

Pathway analysis for Gene Ontology terms changed by diet (p<0.01) in cerebral cortex

Gene Ontology (GO) Term	GO ID	# of Genes	SM_pvalue	SS_pvalue	YS_pvalue	SM_zscore	SS_zscore	YS_zscore	Treatment
regulation of Ras protein signal transduction	GO:0046578	135	0.0000	0.0050	0.0012	4.12	-2.81	-3.24	SM
oxidoreductase activity	GO:0016491	599	0.0000	0.1963	0.0012	-5.56	1.29	-3.23	SM
oxidation reduction	GO:0055114	504	0.0000	0.4432	0.0016	-4.34	0.77	-3.16	SM
small GTPase regulator activity	GO:0005083	183	0.0000	0.0468	0.0017	6.39	-1.99	-3.13	SM
regulation of signal transduction	GO:0009966	400	0.0000	0.1971	0.0030	4.33	-1.29	-2.97	SM
regulation of GTPase activity	GO:0043087	69	0.0001	0.0651	0.0033	3.89	-1.84	-2.94	SM
phosphoric ester hydrolase activity	GO:0042578	270	0.0001	0.4268	0.0036	3.84	-0.79	-2.91	SM
enzyme activator activity	GO:0008047	208	0.0000	0.0898	0.0112	5.77	-1.70	-2.54	SM
regulation of Ras GTPase activity	GO:0032318	58	0.0000	0.1385	0.0119	4.17	-1.48	-2.51	SM
glutamate receptor activity	GO:0008066	26	0.0004	0.3614	0.0147	3.51	-0.91	-2.44	SM
phosphatase activity	GO:0016791	205	0.0004	0.9676	0.0180	3.56	0.04	-2.37	SM
regulation of small GTPase mediated signal transduction	GO:0051056	164	0.0000	0.0269	0.0183	5.38	-2.21	-2.36	SM
regulation of synapse organization and biogenesis	GO:0050807	10	0.0008	0.6563	0.0213	3.34	-0.45	-2.30	SM
iron ion binding	GO:0005506	262	0.0002	0.5211	0.0263	-3.77	-0.64	-2.22	SM
transferase activity, transferring phosphorus-containing groups	GO:0016772	880	0.0000	0.8178	0.0374	6.15	0.23	-2.08	SM
kinase activity	GO:0016301	765	0.0000	0.7258	0.0381	6.65	-0.35	-2.07	SM
GTPase regulator activity	GO:0030695	308	0.0000	0.2787	0.0476	8.24	-1.08	-1.98	SM
GTPase activator activity	GO:0005096	165	0.0000	0.0672	0.0699	6.58	-1.83	-1.81	SM
tubulin binding	GO:0015631	52	0.0007	0.6286	0.0809	3.37	0.48	-1.75	SM
proton-transporting two-sector ATPase complex	GO:0016469	29	0.0001	0.8105	0.0847	-4.03	0.24	-1.72	SM
regulation of synapse structure and activity	GO:0050803	12	0.0007	0.6775	0.0948	3.40	0.42	-1.67	SM
post-translational protein modification	GO:0043687	795	0.0000	0.4095	0.1152	5.89	-0.82	-1.58	SM
phosphotransferase activity, alcohol group as acceptor	GO:0016773	615	0.0000	0.3975	0.1289	7.23	-0.85	-1.52	SM
neurotransmitter transport	GO:0006836	81	0.0000	0.0659	0.1352	4.24	1.84	-1.49	SM
regulation of molecular function	GO:0065009	315	0.0003	0.8409	0.1484	3.60	-0.20	-1.45	SM
actin filament-based process	GO:0030029	135	0.0002	0.2835	0.1580	3.68	-1.07	-1.41	SM
regulation of ARF protein signal transduction	GO:0032012	31	0.0000	0.7990	0.2086	4.15	-0.25	-1.26	SM
purine nucleoside triphosphate metabolic process	GO:0009144	30	0.0005	0.2442	0.2703	-3.47	1.16	-1.10	SM
purine ribonucleoside triphosphate metabolic process	GO:0009205	26	0.0009	0.0922	0.2706	-3.31	1.68	-1.10	SM
purine nucleoside triphosphate biosynthetic process	GO:0009145	21	0.0003	0.0680	0.2728	-3.66	1.82	-1.10	SM
ribonucleoside triphosphate biosynthetic process	GO:0009201	21	0.0003	0.0680	0.2728	-3.66	1.82	-1.10	SM
purine ribonucleoside triphosphate biosynthetic process	GO:0009206	21	0.0003	0.0680	0.2728	-3.66	1.82	-1.10	SM
nucleoside triphosphate biosynthetic process	GO:0009142	23	0.0001	0.0624	0.3023	-3.83	1.86	-1.03	SM
regulation of microtubule-based process	GO:0032886	17	0.0004	0.7277	0.3132	3.52	0.35	-1.01	SM
generation of a signal involved in cell-cell signaling	GO:0003001	65	0.0008	0.0940	0.3157	3.34	1.67	-1.00	SM
phosphoprotein phosphatase activity	GO:0004721	125	0.0003	0.7304	0.3172	3.60	0.34	-1.00	SM
ARF GTPase activator activity	GO:0008060	19	0.0004	0.8734	0.3224	3.52	-0.16	-0.99	SM
regulation of ARF GTPase activity	GO:0032312	19	0.0004	0.8734	0.3224	3.52	-0.16	-0.99	SM
guanyl-nucleotide exchange factor activity	GO:0005085	124	0.0000	0.6720	0.3276	4.20	-0.42	-0.98	SM
phosphorus metabolic process	GO:0006793	681	0.0000	0.7387	0.3547	6.41	0.33	-0.93	SM
phosphate metabolic process	GO:0006796	681	0.0000	0.7387	0.3547	6.41	0.33	-0.93	SM
ribonucleotide biosynthetic process	GO:0009260	36	0.0007	0.1943	0.3778	-3.40	1.30	-0.88	SM
microtubule binding	GO:0008017	45	0.0001	0.2843	0.3931	3.80	1.07	-0.85	SM
regulation of adenylate cyclase activity	GO:0045761	14	0.0006	0.4561	0.4291	3.44	-0.75	-0.79	SM
protein kinase activity	GO:0004672	518	0.0000	0.2531	0.4322	6.45	-1.14	-0.79	SM
phosphorylation	GO:0016310	578	0.0000	0.9748	0.4562	5.26	-0.03	-0.75	SM
protein amino acid phosphorylation	GO:0006468	540	0.0000	0.3746	0.5107	5.96	-0.89	-0.66	SM
dephosphorylation	GO:0016311	106	0.0001	0.3899	0.5319	4.03	0.86	-0.63	SM
protein amino acid dephosphorylation	GO:0006470	91	0.0005	0.1935	0.5919	3.50	1.30	-0.54	SM
protein serine/threonine kinase activity	GO:0004674	368	0.0000	0.2138	0.6364	6.38	-1.24	-0.47	SM
protein tyrosine phosphatase activity	GO:0004725	83	0.0002	0.4835	0.6694	3.68	0.70	-0.43	SM
regulation of cyclase activity	GO:0031279	16	0.0004	0.5517	0.9244	3.57	-0.60	-0.09	SM
regulation of lyase activity	GO:0051339	16	0.0004	0.5517	0.9244	3.57	-0.60	-0.09	SM
regulation of gene expression, epigenetic	GO:0040029	34	0.0003	0.2455	0.3891	3.62	1.16	0.86	SM
DNA alkylation	GO:0006305	10	0.0003	0.2658	0.0038	3.59	1.11	2.90	SM
DNA methylation	GO:0006306	10	0.0003	0.2658	0.0038	3.59	1.11	2.90	SM
organelle envelope	GO:0031967	357	0.0795	0.0000	0.0012	-1.75	4.62	-3.24	SS
cell adhesion	GO:0007155	468	0.7484	0.0003	0.0015	-0.32	-3.62	-3.17	SS
smooth muscle contraction	GO:0006939	15	0.5470	0.0001	0.0021	-0.60	-3.83	-3.08	SS
translation	GO:0006412	216	0.0466	0.0000	0.0046	-1.99	4.61	-2.84	SS
calmodulin binding	GO:0005516	103	0.0055	0.0002	0.0056	2.77	-3.74	-2.77	SS
voltage-gated potassium channel activity	GO:0005249	82	0.1491	0.0004	0.0057	-1.44	-3.57	-2.76	SS
glycoprotein biosynthetic process	GO:0009101	79	0.0376	0.0009	0.0112	-2.08	-3.33	-2.54	SS
axon	GO:0030424	77	0.4666	0.0005	0.0117	0.73	-3.49	-2.52	SS
fatty acid biosynthetic process	GO:0006633	63	0.0544	0.0005	0.1640	-1.92	-3.50	-1.39	SS
organic acid biosynthetic process	GO:0016053	69	0.0921	0.0006	0.1874	-1.68	-3.42	-1.32	SS
carboxylic acid biosynthetic process	GO:0046394	69	0.0921	0.0006	0.1874	-1.68	-3.42	-1.32	SS
ribonucleoprotein complex	GO:0030529	339	0.0152	0.0000	0.2611	-2.43	6.72	-1.12	SS
ATP synthesis coupled electron transport	GO:0042773	12	0.1058	0.0002	0.3196	-1.62	3.69	-1.00	SS
organelle ATP synthesis coupled electron transport	GO:0042775	10	0.2305	0.0002	0.3936	-1.20	3.75	-0.85	SS
oxidative phosphorylation	GO:0006119	24	0.0045	0.0001	0.4328	-2.84	3.99	-0.78	SS
respiratory electron transport chain	GO:0022904	20	0.1982	0.0000	0.6372	-1.29	4.06	-0.47	SS
electron transport chain	GO:0022900	21	0.2141	0.0000	0.7314	-1.24	4.23	-0.34	SS
large ribosomal subunit	GO:0015934	22	0.0153	0.0005	0.7362	-2.43	3.49	-0.34	SS
ribosome	GO:0005840	140	0.0017	0.0000	0.7697	-3.14	7.24	-0.29	SS
tissue homeostasis	GO:0001894	23	0.8617	0.0003	0.9584	0.17	3.65	0.05	SS
multicellular organismal homeostasis	GO:0048871	23	0.8617	0.0003	0.9584	0.17	3.65	0.05	SS
ribosomal subunit	GO:0033279	38	0.0203	0.0001	0.8179	-2.32	3.98	0.23	SS
hydrogen ion transmembrane transporter activity	GO:0015078	67	0.0028	0.0001	0.7380	-2.99	3.95	0.33	SS
response to reactive oxygen species	GO:0000302	21	0.4972	0.0000	0.5399	-0.68	4.77	0.61	SS
hydrogen peroxide metabolic process	GO:0042743	16	0.6935	0.0000	0.4949	-0.39	5.48	0.68	SS
RNA metabolic process	GO:0016070	483	0.4368	0.0007	0.3671	0.78	3.41	0.90	SS
response to hydrogen peroxide	GO:0042542	15	0.9541	0.0000	0.2903	0.06	6.14	1.06	SS
superoxide metabolic process	GO:0006801	11	0.8406	0.0001	0.2791	-0.20	3.91	1.08	SS
oxygen and reactive oxygen species metabolic process	GO:0006800	29	0.5984	0.0000	0.2518	-0.53	5.51	1.15	SS
negative regulation of apoptosis	GO:0043066	163	0.0259	0.0002	0.1756	2.23	3.77	1.35	SS
negative regulation of programmed cell death	GO:0043069	166	0.0168	0.0001	0.1541	2.39	3.82	1.43	SS
RNA binding	GO:0003723	491	0.6438	0.0004	0.1310	0.46	3.57	1.51	SS
apoptotic nuclear changes	GO:0030262	10	0.6882	0.0000	0.0984	0.40	4.34	1.65	SS
negative regulation of neuron apoptosis	GO:0043524	30	0.0651	0.0010	0.0884	1.84	3.30	1.70	SS
RNA processing	GO:0006396	333	0.3941	0.0001	0.0484	0.85	3.98	1.97	SS
RNA splicing	GO:0008380	168	0.6905	0.0006	0.0365	0.40	3.43	2.09	SS
cytochrome-c oxidase activity	GO:0004129	16	0.0433	0.0000	0.0060	-2.02	5.21	2.75	SS
heme-copper terminal oxidase activity	GO:0015002	16	0.0433	0.0000	0.0060	-2.02	5.21	2.75	SS
oxidoreductase activity, acting on heme group of donors	GO:0016675	16	0.0433	0.0000	0.0060	-2.02	5.21	2.75	SS
oxidoreductase activity, acting on heme group of donors, oxygen as acceptor	GO:0016676	16	0.0433	0.0000	0.0060	-2.02	5.21	2.75	SS
organelle membrane	GO:0031090	495	0.1966	0.1090	0.0000	-1.29	1.60	-7.22	YS

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Gene Ontology (GO) Term	GO ID	# of Genes	SM_pvalue	SS_pvalue	YS_pvalue	SM_zscore	SS_zscore	YS_zscore	Treatment
vacuole	GO:0005773	179	0.9255	0.0147	0.0000	0.09	-2.44	-7.03	YS
protein localization	GO:0008104	617	0.5250	0.2265	0.0000	0.64	-1.21	-6.15	YS
lytic vacuole	GO:0000323	165	0.9559	0.1191	0.0000	-0.06	-1.56	-6.13	YS
lysosome	GO:0005764	165	0.9559	0.1191	0.0000	-0.06	-1.56	-6.13	YS
endoplasmic reticulum	GO:0005783	667	0.4763	0.0303	0.0000	-0.71	-2.17	-6.03	YS
vesicle-mediated transport	GO:0016192	368	0.5263	0.0027	0.0000	0.63	-3.00	-6.03	YS
establishment of protein localization	GO:0045184	548	0.3114	0.1860	0.0000	1.01	-1.32	-5.96	YS
protein transport	GO:0015031	547	0.2825	0.2015	0.0000	1.07	-1.28	-5.89	YS
regulation of cellular component organization and biogenesis	GO:0051128	205	0.0030	0.0347	0.0000	2.97	-2.11	-5.86	YS
membrane-bounded vesicle	GO:0031988	189	0.0442	0.0021	0.0000	2.01	-3.08	-5.85	YS
macromolecule localization	GO:0033036	638	0.4429	0.3162	0.0000	0.77	-1.00	-5.80	YS
GTP binding	GO:0005525	286	0.3098	0.0333	0.0000	1.02	-2.13	-5.71	YS
cytoplasmic membrane-bounded vesicle	GO:0016023	182	0.0552	0.0042	0.0000	1.92	-2.86	-5.67	YS
organic acid metabolic process	GO:0006082	378	0.0367	0.0050	0.0000	-2.09	-2.81	-5.62	YS
carboxylic acid metabolic process	GO:0019752	378	0.0367	0.0050	0.0000	-2.09	-2.81	-5.62	YS
cellular biosynthetic process	GO:0044249	801	0.0157	0.8025	0.0000	-2.42	0.25	-5.61	YS
guanyl nucleotide binding	GO:0019001	292	0.2334	0.0536	0.0000	1.19	-1.93	-5.47	YS
guanyl ribonucleotide binding	GO:0032561	292	0.2334	0.0536	0.0000	1.19	-1.93	-5.47	YS
carbohydrate metabolic process	GO:0005975	287	0.6673	0.0492	0.0000	0.43	-1.97	-5.42	YS
organelle organization and biogenesis	GO:0006996	812	0.0055	0.0771	0.0000	2.78	-1.77	-5.40	YS
endomembrane system	GO:0012505	287	0.1615	0.0405	0.0000	1.40	-2.05	-5.37	YS
regulation of neurological system process	GO:0031644	51	0.0104	0.0069	0.0000	2.56	-2.70	-5.22	YS
cellular carbohydrate metabolic process	GO:0044262	197	0.2506	0.3880	0.0000	1.15	-0.86	-5.12	YS
regulation of synaptic transmission	GO:0050804	46	0.0070	0.0067	0.0000	2.70	-2.71	-5.09	YS
regulation of transmission of nerve impulse	GO:0051969	46	0.0070	0.0067	0.0000	2.70	-2.71	-5.09	YS
dendrite	GO:0030425	51	0.0493	0.0012	0.0000	1.97	-3.25	-5.07	YS
cellular localization	GO:0051641	562	0.0177	0.8980	0.0000	2.37	0.13	-5.05	YS
small GTPase mediated signal transduction	GO:007264	221	0.5844	0.0015	0.0000	-0.55	-3.18	-5.01	YS
establishment of localization in cell	GO:0051649	532	0.0186	0.9158	0.0000	2.35	-0.11	-4.91	YS
sulfuric ester hydrolase activity	GO:0008484	11	0.4410	0.0027	0.0000	0.77	-3.00	-4.88	YS
intracellular transport	GO:0046907	422	0.1643	0.8891	0.0000	1.39	-0.14	-4.84	YS
clathrin coat	GO:0030118	30	0.3871	0.0019	0.0000	0.86	-3.11	-4.77	YS
generation of neurons	GO:0048699	342	0.3331	0.0044	0.0000	0.97	-2.85	-4.77	YS
lipid metabolic process	GO:0006629	549	0.7626	0.0070	0.0000	-0.30	-2.70	-4.76	YS
cellular lipid metabolic process	GO:0044255	478	0.6508	0.0066	0.0000	-0.45	-2.71	-4.72	YS
amine metabolic process	GO:0009308	237	0.5650	0.0255	0.0000	-0.58	-2.23	-4.69	YS
learning and/or memory	GO:0007611	69	0.0186	0.0170	0.0000	2.35	-2.39	-4.67	YS
neurogenesis	GO:0022008	363	0.1340	0.0147	0.0000	1.50	-2.44	-4.67	YS
catabolic process	GO:0009056	527	0.3362	0.8529	0.0000	-0.96	0.19	-4.62	YS
memory	GO:0007613	23	0.0352	0.6087	0.0000	2.11	-0.51	-4.60	YS
nitrogen compound metabolic process	GO:0006807	253	0.6742	0.0454	0.0000	-0.42	-2.00	-4.59	YS
cellular catabolic process	GO:0044248	420	0.2997	0.8453	0.0000	-1.04	0.20	-4.58	YS
alcohol metabolic process	GO:0006066	236	0.6639	0.0751	0.0000	0.43	-1.78	-4.57	YS
vesicle organization and biogenesis	GO:0016050	29	0.1095	0.0295	0.0000	1.60	-2.18	-4.57	YS
sensory perception of pain	GO:0019233	25	0.8698	0.0034	0.0000	0.16	-2.93	-4.56	YS
Golgi membrane	GO:0000139	79	0.0997	0.0030	0.0000	-1.65	-2.97	-4.56	YS
cytosol	GO:0005829	293	0.0529	0.9740	0.0000	-1.94	0.03	-4.55	YS
hydrolase activity, acting on acid anhydrides	GO:0016817	395	0.1091	0.0987	0.0000	1.60	-1.65	-4.49	YS
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	GO:0016818	394	0.1087	0.1057	0.0000	1.60	-1.62	-4.49	YS
behavior	GO:0007610	301	0.7503	0.2199	0.0000	0.32	-1.23	-4.47	YS
pyrophosphatase activity	GO:0016462	391	0.0718	0.1073	0.0000	1.80	-1.61	-4.46	YS
cellular nitrogen compound metabolic process	GO:0034641	246	0.7155	0.0522	0.0000	-0.36	-1.94	-4.41	YS
carbohydrate catabolic process	GO:0016052	63	0.7287	0.0464	0.0000	-0.35	-1.99	-4.37	YS
GTPase activity	GO:0003924	101	0.2847	0.0498	0.0000	1.07	-1.96	-4.36	YS
synapse part	GO:0044456	121	0.1642	0.0020	0.0000	1.39	-3.09	-4.27	YS
glucose metabolic process	GO:0006006	88	0.9913	0.3663	0.0000	0.01	-0.90	-4.19	YS
amino acid and derivative metabolic process	GO:0006519	216	0.5526	0.0648	0.0000	-0.59	-1.85	-4.17	YS
nucleoside-triphosphatase activity	GO:0017111	371	0.0401	0.1660	0.0000	2.05	-1.39	-4.14	YS
intracellular signaling cascade	GO:0007242	762	0.0017	0.0310	0.0000	3.14	-2.16	-4.12	YS
learning	GO:0007612	45	0.0845	0.0319	0.0000	1.73	-2.15	-4.11	YS
cellular carbohydrate catabolic process	GO:0044275	57	0.7444	0.0434	0.0000	-0.33	-2.02	-4.11	YS
amino acid metabolic process	GO:0006520	161	0.2251	0.0732	0.0000	-1.21	-1.79	-4.08	YS
vesicle coat	GO:0030120	20	0.4920	0.0073	0.0001	-0.69	-2.68	-4.03	YS
regulation of synaptic plasticity	GO:0048167	27	0.0035	0.1076	0.0001	2.92	-1.61	-4.01	YS
cellular macromolecule biosynthetic process	GO:0034645	351	0.0092	0.0154	0.0001	-2.60	2.42	-4.00	YS
glucose catabolic process	GO:0006007	46	0.9925	0.0943	0.0001	0.01	-1.67	-3.97	YS
hexose catabolic process	GO:0019320	46	0.9925	0.0943	0.0001	0.01	-1.67	-3.97	YS
monosaccharide catabolic process	GO:0046365	46	0.9925	0.0943	0.0001	0.01	-1.67	-3.97	YS
neuron differentiation	GO:0030182	281	0.2660	0.0202	0.0001	1.11	-2.32	-3.97	YS
alcohol catabolic process	GO:0046164	51	0.9281	0.0745	0.0001	-0.09	-1.78	-3.96	YS
presynaptic membrane	GO:0042734	16	0.0109	0.2750	0.0001	2.54	-1.09	-3.94	YS
locomotory behavior	GO:0007626	188	0.5297	0.0844	0.0001	-0.63	-1.73	-3.94	YS
monosaccharide metabolic process	GO:0005996	112	0.3126	0.6542	0.0001	1.01	-0.45	-3.92	YS
hydrolase activity, acting on ester bonds	GO:0016788	544	0.0239	0.0899	0.0001	2.26	-1.70	-3.90	YS
hexose metabolic process	GO:0019318	111	0.2727	0.6827	0.0001	1.10	-0.41	-3.86	YS
postsynaptic membrane	GO:0045211	109	0.3561	0.0038	0.0001	0.92	-2.89	-3.85	YS
transferase activity, transferring groups other than amino-acyl groups	GO:0016747	161	0.9204	0.0056	0.0001	0.10	-2.77	-3.84	YS
AP-type membrane coat adaptor complex	GO:0030119	22	0.2751	0.0015	0.0001	1.09	-3.18	-3.83	YS
clathrin adaptor complex	GO:0030131	22	0.2751	0.0015	0.0001	1.09	-3.18	-3.83	YS
cell morphogenesis	GO:0000902	313	0.0070	0.1388	0.0001	2.70	-1.48	-3.81	YS
cellular structure morphogenesis	GO:0032989	313	0.0070	0.1388	0.0001	2.70	-1.48	-3.81	YS
aminoacyl-tRNA ligase activity	GO:0004812	44	0.3583	0.1605	0.0002	0.92	-1.40	-3.78	YS
ligase activity, forming carbon-oxygen bonds	GO:0016875	44	0.3583	0.1605	0.0002	0.92	-1.40	-3.78	YS
ligase activity, forming aminoacyl-tRNA and related compounds	GO:0016876	44	0.3583	0.1605	0.0002	0.92	-1.40	-3.78	YS
acyltransferase activity	GO:0008415	159	0.9952	0.0063	0.0002	0.01	-2.73	-3.78	YS
microtubule cytoskeleton	GO:0015630	259	0.1974	0.0357	0.0002	1.29	-2.10	-3.76	YS
cell-cell signaling	GO:0007267	274	0.0100	0.1523	0.0002	2.58	-1.43	-3.75	YS
protein polymerization	GO:0051258	23	0.5348	0.0014	0.0002	-0.62	-3.19	-3.74	YS
ligase activity	GO:0016874	307	0.6049	0.0014	0.0002	0.52	-3.19	-3.73	YS
O-acyltransferase activity	GO:0008374	29	0.9713	0.0695	0.0002	0.04	-1.82	-3.72	YS
cation transport	GO:0006812	406	0.4312	0.0148	0.0003	0.79	-2.44	-3.66	YS
microtubule-based process	GO:0007017	141	0.2150	0.0840	0.0003	1.24	-1.73	-3.66	YS
dendritic spine	GO:0043197	11	0.0123	0.0014	0.0003	2.50	-3.20	-3.65	YS
regulation of anatomical structure morphogenesis	GO:0022603	88	0.1955	0.0052	0.0003	1.29	-2.79	-3.64	YS
neuron morphogenesis during differentiation	GO:0048667	154	0.0121	0.2466	0.0003	2.51	-1.16	-3.61	YS
axonogenesis	GO:0007409	144	0.0290	0.0690	0.0003	2.18	-1.82	-3.60	YS
transferase activity, transferring sulfur-containing groups	GO:0016782	44	0.3046	0.0301	0.0003	-1.03	-2.17	-3.59	YS

Pathway analysis for Gene Ontology terms changed by diet (p<0.01) in cerebral cortex

Gene Ontology (GO) Term	GO ID	# of Genes	SM_pvalue	SS_pvalue	YS_pvalue	SM_zscore	SS_zscore	YS_zscore	Treatment
cation transmembrane transporter activity	GO:0008324	427	0.4786	0.0839	0.0003	-0.71	-1.73	-3.58	YS
regulation of neuronal synaptic plasticity	GO:0048168	16	0.0054	0.4112	0.0003	2.78	-0.82	-3.58	YS
regulation of long-term neuronal synaptic plasticity	GO:0048169	13	0.0375	0.0460	0.0004	2.08	-2.00	-3.57	YS
transferase activity, transferring acyl groups	GO:0016746	167	0.8496	0.0183	0.0004	0.19	-2.36	-3.55	YS
substrate-specific transporter activity	GO:0022892	745	0.5321	0.0170	0.0004	0.62	-2.39	-3.55	YS
tRNA aminoacylation for protein translation	GO:0006418	41	0.3932	0.2713	0.0004	0.85	-1.10	-3.55	YS
amino acid activation	GO:0043038	41	0.3932	0.2713	0.0004	0.85	-1.10	-3.55	YS
tRNA aminoacylation	GO:0043039	41	0.3932	0.2713	0.0004	0.85	-1.10	-3.55	YS
cellular macromolecular complex assembly	GO:0034622	158	0.7007	0.6172	0.0004	-0.38	-0.50	-3.53	YS
alkali metal ion binding	GO:0031420	176	0.2725	0.0017	0.0004	1.10	-3.14	-3.53	YS
intracellular protein transport	GO:0006886	258	0.0359	0.9790	0.0004	2.10	-0.03	-3.53	YS
neuron development	GO:0048666	219	0.0124	0.0840	0.0004	2.50	-1.73	-3.52	YS
Golgi-associated vesicle	GO:0005798	25	0.7347	0.0020	0.0004	-0.34	-3.09	-3.52	YS
microtubule associated complex	GO:0005875	74	0.2775	0.0207	0.0004	-1.09	-2.31	-3.52	YS
neurite development	GO:0031175	184	0.0096	0.0859	0.0004	2.59	-1.72	-3.51	YS
voltage-gated ion channel activity	GO:0005244	160	0.4803	0.0023	0.0005	0.71	-3.05	-3.51	YS
voltage-gated channel activity	GO:0022832	160	0.4803	0.0023	0.0005	0.71	-3.05	-3.51	YS
response to organic cyclic substance	GO:0014070	19	0.5074	0.0126	0.0005	0.66	-2.50	-3.51	YS
positive regulation of cellular component organization and biogenesis	GO:0051130	50	0.8797	0.3346	0.0005	-0.15	-0.96	-3.48	YS
Golgi-associated vesicle membrane	GO:0030660	18	0.4608	0.0106	0.0005	-0.74	-2.56	-3.48	YS
neurite morphogenesis	GO:0048812	152	0.0097	0.2617	0.0005	2.59	-1.12	-3.48	YS
sphingolipid catabolic process	GO:0030149	11	0.5754	0.1874	0.0005	-0.56	-1.32	-3.46	YS
cell development	GO:0048468	598	0.2169	0.0346	0.0005	1.23	-2.11	-3.46	YS
membrane lipid metabolic process	GO:0006643	152	0.1478	0.2626	0.0006	1.45	-1.12	-3.44	YS
gated channel activity	GO:0022836	246	0.3381	0.0048	0.0006	0.96	-2.82	-3.43	YS
cell morphogenesis during differentiation	GO:0000904	162	0.0133	0.3559	0.0006	2.48	-0.92	-3.42	YS
regulation of biological quality	GO:0065008	719	0.8717	0.8899	0.0006	0.16	0.14	-3.41	YS
monosaccharide biosynthetic process	GO:0046364	23	0.5283	0.2314	0.0007	-0.63	-1.20	-3.41	YS
cortical actin cytoskeleton	GO:0030864	12	0.9166	0.0167	0.0007	-0.10	-2.39	-3.40	YS
generation of precursor metabolites and energy	GO:0006091	132	0.1307	0.1026	0.0007	-1.51	1.63	-3.39	YS
response to alkaloid	GO:0043279	18	0.9242	0.0249	0.0007	0.10	-2.24	-3.39	YS
cortical cytoskeleton	GO:0030863	18	0.6786	0.0205	0.0007	0.41	-2.32	-3.38	YS
alcohol biosynthetic process	GO:0046165	27	0.8587	0.2340	0.0008	-0.18	-1.19	-3.37	YS
metal ion transport	GO:0030001	355	0.0983	0.0070	0.0009	1.65	-2.70	-3.33	YS
cation channel activity	GO:0005261	213	0.5953	0.0011	0.0009	0.53	-3.26	-3.32	YS
ion transport	GO:0006811	638	0.5296	0.0064	0.0009	0.63	-2.72	-3.32	YS
phosphatase inhibitor activity	GO:0019212	16	0.1927	0.0646	0.0009	1.30	-1.85	-3.32	YS
cell motion	GO:0006928	279	0.6407	0.0102	0.0009	-0.47	-2.57	-3.31	YS
localization of cell	GO:0051674	279	0.6407	0.0102	0.0009	-0.47	-2.57	-3.31	YS
gluconeogenesis	GO:0006094	17	0.2008	0.2976	0.0010	-1.28	-1.04	-3.30	YS
synaptic vesicle transport	GO:0048489	23	0.0930	0.5095	0.0010	1.68	-0.66	-3.29	YS
DNA metabolic process	GO:0006259	310	0.4372	0.0020	0.0006	0.78	3.08	3.43	YS
cell division	GO:0051301	228	0.1172	0.1252	0.0006	1.57	1.53	3.43	YS
mitochondrial respiratory chain	GO:0005746	49	0.0000	0.0000	0.8442	-4.85	6.43	-0.20	SM & SS
mitochondrial membrane part	GO:0044455	59	0.0000	0.0000	0.9628	-4.70	6.17	0.05	SM & SS
structural constituent of ribosome	GO:0003735	92	0.0000	0.0000	0.7603	-4.16	6.57	0.31	SM & SS
cytoskeleton organization and biogenesis	GO:0007010	322	0.0003	0.0260	0.0000	3.66	-2.23	-4.08	SM & YS
transmission of nerve impulse	GO:0019226	196	0.0005	0.4811	0.0001	3.51	-0.70	-4.02	SM & YS
cytoskeletal protein binding	GO:0008092	333	0.0001	0.1430	0.0001	3.90	-1.46	-3.93	SM & YS
synaptic transmission	GO:0007268	160	0.0008	0.5827	0.0002	3.34	-0.55	-3.69	SM & YS
coated vesicle	GO:0030135	83	0.0329	0.0000	0.0000	2.13	-4.83	-7.63	SS & YS
Golgi apparatus	GO:0005794	564	0.4471	0.0000	0.0000	0.76	-4.17	-7.39	SS & YS
clathrin-coated vesicle	GO:0030136	70	0.0110	0.0000	0.0000	2.54	-4.25	-7.00	SS & YS
synaptic vesicle	GO:0008021	54	0.0154	0.0003	0.0000	2.42	-3.65	-6.51	SS & YS
coated vesicle membrane	GO:0030662	34	0.6716	0.0000	0.0000	-0.42	-4.72	-6.24	SS & YS
membrane organization and biogenesis	GO:0016044	217	0.1794	0.0009	0.0000	1.34	-3.33	-6.03	SS & YS
vesicle	GO:0031982	313	0.0345	0.0000	0.0000	2.11	-4.25	-6.02	SS & YS
cytoplasmic vesicle	GO:0031410	304	0.0312	0.0000	0.0000	2.15	-4.24	-5.89	SS & YS
vesicle membrane	GO:0012506	52	0.3167	0.0001	0.0000	1.00	-3.99	-5.84	SS & YS
membrane coat	GO:0030117	49	0.5343	0.0001	0.0000	0.62	-4.02	-5.79	SS & YS
coated membrane	GO:0048475	49	0.5343	0.0001	0.0000	0.62	-4.02	-5.79	SS & YS
cytoplasmic vesicle membrane	GO:0030659	44	0.5127	0.0003	0.0000	0.65	-3.65	-5.68	SS & YS
clathrin coated vesicle membrane	GO:0030665	23	0.8180	0.0000	0.0000	0.23	-4.30	-5.64	SS & YS
Golgi apparatus part	GO:0044431	132	0.5707	0.0000	0.0000	-0.57	-4.46	-5.59	SS & YS
endocytosis	GO:0006897	151	0.5826	0.0000	0.0000	0.55	-4.12	-5.52	SS & YS
membrane invagination	GO:0010324	151	0.5826	0.0000	0.0000	0.55	-4.12	-5.52	SS & YS
plasma membrane part	GO:0044459	977	0.1623	0.0000	0.0000	1.40	-4.75	-5.40	SS & YS
cytoplasmic vesicle part	GO:0044433	45	0.4376	0.0007	0.0000	0.78	-3.39	-5.32	SS & YS
coated pit	GO:0005905	29	0.1616	0.0003	0.0000	1.40	-3.65	-5.27	SS & YS
nervous system development	GO:0007399	628	0.0692	0.0005	0.0000	1.82	-3.48	-5.21	SS & YS
synaptic vesicle membrane	GO:0030672	12	0.7182	0.0002	0.0000	0.36	-3.70	-4.88	SS & YS
cell junction	GO:0030054	392	0.0023	0.0009	0.0000	3.05	-3.33	-4.85	SS & YS
neuron projection	GO:0043005	136	0.1441	0.0000	0.0000	1.46	-5.01	-4.51	SS & YS
microtubule	GO:0005874	179	0.7249	0.0001	0.0000	0.35	-3.90	-4.41	SS & YS
potassium ion binding	GO:0030955	101	0.6790	0.0002	0.0000	0.41	-3.74	-4.40	SS & YS
visual behavior	GO:0007632	23	0.4950	0.0000	0.0000	0.68	-4.15	-4.35	SS & YS
visual learning	GO:0008542	23	0.4950	0.0000	0.0000	0.68	-4.15	-4.35	SS & YS
cell fraction	GO:0000267	411	0.7518	0.0003	0.0000	0.32	-3.63	-4.30	SS & YS
calcium ion binding	GO:0005509	701	0.5972	0.0000	0.0000	0.53	-4.15	-4.23	SS & YS
insoluble fraction	GO:0005626	378	0.7866	0.0002	0.0000	0.27	-3.68	-4.18	SS & YS
membrane fraction	GO:0005624	367	0.8827	0.0003	0.0000	0.15	-3.64	-4.09	SS & YS
lipid biosynthetic process	GO:0008610	227	0.0610	0.0005	0.0001	-1.87	-3.46	-3.99	SS & YS
protein phosphatase regulator activity	GO:0019888	26	0.4313	0.0003	0.0001	0.79	-3.58	-3.90	SS & YS
mitochondrial membrane	GO:0031966	233	0.0011	0.0000	0.0002	-3.26	5.05	-3.73	SS & YS
potassium ion transport	GO:0006813	131	0.9756	0.0008	0.0003	-0.03	-3.34	-3.59	SS & YS
mitochondrial envelope	GO:0005740	252	0.0019	0.0000	0.0004	-3.10	5.18	-3.55	SS & YS
phosphatase regulator activity	GO:0019208	29	0.7515	0.0002	0.0004	0.32	-3.67	-3.55	SS & YS
cytoskeleton	GO:0005856	773	0.0034	0.0006	0.0004	2.93	-3.43	-3.52	SS & YS
adherens junction	GO:0005912	56	0.4463	0.0003	0.0005	-0.76	-3.61	-3.46	SS & YS
potassium channel activity	GO:0005267	104	0.2293	0.0002	0.0009	-1.20	-3.68	-3.31	SS & YS
mitochondrion	GO:0005739	836	0.0000	0.0000	0.0000	-4.31	5.48	-7.51	ALL
organelle inner membrane	GO:0019866	223	0.0003	0.0000	0.0001	-3.66	4.60	-3.93	ALL
mitochondrial inner membrane	GO:0005743	212	0.0001	0.0000	0.0001	-3.85	4.77	-3.80	ALL
mitochondrial part	GO:0044429	290	0.0001	0.0000	0.0002	-3.94	5.72	-3.77	ALL