GO term	GO term ID	GO functional classification	Number of input genes represented by GO term (total: n=61)	Percentage of input genes represented by GO term	PValue	Genes	Population hits	Population total	Fold Enrichment	Bonferroni	Benjamini	FDR
lipid metabolic process	GO:0006629	biological process	21	33.87096774	1.88E-08	PLP1, PSAP, FA2H, ABCD1, HEXA, TTPA, MECP2, STUB1, PNPLA6, GLB1, AUH, CYP7B1, GBA2, NPC1, NPC2, CYP27A1, ARSA, GALC, PLA2G6, ABHD12, PDHX	1332	16651	4.303537144	3.50E-05	3.50E-05	3.20E-05
carboxylic acid metabolic process	GO:0019752	biological process	15	24.19354839	1.04E-06	PLP1, FA2H, ABCD1, MECP2, DARS2, AUH, SDHA, CYP7B1, GBA2, NPC1, CYP27A1, SLC2A1, MARS2, PDHX, SLC25A15	828	16651	4.945058209	0.001930423	9.66E-04	0.00176847
oxoacid metabolic process	GO:0043436	biological process	15	24.19354839	1.11E-06	PLP1, FA2H, ABCD1, MECP2, DARS2, AUH, SDHA, CYP7B1, GBA2, NPC1, CYP27A1, SLC2A1, MARS2, PDHX, SLC25A15	833	16651	4.915375986	0.002073496	6.92E-04	0.00189968
sphingolipid metabolic process	GO:0006665	biological process	8	12.90322581	1.35E-06	GBA2, PSAP, FA2H, HEXA, ARSA, GALC, PLA2G6, GLB1	155	16651	14.08863035	0.002512775	6.29E-04	0.00230263
organic acid metabolic process	GO:0006082	biological process	15	24.19354839	3.28E-06	PLP1, FA2H, ABCD1, MECP2, DARS2, AUH, SDHA, CYP7B1, GBA2, NPC1, CYP27A1, SLC2A1, MARS2, PDHX, SLC25A15	913	16651	4.484674914	0.006087162	0.001220408	0.00558802
glycosphingolipid metabolic process	GO:0006687	biological process	6	9.677419355	5.96E-06	GBA2, PSAP, HEXA, ARSA, GALC, GLB1	72	16651	22.74726776	0.01104261	0.001848961	0.01016223
membrane lipid metabolic process	GO:0006643	biological process	8	12.90322581	8.33E-06	GBA2, PSAP, FA2H, HEXA, ARSA, GALC, PLA2G6, GLB1	204	16651	10.70459659	0.015398325	0.002214417	0.01420163
axo-dendritic transport	GO:0008088	biological process	5	8.064516129	1.03E-05	SPG7, KIF1A, OPA1, UCHL1, SPG11	38	16651	35.91673857	0.018930742	0.002386176	0.01749055
cellular lipid metabolic process	GO:0044255	biological process	15	24.19354839	1.59E-05	PLP1, PSAP, FA2H, ABCD1, HEXA, MECP2, PNPLA6, GLB1, AUH, GBA2, ARSA, GALC, PLA2G6, ABHD12, PDHX	1048	16651	3.90697347	0.029207224	0.003288165	0.02712579
cytoskeleton-dependent intracellular transport	GO:0030705	biological process	6	9.677419355	2.32E-05	KIF1C, SPG7, KIF1A, OPA1, UCHL1, SPG11	95	16651	17.24003451	0.042245922	0.004307121	0.0394974
glycolipid metabolic process	GO:0006664	biological process	6	9.677419355	6.57E-05	GBA2, PSAP, HEXA, ARSA, GALC, GLB1	118	16651	13.8796888	0.115170852	0.011062061	0.1119255
liposaccharide metabolic process	GO:1903509	biological process	6	9.677419355	7.40E-05	GBA2, PSAP, HEXA, ARSA, GALC, GLB1	121	16651	13.53556429	0.128801124	0.011424654	0.12611689
single-organism behavior	GO:0044708	biological process	9	14.51612903	1.11E-04	NPC1, FXN, PSEN1, KCNA2, UCHL1, MECP2, PLA2G6, ABHD12, PRNP	413	16651	5.948438058	0.186465008	0.015749001	0.18869441
transmembrane transport	GO:0055085	biological process	15	24.19354839	1.99E-04	KCND3, ABCD1, KCNA2, AFG3L2, GJC2, ATP13A2, SLC17A5, PSEN1, PEX16, SLC2A1, GRID2, PLA2G6, SCN8A, PRNP, SLC25A15	1322	16651	3.097207411	0.309653912	0.026121504	0.3385752
adult walking behavior	GO:0007628	biological process	4	6.451612903	2.25E-04	NPC1, FXN, UCHL1, ABHD12	33	16651	33.08693492	0.342087601	0.027526285	0.38245844
walking behavior	GO:0090659	biological process	4	6.451612903	2.25E-04	NPC1, FXN, UCHL1, ABHD12	33	16651	33.08693492	0.342087601	0.027526285	0.38245844
axonal transport	GO:0098930	biological process	4	6.451612903	2.25E-04	SPG7, KIF1A, OPA1, UCHL1	33	16651	33.08693492	0.342087601	0.027526285	0.38245844
adult locomotory behavior	GO:0008344	biological process	5	8.064516129	2.48E-04	NPC1, FXN, UCHL1, MECP2, ABHD12	85	16651	16.05689489	0.370080579	0.028472021	0.42209245
regulation of autophagy	GO:0010506	biological process	7	11.29032258	4.05E-04	GFAP, NPC1, PSAP, UCHL1, POLR3A, ATP13A2, CAPN1	269	16651	7.103236029	0.530059375	0.043448381	0.68875209
establishment of localization by movement along microtubule	GO:0010970	biological process	5	8.064516129	4.61E-04	SPG7, KIF1A, OPA1, UCHL1, SPG11	100	16651	13.64836066	0.576782478	0.046647443	0.78388932
cellular catabolic process	GO:0044248	biological process	16	25.80645161	4.63E-04	ABCD1, HEXA, UCHL1, MTPAP, EXOSC3, GAN, ATP13A2, STUB1, PNPLA6, GLB1, CAPN1, AUH, GBA2, PSEN1, GALC, ABHD12	1613	16651	2.707672294	0.578252657	0.044422504	0.78704917
steroid metabolic process	GO:0008202	biological process	7	11.29032258	4.64E-04	CYP7B1, GBA2, NPC1, NPC2, CYP27A1, MECP2, STUB1	276	16651	6.923081492	0.579076661	0.042342641	0.78882498
neuromuscular process	GO:0050905	biological process	5	8.064516129	4.79E-04	OPA3, FXN, UCHL1, GRID2, MECP2	101	16651	13.51322837	0.590550369	0.041629678	0.81391634
bile acid metabolic process	GO:0008206	biological process	4	6.451612903	4.95E-04	CYP7B1, GBA2, NPC1, CYP27A1	43	16651	25.39229889	0.602760015	0.041095991	0.84139405
cellular lipid catabolic process	GO:0044242	biological process	6	9.677419355	5.08E-04	GBA2, ABCD1, GALC, ABHD12, PNPLA6, AUH	183	16651	8.949744692	0.612192959	0.040348104	0.86320203
lipid catabolic process	GO:0016042	biological process	7	11.29032258	6.48E-04	GBA2, ABCD1, GALC, PLA2G6, ABHD12, PNPLA6, AUH	294	16651	6.49921936	0.700821454	0.049036674	1.09834516
monocarboxylic acid metabolic process	GO:0032787	biological process	9	14.51612903	8.34E-04	CYP7B1, GBA2, PLP1, NPC1, CYP27A1, FA2H, ABCD1, PDHX, AUH	558	16651	4.402696986	0.788800247	0.060303225	1.41305893
behavior	GO:0007610	biological process	9	14.51612903	0.00102428	NPC1, FXN, PSEN1, KCNA2, UCHL1, MECP2, PLA2G6, ABHD12, PRNP	576	16651	4.265112705	0.851804057	0.07080024	1.73219725
small molecule binding	GO:0036094	molecular function	20	32.25806452	0.00129164	SPG7, OPA1, ABCD1, MTPAP, TTPA, MECP2, DARS2, AFG3L2, ATP13A2, POLR3B, SETX, SDHA, KIF1C, NPC1, KIF1A, NPC2, MARS2, SPR, SCN8A, TUBB4A	2579	15429	2.099140834	0.36633979	0.36633979	1.75435755
microtubule-based movement	GO:0007018	biological process	6	9.677419355	0.00131179	KIF1C, SPG7, KIF1A, OPA1, UCHL1, SPG11	226	16651	7.246917162	0.913315121	0.08659251	2.2133115
mitochondrion organization	GO:0007005	biological process	10	16.12903226	0.0016858	OPA3, SPG7, OPA1, FXN, PLA2G6, POLR3A, DARS2, AFG3L2, ATP13A2, TTC19	773	16651	3.531270545	0.956859267	0.106188408	2.83584428
adult behavior	GO:0030534	biological process	5	8.064516129	0.00175199	NPC1, FXN, UCHL1, MECP2, ABHD12	143	16651	9.544308151	0.961872805	0.106535989	2.94564313
ion transport	GO:0006811	biological process	14	22.58064516	0.00195235	KCND3, KCNA2, ABCD1, AFG3L2, ATP13A2, SLC17A5, FXN, PSEN1, SLC2A1, GRID2, PLA2G6, SCN8A, PRNP, SLC25A15	1475	16651	2.590875243	0.973768455	0.114284736	3.27725749
regulation of lipid metabolic process	GO:0019216	biological process	6	9.677419355	0.00422009	OPA3, NPC2, PSAP, PLA2G6, PDHX, STUB1	296	16651	5.533119185	0.999621261	0.224424844	6.95694812
autophagy	GO:0006914	biological process	8	12.90322581	0.00426129	GFAP, NPC1, PSEN1, UCHL1, ARSA, POLR3A, ATP13A2, CAPN1	570	16651	3.831118781	0.99964936	0.220121526	7.02256946
nervous system development	GO:0007399	biological process	17	27.41935484	0.00445199	GFAP, SPG7, PLP1, OPA1, FA2H, KCNA2, UCHL1, MECP2, AFG3L2, SETX, SDHA, GBA2, PSEN1, GRID2, ARSA, SCN8A, SPG11	2224	16651	2.086529956	0.99975459	0.222674675	7.3257205
locomotory behavior	GO:0007626	biological process	5	8.064516129	0.00495941	NPC1, FXN, UCHL1, MECP2, ABHD12	191	16651	7.145738563	0.99990507	0.238467739	8.1278286
myelination	GO:0042552	biological process	4	6.451612903	0.00530717	PLP1, FA2H, SCN8A, AFG3L2	98	16651	11.1415189	0.999950502	0.246664989	8.67376494

negative regulation of cell death	GO:0060548	biological process	10	16.12903226	0.00538763	NPC1, OPA1, FXN, PSEN1, PSAP, MECP2, TTPA, PRNP, ATP13A2, SETX	920	16651	2.967034925	0.999957427	0.243886526	8.79965138
ensheathment of neurons	GO:0007272	biological process	4	6.451612903	0.00577088	PLP1, FA2H, SCN8A, AFG3L2	101	16651	10.8105827	0.999979236	0.252793313	9.39699607
axon ensheathment	GO:0008366	biological process	4	6.451612903	0.00577088	PLP1, FA2H, SCN8A, AFG3L2	101	16651	10.8105827	0.999979236	0.252793313	9.39699607
hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0004553	molecular function	4	6.451612903	0.00603298	GBA2, HEXA, GALC, GLB1	102	15429	10.61506708	0.881884554	0.656320722	7.95261977
nucleoside-triphosphatase activity	GO:0017111	molecular function	9	14.51612903	0.00664663	KIF1C, SPG7, KIF1A, OPA1, ABCD1, AFG3L2, ATP13A2, TUBB4A, SETX	777	15429	3.135338346	0.905020216	0.543742105	8.72777706
organic anion transport	GO:0015711	biological process	6	9.677419355	0.00707381	SLC17A5, PSEN1, ABCD1, SLC2A1, PLA2G6, SLC25A15	335	16651	4.888965011	0.999998196	0.293925882	11.4003436
oxidation-reduction process	GO:0055114	biological process	10	16.12903226	0.00816159	SDHA, CYP7B1, GLRX5, FXN, CYP27A1, FA2H, ABCD1, MECP2, SPR, AUH	982	16651	2.779706855	0.999999766	0.323939423	13.0408839
neuron development	GO:0048666	biological process	10	16.12903226	0.00914328	GBA2, PLP1, GFAP, OPA1, PSEN1, UCHL1, MECP2, AFG3L2, SPG11, SETX	1000	16651	2.729672131	0.999999963	0.348062706	14.4968252
regulation of membrane potential	GO:0042391	biological process	6	9.677419355	0.0091744	KCND3, PSEN1, KCNA2, GRID2, MECP2, SCN8A	357	16651	4.587684254	0.999999965	0.342164015	14.5425995
pyrophosphatase activity	GO:0016462	molecular function	9	14.51612903	0.00921161	KIF1C, SPG7, KIF1A, OPA1, ABCD1, AFG3L2, ATP13A2, TUBB4A, SETX	822	15429	2.963695736	0.961870525	0.558108948	11.9028228
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	GO:0016818	molecular function	9	14.51612903	0.00934076	KIF1C, SPG7, KIF1A, OPA1, ABCD1, AFG3L2, ATP13A2, TUBB4A, SETX	824	15429	2.956502299	0.963585344	0.484468457	12.059948
hydrolase activity, acting on acid anhydrides	GO:0016817	molecular function	9	14.51612903	0.00947127	KIF1C, SPG7, KIF1A, OPA1, ABCD1, AFG3L2, ATP13A2, TUBB4A, SETX	826	15429	2.949343698	0.965240107	0.428723439	12.2184645
regulation of mitochondrion organization	GO:0010821	biological process	5	8.064516129	0.00959438	OPA1, FXN, PLA2G6, POLR3A, ATP13A2	231	16651	5.908381236	0.999999984	0.347949954	15.1581318
organonitrogen compound catabolic process	GO:1901565	biological process	6	9.677419355	0.00981492	GBA2, HEXA, GALC, ABHD12, GLB1, AUH	363	16651	4.511854762	0.99999999	0.347756801	15.4796887
single-organism catabolic process	GO:0044712	biological process	9	14.51612903	0.00988448	GBA2, ABCD1, GALC, PLA2G6, ABHD12, STUB1, PNPLA6, GLB1, AUH	836	16651	2.938642246	0.999999991	0.343347402	15.5808732
regulation of macroautophagy	GO:0016241	biological process	4	6.451612903	0.0101311	NPC1, UCHL1, ATP13A2, CAPN1	124	16651	8.805393971	0.999999994	0.343981748	15.9386841
neuron projection development	GO:0031175	biological process	9	14.51612903	0.01093329	PLP1, GFAP, OPA1, PSEN1, UCHL1, MECP2, AFG3L2, SPG11, SETX	851	16651	2.886844792	0.999999999	0.359327468	17.0927174
regulation of release of cytochrome c from mitochondria	GO:0090199	biological process	3	4.838709677	0.01096085	OPA1, FXN, PLA2G6	44	16651	18.61140089	0.999999999	0.353943421	17.1320979
hydrolase activity, acting on glycosyl bonds	GO:0016798	molecular function	4	6.451612903	0.01146553	GBA2, HEXA, GALC, GLB1	129	15429	8.393308854	0.982934811	0.440957994	14.6079939
sterol metabolic process	GO:0016125	biological process	4	6.451612903	0.01151125	CYP7B1, NPC1, NPC2, CYP27A1	130	16651	8.398991173	1	0.361971168	17.9149025
carbohydrate derivative binding	GO:0097367	molecular function	16	25.80645161	0.01187305	GFAP, SPG7, OPA1, ABCD1, MTPAP, DARS2, AFG3L2, ATP13A2, POLR3B, GLB1, SETX, KIF1C, KIF1A, MARS2, SCN8A, TUBB4A	2241	15429	1.932595881	0.985246393	0.409646319	15.0888035
response to inorganic substance	GO:0010035	biological process	7	11.29032258	0.01224667	NPC1, FXN, PSAP, MECP2, PRNP, ATP13A2, SETX	534	16651	3.578221895	1	0.374058352	18.9499993
cellular amino acid metabolic process	GO:0006520	biological process	5	8.064516129	0.01254134	MECP2, MARS2, DARS2, SLC25A15, AUH	250	16651	5.459344262	1	0.375150925	19.3612774
single-organism intracellular transport	GO:1902582	biological process	8	12.90322581	0.01267302	SPG7, KIF1A, NPC2, OPA1, PEX16, UCHL1, AFG3L2, SPG11	701	16651	3.115175043	1	0.372427736	19.5444416
cation transmembrane transport	GO:0098655	biological process	8	12.90322581	0.01323262	KCND3, PSEN1, KCNA2, PLA2G6, SCN8A, AFG3L2, PRNP, ATP13A2	707	16651	3.088737914	1	0.37951176	20.318438
carbohydrate derivative metabolic process	GO:1901135	biological process	11	17.74193548	0.0137444	SDHA, GBA2, NPC1, FXN, PSEN1, PSAP, HEXA, MECP2, ARSA, GALC, GLB1	1258	16651	2.386835727	1	0.385213126	21.0201624
ribonucleoside binding	GO:0032549	molecular function	14	22.58064516	0.01374877	SPG7, OPA1, ABCD1, MTPAP, DARS2, AFG3L2, ATP13A2, POLR3B, SETX, KIF1C, KIF1A, MARS2, SCN8A, TUBB4A	1854	15429	2.04400159	0.992455894	0.418996645	17.2696705
nucleoside binding	GO:0001882	molecular function	14	22.58064516	0.01416147	SPG7, OPA1, ABCD1, MTPAP, DARS2, AFG3L2, ATP13A2, POLR3B, SETX, KIF1C, KIF1A, MARS2, SCN8A, TUBB4A	1861	15429	2.036313244	0.993492061	0.395572317	17.7424841
proprioception	GO:0019230	biological process	2	3.225806452	0.01433711	FXN, MECP2	4	16651	136.4836066	1	0.392382968	21.8255774
neuron differentiation	GO:0030182	biological process	11	17.74193548	0.01461636	GBA2, PLP1, GFAP, OPA1, PSEN1, UCHL1, GRID2, MECP2, AFG3L2, SPG11, SETX	1270	16651	2.364282948	1	0.392710711	22.2023553
cellular localization	GO:0051641	biological process	17	27.41935484	0.01610269	SPG7, OPA1, UCHL1, EXOSC3, POLR3A, AFG3L2, ATP13A2, KIF1C, NPC1, KIF1A, SYNE1, NPC2, PSEN1, PEX16, GRID2, PLA2G6, SPG11	2548	16651	1.821209821	1	0.417287807	24.1791799
neurogenesis	GO:0022008	biological process	12	19.35483871	0.01624123	GBA2, PLP1, GFAP, OPA1, PSEN1, FA2H, UCHL1, GRID2, MECP2, AFG3L2, SPG11, SETX	1489	16651	2.199870086	1	0.414441789	24.3610129
organic hydroxy compound metabolic process	GO:1901615	biological process	6	9.677419355	0.01639106	CYP7B1, NPC1, NPC2, CYP27A1, MECP2, TTPA	413	16651	3.965625372	1	0.411898028	24.5572063
single-organism cellular localization	GO:1902580	biological process	10	16.12903226	0.01642088	SPG7, NPC1, KIF1A, NPC2, OPA1, PSEN1, PEX16, UCHL1, AFG3L2, SPG11	1101	16651	2.479266241	1	0.407150326	24.5961838
nitrogen compound transport	GO:0071705	biological process	8	12.90322581	0.01674691	SLC17A5, PSEN1, KCNA2, SLC2A1, MECP2, PLA2G6, ATP13A2, SLC25A15	741	16651	2.947014447	1	0.408086566	25.0212277
response to oxidative stress	GO:0006979	biological process	6	9.677419355	0.01686039	FXN, PSEN1, PSAP, PRNP, ATP13A2, SETX	416	16651	3.937027112	1	0.405077082	25.1686467
protein maturation	GO:0051604	biological process	5	8.064516129	0.01701994	FXN, PSEN1, AFG3L2, STUB1, CAPN1	274	16651	4.981153524	1	0.402991576	25.3754418
neurological system process	GO:0050877	biological process	11	17.74193548	0.01791415	OPA3, OPA1, FXN, PSEN1, KCNA2, UCHL1, GRID2, MECP2, PLA2G6, SCN8A, PRNP	1311	16651	2.290342749	1	0.414066853	26.5245282
carboxylic acid transport	GO:0046942	biological process	5	8.064516129	0.01806395	SLC17A5, PSEN1, ABCD1, PLA2G6, SLC25A15	279	16651	4.89188554	1	0.411770098	26.7153764
cellular cation homeostasis	GO:0030003	biological process	7	11.29032258	0.01843893	FXN, PSEN1, TTPA, PLA2G6, AFG3L2, PRNP, ATP13A2	585	16651	3.266274345	1	0.413405282	27.1910977
release of cytochrome c from mitochondria	GO:0001836	biological process	3	4.838709677	0.01915325	OPA1, FXN, PLA2G6	59	16651	13.8796888	1	0.4206732	28.0892879

central nervous system development	GO:0007417	biological process	9	14.51612903	0.01916229	GBA2, PLP1, GFAP, PSEN1, FA2H, UCHL1, GRID2, MECP2, ARSA	942	16651	2.607967004	1	0.416083456	28.100587
response to transition metal nanoparticle	GO:1990267	biological process	4	6.451612903	0.02031245	FXN, ARSA, PRNP, ATP13A2	161	16651	6.781794115	1	0.430063982	29.5247188
cellular ion homeostasis	GO:0006873	biological process	7	11.29032258	0.02045908	FXN, PSEN1, TTPA, PLA2G6, AFG3L2, PRNP, ATP13A2	599	16651	3.189934043	1	0.427718386	29.7043453
regulation of cell death	GO:0010941	biological process	12	19.35483871	0.02093873	NPC1, OPA1, FXN, PSEN1, PSAP, GRID2, MECP2, TTPA, PLA2G6, PRNP, ATP13A2, SETX	1546	16651	2.118762327	1	0.430608157	30.2889659
nucleotide binding	GO:0000166	molecular function	16	25.80645161	0.02095895	SPG7, OPA1, ABCD1, MTPAP, MECP2, DARS2, AFG3L2, ATP13A2, SETX, SDHA, KIF1C, KIF1A, MARS2, SPR, SCN8A, TUBB4A	2394	15429	1.809084114	0.999434128	0.493251396	25.1785308
nucleoside phosphate binding	GO:1901265	molecular function	16	25.80645161	0.02103233	SPG7, OPA1, ABCD1, MTPAP, MECP2, DARS2, AFG3L2, ATP13A2, SETX, SDHA, KIF1C, KIF1A, MARS2, SPR, SCN8A, TUBB4A	2395	15429	1.808328755	0.999448903	0.464899113	25.2552852
ATPase activity	GO:0016887	molecular function	6	9.677419355	0.02140164	KIF1C, SPG7, KIF1A, ABCD1, AFG3L2, ATP13A2	440	15429	3.691148325	0.999517627	0.444254934	25.6404983
axonal transport of mitochondrion	GO:0019896	biological process	2	3.225806452	0.02142968	OPA1, UCHL1	6	16651	90.98907104	1	0.43357759	30.8826035
glycosylceramide catabolic process	GO:0046477	biological process	2	3.225806452	0.02142968	GBA2, GALC	6	16651	90.98907104	1	0.43357759	30.8826035
ion transmembrane transport	GO:0034220	biological process	9	14.51612903	0.02192842	KCND3, PSEN1, KCNA2, GRID2, PLA2G6, SCN8A, AFG3L2, PRNP, ATP13A2	966	16651	2.543172793	1	0.43656952	31.4807883
astrocyte differentiation	GO:0048708	biological process	3	4.838709677	0.02296612	PLP1, GFAP, MECP2	65	16651	12.59848676	1	0.447301836	32.7098274
microtubule-based process	GO:0007017	biological process	7	11.29032258	0.02360082	KIF1C, SPG7, KIF1A, OPA1, UCHL1, SPG11, TUBB4A	619	16651	3.086866707	1	0.451896018	33.451286
synaptic signaling	GO:0099536	biological process	7	11.29032258	0.023766	PLP1, GFAP, PSEN1, GRID2, MECP2, PLA2G6, SPG11	620	16651	3.08188789	1	0.449801241	33.6429876
chemical synaptic transmission	GO:0007268	biological process	7	11.29032258	0.023766	PLP1, GFAP, PSEN1, GRID2, MECP2, PLA2G6, SPG11	620	16651	3.08188789	1	0.449801241	33.6429876
trans-synaptic signaling	GO:0099537	biological process	7	11.29032258	0.023766	PLP1, GFAP, PSEN1, GRID2, MECP2, PLA2G6, SPG11	620	16651	3.08188789	1	0.449801241	33.6429876
anterograde trans-synaptic signaling	GO:0098916	biological process	7	11.29032258	0.023766	PLP1, GFAP, PSEN1, GRID2, MECP2, PLA2G6, SPG11	620	16651	3.08188789	1	0.449801241	33.6429876
iron ion binding	GO:0005506	molecular function	4	6.451612903	0.0241525	CYP7B1, FXN, CYP27A1, FA2H	171	15429	6.331794398	0.999821421	0.46014945	28.4524179
phosphatidylcholine metabolic process	GO:0046470	biological process	3	4.838709677	0.0243011	MECP2, PLA2G6, PNPLA6	67	16651	12.22241253	1	0.452861923	34.2604334
cation transport	GO:0006812	biological process	9	14.51612903	0.02470543	KCND3, SLC17A5, PSEN1, KCNA2, PLA2G6, SCN8A, AFG3L2, PRNP, ATP13A2	988	16651	2.486543439	1	0.454062536	34.7234066
peroxisomal membrane transport	GO:0015919	biological process	2	3.225806452	0.02495712	ABCD1, PEX16	7	16651	77.99063232	1	0.453190962	35.0100353
regulation of chaperone-mediated autophagy	GO:1904714	biological process	2	3.225806452	0.02495712	GFAP, ATP13A2	7	16651	77.99063232	1	0.453190962	35.0100353
ATP-dependent protein binding	GO:0043008	molecular function	2	3.225806452	0.02513656	PLA2G6, PRNP	7	15429	77.33834586	0.999874929	0.450699034	29.4341478
establishment of localization in cell	GO:0051649	biological process	14	22.58064516	0.02569538	SPG7, OPA1, UCHL1, POLR3A, AFG3L2, ATP13A2, KIF1C, SYNE1, KIF1A, NPC2, PSEN1, PEX16, PLA2G6, SPG11	2020	16651	1.891851972	1	0.458751427	35.84398
cellular component biogenesis	GO:0044085	biological process	18	29.03225806	0.02652938	KCND3, GFAP, OPA1, KCNA2, SACS, MECP2, EXOSC3, AFG3L2, STUB1, SETX, TTC19, FXN, PSEN1, SLC2A1, PEX16, PLA2G6, PRNP, VAMP1	2928	16651	1.67807713	1	0.465351571	36.7739629
macromolecule catabolic process	GO:0009057	biological process	10	16.12903226	0.02655214	PSEN1, HEXA, UCHL1, MTPAP, EXOSC3, GAN, ATP13A2, STUB1, GLB1, CAPN1	1196	16651	2.282334558	1	0.461492166	36.7991534
generation of neurons	GO:0048699	biological process	11	17.74193548	0.02660021	GBA2, PLP1, GFAP, OPA1, PSEN1, UCHL1, GRID2, MECP2, AFG3L2, SPG11, SETX	1397	16651	2.149348135	1	0.458020485	36.8523515
cofactor biosynthetic process	GO:0051188	biological process	4	6.451612903	0.02673119	FXN, MMADHC, SPR, PDHX	179	16651	6.099825991	1	0.455652661	36.9970781
lipid transport	GO:0006869	biological process	5	8.064516129	0.02730767	NPC1, NPC2, PSAP, ABCD1, PLA2G6	317	16651	4.305476548	1	0.458855076	37.6303501
anion transport	GO:0006820	biological process	6	9.677419355	0.02754093	SLC17A5, PSEN1, ABCD1, SLC2A1, PLA2G6, SLC25A15	473	16651	3.462586213	1	0.457789223	37.8848826
carbohydrate derivative catabolic process	GO:1901136	biological process	4	6.451612903	0.02789492	GBA2, HEXA, GALC, GLB1	182	16651	5.999279409	1	0.458206344	38.2692908
channel activity	GO:0015267	molecular function	6	9.677419355	0.02836335	KCND3, PSEN1, KCNA2, GRID2, SCN8A, GJC2	474	15429	3.426382412	0.999961196	0.469965038	32.5663831
passive transmembrane transporter activity	GO:0022803	molecular function	6	9.677419355	0.02858756	KCND3, PSEN1, KCNA2, GRID2, SCN8A, GJC2	475	15429	3.419168975	0.999964232	0.452428657	32.7791609
monocarboxylic acid biosynthetic process	GO:0072330	biological process	4	6.451612903	0.02868561	CYP7B1, PLP1, CYP27A1, FA2H	184	16651	5.93406985	1	0.463801227	39.1198576
cation homeostasis	GO:0055080	biological process	7	11.29032258	0.0302444	FXN, PSEN1, TTPA, PLA2G6, AFG3L2, PRNP, ATP13A2	656	16651	2.912759896	1	0.478042931	40.7644557
purine ribonucleoside triphosphate binding	GO:0035639	molecular function	13	20.96774194	0.03026718	KIF1C, SPG7, KIF1A, OPA1, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, TUBB4A, SETX	1841	15429	1.911403985	0.999980583	0.452690868	34.3534591
glial cell differentiation	GO:0010001	biological process	4	6.451612903	0.03030266	PLP1, GFAP, FA2H, MECP2	188	16651	5.807813045	1	0.474876766	40.8251073
purine ribonucleoside binding	GO:0032550	molecular function	13	20.96774194	0.03140932	KIF1C, SPG7, KIF1A, OPA1, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, TUBB4A, SETX	1851	15429	1.901077654	0.999987191	0.44728524	35.4043799
purine nucleoside binding	GO:0001883	molecular function	13	20.96774194	0.03175807	KIF1C, SPG7, KIF1A, OPA1, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, TUBB4A, SETX	1854	15429	1.898001476	0.99998872	0.434261739	35.7221549
cellular homeostasis	GO:0019725	biological process	8	12.90322581	0.03280392	GLRX5, FXN, PSEN1, TTPA, PLA2G6, AFG3L2, PRNP, ATP13A2	852	16651	2.563072424	1	0.498638844	43.3745032
inorganic ion homeostasis	GO:0098771	biological process	7	11.29032258	0.03325805	FXN, PSEN1, TTPA, PLA2G6, AFG3L2, PRNP, ATP13A2	671	16651	2.847646038	1	0.499654362	43.8261322
cellular transition metal ion homeostasis	GO:0046916	biological process	3	4.838709677	0.03449059	FXN, PRNP, ATP13A2	81	16651	10.10989678	1	0.508731039	45.0348651

glial cell development	GO:0021782	biological process	3	4.838709677	0.03449059	PLP1, GFAP, FA2H	81	16651	10.10989678	1	0.508731039	45.0348651
cellular metal ion homeostasis	GO:0006875	biological process	6	9.677419355	0.03509182	FXN, PSEN1, PLA2G6, AFG3L2, PRNP, ATP13A2	505	16651	3.243174809	1	0.511100804	45.6155533
organic hydroxy compound transport	GO:0015850	biological process	4	6.451612903	0.03543774	NPC1, NPC2, KCNA2, MECP2	200	16651	5.459344262	1	0.510853249	45.9470381
purine ribonucleotide binding	GO:0032555	molecular function	13	20.96774194	0.03553036	KIF1C, SPG7, KIF1A, OPA1, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, TUBB4A, SETX	1885	15429	1.866787659	0.999997156	0.455625	39.0680188
ATP-dependent peptidase activity	GO:0004176	molecular function	2	3.225806452	0.03571843	SPG7, AFG3L2	10	15429	54.13684211	0.999997346	0.442116085	39.2305254
sensory perception of pain	GO:0019233	biological process	3	4.838709677	0.03606108	KCNA2, UCHL1, MECP2	83	16651	9.866284811	1	0.51336582	46.5395599
lipid localization	GO:0010876	biological process	5	8.064516129	0.03629678	NPC1, NPC2, PSAP, ABCD1, PLA2G6	347	16651	3.933245146	1	0.512022425	46.7620105
purine nucleotide binding	GO:0017076	molecular function	13	20.96774194	0.03720572	KIF1C, SPG7, KIF1A, OPA1, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, TUBB4A, SETX	1898	15429	1.854001442	0.999998461	0.441176027	40.5015834
chemical homeostasis	GO:0048878	biological process	9	14.51612903	0.03725355	NPC1, NPC2, FXN, PSEN1, TTPA, PLA2G6, AFG3L2, PRNP, ATP13A2	1070	16651	2.295985905	1	0.517689223	47.6560845
ribonucleotide binding	GO:0032553	molecular function	13	20.96774194	0.03760035	KIF1C, SPG7, KIF1A, OPA1, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, TUBB4A, SETX	1901	15429	1.851075611	0.999998668	0.430902693	40.8346726
ceramide metabolic process	GO:0006672	biological process	3	4.838709677	0.03765886	GBA2, GALC, PLA2G6	85	16651	9.634136933	1	0.517961346	48.0305545
cellular response to hydrogen peroxide	GO:0070301	biological process	3	4.838709677	0.03765886	FXN, PSAP, SETX	85	16651	9.634136933	1	0.517961346	48.0305545
regulation of postsynaptic membrane potential	GO:0060078	biological process	3	4.838709677	0.03765886	GRID2, MECP2, SCN8A	85	16651	9.634136933	1	0.517961346	48.0305545
outward rectifier potassium channel activity	GO:0015271	molecular function	2	3.225806452	0.03922059	KCND3, KCNA2	11	15429	49.215311	0.999999265	0.431609949	42.1842318
response to metal ion	GO:0010038	biological process	5	8.064516129	0.04032029	NPC1, FXN, MECP2, PRNP, ATP13A2	359	16651	3.80177177	1	0.539054322	50.4275316
amino acid transport	GO:0006865	biological process	3	4.838709677	0.04093447	SLC17A5, PSEN1, SLC25A15	89	16651	9.201142015	1	0.540978046	50.9657154
ATP binding	GO:0005524	molecular function	11	17.74193548	0.04110996	KIF1C, SPG7, KIF1A, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, SETX	1496	15429	1.990325077	0.999999633	0.434442868	43.7218992
glycerophospholipid catabolic process	GO:0046475	biological process	2	3.225806452	0.04240762	ABHD12, PNPLA6	12	16651	45.49453552	1	0.550357422	52.2342277
keratan sulfate catabolic process	GO:0042340	biological process	2	3.225806452	0.04240762	HEXA, GLB1	12	16651	45.49453552	1	0.550357422	52.2342277
glycosphingolipid catabolic process	GO:0046479	biological process	2	3.225806452	0.04240762	GBA2, GALC	12	16651	45.49453552	1	0.550357422	52.2342277
ion homeostasis	GO:0050801	biological process	7	11.29032258	0.04247954	FXN, PSEN1, TTPA, PLA2G6, AFG3L2, PRNP, ATP13A2	712	16651	2.683666421	1	0.547441328	52.2953619
ammonium ion metabolic process	GO:0097164	biological process	3	4.838709677	0.04345945	MECP2, PLA2G6, PNPLA6	92	16651	8.901104775	1	0.552312642	53.1209768
microtubule binding	GO:0008017	molecular function	4	6.451612903	0.04413197	KIF1C, KIF1A, OPA1, PRNP	217	15429	4.989570701	0.99999988	0.445730231	46.1027543
fatty acid metabolic process	GO:0006631	biological process	5	8.064516129	0.04422474	PLP1, FA2H, ABCD1, PDHX, AUH	370	16651	3.688746123	1	0.55526215	53.7563943
central nervous system myelination	GO:0022010	biological process	2	3.225806452	0.04586068	PLP1, FA2H	13	16651	41.99495586	1	0.565234642	55.0876195
axon ensheathment in central nervous system	GO:0032291	biological process	2	3.225806452	0.04586068	PLP1, FA2H	13	16651	41.99495586	1	0.565234642	55.0876195
adenyl ribonucleotide binding	GO:0032559	molecular function	11	17.74193548	0.04732624	KIF1C, SPG7, KIF1A, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, SETX	1533	15429	1.942287225	0.999999963	0.457316567	48.5175839
cell projection organization	GO:0030030	biological process	10	16.12903226	0.04772801	PLP1, GFAP, OPA1, PSEN1, UCHL1, GRID2, MECP2, AFG3L2, SPG11, SETX	1331	16651	2.050843074	1	0.576635196	56.5630183
cellular chemical homeostasis	GO:0055082	biological process	7	11.29032258	0.04777645	FXN, PSEN1, TTPA, PLA2G6, AFG3L2, PRNP, ATP13A2	733	16651	2.606781026	1	0.573598454	56.6006749
adenyl nucleotide binding	GO:0030554	molecular function	11	17.74193548	0.04929298	KIF1C, SPG7, KIF1A, ABCD1, MTPAP, MARS2, SCN8A, DARS2, AFG3L2, ATP13A2, SETX	1544	15429	1.928449686	0.999999982	0.459525342	49.9541158
ceramide catabolic process	GO:0046514	biological process	2	3.225806452	0.0493015	GBA2, GALC	14	16651	38.99531616	1	0.581940188	57.7707145
glycolipid catabolic process	GO:0019377	biological process	2	3.225806452	0.0493015	GBA2, GALC	14	16651	38.99531616	1	0.581940188	57.7707145
glycosylceramide metabolic process	GO:0006677	biological process	2	3.225806452	0.0493015	GBA2, GALC	14	16651	38.99531616	1	0.581940188	57.7707145
protein autoprocessing	GO:0016540	biological process	2	3.225806452	0.0493015	FXN, CAPN1	14	16651	38.99531616	1	0.581940188	57.7707145