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	metID: an R package for automatable compound annotation for LCâˆ'MS-based data. Bioinformatics, 2022, 38, 568-569.	4.1	15
2	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
3	A review of Mendelian randomization in amyotrophic lateral sclerosis. Brain, 2022, 145, 832-842.	7.6	29
4	Heterogeneity of Diabetes: Î²-Cells, Phenotypes, and Precision Medicine: Proceedings of an International Symposium of the Canadian Institutes of Health Researchâ€™s Institute of Nutrition, Metabolism and Diabetes and the U.S. National Institutes of Healthâ€™s National Institute of Diabetes and Digestive and Kidney Diseases. Diabetes Care, 2022, 45, 3-22.	8.6	14
5	Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging. Nature Methods, 2022, 19, 284-295.	19.0	156
6	Real-time alerting system for COVID-19 and other stress events using wearable data. Nature Medicine, 2022, 28, 175-184.	30.7	69
7	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. Neuron, 2022, 110, 992-1008.e11.	8.1	51
8	Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus. Scientific Reports, 2022, 12, 1291.	3.3	3
9	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
10	Elucidating Diversity in Obesity-Related Phenotypes Using Longitudinal and Multi-omic Approaches. , 2022, , 63-75.		0
11	Exerkines in health, resilience and disease. Nature Reviews Endocrinology, 2022, 18, 273-289.	9.6	268
12	Unbiased metabolome screen leads to personalized medicine strategy for amyotrophic lateral sclerosis. Brain Communications, 2022, 4, fcac069.	3.3	10
13	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	19.0	37
14	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
15	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
16	Patient-derived gene and protein expression signatures of NGLY1 deficiency. Journal of Biochemistry, 2022, 171, 187-199.	1.7	9
17	Tet enzymes are essential for early embryogenesis and completion of embryonic genome activation. EMBO Reports, 2022, 23, e53968.	4.5	20
18	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
19	Exploring disease interrelationships in patients with lymphatic disorders: A single center retrospective experience. Clinical and Translational Medicine, 2022, 12, e760.	4.0	9
20	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
21	Prediction of gestational age using urinary metabolites in term and preterm pregnancies. Scientific Reports, 2022, 12, 8033.	3.3	4
22	A cancer-associated RNA polymerase III identity drives robust transcription and expression of snaR-A noncoding RNA. Nature Communications, 2022, 13, .	12.8	12
23	Multiomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity. Cell Systems, 2022, 13, 598-614.e6.	6.2	10
24	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
25	Precision environmental health monitoring by longitudinal exposome and multi-omics profiling. Genome Research, 2022, 32, 1199-1214.	5.5	26
26	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
27	An exercise-inducible metabolite that suppresses feeding and obesity. Nature, 2022, 606, 785-790.	27.8	96
28	Serine biosynthesis as a novel therapeutic target for dilated cardiomyopathy. European Heart Journal, 2022, 43, 3477-3489.	2.2	23
29	KMT2D-NOTCH Mediates Coronary Abnormalities in Hypoplastic Left Heart Syndrome. Circulation Research, 2022, 131, 280-282.	4.5	3
30	Robust identification of temporal biomarkers in longitudinal omics studies. Bioinformatics, 2022, 38, 3802-3811.	4.1	10
31	Towards personalized medicine in maternal and child health: integrating biologic and social determinants. Pediatric Research, 2021, 89, 252-258.	2.3	19
32	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
33	PPARÎ³-p53-Mediated Vasculoregenerative Program to Reverse Pulmonary Hypertension. Circulation Research, 2021, 128, 401-418.	4.5	41
34	RobNorm: model-based robust normalization method for labeled quantitative mass spectrometry proteomics data. Bioinformatics, 2021, 37, 815-821.	4.1	3
35	CTLA-4 expression by B-1a B cells is essential for immune tolerance. Nature Communications, 2021, 12, 525.	12.8	43
36	The gut microbiome: a key player in the complexity of amyotrophic lateral sclerosis (ALS). BMC Medicine, 2021, 19, 13.	5.5	52

#	Article	IF	Citations
37	Decoding personal biotic and abiotic airborne exposome. Nature Protocols, 2021, 16, 1129-1151.	12.0	21
38	An Integrated Sequencing Approach for Updating the Pseudorabies Virus Transcriptome. Pathogens, 2021, 10, 242.	2.8	9
39	Benchmarking workflows to assess performance and suitability of germline variant calling pipelines in clinical diagnostic assays. BMC Bioinformatics, 2021, 22, 85.	2.6	12
40	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
41	Response to Hulman and colleagues regarding â€œGlucotypes reveal new patterns of glucose dysregulationâ€. PLoS Biology, 2021, 19, e3001092.	5.6	3
42	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
43	iNetModels 2.0: an interactive visualization and database of multi-omics data. Nucleic Acids Research, 2021, 49, W271-W276.	14.5	25
44	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. Nature Genetics, 2021, 53, 638-649.	21.4	86
45	ALDH1A3 Coordinates Metabolism With Gene Regulation in Pulmonary Arterial Hypertension. Circulation, 2021, 143, 2074-2090.	1.6	34
46	Swarm: A federated cloud framework for large-scale variant analysis. PLoS Computational Biology, 2021, 17, e1008977.	3.2	2
47	Early detection of SARSâ€CoVâ€2 and other infections in solid organ transplant recipients and household members using wearable devices. Transplant International, 2021, 34, 1019-1031.	1.6	6
48	Wearable sensors enable personalized predictions of clinical laboratory measurements. Nature Medicine, 2021, 27, 1105-1112.	30.7	121
49	Integrated trajectories of the maternal metabolome, proteome, and immunome predict labor onset. Science Translational Medicine, 2021, 13, .	12.4	82
50	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
51	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
52	Precision medicine in women with epilepsy: The challenge, systematic review, and future direction. Epilepsy and Behavior, 2021, 118, 107928.	1.7	13
53	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
54	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

#	Article	IF	Citations
55	AdaTiSS: a novel data-*Ada*ptive robust method for identifying *Ti*ssue *S*pecificity *S*cores. Bioinformatics, 2021, 37, 4469-4476.	4.1	2
56	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
57	Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study. JAMIA Open, 2021, 4, ooab054.	2.0	2
58	Combined nanopore and single-molecule real-time sequencing survey of human betaherpesvirus 5 transcriptome. Scientific Reports, 2021, 11, 14487.	3.3	8
59	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nature Methods, 2021, 18, 747-756.	19.0	403
60	The Exposome in the Era of the Quantified Self. Annual Review of Biomedical Data Science, 2021, 4, 255-277.	6.5	10
61	The X Chromosome from Telomere to Telomere: Key Achievements and Future Opportunities. Faculty Reviews, 2021, 10, 63.	3.9	1
62	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
63	Time-Course Transcriptome Profiling of a Poxvirus Using Long-Read Full-Length Assay. Pathogens, 2021, 10, 919.	2.8	4
64	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
65	Structured elements drive extensive circular RNA translation. Molecular Cell, 2021, 81, 4300-4318.e13.	9.7	108
66	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
67	Divergent patterns of selection on metabolite levels and gene expression. Bmc Ecology and Evolution, 2021, 21, 185.	1.6	4
68	Chromatin accessibility associates with protein-RNA correlation in human cancer. Nature Communications, 2021, 12, 5732.	12.8	18
69	Adapting skills from genetic counseling to wearables technology research during the COVIDâ€19 pandemic: Poised for the pivot. Journal of Genetic Counseling, 2021, 30, 1269-1275.	1.6	0
70	A scalable, secure, and interoperable platform for deep data-driven health management. Nature Communications, 2021, 12, 5757.	12.8	27
71	In-depth triacylglycerol profiling using MS3 Q-Trap mass spectrometry. Analytica Chimica Acta, 2021, 1184, 339023.	5.4	4
72	Precision Neoantigen Discovery Using Large-scale Immunopeptidomes and Composite Modeling of MHC Peptide Presentation. Molecular and Cellular Proteomics, 2021, 20, 100111.	3.8	23

#	Article	IF	Citations
73	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
74	COVID-19–Induced New-Onset Diabetes: Trends and Technologies. Diabetes, 2021, 70, 2733-2744.	0.6	49
75	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
76	Altered Cardiac Energetics and Mitochondrial Dysfunction in Hypertrophic Cardiomyopathy. Circulation, 2021, 144, 1714-1731.	1.6	90
77	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. Nature Genetics, 2021, 53, 1564-1576.	21.4	45
78	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
79	Cross-Laboratory Standardization of Preclinical Lipidomics Using Differential Mobility Spectrometry and Multiple Reaction Monitoring. Analytical Chemistry, 2021, 93, 16369-16378.	6.5	40
80	Human exposome assessment platform. Environmental Epidemiology, 2021, 5, e182.	3.0	7
81	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
82	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
83	Exposome-wide Association Study for Metabolic Syndrome. Frontiers in Genetics, 2021, 12, 783930.	2.3	6
84	Global metabolic profiling to model biological processes of aging in twins. Aging Cell, 2020, 19, e13073.	6.7	38
85	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
86	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	12.8	152
87	iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy. Cell Reports, 2020, 32, 108117.	6.4	40
88	Deep longitudinal multiomics profiling reveals two biological seasonal patterns in California. Nature Communications, 2020, 11, 4933.	12.8	36
89	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
90	Meta-analytic approach for transcriptome profiling of herpes simplex virus type 1. Scientific Data, 2020, 7, 223.	5.3	7

#	Article	IF	Citations
91	Pre-symptomatic detection of COVID-19 from smartwatch data. Nature Biomedical Engineering, 2020, 4, 1208-1220.	22.5	304
92	Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. Cell Reports, 2020, 33, 108456.	6.4	24
93	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. IScience, 2020, 23, 101844.	4.1	31
94	A Customizable Analysis Flow in Integrative Multi-Omics. Biomolecules, 2020, 10, 1606.	4.0	14
95	Multi-faceted epigenetic dysregulation of gene expression promotes esophageal squamous cell carcinoma. Nature Communications, 2020, 11, 3675.	12.8	63
96	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	12.8	95
97	Landscape of cohesin-mediated chromatin loops in the human genome. Nature, 2020, 583, 737-743.	27.8	134
98	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
99	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
100	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	5.5	32
101	Long-read assays shed new light on the transcriptome complexity of a viral pathogen. Scientific Reports, 2020, 10, 13822.	3.3	17
102	Candidate variants in TUB are associated with familial tremor. PLoS Genetics, 2020, 16, e1009010.	3.5	3
103	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
104	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
105	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
106	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
107	Longitudinal Analysis of Serum Cytokine Levels and Gut Microbial Abundance Links IL-17/IL-22 With *Clostridia* and Insulin Sensitivity in Humans. Diabetes, 2020, 69, 1833-1842.	0.6	10
108	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

#	Article	IF	Citations
109	Molecular Choreography of Acute Exercise. Cell, 2020, 181, 1112-1130.e16.	28.9	261
110	Immunologic effects of forest fire exposure show increases in ILâ€‘1Î² and CRP. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 2356-2358.	5.7	14
111	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. Cell, 2020, 181, 1464-1474.	28.9	147
112	Physiological bloodâ€"brain transport is impaired with age by a shift in transcytosis. Nature, 2020, 583, 425-430.	27.8	243
113	Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. Cell, 2020, 181, 1680-1692.e15.	28.9	154
114	Multiomic immune clockworks of pregnancy. Seminars in Immunopathology, 2020, 42, 397-412.	6.1	47
115	Systematic identification of silencers in human cells. Nature Genetics, 2020, 52, 254-263.	21.4	119
116	Personal aging markers and ageotypes revealed by deep longitudinal profiling. Nature Medicine, 2020, 26, 83-90.	30.7	225
117	The MEK5â€"ERK5 Kinase Axis Controls Lipid Metabolism in Small-Cell Lung Cancer. Cancer Research, 2020, 80, 1293-1303.	0.9	49
118	Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension. Nature Communications, 2020, 11, 1673.	12.8	60
119	Humans Are Selectively Exposed to Pneumocystis jirovecii. MBio, 2020, 11, .	4.1	8
120	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
121	Multiomics Characterization of Preterm Birth in Low- and Middle-Income Countries. JAMA Network Open, 2020, 3, e2029655.	5.9	53
122	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
123	Precision Medicine: Role of Proteomics in Changing Clinical Management and Care. Journal of Proteome Research, 2019, 18, 1-6.	3.7	26
124	Multiomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. Bioinformatics, 2019, 35, 95-103.	4.1	162
125	High Throughput Sequencing and Assessing Disease Risk. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a026849.	6.2	23
126	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. Cell, 2019, 178, 1245-1259.e14.	28.9	163

#	Article	IF	Citations
127	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. Frontiers in Genetics, 2019, 10, 834.	2.3	44
128	MISTERMINATE Mechanistically Links Mitochondrial Dysfunction with Proteostasis Failure. Molecular Cell, 2019, 75, 835-848.e8.	9.7	56
129	Chromatin Remodeling in Response to BRCA2-Crisis. Cell Reports, 2019, 28, 2182-2193.e6.	6.4	6
130	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
131	Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. Nature Biomedical Engineering, 2019, 3, 1009-1019.	22.5	135
132	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
133	A machine-compiled database of genome-wide association studies. Nature Communications, 2019, 10, 3341.	12.8	21
134	HAT1 Coordinates Histone Production and Acetylation via H4 Promoter Binding. Molecular Cell, 2019, 75, 711-724.e5.	9.7	55
135	Template-switching artifacts resemble alternative polyadenylation. BMC Genomics, 2019, 20, 824.	2.8	32
136	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
137	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. Nature Communications, 2019, 10, 4063.	12.8	104
138	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
139	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
140	Big data and health. The Lancet Digital Health, 2019, 1, e252-e254.	12.3	28
141	Windows into human health through wearables data analytics. Current Opinion in Biomedical Engineering, 2019, 9, 28-46.	3.4	101
142	Personalized Metabolomics. Methods in Molecular Biology, 2019, 1978, 447-456.	0.9	7
143	Engineering Genetic Predisposition in Human Neuroepithelial Stem Cells Recapitulates Medulloblastoma Tumorigenesis. Cell Stem Cell, 2019, 25, 433-446.e7.	11.1	56
144	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

#	Article	IF	Citations
145	Longitudinal multi-omics of host–microbe dynamics in prediabetes. Nature, 2019, 569, 663-671.	27.8	391
146	Applying circulating tumor DNA methylation in the diagnosis of lung cancer. Precision Clinical Medicine, 2019, 2, 45-56.	3.3	18
147	A longitudinal big data approach for precision health. Nature Medicine, 2019, 25, 792-804.	30.7	329
148	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
149	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	28.9	498
150	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
151	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
152	Gene-Environment Interaction in the Era of Precision Medicine. Cell, 2019, 177, 38-44.	28.9	73
153	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. Science, 2019, 364, .	12.6	576
154	Long-Read Sequencing â€" A Powerful Tool in Viral Transcriptome Research. Trends in Microbiology, 2019, 27, 578-592.	7.7	76
155	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. Nature, 2019, 574, 553-558.	27.8	187
156	Metformin Affects Heme Function as a Possible Mechanism of Action. G3: Genes, Genomes, Genetics, 2019, 9, 513-522.	1.8	12
157	Understanding health disparities. Journal of Perinatology, 2019, 39, 354-358.	2.0	14
158	Macrophage de novo NAD+ synthesis specifies immune function in aging and inflammation. Nature Immunology, 2019, 20, 50-63.	14.5	304
159	Smooth Muscle Contact Drives Endothelial Regeneration by BMPR2-Notch1â€"Mediated Metabolic and Epigenetic Changes. Circulation Research, 2019, 124, 211-224.	4.5	78
160	Whole-exome sequencing data of suicide victims who had suffered from major depressive disorder. Scientific Data, 2019, 6, 190010.	5.3	5
161	Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining. Journal of Proteome Research, 2018, 17, 1383-1396.	3.7	16
162	Integrative omics for health and disease. Nature Reviews Genetics, 2018, 19, 299-310.	16.3	676

#	Article	IF	Citations
163	SETD7 Drives Cardiac Lineage Commitment through Stage-Specific Transcriptional Activation. Cell Stem Cell, 2018, 22, 428-444.e5.	11.1	38
164	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
165	Fast Metagenomic Binning via Hashing and Bayesian Clustering. Journal of Computational Biology, 2018, 25, 677-688.	1.6	5
166	Distinct transcriptomic and exomic abnormalities within myelodysplastic syndrome marrow cells. Leukemia and Lymphoma, 2018, 59, 2952-2962.	1.3	16
167	Comparative analysis of respiratory motion tracking using Microsoft Kinect v2 sensor. Journal of Applied Clinical Medical Physics, 2018, 19, 193-204.	1.9	26
168	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
169	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	8.0	580
170	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. Scientific Reports, 2018, 8, 226.	3.3	37
171	Applying genomics in heart transplantation. Transplant International, 2018, 31, 278-290.	1.6	8
172	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. Cell Systems, 2018, 6, 157-170.e8.	6.2	183
173	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
174	Personal Omics for Precision Health. Circulation Research, 2018, 122, 1169-1171.	4.5	54
175	A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. Nature Genetics, 2018, 50, 613-620.	21.4	116
176	Full Genome Sequence of the Western Reserve Strain of Vaccinia Virus Determined by Third-Generation Sequencing. Genome Announcements, 2018, 6, .	0.8	16
177	Circular DNA elements of chromosomal origin are common in healthy human somatic tissue. Nature Communications, 2018, 9, 1069.	12.8	232
178	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
179	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. Genome Research, 2018, 28, 231-242.	5.5	64
180	*WISP3* mutation associated with pseudorheumatoid dysplasia. Journal of Physical Education and Sports Management, 2018, 4, a001990.	1.2	16

#	Article	IF	Citations
181	Transcriptomic study of Herpes simplex virus type-1 using full-length sequencing techniques. Scientific Data, 2018, 5, 180266.	5.3	27
182	Dynamic transcriptome profiling dataset of vaccinia virus obtained from long-read sequencing techniques. GigaScience, 2018, 7, .	6.4	38
183	Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. Nature Genetics, 2018, 50, 1716-1727.	21.4	135
184	Longitudinal personal DNA methylome dynamics in a human with a chronic condition. Nature Medicine, 2018, 24, 1930-1939.	30.7	55
185	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. PLoS Genetics, 2018, 14, e1007755.	3.5	30
186	Cross-Platform Comparison of Untargeted and Targeted Lipidomics Approaches on Aging Mouse Plasma. Scientific Reports, 2018, 8, 17747.	3.3	81
187	High-frequency actionable pathogenic exome variants in an average-risk cohort. Journal of Physical Education and Sports Management, 2018, 4, a003178.	1.2	23
188	Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome. Frontiers in Genetics, 2018, 9, 432.	2.3	14
189	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
190	Decoding the Genomics of Abdominal Aortic Aneurysm. Cell, 2018, 174, 1361-1372.e10.	28.9	68
191	Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. Cell, 2018, 175, 277-291.e31.	28.9	137
192	Disruption of mesoderm formation during cardiac differentiation due to developmental exposure to 13-cis-retinoic acid. Scientific Reports, 2018, 8, 12960.	3.3	19
193	Natural Selection Has Differentiated the Progesterone Receptor among Human Populations. American Journal of Human Genetics, 2018, 103, 45-57.	6.2	30
194	Glucotypes reveal new patterns of glucose dysregulation. PLoS Biology, 2018, 16, e2005143.	5.6	167
195	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. Frontiers in Microbiology, 2018, 8, 2708.	3.5	64
196	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
197	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
198	Long-Read Sequencing Revealed an Extensive Transcript Complexity in Herpesviruses. Frontiers in Genetics, 2018, 9, 259.	2.3	23

#	Article	IF	Citations
199	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
200	An integrated global regulatory network of hematopoietic precursor cell self-renewal and differentiation. Integrative Biology (United Kingdom), 2018, 10, 390-405.	1.3	4
201	Transcriptome-wide survey of pseudorabies virus using next- and third-generation sequencing platforms. Scientific Data, 2018, 5, 180119.	5.3	31
202	Wearables and the medical revolution. Personalized Medicine, 2018, 15, 429-448.	1.5	361
203	Single cell transcriptomics reveals unanticipated features of early hematopoietic precursors. Nucleic Acids Research, 2017, 45, gkw1214.	14.5	40
204	Association of AHSG with alopecia and mental retardation (APMR) syndrome. Human Genetics, 2017, 136, 287-296.	3.8	14
205	Pharmacological rescue of diabetic skeletal stem cell niches. Science Translational Medicine, 2017, 9, .	12.4	80
206	De novo and rare mutations in the HSPA1L heat shock gene associated with inflammatory bowel disease. Genome Medicine, 2017, 9, 8.	8.2	27
207	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
208	Implementation of facial recognition with Microsoft Kinect v2 sensor for patient verification. Medical Physics, 2017, 44, 2391-2399.	3.0	19
209	Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression. Nature Communications, 2017, 8, 14995.	12.8	131
210	Non-equivalence of Wnt and R-spondin ligands during Lgr5+ intestinal stem-cell self-renewal. Nature, 2017, 545, 238-242.	27.8	327
211	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
212	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. Nature Communications, 2017, 8, 15178.	12.8	284
213	Succinate and its G-protein-coupled receptor stimulates osteoclastogenesis. Nature Communications, 2017, 8, 15621.	12.8	73
214	Multi-platform analysis reveals a complex transcriptome architecture of a circovirus. Virus Research, 2017, 237, 37-46.	2.2	49
215	Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. Nucleic Acids Research, 2017, 45, gkx026.	14.5	31
216	Gpr124 is essential for bloodâ€"brain barrier integrity in central nervous system disease. Nature Medicine, 2017, 23, 450-460.	30.7	177

#	Article	IF	Citations
217	Characterization of the Dynamic Transcriptome of a Herpesvirus with Long-read Single Molecule Real-Time Sequencing. Scientific Reports, 2017, 7, 43751.	3.3	76
218	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
219	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
220	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
221	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
222	Network analyses identify liver‐specific targets for treating liver diseases. Molecular Systems Biology, 2017, 13, 938.	7.2	112
223	Digital Health: Tracking Physiomes and Activity Using Wearable Biosensors Reveals Useful Health-Related Information. PLoS Biology, 2017, 15, e2001402.	5.6	319
224	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. Molecular Cell, 2017, 67, 1037-1048.e6.	9.7	242
225	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
226	Cloud-based interactive analytics for terabytes of genomic variants data. Bioinformatics, 2017, 33, 3709-3715.	4.1	9
227	Isolated Congenital Anosmia and CNGA2 Mutation. Scientific Reports, 2017, 7, 2667.	3.3	14
228	Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis. Scientific Reports, 2017, 7, 5557.	3.3	19
229	High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. Scientific Reports, 2017, 7, 7106.	3.3	56
230	Lineage-specific dynamic and pre-established enhancer‐promoter contacts cooperate in terminal differentiation. Nature Genetics, 2017, 49, 1522-1528.	21.4	255
231	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
232	Long-Read Sequencing of Human Cytomegalovirus Transcriptome Reveals RNA Isoforms Carrying Distinct Coding Potentials. Scientific Reports, 2017, 7, 15989.	3.3	75
233	Association of Omics Features with Histopathology Patterns in Lung Adenocarcinoma. Cell Systems, 2017, 5, 620-627.e3.	6.2	88
234	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. Nature Communications, 2017, 8, 59.	12.8	225

#	Article	IF	Citations
235	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
236	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
237	ChIA-PET2: a versatile and flexible pipeline for ChIA-PET data analysis. Nucleic Acids Research, 2017, 45, e4-e4.	14.5	104
238	Long-read sequencing of the human cytomegalovirus transcriptome with the Pacific Biosciences RSII platform. Scientific Data, 2017, 4, 170194.	5.3	46
239	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
240	Fetal de novo mutations and preterm birth. PLoS Genetics, 2017, 13, e1006689.	3.5	30
241	Topological organization and dynamic regulation of human tRNA genes during macrophage differentiation. Genome Biology, 2017, 18, 180.	8.8	27
242	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
243	Long-Read Sequencing Reveals a GC Pressure during the Evolution of Porcine Endogenous Retrovirus. Genome Announcements, 2017, 5, .	0.8	4
244	Plasma sterols and depressive symptom severity in a population-based cohort. PLoS ONE, 2017, 12, e0184382.	2.5	11
245	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
246	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. PLoS ONE, 2016, 11, e0162868.	2.5	93
247	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
248	Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1. Scientific Reports, 2016, 6, 20104.	3.3	61
249	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. Cell, 2016, 167, 1734-1749.e22.	28.9	195
250	Genome assembly from synthetic long read clouds. Bioinformatics, 2016, 32, i216-i224.	4.1	33
251	Yeast longevity promoted by reversing aging-associated decline in heavy isotope content. Npj Aging and Mechanisms of Disease, 2016, 2, 16004.	4.5	23
252	Omics Profiling in Precision Oncology. Molecular and Cellular Proteomics, 2016, 15, 2525-2536.	3.8	84

#	Article	IF	Citations
253	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
254	Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. Nature Genetics, 2016, 48, 687-693.	21.4	193
255	A proposal for validation of antibodies. Nature Methods, 2016, 13, 823-827.	19.0	473
256	Nat1 Deficiency Is Associated with Mitochondrial Dysfunction and Exercise Intolerance in Mice. Cell Reports, 2016, 17, 527-540.	6.4	35
257	Simul-seq: combined DNA and RNA sequencing for whole-genome and transcriptome profiling. Nature Methods, 2016, 13, 953-958.	19.0	34
258	NIH working group report—using genomic information to guide weight management: From universal to precision treatment. Obesity, 2016, 24, 14-22.	3.0	96
259	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
260	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. Nature Genetics, 2016, 48, 1193-1203.	21.4	952
261	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
262	iPSC-derived cardiomyocytes reveal abnormal TGF-Î² signalling in left ventricular non-compaction cardiomyopathy. Nature Cell Biology, 2016, 18, 1031-1042.	10.3	148
263	Predicting non-small cell lung cancer prognosis by fully automated microscopic pathology image features. Nature Communications, 2016, 7, 12474.	12.8	694
264	Secure cloud computing for genomic data. Nature Biotechnology, 2016, 34, 588-591.	17.5	20
265	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
266	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. Cell Metabolism, 2016, 24, 172-184.	16.2	133
267	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
268	Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. Proteomics, 2016, 16, 465-476.	2.2	8
269	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	28.9	804
270	Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome. Nature Biotechnology, 2016, 34, 64-69.	17.5	93

#	Article	IF	Citations
271	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
272	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
273	Genomics and Personalized Medicine. , 2016, , .		23
274	Effects of cellular origin on differentiation of human induced pluripotent stem cellâ€"derived endothelial cells. JCI Insight, 2016, 1, .	5.0	75
275	Probing High-density Functional Protein Microarrays to Detect Protein-protein Interactions. Journal of Visualized Experiments, 2015, , e51872.	0.3	7
276	Impact of alleleâ€specific peptides in proteome quantification. Proteomics - Clinical Applications, 2015, 9, 432-436.	1.6	4
277	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	5.6	9
278	Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data. PLoS Genetics, 2015, 11, e1005496.	3.5	23
279	Whole-Exome Enrichment with the Agilent SureSelect Human All Exon Platform. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot083659.	0.3	38
280	Whole-Exome Enrichment with the Roche NimbleGen SeqCap EZ Exome Library SR Platform. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot084855.	0.3	13
281	Whole-Exome Enrichment with the Illumina TruSeq Exome Enrichment Platform. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot084863.	0.3	11
282	High-Throughput Sequencing Technologies. Molecular Cell, 2015, 58, 586-597.	9.7	968
283	Recurrent somatic mutations in regulatory regions of human cancer genomes. Nature Genetics, 2015, 47, 710-716.	21.4	225
284	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
285	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
286	Metabolome progression during early gut microbial colonization of gnotobiotic mice. Scientific Reports, 2015, 5, 11589.	3.3	29
287	Mango: a bias-correcting ChIA-PET analysis pipeline. Bioinformatics, 2015, 31, 3092-3098.	4.1	126
288	Transcriptome Signature and Regulation in Human Somatic Cell Reprogramming. Stem Cell Reports, 2015, 4, 1125-1139.	4.8	19

#	Article	IF	Citations
289	Single-cell chromatin accessibility reveals principles of regulatory variation. Nature, 2015, 523, 486-490.	27.8	1,798
290	Transglutaminase 4 as a prostate autoantigen in male subfertility. Science Translational Medicine, 2015, 7, 292ra101.	12.4	60
291	Characterization of Novel Transcripts in Pseudorabies Virus. Viruses, 2015, 7, 2727-2744.	3.3	46
292	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
293	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
294	Reassessment of Piwi Binding to the Genome and Piwi Impact on RNA Polymerase II Distribution. Developmental Cell, 2015, 32, 772-774.	7.0	9
295	Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. Genome Research, 2015, 25, 1610-1621.	5.5	157
296	Genomic analysis of mycosis fungoides and SÃ©zary syndrome identifies recurrent alterations in TNFR2. Nature Genetics, 2015, 47, 1056-1060.	21.4	242
297	Evaluating Common Humoral Responses against Fungal Infections with Yeast Protein Microarrays. Journal of Proteome Research, 2015, 14, 3924-3931.	3.7	10
298	Integrated Proteomic and Genomic Analysis of Gastric Cancer Patient Tissues. Journal of Proteome Research, 2015, 14, 4995-5006.	3.7	7
299	Novel mutations in PIEZO1 cause an autosomal recessive generalized lymphatic dysplasia with non-immune hydrops fetalis. Nature Communications, 2015, 6, 8085.	12.8	247
300	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. Cell, 2015, 162, 1051-1065.	28.9	304
301	Achieving high-sensitivity for clinical applications using augmented exome sequencing. Genome Medicine, 2015, 7, 71.	8.2	46
302	Metformin Improves Diabetic Bone Health by Re-Balancing Catabolism and Nitrogen Disposal. PLoS ONE, 2015, 10, e0146152.	2.5	13
303	Abstract 19076: ATAC-seq Implicates Epigenome-wide CTCF Dissociation in the Progression of Cardiac Ischemia. Circulation, 2015, 132, .	1.6	0
304	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
305	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
306	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

#	Article	IF	Citations
307	Personalized sequencing and the future of medicine: discovery, diagnosis and defeat of disease. Pharmacogenomics, 2014, 15, 1771-1790.	1.3	66
308	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. Molecular Systems Biology, 2014, 10, 774.	7.2	138
309	Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. PLoS Genetics, 2014, 10, e1004549.	3.5	49
310	Coherent Functional Modules Improve Transcription Factor Target Identification, Cooperativity Prediction, and Disease Association. PLoS Genetics, 2014, 10, e1004122.	3.5	29
311	Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues. PLoS Genetics, 2014, 10, e1004304.	3.5	60
312	Strain Kaplan of Pseudorabies Virus Genome Sequenced by PacBio Single-Molecule Real-Time Sequencing Technology. Genome Announcements, 2014, 2, .	0.8	29
313	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
314	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
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	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
317	Haplotype structure and positive selection at TLR1. European Journal of Human Genetics, 2014, 22, 551-557.	2.8	20
318	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
319	Clinical Interpretation and Implications of Whole-Genome Sequencing. JAMA - Journal of the American Medical Association, 2014, 311, 1035.	7.4	398
320	Whole-genome haplotyping using long reads and statistical methods. Nature Biotechnology, 2014, 32, 261-266.	17.5	170
321	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
322	Landscape and variation of RNA secondary structure across the human transcriptome. Nature, 2014, 505, 706-709.	27.8	519
323	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	27.8	259
324	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444

#	Article	IF	Citations
325	Topologically associating domains are stable units of replication-timing regulation. Nature, 2014, 515, 402-405.	27.8	779
326	Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures. Bioinformatics, 2014, 30, 2808-2810.	4.1	182
327	iPOP and its role in participatory medicine. Genome Medicine, 2014, 6, 6.	8.2	7
328	Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulumâ€"associated degradation pathway. Genetics in Medicine, 2014, 16, 751-758.	2.4	191
329	Regulatory analysis of the C. elegans genome with spatiotemporal resolution. Nature, 2014, 512, 400-405.	27.8	115
330	Genome-wide map of regulatory interactions in the human genome. Genome Research, 2014, 24, 1905-1917.	5.5	259
331	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	27.8	184
332	Widespread contribution of transposable elements to the innovation of gene regulatory networks. Genome Research, 2014, 24, 1963-1976.	5.5	408
333	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. Cell, 2014, 158, 673-688.	28.9	404
334	STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. PLoS ONE, 2014, 9, e84860.	2.5	25
335	Identification of STAT5A and STAT5B Target Genes in Human T Cells. PLoS ONE, 2014, 9, e86790.	2.5	67
336	Genomic era diagnosis and management of hereditary and sporadic colon cancer. World Journal of Clinical Oncology, 2014, 5, 1036.	2.3	11
337	Transcriptomic Evaluation of CD34+ Marrow Cells from Myelodysplastic Syndrome (MDS) Patients. Blood, 2014, 124, 1894-1894.	1.4	5
338	Personal genomes, quantitative dynamic omics and personalized medicine. Quantitative Biology, 2013, 1, 71-90.	0.5	29
339	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
340	Dynamic trans-Acting Factor Colocalization in Human Cells. Cell, 2013, 155, 713-724.	28.9	142
341	Extensive Variation in Chromatin States Across Humans. Science, 2013, 342, 750-752.	12.6	338
342	A single-molecule long-read survey of the human transcriptome. Nature Biotechnology, 2013, 31, 1009-1014.	17.5	600

#	Article	IF	Citations
343	Systematic investigation of protein–small molecule interactions. IUBMB Life, 2013, 65, 2-8.	3.4	33
344	Promise of personalized omics to precision medicine. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2013, 5, 73-82.	6.6	245
345	High-throughput sequencing for biology and medicine. Molecular Systems Biology, 2013, 9, 640.	7.2	251
346	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
347	Preparation of Recombinant Protein Spotted Arrays for Proteome-Wide Identification of Kinase Targets. Current Protocols in Protein Science, 2013, 72, Unit 27.4.	2.8	4
348	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
349	Multimodal Dynamic Profiling of Healthy and Diseased States for Future Personalized Health Care. Clinical Pharmacology and Therapeutics, 2013, 93, 29-32.	4.7	7
350	Variation and genetic control of protein abundance in humans. Nature, 2013, 499, 79-82.	27.8	343
351	Centromere-Like Regions in the Budding Yeast Genome. PLoS Genetics, 2013, 9, e1003209.	3.5	38
352	Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 387-397.	1.8	59
353	PATH-SCAN: A REPORTING TOOL FOR IDENTIFYING CLINICALLY ACTIONABLE VARIANTS. , 2013, , .		9
354	Overview of High Throughput Sequencing Technologies to Elucidate Molecular Pathways in Cardiovascular Diseases. Circulation Research, 2013, 112, 1613-1623.	4.5	110
355	Extensive Transcript Diversity and Novel Upstream Open Reading Frame Regulation in Yeast. G3: Genes, Genomes, Genetics, 2013, 3, 343-352.	1.8	59
356	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
357	Metadata Checklist for the Integrated Personal Omics Study: <i>Proteomics and Metabolomics Experiments</i>. Big Data, 2013, 1, 202-206.	3.4	8
358	Integrative Analysis of Longitudinal Metabolomics Data from a Personal Multi-Omics Profile. Metabolites, 2013, 3, 741-760.	2.9	56
359	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
360	Annotation of functional variation in personal genomes using RegulomeDB. Genome Research, 2012, 22, 1790-1797.	5.5	2,335

#	Article	IF	Citations
361	Linking disease associations with regulatory information in the human genome. Genome Research, 2012, 22, 1748-1759.	5.5	657
362	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research, 2012, 22, 1798-1812.	5.5	762
363	Correlation of Global MicroRNA Expression With Basal Cell Carcinoma Subtype. G3: Genes, Genomes, Genetics, 2012, 2, 279-286.	1.8	36
364	Investigating metaboliteâ€"protein interactions: An overview of available techniques. Methods, 2012, 57, 459-466.	3.8	40
365	Systems biology: personalized medicine for the future?. Current Opinion in Pharmacology, 2012, 12, 623-628.	3.5	90
366	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
367	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	5.5	1,708
368	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. Genome Research, 2012, 22, 1735-1747.	5.5	168
369	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	28.9	1,096
370	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	28.9	1,134
371	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	27.8	1,384
372	Detecting and annotating genetic variations using the HugeSeq pipeline. Nature Biotechnology, 2012, 30, 226-229.	17.5	104
373	Performance comparison of whole-genome sequencing platforms. Nature Biotechnology, 2012, 30, 78-82.	17.5	281
374	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223.	17.5	281
375	Whole Genome Sequence Analysis of Primary Myelofibrosis.. Blood, 2012, 120, 2863-2863.	1.4	0
376	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
377	AlleleSeq: analysis of alleleâ€specific expression and binding in a network framework. Molecular Systems Biology, 2011, 7, 522.	7.2	284
378	Dissecting phosphorylation networks: lessons learned from yeast. Expert Review of Proteomics, 2011, 8, 775-786.	3.0	15

#	Article	IF	Citations
379	Regulatory Variation Within and Between Species. Annual Review of Genomics and Human Genetics, 2011, 12, 327-346.	6.2	70
380	Diverse Roles and Interactions of the SWI/SNF Chromatin Remodeling Complex Revealed Using Global Approaches. PLoS Genetics, 2011, 7, e1002008.	3.5	185
381	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
382	Landscape of Next-Generation Sequencing Technologies. Analytical Chemistry, 2011, 83, 4327-4341.	6.5	314
383	Performance comparison of exome DNA sequencing technologies. Nature Biotechnology, 2011, 29, 908-914.	17.5	464
384	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	3.8	294
385	Identification of genomic indels and structural variations using split reads. BMC Genomics, 2011, 12, 375.	2.8	57
386	Metabolites as global regulators: A new view of protein regulation. BioEssays, 2011, 33, 485-489.	2.5	36
387	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. Genes and Development, 2011, 25, 767-778.	5.9	60
388	Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence. PLoS Genetics, 2011, 7, e1002280.	3.5	137
389	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
390	Analyzing In Vivo Metaboliteâ€Protein Interactions by Largeâ€Scale Systematic Analyses. Current Protocols in Chemical Biology, 2011, 3, 181-196.	1.7	5
391	Genome-Wide Mapping of Copy Number Variation in Humans: Comparative Analysis of High Resolution Array Platforms. PLoS ONE, 2011, 6, e27859.	2.5	59
392	Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. Science Signaling, 2010, 3, ra12.	3.6	341
393	Yeast proteomics and protein microarrays. Journal of Proteomics, 2010, 73, 2147-2157.	2.4	31
394	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
395	Genetic analysis of variation in transcription factor binding in yeast. Nature, 2010, 464, 1187-1191.	27.8	162
396	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. Nature Biotechnology, 2010, 28, 47-55.	17.5	158

#	Article	IF	Citations
397	Annotating non-coding regions of the genome. Nature Reviews Genetics, 2010, 11, 559-571.	16.3	398
398	Systems Biology Approaches to Disease Marker Discovery. Disease Markers, 2010, 28, 209-224.	1.3	18
399	Personal genome sequencing: current approaches and challenges. Genes and Development, 2010, 24, 423-431.	5.9	119
400	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
401	Molecular Mechanisms of Ethanol-Induced Pathogenesis Revealed by RNA-Sequencing. PLoS Pathogens, 2010, 6, e1000834.	4.7	142
402	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
403	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
404	Variation in Transcription Factor Binding Among Humans. Science, 2010, 328, 232-235.	12.6	521
405	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	12.6	912
406	ChIPâ€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
407	Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. Cell, 2010, 143, 639-650.	28.9	200
408	Systems biology approaches to disease marker discovery. Disease Markers, 2010, 28, 209-24.	1.3	9
409	MSB: A mean-shift-based approach for the analysis of structural variation in the genome. Genome Research, 2009, 19, 106-117.	5.5	33
410	Personal phenotypes to go with personal genomes. Molecular Systems Biology, 2009, 5, 273.	7.2	41
411	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
412	Integrating Sequencing Technologies in Personal Genomics: Optimal Low Cost Reconstruction of Structural Variants. PLoS Computational Biology, 2009, 5, e1000432.	3.2	14
413	Dynamic and complex transcription factor binding during an inducible response in yeast. Genes and Development, 2009, 23, 1351-1363.	5.9	89
414	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. BMC Genomics, 2009, 10, 37.	2.8	137

#	Article	IF	Citations
415	Systems biology from a yeast omics perspective. FEBS Letters, 2009, 583, 3895-3899.	2.8	46
416	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. Nature Biotechnology, 2009, 27, 66-75.	17.5	514
417	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	27.8	744
418	Global identification of protein kinase substrates by protein microarray analysis. Nature Protocols, 2009, 4, 1820-1827.	12.0	46
419	RNA-Seq: a revolutionary tool for transcriptomics. Nature Reviews Genetics, 2009, 10, 57-63.	16.3	10,529
420	MAPK target networks in <i>Arabidopsis thaliana</i> revealed using functional protein microarrays. Genes and Development, 2009, 23, 80-92.	5.9	438
421	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
422	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
423	Protein Microarrays. Methods in Molecular Biology, 2009, 548, 209-222.	0.9	18
424	The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing. Science, 2008, 320, 1344-1349.	12.6	2,180
425	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. Science, 2008, 322, 104-110.	12.6	1,297
426	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
427	High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. PLoS Genetics, 2008, 4, e1000249.	3.5	99
428	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
429	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
430	Arabidopsis Protein Microarrays for the High-Throughput Identification of Protein-Protein Interactions. Plant Signaling and Behavior, 2007, 2, 416-420.	2.4	30
431	Divergence of Transcription Factor Binding Sites Across Related Yeast Species. Science, 2007, 317, 815-819.	12.6	320
432	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

#	ARTICLE	IF	CITATIONS
433	New insights into *Acinetobacter baumannii* pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. Genes and Development, 2007, 21, 601-614.	5.9	455
434	Getting connected: analysis and principles of biological networks. Genes and Development, 2007, 21, 1010-1024.	5.9	477
435	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. Nature Methods, 2007, 4, 651-657.	19.0	1,254
436	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
437	Paired-End Mapping Reveals Extensive Structural Variation in the Human Genome. Science, 2007, 318, 420-426.	12.6	1,003
438	Proteomics for Elucidating Protein Function, Regulatory Networks and Improving Human Health. FASEB Journal, 2007, 21, A211.	0.5	0
439	ProCAT: a data analysis approach for protein microarrays. Genome Biology, 2006, 7, R110.	9.6	46
440	Yeast as a Model for Human Disease. Current Protocols in Human Genetics, 2006, 48, Unit 15.6.	3.5	36
441	Charging it up: global analysis of protein phosphorylation. Trends in Genetics, 2006, 22, 545-554.	6.7	123
442	Design Issues in Implementing a Portable Sample Tracking and Analysis Research Support (STARS) System for PCR Based Microarray Research. , 2006, , .		0
443	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
444	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
445	Global analysis of protein phosphorylation in yeast. Nature, 2005, 438, 679-684.	27.8	915
446	Global analysis of protein function using protein microarrays. Mechanisms of Ageing and Development, 2005, 126, 171-175.	4.6	35
447	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. Genes and Development, 2005, 19, 2816-2826.	5.9	443
448	Large-Scale Mutagenesis of the Yeast Genome Using a Tn7-Derived Multipurpose Transposon. Genome Research, 2004, 14, 1975-1986.	5.5	52
449	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
450	Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. Science, 2004, 306, 2242-2246.	12.6	983

#	ARTICLE	IF	CITATIONS
451	Regulation of Gene Expression by a Metabolic Enzyme. Science, 2004, 306, 482-484.	12.6	223
452	Protein chip technology. Current Opinion in Chemical Biology, 2003, 7, 55-63.	6.1	861
453	Protein analysis on a proteomic scale. Nature, 2003, 422, 208-215.	27.8	610
454	Analyzing antibody specificity with whole proteome microarrays. Nature Biotechnology, 2003, 21, 1509-1512.	17.5	270
455	Proteomics. Annual Review of Biochemistry, 2003, 72, 783-812.	11.1	332
456	A Bayesian Networks Approach for Predicting Protein-Protein Interactions from Genomic Data. Science, 2003, 302, 449-453.	12.6	1,183
457	Defining Genes in the Genomics Era. Science, 2003, 300, 258-260.	12.6	114
458	Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. Genes and Development, 2003, 17, 2698-2708.	5.9	74
459	Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae. Genes and Development, 2002, 16, 3017-3033.	5.9	236
460	ChIP-chip: A genomic approach for identifying transcription factor binding sites. Methods in Enzymology, 2002, 350, 469-483.	1.0	151
461	Functional profiling of the Saccharomyces cerevisiae genome. Nature, 2002, 418, 387-391.	27.8	3,938
462	Global Analysis of Protein Activities Using Proteome Chips. Science, 2001, 293, 2101-2105.	12.6	2,082
463	Protein arrays and microarrays. Current Opinion in Chemical Biology, 2001, 5, 40-45.	6.1	376
464	Making drug addicts out of yeast. Nature Biotechnology, 2001, 19, 1022-1023.	17.5	3
465	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. Nature, 2001, 409, 533-538.	27.8	1,030
466	Emerging technologies in yeast genomics. Nature Reviews Genetics, 2001, 2, 302-312.	16.3	96
467	A Filamentous Growth Response Mediated by the Yeast Mating Pathway. Genetics, 2001, 159, 919-928.	2.9	82
468	Analysis of yeast protein kinases using protein chips. Nature Genetics, 2000, 26, 283-289.	21.4	810

#	Article	IF	Citations
469	An integrated web interface for large-scale characterization of sequence data. Functional and Integrative Genomics, 2000, 1, 70-75.	3.5	2
470	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
471	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. Nature, 1999, 402, 413-418.	27.8	521
472	Functional Characterization of the S. cerevisiae Genome by Gene Deletion and Parallel Analysis. Science, 1999, 285, 901-906.	12.6	3,761
473	CELL POLARITY AND MORPHOGENESIS IN BUDDING YEAST. Annual Review of Microbiology, 1998, 52, 687-744.	7.3	243
474	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
475	Genome-Wide Identification of the Genetic Basis of Amyotrophic Lateral Sclerosis. SSRN Electronic Journal, 0, , .	0.4	1
476	Wnt Signaling Interactor WTIP (Wilms Tumor Interacting Protein) Underlies Novel Mechanism for Cardiac Hypertrophy. Circulation Genomic and Precision Medicine, 0, , .	3.6	0