

New [Enhancer-Gene Map](#) [PANTHER16.0 Released.](#)

Analysis Summary: Please report in publication [?](#)

**Analysis Type:** PANTHER Overrepresentation Test (Released 20210224)

**Annotation Version and Release Date:** PANTHER version 16.0 Released 2020-12-01

**Analyzed List:** allDEgenes.txt (Homo sapiens)

[Change](#)

**Reference List:** Homo sapiens (all genes in database)

[Change](#)

**Annotation Data Set:** PANTHER GO-Slim Molecular Function [?](#)

**Test Type:** ☒ Fisher's Exact ☐ Binomial

**Correction:** ☒ Calculate False Discovery Rate ☐ Use the Bonferroni correction for multiple testing [?](#) ☐ No correction

Results [?](#)

	Reference list	allDEgenes.txt
Uniquely Mapped IDs:	<a href="#">20595</a> out of 20595	<a href="#">361</a> out of 361
Unmapped IDs:	<a href="#">0</a>	<a href="#">12</a>
Multiple mapping information:	0	<a href="#">0</a>

Export [Table](#) [XML with user input ids](#) [JSON with user input ids](#) View: [-- Please select a chart to display --](#) [?](#)

Displaying only results for FDR P < 0.05, [click here to display all results](#)

	Homo sapiens (REF)	allDEgenes.txt ( <a href="#">Hierarchy</a> <a href="#">NEW!</a> <a href="#">?</a> )					
<a href="#">PANTHER GO-Slim Molecular Function</a>	#	#	<a href="#">expected</a>	<a href="#">Fold Enrichment</a>	<a href="#">+/-</a>	<a href="#">raw P value</a>	<a href="#">FDR</a>
<a href="#">microtubule motor activity</a>	<a href="#">54</a>	<a href="#">7</a>	.95	7.40	+	8.33E-05	2.31E-02
↳ <a href="#">motor activity</a>	<a href="#">70</a>	<a href="#">8</a>	1.23	6.52	+	5.89E-05	3.27E-02
<a href="#">cell adhesion molecule binding</a>	<a href="#">122</a>	<a href="#">10</a>	2.14	4.68	+	9.86E-05	1.82E-02