



Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

417 DAVID IDs

Options

Rerun Using Options

Create Sublist























































850 chart records





























[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of macromolecule metabolic process	RT		95	22.8	2.8E-29	7.8E-26
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of programmed cell death	RT		84	20.1	1.1E-23	1.6E-20
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell death	RT		84	20.1	1.4E-23	1.3E-20
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of apoptosis	RT		83	19.9	2.5E-23	1.8E-20
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of biosynthetic process	RT		75	18.0	3.9E-22	2.2E-19
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cellular biosynthetic process	RT		74	17.7	7.4E-22	3.4E-19
<input type="checkbox"/>	GOTERM_BP_FAT	protein amino acid phosphorylation	RT		72	17.3	3.1E-21	1.3E-18
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of macromolecule biosynthetic process	RT		71	17.0	4.6E-21	1.6E-18
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter	RT		75	18.0	5.7E-21	1.8E-18
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular protein metabolic process	RT		59	14.1	2.6E-20	7.4E-18
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of nitrogen compound metabolic process	RT		69	16.5	3.8E-20	9.6E-18
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of macromolecule metabolic process	RT		72	17.3	6.8E-19	1.6E-16
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transcription from RNA polymerase II promoter	RT		49	11.8	6.5E-18	1.4E-15
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	RT		64	15.3	1.0E-17	2.0E-15
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex assembly	RT		66	15.8	1.5E-17	2.8E-15
<input type="checkbox"/>	GOTERM_BP_FAT	phosphorylation	RT		73	17.5	1.9E-17	3.4E-15
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex subunit organization	RT		67	16.1	1.0E-16	1.8E-14
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of RNA metabolic process	RT		54	12.9	1.3E-16	1.7E-14
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of gene-specific transcription	RT		29	7.0	2.9E-16	4.9E-14
<input type="checkbox"/>	GOTERM_BP_FAT	cell cycle	RT		70	16.8	3.0E-16	4.7E-14
<input type="checkbox"/>	GOTERM_BP_FAT	response to organic substance	RT		67	16.1	3.3E-16	4.4E-14
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of gene expression	RT		59	14.1	4.9E-16	5.6E-14
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transcription, DNA-dependent	RT		53	12.7	5.1E-16	6.7E-14
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex biogenesis	RT		54	12.9	1.3E-15	1.6E-13
<input type="checkbox"/>	GOTERM_BP_FAT	protein complex assembly	RT		54	12.9	1.3E-15	1.6E-13
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transcription	RT		57	13.7	2.2E-15	2.5E-13
<input type="checkbox"/>	GOTERM_BP_FAT	enzyme linked receptor protein signaling pathway	RT		43	10.3	6.7E-15	7.2E-13
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to stress	RT		56	13.4	1.0E-14	1.0E-12
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of apoptosis	RT		48	11.5	1.3E-14	1.3E-12
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of programmed cell death	RT		48	11.5	1.7E-14	1.7E-12
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell death	RT		48	11.5	2.1E-14	1.9E-12
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell proliferation	RT		67	16.1	2.2E-14	2.0E-12
<input type="checkbox"/>	GOTERM_BP_FAT	phosphorus metabolic process	RT		76	18.2	2.4E-14	2.1E-12
<input type="checkbox"/>	GOTERM_BP_FAT	phosphate metabolic process	RT		76	18.2	2.4E-14	2.1E-12
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular signaling cascade	RT		89	21.3	2.5E-14	2.1E-12
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of specific transcription from RNA polymerase II promoter	RT		23	5.5	4.3E-14	3.6E-12
<input type="checkbox"/>	GOTERM_BP_FAT	cell cycle process	RT		54	12.9	1.4E-13	1.1E-11
<input type="checkbox"/>	GOTERM_BP_FAT	death	RT		62	14.9	2.0E-13	1.5E-11
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein metabolic process	RT		34	8.2	3.6E-13	2.7E-11
<input type="checkbox"/>	GOTERM_BP_FAT	chromatin modification	RT		36	8.6	4.2E-13	3.1E-11
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription	RT		140	33.6	4.7E-13	3.4E-11

<input type="checkbox"/>	GOTERM_BP_FAT	cell death		61	14.6	4.9E-13	3.4E-11
<input type="checkbox"/>	GOTERM_BP_FAT	RNA splicing, via transesterification reactions		27	6.5	6.5E-13	4.4E-11
<input type="checkbox"/>	GOTERM_BP_FAT	nuclear mRNA splicing, via spliceosome		27	6.5	6.5E-13	4.4E-11
<input type="checkbox"/>	GOTERM_BP_FAT	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile		27	6.5	6.5E-13	4.4E-11
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cellular biosynthetic process		52	12.5	1.4E-12	9.1E-11
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process		51	12.2	1.9E-12	1.2E-10
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of molecular function		53	12.7	2.1E-12	1.3E-10
<input type="checkbox"/>	GOTERM_BP_FAT	programmed cell death		54	12.9	3.0E-12	1.9E-10
<input type="checkbox"/>	GOTERM_BP_FAT	covalent chromatin modification		24	5.8	3.1E-12	1.9E-10
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of biosynthetic process		52	12.5	3.1E-12	1.8E-10
<input type="checkbox"/>	GOTERM_BP_FAT	chromosome organization		47	11.3	4.4E-12	2.6E-10
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecule catabolic process		62	14.9	5.4E-12	3.1E-10
<input type="checkbox"/>	GOTERM_BP_FAT	apoptosis		53	12.7	5.8E-12	3.2E-10
<input type="checkbox"/>	GOTERM_BP_FAT	protein kinase cascade		40	9.6	8.6E-12	4.7E-10
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell differentiation		31	7.4	1.1E-11	6.0E-10
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein modification process		35	8.4	1.7E-11	9.0E-10
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecule catabolic process		58	13.9	2.3E-11	1.2E-9
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process		47	11.3	2.9E-11	1.5E-9
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of binding		25	6.0	3.0E-11	1.5E-9
<input type="checkbox"/>	GOTERM_BP_FAT	nucleocytoplasmic transport		25	6.0	4.6E-11	2.2E-9
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of nitrogen compound metabolic process		47	11.3	4.6E-11	2.2E-9
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of RNA metabolic process		104	24.9	5.4E-11	2.6E-9
<input type="checkbox"/>	GOTERM_BP_FAT	nuclear transport		25	6.0	6.0E-11	2.8E-9
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell differentiation		29	7.0	7.1E-11	3.3E-9
<input type="checkbox"/>	GOTERM_BP_FAT	histone modification		22	5.3	8.8E-11	3.9E-9
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cellular protein metabolic process		30	7.2	8.8E-11	3.9E-9
<input type="checkbox"/>	GOTERM_BP_FAT	transcription from RNA polymerase II promoter		30	7.2	9.7E-11	4.2E-9
<input type="checkbox"/>	GOTERM_BP_FAT	mitotic cell cycle		38	9.1	1.4E-10	6.0E-9
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of catalytic activity		46	11.0	1.7E-10	7.1E-9
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription, DNA-dependent		101	24.2	1.8E-10	7.3E-9
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of gene expression		45	10.8	2.0E-10	8.3E-9
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of programmed cell death		37	8.9	2.3E-10	9.3E-9
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell death		37	8.9	2.5E-10	1.0E-8
<input type="checkbox"/>	GOTERM_BP_FAT	immune system development		32	7.7	2.7E-10	1.1E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein metabolic process		26	6.2	3.9E-10	1.5E-8
<input type="checkbox"/>	GOTERM_BP_FAT	protein modification by small protein conjugation		22	5.3	4.0E-10	1.5E-8
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein kinase cascade		30	7.2	4.3E-10	1.6E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of transcription		42	10.1	4.4E-10	1.7E-8
<input type="checkbox"/>	GOTERM_BP_FAT	protein modification by small protein conjugation or removal		24	5.8	4.7E-10	1.7E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of transcription from RNA polymerase II promoter		31	7.4	4.7E-10	1.7E-8
<input type="checkbox"/>	GOTERM_BP_FAT	protein amino acid autophosphorylation		18	4.3	4.9E-10	1.8E-8
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of DNA binding		21	5.0	5.2E-10	1.9E-8
<input type="checkbox"/>	GOTERM_BP_FAT	hemopoiesis		29	7.0	5.7E-10	2.0E-8
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular receptor-mediated signaling pathway		17	4.1	5.9E-10	2.0E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of apoptosis		36	8.6	6.1E-10	2.1E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent		36	8.6	7.1E-10	2.4E-8
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of gene-specific transcription		18	4.3	7.3E-10	2.4E-8
<input type="checkbox"/>	GOTERM_BP_FAT	transmembrane receptor protein tyrosine kinase signaling pathway		28	6.7	8.2E-10	2.7E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cellular protein metabolic process		25	6.0	9.4E-10	3.1E-8
<input type="checkbox"/>	GOTERM_BP_FAT	chromatin organization		37	8.9	9.7E-10	3.1E-8
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cellular component organization		25	6.0	1.1E-9	3.4E-8
<input type="checkbox"/>	GOTERM_BP_FAT	transcription, DNA-dependent		32	7.7	1.1E-9	3.4E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of RNA metabolic process		36	8.6	1.1E-9	3.5E-8
<input type="checkbox"/>	GOTERM_BP_FAT	hemopoietic or lymphoid organ development		30	7.2	1.2E-9	3.7E-8

<input type="checkbox"/>	GOTERM_BP_FAT	steroid hormone receptor signaling pathway		15	3.6	1.2E-9	3.8E-8
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell communication		34	8.2	1.3E-9	4.0E-8
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of developmental process		31	7.4	1.4E-9	4.1E-8
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of signal transduction		32	7.7	1.4E-9	4.1E-8
<input type="checkbox"/>	GOTERM_BP_FAT	RNA biosynthetic process		32	7.7	1.5E-9	4.4E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of specific transcription from RNA polymerase II promoter		13	3.1	1.7E-9	5.0E-8
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of molecular function		34	8.2	2.0E-9	5.6E-8
<input type="checkbox"/>	GOTERM_BP_FAT	RNA splicing		31	7.4	2.3E-9	6.5E-8
<input type="checkbox"/>	GOTERM_BP_FAT	cell cycle phase		38	9.1	3.3E-9	9.1E-8
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of fatty acid oxidation		11	2.6	4.5E-9	1.2E-7
<input type="checkbox"/>	GOTERM_BP_FAT	posttranscriptional regulation of gene expression		26	6.2	5.0E-9	1.4E-7
<input type="checkbox"/>	GOTERM_BP_FAT	protein localization		60	14.4	5.4E-9	1.5E-7
<input type="checkbox"/>	GOTERM_BP_FAT	protein catabolic process		48	11.5	5.5E-9	1.5E-7
<input type="checkbox"/>	GOTERM_BP_FAT	peptidyl-tyrosine phosphorylation		13	3.1	7.4E-9	2.0E-7
<input type="checkbox"/>	GOTERM_BP_FAT	DNA metabolic process		42	10.1	7.9E-9	2.1E-7
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecular complex assembly		32	7.7	8.5E-9	2.2E-7
<input type="checkbox"/>	GOTERM_BP_FAT	response to DNA damage stimulus		35	8.4	8.8E-9	2.3E-7
<input type="checkbox"/>	GOTERM_BP_FAT	DNA repair		30	7.2	9.3E-9	2.4E-7
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecular complex subunit organization		34	8.2	1.0E-8	2.7E-7
<input type="checkbox"/>	GOTERM_BP_FAT	interphase of mitotic cell cycle		18	4.3	1.1E-8	2.7E-7
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription factor activity		18	4.3	1.1E-8	2.7E-7
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular transport		49	11.8	1.1E-8	2.8E-7
<input type="checkbox"/>	GOTERM_BP_FAT	peptidyl-tyrosine modification		13	3.1	1.3E-8	3.1E-7
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of gene-specific transcription		13	3.1	1.3E-8	3.1E-7
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell development		15	3.6	1.4E-8	3.4E-7
<input type="checkbox"/>	GOTERM_BP_FAT	interphase		18	4.3	1.7E-8	4.1E-7
<input type="checkbox"/>	GOTERM_BP_FAT	cell division		30	7.2	2.2E-8	5.2E-7
<input type="checkbox"/>	GOTERM_BP_FAT	RNA elongation		13	3.1	2.6E-8	6.3E-7
<input type="checkbox"/>	GOTERM_BP_FAT	cellular protein localization		36	8.6	3.1E-8	7.2E-7
<input type="checkbox"/>	GOTERM_BP_FAT	protein targeting		25	6.0	3.3E-8	7.8E-7
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecule localization		36	8.6	3.6E-8	8.5E-7
<input type="checkbox"/>	GOTERM_BP_FAT	induction of apoptosis		31	7.4	3.7E-8	8.4E-7
<input type="checkbox"/>	GOTERM_BP_FAT	induction of programmed cell death		31	7.4	3.9E-8	8.9E-7
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of lipid metabolic process		18	4.3	3.9E-8	9.0E-7
<input type="checkbox"/>	GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process		45	10.8	4.3E-8	9.6E-7
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell proliferation		33	7.9	4.8E-8	1.1E-6
<input type="checkbox"/>	GOTERM_BP_FAT	cellular protein catabolic process		45	10.8	4.9E-8	1.1E-6
<input type="checkbox"/>	GOTERM_BP_FAT	nuclear import		16	3.8	5.1E-8	1.1E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell development		24	5.8	5.8E-8	1.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	anti-apoptosis		24	5.8	6.4E-8	1.4E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of phosphate metabolic process		39	9.4	7.0E-8	1.5E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of phosphorus metabolic process		39	9.4	7.0E-8	1.5E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell cycle		31	7.4	7.8E-8	1.7E-6
<input type="checkbox"/>	GOTERM_BP_FAT	establishment of protein localization		52	12.5	8.7E-8	1.9E-6
<input type="checkbox"/>	GOTERM_BP_FAT	protein ubiquitination		18	4.3	9.9E-8	2.1E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular ketone metabolic process		13	3.1	1.0E-7	2.1E-6
<input type="checkbox"/>	GOTERM_BP_FAT	cell proliferation		36	8.6	1.3E-7	2.7E-6
<input type="checkbox"/>	GOTERM_BP_FAT	RNA elongation from RNA polymerase II promoter		12	2.9	1.4E-7	2.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	mRNA processing		30	7.2	1.4E-7	2.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	activation of pro-apoptotic gene products		9	2.2	1.4E-7	2.9E-6
<input type="checkbox"/>	GOTERM_BP_FAT	response to UV		13	3.1	1.5E-7	3.0E-6
<input type="checkbox"/>	GOTERM_BP_FAT	protein transport		51	12.2	1.6E-7	3.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of catabolic process		16	3.8	1.7E-7	3.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of fatty acid metabolic process		12	2.9	1.7E-7	3.4E-6

<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein modification process		22	5.3	2.2E-7	4.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	protein import into nucleus		15	3.6	2.6E-7	5.0E-6
<input type="checkbox"/>	GOTERM_BP_FAT	modification-dependent protein catabolic process		42	10.1	2.6E-7	5.0E-6
<input type="checkbox"/>	GOTERM_BP_FAT	modification-dependent macromolecule catabolic process		42	10.1	2.6E-7	5.0E-6
<input type="checkbox"/>	GOTERM_BP_FAT	mRNA metabolic process		32	7.7	2.7E-7	5.3E-6
<input type="checkbox"/>	GOTERM_BP_FAT	cell migration		27	6.5	2.8E-7	5.2E-6
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transferase activity		32	7.7	3.1E-7	5.8E-6
<input type="checkbox"/>	GOTERM_BP_FAT	I-kappaB kinase/NF-kappaB cascade		13	3.1	3.2E-7	6.0E-6
<input type="checkbox"/>	GOTERM_BP_FAT	transcription		103	24.7	3.3E-7	6.1E-6
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell migration		15	3.6	4.0E-7	7.4E-6
<input type="checkbox"/>	GOTERM_BP_FAT	response to dsRNA		9	2.2	4.4E-7	8.1E-6
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein modification process		17	4.1	5.5E-7	1.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of phosphorylation		36	8.6	6.4E-7	1.2E-5
<input type="checkbox"/>	GOTERM_BP_FAT	response to endogenous stimulus		33	7.9	6.5E-7	1.2E-5
<input type="checkbox"/>	GOTERM_BP_FAT	G1/S transition of mitotic cell cycle		12	2.9	7.2E-7	1.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	response to hormone stimulus		31	7.4	7.3E-7	1.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	transcription initiation from RNA polymerase II promoter		13	3.1	7.6E-7	1.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	protein localization in nucleus		15	3.6	8.0E-7	1.4E-5
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell cycle		14	3.4	8.2E-7	1.4E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein localization		18	4.3	8.6E-7	1.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of specific transcription from RNA polymerase II promoter		12	2.9	8.7E-7	1.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of catalytic activity		26	6.2	1.0E-6	1.8E-5
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transport		23	5.5	1.1E-6	1.8E-5
<input type="checkbox"/>	GOTERM_BP_FAT	intracellular protein transport		31	7.4	1.1E-6	1.8E-5
<input type="checkbox"/>	GOTERM_BP_FAT	ubiquitin-dependent protein catabolic process		24	5.8	1.2E-6	2.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	spliceosomal snRNP biogenesis		9	2.2	1.2E-6	2.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	establishment of RNA localization		15	3.6	1.2E-6	2.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	nucleic acid transport		15	3.6	1.2E-6	2.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	RNA transport		15	3.6	1.2E-6	2.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	histone acetylation		11	2.6	1.3E-6	2.2E-5
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of locomotion		15	3.6	1.3E-6	2.2E-5
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell motion		15	3.6	1.3E-6	2.2E-5
<input type="checkbox"/>	GOTERM_BP_FAT	homeostatic process		48	11.5	1.5E-6	2.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of catabolic process		11	2.6	1.6E-6	2.6E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein ubiquitination		15	3.6	1.7E-6	2.8E-5
<input type="checkbox"/>	GOTERM_BP_FAT	RNA localization		15	3.6	1.7E-6	2.8E-5
<input type="checkbox"/>	GOTERM_BP_FAT	cellular protein complex assembly		19	4.6	1.9E-6	3.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	mRNA transport		14	3.4	1.9E-6	3.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	localization of cell		27	6.5	2.1E-6	3.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	cell motility		27	6.5	2.1E-6	3.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	response to nutrient levels		21	5.0	2.1E-6	3.3E-5
<input type="checkbox"/>	GOTERM_BP_FAT	protein amino acid acetylation		11	2.6	2.8E-6	4.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein kinase cascade		19	4.6	2.9E-6	4.6E-5
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell proliferation		32	7.7	3.0E-6	4.7E-5
<input type="checkbox"/>	GOTERM_BP_FAT	response to extracellular stimulus		22	5.3	3.2E-6	4.9E-5
<input type="checkbox"/>	GOTERM_BP_FAT	anatomical structure homeostasis		15	3.6	3.5E-6	5.4E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of translation		17	4.1	3.7E-6	5.6E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of kinase activity		29	7.0	3.8E-6	5.8E-5
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of I-kappaB kinase/NF-kappaB cascade		15	3.6	3.9E-6	5.9E-5
<input type="checkbox"/>	GOTERM_BP_FAT	transcription initiation		13	3.1	6.7E-6	1.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	Wnt receptor signaling pathway through beta-catenin		7	1.7	6.8E-6	1.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	response to abiotic stimulus		29	7.0	6.8E-6	1.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of ubiquitin-protein ligase activity		12	2.9	7.2E-6	1.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	cell motion		34	8.2	7.3E-6	1.1E-4

<input type="checkbox"/>	GOTERM_BP_FAT	nucleobase, nucleoside, nucleotide and nucleic acid transport		15	3.6	7.5E-6	1.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein ubiquitination		13	3.1	7.6E-6	1.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of nucleocytoplasmic transport		11	2.6	8.0E-6	1.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of epithelial cell proliferation		12	2.9	8.3E-6	1.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of intracellular transport		12	2.9	8.3E-6	1.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	chordate embryonic development		27	6.5	8.3E-6	1.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	protein localization in organelle		17	4.1	8.4E-6	1.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of organelle organization		21	5.0	9.2E-6	1.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of neurogenesis		11	2.6	9.3E-6	1.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	protein import		16	3.8	9.4E-6	1.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	embryonic development ending in birth or egg hatching		27	6.5	9.7E-6	1.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of ligase activity		12	2.9	1.1E-5	1.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	protein amino acid acylation		11	2.6	1.1E-5	1.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	nuclear export		11	2.6	1.1E-5	1.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of neurogenesis		18	4.3	1.1E-5	1.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell migration		18	4.3	1.4E-5	1.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	double-strand break repair		11	2.6	1.5E-5	2.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of DNA replication		11	2.6	1.5E-5	2.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	response to peptide hormone stimulus		17	4.1	1.7E-5	2.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein kinase activity		27	6.5	1.7E-5	2.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of carbohydrate metabolic process		9	2.2	1.7E-5	2.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	response to light stimulus		16	3.8	1.8E-5	2.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of DNA binding		10	2.4	1.9E-5	2.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of ubiquitin-protein ligase activity		12	2.9	2.1E-5	2.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of ossification		12	2.9	2.1E-5	2.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein catabolic process		10	2.4	2.2E-5	2.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	protein heterooligomerization		10	2.4	2.2E-5	2.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell motion		19	4.6	2.2E-5	2.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of chromosome organization		8	1.9	2.4E-5	3.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	vasculature development		22	5.3	2.4E-5	3.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of translational initiation		9	2.2	2.5E-5	3.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of ligase activity		12	2.9	3.0E-5	3.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of I-kappaB kinase/NF-kappaB cascade		13	3.1	3.4E-5	4.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle		11	2.6	3.4E-5	4.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of osteoblast differentiation		9	2.2	3.7E-5	4.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of organelle organization		12	2.9	3.8E-5	4.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	tube development		20	4.8	3.8E-5	4.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of DNA metabolic process		14	3.4	3.9E-5	4.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of myeloid cell differentiation		11	2.6	4.4E-5	5.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of DNA binding		11	2.6	4.4E-5	5.5E-4
<input type="checkbox"/>	GOTERM_BP_FAT	reproductive developmental process		22	5.3	4.6E-5	5.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	cell junction organization		10	2.4	4.7E-5	5.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of ubiquitin-protein ligase activity during mitotic cell cycle		11	2.6	5.0E-5	6.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	developmental maturation		13	3.1	5.1E-5	6.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of transcription factor activity		9	2.2	5.2E-5	6.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of fatty acid oxidation		5	1.2	5.2E-5	6.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of fatty acid beta-oxidation		5	1.2	5.2E-5	6.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	SMAD protein complex assembly		5	1.2	5.2E-5	6.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	RNA processing		35	8.4	5.3E-5	6.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	blood vessel development		21	5.0	5.4E-5	6.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	protein import into nucleus, translocation		8	1.9	5.7E-5	6.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	cytoskeleton organization		30	7.2	5.8E-5	6.9E-4
<input type="checkbox"/>	GOTERM_BP_FAT	cell activation		23	5.5	5.9E-5	7.1E-4
<input type="checkbox"/>	GOTERM_BP_FAT	transmembrane receptor protein serine/threonine kinase signaling pathway		13	3.1	6.2E-5	7.3E-4

<input type="checkbox"/>	GOTERM_BP_FAT	cell cycle arrest	RT	13	3.1	6.2E-5	7.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular response to stress	RT	13	3.1	6.2E-5	7.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of caspase activity	RT	10	2.4	6.2E-5	7.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of binding	RT	10	2.4	6.2E-5	7.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of peptidase activity	RT	10	2.4	6.2E-5	7.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of glucose metabolic process	RT	8	1.9	7.0E-5	8.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of nervous system development	RT	18	4.3	7.2E-5	8.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of locomotion	RT	18	4.3	7.2E-5	8.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of establishment of protein localization	RT	14	3.4	7.2E-5	8.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	Ras protein signal transduction	RT	13	3.1	7.5E-5	8.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	cell fate commitment	RT	15	3.6	7.8E-5	9.0E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cytokine production	RT	12	2.9	8.0E-5	9.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	signal complex assembly	RT	6	1.4	8.1E-5	9.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular catabolic process	RT	10	2.4	8.2E-5	9.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of binding	RT	11	2.6	1.1E-4	1.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	response to radiation	RT	18	4.3	1.2E-4	1.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cytokine production	RT	17	4.1	1.2E-4	1.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular carbohydrate metabolic process	RT	8	1.9	1.2E-4	1.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of caspase activity	RT	11	2.6	1.3E-4	1.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	gliogenesis	RT	10	2.4	1.4E-4	1.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of JNK cascade	RT	10	2.4	1.4E-4	1.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of transferase activity	RT	12	2.9	1.4E-4	1.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	immune response-activating signal transduction	RT	9	2.2	1.5E-4	1.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	telomere maintenance	RT	7	1.7	1.6E-4	1.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	embryonic morphogenesis	RT	23	5.5	1.6E-4	1.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	M phase	RT	24	5.8	1.6E-4	1.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell morphogenesis	RT	14	3.4	1.6E-4	1.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	leukocyte differentiation	RT	14	3.4	1.6E-4	1.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of endopeptidase activity	RT	11	2.6	1.7E-4	1.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of intracellular protein transport	RT	9	2.2	1.7E-4	1.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell communication	RT	20	4.8	1.9E-4	2.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	lung development	RT	12	2.9	1.9E-4	2.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	telomere organization	RT	7	1.7	1.9E-4	2.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	activation of caspase activity	RT	9	2.2	2.0E-4	2.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of glucose metabolic process	RT	6	1.4	2.0E-4	2.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	cell junction assembly	RT	8	1.9	2.0E-4	2.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of mitotic cell cycle	RT	15	3.6	2.0E-4	2.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	response to hypoxia	RT	14	3.4	2.0E-4	2.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	ribonucleoprotein complex assembly	RT	10	2.4	2.2E-4	2.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of stress-activated protein kinase signaling pathway	RT	10	2.4	2.2E-4	2.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	response to exogenous dsRNA	RT	5	1.2	2.3E-4	2.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of intracellular transport	RT	7	1.7	2.3E-4	2.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	response to steroid hormone stimulus	RT	17	4.1	2.4E-4	2.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein amino acid phosphorylation	RT	16	3.8	2.4E-4	2.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	gastrulation	RT	10	2.4	2.4E-4	2.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT	proteasomal protein catabolic process	RT	12	2.9	2.5E-4	2.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT	respiratory tube development	RT	12	2.9	2.5E-4	2.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT	proteasomal ubiquitin-dependent protein catabolic process	RT	12	2.9	2.5E-4	2.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT	gene silencing	RT	9	2.2	2.6E-4	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	immune response-regulating signal transduction	RT	9	2.2	2.6E-4	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of peptidase activity	RT	11	2.6	2.6E-4	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of carbohydrate metabolic process	RT	6	1.4	2.6E-4	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cellular carbohydrate metabolic process	RT	6	1.4	2.6E-4	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription in response to stress	RT	4	1.0	2.6E-4	2.6E-3























































<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of telomerase activity		4	1.0	2.6E-4	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter in response to stress		4	1.0	2.6E-4	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	primary microRNA processing		4	1.0	2.6E-4	2.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	viral reproduction		10	2.4	2.7E-4	2.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	proteolysis		53	12.7	2.8E-4	2.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	in utero embryonic development		16	3.8	2.9E-4	2.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein import into nucleus		8	1.9	3.1E-4	3.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	anterior/posterior pattern formation		14	3.4	3.2E-4	3.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of carbohydrate biosynthetic process		6	1.4	3.3E-4	3.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of fatty acid metabolic process		6	1.4	3.3E-4	3.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	stem cell differentiation		7	1.7	3.4E-4	3.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	response to oxygen levels		14	3.4	3.4E-4	3.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	tissue morphogenesis		16	3.8	3.7E-4	3.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein ubiquitination		10	2.4	3.7E-4	3.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of neuron apoptosis		11	2.6	3.7E-4	3.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	response to protein stimulus		12	2.9	3.8E-4	3.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of signal transduction		18	4.3	3.9E-4	3.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	leukocyte activation		19	4.6	4.0E-4	3.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	respiratory system development		12	2.9	4.1E-4	3.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transcription factor activity		9	2.2	4.1E-4	3.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of mitotic cell cycle		6	1.4	4.2E-4	4.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	T cell activation		13	3.1	4.2E-4	4.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of MAPKKK cascade		12	2.9	4.4E-4	4.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	response to oxidative stress		15	3.6	4.5E-4	4.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	tube morphogenesis		13	3.1	4.5E-4	4.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell projection organization		8	1.9	4.8E-4	4.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell morphogenesis involved in differentiation		10	2.4	5.0E-4	4.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of gene expression, epigenetic		10	2.4	5.0E-4	4.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	actin cytoskeleton organization		18	4.3	5.0E-4	4.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of telomere maintenance via telomerase		4	1.0	5.1E-4	4.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	cell surface receptor linked signal transduction		81	19.4	5.1E-4	4.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	viral reproductive process		9	2.2	5.2E-4	4.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT	activation of immune response		11	2.6	5.3E-4	4.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular localization		19	4.6	5.3E-4	4.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	angiogenesis		14	3.4	5.4E-4	4.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	induction of apoptosis by extracellular signals		12	2.9	5.6E-4	5.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	response to cytokine stimulus		10	2.4	6.0E-4	5.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	organ growth		5	1.2	6.4E-4	5.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of homeostatic process		12	2.9	6.5E-4	5.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein transport		12	2.9	6.5E-4	5.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cellular catabolic process		7	1.7	6.6E-4	5.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	gut development		7	1.7	6.6E-4	5.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein kinase cascade		7	1.7	6.6E-4	5.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	blood vessel morphogenesis		17	4.1	6.7E-4	5.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of growth		23	5.5	6.8E-4	6.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of neuron differentiation		13	3.1	6.9E-4	6.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	Wnt receptor signaling pathway		13	3.1	6.9E-4	6.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT	branching morphogenesis of a tube		9	2.2	7.2E-4	6.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	cell-substrate adhesion		11	2.6	7.3E-4	6.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of epithelial cell proliferation		6	1.4	7.9E-4	6.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	stem cell maintenance		6	1.4	7.9E-4	6.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of transport		13	3.1	7.9E-4	6.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	protein oligomerization		15	3.6	8.1E-4	7.0E-3
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of response to stimulus		18	4.3	8.2E-4	7.1E-3

<input type="checkbox"/>	GOTERM_BP_FAT response to drug	RT 	17	4.1	8.6E-4	7.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of response to stimulus	RT 	11	2.6	8.6E-4	7.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT response to insulin stimulus	RT 	11	2.6	8.6E-4	7.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT regulation of cell adhesion	RT 	13	3.1	9.0E-4	7.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT stem cell development	RT 	6	1.4	9.5E-4	8.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT cellular response to insulin stimulus	RT 	9	2.2	9.7E-4	8.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of transferase activity	RT 	18	4.3	9.8E-4	8.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT glial cell differentiation	RT 	8	1.9	1.0E-3	8.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT immune response-activating cell surface receptor signaling pathway	RT 	7	1.7	1.0E-3	8.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT regulation of transforming growth factor beta receptor signaling pathway	RT 	7	1.7	1.0E-3	8.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT actin filament-based process	RT 	18	4.3	1.0E-3	8.7E-3
<input type="checkbox"/>	GOTERM_BP_FAT response to nutrient	RT 	13	3.1	1.1E-3	9.1E-3
<input type="checkbox"/>	GOTERM_BP_FAT regulation of cyclin-dependent protein kinase activity	RT 	8	1.9	1.1E-3	9.4E-3
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of protein catabolic process	RT 	6	1.4	1.1E-3	9.5E-3
<input type="checkbox"/>	GOTERM_BP_FAT cell morphogenesis	RT 	23	5.5	1.2E-3	9.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of multicellular organismal process	RT 	18	4.3	1.2E-3	9.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT regulation of cellular component biogenesis	RT 	13	3.1	1.2E-3	1.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of cellular component organization	RT 	13	3.1	1.2E-3	1.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT pattern specification process	RT 	19	4.6	1.2E-3	1.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT nucleotide-excision repair	RT 	8	1.9	1.3E-3	1.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT response to estrogen stimulus	RT 	11	2.6	1.3E-3	1.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT response to unfolded protein	RT 	9	2.2	1.3E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT RNA export from nucleus	RT 	7	1.7	1.3E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT cellular response to DNA damage stimulus	RT 	4	1.0	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT corticosteroid receptor signaling pathway	RT 	4	1.0	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT nerve growth factor receptor signaling pathway	RT 	4	1.0	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT regulation of telomerase activity	RT 	4	1.0	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT MAPKKK cascade	RT 	15	3.6	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT response to inorganic substance	RT 	16	3.8	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT chromatin remodeling	RT 	8	1.9	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT actin filament organization	RT 	9	2.2	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of MAPKKK cascade	RT 	5	1.2	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT cell-matrix adhesion	RT 	10	2.4	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT regulation of cell projection organization	RT 	10	2.4	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT response to wounding	RT 	30	7.2	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT regulation of cell size	RT 	16	3.8	1.5E-3	1.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT immune response-regulating cell surface receptor signaling pathway	RT 	7	1.7	1.5E-3	1.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT morphogenesis of a branching structure	RT 	9	2.2	1.7E-3	1.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT mRNA catabolic process	RT 	7	1.7	1.7E-3	1.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of kinase activity	RT 	17	4.1	1.7E-3	1.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT embryonic hindlimb morphogenesis	RT 	5	1.2	1.8E-3	1.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT protein export from nucleus	RT 	5	1.2	1.8E-3	1.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT regulation of generation of precursor metabolites and energy	RT 	6	1.4	1.9E-3	1.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	RT 	6	1.4	1.9E-3	1.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT DNA replication	RT 	15	3.6	1.9E-3	1.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT BMP signaling pathway	RT 	7	1.7	1.9E-3	1.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT myeloid cell differentiation	RT 	10	2.4	1.9E-3	1.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT somatic stem cell maintenance	RT 	4	1.0	2.0E-3	1.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT placenta development	RT 	8	1.9	2.1E-3	1.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT DNA catabolic process	RT 	8	1.9	2.1E-3	1.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT transforming growth factor beta receptor signaling pathway	RT 	8	1.9	2.1E-3	1.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT apoptotic mitochondrial changes	RT 	6	1.4	2.2E-3	1.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT neuron apoptosis	RT 	5	1.2	2.2E-3	1.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT platelet-derived growth factor receptor signaling pathway	RT 	5	1.2	2.2E-3	1.7E-2











<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell growth	RT	15	3.6	2.3E-3	1.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of immune system process	RT	17	4.1	2.3E-3	1.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of lipid metabolic process	RT	7	1.7	2.4E-3	1.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of striated muscle cell differentiation	RT	6	1.4	2.5E-3	1.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regionalization	RT	15	3.6	2.6E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	response to UV-A	RT	3	0.7	2.7E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	peptidyl-lysine acetylation	RT	3	0.7	2.7E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	N-terminal peptidyl-lysine acetylation	RT	3	0.7	2.7E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cytoskeleton organization	RT	12	2.9	2.7E-3	2.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of stress-activated protein kinase signaling pathway	RT	4	1.0	2.8E-3	2.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	double-strand break repair via nonhomologous end joining	RT	4	1.0	2.8E-3	2.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of JNK cascade	RT	4	1.0	2.8E-3	2.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	lymphocyte activation	RT	15	3.6	2.8E-3	2.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	antigen receptor-mediated signaling pathway	RT	6	1.4	2.9E-3	2.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of hydrolase activity	RT	14	3.4	3.1E-3	2.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein kinase activity	RT	16	3.8	3.1E-3	2.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of nitric oxide biosynthetic process	RT	5	1.2	3.2E-3	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of lipid storage	RT	5	1.2	3.2E-3	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	gastrulation with mouth forming second	RT	5	1.2	3.2E-3	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	release of cytochrome c from mitochondria	RT	5	1.2	3.2E-3	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	RT	8	1.9	3.3E-3	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	RNA catabolic process	RT	8	1.9	3.3E-3	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	RT	8	1.9	3.3E-3	2.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	establishment or maintenance of cell polarity	RT	7	1.7	3.4E-3	2.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	germ cell development	RT	10	2.4	3.4E-3	2.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cellular component size	RT	18	4.3	3.6E-3	2.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	response to organic cyclic substance	RT	11	2.6	3.6E-3	2.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	response to vitamin	RT	8	1.9	3.6E-3	2.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cell-cell junction organization	RT	6	1.4	3.7E-3	2.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein complex assembly	RT	6	1.4	3.7E-3	2.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	nuclear-transcribed mRNA catabolic process	RT	6	1.4	3.7E-3	2.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of proteasomal ubiquitin-dependent protein catabolic process	RT	4	1.0	3.8E-3	2.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	lipopolysaccharide-mediated signaling pathway	RT	4	1.0	3.8E-3	2.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of glycoprotein biosynthetic process	RT	4	1.0	3.8E-3	2.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of glucose transport	RT	5	1.2	3.9E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of nucleocytoplasmic transport	RT	5	1.2	3.9E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	nucleotide-excision repair, DNA damage removal	RT	5	1.2	3.9E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of glucose import	RT	5	1.2	3.9E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	initiation of viral infection	RT	5	1.2	3.9E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cell projection organization	RT	22	5.3	3.9E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of ligase activity	RT	8	1.9	3.9E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of ubiquitin-protein ligase activity	RT	8	1.9	3.9E-3	2.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	androgen receptor signaling pathway	RT	6	1.4	4.2E-3	3.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	response to molecule of bacterial origin	RT	9	2.2	4.4E-3	3.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of immune response	RT	12	2.9	4.5E-3	3.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cellular component morphogenesis	RT	23	5.5	4.5E-3	3.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	T cell receptor signaling pathway	RT	5	1.2	4.6E-3	3.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cell-substrate junction assembly	RT	5	1.2	4.6E-3	3.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein kinase activity	RT	9	2.2	4.7E-3	3.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of lipid storage	RT	4	1.0	4.9E-3	3.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	telomere maintenance via telomere lengthening	RT	4	1.0	4.9E-3	3.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of foam cell differentiation	RT	4	1.0	4.9E-3	3.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of telomere maintenance	RT	4	1.0	4.9E-3	3.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of hormone metabolic process	RT	4	1.0	4.9E-3	3.4E-2

<input type="checkbox"/>	GOTERM_BP_FAT	gene silencing by miRNA, production of miRNAs	RT 	4	1.0	4.9E-3	3.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	RT 	3	0.7	5.2E-3	3.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of telomere maintenance via telomerase	RT 	3	0.7	5.2E-3	3.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transforming growth factor-beta2 production	RT 	3	0.7	5.2E-3	3.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	induction of apoptosis by intracellular signals	RT 	7	1.7	5.5E-3	3.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	heart development	RT 	15	3.6	5.6E-3	3.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of kinase activity	RT 	9	2.2	5.7E-3	4.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	membrane organization	RT 	22	5.3	5.8E-3	4.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of muscle cell differentiation	RT 	6	1.4	6.0E-3	4.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	sex differentiation	RT 	12	2.9	6.1E-3	4.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cortical actin cytoskeleton organization	RT 	4	1.0	6.2E-3	4.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	dsRNA fragmentation	RT 	4	1.0	6.2E-3	4.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	activation of NF-kappaB-inducing kinase activity	RT 	4	1.0	6.2E-3	4.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of histone modification	RT 	4	1.0	6.2E-3	4.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of skeletal muscle fiber development	RT 	5	1.2	6.2E-3	4.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of foam cell differentiation	RT 	5	1.2	6.2E-3	4.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of monooxygenase activity	RT 	5	1.2	6.2E-3	4.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of DNA metabolic process	RT 	7	1.7	6.6E-3	4.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	response to hydrogen peroxide	RT 	7	1.7	6.6E-3	4.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of oxidoreductase activity	RT 	6	1.4	6.7E-3	4.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to hormone stimulus	RT 	11	2.6	7.0E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of fibroblast proliferation	RT 	5	1.2	7.2E-3	4.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of lipid catabolic process	RT 	5	1.2	7.2E-3	4.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	hindlimb morphogenesis	RT 	5	1.2	7.2E-3	4.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cell maturation	RT 	8	1.9	7.3E-3	4.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	response to reactive oxygen species	RT 	8	1.9	7.3E-3	4.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of NF-kappaB transcription factor activity	RT 	6	1.4	7.5E-3	5.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of myeloid leukocyte differentiation	RT 	6	1.4	7.5E-3	5.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	maintenance of protein location in cell	RT 	6	1.4	7.5E-3	5.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of interleukin-1 beta production	RT 	4	1.0	7.7E-3	5.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cortical cytoskeleton organization	RT 	4	1.0	7.7E-3	5.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	non-recombinational repair	RT 	4	1.0	7.7E-3	5.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of osteoblast differentiation	RT 	4	1.0	7.7E-3	5.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of glucan biosynthetic process	RT 	4	1.0	7.7E-3	5.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of polysaccharide biosynthetic process	RT 	4	1.0	7.7E-3	5.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of glycogen biosynthetic process	RT 	4	1.0	7.7E-3	5.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	skeletal system development	RT 	19	4.6	8.1E-3	5.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of nitric oxide biosynthetic process	RT 	5	1.2	8.3E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell-matrix adhesion	RT 	5	1.2	8.3E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	T cell differentiation in the thymus	RT 	5	1.2	8.3E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	hair cycle process	RT 	6	1.4	8.3E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of microtubule cytoskeleton organization	RT 	6	1.4	8.3E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	hair follicle development	RT 	6	1.4	8.3E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	molting cycle process	RT 	6	1.4	8.3E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	response to starvation	RT 	6	1.4	8.3E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	kidney development	RT 	9	2.2	8.4E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	response to lipopolysaccharide	RT 	8	1.9	8.5E-3	5.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	apical junction assembly	RT 	3	0.7	8.5E-3	5.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of fatty acid beta-oxidation	RT 	3	0.7	8.5E-3	5.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of telomere maintenance	RT	3	0.7	8.5E-3	5.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of phosphorylation	RT	9	2.2	8.9E-3	5.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	epithelium development	RT	15	3.6	9.0E-3	5.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	viral infectious cycle	RT	6	1.4	9.1E-3	5.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	hair cycle	RT	6	1.4	9.1E-3	5.9E-2


<input type="checkbox"/>	GOTERM_BP_FAT	molting cycle	RT	6	1.4	9.1E-3	5.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of DNA replication	RT	5	1.2	9.4E-3	6.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of DNA replication	RT	5	1.2	9.4E-3	6.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	epidermal growth factor receptor signaling pathway	RT	5	1.2	9.4E-3	6.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of lipid transport	RT	4	1.0	9.5E-3	6.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	phosphoinositide phosphorylation	RT	4	1.0	9.5E-3	6.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of polysaccharide metabolic process	RT	4	1.0	9.5E-3	6.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell size	RT	9	2.2	1.0E-2	6.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to nutrient levels	RT	6	1.4	1.0E-2	6.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	homeostasis of number of cells	RT	9	2.2	1.1E-2	6.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of phosphate metabolic process	RT	9	2.2	1.1E-2	6.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of phosphorus metabolic process	RT	9	2.2	1.1E-2	6.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of skeletal muscle tissue development	RT	5	1.2	1.1E-2	6.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	spindle organization	RT	6	1.4	1.1E-2	7.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cytoskeleton organization	RT	6	1.4	1.1E-2	7.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	small GTPase mediated signal transduction	RT	18	4.3	1.1E-2	7.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	morphogenesis of an epithelium	RT	9	2.2	1.1E-2	7.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	lipid phosphorylation	RT	4	1.0	1.1E-2	7.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of fat cell differentiation	RT	4	1.0	1.1E-2	7.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of muscle cell differentiation	RT	4	1.0	1.1E-2	7.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of organelle organization	RT	8	1.9	1.2E-2	7.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	axis specification	RT	5	1.2	1.2E-2	7.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of lipid transport	RT	5	1.2	1.2E-2	7.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of transcription factor import into nucleus	RT	5	1.2	1.2E-2	7.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell-substrate adhesion	RT	6	1.4	1.2E-2	7.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	maintenance of location	RT	7	1.7	1.2E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to extracellular stimulus	RT	7	1.7	1.2E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	neuron migration	RT	7	1.7	1.2E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cholesterol storage	RT	3	0.7	1.3E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	SMAD protein signal transduction	RT	3	0.7	1.3E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	tyrosine phosphorylation of STAT protein	RT	3	0.7	1.3E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of striated muscle cell differentiation	RT	3	0.7	1.3E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of fat cell differentiation	RT	3	0.7	1.3E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	lymphocyte differentiation	RT	9	2.2	1.3E-2	7.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	wound healing	RT	13	3.1	1.3E-2	8.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	T cell differentiation	RT	7	1.7	1.3E-2	8.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	gene silencing by miRNA	RT	4	1.0	1.4E-2	8.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	histone deacetylation	RT	4	1.0	1.4E-2	8.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	nucleotide-excision repair, DNA gap filling	RT	4	1.0	1.4E-2	8.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of interleukin-1 production	RT	4	1.0	1.4E-2	8.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	protein ubiquitination during ubiquitin-dependent protein catabolic process	RT	4	1.0	1.4E-2	8.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	gut morphogenesis	RT	4	1.0	1.4E-2	8.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	peptidyl-lysine modification	RT	4	1.0	1.4E-2	8.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	microtubule cytoskeleton organization	RT	11	2.6	1.4E-2	8.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of hydrolase activity	RT	19	4.6	1.4E-2	8.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	DNA recombination	RT	9	2.2	1.4E-2	8.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	multicellular organismal homeostasis	RT	8	1.9	1.4E-2	8.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	maintenance of protein location	RT	6	1.4	1.4E-2	8.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	maintenance of location in cell	RT	6	1.4	1.4E-2	8.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell size	RT	6	1.4	1.4E-2	8.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cellular response to starvation	RT	5	1.2	1.5E-2	9.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	epithelial tube morphogenesis	RT	7	1.7	1.5E-2	9.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein transport	RT	7	1.7	1.5E-2	9.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	rhythmic process	RT	10	2.4	1.5E-2	9.3E-2

<input type="checkbox"/>	GOTERM_BP_FAT regulation of microtubule-based process	RT 	6	1.4	1.6E-2	9.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT response to lipid	RT 	4	1.0	1.6E-2	9.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT cell-cell junction assembly	RT 	4	1.0	1.6E-2	9.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT chromatin silencing	RT 	4	1.0	1.6E-2	9.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT histone ubiquitination	RT 	4	1.0	1.6E-2	9.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT nuclear division	RT 	14	3.4	1.6E-2	9.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT mitosis	RT 	14	3.4	1.6E-2	9.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT embryonic appendage morphogenesis	RT 	8	1.9	1.6E-2	9.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT embryonic limb morphogenesis	RT 	8	1.9	1.6E-2	9.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT cell morphogenesis involved in differentiation	RT 	15	3.6	1.6E-2	9.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT regulation of peptidyl-tyrosine phosphorylation	RT 	7	1.7	1.6E-2	9.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT regulation of glucose import	RT 	5	1.2	1.7E-2	9.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT cell aging	RT 	5	1.2	1.7E-2	9.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT regulation of striated muscle tissue development	RT 	6	1.4	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of cell activation	RT 	12	2.9	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of histone modification	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT establishment of nucleus localization	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT lymphoid progenitor cell differentiation	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT glucocorticoid receptor signaling pathway	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of epithelial to mesenchymal transition	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT ephrin receptor signaling pathway	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT N-terminal protein amino acid acetylation	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT white fat cell differentiation	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of cell morphogenesis involved in differentiation	RT 	3	0.7	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT response to virus	RT 	9	2.2	1.7E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT regeneration	RT 	7	1.7	1.8E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of protein amino acid phosphorylation	RT 	8	1.9	1.8E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT urogenital system development	RT 	9	2.2	1.8E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of growth	RT 	9	2.2	1.8E-2	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT M phase of mitotic cell cycle	RT 	14	3.4	1.8E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of muscle development	RT 	6	1.4	1.8E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT double-strand break repair via homologous recombination	RT 	4	1.0	1.8E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT recombinational repair	RT 	4	1.0	1.8E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT response to endoplasmic reticulum stress	RT 	5	1.2	1.9E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of glucose transport	RT 	5	1.2	1.9E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT myeloid leukocyte differentiation	RT 	5	1.2	1.9E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT integrin-mediated signaling pathway	RT 	7	1.7	1.9E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of neuron projection development	RT 	7	1.7	1.9E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of protein complex assembly	RT 	8	1.9	1.9E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT inflammatory response	RT 	18	4.3	2.0E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT cell cycle checkpoint	RT 	8	1.9	2.0E-2	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of fibroblast proliferation	RT 	5	1.2	2.0E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT ribonucleoprotein complex biogenesis	RT 	12	2.9	2.1E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of interleukin-1 beta production	RT 	4	1.0	2.1E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of cellular catabolic process	RT 	4	1.0	2.1E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT liver development	RT 	6	1.4	2.1E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of proteolysis	RT 	6	1.4	2.1E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT fat cell differentiation	RT 	6	1.4	2.1E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT organelle fission	RT 	14	3.4	2.1E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of cell cycle process	RT 	9	2.2	2.2E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT leukocyte homeostasis	RT 	5	1.2	2.2E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT provirus integration	RT 	3	0.7	2.3E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of hormone biosynthetic process	RT 	3	0.7	2.3E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of telomere maintenance	RT 	3	0.7	2.3E-2	1.2E-1

<input type="checkbox"/>	GOTERM_BP_FAT	lysogeny		3	0.7	2.3E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cyclin-dependent protein kinase activity		3	0.7	2.3E-2	1.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	growth		12	2.9	2.3E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ossification		9	2.2	2.3E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	mitochondrion organization		10	2.4	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	mesoderm development		7	1.7	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	G1 phase		4	1.0	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	digestive system development		4	1.0	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	posttranscriptional gene silencing		4	1.0	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	posttranscriptional gene silencing by RNA		4	1.0	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	digestive tract morphogenesis		4	1.0	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	G2/M transition of mitotic cell cycle		4	1.0	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of gene expression, epigenetic		4	1.0	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of homeostatic process		4	1.0	2.4E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of catabolic process		5	1.2	2.5E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	insulin receptor signaling pathway		5	1.2	2.5E-2	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	reproductive cellular process		11	2.6	2.5E-2	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of T cell activation		9	2.2	2.5E-2	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	tissue remodeling		6	1.4	2.6E-2	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	vesicle-mediated transport		27	6.5	2.7E-2	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of anti-apoptosis		5	1.2	2.7E-2	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	thymus development		4	1.0	2.7E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of neuron apoptosis		4	1.0	2.7E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ureteric bud morphogenesis		4	1.0	2.7E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	branching involved in ureteric bud morphogenesis		4	1.0	2.7E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein amino acid deacetylation		4	1.0	2.7E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of osteoclast differentiation		4	1.0	2.7E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell cycle		6	1.4	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of axonogenesis		6	1.4	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to host		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of receptor biosynthetic process		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to host defenses		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	insulin-like growth factor receptor signaling pathway		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	anagen		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to defenses of other organism during symbiotic interaction		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of epithelial to mesenchymal transition		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein kinase B signaling cascade		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	B cell receptor signaling pathway		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of retinoic acid receptor signaling pathway		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein import into nucleus, translocation		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	stem cell division		3	0.7	2.8E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of heart contraction		7	1.7	2.9E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of DNA metabolic process		5	1.2	2.9E-2	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	limb morphogenesis		8	1.9	3.0E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	appendage morphogenesis		8	1.9	3.0E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of translation		4	1.0	3.1E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of interleukin-1 production		4	1.0	3.1E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to gamma radiation		4	1.0	3.1E-2	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein transport		5	1.2	3.2E-2	1.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	bone development		9	2.2	3.3E-2	1.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion		31	7.4	3.3E-2	1.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion		31	7.4	3.4E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	hindbrain development		6	1.4	3.4E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of cell adhesion		6	1.4	3.4E-2	1.8E-1

<input type="checkbox"/>	GOTERM_BP_FAT response to ionizing radiation	RT 	6	1.4	3.4E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT ventricular cardiac muscle cell differentiation	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of lipid kinase activity	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT axon regeneration	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of activin receptor signaling pathway	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT ectodermal gut development	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of glycogen biosynthetic process	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of epithelial cell differentiation	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT ectodermal gut morphogenesis	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT nucleus localization	RT 	3	0.7	3.5E-2	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT limb development	RT 	8	1.9	3.6E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT appendage development	RT 	8	1.9	3.6E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT response to vitamin A	RT 	5	1.2	3.7E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of cell growth	RT 	5	1.2	3.7E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of axonogenesis	RT 	4	1.0	3.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of osteoblast differentiation	RT 	4	1.0	3.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT epidermis morphogenesis	RT 	4	1.0	3.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of cell cycle process	RT 	4	1.0	3.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of protein polymerization	RT 	4	1.0	3.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT ectoderm development	RT 	12	2.9	3.9E-2	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT cellular response to oxidative stress	RT 	5	1.2	4.0E-2	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of cell adhesion	RT 	5	1.2	4.0E-2	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT mitotic cell cycle checkpoint	RT 	5	1.2	4.0E-2	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT cell-cell adhesion	RT 	15	3.6	4.0E-2	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT forebrain development	RT 	10	2.4	4.1E-2	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT tissue homeostasis	RT 	6	1.4	4.1E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT hemopoietic progenitor cell differentiation	RT 	3	0.7	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of cell-substrate adhesion	RT 	3	0.7	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of cholesterol storage	RT 	3	0.7	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT negative regulation of cyclin-dependent protein kinase activity	RT 	3	0.7	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT telomere maintenance via telomerase	RT 	3	0.7	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT B cell homeostasis	RT 	3	0.7	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT estrogen receptor signaling pathway	RT 	3	0.7	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT glial cell development	RT 	4	1.0	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of oxidoreductase activity	RT 	4	1.0	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of dephosphorylation	RT 	4	1.0	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT histone H3 acetylation	RT 	4	1.0	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT protein polyubiquitination	RT 	4	1.0	4.2E-2	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT female gonad development	RT 	6	1.4	4.4E-2	2.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT cellular homeostasis	RT 	22	5.3	4.4E-2	2.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT response to glucose stimulus	RT 	5	1.2	4.6E-2	2.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of lipid biosynthetic process	RT 	5	1.2	4.6E-2	2.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT developmental growth	RT 	7	1.7	4.8E-2	2.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT aging	RT 	8	1.9	4.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of phosphoinositide 3-kinase cascade	RT 	3	0.7	4.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT paraxial mesoderm development	RT 	3	0.7	4.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT neuron projection regeneration	RT 	3	0.7	4.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT syncytium formation by plasma membrane fusion	RT 	3	0.7	4.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT positive regulation of stress fiber formation	RT 	3	0.7	4.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT regulation of Wnt receptor signaling pathway	RT	5	1.2	4.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT circadian rhythm	RT	5	1.2	4.9E-2	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT lymphocyte homeostasis	RT	4	1.0	5.1E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT ovulation cycle	RT	6	1.4	5.1E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT gland development	RT	9	2.2	5.2E-2	2.5E-1

<input type="checkbox"/>	GOTERM_BP_FAT	epidermis development		11	2.6	5.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of cell division		5	1.2	5.3E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to hexose stimulus		5	1.2	5.3E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to monosaccharide stimulus		5	1.2	5.3E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of protein polymerization		6	1.4	5.4E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	peptidyl-serine phosphorylation		4	1.0	5.6E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of epithelial cell differentiation		4	1.0	5.6E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of phosphorus metabolic process		5	1.2	5.6E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of phosphate metabolic process		5	1.2	5.6E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of lipid catabolic process		3	0.7	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	hair follicle maturation		3	0.7	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of alpha-beta T cell proliferation		3	0.7	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of microtubule polymerization		3	0.7	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of transcription factor import into nucleus		3	0.7	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of phosphoinositide 3-kinase cascade		3	0.7	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to tumor necrosis factor		3	0.7	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	development of primary female sexual characteristics		6	1.4	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	female sex differentiation		6	1.4	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	lipid modification		6	1.4	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	activation of protein kinase activity		8	1.9	5.7E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of cell growth		7	1.7	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	embryonic genitalia morphogenesis		2	0.5	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of heparan sulfate proteoglycan biosynthetic process		2	0.5	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein heterotrimerization		2	0.5	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of heparan sulfate proteoglycan biosynthetic process		2	0.5	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	establishment of T cell polarity		2	0.5	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	establishment of lymphocyte polarity		2	0.5	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	glucose homeostasis		5	1.2	6.0E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	carbohydrate homeostasis		5	1.2	6.0E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cytokine-mediated signaling pathway		6	1.4	6.0E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of multicellular organismal process		10	2.4	6.1E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of anti-apoptosis		4	1.0	6.1E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of Wnt receptor signaling pathway		4	1.0	6.1E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of myeloid cell differentiation		4	1.0	6.1E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of leukocyte activation		10	2.4	6.4E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	N-terminal protein amino acid modification		3	0.7	6.5E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of actin filament bundle formation		3	0.7	6.5E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cytoplasmic sequestering of protein		3	0.7	6.5E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	neuroprotection		3	0.7	6.5E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	syncytium formation		3	0.7	6.5E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of sodium ion transport		3	0.7	6.5E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	toll-like receptor signaling pathway		3	0.7	6.5E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of smooth muscle cell proliferation		4	1.0	6.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	receptor metabolic process		4	1.0	6.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of microtubule polymerization or depolymerization		4	1.0	6.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	endocytosis		12	2.9	6.9E-2	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	membrane invagination		12	2.9	6.9E-2	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	palate development		4	1.0	7.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	spliceosome assembly		4	1.0	7.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of endothelial cell proliferation		4	1.0	7.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	embryonic pattern specification		4	1.0	7.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	nucleus organization		5	1.2	7.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	muscle cell differentiation		8	1.9	7.3E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to X-ray		3	0.7	7.4E-2	3.3E-1

<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of endothelial cell proliferation		3	0.7	7.4E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of neuron differentiation		4	1.0	7.6E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	gene silencing by RNA		4	1.0	7.6E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of myeloid cell differentiation		4	1.0	7.6E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	mRNA export from nucleus		4	1.0	7.6E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of T cell activation		6	1.4	7.9E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	defense response		26	6.2	7.9E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of lymphocyte activation		9	2.2	7.9E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	odontogenesis		5	1.2	7.9E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of translation		4	1.0	8.2E-2	3.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of S phase of mitotic cell cycle		3	0.7	8.2E-2	3.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of nitric-oxide synthase activity		3	0.7	8.2E-2	3.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	focal adhesion formation		3	0.7	8.2E-2	3.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to calcium ion		5	1.2	8.4E-2	3.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of system process		15	3.6	8.4E-2	3.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	neuron projection development		13	3.1	8.5E-2	3.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	pancreas development		4	1.0	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	glycogen metabolic process		4	1.0	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ureteric bud development		4	1.0	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	metencephalon development		4	1.0	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	ER-nuclear signaling pathway		4	1.0	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	mRNA transcription from RNA polymerase II promoter		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein amino acid dephosphorylation		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of insulin receptor signaling pathway		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of chromatin silencing		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	glial cell fate determination		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of dephosphorylation		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	general transcription from RNA polymerase II promoter		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of sulfur metabolic process		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of T cell anergy		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of telomere maintenance via telomerase		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of lymphocyte anergy		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of lymphocyte anergy		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of T cell anergy		2	0.5	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to mechanical stimulus		5	1.2	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to heat		5	1.2	8.8E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	development of primary sexual characteristics		8	1.9	9.0E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	sensory perception of mechanical stimulus		7	1.7	9.1E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	G1/S transition checkpoint		3	0.7	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	protein import into nucleus, docking		3	0.7	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	pattern recognition receptor signaling pathway		3	0.7	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of protein catabolic process		3	0.7	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	negative regulation of microtubule polymerization or depolymerization		3	0.7	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	RNA-dependent DNA replication		3	0.7	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of protein import into nucleus		3	0.7	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of alpha-beta T cell activation		4	1.0	9.4E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	glucan metabolic process		4	1.0	9.4E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	cellular glucan metabolic process		4	1.0	9.4E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	positive regulation of growth		6	1.4	9.4E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	response to metal ion		8	1.9	9.5E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	chemical homeostasis		22	5.3	9.5E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	DNA-dependent DNA replication		5	1.2	9.7E-2	4.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	regulation of metal ion transport		6	1.4	9.8E-2	4.0E-1

11 gene(s) from your list are not in the output.

Please cite [Nature Protocols 2009; 4\(1\):44](#) & [Genome Biology 2003; 4\(5\):P3](#) within any publication that makes use of any methods inspired by **DAVID**.



[Term of Service](#) | [Contact Us](#) | [Site Map](#)