1639667_at
1630089_at
1624688_at
1639775_at
1633943_at
1634503_at
1631812_at
1637787_a_at
1634482_at
1625330_at
1630416_at
1628337_at
1635177_at
1629708_at
1637723_at
1635815_at
1623695_a_at
1628570_at
1623672_at
1640104_at
1635099_at
1630447_at
1626622_at
1630096_at
1630677_at
1634598_a_at
1625325_s_at
1636207_at
1638494_at
1623633_at
1624870_at
1635595_at
1630683_at
1631909_at
1625204_a_at
1626684_at
1624124_at
1630265_at
1636457_at
1623556_at
1641089_s_at
1635358_at
1636182_a_at
1630780_a_at
1635327_at
1622981_at
1627131_at
1628429_at
1624158_at
1640361_at
1640822_s_at
1628631_at
1625986_at
1623182_at
1625925_at
1623100_at
1634572_at
1639630_at
1639949_s_at
1639614_s_at
1632634_at
1635175_at
1628423_at
1632724_at
1624307_at
1633665_at
1631755_at
1623543_at
1630566_at
1639109_a_at
1636218_at
1626965_at
1627421_at
1626834_at
1630663_a_at
1624981_a_at
1632804_at
1631385_at
1628128_at
1635409_at
1629005_a_at
1630102_at
1623874_at
1636490_at
1633860_at
1632980_at
1641620_s_at
1634082_at
1636039_at
1631458_at

1634628_at
1641192_at
1631480_at
1632802_at
1625488_s_at
1636161_at
1640466_s_at
1632615_at
1636064_at
1633398_at
1636373_at
1624658_at
1636092_a_at
1629324_at
1622956_at
1624932_at
1637887_at
1633220_at
1625706_at
1636811_at
1639874_at
1629091_at
1636308_at
1636299_at
1630453_at
1631733_at
1633479_a_at
1636978_at
1636056_at
1636520_s_at
1640468_a_at
1635718_at
1626433_at
1633464_at
1638382_at
1626556_at
1624353_at
1626657_a_at
1633985_at
1634108_at
1630064_at
1635853_at
1623531_at
1638439_a_at
1634917_at
1636364_a_at
1634515_at
1639319_at
1640559_at
1637256_at
1628504_at
1627333_at
1632152_at
1637602_at
1636784_at
1630165_s_at
1638898_at
1631940_s_at
1639201_at
1627109_at
1624564_s_at
1636575_s_at
1639270_at
1635633_s_at
1634319_at
1634746_at
1623433_at
1627901_a_at
1640214_at
1629584_at
1639644_at
1636234_at
1623638_a_at
1638874_at
1629661_at
1631676_at
1632736_at
1634244_s_at
1634214_a_at
1630056_at
1637440_at
1626248_at
1623914_at
1634855_s_at
1626278_at
1623293_at
1627532_at
1629410_at
1631833_at
1640415_at
1629678_a_at
1633331_at
1628362_s_at
1625214_at
1636868_at
1625904_at
1633701_at
1627470_at
1638133_at
1624262_at
1623579_at
1637584_at
1624732_at
1632717_a_at
1630685_at
1638113_at
1626037_at
1629040_at
1640921_at
1633723_at
1631379_a_at
1625951_at
1639246_at
1629881_at
1636168_s_at
1639782_at
1628643_at
1629743_at
1634201_at
1636943_s_at
1635596_at
1624772_at
1637654_at
1628516_at
1627944_a_at
1633451_at

1638568_s_at
1623928_at
1641315_at
1624284_a_at
1631279_at
1638513_s_at
1641708_at
1623814_at
1627409_at
1629417_s_at
1627020_at
1633147_at
1624551_at
1629418_s_at
1640297_at
1636176_at
1623864_at
1624717_s_at
1624957_a_at
1624478_at
1622892_s_at
1634313_s_at
1638121_at
1634113_at
1636464_at
1625889_at
1626570_s_at
1627744_at
1625758_s_at
1625050_s_at
1639488_at
1629844_s_at
1623294_at
1630657_at
1638964_at
1635863_at
1638581_at
1626619_at
1626441_at
1625291_s_at
1640922_a_at
1638851_at
1633310_at
1636406_at
1639522_at
1632829_at
1627105_at
1633022_at
1630995_at
1632872_at
1625164_at
1632246_at
1628274_a_at
1624143_a_at
1623365_at
1640512_at
1627693_at
1631783_at
1639892_at
1634650_at
1623322_at
1630559_at
1634976_at
1624644_a_at
1635143_at
1639259_at
1629859_s_at
1623842_a_at
1630977_at
1641197_at
1624272_at
1626276_at
1631565_a_at
1627966_s_at
1627371_at
1635427_a_at
1641703_at
1637679_s_at
1635268_at
1636125_a_at
1634321_s_at
1632220_s_at
1637180_at
1623340_at
1627211_at
1625413_s_at
1641204_at
1632811_at
1637600_at
1637509_s_at
1634833_at
1627101_at
1629257_s_at
1630779_s_at
1637848_at
1636305_a_at
1623436_a_at
1634514_at
1625767_at
1626565_at
1633578_a_at
1636666_at
1634814_at
1624901_at
1623257_a_at
1629188_at
1625862_x_at
1632083_at
1634705_at
1636048_at
1639029_at
1635628_s_at
1634079_at
1640966_at
1625499_at
1633800_s_at
1623891_at
1624301_at
1634509_s_at
1641289_at
1624586_a_at
1627999_s_at
1630457_s_at
1637574_at
1636898_at
1640479_at

1639218_s_at
1629378_at
1637022_at
1635667_at
1638762_at
1629911_at
1639074_at
1629549_s_at
1632818_at
1631325_at
1631333_s_at
1630715_at
1633042_at
1640344_at
1638598_at
1640019_at
1628716_at
1635946_at
1634711_at
1627741_at
1640218_at
1624751_at
1633885_s_at
1641011_at
1636822_s_at
1637041_a_at
1624624_at
1629789_at
1623542_at
1636698_at
1638828_a_at
1633512_at
1630358_at
1632402_at
1623813_at
1634934_at
1641363_at
1632834_a_at
1628644_at
1640217_at
1632946_at
1637741_a_at
1630703_at
1639377_at
1638883_at
1635237_at
1634155_at
1640373_at
1626945_at
1637141_at
1637327_at
1634994_a_at
1631738_at
1635587_s_at
1635013_s_at
1628474_at
1633598_at
1625607_s_at
1636620_s_at
1623422_a_at
1632765_at
1625184_at
1635727_a_at
1623783_at
1630323_at
1622917_a_at
1628256_at
1624420_at
1627110_at
1624502_a_at
1626399_at
1634282_s_at
1628112_at
1630667_at
1637782_at
1626879_at
1640938_at
1636248_at
1639787_at
1624916_a_at
1631644_at
1640650_at
1632835_at
1627305_at
1639365_at
1632782_a_at
1635310_s_at
1637904_at
1637328_at
1631195_at
1634295_at
1629007_at
1627737_at
1627911_at
1627204_at
1628984_s_at
1623969_at
1629163_at
1623165_at
1640055_at
1627798_at
1631790_at
1633154_at
1635056_at
1627221_at
1625199_s_at
1626536_at
1626404_a_at
1634614_at
1636084_at
1638524_s_at
1625020_at
1641075_at
1641215_s_at
1633532_at
1636266_at
1631346_a_at
1626881_at
1638664_s_at
1629313_at
1628660_at
1638446_a_at
1623295_at
1637746_at
1625568_a_at
1637854_at

1635046_at
1636957_s_at
1629889_s_at
1628974_at
1638800_a_at
1625650_at
1637169_at
1640582_at
1629104_at
1625487_at
1631772_a_at
1635647_at
1633057_at
1635694_at
1638908_at
1637983_s_at
1637647_at
1626052_at
1634118_at
1638939_at
1627997_at
1630373_at
1641463_at
1631467_at
1633934_at
1627426_at
1635110_at
1623150_at
1640507_s_at
1629854_at
1625922_a_at
1630087_at
1629948_at
1637415_at
1640789_a_at
1638185_at
1639341_at
1623836_at
1631367_at
1627749_at
1634182_at
1633067_at
1626664_at
1632168_at
1631942_at
1633763_at
1625394_at
1637107_at
1630896_at
1638520_at
1624637_at
1637774_s_at
1625519_at
1639093_s_at
1629715_at
1641556_a_at
1628257_s_at
1627118_at
1629240_at
1623896_a_at
1636921_at
1635872_at
1628811_at
1623857_at
1638858_at
1633794_a_at
1628711_at
1622957_s_at
1628980_s_at
1640600_at
1630455_at
1626076_at
1633643_a_at
1633450_at
1632095_at
1636849_at
1641400_at
1634900_at
1640229_at
1624892_s_at
1624605_at
1629207_at
1639253_at
1623032_at
1636502_at
1626797_a_at
1633618_at
1640976_at
1627373_at
1634866_at
1624824_at
1630365_at
1631434_at
1638758_at
1627134_at
1635054_at
1639436_at
1636128_at
1628169_at
1622982_at
1622979_a_at
1627059_at
1634405_s_at
1625060_at
1625816_at
1633654_s_at
1640237_a_at
1638005_s_at
1637136_at
1624632_at
1638861_at
1623459_at
1633477_at
1626006_at
1634962_s_at
1634640_at
1625675_a_at
1634080_at
1630273_at
1637763_a_at
1629574_at
1626002_at
1639079_at
1641564_a_at
1637811_s_at
1628325_at

1625365_at
1631806_at
1633196_at
1627553_at
1633234_at
1630682_at
1635758_s_at
1633669_at
1637515_s_at
1635498_at
1641027_at
1640169_s_at
1623288_at
1633604_at
1624291_at
1631022_at
1638274_s_at
1635300_at
1636296_at
1635971_at
1636253_at
1631101_at
1633960_at
1629972_at
1633435_a_at
1624330_s_at
1627050_at
1628800_at
1625640_a_at

****

Inb Effects DOWN regulated FDR < 0.1

1626166_at
1637239_s_at
1639229_at
1628261_at
1630670_at
1625297_at
1631387_at
1640285_at
1623019_a_at
1631522_x_at
1638554_at
1637123_a_at
1628398_at
1630150_s_at
1624035_a_at
1627583_at
1630402_at
1626953_at
1639979_at
1638327_a_at
1634009_at
1627835_a_at
1634418_at
1623068_at
1639823_at
1639130_a_at
1635793_at
1634165_at
1635639_a_at
1637366_at
1639439_at
1637103_at
1641558_at
1630171_at
1624121_at
1629559_s_at
1637391_at
1624982_s_at
1638240_s_at
1641413_s_at
1623867_at
1634439_at
1628712_at
1641581_at
1640681_at
1632666_at
1637077_s_at
1625409_at
1633303_at
1639317_at
1623238_at
1637701_at
1632964_at
1640223_a_at
1625183_at
1623757_at
1630261_a_at
1625210_a_at
1641607_at
1637097_at
1626893_at
1639838_at
1632032_at
1623452_at
1632328_at
1624525_at
1633355_at
1633033_s_at
1625400_at
1629919_at
1639110_at
1629885_at
1632432_at
1636338_at
1640181_at
1626709_at
1638733_at
1631285_at
1637914_at
1639636_at
1625154_s_at
1640501_at
1633690_at
1625116_at
1641324_at
1639351_at
1625761_a_at
1633882_at
1639469_a_at
1637113_s_at
1637483_at
1632434_at
1630515_s_at
1631280_at
1630252_at
1630065_at
1637504_at
1641325_s_at
1623160_at
1631217_a_at
1626645_at
1637900_at
1632011_at
1640059_at
1630430_a_at
1641442_a_at
1632854_s_at
1640715_at
1631639_at
1634036_at
1640892_a_at
1640107_at
1638207_at
1633740_at
1633272_at
1624979_at
1637194_at
1640224_s_at
1628080_at
1624705_a_at

1625588_s_at
1636775_at
1625071_a_at
1626429_at
1623490_at
1638896_at
1631474_s_at
1634739_a_at
1631380_s_at
1627394_s_at
1632475_at
1623558_at
1634440_s_at
1638475_a_at
1632898_at
1632380_at
1638079_at
1626294_a_at
1628105_a_at
1629876_at
1641310_at
1638004_at
1639928_a_at
1624398_at
1630100_at
1635252_a_at
1623984_s_at
1634269_at
1633285_at
1627352_at
1623252_a_at
1631620_at
1633696_at
1638400_at
1631628_s_at
1629538_s_at
1627287_at
1624432_at
1640991_at
1635398_at
1631724_s_at
1641109_at
1639418_at
1637645_at
1630085_s_at
1640629_s_at
1640462_at
1632091_at
1626442_at
1637335_at
1632967_s_at
1625542_a_at
1636028_at
1635025_a_at
1633452_a_at
1630501_a_at
1630231_at
1631925_at
1634707_s_at
1624340_at
1631302_at
1631468_a_at
1639596_at
1634846_a_at
1624830_at
1623693_a_at
1622974_at
1641291_at
1635253_a_at
1634075_at
1635483_at
1623200_at
1623517_at
1623851_at
1629235_s_at
1633344_at
1632757_a_at
1637634_at
1638472_at
1641018_s_at
1639778_at
1636274_at
1633481_at
1633264_at
1626016_s_at
1624488_a_at
1629551_s_at
1623234_s_at
1629077_s_at
1634955_at
1639252_s_at
1626397_at
1629317_at
1640798_a_at
1637801_at
1635936_at
1624774_a_at
1634162_at
1634188_a_at
1625908_a_at
1634063_a_at
1634156_at
1640754_at
1635678_at
1635161_at
1633167_s_at
1633400_at
1627986_s_at
1632527_at
1635460_a_at
1624826_at
1624157_at
1633434_at
1630044_s_at
1635140_at
1623037_a_at
1632932_a_at
1627818_s_at
1623083_at
1630707_at
1629318_at
1623445_at
1634906_at
1629423_at
1628766_at
1616608_a_at

1635208_at
1635584_s_at
1634310_at
1633293_at
1627493_at
1625752_at
1629446_at
1638067_a_at
1623151_a_at
1640526_at
1626473_a_at
1624929_at
1636461_at
1628909_at
1623957_s_at
1630575_at
1626446_a_at
1626727_at
1625778_at
1638529_at
1640131_a_at
1626740_at
1625312_at
1641598_at
1636414_at
1633480_at
1634417_s_at
1630957_s_at
1638044_a_at
1637943_at
1638681_at
1630201_a_at
1630589_at
1623827_a_at
1639592_at
1639637_a_at
1634684_at
1640854_at
1625211_s_at
1636247_at
1632403_at
1628652_at
1632705_at
1623225_s_at
1637548_at
1630169_a_at
1626521_x_at
1627962_at
1623212_s_at
1632119_s_at
1624776_a_at
1637538_s_at
1634374_at
1636747_at
1641333_s_at
1637813_at
1638365_at
1630160_at
1631524_a_at
1640523_at
1631566_at
1637460_at
1634546_at
1641167_s_at
1638892_at
1638276_at
1641171_at
1627893_at
1640235_at
1634144_at
1633463_s_at
1628235_at
1626088_at
1625992_s_at
1640322_at
1627632_at
1637421_at
1623177_at
1639033_at
1626700_at
1625692_s_at
1631359_s_at
1637133_x_at
1631487_s_at
1638009_s_at
1624505_at
1636813_s_at
1627927_at
1629553_at
1629065_s_at
1637792_at
1630129_at
1624219_s_at
1638050_s_at
1623624_at
1638008_s_at
1629342_s_at
1629015_a_at
1637545_at
1630698_at
1638810_at
1623588_at
1634668_at
1625980_at
1625491_at
1630156_at
1632204_at
1639513_at
1630695_at
1638940_at
1638368_at
1624310_s_at
1640303_a_at
1641474_s_at
1637412_a_at
1634893_at
1634447_at
1640286_at
1635072_at
1636626_s_at
1629396_a_at
1631046_s_at
1641587_at
1639123_at
1631377_a_at
1625652_s_at

1627278_s_at
1637246_a_at
1638457_at
1624029_at
1632317_at
1638515_at
1629944_at
1629798_at
1635538_at
1633290_a_at
1625885_at
1630802_at
1630968_at
1630807_at
1639364_at
1637678_at
1627018_s_at
1636548_at
1639203_at
1628938_at
1641501_a_at
1633597_at
1630979_at
1630563_at
1625584_at
1636961_a_at
1640175_at
1634818_s_at
1625392_at
1633427_at
1623753_at
1626609_at
1632285_at
1636598_s_at
1631765_at
1629837_at
1637669_at
1636348_s_at
1627129_at
1625717_s_at
1624662_at
1630062_a_at
1625442_a_at
1627000_s_at
1623516_s_at
1625401_at
1626431_at
1637018_at
1629034_at
1634170_a_at
1637414_at
1637737_at
1641688_at
1639585_a_at
1637739_at
1625148_s_at
1631318_at
1633752_at
1626323_s_at
1632543_at
1640252_at
1636591_at
1637349_at
1635788_a_at
1633157_a_at
1637057_at
1625215_s_at
1625825_at
1626089_at
1636528_at
1630874_s_at
1634606_a_at
1634794_at
1637531_at
1640838_s_at
1633329_at
1627054_at
1638639_a_at
1629691_at
1634129_at
1629597_a_at
1639255_s_at
1626774_s_at
1639788_at
1624873_at
1635975_s_at
1625370_s_at
1628536_s_at
1635229_at
1634210_at
1630509_at
1634250_at
1640350_at
1629676_at
1633432_at
1629907_at
1636377_at
1638593_a_at
1627963_s_at
1633718_at
1633336_at
1640445_at
1624069_at
1630598_at
1639145_s_at
1626481_a_at
1632117_s_at
1630456_at
1624752_at
1626543_at
1628840_at
1630052_s_at
1632028_a_at
1628927_at
1626694_at
1641049_at
1634329_at
1636057_at
1635861_a_at
1631119_at
1633931_a_at
1635000_at
1631584_at
1634989_at
1637359_at
1627376_at

1632558_at
1634191_at
1631237_s_at
1623714_at
1634458_at
1625537_at
1631695_at
1627430_at
1624256_at
1629648_s_at
1629201_at
1630570_at
1638244_s_at
1629937_a_at
1635730_at
1626077_s_at
1624649_a_at
1627719_at
1639508_a_at
1624407_s_at
1627761_at
1641575_at
1632989_a_at
1635591_at
1630668_a_at
1637109_s_at
1633109_at
1635611_a_at
1629441_at
1641490_s_at
1639233_at
1639338_at
1625857_at
1634961_s_at
1627400_a_at
1635057_s_at
1635376_at
1634654_at
1635661_at
1637481_at
1626509_at
1625434_at
1634783_s_at
1624441_at
1636321_s_at
1626336_at
1636264_at
1630088_at
1636622_at
1630418_s_at
1622906_at
1636902_at
1623884_at
1628668_at
1640375_at
1640159_at
1627834_a_at
1625278_s_at
1630476_s_at
1637971_a_at
1633227_s_at
1628992_at
1632345_at
1628705_at
1638722_at
1638876_at
1639454_at
1639306_s_at
1635226_at
1640472_at
1632455_at
1623446_a_at
1632963_at
1635416_at
1638592_at
1638953_a_at
1624969_s_at
1626513_at
1626025_at
1623398_at
1632596_at
1627855_at
1623164_a_at
1628107_at
1629804_s_at
1637499_s_at
1635352_s_at
1625672_s_at
1639242_a_at
1623073_s_at
1627971_s_at
1629581_at
1637816_s_at
1625412_at
1638721_s_at
1633535_at
1631028_s_at
1638324_s_at
1632409_a_at
1633673_a_at
1623669_at
1640928_at
1639477_s_at
1631402_s_at
1641312_at
1628531_at
1636445_at
1637024_at
1629123_at
1631252_a_at
1625245_at
1630002_s_at
1638736_at
1624517_at
1640465_at
1638703_a_at
1641635_s_at
1629499_at
1633108_at
1635104_s_at
1635677_a_at
1640872_at
1639335_at
1633599_a_at
1632979_at
1636521_at

1641578_at
1638807_s_at
1624273_at
1635745_a_at
1641599_at
1636677_s_at
1624251_a_at
1625023_a_at
1628696_at
1636068_a_at
1634152_at
1625433_at
1625757_at
1626841_s_at
1636302_s_at
1635321_at
1625453_a_at
1634249_s_at
1632734_s_at
1633002_at
1624439_at
1630256_at
1623991_s_at
1629070_at
1626113_at
1641506_at
1623626_a_at
1637341_at
1634364_s_at
1627633_at
1624321_at
1631535_at
1624393_at
1625511_at
1637036_s_at
1640809_at
1626990_s_at
1628867_s_at
1623740_at
1634877_at
1631454_a_at
1625324_at
1638052_at
1634339_at
1623678_at
1636383_at
1627964_s_at
1625076_at
1639660_s_at
1632838_at
1630147_at
1625373_at
1631419_at
1628027_a_at
1637957_s_at
1624715_at
1633965_at
1641464_s_at
1641026_a_at
1628645_at
1631569_s_at
1637076_at
1635728_a_at
1641228_a_at
1630791_a_at
1635828_at
1626143_a_at
1637286_a_at
1623199_a_at
1641495_at
1629345_at
1638246_at
1625471_s_at
1624322_at
1636718_s_at
1630941_s_at
1635500_a_at
1632633_at
1633473_s_at
1626560_at
1635007_at
1624347_s_at
1634148_at
1627256_s_at
1638947_at
1641063_s_at
1634649_at
1625866_at
1632228_at
1637016_at
1626124_at
1639347_s_at
1636112_s_at
1633533_at
1629745_at
1632216_at
1630752_at
1633582_at
1627228_at
1623910_at
1631050_at
1628915_s_at
1638205_s_at
1640409_at
1624695_at
1630034_at
1631055_at
1630946_at
1623274_s_at
1636960_a_at
1630433_at
1623357_at
1637301_a_at
1628323_s_at
1624207_at
1637064_at
1641320_s_at
1626637_a_at
1636603_a_at
1634599_s_at
1636772_s_at
1638109_s_at
1640834_at
1627270_at
1630520_s_at
1636798_at

1625007_a_at
1632916_at
1626534_at
1627043_at
1630788_at
1636669_at
1639245_x_at
1624362_at
1633021_s_at
1628465_a_at
1634096_at
1640710_at
1625637_at
1637172_at
1624971_at
1635210_a_at
1631499_a_at
1630857_s_at
1635681_at
1625544_s_at
1625901_s_at
1624849_at
1627732_s_at
1630984_at
1623503_at
1635188_at
1640162_at
1631323_a_at
1622995_at
1624183_a_at
1640397_at
1625618_at
1622898_a_at
1633088_at
1635583_s_at
1641378_at
1639095_at
1626488_s_at
1634991_at
1626812_at
1624361_s_at
1633553_s_at
1635390_s_at
1628385_a_at
1632790_at
1635998_at
1625897_s_at
1630774_s_at
1623858_at
1634792_s_at
1638100_s_at
1640204_at
1630286_at
1626885_at
1625131_s_at
1632221_at
1626261_s_at
1632943_a_at
1626581_s_at
1628214_at
1633032_s_at
1627636_at
1625264_s_at
1638854_s_at
1636569_a_at
1634270_at
1636682_at
1638818_at
1639305_a_at
1633770_at
1635378_at
1636487_at
1632481_at
1624021_a_at
1640242_s_at
1626743_at
1629981_at
1626666_s_at
1623227_s_at
1629797_at
1637821_at
1630865_s_at
1641328_at
1625880_at
1638154_at
1627515_at
1629566_at
1639946_at
1624851_at
1639363_at
1624012_at
1640952_at
1628489_at
1629086_s_at
1623144_at
1635267_s_at
1635918_at
1635819_at
1634053_at
1631320_at
1635507_at
1640624_s_at
1640534_s_at
1627288_a_at
1637405_at
1641066_s_at
1636762_a_at
1627197_at
1637428_a_at
1633513_a_at
1628469_a_at
1637769_s_at
1635705_at
1626884_a_at
1633732_at
1628573_a_at
1632498_at
1629813_at
1633144_at
1624203_s_at
1639609_s_at
1636026_at
1641118_at
1626303_s_at
1628363_at
1627044_s_at

1628964_at
1634978_at
1629996_at
1631205_a_at
1627500_at
1632568_at
1624132_at
1625445_s_at
1638619_s_at
1640835_a_at
1627651_a_at
1624190_at
1640062_at
1623555_at
1635974_at
1624448_at
1623931_s_at
1625196_a_at
1641542_at
1633594_at
1633745_a_at
1625830_a_at
1628715_a_at
1625476_a_at
1637463_a_at
1628432_at
1637257_at
1623666_at
1624185_at
1635531_at
1633839_at
1638466_a_at
1624410_at
1639437_s_at
1629308_at
1626349_at
1624471_s_at
1626566_at
1625719_at
1632888_s_at
1627452_a_at
1632840_s_at
1640256_at
1627410_at
1636025_at
1624837_at
1625762_s_at
1624122_a_at
1628543_a_at
1624086_at
1638413_at
1635634_at
1634869_at
1629145_at
1638893_at
1637385_a_at
1636689_at
1634187_x_at
1638432_a_at
1629843_s_at
1633935_at
1626759_at
1632676_s_at
1624704_at
1640896_at
1635914_at
1624417_a_at
1628269_at
1635963_a_at
1636103_a_at
1626970_at
1630173_a_at
1628530_at
1639826_at
1637430_s_at
1628950_at
1628475_at
1635065_at
1633471_at
1629511_at
1635619_a_at
1624300_s_at
1637149_s_at
1637478_s_at
1640886_a_at
1631112_at
1639121_at
1640879_at
1639851_at
1640883_a_at
1640729_s_at
1637975_at
1638726_at
1637905_s_at
1636759_at
1628314_a_at
1634733_at
1633446_s_at
1635466_at
1637570_at
1638338_a_at
1636196_s_at
1640405_at
1625780_a_at
1640412_at
1625019_at
1635403_at
1635005_a_at
1633494_at
1625427_at
1629573_at
1633780_at
1623664_at
1639597_at
1623959_at
1630593_at
1627802_s_at
1635375_at
1638558_a_at
1634211_at
1634656_s_at
1640300_at
1633698_at
1636846_at
1627930_s_at
1634574_a_at

1631273_at
1628739_at
1626086_at
1632985_at
1638186_a_at
1631616_at
1628726_s_at
1623514_a_at
1623418_at
1628492_at
1636989_a_at
1639507_at
1640228_at
1641111_s_at
1636337_s_at
1625997_s_at
1635967_at
1630938_a_at
1633983_a_at
1627178_at
1625604_at
1622937_at
1637537_at
1633385_at
1627518_at
1635227_at
1629287_at
1638335_at
1638809_at
1623383_at
1638011_a_at
1637853_a_at
1640470_s_at
1634102_at
1631426_at
1623126_at
1634303_at
1639690_a_at
1623264_at
1637352_a_at
1638418_at
1630313_a_at
1634899_a_at
1631746_a_at
1624142_a_at
1641701_at
1623039_at
1632488_a_at
1634325_a_at
1635501_at
1639257_s_at
1628763_at
1626178_s_at
1625711_at
1626821_s_at
1635298_at
1635997_a_at
1635756_at
1630925_at
1636180_at
1627629_at
1628339_a_at
1623787_at
1630378_at
1630721_s_at
1625173_s_at
1635256_s_at
1632273_at
1629887_at
1626940_at
1641169_s_at
1625369_at
1640491_at
1639482_a_at
1633589_a_at
1623373_at
1629819_s_at
1636157_at
1627491_at
1640372_at
1633206_at
1639900_at
1640918_at
1623952_a_at
1632819_at
1639001_a_at
1631594_s_at
1636436_at
1630027_s_at
1635011_at
1623837_at
1636275_a_at
1636311_at
1623589_a_at
1624675_at
1637492_at
1623379_at
1629890_a_at
1634315_a_at
1634213_at
1638956_at
1639321_s_at
1637190_at
1627886_at
1632841_x_at
1631394_at
1637874_at
1640024_at
1626452_at
1628613_a_at
1632945_at
1629744_a_at
1633515_s_at
1623518_s_at
1640364_at
1631856_a_at
1624044_at
1634573_a_at
1625358_s_at
1632700_a_at
1626875_at
1633149_at
1627220_at
1641191_s_at
1628618_at
1635423_s_at

1627402_a_at
1623261_at
1629803_a_at
1636918_a_at
1640395_a_at
1639091_at
1631388_at
1631399_a_at
1632500_at
1632339_s_at
1641207_s_at
1638412_at
1624331_at
1625847_at
1632196_at
1629129_at
1628207_at
1627024_s_at
1639733_s_at
1640090_a_at
1627984_at
1633319_at
1638716_a_at
1639784_at
1633044_at
1627302_at
1627647_at
1634633_s_at
1638275_at
1625955_a_at
1637393_at
1637772_at
1635976_at
1641202_at
1623849_s_at
1637008_at
1624720_s_at
1630101_s_at
1629858_at
1628328_at
1625594_s_at
1625128_a_at
1637703_a_at
1635800_at
1636853_at
1639502_at
1629169_at
1626805_s_at
1625552_at
1641427_at
1640417_a_at
1628621_at
1627227_at
1628466_s_at
1628032_a_at
1626147_s_at
1639380_a_at
1635711_s_at
1625949_at
1637506_at
1625921_at
1623788_at
1629411_at
1626138_s_at
1632081_s_at
1638937_at
1640917_at
1628743_at
1626163_s_at
1629839_a_at
1634522_s_at
1640142_at
1632670_at
1638866_at
1634512_at
1632395_s_at
1632815_at
1641226_a_at
1631704_at
1638653_a_at
1629647_at
1624429_at
1630249_at
1625249_at
1634343_at
1632163_at
1625556_at
1640555_at
1639722_s_at
1632658_a_at
1637560_at
1633135_s_at
1636316_a_at
1639320_a_at
1633401_s_at
1625686_s_at
1632094_at
1638508_at
1635259_at
1640266_a_at
1623690_at
1634971_at
1627840_a_at
1637148_at
1628146_at
1636651_a_at
1639676_at
1641236_s_at
1633612_at
1636029_s_at
1629806_a_at
1635199_at
1636706_at
1634925_at
1631750_a_at
1639566_s_at
1635266_at
1636219_at
1633280_s_at
1638708_s_at
1628420_s_at
1632852_s_at
1638176_at
1640048_s_at
1628710_at
1637987_at

1626706_at
1637710_at
1631327_at
1636145_at
1636281_at
1630816_at
1631456_at
1638903_at
1626001_at
1640750_at
1639396_s_at
1637155_at
1628488_at
1628208_at
1625950_a_at
1638460_s_at
1628675_at
1634454_at
1630186_at
1636954_at
1636956_at
1640907_at
1635541_s_at
1633956_s_at
1640932_s_at
1626394_at
1626246_s_at
1639763_at
1640092_a_at
1639770_at
1625163_at
1629141_at
1639494_at
1623843_at
1635372_a_at
1624943_at
1626554_at
1623881_s_at
1641504_s_at
1640083_at
1631445_at
1627478_at
1625140_at
1640797_at
1639571_s_at
1641518_a_at
1630688_at
1638727_at
1634675_s_at
1626729_at
1637165_at
1632530_s_at
1633143_s_at
1636431_at
1634065_s_at
1628306_at
1638345_at
1628358_at
1630345_at
1635260_at
1637411_s_at
1636208_a_at
1630901_a_at
1623197_a_at
1640496_at
1634246_at
1623276_at
1633405_s_at
1635652_at
1633801_s_at
1624003_at
1627598_at
1641609_at
1629852_at
1622970_at
1638143_a_at
1626456_at
1629372_a_at
1636183_at
1634452_s_at
1636926_s_at
1628251_at
1624755_a_at
1625750_at
1636947_at
1626038_at
1635173_at
1638673_at
1637684_at
1626449_s_at
1624541_at
1626461_at
1628194_at
1624042_at
1640337_a_at
1626221_at
1630450_s_at
1635638_s_at
1632377_at
1638872_at
1625827_s_at
1634373_a_at
1634525_at
1628758_at
1635961_at
1635340_at
1628873_s_at
1627726_a_at
1638521_a_at
1628149_a_at
1632457_s_at
1630531_at
1623743_at
1623486_at
1631274_at
1635138_at
1623254_s_at
1630611_at
1628360_at
1630415_at
1637294_at
1634667_at
1624240_at
1635023_at
1626390_at
1641297_at

1628458_at
1624976_at
1637652_a_at
1623863_a_at
1626624_s_at
1633370_s_at
1640241_at
1632440_at
1636608_at
1633483_a_at
1628284_at
1634890_at
1628671_a_at
1631340_at
1634043_at
1633729_a_at
1639171_at
1625843_s_at
1638447_s_at
1632961_at
1633112_at
1628777_at
1624447_s_at
1637575_at
1627006_at
1639431_at
1633948_a_at
1632667_s_at
1634704_at
1628143_a_at
1624533_s_at
1633681_at
1640007_at
1624109_s_at
1627420_s_at
1626033_at
1623043_s_at
1630055_a_at
1640386_at
1635393_s_at
1628861_at
1638416_at
1635202_s_at
1629970_s_at
1640833_at
1637778_a_at
1641618_at
1627507_at
1626056_a_at
1628014_at
1639635_s_at
1636728_at
1622932_s_at
1629030_a_at
1627588_at
1632160_s_at
1640672_at
1641544_at
1628498_at
1623648_s_at
1626980_at
1630113_at
1632211_at
1623762_at
1633795_a_at
1635127_at
1633009_a_at
1632225_a_at
1625075_at
1631243_s_at
1633775_at
1625838_at
1634351_at
1629961_s_at
1626174_a_at
1633852_at
1638051_at
1622973_at
1640767_s_at
1633973_at
1624727_s_at
1637770_a_at
1631435_at
1625981_at
1631291_at
1638663_at
1637557_a_at
1632526_s_at
1628990_at
1639985_s_at
1626208_at
1636493_at
1625034_s_at
1630502_at
1627645_at
1633422_a_at
1640736_at
1626528_at
1625065_s_at
1630506_at
1639584_at
1626184_at
1624608_s_at
1639825_at
1632618_a_at
1641004_a_at
1633412_s_at
1629748_s_at
1630280_s_at
1640813_at
1627509_s_at
1624165_a_at
1641104_s_at
1638963_s_at
1633476_at
1630886_at
1634562_s_at
1641303_at
1638063_at
1631183_at
1633081_at
1638875_at
1636496_at
1640060_at
1629877_at
1624970_s_at

1636673_s_at
1636423_at
1626320_at
1624237_at
1634913_s_at
1639897_at
1628691_at
1629898_s_at
1625985_at
1630224_at
1629150_at
1623545_at
1639055_at
1633115_a_at
1625691_at
1641496_a_at
1627668_s_at
1639452_at
1640912_s_at
1632744_a_at
1624212_at
1628888_at
1636530_s_at
1631145_at
1627592_at
1625362_at
1632287_at
1629658_at
1634184_a_at
1632120_at
1626751_at
1628629_at
1636543_a_at
1626331_at
1633499_at
1635103_at
1634020_at
1641486_at
1634222_at
1630824_a_at
1635491_s_at
1626090_at
1640659_s_at
1625515_a_at
1630306_at
1623761_at
1629266_s_at
1640567_at
1636332_at
1634944_at
1641231_at
1635109_at
1641074_s_at
1626239_at
1623012_at
1638409_at
1633386_s_at
1628823_at
1639184_at
1634314_s_at
1623755_at
1639394_at
1641206_at
1627114_at
1635363_a_at
1624119_at
1636946_at
1623048_a_at
1633846_at
1626237_at
1639766_at
1634084_at
1640332_at
1633242_a_at
1624481_a_at
1625281_at
1627568_at
1635910_at
1626523_a_at
1624731_s_at
1639984_at
1638541_at
1639140_at
1629248_at
1636301_s_at
1632297_at
1632678_at
1630650_at
1632129_a_at
1628493_at
1640968_a_at
1637826_at
1635444_at
1626099_s_at
1628931_at
1639911_at
1641676_at
1627282_at
1624437_s_at
1630764_at
1631718_at
1626874_at
1636953_a_at
1624051_at
1634218_at
1634674_at
1625110_at
1629990_at
1640416_at
1631473_at
1640130_at
1629168_s_at
1628482_at
1628155_at
1639117_a_at
1640288_s_at
1635211_at
1634613_s_at
1628285_a_at
1636344_at
1630320_at
1634699_a_at
1635224_s_at
1631798_s_at
1637830_s_at
1627872_at

1627764_at
1624577_at
1628688_at
1632704_at
1632278_s_at
1627497_at
1638931_at
1639133_at
1635589_at
1630935_at
1640889_at
1624908_at
1623647_at
1632485_a_at
1637407_at
1626590_a_at
1622946_at
1631118_s_at
1634878_at
1625638_a_at
1637342_s_at
1641368_at
1635808_s_at
1637442_at
1636681_at
1636647_s_at
1633834_at
1630334_at
1632352_a_at
1638612_at
1628563_at
1634495_s_at
1629020_s_at
1634192_at
1640970_at
1639215_at
1635943_s_at
1636791_s_at
1633870_at
1639047_at
1623424_a_at
1632178_at
1624569_at
1627354_at
1630504_at
1623374_a_at
1640284_at
1634549_at
1626271_at
1637771_s_at
1628008_a_at
1624324_a_at
1624726_s_at
1636872_at
1632975_at
1639671_at
1629767_s_at
1628862_at
1626856_at
1637815_s_at
1635041_at
1628150_a_at
1624326_at
1635818_at
1623216_s_at
1637417_at
1640112_at
1637706_at
1635893_at
1632073_at
1627574_at
1637633_at
1629442_at
1633145_at
1622893_at
1628598_s_at
1633759_s_at
1629357_s_at
1624521_a_at
1629754_s_at
1629732_at
1635329_at
1630094_at
1640457_s_at
1630983_s_at
1638994_at
1625122_at
1639434_at
1636244_s_at
1639326_s_at
1628650_at
1634403_at
1627970_at
1625102_at
1635757_at
1632418_s_at
1633714_at
1636395_at
1629899_at
1628453_at
1629080_at
1625727_at
1628377_s_at
1634291_at
1636703_at
1638033_at
1628390_at
1628296_at
1631121_at
1634972_at
1638377_x_at
1641047_at
1635238_s_at
1636474_at
1639743_s_at
1627915_a_at
1640363_a_at
1627456_s_at
1637612_at
1640557_at
1637913_at
1641330_at
1638783_at
1631779_s_at
1625087_a_at
1631579_a_at

1634952_s_at	1640271_s_at	1641698_at	1636639_at	1641152_at	1628952_s_at

****

Lin Effects FDR < 0.1

1622894_at
1622909_at
1622915_at
1622921_at
1622970_at
1622973_at
1623027_s_at
1623028_at
1623036_a_at
1623040_at
1623058_at
1623080_at
1623088_at
1623094_at
1623097_at
1623113_at
1623133_a_at
1623134_at
1623150_at
1623154_a_at
1623201_at
1623203_at
1623251_at
1623256_at
1623264_at
1623267_at
1623268_a_at
1623281_s_at
1623285_at
1623306_at
1623333_a_at
1623335_a_at
1623353_at
1623357_at
1623436_a_at
1623455_s_at
1623486_at
1623498_at
1623502_at
1623505_s_at
1623510_at
1623513_at
1623518_s_at
1623540_at
1623543_at
1623552_s_at
1623591_a_at
1623631_at
1623633_at
1623645_a_at
1623662_at
1623666_at
1623669_at
1623675_at
1623687_at
1623689_a_at
1623695_a_at
1623698_s_at
1623737_a_at
1623766_at
1623770_at
1623782_at
1623785_a_at
1623789_at
1623817_at
1623819_at
1623826_at
1623849_s_at
1623863_a_at
1623864_at
1623885_at
1623900_a_at
1623916_at
1623934_at
1623998_at
1624015_at
1624027_at
1624042_at
1624054_at
1624069_at
1624083_s_at
1624099_at
1624101_at
1624117_at
1624135_at
1624149_at
1624156_at
1624165_a_at
1624173_at
1624186_at
1624195_at
1624198_at
1624215_s_at
1624252_s_at
1624263_at
1624272_at
1624273_at
1624277_at
1624300_s_at
1624332_s_at
1624347_s_at
1624363_at
1624389_at
1624395_at
1624444_at
1624457_at
1624464_s_at
1624480_at
1624481_a_at
1624484_a_at
1624497_at
1624503_at
1624510_at
1624521_a_at

1624533_s_at
1624535_at
1624539_at
1624555_at
1624569_at
1624577_at
1624580_at
1624581_at
1624583_at
1624589_a_at
1624603_at
1624618_at
1624627_s_at
1624629_at
1624665_at
1624668_s_at
1624678_at
1624683_at
1624688_at
1624692_at
1624717_s_at
1624755_a_at
1624756_at
1624757_at
1624772_at
1624775_at
1624782_a_at
1624795_at
1624815_at
1624847_at
1624863_a_at
1624864_s_at
1624869_at
1624892_s_at
1624908_at
1624929_at
1624935_at
1624953_at
1624957_a_at
1624966_at
1624971_at
1624993_at
1625008_at
1625048_at
1625050_s_at
1625065_s_at
1625099_at
1625102_at
1625114_at
1625120_at
1625129_at
1625134_at
1625137_at
1625144_at
1625162_at
1625163_at
1625164_at
1625165_at
1625166_at
1625184_at
1625185_at
1625193_at
1625211_s_at
1625212_at
1625235_at
1625243_a_at
1625250_at
1625280_at
1625284_at
1625295_at
1625304_s_at
1625314_at
1625323_at
1625325_s_at
1625330_at
1625338_at
1625348_s_at
1625358_s_at
1625359_at
1625362_at
1625374_at
1625375_at
1625388_at
1625393_s_at
1625405_at
1625422_at
1625434_at
1625439_at
1625462_s_at
1625487_at
1625499_at
1625512_s_at
1625514_s_at
1625517_at
1625537_at
1625544_s_at
1625572_s_at
1625589_at
1625595_a_at
1625613_at
1625617_at
1625631_at
1625640_a_at
1625644_at
1625646_at
1625648_at
1625657_at
1625658_at
1625665_at
1625685_at
1625697_at
1625700_a_at
1625727_at
1625742_at
1625744_at
1625755_at
1625770_at
1625793_at
1625801_s_at
1625806_at
1625826_at
1625829_a_at
1625850_at
1625857_at
1625860_s_at
1625862_x_at

1625863_at
1625887_at
1625898_s_at
1625913_at
1625922_a_at
1625954_at
1625967_s_at
1625972_at
1625985_at
1625986_at
1625990_at
1625994_a_at
1626007_at
1626039_at
1626056_a_at
1626074_at
1626079_a_at
1626086_at
1626094_at
1626112_at
1626124_at
1626138_s_at
1626147_s_at
1626148_at
1626154_at
1626156_at
1626168_at
1626175_at
1626198_at
1626201_at
1626217_at
1626251_at
1626257_at
1626261_s_at
1626289_at
1626307_at
1626315_at
1626320_at
1626324_at
1626326_at
1626334_at
1626340_at
1626344_at
1626350_at
1626352_at
1626385_s_at
1626396_s_at
1626399_at
1626407_at
1626412_at
1626414_at
1626433_at
1626435_at
1626482_a_at
1626492_s_at
1626497_at
1626503_at
1626524_at
1626536_at
1626540_at
1626552_at
1626565_at
1626577_at
1626584_a_at
1626588_a_at
1626596_at
1626609_at
1626641_s_at
1626650_at
1626679_at
1626699_at
1626701_at
1626707_a_at
1626718_at
1626734_at
1626740_at
1626745_at
1626749_a_at
1626781_at
1626812_at
1626813_at
1626820_at
1626832_at
1626841_s_at
1626850_s_at
1626856_at
1626857_at
1626864_at
1626881_at
1626906_at
1626933_s_at
1626947_s_at
1626963_at
1626972_at
1627009_at
1627014_a_at
1627041_s_at
1627047_at
1627068_at
1627078_at
1627093_at
1627100_s_at
1627102_at
1627114_at
1627118_at
1627120_at
1627144_at
1627167_a_at
1627172_s_at
1627189_a_at
1627246_at
1627287_at
1627288_a_at
1627297_at
1627301_s_at
1627327_at
1627330_at
1627340_at
1627343_a_at
1627376_at
1627405_at
1627432_at
1627436_s_at
1627448_at
1627459_at
1627460_at

1627470_at
1627473_at
1627495_at
1627498_at
1627507_at
1627552_at
1627565_at
1627574_at
1627598_at
1627620_at
1627633_at
1627640_at
1627656_at
1627657_at
1627660_a_at
1627662_at
1627679_at
1627682_at
1627702_at
1627761_at
1627773_a_at
1627779_at
1627807_at
1627829_at
1627832_at
1627840_a_at
1627844_at
1627847_s_at
1627861_s_at
1627881_at
1627890_at
1627895_at
1627910_s_at
1627938_at
1627939_a_at
1627959_a_at
1627964_s_at
1627971_s_at
1627973_s_at
1627982_at
1628000_s_at
1628018_at
1628030_at
1628040_at
1628053_at
1628080_at
1628083_at
1628092_at
1628100_at
1628129_a_at
1628131_at
1628149_a_at
1628152_at
1628173_at
1628202_at
1628214_at
1628231_at
1628237_s_at
1628257_s_at
1628264_a_at
1628268_at
1628272_a_at
1628282_at
1628309_at
1628320_at
1628328_at
1628332_at
1628339_a_at
1628360_at
1628362_s_at
1628363_at
1628364_at
1628404_at
1628420_s_at
1628428_at
1628432_at
1628444_at
1628446_at
1628469_a_at
1628475_at
1628487_s_at
1628488_at
1628492_at
1628493_at
1628494_a_at
1628500_at
1628507_at
1628539_at
1628550_a_at
1628558_at
1628578_at
1628581_at
1628599_at
1628605_at
1628608_at
1628611_at
1628617_at
1628618_at
1628632_at
1628643_at
1628646_at
1628648_at
1628670_at
1628675_at
1628681_at
1628686_a_at
1628716_at
1628719_at
1628726_s_at
1628734_at
1628743_at
1628744_s_at
1628754_s_at
1628759_a_at
1628760_at
1628763_at
1628764_at
1628798_at
1628818_at
1628821_at
1628828_s_at
1628854_at
1628862_at
1628882_at
1628909_at
1628922_s_at

1628931_at
1628946_at
1628947_s_at
1628977_at
1628984_s_at
1629009_at
1629072_at
1629078_s_at
1629083_at
1629095_a_at
1629098_at
1629106_at
1629113_a_at
1629144_at
1629153_s_at
1629160_s_at
1629168_s_at
1629189_at
1629199_at
1629207_at
1629227_at
1629233_s_at
1629243_at
1629250_at
1629257_s_at
1629271_at
1629285_at
1629307_s_at
1629308_at
1629327_at
1629363_at
1629367_at
1629374_at
1629377_at
1629382_at
1629395_at
1629396_a_at
1629401_s_at
1629413_at
1629427_at
1629442_at
1629464_a_at
1629468_at
1629469_s_at
1629476_at
1629479_a_at
1629487_at
1629496_at
1629510_at
1629515_at
1629520_at
1629565_s_at
1629625_at
1629629_at
1629632_at
1629633_at
1629642_a_at
1629644_s_at
1629661_at
1629670_at
1629685_at
1629698_at
1629705_at
1629718_at
1629766_at
1629788_at
1629806_a_at
1629853_at
1629875_a_at
1629897_a_at
1629936_at
1629972_at
1630003_at
1630005_at
1630008_at
1630024_at
1630067_a_at
1630113_at
1630130_at
1630153_a_at
1630173_a_at
1630206_at
1630208_at
1630209_at
1630212_at
1630227_a_at
1630236_s_at
1630241_at
1630242_at
1630256_at
1630260_at
1630263_at
1630302_at
1630306_at
1630323_at
1630329_at
1630335_s_at
1630359_at
1630363_at
1630365_at
1630393_a_at
1630407_at
1630416_at
1630421_at
1630422_at
1630429_s_at
1630453_at
1630467_a_at
1630469_a_at
1630483_a_at
1630504_at
1630520_s_at
1630539_at
1630590_at
1630605_at
1630606_at
1630635_s_at
1630641_at
1630643_at
1630680_at
1630685_at
1630699_at
1630713_at
1630723_a_at
1630724_at
1630735_at

1630761_at
1630763_at
1630771_s_at
1630773_a_at
1630778_at
1630780_a_at
1630781_at
1630802_at
1630807_at
1630821_at
1630825_at
1630841_at
1630842_s_at
1630870_s_at
1630877_a_at
1630953_at
1630958_at
1630983_s_at
1630990_at
1630996_s_at
1631024_s_at
1631030_at
1631040_at
1631046_s_at
1631055_at
1631058_s_at
1631059_at
1631083_at
1631090_a_at
1631094_s_at
1631128_s_at
1631137_at
1631142_a_at
1631161_at
1631204_at
1631208_at
1631209_at
1631213_at
1631214_at
1631227_at
1631244_a_at
1631303_s_at
1631304_a_at
1631307_at
1631313_at
1631316_a_at
1631319_at
1631325_at
1631354_x_at
1631359_s_at
1631371_s_at
1631374_at
1631399_a_at
1631405_at
1631417_s_at
1631420_at
1631426_at
1631430_at
1631456_at
1631469_at
1631477_a_at
1631479_at
1631515_at
1631525_at
1631526_s_at
1631561_s_at
1631565_a_at
1631568_a_at
1631573_a_at
1631578_s_at
1631584_at
1631603_at
1631622_at
1631633_a_at
1631663_at
1631723_at
1631728_s_at
1631733_at
1631745_at
1631776_at
1631779_s_at
1631784_at
1631800_at
1631806_at
1631873_at
1631891_at
1631915_at
1631942_at
1631971_at
1631984_at
1632003_a_at
1632021_at
1632041_s_at
1632055_at
1632057_at
1632065_at
1632103_at
1632114_at
1632120_at
1632139_at
1632146_a_at
1632185_s_at
1632188_at
1632194_at
1632195_at
1632196_at
1632198_at
1632202_at
1632207_a_at
1632212_at
1632228_at
1632232_at
1632236_at
1632258_s_at
1632261_at
1632280_at
1632297_at
1632317_at
1632319_at
1632335_at
1632338_a_at
1632342_a_at
1632343_at
1632361_at
1632367_at
1632373_s_at

1632387_at
1632390_at
1632400_at
1632409_a_at
1632417_a_at
1632420_at
1632421_at
1632431_s_at
1632446_at
1632462_at
1632478_a_at
1632479_at
1632492_at
1632510_at
1632517_at
1632532_s_at
1632568_at
1632586_at
1632605_at
1632640_at
1632656_at
1632658_a_at
1632695_at
1632705_at
1632710_s_at
1632712_s_at
1632724_at
1632731_at
1632732_at
1632751_at
1632753_a_at
1632755_at
1632758_at
1632762_s_at
1632771_at
1632782_a_at
1632794_a_at
1632802_at
1632809_at
1632818_at
1632821_a_at
1632835_at
1632836_at
1632855_at
1632872_at
1632874_at
1632883_at
1632927_at
1632932_a_at
1632936_at
1632986_a_at
1632989_a_at
1633002_at
1633026_a_at
1633036_s_at
1633060_at
1633067_at
1633086_s_at
1633099_at
1633106_at
1633111_at
1633112_at
1633131_s_at
1633154_at
1633191_at
1633225_at
1633233_a_at
1633237_at
1633266_at
1633268_s_at
1633287_at
1633293_at
1633305_at
1633320_at
1633333_a_at
1633353_s_at
1633362_at
1633378_at
1633380_at
1633415_at
1633422_a_at
1633448_at
1633457_at
1633467_a_at
1633471_at
1633480_at
1633487_at
1633497_s_at
1633501_s_at
1633505_at
1633512_at
1633523_at
1633532_at
1633540_at
1633556_s_at
1633563_at
1633568_s_at
1633573_a_at
1633599_a_at
1633606_s_at
1633612_at
1633631_at
1633641_a_at
1633642_at
1633645_at
1633649_s_at
1633654_s_at
1633658_a_at
1633687_at
1633707_at
1633709_at
1633727_s_at
1633731_at
1633755_at
1633765_at
1633778_at
1633779_s_at
1633780_at
1633784_at
1633846_at
1633856_at
1633857_at
1633886_at
1633914_at
1633915_at
1633947_at

1633949_at
1633957_s_at
1633959_s_at
1633967_at
1633975_s_at
1633997_s_at
1633998_s_at
1634013_at
1634014_at
1634020_at
1634029_at
1634053_at
1634072_s_at
1634076_at
1634102_at
1634113_at
1634117_at
1634131_s_at
1634143_at
1634144_at
1634165_at
1634182_at
1634193_at
1634197_at
1634209_at
1634219_a_at
1634240_at
1634241_at
1634269_at
1634295_at
1634315_a_at
1634321_s_at
1634351_at
1634373_a_at
1634393_s_at
1634396_at
1634401_at
1634429_at
1634430_at
1634433_at
1634443_a_at
1634460_at
1634474_s_at
1634490_at
1634495_s_at
1634496_at
1634509_s_at
1634512_at
1634514_at
1634515_at
1634528_at
1634541_a_at
1634550_at
1634551_at
1634553_at
1634563_at
1634573_a_at
1634592_at
1634594_at
1634625_at
1634630_at
1634633_s_at
1634650_at
1634658_a_at
1634664_at
1634667_at
1634684_at
1634687_at
1634693_at
1634704_at
1634705_at
1634713_at
1634742_at
1634750_at
1634786_at
1634804_at
1634809_s_at
1634815_at
1634823_at
1634861_at
1634878_at
1634883_at
1634904_s_at
1634922_s_at
1634940_at
1634960_at
1634962_s_at
1634971_at
1634978_at
1634979_at
1635003_at
1635007_at
1635008_at
1635013_s_at
1635033_at
1635080_at
1635086_at
1635088_at
1635089_at
1635109_at
1635137_a_at
1635153_at
1635203_at
1635205_at
1635211_at
1635221_at
1635223_at
1635233_at
1635248_at
1635267_s_at
1635271_at
1635290_at
1635293_s_at
1635294_at
1635305_s_at
1635321_at
1635329_at
1635343_a_at
1635361_at
1635363_a_at
1635365_at
1635370_at
1635379_at
1635385_at
1635422_s_at
1635426_at

1635428_at
1635435_at
1635444_at
1635447_at
1635454_a_at
1635481_a_at
1635492_at
1635500_a_at
1635502_at
1635513_at
1635521_at
1635525_at
1635527_at
1635530_at
1635549_at
1635552_s_at
1635581_at
1635588_at
1635589_at
1635607_at
1635645_at
1635647_at
1635654_at
1635666_at
1635667_at
1635695_at
1635701_at
1635706_at
1635724_at
1635728_a_at
1635729_a_at
1635769_at
1635774_at
1635800_at
1635808_s_at
1635813_at
1635828_at
1635840_s_at
1635849_at
1635861_a_at
1635868_at
1635878_s_at
1635881_at
1635886_s_at
1635893_at
1635897_at
1635903_at
1635936_at
1635939_a_at
1635947_at
1635950_at
1635951_at
1635970_at
1635973_at
1635980_s_at
1636006_at
1636020_s_at
1636038_at
1636059_at
1636064_at
1636123_at
1636140_at
1636149_at
1636154_at
1636168_s_at
1636170_at
1636173_s_at
1636174_at
1636193_at
1636198_at
1636202_s_at
1636205_at
1636207_at
1636217_at
1636219_at
1636240_at
1636244_s_at
1636245_at
1636248_at
1636255_s_at
1636257_at
1636275_a_at
1636308_at
1636311_at
1636322_at
1636337_s_at
1636341_at
1636343_at
1636373_at
1636375_at
1636410_at
1636412_at
1636423_at
1636442_at
1636445_at
1636446_at
1636460_at
1636464_at
1636473_at
1636474_at
1636493_at
1636498_at
1636539_at
1636556_at
1636557_a_at
1636564_at
1636567_at
1636575_s_at
1636583_at
1636594_at
1636606_at
1636620_s_at
1636647_s_at
1636656_at
1636674_at
1636694_at
1636695_at
1636703_at
1636705_at
1636743_s_at
1636766_at
1636767_at
1636769_at
1636775_at
1636777_at
1636781_at

1636795_at
1636798_at
1636811_at
1636816_s_at
1636829_at
1636843_a_at
1636845_at
1636848_at
1636877_at
1636894_s_at
1636918_a_at
1636926_s_at
1636943_s_at
1636948_a_at
1636950_at
1636995_at
1637007_s_at
1637008_at
1637027_s_at
1637079_at
1637097_at
1637107_at
1637111_a_at
1637118_at
1637127_at
1637128_a_at
1637129_at
1637141_at
1637175_at
1637189_at
1637191_at
1637192_at
1637255_a_at
1637269_at
1637271_a_at
1637284_at
1637291_at
1637307_at
1637309_a_at
1637314_at
1637317_at
1637319_at
1637321_at
1637346_at
1637352_a_at
1637366_at
1637378_s_at
1637386_at
1637393_at
1637398_a_at
1637403_at
1637417_at
1637429_at
1637461_at
1637466_at
1637469_at
1637481_at
1637499_s_at
1637513_at
1637515_s_at
1637518_at
1637551_at
1637557_a_at
1637575_at
1637587_at
1637598_at
1637612_at
1637620_s_at
1637627_at
1637632_at
1637647_at
1637648_at
1637649_at
1637662_at
1637669_at
1637679_s_at
1637689_at
1637713_at
1637717_at
1637733_at
1637773_s_at
1637780_a_at
1637815_s_at
1637826_at
1637843_at
1637872_at
1637873_at
1637897_at
1637899_at
1637900_at
1637942_at
1637954_at
1637960_at
1637963_at
1637969_at
1637973_a_at
1637983_s_at
1638009_s_at
1638011_a_at
1638020_at
1638053_at
1638080_at
1638092_a_at
1638100_s_at
1638112_at
1638119_at
1638127_s_at
1638143_a_at
1638158_at
1638174_at
1638176_at
1638185_at
1638225_a_at
1638226_at
1638246_at
1638259_s_at
1638265_s_at
1638277_at
1638282_at
1638296_at
1638312_at
1638321_s_at
1638335_at
1638342_at
1638343_at
1638361_at

1638411_at
1638445_a_at
1638447_s_at
1638469_s_at
1638499_s_at
1638523_at
1638526_a_at
1638539_at
1638544_at
1638592_at
1638603_at
1638619_s_at
1638635_at
1638642_at
1638649_at
1638652_at
1638667_a_at
1638670_a_at
1638699_at
1638708_s_at
1638709_at
1638716_a_at
1638758_at
1638763_at
1638770_a_at
1638782_at
1638807_s_at
1638809_at
1638811_at
1638816_at
1638833_at
1638846_at
1638852_at
1638875_at
1638884_at
1638903_at
1638919_at
1638923_at
1638930_s_at
1638963_s_at
1638973_s_at
1638974_at
1638981_at
1639040_s_at
1639046_at
1639072_at
1639075_a_at
1639079_at
1639111_at
1639138_at
1639139_a_at
1639148_at
1639171_at
1639179_at
1639198_at
1639202_a_at
1639203_at
1639211_at
1639215_at
1639222_at
1639236_at
1639255_s_at
1639264_at
1639265_at
1639268_at
1639286_s_at
1639323_at
1639346_at
1639361_a_at
1639366_at
1639374_s_at
1639377_at
1639383_a_at
1639400_at
1639410_at
1639411_at
1639421_at
1639424_at
1639461_a_at
1639494_at
1639519_at
1639527_at
1639566_s_at
1639567_at
1639579_s_at
1639584_at
1639594_at
1639611_at
1639621_at
1639622_at
1639640_at
1639653_at
1639663_at
1639665_at
1639667_at
1639683_at
1639692_s_at
1639721_at
1639737_at
1639748_at
1639757_at
1639762_at
1639787_at
1639816_at
1639842_at
1639856_at
1639862_at
1639868_at
1639874_at
1639891_at
1639898_at
1639903_at
1639911_at
1639913_at
1639927_at
1639932_at
1639937_at
1639972_at
1639974_a_at
1639982_at
1639993_at
1640006_at
1640020_at
1640066_at
1640082_at
1640101_at

1640109_at
1640112_at
1640130_at
1640134_a_at
1640158_at
1640162_at
1640167_s_at
1640169_s_at
1640185_at
1640191_a_at
1640212_at
1640215_at
1640216_at
1640220_a_at
1640228_at
1640242_s_at
1640244_at
1640257_at
1640265_a_at
1640301_a_at
1640303_a_at
1640318_at
1640333_at
1640335_at
1640336_at
1640341_s_at
1640351_s_at
1640355_at
1640365_s_at
1640379_s_at
1640380_a_at
1640425_at
1640426_at
1640445_at
1640451_at
1640486_s_at
1640492_at
1640497_at
1640504_at
1640507_s_at
1640520_at
1640529_at
1640540_at
1640552_at
1640555_at
1640567_at
1640584_at
1640590_at
1640621_at
1640661_at
1640695_at
1640713_at
1640714_at
1640720_a_at
1640732_s_at
1640734_a_at
1640744_a_at
1640746_at
1640754_at
1640755_at
1640759_at
1640762_at
1640765_at
1640781_a_at
1640782_at
1640825_a_at
1640827_at
1640883_a_at
1640886_a_at
1640917_at
1640918_at
1640952_at
1640980_at
1640991_at
1640999_at
1641011_at
1641038_at
1641058_at
1641065_s_at
1641105_at
1641115_at
1641129_at
1641143_s_at
1641178_s_at
1641179_at
1641189_a_at
1641191_s_at
1641212_a_at
1641236_s_at
1641241_at
1641252_at
1641256_at
1641262_at
1641270_at
1641278_at
1641285_at
1641303_at
1641306_at
1641309_s_at
1641320_s_at
1641324_at
1641330_at
1641337_at
1641341_at
1641350_at
1641370_s_at
1641378_at
1641390_at
1641399_at
1641403_at
1641412_at
1641420_s_at
1641424_at
1641427_at
1641445_s_at
1641458_s_at
1641461_at
1641469_at
1641478_s_at
1641479_at
1641481_at
1641486_at
1641496_a_at
1641502_a_at
1641522_at
1641530_s_at

1641537_s_at
1641540_a_at
1641541_a_at
1641549_at
1641570_s_at
1641575_at
1641579_at
1641598_at
1641603_s_at
1641606_s_at
1641624_at
1641626_at
1641634_at
1641642_at
1641653_at
1641660_at
1641664_at
1641681_s_at
1641701_at
1641704_at
1641711_at
1641715_at
1641745_a_at

****

Dep Effects UP regulated FDR < 0.1

1623632_s_at
1623693_a_at
1623782_at
1624042_at
1624464_s_at
1624717_s_at
1624943_at
1625199_s_at
1625264_s_at
1625290_at
1625430_at
1625433_at
1625830_a_at
1625840_at
1626178_s_at
1626385_s_at
1626566_at
1626575_at
1626650_at
1627270_at
1627280_s_at
1627376_at
1627651_a_at
1627702_at
1628172_at
1629357_s_at
1629839_a_at
1629842_at
1629843_s_at
1630280_s_at
1630824_a_at
1630884_at
1630968_at
1631225_at
1631243_s_at
1631374_at
1631385_at
1631426_at
1631527_at
1632146_a_at
1632234_at
1632623_at
1632916_at
1633026_a_at
1633069_s_at
1633391_at
1633563_at
1633654_s_at
1633727_s_at
1633965_at
1634034_at
1634707_s_at
1634814_at
1634869_at
1634877_at
1634904_s_at
1635202_s_at
1635581_at
1635618_at
1635619_a_at
1635711_s_at
1635904_s_at
1636423_at
1636521_at
1636591_at
1636682_at
1636867_s_at
1636896_a_at
1637193_at
1637229_a_at
1637611_at
1637671_a_at
1637872_at
1637940_s_at
1638050_s_at
1638186_a_at
1638290_at
1638325_at
1638727_at
1638875_at
1638994_at
1639321_s_at
1639467_at
1639476_at
1639611_at
1639858_s_at
1640224_s_at
1640296_a_at
1640528_at
1640754_at
1640764_at
1641126_at
1641233_a_at
1641381_s_at
1641506_at

****

Dep Effects DOWN regulated FDR < 0.1

1622935_at
1623032_at
1623069_s_at
1623607_at
1623766_at
1623783_at
1623928_at
1624158_at
1624185_at
1624202_a_at
1624396_at
1624465_at
1624466_a_at
1624560_at
1624699_s_at
1624818_s_at
1624840_at
1624888_at
1624984_at
1625027_a_at
1625250_at
1625351_at
1625375_at
1625519_at
1625814_at
1625954_at
1625991_s_at
1626075_at
1626222_at
1626340_at
1626503_at
1626811_at
1626832_at
1627046_at
1627078_at
1627459_at
1627525_a_at
1627552_at
1627888_at
1628194_at
1628296_at
1628376_x_at
1628429_at
1628598_s_at
1628634_at
1628854_at
1628938_at
1629117_at
1629391_at
1629427_at
1629464_a_at
1629476_at
1629718_at
1629955_at
1630131_at
1630335_s_at
1630408_s_at
1630929_at
1631200_at
1631627_at
1631648_at
1631877_a_at
1631909_at
1631998_at
1632109_s_at
1632318_at
1632374_at
1632461_at
1632583_at
1632677_a_at
1632695_at
1632834_a_at
1633197_at
1633463_s_at
1633810_at
1634575_at
1634672_at
1634697_at
1635065_at
1635305_s_at
1635491_s_at
1635765_at
1635769_at
1635821_at
1635871_at
1635983_a_at
1635987_at
1636014_at
1636131_at
1636142_at
1636257_at
1636337_s_at
1636460_at
1636639_at
1636711_at
1636762_a_at
1636829_at
1636921_at
1636948_a_at
1637124_at
1637392_at
1637465_at
1637547_at
1637778_a_at
1638217_at
1638224_at
1638272_at
1638335_at
1638350_at
1638695_at
1638833_at
1638970_at
1639071_a_at
1639135_at

1639152_at
1639158_at
1639341_at
1639429_at
1639762_at
1639993_at
1640241_at
1640293_s_at
1640332_at
1640635_a_at
1640824_at
1640826_at
1641078_s_at
1641201_at
1641568_a_at
1641630_at

****

Lin x Dep Effects FDR < 0.1

1632492_at

1628404_at

File S2

Functional annotations for probe sets in Figure 6, showing both *Inb* and *Dep* effects

For each pattern we give the list of probe sets and their functional information as provided by the *Functional annotation table* tool in the DAVID web page.

****

+D

C

-D

Probe sets:

1624717_s_at
1625430_at
1625840_at
1631385_at
1631527_at
1632623_at
1635581_at
1636896_a_at
1637193_at
1637940_s_at
1641126_at
1641381_s_at

Functional annotation table:

ID	Gene Name	Species	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1632623_at	Cytochrome b5-related	Drosophila melanogaster	GO:0006631~fatty acid metabolic process,GO:0006633~fatty acid biosynthetic process,GO:0008610~lipid biosynthetic process,GO:0016053~organic acid biosynthetic process,GO:0046394~carboxylic acid biosynthetic process,GO:0055114~oxidation reduction,	GO:0005739~mitochondrion,GO:0005811~lipid particle,	GO:0005506~iron ion binding,GO:0009055~electron carrier activity,GO:0016717~oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water,GO:0020037~heme binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046906~tetrapyrrole binding,GO:0046914~transition metal ion binding,	IPR001199:Cytochrome b5,IPR005804:Fatty acid desaturase, type 1,IPR012171:Fatty acid/sphingolipid desaturase,IPR018506:Cytochrome b5, heme-binding site,		PIRSF015921:fatty acid desaturase/sphingolipid desaturase,PIRSF015921:FA_sphinglp_des,		complete proteome, heme,iron,metal-binding,metalloprotein,	chain:Cytochrome b5-related protein,domain:Cytochrome b5 heme-binding,metal ion-binding site:Iron (heme axial ligand),sequence conflict,sequence variant,
1636896_a_at	Dmel_CG12576	Drosophila melanogaster								complete proteome,	
1641381_s_at	Dmel_CG13213	Drosophila melanogaster				IPR001810:Cyclin-like F-box,IPR018483:Carbohydrate kinase, FGGY, conserved site,		PIRSF036853:conserved protein with F-box/LRR-repeat, AtFBL11 type,	SM00256:FBOX,	complete proteome,	
1625430_at	Dmel_CG14022	Drosophila melanogaster			GO:0003998~acylphosphatase activity,	IPR001792:Acylphosphatase,IPR001792:Acylphosphatase-like,	dme00620:Pyruvate metabolism,	PIRSF001266:acylphosphatase,		complete proteome,hydrolase,	
1631385_at	Dmel_CG2889	Drosophila melanogaster			GO:0008270~zinc ion binding,GO:0043167~ion						

binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR007087:Zinc finger, C2H2-type,IPR012934:Zinc finger, AD-type,IPR015880:Zinc finger, C2H2-like, SM00355:ZnF_C2H2, complete proteome,

1624717_s_at Dmel_CG32647 Drosophila melanogaster IPR001007:von Willebrand factor, type C,IPR002052:N-6 adenine-specific DNA methylase, conserved site, SM00214:VWC, complete proteome,methyltransferase,transferase,

1635581_at Dmel_CG8300 Drosophila melanogaster complete proteome,

1637193_at Eukaryotic translation initiation factor 3 subunit C Drosophila melanogaster GO:0006412~translation,GO:0006413~translational initiation, GO:0005829~cytosol,GO:0005852~eukaryotic translation initiation factor 3 complex, GO:0003743~translation initiation factor activity,GO:0008135~translation factor activity, nucleic acid binding, IPR000717:Proteasome component region PCI,IPR008905:Eukaryotic translation initiation factor 3 subunit 8, N-terminal,IPR011991:Winged helix repressor DNA-binding, PIRSF017001:eukaryotic translation initiation factor 3, subunit 8, SM00088:PINT, complete proteome,cytoplasm,Initiation factor,phosphoprotein,protein biosynthesis, chain:Eukaryotic translation initiation factor 3 subunit C,domain:PCI,modified residue,sequence conflict,

1631527_at Eukaryotic translation initiation factor 3 subunit L Drosophila melanogaster GO:0006412~translation, GO:0003743~translation initiation factor activity,GO:0008135~translation factor activity, nucleic acid binding, IPR019382:RNA polymerase I-associated factor PAF67, complete proteome,cytoplasm,Initiation factor,protein biosynthesis, chain:Eukaryotic translation initiation factor 3 subunit L,

1641126_at Protein LSM12 homolog A Drosophila melanogaster IPR019181:RNA-processing, Lsm domain, complete proteome, chain:Protein LSM12 homolog A,

1625840_at Uncharacterized protein CG12001 Drosophila melanogaster complete proteome,rna editing, chain:Uncharacterized protein CG12001,sequence variant,

****

C

-D

+D

Probe sets:

1624185_at	1628598_s_at	1633463_s_at	1636762_a_at	1638335_at	1640332_at
1628296_at	1628938_at	1636337_s_at	1637778_a_at	1640241_at	

Functional annotation table:

ID	Gene Name	Species	COG_ONTOLOGY	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1624185_at	Dmel_CG1041	Drosophila melanogaster			GO:0005739~mitochondrion,GO:0005777~peroxisome,GO:0042579~microbody,	GO:0004092~carnitine O-acetyltransferase activity,GO:0008374~O-acyltransferase activity,GO:0016406~carnitine O-acyltransferase activity,GO:0016407~acetyltransferase activity,GO:0016413~O-acetyltransferase activity,	IPR000542:Acyltransferase ChoActase/COT/CPT,		PIRSF000430:carnitine O-acetyltransferase,		Acyltransferase,complete proteome,transferase,	
1628938_at	Dmel_CG10882	Drosophila melanogaster		GO:0006886~intracellular protein transport,GO:0006888~ER to Golgi vesicle-mediated transport,GO:0008104~protein localization,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0034613~cellular protein localization,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0048193~Golgi vesicle transport,GO:0070727~cellular macromolecule localization,	GO:0005794~Golgi apparatus,GO:0005811~lipid particle,GO:0012505~endomembrane system,GO:0012506~vesicle membrane,GO:0012507~ER to Golgi transport vesicle membrane,GO:0016023~cytoplasmic membrane-bounded vesicle,GO:0030117~membrane coat,GO:0030120~vesicle coat,GO:0030127~COPII vesicle							

coat,GO:0030133~transport vesicle,GO:0030134~ER to Golgi transport vesicle,GO:0030135~coated vesicle,GO:0030658~transport vesicle membrane,GO:0030659~cytoplasmic vesicle membrane,GO:0030662~coated vesicle membrane,GO:0031090~organelle membrane,GO:0031410~cytoplasmic vesicle,GO:0031982~vesicle,GO:0031988~membrane-bounded vesicle,GO:0044431~Golgi apparatus part,GO:0044433~cytoplasmic vesicle part,GO:0048475~coated membrane,

GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0008270~zinc ion binding,GO:0017171~serine hydrolase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR000183:Orn/DAP/Arg decarboxylase 2,IPR000276:7TM GPCR, rhodopsin-like,IPR006031:XYPPX repeat,IPR006895:Zinc finger, Sec23/Sec24-type,IPR006896:Sec23/Sec24 trunk region,IPR006900:Sec23/Sec24 helical region,IPR007123:Gelsolin region,IPR012990:Sec23/Sec24 beta-sandwich, complete proteome,hydrolase,protein transport,transport,

1628598_s_at Dmel_CG1250 Drosophila melanogaster Intracellular trafficking and secretion, GO:0002164~larval development,GO:0002165~instar larval or pupal development,GO:0002168~instar larval development,GO:0003002~regionalization,GO:0006886~intracellular protein transport,GO:0006888~ER to Golgi vesicle-mediated transport,GO:0007030~Golgi organization,GO:0007389~pattern specification process,GO:0007591~molting cycle, chitin-based cuticle,GO:0007592~protein-based cuticle development,GO:0008104~protein localization,GO:0008363~larval chitin-based cuticle development,GO:0009791~post-embryonic development,GO:0010721~negative regulation of cell development,GO:0010769~regulation of cell morphogenesis involved in differentiation,GO:0010975~regulation of neuron projection development,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0018988~molting cycle, protein-based cuticle,GO:0022404~molting cycle process,GO:0022604~regulation of cell morphogenesis,GO:0031344~regulation of cell projection organization,GO:0031345~negative regulation of cell projection organization,GO:0034613~cellular protein localization,GO:0035017~cuticle pattern formation,GO:0035293~chitin-based larval cuticle pattern formation,GO:0040003~chitin-based cuticle development,GO:0042303~molting cycle,GO:0042335~cuticle development,GO:0042336~protein-based cuticle development during molting,GO:0042337~chitin-based cuticle development during molting,GO:0045184~establishment of protein localization,GO:0045596~negative regulation of cell differentiation,GO:0045664~regulation of neuron differentiation,GO:0046907~intracellular transport,GO:0048193~Golgi vesicle transport,GO:0048814~regulation of dendrite morphogenesis,GO:0050767~regulation of neurogenesis,GO:0050768~negative regulation of neurogenesis,GO:0050773~regulation of dendrite development,GO:0050774~negative regulation of dendrite morphogenesis,GO:0051129~negative regulation of cellular component organization,GO:0051960~regulation of nervous system development,GO:0060284~regulation of cell development,GO:0070727~cellular macromolecule localization, GO:0005783~endoplasmic reticulum,GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0012505~endomembrane system,GO:0012506~vesicle membrane,GO:0012507~ER to Golgi transport vesicle membrane,GO:0016023~cytoplasmic membrane-bounded vesicle,GO:0030117~membrane coat,GO:0030120~vesicle coat,GO:0030127~COPII vesicle coat,GO:0030133~transport vesicle,GO:0030134~ER to Golgi transport vesicle,GO:0030135~coated vesicle,GO:0030658~transport vesicle membrane,GO:0030659~cytoplasmic vesicle membrane,GO:0030662~coated vesicle membrane,GO:0031090~organelle membrane,GO:0031410~cytoplasmic vesicle,GO:0031982~vesicle,GO:0031988~membrane-bounded vesicle,GO:0044431~Golgi apparatus part,GO:0044433~cytoplasmic vesicle part,GO:0048475~coated membrane, GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0008270~zinc ion binding,GO:0030695~GTPase regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding ,GO:0046914~transition metal ion binding,GO:0060589~nucleoside-triphosphatase regulator activity, IPR006895:Zinc finger, Sec23/Sec24-type,IPR006896:Sec23/Sec24 trunk region,IPR006900:Sec23/Sec24 helical region,IPR007123:Gelsolin region,IPR012990:Sec23/Sec24 beta-sandwich, PIRSF003206:SEC23 protein, protein transport,transport,

1638335_at Dmel_CG18493 Drosophila melanogaster GO:0006508~proteolysis, GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR008758:Peptidase S28, PIRSF016539:Lysosomal Pro-X carboxypeptidase / Dipeptidyl-peptidase 2, complete proteome,

1640332_at Dmel_CG6972 Drosophila melanogaster complete proteome,

1640241_at Dmel_CG7008 Drosophila melanogaster GO:0010605~negative regulation of macromolecule metabolic process,GO:0010608~posttranscriptional regulation of gene expression,GO:0010629~negative regulation of gene expression,GO:0016246~RNA interference,GO:0016441~posttranscriptional gene silencing,GO:0016458~gene silencing,GO:0031047~gene silencing by RNA,GO:0035194~posttranscriptional gene silencing by RNA,GO:0040029~regulation of gene expression, epigenetic, GO:0005811~lipid particle,GO:0016442~RNA-induced silencing complex,GO:0030529~ribonucleoprotein complex,GO:0031332~RNAi effector complex, GO:0003712~transcription cofactor activity,GO:0003713~transcription coactivator activity,GO:0008134~transcription factor binding,GO:0016563~transcription activator activity,GO:0030528~transcription regulator activity, IPR002999:Tudor domain,IPR006021:Staphylococcal nuclease (SNase-like),IPR008191:Maternal tudor protein,IPR016685:RNA-induced silencing complex, nuclease component Tudor-SN,IPR018351:Tudor subgroup, PIRS F017179:RISC-Tudor-SN, SM00318:SNc,SM00333:TUDOR, complete proteome,hydrolase, 1637778_a_at Probable glucosamine 6-phosphate N-acetyltransferase Drosophila melanogaster GO:0004343~glucosamine 6-phosphate N-acetyltransferase activity,GO:0008080~N-acetyltransferase activity,GO:0016407~acetyltransferase activity,GO:0016410~N-acyltransferase activity,GO:0042802~identical protein binding, IPR000182:GCN5-related N-acetyltransferase,IPR016181:Acyl-CoA N-acyltransferase, dme00520:Amino sugar and nucleotide sugar metabolism, Acyltransferase,complete proteome,transferase, binding site:Substrate,chain:Probable glucosamine 6-phosphate N- acetyltransferase,domain:N-acetyltransferase,region of interest:Acetyl-CoA binding,region of interest:Substrate binding,

1633463_s_at Putative polypeptide N-acetylgalactosaminyltransferase 9 Drosophila melanogaster GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, alternative splicing,calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:Putative polypeptide N- acetylgalactosaminyltransferase 9,compositionally biased region:Gly-rich,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...) ,region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,sequence conflict,splice variant,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1628296_at polypeptide GalNAc transferase 4 Drosophila melanogaster GO:0009311~oligosaccharide metabolic process,GO:0009312~oligosaccharide biosynthetic process,GO:0016051~carbohydrate biosynthetic process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:N-acetylgalactosaminyltransferase 4,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...),region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1636337_s_at polypeptide GalNAc transferase 6 Drosophila melanogaster GO:0009311~oligosaccharide metabolic process,GO:0009312~oligosaccharide biosynthetic process,GO:0016051~carbohydrate biosynthetic process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:N-acetylgalactosaminyltransfer ase 6,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...),region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,sequence conflict,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1636762_a_at supercoiling factor Drosophila melanogaster Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome partitioning / General function prediction only, GO:0006325~chromatin organization,GO:0007549~dosage compensation,GO:0009047~dosage compensation, by hyperactivation of X chromosome,GO:0040029~regulation of gene expression, epigenetic,GO:0051276~chromosome organization, GO:0005694~chromosome,GO:0005700~polytene chromosome,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0003677~DNA binding,GO:0003916~DNA topoisomerase activity,GO:0005509~calcium ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR002048:Calcium-binding EF-hand,IPR011992:EF-Hand type,IPR018247:EF-HAND 1,IPR018248:EF hand,IPR018249:EF-HAND 2, SM00054:EFh, calcium,

****

-D

+D

C

Probe sets:

1622935_at
1623032_at
1623766_at
1623783_at
1623928_at
1624158_at
1624699_s_at
1624840_at
1624888_at
1624984_at
1625027_a_at
1625375_at
1625814_at
1626075_at
1626222_at
1626503_at
1626811_at
1627078_at
1627459_at
1627888_at
1628376_x_at
1628634_at
1629391_at
1629476_at
1629718_at
1629955_at
1630131_at
1631200_at
1631627_at
1631648_at
1631877_a_at
1631909_at
1631998_at
1632318_at
1632374_at
1632583_at
1633810_at
1634575_at
1634697_at
1635305_s_at
1635821_at
1635983_a_at
1635987_at
1636014_at
1636131_at
1636711_at
1636829_at
1636921_at
1637124_at
1637547_at
1638217_at
1638224_at
1638272_at
1638350_at
1638970_at
1639071_a_at
1639152_at
1639341_at
1639993_at
1640824_at
1640826_at
1641201_at
1641568_a_at

Functional annotation table:

ID	Gene Name	Species	COG_ONTOLOGY	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE

1624840_at Accessory gland-specific peptide 29AB Drosophila melanogaster GO:0007320~insemination,GO:0007321~sperm displacement,GO:0007610~behavior,GO:0007618~mating,GO:0007620~copulation,GO:0019098~reproductive behavior,GO:0032504~multicellular organism reproduction,GO:0045297~post-mating behavior,GO:0046692~sperm competition,GO:0046693~sperm storage,GO:0048609~reproductive process in a multicellular organism, GO:0005576~extracellular region, GO:0005179~hormone activity,GO:0005529~sugar binding,GO:0005534~galactose binding,GO:0030246~carbohydrate binding,GO:0048029~monosaccharide binding, IPR001304:C-type lectin,IPR016186:C-type lectin-like,IPR018378:C-type lectin, conserved site, SM00034:CLECT, behavior,complete proteome,disulfide bond,glycoprotein,Lectin,polymorphism,Secreted,signal, chain:Accessory gland protein Acp29AB,disulfide bond,domain:C-type lectin,glycosylation site:N-linked (GlcNAc...),sequence variant,signal peptide,

1631200_at Accessory gland-specific peptide 32CD Drosophila melanogaster GO:0007610~behavior,GO:0007617~mating behavior,GO:0007618~mating,GO:0007621~negative regulation of female receptivity,GO:0019098~reproductive behavior,GO:0032504~multicellular organism reproduction,GO:0033057~reproductive behavior in a multicellular organism,GO:0045297~post-mating behavior,GO:0045434~negative regulation of female receptivity, post-mating,GO:0045924~regulation of female receptivity,GO:0046008~regulation of female receptivity, post-mating,GO:0048609~reproductive process in a multicellular organism,GO:0051705~behavioral interaction between organisms,GO:0060180~female mating behavior, GO:0005576~extracellular region, GO:0005179~hormone activity, alternative initiation,behavior,complete proteome,polymorphism,Secreted,signal, chain:Accessory gland protein Acp32CD,compositionally biased region:Arg-rich,compositionally biased region:Gly-rich,sequence variant,signal peptide,splice variant,

1628634_at Adenosine 3'-phospho 5'-phosphosulfate transporter 2 Drosophila melanogaster GO:0015858~nucleoside transport,GO:0015860~purine nucleoside transport,GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport,GO:0046963~3'-phosphoadenosine 5'-phosphosulfate transport, GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, GO:0005337~nucleoside transmembrane transporter activity,GO:0015211~purine nucleoside transmembrane transporter activity,GO:0015932~nucleobase, nucleoside, nucleotide and nucleic acid transmembrane transporter activity,GO:0046964~3'-phosphoadenosine 5'-phosphosulfate transmembrane transporter activity, IPR013657:UAA transporter, PIRSF017416:solute carrier family 35, member B type,PIRSF500839:solute carrier family 35, member B3, complete proteome,developmental protein,glycoprotein,golgi apparatus,membrane,phosphoprotein,transmembrane,transport, chain:Adenosine 3'-phospho 5'-phosphosulfate transporter 2,glycosylation site:N-linked (GlcNAc...),modified residue,transmembrane region,

1624699_s_at	Beadex	Drosophila melanogaster	GO:0002165~instar larval or pupal development,GO:0003002~regionalization,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0007389~pattern specification process,GO:0007444~imaginal disc development,GO:0007472~wing disc morphogenesis,GO:0007476~imaginal disc-derived wing morphogenesis,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0007610~behavior,GO:0007622~rhythmic behavior,GO:0007623~circadian rhythm,GO:0007626~locomotory behavior,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0010033~response to organic substance,GO:0010324~membrane invagination,GO:0014070~response to organic cyclic substance,GO:0014073~response to tropane,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0035107~appendage morphogenesis,GO:0035108~limb morphogenesis,GO:0035110~leg morphogenesis,GO:0035114~imaginal disc-derived appendage morphogenesis,GO:0035120~post-embryonic appendage morphogenesis,GO:0035218~leg disc development,GO:0035220~wing disc development,GO:0035282~segmentation,GO:0035285~appendage segmentation,GO:0035286~leg segmentation,GO:0042220~response to cocaine,GO:0043279~response to alkaloid,GO:0045475~locomotor rhythm,GO:0048511~rhythmic process,GO:0048512~circadian behavior,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048707~instar larval or pupal morphogenesis,GO:0048736~appendage development,GO:0048737~imaginal disc-derived appendage development,GO:0060173~limb development,	GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,	IPR001781:Zinc finger, LIM-type,	SM00132:LIM,	complete proteome,LIM domain,metal-binding,zinc,
1636131_at	DNA ligase III	Drosophila melanogaster	GO:0006259~DNA metabolic process,GO:0006260~DNA replication,GO:0006281~DNA repair,GO:0006310~DNA recombination,GO:0006974~response to DNA damage stimulus,GO:0033554~cellular response to stress,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0003677~DNA binding,GO:0003909~DNA ligase activity,GO:0003910~DNA ligase (ATP) activity,GO:0005524~ATP binding,GO:0016886~ligase activity, forming phosphoric ester bonds,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding,	IPR000977:ATP-dependent DNA ligase,IPR001357:BRCT,IPR012308:DNA ligase, N-terminal,IPR012309:ATP dependent DNA ligase, C-terminal,IPR012310:ATP dependent DNA ligase, central,IPR012340:Nucleic acid-binding, OB-fold,IPR016059:ATP-dependent DNA		

ligase, conserved site, dme03410:Base excision repair, SM00292:BRCT, atp-binding,complete proteome,DNA damage,dna recombination,dna repair,dna replication,ligase,nucleotide-binding,

1639071_a_at Death related ced-3/Nedd2-like protein Drosophila melanogaster GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002831~regulation of response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0003006~reproductive developmental process,GO:0006508~proteolysis,GO:0006915~apoptosis,GO:0006952~defense response,GO:0006955~immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007283~spermatogenesis,GO:0007286~spermatid development,GO:0007291~sperm individualization,GO:0007349~cellularization,GO:0008219~cell death,GO:0009617~response to bacterium,GO:0009891~positive regulation of biosynthetic process,GO:0012501~programmed cell death,GO:0016265~death,GO:0016485~protein processing,GO:0019953~sexual reproduction,GO:0031328~positive regulation of cellular biosynthetic process,GO:0032504~multicellular organism reproduction,GO:0042742~defense response to bacterium,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0048232~male gamete generation,GO:0048515~spermatid differentiation,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0050829~defense response to Gram-negative bacterium,GO:0051604~protein maturation,GO:0051605~protein maturation by peptide bond cleavage, GO:0004175~endopeptidase activity,GO:0004197~cysteine-type endopeptidase activity,GO:0008047~enzyme activator activity,GO:0008233~peptidase activity,GO:0008234~cysteine-type peptidase activity,GO:0016504~peptidase activator activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001309:Peptidase C14, ICE, catalytic subunit p20,IPR002138:Peptidase C14, caspase non-catalytic subunit p10,IPR002398:Peptidase C14, caspase precursor p45,IPR011600:Peptidase C14, caspase catalytic,IPR015917:Peptidase C14, caspase precursor p45, core,IPR016129:Peptidase C14, ICE, catalytic subunit p20, active site, SM00115:CASc, alternative splicing,Apoptosis,complete proteome,cytoplasm,hydrolase,immune response,Protease,thiol protease,zymogen, chain:Caspase-8 subunit p10,chain:Caspase-8 subunit p15,sequence conflict,splice variant, 1634575_at Dmel_CG11037 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site, SM00020:Tryp_SPc, complete proteome,hydrolase,

1640824_at Dmel_CG11306 Drosophila melanogaster GO:0000026~alpha-1,2-mannosyltransferase activity,GO:0000030~mannosyltransferase activity, IPR001296:Glycosyl transferase, group 1, dme00510:N-Glycan biosynthesis, complete proteome,glycosyltransferase,transferase,

1626075_at Dmel_CG11664 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin, PIRSF001135:trypsin, SM00020:Tryp_SPc, complete proteome,hydrolase,

1641568_a_at Dmel_CG11790 Drosophila melanogaster GO:0019725~cellular homeostasis,GO:0042592~homeostatic process,GO:0045454~cell redox homeostasis, IPR012335:Thioredoxin fold,IPR013766:Thioredoxin domain, complete proteome,

1635987_at Dmel_CG12116 Drosophila melanogaster Secondary metabolites biosynthesis, transport, and catabolism / General function prediction only, GO:0055114~oxidation reduction, GO:0004757~sepiapterin reductase activity, IPR002198:Short-chain dehydrogenase/reductase SDR,IPR016040:NAD(P)-binding domain, dme00790:Folate biosynthesis, complete proteome,oxidoreductase,

1632318_at Dmel_CG12773 Drosophila melanogaster GO:0006865~amino acid transport,GO:0015837~amine transport,GO:0015849~organic acid transport,GO:0046942~carboxylic acid transport, GO:0005275~amine transmembrane transporter activity,GO:0008509~anion transmembrane transporter activity,GO:0008511~sodium:potassium:chloride symporter activity,GO:0015171~amino acid transmembrane transporter activity,GO:0015293~symporter activity,GO:0015294~solute:cation symporter activity,GO:0015296~anion:cation symporter activity,GO:0015377~cation:chloride symporter activity, IPR004841:Amino acid permease-associated region, complete proteome,

1622935_at Dmel_CG12828 Drosophila melanogaster complete proteome,

1629955_at	Dmel_CG13309	Drosophila melanogaster	GO:0005976~polysaccharide metabolic process,GO:0006022~aminoglycan metabolic process,GO:0006030~chitin metabolic process, GO:0005576~extracellular region, GO:0001871~pattern binding,GO:0008061~chitin binding,GO:0030246~carbohydrate binding,GO:0030247~polysaccharide binding, IPR002557:Chitin binding protein, peritrophin-A, SM00494:ChtBD2, complete proteome,
1632583_at	Dmel_CG13539	Drosophila melanogaster	IPR009961:Protein of unknown function DUF1487, complete proteome,
1628376_x_at	Dmel_CG13947	Drosophila melanogaster	complete proteome,
1623766_at	Dmel_CG14054	Drosophila melanogaster	complete proteome,
1624158_at	Dmel_CG14481	Drosophila melanogaster	complete proteome,
1638970_at	Dmel_CG14543	Drosophila melanogaster	IPR019398:Pre-rRNA-processing protein TSR2, conserved region, complete proteome,
1639341_at	Dmel_CG14971	Drosophila melanogaster	GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, IPR004853:Protein of unknown function DUF250, complete proteome,membrane,transmembrane,
1629391_at	Dmel_CG1656	Drosophila melanogaster	GO:0005529~sugar binding,GO:0005534~galactose binding,GO:0030246~carbohydrate binding,GO:0048029~monosaccharide binding, IPR001304:C-type lectin,IPR016186:C-type lectin-like, SM00034:CLECT, complete proteome,
1629718_at	Dmel_CG16727	Drosophila melanogaster	GO:0015101~organic cation transmembrane transporter activity, IPR011701:Major facilitator superfamily MFS-1, complete proteome,transmembrane,
1625027_a_at	Dmel_CG17035	Drosophila melanogaster	GO:0006644~phospholipid metabolic process,GO:0016042~lipid catabolic process,GO:0019637~organophosphate metabolic process, GO:0005576~extracellular region, GO:0004091~carboxylesterase activity,GO:0004620~phospholipase activity,GO:0004623~phospholipase A2 activity,GO:0005509~calcium ion binding,GO:0016298~lipase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR010711:Phospholipase A2, group XII secretory,IPR013090:Phospholipase A2, active site, dme00564:Glycerophospholipid

metabolism,dme00565:Ether lipid metabolism,dme00590:Arachidonic acid metabolism,dme00591:Linoleic acid metabolism,dme00592:alpha-Linolenic acid metabolism, complete proteome,hydrolase,

1639152_at Dmel_CG18243 Drosophila melanogaster GO:0000902~cell morphogenesis,GO:0000904~cell morphogenesis involved in differentiation,GO:0006470~protein amino acid dephosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0006928~cell motion,GO:0007409~axonogenesis,GO:0007411~axon guidance,GO:0016311~dephosphorylation,GO:0030030~cell projection organization,GO:0030182~neuron differentiation,GO:0031175~neuron projection development,GO:0032989~cellular component morphogenesis,GO:0032990~cell part morphogenesis,GO:0048666~neuron development,GO:0048667~cell morphogenesis involved in neuron differentiation,GO:0048812~neuron projection morphogenesis,GO:0048858~cell projection morphogenesis, GO:0004721~phosphoprotein phosphatase activity,GO:0004725~protein tyrosine phosphatase activity,GO:0016791~phosphatase activity, IPR000242:Protein-tyrosine phosphatase, receptor/non-receptor type,IPR000387:Dual-specific/protein-tyrosine phosphatase, conserved region,IPR000387:Protein - tyrosine phosphatase,IPR000572:Oxidoreductase, molybdopterin binding,IPR003961:Fibronectin, type III,IPR008957:Fibronectin, type III-like fold,IPR016130:Protein-tyrosine phosphatase, active site, SM00060:FN3,SM00194:PTPc, hydrolase,

1626503_at Dmel_CG2254 Drosophila melanogaster GO:0055114~oxidation reduction, GO:0005811~lipid particle, IPR002198:Short-chain dehydrogenase/reductase SDR,IPR002347:Glucose/ribitol dehydrogenase,IPR016040:NAD(P)-binding domain, PIRSF000126:11beta-hydroxysteroid dehydrogenase, complete proteome,oxidoreductase,

1623032_at Dmel_CG2336 Drosophila melanogaster GO:0055114~oxidation reduction, IPR009961:Protein of unknown function DUF1487, complete proteome,oxidoreductase,

1636711_at Dmel_CG31265 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site, PIRSF001135:trypsin, SM00020:Tryp_SPc, complete proteome,hydrolase,Protease,Serine protease,

1636014_at Dmel_CG31419 Drosophila melanogaster complete proteome, 1636829_at Dmel_CG31902 Drosophila melanogaster GO:0004857~enzyme inhibitor activity,GO:0004866~endopeptidase inhibitor activity,GO:0004867~serine-type endopeptidase inhibitor activity,GO:0030414~peptidase inhibitor activity, IPR000215:Protease inhibitor I4, serpin, SM00093:SERPIN, complete proteome,

1625375_at Dmel_CG32201 Drosophila melanogaster GO:0006575~cellular amino acid derivative metabolic process,GO:0018208~peptidyl-proline modification,GO:0018401~peptidyl-proline hydroxylation to 4-hydroxy-L-proline,GO:0019471~4-hydroxyproline metabolic process,GO:0055114~oxidation reduction, GO:0005783~endoplasmic reticulum,GO:0016222~procollagen-proline 4-dioxygenase complex,GO:0044432~endoplasmic reticulum part, GO:0004656~procollagen-proline 4-dioxygenase activity,GO:0005506~iron ion binding,GO:0016706~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,GO:0019798~procollagen-proline dioxygenase activity,GO:0019842~vitamin binding,GO:0031406~carboxylic acid binding,GO:0031418~L-ascorbic acid binding,GO:0031543~peptidyl-proline dioxygenase activity,GO:0031545~peptidyl-proline 4-dioxygenase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR005123:Oxoglutarate and iron-dependent oxygenase,IPR006620:Prolyl 4-hydroxylase, alpha subunit, dme00330:Arginine and proline metabolism, SM00702:P4Hc, oxidoreductase,

1638224_at Dmel_CG32250 Drosophila melanogaster GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005777~peroxisome,GO:0005778~peroxisomal membrane,GO:0005779~integral to peroxisomal membrane,GO:0016021~integral to membrane,GO:0019866~organelle inner membrane,GO:0031090~organelle membrane,GO:0031224~intrinsic to membrane,GO:0031231~intrinsic to peroxisomal membrane,GO:0031300~intrinsic to organelle membrane,GO:0031301~integral to organelle membrane,GO:0031903~microbody membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope,GO:0042579~microbody,GO:0044429~mitochondrial part,GO:0044438~microbody part,GO:0044439~peroxisomal part, IPR001993:Mitochondrial substrate carrier,IPR002113:Adenine nucleotide translocator 1,IPR018108:Mitochondrial substrate/solute carrier, complete proteome,membrane,repeat,transmembrane,transport,

1634697_at Dmel_CG32667 Drosophila melanogaster IPR001007:von Willebrand factor, type C, SM00214:VWC, complete proteome, 1640826_at Dmel_CG3947 Drosophila melanogaster GO:0007031~peroxisome organization, IPR013919:Peroxisome membrane protein, Pex16, complete proteome,

1626222_at Dmel_CG4812 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site, PIRSF001135:trypsin, SM00020:Tryp_SPc, complete proteome,hydrolase,Protease,Serine protease,

1641201_at Dmel_CG5267 Drosophila melanogaster IPR013032:EGF-like region, conserved site,IPR018453:Protease inhibitor I8, cysteine-rich trypsin inhibitor-like subgroup, complete proteome,

1631627_at Dmel_CG5335 Drosophila melanogaster GO:0005529~sugar binding,GO:0030246~carbohydrate binding, IPR001079:Galectin, carbohydrate recognition domain,IPR013320:Concanavalin A-like lectin/glucanase, subgroup, SM00276:GLECT, complete proteome,Lectin,

1626811_at Dmel_CG5510 Drosophila melanogaster IPR005052:Legume-like lectin,IPR013320:Concanavalin A-like lectin/glucanase, subgroup, PIRSF017635:L-type lectin, animal type,PIRSF500265:vesicular integral-membrane protein VIP36, complete proteome,

1623928_at Dmel_CG5910 Drosophila melanogaster complete proteome,

1630131_at Dmel_CG6567 Drosophila melanogaster GO:0004091~carboxylesterase activity,GO:0004620~phospholipase activity,GO:0004622~lysophospholipase activity,GO:0016298~lipase activity, IPR003140:Phospholipase/carboxylesterase, complete proteome,hydrolase,

1627888_at Dmel_CG6672 Drosophila melanogaster GO:0006811~ion transport,GO:0006812~cation transport, GO:0005385~zinc ion transmembrane transporter activity,GO:0015082~di-, tri-valent inorganic cation transmembrane transporter activity,GO:0022890~inorganic cation transmembrane transporter activity,GO:0046873~metal ion transmembrane transporter activity,GO:0046915~transition metal ion transmembrane transporter activity, IPR002524:Cation efflux protein, complete proteome, 1632374_at Dmel_CG6769 Drosophila melanogaster GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR003604:Zinc finger, U1-type,IPR007087:Zinc finger, C2H2-type,IPR015880:Zinc finger, C2H2-like, SM00355:ZnF_C2H2,SM00451:ZnF_U1, complete proteome,

1637124_at Dmel_CG6773 Drosophila melanogaster GO:0002164~larval development,GO:0002165~instar larval or pupal development,GO:0002168~instar larval development,GO:0003002~regionalization,GO:0006900~membrane budding,GO:0007389~pattern specification process,GO:0007591~molting cycle, chitin-based cuticle,GO:0007592~protein-based cuticle development,GO:0008363~larval chitin-based cuticle development,GO:0009791~post-embryonic development,GO:0016044~membrane organization,GO:0016050~vesicle organization,GO:0016192~vesicle-mediated transport,GO:0018988~molting cycle, protein-based cuticle,GO:0022404~molting cycle process,GO:0035017~cuticle pattern formation,GO:0035293~chitin-based larval cuticle pattern formation,GO:0040003~chitin-based cuticle development,GO:0042303~molting cycle,GO:0042335~cuticle development,GO:0042336~protein-based cuticle development during molting,GO:0042337~chitin-based cuticle development during molting, IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like,IPR017986:WD40 repeat, region,IP R019781:WD40 repeat, subgroup,IPR019782:WD40 repeat 2, SM00320:WD40, complete proteome,repeat,wd repeat,

1624888_at Dmel_CG7081 Drosophila melanogaster GO:0007031~peroxisome organization, GO:0005777~peroxisome,GO:0005778~peroxisomal membrane,GO:0031090~organelle membrane,GO:0031903~microbody membrane,GO:0042579~microbody,GO:0044438~microbody part,GO:0044439~peroxisomal part, GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR001841:Zinc finger, RING-type,IPR006845:Pex, N-terminal,IPR017907:Zinc finger, RING-type, conserved site,IPR018957:Zinc finger, C3HC4 RING-type, SM00184:RING, complete proteome,metal-binding,zinc,zinc-finger,

1629476_at Dmel_CG7542 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site, SM00020:Tryp_SPc, complete proteome,hydrolase,Protease,Serine protease, 1624984_at Dmel_CG8021 Drosophila melanogaster GO:0000166~nucleotide binding,GO:0003723~RNA binding,GO:0003729~mRNA binding, IPR000504:RNA recognition motif, RNP-1,IPR012677:Nucleotide-binding, alpha-beta plait, SM00360:RRM, complete proteome,

1637547_at Dmel_CG8199 Drosophila melanogaster Energy production and conversion, GO:0006637~acyl-CoA metabolic process,GO:0006732~coenzyme metabolic process,GO:0009108~coenzyme biosynthetic process,GO:0046949~acyl-CoA biosynthetic process,GO:0051186~cofactor metabolic process,GO:0051188~cofactor biosynthetic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0017086~3-methyl-2-oxobutanoate dehydrogenase (lipoamide) complex,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0003863~3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity,GO:0016624~oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, IPR001017:Dehydrogenase, E1 component, dme00280:Valine, leucine and isoleucine degradation, PIRSF000152:pyruvate dehydrogenase (lipoamide) alpha chain, complete proteome,oxidoreductase,

1623783_at Dmel_CG8489 Drosophila melanogaster GO:0003006~reproductive developmental process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007283~spermatogenesis,GO:0007286~spermatid development,GO:0007291~sperm individualization,GO:0007349~cellularization,GO:0019953~sexual reproduction,GO:0032504~multicellular organism reproduction,GO:0048232~male gamete generation,GO:0048515~spermatid differentiation,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process, complete proteome,developmental protein,differentiation,glycoprotein,spermatogenesis, chain:Male-specific protein scotti,glycosylation site:N-linked (GlcNAc...),

1633810_at Dmel_CG8793 Drosophila melanogaster complete proteome,

1625814_at Dymeclin Drosophila melanogaster IPR019142:Dymeclin, complete proteome,lipoprotein,myristate,phosphoprotein, chain:Dymeclin,lipid moiety-binding region:N-myristoyl glycine,modified residue,

1631877_a_at Histidyl-tRNA synthetase Drosophila melanogaster Translation, ribosomal structure and biogenesis, GO:0006399~tRNA metabolic process,GO:0006412~translation,GO:0006418~tRNA aminoacylation for protein translation,GO:0006427~histidyl-tRNA aminoacylation,GO:0034660~ncRNA metabolic process,GO:0043038~amino acid activation,GO:0043039~tRNA aminoacylation, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0004812~aminoacyl-tRNA ligase activity,GO:0004821~histidine-tRNA ligase activity,GO:0005524~ATP binding,GO:0016875~ligase activity, forming carbon-oxygen bonds,GO:0016876~ligase activity, forming aminoacyl-tRNA and related compounds,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR000738:WHEP-TRS,IPR002314:Aminoacyl-tRNA synthetase, class II (G, H, P and S), conserved region,IPR004154:Anticodon-binding,IPR004516 :Histidyl-tRNA synthetase, class IIa,IPR006195:Aminoacyl-tRNA synthetase, class II, conserved region,IPR009068:S15/NS1, RNA-binding,IPR015807:Histidyl-tRNA synthetase, class IIa, subgroup, dme00970:Aminoacyl-tRNA biosynthesis, PIRSF001549:His-tRNA_synth,PIRSF001549:histidyl-tRNA synthetase, Aminoacyl-tRNA synthetase,complete proteome,ligase,

1635821_at Mediator complex subunit 28 Drosophila melanogaster GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0045449~regulation of transcription,GO:0051252~regulation of RNA metabolic process, GO:0005654~nucleoplasm,GO:0016592~Srb-mediator complex,GO:0031974~membrane-enclosed lumen,GO:0031981~nuclear lumen,GO:0043233~organelle lumen,GO:0044451~nucleoplasm part,GO:0070013~intracellular organelle lumen, GO:0003702~RNA polymerase II transcription factor activity,GO:0016251~general RNA polymerase II transcription factor activity,GO:0016455~RNA polymerase II transcription mediator activity,GO:0030528~transcription regulator activity, activator,coiled coil,complete proteome,nucleus,Transcription,transcription regulation,chain:Mediator of RNA polymerase II transcription subunit 28,compositionally biased region:Pro-rich,

1627459_at N(6)-adenine-specific DNA methyltransferase 2 homolog Drosophila melanogaster GO:0006730~one-carbon metabolic process,GO:0032259~methylation, IPR002052:N-6 adenine-specific DNA methylase, conserved site,IPR019369:N-6 adenine-specific DNA methylase-related, eukaryotic, complete proteome,methyltransferase,transferase, chain:N(6)-adenine-specific DNA methyltransferase 2 homolog,sequence conflict,

1627078_at Organic anion transporting polypeptide 58Dc Drosophila melanogaster GO:0006811~ion transport,GO:0006820~anion transport,GO:0015711~organic anion transport, GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, GO:0008509~anion transmembrane transporter activity,GO:0008514~organic anion transmembrane transporter activity,GO:0015347~sodium-independent organic anion transmembrane transporter activity, IPR002350:Proteinase inhibitor I1, Kazal,IPR004156:Organic anion transporter polypeptide OATP,IPR011497:Protease inhibitor, Kazal-type, SM00280:KAZAL, 1638217_at Probable dolichol-phosphate mannosyltransferase Drosophila melanogaster GO:0006486~protein amino acid glycosylation,GO:0009100~glycoprotein metabolic process,GO:0009101~glycoprotein biosynthetic process,GO:0043413~biopolymer glycosylation,GO:0070085~glycosylation, GO:0005783~endoplasmic reticulum, GO:0000030~mannosyltransferase activity,GO:0004582~dolichyl-phosphate beta-D-mannosyltransferase activity, IPR001173:Glycosyl transferase, family 2, dme00510:N-Glycan biosynthesis, PIRSF005860:dolichyl-phosphate beta-D-mannosyltransferase, complete proteome,endoplasmic reticulum,glycosyltransferase,transferase, chain:Probable dolichol-phosphate mannosyltransferase,

1638350_at Probable ribosome production factor 1 Drosophila melanogaster GO:0006364~rRNA processing,GO:0006396~RNA processing,GO:0016072~rRNA metabolic process,GO:0022613~ribonucleoprotein complex biogenesis,GO:0034470~ncRNA processing,GO:0034660~ncRNA metabolic process,GO:0042254~ribosome biogenesis, GO:0005730~nucleolus,GO:0031974~membrane-enclosed lumen,GO:0031981~nuclear lumen,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0043233~organelle lumen,GO:0070013~intracellular organelle lumen, GO:0003723~RNA binding,GO:0019843~rRNA binding, IPR007109:Brix domain, PIRSF015949:U3 small nucleolar ribonucleoprotein (snoRNP) complex, Imp4p subunit, complete proteome,nucleus,ribosome biogenesis,rna-binding,rrna processing,rrna-binding, chain:Probable ribosome production factor 1,domain:Brix,region of interest:RNA-binding,

1639993_at Protein RFT1 homolog Drosophila melanogaster GO:0006869~lipid transport,GO:0010876~lipid localization, GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, GO:0005319~lipid transporter activity, IPR007594:RFT1, dme00510:N-Glycan biosynthesis, complete proteome,membrane,transmembrane, chain:Protein RFT1 homolog,transmembrane region,

1631648_at Signal recognition particle 9 kDa protein Drosophila melanogaster GO:0006417~regulation of translation,GO:0006448~regulation of translational elongation,GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0008104~protein localization,GO:0009890~negative regulation of biosynthetic process,GO:0010558~negative regulation of macromolecule biosynthetic process,GO:0010605~negative regulation of macromolecule metabolic process,GO:0010608~posttranscriptional regulation of gene expression,GO:0015031~protein transport,GO:0017148~negative regulation of translation,GO:0031327~negative regulation of cellular biosynthetic process,GO:0032268~regulation of cellular protein metabolic process,GO:0032269~negative regulation of cellular protein metabolic process,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0045900~negative regulation of translational elongation,GO:0046907~intracellular transport,GO:0051248~negative regulation of protein metabolic process,GO:0070727~cellular macromolecule localization, GO:0005786~signal recognition particle, endoplasmic reticulum targeting,GO:0030529~ribonucleoprotein complex,GO:0048500~signal recognition particle, GO:0003723~RNA binding,GO:0003729~mRNA binding,GO:0008312~7S RNA binding, IPR008832:Signal recognition particle, SRP9 subunit,IPR009018:Signal recognition particle, SRP9/SRP14 subunit, dme03060:Protein export, PIRSF017029:signal recognition particle, 9 kDa protein,PIRSF017029:Signal_recog_particle_SRP9, complete proteome,cytoplasm,ribonucleoprotein,rna-binding,signal recognition particle, chain:Signal recognition particle 9 kDa protein,

1638272_at Signal recognition particle protein 19 Drosophila melanogaster GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0008104~protein localization,GO:0015031~protein transport,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0070727~cellular macromolecule localization, GO:0005786~signal recognition particle, endoplasmic reticulum targeting,GO:0030529~ribonucleoprotein complex,GO:0048500~signal recognition particle, GO:0003723~RNA binding,GO:0008312~7S RNA binding, IPR002778:Signal recognition particle, SRP19 subunit, dme03060:Protein export, PIRSF006433:Signal recognition particle 19 kDa protein,PIRSF500827:Eukaryota signal recognition particle 19 kDa protein, complete proteome,cytoplasm,ribonucleoprotein,rna-binding,signal recognition particle, chain:Signal recognition particle 19 kDa protein,compositionally biased region:Poly-Gly,region of interest:Basic region, potentially involved in RNA-binding,sequence conflict,

1635305_s_at Trithorax-like Drosophila melanogaster GO:0000087~M phase of mitotic cell cycle,GO:0000278~mitotic cell cycle,GO:0000279~M phase,GO:0000280~nuclear division,GO:0002165~instar larval or pupal development,GO:0006323~DNA packaging,GO:0006325~chromatin organization,GO:0006333~chromatin assembly or disassembly,GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0006461~protein complex assembly,GO:0007049~cell cycle,GO:0007067~mitosis,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007444~imaginal disc development,GO:0007472~wing disc morphogenesis,GO:0007476~imaginal disc-derived wing morphogenesis,GO:0007549~dosage compensation,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0009891~positive regulation of biosynthetic process,GO:0010557~positive regulation of macromolecule biosynthetic process,GO:0010604~positive regulation of macromolecule metabolic process,GO:0010628~positive regulation of gene expression,GO:0016568~chromatin modification,GO:0019953~sexual reproduction,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0031328~positive regulation of cellular biosynthetic process,GO:0031497~chromatin assembly,GO:0032504~multicellular organism reproduction,GO:0033301~cell cycle comprising mitosis without cytokinesis,GO:0035107~appendage morphogenesis,GO:0035114~imaginal disc-derived appendage morphogenesis,GO:0035120~post-embryonic appendage morphogenesis,GO:0035186~syncytial blastoderm mitotic cell cycle,GO:0035220~wing disc development,GO:0040029~regulation of gene expression, epigenetic,GO:0043933~macromolecular complex subunit organization,GO:0045448~mitotic cell cycle, embryonic,GO:0045449~regulation of transcription,GO:0045893~positive regulation of transcription, DNA-dependent,GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,GO:0045941~positive regulation of transcription,GO:0048285~organelle fission,GO:0048477~oogenesis,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048609~reproductive process in a multicellular organism,GO:0048707~instar larval or pupal morphogenesis,GO:0048736~appendage development,GO:0048737~imaginal disc-derived appendage development,GO:0051173~positive regulation of nitrogen compound metabolic process,GO:0051252~regulation of RNA metabolic process,GO:0051254~positive regulation of RNA metabolic process,GO:0051259~protein oligomerization,GO:0051276~chromosome organization,GO:0051301~cell division,GO:0065003~macromolecular complex assembly,GO:0070271~protein complex biogenesis, GO:0000775~chromosome, centromeric region,GO:0000785~chromatin,GO:0000791~euchromatin,GO:0000792~heterochromatin,GO:0005694~chromosome,GO:0005700~polytene chromosome,GO:0005721~centromeric heterochromatin,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0044427~chromosomal part,

GO:0003677~DNA binding,GO:0003702~RNA polymerase II transcription factor activity,GO:0003704~specific RNA polymerase II transcription factor activity,GO:0008270~zinc ion binding,GO:0016563~transcription activator activity,GO:0030528~transcription regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0046982~protein heterodimerization activity,GO:0046983~protein dimerization activity,

IPR000210:BTB/POZ-like,IPR007087:Zinc finger, C2H2-type,IPR011333:BTB/POZ fold,IPR013069:BTB/POZ,IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding,IPR015318:Zinc finger, GAGAG binding factor,IPR015880:Zinc finger, C2H2-like, SM00225:BTB,SM00355:ZnF_C2H2, 3d-structure,activator,alternative splicing,cell cycle,cell division,chromatin regulator,complete proteome,developmental protein,differentiation,direct protein sequencing,DNA binding,dna-binding,metal-binding,mitosis,nucleus,oogenesis,phosphoprotein,repressor,Transcription,transcription factor,transcription regulation,zinc,zinc-finger, chain:Transcription factor GAGA,compositionally biased region:Gln-rich,domain:BTB,helix,modified residue,region of interest:Interaction with E(bx),sequence conflict,splice variant,strand,turn,zinc finger region:C2H2-type; degenerate,

1631998_at Ubiquitin carrier protein Drosophila melanogaster GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process, GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR000608:Ubiquitin-conjugating enzyme, E2,IPR016135:Ubiquitin-conjugating enzyme/RWD-like, dme04120:Ubiquitin mediated proteolysis, PIRSF001567:ubiquitin-protein ligase E2, SM00212:UBCc, complete proteome,ligase,ubl conjugation pathway,

1631909_at baiser Drosophila melanogaster GO:0003002~regionalization,GO:0003006~reproductive developmental process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007292~female gamete generation,GO:0007308~oocyte construction,GO:0007309~oocyte axis specification,GO:0007310~oocyte dorsal/ventral axis specification,GO:0007311~maternal specification of dorsal/ventral axis, oocyte, germ-line encoded,GO:0007389~pattern specification process,GO:0009798~axis specification,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0009994~oocyte differentiation,GO:0016192~vesicle-mediated transport,GO:0019953~sexual reproduction,GO:0021700~developmental maturation,GO:0032504~multicellular organism reproduction,GO:0048469~cell maturation,GO:0048477~oogenesis,GO:0048599~oocyte development,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, IPR000348:emp24/gp25L/p24,IPR009038:GOLD,IPR015720:TMP21 related, PIRSF005359:conserved hypothetical protein YHR110w, complete proteome,membrane,transmembrane,

1636921_at lethal (2) 06496 Drosophila melanogaster GO:0007017~microtubule-based process,GO:0007018~microtubule-based movement, GO:0005856~cytoskeleton,GO:0005869~dynactin complex,GO:0005875~microtubule associated complex,GO:0015629~actin cytoskeleton,GO:0015630~microtubule cytoskeleton,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0044430~cytoskeletal part,

complete proteome,

1635983_a_at no mechanoreceptor potential B Drosophila melanogaster GO:0000902~cell morphogenesis,GO:0007017~microtubule-based process,GO:0007018~microtubule-based movement,GO:0007600~sensory perception,GO:0007605~sensory perception of sound,GO:0009296~flagellum assembly,GO:0010970~microtubule-based transport,GO:0030030~cell projection organization,GO:0030031~cell projection assembly,GO:0030705~cytoskeleton-dependent intracellular transport,GO:0032989~cellular component morphogenesis,GO:0032990~cell part morphogenesis,GO:0035058~sensory cilium assembly,GO:0042073~intraflagellar transport,GO:0042384~cilium assembly,GO:0043064~flagellum organization,GO:0046907~intracellular transport,GO:0048858~cell projection morphogenesis,GO:0050877~neurological system process,GO:0050890~cognition,GO:0050954~sensory perception of mechanical stimulus,GO:0060271~cilium morphogenesis,

IPR001440:Tetratricopeptide TPR-1,IPR011990:Tetratricopeptide-like helical,IPR013026:Tetratricopeptide region,IPR019734:Tetratricopeptide repeat,

SM00028:TPR, complete proteome,receptor,repeat,tpr repeat,

****

C

+D

-D

Probe sets:

1623693_a_at
1624042_at
1624943_at
1625264_s_at
1625433_at
1625830_a_at
1626178_s_at
1626566_at
1627270_at
1627376_at
1627651_a_at
1629357_s_at
1629839_a_at
1629843_s_at
1630280_s_at
1630824_a_at
1630968_at
1631243_s_at

1631426_at
1632916_at
1633965_at
1634707_s_at
1634869_at
1634877_at
1635202_s_at
1635619_a_at
1635711_s_at
1636423_at
1636521_at
1636591_at
1636682_at
1638050_s_at
1638186_a_at
1638727_at
1638994_at
1639321_s_at
1640224_s_at
1640754_at
1641506_at

Functional annotation table:

ID Gene Name Species COG_ONTOLOGY GOTERM_BP_FAT GOTERM_CC_FAT GOTERM_MF_FAT INTERPRO KEGG_PATHWAY PIR_SUPERFAMILY SMART SP_PIR_KEYWORDS UP_SEQ_FEATURE

1635711_s_at Ankyrin Drosophila melanogaster GO:0007010~cytoskeleton organization,GO:0007016~cytoskeletal anchoring at plasma membrane,GO:0008104~protein localization,GO:0032507~maintenance of protein location in cell,GO:0045185~maintenance of protein location,GO:0051235~maintenance of location,GO:0051651~maintenance of location in cell, GO:0005886~plasma membrane,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0045169~fusome,GO:0045170~spectrosome, GO:0005198~structural molecule activity,GO:0005200~structural constituent of cytoskeleton,GO:0008092~cytoskeletal protein binding, IPR000488:Death,IPR000906:ZU5,IPR002110:Ankyrin, SM00005:DEATH,SM00218:ZU5,SM00248:ANK, ank repeat,complete proteome,repeat,

1625264_s_at Cysteine proteinase-1 Drosophila melanogaster GO:0002165~instar larval or pupal development,GO:0006508~proteolysis,GO:0007431~salivary gland development,GO:0007435~salivary gland morphogenesis,GO:0007552~metamorphosis,GO:0007559~histolysis,GO:0007586~digestion,GO:0008219~cell death,GO:0009057~macromolecule catabolic process,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0012501~programmed cell death,GO:0016265~death,GO:0016271~tissue death,GO:0022612~gland morphogenesis,GO:0030163~protein catabolic process,GO:0035070~salivary gland histolysis,GO:0035071~salivary gland cell autophagic cell death,GO:0035272~exocrine system development,GO:0048102~autophagic cell death,GO:0048707~instar larval or pupal morphogenesis,GO:0048732~gland development, GO:0000323~lytic vacuole,GO:0005764~lysosome,GO:0005773~vacuole, GO:0004175~endopeptidase activity,GO:0004197~cysteine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008234~cysteine-type peptidase activity,GO: 0070011~peptidase activity, acting on L-amino acid peptides, IPR000169:Peptidase, cysteine peptidase active site,IPR000668:Peptidase C1A, papain C-terminal,IPR013128:Peptidase C1A, papain,IPR013201:Proteinase inhibitor I29, cathepsin propeptide, dme04142:Lysosome, PIRSF001182:papain, SM00645:Pept_C1, alternative splicing,complete proteome,developmental protein,digestion,disulfide bond,glycoprotein,hydrolase,lysosome,Protease,signal,thiol protease,zymogen, chain:Cathepsin L heavy chain,chain:Cathepsin L light chain,disulfide bond,glycosylation site:N-linked (GlcNAc...),propeptide:Activation peptide,sequence conflict,signal peptide,splice variant,

1638994_at Dmel_CG10627 Drosophila melanogaster GO:0000287~magnesium ion binding,GO:0004610~phosphoacetylglucosamine mutase activity,GO:0016866~intramolecular transferase activity,GO:0016868~intramolecular transferase activity, phosphotransferases,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR005843:Alpha-D-phosphohexomutase, C-terminal,IPR005844:Alpha-D-phosphohexomutase, alpha/beta/alpha domain I,IPR005845:Alpha-D-phosphohexomutase, alpha/beta/alpha domain II,IPR016055:Alpha-D-phosphohexomutase, alpha/beta/alpha I, II and III,IPR016066:Alpha-D-phosphohexomutase, conserved site,IPR016657:Phosphoacetylglucosamine mutase, dme00520:Amino sugar and nucleotide sugar metabolism, PIRSF016408:PAGM,PIRSF016408:phosphoacetylglucosamine mutase, complete proteome,Isomerase,magnesium,metal-binding,

1641506_at Dmel_CG12400 Drosophila melanogaster GO:0006091~generation of precursor metabolites and energy,GO:0006119~oxidative phosphorylation,GO:0006120~mitochondrial electron transport, NADH to ubiquinone,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0015980~energy derivation by oxidation of organic compounds,GO:0016310~phosphorylation,GO:0022900~electron transport chain,GO:0022904~respiratory electron transport chain,GO:0042773~ATP synthesis coupled electron transport,GO:0042775~mitochondrial ATP synthesis coupled electron transport,GO:0045333~cellular respiration,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005746~mitochondrial respiratory chain,GO:0005747~mitochondrial respiratory chain complex I,GO:0019866~organelle inner membrane,GO:0030964~NADH dehydrogenase complex,GO:0031090~organelle membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope,GO:0044429~mitochondrial part,GO:0044455~mitochondrial membrane part,GO:0045271~respiratory chain complex I,GO:0070469~respiratory chain,

			GO:0003954~NADH dehydrogenase activity,GO:0008137~NADH dehydrogenase (ubiquinone) activity,GO:0016651~oxidoreductase activity, acting on NADH or NADPH,GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor,GO:0050136~NADH dehydrogenase (quinone) activity, IPR009423:NADH:ubiquinone oxidoreductase, subunit b14.5b, dme00190:Oxidative phosphorylation, PIRSF017834:NADH-UbQ_OxRdtase_b14.5b, complete proteome,oxidoreductase,
1640224_s_at	Dmel_CG13796	Drosophila melanogaster	GO:0006836~neurotransmitter transport, GO:0005886~plasma membrane,GO:0005887~integral to plasma membrane,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0031226~intrinsic to plasma membrane,GO:0044459~plasma membrane part, GO:0005275~amine transmembrane transporter activity,GO:0005326~neurotransmitter transporter activity,GO:0005328~neurotransmitter:sodium symporter activity,GO:0015171~amino acid transmembrane transporter activity,GO:0015175~neutral amino acid transmembrane transporter activity,GO:0015187~glycine transmembrane transporter activity,GO:0015293~symporter activity,GO:0015294~solute:cation symporter activity,GO:0015370~solute:sodium symporter activity, IPR000175:Sodium:neurotransmitter symporter,IPR000792:Transcription regulator LuxR, C-terminal, SM00421:HTH_LUXR, Symport,transmembrane,transport,
1630968_at	Dmel_CG13907	Drosophila melanogaster	GO:0008028~monocarboxylic acid transmembrane transporter activity,GO:0015355~secondary active monocarboxylate transmembrane transporter activity, IPR011701:Major facilitator superfamily MFS-1, complete proteome,
1634877_at	Dmel_CG15546	Drosophila melanogaster	complete proteome,
1624943_at	Dmel_CG1636	Drosophila melanogaster	complete proteome,
1636521_at	Dmel_CG1981	Drosophila melanogaster	GO:0006259~DNA metabolic process,GO:0006281~DNA repair,GO:0006289~nucleotide-excision repair,GO:0006298~mismatch repair,GO:0006974~response to DNA damage stimulus,GO:0033554~cellular response to stress,GO:0034984~cellular response to DNA damage stimulus, GO:0000700~mismatch base pair DNA N-glycosylase activity,GO:0003677~DNA binding,GO:0003690~double-stranded DNA binding,GO:0008263~pyrimidine-specific mismatch base pair DNA N-glycosylase activity,GO:0016799~hydrolase activity, hydrolyzing N-glycosyl compounds,GO:0019104~DNA N-glycosylase

activity,GO:0043566~structure-specific DNA binding, IPR005122:Uracil-DNA glycosylase-like,IPR015637:DNA glycosylase, G/T mismatch,IPR017956:AT hook, DNA-binding, conserved site, dme03410:Base excision repair, SM00384:AT_hook, complete proteome,

1632916_at Dmel_CG31357 Drosophila melanogaster General function prediction only, IPR006594:LisH dimerisation motif,IPR006595:CTLH, C-terminal to LisH motif,IPR013144:Ran binding protein-like, CRA domain, SM00667:LisH,SM00668:CTLH,SM00757:CRA, complete proteome,

1636682_at Dmel_CG31778 Drosophila melanogaster GO:0004857~enzyme inhibitor activity,GO:0004866~endopeptidase inhibitor activity,GO:0004867~serine-type endopeptidase inhibitor activity,GO:0030414~peptidase inhibitor activity, IPR002223:Proteinase inhibitor I2, Kunitz metazoa, SM00131:KU, complete proteome,

1626178_s_at Dmel_CG32149 Drosophila melanogaster GO:0004427~inorganic diphosphatase activity, IPR000198:RhoGAP,IPR008162:Inorganic pyrophosphatase, SM00324:RhoGAP, complete proteome,hydrolase,

1631426_at Dmel_CG32412 Drosophila melanogaster GO:0006508~proteolysis, GO:0008233~peptidase activity,GO:0016603~glutaminyl-peptide cyclotransferase activity,GO:0016755~transferase activity, transferring amino-acyl groups, IPR007484:Peptidase M28, Acyltransferase,complete proteome,hydrolase,transferase,

1630824_a_at Dmel_CG33145 Drosophila melanogaster GO:0006486~protein amino acid glycosylation,GO:0009100~glycoprotein metabolic process,GO:0009101~glycoprotein biosynthetic process,GO:0043413~biopolymer glycosylation,GO:0070085~glycosylation, GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0008378~galactosyltransferase activity,GO:0008499~UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity,GO:0035250~UDP-galactosyltransferase activity,GO:0048531~beta-1,3-galactosyltransferase activity, IPR002659:Glycosyl transferase, family 31, complete proteome,glycosyltransferase,golgi apparatus,membrane,transferase,transmembrane,

1623693_a_at Dmel_CG3365 Drosophila melanogaster GO:0032012~regulation of ARF protein signal transduction,GO:0032312~regulation of ARF GTPase activity,GO:0032318~regulation of Ras GTPase activity,GO:0043087~regulation of GTPase activity,GO:0046578~regulation of Ras protein signal transduction,GO:0051056~regulation of small GTPase mediated signal transduction,GO:0051336~regulation of hydrolase activity, GO:0005083~small GTPase regulator activity,GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0008060~ARF GTPase activator activity,GO:0008270~zinc ion binding,GO:0030695~GTPase regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0060589~nucleoside-triphosphatase regulator activity, IPR001164:Arf GTPase activating protein, SM00105:ArfGap, complete proteome,

1627270_at Dmel_CG42240 Drosophila melanogaster complete proteome,

1630280_s_at Dmel_CG42353; Dmel_CG42354 Drosophila melanogaster complete proteome,

1634869_at Dmel_CG4581 Drosophila melanogaster GO:0006631~fatty acid metabolic process,GO:0006635~fatty acid beta-oxidation,GO:0009062~fatty acid catabolic process,GO:0016042~lipid catabolic process,GO:0016054~organic acid catabolic process,GO:0019395~fatty acid oxidation,GO:0030258~lipid modification,GO:0034440~lipid oxidation,GO:0044242~cellular lipid catabolic process,GO:0046395~carboxylic acid catabolic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0005811~lipid particle,GO:0016507~fatty acid beta-oxidation multienzyme complex,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0003988~acetyl-CoA C-acyltransferase activity,GO:0016408~C-acyltransferase activity,GO:0016509~long-chain-3-hydroxyacyl-CoA dehydrogenase activity, IPR002155:Thiolase,IPR016038:Thiolase-like, subgroup, dme00062:Fatty acid elongation in mitochondria,dme00071:Fatty acid metabolism,dme00280:Valine, leucine and isoleucine degradation, PIRSF000429:Ac-CoA_Ac_transf, Acyltransferase,complete proteome,oxidoreductase,transferase,

1635202_s_at Dmel_CG5640 Drosophila melanogaster IPR001440:Tetratricopeptide TPR-1,IPR003347:Transcription factor jumonji/aspartyl beta-hydroxylase,IPR011990:Tetratricopeptide-like helical,IPR013026:Tetratricopeptide region,IPR013129:Transcription factor jumonji,IPR019734:Tetratricopeptide repeat, SM00028:TPR,SM00558:JmjC, complete proteome,repeat,tpr repeat,

1633965_at Dmel_CG6020 Drosophila melanogaster GO:0006091~generation of precursor metabolites and energy,GO:0006119~oxidative phosphorylation,GO:0006120~mitochondrial electron transport, NADH to ubiquinone,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0015980~energy derivation by oxidation of organic compounds,GO:0016310~phosphorylation,GO:0022900~electron transport chain,GO:0022904~respiratory electron transport chain,GO:0042773~ATP synthesis coupled electron transport,GO:0042775~mitochondrial ATP synthesis coupled electron transport,GO:0045333~cellular respiration,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005746~mitochondrial respiratory chain,GO:0005747~mitochondrial respiratory chain complex I,GO:0019866~organelle inner membrane,GO:0030964~NADH dehydrogenase complex,GO:0031090~organelle membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope

,GO:0044429~mitochondrial part,GO:0044455~mitochondrial membrane part,GO:0045271~respiratory chain complex I,GO:0070469~respiratory chain,

GO:0003954~NADH dehydrogenase activity,GO:0008137~NADH dehydrogenase (ubiquinone) activity,GO:0016651~oxidoreductase activity, acting on NADH or NADPH,GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor,GO:0048037~cofactor binding,GO:0050136~NADH dehydrogenase (quinone) activity,GO:0050662~coenzyme binding, IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain,

dme00190:Oxidative phosphorylation, complete proteome,oxidoreductase,

1636423_at Dmel_CG8012 Drosophila melanogaster complete proteome,

1636591_at Dmel_CG8881 Drosophila melanogaster Posttranslational modification, protein turnover, chaperones,

GO:0006508~proteolysis,GO:0006511~ubiquitin-dependent protein catabolic process,GO:0009057~macromolecule catabolic process,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process, IPR001232:SKP1 component,IPR011333:BTB/POZ fold,IPR016072:SKP1 component, dimerisation,IPR016073:SKP1 component, POZ,IPR016897:E3 ubiquitin ligase, SCF complex, Skp subunit,

dme04120:Ubiquitin mediated proteolysis,dme04310:Wnt signaling pathway,dme04350:TGF-beta signaling pathway, PIRSF028729:E3_ubiquit_lig_SCF_Skp,

SM00512:Skp1, complete proteome,

1638727_at Dmel_CG9821 Drosophila melanogaster complete proteome,

1629839_a_at G protein gamma 1Drosophila melanogaster GO:0007010~cytoskeleton organization,GO:0007015~actin filament organization,GO:0007155~cell adhesion,GO:0007166~cell surface receptor linked signal transduction,GO:0007186~G-protein coupled receptor protein signaling pathway,GO:0007405~neuroblast proliferation,GO:0007507~heart development,GO:0007584~response to nutrient,GO:0007610~behavior,GO:0007635~chemosensory behavior,GO:0007637~proboscis extension reflex,GO:0008104~protein localization,GO:0008105~asymmetric protein localization,GO:0008283~cell proliferation,GO:0008360~regulation of cell shape,GO:0009991~response to extracellular stimulus,GO:0017145~stem cell division,GO:0022604~regulation of cell morphogenesis,GO:0022610~biological adhesion,GO:0030029~actin filament-based process,GO:0030036~actin cytoskeleton organization,GO:0031667~response to nutrient levels,GO:0035050~embryonic heart tube development,GO:0035295~tube development,GO:0045165~cell fate commitment,GO:0045176~apical protein localizatio n,GO:0048103~somatic stem cell division,GO:0051301~cell division,GO:0051780~behavioral response to nutrient,GO:0055057~neuroblast division,GO:0055059~asymmetric neuroblast division,GO:0060004~reflex,

GO:0005834~heterotrimeric G-protein complex,GO:0005886~plasma membrane,GO:0009898~internal side of plasma membrane,GO:0019897~extrinsic to plasma membrane,GO:0019898~extrinsic to membrane,GO:0044459~plasma membrane part, GO:0003924~GTPase activity, IPR001770:G-protein, gamma subunit,IPR015898:G-protein, gamma-like subunit, PIRSF002398:GTP-binding regulatory protein gamma chain, SM00224:GGL, cell membrane,complete proteome,GTP binding,lipoprotein,membrane,methylated carboxyl end,methylation,prenylated cysteine,prenylation,transducer, chain:Guanine nucleotide-binding protein subunit gamma-1,lipid moiety-binding region:S-geranylgeranyl cysteine,modified residue,propeptide:Removed in mature form,

1624042_at G protein-coupled receptor kinase 2 Drosophila melanogaster GO:0006468~protein amino acid phosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0007166~cell surface receptor linked signal transduction,GO:0007186~G-protein coupled receptor protein signaling pathway,GO:0007224~smoothened signaling pathway,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0008277~regulation of G-protein coupled receptor protein signaling pathway,GO:0016310~phosphorylation,GO:0019953~sexual reproduction,GO:0032504~multicellular organism reproduction,GO:0048477~oogenesis,GO:0048609~reproductive process in a multicellular organism, GO:0005886~plasma membrane, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004703~G-protein coupled receptor kinase activity,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030 554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR000239:GPCR kinase,IPR000342:Regulator of G protein signalling,IPR000719:Protein kinase, core,IPR000961:AGC-kinase, C-terminal,IPR002290:Serine/threonine protein kinase,IPR008271:Serine/threonine protein kinase, active site,IPR017441:Protein kinase, ATP binding site,IPR017442:Serine/threonine protein kinase-related, dme04144:Endocytosis,

SM00133:S_TK_X,SM00220:S_TKc,SM00315:RGS, ATP,atp-binding,complete proteome,developmental protein,differentiation,kinase,membrane,nucleotide-binding,oogenesis,phosphoprotein,phosphotransferase,repeat,serine/threonine-protein kinase,serine/threonine-specific protein kinase,transferase, active site:Proton acceptor,binding site:ATP,chain:G protein-coupled receptor kinase 2,compositionally biased region:Asn-rich,domain:AGC-kinase C-terminal,domain:Protein kinase,domain:RGS 1,domain:RGS 2,modified residue,nucleotide phosphate-bindi ng region:ATP,region of interest:N-terminal,sequence conflict, 1634707_s_at Glutamine:fructose-6-phosphate aminotransferase 1 Drosophila melanogaster Cell envelope biogenesis, outer membrane, GO:0016051~carbohydrate biosynthetic process, GO:0004360~glutamine-fructose-6-phosphate transaminase (isomerizing) activity,GO:0005529~sugar binding,GO:0008483~transaminase activity,GO:0016769~transferase activity, transferring nitrogenous groups,GO:0030246~carbohydrate binding, IPR000583:Glutamine amidotransferase, class-II,IPR001347:Sugar isomerase (SIS),IPR005855:Glucosamine-fructose-6-phosphate aminotransferase, isomerising,IPR017932:Glutamine amidotransferase, type II, dme00250:Alanine, aspartate and glutamate metabolism,dme00520:Amino sugar and nucleotide sugar metabolism, Aminotransferase,complete proteome,transferase,

1626566_at Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial Drosophila melanogaster Lipid metabolism, GO:0006631~fatty acid metabolic process,GO:0006635~fatty acid beta-oxidation,GO:0009062~fatty acid catabolic process,GO:0016042~lipid catabolic process,GO:0016054~organic acid catabolic process,GO:0019395~fatty acid oxidation,GO:0030258~lipid modification,GO:0034440~lipid oxidation,GO:0044242~cellular lipid catabolic process,GO:0046395~carboxylic acid catabolic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0005811~lipid particle,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0003995~acyl-CoA dehydrogenase activity,GO:0009055~electron carrier activity,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding ,GO:0048037~cofactor binding,GO:0050660~FAD binding,GO:0050662~coenzyme binding, IPR006089:Acyl-CoA dehydrogenase, conserved site,IPR006090:Acyl-CoA oxidase/dehydrogenase, type 1,IPR006091:Acyl-CoA oxidase/dehydrogenase, central region,IPR006092:Acyl-CoA dehydrogenase, N-terminal,IPR013764:Acyl-CoA oxidase/dehydrogenase, type1/2, C-terminal,IPR013786:Acyl-CoA dehydrogenase/oxidase, N-terminal, dme00071:Fatty acid metabolism,dme00280:Valine, leucine and isoleucine degradation,dme00410:beta-Alanine metabolism,dme00640:Propanoate metabolism, PIRSF000182:acyl-CoA dehydrogenase, complete proteome,FAD,fatty acid metabolism,Flavoprotein,lipid metabolism,mitochondrion,oxidoreductase,transit peptide, active site:Proton acceptor,binding site:Substrate; via amide nitrogen,binding site:Substrate; via carbonyl oxygen,chain:Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial,nucleotide phosphate-binding region:FAD,region of interest:Substrate binding,transit peptide:Mitochondrion, 1638186_a_at Protein fem-1 homolog B Drosophila melanogaster GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0031396~regulation of protein ubiquitination,GO:0031399~regulation of protein modification process,GO:0032268~regulation of cellular protein metabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051340~regulation of ligase activity,GO:0051438~regulation of ubiquitin-protein ligase activity,GO:0051603~proteolysis involved in cellular protein catabolic process, GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR002110:Ankyrin, SM00248:ANK, alternative splicing,ank repeat,complete proteome,repeat,ubl conjugation pathway, chain:Protein fem-1 homolog B,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5,repeat:ANK 6,repeat:ANK 7,splice variant,

1627376_at Relish Drosophila melanogaster GO:0002684~positive regulation of immune system process,GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002788~regulation of antifungal peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002810~regulation of antifungal peptide biosynthetic process,GO:0002813~regulation of biosynthetic process of antibacterial peptides active against Gram-negative bacteria,GO:0002831~regulation of response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0006952~defense response,GO:0006955~immune response,GO:0006959~humoral immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0006964~positive regulation of biosynthetic process of antibacterial peptides active against Gram-negative bacteria,GO:0006967~positive regulation of antifungal peptide biosynthetic process,GO:0007166~cell surface receptor linked signal transduction,GO:0008063~Toll signaling pathway,GO:0009267~cellular response to starvation,GO:0009617~response to bacterium,GO:0009891~positive regulation of biosynthetic process,GO:0009991~response to extracellular stimulus,GO:0010551~regulation of specific transcription from RNA polymerase II promoter,GO:0010552~positive regulation of specific transcription from RNA polymerase II promoter,GO:0010557~positive regulation of macromolecule biosynthetic process,GO:0010604~positive regulation of macromolecule metabolic process,GO:0010628~positive regulation of gene expression,GO:0019730~antimicrobial humoral response,GO:0031328~positive regulation of cellular biosynthetic process,GO:0031349~positive regulation of defense response,GO:0031667~response to nutrient levels,GO:0031668~cellular response to extracellular stimulus,GO:0031669~cellular response to nutrient levels,GO:0032583~regulation of gene-specific transcription,GO:0033554~cellular response to stress,GO:0034198~cellular response to amino acid starvation,GO:0042594~response to starvation,GO:0042742~defense response to bacterium,GO:0043193~positive regulation of gene-specific transcription,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0045088~regulation of innate immune response,GO:0045089~positive regulation of innate immune response,GO:0045428~regulation of nitric oxide biosynthetic process,GO:0045429~positive regulation of nitric oxide biosynthetic process,GO:0045449~regulation of transcription,GO:0045893~positive regulation of transcription, DNA-dependent,GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,GO:0045941~positive regulation of transcription,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048584~positive regulation of response to stimulus,GO:0050778~positive regulation of immune response,GO:0050829~defense response to Gram-negative bacterium,GO:0051173~positive regulation of nitrogen compound metabolic process,GO:0051252~regulation of RNA metabolic process,GO:0051254~positive regulation of RNA metabolic process, GO:0003677~DNA binding,GO:0003700~transcription factor activity,GO:0030528~transcription regulator activity, IPR000451:NF-kappa-B/Rel/dorsal,IPR002110:Ankyrin,IPR002909:Cell surface receptor IPT/TIG,IPR011539:Rel homology,IPR013783:Immunoglobulin-like fold, SM00248:ANK,SM00429:IPT,activator,alternative splicing,ank repeat,complete proteome,cytoplasm,direct protein sequencing,immune response,innate immunity,nucleus,phosphoprotein,repeat,Transcription,transcription regulation,

chain:Nuclear factor NF-kappa-B p110 subunit,chain:Nuclear factor NF-kappa-B p49 subunit,chain:Nuclear factor NF-kappa-B p68 subunit,domain:RHD,modified residue,mutagenesis site,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5,sequence conflict,sequence variant,short sequence motif:Nuclear localization signal,site:Cleavage (when cotranslationally processed),splice variant,

1629357_s_at SNF1A/AMP-activated protein kinase Drosophila melanogaster GO:0000278~mitotic cell cycle,GO:0000902~cell morphogenesis,GO:0006468~protein amino acid phosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0007049~cell cycle,GO:0007163~establishment or maintenance of cell polarity,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0016310~phosphorylation,GO:0032989~cellular component morphogenesis,GO:0035088~establishment or maintenance of apical/basal cell polarity,GO:0045197~establishment or maintenance of epithelial cell apical/basal polarity, GO:0031588~AMP-activated protein kinase complex, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside

binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004679~AMP-activated protein kinase acti vity,GO:0004703~G-

protein coupled receptor kinase activity,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide

binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR000719:Protein kinase, core,IPR002290:Serine/threonine protein

kinase,IPR008271:Serine/threonine protein kinase, active site,IPR015741:Snf1-like protein AMPK,IPR017441:Protein kinase, ATP binding site,IPR017442:Serine/threonine protein

kinase-related, dme04140:Regulation of autophagy,dme04150:mTOR signaling pathway, PIRSF000590:Snf1/AMPK-type protein kinases, catalytic subunits,

SM00220:S_TKc, atp-binding,complete proteome,kinase,nucleotide-binding,serine/threonine-protein kinase,transferase,

1625433_at Sarcoplasmic calcium-binding protein 1 Drosophila melanogaster GO:0005783~endoplasmic

reticulum,GO:0016528~sarcoplasm,GO:0016529~sarcoplasmic reticulum, GO:0005509~calcium ion binding,GO:0043167~ion binding,GO:0043169~cation

binding,GO:0046872~metal ion binding, IPR002048:Calcium-binding EF-hand,IPR011992:EF-Hand type,IPR018247:EF-HAND 1,IPR018248:EF hand,IPR018249:EF-HAND 2,

SM00054:EFh, calcium,

1638050_s_at Sox box protein 14 Drosophila melanogaster GO:0006350~transcription,GO:0045449~regulation of transcription, GO:0003677~DNA

binding,GO:0003700~transcription factor activity,GO:0030528~transcription regulator activity, IPR000910:High mobility group, HMG1/HMG2, SM00398:HMG,

complete proteome,DNA binding,dna-binding,nucleus,Transcription,transcription regulation, chain:Putative transcription factor SOX-14,compositionally biased

region:Poly-Ala,compositionally biased region:Poly-Asn,DNA-binding region:HMG box,sequence conflict,

1639321_s_at Toll Drosophila melanogaster Function unknown,GO:0000578~embryonic axis specification,GO:0000910~cytokinesis,GO:0002520~immune system

development,GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of

antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002788~regulation of

antifungal peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic

process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002810~regulation of antifungal peptide biosynthetic process,GO:0002831~regulation of

response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0003002~regionalization,GO:0006952~defense response,GO:0006955~immune response,GO:0006959~humoral immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0006967~positive regulation of antifungal peptide biosynthetic process,GO:0007155~cell adhesion,GO:0007166~cell surface receptor linked signal transduction,GO:0007352~zygotic determination of dorsal/ventral axis,GO:0007389~pattern specification process,GO:0007416~synaptogenesis,GO:0008063~Toll signaling pathway,GO:0008283~cell proliferation,GO:0009617~response to bacterium,GO:0009620~response to fungus,GO:0009798~axis specification,GO:0009880~embryonic pattern specification,GO:0009891~positive regulation of biosynthetic process,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0019730~antimicrobial humoral response,GO:0019732~antifungal humoral response,GO:0022610~biological adhesion,GO:0030097~hemopoiesis,GO:0031328~positive regulation of cellular biosynthetic process,GO:0035007~regulation of melanization defense response,GO:0035172~hemocyte proliferation,GO:0042742~defense response to bacterium,GO:0043062~extracellular structure organization,GO:0043455~regulation of secondary metabolic process,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0045088~regulation of innate immune response,GO:0045610~regulation of hemocyte differentiation,GO:0048534~hemopoietic or lymphoid organ development,GO:0050808~synapse organization,GO:0050830~defense response to Gram-positive bacterium,GO:0050832~defense response to fungus,GO:0051301~cell division, GO:0005886~plasma membrane,GO:0005887~integral to plasma membrane,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0031226~intrinsic to plasma membrane,GO:0044459~plasma membrane part,

GO:0019955~cytokine binding,GO:0042802~identical protein binding, IPR000157:Toll-Interleukin receptor,IPR000372:Leucine-rich repeat, cysteine-rich flanking region, N-terminal,IPR000483:Cysteine-rich flanking region, C-terminal,IPR001611:Leucine-rich repeat,IPR003591:Leucine-rich repeat, typical subtype,IPR004075:Interleukin-1 receptor, type I/Toll precursor, SM00013:LRRNT,SM00082:LRRCT,SM00255:TIR,SM00369:LRR_TYP, cell adhesion,cell membrane,complete proteome,developmental protein,disulfide bond,glycoprotein,leucine-rich repeat,membrane,polymorphism,repeat,signal,transmembrane,transmembrane protein, chain:Protein toll,domain:TIR,glycosylation site:N-linked (GlcNAc...),repeat:LRR 1,repeat:LRR 10,repeat:LRR 11,repeat:LRR 12,repeat:LRR 13,repeat:LRR 14,repeat:LRR 15,repeat:LRR 16,repeat:LRR 17,repeat:LRR 18,repeat:LRR 19,repeat:LRR 2,repeat:LRR 20,repeat:LRR 21,repeat:LRR 3,repeat:LRR 4,repeat:LRR 5,repeat:LRR 6,repeat:LRR 7,repeat:LRR 8,repeat:LRR 9,sequence conflict,sequence variant,signal peptide,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,

1629843_s_at Ubiquitin carrier protein Drosophila melanogaster GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0016567~protein ubiquitination,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0032446~protein modification by small protein conjugation,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process,GO:0070647~protein modification by small protein conjugation or removal, GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR000608:Ubiquitin-conjugating enzyme, E2,IPR015581:Ubiquitin-conjugating enzyme,IPR016135:Ubiquitin-conjugating enzyme/RWD-like, dme04120:Ubiquitin mediated proteolysis, SM00212:UBCc, complete proteome,ligase,ubl conjugation pathway,

1640754_at brummer Drosophila melanogaster GO:0006638~neutral lipid metabolic process,GO:0006639~acylglycerol metabolic process,GO:0006641~triglyceride metabolic process,GO:0006642~triglyceride mobilization,GO:0006662~glycerol ether metabolic process,GO:0007568~aging,GO:0008340~determination of adult life span,GO:0010259~multicellular organismal aging,GO:0016042~lipid catabolic process,GO:0018904~organic ether metabolic process,GO:0019433~triglyceride catabolic process,GO:0044242~cellular lipid catabolic process,GO:0044269~glycerol ether catabolic process,GO:0046461~neutral lipid catabolic process,GO:0046464~acylglycerol catabolic process,GO:0046486~glycerolipid metabolic process,GO:0046503~glycerolipid catabolic process,GO:0005811~lipid particle, GO:0004091~carboxylesterase activity,GO:0004806~triacylglycerol lipase activity,GO:0016298~lipase activity, IPR002641:Patatin, complete proteome,hydrolase,lipid degradation,

1635619_a_at centrosomin Drosophila melanogaster GO:0000087~M phase of mitotic cell cycle,GO:0000226~microtubule cytoskeleton organization,GO:0000278~mitotic cell cycle,GO:0000279~M phase,GO:0000280~nuclear division,GO:0007010~cytoskeleton organization,GO:0007017~microtubule-based process,GO:0007049~cell cycle,GO:0007051~spindle organization,GO:0007052~mitotic spindle organization,GO:0007059~chromosome segregation,GO:0007067~mitosis,GO:0007098~centrosome cycle,GO:0007126~meiosis,GO:0007143~female meiosis,GO:0007422~peripheral nervous system development,GO:0007494~midgut development,GO:0016321~female meiosis chromosome segregation,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0031023~microtubule organizing center organization,GO:0045132~meiotic chromosome segregation,GO:0048285~organelle fission,GO:0048565~gut development,GO:0051297~centrosome organization,GO:0051301~cell division,GO:0051321~meiotic cell cycle,GO:0051327~M phase of meiotic cell cycle, GO:0000242~pericentriolar material,GO:0005813~centrosome,GO:0005815~microtubule organizing center,GO:0005856~cytoskeleton,GO:0005875~microtubule associated complex,GO:0005929~cilium,GO:0005932~microtubule basal body,GO:0015629~actin cytoskeleton,GO:0015630~microtubule cytoskeleton,GO:0016459~myosin complex,GO:0019861~flagellum,GO:0042995~cell projection,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0044430~cytoskeletal part,GO:0044450~microtubule organizing center part,GO:0044463~cell projection part, GO:0008017~microtubule binding,GO:0008092~cytoskeletal protein binding,GO:0015631~tubulin binding,GO:0016887~ATPase activity,GO:0042624~ATPase activity, uncoupled, IPR012943:Spindle associated, alternative splicing,cell cycle,cell division,cell projection,cilium,coiled coil,complete proteome,cytoplasm,cytoskeleton,developmental protein,flagellum,hydrolase,leucine zipper,meiosis,mitosis,phosphoprotein, chain:Centrosomin,modified residue,sequence conflict,short sequence motif:Nuclear localization signal,splice variant,

1631243_s_at lethal (3) 05822 Drosophila melanogaster IPR000108:Neutrophil cytosol factor 2,IPR001452:Src homology-3 domain, SM00326:SH3, complete proteome,sh3 domain,

1627651_a_at locomotion defectsDrosophila melanogaster GO:0000902~cell morphogenesis,GO:0001885~endothelial cell development,GO:0002009~morphogenesis of an epithelium,GO:0002064~epithelial cell development,GO:0003002~regionalization,GO:0003006~reproductive developmental process,GO:0007010~cytoskeleton organization,GO:0007043~cell-cell junction assembly,GO:0007163~establishment or maintenance of cell polarity,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007300~ovarian nurse cell to oocyte transport,GO:0007303~cytoplasmic transport, nurse cell to oocyte,GO:0007389~pattern specification process,GO:0007405~neuroblast proliferation,GO:0007419~ventral cord development,GO:0008069~dorsal/ventral axis specification, ovarian follicular epithelium,GO:0008104~protein localization,GO:0008105~asymmetric protein localization,GO:0008277~regulation of G-protein coupled receptor protein signaling pathway,GO:0008283~cell proliferation,GO:0009798~axis specification,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0010001~glial cell differentiation,GO:0014045~establishment of endothelial blood-brain barrier,GO:0016333~morphogenesis of follicular epithelium,GO:0016334~establishment or maintenance of polarity of follicular epithelium,GO:0016482~cytoplasmic transport,GO:0017145~stem cell division,GO:0019953~sexual reproduction,GO:0019991~septate junction assembly,GO:0021782~glial cell development,GO:0030029~actin filament-based process,GO:0030036~actin cytoskeleton organization,GO:0030707~ovarian follicle cell development,GO:0030855~epithelial cell differentiation,GO:0030865~cortical cytoskeleton organization,GO:0030866~cortical actin cytoskeleton organization,GO:0032504~multicellular organism reproduction,GO:0032989~cellular component morphogenesis,GO:0034329~cell junction assembly,GO:0034330~cell junction organization,GO:0042063~gliogenesis,GO:0043297~apical junction assembly,GO:0045165~cell fate commitment,GO:0045216~cell-cell junction organization,GO:0045446~endot helial cell differentiation,GO:0046907~intracellular transport,GO:0048103~somatic stem cell division,GO:0048477~oogenesis,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0048729~tissue morphogenesis,GO:0051301~cell division,GO:0055057~neuroblast division,GO:0055059~asymmetric neuroblast division,GO:0060429~epithelium development,

GO:0005886~plasma membrane,GO:0005938~cell cortex,GO:0044448~cell cortex part,GO:0045177~apical part of cell,GO:0045179~apical cortex, GO:0001965~G-protein alpha-subunit binding,GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0030695~GTPase regulator activity,GO:0060589~nucleoside-triphosphatase regulator activity, IPR000342:Regulator of G protein signalling,IPR001478:PDZ/DHR/GLGF,IPR003109:GoLoco motif,IPR003116:Raf-like Ras-binding,IPR006020:Phosphotyrosine interaction region, SM00228:PDZ,SM00315:RGS,SM00390:GoLoco,SM00455:RBD,SM00462:PTB, complete proteome,

1625830_a_at scruin like at the midline Drosophila melanogaster IPR006652:Kelch repeat type 1,IPR015915:Kelch-type beta propeller, SM00612:Kelch, complete proteome,

****

+D

C

-D

Probe sets:

1625199_s_at	1633654_s_at	1634814_at	1638325_at	1638875_at

Functional annotation table:

-D C +D

ID Gene Name Species GOTERM_BP_FAT GOTERM_CC_FAT GOTERM_MF_FAT INTERPRO KEGG_PATHWAY PIR_SUPERFAMILY SP_PIR_KEYWORDS UP_SEQ_FEATURE

1638875_at Egg-derived tyrosine phosphatase Drosophila melanogaster GO:0006470~protein amino acid dephosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0016311~dephosphorylation, GO:0004721~phosphoprotein phosphatase activity,GO:0004725~protein tyrosine phosphatase activity,GO:0016791~phosphatase activity, IPR016130:Protein-tyrosine phosphatase, active site, complete proteome,hydrolase,

1638325_at Henna Drosophila melanogaster GO:0006558~L-phenylalanine metabolic process,GO:0006559~L-phenylalanine catabolic process,GO:0006575~cellular amino acid derivative metabolic process,GO:0006576~biogenic amine metabolic process,GO:0006586~indolalkylamine metabolic process,GO:0006726~eye pigment biosynthetic process,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0009063~cellular amino acid catabolic process,GO:0009072~aromatic amino acid family metabolic process,GO:0009074~aromatic amino acid family catabolic process,GO:0009309~amine biosynthetic process,GO:0009310~amine catabolic process,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016054~organic acid catabolic process,GO:0016192~vesicle-mediated transport,GO:0018130~heterocycle biosynthetic process,GO:0019439~aromatic compound catabolic process,GO:0042398~cellular amino acid derivative biosynthetic process,GO:0042401~biogenic amine biosynthetic process,GO:0042427~serotonin biosynthetic process,GO:0042428~serotonin metabolic process,GO:0042430~indole and derivative metabolic process,GO:0042434~indole derivative metabolic process,GO:0042435~indole derivative biosynthetic process,GO:0042440~pigment metabolic process,GO:0042441~eye pigment metabolic process,GO:0043473~pigmentation,GO:0044271~nitrogen compound biosynthetic process,GO:0046148~pigment biosynthetic process,GO:0046219~indolalkylamine biosynthetic process,GO:0046395~carboxylic acid catabolic process,GO:0048066~pigmentation during development,GO:0048069~eye pigmentation,GO:0055114~oxidation reduction, GO:0005811~lipid particle, GO:0004505~phenylalanine 4-monooxygenase activity,GO:0004510~tryptophan 5-monooxygenase activity,GO:0005506~iron ion binding,GO:0016597~amino acid binding,GO:0016714~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen,GO:0031406~carboxylic acid binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0043176~amine binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR001273:Aromatic amino acid hydroxylase,IPR002912:Amino acid-binding ACT,IPR005961:Phenylalanine-4-hydroxylase, tetrameric form,IPR018301:Aromatic amino acid hydroxylase, iron/copper binding site,IPR019773:Tyrosine 3-monooxygenase-like,IPR019774:Aromatic amino acid hydroxylase, C-terminal, dme00360:Phenylalanine metabolism,dme00400:Phenylalanine, tyrosine and tryptophan biosynthesis, PIRSF000336:TH,PIRSF000336:tyrosine 3-monooxygenase, allosteric enzyme,biopterin,complete proteome,iron,metal-binding,metalloprotein,Monooxygenase,oxidoreductase,phenylalanine catabolism,phenylketonuria,phosphoprotein,serotonin biosynthesis, chain:Protein henna,domain:ACT,metal ion-binding site:Iron,modified residue,sequence conflict,

1633654_s_at Inositol 1,4,5-triphosphate kinase 2 Drosophila melanogaster GO:0006020~inositol metabolic process,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0016310~phosphorylation,GO:0019751~polyol metabolic process,GO:0046835~carbohydrate phosphorylation,GO:0046853~inositol and derivative phosphorylation, GO:0004428~inositol or phosphatidylinositol kinase activity,GO:0005516~calmodulin binding,GO:0008440~inositol trisphosphate 3-kinase activity,GO:0048306~calcium-dependent protein binding,GO:0051766~inositol trisphosphate kinase activity, IPR005522:Inositol polyphosphate kinase, dme00562:Inositol phosphate metabolism,dme04070:Phosphatidylinositol signaling system, complete proteome,kinase,transferase,

1634814_at UPF0183 protein CG7083 Drosophila melanogaster IPR005373:Uncharacterised protein family UPF0183, PIRSF015809:hypothetical protein, Caenorhabditis elegans T01G9.2b type, complete proteome, chain:UPF0183 protein CG7083,

1625199_s_at dacapo Drosophila melanogaster GO:0000079~regulation of cyclin-dependent protein kinase activity,GO:0000082~G1/S transition of mitotic cell cycle,GO:0000278~mitotic cell cycle,GO:0001709~cell fate determination,GO:0002165~instar larval or pupal development,GO:0003006~reproductive developmental process,GO:0007049~cell cycle,GO:0007050~cell cycle arrest,GO:0007090~regulation of S phase of mitotic cell cycle,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007293~germarium-derived egg chamber formation,GO:0007294~germarium-derived oocyte fate determination,GO:0007346~regulation of mitotic cell cycle,GO:0007423~sensory organ development,GO:0007424~open tracheal system development,GO:0007444~imaginal disc development,GO:0007488~histoblast morphogenesis,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0008356~asymmetric cell division,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0009994~oocyte differentiation,GO:0010563~negative regulation of phosphorus metabolic process,GO:0010564~regulation of cell cycle process,GO:0010605~negative regulation of macromolecule metabolic process,GO:0010948~negative regulation of cell cycle process,GO:0019220~regulation of phosphate metabolic process,GO:0019953~sexual reproduction,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0030706~germarium-derived oocyte differentiation,GO:0030716~oocyte fate determination,GO:0031399~regulation of protein modification process,GO:0031400~negative regulation of protein modification process,GO:0032268~regulation of cellular protein metabolic process,GO:0032269~negative regulation of cellular protein metabolic process,GO:0032504~multicellular organism reproduction,GO:0033261~regulation of S phase,GO:0035303~regulation of dephosphorylation,GO:0035304~regulation of protein amino acid dephosphorylation,GO:0035305~negative regulation of dephosphorylation,GO:0035308~negative regulation of protein amino acid dephosphorylation,GO:0042325~regulation of phosphorylation,GO:0043549~regulation of kinase activity,GO:0045035~sensory organ precursor cell division,GO:0045165~cell fate commitment,GO:0045749~negative regulation of S phase of mitotic cell cycle,GO:0045786~negative regulation of cell cycle,GO:0045859~regulation of protein kinase activity,GO:0045930~negative regulation of mitotic cell cycle,GO:0045936~negative regulation of phosphate metabolic process,GO:0048477~oogenesis,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0048707~instar larval or pupal morphogenesis,GO:0051174~regulation of phosphorus metabolic process,GO:0051248~negative regulation of protein metabolic process,GO:0051301~cell division,GO:0051318~G1 phase,GO:0051325~interphase,GO:0051329~interphase of mitotic cell cycle,GO:0051338~regulation of transferase activity,GO:0051726~regulation of cell cycle,GO:0060541~respiratory system development, GO:0004857~enzyme inhibitor activity,GO:0004860~protein kinase inhibitor activity,GO:0004861~cyclin-dependent protein kinase inhibitor activity,GO:0016538~cyclin-dependent protein kinase regulator activity,GO:0019207~kinase regulator activity,GO:0019210~kinase inhibitor activity,GO:0019887~protein kinase regulator activity,GO:0030291~protein serine/threonine kinase inhibitor activity, IPR003175:Cyclin-dependent kinase inhibitor,

****

-D

C

+D

Probe sets:

1625519_at
1628429_at
1632834_a_at
1639762_at
1628194_at
1635065_at
1635491_s_at
1636639_at

Functional annotation table:

ID	Gene Name	Species	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1635491_s_at	Dmel_CG11642	Drosophila melanogaster	GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0008104~protein localization,GO:0010324~membrane invagination,GO:0015031~protein transport,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0070727~cellular macromolecule localization,	GO:0005783~endoplasmic reticulum,GO:0005811~lipid particle,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,		IPR006634:TRAM, LAG1 and CLN8 homology,IPR013599:TRAM1-like protein,IPR016447:Translocation associated membrane protein,		PIRSF005449:translocation associated membrane protein,PIRSF005449:Translocation_assoc_membrane,	SM00724:TLC,	membrane,transmembrane,	

1628194_at Dmel_CG2918 Drosophila melanogaster GO:0006457~protein folding, GO:0005811~lipid particle, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR001023:Heat shock protein Hsp70,IPR013126:Heat shock protein 70,IPR018181:Heat shock protein 70, conserved site, atp-binding,complete proteome,nucleotide-binding,

1639762_at Dmel_CG3734 Drosophila melanogaster GO:0006508~proteolysis, GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR008758:Peptidase S28, PIRSF016539:Lysosomal Pro-X carboxypeptidase / Dipeptidyl-peptidase 2, complete proteome,

1632834_a_at Dmel_CG5946 Drosophila melanogaster GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0055114~oxidation reduction, GO:0004128~cytochrome-b5 reductase activity,GO:0009055~electron carrier activity,GO:0016651~oxidoreductase activity, acting on NADH or NADPH,GO:0016653~oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor, IPR001433:Oxidoreductase FAD/NAD(P)-binding,IPR001709:Flavoprotein pyridine nucleotide cytochrome reductase,IPR001834:NADH:cytochrome b5 reductase (CBR),IPR008333:Oxidoreductase FAD-binding region,IPR017927:Ferredoxin reductase-type FAD-binding domain, dme00520:Amino sugar and nucleotide sugar metabolism, PIRSF000206:cytochrome-b5 reductase, complete proteome,FAD,Flavoprotein,nad,oxidoreductase,

1625519_at Dmel_CG6453 Drosophila melanogaster GO:0005783~endoplasmic reticulum,GO:0017177~alpha-glucosidase II complex,GO:0044432~endoplasmic reticulum part, GO:0004558~alpha-glucosidase activity,GO:0015926~glucosidase activity, IPR002172:Low density lipoprotein-receptor, class A, cysteine-rich,IPR012913:Glucosidase II beta subunit-like,IPR018247:EF-HAND 1, PIRSF017177:uncharacterized conserved protein, SM00192:LDLa, complete proteome,glycosidase,hydrolase,

1635065_at Dmel_CG7025 Drosophila melanogaster GO:0006508~proteolysis, GO:0004180~carboxypeptidase activity,GO:0004181~metallocarboxypeptidase activity,GO:0008233~peptidase activity,GO:0008235~metalloexopeptidase activity,GO:0008237~metallopeptidase activity,GO:0008238~exopeptidase activity,GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR000834:Peptidase M14, carboxypeptidase A, SM00631:Zn_pept, carboxypeptidase,complete proteome,hydrolase,

1628429_at Protein transport protein Sec61 gamma-2 subunit Drosophila melanogaster GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006616~SRP-dependent cotranslational protein targeting to membrane, translocation,GO:0006886~intracellular protein transport,GO:0007033~vacuole organization,GO:0007040~lysosome organization,GO:0008104~protein localization,GO:0009894~regulation of catabolic process,GO:0009895~negative regulation of catabolic process,GO:0010506~regulation of autophagy,GO:0010507~negative regulation of autophagy,GO:0015031~protein transport,GO:0031329~regulation of cellular catabolic process,GO:0031330~negative regulation of cellular catabolic process,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transp ort,GO:0055085~transmembrane transport,GO:0065002~intracellular protein transmembrane transport,GO:0070727~cellular macromolecule localization, GO:0005783~endoplasmic reticulum,GO:0005784~translocon complex,GO:0005789~endoplasmic reticulum membrane,GO:0005791~rough endoplasmic reticulum,GO:0012505~endomembrane system,GO:0016021~integral to membrane,GO:0030176~integral to endoplasmic reticulum membrane,GO:0030867~rough endoplasmic reticulum membrane,GO:0031090~organelle membrane,GO:0031224~intrinsic to membrane,GO:0031227~intrinsic to endoplasmic reticulum membrane,GO:0031300~intrinsic to organelle membrane,GO:0031301~integral to organelle membrane,GO:0042175~nuclear envelope-endoplasmic reticulum network,GO:0044432~endoplasmic reticulum part, GO:0008320~protein transmembrane transporter activity,GO:0008565~protein transporter activity,GO:0015399~primary active transmembrane transporter activity,GO:0015405~P-P-bond-hydrolysis-driven transmembrane transporter activity,GO:0015450~P-P-bond-hydrolysis-driven prot ein transmembrane transporter activity,GO:0022884~macromolecule transmembrane transporter activity, IPR001901:Protein secE/sec61-gamma protein,IPR008158:Protein translocase SEC61 complex gamma subunit, PIRSF005525:preprotein translocase Sec, SecE/Sec61-gamma subunit,PIRSF500209:preprotein translocase Sec, Sec61-gamma subunit, complete proteome,endoplasmic reticulum,membrane,protein transport,translocation,transmembrane,transport, chain:Protein transport protein Sec61 gamma-2 subunit,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,

1636639_at	Signal peptide protease	Drosophila melanogaster	GO:0006508~proteolysis,GO:0007424~open tracheal system development,GO:0009057~macromolecule catabolic process,GO:0030163~protein catabolic process,GO:0033619~membrane protein proteolysis,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process,GO:0060541~respiratory system development,	GO:0005783~endoplasmic reticulum,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,	GO:0004175~endopeptidase activity,GO:0004190~aspartic-type endopeptidase activity,GO:0008233~peptidase activity,GO:0042500~aspartic endopeptidase activity, intramembrane cleaving,GO:0070001~aspartic-type peptidase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides,	IPR006639:Peptidase A22, presenilin signal peptide,IPR007369:Peptidase A22B, signal peptide peptidase,		SM00730:PSN,	complete proteome,hydrolase,Protease,

File S3

Functional annotations for the probe sets classified in Figure 8

Functional terms enriching the lists of probe sets in each expression pattern, obtained with the DAVID *Functional annotation chart* tool

* * *

C

+D

-D

Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	SP_PIR_KEYWORDS	alternative splicing	RT		167	11.5	1.4E-31	1.9E-28
	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT		85	5.8	5.4E-27	9.5E-24
	GOTERM_BP_FAT	energy derivation by oxidation of organic compounds	RT		58	4.0	2.4E-25	4.3E-22
	UP_SEQ_FEATURE	splice variant	RT		165	11.3	5.1E-25	8.3E-22
	GOTERM_BP_FAT	cellular respiration	RT		54	3.7	6.9E-24	1.2E-20
	GOTERM_CC_FAT	respiratory chain	RT		46	3.2	3.6E-19	5.1E-16
	GOTERM_BP_FAT	electron transport chain	RT		44	3.0	1.9E-18	3.3E-15
	GOTERM_BP_FAT	phosphorus metabolic process	RT		131	9.0	2.7E-18	4.7E-15

GOTERM_BP_FAT	phosphate metabolic process	RT	131	9.0	2.7E-18	4.7E-15
GOTERM_CC_FAT	mitochondrial respiratory chain	RT	44	3.0	3.7E-18	5.2E-15
GOTERM_BP_FAT	respiratory electron transport chain	RT	39	2.7	8.3E-18	1.5E-14
GOTERM_BP_FAT	phosphorylation	RT	109	7.5	9.8E-18	1.7E-14
KEGG_PATHWAY	Oxidative phosphorylation	RT	58	4.0	5.2E-17	5.7E-14
GOTERM_BP_FAT	mitochondrial ATP synthesis coupled electron transport	RT	36	2.5	8.3E-17	1.9E-13
GOTERM_BP_FAT	oxidative phosphorylation	RT	52	3.6	9.2E-17	1.9E-13
GOTERM_BP_FAT	ATP synthesis coupled electron transport	RT	37	2.5	1.0E-16	1.9E-13
GOTERM_CC_FAT	mitochondrial membrane part	RT	55	3.8	6.0E-16	7.9E-13
GOTERM_CC_FAT	mitochondrial inner membrane	RT	68	4.7	1.0E-14	1.4E-11
GOTERM_CC_FAT	mitochondrion	RT	137	9.4	1.2E-14	1.7E-11
GOTERM_CC_FAT	organelle inner membrane	RT	70	4.8	7.6E-14	1.1E-10
GOTERM_BP_FAT	mitochondrial electron transport, NADH to ubiquinone	RT	22	1.5	1.7E-12	3.0E-9
GOTERM_CC_FAT	mitochondrial membrane	RT	72	4.9	2.2E-12	3.1E-9
GOTERM_CC_FAT	mitochondrial envelope	RT	75	5.2	3.1E-12	4.5E-9
GOTERM_CC_FAT	mitochondrial part	RT	103	7.1	3.7E-12	5.2E-9
GOTERM_MF_FAT	cytoskeletal protein binding	RT	64	4.4	1.3E-11	2.0E-8
GOTERM_BP_FAT	epithelium development	RT	63	4.3	3.2E-11	5.6E-8
SP_PIR_KEYWORDS	phosphoprotein	RT	148	10.2	4.2E-11	5.7E-8
GOTERM_CC_FAT	mitochondrial respiratory chain complex I	RT	25	1.7	4.1E-11	5.9E-8
GOTERM_CC_FAT	NADH dehydrogenase complex	RT	25	1.7	4.1E-11	5.9E-8

GOTERM_CC_FAT	respiratory chain complex I	RT	25	1.7	4.1E-11	5.9E-8
GOTERM_MF_FAT	NADH dehydrogenase activity	RT	24	1.6	5.8E-11	9.2E-8
GOTERM_BP_FAT	cellular component morphogenesis	RT	106	7.3	2.5E-10	4.3E-7
GOTERM_CC_FAT	organelle envelope	RT	86	5.9	4.0E-10	5.6E-7
GOTERM_CC_FAT	envelope	RT	86	5.9	4.6E-10	6.6E-7
GOTERM_BP_FAT	cell morphogenesis	RT	94	6.5	3.8E-10	6.7E-7
GOTERM_BP_FAT	establishment or maintenance of cell polarity	RT	37	2.5	7.0E-10	1.2E-6
GOTERM_BP_FAT	transmission of nerve impulse	RT	53	3.6	1.1E-9	1.9E-6
GOTERM_BP_FAT	morphogenesis of an epithelium	RT	58	4.0	1.1E-9	1.9E-6
GOTERM_BP_FAT	actin cytoskeleton organization	RT	43	3.0	1.6E-9	2.8E-6
INTERPRO	PDZ/DHR/GLGF	RT	28	1.9	1.7E-9	2.9E-6
GOTERM_MF_FAT	oxidoreductase activity, acting on NADH or NADPH	RT	25	1.7	1.9E-9	3.0E-6
GOTERM_BP_FAT	actin filament-based process	RT	43	3.0	2.0E-9	3.6E-6
GOTERM_BP_FAT	morphogenesis of embryonic epithelium	RT	38	2.6	3.5E-9	6.2E-6
GOTERM_CC_FAT	lipid particle	RT	66	4.5	5.6E-9	8.0E-6
INTERPRO	Src homology-3 domain	RT	29	2.0	5.2E-9	8.7E-6
GOTERM_BP_FAT	post-embryonic morphogenesis	RT	77	5.3	6.0E-9	1.1E-5
GOTERM_BP_FAT	tissue morphogenesis	RT	60	4.1	6.3E-9	1.1E-5
GOTERM_BP_FAT	metamorphosis	RT	78	5.4	8.4E-9	1.5E-5
GOTERM_CC_FAT	septate junction	RT	15	1.0	1.5E-8	2.1E-5
GOTERM_BP_FAT	instar larval or pupal morphogenesis	RT	75	5.2	1.5E-8	2.6E-5

SMART	PDZ	RT	28	1.9	2.0E-8	2.7E-5
GOTERM_BP_FAT	apical junction assembly	RT	16	1.1	2.1E-8	3.8E-5
GOTERM_BP_FAT	synaptic transmission	RT	49	3.4	2.2E-8	3.8E-5
UP_SEQ_FEATURE	compositionally biased region:Gln-rich	RT	48	3.3	2.8E-8	4.5E-5
GOTERM_MF_FAT	NADH dehydrogenase (quinone) activity	RT	19	1.3	3.0E-8	4.7E-5
GOTERM_MF_FAT	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	RT	19	1.3	3.0E-8	4.7E-5
GOTERM_MF_FAT	NADH dehydrogenase (ubiquinone) activity	RT	19	1.3	3.0E-8	4.7E-5
GOTERM_BP_FAT	cell-cell junction organization	RT	18	1.2	3.5E-8	6.1E-5
SP_PIR_KEYWORDS	muscle protein	RT	12	0.8	5.1E-8	7.0E-5
GOTERM_BP_FAT	neuron differentiation	RT	83	5.7	4.6E-8	8.0E-5
GOTERM_BP_FAT	cell-cell signaling	RT	52	3.6	4.6E-8	8.0E-5
GOTERM_BP_FAT	open tracheal system development	RT	42	2.9	4.7E-8	8.2E-5
GOTERM_BP_FAT	respiratory system development	RT	42	2.9	4.7E-8	8.2E-5
SMART	SH3	RT	29	2.0	6.1E-8	8.2E-5
GOTERM_BP_FAT	dorsal closure	RT	31	2.1	5.9E-8	1.0E-4
GOTERM_BP_FAT	cell junction organization	RT	18	1.2	5.9E-8	1.0E-4
GOTERM_BP_FAT	cell-cell junction assembly	RT	16	1.1	7.7E-8	1.3E-4
GOTERM_BP_FAT	exocrine system development	RT	39	2.7	8.2E-8	1.4E-4
GOTERM_BP_FAT	salivary gland development	RT	39	2.7	8.2E-8	1.4E-4
GOTERM_BP_FAT	cell adhesion	RT	45	3.1	9.7E-8	1.7E-4
SP_PIR_KEYWORDS	calcium	RT	41	2.8	1.3E-7	1.7E-4

GOTERM_CC_FAT	cell junction	RT	41	2.8	1.2E-7	1.8E-4
GOTERM_BP_FAT	instar larval or pupal development	RT	83	5.7	1.2E-7	2.2E-4
GOTERM_BP_FAT	salivary gland morphogenesis	RT	34	2.3	1.4E-7	2.4E-4
GOTERM_BP_FAT	gland morphogenesis	RT	34	2.3	1.4E-7	2.4E-4
GOTERM_CC_FAT	contractile fiber part	RT	13	0.9	1.7E-7	2.4E-4
GOTERM_BP_FAT	cell junction assembly	RT	16	1.1	1.4E-7	2.4E-4
GOTERM_BP_FAT	regulation of tube size	RT	14	1.0	1.5E-7	2.6E-4
GOTERM_BP_FAT	cofactor catabolic process	RT	17	1.2	1.6E-7	2.7E-4
GOTERM_CC_FAT	organelle membrane	RT	94	6.5	2.1E-7	2.9E-4
GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT	30	2.1	1.7E-7	3.0E-4
GOTERM_BP_FAT	neurotransmitter transport	RT	36	2.5	1.7E-7	3.1E-4
GOTERM_BP_FAT	regulation of tube size, open tracheal system	RT	13	0.9	1.8E-7	3.2E-4
GOTERM_BP_FAT	regulation of neurotransmitter levels	RT	33	2.3	1.8E-7	3.2E-4
SP_PIR_KEYWORDS	developmental protein	RT	97	6.7	2.5E-7	3.4E-4
SP_PIR_KEYWORDS	atp-binding	RT	103	7.1	2.7E-7	3.7E-4
KEGG_PATHWAY	Citrate cycle (TCA cycle)	RT	21	1.4	3.6E-7	3.9E-4
GOTERM_MF_FAT	small GTPase regulator activity	RT	34	2.3	2.5E-7	4.0E-4
INTERPRO	EGF-like	RT	26	1.8	2.4E-7	4.0E-4
SP_PIR_KEYWORDS	nucleotide-binding	RT	124	8.5	3.0E-7	4.1E-4
GOTERM_BP_FAT	acetyl-CoA metabolic process	RT	17	1.2	2.6E-7	4.5E-4
GOTERM_BP_FAT	post-embryonic development	RT	84	5.8	3.2E-7	5.6E-4

GOTERM_BP_FAT	neurotransmitter secretion	RT	31	2.1	3.4E-7	6.0E-4
INTERPRO	Pleckstrin homology-type	RT	33	2.3	3.6E-7	6.1E-4
GOTERM_BP_FAT	acetyl-CoA catabolic process	RT	16	1.1	4.1E-7	7.1E-4
GOTERM_BP_FAT	tricarboxylic acid cycle	RT	16	1.1	4.1E-7	7.1E-4
GOTERM_MF_FAT	GTPase regulator activity	RT	40	2.7	4.8E-7	7.5E-4
GOTERM_BP_FAT	generation of a signal involved in cell-cell signaling	RT	31	2.1	4.3E-7	7.6E-4
GOTERM_CC_FAT	cell-cell junction	RT	23	1.6	5.5E-7	7.8E-4
GOTERM_BP_FAT	autophagic cell death	RT	24	1.6	5.3E-7	9.2E-4
GOTERM_BP_FAT	salivary gland cell autophagic cell death	RT	24	1.6	5.3E-7	9.2E-4
GOTERM_BP_FAT	salivary gland histolysis	RT	24	1.6	5.3E-7	9.2E-4
GOTERM_CC_FAT	occluding junction	RT	15	1.0	6.6E-7	9.4E-4
SP_PIR_KEYWORDS	cytoplasm	RT	81	5.6	6.9E-7	9.5E-4
GOTERM_BP_FAT	coenzyme catabolic process	RT	16	1.1	6.7E-7	1.2E-3
GOTERM_CC_FAT	apical junction complex	RT	19	1.3	8.6E-7	1.2E-3
GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT	26	1.8	7.2E-7	1.3E-3
GOTERM_BP_FAT	muscle cell differentiation	RT	25	1.7	7.2E-7	1.3E-3
GOTERM_CC_FAT	contractile fiber	RT	13	0.9	9.0E-7	1.3E-3
GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT	40	2.7	8.6E-7	1.3E-3
GOTERM_BP_FAT	neuron development	RT	70	4.8	7.8E-7	1.4E-3
GOTERM_BP_FAT	tissue death	RT	24	1.6	9.5E-7	1.7E-3
GOTERM_BP_FAT	histolysis	RT	24	1.6	9.5E-7	1.7E-3

GOTERM_BP_FAT	biological adhesion	RT	45	3.1	1.0E-6	1.8E-3
GOTERM_BP_FAT	regulation of tube architecture, open tracheal system	RT	17	1.2	1.0E-6	1.8E-3
GOTERM_BP_FAT	aerobic respiration	RT	16	1.1	1.1E-6	1.9E-3
GOTERM_BP_FAT	programmed cell death	RT	39	2.7	1.2E-6	2.1E-3
GOTERM_BP_FAT	cell motion	RT	63	4.3	1.3E-6	2.3E-3
GOTERM_BP_FAT	negative regulation of cell communication	RT	30	2.1	1.5E-6	2.6E-3
GOTERM_CC_FAT	sarcomere	RT	11	0.8	1.9E-6	2.7E-3
SMART	EGF	RT	26	1.8	2.0E-6	2.8E-3
GOTERM_CC_FAT	actin cytoskeleton	RT	29	2.0	1.9E-6	2.8E-3
GOTERM_MF_FAT	actin binding	RT	35	2.4	1.8E-6	2.8E-3
SP_PIR_KEYWORDS	actin-binding	RT	18	1.2	2.3E-6	3.1E-3
GOTERM_BP_FAT	vesicle-mediated transport	RT	75	5.2	2.2E-6	3.8E-3
GOTERM_BP_FAT	gland development	RT	40	2.7	2.3E-6	4.1E-3
INTERPRO	Variant SH3	RT	11	0.8	2.5E-6	4.2E-3
GOTERM_BP_FAT	septate junction assembly	RT	11	0.8	2.6E-6	4.6E-3
GOTERM_BP_FAT	secretion by cell	RT	32	2.2	3.2E-6	5.7E-3
GOTERM_CC_FAT	apicolateral plasma membrane	RT	19	1.3	4.4E-6	6.2E-3
GOTERM_CC_FAT	myofibril	RT	11	0.8	4.6E-6	6.5E-3
GOTERM_BP_FAT	striated muscle cell differentiation	RT	22	1.5	3.8E-6	6.7E-3
GOTERM_BP_FAT	negative regulation of signal transduction	RT	29	2.0	3.8E-6	6.7E-3
INTERPRO	Pleckstrin homology	RT	25	1.7	4.0E-6	6.7E-3

GOTERM_BP_FAT	regulation of cell morphogenesis	RT	32	2.2	3.9E-6	6.8E-3
SP_PIR_KEYWORDS	sh3 domain	RT	18	1.2	6.2E-6	8.5E-3
GOTERM_BP_FAT	cell death	RT	39	2.7	5.2E-6	9.1E-3
GOTERM_BP_FAT	chitin-based embryonic cuticle biosynthetic process	RT	11	0.8	5.3E-6	9.2E-3
GOTERM_BP_FAT	cell proliferation	RT	33	2.3	5.9E-6	1.0E-2
GOTERM_BP_FAT	cytoskeleton organization	RT	84	5.8	5.9E-6	1.0E-2
GOTERM_BP_FAT	death	RT	39	2.7	6.1E-6	1.1E-2
SP_PIR_KEYWORDS	oxidoreductase	RT	94	6.5	8.3E-6	1.1E-2
GOTERM_BP_FAT	neurological system process	RT	95	6.5	6.7E-6	1.2E-2
GOTERM_CC_FAT	plasma membrane part	RT	83	5.7	8.8E-6	1.2E-2
GOTERM_MF_FAT	calcium ion binding	RT	54	3.7	1.0E-5	1.6E-2
GOTERM_BP_FAT	synaptic vesicle transport	RT	26	1.8	1.0E-5	1.7E-2
GOTERM_BP_FAT	secretion	RT	32	2.2	1.2E-5	2.0E-2
SP_PIR_KEYWORDS	transit peptide	RT	29	2.0	1.7E-5	2.4E-2
GOTERM_BP_FAT	muscle cell development	RT	17	1.2	1.4E-5	2.4E-2
GOTERM_BP_FAT	striated muscle cell development	RT	17	1.2	1.4E-5	2.4E-2
GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	47	3.2	1.5E-5	2.4E-2
GOTERM_BP_FAT	protein amino acid phosphorylation	RT	53	3.6	1.4E-5	2.4E-2
GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	34	2.3	1.6E-5	2.5E-2
INTERPRO	Serine/threonine protein kinase	RT	31	2.1	1.5E-5	2.6E-2
INTERPRO	EGF-like, type 3	RT	20	1.4	1.6E-5	2.6E-2

SP_PIR_KEYWORDS	mitochondrion	RT	40	2.7	2.2E-5	3.0E-2
SP_PIR_KEYWORDS	kinase	RT	44	3.0	2.3E-5	3.2E-2
GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	28	1.9	2.1E-5	3.3E-2
SP_PIR_KEYWORDS	ubl conjugation pathway	RT	26	1.8	2.4E-5	3.3E-2
INTERPRO	Protein kinase, ATP binding site	RT	43	3.0	2.0E-5	3.3E-2
GOTERM_BP_FAT	oxidation reduction	RT	103	7.1	2.0E-5	3.5E-2
GOTERM_CC_FAT	plasma membrane	RT	138	9.5	2.6E-5	3.7E-2
SMART	PH	RT	25	1.7	2.8E-5	3.8E-2
GOTERM_CC_FAT	myosin II complex	RT	7	0.5	2.8E-5	4.0E-2
GOTERM_BP_FAT	cellular protein complex assembly	RT	24	1.6	2.3E-5	4.1E-2
GOTERM_BP_FAT	membrane organization	RT	61	4.2	2.5E-5	4.4E-2
GOTERM_BP_FAT	skeletal muscle organ development	RT	19	1.3	2.7E-5	4.6E-2
GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	27	1.9	4.1E-5	6.4E-2
GOTERM_BP_FAT	myofibril assembly	RT	9	0.6	3.7E-5	6.5E-2
SP_PIR_KEYWORDS	egf-like domain	RT	17	1.2	4.8E-5	6.6E-2
INTERPRO	EF-Hand type	RT	28	1.9	4.2E-5	7.0E-2
SP_PIR_KEYWORDS	transmembrane protein	RT	21	1.4	5.2E-5	7.1E-2
GOTERM_BP_FAT	cuticle development	RT	20	1.4	4.2E-5	7.4E-2
SP_PIR_KEYWORDS	ATP	RT	20	1.4	5.9E-5	8.1E-2
UP_SEQ_FEATURE	mutagenesis site	RT	48	3.3	5.0E-5	8.2E-2
GOTERM_BP_FAT	post-embryonic organ morphogenesis	RT	55	3.8	4.7E-5	8.3E-2

	GOTERM_BP_FAT	imaginal disc morphogenesis	RT		55	3.8	4.7E-5	8.3E-2
	GOTERM_BP_FAT	regulation of cell shape	RT		26	1.8	4.9E-5	8.5E-2
	GOTERM_BP_FAT	protein kinase cascade	RT		19	1.3	5.7E-5	1.0E-1
	GOTERM_CC_FAT	cytoskeleton	RT		71	4.9	7.2E-5	1.0E-1
	GOTERM_CC_FAT	synapse	RT		33	2.3	7.4E-5	1.0E-1

****

-D

C

+D

Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	GOTERM_CC_FAT	Golgi apparatus part	RT		23	3.6	1.9E-10	2.6E-7
	GOTERM_CC_FAT	endoplasmic reticulum part	RT		26	4.1	7.8E-10	1.0E-6
	GOTERM_CC_FAT	endoplasmic reticulum	RT		43	6.8	1.3E-9	1.7E-6
	GOTERM_CC_FAT	Golgi-associated vesicle	RT		12	1.9	2.3E-9	3.1E-6
	GOTERM_CC_FAT	rough endoplasmic reticulum	RT		10	1.6	6.1E-9	8.0E-6
	GOTERM_CC_FAT	endoplasmic reticulum membrane	RT		20	3.2	1.0E-8	1.3E-5

GOTERM_CC_FAT	Golgi apparatus	RT	30	4.7	1.0E-8	1.4E-5
GOTERM_CC_FAT	organelle membrane	RT	54	8.5	1.1E-8	1.5E-5
GOTERM_CC_FAT	endomembrane system	RT	35	5.5	1.5E-8	1.9E-5
GOTERM_CC_FAT	nuclear envelope-endoplasmic reticulum network	RT	20	3.2	1.6E-8	2.1E-5
GOTERM_BP_FAT	cotranslational protein targeting to membrane	RT	10	1.6	2.4E-8	3.9E-5
GOTERM_CC_FAT	rough endoplasmic reticulum membrane	RT	9	1.4	3.0E-8	3.9E-5
GOTERM_CC_FAT	Golgi membrane	RT	14	2.2	1.3E-7	1.7E-4
GOTERM_BP_FAT	protein targeting to ER	RT	9	1.4	2.7E-7	4.4E-4
GOTERM_BP_FAT	SRP-dependent cotranslational protein targeting to membrane	RT	9	1.4	2.7E-7	4.4E-4
GOTERM_MF_FAT	exopeptidase activity	RT	21	3.3	3.1E-7	4.6E-4
GOTERM_BP_FAT	protein targeting to membrane	RT	11	1.7	2.9E-7	4.7E-4
GOTERM_BP_FAT	retrograde vesicle-mediated transport, Golgi to ER	RT	7	1.1	6.0E-7	1.0E-3
GOTERM_BP_FAT	intracellular protein transport	RT	25	3.9	8.5E-7	1.4E-3
GOTERM_CC_FAT	Golgi-associated vesicle membrane	RT	8	1.3	1.8E-6	2.3E-3
GOTERM_BP_FAT	cellular protein localization	RT	25	3.9	1.4E-6	2.4E-3
GOTERM_CC_FAT	COPI coated vesicle membrane	RT	7	1.1	1.9E-6	2.5E-3
GOTERM_CC_FAT	COPI vesicle coat	RT	7	1.1	1.9E-6	2.5E-3
GOTERM_CC_FAT	vesicle coat	RT	9	1.4	2.0E-6	2.6E-3
GOTERM_BP_FAT	protein transport	RT	32	5.1	2.5E-6	4.1E-3
GOTERM_CC_FAT	COPI-coated vesicle	RT	7	1.1	4.4E-6	5.9E-3
GOTERM_BP_FAT	establishment of protein localization	RT	32	5.1	4.2E-6	6.9E-3

GOTERM_CC_FAT	coated vesicle membrane	RT	9	1.4	1.2E-5	1.6E-2
GOTERM_MF_FAT	aminopeptidase activity	RT	12	1.9	1.1E-5	1.7E-2
GOTERM_BP_FAT	intracellular transport	RT	33	5.2	1.1E-5	1.8E-2
GOTERM_BP_FAT	protein localization	RT	38	6.0	1.4E-5	2.3E-2
GOTERM_CC_FAT	cytoplasmic vesicle part	RT	9	1.4	1.7E-5	2.3E-2
GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	9	1.4	1.7E-5	2.3E-2
GOTERM_BP_FAT	Golgi vesicle transport	RT	11	1.7	1.6E-5	2.6E-2
GOTERM_CC_FAT	translocon complex	RT	6	0.9	2.3E-5	3.1E-2
GOTERM_BP_FAT	hexose metabolic process	RT	15	2.4	2.3E-5	3.8E-2
GOTERM_BP_FAT	monosaccharide metabolic process	RT	16	2.5	2.6E-5	4.2E-2
GOTERM_BP_FAT	protein targeting	RT	17	2.7	2.7E-5	4.4E-2
GOTERM_MF_FAT	vitamin binding	RT	17	2.7	3.7E-5	5.4E-2
GOTERM_BP_FAT	mannose metabolic process	RT	6	0.9	3.8E-5	6.2E-2
GOTERM_BP_FAT	protein localization in organelle	RT	15	2.4	5.0E-5	8.3E-2
GOTERM_CC_FAT	vesicle membrane	RT	9	1.4	6.5E-5	8.5E-2
SP_PIR_KEYWORDS	transport	RT	42	6.6	8.2E-5	1.0E-1

****

-D

+D

C

Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	GOTERM_CC_FAT	ribonucleoprotein complex	RT		176	5.3	2.6E-25	3.8E-22
	SP_PIR_KEYWORDS	ribonucleoprotein	RT		88	2.6	6.5E-24	9.0E-21
	GOTERM_CC_FAT	cytosolic part	RT		82	2.5	2.9E-23	4.2E-20
	GOTERM_CC_FAT	cytosolic ribosome	RT		66	2.0	1.6E-22	2.2E-19
	GOTERM_MF_FAT	structural constituent of ribosome	RT		95	2.9	1.3E-18	2.1E-15
	GOTERM_CC_FAT	ribosome	RT		97	2.9	4.0E-18	5.7E-15
	KEGG_PATHWAY	Ribosome	RT		67	2.0	5.4E-18	6.1E-15
	GOTERM_CC_FAT	ribosomal subunit	RT		89	2.7	4.3E-18	6.1E-15
	GOTERM_BP_FAT	RNA processing	RT		129	3.9	2.0E-17	3.5E-14
	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT		57	1.7	8.7E-17	2.0E-13
	GOTERM_CC_FAT	cytosolic large ribosomal subunit	RT		41	1.2	5.7E-15	8.3E-12
	SP_PIR_KEYWORDS	ribosomal protein	RT		85	2.6	9.6E-15	1.3E-11
	GOTERM_BP_FAT	ribosome biogenesis	RT		42	1.3	4.1E-14	7.2E-11
	GOTERM_CC_FAT	large ribosomal subunit	RT		54	1.6	1.4E-10	2.0E-7
	GOTERM_BP_FAT	protein folding	RT		55	1.7	1.5E-10	2.6E-7
	GOTERM_BP_FAT	intracellular transport	RT		112	3.4	2.9E-10	5.1E-7

GOTERM_BP_FAT	mitotic spindle elongation	RT	42	1.3	3.2E-10	5.7E-7
GOTERM_BP_FAT	spindle elongation	RT	42	1.3	5.4E-10	9.5E-7
GOTERM_BP_FAT	mRNA metabolic process	RT	85	2.6	6.2E-10	1.1E-6
GOTERM_BP_FAT	RNA splicing	RT	64	1.9	7.1E-10	1.3E-6
GOTERM_CC_FAT	membrane-enclosed lumen	RT	191	5.8	1.9E-9	2.8E-6
KEGG_PATHWAY	Spliceosome	RT	65	2.0	2.6E-9	2.9E-6
SP_PIR_KEYWORDS	rna-binding	RT	67	2.0	3.6E-9	4.9E-6
GOTERM_BP_FAT	ncRNA metabolic process	RT	58	1.7	3.4E-9	6.0E-6
GOTERM_BP_FAT	mRNA processing	RT	76	2.3	3.5E-9	6.1E-6
GOTERM_BP_FAT	ncRNA processing	RT	45	1.4	3.6E-9	6.4E-6
GOTERM_BP_FAT	post-mating behavior	RT	17	0.5	4.8E-9	8.4E-6
GOTERM_CC_FAT	intracellular organelle lumen	RT	184	5.5	1.1E-8	1.5E-5
GOTERM_CC_FAT	organelle lumen	RT	184	5.5	1.1E-8	1.5E-5
GOTERM_CC_FAT	nuclear lumen	RT	137	4.1	1.3E-8	1.9E-5
GOTERM_CC_FAT	spliceosome	RT	39	1.2	2.1E-8	3.0E-5
GOTERM_BP_FAT	nucleocytoplasmic transport	RT	37	1.1	2.2E-8	3.9E-5
GOTERM_BP_FAT	nuclear transport	RT	37	1.1	2.2E-8	3.9E-5
GOTERM_BP_FAT	mitotic spindle organization	RT	73	2.2	5.2E-8	9.1E-5
SMART	Sm	RT	15	0.5	7.1E-8	9.5E-5
GOTERM_BP_FAT	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT	53	1.6	7.6E-8	1.3E-4
GOTERM_BP_FAT	nuclear mRNA splicing, via spliceosome	RT	53	1.6	7.6E-8	1.3E-4

GOTERM_BP_FAT	RNA splicing, via transesterification reactions	RT	53	1.6	1.0E-7	1.8E-4
GOTERM_CC_FAT	cytosolic small ribosomal subunit	RT	25	0.8	1.4E-7	1.9E-4
GOTERM_CC_FAT	small ribosomal subunit	RT	36	1.1	1.7E-7	2.5E-4
SP_PIR_KEYWORDS	protein biosynthesis	RT	47	1.4	2.4E-7	3.3E-4
GOTERM_BP_FAT	spindle organization	RT	79	2.4	4.0E-7	7.0E-4
GOTERM_CC_FAT	non-membrane-bounded organelle	RT	277	8.3	5.1E-7	7.3E-4
GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	277	8.3	5.1E-7	7.3E-4
SP_PIR_KEYWORDS	ribosome	RT	19	0.6	9.2E-7	1.3E-3
SP_PIR_KEYWORDS	mrna splicing	RT	23	0.7	1.0E-6	1.4E-3
COG_ONTOLOGY	Translation, ribosomal structure and biogenesis	RT	34	1.0	2.2E-6	2.0E-3
INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT	15	0.5	1.2E-6	2.2E-3
INTERPRO	Like-Sm ribonucleoprotein, core	RT	15	0.5	1.2E-6	2.2E-3
GOTERM_MF_FAT	mRNA binding	RT	72	2.2	1.5E-6	2.4E-3
SP_PIR_KEYWORDS	mrna processing	RT	28	0.8	1.8E-6	2.5E-3
GOTERM_BP_FAT	rRNA processing	RT	23	0.7	1.6E-6	2.7E-3
GOTERM_BP_FAT	microtubule-based process	RT	123	3.7	2.0E-6	3.5E-3
GOTERM_BP_FAT	rRNA metabolic process	RT	23	0.7	2.7E-6	4.8E-3
GOTERM_CC_FAT	small nuclear ribonucleoprotein complex	RT	39	1.2	3.7E-6	5.3E-3
GOTERM_BP_FAT	RNA export from nucleus	RT	16	0.5	4.2E-6	7.3E-3
GOTERM_BP_FAT	nuclear export	RT	19	0.6	5.0E-6	8.8E-3
GOTERM_CC_FAT	nucleoplasm part	RT	86	2.6	6.1E-6	8.8E-3

	GOTERM_BP_FAT	microtubule cytoskeleton organization	RT		94	2.8	6.2E-6	1.1E-2
	GOTERM_BP_FAT	translation	RT		148	4.5	8.0E-6	1.4E-2
	GOTERM_CC_FAT	nucleoplasm	RT		92	2.8	1.2E-5	1.7E-2
	GOTERM_BP_FAT	ribonucleoprotein complex assembly	RT		20	0.6	1.0E-5	1.8E-2
	GOTERM_BP_FAT	oxidation reduction	RT		171	5.1	1.1E-5	1.9E-2
	GOTERM_BP_FAT	tRNA metabolic process	RT		38	1.1	2.0E-5	3.6E-2
	SMART	RRM	RT		50	1.5	3.8E-5	5.1E-2
	GOTERM_MF_FAT	unfolded protein binding	RT		34	1.0	3.9E-5	6.2E-2
	GOTERM_BP_FAT	mRNA export from nucleus	RT		14	0.4	4.2E-5	7.4E-2
	GOTERM_BP_FAT	sulfur amino acid metabolic process	RT		11	0.3	5.7E-5	1.0E-1

****

C

-D

+D

Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	GOTERM_CC_FAT	mitochondrial matrix	RT		38	4.3	5.9E-9	8.0E-6

GOTERM_CC_FAT	mitochondrial lumen	RT	38	4.3	5.9E-9	8.0E-6
GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT	32	3.6	1.2E-8	1.8E-5
GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT	32	3.6	1.2E-8	1.8E-5
GOTERM_CC_FAT	mitochondrion	RT	88	10.0	1.4E-8	1.9E-5
GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT	32	3.6	1.7E-8	2.5E-5
GOTERM_CC_FAT	mitochondrial part	RT	69	7.8	2.9E-8	3.9E-5
GOTERM_MF_FAT	primary active transmembrane transporter activity	RT	34	3.9	3.3E-8	5.0E-5
GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT	34	3.9	3.3E-8	5.0E-5
GOTERM_MF_FAT	ATPase activity	RT	54	6.1	4.8E-7	7.3E-4
GOTERM_MF_FAT	actin binding	RT	27	3.1	7.2E-7	1.1E-3
GOTERM_CC_FAT	vacuolar membrane	RT	14	1.6	1.3E-6	1.8E-3
GOTERM_CC_FAT	vacuolar part	RT	14	1.6	1.3E-6	1.8E-3
GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT	20	2.3	1.2E-6	2.0E-3
GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT	20	2.3	1.2E-6	2.0E-3
GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT	20	2.3	1.5E-6	2.3E-3
GOTERM_CC_FAT	vacuolar proton-transporting V-type ATPase complex	RT	13	1.5	1.8E-6	2.4E-3
GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT	20	2.3	1.5E-6	2.5E-3
GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT	20	2.3	1.5E-6	2.5E-3
GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT	23	2.6	1.5E-6	2.6E-3
GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	14	1.6	1.9E-6	2.6E-3
GOTERM_CC_FAT	mitochondrial ribosome	RT	21	2.4	2.2E-6	3.0E-3

GOTERM_CC_FAT	organellar ribosome	RT	21	2.4	2.2E-6	3.0E-3
GOTERM_BP_FAT	ATP biosynthetic process	RT	19	2.2	2.4E-6	4.1E-3
GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	22	2.5	2.6E-6	4.4E-3
GOTERM_MF_FAT	ATPase activity, coupled	RT	47	5.3	3.0E-6	4.6E-3
GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	20	2.3	3.1E-6	5.2E-3
GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	20	2.3	3.1E-6	5.2E-3
GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	20	2.3	3.5E-6	5.3E-3
GOTERM_BP_FAT	ribonucleotide metabolic process	RT	23	2.6	3.4E-6	5.8E-3
GOTERM_BP_FAT	ATP metabolic process	RT	19	2.2	3.6E-6	6.1E-3
GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	20	2.3	3.7E-6	6.3E-3
GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	20	2.3	4.4E-6	7.5E-3
GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	22	2.5	5.8E-6	9.8E-3
SP_PIR_KEYWORDS	transmembrane	RT	104	11.8	1.0E-5	1.3E-2
GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	25	2.8	2.0E-5	3.0E-2
SP_PIR_KEYWORDS	actin-binding	RT	13	1.5	2.8E-5	3.7E-2
GOTERM_CC_FAT	organelle membrane	RT	63	7.1	2.9E-5	4.0E-2
SP_PIR_KEYWORDS	nucleotide-binding	RT	78	8.8	3.4E-5	4.5E-2
GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	32	3.6	3.9E-5	6.6E-2
GOTERM_BP_FAT	transmembrane transport	RT	21	2.4	4.1E-5	6.9E-2
INTERPRO	Major facilitator superfamily MFS-1	RT	22	2.5	4.4E-5	7.1E-2
SMART	AAA	RT	21	2.4	6.8E-5	8.5E-2

GOTERM_BP_FAT proton transport RT 15 1.7 5.0E-5 8.5E-2

SP_PIR_KEYWORDS mitochondrion RT 28 3.2 7.1E-5 9.3E-2

GOTERM_MF_FAT solute:cation symporter activity RT 18 2.0 6.3E-5 9.5E-2

GOTERM_MF_FAT hydrogen-exporting ATPase activity, phosphorylative mechanism RT 14 1.6 6.4E-5 9.6E-2

GOTERM_BP_FAT energy coupled proton transport, down electrochemical gradient RT 14 1.6 5.7E-5 9.7E-2

GOTERM_BP_FAT ATP synthesis coupled proton transport RT 14 1.6 5.7E-5 9.7E-2

GOTERM_BP_FAT hydrogen transport RT 15 1.7 6.1E-5 1.0E-1

****

+D

C

-D

Functional annotation chart:

Sublist Category Term RT Genes Count % P-Value FDR

SP_PIR_KEYWORDS alternative splicing RT 51 10.7 2.9E-8 3.7E-5

GOTERM_BP_FAT phototransduction RT 13 2.7 5.3E-8 8.9E-5

GOTERM_BP_FAT phosphate metabolic process RT 47 9.8 1.3E-7 2.2E-4

GOTERM_BP_FAT phosphorus metabolic process RT 47 9.8 1.3E-7 2.2E-4

GOTERM_BP_FAT	detection of light stimulus	RT	13	2.7	2.4E-7	4.0E-4
GOTERM_BP_FAT	detection of external stimulus	RT	14	2.9	2.6E-7	4.4E-4
GOTERM_BP_FAT	detection of abiotic stimulus	RT	13	2.7	7.2E-7	1.2E-3
SP_PIR_KEYWORDS	phosphoprotein	RT	57	11.9	1.1E-6	1.4E-3
UP_SEQ_FEATURE	splice variant	RT	51	10.7	1.4E-6	2.0E-3
GOTERM_CC_FAT	cell projection	RT	16	3.3	9.0E-6	1.2E-2
GOTERM_BP_FAT	response to radiation	RT	16	3.3	1.7E-5	2.8E-2
GOTERM_BP_FAT	phosphorylation	RT	35	7.3	1.7E-5	2.8E-2
GOTERM_BP_FAT	response to light stimulus	RT	15	3.1	1.7E-5	2.9E-2
SP_PIR_KEYWORDS	rna editing	RT	9	1.9	2.3E-5	2.9E-2
GOTERM_CC_FAT	axon	RT	8	1.7	2.7E-5	3.6E-2
GOTERM_BP_FAT	regulation of cell development	RT	17	3.6	2.6E-5	4.3E-2
GOTERM_BP_FAT	vesicle-mediated transport	RT	32	6.7	4.9E-5	8.2E-2
SP_PIR_KEYWORDS	zinc	RT	40	8.4	7.5E-5	9.6E-2
SP_PIR_KEYWORDS	metal-binding	RT	50	10.5	9.6E-5	1.2E-1
GOTERM_BP_FAT	detection of stimulus	RT	14	2.9	7.7E-5	1.3E-1
GOTERM_BP_FAT	protein amino acid phosphorylation	RT	24	5.0	8.9E-5	1.5E-1
SP_PIR_KEYWORDS	vision	RT	10	2.1	1.2E-4	1.5E-1
GOTERM_BP_FAT	neurological system process	RT	39	8.2	1.2E-4	1.9E-1
GOTERM_CC_FAT	rhabdomere	RT	7	1.5	2.1E-4	2.8E-1
GOTERM_BP_FAT	oogenesis	RT	38	7.9	1.9E-4	3.2E-1

GOTERM_CC_FAT	extrinsic to plasma membrane	RT	8	1.7	2.5E-4	3.3E-1
GOTERM_BP_FAT	visual perception	RT	11	2.3	2.4E-4	3.9E-1
GOTERM_BP_FAT	female gamete generation	RT	38	7.9	2.5E-4	4.1E-1
INTERPRO	Protein kinase, core	RT	21	4.4	2.8E-4	4.2E-1
GOTERM_MF_FAT	protein kinase activity	RT	25	5.2	3.0E-4	4.3E-1
GOTERM_BP_FAT	sensory perception of light stimulus	RT	11	2.3	2.7E-4	4.4E-1
GOTERM_BP_FAT	rhodopsin mediated signaling pathway	RT	6	1.3	2.9E-4	4.9E-1
GOTERM_BP_FAT	regulation of cellular protein metabolic process	RT	15	3.1	3.2E-4	5.3E-1
GOTERM_BP_FAT	response to abiotic stimulus	RT	20	4.2	3.7E-4	6.1E-1
SP_PIR_KEYWORDS	kinase	RT	19	4.0	5.2E-4	6.7E-1
GOTERM_BP_FAT	instar larval or pupal morphogenesis	RT	27	5.6	4.9E-4	8.1E-1
GOTERM_BP_FAT	membrane invagination	RT	22	4.6	5.9E-4	9.8E-1
GOTERM_BP_FAT	endocytosis	RT	22	4.6	5.9E-4	9.8E-1
SP_PIR_KEYWORDS	zinc-finger	RT	24	5.0	7.7E-4	9.9E-1
GOTERM_BP_FAT	post-embryonic morphogenesis	RT	27	5.6	6.3E-4	1.1E0

****

+D

-D

C

Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	GOTERM_BP_FAT	macromolecule catabolic process	RT		73	3.6	4.7E-8	8.3E-5
	GOTERM_BP_FAT	sensory perception of light stimulus	RT		29	1.4	8.7E-8	1.5E-4
	GOTERM_CC_FAT	cell fraction	RT		39	1.9	1.3E-7	1.9E-4
	GOTERM_CC_FAT	rhabdomere	RT		16	0.8	1.5E-7	2.2E-4
	GOTERM_CC_FAT	insoluble fraction	RT		38	1.9	1.9E-7	2.7E-4
	GOTERM_BP_FAT	detection of external stimulus	RT		26	1.3	1.8E-7	3.1E-4
	GOTERM_CC_FAT	chromosome	RT		77	3.8	2.5E-7	3.5E-4
	GOTERM_BP_FAT	visual perception	RT		28	1.4	2.5E-7	4.4E-4
	GOTERM_BP_FAT	detection of light stimulus	RT		23	1.1	3.3E-7	5.8E-4
	GOTERM_BP_FAT	detection of abiotic stimulus	RT		24	1.2	5.3E-7	9.2E-4
	GOTERM_CC_FAT	membrane fraction	RT		36	1.8	6.9E-7	9.8E-4
	SP_PIR_KEYWORDS	phosphoprotein	RT		173	8.5	1.2E-6	1.6E-3
	SP_PIR_KEYWORDS	metal-binding	RT		169	8.3	1.6E-6	2.1E-3
	GOTERM_CC_FAT	extrinsic to membrane	RT		45	2.2	2.5E-6	3.5E-3
	GOTERM_BP_FAT	regulation of cell cycle	RT		47	2.3	2.0E-6	3.5E-3
	GOTERM_BP_FAT	transcription from RNA polymerase II promoter	RT		33	1.6	2.1E-6	3.7E-3
	GOTERM_BP_FAT	chromosome organization	RT		69	3.4	2.2E-6	3.9E-3

GOTERM_BP_FAT	phototransduction	RT	20	1.0	3.1E-6	5.5E-3
GOTERM_CC_FAT	nucleoplasm	RT	66	3.3	4.0E-6	5.7E-3
GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	47	2.3	3.4E-6	6.0E-3
GOTERM_BP_FAT	protein localization	RT	88	4.3	3.5E-6	6.2E-3
GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	47	2.3	4.1E-6	7.1E-3
GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	57	2.8	6.4E-6	1.1E-2
GOTERM_BP_FAT	detection of light stimulus involved in sensory perception	RT	13	0.6	8.5E-6	1.5E-2
GOTERM_MF_FAT	general RNA polymerase II transcription factor activity	RT	31	1.5	9.5E-6	1.5E-2
GOTERM_BP_FAT	intracellular signaling cascade	RT	69	3.4	1.5E-5	2.6E-2
GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	48	2.4	1.5E-5	2.6E-2
GOTERM_BP_FAT	cellular protein catabolic process	RT	48	2.4	1.5E-5	2.6E-2
INTERPRO	Snf7	RT	8	0.4	1.6E-5	2.8E-2
GOTERM_BP_FAT	macromolecular complex subunit organization	RT	66	3.3	1.6E-5	2.8E-2
GOTERM_BP_FAT	protein catabolic process	RT	51	2.5	1.8E-5	3.1E-2
GOTERM_CC_FAT	nucleoplasm part	RT	59	2.9	2.2E-5	3.1E-2
SP_PIR_KEYWORDS	vision	RT	22	1.1	2.3E-5	3.2E-2
GOTERM_CC_FAT	microsome	RT	29	1.4	2.5E-5	3.6E-2
GOTERM_CC_FAT	vesicular fraction	RT	29	1.4	2.5E-5	3.6E-2
SP_PIR_KEYWORDS	nucleus	RT	175	8.6	2.7E-5	3.7E-2
INTERPRO	Cytochrome P450, C-terminal region	RT	30	1.5	2.3E-5	3.8E-2
GOTERM_BP_FAT	establishment of protein localization	RT	66	3.3	2.6E-5	4.5E-2

INTERPRO	Cytochrome P450	RT	30	1.5	2.9E-5	4.9E-2
GOTERM_CC_FAT	spindle	RT	24	1.2	3.7E-5	5.3E-2
SP_PIR_KEYWORDS	zinc-finger	RT	75	3.7	4.0E-5	5.4E-2
COG_ONTOLOGY	Secondary metabolites biosynthesis, transport, and catabolism	RT	32	1.6	6.2E-5	5.6E-2
GOTERM_BP_FAT	phosphate metabolic process	RT	111	5.5	3.2E-5	5.7E-2
GOTERM_BP_FAT	phosphorus metabolic process	RT	111	5.5	3.2E-5	5.7E-2
SP_PIR_KEYWORDS	microsome	RT	27	1.3	4.3E-5	5.9E-2
GOTERM_BP_FAT	detection of light stimulus involved in visual perception	RT	12	0.6	3.4E-5	5.9E-2
GOTERM_BP_FAT	transcription initiation from RNA polymerase II promoter	RT	23	1.1	3.7E-5	6.5E-2
GOTERM_MF_FAT	transition metal ion binding	RT	255	12.6	4.3E-5	6.8E-2
GOTERM_BP_FAT	protein transport	RT	64	3.2	4.2E-5	7.4E-2
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT	34	1.7	4.8E-5	7.8E-2
SP_PIR_KEYWORDS	chromosomal protein	RT	18	0.9	5.8E-5	7.9E-2
GOTERM_BP_FAT	detection of visible light	RT	13	0.6	4.5E-5	8.0E-2
SP_PIR_KEYWORDS	heme	RT	34	1.7	6.1E-5	8.3E-2
GOTERM_BP_FAT	macromolecular complex assembly	RT	58	2.9	5.0E-5	8.8E-2
SP_PIR_KEYWORDS	Monooxygenase	RT	31	1.5	7.1E-5	9.7E-2

File S4

Lists of functional terms common and exclusive to each of the expression patterns shown in Figure 9

****

Common and exclusive to all down regulated protective

```
 [1,] "GOTERM_BP_FAT "   "energy derivation by oxidation of organic compounds "
 [2,] "GOTERM_BP_FAT "   "cellular respiration "
 [3,] "GOTERM_CC_FAT "   "respiratory chain "
 [4,] "GOTERM_BP_FAT "   "electron transport chain "
 [5,] "GOTERM_CC_FAT "   "mitochondrial respiratory chain "
 [6,] "GOTERM_BP_FAT "   "respiratory electron transport chain "
 [7,] "GOTERM_BP_FAT "   "ATP synthesis coupled electron transport "
 [8,] "GOTERM_BP_FAT "   "mitochondrial ATP synthesis coupled electron transport "
 [9,] "GOTERM_CC_FAT "   "mitochondrial membrane part "
[10,] "GOTERM_BP_FAT "   "mitochondrial electron transport, NADH to ubiquinone "
[11,] "GOTERM_CC_FAT "   "NADH dehydrogenase complex "
[12,] "GOTERM_CC_FAT "   "respiratory chain complex I "
[13,] "GOTERM_CC_FAT "   "mitochondrial respiratory chain complex I "
[14,] "GOTERM_MF_FAT "   "NADH dehydrogenase activity "
[15,] "GOTERM_MF_FAT "   "oxidoreductase activity, acting on NADH or NADPH "
```

```
[16,] "GOTERM_MF_FAT "   "NADH dehydrogenase (quinone) activity "
[17,] "GOTERM_MF_FAT "   "NADH dehydrogenase (ubiquinone) activity "
[18,] "GOTERM_MF_FAT "   "oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor "
[19,] "GOTERM_BP_FAT "   "cofactor catabolic process "
[20,] "GOTERM_BP_FAT "   "acetyl-CoA metabolic process "
[21,] "GOTERM_BP_FAT "   "tricarboxylic acid cycle "
[22,] "GOTERM_BP_FAT "   "acetyl-CoA catabolic process "
[23,] "GOTERM_BP_FAT "   "coenzyme catabolic process "
[24,] "GOTERM_BP_FAT "   "aerobic respiration "
[25,] "GOTERM_CC_FAT "   "proton-transporting ATP synthase complex "
[26,] "GOTERM_CC_FAT "   "mitochondrial proton-transporting ATP synthase complex "
[27,] "GOTERM_CC_FAT "   "proton-transporting ATP synthase complex, coupling factor F(o) "
[28,] "GOTERM_CC_FAT "   "mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) "
[29,] "GOTERM_BP_FAT "   "glucose metabolic process "
[30,] "GOTERM_BP_FAT "   "hexose metabolic process "
[31,] "GOTERM_BP_FAT "   "glycolysis "
[32,] "GOTERM_BP_FAT "   "cellular carbohydrate catabolic process "
[33,] "GOTERM_BP_FAT "   "monosaccharide metabolic process "
[34,] "GOTERM_BP_FAT "   "carbohydrate catabolic process "
[35,] "GOTERM_BP_FAT "   "hexose catabolic process "
[36,] "GOTERM_BP_FAT "   "glucose catabolic process "
```

```
[37,] "GOTERM_BP_FAT "   "alcohol catabolic process "
[38,] "GOTERM_BP_FAT "   "monosaccharide catabolic process "
[39,] "GOTERM_BP_FAT "   "regulation of cellular component size "
[40,] "GOTERM_BP_FAT "   "cell growth "
[41,] "GOTERM_BP_FAT "   "regulation of cell size "
[42,] "GOTERM_BP_FAT "   "growth "
[43,] "GOTERM_BP_FAT "   "developmental growth "
[44,] "GOTERM_BP_FAT "   "developmental cell growth "
[45,] "GOTERM_BP_FAT "   "protein amino acid phosphorylation "
[46,] "INTERPRO "        "Protein kinase, ATP binding site "
[47,] "GOTERM_MF_FAT "   "protein serine/threonine kinase activity "
[48,] "SMART "           "S_TKc "
[49,] "INTERPRO "        "Serine/threonine protein kinase "
[50,] "SP_PIR_KEYWORDS " "kinase "
[51,] "SP_PIR_KEYWORDS " "serine/threonine-protein kinase "
[52,] "INTERPRO "        "Serine/threonine protein kinase-related "
[53,] "GOTERM_MF_FAT "   "protein kinase activity "
[54,] "INTERPRO "        "Protein kinase, core "
[55,] "INTERPRO "        "Serine/threonine protein kinase, active site "
[56,] "SP_PIR_KEYWORDS " "atp synthesis "
[57,] "GOTERM_CC_FAT "   "mitochondrial proton-transporting ATP synthase complex, catalytic core F(1) "
```

```
[58,] "GOTERM_CC_FAT "   "proton-transporting ATP synthase complex, catalytic core F(1) "

[59,] "SMART "          "EGF "

[60,] "INTERPRO "       "EGF-like "

[61,] "INTERPRO "       "EGF-like, type 3 "

[62,] "SP_PIR_KEYWORDS " "egf-like domain "

[63,] "GOTERM_BP_FAT "   "olfactory learning "

[64,] "GOTERM_BP_FAT "   "learning or memory "

[65,] "GOTERM_BP_FAT "   "chemosensory behavior "

[66,] "GOTERM_BP_FAT "   "learning "

[67,] "GOTERM_BP_FAT "   "olfactory behavior "

[68,] "GOTERM_BP_FAT "   "circadian rhythm "

[69,] "GOTERM_BP_FAT "   "rhythmic process "

[70,] "GOTERM_BP_FAT "   "circadian behavior "

[71,] "GOTERM_BP_FAT "   "rhythmic behavior "

[72,] "GOTERM_BP_FAT "   "locomotor rhythm "

[73,] "GOTERM_BP_FAT "   "epithelial tube morphogenesis "

[74,] "INTERPRO "       "Pleckstrin homology-type "

[75,] "GOTERM_BP_FAT "   "chitin-based embryonic cuticle biosynthetic process "

[76,] "GOTERM_BP_FAT "   "cuticle development "

[77,] "GOTERM_BP_FAT "   "chitin-based cuticle development "

[78,] "GOTERM_BP_FAT "   "organic acid catabolic process "
```

```
[79,] "GOTERM_BP_FAT "   "carboxylic acid catabolic process "


**********************************************************************************************************************************************
```

Common and exclusive to all up regulated protective

```
 [1,] "GOTERM_MF_FAT "   "RNA polymerase activity "
 [2,] "GOTERM_MF_FAT "   "DNA-directed RNA polymerase activity "
 [3,] "GOTERM_CC_FAT "   "RNA polymerase complex "
 [4,] "GOTERM_CC_FAT "   "DNA-directed RNA polymerase complex "
 [5,] "GOTERM_CC_FAT "   "nuclear DNA-directed RNA polymerase complex "
 [6,] "GOTERM_MF_FAT "   "nucleotidyltransferase activity "
 [7,] "KEGG_PATHWAY "    "RNA polymerase "
 [8,] "GOTERM_CC_FAT "   "DNA-directed RNA polymerase II, core complex "
 [9,] "SP_PIR_KEYWORDS " "nucleotidyltransferase "
[10,] "KEGG_PATHWAY "    "Pyrimidine metabolism "
[11,] "KEGG_PATHWAY "    "Purine metabolism "
[12,] "SMART "           "Sm "
[13,] "INTERPRO "        "Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core "
[14,] "INTERPRO "        "Like-Sm ribonucleoprotein, core "


**********************************************************************************************************************************************
```

Common and exclusive to all down regulated non-protective

None

****

Common and exclusive to all up regulated non-protective

None

****

Common and exclusive to all protective

None

****

Common and exclusive to all non-protective

None

****

Common and exclusive to all down regulated

```
 [1,] "GOTERM_MF_FAT "   "ATPase activity "
 [2,] "GOTERM_CC_FAT "   "mitochondrial part "
 [3,] "GOTERM_CC_FAT "   "mitochondrion "
 [4,] "GOTERM_MF_FAT "   "ATPase activity, coupled to transmembrane movement of substances "
 [5,] "GOTERM_MF_FAT "   "ATPase activity, coupled to movement of substances "
 [6,] "GOTERM_MF_FAT "   "hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances "
 [7,] "GOTERM_MF_FAT "   "P-P-bond-hydrolysis-driven transmembrane transporter activity "
 [8,] "GOTERM_MF_FAT "   "primary active transmembrane transporter activity "
 [9,] "GOTERM_BP_FAT "   "ribonucleotide biosynthetic process "
[10,] "GOTERM_BP_FAT "   "purine nucleoside triphosphate biosynthetic process "
[11,] "GOTERM_BP_FAT "   "purine ribonucleoside triphosphate biosynthetic process "
[12,] "GOTERM_BP_FAT "   "ribonucleotide metabolic process "
[13,] "GOTERM_BP_FAT "   "purine ribonucleotide biosynthetic process "
[14,] "GOTERM_BP_FAT "   "nucleoside triphosphate biosynthetic process "
[15,] "GOTERM_BP_FAT "   "ribonucleoside triphosphate biosynthetic process "
[16,] "GOTERM_MF_FAT "   "ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism "
[17,] "GOTERM_BP_FAT "   "cation transport "
[18,] "GOTERM_BP_FAT "   "purine ribonucleotide metabolic process "
[19,] "GOTERM_BP_FAT "   "purine nucleoside triphosphate metabolic process "
[20,] "GOTERM_BP_FAT "   "purine ribonucleoside triphosphate metabolic process "
```

```
[21,] "GOTERM_BP_FAT "   "ATP biosynthetic process "
[22,] "SP_PIR_KEYWORDS " "Hydrogen ion transport "
[23,] "GOTERM_BP_FAT "   "ribonucleoside triphosphate metabolic process "
[24,] "GOTERM_BP_FAT "   "nucleoside triphosphate metabolic process "
[25,] "GOTERM_MF_FAT "   "ATPase activity, coupled to transmembrane movement of ions "
[26,] "GOTERM_BP_FAT "   "ATP metabolic process "
[27,] "GOTERM_BP_FAT "   "ion transport "
[28,] "GOTERM_BP_FAT "   "purine nucleotide biosynthetic process "
[29,] "GOTERM_MF_FAT "   "ATPase activity, coupled "
[30,] "GOTERM_BP_FAT "   "purine nucleotide metabolic process "
[31,] "GOTERM_MF_FAT "   "hydrogen-exporting ATPase activity, phosphorylative mechanism "
[32,] "GOTERM_BP_FAT "   "nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process "
[33,] "GOTERM_BP_FAT "   "nucleobase, nucleoside and nucleotide biosynthetic process "
[34,] "GOTERM_BP_FAT "   "monovalent inorganic cation transport "
[35,] "GOTERM_BP_FAT "   "nucleotide biosynthetic process "
[36,] "GOTERM_BP_FAT "   "proton transport "
[37,] "GOTERM_BP_FAT "   "hydrogen transport "
[38,] "GOTERM_BP_FAT "   "ATP synthesis coupled proton transport "
[39,] "GOTERM_BP_FAT "   "energy coupled proton transport, down electrochemical gradient "
[40,] "GOTERM_BP_FAT "   "ion transmembrane transport "
[41,] "GOTERM_MF_FAT "   "inorganic cation transmembrane transporter activity "
```

[42,] "GOTERM_CC_FAT " "proton-transporting two-sector ATPase complex "

[43,] "GOTERM_CC_FAT " "proton-transporting two-sector ATPase complex, catalytic domain "

[44,] "GOTERM_MF_FAT " "monovalent inorganic cation transmembrane transporter activity "

[45,] "GOTERM_MF_FAT " "hydrogen ion transmembrane transporter activity "

[46,] "GOTERM_BP_FAT " "transmembrane transport "

[47,] "KEGG_PATHWAY " "Oxidative phosphorylation "

[48,] "GOTERM_BP_FAT " "oxidative phosphorylation "

[49,] "GOTERM_CC_FAT " "proton-transporting two-sector ATPase complex, proton-transporting domain "

****

Common and exclusive to all up regulated

[1,] "GOTERM_CC_FAT " "nucleoplasm part "

[2,] "GOTERM_BP_FAT " "transcription from RNA polymerase II promoter "

[3,] "GOTERM_BP_FAT " "transcription, DNA-dependent "

[4,] "GOTERM_BP_FAT " "RNA biosynthetic process "

[5,] "GOTERM_CC_FAT " "nucleoplasm "

[6,] "GOTERM_CC_FAT " "DNA-directed RNA polymerase II, holoenzyme "

[7,] "GOTERM_BP_FAT " "transcription "

[8,] "GOTERM_CC_FAT " "nuclear lumen "