

Yong Dai

List of Publications by Year in descending order

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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	Comprehensive analysis of microRNA expression patterns in renal biopsies of lupus nephritis patients. <i>Rheumatology International</i> , 2009, 29, 749-754.	3.0	253
2	Circulating microRNAs as candidate biomarkers in patients with systemic lupus erythematosus. <i>Translational Research</i> , 2012, 160, 198-206.	5.0	214
3	Microarray analysis of MicroRNA expression in acute rejection after renal transplantation. <i>Transplant Immunology</i> , 2008, 19, 81-85.	1.2	140
4	Microarray analysis of microRNA expression in hepatocellular carcinoma and non-tumorous tissues without viral hepatitis. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2008, 23, 87-94.	2.8	122
5	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
6	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
7	Controversial treatments: An updated understanding of the coronavirus disease 2019. <i>Journal of Medical Virology</i> , 2020, 92, 1441-1448.	5.0	73
8	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
9	A Pilot Metabolic Profiling Study in Serum of Patients with Chronic Kidney Disease Based on ¹ H-NMR Spectroscopy. <i>Clinical and Translational Science</i> , 2012, 5, 379-385.	3.1	64
10	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
11	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
12	Characters, functions and clinical perspectives of long non-coding RNAs. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1013-1033.	2.1	63
13	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
14	Genome-wide analysis of microRNAs expression profiling in patients with primary IgA nephropathy. <i>Genome</i> , 2013, 56, 161-169.	2.0	48
15	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
16	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
17	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
18	The effect of mycophenolic acid on epigenetic modifications in lupus CD4 ⁺ T cells. <i>Clinical Immunology</i> , 2015, 158, 67-76.	3.2	45

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19	A proton nuclear magnetic resonance-based metabonomics study of metabolic profiling in immunoglobulin a nephropathy. <i>Clinics</i> , 2012, 67, 363-373.	1.5	42
20	Genome-wide analysis of histone H3 lysine 27 trimethylation by ChIP-chip in gastric cancer patients. <i>Journal of Gastroenterology</i> , 2009, 44, 305-312.	5.1	40
21	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
22	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
23	DNA methylation-based classification and identification of renal cell carcinoma prognosis-subgroups. <i>Cancer Cell International</i> , 2019, 19, 185.	4.1	39
24	Generation of systemic lupus erythematosus-specific induced pluripotent stem cells from urine. <i>Rheumatology International</i> , 2013, 33, 2127-2134.	3.0	38
25	¹ H NMR-based serum metabolic profiling in compensated and decompensated cirrhosis. <i>World Journal of Gastroenterology</i> , 2012, 18, 285.	3.3	35
26	Analysis of gut microbiota and metabolites in patients with rheumatoid arthritis and identification of potential biomarkers. <i>Aging</i> , 2021, 13, 23689-23701.	3.1	35
27	Circulating levels of inflammation-associated miR-155 and endothelial-enriched miR-126 in patients with end-stage renal disease. <i>Brazilian Journal of Medical and Biological Research</i> , 2012, 45, 1308-1314.	1.5	34
28	Comparative proteome analysis of peripheral blood mononuclear cells in systemic lupus erythematosus with iTRAQ quantitative proteomics. <i>Rheumatology International</i> , 2012, 32, 585-593.	3.0	34
29	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
30	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
31	Hematopoietic and mesenchymal stem cell transplantation for severe and refractory systemic lupus erythematosus. <i>Clinical Immunology</i> , 2013, 148, 186-197.	3.2	29
32	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
33	Comparison of immunohistochemistry (IHC) and fluorescence in situ hybridization (FISH) assessment for Her-2 status in breast cancer. <i>World Journal of Surgical Oncology</i> , 2009, 7, 83.	1.9	28
34	Proteomic profiling of renal allograft rejection in serum using magnetic bead-based sample fractionation and MALDI-TOF MS. <i>Clinical and Experimental Medicine</i> , 2010, 10, 259-268.	3.6	28
35	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
36	STUB1 suppresses tumorigenesis and chemoresistance through antagonizing YAP1 signaling. <i>Cancer Science</i> , 2019, 110, 3145-3156.	3.9	28

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37	Histone succinylation and its function on the nucleosome. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 7101-7109.	3.6	28
38	Identification of dysregulated microRNAs in lymphocytes from children with Down syndrome. <i>Gene</i> , 2013, 530, 278-286.	2.2	27
39	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
40	<sc>CCDC</sc>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
41	Comprehensive analysis of lysine crotonylation in proteome of maintenance hemodialysis patients. <i>Medicine (United States)</i> , 2018, 97, e12035.	1.0	24
42	High Throughput Sequencing of T Cell Antigen Receptors Reveals a Conserved TCR Repertoire. <i>Medicine (United States)</i> , 2016, 95, e2839.	1.0	23
43	Single-cell transcriptional profiling reveals the heterogeneity in colorectal cancer. <i>Medicine (United States)</i> , 2019, 98, e16916.	1.0	23
44	Targeting the <sc>KDM4</sc> axis promotes sensitivity to androgen receptor-targeted therapy in advanced prostate cancer. <i>Journal of Pathology</i> , 2020, 252, 101-113.	4.5	23
45	Microarray profile of microRNA in tumor tissue from cervical squamous cell carcinoma without human papillomavirus. <i>Journal of Obstetrics and Gynaecology Research</i> , 2009, 35, 842-849.	1.3	22
46	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
47	T cell repertoire following kidney transplantation revealed by high-throughput sequencing. <i>Transplant Immunology</i> , 2016, 39, 34-45.	1.2	22
48	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
49	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
50	Analysis of synovial fluid in knee joint of osteoarthritis:5 proteome patterns of joint inflammation based on matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>International Orthopaedics</i> , 2012, 36, 57-64.	1.9	20
51	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
52	Proteus syndrome: A case report and review of the literature. <i>Molecular and Clinical Oncology</i> , 2017, 6, 381-383.	1.0	20
53	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
54	Rapid gene identification in a Chinese osteopetrosis family by whole exome sequencing. <i>Gene</i> , 2013, 516, 311-315.	2.2	19

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55	Gain of the Human Telomerase RNA Gene TERC at 3q26 is Strongly Associated With Cervical Intraepithelial Neoplasia and Carcinoma. <i>International Journal of Gynecological Cancer</i> , 2009, 19, 1303-1306.	2.5	18
56	The effect of mesenchymal stromal cells on doxorubicin-induced nephropathy in rats. <i>Cytotherapy</i> , 2013, 15, 703-711.	0.7	18
57	Promoter hypermethylation of the CFTR gene as a novel diagnostic and prognostic marker of breast cancer. <i>Cell Biology International</i> , 2020, 44, 603-609.	3.0	18
58	Methyltransferase-like protein 11A promotes migration of cervical cancer cells via up-regulating ELK3. <i>Pharmacological Research</i> , 2021, 172, 105814.	7.1	18
59	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
60	Differential proteomic analysis of renal tissue in lupus nephritis using iTRAQ reagent technology. <i>Rheumatology International</i> , 2012, 32, 3537-3543.	3.0	16
61	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
62	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
63	Identification of a novel interplay between intestinal bacteria and metabolites in Chinese patients with IgA nephropathy via integrated microbiome and metabolome approaches. <i>Annals of Translational Medicine</i> , 2021, 9, 32-32.	1.7	16
64	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
65	Genome-Wide Analysis of Histone H3 Lysine 4 Trimethylation in Peripheral Blood Mononuclear Cells of Minimal Change Nephrotic Syndrome Patients. <i>American Journal of Nephrology</i> , 2009, 30, 505-513.	3.1	15
66	microRNA expression profile of peripheral blood mononuclear cells of Klinefelter syndrome. <i>Experimental and Therapeutic Medicine</i> , 2012, 4, 825-831.	1.8	15
67	Comparison of the metabolic profiling of hepatitis B virus-infected cirrhosis and alcoholic cirrhosis patients by using ¹ H NMR-based metabolomics. <i>Hepatology Research</i> , 2012, 42, 677-685.	3.4	15
68	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
69	Lysine 2-hydroxyisobutyrylation proteomics reveals protein modification alteration in the actin cytoskeleton pathway of oral squamous cell carcinoma. <i>Journal of Proteomics</i> , 2021, 249, 104371.	2.4	15
70	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
71	Histone Demethylase JMJD1A Promotes Tumor Progression via Activating Snail in Prostate Cancer. <i>Molecular Cancer Research</i> , 2020, 18, 698-708.	3.4	14
72	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

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73	Organ Donation in China: Current Status, Challenges, and Future Development. <i>Progress in Transplantation</i> , 2014, 24, 375-380.	0.7	13
74	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
75	Characteristic analysis of TCR β -chain CDR3 repertoire for pre- and post-liver transplantation. <i>Oncotarget</i> , 2018, 9, 34506-34519.	1.8	13
76	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
77	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
78	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
79	Screening Biomarkers for Systemic Lupus Erythematosus Based on Machine Learning and Exploring Their Expression Correlations With the Ratios of Various Immune Cells. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	13
80	New insights for regulatory T cell in lupus nephritis. <i>Autoimmunity Reviews</i> , 2022, 21, 103134.	5.8	13
81	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
82	Identification of microRNAs and their Endonucleolytic Cleaved target mRNAs in colorectal cancer. <i>BMC Cancer</i> , 2020, 20, 242.	2.6	12
83	Integrated analysis of competing endogenous RNA networks in peripheral blood mononuclear cells of systemic lupus erythematosus. <i>Journal of Translational Medicine</i> , 2021, 19, 362.	4.4	12
84	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
85	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
86	Composition and diversity analysis of the B α cell receptor immunoglobulin heavy chain complementarity-determining region 3 repertoire in patients with acute rejection after kidney transplantation using high-throughput sequencing. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 2206-2220.	1.8	10
87	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
88	Kinectin 1 promotes the growth of triple-negative breast cancer via directly co-activating NF-kappaB/p65 and enhancing its transcriptional activity. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 250.	17.1	10
89	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
90	Cytoplasmic PCNA is located in the actin belt and involved in osteoclast differentiation. <i>Aging</i> , 2020, 12, 13297-13317.	3.1	10

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91	Array-CGH detection of three cryptic submicroscopic imbalances in a complex chromosome rearrangement. <i>Journal of Genetics</i> , 2009, 88, 369-372.	0.7	9
92	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
93	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
94	The ubiquitinase ZFP91 promotes tumor cell survival and confers chemoresistance through FOXA1 destabilization. <i>Carcinogenesis</i> , 2020, 41, 56-66.	2.8	9
95	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
96	An Altered Th1/Th2 and Pro-Inflammatory Cytokine Profile in Patients with End-Stage Renal Disease Detected by Suspension Array Technology. <i>Renal Failure</i> , 2009, 31, 1-5.	2.1	8
97	Proteomic profiling of uremia in serum using magnetic bead-based sample fractionation and MALDI-TOF MS. <i>Renal Failure</i> , 2010, 32, 1153-1159.	2.1	8
98	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
99	Association of the characteristics of B α and T α cell repertoires with papillary thyroid carcinoma. <i>Oncology Letters</i> , 2018, 16, 1584-1592.	1.8	8
100	Application of single-cell RNA sequencing in embryonic development. <i>Genomics</i> , 2020, 112, 4547-4551.	2.9	8
101	Quantitative analysis of protein crotonylation identifies its association with immunoglobulin A nephropathy. <i>Molecular Medicine Reports</i> , 2020, 21, 1242-1250.	2.4	8
102	Mining Prognostic Biomarkers of Hepatocellular Carcinoma Based on Immune-Associated Genes. <i>DNA and Cell Biology</i> , 2020, 39, 499-512.	1.9	8
103	Quantitative proteomics analysis of lysine 2-hydroxyisobutyrylation in IgA nephropathy. <i>Clinical Proteomics</i> , 2021, 18, 7.	2.1	8
104	Comparative Proteomic Analysis to Investigate the Pathogenesis of Oral Adenoid Cystic Carcinoma. <i>ACS Omega</i> , 2021, 6, 18623-18634.	3.5	8
105	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
106	Integrated proteome and phosphoproteome analyses of peripheral blood mononuclear cells in primary Sjögren syndrome patients. <i>Aging</i> , 2021, 13, 1071-1095.	3.1	8
107	Characterization of the Phosphoproteome in SLE Patients. <i>PLoS ONE</i> , 2012, 7, e53129.	2.5	7
108	Comprehensive analysis of transcription factor expression patterns in peripheral blood mononuclear cell of systemic lupus erythematosus. <i>International Journal of Rheumatic Diseases</i> , 2012, 15, 212-219.	1.9	7

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109	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
110	Comparative proteomic analysis of renal tissue in IgA nephropathy with iTRAQ quantitative proteomics. <i>Biomedical Reports</i> , 2014, 2, 793-798.	2.0	7
111	Comparative proteomic analysis of membranous nephropathy biopsy tissues using quantitative proteomics. <i>Experimental and Therapeutic Medicine</i> , 2015, 9, 805-810.	1.8	7
112	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
113	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
114	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
115	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
116	Comprehensive Study of Tumor Immune Microenvironment and Relevant Genes in Hepatocellular Carcinoma Identifies Potential Prognostic Significance. <i>Frontiers in Oncology</i> , 2020, 10, 554165.	2.8	7
117	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
118	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
119	Systematic proteomics analysis of lysine acetylation reveals critical features of placental proteins in pregnant women with preeclampsia. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 10614-10626.	3.6	7
120	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
121	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
122	ARHGAP4 mutated in a Chinese intellectually challenged family. <i>Gene</i> , 2016, 578, 205-209.	2.2	6
123	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
124	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
125	Differential expression of transfer RNA-derived small RNAs in IgA nephropathy. <i>Medicine (United States)</i> 100:7843-7854. doi:10.1093/med/100.7843-7854	1.0	6
126	Quantitative ubiquitylomics reveals the ubiquitination regulation landscape in oral adenoid cystic carcinoma. <i>Bioscience Reports</i> , 2021, 41, .	2.4	6

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127	Expression profiling of immune cells in systemic lupus erythematosus by single-cell RNA sequencing. <i>Biocell</i> , 2020, 44, 559-582.	0.7	6
128	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
129	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
130	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
131	Determination of the complexity and diversity of the TCR β -chain CDR3 repertoire in bladder cancer using high-throughput sequencing. <i>Oncology Letters</i> , 2019, 17, 3808-3816.	1.8	5
132	Targeted next generation sequencing identified novel loss-of-function mutations in MERTK gene in Chinese patients with retinitis pigmentosa. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00577.	1.2	5
133	Comprehensive analysis of lysine crotonylation modification in patients with chronic renal failure. <i>BMC Nephrology</i> , 2021, 22, 310.	1.8	5
134	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
135	Targeting KDM6A Suppresses SREBP1c-Dependent Lipid Metabolism and Prostate Tumorigenesis. <i>Cancer Research</i> , 2021, , OF1-OF15.	0.9	5
136	The Univariate and Multiple Linear Regression Analyses for Seventeen SNPs in Thirteen Cardiovascular Disease-Predisposing Genes and Blood Pressure in Chinese Han Males. <i>Clinical and Experimental Hypertension</i> , 2008, 30, 648-661.	1.3	4
137	Array-CGH detection of <i>UGT2B28</i> gene deletion in a girl with primary amenorrhea and hyperandrogenism. <i>International Journal of Gynecology and Obstetrics</i> , 2010, 109, 164-166.	2.3	4
138	CpG Array Analysis of Histone H3 Lysine 4 Trimethylation in Peripheral Blood Mononuclear Cells of Uremia Patients. <i>DNA and Cell Biology</i> , 2011, 30, 179-186.	1.9	4
139	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
140	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
141	A comprehensive immune repertoire study for patients with pulmonary tuberculosis. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00792.	1.2	4
142	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
143	Protease Inhibitor Use in COVID-19. <i>SN Comprehensive Clinical Medicine</i> , 2020, 2, 1436-1443.	0.6	4
144	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

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145	The Landscape and Potential Regulatory Mechanism of Lysine 2-Hydroxyisobutyrylation of Protein in End-Stage Renal Disease. <i>Nephron</i> , 2021, 145, 760-769.	1.8	4
146	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
147	CpG Array Analysis of Histone H3 Lysine 4 Trimethylation by Chromatin Immunoprecipitation Linked to Microarrays Analysis in Peripheral Blood Mononuclear Cells of IgA Nephropathy Patients. <i>Yonsei Medical Journal</i> , 2012, 53, 377.	2.2	3
148	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
149	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
150	A genetic risk factor for thrombophilia in a Han Chinese family. <i>Molecular Medicine Reports</i> , 2017, 15, 1668-1672.	2.4	3
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