

GO_Biological_Process_2023 Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Negative Regulation Of Leukocyte Prolif	-0.4471042	4	1.955e-03	2.522e-01	TNFAIP3:492 IL3:554 ENPP3:986 LYN:1062 NA NA
Nephron Tubule Development (GO:0072080)	-0.4332989	3	9.340e-03	3.466e-01	HNFB1:415 MTSS1:1287 OXSR1:1435 NA NA NA
Cellular Response To Nitrogen Starvation	-0.4312031	4	2.819e-03	2.984e-01	GABARAPL1:550 BECN2:840 ATG7:952 BECN1:1697 NA NA
Cellular Response To Nitrogen Starvation	-0.4312031	4	2.819e-03	2.984e-01	GABARAPL1:550 BECN2:840 ATG7:952 BECN1:1697 NA NA
Positive Regulation Of Intrinsic Apoptot	-0.4135117	2	4.278e-02	4.893e-01	MYC:858 MSX1:1679 NA NA NA NA
Positive Regulation Of Osteoblast Prolif	-0.4095427	3	1.402e-02	3.789e-01	SOX8:277 CCNA2:1839 HPSE:1896 NA NA NA
Response To Peptidoglycan (GO:0032494)	-0.4047233	5	1.723e-03	2.506e-01	INAVA:402 IL6:430 IRAK3:721 IRF5:2460 RELA:2974 NA
Positive Regulation Of Toll-Like Recepto	-0.4033954	3	1.552e-02	3.834e-01	SLC15A4:1238 PTPN22:1240 RSAD2:2062 NA NA NA
Regulation Of Toll-Like Receptor 7 Signa	0.4033954	3	1.552e-02	3.834e-01	SLC15A4:1238 PTPN22:1240 RSAD2:2062 NA NA NA
Cilium Movement Involved In Cell Motilit	0.3980911	7	2.650e-04	1.002e-01	TEKT2:365 TEKT5:791 GAS8:1163 TEKT3:1764 TEKT1:2092 TEKT4:2462
Axonemal Central Apparatus Assembly (GO:	0.3936735	5	2.299e-03	2.689e-01	SPAG17:247 SPEF1:1441 DNAJB13:1934 HYDIN:2157 RSPH9:2559 NA
Valine Metabolic Process (GO:0006573)	-0.3917083	5	2.418e-03	2.711e-01	BCAT2:101 ILVBL5:161 HBCBH:2203 HIBADH:2419 BCAT1:2663 NA
Cell Junction Disassembly (GO:0150146)	-0.3865811	4	7.412e-03	3.416e-01	C1QB:98 CX3CR1:274 C10C:489 DKK1:5797 NA NA
Cellular Response To Potassium Ion (GO:0	0.3816254	4	8.208e-03	3.416e-01	DLG4:135 SLC12A2:756 DLG2:890 CRHPB:5565 NA NA
Response To Potassium Ion (GO:0035864)	0.3816254	4	8.208e-03	3.416e-01	DLG4:135 SLC12A2:756 DLG2:890 CRHPB:5565 NA NA
Protein Retention In ER Lumen (GO:000662	0.3732334	3	2.515e-02	4.371e-01	GPA41:64 KDELR3:927 OS9:4892 NA NA NA
Toll-Like Receptor 9 Signaling Pathway (0.3713153	5	4.034e-03	3.191e-01	IRAK4:591 PIK3AP1:749 IRAK1:2045 UNC93B1:2736 TNIP2:3935 NA
Gastrulation With Mouth Forming Stage (-0.3695565	3	2.663e-02	4.408e-01	LRPS:674 UGDH:2078 MEGF8:3006 NA NA NA
Positive Regulation Of Gastrulation (GO:	0.3684619	2	7.110e-02	5.639e-01	OXSR1:1435 SCX:2683 NA NA NA NA
TRAIL-activated Apoptotic Signaling Path	-0.3657934	3	2.821e-02	4.503e-01	FADD:1220 SP11:1479 ZDHHC3:3229 NA NA NA
Protein Modification By Small Protein Co	-0.3594737	3	3.105e-02	4.695e-01	ATG7:952 UBA6:1503 SENP6:3735 NA NA NA
Regulation Of Translation In Response To	-0.3590882	4	1.287e-02	3.681e-01	EIF4G1:563 SESN2:1036 NCK1:2637 NCK2:4026 NA NA
Regulation Of Cilium Beat Frequency (GO:	0.3519910	5	6.414e-03	3.320e-01	DNAH11:19 CFAP206:481 CFAP43:1915 CVB5D1:2519 CCDC40:6549 NA
snRNA Modification (GO:0040031)	-0.3516117	4	1.487e-02	3.834e-01	MEPCE:290 METTL1:6237 METTL4:2585 NHP2:3460 NA NA
L-phenylalanine Catabolic Process (GO:00	-0.3507499	5	6.604e-03	3.320e-01	TAT:33 HGD:198 OQPR:640 GSTZ1:2049 IL4I1:8036 NA
L-phenylalanine Metabolic Process (GO:00	-0.3507499	5	6.604e-03	3.320e-01	TAT:33 HGD:198 OQPR:640 GSTZ1:2049 IL4I1:8036 NA
Erythrose 4-Phosphate/Phosphoenolpyruvat	-0.3507499	5	6.604e-03	3.320e-01	TAT:33 HGD:198 OQPR:640 GSTZ1:2049 IL4I1:8036 NA
Negative Regulation Of Actin Filament De	0.3475394	4	1.607e-02	3.834e-01	SCIN:355 PLEKHH2:378 VIL1:3087 LIMAI:5643 NA NA
Negative Regulation Of CD8-positve, Alp	0.3473551	6	3.214e-03	3.116e-01	SOC51:275 DAPL1:351 VSIR:1071 HFE:2329 ZBTB7B:3804 SLC4A2:5687
Regulation Of Monoclonal Antigen Transport	-0.3471947	4	1.618e-02	3.834e-01	CA2:263 ATP8B1:359 STC1:2071 PDZK1:5295 NA NA
ATP Synthesis Coupled Electron Transport	0.3460955	5	7.359e-03	3.416e-01	NDUFV1:76 NDUF66:2653 NDUF52:2864 NDUF214:3041 NDUFV3:3480 NA
Positive Regulation Of CD4-positve, CD2	-0.3454843	3	3.821e-02	4.809e-01	KHLH:1525 HLA-DRA:1410 IFNG:5140 NA NA NA
Negative Regulation Of Mitochondrial Fun	-0.3408040	6	3.841e-03	3.191e-01	OMA1:121 SLC18A1:272 HUWE1:288 PRKN:3226 TFR3:3836 MUL1:6284
Signal Complex Assembly (GO:0001712)	-0.3373901	5	8.982e-03	3.466e-01	PXN:835 MAPK8IP2:1323 NCK1:2637 SRC:3111 NCK2:4026 NA
Cellular Response To Histamine (GO:00714	-0.3369591	5	9.070e-03	3.466e-01	GABRB3:1344 DIAPH1:1407 GABRG2:1470 DHX8:3701 GABRB1:4049 NA
Positive Regulation Of Epithelial Cell Di	-0.3366368	3	4.344e-02	4.899e-01	PROM1:269 LIF:566 PAX8:6354 NA NA NA
Positive Regulation Of Translation In Re	-0.3326295	4	1.222e-02	4.167e-01	EIF4G1:563 IMPACT:2587 NCK1:2637 NCK2:4026 NA NA
Regulation Of Lysosomal Protein Cataboli	-0.3311640	6	4.967e-03	3.191e-01	LRP1:91 LAPTM4B:236 USP8:832 MARCF2:2253 MGAT3:2960 LDLR:8535
Mesodermal Cell Differentiation (GO:0048	0.3306751	8	1.201e-03	2.307e-01	ITGA3:358 ITGB4:951 ITGB1:1752 HMG4:2252 ITGB3:2909 KDM6B:3230
Alpha-Amino Acid Biosynthetic Process (G	-0.3304389	10	2.968e-04	1.002e-01	BCAT2:101 SDS:167 SDSL:384 ILVBL5:61 CP51:909 MTHFD1:2006

EnrichmentHsSymbolsFile2 Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_ERYTHROCYTES TAKE UP OXYGEN AND	-0.4066602	6	9.310e-05	1.232e-02	SLC4A1:27 RHAG:75 CA4:132 CA2:263 CA1:1219 AQP1:1829
WP_CELLULAR_PROTEOSTASIS	0.4482417	2	2.811e-02	3.183e-01	VBPI:530 PFDN2:1028 NA NA NA NA
WP_ARACHIDONATE_EPOXYGENASE_EPOKIDE_HYDR	-0.4090380	2	4.511e-02	3.770e-01	EPHX2:1139 COX5A:1574 NA NA NA NA
BIOCARTA_TERT_PATHWAY	-0.4064353	6	5.650e-04	4.071e-02	SP1:558 MZF1:811 MYC:858 SP3:1257 WTT1:1910 TP53:2991
NIKOLSKY_BREAST_CANCER_12024_AMPLICON	0.4059417	15	5.230e-08	2.609e-05	NOC4L:116 GALNT9:313 POLE:580 SFSWAP:595 ULK1:660 CHFR:712
REACTOME_LOSS_OF_FUNCTION_OF_SMAD2_3_IN	-0.4020973	4	5.347e-03	1.425e-01	ZFYVE9:588 TGFBI:994 TGFBR1:1921 TGFBR2:2348 NA NA
REACTOME_SIGNALING_BY_TGFBETA_RECEPTOR	-0.4020973	4	5.347e-03	1.425e-01	ZFYVE9:588 TGFBI:994 TGFBR1:1921 TGFBR2:2348 NA NA
STARK_HYPPOCAMPUS_22Q11_DELETION_DN	-0.3836416	20	2.866e-09	3.098e-06	PRODHB:COMT:10 ARVCF:32 TRMT2A:62 RTNR4:102 TANGO2:251
WP_METHIONINE_METABOLISM_LEADING_TO_SULF	-0.3668945	11	2.514e-05	4.406e-03	BHMT:153 AHCVY:195 CSAD:494 CBS:621 MAT1A:666 GNMT:868
TESAR_ALK_TARGETS_EPISC_4D_UP	-0.3607690	2	7.719e-02	4.657e-01	MSX1:1679 PAX6:2478 NA NA NA NA
TESAR_ALK_AND_JAK_TARGETS_MOUSE_ES_D4_UP	-0.3607690	2	7.719e-02	4.657e-01	MSX1:1679 PAX6:2478 NA NA NA NA
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA	-0.3600579	6	2.255e-03	8.970e-02	HSPB1:301 AKR1B1:559 PGAM1:889 CTSB:2433 CALU:3489 OAT:4869
REACTOME_ABACAVIR_TRANSMEMBRANE_TRANSPOR	-0.3582866	4	1.307e-02	2.202e-01	ABCB1:209 SLC22A1:1671 SLC22A3:1984 SLC22A2:4595 NA NA
BIOCARTA_TERC_PATHWAY	-0.3541296	4	1.416e-02	2.294e-01	SP1:558 SP3:1257 NFYC:2399 RB1:4502 NA NA
RANKIN_ANGIOGENIC_TARGETS_OF_VHL_HIF2A_D	-0.3413519	6	3.782e-03	1.179e-01	VEGFA:446 ANGPTL3:882 PLXND1:1391 CDH5:2731 EGF17:3442 ITGAV:5318
WP_EICOSANOID_METABOLISM_VIA_CYTOCHROME_MANN_RESPONSE_TO_AMIFOSTINE_DN	-0.3398905	3	4.144e-02	3.647e-01	PPARA:715 EPHX2:1139 PPARG:5310 NA NA NA
CASTELLANO_HRAS_TARGETS_UP	-0.3392921	3	4.263e-02	3.682e-01	TWF1:908 BLMH:1352 PRKACB:1473 RRM2:2752 C6NB1:5482 NA
REACTOME_SARS_COV_2_MODULATES_AUTOPHAGY	0.3370961	10	2.231e-04	2.372e-02	VPS11:237 VPS16:578 VPS33B:1304 VPS45:1538 TUFM:2250 VPSA1:2824
WUNDER_INFILMATORY_RESPONSE_AND_CHOLEST	-0.3309688	7	2.425e-03	9.361e-02	ALB:80 ADIPOQ:770 CDKN1C:1457 CXCL9:1604 JCHAIN:2639 MPEG1:5451
REACTOME_HIGHLY_SODIUM_PERMEABLE_POSTSYN	0.3306169	7	2.451e-03	9.405e-02	CHRN2:42 CHRNA4:143 CHRN2:514 CHRNBA3:3111 CHRNA3:4299 CHRG:4724
REACTOME_DOPAMINE_CLEARANCE_FROM_THE_SYN	-0.3299747	4	2.227e-02	2.877e-01	COMT:10 SLC6A3:680 LRTOMT:2240 MAOA:7220 NA NA
CHEN_HOXA5_TARGETS_SHR_DN	-0.3289429	3	4.845e-02	3.841e-01	ZBED8:1791 NPTXR:2422 FXJ1:3450 NA NA NA
SASAI_TARGETS_OF_CXCR6_AND_PTCH1_DN	-0.3252589	7	2.890e-03	1.032e-01	TFPI:1300 MDK:1326 PIPSK1A:1926 OTX1:2352 APOD2:2436 ADAM28:3069
WU_HBX_TARGETS_3_DN	-0.3199754	10	4.586e-04	3.765e-02	IL6:430 TGFBI:994 GLG1:1289 GSTA4:1376 GAS6:1596 MAP2K2:1606
BIOCARTA_VOBEISITY_PATHWAY	-0.3127738	8	2.187e-03	8.809e-02	LPL:67 RXRA:229 ADIPOQ:770 TNF:1662 RETN:1845 HSD11B1:3473
REACTOME_CIPROFLOXACIN_ADME	-0.3123888	4	3.047e-02	3.219e-01	ALB:80 SLC01A2:681 SLC22A1:1671 SLC22A8:8754 NA NA
REACTOME_RUNX3_REGULATES_BCL2L11_BIM_TRA	-0.3116319	3	6.155e-02	4.237e-01	BCL2L1:585 FOXO3:3625 RUNX3:4215 NA NA NA
KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_D	-0.3027063	4	3.601e-02	3.437e-01	VPS35:1269 IGFBP2:2739 LCLAT1:3269 RB1:4502 NA NA
REACTOME_LEUKOTRIENE_RECEPTORS	0.3023814	5	1.919e-02	2.688e-01	LTB4R:329 CYSLTR2:855 LTBR4R2:1490 CYSLTR1:2852 GPR17:9372 NA
MIKELSEN_PLURIPOTENT_STATE_DN	-0.3023770	6	1.031e-02	1.967e-01	CASP8:191 CCND2:1127 TGFBR2:2348 CDK6:2438 JAK2:3096 CAMK2D:8492
REACTOME_ABACAVIR_ADME	-0.3009328	7	5.827e-03	1.482e-01	ABCB1:209 ADLAD:853 NT5C2:1106 SLC22A1:1671 SLC22A3:1984 SLC22A2:4595
CHOI_ATL_ACUTE_STAGE	-0.3008462	3	3.125e-02	4.532e-01	MET:668 ETV1:3177 MBD1:5074 NA NA NA
REACTOME_ACTIVATION_OF_THE_PHOTOTRANSDUC	-0.2979060	5	2.105e-02	2.840e-01	PDE6A:289 CNGA1:443 SAG:1604 RHO:4270 PDE6B:8648 NA
BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULO	-0.2974818	7	6.420e-03	1.549e-01	JAG1:993 MED13L:1282 TBX1:1600 NOTCH1:1701 PTPN11:3352 NOTCH2:3556
REACTOME_RUNX1_REGULATES_ESTROGEN_RECEPT	-0.2941700	4	4.158e-02	3.647e-01	AXIN1:380 GRAM:1197 RUNX1:3974 ESR1:8753 NA NA NA
REACTOME_PP2A_MODIFIED_DEPHOSPHORYLATION	0.2941187	4	4.161e-02	3.647e-01	PPP2R1B:1285 PPP2R5D:2209 MLXIPL:3436 PKFKB1:5540 NA NA
WP_COVID19_THROMBOTIC_AND_ANTIAGOAGULAT	-0.2939023	6	1.266e-02	2.193e-01	FGG:638 F13B:706 PLG:829 FGB:4689 F13A1:4776 F2:6811
REACTOME_SLPB_DEPENDENT_PROCESSING_OF_RE	-0.2910052	4	4.382e-02	3.724e-01	LSM10:1761 LSM11:3384 NCBP1:3576 SLPB:3750 NA NA
AMUNDSON_DNA_DAMAGE_RESPONSE_TP53	-0.2890986	11	8.998e-04	5.453e-02	MDM2:345 LIF:566 BTG2:1699 DDB2:1792 CTS2:2433 XPC:2925

DisGeNET Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Anemia, hereditary spherocytic hemolytic	-0.4941793	5	1.297e-04	4.956e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Spherocytosis	-0.4941793	5	1.297e-04	4.956e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Angiokeratoma	-0.4740601	3	4.457e-03	2.579e-01	MANBA:142 VEGFA:446 GLA:507 NA NA NA NA
Abnormality of cranial vault shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Abnormality of cranium shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Abnormality of head shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Asymmetry of head	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of cranial vault shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of cranium shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of head shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Aase Smith syndrome 2	-0.4099371	3	1.392e-02	3.404e-01	TSR2:1233 RPS10:1273 GATA1:1475 NA NA NA
Monilethrix	0.4092319	2	4.501e-02	4.695e-01	KRT80:954 DSG4:1826 NA NA NA NA
Maple Syrup Urine Disease, Thiamine Resp	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Classic Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Intermediate Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Intermittent Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Heritz Disease	0.4026420	5	1.820e-03	1.959e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 ITGA6:2330 NA
delta beta^alpha Thalassaemia	0.3967382	2	5.197e-02	4.927e-01	PSMB6:543 DSG4:1826 NA NA NA NA
Miller Fisher Syndrome	0.3954018	3	1.769e-02	3.684e-01	PSMB6:543 SMUG1:1645 DLL1:2826 NA NA NA
Junctional split	0.3951658	6	8.020e-04	1.289e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 ITGA6:2330
Desmoplastic infantile astrocytoma	-0.3921741	6	8.787e-04	1.367e-01	HDAC6:158 DIAPH2:411 LUF566 BRAF:2130 TP53:2991 PTPN11:3352
PAROXYSMAL EXTREME PAIN DISORDER	-0.3909838	5	2.464e-03	2.147e-01	SCN8A:735 SCN10A:766 SCN11A:1111 IDS:1200 MCF2L2:4195 NA
Progression of non-small cell lung lance	0.3900721	2	5.604e-02	4.970e-01	CCR7:1133 CD274:2251 NA NA NA NA
Sepsis of the newborn	-0.3898952	3	1.934e-02	3.809e-01	IL6:430 SRAC1:1490 ST14:2980 NA NA NA
Occipital myelomeningocele	-0.3893550	9	5.241e-05	3.022e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
22q11 partial monosomy syndrome	-0.3889745	11	7.942e-06	7.786e-03	COMT:10 ARVCF:32 UFD1:383 PIK4A:789 HIRA:1025 TBX1:1600
Bacterial sepsis of newborn	-0.3852926	2	5.912e-02	5.005e-01	IL6:430 ST14:2980 NA NA NA NA
Visually threatening diabetic retinopath	-0.3811640	4	8.285e-03	3.088e-01	VEGFA:446 TNF:1662 CXCL12:2465 LTA:2524 NA NA
EPIDERMOLYSIS BULLOSA_IJUNCTIONAL_LOCAL	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Adult junctional epidermolysis bullosa (0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Epidermolysis Bullosa Progressiva	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
JEB-I	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Palmar hyperhidrosis	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA</