

GO_Biological_Process_2023 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Very Long-Chain Fatty Acid Catabolic Pro	-0.4422393	6	1.758e-04	2.429e-02	SLC27A2:155 SLC27A4:284 ACOX1:922 ABCD2:1256 ABCD3:1348 ABCD4:1691
Positive Regulation Of Peptidyl–Serine P	0.4105265	4	4.460e-03	2.137e-01	LIF:380 IFNE:766 IFNK:1416 IFNG:3233 NA NA
Regulation Of Peptidyl–Serine Phosphoryl	0.4105265	4	4.460e-03	2.137e-01	LIF:380 IFNE:766 IFNK:1416 IFNG:3233 NA NA
Cellular Response To Histamine (GO:00714	-0.3857041	6	1.068e-03	8.464e-02	DHX8:457 GABRB2:640 GABRB3:914 DIAPH1:1773 GABRB1:2777 GABRG2:4564
Positive Regulation Of Gonad Development	-0.3750494	4	9.379e-03	3.076e-01	SOX9:263 WTI:517 NR5A1:2590 DHX37:4732 NA NA
Positive Regulation Of Male Gonad Develo	-0.3750494	4	9.379e-03	3.076e-01	SOX9:263 WTI:517 NR5A1:2590 DHX37:4732 NA NA
Amino–Acid Betaine Transport (GO:0015838	-0.3722803	7	6.474e-04	6.120e-02	SLC25A29:150 SLC6A20:275 SLC22A4:919 SLC27A6:511 SLC22A5:1473 SLC6A12:5318
Response To Histamine (GO:0034776)	-0.3665382	8	3.306e-04	3.790e-02	DHX8:457 GABRB2:640 GABRB3:914 DRD3:947 DIAPH1:1773 GABRB1:2777
Regulation Of Mitochondrial mRNA Stabili	0.3638544	6	2.025e-03	1.364e-01	FASTKD5:477 FASTKD1:925 FASTKD3:1985 FASTKD2:2508 PDE12:3360 TBRG4:3993
Positive Regulation Of Plasminogen Activ	0.3591537	7	9.995e-04	8.038e-02	ENO1:26 HPN:292 CLEC3B:423 F12:2222 S100A10:2984 MELTF:4877
ATP Synthesis Coupled Electron Transport	0.3548545	5	5.995e-03	2.429e-01	NDUFV1:786 NDUFBE:1014 NDUF42:12770 NDUFV3:3028 NDUF52:4140 NA
Negative Regulation Of B Cell Apoptotic	0.3521520	6	2.815e-03	1.724e-01	BCL6:280 BCL10:527 NOC2L:1085 ORMDL3:1387 FOXP1:2034 IL2:9065
Long–Term Synaptic Depression (GO:006029	-0.3500000	5	6.719e-03	2.577e-01	PLK2:738 SLC24A2:1279 PRRT1:1327 PICK1:3345 SHANK2:5447 NA
Regulation Of Collagen Fibril Organizati	0.3420706	6	3.711e-03	1.970e-01	EMILIN1:158 EFEMP2:180 RB1:753 TNXB:1043 COLGALT1:4751 CHADL:8493
Fatty Acid Elongation, Monounsaturated F	-0.3398303	6	3.942e-03	1.970e-01	ELOVL7:380 ELOVL3:1063 ELOVL4:1247 ELOVL2:3097 ELOVL5:4785 ELOVL6:4982
Fatty Acid Elongation, Polyunsaturated F	-0.3398303	6	3.942e-03	1.970e-01	ELOVL7:380 ELOVL3:1063 ELOVL4:1247 ELOVL2:3097 ELOVL5:4785 ELOVL6:4982
Fatty Acid Elongation, Saturated Fatty A	-0.3398303	6	3.942e-03	1.970e-01	ELOVL7:380 ELOVL3:1063 ELOVL4:1247 ELOVL2:3097 ELOVL5:4785 ELOVL6:4982
Histone Lysine Demethylation (GO:0070076	0.3309140	5	1.039e-02	3.217e-01	KDM4C:744 KDM3B:2629 KDM6B:2798 JMJD1C:3103 KDM3A:4400 NA
Mitochondrial Translational Elongation (0.3302657	5	1.054e-02	3.226e-01	GMF1:592 TSMF:1124 GFMD2:1260 TUFM:4235 MRPL4:6555 NA
Cell Surface Pattern Recognition Recepto	-0.3266644	4	2.366e-02	4.537e-01	COLEC10:754 ERHHAID:2582 COLEC11:3615 FFAR2:4233 NA NA
Positive Regulation Of Sterol Transport	-0.3258953	4	2.398e-02	4.537e-01	ABCBA1:1 NR1H3:1971 LIPG:3257 NR1H2:6000 NA NA
Gamma–Aminobutyric Acid Transport (GO:00	-0.3233178	6	6.094e-03	2.450e-01	SLC6A6:357 SLC6A11:619 SLC6A13:2926 SLC6A1:3482 SLC9A3R1:4439 SLC6A12:5318
Glutamate Catabolic Process (GO:0006538)	-0.3188790	4	2.719e-02	4.726e-01	GLUD1:39 GAD2:1542 GAD1:1704 GLUL:8414 GLYS:5538
Mitochondrial Fragmentation Involved In	-0.3186327	7	3.507e-03	1.948e-01	BAX:80 ERBB4:420 FIS1:481 MFF:963 VPS35:307 CCAR2:5538
Regulation Of Cilium Beat Frequency (GO:	-0.3148482	5	1.476e-02	3.889e-01	CDC40:942 CFAP43:1925 CYBD51:2281 CFAP206:4199 DNAH11:5677 NA
Negative Regulation Of Meiotic Cell Cycl	0.3141750	4	2.954e-02	4.873e-01	DUSP1:38 FBXO5:600 FBXO43:603 NPPC:10850 NA NA
Regulation Of Osteoclast Development (GO	0.3131473	4	3.007e-02	4.881e-01	SIGLEC15:136 TYROBP:2171 NOTCH2:3504 PNBX7:6319 NA NA
Regulation Of Relaxation Of Muscle (GO-1	-0.3120949	3	6.117e-02	4.833e-01	SR1565 TIFAB:2396 NEURON1:6158 NA NA
Neurotransmitter–Gated Ion Channel Clust	-0.3079538	5	1.709e-02	5.136e-01	SHISA7:805 SHANK3:1064 GPHN:2720 NLGN11:4963 LHFPCL4:5954 NA
Intracellular Sequestering Of Iron Ion (-0.3073254	3	6.523e-02	5.873e-01	FTTH:152 SRI565 FTMT:8768 NA NA
Transcription Initiation At RNA Polymera	0.3063045	6	9.367e-03	3.076e-01	TAF1C:1184 RRN3:1372 POLR1E:1835 TAF1B:1908 UBFTE:6172 TAF1:6432
Negative Regulation Of Lymphocyte Apopto	0.3046263	8	2.848e-03	1.724e-01	PIP-21 BCL6:280 NOC2L:1085 ORMDL3:1387 CCCL5:1892 FOXPI1:2034
Cilium Movement Involved In Cell Motilit	0.3032015	7	5.469e-03	2.339e-01	TEKT3:1127 RSPH4:1231 TEKT2:1391 TEKT1:1837 GAS8:2883 TEKT4:3364
Glycerol–3–Phosphate Metabolic Process (-0.3030835	5	1.892e-02	4.203e-01	GPAM:630 GPAT:2336 GKS:2502 GPAT2:3709 GCK:6747 NA
Positive Regulation Of Intracellular Est	-0.3015813	5	1.952e-02	4.275e-01	WBP2:304 KMTD2:700 PAK1:3931 YAP1:4527 PAGR1:6630 NA
Mitochondrial RNA Processing (GO:0009693	-0.3010563	9	1.763e-03	1.250e-01	PNPT1:397 FASTKD5:477 FASTKD1:925 FASTKD3:1985 FASTKD2:2508 TRMT10C:2617
Podocyte Cell Migration (GO:090521)	0.2989089	5	2.062e-02	4.375e-01	KANK2:1771 KANK1:1888 ROCK1:1994 DAAIM2:4924 TSK1:5755 NA
Negative Regulation Of Alpha–Beta T Cell	0.2982921	6	1.139e-02	3.397e-01	HFE:490 VSIR:2438 TWSG1:3129 IHH:3668 DAPL1:4453 GLI3:5442
Regulation Of Glucagon Secretion (GO:007	-0.2965844	5	2.163e-02	4.479e-01	IL6:957 FFAR4:1470 PASK:4169 SYTF:74325 CRH1:5502 NA

EnrichmentHsSymbolsFile2 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_FORMYL_PEPTIDE_RECEPTORS_BIND_F	-0.3863608	4	7.443e-03	2.118e-01	APP:1047 FPR2:1347 HEBP1:2276 ANXA1:2662 NA NA
MATZUK_TRANSDUCTIONSIGNALING	-0.3641491	6	2.007e-03	1.173e-01	VDR:170 STAR:566 DHX24:1391 CYP11A1:2512 CYP19A1:3964 NR5A2:4562
CASTELLANO_HRAS_TARGETS_DN	0.3599077	4	1.266e-02	2.691e-01	OPRM1:583 RAMAC:676 SBF2:3158 C1QTNF12:4671 NA NA
REACTOME_RRNA_PROCESSING_IN_THE_MITOCHON	0.3575435	9	2.036e-04	2.967e-02	PRORP:206 NSUN4:697 MRM1:1141 MRM3:1501 LIOVD7810:2115 TRMT10C:2617
REACTOME_SPERM_MOTILITY_AND_TAXES	0.3533245	8	5.919e-04	5.459e-02	CATSPERB:28 CATSPERG:364 CATSPERA:1342 KNCU1:2451 CATSPER3:3542 CATSPERD:3640
REACTOME_RRNA_MODIFICATION_IN_THE_MITOCH	0.3487287	5	6.191e-03	2.083e-01	NSUN4:697 MRM1:1141 MRM3:1501 TFB1M:4022 MRM2:4915 NA
WP_EFFECT_OF_INTESTINAL_MICROBIOME_ON_AN	-0.3417619	7	1.739e-03	1.085e-01	VDR:170 NR126:265 CD36:694 PPARD:2995 PPARA:3331 SCARB1:4594
REACTOME_DISINHIBITION_OF_SNARE_FORMATIO	-0.3371720	5	9.013e-03	2.364e-01	STX4:106 PRKCB:2222 STXB3:2337 PRKCG:2411 PRKCA:4334 NA
REACTOME_FATTY_ACIDS	-0.3358945	2	9.989e-02	5.730e-01	CYP2F1:1364 CYP4B1:3932 NA NA NA
REACTOME_FLT3_SIGNALING_THROUGH_SRC_FAMI	0.3354586	5	9.378e-03	2.412e-01	LCK:1423 FLT3:1841 HCK:1964 FYN:2208 SYK:5921 NA
REACTOME_ABACAVIR_TRANSMEMBRANE_TRANSPOR	-0.3283157	4	2.295e-02	3.376e-01	ABCB1:580 SLC22A3:2129 SLC22A2:2581 SLC22A1:5789 NA NA
REACTOME_ATORVASTATIN_ADME	-0.3142441	5	1.495e-02	2.795e-01	PON3:159 ABCB1:580 PON1:1819 SLC05A2:2632 SLC01B1:9829 NA
BIOCARTA_BBCELL_PATHWAY	0.3136387	7	4.055e-03	1.656e-01	CD40:604 FASLG:809 IL4A:DR4:947 FAS:3714 CD28:4204 CD40LG:5435
TOMIDA_LUNG_CANCER_POOR_SURVIVAL	-0.2974826	5	2.123e-02	3.295e-01	TYMS:233 KAP4:1274 DNER:1308 DAD1:6311 DLX4:7223 NA
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7	0.2951905	6	1.227e-02	2.672e-01	BCL6:280 MECOM:649 TFCR:1005 LPP:1063 PIK3CA:1960 EIF4A2:15061
HOFFMAN_CLOCK_TARGETS_UP	-0.2919137	7	7.478e-03	2.119e-01	CD36:694 JUN:1202 HOKAT:1767 ANXA1:2662 MIF:2840 TNFRSF11B:5092
CHEN_HOXAS_TARGETS_6HR_DN	0.2909551	5	2.424e-02	3.464e-01	ZBED8:408 TUBA1A:1992 PRPF31:4196 NPTXR:4836 FXJ1:5551 NA
MATZUK_PROVULATORY_FOLLICULAR	-0.2901879	8	4.477e-03	1.741e-01	SOX3:81 SH2B1:615 IMMP2L:1297 SOD1:1571 ESR1:2584 ADAMTS1:5196
REACTOME_ERYTHROCYTES_TAKE_UP_OXYGEN_AND	-0.2883078	6	1.412e-02	2.765e-01	CA2:716 SLC4A1:1754 AQP1:2091 RHAG:2641 CA4:4955 CA1:8255
REACTOME_SYNTHESIS_OF_16_20_HYDROXYEICOS	-0.2881974	4	4.514e-02	4.493e-01	CYP2U1:1554 CYP1A1:2835 CYP1A2:3445 CYP1B1:5768 NA NA
REACTOME_ESTROGEN_STIMULATED_SIGNALING_T	0.2881538	4	4.593e-02	4.535e-01	POPK1:250 NRAS:1928 KRAS:4814 MAPK1:6776 NA NA
WP_PHASE_I_BIOTRANSFORMATIONS_NON_P450	-0.2828663	6	1.641e-02	2.918e-01	PON3:159 PON2:321 ESD:867 PON1:1819 LIPA:3705 CESSA:14219
RAFFEL_YEGFA_TARGETS_DN	-0.2824668	5	2.870e-02	3.731e-01	HEY1:175 TL1:540 IL18R1:2734 HES1:4636 NKX2-5:9498 NA
REACTOME_DEX_H_BOX_HELICASES_ACTIVATE_TY	-0.2780811	7	1.055e-02	2.559e-01	IRF7:1104 NFKB1:1917 DHX36:2638 NFKB2:4401 DHX9:4520 REL4:4722
REACTOME_SIGNALING_BY_MEMBRANE_TETHERED_	0.2782796	5	3.115e-02	3.894e-01	BIN2:108 GOLGA4:113 KANK1:1888 ETVE:5744 KOR:10164 NA
CROSBY_E2F4_TARGETS	0.2763827	6	1.904e-02	3.144e-01	BUB1B:680 NDC80:758 CHEK1:3852 PTTG1:4846 CENPE:5503 CDC6:6164
SASSON_FSH_RESPONSE	-0.2755828	4	6.552e-02	4.892e-01	VEGFA:290 STAR:566 FDX1:5487 GDE1:8175 NA NA
REACTOME_DISEASES_OF_BASE_EXCISION_REPAI	0.2750158	5	3.318e-02	3.972e-01	NEIL3:33 NEIL1:3712 OGG1:4565 MUTYH:4595 NTHL1:5376 NA
WP_CONVERSION_OF_ANGIOGENINNOGEN_TO_ANGI	0.2704697	3	1.047e-01	5.801e-01	CTSD:1168 ACE:4381 REN:5635 NA NA NA
TESAR_ALK_TARGETS_HUMAN_ES_5D_UP	-0.2691208	5	3.714e-02	4.242e-01	SLC25A18:26 SLC17A5:1377 SLC17A1:2067 SLC05A2:2610 SLC17A6:3312 SLC17A7:3958
REACTOME_ORGANIC_ANION_TRANSPORTERS	-0.2690857	10	3.212e-03	1.555e-01	JAK1:12 PTPN11:569 IL6:957 TYK2:1799 MAP2K2:4615 IL6ST:4709
REACTOME_MAPK1_ERK2_ACTIVATION	-0.2690329	9	5.190e-03	1.813e-01	EPHA4:421 CNKSR3:1256 EPHB3:1379 SLC5A3:1949 VVXOC:2290 USP41:3510
GHANDHI_BYSTANDER_IRRADIATION_DN	0.2690113	11	2.005e-03	1.173e-01	CELA1:1591 CELA2A:2183 CELA2B:3179 GRN:3418 ELANE:4118 CELA3B:4415
BIOCARTA_PEPLI_PATHWAY	0.2667094	7	1.453e-02	2.773e-01	ERBB4:420 PSEN1:1449 NRG3:1518 PRKCB:2222 ADAM17:2869 PRKCA:4334
BIOCARTA_ERBB4_PATHWAY	-0.2656069	7	1.494e-02	2.795e-01	SLC6A14:117 SLC6A20:275 SLC6A5:320 SLC6A6:357 SLC6A11:619 SLC18A1:790
REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTE	-0.2646073	19	6.525e-05	1.283e-02	CYP1A2:3445 CYP2E1:4195 NA NA NA
REACTOME_BIOSYNTHESIS_OF_MARENS_LIKE_SPC	-0.2631695	2	1.873e-01	6.806e-01	JAK1:12 PTPN11:569 IL6:957 TYK2:1799 L6ST:4709 MAPK3:5071
REACTOME_MAPK3_ERK1_ACTIVATION	-0.2628479	10	4.050e-03	1.856e-01	JUN:1202 CRYAB:3288 HMOX1:4059 HSPB1:6833 NA NA
STANHILL_HRAS_TRANSFORMATION_UP	-0.2617956	4	6.978e-02	5.225e-01	HM13:509 MAFK:1180 HMOX1:4059 NFE2L2:4315 BACH1:9362 NA
REACTOME_REGULATION_OF_HMOX1_EXPRESSION	-0.2586205	5	4.436e-02	4.493e-01	

DisGeNET Top pathways by permulation

Mitochondrial Complex I Deficiency	-0.3676152	6	1.818e-03	2.903e-01	SDHA:554 SDHB:1050 SDS:1388 SDHD:1694 SARDH:2602 SDHAIF:15504
Campylobacter jejuni infection	0.3626723	3	2.958e-02	5.468e-01	IRF6:1581 CD14:1613 TLR4:3653 NA NA NA
Atrial Flutter	0.3624758	5	4.999e-03	4.457e-01	NUP155:727 SCN3B:1651 TNNI3K:2330 SCN5A:3232 LMNA:3481 NA
Fibrous histiocytoma of tendon sheath	0.3612765	4	1.233e-02	4.841e-01	CSF1R:55 CSF2:739 CSF1:3475 NTRK1:4934 NA NA
Pneumonia, Viral	0.3594260	2	7.827e-02	6.508e-01	BCL6:280 ACE:4381 NA NA NA NA
Obsessions	-0.3570103	7	1.072e-03	2.503e-01	BDNF:3 SLC1A1:494 SLC6A4:1413 ESR1:2584 SCLY:3651 TAL1:3769
Abnormality of the pancreas	0.3568778	5	5.715e-03	4.462e-01	FGFR2:367 NHPH3:798 TTC37:2441 ASXL1:3479 KHLH:4789 NA
Bacterial sepsis of newborn	-0.3542826	2	8.267e-02	6.626e-01	IL6:957 ST14:3741 NA NA NA NA
Hydroa Vacciniforme	-0.3531818	5	6.236e-03	4.462e-01	PLK2:738 CCR4:784 EROCCE:792 UVSSA:3293 EROCCE:6207 NA
Myelitis	0.3516972	5	6.457e-03	4.462e-01	AQP4:360 POU2F3:531 CSF2:739 S100B:4405 LAMC2:6238 NA
Thickening of pleura	-0.3516700	4	1.485e-02	4.913e-01	MTAP:354 SERPINE1:1952 TGFA:2876 TGFBI:4367 NA NA
Hemorrhagic Fever, Crimean	-0.3466692	3	3.755e-02	5.649e-01	CCRS7:51 NFKB1:1917 ISG15:4743 NA NA NA
Intestinal Diseases, Parasitic	-0.3451175	4	1.682e-02	5.129e-01	HSP90AA1:447 MST1:1979 LMN1:3701 L33:3845 NA NA
Central opacification of the cornea	-0.34339191	4	1.721e-02	5.129e-01	PAX6:818 FOXCI:976 PITX2:2494 CYP1B1:5768 NA NA
Thinning of Descemet membrane	-0.34339191	4	1.721e-02	5.129e-01	PAX6:818 FOXCI:976 PITX2:2494 CYP1B1:5768 NA NA
Peroxisome Biogenesis Disorder, Complete	0.3429135	5	7.917e-03	4.541e-01	FGFR1:19 CCND1:638 ERBB2:1624 BRCA1:3438 PEX3:7256 NA
Glycogen Storage Disease Type IV	-0.3404196	8	8.553e-04	2.423e-01	DES:339 GBE1:720 KCNJ6:760 RBCK1:1265 KCNJ3:1506 KCNJ12:3322
Diamond-Blackfan Anemia 1	0.3360263	3	4.382e-02	5.718e-01	RPS7:1743 RPL11:1881 RPS19:4543 NA NA NA
Decreased size of facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Flattening of facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Hypoplastic facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Hypotrophic facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Underdevelopment of facial bones	0.3351659	5	9.443e-03	4.596e-01	ZMPSTE24:1137 DYM:1315 CEP120:2409 LMNA:3481 FIG4:5313 NA
Patchy palmoplantar keratoderma	-0.3339823	5	9.720e-03	4.596e-01	GJB3:47 GJB4:1857 GJA1:2121 DSP:3645 KDSR:5694 NA
Transposition of the Great Arteries, Dextro	0.3323927	3	4.615e-02	5.775e-01	DVL2:17 MED13L:2725 HSPG2:5567 NA NA
Recurrent respiratory papillomatosis	0.3310264	6	4.984e-03	4.457e-01	CCLL2:533 CCCL1:613 CD274:850 CCCL2:1456 TP41:4991 ECR14L:2:8287
Fetal Diseases	0.3271089	5	1.130e-02	4.719e-01	BCSL1:704 CHUK:707 S100AB:1986 BPI:2638 PRSS8:8209 NA
Klippel-Trenaunay-Weber Syndrome	0.3256398	5	1.168e-02	4.773e-01	ROGD1:359 PIK3CA:1860 IGFBP2:4966 AGGF1:3359 SMOC1:6354 NA
Calcium Pyrophosphate Dihydrate Deposition	-0.3239330	4	2.484e-02	5.273e-01	ANKK1:429 CILP:1445 TGFBI:4367 ANKH:5052 NA NA
Ophthalmia, Sympathetic	0.3213816	4	2.600e-02	5.296e-01	MLANA:564 CD274:850 RBMS:5158 PDCD1:5247 NA NA
Vegetative State	-0.3206159	3	5.434e-02	5.595e-01	BDNF:3 NAGA:4223 RUNX1:11408 NA NA NA
Male Germ Cell Tumor	0.3201809	5	1.316e-02	4.913e-01	KIT:436 BCL10:527 FAS:3714 TP53:4018 DICER1:6191 NA
Anterior synchiaria	-0.3190020	6	6.808e-03	4.462e-01	PAX6:818 FOXCI:976 PITX2:2494 OVOL2:2572 VSY1:1483 CYP1B1:5768
Anterior Horn Cell Disease	-0.3184349	6	6.907e-03	4.462e-01	PNPLA6:522 PRD3:864 SOD1:1571 VM1:1865 GLE1:5400 SMN1:7302