Michael Paul Snyder

List of Publications by Year
in descending order

476 papers	103,581 citations	369 135 h-index	261 299 g-index
538 all docs	538 docs citations	538 times ranked	114215 citing authors

#	Article	IF	Citations
1	RNA-Seq: a revolutionary tool for transcriptomics. Nature Reviews Genetics, 2009, 10, 57-63.	16.3	10,529
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
3	Functional profiling of the Saccharomyces cerevisiae genome. Nature, 2002, 418, 387-391.	27.8	3,938
4	Functional Characterization of the S. cerevisiae Genome by Gene Deletion and Parallel Analysis. Science, 1999, 285, 901-906.	12.6	3,761
5	Annotation of functional variation in personal genomes using RegulomeDB. Genome Research, 2012, 22, 1790-1797.	5.5	2,335
6	The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing. Science, 2008, 320, 1344-1349.	12.6	2,180
7	Global Analysis of Protein Activities Using Proteome Chips. Science, 2001, 293, 2101-2105.	12.6	2,082
8	Single-cell chromatin accessibility reveals principles of regulatory variation. Nature, 2015, 523, 486-490.	27.8	1,798
9	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	5.5	1,708
10	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
11	CNVnator: An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. Genome Research, 2011, 21, 974-984.	5.5	1,387
12	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	27.8	1,384
13	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. Science, 2008, 322, 104-110.	12.6	1,297
14	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. Nature Methods, 2007, 4, 651-657.	19.0	1,254
15	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
16	A Bayesian Networks Approach for Predicting Protein-Protein Interactions from Genomic Data. Science, 2003, 302, 449-453.	12.6	1,183
17	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	28.9	1,134
18	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	28.9	1,096

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19	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. Nature, 2001, 409, 533-538.	27.8	1,030
20	Paired-End Mapping Reveals Extensive Structural Variation in the Human Genome. Science, 2007, 318, 420-426.	12.6	1,003
21	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
22	Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. Science, 2004, 306, 2242-2246.	12.6	983
23	High-Throughput Sequencing Technologies. Molecular Cell, 2015, 58, 586-597.	9.7	968
24	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. Nature Genetics, 2016, 48, 1193-1203.	21.4	952
25	Global analysis of protein phosphorylation in yeast. Nature, 2005, 438, 679-684.	27.8	915
26	Integrative Analysis of the *Caenorhabditis elegans* Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	12.6	912
27	Protein chip technology. Current Opinion in Chemical Biology, 2003, 7, 55-63.	6.1	861
28	Analysis of yeast protein kinases using protein chips. Nature Genetics, 2000, 26, 283-289.	21.4	810
29	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	28.9	804
30	Topologically associating domains are stable units of replication-timing regulation. Nature, 2014, 515, 402-405.	27.8	779
31	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research, 2012, 22, 1798-1812.	5.5	762
32	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	27.8	744
33	Predicting non-small cell lung cancer prognosis by fully automated microscopic pathology image features. Nature Communications, 2016, 7, 12474.	12.8	694
34	Integrative omics for health and disease. Nature Reviews Genetics, 2018, 19, 299-310.	16.3	676
35	Linking disease associations with regulatory information in the human genome. Genome Research, 2012, 22, 1748-1759.	5.5	657
36	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	7.1	635

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37	Protein analysis on a proteomic scale. Nature, 2003, 422, 208-215.	27.8	610
38	A single-molecule long-read survey of the human transcriptome. Nature Biotechnology, 2013, 31, 1009-1014.	17.5	600
39	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	8.0	580
40	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. Science, 2019, 364, .	12.6	576
41	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. Nature, 1999, 402, 413-418.	27.8	521
42	Variation in Transcription Factor Binding Among Humans. Science, 2010, 328, 232-235.	12.6	521
43	Landscape and variation of RNA secondary structure across the human transcriptome. Nature, 2014, 505, 706-709.	27.8	519
44	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. Nature Biotechnology, 2009, 27, 66-75.	17.5	514
45	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	28.9	498
46	Getting connected: analysis and principles of biological networks. Genes and Development, 2007, 21, 1010-1024.	5.9	477
47	A proposal for validation of antibodies. Nature Methods, 2016, 13, 823-827.	19.0	473
48	Performance comparison of exome DNA sequencing technologies. Nature Biotechnology, 2011, 29, 908-914.	17.5	464
49	New insights into *Acinetobacter baumannii* pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. Genes and Development, 2007, 21, 601-614.	5.9	455
50	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. Genes and Development, 2005, 19, 2816-2826.	5.9	443
51	MAPK target networks in *Arabidopsis thaliana* revealed using functional protein microarrays. Genes and Development, 2009, 23, 80-92.	5.9	438
52	Widespread contribution of transposable elements to the innovation of gene regulatory networks. Genome Research, 2014, 24, 1963-1976.	5.5	408
53	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. Cell, 2014, 158, 673-688.	28.9	404
54	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nature Methods, 2021, 18, 747-756.	19.0	403

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55	Annotating non-coding regions of the genome. Nature Reviews Genetics, 2010, 11, 559-571.	16.3	398
56	Clinical Interpretation and Implications of Whole-Genome Sequencing. JAMA - Journal of the American Medical Association, 2014, 311, 1035.	7.4	398
57	Longitudinal multi-omics of host–microbe dynamics in prediabetes. Nature, 2019, 569, 663-671.	27.8	391
58	Protein arrays and microarrays. Current Opinion in Chemical Biology, 2001, 5, 40-45.	6.1	376
59	Differential binding of calmodulin-related proteins to their targets revealed through high-density Arabidopsis protein microarrays. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4730-4735.	7.1	369
60	Wearables and the medical revolution. Personalized Medicine, 2018, 15, 429-448.	1.5	361
61	Variation and genetic control of protein abundance in humans. Nature, 2013, 499, 79-82.	27.8	343
62	Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. Science Signaling, 2010, 3, ra12.	3.6	341
63	Extensive Variation in Chromatin States Across Humans. Science, 2013, 342, 750-752.	12.6	338
64	Comparison of the transcriptional landscapes between human and mouse tissues. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17224-17229.	7.1	337
65	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
66	Proteomics. Annual Review of Biochemistry, 2003, 72, 783-812.	11.1	332
67	A longitudinal big data approach for precision health. Nature Medicine, 2019, 25, 792-804.	30.7	329
68	Non-equivalence of Wnt and R-spondin ligands during Lgr5+ intestinal stem-cell self-renewal. Nature, 2017, 545, 238-242.	27.8	327
69	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. Cell Metabolism, 2018, 27, 559-571.e5.	16.2	321
70	Divergence of Transcription Factor Binding Sites Across Related Yeast Species. Science, 2007, 317, 815-819.	12.6	320
71	Digital Health: Tracking Physiomes and Activity Using Wearable Biosensors Reveals Useful Health-Related Information. PLoS Biology, 2017, 15, e2001402.	5.6	319
72	Landscape of Next-Generation Sequencing Technologies. Analytical Chemistry, 2011, 83, 4327-4341.	6.5	314

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73	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	28.9	304
74	Macrophage de novo NAD+ synthesis specifies immune function in aging and inflammation. Nature Immunology, 2019, 20, 50-63.	14.5	304
75	Pre-symptomatic detection of COVID-19 from smartwatch data. Nature Biomedical Engineering, 2020, 4, 1208-1220.	22.5	304
76	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	3.8	294
77	AlleleSeq: analysis of alleleâ€specific expression and binding in a network framework. Molecular Systems Biology, 2011, 7, 522.	7.2	284
78	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. Nature Communications, 2017, 8, 15178.	12.8	284
79	Performance comparison of whole-genome sequencing platforms. Nature Biotechnology, 2012, 30, 78-82.	17.5	281
80	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223.	17.5	281
81	Analyzing antibody specificity with whole proteome microarrays. Nature Biotechnology, 2003, 21, 1509-1512.	17.5	270
82	Exerkines in health, resilience and disease. Nature Reviews Endocrinology, 2022, 18, 273-289.	9.6	268
83	Molecular Choreography of Acute Exercise. Cell, 2020, 181, 1112-1130.e16.	28.9	261
84	Defining a personal, allele-specific, and single-molecule long-read transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9869-9874.	7.1	259
85	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	27.8	259
86	Genome-wide map of regulatory interactions in the human genome. Genome Research, 2014, 24, 1905-1917.	5.5	259
87	Lineage-specific dynamic and pre-established enhancerâ€"promoter contacts cooperate in terminal differentiation. Nature Genetics, 2017, 49, 1522-1528.	21.4	255
88	Highâ€throughput sequencing for biology and medicine. Molecular Systems Biology, 2013, 9, 640.	7.2	251
89	Identification of differentially expressed proteins in ovarian cancer using high-density protein microarrays. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17494-17499.	7.1	250
90	Novel mutations in PIEZO1 cause an autosomal recessive generalized lymphatic dysplasia with non-immune hydrops fetalis. Nature Communications, 2015, 6, 8085.	12.8	247

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91	Promise of personalized omics to precision medicine. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2013, 5, 73-82.	6.6	245
92	CELL POLARITY AND MORPHOGENESIS IN BUDDING YEAST. Annual Review of Microbiology, 1998, 52, 687-744.	7.3	243
93	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
94	Physiological blood–brain transport is impaired with age by a shift in transcytosis. Nature, 2020, 583, 425-430.	27.8	243
95	Genomic analysis of mycosis fungoides and Sézary syndrome identifies recurrent alterations in TNFR2. Nature Genetics, 2015, 47, 1056-1060.	21.4	242
96	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. Molecular Cell, 2017, 67, 1037-1048.e6.	9.7	242
97	Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae. Genes and Development, 2002, 16, 3017-3033.	5.9	236
98	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. Genome Biology, 2012, 13, R48.	9.6	233
99	Circular DNA elements of chromosomal origin are common in healthy human somatic tissue. Nature Communications, 2018, 9, 1069.	12.8	232
100	Finding new components of the target of rapamycin (TOR) signaling network through chemical genetics and proteome chips. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16594-16599.	7.1	225
101	Recurrent somatic mutations in regulatory regions of human cancer genomes. Nature Genetics, 2015, 47, 710-716.	21.4	225
102	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. Nature Communications, 2017, 8, 59.	12.8	225
103	Personal aging markers and ageotypes revealed by deep longitudinal profiling. Nature Medicine, 2020, 26, 83-90.	30.7	225
104	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E440-9.	7.1	224
105	Regulation of Gene Expression by a Metabolic Enzyme. Science, 2004, 306, 482-484.	12.6	223
106	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. Genome Biology, 2009, 10, R23.	9.6	223
107	Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events. Nature Biotechnology, 2015, 33, 736-742.	17.5	205
108	Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. Nature Biotechnology, 2014, 32, 562-568.	17.5	202

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109	Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. Cell, 2010, 143, 639-650.	28.9	200
110	Genomic binding profiles of functionally distinct RNA polymerase III transcription complexes in human cells. Nature Structural and Molecular Biology, 2010, 17, 635-640.	8.2	197
111	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. Cell, 2016, 167, 1734-1749.e22.	28.9	195
112	Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. Nature Genetics, 2016, 48, 687-693.	21.4	193
113	Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulumâ€"associated degradation pathway. Genetics in Medicine, 2014, 16, 751-758.	2.4	191
114	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. Nature, 2019, 574, 553-558.	27.8	187
115	Mapping accessible chromatin regions using Sono-Seq. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14926-14931.	7.1	186
116	Diverse Roles and Interactions of the SWI/SNF Chromatin Remodeling Complex Revealed Using Global Approaches. PLoS Genetics, 2011, 7, e1002008.	3.5	185
117	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	27.8	184
118	Optimized Analytical Procedures for the Untargeted Metabolomic Profiling of Human Urine and Plasma by Combining Hydrophilic Interaction (HILIC) and Reverse-Phase Liquid Chromatography (RPLC)â€"Mass Spectrometry*. Molecular and Cellular Proteomics, 2015, 14, 1684-1695.	3.8	183
119	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. Cell Systems, 2018, 6, 157-170.e8.	6.2	183
120	Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures. Bioinformatics, 2014, 30, 2808-2810.	4.1	182
121	Mapping of transcription factor binding regions in mammalian cells by ChIP: Comparison of array- and sequencing-based technologies. Genome Research, 2007, 17, 898-909.	5.5	181
122	Gpr124 is essential for bloodâ€"brain barrier integrity in central nervous system disease. Nature Medicine, 2017, 23, 450-460.	30.7	177
123	Whole-genome haplotyping using long reads and statistical methods. Nature Biotechnology, 2014, 32, 261-266.	17.5	170
124	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5254-5259.	7.1	168
125	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. Genome Research, 2012, 22, 1735-1747.	5.5	168
126	Close association of RNA polymerase II and many transcription factors with Pol III genes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3639-3644.	7.1	167

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127	Glucotypes reveal new patterns of glucose dysregulation. PLoS Biology, 2018, 16, e2005143.	5.6	167
128	Genome-Wide Identification of Binding Sites Defines Distinct Functions for Caenorhabditis elegans PHA-4/FOXA in Development and Environmental Response. PLoS Genetics, 2010, 6, e1000848.	3.5	165
129	Patient-Specific iPSC-Derived Endothelial Cells Uncover Pathways that Protect against Pulmonary Hypertension in BMPR2 Mutation Carriers. Cell Stem Cell, 2017, 20, 490-504.e5.	11.1	163
130	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. Cell, 2019, 178, 1245-1259.e14.	28.9	163
131	Genetic analysis of variation in transcription factor binding in yeast. Nature, 2010, 464, 1187-1191.	27.8	162
132	Multiomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. Bioinformatics, 2019, 35, 95-103.	4.1	162
133	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. Nature Biotechnology, 2010, 28, 47-55.	17.5	158
134	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
135	Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. Genome Research, 2015, 25, 1610-1621.	5.5	157
136	Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging. Nature Methods, 2022, 19, 284-295.	19.0	156
137	Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. Cell, 2020, 181, 1680-1692.e15.	28.9	154
138	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	12.8	152
139	ChIP-chip: A genomic approach for identifying transcription factor binding sites. Methods in Enzymology, 2002, 350, 469-483.	1.0	151
140	iPSC-derived cardiomyocytes reveal abnormal TGF-β signalling in left ventricular non-compaction cardiomyopathy. Nature Cell Biology, 2016, 18, 1031-1042.	10.3	148
141	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. Cell, 2020, 181, 1464-1474.	28.9	147
142	Molecular Mechanisms of Ethanol-Induced Pathogenesis Revealed by RNA-Sequencing. PLoS Pathogens, 2010, 6, e1000834.	4.7	142
143	Dynamic trans-Acting Factor Colocalization in Human Cells. Cell, 2013, 155, 713-724.	28.9	142
144	Whole-exome sequencing identifies tetratricopeptide repeat domain 7A (TTC7A) mutations for combined immunodeficiency with intestinal atresias. Journal of Allergy and Clinical Immunology, 2013, 132, 656-664.e17.	2.9	140

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145	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. Molecular Systems Biology, 2014, 10, 774.	7.2	138
146	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. BMC Genomics, 2009, 10, 37.	2.8	137
147	Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence. PLoS Genetics, 2011, 7, e1002280.	3.5	137
148	Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. Cell, 2018, 175, 277-291.e31.	28.9	137
149	Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. Nature Genetics, 2018, 50, 1716-1727.	21.4	135
150	Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. Nature Biomedical Engineering, 2019, 3, 1009-1019.	22.5	135
151	Landscape of cohesin-mediated chromatin loops in the human genome. Nature, 2020, 583, 737-743.	27.8	134
152	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. Cell Metabolism, 2016, 24, 172-184.	16.2	133
153	Severe acute respiratory syndrome diagnostics using a coronavirus protein microarray. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4011-4016.	7.1	131
154	Transcriptome Profiling of Patient-Specific Human iPSC-Cardiomyocytes Predicts Individual Drug Safety and Efficacy Responses InÂVitro. Cell Stem Cell, 2016, 19, 311-325.	11.1	131
155	Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression. Nature Communications, 2017, 8, 14995.	12.8	131
156	Mango: a bias-correcting ChIA-PET analysis pipeline. Bioinformatics, 2015, 31, 3092-3098.	4.1	126
157	High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4534-4539.	7.1	125
158	Charging it up: global analysis of protein phosphorylation. Trends in Genetics, 2006, 22, 545-554.	6.7	123
159	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
160	Wearable sensors enable personalized predictions of clinical laboratory measurements. Nature Medicine, 2021, 27, 1105-1112.	30.7	121
161	Personal genome sequencing: current approaches and challenges. Genes and Development, 2010, 24, 423-431.	5.9	119
162	Systematic identification of silencers in human cells. Nature Genetics, 2020, 52, 254-263.	21.4	119

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163	Genome-Wide Temporal Profiling of Transcriptome and Open Chromatin of Early Cardiomyocyte Differentiation Derived From hiPSCs and hESCs. Circulation Research, 2017, 121, 376-391.	4.5	118
164	A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. Nature Genetics, 2018, 50, 613-620.	21.4	116
165	Regulatory analysis of the C. elegans genome with spatiotemporal resolution. Nature, 2014, 512, 400-405.	27.8	115
166	Defining Genes in the Genomics Era. Science, 2003, 300, 258-260.	12.6	114
167	Network analyses identify liver‑specific targets for treating liver diseases. Molecular Systems Biology, 2017, 13, 938.	7.2	112
168	Overview of High Throughput Sequencing Technologies to Elucidate Molecular Pathways in Cardiovascular Diseases. Circulation Research, 2013, 112, 1613-1623.	4.5	110
169	Structured elements drive extensive circular RNA translation. Molecular Cell, 2021, 81, 4300-4318.e13.	9.7	108
170	Detecting and annotating genetic variations using the HugeSeq pipeline. Nature Biotechnology, 2012, 30, 226-229.	17.5	104
171	ChIA-PET2: a versatile and flexible pipeline for ChIA-PET data analysis. Nucleic Acids Research, 2017, 45, e4-e4.	14.5	104
172	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. Nature Communications, 2019, 10, 4063.	12.8	104
173	Windows into human health through wearables data analytics. Current Opinion in Biomedical Engineering, 2019, 9, 28-46.	3.4	101
174	High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. PLoS Genetics, 2008, 4, e1000249.	3.5	99
175	Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. Frontiers in Microbiology, 2017, 8, 1079.	3.5	97
176	Emerging technologies in yeast genomics. Nature Reviews Genetics, 2001, 2, 302-312.	16.3	96
177	NIH working group report—using genomic information to guide weight management: From universal to precision treatment. Obesity, 2016, 24, 14-22.	3.0	96
178	An exercise-inducible metabolite that suppresses feeding and obesity. Nature, 2022, 606, 785-790.	27.8	96
179	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	12.8	95
180	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94

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181	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. PLoS ONE, 2016, 11, e0162868.	2.5	93
182	Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome. Nature Biotechnology, 2016, 34, 64-69.	17.5	93
183	Systems biology: personalized medicine for the future?. Current Opinion in Pharmacology, 2012, 12, 623-628.	3.5	90
184	Altered Cardiac Energetics and Mitochondrial Dysfunction in Hypertrophic Cardiomyopathy. Circulation, 2021, 144, 1714-1731.	1.6	90
185	Dynamic and complex transcription factor binding during an inducible response in yeast. Genes and Development, 2009, 23, 1351-1363.	5.9	89
186	Tcf7 Is an Important Regulator of the Switch of Self-Renewal and Differentiation in a Multipotential Hematopoietic Cell Line. PLoS Genetics, 2012, 8, e1002565.	3.5	88
187	Association of Omics Features with Histopathology Patterns in Lung Adenocarcinoma. Cell Systems, 2017, 5, 620-627.e3.	6.2	88
188	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. Nature Genetics, 2021, 53, 638-649.	21.4	86
189	Systematic functional regulatory assessment of disease-associated variants. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9607-9612.	7.1	85
190	Omics Profiling in Precision Oncology. Molecular and Cellular Proteomics, 2016, 15, 2525-2536.	3.8	84
191	Integrated trajectories of the maternal metabolome, proteome, and immunome predict labor onset. Science Translational Medicine, 2021, 13, .	12.4	82
192	A Filamentous Growth Response Mediated by the Yeast Mating Pathway. Genetics, 2001, 159, 919-928.	2.9	82
193	Cross-Platform Comparison of Untargeted and Targeted Lipidomics Approaches on Aging Mouse Plasma. Scientific Reports, 2018, 8, 17747.	3.3	81
194	Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations. Nature Genetics, 2016, 48, 117-125.	21.4	80
195	Pharmacological rescue of diabetic skeletal stem cell niches. Science Translational Medicine, 2017, 9, .	12.4	80
196	Global analysis of the glycoproteome in <i>Saccharomyces cerevisiae</i> reveals new roles for protein glycosylation in eukaryotes. Molecular Systems Biology, 2009, 5, 308.	7.2	79
197	The Development of Protein Microarrays and Their Applications in DNAâ€"Protein and Proteinâ€"Protein Interaction Analyses of Arabidopsis Transcription Factors. Molecular Plant, 2008, 1, 27-41.	8.3	78
198	Smooth Muscle Contact Drives Endothelial Regeneration by BMPR2-Notch1â€"Mediated Metabolic and Epigenetic Changes. Circulation Research, 2019, 124, 211-224.	4.5	78

#	ARTICLE	IF	CITATIONS
199	Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer. Nature Genetics, 2022, 54, 985-995.	21.4	77
200	Characterization of the Dynamic Transcriptome of a Herpesvirus with Long-read Single Molecule Real-Time Sequencing. Scientific Reports, 2017, 7, 43751.	3.3	76
201	Long-Read Sequencing â€" A Powerful Tool in Viral Transcriptome Research. Trends in Microbiology, 2019, 27, 578-592.	7.7	76
202	Long-Read Sequencing of Human Cytomegalovirus Transcriptome Reveals RNA Isoforms Carrying Distinct Coding Potentials. Scientific Reports, 2017, 7, 15989.	3.3	75
203	Effects of cellular origin on differentiation of human induced pluripotent stem cellâ€"derived endothelial cells. JCI Insight, 2016, 1, .	5.0	75
204	Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. Genes and Development, 2003, 17, 2698-2708.	5.9	74
205	Succinate and its G-protein-coupled receptor stimulates osteoclastogenesis. Nature Communications, 2017, 8, 15621.	12.8	73
206	Gene-Environment Interaction in the Era of Precision Medicine. Cell, 2019, 177, 38-44.	28.9	73
207	Induced Pluripotent Stem Cell Model of Pulmonary Arterial Hypertension Reveals Novel Gene Expression and Patient Specificity. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 930-941.	5.6	72
208	Regulatory Variation Within and Between Species. Annual Review of Genomics and Human Genetics, 2011, 12, 327-346.	6.2	70
209	Classifying non-small cell lung cancer types and transcriptomic subtypes using convolutional neural networks. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 757-769.	4.4	69
210	Real-time alerting system for COVID-19 and other stress events using wearable data. Nature Medicine, 2022, 28, 175-184.	30.7	69
211	Molecular and functional resemblance of differentiated cells derived from isogenic human iPSCs and SCNT-derived ESCs. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E11111-E11120.	7.1	68
212	Decoding the Genomics of Abdominal Aortic Aneurysm. Cell, 2018, 174, 1361-1372.e10.	28.9	68
213	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
214	iPOP Goes the World: Integrated Personalized Omics Profiling and the Road toward Improved Health Care. Chemistry and Biology, 2013, 20, 660-666.	6.0	67
215	Identification of STAT5A and STAT5B Target Genes in Human T Cells. PLoS ONE, 2014, 9, e86790.	2.5	67
216	Personalized sequencing and the future of medicine: discovery, diagnosis and defeat of disease. Pharmacogenomics, 2014, 15, 1771-1790.	1.3	66

#	Article	IF	Citations
217	RNA Sequencing Analysis Detection of a Novel Pathway of Endothelial Dysfunction in Pulmonary Arterial Hypertension. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 356-366.	5.6	66
218	Physical exercise is a risk factor for amyotrophic lateral sclerosis: Convergent evidence from Mendelian randomisation, transcriptomics and risk genotypes. EBioMedicine, 2021, 68, 103397.	6.1	65
219	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. Genome Research, 2018, 28, 231-242.	5.5	64
220	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. Frontiers in Microbiology, 2018, 8, 2708.	3.5	64
221	Lifelong physical activity is associated with promoter hypomethylation of genes involved in metabolism, myogenesis, contractile properties and oxidative stress resistance in aged human skeletal muscle. Scientific Reports, 2019, 9, 3272.	3.3	63
222	Multi-faceted epigenetic dysregulation of gene expression promotes esophageal squamous cell carcinoma. Nature Communications, 2020, 11, 3675.	12.8	63
223	Shared functions of plant and mammalian StAR-related lipid transfer (START) domains in modulating transcription factor activity. BMC Biology, 2014, 12, 70.	3.8	62
224	Systematic Identification of Host Cell Regulators of Legionella pneumophila Pathogenesis Using a Genome-wide CRISPR Screen. Cell Host and Microbe, 2019, 26, 551-563.e6.	11.0	62
225	Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1. Scientific Reports, 2016, 6, 20104.	3.3	61
226	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. Genes and Development, 2011, 25, 767-778.	5.9	60
227	Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues. PLoS Genetics, 2014, 10, e1004304.	3.5	60
228	Transglutaminase 4 as a prostate autoantigen in male subfertility. Science Translational Medicine, 2015, 7, 292ra101.	12.4	60
229	Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension. Nature Communications, 2020, 11, 1673.	12.8	60
230	Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 387-397.	1.8	59
231	Extensive Transcript Diversity and Novel Upstream Open Reading Frame Regulation in Yeast. G3: Genes, Genomes, Genetics, 2013, 3, 343-352.	1.8	59
232	Biallelic Mutations in ATP5F1D, which Encodes a Subunit of ATP Synthase, Cause a Metabolic Disorder. American Journal of Human Genetics, 2018, 102, 494-504.	6.2	59
233	Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2018, 17, 4031-4041.	3.7	59
234	Genome-Wide Mapping of Copy Number Variation in Humans: Comparative Analysis of High Resolution Array Platforms. PLoS ONE, 2011, 6, e27859.	2.5	59

#	Article	IF	Citations
235	Identification of genomic indels and structural variations using split reads. BMC Genomics, 2011, 12, 375.	2.8	57
236	Integrative Analysis of Longitudinal Metabolomics Data from a Personal Multi-Omics Profile. Metabolites, 2013, 3, 741-760.	2.9	56
237	High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. Scientific Reports, 2017, 7, 7106.	3.3	56
238	MISTERMINATE Mechanistically Links Mitochondrial Dysfunction with Proteostasis Failure. Molecular Cell, 2019, 75, 835-848.e8.	9.7	56
239	Engineering Genetic Predisposition in Human Neuroepithelial Stem Cells Recapitulates Medulloblastoma Tumorigenesis. Cell Stem Cell, 2019, 25, 433-446.e7.	11.1	56
240	Longitudinal personal DNA methylome dynamics in a human with a chronic condition. Nature Medicine, 2018, 24, 1930-1939.	30.7	55
241	HAT1 Coordinates Histone Production and Acetylation via H4 Promoter Binding. Molecular Cell, 2019, 75, 711-724.e5.	9.7	55
242	Longitudinal linked-read sequencing reveals ecological and evolutionary responses of a human gut microbiome during antibiotic treatment. Genome Research, 2021, 31, 1433-1446.	5.5	55
243	Personal Omics for Precision Health. Circulation Research, 2018, 122, 1169-1171.	4.5	54
244	Phenotypically Silent Bone Morphogenetic Protein Receptor 2 Mutations Predispose Rats to Inflammation-Induced Pulmonary Arterial Hypertension by Enhancing the Risk for Neointimal Transformation. Circulation, 2019, 140, 1409-1425.	1.6	54
245	Multiomics Characterization of Preterm Birth in Low- and Middle-Income Countries. JAMA Network Open, 2020, 3, e2029655.	5.9	53
246	Large-Scale Mutagenesis of the Yeast Genome Using a Tn7-Derived Multipurpose Transposon. Genome Research, 2004, 14, 1975-1986.	5.5	52
247	The gut microbiome: a key player in the complexity of amyotrophic lateral sclerosis (ALS). BMC Medicine, 2021, 19, 13.	5.5	52
248	The Kar3p Kinesin-related Protein Forms a Novel Heterodimeric Structure with Its Associated Protein Cik1p. Molecular Biology of the Cell, 2000, 11, 2373-2385.	2.1	51
249	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. Neuron, 2022, 110, 992-1008.e11.	8.1	51
250	ChIP€Seq: A Method for Global Identification of Regulatory Elements in the Genome. Current Protocols in Molecular Biology, 2010, 91, Unit 21.19.1-14.	2.9	49
251	Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. PLoS Genetics, 2014, 10, e1004549.	3.5	49
252	Multi-platform analysis reveals a complex transcriptome architecture of a circovirus. Virus Research, 2017, 237, 37-46.	2.2	49

#	Article	IF	Citations
253	The MEK5â€"ERK5 Kinase Axis Controls Lipid Metabolism in Small-Cell Lung Cancer. Cancer Research, 2020, 80, 1293-1303.	0.9	49
254	Systematic Identification of Regulators of Oxidative Stress Reveals Non-canonical Roles for Peroxisomal Import and the Pentose Phosphate Pathway. Cell Reports, 2020, 30, 1417-1433.e7.	6.4	49
255	COVID-19â€"Induced New-Onset Diabetes: Trends and Technologies. Diabetes, 2021, 70, 2733-2744.	0.6	49
256	Global, distinctive, and personal changes in molecular and microbial profiles by specific fibers in humans. Cell Host and Microbe, 2022, 30, 848-862.e7.	11.0	48
257	Multiomic immune clockworks of pregnancy. Seminars in Immunopathology, 2020, 42, 397-412.	6.1	47
258	ProCAT: a data analysis approach for protein microarrays. Genome Biology, 2006, 7, R110.	9.6	46
259	Systems biology from a yeast omics perspective. FEBS Letters, 2009, 583, 3895-3899.	2.8	46
260	Global identification of protein kinase substrates by protein microarray analysis. Nature Protocols, 2009, 4, 1820-1827.	12.0	46
261	Characterization of Novel Transcripts in Pseudorabies Virus. Viruses, 2015, 7, 2727-2744.	3.3	46
262	Achieving high-sensitivity for clinical applications using augmented exome sequencing. Genome Medicine, 2015, 7, 71.	8.2	46
263	Long-read sequencing of the human cytomegalovirus transcriptome with the Pacific Biosciences RSII platform. Scientific Data, 2017, 4, 170194.	5.3	46
264	A DMS Shotgun Lipidomics Workflow Application to Facilitate High-Throughput, Comprehensive Lipidomics. Journal of the American Society for Mass Spectrometry, 2021, 32, 2655-2663.	2.8	46
265	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. Nature Genetics, 2021, 53, 1564-1576.	21.4	45
266	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. Frontiers in Genetics, 2019, 10, 834.	2.3	44
267	CTLA-4 expression by B-1a B cells is essential for immune tolerance. Nature Communications, 2021, 12, 525.	12.8	43
268	Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders. Cell Systems, 2015, 1, 361-374.	6.2	42
269	Disease Variant Landscape of a Large Multiethnic Population of Moyamoya Patients by Exome Sequencing. G3: Genes, Genomes, Genetics, 2016, 6, 41-49.	1.8	42
270	Personal phenotypes to go with personal genomes. Molecular Systems Biology, 2009, 5, 273.	7.2	41

#	Article	IF	Citations
271	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2019, 18, 4098-4107.	3.7	41
272	PPARγ-p53-Mediated Vasculoregenerative Program to Reverse Pulmonary Hypertension. Circulation Research, 2021, 128, 401-418.	4.5	41
273	Investigating metabolite–protein interactions: An overview of available techniques. Methods, 2012, 57, 459-466.	3.8	40
274	Single cell transcriptomics reveals unanticipated features of early hematopoietic precursors. Nucleic Acids Research, 2017, 45, gkw1214.	14.5	40
275	iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy. Cell Reports, 2020, 32, 108117.	6.4	40
276	Cross-Laboratory Standardization of Preclinical Lipidomics Using Differential Mobility Spectrometry and Multiple Reaction Monitoring. Analytical Chemistry, 2021, 93, 16369-16378.	6.5	40
277	Predicting Ovarian Cancer Patients' Clinical Response to Platinum-Based Chemotherapy by Their Tumor Proteomic Signatures. Journal of Proteome Research, 2016, 15, 2455-2465.	3.7	39
278	Quality-control mechanisms targeting translationally stalled and C-terminally extended poly(GR) associated with ALS/FTD. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25104-25115.	7.1	39
279	Centromere-Like Regions in the Budding Yeast Genome. PLoS Genetics, 2013, 9, e1003209.	3.5	38
280	Whole-Exome Enrichment with the Agilent SureSelect Human All Exon Platform. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot083659.	0.3	38
281	Transcriptomic and epigenomic differences in human induced pluripotent stem cells generated from six reprogramming methods. Nature Biomedical Engineering, 2017, 1, 826-837.	22.5	38
282	SETD7 Drives Cardiac Lineage Commitment through Stage-Specific Transcriptional Activation. Cell Stem Cell, 2018, 22, 428-444.e5.	11.1	38
283	Dynamic transcriptome profiling dataset of vaccinia virus obtained from long-read sequencing techniques. GigaScience, 2018, 7, .	6.4	38
284	Global metabolic profiling to model biological processes of aging in twins. Aging Cell, 2020, 19, e13073.	6.7	38
285	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. Journal of Proteome Research, 2020, 19, 4735-4746.	3.7	38
286	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. Scientific Reports, 2018, 8, 226.	3.3	37
287	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	19.0	37
288	Yeast as a Model for Human Disease. Current Protocols in Human Genetics, 2006, 48, Unit 15.6.	3.5	36

#	Article	IF	Citations
289	Metabolites as global regulators: A new view of protein regulation. BioEssays, 2011, 33, 485-489.	2.5	36
290	Correlation of Global MicroRNA Expression With Basal Cell Carcinoma Subtype. G3: Genes, Genomes, Genetics, 2012, 2, 279-286.	1.8	36
291	Deep longitudinal multiomics profiling reveals two biological seasonal patterns in California. Nature Communications, 2020, 11, 4933.	12.8	36
292	Global analysis of protein function using protein microarrays. Mechanisms of Ageing and Development, 2005, 126, 171-175.	4.6	35
293	Nat1 Deficiency Is Associated with Mitochondrial Dysfunction and Exercise Intolerance in Mice. Cell Reports, 2016, 17, 527-540.	6.4	35
294	Simul-seq: combined DNA and RNA sequencing for whole-genome and transcriptome profiling. Nature Methods, 2016, 13, 953-958.	19.0	34
295	ALDH1A3 Coordinates Metabolism With Gene Regulation in Pulmonary Arterial Hypertension. Circulation, 2021, 143, 2074-2090.	1.6	34
296	MSB: A mean-shift-based approach for the analysis of structural variation in the genome. Genome Research, 2009, 19, 106-117.	5.5	33
297	Systematic investigation of protein–small molecule interactions. IUBMB Life, 2013, 65, 2-8.	3.4	33
298	Genome assembly from synthetic long read clouds. Bioinformatics, 2016, 32, i216-i224.	4.1	33
299	Template-switching artifacts resemble alternative polyadenylation. BMC Genomics, 2019, 20, 824.	2.8	32
300	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	5.5	32
301	Yeast proteomics and protein microarrays. Journal of Proteomics, 2010, 73, 2147-2157.	2.4	31
302	Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. Nucleic Acids Research, 2017, 45, gkx026.	14.5	31
303	Transcriptome-wide survey of pseudorabies virus using next- and third-generation sequencing platforms. Scientific Data, 2018, 5, 180119.	5.3	31
304	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. IScience, 2020, 23, 101844.	4.1	31
305	Arabidopsis Protein Microarrays for the High-Throughput Identification of Protein-Protein Interactions. Plant Signaling and Behavior, 2007, 2, 416-420.	2.4	30
306	Fetal de novo mutations and preterm birth. PLoS Genetics, 2017, 13, e1006689.	3.5	30

#	ARTICLE	IF	CITATIONS
307	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. PLoS Genetics, 2018, 14, e1007755.	3.5	30
308	Natural Selection Has Differentiated the Progesterone Receptor among Human Populations. American Journal of Human Genetics, 2018, 103, 45-57.	6.2	30
309	Personal genomes, quantitative dynamic omics and personalized medicine. Quantitative Biology, 2013, 1, 71-90.	0.5	29
310	Coherent Functional Modules Improve Transcription Factor Target Identification, Cooperativity Prediction, and Disease Association. PLoS Genetics, 2014, 10, e1004122.	3.5	29
311	Strain Kaplan of Pseudorabies Virus Genome Sequenced by PacBio Single-Molecule Real-Time Sequencing Technology. Genome Announcements, 2014, 2, .	0.8	29
312	Metabolome progression during early gut microbial colonization of gnotobiotic mice. Scientific Reports, 2015, 5, 11589.	3.3	29
313	A review of Mendelian randomization in amyotrophic lateral sclerosis. Brain, 2022, 145, 832-842.	7.6	29
314	Big data and health. The Lancet Digital Health, 2019, 1, e252-e254.	12.3	28
315	Exome sequencing and genome-wide copy number variant mapping reveal novel associations with sensorineural hereditary hearing loss. BMC Genomics, 2014, 15, 1155.	2.8	27
316	De novo and rare mutations in the HSPA1L heat shock gene associated with inflammatory bowel disease. Genome Medicine, 2017, 9, 8.	8.2	27
317	Topological organization and dynamic regulation of human tRNA genes during macrophage differentiation. Genome Biology, 2017, 18, 180.	8.8	27
318	Transcriptomic study of Herpes simplex virus type-1 using full-length sequencing techniques. Scientific Data, 2018, 5, 180266.	5.3	27
319	A scalable, secure, and interoperable platform for deep data-driven health management. Nature Communications, 2021, 12, 5757.	12.8	27
320	A Case Report of Hypoglycemia and Hypogammaglobulinemia: DAVID Syndrome in a Patient With a Novel <i>NFKB2</i> Mutation. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2127-2130.	3.6	26
321	Comparative analysis of respiratory motion tracking using Microsoft Kinect v2 sensor. Journal of Applied Clinical Medical Physics, 2018, 19, 193-204.	1.9	26
322	Precision Medicine: Role of Proteomics in Changing Clinical Management and Care. Journal of Proteome Research, 2019, 18, 1-6.	3.7	26
323	Precision environmental health monitoring by longitudinal exposome and multi-omics profiling. Genome Research, 2022, 32, 1199-1214.	5.5	26
324	iNetModels 2.0: an interactive visualization and database of multi-omics data. Nucleic Acids Research, 2021, 49, W271-W276.	14.5	25

#	Article	IF	Citations
325	STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. PLoS ONE, 2014, 9, e84860.	2.5	25
326	Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. Cell Reports, 2020, 33, 108456.	6.4	24
327	Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data. PLoS Genetics, 2015, 11, e1005496.	3.5	23
328	Yeast longevity promoted by reversing aging-associated decline in heavy isotope content. Npj Aging and Mechanisms of Disease, 2016, 2, 16004.	4.5	23
329	High-frequency actionable pathogenic exome variants in an average-risk cohort. Journal of Physical Education and Sports Management, 2018, 4, a003178.	1.2	23
330	Long-Read Sequencing Revealed an Extensive Transcript Complexity in Herpesviruses. Frontiers in Genetics, 2018, 9, 259.	2.3	23
331	High Throughput Sequencing and Assessing Disease Risk. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a026849.	6.2	23
332	Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms. Clinical Cancer Research, 2021, 27, 4265-4276.	7.0	23
333	Precision Neoantigen Discovery Using Large-scale Immunopeptidomes and Composite Modeling of MHC Peptide Presentation. Molecular and Cellular Proteomics, 2021, 20, 100111.	3.8	23
334	Genomics and Personalized Medicine. , 2016, , .		23
335	Serine biosynthesis as a novel therapeutic target for dilated cardiomyopathy. European Heart Journal, 2022, 43, 3477-3489.	2.2	23
336	Can Metabolic Profiles Be Used as a Phenotypic Readout of the Genome to Enhance Precision Medicine?. Clinical Chemistry, 2016, 62, 676-678.	3.2	21
337	Multiplatform next-generation sequencing identifies novel RNA molecules and transcript isoforms of the endogenous retrovirus isolated from cultured cells. FEMS Microbiology Letters, 2018, 365, .	1.8	21
338	NF90/ILF3 is a transcription factor that promotes proliferation over differentiation by hierarchical regulation in K562 erythroleukemia cells. PLoS ONE, 2018, 13, e0193126.	2.5	21
339	A machine-compiled database of genome-wide association studies. Nature Communications, 2019, 10, 3341.	12.8	21
340	Decoding personal biotic and abiotic airborne exposome. Nature Protocols, 2021, 16, 1129-1151.	12.0	21
341	Improvement in Glucose Regulation Using a Digital Tracker and Continuous Glucose Monitoring in Healthy Adults and Those with TypeÂ2 Diabetes. Diabetes Therapy, 2021, 12, 1871-1886.	2.5	21
342	Haplotype structure and positive selection at TLR1. European Journal of Human Genetics, 2014, 22, 551-557.	2.8	20

#	Article	IF	Citations
343	Secure cloud computing for genomic data. Nature Biotechnology, 2016, 34, 588-591.	17.5	20
344	Tet enzymes are essential for early embryogenesis and completion of embryonic genome activation. EMBO Reports, 2022, 23, e53968.	4.5	20
345	Transcriptome Signature and Regulation in Human Somatic Cell Reprogramming. Stem Cell Reports, 2015, 4, 1125-1139.	4.8	19
346	Implementation of facial recognition with Microsoft Kinect v2 sensor for patient verification. Medical Physics, 2017, 44, 2391-2399.	3.0	19
347	Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis. Scientific Reports, 2017, 7, 5557.	3.3	19
348	Omics AnalySIs System for PRecision Oncology (OASISPRO): a web-based omics analysis tool for clinical phenotype prediction. Bioinformatics, 2018, 34, 319-320.	4.1	19
349	Disruption of mesoderm formation during cardiac differentiation due to developmental exposure to 13-cis-retinoic acid. Scientific Reports, 2018, 8, 12960.	3.3	19
350	Towards personalized medicine in maternal and child health: integrating biologic and social determinants. Pediatric Research, 2021, 89, 252-258.	2.3	19
351	Systems Biology Approaches to Disease Marker Discovery. Disease Markers, 2010, 28, 209-224.	1.3	18
352	Cell Type-Specific Chromatin Signatures Underline Regulatory DNA Elements in Human Induced Pluripotent Stem Cells and Somatic Cells. Circulation Research, 2017, 121, 1237-1250.	4.5	18
353	Applying circulating tumor DNA methylation in the diagnosis of lung cancer. Precision Clinical Medicine, 2019, 2, 45-56.	3.3	18
354	Chromatin accessibility associates with protein-RNA correlation in human cancer. Nature Communications, 2021, 12, 5732.	12.8	18
355	Protein Microarrays. Methods in Molecular Biology, 2009, 548, 209-222.	0.9	18
356	Long-read assays shed new light on the transcriptome complexity of a viral pathogen. Scientific Reports, 2020, 10, 13822.	3.3	17
357	A common class of transcripts with 5′-intron depletion, distinct early coding sequence features, and N^1-methyladenosine modification. Rna, 2017, 23, 270-283.	3.5	16
358	Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining. Journal of Proteome Research, 2018, 17, 1383-1396.	3.7	16
359	Distinct transcriptomic and exomic abnormalities within myelodysplastic syndrome marrow cells. Leukemia and Lymphoma, 2018, 59, 2952-2962.	1.3	16
360	Full Genome Sequence of the Western Reserve Strain of Vaccinia Virus Determined by Third-Generation Sequencing. Genome Announcements, 2018, 6, .	0.8	16

#	Article	IF	Citations
361	*WISP3* mutation associated with pseudorheumatoid dysplasia. Journal of Physical Education and Sports Management, 2018, 4, a001990.	1.2	16
362	Dissecting phosphorylation networks: lessons learned from yeast. Expert Review of Proteomics, 2011, 8, 775-786.	3.0	15
363	Simultaneous RNA purification and size selection using on-chip isotachophoresis with an ionic spacer. Lab on A Chip, 2019, 19, 2741-2749.	6.0	15
364	Much ado about nothing: A qualitative study of the experiences of an average-risk population receiving results of exome sequencing. Journal of Genetic Counseling, 2019, 28, 428-437.	1.6	15
365	metID: an R package for automatable compound annotation for LC–MS-based data. Bioinformatics, 2022, 38, 568-569.	4.1	15
366	Integrating Sequencing Technologies in Personal Genomics: Optimal Low Cost Reconstruction of Structural Variants. PLoS Computational Biology, 2009, 5, e1000432.	3.2	14
367	Metadata Checklist for the Integrated Personal OMICS Study: Proteomics and Metabolomics Experiments. OMICS A Journal of Integrative Biology, 2014, 18, 81-85.	2.0	14
368	Association of AHSG with alopecia and mental retardation (APMR) syndrome. Human Genetics, 2017, 136, 287-296.	3.8	14
369	Isolated Congenital Anosmia and CNGA2 Mutation. Scientific Reports, 2017, 7, 2667.	3.3	14
370	Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome. Frontiers in Genetics, 2018, 9, 432.	2.3	14
371	Understanding health disparities. Journal of Perinatology, 2019, 39, 354-358.	2.0	14
372	A Customizable Analysis Flow in Integrative Multi-Omics. Biomolecules, 2020, 10, 1606.	4.0	14
373	Immunologic effects of forest fire exposure show increases in IL-1β and CRP. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 2356-2358.	5.7	14
374	Non-invasive wearables for remote monitoring of HbA1c and glucose variability: proof of concept. BMJ Open Diabetes Research and Care, 2021, 9, e002027.	2.8	14
375	Heterogeneity of Diabetes: β-Cells, Phenotypes, and Precision Medicine: Proceedings of an International Symposium of the Canadian Institutes of Health Research's Institute of Nutrition, Metabolism and Diabetes and the U.S. National Institutes of Health's National Institute of Diabetes and Digestive and Kidney Diseases. Diabetes Care, 2022, 45, 3-22.	8.6	14
376	Whole-Exome Enrichment with the Roche NimbleGen SeqCap EZ Exome Library SR Platform. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot084855.	0.3	13
377	Precision medicine in women with epilepsy: The challenge, systematic review, and future direction. Epilepsy and Behavior, 2021, 118, 107928.	1.7	13
378	Metformin Improves Diabetic Bone Health by Re-Balancing Catabolism and Nitrogen Disposal. PLoS ONE, 2015, 10, e0146152.	2.5	13

#	Article	IF	Citations
379	Can heavy isotopes increase lifespan? Studies of relative abundance in various organisms reveal chemical perspectives on aging. BioEssays, 2016, 38, 1093-1101.	2.5	12
380	Metformin Affects Heme Function as a Possible Mechanism of Action. G3: Genes, Genomes, Genetics, 2019, 9, 513-522.	1.8	12
381	Deep Characterization of the Human Antibody Response to Natural Infection Using Longitudinal Immune Repertoire Sequencing. Molecular and Cellular Proteomics, 2020, 19, 278-293.	3.8	12
382	Benchmarking workflows to assess performance and suitability of germline variant calling pipelines in clinical diagnostic assays. BMC Bioinformatics, 2021, 22, 85.	2.6	12
383	Interpretome: a freely available, modular, and secure personal genome interpretation engine. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 339-350.	0.7	12
384	Network biology bridges the gaps between quantitative genetics and multi-omics to map complex diseases. Current Opinion in Chemical Biology, 2022, 66, 102101.	6.1	12
385	A cancer-associated RNA polymerase III identity drives robust transcription and expression of snaR-A noncoding RNA. Nature Communications, 2022, 13, .	12.8	12
386	Whole-Exome Enrichment with the Illumina TruSeq Exome Enrichment Platform. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot084863.	0.3	11
387	Evaluation of whole exome sequencing as an alternative to BeadChip and whole genome sequencing in human population genetic analysis. BMC Genomics, 2018, 19, 778.	2.8	11
388	High-Resolution Bisulfite-Sequencing of Peripheral Blood DNA Methylation in Early-Onset and Familial Risk Breast Cancer Patients. Clinical Cancer Research, 2019, 25, 5301-5314.	7.0	11
389	Plasma sterols and depressive symptom severity in a population-based cohort. PLoS ONE, 2017, 12, e0184382.	2.5	11
390	Genomic era diagnosis and management of hereditary and sporadic colon cancer. World Journal of Clinical Oncology, 2014, 5, 1036.	2.3	11
391	Evaluating Common Humoral Responses against Fungal Infections with Yeast Protein Microarrays. Journal of Proteome Research, 2015, 14, 3924-3931.	3.7	10
392	Genome-wide effects of social status on DNA methylation in the brain of a cichlid fish, Astatotilapia burtoni. BMC Genomics, 2019, 20, 699.	2.8	10
393	Longitudinal Analysis of Serum Cytokine Levels and Gut Microbial Abundance Links IL-17/IL-22 With <i>Clostridia</i> and Insulin Sensitivity in Humans. Diabetes, 2020, 69, 1833-1842.	0.6	10
394	The Exposome in the Era of the Quantified Self. Annual Review of Biomedical Data Science, 2021, 4, 255-277.	6.5	10
395	Unbiased metabolome screen leads to personalized medicine strategy for amyotrophic lateral sclerosis. Brain Communications, 2022, 4, fcac069.	3.3	10
396	Multiomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity. Cell Systems, 2022, 13, 598-614.e6.	6.2	10

#	Article	IF	Citations
397	Endogenous Retroviral Elements Generate Pathologic Neutrophils in Pulmonary Arterial Hypertension. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 1019-1034.	5.6	10
398	Robust identification of temporal biomarkers in longitudinal omics studies. Bioinformatics, 2022, 38, 3802-3811.	4.1	10
399	PATH-SCAN: A REPORTING TOOL FOR IDENTIFYING CLINICALLY ACTIONABLE VARIANTS. , 2013, , .		9
400	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	5.6	9
401	Reassessment of Piwi Binding to the Genome and Piwi Impact on RNA Polymerase II Distribution. Developmental Cell, 2015, 32, 772-774.	7.0	9
402	Cloud-based interactive analytics for terabytes of genomic variants data. Bioinformatics, 2017, 33, 3709-3715.	4.1	9
403	An Integrated Sequencing Approach for Updating the Pseudorabies Virus Transcriptome. Pathogens, 2021, 10, 242.	2.8	9
404	Systems biology approaches to disease marker discovery. Disease Markers, 2010, 28, 209-24.	1.3	9
405	Whole transcriptome profiling of prospective endomyocardial biopsies reveals prognostic and diagnostic signatures of cardiac allograft rejection. Journal of Heart and Lung Transplantation, 2022, 41, 840-848.	0.6	9
406	Patient-derived gene and protein expression signatures of NGLY1 deficiency. Journal of Biochemistry, 2022, 171, 187-199.	1.7	9
407	Exploring disease interrelationships in patients with lymphatic disorders: A single center retrospective experience. Clinical and Translational Medicine, 2022, 12, e760.	4.0	9
408	Metadata Checklist for the Integrated Personal Omics Study: <i>Proteomics and Metabolomics Experiments</i>. Big Data, 2013, 1, 202-206.	3.4	8
409	Multiple Pairwise Analysis of Non-homologous Centromere Coupling Reveals Preferential Chromosome Size-Dependent Interactions and a Role for Bouquet Formation in Establishing the Interaction Pattern. PLoS Genetics, 2016, 12, e1006347.	3.5	8
410	Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. Proteomics, 2016, 16, 465-476.	2.2	8
411	Applying genomics in heart transplantation. Transplant International, 2018, 31, 278-290.	1.6	8
412	Humans Are Selectively Exposed to Pneumocystis jirovecii. MBio, 2020, 11, .	4.1	8
413	Combined nanopore and single-molecule real-time sequencing survey of human betaherpesvirus 5 transcriptome. Scientific Reports, 2021, 11, 14487.	3.3	8
414	A machine learning algorithm with subclonal sensitivity reveals widespread pan-cancer human leukocyte antigen loss of heterozygosity. Nature Communications, 2022, 13, 1925.	12.8	8

#	Article	IF	Citations
415	Multimodal Dynamic Profiling of Healthy and Diseased States for Future Personalized Health Care. Clinical Pharmacology and Therapeutics, 2013, 93, 29-32.	4.7	7
416	Chromatin Immunoprecipitation and Multiplex Sequencing (ChIP-Seq) to Identify Global Transcription Factor Binding Sites in the Nematode Caenorhabditis Elegans. Methods in Enzymology, 2014, 539, 89-111.	1.0	7
417	iPOP and its role in participatory medicine. Genome Medicine, 2014, 6, 6.	8.2	7
418	Probing High-density Functional Protein Microarrays to Detect Protein-protein Interactions. Journal of Visualized Experiments, 2015, , e51872.	0.3	7
419	Integrated Proteomic and Genomic Analysis of Gastric Cancer Patient Tissues. Journal of Proteome Research, 2015, 14, 4995-5006.	3.7	7
420	A Cloud-Based Metabolite and Chemical Prioritization System for the Biology/Disease-Driven Human Proteome Project. Journal of Proteome Research, 2018, 17, 4345-4357.	3.7	7
421	Personalized Metabolomics. Methods in Molecular Biology, 2019, 1978, 447-456.	0.9	7
422	Analysis of the Complete Genome Sequence of a Novel, Pseudorabies Virus Strain Isolated in Southeast Europe. Canadian Journal of Infectious Diseases and Medical Microbiology, 2019, 2019, 1-12.	1.9	7
423	Meta-analytic approach for transcriptome profiling of herpes simplex virus type 1. Scientific Data, 2020, 7, 223.	5.3	7
424	Obesity Drives Delayed Infarct Expansion, Inflammation, and Distinct Gene Networks in a Mouse Stroke Model. Translational Stroke Research, 2021, 12, 331-346.	4.2	7
425	Prevention of Severe Intestinal Barrier Dysfunction Through a Single-Species Probiotics is Associated With the Activation of Microbiome-Mediated Glutamate–Glutamine Biosynthesis. Shock, 2021, 55, 128-137.	2.1	7
426	Master lineage transcription factors anchor trans mega transcriptional complexes at highly accessible enhancer sites to promote long-range chromatin clustering and transcription of distal target genes. Nucleic Acids Research, 2021, 49, 12196-12210.	14.5	7
427	Human exposome assessment platform. Environmental Epidemiology, 2021, 5, e182.	3.0	7
428	Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, and allele-specific binding detection. BMC Bioinformatics, 2016, 17, 96.	2.6	6
429	Chromatin Remodeling in Response to BRCA2-Crisis. Cell Reports, 2019, 28, 2182-2193.e6.	6.4	6
430	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. GigaScience, 2020, 9, .	6.4	6
431	Early detection of SARS–CoV–2 and other infections in solid organ transplant recipients and household members using wearable devices. Transplant International, 2021, 34, 1019-1031.	1.6	6
432	Exposome-wide Association Study for Metabolic Syndrome. Frontiers in Genetics, 2021, 12, 783930.	2.3	6

#	Article	IF	Citations
433	Analyzing In Vivo Metaboliteâ€Protein Interactions by Largeâ€Scale Systematic Analyses. Current Protocols in Chemical Biology, 2011, 3, 181-196.	1.7	5
434	Fast Metagenomic Binning via Hashing and Bayesian Clustering. Journal of Computational Biology, 2018, 25, 677-688.	1.6	5
435	Understanding how biologic and social determinants affect disparities in preterm birth and outcomes of preterm infants in the NICU. Seminars in Perinatology, 2021, 45, 151408.	2.5	5
436	Time-course transcriptome analysis of host cell response to poxvirus infection using a dual long-read sequencing approach. BMC Research Notes, 2021, 14, 239.	1.4	5
437	Evaluation of the impact of ul54 gene-deletion on the global transcription and DNA replication of pseudorabies virus. Archives of Virology, 2017, 162, 2679-2694.	2.1	5
438	Whole-exome sequencing data of suicide victims who had suffered from major depressive disorder. Scientific Data, 2019, 6, 190010.	5.3	5
439	Transcriptomic Evaluation of CD34+ Marrow Cells from Myelodysplastic Syndrome (MDS) Patients. Blood, 2014, 124, 1894-1894.	1.4	5
440	Preparation of Recombinant Protein Spotted Arrays for Proteomeâ€Wide Identification of Kinase Targets. Current Protocols in Protein Science, 2013, 72, Unit 27.4.	2.8	4
441	Impact of alleleâ€specific peptides in proteome quantification. Proteomics - Clinical Applications, 2015, 9, 432-436.	1.6	4
442	An integrated global regulatory network of hematopoietic precursor cell self-renewal and differentiation. Integrative Biology (United Kingdom), 2018, 10, 390-405.	1.3	4
443	Time-Course Transcriptome Profiling of a Poxvirus Using Long-Read Full-Length Assay. Pathogens, 2021, 10, 919.	2.8	4
444	Divergent patterns of selection on metabolite levels and gene expression. Bmc Ecology and Evolution, 2021, 21, 185.	1.6	4
445	In-depth triacylglycerol profiling using MS3 Q-Trap mass spectrometry. Analytica Chimica Acta, 2021, 1184, 339023.	5.4	4
446	Long-Read Sequencing Reveals a GC Pressure during the Evolution of Porcine Endogenous Retrovirus. Genome Announcements, 2017, 5, .	0.8	4
447	Prediction of gestational age using urinary metabolites in term and preterm pregnancies. Scientific Reports, 2022, 12, 8033.	3.3	4
448	Making drug addicts out of yeast. Nature Biotechnology, 2001, 19, 1022-1023.	17.5	3
449	Metabolomics as a robust tool in systems biology and personalized medicine: an open letter to the metabolomics community. Metabolomics, 2013, 9, 532-534.	3.0	3
450	Identification of a novel mutation in the APTX gene associated with ataxia-oculomotor apraxia. Journal of Physical Education and Sports Management, 2017, 3, a002014.	1.2	3

#	Article	IF	Citations
451	Candidate variants in TUB are associated with familial tremor. PLoS Genetics, 2020, 16, e1009010.	3.5	3
452	RobNorm: model-based robust normalization method for labeled quantitative mass spectrometry proteomics data. Bioinformatics, 2021, 37, 815-821.	4.1	3
453	Response to Hulman and colleagues regarding â€œGlucotypes reveal new patterns of glucose dysregulationâ€. PLoS Biology, 2021, 19, e3001092.	5.6	3
454	Temporal changes in soluble angiotensin-converting enzyme 2 associated with metabolic health, body composition, and proteome dynamics during a weight loss diet intervention: a randomized trial with implications for the COVID-19 pandemic. American Journal of Clinical Nutrition, 2021, 114, 1655-1665.	4.7	3
455	Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus. Scientific Reports, 2022, 12, 1291.	3.3	3
456	Adverse childhood experiences, diabetes and associated conditions, preventive care practices and health care access: A population-based study. Preventive Medicine, 2022, 160, 107044.	3.4	3
457	Design and Methods of the Validating Injury to the Renal Transplant Using Urinary Signatures (VIRTUUS) Study in Children. Transplantation Direct, 2021, 7, e791.	1.6	3
458	KMT2D-NOTCH Mediates Coronary Abnormalities in Hypoplastic Left Heart Syndrome. Circulation Research, 2022, 131, 280-282.	4.5	3
459	An integrated web interface for large-scale characterization of sequence data. Functional and Integrative Genomics, 2000, 1, 70-75.	3.5	2
460	Swarm: A federated cloud framework for large-scale variant analysis. PLoS Computational Biology, 2021, 17, e1008977.	3.2	2
461	AdaTiSS: a novel data-*Ada*ptive robust method for identifying *Ti*ssue *S*pecificity *S*cores. Bioinformatics, 2021, 37, 4469-4476.	4.1	2
462	Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study. JAMIA Open, 2021, 4, ooab054.	2.0	2
463	Genetic Adaptation of Porcine Circovirus Type 1 to Cultured Porcine Kidney Cells Revealed by Single-Molecule Long-Read Sequencing Technology. Genome Announcements, 2017, 5, .	0.8	1
464	AdaReg: data adaptive robust estimation in linear regression with application in GTEx gene expressions. Statistical Applications in Genetics and Molecular Biology, 2021, 20, 51-71.	0.6	1
465	The X Chromosome from Telomere to Telomere: Key Achievements and Future Opportunities. Faculty Reviews, 2021, 10, 63.	3.9	1
466	Genome-Wide Identification of the Genetic Basis of Amyotrophic Lateral Sclerosis. SSRN Electronic Journal, 0, , .	0.4	1
467	Effects of an immersive psychosocial training program on depression and well-being: A randomized clinical trial. Journal of Psychiatric Research, 2022, 150, 292-299.	3.1	1
468	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0

#	ARTICLE	IF	CITATIONS
469	Design Issues in Implementing a Portable Sample Tracking and Analysis Research Support (STARS) System for PCR Based Microarray Research. , 2006, , .		0
470	Adapting skills from genetic counseling to wearables technology research during the COVID‑19 pandemic: Poised for the pivot. Journal of Genetic Counseling, 2021, 30, 1269-1275.	1.6	0
471	Proteomics for Elucidating Protein Function, Regulatory Networks and Improving Human Health. FASEB Journal, 2007, 21, A211.	0.5	0
472	Whole Genome Sequence Analysis of Primary Myelofibrosis.. Blood, 2012, 120, 2863-2863.	1.4	0
473	Predictive Signatures for Lung Adenocarcinoma Prognostic Trajectory by Multiomics Data Integration and Ensemble Learning. Lecture Notes in Computer Science, 2021, , 9-23.	1.3	0
474	Elucidating Diversity in Obesity-Related Phenotypes Using Longitudinal and Multi-omic Approaches. , 2022, , 63-75.		0
475	Abstract 19076: ATAC-seq Implicates Epigenome-wide CTCF Dissociation in the Progression of Cardiac Ischemia. Circulation, 2015, 132, .	1.6	0
476	Wnt Signaling Interactor WTIP (Wilms Tumor Interacting Protein) Underlies Novel Mechanism for Cardiac Hypertrophy. Circulation Genomic and Precision Medicine, 0, , .	3.6	0