

GO biological process complete	Homo sapiens - REFLIST (20592)	upload_1 (40)	upload_1 (expected)	upload_1 (over/under)	upload_1 (fold Enrichment)	upload_1 (raw P-value)	upload_1 (FDR)	Column 1
positive regulation of phosphorylation (GO:0042327)	632	19	1.23	+	15.48	1.66E-18	2.54E-14	
regulation of phosphate metabolic process (GO:0019220)	1133	22	2.20	+	10.00	1.02E-17	7.80E-14	
positive regulation of phosphorus metabolic process (GO:0010562)	699	19	1.36	+	13.99	1.02E-17	5.23E-14	
positive regulation of phosphate metabolic process (GO:0045937)	699	19	1.36	+	13.99	1.02E-17	3.92E-14	
regulation of phosphorus metabolic process (GO:0051174)	1134	22	2.20	+	9.99	1.03E-17	3.18E-14	
regulation of phosphorylation (GO:0042325)	1003	21	1.95	+	10.78	1.78E-17	4.57E-14	
regulation of cell migration (GO:0030334)	936	19	1.82	+	10.45	1.93E-15	4.23E-12	
positive regulation of cellular process (GO:0048522)	5698	35	11.07	+	3.16	4.37E-15	8.38E-12	
positive regulation of biological process (GO:0048518)	6211	36	12.06	+	2.98	4.45E-15	7.58E-12	
regulation of cell motility (GO:2000145)	996	19	1.93	+	9.82	5.84E-15	8.97E-12	
positive regulation of protein phosphorylation (GO:0001934)	585	16	1.14	+	14.08	7.26E-15	1.01E-11	
regulation of locomotion (GO:0040012)	1038	19	2.02	+	9.42	1.22E-14	1.56E-11	
phosphorylation (GO:0016310)	744	17	1.45	+	11.76	1.46E-14	1.72E-11	
positive regulation of cell population proliferation (GO:0008284)	1255	20	2.44	+	8.20	2.40E-14	2.63E-11	
regulation of protein phosphorylation (GO:0001932)	926	18	1.80	+	10.01	2.88E-14	2.95E-11	
positive regulation of protein modification process (GO:0031401)	793	17	1.54	+	11.04	4.03E-14	3.87E-11	

protein metabolic process (GO:0019538)	3620	29	7.03	+	4.12	4.14E-14	3.74E-11
positive regulation of cell migration (GO:0030335)	541	15	1.05	+	14.27	5.15E-14	4.39E-11
metabolic process (GO:0008152)	8001	38	15.54	+	2.44	7.96E-14	6.43E-11
positive regulation of cell motility (GO:2000147)	568	15	1.10	+	13.60	1.03E-13	7.87E-11
positive regulation of locomotion (GO:0040017)	583	15	1.13	+	13.25	1.48E-13	1.08E-10
response to stimulus (GO:0050896)	8194	38	15.92	+	2.39	1.91E-13	1.33E-10
protein phosphorylation (GO:0006468)	493	14	.96	+	14.62	3.17E-13	2.11E-10
organonitrogen compound metabolic process (GO:1901564)	4684	31	9.10	+	3.41	3.63E-13	2.32E-10
regulation of protein modification process (GO:0031399)	1272	19	2.47	+	7.69	4.42E-13	2.71E-10
positive regulation of protein metabolic process (GO:0051247)	1285	19	2.50	+	7.61	5.28E-13	3.12E-10
regulation of protein metabolic process (GO:0051246)	2230	23	4.33	+	5.31	9.47E-13	5.39E-10
response to chemical (GO:0042221)	3782	28	7.35	+	3.81	1.43E-12	7.84E-10
response to organic substance (GO:0010033)	2585	24	5.02	+	4.78	2.06E-12	1.09E-09
peptidyl-amino acid modification (GO:0018193)	574	14	1.11	+	12.56	2.35E-12	1.20E-09
cellular response to chemical stimulus (GO:0070887)	2391	23	4.64	+	4.95	4.05E-12	2.01E-09
protein modification process (GO:0036211)	2137	22	4.15	+	5.30	4.28E-12	2.05E-09
response to oxygen-containing compound (GO:1901700)	1670	20	3.24	+	6.17	4.62E-12	2.15E-09
positive regulation of cellular metabolic process (GO:0031325)	3349	26	6.51	+	4.00	7.15E-12	3.23E-09
cellular response to oxygen-containing compound (GO:1901701)	1138	17	2.21	+	7.69	1.21E-11	5.30E-09
response to lipid (GO:0033993)	850	15	1.65	+	9.08	2.91E-11	1.24E-08

macromolecule modification (GO:0043412)	2358	22	4.58	+	4.80	3.00E-11	1.25E-08
regulation of nitrogen compound metabolic process (GO:0051171)	5483	31	10.65	+	2.91	3.03E-11	1.22E-08
primary metabolic process (GO:0044238)	6966	34	13.53	+	2.51	3.66E-11	1.44E-08
response to organic cyclic compound (GO:0014070)	869	15	1.69	+	8.89	3.95E-11	1.52E-08
regulation of multicellular organismal process (GO:0051239)	2965	24	5.76	+	4.17	3.95E-11	1.48E-08
multicellular organism development (GO:0007275)	3953	27	7.68	+	3.52	3.99E-11	1.46E-08
cellular response to stimulus (GO:0051716)	6476	33	12.58	+	2.62	4.05E-11	1.45E-08
regulation of response to stimulus (GO:0048583)	3976	27	7.72	+	3.50	4.58E-11	1.60E-08
response to endogenous stimulus (GO:0009719)	1447	18	2.81	+	6.40	4.78E-11	1.63E-08
positive regulation of molecular function (GO:0044093)	1248	17	2.42	+	7.01	5.07E-11	1.69E-08
positive regulation of nitrogen compound metabolic process (GO:0051173)	3015	24	5.86	+	4.10	5.64E-11	1.84E-08
regulation of cellular metabolic process (GO:0031323)	6066	32	11.78	+	2.72	5.69E-11	1.82E-08
phosphate-containing compound metabolic process (GO:0006796)	1686	19	3.28	+	5.80	5.86E-11	1.84E-08
regulation of metabolic process (GO:0019222)	6584	33	12.79	+	2.58	6.63E-11	2.03E-08
regulation of primary metabolic process (GO:0080090)	5649	31	10.97	+	2.83	6.92E-11	2.08E-08
regulation of cell population proliferation (GO:0042127)	2198	21	4.27	+	4.92	7.26E-11	2.14E-08
phosphorus metabolic process (GO:0006793)	1712	19	3.33	+	5.71	7.62E-11	2.21E-08
positive regulation of metabolic process (GO:0009893)	3736	26	7.26	+	3.58	8.98E-11	2.55E-08
regulation of molecular function (GO:0065009)	2050	20	3.98	+	5.02	1.86E-10	5.19E-08

regulation of cellular component biogenesis (GO:0044087)	973	15	1.89	+	7.94	1.88E-10	5.14E-08
system development (GO:0048731)	3538	25	6.87	+	3.64	2.15E-10	5.80E-08
regulation of kinase activity (GO:0043549)	537	12	1.04	+	11.50	3.17E-10	8.39E-08
organic substance metabolic process (GO:0071704)	7478	34	14.53	+	2.34	3.26E-10	8.48E-08
positive regulation of multicellular organismal process (GO:0051240)	1647	18	3.20	+	5.63	3.90E-10	9.98E-08
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	420	11	.82	+	13.48	3.90E-10	9.82E-08
regulation of catalytic activity (GO:0050790)	1433	17	2.78	+	6.11	4.26E-10	1.05E-07
regulation of macromolecule metabolic process (GO:0060255)	6058	31	11.77	+	2.63	4.73E-10	1.15E-07
regulation of cellular component organization (GO:0051128)	2436	21	4.73	+	4.44	4.93E-10	1.18E-07
regulation of response to stress (GO:0080134)	1452	17	2.82	+	6.03	5.21E-10	1.23E-07
anatomical structure development (GO:0048856)	5214	29	10.13	+	2.86	5.59E-10	1.30E-07
response to nitrogen compound (GO:1901698)	1060	15	2.06	+	7.28	6.05E-10	1.39E-07
developmental process (GO:0032502)	5723	30	11.12	+	2.70	8.09E-10	1.83E-07
regulation of response to external stimulus (GO:0032101)	1086	15	2.11	+	7.11	8.42E-10	1.87E-07
regulation of signaling (GO:0023051)	3428	24	6.66	+	3.60	8.47E-10	1.86E-07
positive regulation of macromolecule metabolic process (GO:0010604)	3431	24	6.66	+	3.60	8.63E-10	1.87E-07
regulation of cell communication (GO:0010646)	3433	24	6.67	+	3.60	8.73E-10	1.86E-07
positive regulation of cellular component organization (GO:0051130)	1118	15	2.17	+	6.91	1.25E-09	2.63E-07
regulation of intracellular signal transduction (GO:1902531)	1773	18	3.44	+	5.23	1.27E-09	2.64E-07

animal organ development (GO:0048513)	2859	22	5.55	+	3.96	1.27E-09	2.60E-07
regulation of cellular process (GO:0050794)	11189	39	21.73	+	1.79	1.29E-09	2.61E-07
regulation of localization (GO:0032879)	2039	19	3.96	+	4.80	1.47E-09	2.93E-07
cellular metabolic process (GO:0044237)	6383	31	12.40	+	2.50	1.96E-09	3.86E-07
nitrogen compound metabolic process (GO:0006807)	6402	31	12.44	+	2.49	2.13E-09	4.14E-07
regulation of MAPK cascade (GO:0043408)	649	12	1.26	+	9.52	2.60E-09	4.99E-07
response to organonitrogen compound (GO:0010243)	988	14	1.92	+	7.29	2.64E-09	5.00E-07
regulation of transferase activity (GO:0051338)	652	12	1.27	+	9.47	2.74E-09	5.12E-07
cellular response to endogenous stimulus (GO:0071495)	1187	15	2.31	+	6.51	2.81E-09	5.19E-07
protein deacetylation (GO:0006476)	25	5	.05	+	> 100	2.91E-09	5.31E-07
positive regulation of transferase activity (GO:0051347)	384	10	.75	+	13.41	2.93E-09	5.29E-07
regulation of signal transduction (GO:0009966)	3018	22	5.86	+	3.75	3.57E-09	6.38E-07
macromolecule metabolic process (GO:0043170)	5672	29	11.02	+	2.63	4.65E-09	8.21E-07
peptidyl-tyrosine phosphorylation (GO:0018108)	65	6	.13	+	47.52	4.68E-09	8.17E-07
peptidyl-tyrosine modification (GO:0018212)	67	6	.13	+	46.10	5.55E-09	9.58E-07
regulation of biological process (GO:0050789)	11738	39	22.80	+	1.71	6.12E-09	1.04E-06
response to stress (GO:0006950)	3436	23	6.67	+	3.45	6.33E-09	1.07E-06
multicellular organismal process (GO:0032501)	6730	31	13.07	+	2.37	8.17E-09	1.36E-06
anatomical structure morphogenesis (GO:0009653)	2261	19	4.39	+	4.33	8.18E-09	1.35E-06
positive regulation of kinase activity (GO:0033674)	311	9	.60	+	14.90	8.32E-09	1.36E-06
regulation of programmed cell death (GO:0043067)	1522	16	2.96	+	5.41	9.48E-09	1.53E-06
positive regulation of catalytic activity (GO:0043085)	905	13	1.76	+	7.39	9.69E-09	1.55E-06

cellular response to organic substance (GO:0071310)	1764	17	3.43	+	4.96	9.83E-09	1.56E-06
response to external stimulus (GO:0009605)	2290	19	4.45	+	4.27	1.01E-08	1.58E-06
protein deacylation (GO:0035601)	34	5	.07	+	75.71	1.16E-08	1.80E-06
regulation of macromolecule biosynthetic process (GO:0010556)	5036	27	9.78	+	2.76	1.18E-08	1.81E-06
response to abiotic stimulus (GO:0009628)	1114	14	2.16	+	6.47	1.20E-08	1.82E-06
response to peptide (GO:1901652)	459	10	.89	+	11.22	1.54E-08	2.32E-06
regulation of proteolysis (GO:0030162)	605	11	1.18	+	9.36	1.62E-08	2.41E-06
macromolecule deacylation (GO:0098732)	37	5	.07	+	69.57	1.71E-08	2.52E-06
positive regulation of epithelial cell migration (GO:0010634)	151	7	.29	+	23.86	2.04E-08	2.98E-06
positive regulation of proteolysis (GO:0045862)	347	9	.67	+	13.35	2.09E-08	3.03E-06
regulation of cellular biosynthetic process (GO:0031326)	5167	27	10.04	+	2.69	2.12E-08	3.04E-06
cellular response to nitrogen compound (GO:1901699)	625	11	1.21	+	9.06	2.25E-08	3.19E-06
enzyme-linked receptor protein signaling pathway (GO:0007167)	626	11	1.22	+	9.05	2.28E-08	3.21E-06
regulation of biosynthetic process (GO:0009889)	5198	27	10.10	+	2.67	2.43E-08	3.39E-06
regulation of nucleobase-containing compound metabolic process (GO:0019219)	4055	24	7.88	+	3.05	2.68E-08	3.71E-06
biological regulation (GO:0065007)	12153	39	23.61	+	1.65	3.17E-08	4.35E-06
regulation of mitotic cell cycle (GO:0007346)	497	10	.97	+	10.36	3.21E-08	4.37E-06
regulation of developmental process (GO:0050793)	2466	19	4.79	+	3.97	3.39E-08	4.56E-06
negative regulation of biological process (GO:0048519)	5284	27	10.26	+	2.63	3.52E-08	4.70E-06
response to growth factor (GO:0070848)	505	10	.98	+	10.19	3.72E-08	4.93E-06

response to oxidative stress (GO:0006979)	372	9	.72	+	12.45	3.75E-08	4.92E-06
regulation of gene expression (GO:0010468)	4909	26	9.54	+	2.73	4.09E-08	5.32E-06
positive regulation of protein localization to nucleus (GO:1900182)	96	6	.19	+	32.17	4.21E-08	5.44E-06
cellular response to lipid (GO:0071396)	527	10	1.02	+	9.77	5.51E-08	7.05E-06
positive regulation of cell communication (GO:0010647)	1748	16	3.40	+	4.71	6.59E-08	8.36E-06
positive regulation of signaling (GO:0023056)	1750	16	3.40	+	4.71	6.69E-08	8.42E-06
intracellular signal transduction (GO:0035556)	1525	15	2.96	+	5.06	7.83E-08	9.78E-06
positive regulation of macromolecule biosynthetic process (GO:0010557)	2608	19	5.07	+	3.75	8.38E-08	1.04E-05
positive regulation of transport (GO:0051050)	903	12	1.75	+	6.84	9.54E-08	1.17E-05
histone deacetylation (GO:0016575)	19	4	.04	+	> 100	1.04E-07	1.27E-05
signaling (GO:0023052)	5133	26	9.97	+	2.61	1.07E-07	1.30E-05
positive regulation of developmental process (GO:0051094)	1332	14	2.59	+	5.41	1.10E-07	1.32E-05
response to xenobiotic stimulus (GO:0009410)	431	9	.84	+	10.75	1.28E-07	1.52E-05
regulation of nitric oxide biosynthetic process (GO:0045428)	58	5	.11	+	44.38	1.37E-07	1.62E-05
positive regulation of cellular biosynthetic process (GO:0031328)	2690	19	5.23	+	3.64	1.38E-07	1.61E-05
positive regulation of biosynthetic process (GO:0009891)	2710	19	5.26	+	3.61	1.55E-07	1.80E-05
regulation of nitric oxide metabolic process (GO:0080164)	60	5	.12	+	42.90	1.60E-07	1.85E-05
signal transduction (GO:0007165)	4829	25	9.38	+	2.67	1.64E-07	1.88E-05
cell communication (GO:0007154)	5285	26	10.27	+	2.53	2.01E-07	2.29E-05
regulation of focal adhesion assembly (GO:0051893)	63	5	.12	+	40.86	2.01E-07	2.27E-05

regulation of cell-substrate junction assembly (GO:0090109)	63	5	.12	+	40.86	2.01E-07	2.26E-05
response to ketone (GO:1901654)	214	7	.42	+	16.84	2.03E-07	2.26E-05
response to hormone (GO:0009725)	780	11	1.52	+	7.26	2.05E-07	2.26E-05
positive regulation of cell cycle (GO:0045787)	326	8	.63	+	12.63	2.12E-07	2.33E-05
regulation of cytokine production (GO:0001817)	784	11	1.52	+	7.22	2.16E-07	2.35E-05
positive regulation of gene expression (GO:0010628)	1183	13	2.30	+	5.66	2.16E-07	2.34E-05
positive regulation of nucleocytoplasmic transport (GO:0046824)	64	5	.12	+	40.22	2.17E-07	2.33E-05
regulation of cell-substrate adhesion (GO:0010810)	217	7	.42	+	16.61	2.23E-07	2.37E-05
positive regulation of MAPK cascade (GO:0043410)	464	9	.90	+	9.99	2.36E-07	2.50E-05
negative regulation of cellular process (GO:0048523)	4926	25	9.57	+	2.61	2.47E-07	2.60E-05
cellular response to hydrogen peroxide (GO:0070301)	66	5	.13	+	39.00	2.51E-07	2.62E-05
regulation of transport (GO:0051049)	1668	15	3.24	+	4.63	2.51E-07	2.60E-05
cellular response to reactive oxygen species (GO:0034614)	133	6	.26	+	23.22	2.67E-07	2.75E-05
regulation of cell-substrate junction organization (GO:0150116)	68	5	.13	+	37.85	2.88E-07	2.95E-05
positive regulation of response to stimulus (GO:0048584)	2229	17	4.33	+	3.93	3.02E-07	3.07E-05
regulation of epithelial cell migration (GO:0010632)	229	7	.44	+	15.74	3.17E-07	3.20E-05
cellular response to organic cyclic compound (GO:0071407)	490	9	.95	+	9.46	3.70E-07	3.71E-05
regulation of apoptotic process (GO:0042981)	1477	14	2.87	+	4.88	3.87E-07	3.86E-05
positive regulation of cytokine production (GO:0001819)	494	9	.96	+	9.38	3.95E-07	3.92E-05
regulation of cellular response to stress (GO:0080135)	657	10	1.28	+	7.84	4.11E-07	4.05E-05

positive regulation of intracellular signal transduction (GO:1902533)	1037	12	2.01	+	5.96	4.17E-07	4.08E-05
regulation of reactive oxygen species metabolic process (GO:2000377)	144	6	.28	+	21.45	4.18E-07	4.06E-05
positive regulation of cellular component biogenesis (GO:0044089)	509	9	.99	+	9.10	5.06E-07	4.88E-05
regulation of protein localization to nucleus (GO:1900180)	149	6	.29	+	20.73	5.07E-07	4.87E-05
response to peptide hormone (GO:0043434)	377	8	.73	+	10.92	6.24E-07	5.95E-05
regulation of inflammatory response (GO:0050727)	378	8	.73	+	10.90	6.36E-07	6.03E-05
protein autophosphorylation (GO:0046777)	156	6	.30	+	19.80	6.57E-07	6.19E-05
response to inorganic substance (GO:0010035)	528	9	1.03	+	8.78	6.83E-07	6.39E-05
blood vessel development (GO:0001568)	529	9	1.03	+	8.76	6.94E-07	6.45E-05
regulation of cell cycle (GO:0051726)	1094	12	2.13	+	5.65	7.33E-07	6.78E-05
regulation of cell differentiation (GO:0045595)	1563	14	3.04	+	4.61	7.64E-07	7.03E-05
peptidyl-lysine deacetylation (GO:0034983)	7	3	.01	+	> 100	8.02E-07	7.33E-05
negative regulation of cellular component organization (GO:0051129)	708	10	1.38	+	7.27	8.05E-07	7.32E-05
positive regulation of smooth muscle cell proliferation (GO:0048661)	85	5	.17	+	30.28	8.23E-07	7.44E-05
positive regulation of response to external stimulus (GO:0032103)	548	9	1.06	+	8.45	9.26E-07	8.31E-05
vasculature development (GO:0001944)	550	9	1.07	+	8.42	9.53E-07	8.51E-05
negative regulation of programmed cell death (GO:0043069)	923	11	1.79	+	6.14	1.07E-06	9.46E-05
circulatory system development (GO:0072359)	926	11	1.80	+	6.12	1.10E-06	9.71E-05
regulation of leukocyte activation (GO:0002694)	566	9	1.10	+	8.19	1.20E-06	1.06E-04
cellular response to stress (GO:0033554)	1630	14	3.17	+	4.42	1.26E-06	1.10E-04

response to angiotensin (GO:1990776)	38	4	.07	+	54.19	1.29E-06	1.11E-04
cellular response to chemical stress (GO:0062197)	285	7	.55	+	12.64	1.32E-06	1.14E-04
chromatin organization (GO:0006325)	751	10	1.46	+	6.85	1.36E-06	1.17E-04
response to reactive oxygen species (GO:0000302)	179	6	.35	+	17.26	1.43E-06	1.22E-04
cellular response to organonitrogen compound (GO:0071417)	587	9	1.14	+	7.89	1.62E-06	1.37E-04
response to hydrogen peroxide (GO:0042542)	99	5	.19	+	26.00	1.69E-06	1.42E-04
regulation of G2/M transition of mitotic cell cycle (GO:0010389)	101	5	.20	+	25.49	1.86E-06	1.56E-04
positive regulation of protein import into nucleus (GO:0042307)	42	4	.08	+	49.03	1.86E-06	1.55E-04
epigenetic regulation of gene expression (GO:0040029)	189	6	.37	+	16.34	1.94E-06	1.61E-04
chromatin remodeling (GO:0006338)	602	9	1.17	+	7.70	1.99E-06	1.64E-04
positive regulation of endothelial cell migration (GO:0010595)	106	5	.21	+	24.28	2.33E-06	1.91E-04
cellular response to ketone (GO:1901655)	107	5	.21	+	24.06	2.44E-06	1.99E-04
negative regulation of metabolic process (GO:0009892)	2902	18	5.64	+	3.19	2.45E-06	1.99E-04
regulation of cell activation (GO:0050865)	623	9	1.21	+	7.44	2.62E-06	2.12E-04
positive regulation of protein-containing complex assembly (GO:0031334)	200	6	.39	+	15.44	2.66E-06	2.14E-04
negative regulation of gene expression, epigenetic (GO:0045814)	110	5	.21	+	23.40	2.78E-06	2.22E-04
regulation of catabolic process (GO:0009894)	1026	11	1.99	+	5.52	2.95E-06	2.35E-04
response to amine (GO:0014075)	48	4	.09	+	42.90	3.07E-06	2.43E-04
regulation of cell cycle G2/M phase transition (GO:1902749)	114	5	.22	+	22.58	3.28E-06	2.59E-04
regulation of protein kinase activity (GO:0045859)	473	8	.92	+	8.71	3.29E-06	2.57E-04

tissue development (GO:0009888)	1768	14	3.43	+	4.08	3.29E-06	2.56E-04
cell differentiation (GO:0030154)	3648	20	7.09	+	2.82	3.33E-06	2.59E-04
cellular developmental process (GO:0048869)	3651	20	7.09	+	2.82	3.38E-06	2.61E-04
cellular response to growth factor stimulus (GO:0071363)	475	8	.92	+	8.67	3.39E-06	2.60E-04
cellular process (GO:0009987)	14924	40	28.99	+	1.38	3.40E-06	2.59E-04
negative regulation of cellular metabolic process (GO:0031324)	2648	17	5.14	+	3.30	3.41E-06	2.59E-04
regulation of nucleocytoplasmic transport (GO:0046822)	116	5	.23	+	22.19	3.56E-06	2.70E-04
G2/M transition of mitotic cell cycle (GO:0000086)	50	4	.10	+	41.18	3.57E-06	2.69E-04
protein-DNA complex organization (GO:0071824)	839	10	1.63	+	6.14	3.64E-06	2.72E-04
response to oxygen levels (GO:0070482)	336	7	.65	+	10.72	3.84E-06	2.86E-04
protein destabilization (GO:0031648)	51	4	.10	+	40.38	3.85E-06	2.85E-04
regulation of plasma membrane bounded cell projection organization (GO:0120035)	654	9	1.27	+	7.08	3.88E-06	2.86E-04
positive regulation of mitotic cell cycle (GO:0045931)	120	5	.23	+	21.45	4.18E-06	3.07E-04
regulation of cell-matrix adhesion (GO:0001952)	122	5	.24	+	21.10	4.52E-06	3.30E-04
positive regulation of protein localization (GO:1903829)	496	8	.96	+	8.30	4.64E-06	3.37E-04
regulation of cell projection organization (GO:0031344)	669	9	1.30	+	6.93	4.65E-06	3.37E-04
cell population proliferation (GO:0008283)	1823	14	3.54	+	3.95	4.70E-06	3.39E-04
cell cycle G2/M phase transition (GO:0044839)	55	4	.11	+	37.44	5.10E-06	3.66E-04
positive regulation of organelle organization (GO:0010638)	505	8	.98	+	8.16	5.28E-06	3.77E-04
sphingosine-1-phosphate receptor signaling pathway (GO:0003376)	15	3	.03	+	> 100	5.40E-06	3.84E-04
regulation of chemotaxis (GO:0050920)	228	6	.44	+	13.55	5.55E-06	3.93E-04

tube morphogenesis (GO:0035239)	684	9	1.33	+	6.77	5.55E-06	3.91E-04
mitotic cell cycle process (GO:1903047)	509	8	.99	+	8.09	5.59E-06	3.92E-04
positive regulation of cell projection organization (GO:0031346)	358	7	.70	+	10.07	5.77E-06	4.03E-04
cellular response to oxidative stress (GO:0034599)	230	6	.45	+	13.43	5.83E-06	4.05E-04
cellular response to heat (GO:0034605)	57	4	.11	+	36.13	5.84E-06	4.04E-04
regulation of protein localization (GO:0032880)	892	10	1.73	+	5.77	6.22E-06	4.28E-04
sphingolipid mediated signaling pathway (GO:0090520)	16	3	.03	+	96.53	6.40E-06	4.39E-04
negative regulation of apoptotic process (GO:0043066)	896	10	1.74	+	5.75	6.47E-06	4.41E-04
cell migration (GO:0016477)	899	10	1.75	+	5.73	6.66E-06	4.52E-04
regulation of protein import into nucleus (GO:0042306)	61	4	.12	+	33.76	7.53E-06	5.09E-04
regulation of smooth muscle cell proliferation (GO:0048660)	139	5	.27	+	18.52	8.35E-06	5.62E-04
regulation of cell cycle process (GO:0010564)	726	9	1.41	+	6.38	8.92E-06	5.98E-04
regulation of muscle cell differentiation (GO:0051147)	142	5	.28	+	18.13	9.23E-06	6.16E-04
regulation of system process (GO:0044057)	547	8	1.06	+	7.53	9.38E-06	6.24E-04
negative regulation of molecular function (GO:0044092)	736	9	1.43	+	6.30	9.95E-06	6.58E-04
mitotic cell cycle phase transition (GO:0044772)	145	5	.28	+	17.75	1.02E-05	6.71E-04
positive regulation of cell cycle process (GO:0090068)	256	6	.50	+	12.07	1.06E-05	6.94E-04
regulation of organelle organization (GO:0033043)	1181	11	2.29	+	4.79	1.12E-05	7.31E-04
cellular response to fluid shear stress (GO:0071498)	20	3	.04	+	77.22	1.16E-05	7.57E-04
protein-containing complex organization (GO:0043933)	2006	14	3.90	+	3.59	1.41E-05	9.16E-04
regulation of defense response (GO:0031347)	774	9	1.50	+	5.99	1.48E-05	9.55E-04

cell cycle phase transition (GO:0044770)	158	5	.31	+	16.29	1.52E-05	9.78E-04
regulation of protein-containing complex assembly (GO:0043254)	421	7	.82	+	8.56	1.62E-05	1.04E-03
regulation of cellular localization (GO:0060341)	999	10	1.94	+	5.15	1.66E-05	1.06E-03
supramolecular fiber organization (GO:0097435)	593	8	1.15	+	6.95	1.67E-05	1.06E-03
mitotic cell cycle (GO:0000278)	594	8	1.15	+	6.93	1.69E-05	1.07E-03
regulation of cell adhesion (GO:0030155)	788	9	1.53	+	5.88	1.70E-05	1.07E-03
positive regulation of intracellular protein transport (GO:0090316)	162	5	.31	+	15.89	1.71E-05	1.07E-03
cellular component organization (GO:0016043)	5610	24	10.90	+	2.20	1.73E-05	1.08E-03
cytoskeleton organization (GO:0007010)	1256	11	2.44	+	4.51	1.98E-05	1.23E-03
regulation of endothelial cell migration (GO:0010594)	168	5	.33	+	15.32	2.03E-05	1.26E-03
response to hypoxia (GO:0001666)	294	6	.57	+	10.51	2.28E-05	1.40E-03
regulation of immune system process (GO:0002682)	1531	12	2.97	+	4.04	2.28E-05	1.40E-03
mitotic DNA damage checkpoint signaling (GO:0044773)	85	4	.17	+	24.23	2.63E-05	1.61E-03
regulation of striated muscle cell differentiation (GO:0051153)	85	4	.17	+	24.23	2.63E-05	1.60E-03
regulation of cell development (GO:0060284)	834	9	1.62	+	5.56	2.66E-05	1.61E-03
histone modification (GO:0016570)	86	4	.17	+	23.94	2.74E-05	1.66E-03
positive regulation of signal transduction (GO:0009967)	1563	12	3.04	+	3.95	2.80E-05	1.68E-03
response to decreased oxygen levels (GO:0036293)	307	6	.60	+	10.06	2.89E-05	1.73E-03
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction (GO:0051897)	182	5	.35	+	14.14	2.95E-05	1.76E-03
cellular component organization or biogenesis (GO:0071840)	5824	24	11.31	+	2.12	3.02E-05	1.79E-03

cell motility (GO:0048870)	1075	10	2.09	+	4.79	3.10E-05	1.84E-03
mitotic DNA integrity checkpoint signaling (GO:0044774)	89	4	.17	+	23.14	3.12E-05	1.84E-03
positive regulation of cell differentiation (GO:0045597)	865	9	1.68	+	5.36	3.53E-05	2.07E-03
regulation of stress fiber assembly (GO:0051492)	92	4	.18	+	22.38	3.54E-05	2.07E-03
positive regulation of protein transport (GO:0051222)	319	6	.62	+	9.68	3.57E-05	2.08E-03
response to lipopolysaccharide (GO:0032496)	320	6	.62	+	9.65	3.63E-05	2.11E-03
negative regulation of cellular biosynthetic process (GO:0031327)	2189	14	4.25	+	3.29	3.78E-05	2.19E-03
positive regulation of peptidyl-serine phosphorylation (GO:0033138)	94	4	.18	+	21.91	3.84E-05	2.21E-03
negative regulation of cell junction assembly (GO:1901889)	31	3	.06	+	49.82	3.87E-05	2.23E-03
positive regulation of signaling receptor activity (GO:2000273)	31	3	.06	+	49.82	3.87E-05	2.22E-03
response to heat (GO:0009408)	95	4	.18	+	21.68	3.99E-05	2.28E-03
nervous system development (GO:0007399)	2200	14	4.27	+	3.28	4.00E-05	2.27E-03
negative regulation of biosynthetic process (GO:0009890)	2203	14	4.28	+	3.27	4.06E-05	2.30E-03
response to alkaloid (GO:0043279)	96	4	.19	+	21.45	4.15E-05	2.34E-03
cell cycle process (GO:0022402)	884	9	1.72	+	5.24	4.17E-05	2.35E-03
response to amphetamine (GO:0001975)	32	3	.06	+	48.26	4.23E-05	2.37E-03
regulation of mitotic cell cycle phase transition (GO:1901990)	332	6	.64	+	9.30	4.44E-05	2.48E-03
regulation of protein stability (GO:0031647)	334	6	.65	+	9.25	4.58E-05	2.55E-03
positive regulation of establishment of protein localization (GO:1904951)	335	6	.65	+	9.22	4.66E-05	2.58E-03

negative regulation of locomotion (GO:0040013)	336	6	.65	+	9.19	4.74E-05	2.62E-03
response to molecule of bacterial origin (GO:0002237)	338	6	.66	+	9.14	4.89E-05	2.69E-03
tube development (GO:0035295)	904	9	1.76	+	5.13	4.96E-05	2.72E-03
regulation of neuroinflammatory response (GO:0150077)	34	3	.07	+	45.42	5.01E-05	2.74E-03
response to fluid shear stress (GO:0034405)	34	3	.07	+	45.42	5.01E-05	2.73E-03
angiogenesis (GO:0001525)	340	6	.66	+	9.08	5.05E-05	2.74E-03
negative regulation of response to stimulus (GO:0048585)	1662	12	3.23	+	3.72	5.11E-05	2.76E-03
positive regulation of intracellular transport (GO:0032388)	205	5	.40	+	12.56	5.13E-05	2.76E-03
regulation of actomyosin structure organization (GO:0110020)	102	4	.20	+	20.19	5.22E-05	2.80E-03
positive regulation of tumor necrosis factor production (GO:0032760)	102	4	.20	+	20.19	5.22E-05	2.79E-03
positive regulation of fibroblast growth factor production (GO:0090271)	4	2	.01	+	> 100	5.47E-05	2.92E-03
regulation of intracellular transport (GO:0032386)	345	6	.67	+	8.95	5.47E-05	2.91E-03
regulation of actin filament bundle assembly (GO:0032231)	104	4	.20	+	19.80	5.61E-05	2.97E-03
regulation of cell junction assembly (GO:1901888)	211	5	.41	+	12.20	5.86E-05	3.09E-03
positive regulation of lamellipodium organization (GO:1902745)	36	3	.07	+	42.90	5.88E-05	3.09E-03
negative regulation of JNK cascade (GO:0046329)	36	3	.07	+	42.90	5.88E-05	3.08E-03
regulation of cytoskeleton organization (GO:0051493)	518	7	1.01	+	6.96	5.97E-05	3.12E-03
positive regulation of tumor necrosis factor superfamily cytokine production (GO:1903557)	106	4	.21	+	19.43	6.03E-05	3.14E-03
positive regulation of vascular associated smooth	37	3	.07	+	41.74	6.35E-05	3.29E-03

muscle cell proliferation (GO:1904707)							
platelet-derived growth factor receptor signaling pathway (GO:0048008)	37	3	.07	+	41.74	6.35E- 05	3.28 E-03
negative regulation of nitrogen compound metabolic process (GO:0051172)	2294	14	4.46	+	3.14	6.35E- 05	3.27 E-03
membrane protein proteolysis (GO:0033619)	38	3	.07	+	40.64	6.84E- 05	3.51 E-03
positive regulation of leukocyte activation (GO:0002696)	360	6	.70	+	8.58	6.90E- 05	3.53 E-03
cell activation (GO:0001775)	731	8	1.42	+	5.63	7.26E- 05	3.70 E-03
response to antibiotic (GO:0046677)	39	3	.08	+	39.60	7.35E- 05	3.74 E-03
positive regulation of smooth muscle cell migration (GO:0014911)	39	3	.08	+	39.60	7.35E- 05	3.73 E-03
DNA damage checkpoint signaling (GO:0000077)	112	4	.22	+	18.39	7.42E- 05	3.74 E-03
regulation of anaphase- promoting complex- dependent catabolic process (GO:1905784)	5	2	.01	+	> 100	7.65E- 05	3.85 E-03
positive regulation of nitric oxide biosynthetic process (GO:0045429)	40	3	.08	+	38.61	7.89E- 05	3.96 E-03
regulation of establishment of protein localization (GO:0070201)	542	7	1.05	+	6.65	7.91E- 05	3.95 E-03
actin cytoskeleton organization (GO:0030036)	543	7	1.05	+	6.64	8.00E- 05	3.99 E-03
anatomical structure formation involved in morphogenesis (GO:0048646)	964	9	1.87	+	4.81	8.11E- 05	4.03 E-03
regulation of muscle system process (GO:0090257)	228	5	.44	+	11.29	8.39E- 05	4.15 E-03
collagen catabolic process (GO:0030574)	41	3	.08	+	37.67	8.46E- 05	4.18 E-03
positive regulation of nitric oxide metabolic process (GO:1904407)	41	3	.08	+	37.67	8.46E- 05	4.16 E-03
negative regulation of intracellular signal transduction (GO:1902532)	548	7	1.06	+	6.58	8.46E- 05	4.15 E-03

response to salt (GO:1902074)	374	6	.73	+	8.26	8.48E-05	4.15E-03
regulation of DNA biosynthetic process (GO:2000278)	117	4	.23	+	17.60	8.74E-05	4.26E-03
actomyosin structure organization (GO:0031032)	117	4	.23	+	17.60	8.74E-05	4.24E-03
positive regulation of cell activation (GO:0050867)	378	6	.73	+	8.17	8.99E-05	4.35E-03
regulation of mitotic nuclear division (GO:0007088)	118	4	.23	+	17.45	9.02E-05	4.35E-03
regulation of hydrolase activity (GO:0051336)	755	8	1.47	+	5.45	9.07E-05	4.36E-03
cellular response to biotic stimulus (GO:0071216)	233	5	.45	+	11.05	9.27E-05	4.45E-03
regulation of intracellular protein transport (GO:0033157)	234	5	.45	+	11.00	9.45E-05	4.52E-03
negative regulation of gene expression (GO:0010629)	985	9	1.91	+	4.70	9.55E-05	4.55E-03
regulation of myotube differentiation (GO:0010830)	43	3	.08	+	35.92	9.67E-05	4.60E-03
regulation of inflammatory response to antigenic stimulus (GO:0002861)	43	3	.08	+	35.92	9.67E-05	4.58E-03
regulation of RNA metabolic process (GO:0051252)	3773	18	7.33	+	2.46	9.76E-05	4.61E-03
DNA integrity checkpoint signaling (GO:0031570)	121	4	.24	+	17.02	9.91E-05	4.67E-03
positive regulation of immune system process (GO:0002684)	995	9	1.93	+	4.66	1.03E-04	4.84E-03
cell surface receptor signaling pathway (GO:0007166)	2092	13	4.06	+	3.20	1.07E-04	4.99E-03
negative regulation of transcription by RNA polymerase II (GO:0000122)	1000	9	1.94	+	4.63	1.07E-04	5.00E-03
regulation of protein modification by small protein conjugation or removal (GO:1903320)	241	5	.47	+	10.68	1.08E-04	5.04E-03
cellular response to vascular endothelial growth factor stimulus (GO:0035924)	45	3	.09	+	34.32	1.10E-04	5.10E-03
positive regulation of muscle contraction (GO:0045933)	45	3	.09	+	34.32	1.10E-04	5.08E-03
tissue morphogenesis (GO:0048729)	572	7	1.11	+	6.30	1.10E-04	5.08E-03

regulation of peptidyl-serine phosphorylation (GO:0033135)	126	4	.24	+	16.34	1.15E-04	5.30E-03
substrate adhesion-dependent cell spreading (GO:0034446)	46	3	.09	+	33.57	1.17E-04	5.36E-03
regulation of DNA-templated transcription (GO:0006355)	3459	17	6.72	+	2.53	1.19E-04	5.42E-03
cellular response to peptide hormone stimulus (GO:0071375)	246	5	.48	+	10.46	1.19E-04	5.42E-03
cell cycle (GO:0007049)	1265	10	2.46	+	4.07	1.21E-04	5.48E-03
negative regulation of stress-activated MAPK cascade (GO:0032873)	47	3	.09	+	32.86	1.24E-04	5.63E-03
extracellular matrix disassembly (GO:0022617)	47	3	.09	+	32.86	1.24E-04	5.61E-03
regulation of RNA biosynthetic process (GO:2001141)	3477	17	6.75	+	2.52	1.27E-04	5.71E-03
regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction (GO:0051896)	250	5	.49	+	10.30	1.28E-04	5.75E-03
mitotic cell cycle checkpoint signaling (GO:0007093)	130	4	.25	+	15.84	1.30E-04	5.80E-03
interleukin-3-mediated signaling pathway (GO:0038156)	7	2	.01	+	> 100	1.31E-04	5.84E-03
regulation of fibroblast growth factor production (GO:0090270)	7	2	.01	+	> 100	1.31E-04	5.82E-03
negative regulation of stress-activated protein kinase signaling cascade (GO:0070303)	48	3	.09	+	32.17	1.32E-04	5.85E-03
negative regulation of macromolecule biosynthetic process (GO:0010558)	2138	13	4.15	+	3.13	1.33E-04	5.88E-03
regulation of blood circulation (GO:1903522)	252	5	.49	+	10.21	1.33E-04	5.86E-03
positive regulation of protein modification by small protein conjugation or removal (GO:1903322)	133	4	.26	+	15.48	1.41E-04	6.21E-03
biological process involved in interspecies interaction	1562	11	3.03	+	3.63	1.43E-04	6.26E-03

between organisms (GO:0044419)							
response to alcohol (GO:0097305)	260	5	.51	+	9.90	1.53E-04	6.71E-03
actin filament-based process (GO:0030029)	605	7	1.18	+	5.96	1.55E-04	6.77E-03
regulation of lamellipodium organization (GO:1902743)	51	3	.10	+	30.28	1.56E-04	6.80E-03
response to cocaine (GO:0042220)	51	3	.10	+	30.28	1.56E-04	6.78E-03
positive regulation of protein kinase activity (GO:0045860)	263	5	.51	+	9.79	1.62E-04	6.99E-03
hepatocyte growth factor receptor signaling pathway (GO:0048012)	8	2	.02	+	> 100	1.63E-04	7.04E-03
negative regulation of nucleobase-containing compound metabolic process (GO:0045934)	1587	11	3.08	+	3.57	1.64E-04	7.06E-03
positive regulation of stress fiber assembly (GO:0051496)	52	3	.10	+	29.70	1.65E-04	7.08E-03
regulation of biological quality (GO:0065008)	2846	15	5.53	+	2.71	1.69E-04	7.22E-03
regulation of microtubule- based process (GO:0032886)	266	5	.52	+	9.68	1.70E-04	7.26E-03
positive regulation of synaptic transmission (GO:0050806)	141	4	.27	+	14.60	1.76E-04	7.47E-03
rhythmic process (GO:0048511)	268	5	.52	+	9.60	1.76E-04	7.47E-03
blood vessel morphogenesis (GO:0048514)	431	6	.84	+	7.17	1.82E-04	7.69E-03
regulation of protein serine/threonine kinase activity (GO:0071900)	270	5	.52	+	9.53	1.82E-04	7.69E-03
regulation of cell cycle phase transition (GO:1901987)	434	6	.84	+	7.12	1.89E-04	7.94E-03
signal transduction in response to DNA damage (GO:0042770)	145	4	.28	+	14.20	1.95E-04	8.18E-03
cellular response to phorbol 13-acetate 12-myristate (GO:1904628)	9	2	.02	+	> 100	1.99E-04	8.34E-03
response to phorbol 13-acetate 12-myristate (GO:1904627)	9	2	.02	+	> 100	1.99E-04	8.32E-03
neurogenesis (GO:0022008)	1348	10	2.62	+	3.82	2.03E-04	8.43E-03

regulation of nuclear division (GO:0051783)	147	4	.29	+	14.01	2.05E-04	8.52E-03
regulation of endopeptidase activity (GO:0052548)	278	5	.54	+	9.26	2.08E-04	8.61E-03
cell development (GO:0048468)	2237	13	4.35	+	2.99	2.10E-04	8.65E-03
response to purine-containing compound (GO:0014074)	148	4	.29	+	13.91	2.11E-04	8.66E-03
response to fatty acid (GO:0070542)	57	3	.11	+	27.09	2.14E-04	8.78E-03
actin filament organization (GO:0007015)	280	5	.54	+	9.19	2.15E-04	8.81E-03
response to steroid hormone (GO:0048545)	281	5	.55	+	9.16	2.19E-04	8.93E-03
positive regulation of cell development (GO:0010720)	450	6	.87	+	6.86	2.29E-04	9.32E-03
epithelium development (GO:0060429)	1107	9	2.15	+	4.19	2.29E-04	9.31E-03
regulation of post-translational protein modification (GO:1901873)	285	5	.55	+	9.03	2.33E-04	9.44E-03
positive regulation of immune response (GO:0050778)	648	7	1.26	+	5.56	2.36E-04	9.52E-03
negative regulation of cell migration (GO:0030336)	286	5	.56	+	9.00	2.37E-04	9.54E-03
negative regulation of protein acetylation (GO:1901984)	10	2	.02	+	> 100	2.39E-04	9.60E-03
response to other organism (GO:0051707)	1379	10	2.68	+	3.73	2.43E-04	9.75E-03
response to corticosteroid (GO:0031960)	154	4	.30	+	13.37	2.44E-04	9.76E-03
positive regulation of endopeptidase activity (GO:0010950)	154	4	.30	+	13.37	2.44E-04	9.73E-03
regulation of anatomical structure morphogenesis (GO:0022603)	874	8	1.70	+	4.71	2.46E-04	9.78E-03
regulation of vascular associated smooth muscle cell proliferation (GO:1904705)	60	3	.12	+	25.74	2.47E-04	9.81E-03
response to external biotic stimulus (GO:0043207)	1382	10	2.68	+	3.73	2.48E-04	9.80E-03
regulation of neuron projection development (GO:0010975)	458	6	.89	+	6.74	2.51E-04	9.92E-03
morphogenesis of an epithelium (GO:0002009)	460	6	.89	+	6.71	2.57E-04	1.01E-02

ossification (GO:0001503)	293	5	.57	+	8.78	2.64E-04	1.04E-02
collagen metabolic process (GO:0032963)	62	3	.12	+	24.91	2.71E-04	1.06E-02
negative regulation of chemotaxis (GO:0050922)	62	3	.12	+	24.91	2.71E-04	1.06E-02
positive regulation of actin filament bundle assembly (GO:0032233)	62	3	.12	+	24.91	2.71E-04	1.06E-02
phagocytosis (GO:0006909)	159	4	.31	+	12.95	2.75E-04	1.07E-02
regulation of ERK1 and ERK2 cascade (GO:0070372)	296	5	.57	+	8.70	2.77E-04	1.07E-02
negative regulation of fibroblast migration (GO:0010764)	11	2	.02	+	93.60	2.82E-04	1.09E-02
regulation of peptidase activity (GO:0052547)	301	5	.58	+	8.55	2.99E-04	1.15E-02
negative regulation of cell motility (GO:2000146)	301	5	.58	+	8.55	2.99E-04	1.15E-02
regulation of muscle contraction (GO:0006937)	163	4	.32	+	12.63	3.01E-04	1.16E-02
regulation of microtubule cytoskeleton organization (GO:0070507)	163	4	.32	+	12.63	3.01E-04	1.15E-02
positive regulation of post-translational protein modification (GO:1901875)	164	4	.32	+	12.56	3.08E-04	1.18E-02
cell cycle checkpoint signaling (GO:0000075)	164	4	.32	+	12.56	3.08E-04	1.17E-02
regulation of smooth muscle cell migration (GO:0014910)	65	3	.13	+	23.76	3.10E-04	1.18E-02
regulation of tumor necrosis factor production (GO:0032680)	165	4	.32	+	12.48	3.15E-04	1.20E-02
positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	165	4	.32	+	12.48	3.15E-04	1.19E-02
regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043281)	165	4	.32	+	12.48	3.15E-04	1.19E-02
regulation of immune response (GO:0050776)	908	8	1.76	+	4.54	3.17E-04	1.19E-02
response to biotic stimulus (GO:0009607)	1426	10	2.77	+	3.61	3.18E-04	1.20E-02

cellular response to peptide (GO:1901653)	306	5	.59	+	8.41	3.22E-04	1.20E-02
G1/S transition of mitotic cell cycle (GO:0000082)	66	3	.13	+	23.40	3.24E-04	1.21E-02
regulation of ceramide biosynthetic process (GO:2000303)	12	2	.02	+	85.80	3.29E-04	1.22E-02
regulation of sphingolipid biosynthetic process (GO:0090153)	12	2	.02	+	85.80	3.29E-04	1.22E-02
regulation of membrane lipid metabolic process (GO:1905038)	12	2	.02	+	85.80	3.29E-04	1.22E-02
response to temperature stimulus (GO:0009266)	167	4	.32	+	12.33	3.30E-04	1.22E-02
response to bacterium (GO:0009617)	687	7	1.33	+	5.25	3.35E-04	1.24E-02
negative regulation of mitotic cell cycle phase transition (GO:1901991)	168	4	.33	+	12.26	3.37E-04	1.24E-02
positive regulation of peptidase activity (GO:0010952)	168	4	.33	+	12.26	3.37E-04	1.24E-02
regulation of protein processing (GO:0070613)	67	3	.13	+	23.05	3.38E-04	1.24E-02
positive regulation of cell adhesion (GO:0045785)	485	6	.94	+	6.37	3.40E-04	1.24E-02
negative regulation of macromolecule metabolic process (GO:0010605)	2685	14	5.22	+	2.68	3.43E-04	1.25E-02
generation of neurons (GO:0048699)	1172	9	2.28	+	3.95	3.49E-04	1.27E-02
cell cycle G1/S phase transition (GO:0044843)	68	3	.13	+	22.71	3.52E-04	1.28E-02
regulation of tumor necrosis factor superfamily cytokine production (GO:1903555)	170	4	.33	+	12.11	3.52E-04	1.28E-02
peptidyl-lysine modification (GO:0018205)	171	4	.33	+	12.04	3.60E-04	1.30E-02
hemopoiesis (GO:0030097)	696	7	1.35	+	5.18	3.62E-04	1.30E-02
regulation of lipid metabolic process (GO:0019216)	315	5	.61	+	8.17	3.67E-04	1.32E-02
positive regulation of hydrolase activity (GO:0051345)	494	6	.96	+	6.25	3.75E-04	1.34E-02
positive regulation of nucleobase-containing	2052	12	3.99	+	3.01	3.76E-04	1.35E-02

compound metabolic process (GO:0045935)							
positive regulation of cell size (GO:0045793)	13	2	.03	+	79.20	3.79E-04	1.35E-02
regulation of skeletal muscle fiber development (GO:0048742)	13	2	.03	+	79.20	3.79E-04	1.35E-02
negative regulation of transcription by competitive promoter binding (GO:0010944)	13	2	.03	+	79.20	3.79E-04	1.35E-02
positive regulation of supramolecular fiber organization (GO:1902905)	175	4	.34	+	11.77	3.92E-04	1.39E-02
response to estrogen (GO:0043627)	71	3	.14	+	21.75	3.98E-04	1.41E-02
cellular response to abiotic stimulus (GO:0071214)	323	5	.63	+	7.97	4.11E-04	1.45E-02
cellular response to environmental stimulus (GO:0104004)	323	5	.63	+	7.97	4.11E-04	1.45E-02
cellular response to hormone stimulus (GO:0032870)	503	6	.98	+	6.14	4.12E-04	1.45E-02
regulation of lymphocyte activation (GO:0051249)	503	6	.98	+	6.14	4.12E-04	1.44E-02
positive regulation of TOR signaling (GO:0032008)	72	3	.14	+	21.45	4.14E-04	1.45E-02
regulation of protein maturation (GO:1903317)	72	3	.14	+	21.45	4.14E-04	1.44E-02
post-translational protein modification (GO:0043687)	946	8	1.84	+	4.35	4.17E-04	1.45E-02
interleukin-6-mediated signaling pathway (GO:0070102)	14	2	.03	+	73.54	4.32E-04	1.50E-02
sphingoid biosynthetic process (GO:0046520)	14	2	.03	+	73.54	4.32E-04	1.50E-02
sphingosine biosynthetic process (GO:0046512)	14	2	.03	+	73.54	4.32E-04	1.49E-02
regulation of small molecule metabolic process (GO:0062012)	327	5	.64	+	7.87	4.34E-04	1.50E-02
regulation of intracellular steroid hormone receptor signaling pathway (GO:0033143)	74	3	.14	+	20.87	4.47E-04	1.54E-02
cellular component disassembly (GO:0022411)	330	5	.64	+	7.80	4.52E-04	1.55E-02

positive regulation of cytoskeleton organization (GO:0051495)	184	4	.36	+	11.19	4.72E-04	1.62E-02
regulation of protein transport (GO:0051223)	517	6	1.00	+	5.97	4.76E-04	1.63E-02
cellular response to nitric oxide (GO:0071732)	15	2	.03	+	68.64	4.89E-04	1.67E-02
angiotensin-activated signaling pathway (GO:0038166)	15	2	.03	+	68.64	4.89E-04	1.67E-02
collagen-activated signaling pathway (GO:0038065)	15	2	.03	+	68.64	4.89E-04	1.66E-02
positive regulation of mast cell degranulation (GO:0043306)	15	2	.03	+	68.64	4.89E-04	1.66E-02
regulation of anatomical structure size (GO:0090066)	520	6	1.01	+	5.94	4.90E-04	1.66E-02
regulation of actin cytoskeleton organization (GO:0032956)	337	5	.65	+	7.64	4.97E-04	1.68E-02
regulation of tissue remodeling (GO:0034103)	77	3	.15	+	20.06	5.00E-04	1.68E-02
regulation of DNA metabolic process (GO:0051052)	526	6	1.02	+	5.87	5.21E-04	1.75E-02
regulation of stress-activated MAPK cascade (GO:0032872)	189	4	.37	+	10.90	5.21E-04	1.75E-02
negative regulation of organelle organization (GO:0010639)	342	5	.66	+	7.53	5.30E-04	1.77E-02
regulation of vesicle-mediated transport (GO:0060627)	529	6	1.03	+	5.84	5.36E-04	1.79E-02
positive regulation of programmed cell death (GO:0043068)	530	6	1.03	+	5.83	5.42E-04	1.80E-02
response to ether (GO:0045472)	16	2	.03	+	64.35	5.50E-04	1.83E-02
negative regulation of focal adhesion assembly (GO:0051895)	16	2	.03	+	64.35	5.50E-04	1.82E-02
positive regulation of calcium ion import (GO:0090280)	16	2	.03	+	64.35	5.50E-04	1.82E-02
response to caffeine (GO:0031000)	16	2	.03	+	64.35	5.50E-04	1.82E-02
negative regulation of cell-substrate junction organization (GO:0150118)	16	2	.03	+	64.35	5.50E-04	1.81E-02

chemotaxis (GO:0006935)	345	5	.67	+	7.46	5.52E-04	1.81E-02
regulation of stress-activated protein kinase signaling cascade (GO:0070302)	193	4	.37	+	10.67	5.63E-04	1.85E-02
taxis (GO:0042330)	347	5	.67	+	7.42	5.66E-04	1.85E-02
animal organ morphogenesis (GO:0009887)	994	8	1.93	+	4.14	5.78E-04	1.89E-02
regulation of cysteine-type endopeptidase activity (GO:2000116)	195	4	.38	+	10.56	5.85E-04	1.91E-02
regulation of cell size (GO:0008361)	195	4	.38	+	10.56	5.85E-04	1.90E-02
cellular response to lipopolysaccharide (GO:0071222)	196	4	.38	+	10.51	5.96E-04	1.93E-02
positive regulation of B cell differentiation (GO:0045579)	17	2	.03	+	60.56	6.14E-04	1.99E-02
cellular response to reactive nitrogen species (GO:1902170)	17	2	.03	+	60.56	6.14E-04	1.98E-02
response to vitamin (GO:0033273)	83	3	.16	+	18.61	6.18E-04	1.99E-02
regulation of protein ubiquitination (GO:0031396)	198	4	.38	+	10.40	6.19E-04	1.99E-02
regulation of heart contraction (GO:0008016)	199	4	.39	+	10.35	6.30E-04	2.02E-02
regulation of hydrogen peroxide metabolic process (GO:0010310)	18	2	.03	+	57.20	6.81E-04	2.18E-02
negative regulation of glycolytic process (GO:0045820)	18	2	.03	+	57.20	6.81E-04	2.18E-02
inflammatory response (GO:0006954)	554	6	1.08	+	5.58	6.82E-04	2.18E-02
cellular response to salt (GO:1902075)	204	4	.40	+	10.09	6.90E-04	2.20E-02
negative regulation of cell cycle (GO:0045786)	363	5	.71	+	7.09	6.92E-04	2.20E-02
locomotion (GO:0040011)	367	5	.71	+	7.01	7.27E-04	2.30E-02
cellular response to molecule of bacterial origin (GO:0071219)	207	4	.40	+	9.95	7.28E-04	2.31E-02
negative regulation of signal transduction (GO:0009968)	1300	9	2.53	+	3.56	7.39E-04	2.33E-02

regulation of MHC class II biosynthetic process (GO:0045346)	19	2	.04	+	54.19	7.52E-04	2.37E-02
stress fiber assembly (GO:0043149)	19	2	.04	+	54.19	7.52E-04	2.37E-02
contractile actin filament bundle assembly (GO:0030038)	19	2	.04	+	54.19	7.52E-04	2.36E-02
positive regulation of mitotic cell cycle phase transition (GO:1901992)	89	3	.17	+	17.35	7.52E-04	2.36E-02
regulation of DNA-binding transcription factor activity (GO:0051090)	373	5	.72	+	6.90	7.81E-04	2.44E-02
regulation of protein catabolic process (GO:0042176)	373	5	.72	+	6.90	7.81E-04	2.44E-02
positive regulation of protein polymerization (GO:0032273)	91	3	.18	+	16.97	8.01E-04	2.49E-02
cellular response to UV (GO:0034644)	91	3	.18	+	16.97	8.01E-04	2.49E-02
centrosome cycle (GO:0007098)	92	3	.18	+	16.79	8.26E-04	2.56E-02
positive regulation of reproductive process (GO:2000243)	92	3	.18	+	16.79	8.26E-04	2.56E-02
positive regulation of bone resorption (GO:0045780)	20	2	.04	+	51.48	8.26E-04	2.55E-02
immune response-regulating cell surface receptor signaling pathway involved in phagocytosis (GO:0002433)	20	2	.04	+	51.48	8.26E-04	2.55E-02
response to nitric oxide (GO:0071731)	20	2	.04	+	51.48	8.26E-04	2.54E-02
sphingosine metabolic process (GO:0006670)	20	2	.04	+	51.48	8.26E-04	2.54E-02
Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)	20	2	.04	+	51.48	8.26E-04	2.53E-02
cell chemotaxis (GO:0060326)	215	4	.42	+	9.58	8.37E-04	2.56E-02
regulation of actin filament-based process (GO:0032970)	379	5	.74	+	6.79	8.38E-04	2.56E-02
regulation of T cell activation (GO:0050863)	379	5	.74	+	6.79	8.38E-04	2.55E-02
female gonad development (GO:0008585)	93	3	.18	+	16.61	8.51E-04	2.59E-02
negative regulation of mitotic cell cycle (GO:0045930)	217	4	.42	+	9.49	8.65E-04	2.63E-02

regulation of apoptotic signaling pathway (GO:2001233)	382	5	.74	+	6.74	8.68E-04	2.63E-02
cellular response to platelet-derived growth factor stimulus (GO:0036120)	21	2	.04	+	49.03	9.04E-04	2.73E-02
diol biosynthetic process (GO:0034312)	21	2	.04	+	49.03	9.04E-04	2.73E-02
response to mechanical stimulus (GO:0009612)	220	4	.43	+	9.36	9.10E-04	2.74E-02
regulation of microtubule polymerization or depolymerization (GO:0031110)	96	3	.19	+	16.09	9.31E-04	2.80E-02
negative regulation of DNA-templated transcription (GO:0045892)	1343	9	2.61	+	3.45	9.31E-04	2.79E-02
regulation of supramolecular fiber organization (GO:1902903)	389	5	.76	+	6.62	9.40E-04	2.81E-02
development of primary female sexual characteristics (GO:0046545)	97	3	.19	+	15.92	9.58E-04	2.86E-02
response to cytokine (GO:0034097)	825	7	1.60	+	4.37	9.85E-04	2.93E-02
positive regulation of cell adhesion mediated by integrin (GO:0033630)	22	2	.04	+	46.80	9.85E-04	2.93E-02
Fc receptor mediated stimulatory signaling pathway (GO:0002431)	22	2	.04	+	46.80	9.85E-04	2.92E-02
stimulatory C-type lectin receptor signaling pathway (GO:0002223)	22	2	.04	+	46.80	9.85E-04	2.92E-02
cellular response to lectin (GO:1990858)	22	2	.04	+	46.80	9.85E-04	2.91E-02
response to lectin (GO:1990840)	22	2	.04	+	46.80	9.85E-04	2.91E-02
cellular response to vitamin (GO:0071295)	22	2	.04	+	46.80	9.85E-04	2.90E-02
positive regulation of cell migration involved in sprouting angiogenesis (GO:0090050)	22	2	.04	+	46.80	9.85E-04	2.90E-02
sphingoid metabolic process (GO:0046519)	22	2	.04	+	46.80	9.85E-04	2.89E-02
DNA biosynthetic process (GO:0071897)	98	3	.19	+	15.76	9.86E-04	2.89E-02

regulation of peptidyl-tyrosine phosphorylation (GO:0050730)	225	4	.44	+	9.15	9.88E-04	2.89E-02
negative regulation of RNA biosynthetic process (GO:1902679)	1357	9	2.64	+	3.41	1.00E-03	2.92E-02
immune system process (GO:0002376)	2293	12	4.45	+	2.69	1.02E-03	2.98E-02
negative regulation of cell cycle phase transition (GO:1901988)	229	4	.44	+	8.99	1.05E-03	3.06E-02
membrane protein ectodomain proteolysis (GO:0006509)	23	2	.04	+	44.77	1.07E-03	3.10E-02
response to platelet-derived growth factor (GO:0036119)	23	2	.04	+	44.77	1.07E-03	3.10E-02
positive regulation of cold-induced thermogenesis (GO:0120162)	101	3	.20	+	15.29	1.07E-03	3.10E-02
cellular response to inorganic substance (GO:0071241)	231	4	.45	+	8.91	1.09E-03	3.14E-02
leukocyte activation (GO:0045321)	607	6	1.18	+	5.09	1.09E-03	3.14E-02
neuron differentiation (GO:0030182)	1099	8	2.13	+	3.75	1.11E-03	3.19E-02
negative regulation of lipid metabolic process (GO:0045833)	103	3	.20	+	14.99	1.13E-03	3.25E-02
negative regulation of response to external stimulus (GO:0032102)	406	5	.79	+	6.34	1.13E-03	3.25E-02
positive regulation of defense response (GO:0031349)	407	5	.79	+	6.32	1.15E-03	3.28E-02
positive regulation of protein processing (GO:0010954)	24	2	.05	+	42.90	1.16E-03	3.30E-02
cellular response to alcohol (GO:0097306)	104	3	.20	+	14.85	1.17E-03	3.32E-02
small molecule metabolic process (GO:0044281)	1684	10	3.27	+	3.06	1.17E-03	3.32E-02
negative regulation of cell communication (GO:0010648)	1396	9	2.71	+	3.32	1.22E-03	3.47E-02
negative regulation of signaling (GO:0023057)	1397	9	2.71	+	3.32	1.23E-03	3.48E-02
regulation of dephosphorylation (GO:0035303)	106	3	.21	+	14.57	1.23E-03	3.48E-02

negative regulation of multicellular organismal process (GO:0051241)	1117	8	2.17	+	3.69	1.23E-03	3.47E-02
organic cyclic compound biosynthetic process (GO:1901362)	1119	8	2.17	+	3.68	1.24E-03	3.50E-02
steroid catabolic process (GO:0006706)	25	2	.05	+	41.18	1.25E-03	3.51E-02
vascular endothelial growth factor signaling pathway (GO:0038084)	25	2	.05	+	41.18	1.25E-03	3.50E-02
positive regulation of alpha-beta T cell proliferation (GO:0046641)	25	2	.05	+	41.18	1.25E-03	3.50E-02
regulation of multicellular organismal development (GO:2000026)	1401	9	2.72	+	3.31	1.25E-03	3.51E-02
negative regulation of protein modification process (GO:0031400)	417	5	.81	+	6.17	1.28E-03	3.56E-02
negative regulation of intrinsic apoptotic signaling pathway (GO:2001243)	108	3	.21	+	14.30	1.30E-03	3.61E-02
tissue remodeling (GO:0048771)	108	3	.21	+	14.30	1.30E-03	3.60E-02
behavior (GO:0007610)	629	6	1.22	+	4.91	1.31E-03	3.63E-02
microtubule organizing center organization (GO:0031023)	109	3	.21	+	14.17	1.33E-03	3.68E-02
uterus development (GO:0060065)	26	2	.05	+	39.60	1.34E-03	3.71E-02
positive regulation of leukocyte degranulation (GO:0043302)	26	2	.05	+	39.60	1.34E-03	3.71E-02
positive regulation of protein maturation (GO:1903319)	26	2	.05	+	39.60	1.34E-03	3.70E-02
positive regulation of protein ubiquitination (GO:0031398)	110	3	.21	+	14.04	1.36E-03	3.75E-02
regulation of signaling receptor activity (GO:0010469)	110	3	.21	+	14.04	1.36E-03	3.75E-02
negative regulation of protein metabolic process (GO:0051248)	874	7	1.70	+	4.12	1.37E-03	3.76E-02
regulation of calcium ion transport (GO:0051924)	247	4	.48	+	8.34	1.39E-03	3.79E-02
response to radiation (GO:0009314)	425	5	.83	+	6.06	1.39E-03	3.79E-02

leukocyte migration (GO:0050900)	248	4	.48	+	8.30	1.41E-03	3.83E-02
regulation of binding (GO:0051098)	249	4	.48	+	8.27	1.43E-03	3.88E-02
negative regulation of cell population proliferation (GO:0008285)	880	7	1.71	+	4.09	1.43E-03	3.88E-02
positive regulation of cell cycle phase transition (GO:1901989)	112	3	.22	+	13.79	1.43E-03	3.89E-02
female sex differentiation (GO:0046660)	112	3	.22	+	13.79	1.43E-03	3.88E-02
positive regulation of interleukin-17 production (GO:0032740)	27	2	.05	+	38.13	1.44E-03	3.89E-02
leukocyte differentiation (GO:0002521)	430	5	.84	+	5.99	1.46E-03	3.94E-02
regulation of interleukin-1 production (GO:0032652)	113	3	.22	+	13.67	1.47E-03	3.96E-02
gland development (GO:0048732)	431	5	.84	+	5.97	1.47E-03	3.96E-02
cellular response to interleukin-6 (GO:0071354)	28	2	.05	+	36.77	1.54E-03	4.13E-02
response to immobilization stress (GO:0035902)	28	2	.05	+	36.77	1.54E-03	4.13E-02
positive regulation of G2/M transition of mitotic cell cycle (GO:0010971)	28	2	.05	+	36.77	1.54E-03	4.12E-02
positive regulation of peptidyl-threonine phosphorylation (GO:0010800)	28	2	.05	+	36.77	1.54E-03	4.11E-02
positive regulation of lamellipodium assembly (GO:0010592)	28	2	.05	+	36.77	1.54E-03	4.11E-02
negative regulation of inflammatory response to antigenic stimulus (GO:0002862)	28	2	.05	+	36.77	1.54E-03	4.10E-02
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043280)	115	3	.22	+	13.43	1.54E-03	4.10E-02
cellular response to light stimulus (GO:0071482)	116	3	.23	+	13.31	1.58E-03	4.19E-02
Fc-gamma receptor signaling pathway (GO:0038094)	29	2	.06	+	35.50	1.64E-03	4.35E-02

regulation of platelet aggregation (GO:0090330)	29	2	.06	+	35.50	1.64E-03	4.35E-02
regulation of androgen receptor signaling pathway (GO:0060765)	29	2	.06	+	35.50	1.64E-03	4.34E-02
positive regulation of smooth muscle contraction (GO:0045987)	29	2	.06	+	35.50	1.64E-03	4.33E-02
negative regulation of miRNA transcription (GO:1902894)	29	2	.06	+	35.50	1.64E-03	4.32E-02
skin epidermis development (GO:0098773)	119	3	.23	+	12.98	1.70E-03	4.46E-02
nucleobase-containing compound biosynthetic process (GO:0034654)	908	7	1.76	+	3.97	1.71E-03	4.47E-02
response to vitamin D (GO:0033280)	30	2	.06	+	34.32	1.75E-03	4.58E-02
regulation of mast cell degranulation (GO:0043304)	30	2	.06	+	34.32	1.75E-03	4.57E-02
diol metabolic process (GO:0034311)	30	2	.06	+	34.32	1.75E-03	4.57E-02
negative regulation of RNA metabolic process (GO:0051253)	1472	9	2.86	+	3.15	1.77E-03	4.60E-02
negative regulation of catalytic activity (GO:0043086)	451	5	.88	+	5.71	1.79E-03	4.66E-02
proteolysis (GO:0006508)	1187	8	2.31	+	3.47	1.81E-03	4.69E-02
positive regulation of cell cycle G2/M phase transition (GO:1902751)	31	2	.06	+	33.21	1.86E-03	4.82E-02
negative regulation of miRNA metabolic process (GO:2000629)	31	2	.06	+	33.21	1.86E-03	4.81E-02
positive regulation of cell-substrate junction organization (GO:0150117)	31	2	.06	+	33.21	1.86E-03	4.81E-02
cellular response to angiotensin (GO:1904385)	31	2	.06	+	33.21	1.86E-03	4.80E-02
regulation of actin filament organization (GO:0110053)	271	4	.53	+	7.60	1.94E-03	4.98E-02

Analysis Type: PANTHER Overrepresentation Test (Released 20231017)

Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.8436609 Released 2023-10-09

Analyzed List: upload_1 (Homo sapiens)

Reference List: Homo sapiens (all genes in database)

Test Type: FISHER

Correction: FDR