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Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles

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267	Long-term organoid culture of a small intestinal neuroendocrine tumor. 14,	O
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27	Network connectivity and local transcriptomic vulnerability underpin cortical atrophy progression in Parkinson disease.	O
26	Systematic Pan-cancer Functional Inference and Validation of Hyper, Hypo and Neomorphic Mutations.	O
25	Activation of the integrated stress response (ISR) pathways in response to Ref-1 inhibition in human pancreatic cancer and its tumor microenvironment. 10,	O
24	Perivascular localized cells commit erythropoiesis in PDGF-B-expressing solid tumors.	О
23	Identifying Key Genes and Related Molecules as Potential Biomarkers in Human Dilated Cardiomyopathy by Comprehensive Bioinformatics Analysis. 2023 , 8,	O
22	Apoe-knockout induces strong vascular oxidative stress and significant changes in the gene expression profile related to the pathways implicated in redox, inflammation, and endothelial function. 2023 , 108, 110696	O
21	Progranulin deficiency results in sex-dependent alterations in microglia in response to demyelination.	O
20	BCAT1 regulates glioblastoma cell plasticity and contributes to immunosuppression.	O
19	Topical GZ21T inhibits the growth of actinic keratoses in a UVB induced model of skin carcinogenesis. 2023 , 100206	O
18	A Novel Assessment of Metabolic Pathways in Peritoneal Metastases from Low-Grade Appendiceal Mucinous Neoplasms.	O
17	Methadone alters transcriptional programs associated with synapse formation in human cortical organoids. 2023 , 13,	O
16	An RNA Damage Response Network Mediates the Lethality of 5-FU in Clinically Relevant Tumor Types.	О
15	Protein interactome homeostasis through an N-recognin E3 ligase is a vulnerability in aneuploid cancer.	O
14	Glial progenitor heterogeneity and key regulators revealed by single-cell RNA sequencing provide insight to regeneration in spinal cord injury. 2023 , 42, 112486	O
13	DNA methylation, combined with RNA sequencing, provide novel insight into molecular classification of chordomas and their microenvironment.	O

12	Vaginal epithelial dysfunction is mediated by the microbiome, metabolome, and mTOR signaling. 2023 , 42, 112474	Ο
11	MetaTiME integrates single-cell gene expression to characterize the meta-components of the tumor immune microenvironment. 2023 , 14,	O
10	B cells require licensing by dendritic cells to serve as primary antigen-presenting cells for plasmid DNA. 2023 , 12,	O
9	Shared diagnostic genes and potential mechanism between PCOS and recurrent implantation failure revealed by integrated transcriptomic analysis and machine learning. 14,	O
8	The Glomerulus Multiomics Analysis Provides Deeper Insights into Diabetic Nephropathy.	0
7	Integration of Single-Cell RNA-Sequencing and Network Analysis to Investigate Mechanisms of Drug Resistance. 2023 , 85-94	O
6	Cell-type-specific nuclear morphology predicts genomic instability and prognosis in multiple cancer types.	0
5	Sample Preparation and Differential Gene Expression Analysis of Human Cancer Cell Lines by RNA Sequencing. 2023 , 23-41	O
4	LINC00426 is a potential immune phenotype-related biomarker and an overall survival predictor in PAM50 luminal B breast cancer. 14,	O
3	Implications of CRNDE in prognosis, tumor immunity, and therapeutic sensitivity in low grade glioma patients. 2023 , 23,	O
2	Identification of fatty acid-related subtypes, the establishment of a prognostic signature, and immune infiltration characteristics in lung adenocarcinoma.	0
1	Identification of Age-Related Characteristic Genes Involved in Severe COVID-19 Infection Among Elderly Patients using Machine Learning and Immune Cell Infiltration Analysis.	O