



Functional Annotation Chart

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Current Gene List: condition_specific_gene_list
Current Background: Homo sapiens
2052 DAVID IDs

Options

Rerun Using Options

Create Sublist

348 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	cytosol	RT	<div></div>	999	48.7	5.9E-83	7.1E-80
<input type="checkbox"/>	GOTERM_CC_FAT	nucleoplasm	RT	<div></div>	816	39.8	1.9E-75	1.2E-72
<input type="checkbox"/>	GOTERM_CC_FAT	cytosolic ribosome	RT	<div></div>	82	4.0	5.4E-48	2.2E-45
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular exosome	RT	<div></div>	443	21.6	6.5E-40	2.0E-37
<input type="checkbox"/>	GOTERM_CC_FAT	ribosomal subunit	RT	<div></div>	93	4.5	4.4E-37	1.1E-34
<input type="checkbox"/>	GOTERM_CC_FAT	ribosome	RT	<div></div>	111	5.4	1.1E-35	2.2E-33
<input type="checkbox"/>	GOTERM_CC_FAT	cytosolic large ribosomal subunit	RT	<div></div>	49	2.4	1.8E-35	3.1E-33
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular vesicle	RT	<div></div>	443	21.6	3.9E-35	5.8E-33
<input type="checkbox"/>	GOTERM_CC_FAT	extracellular organelle	RT	<div></div>	443	21.6	4.3E-35	5.8E-33
<input type="checkbox"/>	GOTERM_CC_FAT	cytosolic part	RT	<div></div>	110	5.4	5.7E-34	6.9E-32
<input type="checkbox"/>	GOTERM_CC_FAT	nucleoplasm part	RT	<div></div>	283	13.8	2.0E-32	2.2E-30
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear body	RT	<div></div>	208	10.1	1.1E-27	1.1E-25
<input type="checkbox"/>	GOTERM_CC_FAT	ribonucleoprotein complex	RT	<div></div>	287	14.0	9.3E-25	8.7E-23
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear speck	RT	<div></div>	124	6.0	1.1E-24	9.2E-23
<input type="checkbox"/>	GOTERM_CC_FAT	large ribosomal subunit	RT	<div></div>	58	2.8	6.2E-24	5.0E-22
<input type="checkbox"/>	GOTERM_CC_FAT	focal adhesion	RT	<div></div>	122	5.9	9.8E-24	7.4E-22
<input type="checkbox"/>	GOTERM_CC_FAT	cell-substrate adherens junction	RT	<div></div>	122	5.9	2.3E-23	1.7E-21
<input type="checkbox"/>	GOTERM_CC_FAT	cell-substrate junction	RT	<div></div>	123	6.0	2.6E-23	1.7E-21
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular ribonucleoprotein complex	RT	<div></div>	268	13.1	6.5E-23	4.1E-21
<input type="checkbox"/>	GOTERM_CC_FAT	polysome	RT	<div></div>	42	2.0	2.1E-22	1.3E-20
<input type="checkbox"/>	GOTERM_CC_FAT	polysomal ribosome	RT	<div></div>	26	1.3	3.3E-19	1.9E-17
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic vesicle part	RT	<div></div>	297	14.5	9.8E-19	5.4E-17
<input type="checkbox"/>	GOTERM_CC_FAT	cytosolic small ribosomal subunit	RT	<div></div>	30	1.5	3.0E-17	1.6E-15
<input type="checkbox"/>	GOTERM_CC_FAT	vacuole	RT	<div></div>	178	8.7	5.1E-16	2.5E-14
<input type="checkbox"/>	GOTERM_CC_FAT	lytic vacuole	RT	<div></div>	163	7.9	5.7E-16	2.6E-14
<input type="checkbox"/>	GOTERM_CC_FAT	lysosome	RT	<div></div>	163	7.9	5.7E-16	2.6E-14
<input type="checkbox"/>	GOTERM_CC_FAT	adherens junction	RT	<div></div>	129	6.3	3.8E-15	1.7E-13
<input type="checkbox"/>	GOTERM_CC_FAT	vacuolar part	RT	<div></div>	142	6.9	6.6E-15	2.8E-13
<input type="checkbox"/>	GOTERM_CC_FAT	small ribosomal subunit	RT	<div></div>	37	1.8	1.9E-14	7.8E-13
<input type="checkbox"/>	GOTERM_CC_FAT	envelope	RT	<div></div>	236	11.5	4.6E-14	1.8E-12
<input type="checkbox"/>	GOTERM_CC_FAT	organelle envelope	RT	<div></div>	236	11.5	4.6E-14	1.8E-12
<input type="checkbox"/>	GOTERM_CC_FAT	anchoring junction	RT	<div></div>	135	6.6	8.9E-14	3.4E-12
<input type="checkbox"/>	GOTERM_CC_FAT	ficolin-1-rich granule lumen	RT	<div></div>	46	2.2	1.3E-13	4.5E-12
<input type="checkbox"/>	GOTERM_CC_FAT	ficolin-1-rich granule	RT	<div></div>	46	2.2	1.3E-13	4.5E-12
<input type="checkbox"/>	GOTERM_CC_FAT	melanosome	RT	<div></div>	43	2.1	1.6E-13	5.5E-12
<input type="checkbox"/>	GOTERM_CC_FAT	pigment granule	RT	<div></div>	43	2.1	1.6E-13	5.5E-12
<input type="checkbox"/>	GOTERM_CC_FAT	vacuolar membrane	RT	<div></div>	113	5.5	2.0E-13	6.4E-12
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear envelope	RT	<div></div>	111	5.4	3.6E-12	1.2E-10
<input type="checkbox"/>	GOTERM_CC_FAT	coated vesicle	RT	<div></div>	80	3.9	4.4E-12	1.4E-10
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum	RT	<div></div>	328	16.0	6.8E-12	2.1E-10
<input type="checkbox"/>	GOTERM_CC_FAT	lysosomal membrane	RT	<div></div>	101	4.9	1.4E-11	4.0E-10
<input type="checkbox"/>	GOTERM_CC_FAT	lytic vacuole membrane	RT	<div></div>	101	4.9	1.4E-11	4.0E-10
<input type="checkbox"/>	GOTERM_CC_FAT	coated vesicle membrane	RT	<div></div>	58	2.8	2.2E-11	6.3E-10
<input type="checkbox"/>	GOTERM_CC_FAT	secretory granule	RT	<div></div>	167	8.1	2.4E-11	6.7E-10
<input type="checkbox"/>	GOTERM_CC_FAT	spliceosomal complex	RT	<div></div>	59	2.9	3.0E-11	8.1E-10
<input type="checkbox"/>	GOTERM_CC_FAT	endosomal part	RT	<div></div>	128	6.2	4.2E-11	1.1E-9
<input type="checkbox"/>	GOTERM_CC_FAT	immunological synapse	RT	<div></div>	24	1.2	5.0E-11	1.3E-9
<input type="checkbox"/>	GOTERM_CC_FAT	endosome	RT	<div></div>	191	9.3	5.1E-11	1.3E-9
<input type="checkbox"/>	GOTERM_CC_FAT	endosome membrane	RT	<div></div>	119	5.8	5.2E-11	1.3E-9
<input type="checkbox"/>	GOTERM_CC_FAT	secretory vesicle	RT	<div></div>	189	9.2	1.3E-10	3.1E-9
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	<div></div>	149	7.3	9.2E-10	2.2E-8
<input type="checkbox"/>	GOTERM_CC_FAT	vesicle membrane	RT	<div></div>	151	7.4	1.1E-9	2.4E-8
<input type="checkbox"/>	GOTERM_CC_FAT	secretory granule lumen	RT	<div></div>	74	3.6	1.5E-9	3.4E-8
<input type="checkbox"/>	GOTERM_CC_FAT	cell junction	RT	<div></div>	173	8.4	1.7E-9	3.8E-8
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic vesicle lumen	RT	<div></div>	77	3.8	1.8E-9	3.9E-8
<input type="checkbox"/>	GOTERM_CC_FAT	vesicle lumen	RT	<div></div>	77	3.8	2.0E-9	4.4E-8
<input type="checkbox"/>	GOTERM_CC_FAT	chaperone complex	RT	<div></div>	21	1.0	2.7E-9	5.8E-8
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear outer membrane-endoplasmic reticulum membrane network	RT	<div></div>	205	10.0	2.9E-9	6.1E-8
<input type="checkbox"/>	GOTERM_CC_FAT	midbody	RT	<div></div>	53	2.6	9.6E-9	2.0E-7
<input type="checkbox"/>	GOTERM_CC_FAT	small-subunit processome	RT	<div></div>	28	1.4	9.7E-9	2.0E-7
<input type="checkbox"/>	GOTERM_CC_FAT	eukaryotic translation initiation factor 3 complex	RT	<div></div>	13	0.6	1.1E-8	2.1E-7
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum membrane	RT	<div></div>	199	9.7	1.2E-8	2.4E-7
<input type="checkbox"/>	GOTERM_CC_FAT	perinuclear region of cytoplasm	RT	<div></div>	136	6.6	1.3E-8	2.5E-7
<input type="checkbox"/>	GOTERM_CC_FAT	ER to Golgi transport vesicle membrane	RT	<div></div>	25	1.2	2.5E-8	4.8E-7
<input type="checkbox"/>	GOTERM_CC_FAT	ER to Golgi transport vesicle	RT	<div></div>	31	1.5	3.7E-8	6.8E-7
<input type="checkbox"/>	GOTERM_CC_FAT	ribonucleoprotein granule	RT	<div></div>	63	3.1	3.9E-8	7.2E-7
<input type="checkbox"/>	GOTERM_CC_FAT	phagocytic vesicle	RT	<div></div>	41	2.0	6.4E-8	1.2E-6
<input type="checkbox"/>	GOTERM_CC_FAT	lumenal side of endoplasmic reticulum membrane	RT	<div></div>	16	0.8	6.6E-8	1.2E-6
<input type="checkbox"/>	GOTERM_CC_FAT	azurophil granule	RT	<div></div>	42	2.0	6.8E-8	1.2E-6
<input type="checkbox"/>	GOTERM_CC_FAT	primary lysosome	RT	<div></div>	42	2.0	6.8E-8	1.2E-6
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrion	RT	<div></div>	262	12.8	8.1E-8	1.4E-6
<input type="checkbox"/>	GOTERM_CC_FAT	U2-type spliceosomal complex	RT	<div></div>	31	1.5	8.1E-8	1.4E-6
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic side of membrane	RT	<div></div>	52	2.5	8.3E-8	1.4E-6
<input type="checkbox"/>	GOTERM_CC_FAT	chromosomal region	RT	<div></div>	83	4.0	8.4E-8	1.4E-6
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic ribonucleoprotein granule	RT	<div></div>	59	2.9	1.2E-7	2.0E-6
<input type="checkbox"/>	GOTERM_CC_FAT	autophagosome membrane	RT	<div></div>	22	1.1	1.3E-7	2.1E-6
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum part	RT	<div></div>	231	11.3	1.5E-7	2.4E-6
<input type="checkbox"/>	GOTERM_CC_FAT	late endosome	RT	<div></div>	68	3.3	1.9E-7	2.9E-6

Sublist	Category	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT secretory granule membrane	RT	<div></div>	68	3.3	2.9E-7	4.5E-6
<input type="checkbox"/>	GOTERM_CC_FAT transport vesicle	RT	<div></div>	89	4.3	3.5E-7	5.3E-6
<input type="checkbox"/>	GOTERM_CC_FAT spindle	RT	<div></div>	85	4.1	3.7E-7	5.6E-6
<input type="checkbox"/>	GOTERM_CC_FAT catalytic step 2 spliceosome	RT	<div></div>	29	1.4	4.1E-7	6.0E-6
<input type="checkbox"/>	GOTERM_CC_FAT nucleolus	RT	<div></div>	226	11.0	7.0E-7	1.0E-5
<input type="checkbox"/>	GOTERM_CC_FAT eukaryotic 43S preinitiation complex	RT	<div></div>	12	0.6	8.8E-7	1.3E-5
<input type="checkbox"/>	GOTERM_CC_FAT phagocytic vesicle membrane	RT	<div></div>	27	1.3	1.2E-6	1.7E-5
<input type="checkbox"/>	GOTERM_CC_FAT RNA polymerase II transcription factor complex	RT	<div></div>	53	2.6	1.2E-6	1.7E-5
<input type="checkbox"/>	GOTERM_CC_FAT translation preinitiation complex	RT	<div></div>	12	0.6	1.8E-6	2.5E-5
<input type="checkbox"/>	GOTERM_CC_FAT centrosome	RT	<div></div>	131	6.4	2.3E-6	3.2E-5
<input type="checkbox"/>	GOTERM_CC_FAT rough endoplasmic reticulum	RT	<div></div>	21	1.0	2.4E-6	3.2E-5
<input type="checkbox"/>	GOTERM_CC_FAT preribosome	RT	<div></div>	31	1.5	2.5E-6	3.3E-5
<input type="checkbox"/>	GOTERM_CC_FAT tertiary granule	RT	<div></div>	40	1.9	2.6E-6	3.4E-5
<input type="checkbox"/>	GOTERM_CC_FAT peptidase complex	RT	<div></div>	32	1.6	2.6E-6	3.5E-5
<input type="checkbox"/>	GOTERM_CC_FAT microtubule cytoskeleton	RT	<div></div>	214	10.4	2.7E-6	3.6E-5
<input type="checkbox"/>	GOTERM_CC_FAT recycling endosome membrane	RT	<div></div>	31	1.5	3.7E-6	4.7E-5
<input type="checkbox"/>	GOTERM_CC_FAT nuclear transcription factor complex	RT	<div></div>	55	2.7	3.8E-6	4.9E-5
<input type="checkbox"/>	GOTERM_CC_FAT late endosome membrane	RT	<div></div>	42	2.0	3.9E-6	5.0E-5
<input type="checkbox"/>	GOTERM_CC_FAT clathrin-coated vesicle	RT	<div></div>	49	2.4	4.4E-6	5.5E-5
<input type="checkbox"/>	GOTERM_CC_FAT autophagosome	RT	<div></div>	32	1.6	4.7E-6	5.7E-5
<input type="checkbox"/>	GOTERM_CC_FAT eukaryotic 48S preinitiation complex	RT	<div></div>	11	0.5	4.7E-6	5.7E-5
<input type="checkbox"/>	GOTERM_CC_FAT protein serine/threonine phosphatase complex	RT	<div></div>	19	0.9	7.3E-6	8.8E-5
<input type="checkbox"/>	GOTERM_CC_FAT mitochondrial part	RT	<div></div>	177	8.6	9.2E-6	1.1E-4
<input type="checkbox"/>	GOTERM_CC_FAT MHC protein complex	RT	<div></div>	14	0.7	9.8E-6	1.2E-4
<input type="checkbox"/>	GOTERM_CC_FAT cytoplasmic side of plasma membrane	RT	<div></div>	40	1.9	1.2E-5	1.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT transcription factor complex	RT	<div></div>	79	3.8	1.3E-5	1.5E-4
<input type="checkbox"/>	GOTERM_CC_FAT phosphatase complex	RT	<div></div>	19	0.9	1.3E-5	1.5E-4
<input type="checkbox"/>	GOTERM_CC_FAT microtubule organizing center	RT	<div></div>	140	6.8	1.3E-5	1.5E-4
<input type="checkbox"/>	GOTERM_CC_FAT clathrin-coated vesicle membrane	RT	<div></div>	34	1.7	1.3E-5	1.5E-4
<input type="checkbox"/>	GOTERM_CC_FAT nuclear membrane	RT	<div></div>	62	3.0	1.5E-5	1.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT extracellular region part	RT	<div></div>	498	24.3	2.0E-5	2.2E-4
<input type="checkbox"/>	GOTERM_CC_FAT ubiquitin ligase complex	RT	<div></div>	61	3.0	2.5E-5	2.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT chromosome	RT	<div></div>	271	13.2	2.9E-5	3.2E-4
<input type="checkbox"/>	GOTERM_CC_FAT endocytic vesicle membrane	RT	<div></div>	44	2.1	3.4E-5	3.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT endoplasmic reticulum-Golgi intermediate compartment	RT	<div></div>	33	1.6	3.5E-5	3.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT endocytic vesicle	RT	<div></div>	66	3.2	3.5E-5	3.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT azurophil granule membrane	RT	<div></div>	19	0.9	3.8E-5	4.0E-4
<input type="checkbox"/>	GOTERM_CC_FAT PML body	RT	<div></div>	28	1.4	4.3E-5	4.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT MHC class II protein complex	RT	<div></div>	12	0.6	4.3E-5	4.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT rough endoplasmic reticulum membrane	RT	<div></div>	12	0.6	4.3E-5	4.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT Golgi apparatus	RT	<div></div>	235	11.5	4.5E-5	4.5E-4
<input type="checkbox"/>	GOTERM_CC_FAT mitochondrial protein complex	RT	<div></div>	41	2.0	4.7E-5	4.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT mitochondrial envelope	RT	<div></div>	132	6.4	4.7E-5	4.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT nuclear pore	RT	<div></div>	27	1.3	5.9E-5	5.9E-4
<input type="checkbox"/>	GOTERM_CC_FAT Golgi membrane	RT	<div></div>	121	5.9	6.7E-5	6.6E-4
<input type="checkbox"/>	GOTERM_CC_FAT proteasome complex	RT	<div></div>	20	1.0	7.2E-5	7.0E-4
<input type="checkbox"/>	GOTERM_CC_FAT chromosome, centromeric region	RT	<div></div>	51	2.5	7.3E-5	7.0E-4
<input type="checkbox"/>	GOTERM_CC_FAT cytoplasmic stress granule	RT	<div></div>	25	1.2	9.7E-5	9.3E-4
<input type="checkbox"/>	GOTERM_CC_FAT side of membrane	RT	<div></div>	118	5.8	1.0E-4	9.5E-4
<input type="checkbox"/>	GOTERM_CC_FAT specific granule	RT	<div></div>	35	1.7	1.3E-4	1.2E-3
<input type="checkbox"/>	GOTERM_CC_FAT ESCRT complex	RT	<div></div>	12	0.6	1.4E-4	1.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT Flemming body	RT	<div></div>	13	0.6	1.6E-4	1.5E-3
<input type="checkbox"/>	GOTERM_CC_FAT respiratory chain complex	RT	<div></div>	24	1.2	1.9E-4	1.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT U2-type catalytic step 2 spliceosome	RT	<div></div>	12	0.6	2.0E-4	1.9E-3
<input type="checkbox"/>	GOTERM_CC_FAT chromosome, telomeric region	RT	<div></div>	36	1.8	2.5E-4	2.2E-3
<input type="checkbox"/>	GOTERM_CC_FAT transport vesicle membrane	RT	<div></div>	46	2.2	2.7E-4	2.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT transferase complex, transferring phosphorus-containing groups	RT	<div></div>	61	3.0	2.7E-4	2.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT eukaryotic translation initiation factor 3 complex, eIF3m	RT	<div></div>	6	0.3	2.7E-4	2.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT mitochondrial respiratory chain	RT	<div></div>	24	1.2	3.1E-4	2.7E-3
<input type="checkbox"/>	GOTERM_CC_FAT Golgi apparatus part	RT	<div></div>	150	7.3	3.6E-4	3.2E-3
<input type="checkbox"/>	GOTERM_CC_FAT oxidoreductase complex	RT	<div></div>	30	1.5	3.7E-4	3.2E-3
<input type="checkbox"/>	GOTERM_CC_FAT inner mitochondrial membrane protein complex	RT	<div></div>	33	1.6	3.9E-4	3.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT respiratory chain	RT	<div></div>	25	1.2	4.1E-4	3.5E-3
<input type="checkbox"/>	GOTERM_CC_FAT P-body	RT	<div></div>	24	1.2	4.2E-4	3.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT mitochondrial membrane	RT	<div></div>	120	5.8	4.3E-4	3.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT vacuolar lumen	RT	<div></div>	36	1.8	4.3E-4	3.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT endopeptidase complex	RT	<div></div>	21	1.0	4.4E-4	3.7E-3
<input type="checkbox"/>	GOTERM_CC_FAT chromosomal part	RT	<div></div>	240	11.7	4.8E-4	4.0E-3
<input type="checkbox"/>	GOTERM_CC_FAT Prp19 complex	RT	<div></div>	8	0.4	5.5E-4	4.5E-3
<input type="checkbox"/>	GOTERM_CC_FAT inclusion body	RT	<div></div>	19	0.9	6.1E-4	5.0E-3
<input type="checkbox"/>	GOTERM_CC_FAT transcription factor AP-1 complex	RT	<div></div>	5	0.2	6.6E-4	5.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT nuclear periphery	RT	<div></div>	32	1.6	6.7E-4	5.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT F-actin capping protein complex	RT	<div></div>	6	0.3	6.7E-4	5.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT azurophil granule lumen	RT	<div></div>	22	1.1	7.1E-4	5.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT specific granule membrane	RT	<div></div>	22	1.1	7.1E-4	5.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT ruffle	RT	<div></div>	36	1.8	7.4E-4	5.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT organelle subcompartment	RT	<div></div>	69	3.4	7.8E-4	6.1E-3
<input type="checkbox"/>	GOTERM_CC_FAT serine/threonine protein kinase complex	RT	<div></div>	26	1.3	7.9E-4	6.1E-3
<input type="checkbox"/>	GOTERM_CC_FAT mitotic spindle	RT	<div></div>	37	1.8	8.2E-4	6.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT CCR4-NOT complex	RT	<div></div>	8	0.4	8.8E-4	6.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT membrane coat	RT	<div></div>	23	1.1	1.1E-3	8.0E-3
<input type="checkbox"/>	GOTERM_CC_FAT coated membrane	RT	<div></div>	23	1.1	1.1E-3	8.0E-3
<input type="checkbox"/>	GOTERM_CC_FAT clathrin-coated endocytic vesicle	RT	<div></div>	22	1.1	1.1E-3	8.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT retromer complex	RT	<div></div>	9	0.4	1.1E-3	8.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT vesicle coat	RT	<div></div>	17	0.8	1.2E-3	8.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT clathrin-coated endocytic vesicle membrane	RT	<div></div>	19	0.9	1.2E-3	8.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT recycling endosome	RT	<div></div>	40	1.9	1.2E-3	8.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT nuclear chromosome	RT	<div></div>	46	2.2	1.2E-3	8.9E-3
<input type="checkbox"/>	GOTERM_CC_FAT precatalytic spliceosome	RT	<div></div>	15	0.7	1.3E-3	9.7E-3
<input type="checkbox"/>	GOTERM_CC_FAT MHC class I protein complex	RT	<div></div>	6	0.3	1.4E-3	9.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT endoplasmic reticulum-Golgi intermediate compartment membrane	RT	<div></div>	20	1.0	1.4E-3	9.8E-3
<input type="checkbox"/>	GOTERM_CC_FAT multivesicular body	RT	<div></div>	18	0.9	1.4E-3	1.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT cytoplasmic region	RT	<div></div>	64	3.1	1.5E-3	1.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT small nuclear ribonucleoprotein complex	RT	<div></div>	23	1.1	1.6E-3	1.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT mitochondrial membrane part	RT	<div></div>	38	1.9	1.6E-3	1.1E-2

Sublist	Category		RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	cyclin-dependent protein kinase holoenzyme complex	RT	<div></div>	16	0.8	1.7E-3	1.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	CRD-mediated mRNA stability complex	RT	<div></div>	5	0.2	1.8E-3	1.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial nucleoid	RT	<div></div>	14	0.7	1.9E-3	1.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nucleoid	RT	<div></div>	14	0.7	1.9E-3	1.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	protein acetyltransferase complex	RT	<div></div>	22	1.1	1.9E-3	1.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	tertiary granule membrane	RT	<div></div>	18	0.9	2.0E-3	1.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	ficolin-1-rich granule membrane	RT	<div></div>	16	0.8	2.0E-3	1.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	organelle inner membrane	RT	<div></div>	87	4.2	2.1E-3	1.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	kinetochore	RT	<div></div>	33	1.6	2.1E-3	1.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	synapse	RT	<div></div>	199	9.7	2.2E-3	1.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	acetyltransferase complex	RT	<div></div>	22	1.1	2.2E-3	1.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	oligosaccharyltransferase complex	RT	<div></div>	7	0.3	2.4E-3	1.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	amphisome membrane	RT	<div></div>	7	0.3	2.4E-3	1.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	histone acetyltransferase complex	RT	<div></div>	20	1.0	2.5E-3	1.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	protein kinase complex	RT	<div></div>	28	1.4	2.8E-3	1.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	heterochromatin	RT	<div></div>	20	1.0	2.8E-3	1.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear matrix	RT	<div></div>	26	1.3	3.3E-3	2.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	transcription elongation factor complex	RT	<div></div>	14	0.7	3.4E-3	2.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear inner membrane	RT	<div></div>	15	0.7	3.4E-3	2.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nucleolar part	RT	<div></div>	37	1.8	3.8E-3	2.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT	<div></div>	10	0.5	3.8E-3	2.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	PTW/PP1 phosphatase complex	RT	<div></div>	5	0.2	3.8E-3	2.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	axon cytoplasm	RT	<div></div>	16	0.8	3.9E-3	2.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	spliceosomal snRNP complex	RT	<div></div>	21	1.0	3.9E-3	2.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	proteasome accessory complex	RT	<div></div>	9	0.4	4.0E-3	2.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	fibrillar center	RT	<div></div>	29	1.4	4.1E-3	2.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cytolytic granule	RT	<div></div>	6	0.3	4.1E-3	2.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	ESCRT III complex	RT	<div></div>	6	0.3	4.1E-3	2.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cell projection cytoplasm	RT	<div></div>	20	1.0	4.2E-3	2.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	multivesicular body membrane	RT	<div></div>	10	0.5	4.8E-3	2.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	early endosome	RT	<div></div>	68	3.3	4.8E-3	2.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cytolytic granule membrane	RT	<div></div>	4	0.2	4.8E-3	2.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	ASAP complex	RT	<div></div>	4	0.2	4.8E-3	2.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial matrix	RT	<div></div>	76	3.7	4.9E-3	2.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	lysosomal lumen	RT	<div></div>	21	1.0	5.6E-3	3.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	membrane region	RT	<div></div>	60	2.9	6.2E-3	3.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	U2-type precatalytic spliceosome	RT	<div></div>	13	0.6	6.7E-3	3.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	vacuolar proton-transporting V-type ATPase complex	RT	<div></div>	9	0.4	6.8E-3	3.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	spindle pole	RT	<div></div>	32	1.6	6.8E-3	3.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear chromatin	RT	<div></div>	16	0.8	7.0E-3	4.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	ubiquitin conjugating enzyme complex	RT	<div></div>	5	0.2	7.0E-3	4.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	proteasome regulatory particle	RT	<div></div>	8	0.4	7.3E-3	4.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	Golgi subcompartment	RT	<div></div>	60	2.9	7.4E-3	4.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum subcompartment	RT	<div></div>	10	0.5	7.6E-3	4.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	Golgi-associated vesicle	RT	<div></div>	20	1.0	8.5E-3	4.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum tubular network	RT	<div></div>	9	0.4	8.6E-3	4.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	NADH dehydrogenase complex	RT	<div></div>	13	0.6	9.3E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial respiratory chain complex I	RT	<div></div>	13	0.6	9.3E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	respiratory chain complex I	RT	<div></div>	13	0.6	9.3E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	kinetochore microtubule	RT	<div></div>	8	0.4	9.5E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear chromosome, telomeric region	RT	<div></div>	6	0.3	9.6E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear telomere cap complex	RT	<div></div>	6	0.3	9.6E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	alpha-beta T cell receptor complex	RT	<div></div>	6	0.3	9.6E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	telomere cap complex	RT	<div></div>	6	0.3	9.6E-3	5.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	secondary lysosome	RT	<div></div>	7	0.3	1.0E-2	5.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	trans-Golgi network	RT	<div></div>	43	2.1	1.0E-2	5.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	DNA-directed RNA polymerase II, holoenzyme	RT	<div></div>	25	1.2	1.1E-2	5.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cortical cytoskeleton	RT	<div></div>	21	1.0	1.1E-2	5.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	NF-kappaB complex	RT	<div></div>	4	0.2	1.1E-2	5.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic side of rough endoplasmic reticulum membrane	RT	<div></div>	4	0.2	1.1E-2	5.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	ISWI-type complex	RT	<div></div>	6	0.3	1.4E-2	7.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	Cul4A-RING E3 ubiquitin ligase complex	RT	<div></div>	6	0.3	1.4E-2	7.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	organelle envelope lumen	RT	<div></div>	19	0.9	1.4E-2	7.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	early endosome membrane	RT	<div></div>	34	1.7	1.5E-2	7.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	COPI-coated vesicle	RT	<div></div>	8	0.4	1.5E-2	7.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	PcG protein complex	RT	<div></div>	12	0.6	1.5E-2	7.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	COP9 signalosome	RT	<div></div>	10	0.5	1.6E-2	8.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	tertiary granule lumen	RT	<div></div>	13	0.6	1.7E-2	8.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	MHC class I peptide loading complex	RT	<div></div>	5	0.2	1.8E-2	8.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	core mediator complex	RT	<div></div>	8	0.4	1.9E-2	9.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	outer membrane	RT	<div></div>	41	2.0	1.9E-2	9.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	sex chromosome	RT	<div></div>	9	0.4	2.0E-2	9.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	signal peptidase complex	RT	<div></div>	4	0.2	2.0E-2	1.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	protein phosphatase 4 complex	RT	<div></div>	4	0.2	2.0E-2	1.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	methyltransferase complex	RT	<div></div>	20	1.0	2.1E-2	1.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial intermembrane space	RT	<div></div>	17	0.8	2.1E-2	1.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	pre-autophagosomal structure	RT	<div></div>	10	0.5	2.3E-2	1.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	membrane microdomain	RT	<div></div>	46	2.2	2.3E-2	1.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell leading edge	RT	<div></div>	62	3.0	2.3E-2	1.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	histone deacetylase complex	RT	<div></div>	15	0.7	2.3E-2	1.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum quality control compartment	RT	<div></div>	6	0.3	2.5E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear chromosome part	RT	<div></div>	32	1.6	2.5E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	chaperonin-containing T-complex	RT	<div></div>	5	0.2	2.5E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum chaperone complex	RT	<div></div>	5	0.2	2.5E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	autolysosome	RT	<div></div>	5	0.2	2.5E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	NSL complex	RT	<div></div>	5	0.2	2.5E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	GTPase activator complex	RT	<div></div>	5	0.2	2.5E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	histone methyltransferase complex	RT	<div></div>	15	0.7	2.6E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endosome lumen	RT	<div></div>	10	0.5	2.7E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	trans-Golgi network transport vesicle	RT	<div></div>	10	0.5	2.7E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	organelle outer membrane	RT	<div></div>	40	1.9	2.7E-2	1.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Sin3-type complex	RT	<div></div>	7	0.3	2.8E-2	1.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endoribonuclease complex	RT	<div></div>	9	0.4	2.8E-2	1.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear transcriptional repressor complex	RT	<div></div>	11	0.5	2.9E-2	1.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell cortex part	RT	<div></div>	28	1.4	2.9E-2	1.3E-1

Sublist	Category		RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	trans-Golgi network membrane	RT	<div></div>	20	1.0	3.0E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear cyclin-dependent protein kinase holoenzyme complex	RT	<div></div>	6	0.3	3.2E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial inner membrane	RT	<div></div>	72	3.5	3.2E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	membrane raft	RT	<div></div>	45	2.2	3.2E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	integral component of endoplasmic reticulum membrane	RT	<div></div>	9	0.4	3.3E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	intrinsic component of endoplasmic reticulum membrane	RT	<div></div>	9	0.4	3.3E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	aggresome	RT	<div></div>	9	0.4	3.3E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	pre-snoRNP complex	RT	<div></div>	4	0.2	3.3E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	shelterin complex	RT	<div></div>	4	0.2	3.3E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial permeability transition pore complex	RT	<div></div>	4	0.2	3.3E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Lewy body core	RT	<div></div>	3	0.1	3.3E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell cortex	RT	<div></div>	46	2.2	3.4E-2	1.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear inclusion body	RT	<div></div>	5	0.2	3.5E-2	1.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	proton-transporting V-type ATPase, V0 domain	RT	<div></div>	5	0.2	3.5E-2	1.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	euchromatin	RT	<div></div>	13	0.6	3.5E-2	1.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	centriolar satellite	RT	<div></div>	22	1.1	3.6E-2	1.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	SWI/SNF superfamily-type complex	RT	<div></div>	17	0.8	3.8E-2	1.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear DNA-directed RNA polymerase complex	RT	<div></div>	26	1.3	3.8E-2	1.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic side of endoplasmic reticulum membrane	RT	<div></div>	6	0.3	4.0E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	COPI-coated vesicle membrane	RT	<div></div>	6	0.3	4.0E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	spindle microtubule	RT	<div></div>	16	0.8	4.3E-2	1.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	transcriptional repressor complex	RT	<div></div>	19	0.9	4.3E-2	1.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex	RT	<div></div>	12	0.6	4.3E-2	1.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	site of double-strand break	RT	<div></div>	17	0.8	4.5E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	DNA replication factor A complex	RT	<div></div>	5	0.2	4.6E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	chromatin silencing complex	RT	<div></div>	5	0.2	4.6E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	eukaryotic translation initiation factor 4F complex	RT	<div></div>	5	0.2	4.6E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial outer membrane	RT	<div></div>	35	1.7	4.6E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	pericentric heterochromatin	RT	<div></div>	8	0.4	4.7E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	proteasome regulatory particle, lid subcomplex	RT	<div></div>	4	0.2	4.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	postsynaptic recycling endosome	RT	<div></div>	4	0.2	4.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	zona pellucida receptor complex	RT	<div></div>	4	0.2	4.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Lewy body	RT	<div></div>	4	0.2	4.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cyclin/CDK positive transcription elongation factor complex	RT	<div></div>	4	0.2	4.8E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Golgi-associated vesicle membrane	RT	<div></div>	12	0.6	4.9E-2	1.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	clathrin coat of coated pit	RT	<div></div>	6	0.3	5.0E-2	2.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Cajal body	RT	<div></div>	16	0.8	5.1E-2	2.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Cul4-RING E3 ubiquitin ligase complex	RT	<div></div>	9	0.4	5.1E-2	2.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endonuclease complex	RT	<div></div>	9	0.4	5.1E-2	2.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	DNA-directed RNA polymerase complex	RT	<div></div>	26	1.3	5.3E-2	2.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	H4 histone acetyltransferase complex	RT	<div></div>	10	0.5	5.3E-2	2.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cortical actin cytoskeleton	RT	<div></div>	14	0.7	5.3E-2	2.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	smooth endoplasmic reticulum	RT	<div></div>	8	0.4	5.5E-2	2.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endoplasmic reticulum exit site	RT	<div></div>	8	0.4	5.5E-2	2.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mediator complex	RT	<div></div>	9	0.4	5.8E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitotic spindle pole	RT	<div></div>	9	0.4	5.8E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	chromatin	RT	<div></div>	167	8.1	5.8E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic side of lysosomal membrane	RT	<div></div>	5	0.2	5.9E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	uropod	RT	<div></div>	5	0.2	5.9E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cullin-RING ubiquitin ligase complex	RT	<div></div>	29	1.4	6.1E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	NELF complex	RT	<div></div>	3	0.1	6.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	retromer, cargo-selective complex	RT	<div></div>	3	0.1	6.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	ATF4-CREB1 transcription factor complex	RT	<div></div>	3	0.1	6.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	HULC complex	RT	<div></div>	3	0.1	6.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	SPOTS complex	RT	<div></div>	3	0.1	6.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	eukaryotic translation elongation factor 1 complex	RT	<div></div>	3	0.1	6.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	I-kappaB/NF-kappaB complex	RT	<div></div>	3	0.1	6.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	retromer, tubulation complex	RT	<div></div>	3	0.1	6.2E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	RNA polymerase complex	RT	<div></div>	26	1.3	6.3E-2	2.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	death-inducing signaling complex	RT	<div></div>	4	0.2	6.7E-2	2.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Sin3 complex	RT	<div></div>	6	0.3	7.2E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	exon-exon junction complex	RT	<div></div>	6	0.3	7.2E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell trailing edge	RT	<div></div>	5	0.2	7.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mitochondrial respiratory chain complex III	RT	<div></div>	5	0.2	7.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	respiratory chain complex III	RT	<div></div>	5	0.2	7.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	U2 snRNP	RT	<div></div>	7	0.3	7.9E-2	2.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	specific granule lumen	RT	<div></div>	12	0.6	8.0E-2	2.9E-1
<input type="checkbox"/>	GOTERM_CC_FAT	clathrin vesicle coat	RT	<div></div>	8	0.4	8.2E-2	3.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	perinuclear endoplasmic reticulum	RT	<div></div>	6	0.3	8.6E-2	3.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	vacuolar proton-transporting V-type ATPase, V0 domain	RT	<div></div>	4	0.2	8.8E-2	3.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Lst4-Lst7 complex	RT	<div></div>	4	0.2	8.8E-2	3.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	site of DNA damage	RT	<div></div>	20	1.0	8.9E-2	3.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	COPII vesicle coat	RT	<div></div>	5	0.2	9.0E-2	3.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	mRNA cleavage factor complex	RT	<div></div>	7	0.3	9.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	proton-transporting two-sector ATPase complex, proton-transporting domain	RT	<div></div>	7	0.3	9.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endolysosome	RT	<div></div>	7	0.3	9.1E-2	3.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	SNARE complex	RT	<div></div>	10	0.5	9.2E-2	3.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytochrome complex	RT	<div></div>	9	0.4	9.3E-2	3.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	DNA-dependent protein kinase complex	RT	<div></div>	3	0.1	9.6E-2	3.3E-1
<input type="checkbox"/>	GOTERM_CC_FAT	exocytic vesicle	RT	<div></div>	34	1.7	9.8E-2	3.4E-1

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

Please [cite DAVID](#) within any publication that makes use of any methods inspired by **DAVID**.