

Yong Dai

List of Publications by Year in descending order

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Version: 2024-02-01

187
papers

3,550
citations

172457

29
h-index

197818

49
g-index

193
all docs

193
docs citations

193
times ranked

5350
citing authors

#	ARTICLE	IF	CITATIONS
1	Label-free quantitative proteomic and phosphoproteomic analyses of renal biopsy tissues in membranous nephropathy. <i>Proteomics - Clinical Applications</i> , 2022, 16, e2000069.	1.6	0
2	Identification of exosomal mRNA, lncRNA and circRNA signatures in an osteoarthritis synovial fluid-exosomal study. <i>Experimental Cell Research</i> , 2022, 410, 112881.	2.6	15
3	A preliminary analysis of mitochondrial DNA atlas in the type 2 diabetes patients. <i>International Journal of Diabetes in Developing Countries</i> , 2022, 42, 713-720.	0.8	2
4	Exosomal circSHKBP1 participates in non-small cell lung cancer progression through PKM2-mediated glycolysis. <i>Molecular Therapy - Oncolytics</i> , 2022, 24, 470-485.	4.4	17
5	Global Proteomic Analyses Reveals Abnormal Immune Regulation in Patients With New Onset Ankylosing Spondylitis. <i>Frontiers in Immunology</i> , 2022, 13, 838891.	4.8	6
6	Metabolomics study reveals the alteration of fatty acid oxidation in the hearts of diabetic mice by empagliflozin. <i>Molecular Omics</i> , 2022, 18, 643-651.	2.8	7
7	New insights for regulatory T cell in lupus nephritis. <i>Autoimmunity Reviews</i> , 2022, 21, 103134.	5.8	13
8	Antibody responses to SARS-CoV-2 in healthy individuals returning to Shenzhen. <i>Journal of Medical Virology</i> , 2021, 93, 1154-1157.	5.0	2
9	A single-cell map for the transcriptomic signatures of peripheral blood mononuclear cells in end-stage renal disease. <i>Nephrology Dialysis Transplantation</i> , 2021, 36, 599-608.	0.7	13
10	Intestinal microbiome and metabolome analyses reveal metabolic disorders in the early stage of renal transplantation. <i>Molecular Omics</i> , 2021, 17, 985-996.	2.8	2
11	A report on seven fetal cases associated with 15q11-q13 microdeletion and microduplication. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1605.	1.2	3
12	Quantitative proteomics analysis of lysine 2-hydroxyisobutyrylation in IgA nephropathy. <i>Clinical Proteomics</i> , 2021, 18, 7.	2.1	8
13	Generation of Systemic Lupus Erythematosus Patient-Derived Induced Pluripotent Stem Cells from Blood. <i>Stem Cells and Development</i> , 2021, 30, 227-233.	2.1	3
14	Co-occurrence of Protein Crotonylation and 2-Hydroxyisobutyrylation in the Proteome of End-Stage Renal Disease. <i>ACS Omega</i> , 2021, 6, 15782-15793.	3.5	7
15	Histone succinylation and its function on the nucleosome. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 7101-7109.	3.6	28
16	Single-cell chromatin accessibility landscape of human umbilical cord blood in trisomy 18 syndrome. <i>Human Genomics</i> , 2021, 15, 40.	2.9	2
17	Kinectin 1 promotes the growth of triple-negative breast cancer via directly co-activating NF- κ B/p65 and enhancing its transcriptional activity. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 250.	17.1	10
18	Comparative Proteomic Analysis to Investigate the Pathogenesis of Oral Adenoid Cystic Carcinoma. <i>ACS Omega</i> , 2021, 6, 18623-18634.	3.5	8

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19	Advances in antigens associated with Idiopathic Membranous Nephropathy. Journal of the Formosan Medical Association, 2021, 120, 1941-1948.	1.7	1
20	Quantitative ubiquitylomics reveals the ubiquitination regulation landscape in oral adenoid cystic carcinoma. Bioscience Reports, 2021, 41, .	2.4	6
21	Integrated analysis of competing endogenous RNA networks in peripheral blood mononuclear cells of systemic lupus erythematosus. Journal of Translational Medicine, 2021, 19, 362.	4.4	12
22	The Landscape and Potential Regulatory Mechanism of Lysine 2-Hydroxyisobutyrylation of Protein in End-Stage Renal Disease. Nephron, 2021, 145, 760-769.	1.8	4
23	Comprehensive analysis of lysine crotonylation modification in patients with chronic renal failure. BMC Nephrology, 2021, 22, 310.	1.8	5
24	Methyltransferase-like protein 11A promotes migration of cervical cancer cells via up-regulating ELK3. Pharmacological Research, 2021, 172, 105814.	7.1	18
25	Lysine 2-hydroxyisobutyrylation proteomics reveals protein modification alteration in the actin cytoskeleton pathway of oral squamous cell carcinoma. Journal of Proteomics, 2021, 249, 104371.	2.4	15
26	Identification of a novel interplay between intestinal bacteria and metabolites in Chinese patients with IgA nephropathy via integrated microbiome and metabolome approaches. Annals of Translational Medicine, 2021, 9, 32-32.	1.7	16
27	Targeting KDM6A Suppresses SREBP1c-Dependent Lipid Metabolism and Prostate Tumorigenesis. Cancer Research, 2021, , OF1-OF15.	0.9	5
28	Systematic proteomics analysis of lysine acetylation reveals critical features of placental proteins in pregnant women with preeclampsia. Journal of Cellular and Molecular Medicine, 2021, 25, 10614-10626.	3.6	7
29	Multiomics landscape of the autosomal dominant osteopetrosis type II disease-specific induced pluripotent stem cells. Hereditas, 2021, 158, 40.	1.4	2
30	Integrated proteome and phosphoproteome analyses of peripheral blood mononuclear cells in primary Sjögren syndrome patients. Aging, 2021, 13, 1071-1095.	3.1	8
31	Analysis of gut microbiota and metabolites in patients with rheumatoid arthritis and identification of potential biomarkers. Aging, 2021, 13, 23689-23701.	3.1	35
32	Multi-Omics Analyses Revealed GOL1B as a Potential Prognostic Gene in Breast Cancer Probably Regulating the Immune Microenvironment. Frontiers in Oncology, 2021, 11, 805273.	2.8	3
33	Analysis of transcription factors in accessible open chromatin in the 18-trisomy syndrome based on single cell ATAC sequencing technique. Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji, 2021, 43, 74-83.	0.2	1
34	The ubiquitinase ZFP91 promotes tumor cell survival and confers chemoresistance through FOXA1 destabilization. Carcinogenesis, 2020, 41, 56-66.	2.8	9
35	Promoter hypermethylation of the CFTR gene as a novel diagnostic and prognostic marker of breast cancer. Cell Biology International, 2020, 44, 603-609.	3.0	18
36	Comprehensive Study of Tumor Immune Microenvironment and Relevant Genes in Hepatocellular Carcinoma Identifies Potential Prognostic Significance. Frontiers in Oncology, 2020, 10, 554165.	2.8	7

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37	Differential expression of transfer RNA-derived small RNAs in IgA nephropathy. <i>Medicine (United States)</i> , 2020, 99, 1007-1014.	1.0	6
38	Application of single-cell RNA sequencing in embryonic development. <i>Genomics</i> , 2020, 112, 4547-4551.	2.9	8
39	Protease Inhibitor Use in COVID-19. <i>SN Comprehensive Clinical Medicine</i> , 2020, 2, 1436-1443.	0.6	4
40	Epigenetic silencing of ZIC4 contributes to cancer progression in hepatocellular carcinoma. <i>Cell Death and Disease</i> , 2020, 11, 906.	6.3	3
41	Quantitative Proteomic Analyses To Reveal the Key Features of Proteins in New Onset Ankylosing Spondylitis Patients. <i>ACS Omega</i> , 2020, 5, 20153-20161.	3.5	4
42	Histone Demethylase JMJD1A Promotes Tumor Progression via Activating Snail in Prostate Cancer. <i>Molecular Cancer Research</i> , 2020, 18, 698-708.	3.4	14
43	The potential role of tRNAs and small RNAs derived from tRNAs in the occurrence and development of systemic lupus erythematosus. <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 561-567.	2.1	15
44	Targeting prostate cancer stem-like cells by an immunotherapeutic platform based on immunogenic peptide-sensitized dendritic cells-cytokine-induced killer cells. <i>Stem Cell Research and Therapy</i> , 2020, 11, 123.	5.5	16
45	Identification and Validation of Immune-Related Gene Prognostic Signature for Hepatocellular Carcinoma. <i>Journal of Immunology Research</i> , 2020, 2020, 1-14.	2.2	50
46	Quantitative analysis of protein crotonylation identifies its association with immunoglobulin A nephropathy. <i>Molecular Medicine Reports</i> , 2020, 21, 1242-1250.	2.4	8
47	Advances in applying of multi-omics approaches in the research of systemic lupus erythematosus. <i>International Reviews of Immunology</i> , 2020, 39, 163-173.	3.3	9
48	Controversial treatments: An updated understanding of the coronavirus disease 2019. <i>Journal of Medical Virology</i> , 2020, 92, 1441-1448.	5.0	73
49	Targeting the KDM4/AR/c-Myc axis promotes sensitivity to androgen receptor-targeted therapy in advanced prostate cancer. <i>Journal of Pathology</i> , 2020, 252, 101-113.	4.5	23
50	Mining Prognostic Biomarkers of Hepatocellular Carcinoma Based on Immune-Associated Genes. <i>DNA and Cell Biology</i> , 2020, 39, 499-512.	1.9	8
51	Identification of microRNAs and their Endonucleolytic Cleavaged target mRNAs in colorectal cancer. <i>BMC Cancer</i> , 2020, 20, 242.	2.6	12
52	Single-Cell RNA Sequencing Reveals the Expansion of Cytotoxic CD4+ T Lymphocytes and a Landscape of Immune Cells in Primary Sjögren's Syndrome. <i>Frontiers in Immunology</i> , 2020, 11, 594658.	4.8	47
53	Cytoplasmic PCNA is located in the actin belt and involved in osteoclast differentiation. <i>Aging</i> , 2020, 12, 13297-13317.	3.1	10
54	Expression profiling of immune cells in systemic lupus erythematosus by single-cell RNA sequencing. <i>Biocell</i> , 2020, 44, 559-582.	0.7	6

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55	Differential expression profile study and gene function analysis of maternal foetalâ€derived circRNA for screening for Down's syndrome. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 1006-1016.	1.8	3
56	Proteomic analysis of differentially expressed proteins in the serum of patients with acute renal allograft rejection using iTRAQ labelling technology. <i>Molecular Medicine Reports</i> , 2020, 22, 2329-2341.	2.4	7
57	Next generation sequencing reveals novel alterations in B-cell heavy chain receptor repertoires associated with acute-on-chronic liver failure. <i>International Journal of Molecular Medicine</i> , 2019, 43, 243-255.	4.0	11
58	Genotyping, generation and proteomic profiling of the first human autosomal dominant osteopetrosis type II-specific induced pluripotent stem cells. <i>Stem Cell Research and Therapy</i> , 2019, 10, 251.	5.5	6
59	DNA methylation-based classification and identification of renal cell carcinoma prognosis-subgroups. <i>Cancer Cell International</i> , 2019, 19, 185.	4.1	39
60	Establishment and Characterization of a CTC Cell Line from Peripheral Blood of Breast Cancer Patient. <i>Journal of Cancer</i> , 2019, 10, 6095-6104.	2.5	20
61	STUB1 suppresses tumorigenesis and chemoresistance through antagonizing YAP1 signaling. <i>Cancer Science</i> , 2019, 110, 3145-3156.	3.9	28
62	Single-Cell Sequencing Reveals the Relationship between Phenotypes and Genotypes of Klinefelter Syndrome. <i>Cytogenetic and Genome Research</i> , 2019, 159, 55-65.	1.1	9
63	Integrated analysis of quantitative proteome and transcriptional profiles reveals abnormal gene expression and signal pathway in bladder cancer. <i>Genes and Genomics</i> , 2019, 41, 1493-1503.	1.4	3
64	A comprehensive immune repertoire study for patients with pulmonary tuberculosis. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00792.	1.2	4
65	Profiling the TRB and IGH repertoire of patients with H5N6 Avian Influenza Virus Infection by high-throughput sequencing. <i>Scientific Reports</i> , 2019, 9, 7429.	3.3	13
66	Bioinformatics Analysis of the Core Genes Related to Lupus Nephritis Through a Network and Pathway-Based Approach. <i>DNA and Cell Biology</i> , 2019, 38, 639-650.	1.9	4
67	CFTR interacts with Hsp90 and regulates the phosphorylation of AKT and ERK1/2 in colorectal cancer cells. <i>FEBS Open Bio</i> , 2019, 9, 1119-1127.	2.3	13
68	Composition and diversity analysis of the Bâ€cell receptor immunoglobulin heavy chain complementarityâ€determining region 3 repertoire in patients with acute rejection after kidney transplantation using highâ€throughput sequencing. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 2206-2220.	1.8	10
69	Determination of the complexity and diversity of the TCR Î²â€chain CDR3 repertoire in bladder cancer using highâ€throughput sequencing. <i>Oncology Letters</i> , 2019, 17, 3808-3816.	1.8	5
70	Assessment of variation in B-cell receptor heavy chain repertoire in patients with end-stage renal disease by high-throughput sequencing. <i>Renal Failure</i> , 2019, 41, 1-13.	2.1	6
71	Targeted next generation sequencing identified novel lossâ€ofâ€function mutations in MERTK gene in Chinese patients with retinitis pigmentosa. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00577.	1.2	5
72	iTRAQâ€based proteomic analysis of human umbilical vein endothelial cells with platelet endothelial aggregation receptorâ€1 knockdown. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 12300-12310.	2.6	0

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73	Analysis of autophagy-related genes and associated noncoding RNAs and transcription factors in digestive system tumors. <i>Future Oncology</i> , 2019, 15, 4141-4154.	2.4	3
74	Single-cell transcriptional profiling reveals the heterogeneity in colorectal cancer. <i>Medicine (United States)</i> , 2019, 98, e16916.	1.0	23
75	Defective CFTR promotes intestinal proliferation via inhibition of the hedgehog pathway during cystic fibrosis. <i>Cancer Letters</i> , 2019, 446, 15-24.	7.2	10
76	Comparative proteomic analysis of human serum before and after liver transplantation using quantitative proteomics. <i>Oncotarget</i> , 2019, 10, 2508-2514.	1.8	1
77	Investigating the dysfunctional pathogenesis of Wilms's tumor through a multidimensional integration strategy. <i>Annals of Translational Medicine</i> , 2019, 7, 136-136.	1.7	7
78	Integrated analysis of B cell and T cell receptors by high-throughput sequencing reveals conserved repertoires in IgA nephropathy. <i>Molecular Medicine Reports</i> , 2018, 17, 7027-7036.	2.4	3
79	The differentially expressed circular ribonucleic acids of primary hepatic carcinoma following liver transplantation as new diagnostic biomarkers for primary hepatic carcinoma. <i>Tumor Biology</i> , 2018, 40, 101042831876692.	1.8	7
80	Verification of foetal Down syndrome biomarker proteins in maternal plasma and applications in prenatal screening for Down syndrome. <i>Translational Medicine Communications</i> , 2018, 3, .	1.4	2
81	Identification of 11 potentially relevant gene mutations involved in growth retardation, intellectual disability, joint contracture, and hepatopathy. <i>Medicine (United States)</i> , 2018, 97, e13117.	1.0	3
82	Characteristic analysis of TCR β -chain CDR3 repertoire for pre- and post-liver transplantation. <i>Oncotarget</i> , 2018, 9, 34506-34519.	1.8	13
83	Establishment of microRNA, transcript and protein regulatory networks in Alport syndrome induced pluripotent stem cells. <i>Molecular Medicine Reports</i> , 2018, 19, 238-250.	2.4	7
84	The composition and variation of the BCR CDR3s in gastric cancer. <i>Oncology Letters</i> , 2018, 16, 239-246.	1.8	1
85	Development of a novel and economical agar-based non-adherent three-dimensional culture method for enrichment of cancer stem-like cells. <i>Stem Cell Research and Therapy</i> , 2018, 9, 243.	5.5	48
86	Comprehensive analysis of lysine crotonylation in proteome of maintenance hemodialysis patients. <i>Medicine (United States)</i> , 2018, 97, e12035.	1.0	24
87	Association of the characteristics of B cell and T cell repertoires with papillary thyroid carcinoma. <i>Oncology Letters</i> , 2018, 16, 1584-1592.	1.8	8
88	Proteus syndrome: A case report and review of the literature. <i>Molecular and Clinical Oncology</i> , 2017, 6, 381-383.	1.0	20
89	Circular RNA and gene expression profiles in gastric cancer based on microarray chip technology. <i>Oncology Reports</i> , 2017, 37, 1804-1814.	2.6	71
90	Integrated analysis of microRNA and transcription factor reveals important regulators and regulatory motifs in adult B-cell acute lymphoblastic leukemia. <i>International Journal of Oncology</i> , 2017, 50, 671-683.	3.3	7

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91	Differential proteomics analysis of liver failure in peripheral blood mononuclear cells using isobaric tags for relative and absolute quantitation. <i>Biomedical Reports</i> , 2017, 6, 167-174.	2.0	0
92	A genetic risk factor for thrombophilia in a Han Chinese family. <i>Molecular Medicine Reports</i> , 2017, 15, 1668-1672.	2.4	3
93	Circular RNA expression profiles of peripheral blood mononuclear cells in rheumatoid arthritis patients, based on microarray chip technology. <i>Molecular Medicine Reports</i> , 2017, 16, 8029-8036.	2.4	102
94	Characterization of the T cell receptor repertoire by deep T cell receptor sequencing in tissues from patients with prostate cancer. <i>Oncology Letters</i> , 2017, 15, 1744-1752.	1.8	4
95	Down-regulation of MBD4 contributes to hypomethylation and overexpression of CD70 in CD4+ T cells in systemic lupus erythematosus. <i>Clinical Epigenetics</i> , 2017, 9, 104.	4.1	22
96	Immunology repertoire study of pulmonary sarcoidosis T cells in CD4+, CD8+ PBMC and tissue. <i>Oncotarget</i> , 2017, 8, 89515-89526.	1.8	3
97	Microarray based circRNA expression profiles in uremic plasma and PBMCs due to chronic glomerulonephritis. <i>Archives of Biological Sciences</i> , 2017, 69, 523-534.	0.5	2
98	Method Comparison and Bias Estimation of Blood Urea Nitrogen (BUN), Creatinine (Cr), and Uric Acid (UA) Measurements between Two Analytical Methods. <i>Clinical Laboratory</i> , 2017, 63, 73-77.	0.5	3
99	High Throughput Sequencing of T Cell Antigen Receptors Reveals a Conserved TCR Repertoire. <i>Medicine (United States)</i> , 2016, 95, e2839.	1.0	23
100	High salt promotes autoimmunity by TET2-induced DNA demethylation and driving the differentiation of Tfh cells. <i>Scientific Reports</i> , 2016, 6, 28065.	3.3	63
101	T cell repertoire following kidney transplantation revealed by high-throughput sequencing. <i>Transplant Immunology</i> , 2016, 39, 34-45.	1.2	22
102	Analysis of the Repertoire Features of TCR Beta Chain CDR3 in Human by High-Throughput Sequencing. <i>Cellular Physiology and Biochemistry</i> , 2016, 39, 651-667.	1.6	39
103	Integrated microRNA and protein expression analysis reveals novel microRNA regulation of targets in fetal down syndrome. <i>Molecular Medicine Reports</i> , 2016, 14, 4109-4118.	2.4	7
104	Integrated analysis of mRNA, microRNA and protein in systemic lupus erythematosus-specific induced pluripotent stem cells from urine. <i>BMC Genomics</i> , 2016, 17, 488.	2.8	16
105	Whole-genome resequencing of 100 healthy individuals using DNA pooling. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 3143-3150.	1.8	2
106	Differential proteomic analysis of respiratory failure in peripheral blood mononuclear cells using iTRAQ technology. <i>Biomedical Reports</i> , 2016, 4, 573-577.	2.0	0
107	Molecular dysfunctions in acute myeloid leukemia revealed by integrated analysis of microRNA and transcription factor. <i>International Journal of Oncology</i> , 2016, 48, 2367-2380.	3.3	5
108	Whole-genome re-sequencing for the identification of high contribution susceptibility gene variants in patients with type 2 diabetes. <i>Molecular Medicine Reports</i> , 2016, 13, 3735-3746.	2.4	5

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109	ARHGAP4 mutated in a Chinese intellectually challenged family. <i>Gene</i> , 2016, 578, 205-209.	2.2	6
110	<scp>CCDC</scp>40 mutation as a cause of primary ciliary dyskinesia: a case report and review of literature. <i>Clinical Respiratory Journal</i> , 2016, 10, 614-621.	1.6	26
111	Integrated analyses of a major histocompatibility complex, methylation and transcribed ultra-conserved regions in systemic lupus erythematosus. <i>International Journal of Molecular Medicine</i> , 2016, 37, 139-148.	4.0	3
112	Characters, functions and clinical perspectives of long non-coding RNAs. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1013-1033.	2.1	63
113	Study on 3' UTR length polymorphism in peripheral blood mononuclear cells of uremia patient. <i>Renal Failure</i> , 2016, 38, 96-99.	2.1	2
114	The role of icaritin in regulating Foxp3/IL17a balance in systemic lupus erythematosus and its effects on the treatment of MRL/lpr mice. <i>Clinical Immunology</i> , 2016, 162, 74-83.	3.2	29
115	Quantitative Proteomic Analysis of Peripheral Blood Mononuclear Cells in Ankylosing Spondylitis by iTRAQ. <i>Clinical and Translational Science</i> , 2015, 8, 579-583.	3.1	10
116	Quantitative proteomic analysis of Down syndrome in the umbilical cord blood using iTRAQ. <i>Molecular Medicine Reports</i> , 2015, 11, 1391-1399.	2.4	13
117	Tripterygium glycosides inhibit inflammatory mediators in the rat synovial RSC-364 cell line stimulated with interleukin-1 β . <i>Biomedical Reports</i> , 2015, 3, 763-766.	2.0	20
118	Generation of induced pluripotent stem cells from renal tubular cells of a patient with Alport syndrome. <i>International Journal of Nephrology and Renovascular Disease</i> , 2015, 8, 101.	1.8	12
119	Identification of microRNAs and their target genes in Alport syndrome using deep sequencing of iPSCs samples. <i>Journal of Zhejiang University: Science B</i> , 2015, 16, 235-250.	2.8	4
120	Comparative proteomic analysis of membranous nephropathy biopsy tissues using quantitative proteomics. <i>Experimental and Therapeutic Medicine</i> , 2015, 9, 805-810.	1.8	7
121	Genome-wide analysis of 5-hmC in the peripheral blood of systemic lupus erythematosus patients using an hMeDIP-chip. <i>International Journal of Molecular Medicine</i> , 2015, 35, 1467-1479.	4.0	22
122	The role of microRNA-1246 in the regulation of B cell activation and the pathogenesis of systemic lupus erythematosus. <i>Clinical Epigenetics</i> , 2015, 7, 24.	4.1	81
123	The effect of mycophenolic acid on epigenetic modifications in lupus CD4+T cells. <i>Clinical Immunology</i> , 2015, 158, 67-76.	3.2	45
124	Composition and variation analysis of the TCR β -chain CDR3 repertoire in systemic lupus erythematosus using high-throughput sequencing. <i>Molecular Immunology</i> , 2015, 67, 455-464.	2.2	47
125	Microarray analysis of long non-coding RNA expression in Ankylosing Spondylitis. <i>Integrative Molecular Medicine</i> , 2015, 2, .	0.3	0
126	Integration of major histocompatibility complex, methylation, and transcribed ultra-conserved regions analyses in uremia. <i>Integrative Molecular Medicine</i> , 2015, 2, .	0.3	0

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127	Exome sequencing identifies mutations in ABCD1 and DACH2 in two brothers with a distinct phenotype. <i>BMC Medical Genetics</i> , 2014, 15, 105.	2.1	7
128	Comparative proteomic analysis of renal tissue in IgA nephropathy with iTRAQ quantitative proteomics. <i>Biomedical Reports</i> , 2014, 2, 793-798.	2.0	7
129	Microarray analysis of long non-coding RNA expression in human acute rejection biopsy samples following renal transplantation. <i>Molecular Medicine Reports</i> , 2014, 10, 2210-2216.	2.4	28
130	Genome-wide analysis of DNA 5-hmC in peripheral blood of uremia by hMeDIP-chip. <i>Renal Failure</i> , 2014, 36, 937-945.	2.1	1
131	Analysis of microRNAs in patients with systemic lupus erythematosus, using Solexa deep sequencing. <i>Connective Tissue Research</i> , 2014, 55, 187-196.	2.3	9
132	Identification of potential microRNA-target pairs associated with osteopetrosis by deep sequencing, iTRAQ proteomics and bioinformatics. <i>European Journal of Human Genetics</i> , 2014, 22, 625-632.	2.8	32
133	Organ Donation in China: Current Status, Challenges, and Future Development. <i>Progress in Transplantation</i> , 2014, 24, 375-380.	0.7	13
134	Integrated profiling of microRNA expression in membranous nephropathy using high-throughput sequencing technology. <i>International Journal of Molecular Medicine</i> , 2014, 33, 25-34.	4.0	26
135	Integrated analysis of long non-coding RNAs and mRNA expression profiles reveals the potential role of lncRNAs in gastric cancer pathogenesis. <i>International Journal of Oncology</i> , 2014, 45, 619-628.	3.3	64
136	Evaluating a Particular Circulating MicroRNA Species from an SLE Patient Using Stem-Loop qRT-PCR. <i>Methods in Molecular Biology</i> , 2014, 1134, 201-209.	0.9	4
137	Microarray Technology for Analysis of MicroRNA Expression in Renal Biopsies of Lupus Nephritis Patients. <i>Methods in Molecular Biology</i> , 2014, 1134, 211-220.	0.9	10
138	Univariate and multiple linear regression analyses for 23 single nucleotide polymorphisms in 14 genes predisposing to chronic glomerular diseases and IgA nephropathy in Han Chinese. <i>Saudi Journal of Kidney Diseases and Transplantation: an Official Publication of the Saudi Center for Organ Transplantation, Saudi Arabia</i> , 2014, 25, 992.	0.3	5
139	Hematopoietic and mesenchymal stem cell transplantation for severe and refractory systemic lupus erythematosus. <i>Clinical Immunology</i> , 2013, 148, 186-197.	3.2	29
140	The effect of mesenchymal stromal cells on doxorubicin-induced nephropathy in rats. <i>Cytotherapy</i> , 2013, 15, 703-711.	0.7	18
141	Genome-wide analysis of histone H3 lysine9 trimethylation by ChIP-seq in peripheral blood mononuclear cells of uremia patients. <i>Hemodialysis International</i> , 2013, 17, 493-501.	0.9	3
142	Molecular dysfunctions in acute rejection after renal transplantation revealed by integrated analysis of transcription factor, microRNA and long noncoding RNA. <i>Genomics</i> , 2013, 102, 310-322.	2.9	40
143	Identification of dysregulated microRNAs in lymphocytes from children with Down syndrome. <i>Gene</i> , 2013, 530, 278-286.	2.2	27
144	Generation of systemic lupus erythematosus-specific induced pluripotent stem cells from urine. <i>Rheumatology International</i> , 2013, 33, 2127-2134.	3.0	38

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145	Rapid gene identification in a Chinese osteopetrosis family by whole exome sequencing. <i>Gene</i> , 2013, 516, 311-315.	2.2	19
146	Genome-wide analysis of microRNAs expression profiling in patients with primary IgA nephropathy. <i>Genome</i> , 2013, 56, 161-169.	2.0	48
147	¹ H NMR-Based Metabolic Profiling of Human Serum Before and After Renal Transplantation. <i>ASAIO Journal</i> , 2013, 59, 286-293.	1.6	8
148	Analysis of microRNA expression profile by small RNA sequencing in Down syndrome fetuses. <i>International Journal of Molecular Medicine</i> , 2013, 32, 1115-1125.	4.0	32
149	Differential proteomic analysis of renal tissue in mesangial proliferative glomerulonephritis using iTRAQ technology. <i>Journal of Nephrology</i> , 2013, 26, 191-198.	2.0	8
150	Genome-wide analysis of long noncoding RNA expression in peripheral blood mononuclear cells of uremia patients. <i>Journal of Nephrology</i> , 2013, 26, 731-738.	2.0	16
151	Transcription factor activity profile of acute rejection after kidney transplantation. <i>Saudi Journal of Kidney Diseases and Transplantation: an Official Publication of the Saudi Center for Organ Transplantation, Saudi Arabia</i> , 2013, 24, 480.	0.3	1
152	Altered long non-coding RNA expression profile in patients with IgA-negative mesangial proliferative glomerulonephritis. <i>International Journal of Molecular Medicine</i> , 2012, 30, 173-8.	4.0	13
153	Circulating microRNAs as candidate biomarkers in patients with systemic lupus erythematosus. <i>Translational Research</i> , 2012, 160, 198-206.	5.0	214
154	Reduced Circulating miR-15b Is Correlated with Phosphate Metabolism in Patients with End-Stage Renal Disease on Maintenance Hemodialysis. <i>Renal Failure</i> , 2012, 34, 685-690.	2.1	20
155	Differential proteomic analysis of renal tissue in lupus nephritis using iTRAQ reagent technology. <i>Rheumatology International</i> , 2012, 32, 3537-3543.	3.0	16
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