



Neely, 2021; suppl Table 5A : cluster 0 at E 0.1 μM

	Homo sapiens (REF)	#	expected	upload_1 (▼ hierarchy)	NEW! (▼)	EDR
GO:biological_process_complete						
SRB-dependent cotranslational protein_targeting_to_membrane	958	58	6.67	8.40	+ 4.98e-28	3.35e-25
protein_targeting_to_ER	113	60	7.71	7.78	+ 1.32e-28	9.93e-26
protein_targeting	320	85	25.71	3.31	+ 5.87e-19	1.30e-16
intracellular_protein_transport	974	153	67.68	2.26	+ 1.28e-18	2.72e-16
intracellular_protein_localization	1643	215	114.16	1.88	+ 1.72e-17	3.40e-15
intracellular_macromolecule_localization	1649	217	114.58	1.89	+ 8.10e-18	1.64e-15
intracellular_localization	3006	340	208.87	1.63	+ 1.53e-18	3.21e-16
intracellular_process	15487	1222	1076.08	1.14	+ 5.59e-20	1.39e-17
localization	5805	482	403.55	1.21	+ 3.10e-06	2.22e-04
macromolecule_localization	2563	285	177.39	1.61	+ 1.14e-14	1.94e-13
protein_localization	2161	256	150.15	1.70	+ 6.97e-16	1.28e-13
intracellular_transport	1500	214	104.22	2.05	+ 2.34e-21	6.82e-19
establishment_of_localization_in_cell	2365	276	164.33	1.68	+ 1.91e-16	3.59e-14
establishment_of_localization	4853	329	232.30	1.23	+ 7.02e-06	4.75e-04
transport	4592	382	312.81	1.22	+ 2.69e-05	1.77e-03
protein_transport	1494	192	101.72	1.89	+ 1.03e-11	1.86e-13
establishment_of_protein_localization	1559	191	108.32	1.83	+ 6.27e-15	1.09e-12
peptide_transport	1493	193	103.74	1.86	+ 2.89e-15	5.06e-13
amino_acid_transport	1627	195	106.10	1.84	+ 7.67e-13	1.91e-12
hydrogen_compound_transport	1802	205	126.21	1.64	+ 3.04e-11	3.99e-09
organic_substance_transport	2121	218	150.85	1.45	+ 1.52e-07	1.38e-05
ion_transport	2288	223	158.98	1.40	+ 8.72e-07	7.05e-05
ion_transport	2882	262	200.25	1.31	+ 1.17e-05	7.67e-04
establishment_of_protein_localization_to_endoplasmic_reticulum	115	60	7.99	7.51	+ 5.60e-28	3.69e-25
protein_localization_to_endoplasmic_reticulum	142	61	9.87	6.18	+ 6.48e-25	2.62e-22
protein_localization_to_organelle	751	134	54.96	2.44	+ 1.10e-18	2.37e-16
establishment_of_protein_localization_to_organelle	449	97	31.20	3.11	+ 7.02e-20	1.70e-17
cotranslational_protein_targeting_to_membrane	101	57	7.02	8.12	+ 5.82e-28	3.67e-25
protein_targeting_to_membrane	1823	63	12.72	4.95	+ 1.39e-21	4.15e-19
establishment_of_protein_localization_to_membrane	302	71	21.33	3.33	+ 3.65e-16	5.77e-14
protein_localization_to_membrane	537	85	37.31	2.28	+ 8.39e-11	1.04e-08
maturatation_of_lsuv_rna_from_tricistronic_rna_transcript_(lsu_rna_5.8s_rna_lsuv_rna)	16	8	1.04	7.68	+ 6.32e-05	3.64e-03
maturatation_of_lsuv_rna	28	16	1.95	8.22	+ 6.79e-09	7.29e-07
rna_processing	260	80	18.07	4.43	+ 1.80e-24	6.62e-22
ncrna_processing	432	95	30.02	3.16	+ 6.09e-20	1.50e-17
rrna_processing	923	218	64.13	3.40	+ 8.25e-50	3.52e-46
gene_expression	2187	36	151.96	2.40	+ 1.39e-51	1.10e-47
macromolecule_metabolic_process	6194	656	430.38	1.52	+ 1.64e-33	1.73e-30
intracellular_molecular_process	7879	756	547.46	1.38	+ 5.21e-27	2.74e-24
metabolic_process	8334	816	579.07	1.41	+ 5.04e-34	5.67e-31
RNA_molecular_process	1599	296	111.10	2.66	+ 4.69e-49	1.48e-45
nucleic_acid_molecular_process	2232	362	155.09	2.33	+ 6.55e-49	1.73e-45
nucleic_acid-containing_compound_molecular_process	2720	413	188.99	2.19	+ 4.70e-50	2.47e-46
heterocycle_molecular_process	2904	421	201.78	2.09	+ 1.85e-46	3.65e-43
cellular_molecular_process	2571	781	526.05	1.48	+ 9.19e-40	1.32e-36
primary_molecular_process	7365	725	511.74	1.42	+ 1.20e-28	9.49e-26
cellular_aromatic_compound_molecular_process	2949	422	204.91	2.06	+ 3.63e-45	4.35e-42
cellular_nitrogen_compound_molecular_process	3407	468	236.73	1.98	+ 8.49e-47	1.91e-43
organic_sulfur_compound_molecular_process	6898	701	479.29	1.46	+ 2.36e-31	1.96e-28
organic_cyclic_compound_molecular_process	3190	435	221.85	1.96	+ 5.28e-42	8.29e-39
riboisomal_large_subunit_biosynthesis	517	104	35.92	2.90	+ 2.71e-19	6.19e-17
viral_transcription	270	80	18.76	4.26	+ 1.33e-23	4.48e-21
viral_process	937	164	65.11	2.52	+ 3.30e-24	1.18e-21
virological_process_involved_in_symbiotic_interaction	2118	224	147.16	1.52	+ 1.79e-09	2.02e-07
virological_process_involved_in_interspecies_interaction_between_organisms	172	68	11.95	5.52	+ 1.18e-24	4.48e-22
viral_genome_expression	1722	50	8.34	7.08	+ 1.69e-26	8.62e-24
noncoding_rna_catobolic_process	196	73	13.62	5.21	+ 3.17e-25	1.35e-22
ribonucleic_acid_catobolic_process	216	74	15.01	4.93	+ 4.95e-25	2.06e-22
negative_regulation_of_gene_expression	2039	286	141.33	1.81	+ 7.01e-19	1.56e-16
negative_regulation_of_macromolecule_molecular_process	2862	326	198.86	1.64	+ 3.59e-16	7.34e-13
negative_regulation_of_protein_molecular_process	3105	343	215.74	1.59	+ 2.26e-17	4.34e-15
negative_regulation_of_biological_process	5544	518	385.21	1.34	+ 1.36e-13	2.12e-11
regulation_of_biological_process	11860	915	824.07	1.11	+ 2.44e-06	1.76e-04
regulation_of_protein_localization	1257	947	67.82	1.08	+ 1.18e-06	4.38e-05
regulation_of_protein_localization_to_endoplasmic_reticulum	6854	653	476.24	1.37	+ 1.04e-20	2.94e-18
regulation_of_protein_localization_to_organelle	7365	725	511.74	1.42	+ 1.20e-28	9.49e-26
primary_molecular_process	2949	422	204.91	2.06	+ 3.63e-45	4.35e-42
cellular_aromatic_compound_molecular_process	3407	468	236.73	1.98	+ 8.49e-47	1.91e-43
cellular_nitrogen_compound_molecular_process	6898	701	479.29	1.46	+ 2.36e-31	1.96e-28
organic_sulfur_compound_molecular_process	3190	435	221.85	1.96	+ 5.28e-42	8.29e-39
organic_cyclic_compound_molecular_process	3406	416	240.89	1.31	+ 2.77e-20	7.16e-18
organic_nitrogen_compound_molecular_process	3105	343	215.74	1.59	+ 2.26e-17	4.34e-15
organic_sulfur_molecular_process	5544	518	385.21	1.34	+ 1.36e-13	2.12e-11
organic_sulfur-containing_compound_molecular_process	2720	413	188.99	2.19	+ 4.70e-07	3.95e-05
organic_sulfur-containing_compound_molecular_process	2904	421	201.78	2.09	+ 1.85e-06	3.65e-04
organic_sulfur-containing_compound_molecular_process	3190	435	221.85	1.96	+ 5.28e-42	8.29e-39
organic_sulfur-containing_compound_molecular_process	3406	416	240.89	1.31		

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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/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 - Binomial

Correction: Calculate False Discovery Rate Use the Bonferroni correction for multiple testing [⑤](#) No correction

Results [⑥](#)

Uniquely Mapped IDs: 20595 out of 20595 [⑦](#) 064 out of 1241

Unmapped IDs: 0 [⑧](#) 63

Multiple mapping information: 0 [⑨](#) 105

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

Table XML with user input IDs JSON with user input IDs

Neely, 2021 Suppl. Table 5B: cluster 1 at E 0.1 PM

Homo sapiens (REF)	#	expected	Fold Enrichment	adj. p-value	FDR
upload_1 (V7 Hierarch)					
20	9	1.21	7.47	+ 2.14E-05	1.29E-03
89	35	5.36	6.53	+ 1.05E-15	2.72E-13
92	35	5.32	6.45	+ 1.38E-15	3.72E-13
108	32	6.51	5.69	+ 5.62E-15	1.27E-12
170	60	10.24	3.92	+ 1.24E-11	2.00E-09
402	61	24.22	2.68	+ 2.14E-11	3.21E-09
571	672	456.21	1.47	+ 1.95E-33	4.40E-30
834	688	502.18	1.37	+ 6.77E-25	6.68E-22
15487	1064	932.21	1.12	+ 8.23E-19	3.61E-16
162	41	9.46	4.33	+ 3.97E-13	7.37E-11
227	45	13.68	3.29	+ 9.57E-11	1.28E-08
320	46	7.23	6.04	+ 1.88E-18	7.40E-16
1023	99	61.64	1.81	+ 1.14E-05	7.16E-04
206	50	12.41	4.03	+ 1.21E-14	2.62E-12
39	9	1.21	7.47	+ 2.14E-05	1.28E-03
72	19	4.64	4.09	+ 1.62E-06	1.26E-04
22	9	2.17	4.19	+ 8.32E-04	3.45E-02
1222	104	73.63	1.41	+ 7.47E-04	3.17E-02
3190	349	192.22	1.82	+ 9.19E-28	1.11E-24
2879	628	474.77	1.32	+ 1.24E-17	4.35E-15
2804	273	168.96	1.62	+ 9.70E-15	2.12E-12
2882	278	172.46	1.60	+ 1.65E-14	3.51E-12
1076	98	64.84	1.51	+ 1.24E-04	6.42E-03
2904	341	174.99	1.95	+ 2.96E-32	5.18E-29
2709	29	163.24	1.65	+ 1.46E-15	3.59E-13
1575	185	94.91	1.95	+ 8.70E-17	2.75E-14
3407	382	205.30	1.86	+ 6.71E-33	1.32E-29
6388	585	416.68	1.41	+ 5.91E-22	4.44E-19
5254	276	316.59	1.19	+ 2.35E-04	1.13E-02
2949	343	177.70	1.93	+ 7.78E-32	1.23E-28
1088	91	65.44	1.51	+ 1.03E-04	5.45E-03
1380	149	83.16	1.79	+ 6.31E-11	8.81E-09
2720	332	163.90	2.06	+ 4.25E-36	1.12E-32
7365	608	443.80	1.37	+ 7.23E-20	3.68E-17
1003	97	60.44	1.51	+ 2.35E-05	1.39E-03
47	10	2.83	3.53	+ 1.27E-03	4.90E-02
24	9	1.45	6.22	+ 6.69E-05	3.70E-03
134	22	8.07	2.72	+ 7.42E-05	4.06E-03
2882	220	173.66	1.27	+ 3.67E-04	1.68E-02
4653	332	280.33	1.20	+ 2.55E-04	1.22E-02
5805	822	349.79	1.21	+ 1.41E-05	8.77E-04
1500	168	90.39	1.86	+ 1.40E-13	2.69E-11
2395	220	142.51	1.54	+ 4.61E-10	5.63E-08
3006	276	181.13	1.52	+ 3.69E-12	6.07E-10
229	33	13.80	2.39	+ 1.90E-05	1.16E-03
2805	214	155.97	1.36	+ 6.75E-06	4.51E-04
5895	478	355.22	1.35	+ 3.89E-13	7.31E-11
6854	561	413.00	1.38	+ 7.32E-19	3.30E-16
11860	784	714.65	1.16	+ 1.04E-04	5.48E-03
6308	539	380.10	1.42	+ 4.00E-20	2.10E-17
5692	470	342.98	1.37	+ 3.90E-14	7.99E-12
2633	202	142.39	1.45	+ 1.30E-07	1.15E-05
966	38	5.78	6.57	+ 5.25E-17	1.72E-14
2720	33	163.90	2.06	+ 4.25E-36	1.12E-32
5855	608	443.80	1.37	+ 6.92E-20	3.48E-17
1003	97	60.44	1.51	+ 2.35E-05	1.39E-03
47	10	2.83	3.53	+ 1.27E-03	4.90E-02
24	9	1.45	6.22	+ 6.69E-05	3.70E-03
134	22	8.07	2.72	+ 7.42E-05	4.06E-03
2882	220	173.66	1.27	+ 3.67E-04	1.68E-02
4653	332	280.33	1.20	+ 2.55E-04	1.22E-02
5805	822	349.79	1.21	+ 1.41E-05	8.77E-04
1500	168	90.39	1.86	+ 1.40E-13	2.69E-11
2395	220	142.51	1.54	+ 4.61E-10	5.63E-08
3006	276	181.13	1.52	+ 3.69E-12	6.07E-10
229	33	13.80	2.39	+ 1.90E-05	1.16E-03
2805	214	155.97	1.36	+ 6.75E-06	4.51E-04
5895	478	355.22	1.35	+ 3.89E-13	7.31E-11
6854	561	413.00	1.38	+ 7.32E-19	3.30E-16
11860	784	714.65	1.16	+ 1.04E-04	5.48E-03
6308	539	380.10	1.42	+ 4.00E-20	2.10E-17
5692	470	342.98	1.37	+ 3.90E-14	7.99E-12
2633	202	142.39	1.45	+ 1.30E-07	1.15E-05
966	38	5.78	6.57	+ 5.25E-17	1.72E-14
2720	33	163.90	2.06	+ 3.67E-04	1.37E-02
5855	608	443.80	1.37	+ 6.92E-20	3.48E-17
1003	97	60.44	1.51	+ 2.35E-05	1.39E-03
47	10	2.83	3.53	+ 1.27E-03	4.90E-02
24	9	1.45	6.22	+ 6.69E-05	3.70E-03
134	22	8.07	2.72	+ 7.42E-05	4.06E-03
2882	220	173.66	1.27	+ 3.67E-04	1.68E-02
4653	332	280.33	1.20	+ 2.55E-04	1.22E-02
5805	822	349.79	1.21	+ 1.41E-05	8.77E-04
1500	168	90.39	1.86	+ 1.40E-13	2.69E-11
2395	220	142.51	1.54	+ 4.61E-10	5.63E-08
3006	276	181.13	1.52	+ 3.69E-12	6.07E-10
229	33	13.80	2.39	+ 1.90E-05	1.16E-03
2805	214	155.97	1.36	+ 6.75E-06	4.51E-04
5895	478	355.22	1.35	+ 3.89E-13	7.31E-11
6854	561	413.00	1.38	+ 7.32E-19	3.30E-16
11860	784	714.65	1.16	+ 1.04E-04	5.48E-03
6308	539	380.10	1.42	+ 4.00E-20	2.10E-17
5692	470	342.98	1.37	+ 3.90E-14	7.99E-12
2633	202	142.39	1.45	+ 1.30E-07	1.15E-05
966	38	5.78	6.57	+ 5.25E-17	1.72E-14
2720	33	163.90	2.06	+ 3.67E-04	1.37E-02
5855	608	443.80	1.37	+ 6.92E-20	3.48E-17
1003	97	60.44	1.51	+ 2.35E-05	1.39E-03
47	10	2.83	3.53	+ 1.27E-03	4.90E-02</td

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 BinomialCorrection: Calculate False Discovery Rate Use the Bonferroni correction for multiple testing [?](#) No correctionResults [?](#)Reference list upload_1
Uniquely Mapped IDs: 20595 out of 20595 218 out of 224
Unmapped IDs: 0 6
Multiple mapping information: 0 11**Neely, 2021, suppl. Table 5C: cluster 5 at E 0.1 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 ATP synthesis coupled proton transport	19	5	.21	24.20	+	4.96E-06	6.69E-04
↳ATP synthesis_coupled_proton_transport	24	5	.26	19.15	+	1.33E-05	1.66E-03
↳ATP biosynthetic process	36	5	.39	12.77	+	7.54E-05	8.31E-03
↳organic cyclic compound metabolic process	3190	89	34.70	2.57	+	3.34E-18	2.40E-15
↳organic substance metabolic process	2879	122	85.70	1.42	+	1.12E-06	1.63E-04
↳metabolic_process	8334	141	90.64	1.56	+	2.47E-11	6.60E-09
↳organic substance biosynthetic process	2804	63	30.50	2.07	+	1.42E-08	2.58E-06
↳biosynthetic process	2862	63	31.13	2.02	+	3.28E-08	5.82E-06
↳heterocycle metabolic process	2904	89	31.59	2.82	+	7.61E-21	1.00E-17
↳cellular metabolic process	7571	141	82.35	1.71	+	4.48E-15	1.77E-12
↳cellular process	15487	205	168.44	1.22	+	6.22E-10	1.31E-07
↳cellular biosynthetic process	2709	62	29.46	2.10	+	1.35E-08	2.48E-06
↳cellular nitrogen compound biosynthetic process	1575	51	17.13	2.98	+	2.43E-12	7.82E-10
↳cellular_nitrogen_compound_metallic_process	3407	99	37.06	2.67	+	5.56E-22	1.10E-18
↳nitrogen compound metabolic process	6898	121	75.03	1.61	+	3.74E-10	8.20E-08
↳cellular aromatic compound metabolic process	2949	89	32.07	2.77	+	2.09E-20	2.36E-17
↳organonitrogen compound biosynthetic process	1380	48	15.01	3.20	+	1.06E-12	3.56E-10
↳nucleobase-containing compound metabolic process	2720	89	29.58	3.01	+	9.66E-23	3.05E-19
↳primary metabolic process	7365	122	80.10	1.52	+	1.51E-08	2.71E-06
↳ATP metabolic process	206	23	2.24	10.27	+	5.77E-16	2.93E-13
↳purine ribonucleoside triphosphate biosynthetic process	47	6	.51	11.74	+	2.18E-05	2.67E-03
↳purine nucleoside triphosphate biosynthetic process	48	6	.52	11.49	+	2.43E-05	2.95E-03
↳nucleoside triphosphate biosynthetic process	65	6	.71	8.49	+	1.16E-04	1.25E-02
↳purine nucleoside triphosphate metabolic process	67	6	.73	8.23	+	1.35E-04	1.41E-02
↳ribonucleoside triphosphate biosynthetic process	53	6	.58	10.41	+	4.06E-05	4.75E-03
↳ribonucleoside triphosphate metabolic process	68	6	.74	8.11	+	1.46E-04	1.49E-02
↳purine ribonucleoside triphosphate metabolic process	61	6	.66	9.04	+	8.38E-05	9.11E-03
↳energy_coupled_proton_transport_down_electrochemical_gradient	24	5	.26	19.15	+	1.33E-05	1.65E-03
↳proton_transmembrane_transport	134	10	1.46	6.86	+	3.72E-06	5.10E-04
↳ion_transport	2882	57	31.35	1.82	+	6.76E-06	8.74E-04
↳transport	4502	73	48.97	1.49	+	2.39E-04	2.40E-02
↳establishment_of_localization	4653	75	50.61	1.48	+	2.09E-04	2.11E-02
↳localization	5805	89	63.14	1.41	+	2.39E-04	2.39E-02
↳oxidative_phosphorylation	120	20	1.31	15.32	+	4.87E-17	3.20E-14
↳generation_of_precursor_metabolites_and_energy	402	24	4.37	5.49	+	4.08E-11	1.06E-08
↳phosphorylation	1023	29	11.13	2.61	+	3.26E-06	4.55E-04
↳intracellular_transport	1500	49	16.31	3.00	+	5.35E-12	1.65E-09
↳establishment_of_localization_in_cell	2365	55	25.72	2.14	+	7.66E-08	1.29E-05
↳cellular_localization	3006	65	32.69	1.99	+	3.64E-08	6.38E-06
↳mitochondrial_transmembrane_transport	105	11	1.14	9.63	+	5.11E-08	8.76E-06
↳mitochondrial_transport	229	18	2.49	7.23	+	2.08E-10	4.82E-08
SRP-dependent_cotranslational_protein_targeting_to_membrane	96	21	1.04	20.11	+	5.69E-20	5.61E-17
↳protein_targeting_to_ER	111	23	1.21	19.05	+	2.63E-21	4.61E-18
↳protein_targeting	370	33	4.02	8.20	+	9.65E-20	8.95E-17
↳intracellular_protein_transport	974	39	10.59	3.68	+	3.57E-12	1.13E-09
↳cellular_protein_localization	1643	49	17.87	2.74	+	1.21E-10	2.94E-08
↳cellular_macromolecule_localization	1649	49	17.94	2.73	+	1.37E-10	3.23E-08
↳macromolecule_localization	2553	52	27.77	1.87	+	9.19E-06	1.17E-03
↳protein_localization	2161	51	23.50	2.17	+	1.43E-07	2.33E-05
↳protein_transport	1464	40	15.92	2.51	+	1.34E-07	2.20E-05
↳establishment_of_protein_localization	1559	41	16.96	2.42	+	1.76E-07	2.83E-05
↳peptide_transport	1493	40	16.24	2.46	+	1.79E-07	2.84E-05
↳amino_transport	1527	40	16.61	2.41	+	2.81E-07	4.30E-05
↳nitrogen_compound_transport	1802	41	19.60	2.09	+	7.72E-06	9.90E-04
↳establishment_of_protein_localization_to_endoplasmic_reticulum	115	23	1.25	18.39	+	5.30E-21	7.60E-18
↳protein_localization_to_endoplasmic_reticulum	142	24	1.54	15.54	+	2.35E-20	2.47E-17
↳protein_localization_to_organelle	791	40	8.60	4.65	+	1.28E-15	6.10E-13
↳establishment_of_protein_localization_to_organelle	449	21	4.88	6.35	+	1.11E-15	5.49E-13
↳cotranslational_protein_targeting_to_membrane	101	22	1.10	20.03	+	7.77E-21	9.43E-18
↳protein_targeting_to_membrane	183	25	1.99	12.56	+	3.70E-19	3.07E-16
↳establishment_of_protein_localization_to_membrane	307	27	3.34	8.09	+	3.64E-16	1.92E-13
↳protein_localization_to_membrane	537	28	5.84	4.79	+	1.81E-11	4.93E-09
cytoplasmic_translation	75	15	.82	18.39	+	4.20E-14	1.44E-11
↳translation	384	33	4.18	7.90	+	2.75E-19	2.41E-16
↳peptide_biosynthetic_process	409	33	4.45	7.42	+	1.61E-18	1.27E-15
↳peptide_metallic_process	537	33	5.84	5.65	+	2.93E-15	1.19E-12
↳cellular_amide_metallic_process	808	33	8.79	3.76	+	1.24E-10	2.97E-08
↳amide_biosynthetic_process	528	33	5.74	5.75	+	1.85E-15	8.12E-13
↳gene_expression	2187	82	23.79	3.45	+	2.14E-24	8.45E-21
↳macromolecule_metallic_process	6194	111	67.37	1.65	+	1.82E-09	3.60E-07
↳cellular_macromolecule_biosynthetic_process	1655	51	18.00	2.83	+	1.44E-11	3.99E-09
↳cellular_macromolecule_metallic_process	4964	78	53.99	1.44	+	3.86E-04	3.69E-02
↳macromolecule_biosynthetic_process	1696	51	18.45	2.76	+	3.43E-11	9.02E-09
↳cellular_protein_metallic_process	3644	66	39.63	1.67	+	2.05E-05	2.52E-03
mitochondrial_electron_transport_cytochrome_c_to_oxygen	20	4	.22	18.39	+	1.17E-04	1.26E-02
mitochondrial_ATP_syn							

Neely 2021, suppl. Table 5D cluster 2 at E 0.1 μM

Homo sapiens (REF)	#	expected	Fold Enrichment	n/c	raw P-value	EDR
GO:biological_process_complete	133	52.73	2.52	+ 2.85E-20	1.7E-17	
viral_release_from_host_cell	6	.34	1.85	+ 1.30E-03	4.6E-02	
viral_life_cycle	225	32.12E-06	2.53	+ 7.98E-06	5.94E-04	
viral_process	849	124.47E-06	2.60	+ 6.76E-02	3.8E-17	
virological_process_involved_in_symbiotic_interaction	937	13.20E-06	2.52	+ 2.85E-20	1.7E-17	
virological_process_involved_in_interspecies_interaction_between_organisms	2118	174.11E-06	1.46	+ 1.31E-04	1.14E-04	
exit_from_host_cell	6	.34	1.84	+ 1.30E-03	4.6E-02	
exit_from_host	6	.34	1.84	+ 1.30E-03	4.6E-02	
positive regulation_of_protein_localization_to_Cajal_body	11	.62	0.69	+ 1.68E-04	8.63E-03	
regulation_of_protein_localization_to_Cajal_body	11	.62	0.69	+ 1.68E-04	8.63E-03	
regulation_of_cellular_protein_localization	566	62.31E-06	1.95	+ 3.17E-04	2.56E-04	
regulation_of_cellular_localization	838	82.47E-06	1.74	+ 4.07E-04	3.16E-04	
regulation_of_biological_process	11860	744.66E-03	1.11	+ 9.04E-05	6.51E-04	
biological_process_reproduction	12526	760.70E-02	1.09	+ 3.20E-04	1.51E-02	
regulation_of_localization	2734	293.15E-06	1.36	+ 9.64E-06	6.91E-04	
regulation_of_protein_localization	893	93.50E-06	1.89	+ 9.88E-06	1.02E-05	
positive regulation_of_protein_localization_to_nucleus	89	14.50E-01	2.80	+ 1.12E-03	4.16E-02	
positive regulation_of_cellular_protein_localization	301	32.16E-04	2.01	+ 3.89E-05	2.39E-03	
positive regulation_of_cellular_processor	5652	320.31E-05	1.24	+ 1.19E-06	1.05E-04	
positive regulation_of_biological_process	6245	422.35E-04	1.20	+ 1.75E-05	1.19E-03	
mitochondrial_electron_transport_irreducibly_in_cytochrome_c	14	.74	0.79	+ 8.88E-03	4.96E-02	
respiratory_electron_transport_chain	108	45.76E-06	5.62	+ 1.75E-04	4.46E-02	
electron_transport_chain	120	41.95E-06	4.29	+ 4.43E-13	9.08E-11	
generation_of_precursor_metabolites_and_energy	402	62.22E-06	2.96	+ 1.56E-05	3.41E-04	
cellular_mitochondrial_processes	7521	62.42E-06	1.48	+ 7.80E-03	1.76E-02	
metabolic_process	8324	849.46E-03	1.38	+ 4.57E-05	4.80E-02	
cellular_process	5462	1008.87E-04	1.95	+ 1.75E-05	1.21E-04	
cellular_respiration	152	64.88E-06	4.98	+ 6.56E-16	1.88E-13	
energy_derivation_by_oxidation_of_organic_compounds	222	51.12E-07	3.90	+ 7.05E-16	1.85E-12	
mitochondrial_ATP_synthesis_coupled_electron_transport	89	34.50E-01	6.79	+ 8.00E-16	2.21E-13	
ATP_syntase_coupled_electron_transport	90	33.50E-06	6.71	+ 1.05E-05	2.84E-03	
oxidative_phosphorylation	120	41.67E-06	6.07	+ 2.16E-17	8.31E-15	
phosphorylation	1023	84.57E-06	1.49	+ 4.44E-04	1.99E-02	
ATP_metabolic_process	208	68.11E-05	4.14	+ 1.36E-05	3.51E-12	
positive regulation_ofEstablishment_of_protein_localization_to_telomere	101	5.56E-06	8.88	+ 8.16E-04	3.22E-02	
positive regulation_of_protein_localization_to_chromosome_telegomeric_region	13	6.73E-06	8.20	+ 3.36E-04	1.56E-02	
regulation_of_protein_localization_to_chromosome_telegomeric_region	15	6.84E-06	7.11	+ 6.13E-04	2.56E-02	
regulation_ofEstablishment_of_protein_localization_to_telomere	31	5.62E-06	8.08	+ 1.13E-03	4.17E-02	
positive regulation_ofEstablishment_of_protein_localization	593	64.33E-06	1.92	+ 3.41E-04	2.76E-04	
positive regulation_ofEstablishment_of_protein_localization_to_nucleus	349	62.19E-02	2.16	+ 1.64E-05	1.11E-03	
positive regulation_ofEstablishment_of_protein_localization_to_nucleoplasm	5652	320.31E-05	1.24	+ 1.19E-06	1.05E-04	
positive regulation_ofEstablishment_of_protein_localization_to_nucleoplasm	6245	422.35E-04	1.20	+ 1.75E-05	1.19E-03	
mitochondrial_electron_transport_irreducibly_in_cytochrome_c	14	.74	0.79	+ 8.88E-03	4.96E-02	
respiratory_electron_transport_chain	108	45.76E-06	5.62	+ 1.75E-04	4.46E-02	
electron_transport_chain	120	41.95E-06	4.29	+ 4.43E-13	9.08E-11	
generation_of_precursor_metabolites_and_energy	402	62.22E-06	2.96	+ 1.56E-05	3.41E-04	
cellular_mitochondrial_processes	7521	62.42E-06	1.48	+ 7.80E-03	1.76E-02	
metabolic_process	8324	849.46E-03	1.38	+ 4.57E-05	4.80E-02	
cellular_process	5462	1008.87E-04	1.95	+ 1.75E-05	1.21E-04	
cellular_respiration	152	64.88E-06	4.98	+ 6.56E-16	1.88E-13	
energy_derivation_by_oxidation_of_organic_compounds	222	51.12E-07	3.90	+ 7.05E-16	1.85E-12	
mitochondrial_ATP_synthesis_coupled_electron_transport	89	34.50E-01	6.79	+ 8.00E-16	2.21E-13	
ATP_syntase_coupled_electron_transport	90	33.50E-06	6.71	+ 1.05E-05	2.84E-03	
oxidative_phosphorylation	120	41.67E-06	6.07	+ 2.16E-17	8.31E-15	
phosphorylation	1023	84.57E-06	1.49	+ 4.44E-04	1.99E-02	
ATP_metabolic_process	208	68.11E-05	4.14	+ 1.36E-05	3.51E-12	
positive regulation_ofEstablishment_of_protein_localization	101	5.56E-06	8.88	+ 8.16E-04	3.22E-02	
positive regulation_of_protein_localization_to_chromosome_telegomeric_region	13	6.73E-06	8.20	+ 3.36E-04	1.56E-02	
regulation_of_protein_localization_to_chromosome_telegomeric_region	15	6.84E-06	7.11	+ 6.13E-04	2.56E-02	
regulation_ofEstablishment_of_protein_localization_to_telomere	31	5.62E-06	8.08	+ 1.13E-03	4.17E-02	
positive regulation_ofEstablishment_of_protein_localization	593	64.33E-06	1.92	+ 3.41E-04	2.76E-04	
positive regulation_ofEstablishment_of_protein_localization_to_nucleus	349	62.19E-02	2.16	+ 1.64E-05	1.11E-03	
positive regulation_ofEstablishment_of_protein_localization_to_nucleoplasm	5652	320.31E-05	1.24	+ 1.19E-06	1.05E-04	
positive regulation_ofEstablishment_of_protein_localization_to_nucleoplasm	6245	422.35E-04	1.20	+ 1.75E-05	1.19E-03	
mitochondrial_electron_transport_irreducibly_in_cytochrome_c	14	.74	0.79	+ 8.88E-03	4.96E-02	
respiratory_electron_transport_chain	108	45.76E-06	5.62	+ 1.75E-04	4.46E-02	
electron_transport_chain	120	41.95E-06	4.29	+ 4.43E-13	9.08E-11	
generation_of_precursor_metabolites_and_energy	402	62.22E-06	2.96	+ 1.56E-05	3.41E-04	
cellular_mitochondrial_processes	7521	62.42E-06	1.48	+ 7.80E-03	1.76E-02	
metabolic_process	8324	849.46E-03	1.38	+ 4.57E-05	4.80E-02	
cellular_process	5462	1008.87E-04	1.95	+ 1.75E-05	1.21E-04	
cellular_respiration	152	64.88E-06	4.98	+ 6.56E-16	1.88E-13	
energy_derivation_by_oxidation_of_organic_compounds	222	51.12E-07	3.90	+ 7.05E-16	1.85E-12	
mitochondrial_ATP_synthesis_coupled_electron_transport	89	34.50E-01	6.79	+ 8.00E-16	2.21E-13	
ATP_syntase_coupled_electron_transport	90	33.50E-06	6.71	+ 1.05E-05	2.84E-03	
oxidative_phosphorylation	120	41.67E-06	6.07	+ 2.16E-17	8.31E-15	
phosphorylation	1023	84.57E-06	1.49	+ 4.44E-04	1.99E-02	
ATP_metabolic_process	208	68.11E-05	4.14	+ 1.36E-05	3.51E-12	
positive regulation_ofEstablishment_of_protein_localization	101	5.56E-06	8.88	+ 8.16E-04	3.22E-02	
positive regulation_of_protein_localization_to_chromosome_telegomeric_region	13	6.73E-06	8.20	+ 3.36E-04	1.56E-02	
regulation_of_protein_localization_to_chromosome_telegomeric_region	15	6.84E-06	7.11	+ 6.13E-04	2.56E-02	
regulation_ofEstablishment_of_protein_localization_to_telomere	31	5.62E-06	8.08	+ 1.13E-03	4.17E-02	
positive regulation_ofEstablishment_of_protein_localization	593	64.33E-06</				

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 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 138 out of 142
Unmapped IDs:	0 8
Multiple mapping information:	0 2

Neely 2021, suppl. Table 5F cluster 4 at E 0.1 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								
regulation of mRNA stability involved in response to oxidative stress	2	2	.01	> 100	+	2.77E-04	3.28E-02	
↳ regulation of gene expression	4880	57	33.65	1.69	+	1.63E-05	2.68E-03	
↳ cellular process	15487	127	106.78	1.19	+	3.32E-05	4.94E-03	
mitochondrial ATP synthesis coupled proton transport	19	4	.13	30.53	+	1.69E-05	2.74E-03	
↳ ATP synthesis coupled proton transport	24	4	.17	24.17	+	3.80E-05	5.49E-03	
↳ ATP biosynthetic process	36	4	.25	16.12	+	1.59E-04	1.93E-02	
↳ organic cyclic compound metabolic process	3190	55	21.99	2.50	+	2.14E-11	9.91E-09	
↳ organic substance metabolic process	2879	78	54.32	1.44	+	6.19E-05	8.35E-03	
↳ metabolic process	8334	91	57.46	1.58	+	2.27E-08	6.40E-06	
↳ organic substance biosynthetic process	2804	43	19.33	2.22	+	2.62E-07	5.82E-05	
↳ biosynthetic process	2862	44	19.73	2.23	+	1.66E-07	3.74E-05	
↳ heterocycle metabolic process	2904	53	20.02	2.65	+	7.07E-12	3.98E-09	
↳ cellular metabolic process	2521	89	52.20	1.70	+	7.04E-10	2.53E-07	
↳ cellular biosynthetic process	2709	43	18.68	2.30	+	1.28E-07	2.98E-05	
↳ cellular nitrogen compound biosynthetic process	1575	36	10.86	3.32	+	1.44E-10	5.83E-08	
↳ cellular nitrogen compound metabolic process	3407	59	23.49	2.51	+	2.03E-12	1.28E-09	
↳ nitrogen compound metabolic process	6898	73	47.56	1.53	+	1.50E-05	2.50E-03	
↳ cellular aromatic compound metabolic process	2949	53	20.33	2.61	+	1.27E-11	6.69E-09	
↳ organonitrogen compound biosynthetic process	1380	32	9.51	3.36	+	1.37E-09	4.71E-07	
↳ nucleobase-containing compound metabolic process	2720	52	18.75	2.77	+	2.14E-12	1.30E-09	
↳ primary metabolic process	7365	76	50.78	1.50	+	2.06E-05	3.19E-03	
↳ ATP metabolic process	206	13	1.42	9.15	+	3.73E-09	1.18E-06	
↳ purine ribonucleoside triphosphate biosynthetic process	47	5	.32	15.43	+	2.81E-05	4.27E-03	
↳ purine nucleoside triphosphate biosynthetic process	48	5	.33	15.11	+	3.09E-05	4.64E-03	
↳ nucleoside triphosphate biosynthetic process	65	5	.45	11.16	+	1.19E-04	1.51E-02	
↳ purine nucleoside triphosphate metabolic process	67	5	.46	10.82	+	1.36E-04	1.67E-02	
↳ ribonucleoside triphosphate biosynthetic process	53	5	.37	13.68	+	4.80E-05	6.76E-03	
↳ ribonucleoside triphosphate metabolic process	68	5	.47	10.66	+	1.45E-04	1.77E-02	
↳ purine ribonucleoside triphosphate metabolic process	61	5	.42	11.89	+	8.96E-05	1.17E-02	
↳ energy coupled proton transport, down electrochemical gradient	24	4	.17	24.17	+	3.80E-05	5.44E-03	
↳ proton transmembrane transport	134	6	.92	6.49	+	4.10E-04	4.76E-02	
↳ ion transport	2882	41	19.87	2.06	+	4.53E-06	8.22E-04	
↳ transport	4502	53	31.04	1.71	+	3.70E-05	5.45E-03	
↳ establishment of localization	4653	53	32.08	1.65	+	7.57E-05	1.00E-02	
↳ localization	5805	62	40.02	1.55	+	1.08E-04	1.38E-02	
↳ oxidative phosphorylation	120	13	.83	15.71	+	7.38E-12	4.01E-09	
↳ generation of precursor metabolites and energy	402	14	2.77	5.05	+	1.07E-06	2.19E-04	
↳ phosphorylation	1023	18	7.05	2.55	+	2.74E-04	3.28E-02	
↳ intracellular transport	1500	33	10.34	3.19	+	2.61E-09	8.42E-07	
↳ establishment of localization in cell	2365	42	16.31	2.58	+	5.80E-09	1.79E-06	
↳ cellular localization	3006	46	20.73	2.22	+	1.27E-07	2.99E-05	
↳ mitochondrial transmembrane transport	105	7	.72	9.67	+	1.21E-05	2.03E-03	
↳ mitochondrial transport	229	12	1.58	7.60	+	1.06E-07	2.61E-05	
ribosomal small subunit assembly	21	4	.14	27.63	+	2.38E-05	3.65E-03	
↳ cellular component organization or biogenesis	6000	68	41.37	1.64	+	2.80E-06	5.31E-04	
↳ cellular component biogenesis	2701	44	18.62	2.36	+	3.06E-08	8.18E-06	
↳ ribosome biogenesis	332	17	2.29	7.43	+	2.83E-10	1.06E-07	
↳ ribonucleoprotein complex biogenesis	465	21	3.21	6.55	+	1.81E-11	8.65E-09	
↳ ribosomal small subunit biogenesis	75	6	.52	11.60	+	1.97E-05	3.14E-03	
↳ ribonucleoprotein complex assembly	190	8	1.31	6.11	+	6.75E-05	9.02E-03	
↳ ribonucleoprotein complex subunit organization	197	8	1.36	5.89	+	8.61E-05	1.13E-02	
↳ protein-containing complex subunit organization	1582	24	10.91	2.20	+	3.62E-04	4.23E-02	
↳ cellular protein-containing complex assembly	860	19	5.93	3.20	+	9.08E-06	1.56E-03	
↳ protein-containing complex assembly	1338	23	9.23	2.49	+	5.09E-05	7.10E-03	
SRP-dependent cotranslational protein targeting to membrane	96	18	.66	27.19	+	8.32E-20	3.28E-16	
↳ protein targeting to ER	111	19	.77	24.83	+	3.45E-20	2.72E-16	
↳ protein targeting	370	24	2.55	9.41	+	2.92E-16	4.19E-13	
↳ intracellular protein transport	974	25	6.72	3.72	+	1.74E-08	4.98E-06	
↳ cellular protein localization	1643	31	11.33	2.74	+	2.70E-07	5.91E-05	
↳ cellular macromolecule localization	1649	31	11.37	2.73	+	2.92E-07	6.30E-05	
↳ macromolecule localization	2553	35	17.60	1.99	+	5.97E-05	8.18E-03	
↳ protein localization	2161	34	14.90	2.28	+	5.97E-06	1.07E-03	
↳ protein transport	1464	27	10.09	2.67	+	2.83E-06	5.32E-04	
↳ establishment of protein localization	1559	27	10.75	2.51	+	8.87E-06	1.54E-03	
↳ peptide transport	1493	27	10.29	2.62	+	4.06E-06	7.53E-04	
↳ amide transport	1527	27	10.53	2.56	+	6.11E-06	1.08E-03	
↳ nitrogen compound transport	1802	29	12.42	2.33	+	1.73E-05	2.79E-03	
↳ establishment of protein localization to endoplasmic reticulum	115	19	.79	23.96	+	6.26E-20	3.29E-16	
↳ protein localization to endoplasmic reticulum	142	19	.98	19.41	+	2.22E-18	7.01E-15	
↳ protein localization to organelle	791	29	5.45	5.32	+	2.48E-13	1.78E-10	
↳ establishment of protein localization to organelle	449	25	3.10	8.08	+	1.87E-15	2.27E-12	
↳ cotranslational protein targeting to membrane	101	19	.70	27.28	+	7.06E-21	1.11E-16	
↳ protein targeting to membrane	183	19	1.26	15.06	+	1.65E-16	2.61E-13	
↳ establishment of protein localization to membrane	307	20	2.12	9.45	+	9.97E-14	7.86E-11	
↳ protein localization								