

DAVID Bioinformatics Resources 6.7

National Institute of Allergy and Infectious Diseases (NIAID), NIH

Functional Annotation Chart

Current Gene List: List_1
Current Background: Homo sapiens
417 DAVID IDs

Options

117 chart records

Rerun Using Options Create Sublist

Help and Manual

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Subl	st Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	SP_PIR_KEYWORDS	phosphoprotein	RT		312	74.8	2.5E-54	9.7E-52
	SP_PIR_KEYWORDS	acetylation	RT		174	41.7	1.1E-45	2.1E-43
	SP_PIR_KEYWORDS	ubl conjugation	RT		77	18.5	2.0E-37	2.7E-35
	SP_PIR_KEYWORDS	host-virus interaction	RT		57	13.7	2.1E-37	2.0E-35
	SP_PIR_KEYWORDS	nucleus	RT		211	50.6	2.3E-37	1.8E-35
	SP_PIR_KEYWORDS	<u>cytoplasm</u>	RT		164	39.3	8.0E-27	5.2E-25
	SP_PIR_KEYWORDS	atp-binding	RT		97	23.3	1.0E-26	5.8E-25
	SP_PIR_KEYWORDS	<u>kinase</u>	RT		68	16.3	1.3E-25	6.5E-24
	SP_PIR_KEYWORDS	nucleotide-binding	RT		106	25.4	4.5E-24	1.9E-22
	SP_PIR_KEYWORDS	isopeptide bond	RT		42	10.1	2.7E-20	1.1E-18
	SP_PIR_KEYWORDS	<u>Proto-oncogene</u>	RT ==		34	8.2	5.2E-18	1.9E-16
	SP_PIR_KEYWORDS	tyrosine-protein kinase	RT =		24	5.8	1.6E-16	3.6E-15
	SP_PIR_KEYWORDS	transcription regulation	RT		102	24.5	4.0E-16	1.3E-14
	SP_PIR_KEYWORDS	<u>Transcription</u>	RT		102	24.5	1.9E-15	5.3E-14
	SP_PIR_KEYWORDS	<u>transferase</u>	RT	i	79	18.9	5.2E-15	1.4E-13
	SP_PIR_KEYWORDS	<u>ATP</u>	RT =		30	7.2	4.0E-14	9.8E-13
	SP_PIR_KEYWORDS	serine/threonine-protein kinase	RT ==		35	8.4	2.9E-12	6.7E-11
	SP_PIR_KEYWORDS	disease mutation	RT	i	79	18.9	5.1E-12	1.1E-10
	SP_PIR_KEYWORDS	<u>phosphotransferase</u>	RT 🚃		25	6.0	1.2E-11	2.5E-10
	SP_PIR_KEYWORDS	SH2 domain	RT =		19	4.6	2.8E-11	5.5E-10
	SP_PIR_KEYWORDS	zinc finger	RT =		21	5.0	1.3E-10	2.3E-9
	SP_PIR_KEYWORDS	ubl conjugation pathway	RT ===		38	9.1	1.3E-10	2.3E-9
	SP_PIR_KEYWORDS	<u>Apoptosis</u>	RT =		32	7.7	2.8E-10	4.8E-9
	SP_PIR_KEYWORDS	<u>chromatin regulator</u>	RT 🚃		23	5.5	1.5E-9	2.4E-8
	SP_PIR_KEYWORDS	mRNA transport	RT 🚃		14	3.4	5.9E-9	9.3E-8
	SP_PIR_KEYWORDS	cell cycle	RT ==		32	7.7	2.7E-8	4.0E-7
	SP_PIR_KEYWORDS	steroid hormone receptor	RT 🖥		6	1.4	2.7E-8	3.9E-7
	SP_PIR_KEYWORDS	DNA binding	RT =		27	6.5	2.9E-8	4.0E-7
	SP_PIR_KEYWORDS	sh3 domain	RT 🚃		21	5.0	3.3E-8	4.5E-7
	SP_PIR_KEYWORDS	activator	RT =		34	8.2	3.7E-8	4.8E-7
	SP_PIR_KEYWORDS	<u>Spliceosome</u>	RT 🚃		16	3.8	4.9E-8	6.2E-7
	SP_PIR_KEYWORDS	mrna splicing	RT 🚃		20	4.8	1.5E-7	1.9E-6
	SP_PIR_KEYWORDS	cell cycle control	RT 🖥		9	2.2	2.3E-7	2.7E-6
	SP_PIR_KEYWORDS	serine/threonine-specific protein kinase	RT 🔳		11	2.6	5.8E-7	6.6E-6
	SP_PIR_KEYWORDS	duplication	RT 🚃		20	4.8	5.9E-7	6.6E-6
	SP_PIR_KEYWORDS	<u>chromosomal rearrangement</u>	RT 🚃		22	5.3	8.1E-7	8.8E-6
	SP_PIR_KEYWORDS	<u>rna-binding</u>	RT =		32	7.7	8.7E-7	9.2E-6
	SP_PIR_KEYWORDS	mrna processing	RT 🔤		21	5.0	1.1E-6	1.1E-5
	SP_PIR_KEYWORDS	cell division	RT 🔤		21	5.0	1.3E-6	1.3E-5
	SP_PIR_KEYWORDS	repressor	RT 🚃		26	6.2	9.9E-6	9.7E-5
	SP_PIR_KEYWORDS	transcription factor	RT 📱		10	2.4	1.0E-5	9.9E-5

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SP_PIR_KEYWORDS	<u>DNA damage</u>	RT =	17	4.1	1.1E-5	9.8E-5
SP_PIR_KEYWORDS	dna repair	RT =	16	3.8	1.8E-5	1.7E-4
SP_PIR_KEYWORDS	protein transport	RT =	27	6.5	2.2E-5	2.0E-4
SP_PIR_KEYWORDS	<u>dna-binding</u>	RT	67	16.1	4.5E-5	3.9E-4
SP_PIR_KEYWORDS	<u>cytoskeleton</u>	RT =	31	7.4	5.9E-5	5.0E-4
SP_PIR_KEYWORDS	tyrosine-specific protein kinase	RT	8	1.9	7.2E-5	6.0E-4
SP_PIR_KEYWORDS	transforming protein	RT	7	1.7	7.9E-5	6.5E-4
SP_PIR_KEYWORDS	translation regulation	RT	9	2.2	9.6E-5	7.6E-4
SP_PIR_KEYWORDS	<u>Initiation factor</u>	RT	8	1.9	1.2E-4	9.5E-4
SP_PIR_KEYWORDS	helicase	RT =	12	2.9	1.6E-4	1.2E-3
SP_PIR_KEYWORDS	nonsense-mediated mrna decay	RT	6	1.4	3.0E-4	2.3E-3
SP_PIR_KEYWORDS	<u>ligase</u>	RT =	18	4.3	3.7E-4	2.7E-3
SP_PIR_KEYWORDS	stress response	RT	8	1.9	5.5E-4	3.9E-3
SP_PIR_KEYWORDS	receptor	RT ===	55	13.2	5.6E-4	3.9E-3
SP_PIR_KEYWORDS	ADP-ribosylation	RT	6	1.4	6.7E-4	4.6E-3
SP_PIR_KEYWORDS	signal transduction	RT	6	1.4	8.8E-4	6.0E-3
SP_PIR_KEYWORDS	<u>myristate</u>	RT =	10	2.4	1.1E-3	7.6E-3
SP_PIR_KEYWORDS	wnt signaling pathway	RT	10	2.4	1.3E-3	8.9E-3
SP_PIR_KEYWORDS	bromodomain	RT	6	1.4	1.5E-3	9.4E-3
SP_PIR_KEYWORDS	nuclear pore complex	RT	6	1.4	1.6E-3	1.0E-2
SP_PIR_KEYWORDS	<u>s-nitrosylation</u>	RT	4	1.0	2.4E-3	1.5E-2
SP_PIR_KEYWORDS	protein biosynthesis	RT =	12	2.9	2.7E-3	1.7E-2
SP_PIR_KEYWORDS	RNA binding	RT	5	1.2	2.9E-3	1.8E-2
SP_PIR_KEYWORDS	steroid-binding	RT	4	1.0	3.8E-3	2.2E-2
SP_PIR_KEYWORDS	autophosphorylation	RT	6	1.4	4.0E-3	2.4E-2
SP_PIR_KEYWORDS	cyclin	RT	6	1.4	4.4E-3	2.5E-2
SP_PIR_KEYWORDS	<u>telomere</u>	RT I	4	1.0	4.6E-3	2.6E-2
SP_PIR_KEYWORDS	<u>zinc-finger</u>	RT ===	54	12.9	5.4E-3	3.0E-2
SP_PIR_KEYWORDS	<u>deafness</u>	RT	8	1.9	6.0E-3	3.3E-2
SP_PIR_KEYWORDS	<u>Chaperone</u>	RT	10	2.4	7.5E-3	4.1E-2
SP_PIR_KEYWORDS	<u>zinc</u>	RT	65	15.6	7.6E-3	4.0E-2
SP_PIR_KEYWORDS	myristylation	RT	5	1.2	9.8E-3	5.1E-2
SP_PIR_KEYWORDS	tumor suppressor	RT 🖥	9	2.2	1.0E-2	5.1E-2
SP_PIR_KEYWORDS	actin binding	RT	5	1.2	1.1E-2	5.4E-2
SP_PIR_KEYWORDS	<u>homodimer</u>	RT	7	1.7	1.3E-2	6.4E-2
SP_PIR_KEYWORDS	<u>angiogenesis</u>	RT	6	1.4	1.4E-2	6.9E-2
SP_PIR_KEYWORDS	<u>lipid-binding</u>	RT	7	1.7	1.4E-2	6.8E-2
SP_PIR_KEYWORDS	transcription initiation	RT I	3	0.7	1.5E-2	7.3E-2
SP_PIR_KEYWORDS	<u>endosome</u>	RT 🔳	11	2.6	1.6E-2	7.5E-2
SP_PIR_KEYWORDS	<u>mitosis</u>	RT 🔳	10	2.4	1.8E-2	8.5E-2
SP_PIR_KEYWORDS	carcinogenesis	RT I	3	0.7	1.9E-2	8.6E-2
SP_PIR_KEYWORDS	systemic lupus erythematosus	RT	4	1.0	2.0E-2	9.1E-2
SP_PIR_KEYWORDS	<u>translocation</u>	RT	6	1.4	2.2E-2	9.8E-2
SP_PIR_KEYWORDS	calcium binding	RT	7	1.7	2.4E-2	1.1E-1
SP_PIR_KEYWORDS	heterodimer	RT	7	1.7	2.4E-2	1.1E-1
SP_PIR_KEYWORDS	innate immunity	RT	6	1.4	2.7E-2	1.2E-1
SP_PIR_KEYWORDS	metal-binding	RT	80	19.2	2.8E-2	1.2E-1
SP_PIR_KEYWORDS	neurodegeneration	RT 🖥	6	1.4	3.0E-2	1.2E-1
SP_PIR_KEYWORDS	<u>Fanconi anemia</u>	RT .	3	0.7	3.1E-2	1.3E-1
SP_PIR_KEYWORDS	molecular chaperone	RT .	3	0.7	3.1E-2	1.3E-1
SP_PIR_KEYWORDS	cysteine proteinase	RT	3	0.7	3.6E-2	1.5E-1
SP_PIR_KEYWORDS	<u>polymorphism</u>	RT	269	64.5	3.6E-2	1.5E-1
SP_PIR_KEYWORDS	chromosomal protein	RI	8	1.9	3.8E-2	1.5E-1
SP_PIR_KEYWORDS	wd repeat	RI	12	2.9	3.8E-2	1.5E-1
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SP_PIR_KEYWORDS	<u>EF hand</u>	<u>RT</u>	i	5	1.2	4.1E-2	1.6E-1
SP_PIR_KEYWORDS	thyroid hormone receptor	RT	i	2	0.5	4.3E-2	1.6E-1
SP_PIR_KEYWORDS	Antiviral defense	RT	i .	5	1.2	4.5E-2	1.7E-1
SP_PIR_KEYWORDS	dna recombination	RT		4	1.0	4.5E-2	1.7E-1
SP_PIR_KEYWORDS	<u>leukodystrophy</u>	RT	i	3	0.7	4.6E-2	1.7E-1
SP_PIR_KEYWORDS	kinetochore	<u>RT</u>	•	5	1.2	4.7E-2	1.7E-1
SP_PIR_KEYWORDS	<u>manganese</u>	<u>RT</u>	=	8	1.9	4.8E-2	1.7E-1
SP_PIR_KEYWORDS	blocked amino end	<u>RT</u>	=	6	1.4	4.9E-2	1.8E-1
SP_PIR_KEYWORDS	alternative initiation	<u>RT</u>	•	5	1.2	5.0E-2	1.8E-1
SP_PIR_KEYWORDS	fusion protein	<u>RT</u>	i	3	0.7	6.3E-2	2.2E-1
SP_PIR_KEYWORDS	Short OT syndrome	<u>RT</u>	•	2	0.5	6.3E-2	2.2E-1
SP_PIR_KEYWORDS	acetylated amino end	<u>RT</u>	=	6	1.4	6.6E-2	2.2E-1
SP_PIR_KEYWORDS	hydroxylation	<u>RT</u>	i	5	1.2	6.8E-2	2.3E-1
SP_PIR_KEYWORDS	alternative splicing	<u>RT</u>		178	42.7	7.0E-2	2.3E-1
SP_PIR_KEYWORDS	tandem repeat	<u>RT</u>	•	5	1.2	7.9E-2	2.6E-1
SP_PIR_KEYWORDS	methylation	<u>RT</u>	=	10	2.4	8.1E-2	2.6E-1
SP_PIR_KEYWORDS	<u>alycogen metabolism</u>	RT	i	3	0.7	8.1E-2	2.6E-1
SP_PIR_KEYWORDS	nucleotide binding	<u>RT</u>	•	6	1.4	8.3E-2	2.6E-1
SP_PIR_KEYWORDS	mrna capping	RT	•	2	0.5	8.4E-2	2.6E-1
SP_PIR_KEYWORDS	Cardiomyopathy	<u>RT</u>	•	4	1.0	8.5E-2	2.6E-1
SP_PIR_KEYWORDS	cell junction	RT		14	3.4	9.4E-2	2.9E-1
SP_PIR_KEYWORDS	<u>cell shape</u>	RT	i	3	0.7	9.4E-2	2.9E-1

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