

Table 1: Ontology for the positively correlated genes with the lowest p-values for expression correlations with COMT: Prefrontal Cortex

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:1901575	0.00000000000024193	2.83	36.66	83	1755	organic substance catabolic process
GO:0019752	0.000000000000191738	3.40	18.94	54	907	carboxylic acid metabolic process
GO:0006614	0.000000000000199244	13.60	1.55	16	74	SRP-dependent cotranslational protein targeting to membrane
GO:0009056	0.000000000000242965	2.58	44.82	92	2146	catabolic process
GO:0006613	0.000000000000581534	12.52	1.65	16	79	cotranslational protein targeting to membrane
GO:0045047	0.000000000000872417	12.13	1.69	16	81	protein targeting to ER
GO:0072599	0.000000000001895280	11.42	1.78	16	85	establishment of protein localization to endoplasmic reticulum
GO:0044248	0.000000000003370001	2.57	38.01	80	1820	cellular catabolic process
GO:0000184	0.000000000003385265	9.88	2.13	17	102	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0006082	0.000000000004961424	3.06	21.24	55	1017	organic acid metabolic process
GO:0043436	0.000000000008769477	3.04	20.93	54	1002	oxoacid metabolic process
GO:0019080	0.000000000033370798	6.71	3.51	20	168	viral gene expression
GO:0006612	0.000000000045646174	7.54	2.84	18	136	protein targeting to membrane
GO:0019083	0.000000000050474691	6.97	3.22	19	154	viral transcription
GO:0070972	0.000000000051781086	8.84	2.19	16	105	protein localization to endoplasmic reticulum
GO:0006413	0.000000000078566674	6.77	3.30	19	158	translational initiation
GO:0055114	0.00000000297762366	2.96	17.88	46	856	oxidation-reduction process
GO:0044281	0.00000000978573710	2.27	39.73	76	1902	small molecule metabolic process
GO:0032787	0.00000001125057791	3.47	10.80	33	517	monocarboxylic acid metabolic process
GO:0044282	0.00000001362950854	4.13	7.14	26	342	small molecule catabolic process

GO:0019439	0.00000002466999636	3.49	10.03	31	480	aromatic compound catabolic process
GO:1901361	0.00000002991530197	3.39	10.67	32	511	organic cyclic compound catabolic process
GO:0006631	0.00000003146332822	4.22	6.43	24	308	fatty acid metabolic process
GO:0044255	0.00000006767057561	2.64	19.80	46	948	cellular lipid metabolic process
GO:0016054	0.00000008280514962	4.69	4.82	20	231	organic acid catabolic process
GO:0046395	0.00000008280514962	4.69	4.82	20	231	carboxylic acid catabolic process
GO:0000956	0.00000021157616676	5.15	3.74	17	179	nuclear-transcribed mRNA catabolic process
GO:0006629	0.00000036745895145	2.33	25.90	53	1240	lipid metabolic process
GO:0090150	0.00000065868607103	4.25	4.99	19	239	establishment of protein localization to membrane
GO:0006402	0.00000078905642861	3.86	6.06	21	290	mRNA catabolic process
GO:0030258	0.00000115353279079	4.08	5.18	19	248	lipid modification
GO:0034655	0.00000117728275825	3.22	8.96	26	429	nucleobase-containing compound catabolic process
GO:0044270	0.00000187266403650	3.05	9.78	27	468	cellular nitrogen compound catabolic process
GO:0016053	0.00000200419624676	3.76	5.89	20	282	organic acid biosynthetic process
GO:0046394	0.00000200419624676	3.76	5.89	20	282	carboxylic acid biosynthetic process
GO:0051234	0.00000202307409344	1.75	92.93	131	4449	establishment of localization
GO:0006605	0.00000209509939742	3.49	6.98	22	334	protein targeting
GO:1901566	0.00000303378625602	2.03	35.36	63	1693	organonitrogen compound biosynthetic process
GO:0006401	0.00000328286130842	3.50	6.62	21	317	RNA catabolic process
GO:0006810	0.00000348431672061	1.73	91.05	128	4359	transport
GO:0006364	0.00000379081285321	4.10	4.60	17	220	rRNA processing
GO:0072329	0.00000379591290085	5.82	2.34	12	112	monocarboxylic acid catabolic process
GO:0043603	0.00000468363764893	2.39	18.09	39	866	cellular amide metabolic process
GO:0043299	0.00000557665386815	2.93	9.75	26	467	leukocyte degranulation

GO:0046700	0.00000557665386815	2.93	9.75	26	467	heterocycle catabolic process
GO:0006518	0.00000702306767847	2.50	15.00	34	718	peptide metabolic process
GO:0002275	0.00000783850054355	2.87	9.94	26	476	myeloid cell activation involved in immune response
GO:0006081	0.00000874441662305	7.60	1.38	9	66	cellular aldehyde metabolic process
GO:0002444	0.00000876117203988	2.85	10.00	26	479	myeloid leukocyte mediated immunity
GO:0001676	0.00001067388699925	6.43	1.78	10	85	long-chain fatty acid metabolic process
GO:0002366	0.00001078942808552	2.60	12.66	30	606	leukocyte activation involved in immune response
GO:0002263	0.00001225012722955	2.58	12.74	30	610	cell activation involved in immune response
GO:0044403	0.00001571079899728	2.40	15.58	34	746	symbiosis, encompassing mutualism through parasitism
GO:0000038	0.00001615201848180	13.65	0.56	6	27	very long-chain fatty acid metabolic process
GO:0044283	0.00001670735166018	2.74	10.38	26	497	small molecule biosynthetic process
GO:0044242	0.00001737558853057	4.25	3.63	14	174	cellular lipid catabolic process
GO:0009062	0.00001963375176913	5.95	1.90	10	91	fatty acid catabolic process
GO:0016032	0.00002075292429055	2.43	14.43	32	691	viral process
GO:0016072	0.00002271139713252	3.53	5.26	17	252	rRNA metabolic process
GO:0046907	0.00002387382240916	1.91	34.53	59	1653	intracellular transport
GO:0051179	0.00002459990279365	1.62	114.23	149	5469	localization
GO:1901568	0.00002593180098853	4.72	2.82	12	135	fatty acid derivative metabolic process
GO:0008610	0.00002767454256694	2.51	12.64	29	605	lipid biosynthetic process
GO:0002274	0.00003401411595666	2.57	11.47	27	549	myeloid leukocyte activation
GO:0043312	0.00003430325935856	2.80	8.94	23	428	neutrophil degranulation
GO:0002283	0.00003557011686050	2.79	8.96	23	429	neutrophil activation involved in immune response
GO:0044419	0.00003612233331953	2.29	16.23	34	777	interspecies interaction between organisms
GO:0051186	0.00004340624927149	2.91	7.85	21	376	cofactor metabolic process

GO:0042119	0.00004901091570909	2.73	9.15	23	438	neutrophil activation
GO:0016042	0.00004954448917884	3.31	5.60	17	268	lipid catabolic process
GO:0016192	0.00004985050637865	1.88	33.82	57	1619	vesicle-mediated transport
GO:0045055	0.00005080190280752	2.38	13.74	30	658	regulated exocytosis
GO:0072594	0.00005085501381566	2.50	11.74	27	562	establishment of protein localization to organelle
GO:0002446	0.00005441258899407	2.71	9.21	23	441	neutrophil mediated immunity
GO:0036230	0.00005441258899407	2.71	9.21	23	441	granulocyte activation
GO:0006635	0.00006622525337620	6.62	1.38	8	66	fatty acid beta-oxidation
GO:0042254	0.00008155706593479	3.16	5.83	17	279	ribosome biogenesis
GO:0044265	0.00008721929473351	2.11	19.13	37	916	cellular macromolecule catabolic process
GO:0006102	0.00008745697910502	71.01	0.10	3	5	isocitrate metabolic process
GO:0006887	0.00008803494957000	2.24	15.56	32	745	exocytosis
GO:0042063	0.00009589960967303	3.41	4.78	15	229	gliogenesis
GO:0006637	0.00009873074294533	5.41	1.86	9	89	acyl-CoA metabolic process
GO:0035383	0.00009873074294533	5.41	1.86	9	89	thioester metabolic process

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