



Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

417 DAVID IDs

Options

Rerun Using Options

Create Sublist

141 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_CC_FAT	cytosol	RT		153	36.7	4.3E-56	1.8E-53
<input type="checkbox"/>	GOTERM_CC_FAT	nucleoplasm	RT		122	29.3	1.0E-51	2.2E-49
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear lumen	RT		143	34.3	1.7E-43	2.5E-41
<input type="checkbox"/>	GOTERM_CC_FAT	organelle lumen	RT		151	36.2	4.0E-37	4.3E-35
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular organelle lumen	RT		149	35.7	5.3E-37	4.5E-35
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-enclosed lumen	RT		151	36.2	4.2E-36	3.0E-34
<input type="checkbox"/>	GOTERM_CC_FAT	nucleoplasm part	RT		75	18.0	8.5E-30	5.2E-28
<input type="checkbox"/>	GOTERM_CC_FAT	transcription factor complex	RT		35	8.4	1.3E-16	5.9E-15
<input type="checkbox"/>	GOTERM_CC_FAT	chromosomal part	RT		44	10.6	1.6E-14	7.7E-13
<input type="checkbox"/>	GOTERM_CC_FAT	non-membrane-bounded organelle	RT		137	32.9	4.1E-14	1.8E-12
<input type="checkbox"/>	GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT		137	32.9	4.1E-14	1.8E-12
<input type="checkbox"/>	GOTERM_CC_FAT	chromosome	RT		46	11.0	4.3E-13	1.7E-11
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear envelope	RT		25	6.0	4.9E-9	1.7E-7
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear chromosome part	RT		18	4.3	7.0E-8	2.3E-6
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear body	RT		21	5.0	7.3E-8	2.2E-6
<input type="checkbox"/>	GOTERM_CC_FAT	transcriptional repressor complex	RT		11	2.6	1.7E-7	4.9E-6
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear chromosome	RT		20	4.8	2.0E-7	5.2E-6
<input type="checkbox"/>	GOTERM_CC_FAT	melanosome	RT		15	3.6	2.2E-7	5.5E-6
<input type="checkbox"/>	GOTERM_CC_FAT	pigment granule	RT		15	3.6	2.2E-7	5.5E-6
<input type="checkbox"/>	GOTERM_CC_FAT	ubiquitin ligase complex	RT		15	3.6	2.5E-7	6.0E-6
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear pore	RT		14	3.4	3.5E-7	7.8E-6
<input type="checkbox"/>	GOTERM_CC_FAT	adherens junction	RT		19	4.6	4.8E-7	1.0E-5
<input type="checkbox"/>	GOTERM_CC_FAT	chromatin remodeling complex	RT		13	3.1	7.3E-7	1.5E-5
<input type="checkbox"/>	GOTERM_CC_FAT	chromosome, telomeric region	RT		9	2.2	1.1E-6	2.1E-5
<input type="checkbox"/>	GOTERM_CC_FAT	histone acetyltransferase complex	RT		11	2.6	1.2E-6	2.3E-5
<input type="checkbox"/>	GOTERM_CC_FAT	kinetochore	RT		13	3.1	1.8E-6	3.2E-5
<input type="checkbox"/>	GOTERM_CC_FAT	anchoring junction	RT		19	4.6	2.2E-6	3.8E-5
<input type="checkbox"/>	GOTERM_CC_FAT	cytoskeleton	RT		70	16.8	2.7E-6	4.5E-5
<input type="checkbox"/>	GOTERM_CC_FAT	pore complex	RT		14	3.4	3.0E-6	4.8E-5
<input type="checkbox"/>	GOTERM_CC_FAT	DNA-directed RNA polymerase II, holoenzyme	RT		13	3.1	3.1E-6	4.8E-5
<input type="checkbox"/>	GOTERM_CC_FAT	spliceosome	RT		16	3.8	5.7E-6	8.4E-5
<input type="checkbox"/>	GOTERM_CC_FAT	basolateral plasma membrane	RT		20	4.8	6.1E-6	8.7E-5
<input type="checkbox"/>	GOTERM_CC_FAT	focal adhesion	RT		14	3.4	6.8E-6	9.3E-5
<input type="checkbox"/>	GOTERM_CC_FAT	cyclin-dependent protein kinase holoenzyme complex	RT		6	1.4	7.6E-6	1.0E-4
<input type="checkbox"/>	GOTERM_CC_FAT	cell-substrate adherens junction	RT		14	3.4	1.0E-5	1.3E-4
<input type="checkbox"/>	GOTERM_CC_FAT	spindle microtubule	RT		8	1.9	1.4E-5	1.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT	chromatin	RT		19	4.6	1.8E-5	2.2E-4
<input type="checkbox"/>	GOTERM_CC_FAT	cell-substrate junction	RT		14	3.4	1.9E-5	2.3E-4
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear chromosome, telomeric region	RT		7	1.7	2.0E-5	2.3E-4
<input type="checkbox"/>	GOTERM_CC_FAT	spindle	RT		16	3.8	2.1E-5	2.4E-4
<input type="checkbox"/>	GOTERM_CC_FAT	nucleolus	RT		41	9.8	2.3E-5	2.5E-4

<input type="checkbox"/>	GOTERM_CC_FAT	transcription factor TFIID complex	RT 	7	1.7	2.7E-5	2.9E-4
<input type="checkbox"/>	GOTERM_CC_FAT	chromosome, centromeric region	RT 	14	3.4	5.6E-5	5.9E-4
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear telomere cap complex	RT 	5	1.2	7.5E-5	7.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT	eukaryotic translation initiation factor 4F complex	RT 	5	1.2	7.5E-5	7.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT	telomere cap complex	RT 	5	1.2	7.5E-5	7.7E-4
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic vesicle	RT 	37	8.9	9.3E-5	9.3E-4
<input type="checkbox"/>	GOTERM_CC_FAT	vesicle	RT 	38	9.1	1.0E-4	9.8E-4
<input type="checkbox"/>	GOTERM_CC_FAT	Nup107-160 complex	RT 	5	1.2	1.2E-4	1.2E-3
<input type="checkbox"/>	GOTERM_CC_FAT	cell leading edge	RT 	14	3.4	1.7E-4	1.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT	membrane-bounded vesicle	RT 	33	7.9	2.1E-4	1.9E-3
<input type="checkbox"/>	GOTERM_CC_FAT	microtubule cytoskeleton	RT 	32	7.7	2.6E-4	2.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT	methyltransferase complex	RT 	6	1.4	2.6E-4	2.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT	histone methyltransferase complex	RT 	6	1.4	2.6E-4	2.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	RT 	32	7.7	2.7E-4	2.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT	endomembrane system	RT 	41	9.8	2.7E-4	2.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT	phosphoinositide 3-kinase complex	RT 	5	1.2	2.8E-4	2.3E-3
<input type="checkbox"/>	GOTERM_CC_FAT	SAGA-type complex	RT 	6	1.4	4.2E-4	3.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT	ribonucleoprotein complex	RT 	30	7.2	4.2E-4	3.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT	PCAF complex	RT 	4	1.0	4.4E-4	3.4E-3
<input type="checkbox"/>	GOTERM_CC_FAT	transcription factor TIFC complex	RT 	5	1.2	5.3E-4	4.1E-3
<input type="checkbox"/>	GOTERM_CC_FAT	centrosome	RT 	17	4.1	7.5E-4	5.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear chromatin	RT 	8	1.9	9.4E-4	6.9E-3
<input type="checkbox"/>	GOTERM_CC_FAT	histone deacetylase complex	RT 	7	1.7	1.0E-3	7.5E-3
<input type="checkbox"/>	GOTERM_CC_FAT	condensed chromosome	RT 	12	2.9	1.2E-3	8.6E-3
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic microtubule	RT 	5	1.2	1.5E-3	1.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	PML body	RT 	6	1.4	2.3E-3	1.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	PcG protein complex	RT 	4	1.0	2.4E-3	1.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	contractile fiber	RT 	11	2.6	2.5E-3	1.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	microtubule organizing center	RT 	17	4.1	2.7E-3	1.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	membrane raft	RT 	12	2.9	2.8E-3	1.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear speck	RT 	10	2.4	2.8E-3	1.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cell-cell adherens junction	RT 	6	1.4	3.0E-3	1.9E-2
<input type="checkbox"/>	GOTERM_CC_FAT	organelle envelope	RT 	31	7.4	3.6E-3	2.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	envelope	RT 	31	7.4	3.8E-3	2.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	lamellipodium	RT 	8	1.9	3.9E-3	2.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	perinuclear region of cytoplasm	RT 	18	4.3	4.0E-3	2.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	STAGA complex	RT 	4	1.0	4.3E-3	2.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	small nuclear ribonucleoprotein complex	RT 	5	1.2	4.5E-3	2.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	beta-catenin destruction complex	RT 	3	0.7	4.7E-3	2.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	I-kappaB/NF-kappaB complex	RT 	3	0.7	4.7E-3	2.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	lateral plasma membrane	RT 	4	1.0	6.8E-3	3.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	death-inducing signaling complex	RT 	3	0.7	7.8E-3	4.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cullin-RING ubiquitin ligase complex	RT 	4	1.0	8.3E-3	4.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	soluble fraction	RT 	18	4.3	9.0E-3	4.8E-2
<input type="checkbox"/>	GOTERM_CC_FAT	internal side of plasma membrane	RT 	18	4.3	9.9E-3	5.2E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cell projection	RT 	32	7.7	1.0E-2	5.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	protein-DNA complex	RT 	8	1.9	1.2E-2	6.0E-2
<input type="checkbox"/>	GOTERM_CC_FAT	Cajal body	RT 	5	1.2	1.3E-2	6.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	microtubule	RT 	16	3.8	1.3E-2	6.4E-2
<input type="checkbox"/>	GOTERM_CC_FAT	myofibril	RT	9	2.2	1.5E-2	7.1E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cytoplasmic ubiquitin ligase complex	RT	3	0.7	1.6E-2	7.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	contractile fiber part	RT	9	2.2	1.6E-2	7.7E-2
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear membrane	RT	7	1.7	1.8E-2	8.6E-2
<input type="checkbox"/>	GOTERM_CC_FAT	cell fraction	RT	44	10.6	1.8E-2	8.5E-2

<input type="checkbox"/>	GOTERM_CC_FAT	receptor complex	RT	9	2.2	1.9E-2	8.5E-2
<input type="checkbox"/>	GOTERM_CC_FAT	MLL5-L complex	RT	3	0.7	2.1E-2	9.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	Sin3-type complex	RT	3	0.7	2.1E-2	9.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	Sin3 complex	RT	3	0.7	2.1E-2	9.3E-2
<input type="checkbox"/>	GOTERM_CC_FAT	sarcomere	RT	8	1.9	2.3E-2	1.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell soma	RT	11	2.6	2.3E-2	1.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	condensed chromosome kinetochore	RT	6	1.4	2.5E-2	1.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	fascia adherens	RT	3	0.7	3.2E-2	1.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	secretory granule	RT	11	2.6	3.5E-2	1.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytoskeletal part	RT	38	9.1	3.6E-2	1.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endosome	RT	16	3.8	3.9E-2	1.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	condensed chromosome, centromeric region	RT	6	1.4	4.1E-2	1.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Z disc	RT	5	1.2	4.2E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	ruffle	RT	6	1.4	4.3E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell junction	RT	23	5.5	4.3E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	pericentriolar material	RT	3	0.7	4.5E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	plasma membrane part	RT	77	18.5	4.5E-2	1.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	NuRD complex	RT	3	0.7	5.2E-2	2.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	pronucleus	RT	3	0.7	5.2E-2	2.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	beta-catenin-TCF7L2 complex	RT	2	0.5	5.7E-2	2.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cortical microtubule cytoskeleton	RT	2	0.5	5.7E-2	2.1E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell cortex	RT	9	2.2	6.0E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear replisome	RT	3	0.7	6.0E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	NuA4 histone acetyltransferase complex	RT	3	0.7	6.0E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	replisome	RT	3	0.7	6.0E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	caveola	RT	5	1.2	6.2E-2	2.2E-1
<input type="checkbox"/>	GOTERM_CC_FAT	H4/H2A histone acetyltransferase complex	RT	3	0.7	6.7E-2	2.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear replication fork	RT	3	0.7	6.7E-2	2.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	intercalated disc	RT	3	0.7	6.7E-2	2.4E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cytosolic part	RT	9	2.2	7.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	I band	RT	5	1.2	7.3E-2	2.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	spindle pole	RT	4	1.0	7.3E-2	2.5E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear matrix	RT	5	1.2	7.7E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	microtubule organizing center part	RT	5	1.2	7.7E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell surface	RT	16	3.8	7.7E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	extrinsic to membrane	RT	21	5.0	7.7E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endosome membrane	RT	5	1.2	8.1E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	endosomal part	RT	5	1.2	8.1E-2	2.6E-1
<input type="checkbox"/>	GOTERM_CC_FAT	actin responsive factor complex	RT	2	0.5	8.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cyclin-dependent protein kinase 5 activator complex	RT	2	0.5	8.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	Axin-APC-beta-catenin-GSK3B complex	RT	2	0.5	8.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	heterogeneous nuclear ribonucleoprotein complex	RT	3	0.7	8.4E-2	2.7E-1
<input type="checkbox"/>	GOTERM_CC_FAT	axon	RT	9	2.2	8.8E-2	2.8E-1
<input type="checkbox"/>	GOTERM_CC_FAT	cell-cell junction	RT	10	2.4	9.7E-2	3.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	nuclear periphery	RT	5	1.2	9.8E-2	3.0E-1
<input type="checkbox"/>	GOTERM_CC_FAT	dendrite	RT	9	2.2	9.8E-2	3.0E-1

66 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](#)