



Functional Annotation Chart

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Current Gene List: List\_1  
Current Background: Homo sapiens  
417 DAVID IDs  
Options

Rerun Using Options   Create Sublist

36 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	SMART	<a href="#">HOLI</a>	<a href="#">RT</a>		24	5.8	8.4E-22	1.6E-19
<input type="checkbox"/>	SMART	<a href="#">ZnF_C4</a>	<a href="#">RT</a>		23	5.5	7.1E-21	6.7E-19
<input type="checkbox"/>	SMART	<a href="#">TyrKc</a>	<a href="#">RT</a>		24	5.8	5.9E-12	3.7E-10
<input type="checkbox"/>	SMART	<a href="#">SH2</a>	<a href="#">RT</a>		18	4.3	1.6E-7	7.4E-6
<input type="checkbox"/>	SMART	<a href="#">SH3</a>	<a href="#">RT</a>		21	5.0	3.2E-5	1.2E-3
<input type="checkbox"/>	SMART	<a href="#">S_TKc</a>	<a href="#">RT</a>		23	5.5	6.0E-5	1.9E-3
<input type="checkbox"/>	SMART	<a href="#">PAS</a>	<a href="#">RT</a>		7	1.7	7.2E-4	1.9E-2
<input type="checkbox"/>	SMART	<a href="#">DEATH</a>	<a href="#">RT</a>		7	1.7	8.5E-4	2.0E-2
<input type="checkbox"/>	SMART	<a href="#">eIF5C</a>	<a href="#">RT</a>		4	1.0	1.2E-3	2.5E-2
<input type="checkbox"/>	SMART	<a href="#">14_3_3</a>	<a href="#">RT</a>		4	1.0	1.2E-3	2.5E-2
<input type="checkbox"/>	SMART	<a href="#">PAC</a>	<a href="#">RT</a>		6	1.4	1.5E-3	2.9E-2
<input type="checkbox"/>	SMART	<a href="#">DWB</a>	<a href="#">RT</a>		4	1.0	1.9E-3	3.2E-2
<input type="checkbox"/>	SMART	<a href="#">MIF4G</a>	<a href="#">RT</a>		4	1.0	3.8E-3	5.9E-2
<input type="checkbox"/>	SMART	<a href="#">DWA</a>	<a href="#">RT</a>		4	1.0	6.7E-3	9.3E-2
<input type="checkbox"/>	SMART	<a href="#">CASC</a>	<a href="#">RT</a>		4	1.0	1.0E-2	1.3E-1
<input type="checkbox"/>	SMART	<a href="#">EPH_Ibd</a>	<a href="#">RT</a>		4	1.0	1.0E-2	1.3E-1
<input type="checkbox"/>	SMART	<a href="#">MA3</a>	<a href="#">RT</a>		3	0.7	1.6E-2	1.8E-1
<input type="checkbox"/>	SMART	<a href="#">SPEC</a>	<a href="#">RT</a>		5	1.2	1.9E-2	2.1E-1
<input type="checkbox"/>	SMART	<a href="#">PI3Kc</a>	<a href="#">RT</a>		4	1.0	2.1E-2	2.1E-1
<input type="checkbox"/>	SMART	<a href="#">CHROMO</a>	<a href="#">RT</a>		5	1.2	2.2E-2	2.1E-1
<input type="checkbox"/>	SMART	<a href="#">HELICc</a>	<a href="#">RT</a>		9	2.2	2.6E-2	2.4E-1
<input type="checkbox"/>	SMART	<a href="#">PI3K_C2</a>	<a href="#">RT</a>		3	0.7	2.8E-2	2.3E-1
<input type="checkbox"/>	SMART	<a href="#">CH</a>	<a href="#">RT</a>		7	1.7	3.0E-2	2.4E-1
<input type="checkbox"/>	SMART	<a href="#">DEXDc</a>	<a href="#">RT</a>		9	2.2	3.1E-2	2.4E-1
<input type="checkbox"/>	SMART	<a href="#">WW</a>	<a href="#">RT</a>		6	1.4	3.2E-2	2.4E-1
<input type="checkbox"/>	SMART	<a href="#">CULLIN</a>	<a href="#">RT</a>		3	0.7	3.5E-2	2.4E-1
<input type="checkbox"/>	SMART	<a href="#">ARM</a>	<a href="#">RT</a>		5	1.2	3.5E-2	2.4E-1
<input type="checkbox"/>	SMART	<a href="#">PI3Ka</a>	<a href="#">RT</a>		3	0.7	4.3E-2	2.7E-1
<input type="checkbox"/>	SMART	<a href="#">BROMO</a>	<a href="#">RT</a>		5	1.2	4.5E-2	2.7E-1
<input type="checkbox"/>	SMART	<a href="#">CYCLIN</a>	<a href="#">RT</a>		5	1.2	4.5E-2	2.7E-1
<input type="checkbox"/>	SMART	<a href="#">UBCc</a>	<a href="#">RT</a>		5	1.2	4.8E-2	2.8E-1
<input type="checkbox"/>	SMART	<a href="#">ZnF_TAZ</a>	<a href="#">RT</a>		2	0.5	6.6E-2	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">Ku78</a>	<a href="#">RT</a>		2	0.5	6.6E-2	3.6E-1
<input type="checkbox"/>	SMART	<a href="#">HECTc</a>	<a href="#">RT</a>		4	1.0	6.7E-2	3.5E-1
<input type="checkbox"/>	SMART	<a href="#">UBO</a>	<a href="#">RT</a>		5	1.2	6.8E-2	3.5E-1
<input type="checkbox"/>	SMART	<a href="#">B41</a>	<a href="#">RT</a>		5	1.2	8.7E-2	4.2E-1

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

Please cite [Nature Protocols 2009; 4\(1\):44](#) & [Genome Biology 2003; 4\(5\):P3](#) within any publication that makes use of any methods inspired by **DAVID**.



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