

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:** DE50KB.txt (Homo sapiens)

[Change](#)

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

[Change](#)

**Annotation Data Set:** PANTHER GO-Slim Cellular Component ▾ [?](#)

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

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

Results [?](#)

	Reference list	DE50KB.txt
Uniquely Mapped IDs:	<a href="#">20595</a> out of 20595	<a href="#">216</a> out of 216
Unmapped IDs:	<a href="#">0</a>	<a href="#">7</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](#)

	<a href="#">Homo sapiens</a> (REF)	<a href="#">DE50KB.txt</a> (▼ <a href="#">Hierarchy</a> <b>NEW!</b> <a href="#">?</a> )					
<a href="#">PANTHER GO-Slim Cellular Component</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="#">anchoring junction</a>	<a href="#">168</a>	<a href="#">9</a>	1.76	5.11	+	1.00E-04	5.10E-02
<a href="#">receptor complex</a>	<a href="#">213</a>	<a href="#">10</a>	2.23	4.48	+	1.18E-04	3.00E-02