

GO_Biological_Process_2023 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cilium Movement (GO:0003341)	0.25969962	47	7.519e-10	4.045e-06	DNAH11:19 DNAI2:36 SPAG17:247 TEK2:365 DNAH9:435 CFAP206:481
Axoneme Assembly (GO:0035082)	0.25692897	30	1.125e-06	3.027e-03	LRGUK:141 SPAG17:247 CCDC65:326 CFAP206:481 SPACA9:748 STK36:928
Axonemal Dynein Complex Assembly (GO:007	0.26722391	23	9.213e-06	9.913e-03	DNAI2:36 CCDC65:326 DNAH5:728 DNAH17:1027 TTC12:1033 DNAH1:1176
Cilium-Dependent Cell Motility (GO:00602	0.31091204	17	9.111e-06	9.913e-03	DNAH3:232 CCDC65:326 TEK2:365 TEK5:791 DNAH17:1027 GAS8:1163
Regulation Of DNA-templated Transcriptio	-0.03634291	1447	7.452e-06	9.913e-03	CARM1:18 TCF15:19 GTF2IRD1:54 NUP62:63 NSD1:106 ZNF628:149
Neuropeptide Signaling Pathway (GO:00072	0.15797528	63	1.480e-05	1.327e-02	SORCS1:16 RXFP3:35 GPR37:226 LTB4R:329 OPRK1:635 GALR3:697
Regulation Of Heart Rate By Cardiac Cond	0.20221682	37	2.100e-05	1.614e-02	SCN5A:49 KCND3:97 HCN3:311 KCNE4:554 KCNE2:821 KCNH2:878
Muscle Contraction (GO:0006936)	0.12909370	82	5.460e-05	3.672e-02	CHRNE:42 EMD:104 LMOD3:204 CASQ2:245 LTB4R:329 CHRND:514
Regulation Of DNA Metabolic Process (GO:	-0.11567172	97	8.504e-05	5.084e-02	TERF2:152 USP37:477 RBBP6:587 ESCO1:647 MYC:858 ACTR5:1006
Fatty Acid Transport (GO:0015908)	-0.18547566	36	1.187e-04	5.803e-02	SLCO2A1:46 SLC27A4:141 SLC22A6:660 FABP6:916 ACSL1:1041 PPARD:1166
Positive Regulation Of Chemotaxis (GO:00	-0.17416692	41	1.152e-04	5.803e-02	LGMN:174 HSPB1:301 CCL19:329 PPM1F:339 IL6:430 VEGFA:446
Cardiac Conduction (GO:0061337)	0.16773310	42	1.709e-04	7.071e-02	SCN5A:49 KCND3:97 HCN3:311 KCNE4:554 KCNE2:821 KCNH2:878
Regulation Of Gene Expression (GO:001046	-0.03928959	829	1.593e-04	7.071e-02	CARM1:18 BTNL9:36 GTF2IRD1:54 LRP1:91 NSD1:106 PRKAG1:107
Alpha-Amino Acid Biosynthetic Process (G	-0.33043891	10	2.968e-04	1.002e-01	BCAT2:101 SDS:167 SDSL:384 ILVBL:561 CPS1:909 MTHFD1:2006
Cilium Movement Involved In Cell Motilit	0.39809113	7	2.650e-04	1.002e-01	TEK2:365 TEK5:791 GAS8:1163 TEK3:1764 TEK1:2092 TEK4:2462
Protein Modification By Small Protein Co	-0.06407081	272	2.979e-04	1.002e-01	ATG3:59 CUL4B:96 KLHL2:97 DTX2:234 UBR1:241 KLHL25:255
Cilium Assembly (GO:0060271)	0.06933779	218	4.434e-04	1.403e-01	CEP19:2 TMEM216:3 DZIP1:6 DNAI2:36 E2F4:92 AVIL:112
Motile Cilium Assembly (GO:0044458)	0.26330544	14	6.481e-04	1.763e-01	E2F4:92 SPAG17:247 BBOF1:1683 RSPH9:2559 CCDC39:2623 MCIDAS:2794
Positive Regulation Of Cellular Componen	-0.10187651	94	6.555e-04	1.763e-01	LRP1:91 ASAP1:100 CLU:114 TPPP:127 CCL19:329 CRB3:344
Vesicle-Mediated Transport Between Endos	-0.20597376	23	6.300e-04	1.763e-01	SNX16:367 PTPN23:1022 RAB7A:1088 HOOK2:1270 PIK3R4:1354 BECN1:1697
Nitrogen Compound Transport (GO:0071705)	-0.08130372	146	7.209e-04	1.847e-01	SLC38A3:38 SLC6A6:53 RHAG:75 SLC7A4:87 ATP11B:139 RHCG:202
Early Endosome To Late Endosome Transpor	-0.20452387	22	9.007e-04	1.959e-01	SNX16:367 PTPN23:1022 RAB7A:1088 HOOK2:1270 PIK3R4:1354 BECN1:1697
Fatty Acid Catabolic Process (GO:0009062	-0.12524595	58	9.814e-04	1.959e-01	HADHB:24 NUDT7:86 SLC27A4:141 EHHADH:260 PEX2:407 PLA2G15:422
Negative Regulation Of Apoptotic Process	-0.05015361	375	9.347e-04	1.959e-01	NUP62:63 ALB:80 TMBIM4:110 CLU:114 LGMN:174 GCLC:215
Negative Regulation Of Macromolecule Bio	-0.11020580	75	9.831e-04	1.959e-01	RIDA:65 EIF2AK2:183 CAPRIN1:443 AKR1B1:559 PATL2:603 TSPO:722
Regulation Of Protein Phosphorylation (G	-0.06464198	221	9.775e-04	1.959e-01	NSD1:106 HSPB1:301 PECAM1:312 TSPYL2:359 AXIN1:360 FKBP8:382
Ventricular Cardiac Muscle Cell Action P	0.25589950	14	9.174e-04	1.959e-01	SCN5A:49 KCNE4:554 KCNE2:821 KCNH2:878 PKP2:1022 KCNQ1:1830
Mesodermal Cell Differentiation (GO:0048	0.33067506	8	1.201e-03	2.307e-01	ITGA3:358 ITGB4:951 ITGB1:1752 HMGA2:2252 ITGB3:2909 KDM6B:3230
Anterograde Trans-Synaptic Signaling (GO	0.07241974	166	1.332e-03	2.390e-01	CHRNE:42 DLG4:135 CHRNA4:143 RPS6KA1:154 CHRNA2:167 GABRR2:179
Diol Biosynthetic Process (GO:0034312)	-0.24836416	14	1.295e-03	2.390e-01	ACER1:184 QDPR:640 SPHK1:725 SPHK2:943 SPTLC2:1933 ACER2:2283
Positive Regulation Of Receptor-Mediated	-0.15114112	37	1.475e-03	2.405e-01	CLU:114 CD63:326 CCL19:329 VEGFA:446 RAB21:989 FMR1:1021
Regulation Of Interleukin-2 Production (-0.14541368	40	1.472e-03	2.405e-01	HOMER3:111 CD80:172 IL17F:214 TNFAIP3:492 CD86:503 RPS3:907
Striated Muscle Contraction (GO:0006941)	0.13276812	48	1.474e-03	2.405e-01	SCN5A:49 TCAP:145 LMOD3:204 DMD:228 CASQ2:245 TNNI3:582
Branched-Chain Amino Acid Metabolic Proc	-0.23496089	15	1.632e-03	2.492e-01	BCAT2:101 BCKDHA:1038 DBT:1399 PCCB:2152 HIBCH:2203 MCCC1:2244
Cellular Response To Acetylcholine (GO:1	0.30402751	9	1.588e-03	2.492e-01	LY6G6D:430 CHRND:514 CHRM3:1023 LY6H:1052 ROCK2:1193 LYPD1:2631
Positive Regulation Of Endothelial Cell	-0.26213167	12	1.668e-03	2.492e-01	LGMN:174 HSPB1:301 VEGFA:446 MET:668 P2RX4:2164 KDR:2810
Response To Peptidoglycan (GO:0032494)	-0.40472332	5	1.723e-03	2.506e-01	INAVA:402 IL6:430 IRAK3:721 IRF5:2460 RELA:2974 NA
Monocarboxylic Acid Transport (GO:001571	-0.11458389	62	1.827e-03	2.521e-01	SLC10A2:95 SLC27A4:141 SLC10A1:369 UGT1A6:625 SLCO1A2:681 FABP6:916
Protein Ubiquitination (GO:0016567)	-0.05041259	329	1.795e-03	2.521e-01	ATG3:59 CUL4B:96 KLHL2:97 PPIL2:154 RNF8:228 DTX2:234
Cytosolic Transport (GO:0016482)	-0.08698341	106	2.015e-03	2.522e-01	VPS13C:364 SNX16:367 CLTCL1:418 CLN3:481 EPS15:645 VPS26B:823