



Functional Annotation Chart

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Current Gene List: List_1

Current Background: Homo sapiens

417 DAVID IDs

Options


Rerun Using Options

Create Sublist

144 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	transcription factor binding	RT		67	16.1	1.4E-24	8.4E-22
<input type="checkbox"/>	GOTERM_MF_FAT	steroid hormone receptor activity	RT		24	5.8	1.3E-22	3.7E-20
<input type="checkbox"/>	GOTERM_MF_FAT	ligand-dependent nuclear receptor activity	RT		24	5.8	1.5E-20	2.9E-18
<input type="checkbox"/>	GOTERM_MF_FAT	protein kinase activity	RT		67	16.1	1.5E-20	2.2E-18
<input type="checkbox"/>	GOTERM_MF_FAT	transcription activator activity	RT		51	12.2	9.6E-18	1.1E-15
<input type="checkbox"/>	GOTERM_MF_FAT	transcription regulator activity	RT		104	24.9	2.4E-16	2.2E-14
<input type="checkbox"/>	GOTERM_MF_FAT	enzyme binding	RT		54	12.9	3.6E-15	3.0E-13
<input type="checkbox"/>	GOTERM_MF_FAT	transcription cofactor activity	RT		44	10.6	7.7E-15	5.8E-13
<input type="checkbox"/>	GOTERM_MF_FAT	ATP binding	RT		98	23.5	2.1E-14	1.4E-12
<input type="checkbox"/>	GOTERM_MF_FAT	promoter binding	RT		19	4.6	2.6E-14	1.6E-12
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl ribonucleotide binding	RT		98	23.5	4.9E-14	2.7E-12
<input type="checkbox"/>	GOTERM_MF_FAT	protein domain specific binding	RT		40	9.6	1.8E-13	8.9E-12
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleoside binding	RT		101	24.2	1.8E-13	8.2E-12
<input type="checkbox"/>	GOTERM_MF_FAT	nucleoside binding	RT		101	24.2	2.8E-13	1.2E-11
<input type="checkbox"/>	GOTERM_MF_FAT	adenyl nucleotide binding	RT		99	23.7	4.7E-13	1.9E-11
<input type="checkbox"/>	GOTERM_MF_FAT	nucleotide binding	RT		125	30.0	6.3E-13	2.3E-11
<input type="checkbox"/>	GOTERM_MF_FAT	transcription coactivator activity	RT		31	7.4	1.5E-12	5.1E-11
<input type="checkbox"/>	GOTERM_MF_FAT	ribonucleotide binding	RT		108	25.9	1.8E-12	5.8E-11
<input type="checkbox"/>	GOTERM_MF_FAT	purine ribonucleotide binding	RT		108	25.9	1.8E-12	5.8E-11
<input type="checkbox"/>	GOTERM_MF_FAT	purine nucleotide binding	RT		109	26.1	1.2E-11	3.7E-10
<input type="checkbox"/>	GOTERM_MF_FAT	sequence-specific DNA binding	RT		51	12.2	5.9E-11	1.7E-9
<input type="checkbox"/>	GOTERM_MF_FAT	non-membrane spanning protein tyrosine kinase activity	RT		14	3.4	1.0E-10	2.9E-9
<input type="checkbox"/>	GOTERM_MF_FAT	protein tyrosine kinase activity	RT		25	6.0	1.4E-10	3.8E-9
<input type="checkbox"/>	GOTERM_MF_FAT	protein serine/threonine kinase activity	RT		40	9.6	5.8E-10	1.5E-8
<input type="checkbox"/>	GOTERM_MF_FAT	lysine N-acetyltransferase activity	RT		13	3.1	5.8E-10	1.4E-8
<input type="checkbox"/>	GOTERM_MF_FAT	histone acetyltransferase activity	RT		13	3.1	5.8E-10	1.4E-8
<input type="checkbox"/>	GOTERM_MF_FAT	protein C-terminus binding	RT		22	5.3	1.2E-9	2.8E-8
<input type="checkbox"/>	GOTERM_MF_FAT	structure-specific DNA binding	RT		22	5.3	2.0E-9	4.5E-8
<input type="checkbox"/>	GOTERM_MF_FAT	transcription factor activity	RT		64	15.3	3.8E-9	8.3E-8
<input type="checkbox"/>	GOTERM_MF_FAT	transcription repressor activity	RT		31	7.4	2.2E-8	4.7E-7
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<input type="checkbox"/>	GOTERM_MF_FAT	hormone receptor binding	RT		15	3.6	3.1E-7	6.1E-6
<input type="checkbox"/>	GOTERM_MF_FAT	kinase binding	RT		21	5.0	4.0E-7	7.6E-6
<input type="checkbox"/>	GOTERM_MF_FAT	chromatin binding	RT		19	4.6	5.3E-7	9.8E-6
<input type="checkbox"/>	GOTERM_MF_FAT	SMAD binding	RT		11	2.6	7.9E-7	1.4E-5
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<input type="checkbox"/>	GOTERM_MF_FAT	N-acetyltransferase activity	RT		13	3.1	8.1E-7	1.4E-5
<input type="checkbox"/>	GOTERM_MF_FAT	double-stranded DNA binding	RT		15	3.6	1.1E-6	1.7E-5
<input type="checkbox"/>	GOTERM_MF_FAT	RNA polymerase II transcription factor activity	RT		24	5.8	1.1E-6	1.8E-5
<input type="checkbox"/>	GOTERM_MF_FAT	identical protein binding	RT		43	10.3	1.3E-6	2.1E-5
<input type="checkbox"/>	GOTERM_MF_FAT	protein kinase binding	RT		18	4.3	1.8E-6	2.8E-5

<input type="checkbox"/>	GOTERM_MF_FAT	histone deacetylase binding	RT 	9	2.2	2.6E-6	3.8E-5
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<input type="checkbox"/>	GOTERM_MF_FAT	nitric-oxide synthase regulator activity	RT 	5	1.2	3.8E-6	5.5E-5
<input type="checkbox"/>	GOTERM_MF_FAT	acetyltransferase activity	RT 	13	3.1	5.4E-6	7.5E-5
<input type="checkbox"/>	GOTERM_MF_FAT	N-acyltransferase activity	RT 	13	3.1	6.1E-6	8.3E-5
<input type="checkbox"/>	GOTERM_MF_FAT	ubiquitin protein ligase binding	RT 	9	2.2	8.6E-6	1.1E-4
<input type="checkbox"/>	GOTERM_MF_FAT	small conjugating protein ligase activity	RT 	18	4.3	9.7E-6	1.3E-4
<input type="checkbox"/>	GOTERM_MF_FAT	steroid hormone receptor binding	RT 	9	2.2	1.3E-5	1.7E-4
<input type="checkbox"/>	GOTERM_MF_FAT	protein dimerization activity	RT 	36	8.6	1.5E-5	1.9E-4
<input type="checkbox"/>	GOTERM_MF_FAT	transmembrane receptor protein tyrosine kinase activity	RT 	11	2.6	2.7E-5	3.3E-4
<input type="checkbox"/>	GOTERM_MF_FAT	ubiquitin-protein ligase activity	RT 	16	3.8	3.4E-5	4.0E-4
<input type="checkbox"/>	GOTERM_MF_FAT	peptidase activator activity	RT 	7	1.7	4.5E-5	5.3E-4
<input type="checkbox"/>	GOTERM_MF_FAT	protein heterodimerization activity	RT 	19	4.6	5.3E-5	6.1E-4
<input type="checkbox"/>	GOTERM_MF_FAT	protein N-terminus binding	RT 	11	2.6	6.6E-5	7.4E-4
<input type="checkbox"/>	GOTERM_MF_FAT	androgen receptor binding	RT 	7	1.7	9.5E-5	1.0E-3
<input type="checkbox"/>	GOTERM_MF_FAT	p53 binding	RT 	6	1.4	1.1E-4	1.2E-3
<input type="checkbox"/>	GOTERM_MF_FAT	acid-amino acid ligase activity	RT 	18	4.3	1.1E-4	1.2E-3
<input type="checkbox"/>	GOTERM_MF_FAT	R-SMAD binding	RT 	5	1.2	1.4E-4	1.5E-3
<input type="checkbox"/>	GOTERM_MF_FAT	caspase regulator activity	RT 	7	1.7	1.8E-4	1.9E-3
<input type="checkbox"/>	GOTERM_MF_FAT	transforming growth factor beta receptor, cytoplasmic mediator activity	RT 	5	1.2	2.2E-4	2.2E-3
<input type="checkbox"/>	GOTERM_MF_FAT	cyclin-dependent protein kinase activity	RT 	7	1.7	2.2E-4	2.2E-3
<input type="checkbox"/>	GOTERM_MF_FAT	transcription corepressor activity	RT 	14	3.4	4.1E-4	4.0E-3
<input type="checkbox"/>	GOTERM_MF_FAT	cytoskeletal protein binding	RT 	30	7.2	5.7E-4	5.5E-3
<input type="checkbox"/>	GOTERM_MF_FAT	ligase activity, forming carbon-nitrogen bonds	RT 	18	4.3	5.8E-4	5.5E-3
<input type="checkbox"/>	GOTERM_MF_FAT	steroid binding	RT 	9	2.2	6.1E-4	5.6E-3
<input type="checkbox"/>	GOTERM_MF_FAT	general RNA polymerase II transcription factor activity	RT 	8	1.9	6.6E-4	6.1E-3
<input type="checkbox"/>	GOTERM_MF_FAT	ATP-dependent helicase activity	RT 	11	2.6	6.8E-4	6.2E-3
<input type="checkbox"/>	GOTERM_MF_FAT	purine NTP-dependent helicase activity	RT 	11	2.6	6.8E-4	6.2E-3
<input type="checkbox"/>	GOTERM_MF_FAT	telomeric DNA binding	RT 	5	1.2	8.3E-4	7.3E-3
<input type="checkbox"/>	GOTERM_MF_FAT	vinculin binding	RT 	4	1.0	8.5E-4	7.4E-3
<input type="checkbox"/>	GOTERM_MF_FAT	caspase activator activity	RT 	5	1.2	1.1E-3	9.3E-3
<input type="checkbox"/>	GOTERM_MF_FAT	RNA cap binding	RT 	4	1.0	1.3E-3	1.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	cadherin binding	RT 	5	1.2	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	histone binding	RT 	7	1.7	1.9E-3	1.5E-2
<input type="checkbox"/>	GOTERM_MF_FAT	phosphatase binding	RT 	7	1.7	1.9E-3	1.5E-2
<input type="checkbox"/>	GOTERM_MF_FAT	nucleocytoplasmic transporter activity	RT 	4	1.0	1.9E-3	1.6E-2
<input type="checkbox"/>	GOTERM_MF_FAT	translation initiation factor activity	RT 	8	1.9	2.2E-3	1.8E-2
<input type="checkbox"/>	GOTERM_MF_FAT	unfolded protein binding	RT 	11	2.6	2.3E-3	1.8E-2
<input type="checkbox"/>	GOTERM_MF_FAT	RNA binding	RT 	36	8.6	3.0E-3	2.3E-2
<input type="checkbox"/>	GOTERM_MF_FAT	helicase activity	RT 	12	2.9	3.2E-3	2.4E-2
<input type="checkbox"/>	GOTERM_MF_FAT	protein phosphorylated amino acid binding	RT 	4	1.0	4.8E-3	3.6E-2
<input type="checkbox"/>	GOTERM_MF_FAT	phosphoserine binding	RT 	3	0.7	5.1E-3	3.8E-2
<input type="checkbox"/>	GOTERM_MF_FAT	SH2 domain binding	RT 	5	1.2	5.2E-3	3.8E-2
<input type="checkbox"/>	GOTERM_MF_FAT	protein phosphatase binding	RT 	6	1.4	5.8E-3	4.2E-2
<input type="checkbox"/>	GOTERM_MF_FAT	single-stranded RNA binding	RT 	5	1.2	8.0E-3	5.7E-2
<input type="checkbox"/>	GOTERM_MF_FAT	transforming growth factor beta receptor, pathway-specific cytoplasmic mediator activity	RT 	3	0.7	8.4E-3	5.9E-2
<input type="checkbox"/>	GOTERM_MF_FAT	double-stranded telomeric DNA binding	RT 	3	0.7	8.4E-3	5.9E-2
<input type="checkbox"/>	GOTERM_MF_FAT	specific RNA polymerase II transcription factor activity	RT 	6	1.4	8.8E-3	6.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	translation factor activity, nucleic acid binding	RT 	9	2.2	9.0E-3	6.1E-2
<input type="checkbox"/>	GOTERM_MF_FAT	tubulin binding	RT	9	2.2	1.0E-2	6.8E-2
<input type="checkbox"/>	GOTERM_MF_FAT	cell adhesion molecule binding	RT	5	1.2	1.2E-2	7.7E-2
<input type="checkbox"/>	GOTERM_MF_FAT	protein homodimerization activity	RT	19	4.6	1.2E-2	7.7E-2
<input type="checkbox"/>	GOTERM_MF_FAT	ephrin receptor activity	RT	4	1.0	1.3E-2	8.5E-2
<input type="checkbox"/>	GOTERM_MF_FAT	ATPase activity, coupled	RT	16	3.8	1.7E-2	1.1E-1

<input type="checkbox"/>	GOTERM_MF_FAT	thyroid hormone receptor activity	RT	3	0.7	1.7E-2	1.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	microtubule plus-end binding	RT	3	0.7	1.7E-2	1.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	nuclear localization sequence binding	RT	3	0.7	1.7E-2	1.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	MAP kinase kinase kinase activity	RT	4	1.0	1.8E-2	1.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	signal sequence binding	RT	4	1.0	2.1E-2	1.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	kinase regulator activity	RT	8	1.9	2.1E-2	1.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	collagen binding	RT	5	1.2	2.2E-2	1.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	co-SMAD binding	RT	3	0.7	2.2E-2	1.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	ATPase activity	RT	18	4.3	2.3E-2	1.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	single-stranded DNA binding	RT	6	1.4	2.4E-2	1.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	drug binding	RT	6	1.4	2.7E-2	1.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	DNA-dependent ATPase activity	RT	6	1.4	2.7E-2	1.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	lipid binding	RT	22	5.3	2.9E-2	1.6E-1
<input type="checkbox"/>	GOTERM_MF_FAT	nucleotide kinase activity	RT	4	1.0	3.0E-2	1.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	protein complex binding	RT	12	2.9	3.4E-2	1.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	phosphoinositide 3-kinase binding	RT	3	0.7	3.4E-2	1.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	ATP-dependent DNA helicase activity	RT	4	1.0	3.7E-2	2.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	1-phosphatidylinositol-3-kinase activity	RT	3	0.7	4.1E-2	2.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	guanylate kinase activity	RT	3	0.7	4.1E-2	2.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	insulin receptor substrate binding	RT	3	0.7	4.1E-2	2.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	platelet-derived growth factor binding	RT	3	0.7	4.1E-2	2.1E-1
<input type="checkbox"/>	GOTERM_MF_FAT	mRNA binding	RT	6	1.4	4.7E-2	2.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	RNA polymerase II carboxy-terminal domain kinase activity	RT	3	0.7	4.8E-2	2.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	phosphoinositide 3-kinase activity	RT	3	0.7	4.8E-2	2.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	retinoic acid receptor activity	RT	3	0.7	4.8E-2	2.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	insulin-like growth factor receptor binding	RT	3	0.7	4.8E-2	2.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	cytoskeletal adaptor activity	RT	3	0.7	5.6E-2	2.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	estrogen receptor activity	RT	2	0.5	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	beta-catenin binding	RT	4	1.0	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	receptor regulator activity	RT	4	1.0	5.9E-2	2.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	damaged DNA binding	RT	5	1.2	6.2E-2	2.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	microtubule binding	RT	6	1.4	6.4E-2	3.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	cysteine-type endopeptidase activity	RT	6	1.4	6.4E-2	3.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	protein deacetylase activity	RT	3	0.7	7.2E-2	3.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	histone deacetylase activity	RT	3	0.7	7.2E-2	3.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	actin filament binding	RT	5	1.2	7.3E-2	3.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	phosphotransferase activity, phosphate group as acceptor	RT	4	1.0	7.5E-2	3.3E-1
<input type="checkbox"/>	GOTERM_MF_FAT	enzyme activator activity	RT	16	3.8	7.7E-2	3.4E-1
<input type="checkbox"/>	GOTERM_MF_FAT	peroxisome proliferator activated receptor binding	RT	2	0.5	8.7E-2	3.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	TPR domain binding	RT	2	0.5	8.7E-2	3.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	telomerase inhibitor activity	RT	2	0.5	8.7E-2	3.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	vitamin D response element binding	RT	2	0.5	8.7E-2	3.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	receptor activator activity	RT	3	0.7	9.0E-2	3.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	manganese ion binding	RT	9	2.2	9.1E-2	3.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	ligand-dependent nuclear receptor transcription coactivator activity	RT	4	1.0	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	specific transcriptional repressor activity	RT	4	1.0	9.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	protein kinase regulator activity	RT	6	1.4	9.5E-2	3.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	glycoprotein binding	RT	4	1.0	9.8E-2	4.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	deacetylase activity	RT	3	0.7	1.0E-1	4.0E-1

71 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**.



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