List of Publications by Year in descending order

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LERON HOOD

#	Article	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	A distinct lineage of CD4 T cells regulates tissue inflammation by producing interleukin 17. Nature Immunology, 2005, 6, 1133-1141.	14.5	3,869
3	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	12.0	2,275
4	Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network. Science, 2001, 292, 929-934.	12.6	1,921
5	Direct multiplexed measurement of gene expression with color-coded probe pairs. Nature Biotechnology, 2008, 26, 317-325.	17.5	1,832
6	A NEWAPPROACH TODECODINGLIFE: Systems Biology. Annual Review of Genomics and Human Genetics, 2001, 2, 343-372.	6.2	1,455
7	Whole-Genome Shotgun Assembly and Analysis of the Genome of <i>Fugu rubripes</i> . Science, 2002, 297, 1301-1310.	12.6	1,432
8	A Genomic Regulatory Network for Development. Science, 2002, 295, 1669-1678.	12.6	1,399
9	Alagille syndrome is caused by mutations in human Jagged1, which encodes a ligand for Notch1. Nature Genetics, 1997, 16, 243-251.	21.4	1,184
10	Analysis of Genetic Inheritance in a Family Quartet by Whole-Genome Sequencing. Science, 2010, 328, 636-639.	12.6	979
11	Systems Biology and New Technologies Enable Predictive and Preventative Medicine. Science, 2004, 306, 640-643.	12.6	977
12	Systems Biology, Proteomics, and the Future of Health Care:Â Toward Predictive, Preventative, and Personalized Medicine. Journal of Proteome Research, 2004, 3, 179-196.	3.7	680
13	Transgenic mice that express a myelin basic protein-specific T cell receptor develop spontaneous autoimmunity. Cell, 1993, 72, 551-560.	28.9	657
14	Death Receptor 5, a New Member of the TNFR Family, and DR4 Induce FADD-Dependent Apoptosis and Activate the NF-κB Pathway. Immunity, 1997, 7, 821-830.	14.3	656
15	Predictive, personalized, preventive, participatory (P4) cancer medicine. Nature Reviews Clinical Oncology, 2011, 8, 184-187.	27.6	628
16	Multiple early factors anticipate post-acute COVID-19 sequelae. Cell, 2022, 185, 881-895.e20.	28.9	605
17	Restricted use of T cell receptor V genes in murine autoimmune encephalomyelitis raises possibilities for antibody therapy. Cell, 1988, 54, 577-592.	28.9	596
18	Complementary Profiling of Gene Expression at the Transcriptome and Proteome Levels in Saccharomyces cerevisiae. Molecular and Cellular Proteomics, 2002, 1, 323-333.	3.8	591

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19	Integrated barcode chips for rapid, multiplexed analysis of proteins in microliter quantities of blood. Nature Biotechnology, 2008, 26, 1373-1378.	17.5	507
20	A single VH gene segment encodes the immune response to phosphorylcholine: Somatic mutation is correlated with the class of the antibody. Cell, 1981, 25, 59-66.	28.9	496
21	lgC antibodies to phosphorylcholine exhibit more diversity than their IgM counterparts. Nature, 1981, 291, 29-34.	27.8	492
22	A molecular map of the immune response region from the major histocompatibility complex of the mouse. Nature, 1982, 300, 35-42.	27.8	460
23	The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. Genome Biology, 2006, 7, R36.	9.6	456
24	Introduced T cell receptor variable region gene segments recombine in pre-B cells: Evidence that B and T cells use a common recombinase. Cell, 1986, 44, 251-259.	28.9	455
25	Clusters of genes encoding mouse transplantation antigens. Cell, 1982, 28, 489-498.	28.9	449
26	Multi-Omics Resolves a Sharp Disease-State Shift between Mild and Moderate COVID-19. Cell, 2020, 183, 1479-1495.e20.	28.9	449
27	A personal view on systems medicine and the emergence of proactive P4 medicine: predictive, preventive, personalized and participatory. New Biotechnology, 2012, 29, 613-624.	4.4	442
28	Mouse T cell antigen receptor: Structure and organization of constant and joining gene segments encoding the β polypeptide. Cell, 1984, 37, 1101-1110.	28.9	422
29	P4 medicine: how systems medicine will transform the healthcare sector and society. Personalized Medicine, 2013, 10, 565-576.	1.5	422
30	The program of androgen-responsive genes in neoplastic prostate epithelium. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11890-11895.	7.1	407
31	PTEN-deficient intestinal stem cells initiate intestinal polyposis. Nature Genetics, 2007, 39, 189-198.	21.4	391
32	Hematopoietic Stem Cells Contribute to the Regeneration of Renal Tubules after Renal Ischemia-Reperfusion Injury in Mice. Journal of the American Society of Nephrology: JASN, 2003, 14, 1188-1199.	6.1	387
33	Conserved organization of the human and murine T-cell receptor Î ² -gene families. Nature, 1988, 331, 543-546.	27.8	374
34	Gene Families: The Taxonomy of Protein Paralogs and Chimeras. Science, 1997, 278, 609-614.	12.6	362
35	Comparative hybridization of an array of 21 500 ovarian cDNAs for the discovery of genes overexpressed in ovarian carcinomas. Gene, 1999, 238, 375-385.	2.2	342
36	Antibody diversity: Somatic hypermutation of rearranged VH genes. Cell, 1981, 27, 573-581.	28.9	340

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37	A pseudogene homologous to mouse transplantation antigens: Transplantation antigens are encoded by eight exons that correlate with protein domains. Cell, 1981, 25, 683-692.	28.9	340
38	A wellness study of 108 individuals using personal, dense, dynamic data clouds. Nature Biotechnology, 2017, 35, 747-756.	17.5	340
39	A new strategy for genome sequencing. Nature, 1996, 381, 364-366.	27.8	338
40	Systems medicine: the future of medical genomics and healthcare. Genome Medicine, 2009, 1, 2.	8.2	333
41	A Provisional Regulatory Gene Network for Specification of Endomesoderm in the Sea Urchin Embryo. Developmental Biology, 2002, 246, 162-190.	2.0	319
42	An immunoglobulin heavy-chain gene is formed by at least two recombinational events. Nature, 1980, 283, 733-739.	27.8	305
43	Quantitative phosphoproteome analysis using a dendrimer conjugation chemistry and tandem mass spectrometry. Nature Methods, 2005, 2, 591-598.	19.0	302
44	The human t cell antigen receptor is encoded by variable, diversity, and joining gene segments that rearrange to generate a complete V gene. Cell, 1984, 37, 393-401.	28.9	300
45	Single-cell proteomic chip for profiling intracellular signaling pathways in single tumor cells. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 419-424.	7.1	300
46	The structure, rearrangement and expression of $\hat{D^2}$ gene segments of the murine T-cell antigen receptor. Nature, 1984, 311, 344-349.	27.8	299
47	Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. Cell, 2016, 166, 766-778.	28.9	295
48	The murine T-cell receptor uses a limited repertoire of expressed VÎ ² gene segments. Nature, 1985, 316, 517-523.	27.8	294
49	Understanding the Adaptation of Halobacterium Species NRC-1 to Its Extreme Environment through Computational Analysis of Its Genome Sequence. Genome Research, 2001, 11, 1641-1650.	5.5	294
50	A data integration methodology for systems biology. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17296-17301.	7.1	293
51	Evidence for a Rare Prostate Cancer–Susceptibility Locus at Chromosome 1p36. American Journal of Human Genetics, 1999, 64, 776-787.	6.2	292
52	A Predictive Model for Transcriptional Control of Physiology in a Free Living Cell. Cell, 2007, 131, 1354-1365.	28.9	284
53	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. Nature Metabolism, 2021, 3, 274-286.	11.9	278
54	Monitoring gene expression profile changes in ovarian carcinomas using cDNA microarray. Gene, 1999, 229, 101-108.	2.2	277

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55	Diversity of the Immunoglobulin Gene Superfamily. Advances in Immunology, 1989, 44, 1-63.	2.2	274
56	Modulation of the NF-κB pathway by virally encoded Death Effector Domains-containing proteins. Oncogene, 1999, 18, 5738-5746.	5.9	271
57	Genome sequence of Haloarcula marismortui: A halophilic archaeon from the Dead Sea. Genome Research, 2004, 14, 2221-2234.	5.5	268
58	The Human Homolog of Rat Jagged1Expressed by Marrow Stroma Inhibits Differentiation of 32D Cells through Interaction with Notch1. Immunity, 1998, 8, 43-55.	14.3	261
59	A molecular correlate to the Gleason grading system for prostate adenocarcinoma. Proceedings of the United States of America, 2006, 103, 10991-10996.	7.1	261
60	Dysregulated gene expression networks in human acute myelogenous leukemia stem cells. Proceedings of the United States of America, 2009, 106, 3396-3401.	7.1	253
61	Asparagine-linked glycosylation of the scrapie and cellular prion proteins. Archives of Biochemistry and Biophysics, 1989, 274, 1-13.	3.0	246
62	Systems biology: integrating technology, biology, and computation. Mechanisms of Ageing and Development, 2003, 124, 9-16.	4.6	235
63	Proteomic analysis of human prostasomes. Prostate, 2003, 56, 150-161.	2.3	226
64	The digital code of DNA. Nature, 2003, 421, 444-448.	27.8	226
65	The T cell receptor β chain genes are located on chromosome 6 in mice and chromosome 7 in humans. Cell, 1984, 37, 1091-1099.	28.9	225
66	Revolutionizing medicine in the 21 st century through systems approaches. Biotechnology Journal, 2012, 7, 992-1001.	3.5	225
67	Activation of the NF- \hat{I}^{e} B pathway by Caspase 8 and its homologs. Oncogene, 2000, 19, 4451-4460.	5.9	219
68	Genomic organization of the genes encoding mouse T-cell receptor α-chain. Nature, 1985, 316, 832-836.	27.8	216
69	Predominant use of a Vα gene segment in mouse T-cell receptors for cytochrome c. Nature, 1986, 324, 679-682.	27.8	214
70	The impact of systems approaches on biological problems in drug discovery. Nature Biotechnology, 2004, 22, 1215-1217.	17.5	213
71	Blood metabolome predicts gut microbiome α-diversity in humans. Nature Biotechnology, 2019, 37, 1217-1228.	17.5	213
72	Regulatory gene networks and the properties of the developmental process. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1475-1480	7.1	211

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73	Label-Free Quantitative Detection of Tumor-Derived Exosomes through Surface Plasmon Resonance Imaging. Analytical Chemistry, 2014, 86, 8857-8864.	6.5	211
74	Systems Biology and P4 Medicine: Past, Present, and Future. Rambam Maimonides Medical Journal, 2013, 4, e0012.	1.0	208
75	Genetic Effects on Age-Dependent Onset and Islet Cell Autoantibody Markers in Type 1 Diabetes. Diabetes, 2002, 51, 1346-1355.	0.6	203
76	Mouse epidermal la molecules have a bone marrow origin. Nature, 1979, 282, 321-323.	27.8	194
77	A T cell clone expresses two T cell receptor α genes but uses one αβ heterodimer for allorecognition and self MHC-restricted antigen recognition. Cell, 1988, 55, 49-59.	28.9	190
78	The human genome project: big science transforms biology and medicine. Genome Medicine, 2013, 5, 79.	8.2	184
79	Rearrangement and transcription of the β-chain genes of the T-cell antigen receptor in different types of murine lymphocytes. Nature, 1985, 313, 647-653.	27.8	183
80	Systems medicine and integrated care to combat chronic noncommunicable diseases. Genome Medicine, 2011, 3, 43.	8.2	181
81	Mutations in STX1B, encoding a presynaptic protein, cause fever-associated epilepsy syndromes. Nature Genetics, 2014, 46, 1327-1332.	21.4	178
82	The P4 Health Spectrum – A Predictive, Preventive, Personalized and Participatory Continuum for Promoting Healthspan. Progress in Cardiovascular Diseases, 2017, 59, 506-521.	3.1	178
83	The Human T-Cell Receptor TCRAC/TCRDC (Cα/Cdelta;) Region: Organization, Sequence, and Evolution of 97.6 kb of DNA. Genomics, 1994, 19, 478-493.	2.9	171
84	Differential gene expression profiling of adult murine hematopoietic stem cells. Blood, 2002, 99, 488-498.	1.4	168
85	Boosting Signal-to-Noise in Complex Biology: Prior Knowledge Is Power. Cell, 2011, 144, 860-863.	28.9	167
86	A Blood-Based Proteomic Classifier for the Molecular Characterization of Pulmonary Nodules. Science Translational Medicine, 2013, 5, 207ra142.	12.4	165
87	Analysis of the Human Neurexin Genes: Alternative Splicing and the Generation of Protein Diversity. Genomics, 2002, 79, 587-597.	2.9	164
88	Comparative Genomics of the Human and Mouse T Cell Receptor Loci. Immunity, 2001, 15, 337-349.	14.3	163
89	Identification of the class I genes of the mouse major histocompatibility complex by DNA-mediated gene transfer. Nature, 1982, 300, 231-237.	27.8	160
90	Striking sequence similarity over almost 100 kilobases of human and mouse T–cell receptor DNA. Nature Genetics, 1994, 7, 48-53.	21.4	160

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91	Activated Notch4 Inhibits Angiogenesis: Role of β1-Integrin Activation. Molecular and Cellular Biology, 2002, 22, 2830-2841.	2.3	157
92	Direct evidence for chromosomal inversion during T-cell receptor Î ² -gene rearrangements. Nature, 1986, 319, 28-33.	27.8	152
93	Shotgun Glycopeptide Capture Approach Coupled with Mass Spectrometry for Comprehensive Glycoproteomics. Molecular and Cellular Proteomics, 2007, 6, 141-149.	3.8	152
94	Rare variants in neuronal excitability genes influence risk for bipolar disorder. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3576-3581.	7.1	152
95	Highly accurate two-gene classifier for differentiating gastrointestinal stromal tumors and leiomyosarcomas. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3414-3419.	7.1	144
96	Predictive, preventive, personalized and participatory medicine: back to the future. Genome Medicine, 2010, 2, 57.	8.2	144
97	Lipopolysaccharide Mediates Endothelial Apoptosis by a FADD-dependent Pathway. Journal of Biological Chemistry, 1998, 273, 20185-20188.	3.4	141
98	Cancer as robust intrinsic state of endogenous molecular-cellular network shaped by evolution. Medical Hypotheses, 2008, 70, 678-684.	1.5	141
99	Organization, structure, and function of 95 kb of DNA spanning the murine T-cell receptor CαCδ region. Genomics, 1992, 13, 1209-1230.	2.9	139
100	One heavy chain variable region gene segment subfamily in the BALBc mouse contains 500–1000 or more members. Cell, 1986, 47, 461-470.	28.9	138
101	Optimized conditions for pulsed field gel electrophoretic separations of DNA. Nucleic Acids Research, 1988, 16, 7563-7582.	14.5	138
102	Proteomic analysis identifies that 14-3-3Â interacts with Â-catenin and facilitates its activation by Akt. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15370-15375.	7.1	138
103	A Combined Genomewide Linkage Scan of 1,233 Families for Prostate Cancer–Susceptibility Genes Conducted by the International Consortium for Prostate Cancer Genetics. American Journal of Human Genetics, 2005, 77, 219-229.	6.2	138
104	Participatory medicine: a driving force for revolutionizing healthcare. Genome Medicine, 2013, 5, 110.	8.2	137
105	The Generation of Diversity in Phosphorylcholine-Binding Antibodies. Advances in Immunology, 1984, 35, 1-37.	2.2	136
106	Genome-Wide Analysis of Epigenetic Silencing Identifies BEX1 and BEX2 as Candidate Tumor Suppressor Genes in Malignant Glioma. Cancer Research, 2006, 66, 6665-6674.	0.9	135
107	Elevated expression of DKK1 is associated with cytoplasmic/nuclear β-catenin accumulation and poor prognosis in hepatocellular carcinomas. Journal of Hepatology, 2009, 50, 948-957.	3.7	131
108	Systems Level Insights Into the Stress Response to UV Radiation in the Halophilic Archaeon Halobacterium NRC-1. Genome Research, 2004, 14, 1025-1035.	5.5	130

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109	A novel Fanconi anaemia subtype associated with a dominant-negative mutation in RAD51. Nature Communications, 2015, 6, 8829.	12.8	130
110	The joining of V and J gene segments creates antibody diversity. Nature, 1980, 283, 497-499.	27.8	129
111	Rearranged \hat{l}^2 t cell receptor genes in a helper t cell clone specific for lysozyme: No correlation between VÎ ² and MHC restriction. Cell, 1985, 40, 859-867.	28.9	128
112	GrpL, a Grb2-related Adaptor Protein, Interacts with SLP-76 to Regulate Nuclear Factor of Activated T Cell Activation. Journal of Experimental Medicine, 1999, 189, 1243-1253.	8.5	128
113	A single gene encodes soluble and membrane-bound forms of the major histocompatibility Qa-2 antigen: Anchoring of the product by a phospholipid tail. Cell, 1987, 50, 759-768.	28.9	125
114	Identification of a diversity segment of human T-cell receptor \hat{I}^2 -chain, and comparison with the analogous murine element. Nature, 1984, 311, 387-389.	27.8	124
115	Coordinate regulation of energy transduction modules in Halobacterium sp. analyzed by a global systems approach. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14913-14918.	7.1	123
116	Parallel microfluidic surface plasmon resonance imaging arrays. Lab on A Chip, 2010, 10, 581.	6.0	123
117	The dysmyelinating mouse mutations shiverer (shi) and myelin deficient (shi mld). Behavior Genetics, 1990, 20, 213-234.	2.1	122
118	Sequencing the Human Genome. Science, 1997, 278, 605-607.	12.6	121
119	Proteins Associated with Cisplatin Resistance in Ovarian Cancer Cells Identified by Quantitative Proteomic Technology and Integrated with mRNA Expression Levels. Molecular and Cellular Proteomics, 2006, 5, 433-443.	3.8	118
120	A speculative view of the multicomponent nature of T cell antigen recognition. Cell, 1986, 45, 475-484.	28.9	117
121	Linkage Analysis of 49 High-Risk Families Does Not Support a Common Familial Prostate Cancer—Susceptibility Gene at 1q24-25. American Journal of Human Genetics, 1997, 61, 347-353.	6.2	114
122	Expression and function of transplantation antigens with altered or deleted cytoplasmic domains. Cell, 1983, 34, 535-544.	28.9	113
123	Snapshot of a Large Dynamic Replicon in a Halophilic Archaeon: Megaplasmid or Minichromosome?. Genome Research, 1998, 8, 1131-1141.	5.5	113
124	The DNA sequence and analysis of human chromosome 14. Nature, 2003, 421, 601-607.	27.8	108
125		27.8	105
	Immunology: The growing immunoglobulin gene superfamily. Nature, 1986, 323, 15-16.	27.0	100

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127	From functional genomics to systems biology: concepts and practices. Comptes Rendus - Biologies, 2003, 326, 879-892.	0.2	103
128	Electrochemically Programmed, Spatially Selective Biofunctionalization of Silicon Wires. Langmuir, 2004, 20, 10630-10638.	3.5	102
129	Detailed transcriptome atlas of the pancreatic beta cell. BMC Medical Genomics, 2009, 2, 3.	1.5	102
130	Morphometric Analysis of Normal, Mutant, and Transgenic CNS: Correlation of Myelin Basic Protein Expression to Myelinogenesis. Journal of Neurochemistry, 1992, 58, 342-349.	3.9	101
131	Pairwise end sequencing: a unified approach to genomic mapping and sequencing. Genomics, 1995, 26, 345-353.	2.9	101
132	Rabbit Antibody Light Chains and Gene Evolution. Nature, 1970, 228, 1040-1044.	27.8	98
133	Toxoplasma Modulates Signature Pathways of Human Epilepsy, Neurodegeneration & Cancer. Scientific Reports, 2017, 7, 11496.	3.3	97
134	Cell population structure prior to bifurcation predicts efficiency of directed differentiation in human induced pluripotent cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2271-2276.	7.1	96
135	Is gene expression in Halobacterium NRC-1 regulated by multiple TBP and TFB transcription factors?. MicroCorrespondence. Molecular Microbiology, 2000, 36, 1184-1185.	2.5	94
136	Analysis of the Gene-Dense Major Histocompatibility Complex Class III Region and Its Comparison to Mouse. Genome Research, 2003, 13, 2621-2636.	5.5	94
137	Predictive Big Data Analytics: A Study of Parkinson's Disease Using Large, Complex, Heterogeneous, Incongruent, Multi-Source and Incomplete Observations. PLoS ONE, 2016, 11, e0157077.	2.5	94
138	A unified test of linkage analysis and rare-variant association for analysis of pedigree sequence data. Nature Biotechnology, 2014, 32, 663-669.	17.5	93
139	Autoimmune T cells: Immune recognition of normal and variant peptide epitopes and peptide-based therapy. Cell, 1989, 59, 257-271.	28.9	90
140	Evolutionary history of Tibetans inferred from whole-genome sequencing. PLoS Genetics, 2017, 13, e1006675.	3.5	89
141	A Genomic Scan of Families with Prostate Cancer Identifies Multiple Regions of Interest. American Journal of Human Genetics, 2000, 67, 100-109.	6.2	88
142	brp and blh Are Required for Synthesis of the Retinal Cofactor of Bacteriorhodopsin in Halobacterium salinarum. Journal of Biological Chemistry, 2001, 276, 5739-5744.	3.4	87
143	A Review of Computational Tools in microRNA Discovery. Frontiers in Genetics, 2013, 4, 81.	2.3	86
144	The myelin proteins of the shark brain are similar to the myelin proteins of the mammalian peripheral nervous system. Journal of Molecular Evolution, 1989, 29, 149-156.	1.8	84

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145	The Molecular Evolution of the Vertebrate Trypsinogens. Journal of Molecular Evolution, 1997, 45, 640-652.	1.8	84
146	Proteomics Analysis of the Interactome of N-myc Downstream Regulated Gene 1 and Its Interactions with the Androgen Response Program in Prostate Cancer Cells. Molecular and Cellular Proteomics, 2007, 6, 575-588.	3.8	83
147	Systems Approaches to Biology and Disease Enable Translational Systems Medicine. Genomics, Proteomics and Bioinformatics, 2012, 10, 181-185.	6.9	83
148	Integrated analysis of plasma and single immune cells uncovers metabolic changes in individuals with COVID-19. Nature Biotechnology, 2022, 40, 110-120.	17.5	81
149	The effect of maternal SARS-CoV-2 infection timing on birth outcomes: a retrospective multicentre cohort study. The Lancet Digital Health, 2022, 4, e95-e104.	12.3	81
150	Novel submicroscopic extrachromosomal elements containing amplified genes in human cells. Nature, 1987, 327, 434-437.	27.8	79
151	Massively Parallel Signature Sequencing and Bioinformatics Analysis Identifies Up-Regulation of TGFBI and SOX4 in Human Glioblastoma. PLoS ONE, 2010, 5, e10210.	2.5	77
152	Integrated Expression Profiling and ChIP-seq Analyses of the Growth Inhibition Response Program of the Androgen Receptor. PLoS ONE, 2009, 4, e6589.	2.5	77
153	Quantitative Proteomics Analysis Integrated with Microarray Data Reveals That Extracellular Matrix Proteins, Catenins, and P53 Binding Protein 1 Are Important for Chemotherapy Response in Ovarian Cancers. OMICS A Journal of Integrative Biology, 2009, 13, 345-354.	2.0	76
154	Immunoglobulin Lambda Chain Structure: Two Genes, One Polypeptide Chain. Nature, 1968, 220, 764-767.	27.8	75
155	Identifying Tightly Regulated and Variably Expressed Networks by Differential Rank Conservation (DIRAC). PLoS Computational Biology, 2010, 6, e1000792.	3.2	73
156	Quantitative Serum Proteomics from Surface Plasmon Resonance Imaging. Molecular and Cellular Proteomics, 2008, 7, 2464-2474.	3.8	71
157	Product of a transferred H–2Ld gene acts as restriction element for LCMV-specific killer T cells. Nature, 1982, 297, 415-417.	27.8	70
158	Analysis of Chromosome 1q42.2-43 in 152 Families with High Risk of Prostate Cancer. American Journal of Human Genetics, 1999, 64, 1087-1095.	6.2	70
159	Big biomedical data as the key resource for discovery science. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1126-1131.	4.4	70
160	Genetic Evaluation of Suspected Cases of Transient HIV-1 Infection of Infants. Science, 1998, 280, 1073-1077.	12.6	68
161	Multi-omic biomarker identification and validation for diagnosing warzone-related post-traumatic stress disorder. Molecular Psychiatry, 2020, 25, 3337-3349.	7.9	68
162	Sequence analysis of mouse vomeronasal receptor gene clusters reveals common promoter motifs and a history of recent expansion. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 291-296.	7.1	67

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163	Analysis of the DNA sequence and duplication history of human chromosome 15. Nature, 2006, 440, 671-675.	27.8	67
164	Relationship Estimation from Whole-Genome Sequence Data. PLoS Genetics, 2014, 10, e1004144.	3.5	67
165	Demystifying Disease, Democratizing Health Care. Science Translational Medicine, 2014, 6, 225ed5.	12.4	67
166	Low Fidelity Mutants in the O-Helix of Thermus aquaticus DNA Polymerase I. Journal of Biological Chemistry, 1997, 272, 11228-11235.	3.4	66
167	Initial Proteome Analysis of Model Microorganism <i>Haemophilus influenzae</i> Strain Rd KW20. Journal of Bacteriology, 2003, 185, 4593-4602.	2.2	66
168	Landscape of the SOX2 protein–protein interactome. Proteomics, 2011, 11, 921-934.	2.2	66
169	Integrating big data and actionable health coaching to optimize wellness. BMC Medicine, 2015, 13, 4.	5.5	66
170	Testing the Hypothesis of a Recombinant Origin of Human Immunodeficiency Virus Type 1 Subtype E. Journal of Virology, 2000, 74, 10752-10765.	3.4	65
171	Systems biology at the Institute for Systems Biology. Briefings in Functional Genomics & Proteomics, 2008, 7, 239-248.	3.8	65
172	Global analysis of H3K4me3 and H3K27me3 profiles in glioblastoma stem cells and identification of SLC17A7 as a bivalent tumor suppressor gene. Oncotarget, 2015, 6, 5369-5381.	1.8	65
173	Expression of complete transplantation antigens by mammalian cells transformed with truncated class I genes. Nature, 1983, 301, 388-394.	27.8	64
174	Bridging the BMP and Wnt Pathways by PI3 Kinase/Akt and 14-3-3?. Cell Cycle, 2005, 4, 218-219.	2.6	64
175	Analysis of chemotherapy response programs in ovarian cancers by the next-generation sequencing technologies. Gynecologic Oncology, 2010, 117, 159-169.	1.4	64
176	Chromosomal Haplotypes by Genetic Phasing of Human Families. American Journal of Human Genetics, 2011, 89, 382-397.	6.2	63
177	Expression of l–Ak class II genes in mouse L cells after DNA-mediated gene transfer. Nature, 1983, 305, 440-443.	27.8	62
178	Extracellular vesicle <scp>RNA</scp> s reflect placenta dysfunction and are a biomarker source for preterm labour. Journal of Cellular and Molecular Medicine, 2018, 22, 2760-2773.	3.6	62
179	Cell type-specific genes show striking and distinct patterns of spatial expression in the mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3095-3100.	7.1	61
180	Genomic scan of 254 hereditary prostate cancer families. Prostate, 2003, 57, 309-319.	2.3	59

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181	INDUCTION OF RABBIT ANTIBODY WITH MOLECULAR UNIFORMITY AFTER IMMUNIZATION WITH GROUP C STREPTOCOCCI. Journal of Experimental Medicine, 1970, 131, 207-221.	8.5	58
182	Genetic Mapping at 3-Kilobase Resolution Reveals Inositol 1,4,5-Triphosphate Receptor 3 as a Risk Factor for Type 1 Diabetes in Sweden. American Journal of Human Genetics, 2006, 79, 614-627.	6.2	58
183	A Personal View of Molecular Technology and How It Has Changed Biology. Journal of Proteome Research, 2002, 1, 399-409.	3.7	57
184	New and improved proteomics technologies for understanding complex biological systems: Addressing a grand challenge in the life sciences. Proteomics, 2012, 12, 2773-2783.	2.2	57
185	Whole-Genome Sequencing of the World's Oldest People. PLoS ONE, 2014, 9, e112430.	2.5	57
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