

CITATION REPORT

List of articles citing

NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data

DOI: 10.1038/nprot.2015.052
Nature Protocols, 2015, 10, 823-44.

Source: <https://exaly.com/paper-pdf/62320225/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
673	Microarray Meta-Analysis and Cross-Platform Normalization: Integrative Genomics for Robust Biomarker Discovery. 2015 , 4, 389-406		60
672	Comparative Study of Web-Based Gene Expression Analysis Tools for Biomarkers Identification. 2015 , 214-222		
671	Mitochondrial Citrate Transporter-dependent Metabolic Signature in the 22q11.2 Deletion Syndrome. 2015 , 290, 23240-53		34
670	Antimicrobial peptide LL-37 participates in the transcriptional regulation of melanoma cells. 2016 , 7, 2341-2345		12
669	Gene Expression Profile in Patients with Axial Spondyloarthritis: Meta-analysis of Publicly Accessible Microarray Datasets. 2016 , 23, 363		7
668	The Effects of Ivermectin on <i>Brugia malayi</i> Females In Vitro: A Transcriptomic Approach. 2016 , 10, e0004929		17
667	Transcriptome Profiling Reveals Disruption of Innate Immunity in Chronic Heavy Ethanol Consuming Female Rhesus Macaques. 2016 , 11, e0159295		17
666	Computational challenges in modeling gene regulatory events. 2016 , 7, 188-195		6
665	The Clathrin-dependent Spindle Proteome. 2016 , 15, 2537-53		7
664	Unique gene expression profile in osteoarthritis synovium compared with cartilage: analysis of publicly accessible microarray datasets. 2016 , 36, 819-27		9
663	The immunology of host defence peptides: beyond antimicrobial activity. 2016 , 16, 321-34		477
662	Using biological networks to integrate, visualize and analyze genomics data. 2016 , 48, 27		39
661	Profiling the macrofilaricidal effects of flubendazole on adult female <i>Brugia malayi</i> using RNAseq. 2016 , 6, 288-296		11
660	Functional and Proteomic Investigations Reveal Major Royal Jelly Protein 1 Associated with Anti-hypertension Activity in Mouse Vascular Smooth Muscle Cells. 2016 , 6, 30230		27
659	Transcriptome meta-analysis of three follicular compartments and its correlation with ovarian follicle maturity and oocyte developmental competence in cows. 2016 , 48, 633-43		16
658	AllerGen 8th research conference. 2016 , 12,		78
657	Autoimmune Regulator (AIRE) Is Expressed in Spermatogenic Cells, and It Altered the Expression of Several Nucleic-Acid-Binding and Cytoskeletal Proteins in Germ Cell 1 Spermatogonial (GC1-spg) Cells. 2016 , 15, 2686-98		5

656	miRNet - dissecting miRNA-target interactions and functional associations through network-based visual analysis. 2016 , 44, W135-41	265
655	Bioinformatics-Driven New Immune Target Discovery in Disease. 2016 , 84, 130-6	1
654	Comparative proteomic profiling of Hodgkin lymphoma cell lines. 2016 , 12, 219-32	7
653	Transcriptomics and Gene Regulation. 2016 ,	1
652	An overview of bioinformatics methods for modeling biological pathways in yeast. 2016 , 15, 95-108	13
651	Tumor-induced Stromal STAT1 Accelerates Breast Cancer via Deregulating Tissue Homeostasis. 2017 , 15, 585-597	9
650	GAD1 Upregulation Programs Aggressive Features of Cancer Cell Metabolism in the Brain Metastatic Microenvironment. 2017 , 77, 2844-2856	20
649	PEGylation of a TLR2-agonist-based vaccine delivery system improves antigen trafficking and the magnitude of ensuing antibody and CD8 T cell responses. 2017 , 137, 61-72	25
648	Exploiting induced pluripotent stem cell-derived macrophages to unravel host factors influencing Chlamydia trachomatis pathogenesis. 2017 , 8, 15013	36
647	MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. 2017 , 45, W180-W188	706
646	Inflammation related genes are upregulated in surgical margins of advanced stage oral squamous cell carcinoma. 2017 , 7, 193-197	5
645	Molecular indicators of stress-induced neuroinflammation in a mouse model simulating features of post-traumatic stress disorder. 2017 , 7, e1135	32
644	STAT3 and NF- κ B are Simultaneously Suppressed in Dendritic Cells in Lung Cancer. 2017 , 7, 45395	20
643	A Rough Based Hybrid Binary PSO Algorithm for Flat Feature Selection and Classification in Gene Expression Data. 2017 , 4, 341-360	8
642	Cross platform analysis of transcriptomic data identifies ageing has distinct and opposite effects on tendon in males and females. 2017 , 7, 14443	13
641	Molecular mechanisms underlying gliomas and glioblastoma pathogenesis revealed by bioinformatics analysis of microarray data. 2017 , 34, 182	31
640	Mechanisms of the Innate Defense Regulator Peptide-1002 Anti-Inflammatory Activity in a Sterile Inflammation Mouse Model. 2017 , 199, 3592-3603	33
639	Gene expression associated with suicide attempts in US veterans. 2017 , 7, e1226	14

638	Dysregulation of Notch signaling related genes in oral lichen planus. 2017 , 7, 666-669	1
637	Transcriptional profiles for distinct aggregation states of mutant Huntingtin exon 1 protein unmask new Huntington's disease pathways. 2017 , 83, 103-112	15
636	Accumulation of Chromatin Remodelling Enzyme and Histone Transcripts in Bovine Oocytes. 2017 , 63, 223-255	9
635	An IRF-3-, IRF-5-, and IRF-7-Independent Pathway of Dengue Viral Resistance Utilizes IRF-1 to Stimulate Type I and II Interferon Responses. 2017 , 21, 1600-1612	32
634	Profiling conserved biological pathways in Autosomal Dominant Polycystic Kidney Disorder (ADPKD) to elucidate key transcriptomic alterations regulating cystogenesis: A cross-species meta-analysis approach. 2017 , 627, 434-450	8
633	Dynamic changes in murine forebrain miR-211 expression associate with cholinergic imbalances and epileptiform activity. 2017 , 114, E4996-E5005	33
632	Combined GWAS and 'guilt by association'-based prioritization analysis identifies functional candidate genes for body size in sheep. 2017 , 49, 41	43
631	NFPscanner: a webtool for knowledge-based deciphering of biomedical networks. 2017 , 18, 262	
630	The timeline of corona formation around silica nanocarriers highlights the role of the protein interactome. 2017 , 9, 1840-1851	45
629	Systematic assessment of cervical cancer initiation and progression uncovers genetic panels for deep learning-based early diagnosis and proposes novel diagnostic and prognostic biomarkers. 2017 , 8, 109436-109456	25
628	Equine skeletal muscle adaptations to exercise and training: evidence of differential regulation of autophagosomal and mitochondrial components. 2017 , 18, 595	16
627	Network Analysis of the Systemic Response to Infection in Sheep Reveals Changes in Fibrosis, Apoptosis, Toll-Like Receptors 3/4, and B Cell Function. 2017 , 8, 485	9
626	RNA-Sequencing Analysis Reveals a Regulatory Role for Transcription Factor in the Mature Motor Cortex. 2017 , 10, 283	5
625	Identification and validation of a 44-gene expression signature for the classification of renal cell carcinomas. 2017 , 36, 176	12
624	Oncogenic Protein Kinase D3 Regulating Networks in Invasive Breast Cancer. 2017 , 13, 748-758	12
623	A 16-gene signature predicting prognosis of patients with oral tongue squamous cell carcinoma. 2017 , 5, e4062	15
622	Suppression of dsRNA response genes and innate immunity following Oct4, Stella, and Nanos2 overexpression in mouse embryonic fibroblasts. 2018 , 106, 1-11	5
621	From gene networks to drugs: systems pharmacology approaches for AUD. 2018 , 235, 1635-1662	11

620	Gene Expression Analysis in Human Peripheral Blood Cells after 900 MHz RF-EMF Short-Term Exposure. 2018 , 189, 529-540	5
619	A novel long non-coding RNA Myolinc regulates myogenesis through TDP-43 and Filip1. 2018 , 10, 102-117	38
618	Follicle capacitation: a meta-analysis to investigate the transcriptome dynamics following follicle-stimulating hormone decline in bovine granulosa cells. 2018 , 99, 877-887	6
617	The PPI network analysis of mRNA expression profile of uterus from primary dysmenorrheal rats. 2018 , 8, 351	5
616	Transcriptional profiling of primary endometrial epithelial cells following acute HIV-1 exposure reveals gene signatures related to innate immunity. 2018 , 79, e12822	2
615	The Orphan Nuclear Receptor Liver Homolog Receptor-1 (Nr5a2) Regulates Ovarian Granulosa Cell Proliferation. 2018 , 2, 24-41	22
614	Network-based technologies for early drug discovery. 2018 , 23, 626-635	39
613	Host Transcription Profile in Nasal Epithelium and Whole Blood of Hospitalized Children Under 2 Years of Age With Respiratory Syncytial Virus Infection. 2017 , 217, 134-146	23
612	Meta-analysis of human gene expression in response to Mycobacterium tuberculosis infection reveals potential therapeutic targets. 2018 , 12, 3	35
611	Epigenome-wide DNA methylation profiling of periprostatic adipose tissue in prostate cancer patients with excess adiposity-a pilot study. 2018 , 10, 54	12
610	Identifying condition-specific modules by clustering multiple networks. 2017 ,	14
609	The senescence-associated secretory phenotype is potentiated by feedforward regulatory mechanisms involving Zscan4 and TAK1. 2018 , 9, 1723	58
608	Transcriptome Network Analysis Reveals Aging-Related Mitochondrial and Proteasomal Dysfunction and Immune Activation in Human Thyroid. 2018 , 28, 656-666	15
607	Differential expression analysis of JAK/STAT pathway related genes in breast cancer. 2018 , 16, 122-129	3
606	Pre-operative progesterone benefits operable breast cancer patients by modulating surgical stress. 2018 , 170, 431-438	7
605	Cholangiocarcinoma-associated genes identified by integrative analysis of gene expression data. 2018 , 17, 5744-5753	6
604	Extracting Stage-Specific and Dynamic Modules Through Analyzing Multiple Networks Associated with Cancer Progression. 2018 , 15, 647-658	18
603	The Key Genes of Chronic Pancreatitis which Bridge Chronic Pancreatitis and Pancreatic Cancer Can be Therapeutic Targets. 2018 , 24, 215-222	2

602	Identification of differentially expressed genes regulated by molecular signature in breast cancer-associated fibroblasts by bioinformatics analysis. 2018 , 297, 161-183	7
601	Differential expression of genes in fetal brain as a consequence of maternal protein deficiency and nematode infection. 2018 , 48, 51-58	7
600	Medroxyprogesterone acetate-treated human, primary endometrial epithelial cells reveal unique gene expression signature linked to innate immunity and HIV-1 susceptibility. 2018 , 79, e12781	7
599	NK-lysin from <i>Oreochromis niloticus</i> improves antimicrobial defence against bacterial pathogens. 2018 , 72, 259-265	26
598	Global Transcriptome Sequencing Reveals Molecular Profiles of Summer Diapause Induction Stage of Onion Maggot, (Diptera: Anthomyiidae). 2018 , 8, 207-217	23
597	TAK1 regulates skeletal muscle mass and mitochondrial function. 2018 , 3,	25
596	Bayesian Modeling Approaches for Temporal Dynamics in RNA-seq Data. 2018 ,	2
595	Computational Cell Biology. 2018 ,	
594	Biosafety of Mesoporous Silica Nanoparticles. 2018 , 3,	8
593	Unified Transcriptomic Signature of Arbuscular Mycorrhiza Colonization in Roots of by Integration of Machine Learning, Promoter Analysis, and Direct Merging Meta-Analysis. 2018 , 9, 1550	12
592	miRNet-Functional Analysis and Visual Exploration of miRNA-Target Interactions in a Network Context. 2018 , 1819, 215-233	95
591	Bovine Neonatal Monocytes Display Phenotypic Differences Compared With Adults After Challenge With the Infectious Abortifacient Agent. 2018 , 9, 3011	5
590	Biological links in periodontitis and rheumatoid arthritis: Discovery via text-mining PubMed abstracts. 2019 , 54, 318-328	3
589	Fold change based approach for identification of significant network markers in breast, lung and prostate cancer. 2018 , 12, 213-218	4
588	Honey bee Royalactin unlocks conserved pluripotency pathway in mammals. 2018 , 9, 5078	13
587	Genetic basis of thermal plasticity variation in <i>Drosophila melanogaster</i> body size. 2018 , 14, e1007686	24
586	Integrative Omics for Interactomes. 2018 , 39-49	1
585	Synthetic Biology. 2018 ,	

584	Gene expression changes in human iPSC-derived cardiomyocytes after X-ray irradiation. 2018 , 94, 1095-1103	6
583	Genome-Wide Transcriptomic Analysis Reveals Insights into the Response to (CBCVd) in Hop (L.). 2018 , 10,	17
582	Transcriptional Regulation of Lipophorin Receptors Supports Neuronal Adaptation to Chronic Elevations of Activity. 2018 , 25, 1181-1192.e4	7
581	Integrated bioinformatic analysis of microarray data reveals shared gene signature between MDS and AML. 2018 , 16, 5147-5159	5
580	Identification of target gene and prognostic evaluation for lung adenocarcinoma using gene expression meta-analysis, network analysis and neural network algorithms. 2018 , 86, 120-134	38
579	The NFB subunit RELA is a master transcriptional regulator of the committed epithelial-mesenchymal transition in airway epithelial cells. 2018 , 293, 16528-16545	28
578	Photodynamic therapy corrects abnormal cancer-associated gene expression observed in actinic keratosis lesions and induces a remodeling effect in photodamaged skin. 2018 ,	5
577	Impact of Ionizing Radiation on Electrophysiological Behavior of Human-induced Ipsc-derived Cardiomyocytes on Multielectrode Arrays. 2018 , 115, 21-28	7
576	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. 2018 , 46, W486-W494	2157
575	Retinoic acid elicits a coordinated expression of gut homing markers on T lymphocytes of Zambian men receiving oral Vivotif, but not Rotarix, Dukoral or OPVERO vaccines. 2018 , 36, 4134-4141	4
574	Time- and polarity-dependent proteomic changes associated with homeostatic scaling at central synapses. 2018 , 7,	33
573	Transcriptome analysis identifies the potential roles of long non-coding RNAs during parainfluenza virus infection. 2018 , 592, 2444-2457	2
572	In vitro characterization of neonatal, juvenile, and adult porcine islet oxygen demand, Ecell function, and transcriptomes. 2018 , 25, e12432	14
571	Precision Medicine for Neonatal Sepsis. 2018 , 5, 70	25
570	Bioinformatics analysis of gene expression profiles to diagnose crucial and novel genes in glioblastoma multiform. 2018 , 214, 1395-1461	5
569	Identification of Shared Molecular Signatures Indicate the Susceptibility of Endometriosis to Multiple Sclerosis. 2018 , 9, 42	12
568	Cerebrospinal Fluid Concentrations of Neuronal Proteins Are Reduced in Primary Angiitis of the Central Nervous System. 2018 , 9, 407	10
567	A common molecular signature of patients with sickle cell disease revealed by microarray meta-analysis and a genome-wide association study. 2018 , 13, e0199461	8

566	Identification of hub genes with prognostic values in gastric cancer by bioinformatics analysis. 2018 , 16, 114	41
565	A coding and non-coding transcriptomic perspective on the genomics of human metabolic disease. 2018 , 46, 7772-7792	22
564	Structure Optimization for Large Gene Networks Based on Greedy Strategy. 2018 , 2018, 9674108	6
563	Systematic bioinformatic approaches reveal novel gene expression signatures associated with acquired resistance to EGFR targeted therapy in lung cancer. 2018 , 667, 62-69	6
562	LYL1 gene amplification predicts poor survival of patients with uterine corpus endometrial carcinoma: analysis of the Cancer genome atlas data. 2018 , 18, 494	6
561	Time-course transcriptome analysis of medullary thymic epithelial cells in the early phase of thymic involution. 2018 , 99, 87-94	10
560	Distinctive Roles for Type I and Type II Interferons and Interferon Regulatory Factors in the Host Cell Defense against Varicella-Zoster Virus. 2018 , 92,	21
559	Analysis of Gene Expression Changes in PHA-M Stimulated Lymphocytes - Unraveling PHA Activity as Prerequisite for Dicentric Chromosome Analysis. 2018 , 189, 579-596	2
558	Effect of heifer age on the granulosa cell transcriptome after ovarian stimulation. 2018 , 30, 980-990	3
557	OmicsNet: a web-based tool for creation and visual analysis of biological networks in 3D space. 2018 , 46, W514-W522	78
556	Comprehensive meta-analysis and co-expression network analysis identify candidate genes for salt stress response in Arabidopsis. 2019 , 153, 367-377	4
555	DNA Methylation Changes in Lung Immune Cells Are Associated with Granulomatous Lung Disease. 2019 , 60, 96-105	15
554	The metastatic microenvironment: Melanoma-microglia cross-talk promotes the malignant phenotype of melanoma cells. 2019 , 144, 802-817	21
553	Characterization of the prognostic values of the family in gastric cancer. 2019 , 12, 1756284819858507	14
552	Identification of CXCL13 as a potential biomarker in clear cell renal cell carcinoma via comprehensive bioinformatics analysis. 2019 , 118, 109264	18
551	Characteristic genes in THP-1 derived macrophages infected with Mycobacterium tuberculosis H37Rv strain identified by integrating bioinformatics methods. 2019 , 44, 1243-1254	5
550	Shared gene signature between pterygium and meibomian gland dysfunction uncovered through gene-expression meta-analysis. 2019 , 83, 397-404	
549	Dynamic Quantum Proxy Blind Signature Scheme with Cluster State. 2019 ,	

548	BRCA2 abrogation triggers innate immune responses potentiated by treatment with PARP inhibitors. 2019 , 10, 3143	75
547	The influence of depression on ovarian cancer: Discovering molecular pathways that identify novel biomarkers and therapeutic targets. 2019 , 16, 100207	13
546	Detection of multiple sclerosis using blood and brain cells transcript profiles: Insights from comprehensive bioinformatics approach. 2019 , 16, 100201	12
545	Salivary Flow Alteration in Patients Undergoing Treatment for Schizophrenia: Disease-Drug-Target Gene/Protein Association Study for Side-effects. 2019 , 9, 286-293	2
544	Therapeutic Targeting of Casein Kinase 1 β in an Alzheimer's Disease Mouse Model. 2019 , 18, 3383-3393	15
543	OMICs approaches-assisted identification of macrophages-derived MIP-1 β s the therapeutic target of botanical products TNTL in diabetic retinopathy. 2019 , 17, 81	6
542	Genetic Associations between Voltage-Gated Calcium Channels and Psychiatric Disorders. 2019 , 20,	29
541	Identification and Interaction Analysis of Key Genes and MicroRNAs in Systemic Sclerosis by Bioinformatics Approaches. 2019 , 39, 645-652	6
540	HOXA10 induces BCL2 expression, inhibits apoptosis, and promotes cell proliferation in gastric cancer. 2019 , 8, 5651-5661	22
539	Gene expression signature of atypical breast hyperplasia and regulation by SFRP1. 2019 , 21, 76	5
538	Leveraging the Role of the Metastatic Associated Protein Anterior Gradient Homologue 2 in Unfolded Protein Degradation: A Novel Therapeutic Biomarker for Cancer. 2019 , 11,	2
537	STAT3 induces G9a to exacerbate HER3 expression for the survival of epidermal growth factor receptor-tyrosine kinase inhibitors in lung cancers. 2019 , 19, 959	8
536	Distinct molecular etiologies of male and female hepatocellular carcinoma. 2019 , 19, 951	25
535	Drug repositioning and biomarkers in low-grade glioma via bioinformatics approach. 2019 , 17, 100250	5
534	G-quadruplexes Sequester Free Heme in Living Cells. 2019 , 26, 1681-1691.e5	35
533	Meta-Analysis of Gene Expression Changes in the Blood of Patients with Mild Cognitive Impairment and Alzheimer's Disease Dementia. 2019 , 20,	15
532	Assessing the Impact of Sample Heterogeneity on Transcriptome Analysis of Human Diseases Using MDP Webtool. 2019 , 10, 971	9
531	Target Genes of Autism Risk Loci in Brain Frontal Cortex. 2019 , 10, 707	8

530	STAT3 operates as a novel transcription factor that regulates NEDD4 in Keloid. 2019 , 518, 638-643	3
529	Identification and interaction analysis of key miRNAs in medullary thyroid carcinoma by bioinformatics analysis. 2019 , 20, 2316-2324	4
528	Identification of Transcriptional Markers and microRNA-mRNA Regulatory Networks in Colon Cancer by Integrative Analysis of mRNA and microRNA Expression Profiles in Colon Tumor Stroma. 2019 , 8,	14
527	Network-based approach to identify key candidate genes and pathways shared by thyroid cancer and chronic kidney disease. 2019 , 16, 100240	13
526	iPSC-Derived Embryoid Bodies as Models of c-Mutated Hereditary Papillary Renal Cell Carcinoma. 2019 , 20,	11
525	Genome-wide association study on antipsychotic-induced weight gain in Europeans and African-Americans. 2019 , 212, 204-212	5
524	P2Y2 purinergic receptor modulates virus yield, calcium homeostasis, and cell motility in human cytomegalovirus-infected cells. 2019 , 116, 18971-18982	10
523	Computational identification of key genes that may regulate gene expression reprogramming in Alzheimer's patients. 2019 , 14, e0222921	15
522	Temporal dynamics in meta longitudinal RNA-Seq data. 2019 , 9, 763	1
521	Integrative Analyses of Genes Associated with Subcutaneous Insulin Resistance. 2019 , 9,	8
520	EcoToxChip: A next-generation toxicogenomics tool for chemical prioritization and environmental management. 2019 , 38, 279-288	26
519	An Integrative Data Mining and Omics-Based Translational Model for the Identification and Validation of Oncogenic Biomarkers of Pancreatic Cancer. 2019 , 11,	21
518	VCAN Canonical Splice Site Mutation is Associated With Vitreoretinal Degeneration and Disrupts an MMP Proteolytic Site. 2019 , 60, 282-293	7
517	High-Throughput Omics and Statistical Learning Integration for the Discovery and Validation of Novel Diagnostic Signatures in Colorectal Cancer. 2019 , 20,	20
516	Jagged1 promotes mineralization in human bone-derived cells. 2019 , 99, 134-140	12
515	First step toward gene expression data integration: transcriptomic data acquisition with COMMAND>_. 2019 , 20, 54	5
514	Identification of molecular signatures and pathways common to blood cells and brain tissue of amyotrophic lateral sclerosis patients. 2019 , 16, 100193	15
513	The State of the Art in Multilayer Network Visualization. 2019 , 38, 125-149	25

512	Systematic profiling identifies PDLIM2 as a novel prognostic predictor for oesophageal squamous cell carcinoma (ESCC). 2019 , 23, 5751-5761	8
511	A Novel Set of WNT Pathway Effectors as a Predictive Marker of Uterine Corpus Endometrial Carcinoma-Study Based on Weighted Co-expression Matrices. 2019 , 9, 360	2
510	LC-MS/MS analysis and network pharmacology of Trigonella foenum-graecum - A plant from Ayurveda against hyperlipidemia and hyperglycemia with combination synergy. 2019 , 60, 152944	29
509	Oxygen Regulates Human Pluripotent Stem Cell Metabolic Flux. 2019 , 2019, 8195614	13
508	Key candidate genes associated with BRAF in papillary thyroid carcinoma on microarray analysis. 2019 , 234, 23369-23378	10
507	Discovering Biomarkers and Pathways Shared by Alzheimer's Disease and Ischemic Stroke to Identify Novel Therapeutic Targets. 2019 , 55,	18
506	Identification of Transcriptional Signatures of Colon Tumor Stroma by a Meta-Analysis. 2019 , 2019, 8752862	15
505	Meta-analysis of mammary RNA seq datasets reveals the molecular understanding of bovine lactation biology. 2019 , 62, 489-501	4
504	Integrated proteomics and metabolomics analysis reveals differential lipid metabolism in human umbilical vein endothelial cells under high and low shear stress. 2019 , 317, C326-C338	10
503	TET1 contributes to allergic airway inflammation and regulates interferon and aryl hydrocarbon receptor signaling pathways in bronchial epithelial cells. 2019 , 9, 7361	19
502	Molecular alterations induced by Yersinia pestis, dengue virus and Staphylococcal enterotoxin B under severe stress. 2019 , 80, 725-741	2
501	Galectin-3, a novel endogenous TREM2 ligand, detrimentally regulates inflammatory response in Alzheimer's disease. 2019 , 138, 251-273	91
500	Metabolomic and Transcriptional Analyses Reveal Atmospheric Oxygen During Human Induced Pluripotent Stem Cell Generation Impairs Metabolic Reprogramming. 2019 , 37, 1042-1056	8
499	NR4A3 fusion proteins trigger an axon guidance switch that marks the difference between EWSR1 and TAF15 translocated extraskeletal myxoid chondrosarcomas. 2019 , 249, 90-101	13
498	Maternal Gastrointestinal Nematode Infection Up-regulates Expression of Genes Associated with Long-Term Potentiation in Perinatal Brains of Uninfected Developing Pups. 2019 , 9, 4165	3
497	Investigation into the underlying molecular mechanisms of non-small cell lung cancer using bioinformatics analysis. 2019 , 15, 100394	2
496	Gene expression profiling meta-analysis reveals novel gene signatures and pathways shared between tuberculosis and rheumatoid arthritis. 2019 , 14, e0213470	13
495	Dynamic molecular changes during the first week of human life follow a robust developmental trajectory. 2019 , 10, 1092	79

494	A Systematic Workflow for Design and Computational Analysis of Protein Microarrays. 2019 , 213-222	1
493	Mining Featured Biomarkers Linked with Epithelial Ovarian CancerBased on Bioinformatics. 2019 , 9,	1
492	NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. 2019 , 47, W234-W241	491
491	Spatial and Temporal Mapping of Human Innate Lymphoid Cells Reveals Elements of Tissue Specificity. 2019 , 50, 505-519.e4	91
490	Identifying novel biomarkers in hepatocellular carcinoma by weighted gene co-expression network analysis. 2019 , 120, 11418	26
489	Mining conditions specific hub genes from RNA-Seq gene-expression data via biclustering and their application to drug discovery. 2019 , 13, 194-203	6
488	Irradiated Human Fibroblasts as a Substitute Feeder Layer to Irradiated Mouse 3T3 for the Culture of Human Corneal Epithelial Cells: Impact on the Stability of the Transcription Factors Sp1 and NFI. 2019 , 20,	2
487	Transcriptomic and Network Analysis Highlight the Association of Diabetes at Different Stages of Alzheimer's Disease. 2019 , 13, 1273	18
486	Nucleated Red Blood Cells Contribute to the Host Immune Response Against Pathogens. 2019 ,	2
485	Lithium alters expression of RNAs in a type-specific manner in differentiated human neuroblastoma neuronal cultures, including specific genes involved in Alzheimer's disease. 2019 , 9, 18261	9
484	IL-17A is functionally relevant and a potential therapeutic target in bullous pemphigoid. 2019 , 96, 104-112	39
483	Network-based approach to identify molecular signatures and therapeutic agents in Alzheimer's disease. 2019 , 78, 431-439	66
482	Using OmicsNet for Network Integration and 3D Visualization. 2019 , 65, e69	27
481	Not only cancer: the long non-coding RNA MALAT1 affects the repertoire of alternatively spliced transcripts and circular RNAs in multiple sclerosis. 2019 , 28, 1414-1428	31
480	Chorioamnionitis exposure remodels the unique histone modification landscape of neonatal monocytes and alters the expression of immune pathway genes. 2019 , 286, 82-109	7
479	PPIExp: A Web-Based Platform for Integration and Visualization of Protein-Protein Interaction Data and Spatiotemporal Proteomics Data. 2019 , 18, 633-641	3
478	Integrative meta-analysis of publically available microarray datasets of several epithelial cell lines identifies biological processes affected by silver nanoparticles exposure. 2019 , 216, 67-74	2
477	Long non-coding RNAs influence the transcriptome in pulmonary arterial hypertension: the role of PAXIP1-AS1. 2019 , 247, 357-370	26

476	Environmental Control of Astrocyte Pathogenic Activities in CNS Inflammation. 2019 , 176, 581-596.e18	74
475	Efficacy of Integrating a Novel 16-Gene Biomarker Panel and Intelligence Classifiers for Differential Diagnosis of Rheumatoid Arthritis and Osteoarthritis. 2019 , 8,	17
474	The Potential Mechanism of Bufadienolide-Like Chemicals on Breast Cancer via Bioinformatics Analysis. 2019 , 11,	3
473	Deduction of Novel Genes Potentially Involved in Keratinocytes of Type 2 Diabetes Using Next-Generation Sequencing and Bioinformatics Approaches. 2019 , 8,	6
472	The human placental proteome secreted into the maternal and fetal circulations in normal pregnancy based on 4-vessel sampling. 2019 , 33, 2944-2956	15
471	Genes interconnecting AMPK and TREM-1 and associated microRNAs in rotator cuff tendon injury. 2019 , 454, 97-109	9
470	MetaOmics: analysis pipeline and browser-based software suite for transcriptomic meta-analysis. 2019 , 35, 1597-1599	14
469	Polygenic analysis suggests the involvement of calcium signaling in executive function in schizophrenia patients. 2020 , 270, 425-431	3
468	Perimatrix of middle ear cholesteatoma: A granulation tissue with a specific transcriptomic signature. 2020 , 130, E220-E227	4
467	LEF1 supports metastatic brain colonization by regulating glutathione metabolism and increasing ROS resistance in breast cancer. 2020 , 146, 3170-3183	8
466	Identification of molecular signatures and pathways to identify novel therapeutic targets in Alzheimer's disease: Insights from a systems biomedicine perspective. 2020 , 112, 1290-1299	55
465	Bioinformatics identification of key candidate genes and pathways associated with systemic lupus erythematosus. 2020 , 39, 425-434	11
464	Identification of Acute Pancreatitis-Related Genes and Pathways by Integrated Bioinformatics Analysis. 2020 , 65, 1720-1732	3
463	Adaptive Sparse Estimation With Side Information. 2020 , 115, 2053-2067	2
462	The Potential Role of Claudins in Regulation of Metastasis and Development of Drug Resistance in Breast Cancer. 2020 , 7, 25-43	
461	Effects of left ventricular assist device on heart failure patients: A bioinformatics analysis. 2020 , 44, 577-583	3
460	Integrated Microarray and RNAseq Transcriptomic Analysis of Retinal Pigment Epithelium/Choroid in Age-Related Macular Degeneration. 2020 , 8, 808	5
459	Integrative Analyses of Genes Associated with Fulminant Type 1 Diabetes. 2020 , 2020, 1025857	3

458	Comprehensive Analysis of RNA-Seq Gene Expression Profiling of Brain Transcriptomes Reveals Novel Genes, Regulators, and Pathways in Autism Spectrum Disorder. 2020 , 10,	16
457	Fisetin inhibits proliferation of pancreatic adenocarcinoma by inducing DNA damage via RFXAP/KDM4A-dependent histone H3K36 demethylation. 2020 , 11, 893	17
456	Integrative analyses of biomarkers and pathways for adipose tissue after bariatric surgery. 2020 , 9, 384-400	7
455	SLC12A2 variants cause a neurodevelopmental disorder or cochleovestibular defect. 2020 , 143, 2380-2387	15
454	Rhinovirus Infection Drives Complex Host Airway Molecular Responses in Children With Cystic Fibrosis. 2020 , 11, 1327	6
453	Prediction of biomarker signatures and therapeutic agents from blood sample against Pancreatic Ductal Adenocarcinoma (PDAC): A network-based study. 2020 , 19, 100346	0
452	Identification of vital regulatory genes with network pathways among Huntington's, Parkinson's, and Alzheimer's diseases. 2020 , 9, 1	2
451	Transcriptomic profiling of adipose tissue inflammation, remodeling, and lipid metabolism in periparturient dairy cows (<i>Bos taurus</i>). 2020 , 21, 824	4
450	Identification and Validation of MSX1 as a Key Candidate for Progesterin Resistance in Endometrial Cancer. 2020 , 13, 11669-11688	5
449	Transcriptome of Two Canine Prostate Cancer Cells Treated With Toseranib Phosphate Reveals Distinct Antitumor Profiles Associated With the PDGFR Pathway. 2020 , 7, 561212	4
448	Genome-wide association study to identify genomic regions and positional candidate genes associated with male fertility in beef cattle. 2020 , 10, 20102	8
447	Morphing projections: a new visual technique for fast and interactive large-scale analysis of biomedical datasets. 2021 , 37, 1571-1580	0
446	A machine learning approach identified a diagnostic model for pancreatic cancer through using circulating microRNA signatures. 2020 , 20, 1195-1204	14
445	Integrated Bioinformatics Analysis Identifies ELAVL1 and APP as Candidate Crucial Genes for Crohn's Disease. 2020 , 2020, 3067273	4
444	Systems Biology Approaches to Understanding the Human Immune System. 2020 , 11, 1683	6
443	Integrated PPI- and WGCNA-Retrieval of Hub Gene Signatures Shared Between Barrett's Esophagus and Esophageal Adenocarcinoma. 2020 , 11, 881	27
442	Identification of biomarkers associated with extracellular vesicles based on an integrative pan-cancer bioinformatics analysis. 2020 , 37, 79	1
441	Transcriptome analysis of basic fibroblast growth factor treated stem cells isolated from human exfoliated deciduous teeth. 2020 , 6, e04246	3

440	Identifying functionally relevant candidate genes for inflexible ethanol intake in mice and humans using a guilt-by-association approach. 2020 , 10, e01879	2
439	IFN- Mediates the Development of Systemic Lupus Erythematosus. 2020 , 2020, 7176515	7
438	Multi-omic studies on missense PLG variants in families with otitis media. 2020 , 10, 15035	2
437	Comprehensive analysis of key genes associated with ceRNA networks in nasopharyngeal carcinoma based on bioinformatics analysis. 2020 , 20, 408	4
436	MDA-MB-231 Breast Cancer Cells Resistant to Pleurocidin-Family Lytic Peptides Are Chemosensitive and Exhibit Reduced Tumor-Forming Capacity. 2020 , 10,	2
435	Genome Wide Analysis Points towards Subtype-Specific Diseases in Different Genetic Forms of Amyotrophic Lateral Sclerosis. 2020 , 21,	2
434	A meta-analysis of microRNA networks regulated by melatonin in cancer: Portrait of potential candidates for breast cancer treatment. 2020 , 69, e12693	15
433	Global analysis of FSH-regulated gene expression and histone modification in mouse granulosa cells. 2020 , 87, 1082-1096	2
432	Decoding Susceptibility to Respiratory Viral Infections and Asthma Inception in Children. 2020 , 21,	3
431	Improved identification of core biomarkers and drug repositioning for ovarian cancer: an integrated bioinformatics approach. 2020 , 9, 1	0
430	Identification of FMRP target mRNAs in the developmental brain: FMRP might coordinate Ras/MAPK, Wnt/ β -catenin, and mTOR signaling during corticogenesis. 2020 , 13, 167	12
429	Identification of a Ubiquitination-Related Gene Risk Model for Predicting Survival in Patients With Pancreatic Cancer. 2020 , 11, 612196	4
428	Meta-Analysis of Differentially Expressed Genes in the Substantia Nigra in Parkinson's Disease Supports Phenotype-Specific Transcriptome Changes. 2020 , 14, 596105	1
427	Multi-Omic Data Integration Allows Baseline Immune Signatures to Predict Hepatitis B Vaccine Response in a Small Cohort. 2020 , 11, 578801	9
426	A Comparison of Gene Expression Changes in the Blood of Individuals Consuming Diets Supplemented with Olives, Nuts or Long-Chain Omega-3 Fatty Acids. 2020 , 12,	5
425	Research Status and Future Expectation of Agricultural Big Data Technology. 2020 ,	0
424	A combination of growth factors and cytokines alter preimplantation mouse embryo development, foetal development and gene expression profiles. 2020 , 26, 953-970	2
423	Immune-profiling of ZIKV-infected patients identifies a distinct function of plasmacytoid dendritic cells for immune cross-regulation. 2020 , 11, 2421	2

422	TNF β Rescues Dendritic Cell Development in Hematopoietic Stem and Progenitor Cells Lacking C/EBP β . 2020 , 9,	1
421	Bioinformatic Analysis Reveals Phosphodiesterase 4D-Interacting Protein as a Key Frontal Cortex Dementia Switch Gene. 2020 , 21,	6
420	Whole blood transcriptional responses of very preterm infants during late-onset sepsis. 2020 , 15, e0233841	10
419	Whole transcriptome analysis of human lung tissue to identify COPD-associated genes. 2020 , 112, 3135-3141	2
418	Integrative meta-analysis for the identification of hub genes in chemoresistant colorectal cancer. 2020 , 14, 525-537	0
417	Omics Integration Analyses Reveal the Early Evolution of Malignancy in Breast Cancer. 2020 , 12,	1
416	Detection of molecular signatures and pathways shared in inflammatory bowel disease and colorectal cancer: A bioinformatics and systems biology approach. 2020 , 112, 3416-3426	12
415	Mining and predicting protein-drug interaction network of breast cancer risk genes. 2020 , 20, 100753	
414	Analysis of gene network model of Thyroid Disorder and associated diseases: A bioinformatics approach. 2020 , 20, 100381	
413	Effect of Jagged1 on the expression of genes in regulation of osteoblast differentiation and bone mineralization ontology in human dental pulp and periodontal ligament cells. 2020 , 10, 233-237	6
412	Cell-of-Origin Subtyping of Diffuse Large B-Cell Lymphoma by Using a qPCR-based Gene Expression Assay on Formalin-Fixed Paraffin-Embedded Tissues. 2020 , 10, 803	6
411	Regional Dichotomy in Enteric Mucosal Immune Responses to a Persistent ssp. Infection. 2020 , 11, 1020	5
410	Cancer bioMarker Prediction Pipeline (CAMPP)-A standardized framework for the analysis of quantitative biological data. 2020 , 16, e1007665	2
409	Characterizing topological properties and network pathway model among vector borne diseases. 2020 , 18, 100312	1
408	Transcriptome hallmarks in infection influence gastric cancer and MALT lymphoma. 2020 , 12, 661-671	7
407	Transcriptomic and Network Analysis Identifies Shared and Unique Pathways across Dementia Spectrum Disorders. 2020 , 21,	7
406	Design protein-protein interaction network and protein-drug interaction network for common cancer diseases: A bioinformatics approach. 2020 , 18, 100311	2
405	Analysis of Dual Class I Histone Deacetylase and Lysine Demethylase Inhibitor Domatinostat (4SC-202) on Growth and Cellular and Genomic Landscape of Atypical Teratoid/Rhabdoid. 2020 , 12,	12

404	MetaBridge: An Integrative Multi-Omics Tool for Metabolite-Enzyme Mapping. 2020 , 70, e98	6
403	Integrated Gene Expression Profiling Analysis Reveals Probable Molecular Mechanism and Candidate Biomarker in Anti-TNF Non-Response IBD Patients. 2020 , 13, 81-95	6
402	Small RNA technology for plant abiotic stress tolerance. 2020 , 521-541	1
401	Biomarker development for axial spondyloarthritis. 2020 , 16, 448-463	20
400	Development and Clinical Validation of a 90-Gene Expression Assay for Identifying Tumor Tissue Origin. 2020 , 22, 1139-1150	5
399	Bioinformatics Approach for Identifying Novel Biomarkers and Their Signaling Pathways Involved in Interstitial Cystitis/Bladder Pain Syndrome with Hunner Lesion. 2020 , 9,	7
398	Dysregulated NF- κ B signal promotes the hub gene PCLAF expression to facilitate nasopharyngeal carcinoma proliferation and metastasis. 2020 , 125, 109905	4
397	Network-Based Genetic Profiling Reveals Cellular Pathway Differences Between Follicular Thyroid Carcinoma and Follicular Thyroid Adenoma. 2020 , 17,	11
396	Transcript profiling reveals potential regulators for oxidative stress response of a necrotrophic chickpea pathogen. 2020 , 10, 117	4
395	Proteome of thymus and spleen reveals that 10-hydroxydec-2-enoic acid could enhance immunity in mice. 2020 , 24, 267-279	4
394	Doxycycline-induced exogenous Bmi-1 expression enhances tumor formation in a murine model of oral squamous cell carcinoma. 2020 , 21, 400-411	4
393	An Integrated Systems Biology and Network-Based Approaches to Identify Novel Biomarkers in Breast Cancer Cell Lines Using Gene Expression Data. 2020 , 12, 155-168	16
392	Immunomodulatory function of the cystic fibrosis modifier gene BPIFA1. 2020 , 15, e0227067	5
391	Dysregulation of the Wnt Signaling Pathway and Synovial Stem Cell Dysfunction in Osteoarthritis Development. 2020 , 29, 401-413	10
390	ID1 overexpression increases gefitinib sensitivity in non-small cell lung cancer by activating RIP3/MLKL-dependent necroptosis. 2020 , 475, 109-118	6
389	Network-Based Computational Approach to Identify Delineating Common Cell Pathways Influencing Type 2 Diabetes and Diseases of Bone and Joints. 2020 , 8, 1486-1497	8
388	Open Data for Differential Network Analysis in Glioma. 2020 , 21,	5
387	In silico identification of novel transcription factors associated with CYP27B1 transcriptional regulation in LPS-challenged mononuclear phagocytes. 2020 , 199, 105590	1

386	Functional Genomics of the Pediatric Obese Asthma Phenotype Reveal Enrichment of Rho-GTPase Pathways. 2020 , 202, 259-274	6
385	RNA-Seq transcriptome profiling in three liver regeneration models in rats: comparative analysis of partial hepatectomy, ALLPS, and PVL. 2020 , 10, 5213	10
384	The importance of reporting house dust mite endotoxin abundance: impact on the lung transcriptome. 2020 , 318, L1229-L1236	8
383	Protein Kinase A Is Involved in Neuropathic Pain by Activating the p38MAPK Pathway to Mediate Spinal Cord Cell Apoptosis. 2020 , 2020, 6420425	5
382	Decreased Expression of NUSAP1 Predicts Poor Overall Survival in Cervical Cancer. 2020 , 11, 2852-2863	12
381	Network-based identification genetic effect of SARS-CoV-2 infections to Idiopathic pulmonary fibrosis (IPF) patients. 2021 , 22, 1254-1266	33
380	Immunoprotective potential of Ayurvedic herb Kalmegh (<i>Andrographis paniculata</i>) against respiratory viral infections - LC-MS/MS and network pharmacology analysis. 2021 , 32, 629-639	13
379	Mitochondria-related core genes and TF-miRNA-hub mrDEGs network in breast cancer. 2021 , 41,	2
378	Identification of an immune-related risk signature and nomogram predicting the overall survival in patients with endometrial cancer. 2021 , 32, e30	4
377	Bioinformatics and system biology approach to identify the influences of COVID-19 on cardiovascular and hypertensive comorbidities. 2021 , 22, 1387-1401	17
376	GPRC5A: An emerging prognostic biomarker for predicting malignancy of Pancreatic Cancer based on bioinformatics analysis. 2021 , 12, 2010-2022	4
375	Meta-analysis identifying epithelial-derived transcriptomes predicts poor clinical outcome and immune infiltrations in ovarian cancer. 2021 , 18, 6527-6551	1
374	Weighted gene co-expression network analysis of the salt-responsive transcriptomes reveals novel hub genes in green halophytic microalgae <i>Dunaliella salina</i> . 2021 , 11, 1607	11
373	Increased gene expression associated with poor prognosis in breast cancer.. 2021 , 10, 4009-4019	0
372	Identification of biomarkers and pathways for the SARS-CoV-2 infections that make complexities in pulmonary arterial hypertension patients. 2021 , 22, 1451-1465	19
371	Different Disease Endotypes in Phenotypically Similar Vasculitides Affecting Small-to-Medium Sized Blood Vessels. 2021 , 12, 638571	2
370	Integrative Transcriptomic Network Analysis of Butyrate Treated Colorectal Cancer Cells. 2021 , 13,	4
369	Expression of SARS-COV-2 cell receptor gene ACE2 is associated with immunosuppression and metabolic reprogramming in lung adenocarcinoma based on bioinformatics analyses of gene expression profiles. 2021 , 335, 109370	5

368	Identifying potential drug targets and candidate drugs for COVID-19: biological networks and structural modeling approaches. 2021 , 10, 127	5
367	Comprehensive Integration of Genome-Wide Association and Gene Expression Studies Reveals Novel Gene Signatures and Potential Therapeutic Targets for -Induced Gastric Disease. 2021 , 12, 624117	4
366	Concomitant gain and loss of function pathomechanisms in C9ORF72 amyotrophic lateral sclerosis. 2021 , 4,	1
365	Identification of functional candidate variants and genes for feed efficiency in Holstein and Jersey cattle breeds using RNA-sequencing. 2021 , 104, 1928-1950	6
364	Network-based gene deletion analysis identifies candidate genes and molecular mechanism involved in clear cell renal cell carcinoma. 2021 , 100, 1	0
363	Mechanism and reversal of drug-induced nephrotoxicity on a chip. 2021 , 13,	15
362	Multiple criteria analysis of the popularity and growth of research and practice of visual analytics, and a forecast of the future trajectory. 2021 , 28, 2275-2298	5
361	Single-cell transcriptomic profiling and characterization of endothelial progenitor cells: new approach for finding novel markers. 2021 , 12, 145	6
360	Identifying Molecular Signatures of Distinct Modes of Collective Migration in Response to the Microenvironment Using Three-Dimensional Breast Cancer Models. 2021 , 13,	0
359	Analysis of MCM Proteins' Role as a Potential Target of Statins in Patients with Acute Type A Aortic Dissection through Bioinformatics. 2021 , 12,	0
358	Noninvasive Analysis Using Data-Independent Acquisition Mass Spectrometry: New Epidermal Proteins That Reveal Sex Differences in the Aging Process. 2021 , 2021, 1-17	
357	MicroRNA-29c Acting on FOS Plays a Significant Role in Nonalcoholic Steatohepatitis Through the Interleukin-17 Signaling Pathway. 2021 , 12, 597449	1
356	Bioinformatics analysis of mRNA and miRNA microarray to identify the key miRNA-mRNA pairs in cisplatin-resistant ovarian cancer. 2021 , 21, 452	1
355	An Overview of Biological and Computational Methods for Designing Mechanism-Informed Anti-biofilm Agents. 2021 , 12, 640787	7
354	Bioinformatics and machine learning approach identifies potential drug targets and pathways in COVID-19. 2021 , 22,	22
353	Evidence of a dysregulated vitamin D endocrine system in SARS-CoV-2 infected patient's lung cells. 2021 , 11, 8570	5
352	Integrative Systems Biology Approaches to Identify Potential Biomarkers and Pathways of Cervical Cancer. 2021 , 11,	3
351	Identifying potential drug targets and candidate drugs for COVID-19: biological networks and structural modeling approaches. 10, 127	5

350	Bioinformatics and system biology approach to identify the influences of SARS-CoV-2 infections to idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease patients. 2021 , 22,	17
349	Bioinformatics and system biology approaches to identify the diseasome and comorbidities complexities of SARS-CoV-2 infection with the digestive tract disorders. 2021 , 22,	7
348	Identifying potential drug targets and candidate drugs for COVID-19: biological networks and structural modeling approaches. 2021 , 10, 127	5
347	Evaluation of Antibiotic Tolerance in <i>Pseudomonas aeruginosa</i> for Aminoglycosides and its Predicted Gene Regulations Through In-silico Transcriptomic Analysis.	
346	Proteomic profiling of soft tissue sarcomas with SWATH mass spectrometry. 2021 , 241, 104236	4
345	Identification of Novel Alternative Splicing Events Associated With Tumorigenesis, Protein Modification, and Immune Microenvironment in Early-Onset Gastric Cancer. 2021 , 11, 640272	0
344	Identification of Potential Biomarkers and Biological Pathways for Poor Clinical Outcome in Mucinous Colorectal Adenocarcinoma. 2021 , 13,	1
343	Visual Analysis of Multilayer Networks. 2021 , 8, 1-150	
342	How does the early life environment influence the oral microbiome and determine oral health outcomes in childhood?. 2021 , 43, e2000314	0
341	Multiple allelic associations from genes involved in energy metabolism were identified in celiac disease. 2021 , 46, 1	1
340	Proteasome activity contributes to pro-survival response upon mild mitochondrial stress in <i>Caenorhabditis elegans</i> . 2021 , 19, e3001302	4
339	Evaluation of Antibiotic Tolerance in <i>Pseudomonas aeruginosa</i> for Aminoglycosides and Its Predicted Gene Regulations through In-Silico Transcriptomic Analysis. 2021 , 12, 630-645	1
338	Roles of tetraspanins during trophoblast development: bioinformatics and new perspectives. 2021 , 386, 157-171	
337	Identification of Hub Genes Associated with Diabetes Mellitus and Tuberculosis Using Bioinformatic Analysis. 2021 , 14, 4061-4072	1
336	Integration of RNA-Seq and proteomics data identifies glioblastoma multiforme surfaceome signature. 2021 , 21, 850	3
335	The transcription factor RUNX2 fuels YAP1 signaling and gastric cancer tumorigenesis. 2021 , 112, 3533-3544	3
334	Molecular Characterization and Elucidation of Pathways to Identify Novel Therapeutic Targets in Pulmonary Arterial Hypertension. 2021 , 12, 694702	1
333	Hyperleptinemia in obese state renders luminal breast cancers refractory to tamoxifen by coordinating a crosstalk between Med1, miR205 and ErbB. 2021 , 7, 105	1

- 332 Interleukin 15 participates in Jagged1-induced mineralization in human dental pulp cells. **2021**, 128, 105163 0
- 331 Promising Anticancer Activity of [Bis(1,8-quinolato)palladium (II)] Alone and in Combination. **2021**, 22, 0
- 330 Modulation of Synthetic Tracheal Grafts with Extracellular Matrix Coatings. **2021**, 8, 1
- 329 Screening and identification of NOTCH1, CDKN2A, and NOS3 as differentially expressed autophagy-related genes in erectile dysfunction. **2021**, 9, e11986 0
- 328 Sex- and Developmental Stage-Related Differences in the Hepatic Transcriptome of Japanese Quail (*Coturnix japonica*) Exposed to 17 β Trenbolone. **2021**, 40, 2559-2570 1
- 327 Leber's hereditary optic neuropathy: Current approaches and future perspectives on Mesenchymal stem cell-mediated rescue. **2021**, 60, 201-218 3
- 326 Expression as a Prognostic Marker in Gastric Cancer: A Bioinformatics-Based Analysis. **2021**, 14, 1151-1168 1
- 325 Quantitative global lipidomics analysis of patients with ovarian cancer versus benign adnexal mass. **2021**, 11, 18156 1
- 324 NR0B2 regulation during Primary Sclerosing Cholangitis defines a metabolic and pre-malignant reprogramming of Cholangiocyte.
- 323 Searching for a technology-driven acute rheumatic fever test: the START study protocol. **2021**, 11, e053720 0
- 322 Brown adipocyte ATF4 activation improves thermoregulation and systemic metabolism. **2021**, 36, 109742 2
- 321 Inflammatory signature in acute-on-chronic liver failure includes increased expression of granulocyte genes ELANE, MPO and CD177. **2021**, 11, 18849 2
- 320 Identification of Gene Signature as Diagnostic and Prognostic Blood Biomarker for Early Hepatocellular Carcinoma Using Integrated Cross-Species Transcriptomic and Network Analyses. **2021**, 12, 710049 2
- 319 Bioinformatics analyses of gene expression profile identify key genes and functional pathways involved in cutaneous lupus erythematosus. **2021**, 1 2
- 318 Dorsomorphin attenuates Jagged1-induced mineralization in human dental pulp cells. **2021**, 54, 2229-2242 0
- 317 Identifying key genes and screening therapeutic agents associated with diabetes mellitus and HCV-related hepatocellular carcinoma by bioinformatics analysis. **2021**, 28, 5518-5525 3
- 316 Network-based transcriptomic analysis identifies the genetic effect of COVID-19 to chronic kidney disease patients: A bioinformatics approach. **2021**, 28, 5647-5656 3
- 315 Adenoma to carcinoma: A portrait of molecular and immunological profiles of colorectal sporadic tumors. **2021**, 100, 108168

314	Identifying the function of methylated genes in Alzheimer's disease to determine epigenetic signatures: a comprehensive bioinformatics analysis. 2021 , 2,	
313	NetMix: A Network-Structured Mixture Model for Reduced-Bias Estimation of Altered Subnetworks. 2021 , 28, 469-484	3
312	Systematic Construction and Validation of an RNA-Binding Protein-Associated Model for Prognosis Prediction in Hepatocellular Carcinoma. 2020 , 10, 597996	3
311	Contribution of endothelial cell-derived transcriptomes to the colon cancer based on bioinformatics analysis. 2021 , 18, 7280-7300	2
310	Bioinformatics and machine learning methodologies to identify the effects of central nervous system disorders on glioblastoma progression. 2021 , 22,	9
309	Mapping Biological Networks from Quantitative Data-Independent Acquisition Mass Spectrometry: Data to Knowledge Pipelines. 2017 , 1558, 395-413	5
308	Plant Adaptation and Tolerance to Environmental Stresses: Mechanisms and Perspectives. 2020 , 117-145	22
307	Bioinformatics-based analysis of the lncRNA-miRNA-mRNA and TF regulatory networks reveals functional genes in esophageal squamous cell carcinoma. 2020 , 40,	4
306	Meta-analysis based gene expression profiling reveals functional genes in ovarian cancer. 2020 , 40,	6
305	Integrated Bioinformatic Approach to Identify Potential Biomarkers against Idiopathic Pulmonary Fibrosis.	0
304	NetMix: A network-structured mixture model for reduced-bias estimation of altered subnetworks.	1
303	Evaluation of CRISPR gene-editing tools in zebrafish.	1
302	Evidence of a dysregulated Vitamin D pathway in SARS-CoV-2 infected patient's lung cells.	1
301	A system biology approach reveals cellular pathway differences between follicular thyroid carcinoma and follicular thyroid adenoma.	3
300	Identification of biomarkers and pathways to identify novel therapeutic targets in Alzheimer's disease: Insights from a systems biomedicine perspective.	3
299	Identification of common molecular biomarker signatures in blood and brain of Alzheimer's disease.	6
298	iPSC-derived Cancer Organoids Recapitulate Genomic and Phenotypic Alterations of c-met-mutated Hereditary Kidney Cancer.	2
297	STAT1 and its related molecules as potential biomarkers in Mycobacterium tuberculosis infection. 2020 , 24, 2866-2878	19

296	Aberrant cell migration contributes to defective airway epithelial repair in childhood wheeze. 2020 , 5,	8
295	Preexisting antibodies can protect against congenital cytomegalovirus infection in monkeys. 2017 , 2,	39
294	The Effect of In Vitro Cultivation on the Transcriptome of Adult <i>Brugia malayi</i> . 2016 , 10, e0004311	15
293	RNA-Seq Transcriptomic Responses of Full-Thickness Dermal Excision Wounds to <i>Pseudomonas aeruginosa</i> Acute and Biofilm Infection. 2016 , 11, e0165312	7
292	MicroRNAs Associated with Shoulder Tendon Matrisome Disorganization in Glenohumeral Arthritis. 2016 , 11, e0168077	26
291	NCOA1 is a novel susceptibility gene for multiple myeloma in the Chinese population: A case-control study. 2017 , 12, e0173298	5
290	Prognostic value of circulating microRNAs in upper tract urinary carcinoma. 2018 , 9, 16691-16700	11
289	Down syndrome iPSC model: endothelial perspective on tumor development. 2020 , 11, 3387-3404	2
288	Available Software for Meta-analyses of Genome-wide Expression Studies. 2019 , 20, 325-331	5
287	Integrated System Pharmacology and Analysis Elucidating Neuropharmacological Actions of in the Treatment of Alzheimer's Disease. 2020 , 19, 541-556	3
286	Omics Integration Analysis Unravel the Landscape of Driving Mechanisms of Colorectal Cancer. 2020 , 21, 3539-3549	2
285	Identification of Novel Genes and Biological Pathways That Overlap in Infectious and Nonallergic Diseases of the Upper and Lower Airways Using Network Analyses. 2019 , 10, 1352	7
284	A Network-Based Bioinformatics Approach to Identify Molecular Biomarkers for Type 2 Diabetes that Are Linked to the Progression of Neurological Diseases. 2020 , 17,	25
283	Identification of potential markers for type 2 diabetes mellitus via bioinformatics analysis. 2020 , 22, 1868-1882	5
282	Molecular markers associated with perineural invasion in pancreatic ductal adenocarcinoma. 2020 , 20, 5	4
281	Meta-analysis of microarray datasets identify several chromosome segregation-related cancer/testis genes potentially contributing to anaplastic thyroid carcinoma. 2018 , 6, e5822	8
280	Identification of diagnostic markers for major depressive disorder by cross-validation of data from whole blood samples. 2019 , 7, e7171	6
279	Host transcriptome-guided drug repurposing for COVID-19 treatment: a meta-analysis based approach. 2020 , 8, e9357	24

278	Convergent Canonical Pathways in Autism Spectrum Disorder from Proteomic, Transcriptomic and DNA Methylation Data. 2021 , 22,	1
277	Integrative meta-analysis of gene expression profiles identifies FEN1 and ENDOU as potential diagnostic biomarkers for cervical squamous cell carcinoma. 2021 , 22, 840	1
276	Fasting drives the metabolic, molecular and geroprotective effects of a calorie-restricted diet in mice. 2021 , 3, 1327-1341	18
275	Plexin-B2 orchestrates collective stem cell dynamics via actomyosin contractility, cytoskeletal tension and adhesion. 2021 , 12, 6019	2
274	RNF2 ablation reprograms the tumor-immune microenvironment and stimulates durable NK and CD4 T-cell-dependent antitumor immunity.. 2021 , 2, 1018-1038	0
273	A 10-gene biosignature of tuberculosis treatment monitoring and treatment outcome prediction. 2021 , 131, 102138	0
272	From Gene Expression to Disease Phenotypes: Network-Based Approaches to Study Complex Human Diseases. 2016 , 115-140	
271	Preexisting antibodies can protect against congenital cytomegalovirus infection in monkeys.	
270	Genetic basis of thermal plasticity variation in <i>Drosophila melanogaster</i> body size.	0
269	A Network Biology Approach for Assessing the Role of Pathologic Adipose Tissues in Insulin Resistance Using Meta-analysis of Microarray Datasets. 2018 , 19, 630-666	3
268	BRCA2 abrogation triggers innate immune responses potentiated by treatment with PARP inhibitors.	
267	Galectin-3, A Novel Endogenous Trem2 Ligand, Regulates Inflammatory Response and A β Fibrillation in Alzheimer's Disease.	
266	Distinct molecular etiologies of male and female hepatocellular carcinoma.	0
265	Therapeutic Targeting of Casein Kinase 1 γ in an Alzheimer's Disease Mouse Model.	
264	CANcer bioMarker Prediction Pipeline (CAMPP) - A standardised and user-friendly framework for the analysis of quantitative biological data.	
263	G-quadruplexes sequester free heme in living cells.	
262	Identification of Blood-based Non-invasive Biomarkers and Therapeutic Agents against Pancreatic Ductal Adenocarcinoma (PDAC): A Network-based Study.	
261	Proteomic profiling of soft tissue sarcomas with SWATH mass spectrometry.	

- 260 Constitutive activation of the PI3K-Akt-mTORC1 pathway sustains the m.3243A>G mtDNA mutation.
- 259 Identifying novel high-impact rare disease-causing mutations, genes and pathways in exomes of Ashkenazi Jewish inflammatory bowel disease patients.
- 258 Gel Balıng Alzheimer Hastalığı ve Hepatosellüler Karsinom ile İlgili Ortak Moleküler Yolakların ve Anahtar Biyobelirteçlerin Biyoinformatik Analizlerle Araştırılması
- 257 Identification of novel alternative splicing events associated with tumorigenesis, protein modification, and immune microenvironment in early-onset gastric cancer.
- 256 Glia Maturation Factor Beta as a Novel Biomarker and Therapeutic Target for Hepatocellular Carcinoma. **2021**, 11, 744331 1
- 255 Dynamic methylome modification is associated with mutational signatures in aging and the etiology of disease.
- 254 Analysis of PPI networks of transcriptomic expression identifies hub genes associated with Newcastle disease virus persistent infection in bladder cancer.
- 253 Changes in microbial community diversity, composition, and functions upon nitrate and Cr(VI) contaminated groundwater. **2021**, 288, 132476 2
- 252 Drug-Protein Interaction Network Detection and Analysis of Cardiovascular Disease-Related Genes: A Bioinformatics Approach. **2020**, 243-252
- 251 Senescent stromal cells promote cancer resistance through SIRT1 loss-potentiated overproduction of small extracellular vesicles. 1
- 250 Omics integration analyses reveal the early evolution of malignancy in breast cancer.
- 249 Constitutive activation of the PI3K-Akt-mTORC1 pathway sustains the m.3243 A > G mtDNA mutation. **2021**, 12, 6409 2
- 248 RHBDF2 gene functions are correlated to facilitated renal clear cell carcinoma progression. **2021**, 21, 590 1
- 247 The Proteomic Signature of Recombinant Growth Hormone in Recreational Athletes. **2021**, 5, bvab156 0
- 246 NetMix: A Network-Structured Mixture Model for Reduced-Bias Estimation of Altered Subnetworks. **2020**, 169-185
- 245 Promising diagnostic and prognostic value of six genes in human hepatocellular carcinoma. **2020**, 12, 1239-1254 3
- 244 Development and validation of a survival model based on autophagy-associated genes for predicting prognosis of hepatocellular carcinoma. **2020**, 12, 6705-6722 3
- 243 Identification of Alzheimer associated differentially expressed gene through microarray data and transfer learning-based image analysis. **2022**, 766, 136357 0

242	Microplastic-associated pathogens and antimicrobial resistance in environment. 2021 , 133005	2
241	Detection of molecular signatures and pathways shared by Alzheimer's disease and type 2 diabetes. 2021 , 810, 146070	0
240	Identification of Immunological Biomarkers of Atopic Dermatitis by Integrated Analysis to Determine Molecular Targets for Diagnosis and Therapy. 2021 , 14, 8193-8209	0
239	Maternal nematode infection upregulates expression of Th2/Treg and diapycosis related genes in the neonatal brain. 2021 , 11, 22082	0
238	Altered neurogenic pathways in experimental rat models of ischemic cerebral stroke: A transcriptome based meta-analysis.	
237	Antioxidant supplementation of mouse embryo culture or vitrification media support more in-vivo-like gene expression post-transfer.. 2021 ,	1
236	Comprehensive Analyses of Type 1 Diabetes Ketosis- or Ketoacidosis-Related Genes in Activated CD56CD16 NK Cells.. 2021 , 12, 750135	1
235	Non-coding RNAs and related molecules associated with form-deprivation myopia in mice. 2021 ,	2
234	A transcriptomic analysis based on aberrant methylation levels revealed potential novel therapeutic targets for nasopharyngeal carcinoma.. 2022 , 10, 47	
233	Identification of the GTPase IMAF family as an immune-related prognostic biomarker in the breast cancer tumor microenvironment.. 2021 , 812, 146094	0
232	Unraveling molecular mechanism underlying biomaterial and stem cells interaction during cell fate commitment using high throughput data analysis.. 2021 , 812, 146111	
231	EXTRACELLULAR MATRIX REMODELING IN ATOPIC DERMATITIS HARNESSSES THE ONSET OF AN ASTHMATIC PHENOTYPE AND IS A POTENTIAL CONTRIBUTOR TO THE ATOPIC MARCH.	1
230	Evaluation of CRISPR gene-editing tools in zebrafish.. 2022 , 23, 12	3
229	Host T cell dedifferentiation effects drive HIV-1 latency stability.. 2022 , jvi0197421	0
228	Identification of key tumor stroma-associated transcriptional signatures correlated with survival prognosis and tumor progression in breast cancer.. 2022 , 1	1
227	The Variant c.461G>A (p.Trp154*) Is Associated With Differentially Expressed Genes and Nasopharyngeal Microbiota Shifts in Patients With Otitis Media.. 2021 , 11, 798246	2
226	Identification of key regulators in Sarcoidosis through multidimensional systems biological approach.. 2022 , 12, 1236	0
225	Systems Biology and Bioinformatics approach to Identify blood based signatures molecules and drug targets of patient with COVID-19.. 2021 , 28, 100840	5

224	Immune Response Is Key to Genetic Mechanisms of SARS-CoV-2 Infection With Psychiatric Disorders Based on Differential Gene Expression Pattern Analysis.. 2022 , 13, 798538	0
223	NetMix2: Unifying network propagation and altered subnetworks.	
222	Protocol for inducing inflammation and acute myelin degeneration in larval zebrafish.. 2022 , 3, 101134	0
221	Determination of molecular signatures and pathways common to brain tissues of autism spectrum disorder: Insights from comprehensive bioinformatics approach. 2022 , 29, 100871	3
220	Comprehensive investigation of molecular signatures and pathways linking Alzheimer's disease and Epilepsy via bioinformatic approaches.. 2022 ,	1
219	Bioinformatics analysis deciphering the transcriptomic signatures associated with signalling pathways and prognosis in the myelodysplastic syndromes.. 2022 , 27, 214-231	1
218	Identification of Molecular Signatures and Candidate Drugs in Vascular Dementia by Bioinformatics Analyses.. 2022 , 15, 751044	1
217	Unlocking the Memory Component of Alzheimer's Disease: Biological Processes and Pathways across Brain Regions.. 2022 , 12,	0
216	Identification of molecular signatures and pathways common to blood cells and brain tissue based RNA-Seq datasets of bipolar disorder: Insights from comprehensive bioinformatics approach. 2022 , 29, 100881	4
215	Identifying molecular signatures and pathways shared between Alzheimer's and Huntington's disorders: A bioinformatics and systems biology approach. 2022 , 30, 100888	1
214	Bioinformatics Approach to Identify Significant Biomarkers, Drug Targets Shared Between Parkinson's Disease and Bipolar Disorder: A Pilot Study.. 2022 , 16, 11779322221079232	1
213	Comprehensive pan-cancer analysis on CBX3 as a prognostic and immunological biomarker.. 2022 , 15, 29	2
212	Identification of the shared gene signatures and pathways between sarcopenia and type 2 diabetes mellitus.. 2022 , 17, e0265221	0
211	Reduction of Metastasis via Epigenetic Modulation in a Murine Model of Metastatic Triple Negative Breast Cancer (TNBC).. 2022 , 14,	0
210	Identification of novel alternative splicing associated with mastitis disease in Holstein dairy cows using large gap read mapping.. 2022 , 23, 222	1
209	The Key Genes Underlying Pathophysiology Correlation Between the Acute Myocardial Infarction and COVID-19.. 2022 , 15, 2479-2490	2
208	Computational identification of host genomic biomarkers highlighting their functions, pathways and regulators that influence SARS-CoV-2 infections and drug repurposing.. 2022 , 12, 4279	8
207	An investigation of 6-Shogaol effects on MCF7 cell lines through a systems biology approach. 2022 , 23,	0

206 Identifying the *C. elegans* vulval transcriptome.

205 Identification of Breast Cancer Subtypes Based on Gene Expression Profiles in Breast Cancer Stroma.. **2022**, 0

204 Bioinformatics and System Biology Approach to Identify the Influences of COVID-19 on Rheumatoid Arthritis.. **2022**, 13, 860676 0

203 Autophagy Induced by BCL2-Related ceRNA Network Participates in the Occurrence of COPD.. **2022**, 17, 791-808 0

202 Identification of host transcriptome-guided repurposable drugs for SARS-CoV-1 infections and their validation with SARS-CoV-2 infections by using the integrated bioinformatics approaches.. **2022**, 17, e0266124 1

201 A system biology approach to determine therapeutic targets by identifying molecular mechanisms and key pathways for type 2 diabetes that are linked to the development of tuberculosis and rheumatoid arthritis.. **2022**, 120483 2

200 Transcriptome profiling of curcumin-treated T47D human breast cancer cells by a system-based approach. **2022**, 27, 101556 0

199 Hsa_circ_0087352 promotes the inflammatory response of macrophages in abdominal aortic aneurysm by adsorbing hsa-miR-149-5p.. **2022**, 107, 108691 2

198 A Bioinformatics Approach for Deciphering the Pathogenic Processes of COPD. **2021**, 0

197 A Transcriptomic and Proteomic Atlas of Obesity and Type 2 Diabetes in Cynomolgus Monkeys.

196 Genome-Wide DNA Methylation Signatures Predict the Early Asymptomatic Doxorubicin-Induced Cardiotoxicity in Breast Cancer.. **2021**, 13, 0

195 Computational Prediction of Biomarkers, Pathways, and New Target Drugs in the Pathogenesis of Immune-Based Diseases Regarding Kidney Transplantation Rejection.. **2021**, 12, 800968 1

194 A hybrid systems biology and systems pharmacology investigation of Zingerone's effects on reconstructed human epidermal tissues. **2021**, 22,

193 Intellectual disability associated with craniofacial dysmorphism due to POLR3B mutation and defect in spliceosomal machinery.. **2022**, 15, 89

192 An updated *C. elegans* body muscle transcriptome for studies in muscle formation and function.

191 Characterization of Altered Molecular Pathways in the Entorhinal Cortex of Alzheimer's Disease Patients and In Silico Prediction of Potential Repurposable Drugs.. **2022**, 13, 1

190 Identification of Immune-Related Key Genes as Potential Diagnostic Biomarkers of Sepsis in Children.. **2022**, 15, 2441-2459 0

189 Image_1.JPEG. **2020**,

188 Image_2.JPEG. 2020,

187 Image_3.JPEG. 2020,

186 Table_1.xlsx. 2020,

185 Image1.PDF. 2018,

184 Table1.XLSX. 2018,

183 Image_1.TIF. 2020,

182 Image_2.TIF. 2020,

181 Table_1.XLSX. 2020,

180 Table_2.XLSX. 2020,

179 Table_3.XLSX. 2020,

178 Table_4.XLSX. 2020,

177 DataSheet_1.zip. 2020,

176 Data_Sheet_1.docx. 2020,

175 Table_1.XLSX. 2020,

174 DataSheet_1.pdf. 2020,

173 Table_1.xlsx. 2020,

172 Table_10.xlsx. 2020,

171 Table_11.xlsx. 2020,

170 Table_12.xlsx. 2020,

169 Table_13.xlsx. 2020,

168 Table_14.xlsx. 2020,

167 Table_2.xlsx. 2020,

166 Table_3.xlsx. 2020,

165 Table_4.xlsx. 2020,

164 Table_5.xlsx. 2020,

163 Table_6.xlsx. 2020,

162 Table_7.xlsx. 2020,

161 Table_8.xlsx. 2020,

160 Table_9.xlsx. 2020,

159 Image_1.TIF. 2020,

158 DataSheet_1.pdf. 2019,

157 DataSheet_1.xlsx. 2019,

156 Image_1.pdf. 2019,

155 Image_2.pdf. 2019,

154 Data_Sheet_1.docx. 2018,

153 Table_1.XLSX. 2018,

152 Table_2.XLSX. 2018,

151 Table_3.XLSX. 2018,

150 Table_4.DOCX. 2018,

149 Table_5.XLSX. 2018,

148 Data_Sheet_1.docx. 2019,

147 Image_1.TIFF. 2020,

146 Image_2.TIFF. 2020,

145 Table_1.DOCX. 2020,

144 Table_2.XLSX. 2020,

143 Table_3.XLSX. 2020,

142 Table_1.xlsx. 2019,

141 Table_2.xlsx. 2019,

140 Table_3.xlsx. 2019,

139 Table_4.xlsx. 2019,

138 Table_5.xlsx. 2019,

137 Table_6.xlsx. 2019,

136 Table_7.xlsx. 2019,

135 Table_8.docx. 2019,

134 Image_1.PNG. 2020,

133 Image_2.PNG. 2020,

132 Image_1.TIF. 2018,

131 Table_1.XLSX. 2018,

130 Table_2.XLS. 2018,

129 Table_3.XLSX. 2018,

128 Table_4.XLS. 2018,

127 Table_5.XLSX. 2018,

126 Table_6.XLS. 2018,

125 Table_7.XLSX. 2018,

124 Table_8.XLSX. 2018,

123 DataSheet_1.pdf. 2020,

122 Table_1.DOCX. 2020,

121 Table_2.DOCX. 2020,

120 Table_3.DOCX. 2020,

119 Table_4.DOCX. 2020,

118 Table_5.DOCX. 2020,

117 Immune-related biomarkers shared by inflammatory bowel disease and liver cancer.. 2022, 17, e0267358

2

116	NetMix2: Unifying Network Propagation and Altered Subnetworks. 2022 , 193-208	0
115	Discovering Common Pathophysiological Processes between COVID-19 and Cystic Fibrosis by Differential Gene Expression Pattern Analysis.. 2022 , 2022, 8078259	0
114	Comprehensive Analysis of N6-Methyladenosine Regulators in the Subcluster Classification and Drug Candidates Prediction of Severe Obstructive Sleep Apnea.. 2022 , 13, 862972	
113	Identifying the <i>C. elegans</i> vulval transcriptome.. 2022 ,	
112	Identification of key genes and miRNA-mRNA regulatory networks associated with bone marrow immune microenvironment regulations in multiple myeloma by integrative bioinformatics analysis.. 2022 , 27, 506-517	0
111	Identification of Immune Hub Genes Associated With Braak Stages in Alzheimer's Disease and Their Correlation of Immune Infiltration. 2022 , 14,	0
110	Non-canonical Wnt signaling participates in Jagged1-induced osteo/odontogenic differentiation in human dental pulp stem cells.. 2022 , 12, 7583	1
109	Disclosing Potential Key Genes, Therapeutic Targets and Agents for Non-Small Cell Lung Cancer: Evidence from Integrative Bioinformatics Analysis. 2022 , 10, 771	0
108	RNA-seq based integrative analysis of potential crucial genes and pathways associated with patellar instability.. 2022 , 13, 11402-11416	
107	A Computational Approach to Justifying Stratifin as a Candidate Diagnostic and Prognostic Biomarker for Pancreatic Cancer.. 2022 , 2022, 1617989	0
106	JUN and PDGFRA as Crucial Candidate Genes for Childhood Autism Spectrum Disorder. 2022 , 16,	0
105	Musashi1 and its short C-terminal variants regulate pluripotency states in embryonic stem cells.	
104	Aberrant methylmalonylation underlies methylmalonic acidemia and is attenuated by an engineered sirtuin. 2022 , 14,	0
103	MLBioIGE: Integration and Interplay of Machine Learning and Bioinformatics Approach to Identify the Genetic Effect of SARS-COV-2 on Idiopathic Pulmonary Fibrosis Patients.	3
102	Endotyping pediatric obesity-related asthma: contribution of anthropometrics, metabolism, nutrients, and CD4+ lymphocytes, to pulmonary function. 2022 ,	1
101	Target and drug predictions for SARS-CoV-2 infection in hepatocellular carcinoma patients. 2022 , 17, e0269249	0
100	Identification of biomarkers, immune infiltration landscape, and treatment targets of ischemia-reperfusion acute kidney injury at an early stage by bioinformatics methods. 2022 , 159,	
99	Physical Activity Rewires the Human Brain against Neurodegeneration. 2022 , 23, 6223	2

- 98 A review of bioinformatics tools and web servers in different microarray platforms used in cancer research. **2022**, 0
- 97 MAP Kinase and mammalian target of rapamycin are main pathways of gallbladder carcinogenesis: Results from bioinformatic analysis of Next Generation Sequencing data from a hospital-based cohort. 3
- 96 Dietary polyphenols drive alterations in behavior, transcriptional regulation, and commensal microbiota in models of opioid use. 0
- 95 Integrated multi-omic data analysis and validation with yeast model show oxidative phosphorylation modulates protein aggregation in amyotrophic lateral sclerosis. 1-20 3
- 94 Gravity++: A graph-based framework for constructing interactive visualization narratives. **2022**, 71, 101125 0
- 93 Deep learning-based microarray cancer classification and ensemble gene selection approach. **2022**, 16, 120-131 3
- 92 Identifying Potential Effective Diagnostic and Prognostic Biomarkers in Sepsis by Bioinformatics Analysis and Validation. Volume 15, 6055-6071 0
- 91 Statistical Bioinformatics to Uncover the Underlying Biological Mechanisms That Linked Smoking with Type 2 Diabetes Patients Using Transcriptomic and GWAS Analysis. **2022**, 27, 4390 1
- 90 Integrated ONT Full-Length Transcriptome and Metabolism Reveal the Mechanism Affecting Ovulation in Muscovy Duck (*Cairina moschata*). 9, 0
- 89 Identification of core genes associated with the anti-atherosclerotic effects of Salvianolic acid B and immune cell infiltration characteristics using bioinformatics analysis. **2022**, 22, 0
- 88 Network analysis reveals the molecular bases of statin pleiotropy that vary with genetic background. 0
- 87 Role of Shankpushpi (*Convolvulus pluricaulis*) in Neurological Disorders: An Umbrella Review Covering Evidence from Ethnopharmacology to Clinical Studies. **2022**, 104795 3
- 86 Integrative study of gene expression datasets in retinal samples of Diabetic Retinopathy. **2022**, 109194 0
- 85 OMiCC: An expanded and enhanced platform for meta-analysis of public gene expression data. **2022**, 3, 101474 0
- 84 Bioinformatics Strategies to Identify Shared Molecular Biomarkers That Link Ischemic Stroke and Moyamoya Disease with Glioblastoma. **2022**, 14, 1573 0
- 83 Identification of key genes and pathways in chronic rhinosinusitis with nasal polyps and asthma comorbidity using bioinformatics approaches. 13, 1
- 82 Meta-Data Analysis to Explore the Hub of the Hub-Genes That Influence SARS-CoV-2 Infections Highlighting Their Pathogenetic Processes and Drugs Repurposing. **2022**, 10, 1248 1
- 81 Early Deregulation Of Cholangiocyte NR0B2 During Primary Sclerosing Cholangitis. **2022**, 0

80	Identification of novel long noncoding RNA with distinct expression patterns in different subtypes of multiple myeloma.	
79	Effects of decellularized extracellular matrix derived from Jagged1-treated human dental pulp stem cells on biological responses of stem cells isolated from apical papilla. 10,	o
78	MAP kinase and mammalian target of rapamycin are main pathways of gallbladder carcinogenesis: results from bioinformatic analysis of next generation sequencing data from a hospital-based cohort (NCT05404347).	o
77	Identification of Key Gene Network Modules and Hub Genes Associated with Wheat Response to Biotic Stress Using Combined Microarray Meta-analysis and WGCN Analysis.	o
76	Network-Based Data Analysis Reveals Ion Channel-Related Gene Features in COVID-19: A Bioinformatic Approach.	1
75	Identification of potential crucial genes and key pathways shared in Inflammatory Bowel Disease and cervical cancer by machine learning and integrated bioinformatics. 2022 , 149, 105996	1
74	Combining LC-MS/MS profiles with network pharmacology to predict molecular mechanisms of the hyperlipidemic activity of <i>Lagenaria siceraria</i> stand. 2023 , 300, 115633	o
73	To investigate the internal association between SARS-CoV-2 infections and cancer through bioinformatics. 2022 , 19, 11172-11194	1
72	Prognostic and immunological role of SERPINH1 in pan-cancer. 13,	o
71	The angiogenic genes predict prognosis and immune characteristics in esophageal squamous cell carcinoma: Evidence from multi-omics and experimental verification. 12,	o
70	Comprehensive analysis and validation of novel immune and vascular remodeling related genes signature associated with drug interactions in pulmonary arterial hypertension. 13,	o
69	Exploration of Hub Genes in Retinopathy of Prematurity Based on Bioinformatics Analysis of the Oxygen-Induced Retinopathy Model. 2022 , 2022, 1-12	o
68	Integrating peripheral blood and brain transcriptomics to identify immunological features associated with Alzheimer's disease in mild cognitive impairment patients. 13,	o
67	Gene Expression Profiles Reveal Potential Targets for Breast Cancer Diagnosis and Treatment.	o
66	A Bioinformatic Approach Based on Systems Biology to Determine the Effects of SARS-CoV-2 Infection in Patients with Hypertrophic Cardiomyopathy. 2022 , 2022, 1-13	o
65	Bioinformatics and systems-biology analysis to determine the effects of Coronavirus disease 2019 on patients with allergic asthma. 13,	o
64	Evaluation and assessment of nutritional composition for quality profiling of <i>Phoenix dactylifera</i> cultivars using multivariate analytical tools.	o
63	Identification of key molecular signatures in epithelial ovarian cancer by integrated bioinformatics analysis.	o

62	Protective Mechanisms of Nootropic Herb Shankpushpi (<i>Convolvulus pluricaulis</i>) against Dementia: Network Pharmacology and Computational Approach. 2022 , 2022, 1-18	0
61	Crosstalk Between CD4+ T Cells and Airway Smooth Muscle in Pediatric Obesity-related Asthma.	0
60	Impact of Exosomes Released by Different Corneal Cell Types on the Wound Healing Properties of Human Corneal Epithelial Cells. 2022 , 23, 12201	0
59	Central gene transcriptional regulatory networks shaping monocyte development in bone marrow. 13,	0
58	System Biology Approaches Identified Novel Biomarkers and their Signaling Pathways Involved in Renal Cell Carcinoma (RCC) with Different Human Diseases.	1
57	miR-495-3p Sensitizes BCR::ABL1 Expressing Leukemic cells to Tyrosine Kinase Inhibitors by Targeting Multidrug Resistance 1 Gene including in T315I Mutated cells.	0
56	A multi-omics analysis of glioma chemoresistance using a hybrid microphysiological model of glioblastoma.	0
55	A bioinformatics approach to systematically analyze the molecular patterns of monkeypox virus-host cell interactions.	0
54	miRNA Expression May Have Implications for Immunotherapy in PDGFRA Mutant GISTs. 2022 , 23, 12248	0
53	Characterization of hepatic inflammatory changes in a C57BL/6J mouse model of alpha-1 antitrypsin deficiency.	0
52	Severity of COVID-19 patients with coexistence of asthma and vitamin D deficiency. 2022 , 101116	0
51	Host Response of Human Epidermis to Methicillin-Resistant <i>Staphylococcus aureus</i> Biofilm Infection and Synthetic Antibiofilm Peptide Treatment. 2022 , 11, 3459	2
50	A broad cuproptosis landscape in inflammatory bowel disease. 13,	0
49	Bioinformatics and systems biology approaches to identify molecular targeting mechanism influenced by COVID-19 on heart failure. 13,	0
48	Identification of GLS as a cuproptosis-related diagnosis gene in acute myocardial infarction. 9,	1
47	A meta-analysis of differentially expressed and regulatory genes with their functional enrichment analysis for brain transcriptome data in autism spectrum disorder. 1-7	0
46	Transcriptional profiles and common genes link lung cancer with the development and severity of COVID-19. 2022 , 147047	0
45	FABP5 controls macrophage alternative activation and allergic asthma by selectively programming long-chain unsaturated fatty acid metabolism. 2022 , 41, 111668	0

- 44 A systems biology approach towards oral cancer using computational tools and techniques. **2022**, 231, 104709 ○
- 43 Network analysis of long non-coding RNA expression profiles in common warts. **2022**, e11790 ○
- 42 Bioinformatics and System Biology Techniques to Determine Biomolecular Signatures and Pathways of Prion Disorder. **2022**, 16, 117793222211453 ○
- 41 Identifying key transcription factors and miRNAs coregulatory networks associated with immune infiltrations and drug interactions in idiopathic pulmonary arterial hypertension. **2022**, 20, 4153-4177 ○
- 40 Ethnopharmacological review of *Tkalmegh* for anticancer activity. **2022**, 4, 152-157 ○
- 39 Tsukushi proteoglycan maintains RNA splicing and developmental signaling network in GFAP-expressing subventricular zone neural stem/progenitor cells. 10, ○
- 38 Pathogen-driven gene expression patterns lead to a novel approach to the identification of common therapeutic targets. **2022**, 12, ○
- 37 Extracellular vesicles improve GABAergic transmission in Huntington's disease iPSC-derived neurons. ○
- 36 Spontaneous immortalization of chicken fibroblasts generates stable, high-yield cell lines for serum-free production of cultured meat. ○
- 35 Co-expression of fibrotic genes in inflammatory bowel disease; A localized event?. 13, ○
- 34 miR-495-3p sensitizes BCR-ABL1-expressing leukemic cells to tyrosine kinase inhibitors by targeting multidrug resistance 1 gene in T315I mutated cells. **2022**, ○
- 33 Identification of immunogenic cell death-related gene classification patterns and immune infiltration characterization in ischemic stroke based on machine learning. 16, ○
- 32 Identification of perturbed pathways rendering susceptibility to tuberculosis in type 2 diabetes mellitus patients using BioNSi simulation of integrated networks of implicated human genes. **2022**, 47, ○
- 31 Harshening stem cell research and precision medicine: The states of human pluripotent cells stem cell repository diversity, and racial and sex differences in transcriptomes. 10, ○
- 30 A Newly Developed Chemically Defined Serum-Free Medium Suitable for Human Primary Keratinocyte Culture and Tissue Engineering Applications. **2023**, 24, 1821 ○
- 29 Bioinformatics Prediction and Experimental Validation Identify a Novel Cuproptosis-Related Gene Signature in Human Synovial Inflammation during Osteoarthritis Progression. **2023**, 13, 127 ○
- 28 Novel candidate genes for cholesteatoma in chronic otitis media. 13, ○
- 27 A novel risk model based on the correlation between the expression of basement membrane genes and immune infiltration to predict the invasiveness of pituitary adenomas. 13, ○

- 26 Exploration of the Link Between COVID-19 and Alcoholic Hepatitis from the Perspective of Bioinformatics and Systems Biology. ○
- 25 An evaluation of gastric adenocarcinoma-associated CircRNAs based on microarray meta-analysis and ceRNA networks. **2023**, 28, 101611 ○
- 24 Bioinformatics and systems biology approaches to identify the effects of COVID-19 on neurodegenerative diseases: A review. **2022**, 101, e32100 ○
- 23 Efficacy and safety of metabolic interventions for the treatment of severe COVID-19: in vitro, observational, and non-randomized open label interventional study. 12, 1
- 22 Identification of drug and protein-protein interaction network among stress and depression: A bioinformatics approach. **2023**, 37, 101174 ○
- 21 A bioinformatics approach to identify candidate biomarkers and common pathways between bipolar disorder and stroke. **2022**, ○
- 20 The use of bioinformatics methods to identify the effects of SARS-CoV-2 and influenza viruses on the regulation of gene expression in patients. 14, ○
- 19 *Akkermansia muciniphila* plays a neuroprotective role in HMC3 cells through the gut-brain axis. ○
- 18 Evaluation and assessment of nutritional composition for quality profiling of *Phoenix dactylifera* cultivars using multivariate analytical tools. **2023**, 27, 100173 ○
- 17 Pathogenomic Signature and Aberrant Neurogenic Events in Experimental Cerebral Ischemic Stroke: A Neurotranscriptomic-Based Implication for Dementia. **2023**, 1-20 ○
- 16 Integrated bioinformatics analyses identifying key transcriptomes correlated with prognosis and immune infiltrations in lung squamous cell carcinoma. **2023**, 30, 103596 ○
- 15 In silico Identification of Hypoxic Signature followed by reverse transcription-quantitative PCR Validation in Cancer Cell Lines. **2023**, 27, 23-33 ○
- 14 Exploring Core Genes by Comparative Transcriptomics Analysis for Early Diagnosis, Prognosis, and Therapies of Colorectal Cancer. **2023**, 15, 1369 ○
- 13 Vitamin B6, B12 and folate modulate deregulated pathways and protein aggregation in yeast model of Huntington disease. **2023**, 13, ○
- 12 Identification of a necroptosis-related gene signature as a novel prognostic biomarker of cholangiocarcinoma. 14, ○
- 11 Identification microenvironment immune features and key genes in elderly stroke patients. **2023**, 102, e33108 ○
- 10 An updated *C. elegans* nuclear body muscle transcriptome for studies in muscle formation and function. **2023**, 13, ○
- 9 Bulk RNA-Sequencing of small airway cell cultures from IPF and post-COVID lung fibrosis patients illustrates disease signatures and differential responses to TGF- β treatment. ○

- 8 Identification and Analysis of Necroptosis-Related Genes in COPD by Bioinformatics and Experimental Verification. **2023**, 13, 482
- 7 Molecular and network-level mechanisms explaining individual differences in autism spectrum disorder. **2023**, 26, 650-663
- 6 Network Analysis Reveals the Molecular Bases of Statin Pleiotropy That Vary with Genetic Background. **2023**, 11,
- 5 The pathogenetic influence of smoking on SARS-CoV-2 infection: Integrative transcriptome and regulomics analysis of lung epithelial cells. **2023**, 159, 106885
- 4 Integrated analysis of endoplasmic reticulum stress regulators expression identifies distinct subtypes of autism spectrum disorder. 14,
- 3 Identifying high-impact variants and genes in exomes of Ashkenazi Jewish inflammatory bowel disease patients. **2023**, 14,
- 2 Prognostic role and immune infiltration characteristics of E124 in multiple cancer types.
- 1 Analysis of N-glycosylation protein of KashinBeck disease chondrocytes derived from induced pluripotent stem cells based on label-free strategies with LC-MS/MS.