



Functional Annotation Chart

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

Options

Rerun Using Options

Create Sublist

32 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Host-virus interaction	RT	<div></div>	213	10.4	1.7E-45	2.3E-43
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	mRNA processing	RT	<div></div>	118	5.8	4.7E-23	3.2E-21
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	mRNA splicing	RT	<div></div>	97	4.7	6.1E-21	2.8E-19
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Apoptosis	RT	<div></div>	121	5.9	1.5E-12	5.1E-11
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Protein transport	RT	<div></div>	134	6.5	8.1E-12	2.2E-10
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Cell cycle	RT	<div></div>	126	6.1	8.4E-8	1.9E-6
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Ubl conjugation pathway	RT	<div></div>	131	6.4	8.9E-7	1.7E-5
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Innate immunity	RT	<div></div>	81	3.9	4.9E-6	7.4E-5
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Biological rhythms	RT	<div></div>	38	1.9	4.9E-6	7.4E-5
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	ER-Golgi transport	RT	<div></div>	29	1.4	6.5E-6	8.4E-5
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Unfolded protein response	RT	<div></div>	18	0.9	6.8E-6	8.4E-5
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Autophagy	RT	<div></div>	40	1.9	1.5E-5	1.7E-4
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Electron transport	RT	<div></div>	30	1.5	1.6E-5	1.7E-4
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Cell division	RT	<div></div>	75	3.7	1.0E-4	9.7E-4
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Antiviral defense	RT	<div></div>	32	1.6	1.4E-4	1.2E-3
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Respiratory chain	RT	<div></div>	20	1.0	1.4E-4	1.2E-3
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Translation regulation	RT	<div></div>	31	1.5	3.2E-4	2.6E-3
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Protein biosynthesis	RT	<div></div>	33	1.6	5.7E-4	4.3E-3
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Tricarboxylic acid cycle	RT	<div></div>	10	0.5	1.3E-3	9.2E-3
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Chromosome partition	RT	<div></div>	14	0.7	2.4E-3	1.6E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Stress response	RT	<div></div>	24	1.2	4.6E-3	3.0E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription regulation	RT	<div></div>	313	15.3	9.7E-3	6.0E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Purine salvage	RT	<div></div>	4	0.2	1.3E-2	7.6E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	mRNA transport	RT	<div></div>	23	1.1	1.5E-2	8.7E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transcription	RT	<div></div>	319	15.5	1.6E-2	8.9E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	DNA damage	RT	<div></div>	66	3.2	1.8E-2	9.3E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transport	RT	<div></div>	274	13.4	1.9E-2	9.8E-2
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Immunity	RT	<div></div>	132	6.4	2.2E-2	1.1E-1
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	DNA repair	RT	<div></div>	56	2.7	2.3E-2	1.1E-1
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Ribosome biogenesis	RT	<div></div>	19	0.9	3.6E-2	1.6E-1
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Mitosis	RT	<div></div>	45	2.2	4.0E-2	1.8E-1
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Polyamine biosynthesis	RT	<div></div>	4	0.2	7.6E-2	3.2E-1

905 gene(s)

 from your list are not in the output.

Please [cite DAVID](#) within any publication that makes use of any methods inspired by **DAVID**.