

Home	About	PANTHER Data	PANTHER Tools	PANTHER Services	Workspaces	Downloads	Help/Tutorial
New: Enhancer-Gene Map PANTHER16.0 Released.							
Analysis Summary: Please report in publication (1)							
Analysis Type: PANTHER overrepresentation Test (Released 20210224)							
Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.4437524 Released 2021-01-01							
Analyzed List: upload_1 (Home sapiens) Change							
Reference List: Home sapiens (all genes in database) Change							
Annotation Data Set: Ecological process complete ? Change							
Test Type: Fisher's Exact - Binomial							
Correction: Calculate False Discovery Rate <input checked="" type="checkbox"/> Use the Bonferroni correction for multiple testing ? <input type="checkbox"/> No correction							

Results (1)
Uniquely Mapped IDs: 20585 out of 20595 1529 out of 1646
Unmapped IDs: 0 68
Multiple mapping information: 0 80
Export [Table](#) [XML with user input IDs](#) [JSON with user input IDs](#)

Displaying only results for FDR P < 0.05, click here to display all results

Neely 2021, suppl. Table 6A: cluster 0 at E 1.0 pM

Hom sapiens (REF)	#	upload_1 (Hierarchy, NEW!?)	# expected	Fold Enrichment	+/-	raw P-value	EDR
GO_biological_process	26	cerebral cortex regionalization	548	10.43	+	5.98E-04	3.2E-02
anatomical_structure_development	5264	497 420.71	1.18	+ 4.77E-05	3.1E-03		
developmental_process	5233	543 458.19	1.19	+ 1.02E-05	8.49E-04		
cellular_development	169	31 13.51	2.30	+ 9.93E-05	8.2E-03		
telencephalon_development	252	43 20.14	2.14	+ 2.48E-05	1.81E-03		
forebrain_development	380	53 36.37	1.94	+ 7.98E-06	6.91E-04		
brain_development	745	102 56.54	1.80	+ 7.01E-08	9.41E-06		
central_nervous_system_development	991	135 79.20	1.70	+ 2.24E-05	3.57E-06		
nervous_system_development	2183	269 174.95	1.54	+ 1.66E-10	4.94E-09		
system_development	4275	426 341.67	1.25	+ 1.80E-05	1.77E-04		
multicellular_organism_development	4875	426 389.62	1.22	+ 2.49E-06	2.40E-04		
head_development	788	116 62.98	1.81	+ 1.72E-04	2.83E-06		
animal_organ_development	3186	310 254.63	1.22	+ 4.28E-04	2.17E-02		
telencephalon_regionization	12	2 9.98	7.30	+ 2.73E-04	1.51E-02		
regionalization	218	48 25.42	1.89	+ 1.01E-04	7.00E-03		
forebrain_regionization	22	9 1.76	5.12	+ 2.95E-04	1.59E-02		
mitochondrial_electron_transport_NADH_to ubiquinone	49	20 39.92	5.36	+ 1.80E-05	3.29E-06		
mitochondrial_ATP_synthesis_coupled_electron_transport	89	30 21.11	4.22	+ 1.82E-09	3.59E-07		
ATP_synthesis_coupled_electron_transport	90	31 71.19	4.31	+ 3.38E-04	1.40E-07		
respiratory_electron_transport_chain	108	32 86.3	3.71	+ 1.72E-09	1.33E-06		
electron_transport_chain	120	40 13.59	2.94	+ 3.70E-04	4.12E-06		
generation_of_precursor_molecules_and_energy	402	65 31.23	2.02	+ 9.82E-07	1.05E-04		
cellular_mitochondrial_process	7571	805 605.00	1.33	+ 5.64E-02	8.89E-08		
metabolic_process	8324	856 666.07	1.29	+ 1.35E-10	6.97E-16		
caricular_process	15487	1387 1237.76	1.12	+ 3.10E-10	3.19E-14		
cellular_respiration	157	37 12.55	2.95	+ 8.60E-05	1.12E-05		
energy_stabilization_by_oxidation_of_organic_compounds	222	40 16.14	2.20	+ 1.76E-05	1.35E-03		
oxidative_phosphorylation	120	38 9.59	3.30	+ 5.93E-04	1.81E-08		
ATP_metabolic_process	208	50 16.46	3.04	+ 2.07E-10	4.88E-08		
SRB-dependent cotranslational protein targeting to membrane	98	37 7.67	4.82	+ 9.73E-13	4.51E-10		
protein_targeting_to_ER	111	40 8.87	4.51	+ 5.76E-13	3.33E-10		
protein_targeting	370	68 29.57	2.30	+ 5.40E-09	1.03E-06		
intracellular_protein_translocation	978	128 77.84	1.64	+ 3.24E-07	3.63E-05		
cellular_protein_localization	1643	202 131.31	1.54	+ 5.91E-09	1.65E-06		
cellular_macromolecule_localization	1649	203 131.79	1.54	+ 7.66E-09	1.36E-06		
cellular_localization	3006	325 240.25	1.35	+ 5.54E-08	7.54E-06		
localization	5805	532 463.95	1.15	+ 4.31E-04	2.17E-02		
macromolecule_localization	2553	262 204.00	1.28	+ 6.02E-05	4.06E-03		
protein_localization	2161	234 17.71	1.35	+ 6.36E-06	5.70E-04		
intracellular_transport	1500	193 119.88	1.61	+ 9.23E-10	1.99E-07		
establishment_of_localization_in_cell	2368	262 189.02	1.41	+ 4.06E-05	5.20E-06		
establishment_of_localization	4653	434 371.88	1.17	+ 6.65E-04	2.72E-02		
transport	4502	422 39.81	1.17	+ 4.86E-04	2.38E-02		
protein_transport	1464	165 117.01	1.41	+ 2.80E-05	2.02E-03		
establishment_of_protein_localization	1659	208 124.60	1.42	+ 1.05E-05	5.68E-04		
peptide_transport	1493	168 113.32	1.41	+ 2.65E-05	1.92E-03		
amide_transport	1527	169 120.4	1.38	+ 5.92E-04	4.02E-03		
nitrogen_compound_transport	1802	191 14.20	1.32	+ 2.92E-04	1.28E-02		
establishment_of_protein_localization_to_endoplasmic_reticulum	115	40 9.19	4.35	+ 1.69E-12	7.61E-10		
protein_localization_to_endoplasmic_reticulum	142	43 11.35	3.79	+ 1.11E-11	3.52E-09		
protein_localization_to_golgi	291	118 63.22	1.80	+ 1.85E-08	2.98E-06		
establishment_of_protein_localization_to_golgi	449	80 36.89	2.23	+ 1.86E-09	2.43E-07		
translational_protein_targeting_to_membrane	101	38 6.07	4.71	+ 3.74E-13	4.19E-10		
protein_targeting_to_membrane	183	42 14.63	3.21	+ 1.47E-10	3.62E-08		
establishment_of_protein_localization_to_membrane	207	68 24.54	2.77	+ 3.61E-02	1.77E-09		
protein_localization_to_membrane	532	92 42.92	2.26	+ 3.14E-12	2.68E-09		
cytoplasmic_translation	75	26 5.99	4.34	+ 1.35E-05	2.27E-06		
translation	384	82 30.69	2.67	+ 1.52E-13	1.01E-10		
peptide_biosynthetic_process	409	82 32.69	2.63	+ 3.84E-05	7.05E-01		
protein_biosynthetic_process	297	100 42.92	2.33	+ 5.62E-13	2.86E-10		
protein_localization	1696	239 135.55	1.76	+ 5.93E-16	3.70E-02		
intracellular_protein_localization	1698	534 419.91	1.27	+ 1.06E-15	1.86E-12		
protein_localization_to_endoplasmic_reticulum	115	40 9.19	4.35	+ 1.69E-12	7.61E-10		
protein_localization_to_golgi	142	43 11.35	3.79	+ 1.11E-11	3.52E-09		
establishment_of_protein_localization_to_golgi	291	118 63.22	1.80	+ 1.85E-08	2.98E-06		
establishment_of_protein_localization_to_golgi	449	80 36.89	2.23	+ 1.86E-09	2.43E-07		
translational_protein_targeting	101	28 10.7	4.71	+ 3.74E-13	4.19E-10		
protein_targeting	223	45 12.9	2.50	+ 3.73E-04	1.93E-02		
regulation_of_protein_localization	400	55 31.97	1.72	+ 3.73E-04	1.93E-02		
regulation_of_protein_localization_to_golgi	576	620 461.63	1.34	+ 5.91E-09	1.65E-06		
autophagy	6000	660 479.53	1.38	+ 7.28E-20	5.74E-16		
protein_catalytic_process	1582	213 125.44	1.68	+ 1.77E-12	7.47E-10		

Analysis summary: Please report in publication [①](#)

Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zendo.4437524 Released 2021-01-01

Analyzed List: upload_1 (Homo sapiens) [Change](#)Reference List: Homo sapiens (all genes in database) [Change](#)Annotation Data Set: [②](#) biological process complete [③](#) [④](#)Test Type: Fisher's exact BinomialCorrection: Calculate False Discovery Rate Use the Bonferroni correction for multiple testing [⑤](#) [⑥](#) - No correctionResults [⑦](#)

Uniquely Mapped IDs: 20595 out of 20595 902 out of 944

Unmapped IDs: 0 32

Multiple mapping information: 0 47

Export [Table](#) XML with user input [⑧](#) XML with user input [⑨](#)

Displaying only results for FDR P < 0.05, click here to display all results

Neely 2021, suppl. Table 6B: Cluster 1 at E 1.0 μM

Homo sapiens (REF)		#	expected	upload 1 (Y) Hierarchy, NEW! ⑩
		#	Fold Enrichment	+/- raw P-value FDR
GO:biological_process_complete	cerebral cortex regionalization	6	4.28	14.54 + 6.23E-04 2.91E-02
↳ anatomical_structure_development	↳ developmental_process	5264	339 241.28	1.40 + 6.92E-12 9.09E-09
↳ cell_adhesion	↳ cell_morphogenesis	5733	358 262.78	1.36 + 6.55E-11 4.49E-08
↳ cell_cycle	↳ cell_death	169	19 7.76	2.49 + 8.37E-04 3.80E-02
↳ cell_mitosis	↳ cell_regeneration	252	29 11.55	2.51 + 2.14E-05 1.69E-03
↳ cell_proliferation	↳ cell_subdivision	380	41 17.42	2.35 + 1.75E-06 1.95E-04
↳ cell_development	↳ cell_division	745	75 34.15	2.20 + 1.64E-09 6.29E-07
↳ cell_differentiation	↳ cell_regeneration	951	97 45.42	2.14 + 2.72E-11 2.05E-08
↳ cell_morphogenesis	↳ nervous_system_development	2189	184 100.34	1.83 + 6.10E-15 3.21E-11
↳ cell_death	↳ system_development	4275	286 195.95	1.46 + 1.87E-11 1.64E-08
↳ cell_division	↳ multicellular_organism_development	4875	321 223.45	1.44 + 2.62E-12 4.14E-09
↳ cell_regeneration	↳ multicellular_organismal_process	6998	376 316.84	1.19 + 8.01E-05 5.29E-03
↳ cell_subdivision	↳ nervous_system_development	788	80 36.12	2.21 + 2.99E-10 1.52E-07
↳ cell_development	↳ animal_organ_development	3186	203 146.03	1.39 + 1.85E-06 2.02E-04
↳ cell_regeneration	↳ brain_development	12	6 5.55	10.91 + 8.22E-05 5.38E-03
↳ cell_differentiation	↳ regionalization	318	33 14.58	2.26 + 5.35E-05 3.73E-03
↳ cell_death	↳ pattern_specification_process	423	39 19.39	2.01 + 1.16E-04 7.33E-03
↳ cell_regeneration	↳ forebrain_regeneration	22	7 1.01	6.94 + 2.03E-04 1.19E-02
↳ cell_subdivision	↳ radial_glia_cell_differentiation	11	5 5.50	9.92 + 4.66E-04 2.33E-02
↳ cell_development	↳ glial_cell_differentiation	171	20 7.84	2.55 + 2.97E-04 1.59E-02
↳ cell_regeneration	↳ head_development	3512	222 160.98	1.38 + 7.88E-07 9.54E-05
↳ cell_differentiation	↳ cerebellar_development	3565	228 163.41	1.40 + 2.29E-07 3.25E-05
↳ cell_regeneration	↳ cellular_process	15487	797 709.87	1.12 + 1.66E-11 1.54E-08
↳ cell_death	↳ gliogenesis	222	26 10.18	2.56 + 5.11E-05 3.62E-03
↳ cell_regeneration	↳ neurogenesis	1369	127 62.75	2.02 + 4.19E-13 1.10E-09
↳ cell_subdivision	positive regulation_of_nuclear_rna_transcribed_mRNA_catabolic_process, deadenylation-dependent_decay	16	6 7.33	8.18 + 2.84E-04 1.58E-02
↳ cell_regeneration	regulation_of_mRNA_catabolic_process	214	22 9.81	2.24 + 1.02E-03 4.50E-02
↳ cell_regeneration	regulation_of_metabolic_process	6854	423 914.16	1.35 + 7.32E-13 4.44E-09
↳ cell_regeneration	regulation_of_biological_process	1060	619 543.62	1.14 + 9.80E-07 1.14E-04
↳ cell_regeneration	biological_regulation	12576	637 576.44	1.11 + 7.21E-05 4.88E-03
↳ cell_regeneration	regulation_of_cellular_metabolic_process	6110	377 280.06	1.35 + 5.56E-11 3.99E-08
↳ cell_regeneration	regulation_of_cellular_process	11308	582 518.32	1.12 + 4.37E-05 3.19E-03
↳ cell_regeneration	regulation_of_mRNA_cathepsin	341	36 15.63	2.30 + 1.78E-05 1.43E-03
↳ cell_regeneration	regulation_of_RNA_cathepsin	3738	252 171.34	1.47 + 2.53E-10 1.33E-07
↳ cell_regeneration	regulation_of_mRNA_cathepsin	6308	402 289.14	1.39 + 4.37E-14 1.72E-10
↳ cell_regeneration	regulation_of_macromolecule_cathepsin	4007	266 183.67	1.45 + 3.18E-10 1.57E-07
↳ cell_regeneration	regulation_of_nucleotide-containing_compound_cathepsin	5882	362 260.90	1.39 + 3.57E-12 5.12E-09
↳ cell_regeneration	regulation_of_nitrogen_compound_cathepsin	5895	368 270.21	1.36 + 2.72E-11 2.14E-08
↳ cell_regeneration	regulation_of_gene_expression	4880	324 223.68	1.45 + 6.52E-13 4.17E-09
↳ cell_regeneration	positive regulation_of_mRNA_cathepsin	85	13 3.96	3.34 + 3.46E-04 1.85E-02
↳ cell_regeneration	positive regulation_of_tRNA_cathepsin	1719	129 78.79	1.64 + 1.01E-07 1.58E-05
↳ cell_regeneration	positive regulation_of_nucleobase-containing_compound_cathepsin	1892	142 86.72	1.64 + 1.95E-08 3.66E-06
↳ cell_regeneration	positive regulation_of_nitrogen_compound_cathepsin	3059	208 140.21	1.48 + 9.94E-09 2.18E-06
↳ cell_regeneration	positive regulation_of_nucleobase-containing_compound_cathepsin	3720	253 170.51	1.43 + 1.24E-08 2.62E-06
↳ cell_regeneration	positive regulation_of_biological_process	6245	369 286.25	1.29 + 2.52E-08 4.56E-06
↳ cell_regeneration	positive regulation_of_cellular_process	3239	129 148.46	1.48 + 5.65E-09 4.14E-06
↳ cell_regeneration	positive regulation_of_cellular_process	5657	351 259.30	1.35 + 2.43E-10 1.32E-07
↳ cell_regeneration	positive regulation_of_macromolecule_cathepsin	3432	229 157.31	1.46 + 7.17E-09 1.62E-06
↳ cell_regeneration	regulation_of_nuclear_transcribed_mRNA_cathepsin,deadenylation-dependent_decay	18	6 8.33	7.27 + 4.76E-04 2.36E-02
↳ cell_regeneration	negative regulation_of_membrane_potential	14	5 6.44	7.79 + 1.11E-03 4.79E-02
↳ cell_regeneration	mitochondrial_ATP_synthase_coupled_proton_transport	19	6 8.77	6.89 + 6.03E-04 2.86E-02
↳ cell_regeneration	organic_cyclic_compound_biosynthetic_process	1224	82 56.01	1.46 + 9.92E-04 4.41E-02
↳ cell_regeneration	organic_cyclic_compound_cathepsin	3190	214 146.22	1.46 + 1.73E-08 3.29E-06
↳ cell_regeneration	organic_substance_cathepsin	7879	432 361.34	1.20 + 4.49E-06 4.51E-04
↳ cell_regeneration	organic_substance_cathepsin	8334	475 382.00	1.24 + 2.35E-06 8.22E-07
↳ cell_regeneration	organic_substance_cathepsin	2804	197 128.53	1.53 + 2.76E-09 9.07E-07
↳ cell_regeneration	organic_substance_cathepsin	2862	198 131.38	1.51 + 6.90E-09 1.58E-06
↳ cell_regeneration	organic_substance_cathepsin	1076	74 49.32	1.50 + 1.06E-03 4.65E-02
↳ cell_regeneration	organic_substance_cathepsin	2904	198 133.11	1.49 + 2.50E-08 4.58E-06
↳ cell_regeneration	organic_substance_cathepsin	7571	450 347.03	1.30 + 2.59E-11 2.14E-08
↳ cell_regeneration	organic_substance_cathepsin	2709	185 124.37	1.49 + 6.94E-08 1.16E-05
↳ cell_regeneration	organic_substance_cathepsin	1975	126 72.19	1.75 + 4.78E-09 1.30E-06
↳ cell_regeneration	organic_substance_cathepsin	3407	222 156.91	1.42 + 8.48E-08 1.37E-05
↳ cell_regeneration	regulation_of_nuclear_transcribed_mRNA_cathepsin,deadenylation-dependent_decay	18	6 8.33	7.27 + 4.76E-04 2.36E-02
↳ cell_regeneration	negative regulation_of_membrane_potential	14	5 6.44	7.79 + 1.11E-03 4.79E-02
↳ cell_regeneration	mitochondrial_ATP_synthase_coupled_proton_transport	19	6 8.77	6.89 + 6.03E-04 2.86E-02
↳ cell_regeneration	organic_cyclic_compound_cathepsin	1224	82 56.01	1.46 + 9.92E-04 4.41E-02
↳ cell_regeneration	organic_substance_cathepsin	3190	214 146.22	1.46 + 1.73E-08 3.29E-06
↳ cell_regeneration	organic_substance_cathepsin	7879	432 361.34	1.20 + 4.49E-06 4.51E-04
↳ cell_regeneration	organic_substance_cathepsin	8334	475 382.00	1.24 + 2.35E-06 8.22E-07
↳ cell_regeneration	organic_substance_cathepsin	2804	197 128.53	1.53 + 2.76E-09 9.07E-07
↳ cell_regeneration	organic_substance_cathepsin	2862	198 131.38	1.51 + 6.90E-09 1.58E-06
↳ cell_regeneration	organic_substance_cathepsin	1076	74 49.32	1.50 + 1.06E-03 4.65E-02
↳ cell_regeneration	organic_substance_cathepsin	2904	198 133.11	1.49 + 2.50E-08 4.58E-06
↳ cell_regeneration	organic_substance_cathepsin	7571	450 347.03	1.30 + 2.59E-11 2.14E-08
↳ cell_regeneration	organic_substance_cathepsin	2709	185 124.37	1.49 + 6.94E-08 1.16E-05
↳ cell_regeneration	organic_substance_cathepsin	1975	126 72.19	1.75 + 4.78E-09 1.30E-06
↳ cell_regeneration	organic_substance_cathepsin	3407	222 156.91	1.42 + 8.48E-08 1.37E-05
↳ cell_regeneration	positive regulation_of_protein_kinase_B_activity	33	8 1.51	5.29 + 3.48E-04 1.85E-02
↳ cell_regeneration	regulation_of_protein_modification	1638	106 74.99	1.41 + 6.03E-04 2.85E-02
↳ cell_regeneration	regulation_of_cellular_protein_modification	2447	165 112.16	1.47 + 9.04E-07 1.07E-04
↳ cell_regeneration	regulation_of_protein_modification	2605	174 119.40	1.46 + 8.02E-07 9.58E-05
↳ cell_regeneration	positive regulation_of_protein_modification	1452	97 66.78	1.45 + 3.88E-04 2.01E-02
↳ cell_regeneration	positive regulation_of_protein_modification	1539	101 70.54	1.43 + 5.32E-04 2.57E-02
↳ cell_regeneration	regulation_of_protein_modification	3006	198 137.78	1.42 + 6.45E-07 8.07E-05
↳ cell_regeneration	regulation_of_protein_modification	33	8 1.51	5.29 + 3.4

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

Analysis Type: PANTHER Overrepresentation Test (Released 20210224)	
Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.4437524 Released 2021-01-01	
Analyzed List:	upload_1 (Homo sapiens) Change
Reference List:	Homo sapiens (all genes in database) Change
Annotation Data Set:	GO biological process complete ? ②
Test Type:	Fisher's Exact <input type="radio"/> Binomial
Correction:	Calculate False Discovery Rate <input type="radio"/> Use the Bonferroni correction for multiple testing ? <input type="radio"/> No correction

Results [?](#)

Reference list	upload_1
Uniquely Mapped IDs:	20595 out of 20595 49 out of 50
Unmapped IDs:	0 4
Multiple mapping information:	0 1

Export [Table](#) [XML with user input ids](#) [JSON with user input ids](#)Displaying only results for FDR P < 0.05, [click here to display all results](#)**Neely 2021, suppl Table 6C: Cluster 5 at E 1.0 μM**

	Homo sapiens (REF)	#	upload_1 (▼ Hierarchy NEW! ?)				
			#	expected	Fold Enrichment	+/-	raw P value
GO biological process complete							
umbilical cord morphogenesis		2	2	.00	> 100	+	3.44E-05 7.14E-03
↳ umbilical cord development		2	2	.00	> 100	+	3.44E-05 7.04E-03
negative regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation		3	2	.01	> 100	+	5.72E-05 1.00E-02
↳ negative regulation of transcription by RNA polymerase II		903	10	2.19	4.56	+	5.59E-05 9.90E-03
↳ negative regulation of transcription, DNA-templated		1289	11	3.13	3.52	+	2.26E-04 2.93E-02
↳ regulation of macromolecule metabolic process		6308	31	15.31	2.02	+	7.55E-06 2.05E-03
↳ regulation of metabolic process		6854	31	16.64	1.86	+	3.51E-05 7.09E-03
↳ negative regulation of macromolecule biosynthetic process		1499	12	3.64	3.30	+	2.01E-04 2.65E-02
↳ negative regulation of macromolecule metabolic process		2862	26	6.95	3.74	+	2.19E-10 1.44E-07
↳ negative regulation of metabolic process		3105	26	7.54	3.45	+	1.32E-09 6.30E-07
↳ negative regulation of biological process		5544	28	13.46	2.08	+	1.67E-05 4.06E-03
↳ negative regulation of biosynthetic process		1589	12	3.86	3.11	+	3.44E-04 4.08E-02
↳ negative regulation of cellular biosynthetic process		1557	12	3.78	3.17	+	2.86E-04 3.44E-02
↳ negative regulation of gene expression		2034	24	4.94	4.86	+	7.55E-12 6.61E-09
↳ regulation of gene expression		4880	31	11.85	2.62	+	9.44E-09 4.02E-06
↳ regulation of nucleic acid-templated transcription		3465	19	8.41	2.26	+	3.86E-04 4.47E-02
↳ regulation of RNA biosynthetic process		3470	19	8.42	2.26	+	3.90E-04 4.49E-02
↳ negative regulation of nucleic acid-templated transcription		1291	12	3.13	3.83	+	4.90E-05 9.20E-03
↳ negative regulation of RNA biosynthetic process		1293	12	3.14	3.82	+	4.97E-05 9.22E-03
↳ negative regulation of RNA metabolic process		1395	12	3.39	3.54	+	1.03E-04 1.53E-02
↳ negative regulation of nucleobase-containing compound metabolic process		1515	13	3.68	3.53	+	5.05E-05 9.27E-03
↳ regulation of transcription by RNA polymerase II		2586	17	6.28	2.71	+	7.80E-05 1.24E-02
negative regulation of transcription by transcription factor localization		3	2	.01	> 100	+	5.72E-05 9.92E-03
↳ cellular protein localization		1643	16	3.99	4.01	+	9.96E-07 3.14E-04
↳ cellular macromolecule localization		1649	16	4.00	4.00	+	1.05E-06 3.23E-04
↳ cellular localization		3006	19	7.30	2.60	+	4.18E-05 8.15E-03
↳ localization		5805	22	14.09	1.92	+	1.98E-04 2.64E-02
↳ macromolecule localization		2553	16	6.20	2.58	+	2.40E-04 3.03E-02
↳ protein localization		2161	16	5.25	3.05	+	3.29E-05 6.92E-03
arterial endothelial cell differentiation		6	2	.01	> 100	+	1.59E-04 2.21E-02
↳ blood vessel endothelial cell differentiation		8	2	.02	> 100	+	2.55E-04 3.15E-02
dorsal aorta morphogenesis		8	2	.02	> 100	+	2.55E-04 3.17E-02
↳ tube morphogenesis		644	9	1.56	5.76	+	2.35E-05 5.54E-03
↳ tube development		840	9	2.04	4.41	+	1.77E-04 2.41E-02
↳ dorsal aorta development		10	2	.02	82.38	+	3.74E-04 4.36E-02
atrioventricular valve formation		8	2	.02	> 100	+	2.55E-04 3.12E-02
Notch signaling involved in heart development		11	2	.03	74.89	+	4.41E-04 4.93E-02
ribosomal small subunit assembly		21	3	.05	58.84	+	2.61E-05 5.97E-03
↳ ribosome biogenesis		332	11	.81	13.65	+	4.75E-10 2.50E-07
↳ ribonucleoprotein complex biogenesis		465	11	1.13	9.74	+	1.45E-08 5.86E-06
↳ ribosomal small subunit biogenesis		75	4	.18	21.97	+	4.00E-05 7.89E-03
negative regulation of transcription regulatory region DNA binding		22	3	.05	56.17	+	2.96E-05 6.49E-03
↳ negative regulation of DNA binding		55	4	.13	29.96	+	1.26E-05 3.09E-03
↳ regulation of DNA binding		123	4	.30	13.40	+	2.53E-04 3.16E-02
↳ negative regulation of binding		163	5	.40	12.63	+	5.30E-05 9.60E-03
↳ regulation of transcription regulatory region DNA binding		54	3	.13	22.88	+	3.57E-04 4.20E-02
forebrain regionalization		22	3	.05	56.17	+	2.96E-05 6.49E-03
↳ brain development		745	10	1.81	5.53	+	1.10E-05 2.80E-03
↳ central nervous system development		991	10	2.41	4.16	+	1.20E-04 1.75E-02
↳ nervous system development		2189	15	5.31	2.82	+	1.51E-04 2.13E-02
↳ head development		788	10	1.91	5.23	+	1.78E-05 4.24E-03
↳ regionalization		318	6	.77	7.77	+	1.27E-04 1.83E-02
↳ pattern specification process		423	8	1.03	7.79	+	8.42E-06 2.25E-03
SRP-dependent cotranslational protein targeting to membrane		96	12	.23	51.49	+	2.30E-17 1.21E-13
↳ protein targeting to ER		111	13	.27	48.24	+	2.04E-18 3.22E-14
↳ protein targeting		370	13	.90	14.47	+	4.80E-12 4.74E-09
↳ intracellular protein transport		974	13	2.36	5.50	+	4.30E-07 1.44E-04
↳ intracellular transport		1500	15	3.64	4.12	+	1.74E-06 5.08E-04
↳ establishment of localization in cell		2365	16	5.74	2.79	+	9.79E-05 1.47E-02
↳ protein transport		1464	13	3.55	3.66	+	3.55E-05 7.08E-03
↳ establishment of protein localization		1559	13	3.78	3.43	+	6.77E-05 1.12E-02
↳ peptide transport		1493	13	3.62	3.59	+	4.35E-05 8.36E-03
↳ amide transport		1527	13	3.71	3.51	+	5.48E-05 9.82E-03
↳ nitrogen compound transport		1802	13	4.37	2.97	+	2.88E-04 3.44E-02
↳ ion transport		2882	18	7.00	2.57	+	8.60E-05 1.33E-02
↳ establishment of protein localization to endoplasmic reticulum		115	13	.28	46.56	+	3.13E-18 2.47E-14
↳ protein localization to endoplasmic reticulum		142	13	.34	37.71	+	4.03E-17 1.59E-13
↳ protein localization to organelle		791	14	1.92	7.29	+	4.27E-09 1.92E-06
↳ establishment of protein localization to organelle		449	13	1.09	11.93	+	4.99E-11 3.75E-08
↳ cotranslational protein targeting to membrane		101	12	.25	48.94	+	4.05E-17 1.28E-13
↳ protein targeting to membrane		183	13	.44	29.26	+	8.89E-16 1.56E-12
↳ establishment of protein localization to membrane		307	13	.75	17.44	+	4.96E-13 5.59E-10
↳ protein localization to membrane		537	13	1.30	9.97	+	4.26E-10 2.32E-07
cytoplasmic translation		75	9	.18	49.43	+	4.30E-13 5.22E-10
↳ translation		384	13	.93	13.94	+	7.54E-12 6.99E-09
↳ peptide biosynthetic process		409	13	.99	13.09	+	1.62E-11 1.34E-08
↳ peptide metabolic process		53					

New Enhancer-Gene Panther 16.0 Released.

Analysis Summary: Please report in publication ①	
Annotation Type: PANTHER Overrepresentation Test (Released 20210224)	
Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.4437524 Released 2021-01-01	
Analyzed List: upload_1 (Homo sapiens) Change	
Reference List: Homo sapiens (all genes in database) Change	
Annotation Data Set: GO biological process complete ②	
Test Type: Fisher's Exact / Binomial	
Correction: Calculate False Discovery Rate <input checked="" type="checkbox"/> Use the Bonferroni correction for multiple testing ③ - No correction	

Results ④
Uniquely Mapped IDs: 30585 out of 20995 ⑤ 1541 out of 1590
Unmapped IDs: 0 ⑥ 41
Multiple mapping information: 0 ⑦ 62
Export FASTA XLSX CSV JSON with user meta ⑧

Displaying only results for FDR P < 0.05, click here to display all results

GO biological process complete

mitochondrial electron transport,ubiquinol to cytochrome.c

respiratory electron transport chain

electron transport chain

generation of precursor metabolites and energy

cellular metabolic process

intracellular process

cellular processes

cellular respiration

energy derivation by oxidation of organic compounds

mitochondrial ATP synthase,coupled electron transport

ATP synthase,coupled electron transport

oxidative phosphorylation

respiration

phosphate-containing compound,metabolic process

cellular respiration,metabolic process

ATP metabolic process

mitochondrial electron transport, cytochrome.c to oxygen

aerobic electron transport chain

aerobic respiration

IRES-dependent viral translational initiation

liver process

biological processes involved in symbiotic interaction

biological processes involved in interspecies interaction,between organisms

mitochondrial gene expression

mitochondrial electron transport,NADH to ubiquinone

mitochondrial ATP synthase,coupled proton transport

ATP synthase,coupled proton transport

ATP biosynthetic process

uridine ribonucleotide biosynthetic process

uridine nucleotide biosynthetic process

uridine-containing compound biosynthetic process

organic cyclic compound biosynthetic process

organic substance,metabolic process

organic substance biosynthetic process

biosynthesis process

heterocyclic biosynthetic process

uridine nucleotide biosynthetic process

uridine nucleotide triphosphate biosynthetic

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

Analysis Type: PANTHER Overrepresentation Test (Released 20210224)	
Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.4437524 Released 2021-01-01	
Analyzed List:	upload_1 (Homo sapiens) Change
Reference List:	Homo sapiens (all genes in database) Change
Annotation Data Set:	GO biological process complete ?
Test Type:	Fisher's Exact <input checked="" type="radio"/> Binomial
Correction:	Calculate False Discovery Rate <input checked="" type="radio"/> Use the Bonferroni correction for multiple testing ? <input type="radio"/> No correction

Results [?](#)

	Reference list	upload_1
Uniquely Mapped IDs:	20595 out of 20595	72 out of 74
Unmapped IDs:	0	5
Multiple mapping information:	0	2

Neely 2021, suppl. Table 6E: Cluster 3 at E 1.0 μM

Export [Table](#) [XML with user input ids](#) [JSON with user input ids](#)Displaying only results for FDR P < 0.05, [click here to display all results](#)

	Homo sapiens (REF)	upload_1 (▼ Hierarchy NEW! ?)					
		#	# expected	Fold Enrichment	+/-	raw P value	FDR
GO biological process complete							
mitochondrial electron transport, cytochrome c to oxygen	20	3	.07	41.75	+	7.41E-05	1.37E-02
↳ mitochondrial ATP synthesis coupled electron transport	89	6	.32	18.76	+	1.16E-06	2.99E-04
↳ ATP synthesis coupled electron transport	90	6	.32	18.55	+	1.23E-06	3.13E-04
↳ respiratory electron transport chain	108	6	.39	15.46	+	3.37E-06	8.04E-04
↳ electron transport chain	170	6	.61	9.82	+	4.01E-05	7.82E-03
↳ generation_of_precursor_metabolites_and_energy	402	8	1.44	5.54	+	1.08E-04	1.89E-02
↳ cellular_process	15487	69	55.65	1.24	+	1.13E-04	1.96E-02
↳ cellular_respiration	157	6	.56	10.64	+	2.61E-05	5.21E-03
↳ energy_derivation_by_oxidation_of_organic_compounds	227	6	.82	7.36	+	1.88E-04	3.12E-02
↳ oxidative_phosphorylation	120	8	.43	18.55	+	1.86E-08	7.32E-06
↳ ATP_metabolic_process	206	8	.74	10.81	+	9.71E-07	2.60E-04
↳ aerobic_electron_transport_chain	20	3	.07	41.75	+	7.41E-05	1.36E-02
SRP-dependent cotranslational protein targeting to membrane	96	14	.34	40.59	+	2.18E-18	1.14E-14
↳ protein_targeting_to_ER	111	15	.40	37.61	+	3.41E-19	5.38E-15
↳ protein_targeting	370	15	1.33	11.28	+	5.78E-12	4.56E-09
↳ intracellular_protein_transport	974	18	3.50	5.14	+	8.91E-09	3.60E-06
↳ cellular_protein_localization	1643	22	5.90	3.73	+	4.56E-08	1.71E-05
↳ cellular_monomolecule_localization	1649	22	5.93	3.71	+	4.86E-08	1.78E-05
↳ cellular_localization	3006	26	10.80	2.41	+	9.44E-06	2.04E-03
↳ localization	5805	37	20.86	1.77	+	7.96E-05	1.43E-02
↳ macromolecule_localization	2553	23	9.17	2.51	+	2.00E-05	4.11E-03
↳ protein_localization	2161	23	7.76	2.96	+	1.23E-06	3.09E-04
↳ intracellular_transport	1500	20	5.39	3.71	+	2.37E-07	7.06E-05
↳ establishment_of_localization_in_cell	2365	21	8.50	2.47	+	6.45E-05	1.21E-02
↳ protein_transport	1464	19	5.26	3.61	+	7.70E-07	2.17E-04
↳ establishment_of_protein_localization	1559	19	5.60	3.39	+	1.95E-06	4.74E-04
↳ peptide_transport	1493	19	5.36	3.54	+	1.03E-06	2.71E-04
↳ amide_transport	1527	19	5.49	3.46	+	1.44E-06	3.55E-04
↳ nitrogen_compound_transport	1802	20	6.47	3.09	+	4.07E-06	9.43E-04
↳ organic_substance_transport	2171	20	7.80	2.56	+	6.11E-05	1.18E-02
↳ anion_transport	2288	20	8.22	2.43	+	1.26E-04	2.17E-02
↳ ion_transport	2882	26	10.36	2.51	+	4.36E-06	9.82E-04
↳ establishment_of_protein_localization_to_endoplasmic_reticulum	115	15	.41	36.30	+	5.54E-19	4.37E-15
↳ protein_localization_to_endoplasmic_reticulum	142	15	.51	29.40	+	1.01E-17	3.20E-14
↳ protein_localization_to_organelle	791	16	2.84	5.63	+	2.03E-08	7.82E-06
↳ establishment_of_protein_localization_to_organelle	449	15	1.61	9.30	+	8.03E-11	4.69E-08
↳ cotranslational_protein_targeting_to_membrane	101	14	.36	38.58	+	4.16E-18	1.64E-14
↳ protein_targeting_to_membrane	183	15	.66	22.81	+	3.42E-16	5.99E-13
↳ establishment_of_protein_localization_to_membrane	307	15	1.10	13.60	+	4.45E-13	4.13E-10
↳ protein_localization_to_membrane	537	16	1.93	8.29	+	8.92E-11	5.02E-08
ribosomal small subunit assembly	21	3	.08	39.76	+	8.45E-05	1.50E-02
↳ cellular_component_organization_or_biogenesis	6000	40	21.56	1.86	+	8.39E-06	1.84E-03
↳ cellular_component_biogenesis	2701	24	9.70	2.47	+	1.55E-05	3.25E-03
↳ ribosome_biogenesis	332	12	1.19	10.06	+	3.25E-09	1.35E-06
↳ ribonucleoprotein_complex_biogenesis	465	12	1.67	7.18	+	1.19E-07	3.92E-05
↳ ribosomal_small_subunit_biogenesis	75	5	.27	18.55	+	1.00E-05	2.13E-03
cytoplasmic translation	75	10	.27	37.11	+	4.65E-13	4.07E-10
↳ translation	384	18	1.38	13.05	+	2.92E-15	4.18E-12
↳ peptide_biosynthetic_process	409	18	1.47	12.25	+	8.28E-15	9.33E-12
↳ peptide_metabolic_process	537	19	1.93	9.85	+	5.85E-14	5.77E-11
↳ cellular_amide_metabolic_process	808	19	2.90	6.54	+	6.05E-11	3.82E-08
↳ cellular_nitrogen_compound_metabolic_process	3407	30	12.24	2.45	+	8.71E-07	2.37E-04
↳ amide_biosynthetic_process	528	18	1.90	9.49	+	5.49E-13	4.55E-10
↳ cellular_nitrogen_compound_biosynthetic_process	1575	25	5.66	4.42	+	1.18E-10	6.41E-08
↳ cellular_biosynthetic_process	2709	28	9.73	2.88	+	9.13E-08	3.13E-05
↳ biosynthetic_process	2862	28	10.28	2.72	+	2.90E-07	8.47E-05
↳ organonitrogen_compound_biosynthetic_process	1380	23	4.96	4.64	+	3.24E-10	1.59E-07
↳ organic_substance_biosynthetic_process	2804	28	10.08	2.78	+	1.89E-07	5.85E-05
↳ gene_expression	2187	25	7.86	3.18	+	8.93E-08	3.13E-05
↳ cellular_macromolecule_biosynthetic_process	1655	24	5.95	4.04	+	1.89E-09	8.29E-07
↳ macromolecule_biosynthetic_process	1696	24	6.09	3.94	+	3.06E-09	1.30E-06
viral transcription	116	14	.42	33.59	+	2.45E-17	5.52E-14
↳ viral_process	849	18	3.05	5.90	+	1.08E-09	4.85E-07
↳ biological_process_involved_in_symbiotic_interaction	937	19	3.37	5.64	+	6.97E-10	3.24E-07
↳ biological_process_involved_in_interspecies_interaction_between_organisms	2118	24	7.61	3.15	+	2.10E-07	6.38E-05
↳ viral_gene_expression	172	14	.62	22.65	+	3.97E-15	4.81E-12
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	120	14	.43	32.47	+	3.79E-17	7.47E-14
↳ nuclear-transcribed mRNA catabolic process	196	15	.70	21.30	+	8.86E-16	1.40E-12
↳ mRNA_catabolic_process	216	15	.78	19.33	+	3.42E-15	4.49E-12
↳ negative_regulation_of_gene_expression	2034						

Home	About	PANTHER Data	PANTHER Tools	PANTHER Services	Workspace	Downloads	Help/Tutorial
New Enhancer-Genome Map PANTHER16.0 Released.							
Analysis Summary: Please report in publication ①							
Analysis Type: PANTHER Overrepresentation Test (Released 20210224)							
Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.4437524 Released 2021-01-01							
Analyzed List: upload_1 (Homo sapiens) [Change]							
Reference List: Homo sapiens (all genes in database) [Change]							
Annotation Data Set: GO biological process complete ②							
Test Type: Fisher's Exact <input checked="" type="radio"/> Binomial							
Correction: Calculate False Discovery Rate <input checked="" type="radio"/> Use the Bonferroni correction for multiple testing ③ <input type="radio"/> No correction							

Results [④](#)

Reference list	upload_1
Uniquely Mapped IDs: 20585 out of 20595	234 out of 245
Unmapped IDs: 0	6
Multiple mapping information: 0	9

Export [Table](#) [XML with user input ids](#) [JSON with user input ids](#)

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

GO biological process complete	Homo sapiens (REF)	#	# expected	upload_1 [Hierarchy]	NEW! [?]	FDR
cardiac_neural_crest_cell_development_involved_in_outflow_tract_morphogenesis	6	3	.07	42.03	+	1.28E-04 1.34E-02
heart_development	508	16	6.04	2.65	+	5.04E-04 3.61E-02
animal_organ_development	3186	63	37.90	1.82	+	5.02E-04 9.43E-05
anatomical_structure_development	5264	103	62.62	1.64	+	2.46E-08 6.69E-06
developmental_process	5733	111	68.20	1.63	+	7.09E-09 2.15E-06
system_development	4275	92	50.86	1.81	+	2.78E-09 9.13E-07
multicellular_organism_development	4875	101	57.99	1.74	+	1.55E-09 5.68E-07
multicellular_organismal_process	6908	120	82.18	1.46	+	8.08E-07 1.42E-04
circulatory_system_development	852	23	10.14	2.27	+	3.06E-04 2.53E-02
animal_organ_morphogenesis	945	31	11.24	2.76	+	5.00E-07 9.50E-05
anatomical_structure_morphogenesis	2134	58	25.39	2.28	+	2.76E-09 9.27E-07
cardiac_neural_crest_cell_development_involved_in_heart_development	9	3	.11	28.02	+	3.26E-04 2.67E-02
cardiac_neural_crest_cell_differentiation_involved_in_heart_development	9	3	.11	28.02	+	3.26E-04 2.65E-02
cell_differentiation	3512	81	41.78	1.94	+	1.36E-09 5.10E-07
cellular_developmental_process	3565	83	42.41	1.96	+	5.15E-10 2.14E-07
cellular_process	15482	218	184.23	1.18	+	8.98E-08 2.05E-05
mesenchyme_development	212	11	2.58	4.26	+	8.58E-05 9.27E-03
tissue_development	1731	42	20.59	2.28	+	1.15E-07 2.52E-05
cell_development	1616	36	19.21	1.87	+	3.01E-04 2.54E-02
anterior/posterior_axon_guidance	7	3	.08	36.03	+	1.81E-04 1.76E-02
axon_guidance	278	11	3.31	3.33	+	6.57E-04 4.37E-02
neuron_projection_guidance	279	11	3.32	3.31	+	6.76E-04 4.44E-02
neuron_projection_morphogenesis	495	16	5.89	2.72	+	3.84E-04 3.01E-02
neuron_differentiation	1028	29	12.23	2.37	+	2.28E-05 2.97E-03
generation_of_neurons	1249	37	14.86	2.49	+	5.59E-07 1.01E-04
neurogenesis	1369	39	16.29	2.39	+	5.28E-07 9.69E-05
nervous_system_development	2189	58	26.04	2.23	+	8.48E-09 2.48E-06
cellular_component_organization	5776	99	68.71	1.44	+	4.17E-04 4.91E-03
cellular_component_organization_or_biogenesis	6000	113	71.38	1.58	+	2.58E-08 6.91E-06
plasma_membrane_bounded_cell_projection_morphogenesis	499	16	5.94	2.70	+	4.18E-04 3.18E-02
cell_projection_morphogenesis	503	17	5.98	2.84	+	1.52E-04 1.52E-02
cellular_component_morphogenesis	522	17	6.21	2.74	+	2.32E-04 2.13E-02
chemotaxis	604	19	7.19	2.64	+	1.54E-04 1.53E-02
taxis	546	17	6.50	2.62	+	3.84E-04 3.00E-02
response_to_external_stimulus	549	17	6.53	2.60	+	4.08E-04 3.12E-02
locomotion	2508	52	29.84	1.78	+	3.29E-05 3.97E-03
movement_of_cell_or_subcellular_component	1336	33	15.89	2.08	+	7.81E-05 8.68E-03
axonogenesis	1588	36	18.89	1.91	+	2.57E-04 2.29E-02
cell_morphogenesis_involved_in_neuron_differentiation	384	14	4.57	3.06	+	2.80E-04 2.43E-02
cell_morphogenesis_involved_in_differentiation	449	15	5.34	2.81	+	4.18E-04 3.17E-02
axon_development	554	17	6.59	2.58	+	4.51E-04 3.35E-02
protein_targeting_to_ER	419	14	4.98	2.81	+	6.47E-04 4.34E-02
protein_targeting	111	24	1.32	18.18	+	1.21E-21 4.77E-18
intracellular_protein_transport	370	31	4.40	7.04	+	9.40E-17 1.24E-13
cellular_protein_localization	974	38	11.59	3.28	+	2.19E-10 9.60E-08
establishment_of_localization_in_cell	1643	46	19.55	2.35	+	8.38E-08 2.00E-05
establishment_of_localization	1649	46	19.62	2.34	+	8.93E-08 2.07E-05
cellular_localization	3006	70	35.76	1.96	+	2.96E-08 7.77E-06
localization	5805	105	69.06	1.52	+	1.05E-06 1.82E-04
macromolecule_localization	2553	58	30.37	1.94	+	5.23E-07 9.71E-05
protein_localization	2161	54	25.71	2.10	+	1.76E-07 3.71E-05
intracellular_transport	1500	58	17.84	2.80	+	4.69E-11 2.39E-08
establishment_of_localization_in_cell	2365	66	28.13	2.35	+	3.89E-11 2.12E-08
establishment_of_localization	4653	83	55.35	1.59	+	2.47E-06 4.01E-04
transport	4502	87	53.56	1.62	+	1.21E-06 2.04E-04
protein_transport	1464	43	17.42	2.47	+	5.95E-08 1.54E-05
establishment_of_protein_localization	1559	44	18.55	2.37	+	1.62E-07 3.51E-05
peptide_transport	1493	43	17.76	2.42	+	9.25E-08 2.08E-05
amide_transport	1527	43	18.17	2.37	+	2.46E-07 5.04E-05
nitrogen_compound_transport	1802	48	21.44	2.24	+	1.70E-07 3.62E-05
organic_substance_transport	2171	52	25.83	2.01	+	1.11E-06 1.90E-04
anion_transport	2288	52	27.22	1.91	+	5.46E-06 8.44E-04
ion_transport	2882	64	34.28	1.90	+	2.72E-07 5.49E-05
establishment_of_protein_localization_to_endoplasmic_reticulum	115	24	1.37	17.54	+	2.50E-21 7.89E-18
protein_localization_to_endoplasmic_reticulum	142	24	1.69	14.21	+	1.93E-19 3.80E-16
establishment_of_protein_localization_to_organelle	791	32	9.41	3.40	+	2.96E-09 9.52E-07
establishment_of_protein_localization_to_organelle	449	32	5.34	5.99	+	2.13E-15 2.24E-12
cotransportin_protein_targeting_to_membrane	101	24	1.20	19.97	+	1.75E-22 1.38E-18
protein_targeting_to_membrane	183	25	2.18	11.48	+	3.21E-18 5.07E-15
establishment_of_protein_localization_to_membrane	307	26	3.65	7.12	+	2.60E-14 2.56E-11
protein_localization_to_membrane	537	31	6.39	4.85	+	1.19E-12 9.42E-10
mitochondrial_ATP_synthesis_coupled_proton_transport	19	4	.23	17.70	+	1.38E-04 1.43E-02
ATP_synthesis_coupled_proton_transport	24	4	.29	14.01	+	3.06E-04 2.54E-02
organic_substance_biosynthetic_process	2804	68	33.36	2.04	+	1.07E-08 3.02E-06
biosynthetic_process	2862	68	34.05	2.00	+	1.64E-08 4.54E-06
cellular_biosynthetic_process	2709	67	32.23	2.08	+	6.