Functional Annotation Chart

Help and Manual

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

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Options									
Rerun Using Options Create Sublist									
201 c	hart reco	rds			. —		oad File		
	Category		'	1		1	Benjamini		
		Nucleotide-bd a/b plait sf RBD domain sf	RT RT	76 73		4.6E-17 9.1E-16			
	INTERPRO		RT =	65		2.3E-14			
		Thioredoxin-like sf	RT	31		1.0E-5			
	INTERPRO	Znf_RING/FYVE/PHD	RT =	79	3.8	1.4E-5	1.1E-2		
	INTERPRO	Thioredoxin domain	RT	15	0.7	1.5E-5	1.1E-2		
		MHC I a C	RT	7		2.1E-5	1.3E-2		
		RNA-helicase DEAD-box CS	RT	12		2.4E-5	1.3E-2		
		Ribosomal zn-bd Znf PHD-finger	RT I	8 21		4.5E-5 4.9E-5	2.0E-2 2.0E-2		
		<u>Ubiquitin-like domsf</u>	RT	38		5.3E-5	2.0E-2		
	INTERPRO	· · · · · · · · · · · · · · · · · · ·	RT	23	1.1	5.6E-5	2.0E-2		
	INTERPRO	Znf_FYVE_PHD	RT	30	1.5	8.7E-5	2.7E-2		
		MHC I a a1/a2	RT	8		9.0E-5	2.7E-2		
		Thioredoxin CS RHD DNA bind dom	RT I	9 7		9.4E-5 1.3E-4	2.7E-2 3.3E-2		
		RHD DNA bind dom sf	RT	, 7		1.3E-4	3.3E-2		
		RHD dimer	RT	7		1.3E-4	3.3E-2		
	INTERPRO	SAP dom sf	RT	11	0.5	1.5E-4	3.4E-2		
		Zinc finger PHD-type CS	RT	19	0.9	1.6E-4	3.6E-2		
		Small_GTP-bd_dom	RT =	34		2.2E-4	4.6E-2		
		RNA helicase DEAD Q motif	RT	12		2.8E-4	4.8E-2		
	INTERPRO	ARM-type_fold SAP_dom	RT RT	58 10		2.8E-4 2.8E-4	4.8E-2 4.8E-2		
		MHC II a/b N	RT	10		2.8E-4	4.8E-2		
	INTERPRO		RT	10	0.5	2.8E-4	4.8E-2		
	INTERPRO	Helicase_C	RT	24	1.2	3.4E-4	5.5E-2		
	INTERPRO		RT	6		4.0E-4	6.3E-2		
		DEAD/DEAH box helicase dom	RT	18		4.2E-4	6.4E-2		
		Translation prot SH3-like sf Helicase ATP-bd	RT I	8 24		4.6E-4 5.1E-4	6.7E-2 7.2E-2		
		Ubiquitin-like_dom	RT	16		6.7E-4			
	INTERPRO		RT	15		6.9E-4			
	INTERPRO	<u>bZIP</u>	RT	15		8.4E-4			
		Longin-like dom sf	RT	10		1.0E-3			
		Rib_uL2_dom2	RT I	9		1.1E-3			
		Znf_RanBP2_sf P-loop_NTPase	RT I	9 119		1.1E-3 1.3E-3			
		Ser/Thr-sp_prot-phosphatase	RT I	7		1.4E-3			
		HSP70_C_sf	RT	7		1.4E-3			
	INTERPRO	Snf7_fam	RT	7	0.3	1.4E-3	1.4E-1		
		Znf RanBP2	RT	9		2.0E-3			
		ARID dom	RT	7		2.1E-3			
		ARID dom sf Znf RING	RT I	7 48		2.1E-3 2.3E-3			
	INTERPRO		RT	6		2.6E-3			
	INTERPRO	Ribosomal eL8/eL30/eS12/Gad45	_	6	0.3	2.6E-3	1.9E-1		
	INTERPRO		RT	6	0.3	2.6E-3	1.9E-1		
		STAT_TF_alpha	RT			2.6E-3			
		STAT_N_sf	RT I	5		2.6E-3			
	INTERPRO	STAT TF DNA-bd	RT I	5 5		2.6E-3 2.6E-3			
		STAT TF coiled-coil	RT	5		2.6E-3			
		MHC_II_a_N	RT	5	0.2	2.6E-3	1.9E-1		
	INTERPRO	STAT_TF_prot_interaction	RT	5	0.2	2.6E-3	1.9E-1		
		DUSP-like sf	<u>RT</u>			2.6E-3			
		STAT TF DNA-bd N Pept C19 DUSP	RT I	5 5		2.6E-3 2.6E-3			
		STAT_linker	RT	5		2.6E-3			
		p53-like TF DNA-bd sf	RT	12		3.0E-3			
		Chaperone TCP-1	RT	6		4.0E-3			
	INTERPRO	NA-bd OB-fold	RT	19	0.9	4.4E-3	3.1E-1		
		AN1-like_Znf	RT	5		4.7E-3			
	INTERPRO		RT			4.7E-3 5.1E-3			
	INTERPRO	MHC I/II-like Ag-recog WD40 rpt	RT RT			5.4E-3			
		HSP70_peptide-bd_sf	RT			6.0E-3			
		G-protein beta WD-40 rep				6.9E-3			
		Small_GTPase	RT	25		7.2E-3	4.6E-1		
		Znf CCCH	RT	14		7.6E-3	4.7E-1		
		Bromodomain Chaperonin TCP-1 CS	RT	11 5		7.8E-3	4.7E-1 4.7E-1		
	INTERPRO		RT I	5 4		7.9E-3 8.2E-3	4.7E-1 4.7E-1		
		PTBP1-like_RRM2	RT	4		8.2E-3	4.7E-1		
		IPT NFkappaB	RT	4		8.2E-3			
	INTERPRO	NFkB/Dor	RT	4		8.2E-3			
		HnRNP-L/PTB TNER/NGER Cys rich rea	RT	4 8		8.2E-3 8.7F-3			

INTERPRO TNFR/NGFR Cys rich reg 8 0.4 8.7E-3 4.8E-1

0	0-4	T	DT	0	0	0/	D Value	Daniamini
Sublist	Category INTERPRO			'_	9	1	8.7E-3	Benjamini
		WD40 repeat dom sf	RT RT	_	45		9.2E-3	
		Bromodomain-like sf	RT		11		9.2E-3	
		WD40 repeat CS	RT		25		1.1E-2	
		ADF-H/Gelsolin-like dom sf	RT		8		1.1E-2	
	INTERPRO	Znf_CCCH_sf	<u>RT</u>		10	0.5	1.2E-2	6.0E-1
	INTERPRO	Heat shock 70 CS	<u>RT</u>		6	0.3	1.2E-2	6.0E-1
	INTERPRO	<u>Hsp 70 fam</u>	<u>RT</u>		6	0.3	1.2E-2	6.0E-1
		Ribosomal_eL30-like_sf	<u>RT</u>		6		1.2E-2	
		Chromo-like dom sf	RT	_	9		1.3E-2	
		ATPase_NBD	RT	_	15		1.4E-2	
		Tudor-knot ENTH VHS	RT RT	_	4 8		1.5E-2 1.7E-2	7.4E-1 7.9E-1
		TPR-like helical dom sf	RT		34		1.7E-2	8.5E-1
		SH2 dom sf	RT	_	20		1.9E-2	
		MHC I-like Ag-recog	RT	_	8		2.0E-2	
	INTERPRO	MHC I-like Ag-recog sf	RT		8	0.4	2.0E-2	9.2E-1
	INTERPRO	GROEL-like equatorial sf	<u>RT</u>		6	0.3	2.1E-2	9.5E-1
	INTERPRO	<u>SH2</u>	<u>RT</u>		19	0.9	2.4E-2	9.9E-1
	INTERPRO	Calcineurin-like PHP ApaH	RT		8		2.4E-2	
	INTERPRO		RT	_	8		2.4E-2	
		Metallo-depent PP-like	RT	_	8		2.4E-2	
	INTERPRO		RT DT		8		2.4E-2	
	INTERPRO INTERPRO		RT RT	_	5 4		2.4E-2 2.5E-2	
		Di19 Zn-bd	RT	_	4		2.5E-2	
		DEATH-like dom sf	RT		18		2.5E-2	
		MHC II b N	RT	_	6		2.7E-2	
		GroEL-like apical dom sf	RT		6	0.3	2.7E-2	9.9E-1
	INTERPRO	Cpn60/GroEL/TCP-1	RT		6	0.3	2.7E-2	9.9E-1
		TCP-1-like intermed sf	RT		6	0.3	2.7E-2	9.9E-1
		STPPase N	<u>RT</u>		3	0.1	2.7E-2	9.9E-1
	INTERPRO		<u>RT</u>		3		2.7E-2	9.9E-1
	INTERPRO		<u>RT</u>		3		2.7E-2	9.9E-1
	INTERPRO		RT	_			2.7E-2	
		<u>Leuzip Jun</u>	RT		3		2.7E-2	
	INTERPRO		RT		3		2.7E-2	
	INTERPRO		RT DT	_	3		2.7E-2	
		OS9-like dom ZFP36-like	RT DT	_	3		2.7E-2 2.7E-2	
	INTERPRO		RT RT		3		2.7E-2	
	INTERPRO		RT		3		2.7E-2	
		Cyclin-like dom	RT		9		2.9E-2	
		WWE dom sf			5		3.3E-2	
	INTERPRO	V SNARE CC			5	0.2	3.3E-2	1.0E0
	INTERPRO	Znf CXXC	RT		5	0.2	3.3E-2	1.0E0
	INTERPRO	Papain-like cys pep sf	<u>RT</u>		23	1.1	3.3E-2	1.0E0
	INTERPRO				13	0.6	3.6E-2	1.0E0
		Ig/MHC_CS			13		3.6E-2	
		Man6P isomerase rcpt-bd dom sf			4		3.7E-2	
		Cyclin/Ssn8	RT DT		4		3.7E-2 3.7E-2	
	INTERPRO INTERPRO		RT RT	_	4		3.7E-2	1.0E0 1.0E0
		TRASH_dom	RT		4		3.7E-2	1.0E0
	INTERPRO		RT		7		3.7E-2	1.0E0
		Bromodomain CS	RT		7	0.3	3.7E-2	1.0E0
	INTERPRO	RRM_dom_euk	RT		7	0.3	3.7E-2	1.0E0
	INTERPRO	WD40/YVTN_repeat-like_dom_sf	<u>RT</u>		47	2.3	3.9E-2	1.0E0
	INTERPRO	<u>Ig C1-set</u>	<u>RT</u>		14	0.7	4.1E-2	1.0E0
	INTERPRO		RT		6		4.1E-2	
		Chromo/chromo_shadow_dom	RT		8		4.5E-2	
	INTERPRO INTERPRO		RT RT		6 3		4.9E-2 5.1E-2	
		ZF C2HC RNF			3		5.1E-2 5.1E-2	
	INTERPRO				3		5.1E-2	
		Ribosomal uL23/eL15/eS24_sf			3		5.1E-2	
		CapZ_alpha/beta		i	3		5.1E-2	
	INTERPRO	CapZ alpha/beta 2		i	3	0.1	5.1E-2	1.0E0
		CC2-LZ dom					5.1E-2	
		CD3 esu/gsu/dsu					5.1E-2	
	INTERPRO				3		5.1E-2	
		WHIM1 dom	RT DT		3		5.1E-2	1.0E0
		LMBR1-like membr prot Synaptobrevin-like	RT RT		3 4		5.1E-2 5.1E-2	1.0E0 1.0E0
	INTERPRO		RT	_	4		5.1E-2 5.1E-2	1.0E0 1.0E0
		Nuclear_transport_factor_2_euk	RT	_	4		5.1E-2	1.0E0
		NTF2 dom	RT	_	4		5.1E-2	
	INTERPRO		RT	_	4		5.1E-2	
	INTERPRO	Peptidase C19 UCH	<u>RT</u>		13	0.6	5.2E-2	1.0E0
	INTERPRO	WH_DNA-bd_sf	<u>RT</u>		31	1.5	5.4E-2	1.0E0
		ArfGAP dom sf	RT		7		6.0E-2	
		ARFGAP/RecO	RT		7		6.0E-2	
		ArfGAP dom	RT DT		7		6.0E-2	
	INTERPRO		RT DT		13		6.2E-2	
	INTERPRO		RT DT	_	10 4		6.6E-2 6.8E-2	
	INTERPRO	Pept asp AS G TR CS	RT RT		4		6.8E-2	
		MIF4G-like_typ-3	RT	_	4		6.8E-2	
		Znf C2H2 jaz	RT	_	4		6.8E-2	
		Phos immunorcpt sig ITAM	RT	_	4		6.8E-2	
	INTERPRO	<u>HAT</u>	<u>RT</u>	i	4	0.2	6.8E-2	1.0E0
		Actinin actin-bd CS	<u>RT</u>	_	6	0.3	6.9E-2	1.0E0
		NTF2-like dom sf	RT	_	5		7.9E-2	
		TF_DNA-bd_sf	RT	_	5		7.9E-2	
	INTERPRO	Poly(ADP-ribose)pol cat dom	<u>RT</u>	•	5	υ.2	7.9E-2	1.0E0

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	INTERPRO	HMGN fam	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	<u>NFAT</u>	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	<u>SKICH</u>	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	S4 RNA-bd	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	Vps5_C	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	<u>Longin_dom</u>	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	<u>Ub_USP-typ</u>	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	PPA2-like	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	CALCOCO1/2 Zn UBZ1	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	DDT_dom	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	PDI thioredoxin-like dom	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	Thiolase acyl enz int AS	<u>RT</u>		3	0.1	7.9E-2	1.0E0
		WHIM2 dom	<u>RT</u>		3	0.1	7.9E-2	1.0E0
	INTERPRO	Cyclophilin-like dom sf	<u>RT</u>		6	0.3	8.1E-2	1.0E0
	INTERPRO	Cyclophilin-type PPIase dom	<u>RT</u>		6	0.3	8.1E-2	1.0E0
	INTERPRO	<u>Proteasome_suB-type</u>	<u>RT</u>		4	0.2	8.6E-2	1.0E0
	INTERPRO	Pept his AS	<u>RT</u>		4	0.2	8.6E-2	1.0E0
	INTERPRO	Hempt rcpt S F1 CS	<u>RT</u>		4	0.2	8.6E-2	1.0E0
	INTERPRO	Cyclin-like_sf	<u>RT</u>		9	0.4	8.7E-2	1.0E0
	INTERPRO	<u>Ig_E-set</u>	<u>RT</u>		17	0.8	8.8E-2	1.0E0
	INTERPRO	HSP20-like chaperone	<u>RT</u>		7	0.3	8.9E-2	1.0E0
	INTERPRO	GTP-bd	<u>RT</u>		5	0.2	9.4E-2	1.0E0
	INTERPRO	Post-SET_dom	<u>RT</u>		5	0.2	9.4E-2	1.0E0
	INTERPRO	<u>MPN</u>	<u>RT</u>		5	0.2	9.4E-2	1.0E0
	INTERPRO	TPR_repeat	<u>RT</u>		20	1.0	9.4E-2	1.0E0
	INTERPRO	WW dom sf	<u>RT</u>		9	0.4	9.5E-2	1.0E0
	INTERPRO	SH3-like dom sf	<u>RT</u>		29	1.4	9.6E-2	1.0E0
	INTERPRO	SH3_domain	<u>RT</u>		30	1.5	9.6E-2	1.0E0

1206 gene(s) from your list are not in the output.

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