



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

13 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	HIV_INTERACTION	Pr55(Gag)	RT	<div></div>	258	12.6	5.7E-27	1.2E-25
<input type="checkbox"/>	HIV_INTERACTION	Gag-Pol	RT	<div></div>	113	5.5	1.1E-21	1.3E-20
<input type="checkbox"/>	HIV_INTERACTION	Nef	RT	<div></div>	270	13.2	2.6E-16	1.9E-15
<input type="checkbox"/>	HIV_INTERACTION	Vpu	RT	<div></div>	101	4.9	2.7E-10	1.5E-9
<input type="checkbox"/>	HIV_INTERACTION	Rev	RT	<div></div>	114	5.6	1.3E-9	5.8E-9
<input type="checkbox"/>	HIV_INTERACTION	retropepsin	RT	<div></div>	99	4.8	5.4E-7	2.0E-6
<input type="checkbox"/>	HIV_INTERACTION	integrase	RT	<div></div>	75	3.7	3.8E-6	1.2E-5
<input type="checkbox"/>	HIV_INTERACTION	Vpr	RT	<div></div>	190	9.3	7.8E-6	2.2E-5
<input type="checkbox"/>	HIV_INTERACTION	Envelope surface glycoprotein gp120	RT	<div></div>	309	15.1	7.1E-5	1.7E-4
<input type="checkbox"/>	HIV_INTERACTION	matrix	RT	<div></div>	70	3.4	1.8E-3	4.0E-3
<input type="checkbox"/>	HIV_INTERACTION	Envelope surface glycoprotein gp160_precursor	RT	<div></div>	123	6.0	6.0E-3	1.2E-2
<input type="checkbox"/>	HIV_INTERACTION	Pol	RT	<div></div>	22	1.1	1.5E-2	2.8E-2
<input type="checkbox"/>	HIV_INTERACTION	capsid	RT	<div></div>	70	3.4	3.0E-2	5.1E-2

1309 gene(s)

 from your list are not in the output.

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