

Term	P-value	Adjusted P	Odds Ratio	Combined
Parkinson disease	9.11E-10	1.32E-07	11.39732	237.2511
Prion disease	2.79E-09	2.02E-07	10.33263	203.5364
Salmonella infection	9.93E-07	4.80E-05	8.390829	115.9792
Pathways of neurodegeneration	1.72E-06	6.23E-05	5.755069	76.39387
Antigen processing and presentation	4.04E-06	9.97E-05	16.19281	201.1103
Protein processing in endoplasmic reticulum	4.13E-06	9.97E-05	9.682945	120.0495
Alzheimer disease	5.07E-06	1.05E-04	6.187698	75.4427
Pathogenic Escherichia coli infection	1.17E-05	2.10E-04	8.339894	94.73312
Legionellosis	1.40E-05	2.10E-04	18.52128	206.9931
Diabetic cardiomyopathy	1.45E-05	2.10E-04	8.080821	90.03131
Lipid and atherosclerosis	2.19E-05	2.89E-04	7.607729	81.61047
Huntington disease	4.25E-05	5.13E-04	5.997857	60.38144
Estrogen signaling pathway	9.99E-05	0.001114	8.873372	81.73472
Amyotrophic lateral sclerosis	1.59E-04	0.00165	5.003073	43.74935
Ribosome	2.18E-04	0.001961	7.639319	64.41426
Necroptosis	2.25E-04	0.001961	7.589004	63.73107
Amoebiasis	2.30E-04	0.001961	9.906416	82.99555
Fluid shear stress and atherosclerosis	9.48E-04	0.007636	7.157658	49.82603
Gap junction	0.001324	0.010102	9.069597	60.10746
Phagosome	0.001411	0.010233	6.520375	42.79401
Coronavirus disease	0.001634	0.01113	5.118688	32.84652
IL-17 signaling pathway	0.001689	0.01113	8.462393	54.02196
cGMP-PKG signaling pathway	0.002133	0.013207	5.912142	36.36059
Tight junction	0.002246	0.013207	5.839451	35.61122
Longevity regulating pathway	0.002277	0.013207	7.768446	47.26975
Arginine biosynthesis	0.006219	0.034685	18.74717	95.23721
Measles	0.006857	0.036822	5.628775	28.04564
Apoptosis	0.007384	0.038237	5.505574	27.02394
Arrhythmogenic right ventricular cardiomyopathy	0.008386	0.04193	7.651737	36.58443
Peroxisome	0.009958	0.047697	7.165642	33.02932
Cellular senescence	0.010197	0.047697	4.994939	22.90496
Tuberculosis	0.016479	0.074671	4.308566	17.68951
Neutrophil extracellular trap formation	0.019343	0.084994	4.097089	16.16466
Toxoplasmosis	0.022826	0.097348	5.185583	19.60064
D-Glutamine and D-glutamate metabolism	0.026712	0.110666	46.46729	168.3336
Glutathione metabolism	0.038035	0.153198	6.805146	22.24765
Calcium signaling pathway	0.041222	0.157805	3.20339	10.21494
Viral myocarditis	0.041747	0.157805	6.45218	20.49298
Spinocerebellar ataxia	0.042444	0.157805	4.03102	12.73627
Spliceosome	0.047746	0.173079	3.837707	11.67376
Glycolysis / Gluconeogenesis	0.050904	0.180026	5.755298	17.13821
Gastric acid secretion	0.063617	0.214522	5.053034	13.92049
Pertussis	0.063617	0.214522	5.053034	13.92049
Influenza A	0.066395	0.218801	3.334404	9.043358
RNA degradation	0.06807	0.219335	4.855428	13.04763
NOD-like receptor signaling pathway	0.074852	0.231876	3.164366	8.202791

MAPK signaling pathway	0.07516	0.231876	2.599735	6.728471
Cardiac muscle contraction	0.080421	0.242937	4.39667	11.08174
Hypertrophic cardiomyopathy	0.085219	0.252179	4.246141	10.45624
Nitrogen metabolism	0.087973	0.255121	11.60981	28.22031
Dilated cardiomyopathy	0.095067	0.270288	3.973906	9.351295
Histidine metabolism	0.112356	0.293555	8.843347	19.3323
Regulation of actin cytoskeleton	0.114155	0.293555	2.614884	5.674804
Human T-cell leukemia virus 1 infection	0.11531	0.293555	2.602646	5.622054
Drug metabolism	0.115658	0.293555	3.521894	7.597153
Protein export	0.117154	0.293555	8.440952	18.09962
Proximal tubule bicarbonate reclamation	0.117154	0.293555	8.440952	18.09962
HIF-1 signaling pathway	0.117422	0.293555	3.488803	7.472954
Thermogenesis	0.130714	0.321246	2.453275	4.99179
Thyroid hormone signaling pathway	0.139093	0.334604	3.135088	6.184323
Phototransduction	0.140764	0.334604	6.876082	13.48172
Platelet activation	0.14464	0.338272	3.057532	5.911753
Glyoxylate and dicarboxylate metabolism	0.150032	0.339917	6.401225	12.14252
Pentose phosphate pathway	0.150032	0.339917	6.401225	12.14252
Endocytosis	0.15572	0.347374	2.25393	4.191631
Vascular smooth muscle contraction	0.161548	0.34917	2.846176	5.188447
Oxidative phosphorylation	0.161548	0.34917	2.846176	5.188447
Fructose and mannose metabolism	0.163749	0.34917	5.800234	10.49508
Ubiquitin mediated proteolysis	0.174936	0.367619	2.700848	4.708485
Alanine, aspartate and glutamate metabolism	0.181696	0.376371	5.154725	8.79096
Adrenergic signaling in cardiomyocytes	0.194351	0.394715	2.517083	4.123201
Ferroptosis	0.199263	0.394715	4.638318	7.482216
Oxytocin signaling pathway	0.202196	0.394715	2.450348	3.916928
Tryptophan metabolism	0.203596	0.394715	4.52496	7.202017
Non-alcoholic fatty liver disease	0.204163	0.394715	2.434209	3.867564
Type I diabetes mellitus	0.207905	0.396661	4.417	6.937665
Hepatocellular carcinoma	0.229905	0.430346	2.2421	3.29609
Arginine and proline metabolism	0.237432	0.430346	3.784665	5.441865
Vibrio cholerae infection	0.237432	0.430346	3.784665	5.441865
Cholesterol metabolism	0.237432	0.430346	3.784665	5.441865
Pyrimidine metabolism	0.261872	0.468783	3.370773	4.516501
VEGF signaling pathway	0.273799	0.484156	3.195939	4.139899
Kaposi sarcoma-associated herpesvirus infection	0.279865	0.48892	1.946162	2.478338
Focal adhesion	0.295851	0.49511	1.867166	2.274021
Proteoglycans in cancer	0.303827	0.49511	1.830003	2.180075
Acute myeloid leukemia	0.304679	0.49511	2.80742	3.336612
Long-term potentiation	0.304679	0.49511	2.80742	3.336612
Mitophagy	0.308446	0.49511	2.765379	3.252662
Amphetamine addiction	0.312193	0.49511	2.724574	3.171767
Renin secretion	0.312193	0.49511	2.724574	3.171767
Rap1 signaling pathway	0.313776	0.49511	1.785559	2.069598
Human immunodeficiency virus 1 infection	0.317747	0.49511	1.768374	2.027437
Adherens junction	0.319627	0.49511	2.646462	3.018555

Pathways in cancer	0.322575	0.49511	1.413297	1.599031
PPAR signaling pathway	0.330629	0.49511	2.537319	2.808198
Thyroid hormone synthesis	0.334257	0.49511	2.502905	2.742795
Glioma	0.334257	0.49511	2.502905	2.742795
Metabolism of xenobiotics by cytochrome P450	0.337866	0.49511	2.469408	2.679571
Bacterial invasion of epithelial cells	0.341455	0.49511	2.436793	2.618431
Leishmaniasis	0.341455	0.49511	2.436793	2.618431
Chemical carcinogenesis	0.37073	0.532139	1.564764	1.552686
ECM-receptor interaction	0.379686	0.532139	2.127511	2.060306
Shigellosis	0.384221	0.532139	1.519332	1.453298
Salivary secretion	0.396328	0.532139	2.011377	1.861555
GnRH signaling pathway	0.396328	0.532139	2.011377	1.861555
Staphylococcus aureus infection	0.402861	0.532139	1.968383	1.789584
Circadian entrainment	0.409323	0.532139	1.927181	1.721454
Fc gamma R-mediated phagocytosis	0.409323	0.532139	1.927181	1.721454
Phosphatidylinositol signaling system	0.409323	0.532139	1.927181	1.721454
Prostate cancer	0.409323	0.532139	1.927181	1.721454
Aldosterone synthesis and secretion	0.412528	0.532139	1.907216	1.688745
Inflammatory mediator regulation of TRP channels	0.412528	0.532139	1.907216	1.688745
AGE-RAGE signaling pathway in diabetic complications	0.418887	0.532139	1.868498	1.62588
Progesterone-mediated oocyte maturation	0.418887	0.532139	1.868498	1.62588
Melanogenesis	0.422041	0.532139	1.84972	1.595666
Protein digestion and absorption	0.428298	0.534642	1.813267	1.537536
C-type lectin receptor signaling pathway	0.431401	0.534642	1.795572	1.509569
Th17 cell differentiation	0.440611	0.536879	1.74449	1.429773
Glucagon signaling pathway	0.440611	0.536879	1.74449	1.429773
Leukocyte transendothelial migration	0.461529	0.557681	1.635845	1.264851
Sphingolipid signaling pathway	0.475995	0.565731	1.566133	1.162617
Neurotrophin signaling pathway	0.475995	0.565731	1.566133	1.162617
Lysosome	0.501069	0.576654	1.454485	1.005066
Oocyte meiosis	0.503781	0.576654	1.443049	0.989375
Purine metabolism	0.503781	0.576654	1.443049	0.989375
Relaxin signaling pathway	0.503781	0.576654	1.443049	0.989375
FoxO signaling pathway	0.50916	0.576654	1.420705	0.958965
Dopaminergic synapse	0.511828	0.576654	1.409788	0.944229
Apelin signaling pathway	0.524954	0.576654	1.357614	0.874907
Autophagy	0.524954	0.576654	1.357614	0.874907
Yersinia infection	0.524954	0.576654	1.357614	0.874907
Insulin signaling pathway	0.524954	0.576654	1.357614	0.874907
Retrograde endocannabinoid signaling	0.552613	0.600611	1.255325	0.744529
Gastric cancer	0.555047	0.600611	1.246779	0.733982
PI3K-Akt signaling pathway	0.572528	0.614938	1.047384	0.584119
Hippo signaling pathway	0.587775	0.626672	1.138225	0.604865
Axon guidance	0.628408	0.663915	1.017762	0.472817
Alcoholism	0.636443	0.663915	0.995554	0.449852
RNA transport	0.636443	0.663915	0.995554	0.449852
Transcriptional misregulation in cancer	0.648173	0.671322	0.963987	0.417982

cAMP signaling pathway	0.691461	0.711077	0.855336	0.315575
Human cytomegalovirus infection	0.706296	0.721217	0.820594	0.285338
Ras signaling pathway	0.717343	0.727376	0.795444	0.264247
Human papillomavirus infection	0.835892	0.841696	0.554007	0.099309
Olfactory transduction	0.910098	0.910098	0.414132	0.039013

Genes

CALML5;HSPA5;NDUFA4;TUBB;TXN;TUBB4B;TUBA4A;TUBA1B;VDAC2;UQCRC2;RPS27A;SLC25A4;SLC25A6;HSPA8;HSPA5;NDUFA4;TUBB;TUBB4B;TUBA4A;TUBA1B;VDAC2;UQCRC2;SLC25A4;HSPA1B;SLC25A6;HSPA1B;HSP90AA1;ANXA2;TUBB;RPS3;TXN;TUBB4B;GAPDH;ACTB;TUBA4A

CALML5;HSPA5;NDUFA4;TUBB;TUBB4B;TUBA4A;TUBA1B;CAT;VDAC2;UQCRC2;RPS27A;SLC25A4;SLC25A6;HSPA8;HSP90AA1;HSPA5;HSPA4;HSPA1B;HSPA1A

HSPA8;HSP90AA1;HSPA5;SSR1;STUB1;HSPBP1;HSPA1B;HSPA1A

TUBA1B;CALML5;NDUFA4;TUBB;VDAC2;UQCRC2;TUBB4B;GAPDH;SLC25A4;TUBA4A;SLC25A6

TUBA1B;TUBB;RPS3;MYH9;TUBB4B;GAPDH;ACTB;TUBA4A

EEF1A1;HSPA8;HSPA1B;HSPD1;HSPA1A

COL1A2;NDUFA4;VDAC2;UQCRC2;CTSD;GAPDH;SLC25A4;SLC25A6

HSPA8;HSP90AA1;CALML5;HSPA5;HSPA4;HSPA1B;HSPD1;HSPA1A

TUBA1B;NDUFA4;TUBB;VDAC2;UQCRC2;TUBB4B;SLC25A4;TUBA4A;SLC25A6

HSPA8;HSP90AA1;CALML5;CTSD;HSPA1B;HSPA1A

TUBA1B;HSPA5;NDUFA4;TUBB;CAT;UQCRC2;TUBB4B;ACTB;TUBA4A

RPL12;RPL11;RPS3;RPLP2;RPS20;RPS27A

GLUD1;HSP90AA1;VDAC2;PPIA;SLC25A4;SLC25A6

SERPINB3;COL1A2;ARG1;PRDX1;HSPB1

HSP90AA1;CALML5;MGST1;TXN;ACTB

TUBA1B;TUBB;TUBB4B;TUBA4A

TUBA1B;TUBB;TUBB4B;ACTB;TUBA4A

RPL12;RPL11;RPS3;RPLP2;RPS20;RPS27A

HSP90AA1;S100A9;S100A8;S100A7

CALML5;VDAC2;SLC25A4;MYH6;SLC25A6

TUBA1B;HSPA4;MYH9;ACTB;TUBA4A

HSPA8;CAT;HSPA1B;HSPA1A

GLUD1;ARG1

HSPA8;RACK1;HSPA1B;HSPA1A

TUBA1B;CTSD;ACTB;TUBA4A

DSP;JUP;ACTB

PRDX1;ECH1;CAT

CALML5;VDAC2;SLC25A4;SLC25A6

HSPA9;CALML5;CTSD;HSPD1

VDAC2;SLC25A4;ACTB;SLC25A6

HSPA8;HSPA1B;HSPA1A

GLUD1

GGCT;MGST1

CALML5;VDAC2;SLC25A4;SLC25A6

ACTB;MYH6

VDAC2;SLC25A4;SLC25A6

HSPA8;HSPA1B;HSPA1A

ALDOA;GAPDH

CALML5;ACTB

CALML5;CFL1

SLC25A4;ACTB;SLC25A6

HSPA9;HSPD1

HSP90AA1;VDAC2;TXN

HSPA8;HSPB1;HSPA1B;HSPA1A
UQCRC2;MYH6
ACTB;MYH6
GLUD1
ACTB;MYH6
HAL
CFL1;MYH9;ACTB
VDAC2;SLC25A4;SLC25A6
MGST1;NME1
HSPA5
GLUD1
ALDOA;GAPDH
NDUFA4;UQCRC2;ACTB
ACTB;MYH6
CALML5
COL1A2;ACTB
CAT
ALDOA
HSPA8;HSPA1B;HSPA1A
CALML5;MYH9
NDUFA4;UQCRC2
ALDOA
STUB1;RPS27A
GLUD1
CALML5;MYH6
VDAC2
CALML5;ACTB
CAT
NDUFA4;UQCRC2
HSPD1
MGST1;ACTB
ARG1
ACTB
VDAC2
NME1
HSPB1
CALML5;RPS27A
COL1A2;ACTB
COL1A2;ACTB
JUP
CALML5
RPS27A
CALML5
CALML5
CALML5;ACTB
CALML5;CFL1
ACTB

HSP90AA1;CALML5;JUP;MGST1
FABP5
HSPA5
CALML5
MGST1
ACTB
EEF1A1
HSP90AA1;MGST1
COL1A2
RPS27A;ACTB
CALML5
CALML5
DSG1
CALML5
CFL1
CALML5
HSP90AA1
CALML5
CALML5
COL1A2
HSP90AA1
CALML5
COL1A2
CALML5
HSP90AA1
CALML5
ACTB
CTSD
CALML5
CTSD
CALML5
NME1
COL1A2
CAT
CALML5
CALML5
CTSD
ACTB
CALML5
NDUFA4
JUP
HSP90AA1;COL1A2
ACTB
CFL1
CALML5
EEF1A1
JUP

CALML5
CALML5
CALML5
COL1A2
CALML5

A6
PA1A

A6