


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:

Reference List:

Annotation Data Set: GO biological process complete 

Test Type: Fisher's Exact Binomial

Correction: Calculate False Discovery Rate Use the Bonferroni correction for multiple testing No correction

Results 


Reference list	upload_1
Uniquely Mapped IDs:	20595 out of 20595 552 out of 467
Unmapped IDs:	0 9
Multiple mapping information:	0 15

Neely 2021, suppl. Table 7A: Cluster 0 at E+L 0.1 μM

Export

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

GO biological process complete	Homo sapiens (REF)	#	expected	Fold Enrichment	z/ z	raw P value	FDR
SRP-dependent cotranslational protein targeting to membrane		96	75	2.18	34.45	+ 1.55E-78	6.09E-75
protein targeting to ER		133	79	2.52	31.39	+ 1.74E-80	2.74E-76
protein targeting		370	90	8.39	10.73	+ 5.42E-59	4.50E-56
intracellular protein transport		974	104	22.09	4.71	+ 2.19E-38	7.06E-36
cellular protein localization		1643	122	37.26	3.27	+ 6.47E-31	1.48E-28
cellular macromolecule localization		1649	123	37.39	3.29	+ 2.29E-31	5.32E-29
cellular localization		3006	167	68.16	2.45	+ 7.80E-29	1.71E-26
cellular process		15487	421	351.17	1.20	+ 7.42E-16	1.06E-13
localization		5805	217	131.63	1.85	+ 1.66E-16	2.29E-14
macromolecule localization		2553	136	57.89	2.35	+ 3.78E-21	8.41E-19
protein localization		2161	131	49.00	2.67	+ 2.68E-25	6.03E-23
intracellular transport		1500	129	34.01	3.79	+ 5.68E-39	1.87E-36
establishment of localization in cell		2365	155	53.63	2.89	+ 2.76E-34	6.92E-32
establishment of localization		4653	198	105.51	1.88	+ 7.75E-21	1.27E-18
transport		4502	194	102.08	1.90	+ 5.02E-21	8.34E-19
protein transport		1464	110	33.20	3.31	+ 4.57E-28	9.62E-26
reestablishment of protein localization		1559	111	35.35	3.14	+ 1.76E-26	3.42E-24
peptide transport		1493	110	33.85	3.25	+ 2.16E-27	4.42E-25
amide transport		1527	110	34.63	3.18	+ 1.26E-26	2.52E-24
nitrogen compound transport		1802	114	40.86	2.79	+ 3.53E-23	6.33E-21
organic substance transport		2171	115	49.23	2.34	+ 1.43E-17	2.07E-15
anion transport		2288	119	51.88	2.29	+ 1.21E-17	1.77E-16
ion transport		2882	149	65.35	2.28	+ 2.59E-22	4.54E-20
establishment of protein localization to endoplasmic reticulum		115	79	2.61	30.30	+ 1.33E-79	1.05E-75
protein localization to endoplasmic reticulum		142	79	3.22	24.53	+ 3.34E-74	8.77E-71
protein localization to organelle		781	104	17.94	5.80	+ 7.87E-46	3.55E-43
establishment of protein localization to organelle		449	95	10.18	9.33	+ 1.17E-57	9.20E-55
cotranslational protein targeting to membrane		101	76	2.29	39.14	+ 1.03E-78	5.43E-75
protein targeting to membrane		183	79	4.15	10.08	+ 1.80E-67	2.58E-64
establishment of protein localization to membrane		307	83	6.96	11.92	+ 2.12E-57	1.59E-54
protein localization to membrane		537	88	12.18	7.23	+ 2.66E-45	1.10E-42
mitochondrial electron transport, cytochrome c to oxygen		20	13	45	28.67	+ 1.02E-13	1.32E-11
mitochondrial ATP synthesis coupled electron transport		89	41	2.02	20.32	+ 5.07E-36	1.48E-33
ATP synthesis coupled electron transport		90	41	2.04	20.09	+ 7.23E-36	2.07E-33
respiratory electron transport chain		108	41	2.45	16.74	+ 2.54E-33	6.07E-31
electron transport chain		170	43	3.85	11.15	+ 8.12E-29	1.75E-26
generation of precursor metabolites and energy		402	59	9.12	6.47	+ 5.16E-28	1.07E-25
cellular metabolic process		7571	315	171.68	1.83	+ 4.50E-40	1.51E-37
metabolic process		8334	317	188.98	1.68	+ 3.89E-32	9.17E-30
cellular respiration		157	42	3.56	11.80	+ 5.39E-29	1.20E-26
energy derivation by oxidation of organic compounds		227	45	5.15	8.74	+ 2.95E-26	5.61E-24
oxidative phosphorylation		120	51	2.72	18.74	+ 3.06E-43	1.12E-40
phosphorylation		1023	60	23.20	2.59	+ 7.34E-11	8.84E-09
phosphate-containing compound metabolic process		1907	75	43.24	1.73	+ 4.06E-06	3.77E-04
sulfur metabolic process		1934	75	43.85	1.71	+ 6.82E-06	6.11E-04
ATP metabolic process		206	53	4.67	11.35	+ 1.15E-35	3.23E-33
aerobic electron transport chain		20	13	45	28.67	+ 1.02E-13	1.31E-11
aerobic respiration		77	18	1.75	10.31	+ 2.80E-12	3.32E-10
viral transcription		118	73	2.83	27.75	+ 1.99E-71	3.50E-68
viral process		849	115	19.25	5.97	+ 3.50E-52	2.21E-49
biological process involved in symbiotic interaction		937	117	21.25	5.51	+ 8.05E-50	4.53E-47
biological process involved in interspecies interaction between organisms		2118	132	48.03	2.75	+ 1.36E-26	2.68E-24
viral gene expression		172	78	3.90	19.49	+ 1.79E-65	2.18E-62
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay		120	75	2.72	27.56	+ 3.06E-73	6.88E-70
nuclear-transcribed mRNA catabolic process		196	79	4.44	17.88	+ 1.30E-65	1.71E-62
mRNA catabolic process		216	79	4.90	16.13	+ 5.85E-63	5.77E-60
negative regulation of gene expression		2034	136	46.12	2.95	+ 2.19E-30	4.94E-28
negative regulation of macromolecule metabolic process		2682	158	64.90	2.43	+ 7.69E-27	1.55E-24
negative regulation of metabolic process		3105	161	70.41	2.29	+ 1.36E-24	2.50E-22
negative regulation of biological process		5544	210	125.71	1.67	+ 1.59E-16	2.21E-14
regulation of metabolic process		6854	244	155.42	1.57	+ 8.83E-17	1.26E-14
regulation of macromolecule metabolic process		6308	236	143.04	1.65	+ 1.05E-18	1.61E-16
regulation of gene expression		4880	207	110.66	1.87	+ 4.89E-22	8.47E-20
mRNA catabolic process		246	80	5.58	14.34	+ 1.72E-60	1.51E-57
mRNA metabolic process		1599	144	36.26	3.97	+ 3.00E-46	1.39E-43
nucleic acid metabolic process		2232	161	50.61	3.18	+ 1.04E-40	3.58E-38
nucleobase-containing compound metabolic process		2720	179	61.68	2.90	+ 7.07E-41	2.48E-38
nucleotide metabolic process		2904	180	65.85	2.73	+ 8.83E-38	2.78E-35
primary metabolic process		7365	261	167.00	1.56	+ 2.46E-18	3.73E-16
cellular aromatic compound metabolic process		2949	180	68.87	2.69	+ 6.31E-37	1.88E-34
cellular nitrogen compound metabolic process		3407	213	77.26	1.76	+ 2.97E-47	1.46E-44
nitrogen compound metabolic process		6898	254	156.41	1.62	+ 6.67E-20	1.06E-17
organic cyclic compound metabolic process		3190	182	72.33	2.52	+ 1.22E-33	2.97E-31
organic substance metabolic process		7879	269	178.66	1.51	+ 8.95E-17	1.26E-14
macromolecule metabolic process		6194	237	140.45	1.69	+ 3.77E-20	6.08E-18
cellular macromolecule catabolic process		912	100	20.68	4.84	+ 9.78E-38	3.02E-35
macromolecule catabolic process		1046	102	23.72	4.30	+ 1.68E-34	4.40E-32
organic substance catabolic process		1762	111	39.95	2.78	+ 2.16E-22	3.83E-20
catabolic process		2085	119	47.28	2.52	+ 1.12E-20	1.82E-18
cellular macromolecule metabolic process		4964	201	112.56	1.79	+ 8.53E-19	1.32E-16
cellular catabolic process		1798	117	40.77	2.87	+ 8.18E-25	1.52E-22
nucleobase-containing compound catabolic process		175	84	8.50	9.88	+ 1.69E-52	1.11E-49
cellular nitrogen compound catabolic process		425	84	9.64	8.72	+ 9.23E-49	4.85E-46
heterocycle catabolic process		419	84	9.50	8.84	+ 3.48E-49	1.89E-46
aromatic compound catabolic process		441	84	10.00	8.40	+ 1.17E-47	5.94E-45
organic cyclic compound catabolic process		469	84	10.63	7.90	+ 7.94E-46	3.48E-43
mRNA metabolic process		624	119	15.74	7.56	+ 4.46E-64	4.69E-61
negative regulation of protein neddylation		5	3	11	26.46	+ 5.58E-04	3.20E-02
regulation of cellular metabolic process		8110	126	138.55	1.27	+ 2.73E-04	1.74E-02
regulation of protein metabolic process		2605	87	59.07	1.47	+ 2.56E-04	1.66E-02
regulation of primary metabolic process		5895	122	133.67	1.29	+ 1.56E-04	1.09E-02
regulation of nitrogen compound metabolic process		5692	168	129.07	1.30	+ 1.07E-04	7.68E-03
negative regulation of protein modification by small protein conjugation or removal		91	9	2.05	4.36	+ 3.83E-04	2.33E-02
negative regulation of nitrogen compound metabolic process		2392	86	54.24	1.59	+ 2.25E-05	1.90E-03
negative regulation of cellular metabolic process		2582	89	58.55	1.52	+ 7.53E-05	6.60E-03
positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator		5	3	11	26.46	+ 5.58E-04	3.19E-02
positive regulation of signal transduction by p53 class mediator		23	5	5.2	9.59	+ 3.38E-04	2.10E-02
regulation of apoptotic signaling pathway		347	20	7.87	2.54	+ 2.22E-04	1.47E-02
regulation of intrinsic apoptotic signaling pathway		158	14	3.58	3.91	+ 3.11E-05	2.54E-03
regulation of intrinsic apoptotic signaling pathway by bax class mediator		28	5	6.3	7.88	+ 7.46E-04	4.04E-02
cerebral cortex regionalization		6	3	14	22.05	+ 8.24E-04	4.39E-02
mitochondrial electron transport, ubiquinol to cytochrome c		14	7	3.2	22.05	+ 2.24E-07	2.15E-05
regulation of development, heterochromatin		8	4	18	22.05	+ 1.03E-04	7.42E-03
ribosomal small subunit assembly		21	10	48	21.00	+ 7.63E-10	8.65E-08
ribosome assembly		64	19	145	13.09	+ 1.79E-14	2.37E-12
organelle assembly		781	33	17.71	1.86	+ 9.04E-04	4.75E-02
organelle organization		3574	144	81.04	1.78	+ 2.12E-12	2.54E-10
cellular component organization		5776	198	130.97	1.51	+ 6.02E-11	6.98E-09
cellular component organization or biogenesis		6000	248	136.05	1.82	+ 1.83E-26	3.52E-24
cellular component assembly		2438	114	55.28	2.06	+ 1.38E-13	1.76E-11
cellular component biogenesis		2201	167	61.25	2.73	+ 2.11E-34	5.38E-32
ribosome biogenesis		332	75	75.3	9.96	+ 5.32E-47	2.54E-44
ribonucleoprotein complex biogenesis		465	94	10.54	8.91	+ 1.67E-55	1.20E-52
ribosomal small subunit biogenesis		75	19	1.70	11.17	+ 2.01E-13	2.50E-11
ribonucleoprotein complex assembly		190	37	4.31	8.29	+ 1.56E-21	2.68E-19
ribonucleoprotein complex subunit organization		197	37	4.47	8.58	+ 4.60E-21	7.72E-19
protein-containing complex subunit organization		1582	107	35.87	2.98	+ 8.44E-24	1.53E-21
cellular protein-containing complex assembly		860	84	19.50	4.31	+ 2.86E-28	6.10E-26
protein-containing complex assembly		1338	89	30.34	2.93	+ 3.13E-19	4.89E-17
mitochondrial ATP synthesis coupled proton transport		19	9	4.3	20.89	+ 5.70E-09	6.24E-07
ATP synthesis coupled proton transport		24	9	5.4	16.54	+ 2.88E-08	2.95E-06
ATP biosynthetic process		36	9	8.2	11.03	+ 5.23E-07	4.97E-05
purine ribonucleotide biosynthetic process		150	13	3.40	3.82	+ 7.32E-05	5.60E-03
purine nucleotide biosynthetic process		161	14	3.65	3.83	+ 3.77E-05	3.02E-03
purine-containing compound biosynthetic process		172	14	3.90	3.59	+ 7.33E-05	5.48E-03
organic cyclic compound biosynthetic process		1222	50	27.71	1.80	+ 1.06E-04	7.66E-03
organic substance biosynthetic process		2804	171	63.58	2.69	+ 1.15E-34	3.08E-32
biosynthetic process		2862	172	64.90	2.65	+ 3.85E-34	9.49E-32
heterocycle biosynthetic process		1076	48	24.40	1.97	+ 1.47E-05	1.26E-03
cellular biosynthetic process		2709	169	61.43	2.75	+ 2.35E-35	6.39E-33
cellular nitrogen compound biosynthetic process		1575	149	35.71	4.17	+ 1.53E-50	8.95E-48
organonitrogen compound metabolic process		5254	188	119.14	1.58	+ 7.02E-12	8.26E-10
aromatic compound biosynthetic process		1056	48	24.63	1.95	+ 1.69E-05	1.43E-03
organonitrogen compound biosynthetic process		1380	127	31.29	4.06	+ 3.70E-41	1.33E-38
nucleobase-containing compound biosynthetic process		1003	47	22.74	2.07	+ 4.63E-06	4.25E-04
purine nucleotide metabolic process		337	19	7.64	2.49	+ 4.10E-04	2.48E-02
purine ribonucleotide metabolic process		314	18	7.12	2.53	+ 4.80E-04	2.81E-02
ribose phosphate metabolic process		342	19	7.75	2.45	+ 7.71E-04	4.14E-02
ribonucleotide biosynthetic process		164	13	3.72	3.50	+ 1.68E-04	1.16E-02
ribose phosphate biosynthetic process		171	14	3.88	3.61	+ 6.92E-05	5.27



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


Analyzed List: [Change](#)

Reference List: [Change](#)

Annotation Data Set:  

Test Type: Fisher's Exact Binomial

Correction: Calculate False Discovery Rate Use the Bonferroni correction for multiple testing  No correction

Results 

Uniquely Mapped IDs:	Reference list	upload_1
20585	Out of 20595	330 out of 349
Unmapped IDs:	0	7
Multiple mapping information:	0	14

Neely 2021, suppl. Table 7B: Cluster 1 at E+L 0.1 µM

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

GO biological process complete	Homo sapiens (REF)	#	expected	observed	Fold Enrichment	z-score	raw P-value	FDR
negative regulation of protein neddylation	5	3	.08	35.41	+ 2.41E-04	1.61E-02		
regulation of metabolic process	6854	178	116.15	1.52	+ 6.77E-11	8.89E-09		
regulation of macromolecule metabolic process	6308	172	106.89	1.61	+ 7.93E-13	1.13E-10		
regulation of macromolecule metabolic process	5692	126	96.46	1.31	+ 7.12E-04	4.10E-02		
negative regulation of macromolecule metabolic process	2862	118	48.50	2.43	+ 1.76E-20	3.42E-18		
negative regulation of metabolic process	3105	118	52.62	2.24	+ 9.30E-18	1.61E-15		
negative regulation of biological process	5544	158	93.95	1.68	+ 3.86E-13	5.58E-11		
negative regulation of nitrogen compound metabolic process	2392	70	40.53	1.73	+ 7.18E-06	6.47E-04		
negative regulation of cellular metabolic process	2582	68	43.75	1.55	+ 2.43E-04	1.61E-02		
negative regulation of cellular process	4312	112	83.24	1.35	+ 4.97E-04	3.06E-02		
positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator	5	3	.08	35.41	+ 2.41E-04	1.61E-02		
regulation of apoptotic process	1479	43	25.06	1.72	+ 7.74E-04	4.41E-02		
regulation of programmed cell death	1517	45	25.71	1.75	+ 2.93E-04	1.88E-02		
regulation of cell death	1654	47	28.03	1.68	+ 6.96E-04	4.03E-02		
regulation of intrinsic apoptotic signaling pathway	158	10	2.68	3.73	+ 5.33E-04	3.25E-02		
regulation of intrinsic apoptotic signaling pathway by p53 class mediator	28	5	.47	10.54	+ 2.02E-04	1.40E-02		
SRP-dependent cotranslational protein targeting to membrane	96	52	1.63	31.96	+ 5.49E-55	2.61E-51		
protein targeting to ER	111	55	1.88	29.34	+ 1.61E-56	2.54E-52		
protein targeting	320	67	6.27	10.69	+ 6.62E-45	9.49E-42		
intracellular protein transport	974	77	16.51	4.67	+ 7.17E-29	2.02E-26		
cellular protein localization	1643	84	27.84	3.02	+ 1.32E-19	2.48E-17		
cellular macromolecule localization	1649	84	27.94	3.01	+ 1.64E-19	3.01E-17		
cellular localization	3006	122	50.94	2.40	+ 6.87E-21	1.39E-18		
cellular process	16487	329	262.44	1.25	+ 9.00E-21	1.80E-18		
localization	5805	156	98.37	1.59	+ 9.51E-11	1.24E-08		
macromolecule localization	2553	95	43.26	2.20	+ 1.98E-13	2.89E-11		
protein localization	2161	93	36.62	2.54	+ 5.31E-17	9.11E-15		
intracellular transport	1500	100	25.42	3.93	+ 2.99E-32	1.37E-29		
reestablishment of localization in cell	2365	116	40.08	2.89	+ 2.38E-26	5.61E-24		
establishment of localization	4653	143	78.85	1.81	+ 3.37E-14	5.02E-12		
transport	4502	140	76.29	1.84	+ 2.87E-14	4.31E-12		
protein transport	1464	82	24.81	3.31	+ 1.87E-21	3.94E-19		
establishment of protein localization	1559	82	26.42	3.10	+ 7.75E-20	1.47E-17		
vesicle transport	1493	82	25.30	3.24	+ 6.04E-21	1.24E-18		
amide transport	1522	82	25.88	3.17	+ 2.29E-20	4.40E-18		
nitrogen compound transport	1802	83	30.54	2.72	+ 9.36E-17	1.59E-14		
organic substance transport	2171	84	36.79	2.28	+ 8.40E-13	1.18E-10		
anion transport	2288	85	38.77	2.19	+ 5.27E-12	7.16E-10		
ion transport	2882	110	48.84	2.25	+ 1.26E-16	2.09E-14		
establishment of protein localization to endoplasmic reticulum	115	55	1.95	28.22	+ 7.41E-56	5.84E-52		
protein localization to endoplasmic reticulum	142	55	2.41	22.86	+ 7.60E-52	2.40E-48		
protein localization to organelle	791	68	13.40	5.07	+ 2.26E-27	5.66E-25		
establishment of protein localization to organelle	449	64	7.61	8.41	+ 2.86E-37	2.05E-34		
cotranslational protein targeting to membrane	101	53	1.71	30.97	+ 1.75E-55	9.21E-52		
protein targeting to membrane	183	55	3.10	17.74	+ 6.74E-47	1.18E-43		
establishment of protein localization to membrane	302	58	5.20	11.15	+ 1.07E-39	9.35E-37		
protein localization to membrane	537	59	9.10	6.48	+ 4.40E-29	2.32E-26		
mitochondrial ATP synthesis coupled proton transport	19	9	.32	27.95	+ 4.67E-10	5.58E-08		
ATP synthesis coupled proton transport	24	9	.41	22.13	+ 2.42E-09	2.79E-07		
ATP biosynthetic process	36	10	.61	16.39	+ 3.47E-09	3.89E-07		
purine ribonucleotide biosynthetic process	150	10	2.54	3.93	+ 3.63E-04	2.30E-02		
purine nucleotide biosynthetic process	161	10	2.73	3.67	+ 6.12E-04	3.66E-02		
purine-containing compound biosynthetic process	122	51	2.91	3.77	+ 2.62E-04	1.72E-02		
organic cyclic compound biosynthetic process	1222	44	20.71	2.12	+ 3.81E-06	3.55E-04		
organic cyclic compound metabolic process	3190	145	54.06	2.68	+ 8.92E-31	3.13E-28		
organic substance metabolic process	2879	208	133.52	1.56	+ 2.05E-15	3.37E-13		
metabolic process	8334	251	141.23	1.78	+ 6.21E-32	2.80E-29		
organic substance biosynthetic process	2804	130	47.52	2.74	+ 9.10E-28	2.31E-25		
biosynthetic process	2862	130	48.50	2.68	+ 6.08E-27	1.48E-24		
heterocycle biosynthetic process	1076	42	18.23	2.30	+ 8.38E-07	8.11E-05		
heterocycle metabolic process	2904	162	49.21	2.89	+ 2.74E-33	1.44E-30		
cellular metabolic process	2671	248	128.30	1.93	+ 6.38E-38	4.79E-35		
cellular biosynthetic process	2709	128	45.91	2.79	+ 5.08E-28	1.31E-25		
cellular nitrogen compound biosynthetic process	1676	108	26.69	4.05	+ 3.84E-36	2.42E-33		
cellular nitrogen compound metabolic process	3402	161	57.73	2.79	+ 3.84E-37	2.64E-34		
nitrogen compound metabolic process	6888	199	116.89	1.70	+ 5.61E-19	1.02E-16		
purine-containing compound metabolic process	359	16	6.08	2.63	+ 6.00E-04	3.60E-02		
organonitrogen compound metabolic process	5254	145	89.03	1.63	+ 1.25E-10	1.62E-08		
cellular aromatic compound metabolic process	2849	143	49.07	2.86	+ 3.44E-33	1.75E-30		
aromatic compound biosynthetic process	1086	42	18.40	2.28	+ 1.02E-06	9.76E-05		
organonitrogen compound biosynthetic process	1380	91	23.09	3.89	+ 8.41E-29	2.29E-26		
nucleobase-containing compound metabolic process	2720	138	46.99	2.99	+ 8.53E-34	4.80E-31		
primary metabolic process	2365	202	124.81	1.62	+ 1.15E-16	1.92E-14		
phosphate-containing compound metabolic process	1902	58	32.32	1.79	+ 1.68E-05	1.46E-03		
phosphorus metabolic process	1934	58	32.77	1.77	+ 2.82E-05	2.30E-03		
nucleobase-containing compound biosynthetic process	1003	38	17.00	2.24	+ 8.23E-06	7.34E-04		
ribonucleotide biosynthetic process	164	10	2.78	3.60	+ 7.01E-04	4.05E-02		
ATP metabolic process	206	46	3.49	13.18	+ 2.59E-34	1.51E-31		
purine ribonucleoside triphosphate biosynthetic process	47	10	.80	12.56	+ 3.13E-08	3.40E-06		
purine nucleoside triphosphate biosynthetic process	48	10	.81	12.29	+ 3.72E-08	4.02E-06		
nucleoside triphosphate biosynthetic process	66	10	1.10	9.08	+ 4.60E-07	4.62E-05		
nucleoside triphosphate metabolic process	91	10	1.54	6.48	+ 7.28E-06	6.52E-04		
purine nucleoside triphosphate metabolic process	67	10	1.14	8.81	+ 5.92E-07	5.90E-05		
ribonucleoside triphosphate biosynthetic process	53	10	.90	11.13	+ 8.47E-08	8.97E-06		
ribonucleoside triphosphate metabolic process	68	10	1.15	8.68	+ 6.69E-07	6.55E-05		
purine ribonucleoside triphosphate metabolic process	61	10	1.03	9.67	+ 2.72E-07	2.79E-05		
energy coupled proton transport, down electrochemical gradient	24	9	.41	22.13	+ 2.42E-09	2.77E-07		
nitron transmembrane transport	134	19	2.27	8.37	+ 1.10E-11	1.48E-09		
inorganic cation transmembrane transport	672	23	9.69	2.37	+ 2.17E-04	1.48E-02		
transmembrane transport	1292	39	21.89	1.78	+ 5.53E-04	3.36E-02		
oxidative phosphorylation	120	43	2.03	21.15	+ 2.11E-39	1.75E-36		
generation of exocyclic metabolites and energy	402	53	6.81	7.78	+ 2.42E-29	7.19E-27		
phosphorylation	1023	47	17.34	2.71	+ 1.25E-09	1.46E-07		
mitochondrial transmembrane transport	105	12	1.78	6.74	+ 6.07E-07	6.02E-05		
mitochondrial transport	229	18	3.88	4.64	+ 1.94E-07	1.99E-05		
viral transcription	116	51	1.97	25.94	+ 2.58E-50	5.09E-47		
viral process	849	76	14.39	5.28	+ 9.30E-32	3.96E-29		
biological process involved in symbiotic interaction	937	79	15.88	4.98	+ 2.08E-31	8.19E-29		
biological process involved in interspecies interaction between organisms	2118	97	35.89	2.70	+ 1.36E-19	2.52E-17		
viral gene expression	172	51	2.91	17.50	+ 3.08E-43	3.74E-40		
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	120	52	2.03	25.57	+ 4.84E-51	1.27E-47		
nuclear-transcribed mRNA catabolic process	198	53	3.32	15.96	+ 3.57E-43	4.02E-40		
mRNA catabolic process	216	53	3.66	14.48	+ 2.60E-41	2.56E-38		
negative regulation of gene expression	2034	98	34.47	2.84	+ 2.60E-21	5.39E-19		
regulation of gene expression	4880	150	82.70	1.81	+ 4.21E-15	6.45E-13		
RNA catabolic process	246	53	4.17	12.71	+ 8.31E-39	6.56E-36		
RNA metabolic process	1599	102	27.10	3.76	+ 1.88E-31	7.61E-29		
nucleic acid metabolic process	2232	118	37.82	3.12	+ 1.11E-29	3.45E-27		
macromolecule metabolic process	6194	177	104.96	1.69	+ 2.07E-15	3.37E-13		
cellular macromolecule catabolic process	912	68	15.45	4.40	+ 4.64E-24	1.05E-21		
macromolecule catabolic process	1046	70	17.73	3.95	+ 2.98E-22	6.35E-20		
organic substance catabolic process	1762	79	29.86	2.65	+ 2.64E-15	4.13E-13		
catabolic process	2085	88	35.33	2.49	+ 2.15E-15	3.46E-13		
cellular macromolecule metabolic process	4964	149	84.12	1.77	+ 4.69E-14	6.91E-12		
cellular catabolic process	1798	85	30.47	2.79	+ 7.85E-18	1.38E-15		
nucleobase-containing compound catabolic process	375	56	6.35	8.81	+ 1.59E-33	8.65E-31		
cellular nitrogen compound catabolic process	425	56	7.20	7.78	+ 5.50E-31	2.02E-28		
heterocycle catabolic process	419	56	7.10	7.89	+ 2.84E-31	1.09E-28		
aromatic compound catabolic process	441	56	7.47	7.49	+ 3.06E-30	9.86E-28		
organic cyclic compound catabolic process	469	56	7.95	7.05	+ 5.30E-29	1.52E-26		
mRNA catabolic process	694	81	11.76	6.89	+ 1.33E-41	1.40E-38		
mitochondrial electron transport, ubiquinol to cytochrome c	14	6	.24	25.29	+ 6.53E-07	6.43E-05		
respiratory electron transport chain	108	34	1.83	18.58	+ 9.46E-30	2.98E-27		
electron transport chain	170	38	2.88	13.19	+ 1.80E-28	4.73E-26		
cellular respiration	157	3						

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: 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:	<input type="text" value="GO biological process complete"/> ?
Test Type:	<input type="radio"/> Fisher's Exact <input type="radio"/> Binomial
Correction:	<input type="radio"/> 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	5 out of 5
Unmapped IDs:	0	0
Multiple mapping information:	0	0

Neely 2021, suppl. Table 7C: Cluster 5 at E+L 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							
SRP-dependent cotranslational protein targeting to membrane	96	3	.02	> 100	+	1.07E-06	1.69E-02
↳ protein targeting to ER	111	3	.03	> 100	+	1.64E-06	8.61E-03
↳ protein targeting	370	3	.09	33.40	+	5.73E-05	5.02E-02
↳ establishment of protein localization to endoplasmic reticulum	115	3	.03	> 100	+	1.82E-06	7.16E-03
↳ protein localization to endoplasmic reticulum	142	3	.03	87.02	+	3.38E-06	7.62E-03
↳ cotranslational protein targeting to membrane	101	3	.02	> 100	+	1.24E-06	9.79E-03
↳ protein targeting to membrane	183	3	.04	67.52	+	7.15E-06	1.13E-02
↳ establishment of protein localization to membrane	307	3	.07	40.25	+	3.30E-05	3.25E-02
viral transcription	116	3	.03	> 100	+	1.86E-06	5.88E-03
↳ viral gene expression	172	3	.04	71.84	+	5.95E-06	1.04E-02
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	120	3	.03	> 100	+	2.06E-06	5.41E-03
↳ nuclear-transcribed mRNA catabolic process	196	3	.05	63.05	+	8.75E-06	1.26E-02
↳ mRNA catabolic process	216	3	.05	57.21	+	1.17E-05	1.53E-02
↳ RNA catabolic process	246	3	.06	50.23	+	1.71E-05	2.08E-02
↳ nucleobase-containing compound catabolic process	375	3	.09	32.95	+	5.96E-05	4.95E-02
translational initiation	143	3	.03	86.41	+	3.45E-06	6.80E-03
rRNA processing	260	3	.06	47.53	+	2.02E-05	2.27E-02
↳ rRNA metabolic process	270	3	.07	45.77	+	2.26E-05	2.37E-02
↳ ribosome biogenesis	332	3	.08	37.22	+	4.16E-05	3.86E-02

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:	<input checked="" type="checkbox"/> GO biological process complete ?
Test Type:	<input checked="" type="radio"/> Fisher's Exact <input type="radio"/> Binomial
Correction:	<input checked="" type="radio"/> Calculate False Discovery Rate <input type="radio"/> Use the Bonferroni correction for multiple testing ? <input type="radio"/> No correction

Results [?](#)

Uniquely Mapped IDs:	Reference list 20595 out of 20595	upload_1 60 out of 60
Unmapped IDs:	0	0
Multiple mapping information:	0	0

Neely 2021, suppl. Table 7D: Cluster 2 at E+L 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						
compartment pattern specification	4	2	.01	> 100	+ 1.24E-04	1.71E-02
SRP-dependent cotranslational protein targeting to membrane	96	23	.28	82.24	+ 6.41E-37	1.01E-32
↳ protein targeting to ER	111	23	.32	71.12	+ 1.26E-35	6.60E-32
↳ protein targeting	370	24	1.08	22.26	+ 5.15E-26	5.42E-23
↳ intracellular protein transport	974	24	2.84	8.46	+ 1.37E-16	5.67E-14
↳ cellular protein localization	1643	25	4.79	5.22	+ 1.30E-12	3.86E-10
↳ cellular macromolecule localization	1649	25	4.80	5.20	+ 1.41E-12	3.96E-10
↳ cellular localization	3006	28	8.76	3.20	+ 3.50E-09	6.73E-07
↳ localization	5805	35	16.91	2.07	+ 1.70E-06	2.70E-04
↳ macromolecule localization	2553	26	7.44	3.50	+ 2.72E-09	5.43E-07
↳ protein localization	2161	26	6.30	4.13	+ 7.33E-11	1.73E-08
↳ intracellular transport	1500	27	4.37	6.18	+ 1.86E-15	7.14E-13
↳ establishment of localization in cell	2385	27	6.89	3.92	+ 8.58E-11	1.96E-08
↳ establishment of localization	4653	33	13.56	2.43	+ 5.74E-08	1.01E-05
↳ transport	4502	33	13.12	2.52	+ 2.47E-08	4.53E-06
↳ protein transport	1464	24	4.27	5.63	+ 9.16E-13	2.89E-10
↳ establishment of protein localization	1559	24	4.54	5.28	+ 3.45E-12	8.92E-10
↳ peptide transport	1493	24	4.35	5.52	+ 1.39E-12	3.98E-10
↳ amide transport	1527	24	4.45	5.39	+ 2.23E-12	6.07E-10
↳ nitrogen compound transport	1802	24	5.25	4.57	+ 7.01E-11	1.68E-08
↳ organic substance transport	2171	24	6.32	3.79	+ 3.03E-09	5.90E-07
↳ anion transport	2288	24	6.67	3.60	+ 8.54E-09	1.60E-06
↳ ion transport	2882	31	8.40	3.69	+ 6.29E-12	1.58E-09
↳ establishment of protein localization to endoplasmic reticulum	115	23	.34	68.65	+ 2.61E-35	1.03E-31
↳ protein localization to endoplasmic reticulum	142	23	.41	55.60	+ 2.12E-33	6.68E-30
↳ protein localization to organelle	791	24	2.30	10.41	+ 1.37E-18	6.95E-16
↳ establishment of protein localization to organelle	449	24	1.31	18.35	+ 4.08E-24	3.58E-21
↳ cotranslational protein targeting to membrane	101	23	.29	78.17	+ 1.81E-36	1.42E-32
↳ protein targeting to membrane	183	23	.53	43.14	+ 4.53E-31	7.94E-28
↳ establishment of protein localization to membrane	307	24	.89	26.83	+ 7.62E-28	1.00E-24
↳ protein localization to membrane	537	24	1.56	15.34	+ 2.32E-22	1.66E-19
ribosomal small subunit assembly	21	4	.06	65.38	+ 7.77E-07	1.28E-04
↳ ribosome assembly	64	4	.19	21.45	+ 4.56E-05	6.60E-03
↳ cellular component organization or biogenesis	6000	34	17.48	1.95	+ 1.08E-05	1.64E-03
↳ cellular component biogenesis	2701	26	7.87	3.30	+ 8.97E-09	1.66E-06
↳ ribosome biogenesis	332	19	.97	19.64	+ 1.58E-19	8.33E-17
↳ ribonucleoprotein complex biogenesis	465	19	1.35	14.03	+ 6.31E-17	2.77E-14
↳ ribosomal small subunit biogenesis	75	6	.22	27.46	+ 1.27E-07	2.18E-05
viral transcription	116	22	.34	65.10	+ 2.79E-33	7.33E-30
↳ viral process	849	23	2.47	9.30	+ 9.71E-17	4.14E-14
↳ biological process involved in symbiotic interaction	937	23	2.73	8.43	+ 7.78E-16	3.07E-13
↳ biological process involved in interspecies interaction between organisms	2118	24	6.17	3.89	+ 1.85E-09	3.95E-07
↳ viral gene expression	172	22	.50	43.90	+ 7.71E-30	1.22E-26
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	120	22	.35	62.93	+ 5.47E-33	1.23E-29
↳ nuclear-transcribed mRNA catabolic process	196	22	.57	38.53	+ 1.11E-28	1.59E-25
↳ mRNA catabolic process	216	22	.63	34.96	+ 8.11E-28	9.84E-25
↳ negative regulation of gene expression	2034	23	5.93	3.88	+ 4.89E-09	9.29E-07
↳ negative regulation of macromolecule metabolic process	2862	26	8.34	3.12	+ 3.00E-08	5.37E-06
↳ negative regulation of metabolic process	3105	26	9.05	2.87	+ 1.58E-07	2.69E-05
↳ negative regulation of biological process	5544	30	16.15	1.86	+ 1.91E-04	2.59E-02
↳ regulation of gene expression	4880	30	14.22	2.11	+ 1.07E-05	1.63E-03
↳ RNA catabolic process	246	22	.72	30.70	+ 1.17E-26	1.32E-23
↳ RNA metabolic process	1599	27	4.66	5.80	+ 8.71E-15	2.92E-12
↳ nucleic acid metabolic process	2232	28	6.50	4.31	+ 3.27E-12	8.59E-10
↳ nucleobase-containing compound metabolic process	2720	31	7.92	3.91	+ 1.36E-12	3.98E-10
↳ heterocycle metabolic process	2904	31	8.46	3.66	+ 7.69E-12	1.89E-09
↳ cellular metabolic process	7571	45	22.06	2.04	+ 2.62E-09	5.29E-07
↳ metabolic process	8334	45	24.28	1.85	+ 8.66E-08	1.50E-05
↳ cellular aromatic compound metabolic process	2949	31	8.59	3.61	+ 1.15E-11	2.79E-09
↳ cellular nitrogen compound metabolic process	3407	32	9.93	3.22	+ 8.51E-11	1.97E-08
↳ nitrogen compound metabolic process	6898	35	20.10	1.74	+ 9.37E-05	1.31E-02
↳ organic cyclic compound metabolic process	3190	31	9.29	3.34	+ 8.86E-11	2.00E-08
↳ macromolecule metabolic process	6194	33	18.05	1.83	+ 6.09E-05	8.73E-03
↳ cellular macromolecule catabolic process	912	22	2.66	8.28	+ 5.65E-15	1.98E-12
↳ macromolecule catabolic process	1046	22	3.05	7.22	+ 8.70E-14	2.80E-11
↳ organic substance catabolic process	1762	22	5.13	4.29	+ 1.98E-09	4.17E-07
↳ catabolic process	2085	22	6.07	3.62	+ 4.23E-08	7.49E-06
↳ cellular macromolecule metabolic process	4964	32	14.46	2.21	+ 1.16E-06	1.86E-04
↳ cellular catabolic process	1798	22	5.24	4.20	+ 2.88E-09	5.67E-07
↳ nucleobase-containing compound catabolic process	375	22	1.09	20.14	+ 7.11E-23	5.90E-20
↳ cellular nitrogen compound catabolic process	425	22	1.24	17.77	+ 9.45E-22	6.21E-19
↳ heterocycle catabolic process	419	22	1.22	18.02	+ 7.04E-22	4.83E-19
↳ aromatic compound catabolic process	441	22	1.28	17.12	+ 2.03E-21	1.28E-18
↳ organic cyclic compound catabolic process	469	22	1.37	16.10	+ 7.22E-21	4.22E-18
↳ mRNA metabolic process	694	25	2.02	12.36	+ 3.81E-21	2.31E-18
cytoplasmic translation	75	12	.22	54.92	+ 1.68E-17	8.04E-15
↳ translation	384	24	1.12	21.45	+ 1.19E-25	1.18E-22
↳ peptide biosynthetic process	409	24	1.19	20.14	+ 4.96E-25	4.60E-22
↳ peptide metabolic process	537	24	1.56	15.34	+ 2.32E-22	1.74E-19
↳ organonitrogen compound metabolic process	5254	31	15.31	2.03	+ 1.79E-05	2.67E-03
↳ cellular amide metabolic process	808	24	2.35	10.20	+ 2.19E-18	1.08E-15
↳ amide biosynthetic process	528	24	1.54	15.60	+ 1.58E-22	1.25E-19
↳ cellular nitrogen compound biosynthetic process	1575	29	4.59	6.32	+ 5.50E-17	2.48E-14
↳ cellular biosynthetic process	2709	31	7.89	3.93	+ 1.22E-12	3.78E-10
↳ biosynthetic process	2862	31	8.34	3.72	+ 5.24E-12	1.33E-09
↳ organonitrogen compound biosynthetic process	1380	28	4.02	6.96	+ 2.09E-17	9.67E-15
↳ organic substance biosynthetic process	2804	31	8.17	3.79	+ 3.05E-12	8.16E-10
↳ gene expression	2187	28	6.37	4.39	+ 2.00E-12	5.53E-10
↳ cellular macromolecule biosynthetic process	1655	28	4.82	5.81	+ 2.07E-15	7.77E-13
↳ macromolecule biosynthetic process	1696	28	4.94	5.67	+ 3.82E-15	1.37E-12
↳ cellular protein metabolic process	3644	28	10.62	2.64	+ 2.44E-07	4.09E-05
↳ protein metabolic process	4219	28	12.29	2.28	+ 6.10E-06	9.53E-04
mitochondrial ATP synthesis coupled proton transport	19	3	.06	54.20	+ 3.45E-05	5.04E-03
↳ ATP synthesis coupled proton transport	24	3	.07	42.91	+ 6.49E-05	9.22E-03
↳ ATP biosynthetic process	36	3	.10	28.60	+ 1.98E-04	2.66E-02
↳ ATP metabolic process	206	12	.60	20.00	+ 1.26E-12	3.83E-10
↳ energy coupled proton transport, down electrochemical gradient	24	3	.07	42.91	+ 6.49E-05	9.13E-03
↳ proton transmembrane transport	134	6	.39	15.37	+ 3.23E-06	5.09E-04
↳ oxidative phosphorylation	120	12	.35	34.33	+ 3.01E-15	1.10E-12
↳ generation of precursor metabolites and energy	402	12	1.17	10.25	+ 2.11E-09	4.37E-07
↳ phosphorylation	1023	13	2.98	4.36	+ 6.76E-06	1.05E-03
translational initiation	143	22	.42	52.81	+ 1.84E-31	3.62E-28
cristae formation	31	3	.09	33.22	+ 1.31E-04	1.79E-02
↳ inner mitochondrial membrane organization	52	4	.15	26.40	+ 2.11E-05	3.11E-03
↳ mitochondrion organization	457	10	1.33	7.51	+ 8.69E-07	1.41E-04
mitochondrial electron transport, NADH to ubiquinone	49	4	.14	28.02	+ 1.69E-05	2.54E-03
↳ mitochondrial ATP synthesis coupled electron transport	89	8	.26	30.85	+ 3.69E-10	8.20E-08
↳ ATP synthesis coupled electron transport	90	8	.26	30.51	+ 4.01E-10	8.78E-08
↳ respiratory electron transport chain	108	8	.31	25.43	+ 1.55E-09	3.36E-07
↳ electron transport chain	170	9	.50	18.17	+ 2.28E-09	4.67E-07
↳ cellular respiration	157	8	.46	17.49	+ 2.51E-08	4.56E-06
↳ energy derivation by oxidation of organic compounds	227	8	.66	12.10	+ 3.83E-07	6.36E-05
rRNA processing	260	18	.76	23.76	+ 6.74E-20	3.79E-17
↳ ncRNA processing	432	18	1.26	14.30	+ 3.48E-16	1.41E-13
↳ RNA processing	923	21	2.69	7.81	+ 8.51E-14	2.80E-11
↳ ncRNA metabolic process	517	18	1.51	11.95	+ 7.01E-15	2.40E-12
↳ rRNA metabolic process	270	18	.79	22.88	+ 1.27E-19	6.92E-17
mitochondrial respiratory chain complex assembly	101	4	.29	13.59	+ 2.47E-04	3.30E-02
regulation of cellular process	11308	19	32.94	.58	- 3.73E-04	4.94E-02

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: 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 Binomial

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

Results [?](#)

	Reference list	upload_1
Uniquely Mapped IDs:	20595 out of 20595	21 out of 22
Unmapped IDs:	0	0
Multiple mapping information:	0	1

Neely 2021, suppl. Table 7E: Cluster 3 at E+L 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](#)

GO biological process complete	Homo sapiens (REF)		upload_1 (Hierarchy NEW! ?)				
	#	#	expected	Fold Enrichment	+/-	raw P value	FDR
SRP-dependent cotranslational protein targeting to membrane	96	7	.10	68.26	+	1.01E-11	1.60E-07
↳protein targeting to ER	111	7	.12	59.04	+	2.67E-11	1.40E-07
↳protein targeting	370	8	.40	20.24	+	3.03E-09	3.68E-06
↳intracellular protein transport	974	8	1.04	7.69	+	4.53E-06	1.79E-03
↳macromolecule localization	2553	10	2.73	3.67	+	1.35E-04	3.61E-02
↳protein localization	2161	10	2.31	4.33	+	3.22E-05	1.04E-02
↳intracellular transport	1500	9	1.60	5.62	+	1.22E-05	4.37E-03
↳protein transport	1464	9	1.56	5.75	+	1.00E-05	3.77E-03
↳establishment of protein localization	1559	9	1.67	5.40	+	1.66E-05	5.71E-03
↳peptide transport	1493	9	1.59	5.64	+	1.17E-05	4.31E-03
↳amide transport	1527	9	1.63	5.52	+	1.41E-05	4.94E-03
↳nitrogen compound transport	1802	9	1.92	4.68	+	5.27E-05	1.57E-02
↳establishment of protein localization to endoplasmic reticulum	115	7	.12	56.98	+	3.38E-11	1.33E-07
↳protein localization to endoplasmic reticulum	142	7	.15	46.15	+	1.39E-10	3.14E-07
↳protein localization to organelle	791	8	.84	9.47	+	9.69E-07	4.37E-04
↳establishment of protein localization to organelle	449	8	.48	16.68	+	1.33E-08	1.11E-05
↳cotranslational protein targeting to membrane	101	7	.11	64.88	+	1.42E-11	1.12E-07
↳protein targeting to membrane	183	7	.20	35.81	+	7.67E-10	1.21E-06
↳establishment of protein localization to membrane	307	7	.33	21.35	+	2.49E-08	1.87E-05
↳protein localization to membrane	537	7	.57	12.20	+	1.04E-06	4.54E-04
cytoplasmic translation	75	5	.08	62.41	+	1.94E-08	1.53E-05
↳translation	384	8	.41	19.50	+	4.03E-09	4.54E-06
↳peptide biosynthetic process	409	8	.44	18.31	+	6.54E-09	6.44E-06
↳peptide metabolic process	537	8	.57	13.95	+	5.23E-08	3.43E-05
↳cellular amide metabolic process	808	8	.86	9.27	+	1.14E-06	4.84E-04
↳cellular nitrogen compound metabolic process	3407	12	3.64	3.30	+	5.30E-05	1.55E-02
↳amide biosynthetic process	528	8	.56	14.18	+	4.60E-08	3.15E-05
↳cellular nitrogen compound biosynthetic process	1575	10	1.68	5.94	+	1.92E-06	7.97E-04
↳organonitrogen compound biosynthetic process	1380	10	1.47	6.78	+	5.74E-07	2.74E-04
↳gene expression	2187	10	2.34	4.28	+	3.57E-05	1.10E-02
viral transcription	116	7	.12	56.49	+	3.58E-11	1.13E-07
↳viral process	849	7	.91	7.72	+	2.05E-05	6.73E-03
↳biological process involved in symbiotic interaction	937	7	1.00	6.99	+	3.84E-05	1.17E-02
↳viral gene expression	172	7	.18	38.10	+	5.05E-10	8.85E-07
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	120	7	.13	54.61	+	4.50E-11	1.18E-07
↳nuclear-transcribed mRNA catabolic process	196	7	.21	33.43	+	1.22E-09	1.75E-06
↳mRNA catabolic process	216	7	.23	30.34	+	2.34E-09	3.08E-06
↳RNA catabolic process	246	7	.26	26.64	+	5.62E-09	5.91E-06
↳RNA metabolic process	1599	9	1.71	5.27	+	2.04E-05	6.84E-03
↳cellular macromolecule catabolic process	912	7	.97	7.19	+	3.23E-05	1.02E-02
↳macromolecule catabolic process	1046	7	1.12	6.26	+	7.70E-05	2.17E-02
↳nucleobase-containing compound catabolic process	375	7	.40	17.47	+	9.52E-08	6.01E-05
↳cellular nitrogen compound catabolic process	425	7	.45	15.42	+	2.20E-07	1.28E-04
↳heterocycle catabolic process	419	7	.45	15.64	+	2.00E-07	1.21E-04
↳aromatic compound catabolic process	441	7	.47	14.86	+	2.81E-07	1.53E-04
↳organic cyclic compound catabolic process	469	7	.50	13.97	+	4.23E-07	2.08E-04
↳mRNA metabolic process	694	8	.74	10.79	+	3.64E-07	1.91E-04
translational initiation	143	7	.15	45.82	+	1.46E-10	2.88E-07
mitochondrial ATP synthesis coupled electron transport	89	3	.10	31.56	+	1.25E-04	3.45E-02
↳ATP synthesis coupled electron transport	90	3	.10	31.20	+	1.29E-04	3.50E-02
↳oxidative phosphorylation	120	4	.13	31.20	+	8.38E-06	3.23E-03
↳ATP metabolic process	206	4	.22	18.18	+	6.63E-05	1.90E-02
rRNA processing	260	7	.28	25.20	+	8.16E-09	7.57E-06
↳ncRNA processing	432	7	.46	15.17	+	2.45E-07	1.38E-04
↳RNA processing	923	8	.99	8.11	+	3.05E-06	1.23E-03
↳ncRNA metabolic process	517	7	.55	12.67	+	8.06E-07	3.74E-04
↳rRNA metabolic process	270	7	.29	24.27	+	1.05E-08	9.21E-06
↳ribosome biogenesis	332	7	.35	19.74	+	4.21E-08	3.02E-05
↳ribonucleoprotein complex biogenesis	465	7	.50	14.09	+	3.99E-07	2.03E-04

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	121 out of 129
Unmapped IDs:	0	1
Multiple mapping information:	0	3

Neely 2021, suppl. Table 7F: Cluster 4 at E+L 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! ?)				
GO biological process complete	#	#	expected	Fold Enrichment	+/-	raw P value	FDR
putrescine catabolic process	3	2	.02	> 100	+	3.80E-04	4.22E-02
↳organonitrogen compound metabolic process	5254	56	32.91	1.70	+	1.06E-05	1.48E-03
↳↳metabolic process	8334	80	52.20	1.53	+	1.30E-06	1.96E-04
↳↳cellular nitrogen compound metabolic process	3407	47	21.34	2.20	+	6.72E-08	1.23E-05
↳↳cellular metabolic process	7571	78	47.42	1.64	+	6.39E-08	1.20E-05
↳↳cellular process	15487	116	97.01	1.20	+	3.50E-05	4.56E-03
↳↳organic substance catabolic process	1762	36	11.04	3.26	+	1.64E-10	4.45E-08
↳↳catabolic process	2085	36	13.06	2.76	+	1.41E-08	3.19E-06
ribosomal small subunit assembly	21	6	.13	45.61	+	1.38E-08	3.15E-06
↳ribosome assembly	64	6	.40	14.97	+	4.90E-06	7.02E-04
↳cellular component organization or biogenesis	6000	68	37.58	1.81	+	2.71E-08	5.63E-06
↳cellular component assembly	2438	30	15.27	1.96	+	2.99E-04	3.41E-02
↳cellular component biogenesis	2701	44	16.92	2.60	+	1.07E-09	2.67E-07
↳ribosome biogenesis	332	20	2.08	9.62	+	6.15E-14	2.69E-11
↳ribonucleoprotein complex biogenesis	465	20	2.91	6.87	+	2.21E-11	6.98E-09
↳ribosomal small subunit biogenesis	75	7	.47	14.90	+	7.93E-07	1.20E-04
↳protein-containing complex subunit organization	1582	31	9.91	3.13	+	1.12E-08	2.60E-06
↳cellular protein-containing complex assembly	860	23	5.39	4.27	+	5.20E-09	1.24E-06
↳protein-containing complex assembly	1338	29	8.38	3.46	+	4.18E-09	1.01E-06
protein insertion into mitochondrial inner membrane	11	3	.07	43.54	+	8.16E-05	1.02E-02
↳inner mitochondrial membrane organization	52	7	.33	21.49	+	8.01E-08	1.44E-05
↳mitochondrial membrane organization	140	8	.88	9.12	+	4.12E-06	5.95E-04
↳mitochondrion organization	457	21	2.86	7.34	+	2.00E-12	6.70E-10
↳cellular protein localization	1643	31	10.29	3.01	+	2.65E-08	5.58E-06
↳cellular macromolecule localization	1649	31	10.33	3.00	+	2.88E-08	5.90E-06
↳cellular localization	3006	44	18.83	2.34	+	2.91E-08	5.88E-06
↳localization	5805	62	36.36	1.71	+	1.87E-06	2.78E-04
↳macromolecule localization	2553	34	15.99	2.13	+	2.06E-05	2.75E-03
↳protein localization	2161	32	13.54	2.36	+	3.77E-06	5.56E-04
↳establishment of protein localization to membrane	307	26	1.92	13.52	+	2.39E-21	2.90E-18
↳protein localization to membrane	537	27	3.36	8.03	+	1.06E-16	6.44E-14
↳establishment of protein localization	1559	28	9.77	2.87	+	3.95E-07	6.35E-05
↳establishment of localization	4653	56	29.14	1.92	+	2.18E-07	3.61E-05
↳intracellular protein transport	974	28	6.10	4.59	+	1.61E-11	5.17E-09
↳intracellular transport	1500	34	9.40	3.62	+	4.10E-11	1.24E-08
↳establishment of localization in cell	2365	41	14.81	2.77	+	8.22E-10	2.16E-07
↳transport	4502	55	28.20	1.95	+	1.56E-07	2.68E-05
↳protein transport	1464	28	9.17	3.05	+	1.11E-07	1.93E-05
↳peptide transport	1493	28	9.35	2.99	+	1.66E-07	2.81E-05
↳amide transport	1527	28	9.56	2.93	+	2.61E-07	4.28E-05
↳nitrogen compound transport	1802	30	11.29	2.66	+	6.77E-07	1.04E-04
↳organic substance transport	2171	32	13.60	2.35	+	4.06E-06	5.94E-04
↳anion transport	2288	32	14.33	2.23	+	1.43E-05	1.94E-03
↳ion transport	2882	44	18.05	2.44	+	1.07E-08	2.51E-06
↳establishment of protein localization to organelle	449	26	2.81	9.24	+	1.66E-17	1.25E-14
↳protein localization to organelle	791	27	4.95	5.45	+	8.56E-13	3.14E-10
↳mitochondrial transport	229	8	1.43	5.58	+	1.21E-04	1.46E-02
↳protein targeting	370	27	2.32	11.65	+	1.39E-20	1.46E-17
mitochondrial electron transport, cytochrome c to oxygen	20	5	.13	39.91	+	4.16E-07	6.62E-05
↳mitochondrial ATP synthesis coupled electron transport	89	13	.56	23.32	+	6.65E-14	2.84E-11
↳ATP synthesis coupled electron transport	90	13	.56	23.06	+	7.57E-14	3.14E-11
↳respiratory electron transport chain	108	13	.68	19.22	+	6.32E-13	2.37E-10
↳electron transport chain	170	13	1.06	12.21	+	1.25E-10	3.51E-08
↳generation of precursor metabolites and energy	402	18	2.52	7.15	+	1.30E-10	3.60E-08
↳cellular respiration	157	13	.98	13.22	+	4.95E-11	1.47E-08
↳energy derivation by oxidation of organic compounds	227	13	1.42	9.14	+	3.49E-09	8.61E-07
↳oxidative phosphorylation	120	17	.75	22.62	+	1.20E-17	9.49E-15
↳phosphorylation	1023	22	6.41	3.43	+	4.80E-07	7.50E-05
↳phosphate-containing compound metabolic process	1907	27	11.94	2.26	+	5.29E-05	6.84E-03
↳phosphorus metabolic process	1934	27	12.11	2.23	+	1.01E-04	1.24E-02
↳ATP metabolic process	206	18	1.29	13.95	+	3.12E-15	1.54E-12
↳aerobic electron transport chain	20	5	.13	39.91	+	4.16E-07	6.55E-05
↳aerobic respiration	77	6	.48	12.44	+	1.32E-05	1.81E-03
SRP-dependent cotranslational protein targeting to membrane	96	23	.60	38.25	+	3.13E-28	4.94E-24
↳protein targeting to ER	111	23	.70	33.08	+	5.85E-27	3.07E-23
↳establishment of protein localization to endoplasmic reticulum	115	23	.72	31.93	+	1.20E-26	4.73E-23
↳protein localization to endoplasmic reticulum	142	23	.89	25.86	+	8.93E-25	2.01E-21
↳cotranslational protein targeting to membrane	101	23	.63	36.36	+	8.68E-28	6.85E-24
↳protein targeting to membrane	183	23	1.15	20.07	+	1.68E-22	2.40E-19
mitochondrial ATP synthesis coupled proton transport	19	4	.12	33.61	+	1.16E-05	1.60E-03
↳ATP synthesis coupled proton transport	24	4	.15	26.61	+	2.61E-05	3.46E-03
↳ATP biosynthetic process	36	4	.23	17.74	+	1.10E-04	1.35E-02
↳purine ribonucleotide biosynthetic process	150	6	.94	6.39	+	4.39E-04	4.81E-02
↳purine nucleotide biosynthetic process	161	7	1.01	6.94	+	8.85E-05	1.10E-02
↳purine-containing compound biosynthetic process	172	7	1.08	6.50	+	1.31E-04	1.58E-02
↳organic cyclic compound metabolic process	3190	45	19.98	2.25	+	6.18E-08	1.17E-05
↳organic substance biosynthetic process	2804	50	17.56	2.85	+	1.44E-12	5.05E-10
↳biosynthetic process	2862	50	17.93	2.79	+	3.10E-12	1.02E-09
↳heterocycle metabolic process	2904	41	18.19	2.25	+	3.30E-07	5.37E-05
↳cellular biosynthetic process	2709	49	16.97	2.89	+	1.61E-12	5.53E-10
↳cellular nitrogen compound biosynthetic process	1575	41	9.87	4.16	+	2.08E-15	1.06E-12
↳cellular aromatic compound metabolic process	2949	42	18.47	2.27	+	1.84E-07	3.09E-05
↳organonitrogen compound biosynthetic process	1380	39	8.64	4.51	+	9.08E-16	4.94E-13
↳nucleobase-containing compound metabolic process	2720	41	17.04	2.41	+	5.52E-08	1.09E-05
↳purine nucleotide metabolic process	337	9	2.11	4.26	+	3.21E-04	3.62E-02
↳purine ribonucleotide metabolic process	314	9	1.97	4.58	+	1.94E-04	2.28E-02
↳ribonucleotide metabolic process	332	9	2.08	4.33	+	2.89E-04	3.33E-02
↳ribose phosphate metabolic process	342	9	2.14	4.20	+	3.57E-04	3.99E-02
↳purine ribonucleoside triphosphate biosynthetic process	47	4	.29	13.59	+	2.85E-04	3.34E-02
↳purine nucleoside triphosphate biosynthetic process	48	4	.30	13.30	+	3.08E-04	3.49E-02
↳ribonucleoside triphosphate biosynthetic process	53	4	.33	12.05	+	4.38E-04	4.84E-02
↳energy coupled proton transport, down electrochemical gradient	24	4	.15	26.61	+	2.61E-05	3.43E-03
↳proton transmembrane transport	134	10	.84	11.91	+	2.33E-08	5.03E-06
viral transcription	116	23	.73	31.65	+	1.43E-26	4.51E-23
↳viral process	849	33	5.32	6.21	+	3.73E-17	2.67E-14
↳biological process involved in symbiotic interaction	937	35	5.87	5.96	+	1.10E-17	9.15E-15
↳biological process involved in interspecies interaction between organisms	2118	41	13.27	3.09	+	2.91E-11	9.00E-09
↳viral gene expression	172	23	1.08	21.35	+	4.65E-23	7.33E-20
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	120	23	.75	30.60	+	2.85E-26	7.49E-23
↳nuclear-transcribed mRNA catabolic process	196	24	1.23	19.55	+	3.28E-23	5.75E-20
↳mRNA catabolic process	216	24	1.35	17.74	+	2.69E-22	3.53E-19
↳negative regulation of gene expression	2034	35	12.74	2.75	+	2.61E-08	5.57E-06
↳negative regulation of macromolecule metabolic process	2862	42	17.93	2.34	+	6.58E-08	1.22E-05
↳negative regulation of metabolic process	3105	44	19.45	2.26	+	8.58E-08	1.50E-05
↳negative regulation of biological process	5544	64	34.73	1.84	+	6.92E-08	1.26E-05
↳regulation of metabolic process	6854	65	42.93	1.51	+	7.18E-05	9.13E-03
↳regulation of macromolecule metabolic process	6308	61	39.51	1.54	+	7.72E-05	9.74E-03
↳regulation of gene expression	4880	53	30.57	1.73	+	1.56E-05	2.11E-03
↳RNA catabolic process	246	24	1.54	15.58	+	4.49E-21	5.05E-18
↳RNA metabolic process	1599	30	10.02	3.00	+	5.33E-08	1.06E-05
↳nucleic acid metabolic process	2232	32	13.98	2.29	+	6.68E-06	9.50E-04
↳cellular macromolecule catabolic process	912	30	5.71	5.25	+	9.19E-14	3.72E-11
↳macromolecule catabolic process	1046	31	6.55	4.73	+	4.78E-13	1.84E-10
↳cellular catabolic process	1798	32	11.26	2.84	+	5.74E-08	1.10E-05
↳nucleobase-containing compound catabolic process	375	25	2.35	10.64	+	3.25E-18	2.85E-15
↳cellular nitrogen compound catabolic process	425	25	2.66	9.39	+	5.27E-17	3.46E-14
↳heterocycle catabolic process	419	25	2.62	9.53	+	3.84E-17	2.64E-14
↳aromatic compound catabolic process	441	25	2.76	9.05	+	1.19E-16	6.98E-14
↳organic cyclic compound catabolic process	469	25	2.94	8.51	+	4.65E-16	2.62E-13
↳mRNA metabolic process	694	26	4.35	5.98	+	3.15E-13	1.24E-10
cytoplasmic translation	75	13	.47	27.67	+	9.19E-15	4.39E-12
↳translation	384	26	2.41	10.81	+	4.44E-19	4.38E-16
↳peptide biosynthetic process	409	26	2.56	10.15	+	1.92E-18	1.78E-15
↳peptide metabolic process	537	26	3.				