

Current Gene List: z.motif.list

Current Background: Homo sapiens

11 DAVID IDs

+ Options

Rerun Using Options

Create Sublist

1 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	p53 signaling pathway	RT		2	18.2	6.5E-2	4.5E-1

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

Current Background: Homo sapiens
702 DAVID IDs

Options

Rerun Using Options Create Sublist

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231 chart records

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	polymorphism	RT		556	79.2	5.1E-32	2.5E-29
<input type="checkbox"/>	SP_PIR_KEYWORDS	alternative splicing	RT		338	48.1	3.8E-8	9.3E-6
<input type="checkbox"/>	SP_PIR_KEYWORDS	glycoprotein	RT		215	30.6	6.7E-8	1.1E-5
<input type="checkbox"/>	INTERPRO	EGF-like region, conserved site	RT		32	4.6	9.6E-8	9.4E-5
<input type="checkbox"/>	GOTERM_BP_FAT	cell adhesion	RT		54	7.7	1.1E-7	2.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	biological adhesion	RT		54	7.7	1.1E-7	1.1E-4
<input type="checkbox"/>	GOTERM_MF_FAT	extracellular matrix structural constituent	RT		16	2.3	4.3E-7	2.7E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	cell adhesion	RT		38	5.4	5.5E-7	6.6E-5
<input type="checkbox"/>	GOTERM_CC_FAT	plasma membrane	RT		180	25.6	2.1E-6	8.3E-4
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF038286:preferentially expressed antigen of melanoma (PRAME) family protein	RT		8	1.1	3.3E-6	7.5E-4
<input type="checkbox"/>	SP_PIR_KEYWORDS	disulfide bond	RT		149	21.2	4.8E-6	4.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	homophilic cell adhesion	RT		17	2.4	1.5E-5	9.6E-3
<input type="checkbox"/>	GOTERM_BP_FAT	cell-cell adhesion	RT		26	3.7	1.5E-5	7.6E-3
<input type="checkbox"/>	INTERPRO	EGF-like, type 3	RT		21	3.0	2.7E-5	1.3E-2
<input type="checkbox"/>	INTERPRO	MAGE protein	RT		9	1.3	2.8E-5	9.2E-3
<input type="checkbox"/>	KEGG_PATHWAY	Graft-versus-host disease	RT		9	1.3	4.0E-5	5.3E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	tumor antigen	RT		9	1.3	4.9E-5	4.0E-3
<input type="checkbox"/>	SP_PIR_KEYWORDS	egf-like domain	RT		22	3.1	8.7E-5	6.0E-3
<input type="checkbox"/>	INTERPRO	Neuroblastoma breakpoint family	RT		5	0.7	1.1E-4	2.6E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cellular component morphogenesis	RT		30	4.3	1.7E-4	6.6E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF003152:G protein-coupled olfactory receptor, class II	RT		26	3.7	2.8E-4	3.2E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF800006:rhodopsin-like G protein-coupled receptors	RT		41	5.8	3.1E-4	2.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	sensory perception of smell	RT		31	4.4	3.1E-4	9.7E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	coiled coil	RT		102	14.5	3.2E-4	1.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cell morphogenesis	RT		27	3.8	3.7E-4	1.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	sensory perception of chemical stimulus	RT		33	4.7	4.0E-4	9.3E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	olfaction	RT		30	4.3	4.0E-4	2.1E-2
<input type="checkbox"/>	KEGG_PATHWAY	Olfactory transduction	RT		27	3.8	4.3E-4	2.8E-2
<input type="checkbox"/>	KEGG_PATHWAY	Antigen processing and presentation	RT		11	1.6	4.7E-4	2.1E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF005491:tumor associated protein MAGE	RT		6	0.9	5.2E-4	2.9E-2

Current Gene List: z.premature.list**Current Background: Homo sapiens****86 DAVID IDs****Options**

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Create Sublist

43 chart records[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF800006:rhodopsin-like G protein-coupled receptors	RT		12	14.0	1.3E-5	3.2E-4
<input type="checkbox"/>	GOTERM_MF_FAT	olfactory receptor activity	RT		10	11.6	4.0E-5	5.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	sensory perception of smell	RT		10	11.6	5.4E-5	1.7E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	olfaction	RT		10	11.6	7.3E-5	9.2E-3
<input type="checkbox"/>	GOTERM_BP_FAT	sensory perception of chemical stimulus	RT		10	11.6	1.2E-4	1.9E-2
<input type="checkbox"/>	INTERPRO	Olfactory receptor	RT		10	11.6	1.4E-4	2.4E-2
<input type="checkbox"/>	PIR_SUPERFAMILY	PIRSF003152:G protein-coupled olfactory receptor, class II	RT		8	9.3	2.1E-4	2.5E-3
<input type="checkbox"/>	KEGG_PATHWAY	Olfactory transduction	RT		9	10.5	4.2E-4	1.7E-2
<input type="checkbox"/>	INTERPRO	GPCR, rhodopsin-like superfamily	RT		12	14.0	4.3E-4	3.7E-2
<input type="checkbox"/>	INTERPRO	7TM GPCR, rhodopsin-like	RT		12	14.0	4.4E-4	2.5E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	g-protein coupled receptor	RT		12	14.0	8.2E-4	5.1E-2
<input type="checkbox"/>	SP_PIR_KEYWORDS	sensory transduction	RT		10	11.6	1.1E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_FAT	sensory perception	RT		11	12.8	1.4E-3	1.4E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	transducer	RT		12	14.0	1.4E-3	4.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	G-protein coupled receptor protein signaling pathway	RT		13	15.1	1.6E-3	1.2E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	disulfide bond	RT		24	27.9	2.9E-3	7.0E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cognition	RT		11	12.8	3.3E-3	1.9E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	RT		30	34.9	3.6E-3	7.1E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	disulfide bond	RT		23	26.7	3.7E-3	4.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	glycoprotein	RT		31	36.0	3.9E-3	7.8E-2
<input type="checkbox"/>	UP_SEQ_FEATURE	transmembrane region	RT		33	38.4	6.7E-3	5.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	neurological system process	RT		12	14.0	8.5E-3	3.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	transmembrane	RT		33	38.4	9.0E-3	1.5E-1