

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa01100	Metabolic pathways	45/173	68/361	0.000632	0.033515046	0.03261643	B3GNT3/PLA2G10/PLA	45
hsa04360	Axon guidance	10/173	11/361	0.003533	0.062410924	0.060737543	SEMA4G/BNC1/EFNA1,	10
hsa05204	Chemical carcinogenesis	10/173	11/361	0.003533	0.062410924	0.060737543	CYP3A5/CYP2C18/UGT	10
hsa00980	Metabolism of xenobiotics by	9/173	10/361	0.006927	0.091783891	0.089322953	CYP3A/5AKR7A3/UGT1	9
hsa05206	MicroRNAs in cancer	8/173	11/361	0.085338	0.774334299	0.753572605	ERBB3/SERPINB5/EFNA	8
hsa04530	Tight junction	9/173	13/361	0.099298	0.774334299	0.753572605	MYH14/CGN/CLDN7/CI	9
hsa04151	PI3K-Akt signaling pathway	15/173	24/361	0.102271	0.774334299	0.753572605	ERBB3/CREB3L1/EFNA1	15
hsa04261	Adrenergic signaling in cardior	7/173	10/361	0.13651	0.904378514	0.880130034	CREB3L1/ATP1B1/TNN	7
hsa04970	Salivary secretion	7/173	11/361	0.226062	0.999831314	0.973023523	KCNN4/ATP1B1/MUC5	7
hsa04010	MAPK signaling pathway	10/173	17/361	0.250511	0.999831314	0.973023523	ERBB3/PLA2G4F/EFNA:	10
hsa05016	Huntington disease	6/173	10/361	0.324729	0.999831314	0.973023523	CREB3L1/GPX2/DNAH3	6
hsa05205	Proteoglycans in cancer	6/173	10/361	0.324729	0.999831314	0.973023523	ERBB3/ SHH/IHH/MET/	6
hsa01240	Biosynthesis of cofactors	7/173	12/361	0.329635	0.999831314	0.973023523	SDR16C5/BCO1/UGT1A	7
hsa05165	Human papillomavirus infectio	7/173	12/361	0.329635	0.999831314	0.973023523	CRB3/CREB3L1/ITGA3/	7
hsa04080	Neuroactive ligand-receptor ir	9/173	16/361	0.334689	0.999831314	0.973023523	GPR35/CHRNA5/HTR1E	9
hsa05022	Pathways of neurodegenerati	9/173	16/361	0.334689	0.999831314	0.973023523	GPX2/DNAH3/DKK4/ST	9
hsa05418	Fluid shear stress and atheros	6/173	11/361	0.443131	0.999831314	0.973023523	SDC1/GSTO2/MGST1/T	6
hsa05200	Pathways in cancer	11/173	22/361	0.506426	0.999831314	0.973023523	SHH/MET/SLC2A1/ITGA	11
hsa04510	Focal adhesion	5/173	10/361	0.572104	0.999831314	0.973023523	MET/ITGA3/LAMA3/ITC	5
hsa05166	Human T-cell leukemia virus 1	5/173	10/361	0.572104	0.999831314	0.973023523	CREB3L1/SLC2A1/MSX:	5
hsa04810	Regulation of actin cytoskelet	6/173	13/361	0.658091	0.999831314	0.973023523	MYH14/ITGA3/IQGAP3	6
hsa05202	Transcriptional misregulation i	6/173	13/361	0.658091	0.999831314	0.973023523	TMPRSS2/MET/H3C10/	6
hsa04064	NF-kappa B signaling pathway	5/173	11/361	0.679581	0.999831314	0.973023523	CCL4/TNF/BCL2/PTGS2	5
hsa05010	Alzheimer disease	5/173	11/361	0.679581	0.999831314	0.973023523	DKK4/COX6B2/TNF/PTC	5
hsa05034	Alcoholism	5/173	11/361	0.679581	0.999831314	0.973023523	CREB3L1/H3C10/H2BC:	5
hsa05164	Influenza A	5/173	11/361	0.679581	0.999831314	0.973023523	TMPRSS4/TMPRSS2/PR	5
hsa04014	Ras signaling pathway	7/173	16/361	0.723547	0.999831314	0.973023523	PLA2G10/PLA2G4F/EFN	7
hsa05130	Pathogenic Escherichia coli inf	7/173	16/361	0.723547	0.999831314	0.973023523	BAIAP2L1/MYH14/CLDI	7
hsa05163	Human cytomegalovirus infecti	6/173	15/361	0.813044	0.999831314	0.973023523	CREB3L1/CCL4/TNF/PT	6
hsa05322	Systemic lupus erythematosus	5/173	13/361	0.835727	0.999831314	0.973023523	H3C10/H2BC5/H2BC11	5
hsa04514	Cell adhesion molecules	6/173	16/361	0.866742	0.999831314	0.973023523	CLDN7/CLDN4/SDC1/C	6
hsa04015	Rap1 signaling pathway	7/173	19/361	0.891197	0.999831314	0.973023523	EFNA1/EPHA2/MET/EF	7

hsa04610	Complement and coagulation	3/173	10/361	0.931885	0.999831314	0.973023523	C4BPB/F3/F12	3
hsa04670	Leukocyte transendothelial mi	4/173	13/361	0.940838	0.999831314	0.973023523	CLDN7/CLDN4/CLDN18	4
hsa05020	Prion disease	4/173	13/361	0.940838	0.999831314	0.973023523	CREB3L1/COX6B2/TNF,	4
hsa05171	Coronavirus disease - COVID-15	173	16/361	0.949498	0.999831314	0.973023523	TMPRSS2/MMP1/ACE2	5
hsa04621	NOD-like receptor signaling p	3/173	11/361	0.958293	0.999831314	0.973023523	TNF/BCL2/PLCB2	3
hsa04666	Fc gamma R-mediated phagoc	3/173	11/361	0.958293	0.999831314	0.973023523	PLA2G4F/SCIN/NCF1	3
hsa05144	Malaria	3/173	12/361	0.974892	0.999831314	0.973023523	MET/SDC1/TNF	3
hsa04061	Viral protein interaction with	6/173	21/361	0.981638	0.999831314	0.973023523	IL22RA1/IL20RA/CCL15	6
hsa04640	Hematopoietic cell lineage	3/173	13/361	0.985108	0.999831314	0.973023523	ITGA3/TNF/CD22	3
hsa05140	Leishmaniasis	3/173	13/361	0.985108	0.999831314	0.973023523	TNF/PTGS2/NCF1	3
hsa05323	Rheumatoid arthritis	2/173	10/361	0.98609	0.999831314	0.973023523	MMP1/TNF	2
hsa05135	Yersinia infection	2/173	11/361	0.992267	0.999831314	0.973023523	BAIAP2/TNF	2
hsa05142	Chagas disease	2/173	11/361	0.992267	0.999831314	0.973023523	TNF/PLCB2	2
hsa04062	Chemokine signaling pathway	6/173	25/361	0.997123	0.999831314	0.973023523	CCL15/CCL4/PIK3R5/PL	6
hsa04380	Osteoclast differentiation	5/173	23/361	0.99817	0.999831314	0.973023523	FHL2/FOSL1/TNF/LILRB	5
hsa04662	B cell receptor signaling pathw	3/173	17/361	0.998366	0.999831314	0.973023523	CD22/LILRB3/PIK3AP1	3
hsa05150	Staphylococcus aureus infecti	2/173	14/361	0.998741	0.999831314	0.973023523	KRT18/KRT15	2
hsa04650	Natural killer cell mediated cy	2/173	15/361	0.999323	0.999831314	0.973023523	TNF/ULBP2	2
hsa05152	Tuberculosis	2/173	15/361	0.999323	0.999831314	0.973023523	TNF/BCL2	2
hsa04060	Cytokine-cytokine receptor int	7/173	33/361	0.999783	0.999831314	0.973023523	IL22RA1/IL20RA/CCL15	7
hsa04145	Phagosome	1/173	13/361	0.999831	0.999831314	0.973023523	NCF1	1