

Now includes comprehensive GO annotations directly imported from the GO database

Analysis Summary: Please report in publication ?

Analysis Type: PANTHER Overrepresentation Test (release 20160321)

Annotation Version and Release Date: PANTHER version 10.0 Released 2015-05-15

Analyzed List: Client Text Box Input (Homo sapiens)Change

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

Annotation Data Set: PANTHER GO-Slim Biological Process MUSE CELLS

☒ Use the Bonferroni correction for multiple testing ?

Results ?

	Reference list	Client Text Box Input
Mapped IDs:	20814	187
Unmapped IDs:	0	7

Export resultsView: -- Please select a chart to display --

Displaying only results with P<0.05; [click here to display all results](#)

	Homo sapiens (REF)	Client Text Box Input (▼ Hierarchy NEW! ?)				
PANTHER GO-Slim Biological Process	#	#	expected	Fold Enrichment	+/-	P value
glycolysis	25	6	.22	26.71	+	3.02E-05
↳ monosaccharide metabolic process	143	8	1.28	6.23	+	1.18E-02
↳ generation of precursor metabolites and energy	274	10	2.46	4.06	+	4.72E-02
regulation of liquid surface tension	56	8	.50	15.90	+	1.26E-05
↳ homeostatic process	209	11	1.88	5.86	+	8.33E-04
cell-matrix adhesion	89	7	.80	8.75	+	4.18E-03
↳ cell adhesion	579	18	5.20	3.46	+	1.31E-03
↳ biological adhesion	606	20	5.44	3.67	+	1.56E-04
cellular component morphogenesis	478	31	4.29	7.22	+	2.42E-15
↳ anatomical structure morphogenesis	596	35	5.35	6.54	+	3.16E-16
↳ developmental process	2456	54	22.07	2.45	+	5.77E-08
↳ cellular component organization	1206	37	10.84	3.41	+	1.17E-08
↳ cellular component organization or biogenesis	1316	39	11.82	3.30	+	8.79E-09
macrophage activation	167	10	1.50	6.66	+	7.60E-04
↳ immune system process	1391	28	12.50	2.24	+	1.20E-02
blood circulation	154	8	1.38	5.78	+	1.96E-02
protein folding	155	8	1.39	5.74	+	2.05E-02
cell-cell adhesion	391	16	3.51	4.55	+	1.42E-04
regulation of catalytic activity	1073	26	9.64	2.70	+	9.97E-04

↳ regulation of molecular function	1096	26	9.85	2.64	+	1.45E-03
cellular process	6708	93	60.27	1.54	+	1.15E-04
Unclassified	8629	36	77.53	.46	-	0.00E00
regulation of transcription from RNA polymerase II promoter	1319	1	11.85	< 0.2	-	1.45E-02
↳ transcription from RNA polymerase II promoter	1723	1	15.48	< 0.2	-	3.79E-04
↳ transcription, DNA-dependent	1941	1	17.44	< 0.2	-	5.01E-05
↳ RNA metabolic process	2360	2	21.20	< 0.2	-	1.15E-05
↳ regulation of nucleobase-containing compound metabolic process	1700	2	15.27	< 0.2	-	4.13E-03

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Analized List: Client Text Box Input (Homo sapiens)Change

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

Annotation Data Set: PANTHER GO-Slim Molecular Function MUSE CELLS

☒ Use the Bonferroni correction for multiple testing ?

Results ?

	Reference list	Client Text Box Input
Mapped IDs:	20814	187
Unmapped IDs:	0	7

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Displaying only results with P<0.05; [click here to display all results](#)

	Homo sapiens (REF)	Client Text Box Input (▼ Hierarchy NEW! ?)				
PANTHER GO-Slim Molecular Function	#	#	expected	Fold Enrichment	±/-	P value
peroxidase activity	27	4	.24	16.49	+	1.95E-02
↳ antioxidant activity	30	4	.27	14.84	+	2.92E-02
extracellular matrix structural constituent	76	9	.68	13.18	+	6.89E-06
↳ structural molecule activity	1034	40	9.29	4.31	+	8.29E-13
peptidase inhibitor activity	226	20	2.03	9.85	+	6.08E-12
↳ enzyme inhibitor activity	362	20	3.25	6.15	+	2.64E-08
↳ enzyme regulator activity	1002	24	9.00	2.67	+	2.22E-03
↳ peptidase activity	630	29	5.66	5.12	+	1.22E-10
cysteine-type peptidase activity	92	7	.83	8.47	+	3.94E-03
isomerase activity	166	9	1.49	6.03	+	3.91E-03
structural constituent of cytoskeleton	663	29	5.96	4.87	+	4.19E-10
serine-type peptidase activity	322	14	2.89	4.84	+	2.78E-04
Unclassified	10020	52	90.02	.58	-	0.00E00

DNA binding	1878	1	16.87	< 0.2	-	6.91E-05
↳nucleic acid binding	2915	4	26.19	< 0.2	-	3.75E-06

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Analzyed List: Client Text Box Input (Homo sapiens)

Change

Reference List: Homo sapiens (all genes in database)

Change

Annotation Data Set:

PANTHER GO-Slim Biological Process

BONE MARROW MSCs

☒ Use the Bonferroni correction for multiple testing ?

Results ?

	Reference list	Client Text Box Input
Mapped IDs:	20814	361
Unmapped IDs:	0	5

Export results

View:

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	Homo sapiens (REF)	Client Text Box Input (▼ Hierarchy NEW! ?)				
PANTHER GO-Slim Biological Process	#	#	expected	Fold Enrichment	+/-	P value
tricarboxylic acid cycle	20	5	.35	14.41	+	6.77E-03
↳ metabolic process	8247	180	143.04	1.26	+	1.13E-02
glycolysis	25	6	.43	13.84	+	1.36E-03
↳ monosaccharide metabolic process	143	11	2.48	4.44	+	1.16E-02
↳ generation of precursor metabolites and energy	274	16	4.75	3.37	+	7.18E-03
regulation of liquid surface tension	56	13	.97	13.38	+	8.19E-09
↳ homeostatic process	209	19	3.62	5.24	+	1.82E-06
protein folding	155	21	2.69	7.81	+	2.22E-10
↳ protein metabolic process	2692	103	46.69	2.21	+	8.66E-13
cellular component morphogenesis	478	50	8.29	6.03	+	1.49E-21
↳ anatomical structure morphogenesis	596	55	10.34	5.32	+	2.31E-21
↳ developmental process	2456	105	42.60	2.46	+	1.95E-16
↳ cellular component organization	1206	64	20.92	3.06	+	4.12E-13
↳ cellular component organization or biogenesis	1316	71	22.82	3.11	+	3.69E-15
cell-matrix adhesion	89	9	1.54	5.83	+	7.12E-03
↳ cell adhesion	579	37	10.04	3.68	+	3.93E-09
↳ biological adhesion	606	41	10.51	3.90	+	4.86E-11
protein complex assembly	107	10	1.86	5.39	+	5.09E-03
↳ protein complex biogenesis	108	10	1.87	5.34	+	5.50E-03

cell-cell adhesion	391	33	6.78	4.87	+	3.72E-11
macrophage activation	167	14	2.90	4.83	+	4.30E-04
↳ immune system process	1391	50	24.13	2.07	+	2.19E-04
receptor-mediated endocytosis	205	16	3.56	4.50	+	2.02E-04
↳ endocytosis	373	25	6.47	3.86	+	3.41E-06
regulation of translation	148	11	2.57	4.29	+	1.57E-02
muscle contraction	217	14	3.76	3.72	+	7.78E-03
↳ system process	1296	48	22.48	2.14	+	1.62E-04
↳ single-multicellular organism process	1636	52	28.37	1.83	+	4.15E-03
↳ multicellular organismal process	1640	52	28.44	1.83	+	4.43E-03
proteolysis	719	36	12.47	2.89	+	4.37E-06
mesoderm development	671	31	11.64	2.66	+	2.39E-04
response to stimulus	2170	65	37.64	1.73	+	2.16E-03
cellular process	6708	188	116.34	1.62	+	1.17E-12
Unclassified	8629	61	149.66	.41	-	0.00E00
regulation of transcription from RNA polymerase II promoter	1319	7	22.88	.31	-	1.61E-02
↳ transcription from RNA polymerase II promoter	1723	10	29.88	.33	-	2.94E-03
↳ transcription, DNA-dependent	1941	10	33.66	.30	-	1.64E-04
↳ RNA metabolic process	2360	17	40.93	.42	-	1.80E-03
↳ regulation of nucleobase-containing compound metabolic process	1700	8	29.48	.27	-	3.32E-04

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Homo sapiens (all genes in database)

Change

Annotation Data Set:

PANTHER GO-Slim Molecular Function

BONE MARROW MSCs

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	Reference list	Client Text Box Input
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	Homo sapiens (REF)	Client Text Box Input (▼ Hierarchy NEW! ?)				
PANTHER GO-Slim Molecular Function	#	#	expected	Fold Enrichment	+/-	P value
peroxidase activity	27	6	.47	12.81	+	1.60E-03
↳ antioxidant activity	30	6	.52	11.53	+	2.89E-03
extracellular matrix structural constituent	76	16	1.32	12.14	+	1.46E-10
↳ structural molecule activity	1034	80	17.93	4.46	+	2.62E-27
actin binding	176	27	3.05	8.85	+	4.55E-15
↳ cytoskeletal protein binding	251	29	4.35	6.66	+	4.16E-13
↳ protein binding	2819	100	48.89	2.05	+	2.07E-10
translation elongation factor activity	46	6	.80	7.52	+	2.98E-02
↳ translation factor activity, nucleic acid binding	136	11	2.36	4.66	+	5.67E-03
↳ translation regulator activity	128	10	2.22	4.50	+	1.70E-02
isomerase activity	166	18	2.88	6.25	+	2.38E-07
↳ catalytic activity	5209	127	90.35	1.41	+	1.88E-03
structural constituent of cytoskeleton	663	55	11.50	4.78	+	2.29E-19
metallopeptidase activity	170	13	2.95	4.41	+	2.00E-03
↳ peptidase activity	630	38	10.93	3.48	+	8.17E-09
↳ hydrolase activity	2205	62	38.24	1.62	+	1.73E-02

serine-type peptidase activity	322	22	5.58	3.94	+	1.40E-05
peptidase inhibitor activity	226	15	3.92	3.83	+	2.28E-03
oxidoreductase activity	626	40	10.86	3.68	+	4.30E-10
receptor binding	980	34	17.00	2.00	+	2.02E-02
Unclassified	10020	100	173.79	.58	-	0.00E00
sequence-specific DNA binding transcription factor activity	1462	7	25.36	.28	-	1.80E-03
↳ nucleic acid binding transcription factor activity	1646	7	28.55	.25	-	1.35E-04
↳ DNA binding	1878	9	32.57	.28	-	8.09E-05

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Change

Reference List:

Homo sapiens (all genes in database)

Change

Annotation Data Set:

PANTHER GO-Slim Biological Process

ADIPOSE MSCs

☒ Use the Bonferroni correction for multiple testing ?

Results ?

	Reference list	Client Text Box Input
Mapped IDs:	20814	247
Unmapped IDs:	0	2

Export results

View: -- Please select a chart to display --

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	Homo sapiens (REF)	Client Text Box Input (▼ Hierarchy NEW! ?)				
PANTHER GO-Slim Biological Process	#	#	expected	Fold Enrichment	+/-	P value
tricarboxylic acid cycle	20	5	.24	21.07	+	1.10E-03
↳ primary metabolic process	6825	108	80.99	1.33	+	4.79E-02
↳ metabolic process	8247	127	97.87	1.30	+	2.54E-02
glycolysis	25	6	.30	20.22	+	1.54E-04
↳ monosaccharide metabolic process	143	10	1.70	5.89	+	2.29E-03
↳ carbohydrate metabolic process	573	21	6.80	3.09	+	1.40E-03
↳ generation of precursor metabolites and energy	274	14	3.25	4.31	+	1.47E-03
regulation of liquid surface tension	56	8	.66	12.04	+	1.05E-04
↳ homeostatic process	209	14	2.48	5.64	+	6.55E-05
protein folding	155	22	1.84	11.96	+	1.00E-14
↳ protein metabolic process	2692	73	31.95	2.29	+	1.21E-09
cell-matrix adhesion	89	9	1.06	8.52	+	3.45E-04
↳ cell adhesion	579	30	6.87	4.37	+	4.69E-09
↳ biological adhesion	606	32	7.19	4.45	+	5.82E-10
protein complex assembly	107	9	1.27	7.09	+	1.51E-03
↳ protein complex biogenesis	108	9	1.28	7.02	+	1.62E-03
↳ cellular component organization or biogenesis	1316	47	15.62	3.01	+	2.93E-09
cell-cell adhesion	391	27	4.64	5.82	+	8.34E-11
cellular component morphogenesis	478	29	5.67	5.11	+	2.48E-10

↳anatomical structure morphogenesis	596	35	7.07	4.95	+	2.37E-12
↳developmental process	2456	69	29.15	2.37	+	1.17E-09
↳cellular component organization	1206	39	14.31	2.73	+	3.19E-06
blood coagulation	168	9	1.99	4.51	+	4.69E-02
↳response to stimulus	2170	46	25.75	1.79	+	1.72E-02
endocytosis	373	15	4.43	3.39	+	1.09E-02
proteolysis	719	25	8.53	2.93	+	4.47E-04
mesoderm development	671	20	7.96	2.51	+	3.92E-02
immune system process	1391	39	16.51	2.36	+	1.25E-04
system process	1296	32	15.38	2.08	+	1.70E-02
cell communication	3006	61	35.67	1.71	+	3.24E-03
↳cellular process	6708	127	79.60	1.60	+	7.68E-08
Unclassified	8629	43	102.40	.42	-	0.00E00
regulation of transcription from RNA polymerase II promoter	1319	2	15.65	< 0.2	-	3.29E-03
↳transcription from RNA polymerase II promoter	1723	4	20.45	< 0.2	-	1.44E-03
↳transcription, DNA-dependent	1941	4	23.03	< 0.2	-	1.39E-04
↳RNA metabolic process	2360	7	28.01	.25	-	1.99E-04
↳nucleobase-containing compound metabolic process	3467	18	41.14	.44	-	2.54E-03
↳regulation of nucleobase-containing compound metabolic process	1700	3	20.17	< 0.2	-	3.22E-04

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	Reference list	Client Text Box Input
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	Homo sapiens (REF)	Client Text Box Input (▼ Hierarchy NEW! ?)				
PANTHER GO-Slim Molecular Function	#	#	expected	Fold Enrichment	+/-	P value
peroxidase activity	27	5	.32	15.61	+	3.52E-03
↳ antioxidant activity	30	6	.36	16.85	+	3.34E-04
extracellular matrix structural constituent	76	13	.90	14.41	+	2.33E-09
↳ structural molecule activity	1034	53	12.27	4.32	+	3.08E-17
translation elongation factor activity	46	5	.55	9.16	+	4.21E-02
metallopeptidase activity	170	13	2.02	6.44	+	3.07E-05
↳ peptidase activity	630	29	7.48	3.88	+	1.19E-07
↳ catalytic activity	5209	90	61.82	1.46	+	7.67E-03
isomerase activity	166	12	1.97	6.09	+	1.63E-04
lipid transporter activity	112	8	1.33	6.02	+	1.17E-02
actin binding	176	12	2.09	5.75	+	2.97E-04
↳ cytoskeletal protein binding	251	12	2.98	4.03	+	9.67E-03
↳ protein binding	2819	66	33.45	1.97	+	5.52E-06
peptidase inhibitor activity	226	14	2.68	5.22	+	1.25E-04
↳ enzyme inhibitor activity	362	14	4.30	3.26	+	2.23E-02
serine-type peptidase activity	322	18	3.82	4.71	+	1.46E-05

structural constituent of cytoskeleton	663	34	7.87	4.32	+	1.92E-10
oxidoreductase activity	626	31	7.43	4.17	+	4.94E-09
calmodulin binding	282	12	3.35	3.59	+	2.84E-02
calcium ion binding	449	17	5.33	3.19	+	5.57E-03
receptor binding	980	26	11.63	2.24	+	2.11E-02
Unclassified	10020	67	118.91	.56	-	0.00E00
sequence-specific DNA binding transcription factor activity	1462	2	17.35	< 0.2	-	5.02E-04
↳ nucleic acid binding transcription factor activity	1646	2	19.53	< 0.2	-	6.05E-05
↳ DNA binding	1878	5	22.29	.22	-	1.07E-03