



Functional Annotation Chart

[Help and Manual](#)

Current Gene List: condition\_specific\_gene\_list  
Current Background: Homo sapiens  
2052 DAVID IDs

Options

Rerun Using Options    Create Sublist

4 chart records

[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GAD_DISEASE_CLASS	INFECTION	<a href="#">RT</a>		306	14.9	3.9E-10	7.1E-9
<input type="checkbox"/>	GAD_DISEASE_CLASS	IMMUNE	<a href="#">RT</a>		364	17.7	1.2E-4	1.0E-3
<input type="checkbox"/>	GAD_DISEASE_CLASS	CANCER	<a href="#">RT</a>		384	18.7	2.3E-4	1.4E-3
<input type="checkbox"/>	GAD_DISEASE_CLASS	PHARMACOGENOMIC	<a href="#">RT</a>		314	15.3	1.2E-2	5.6E-2

1210 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**.