

Michael Paul Snyder

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7556462/publications.pdf>

Version: 2024-02-01

476
papers

103,581
citations

439

135
h-index

305

299
g-index

538
all docs

538
docs citations

538
times ranked

126597
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | metID: an R package for automatable compound annotation for LC-MS-based data. <i>Bioinformatics</i> , 2022, 38, 568-569. | 1.8 | 15 |
| 2 | Network biology bridges the gaps between quantitative genetics and multi-omics to map complex diseases. <i>Current Opinion in Chemical Biology</i> , 2022, 66, 102101. | 2.8 | 12 |
| 3 | A review of Mendelian randomization in amyotrophic lateral sclerosis. <i>Brain</i> , 2022, 145, 832-842. | 3.7 | 29 |
| 4 | Heterogeneity of Diabetes: Î²-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. <i>Diabetes Care</i> , 2022, 45, 3-22. | 4.3 | 14 |
| 5 | Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging. <i>Nature Methods</i> , 2022, 19, 284-295. | 9.0 | 156 |
| 6 | Real-time alerting system for COVID-19 and other stress events using wearable data. <i>Nature Medicine</i> , 2022, 28, 175-184. | 15.2 | 69 |
| 7 | Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. <i>Neuron</i> , 2022, 110, 992-1008.e11. | 3.8 | 51 |
| 8 | Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus. <i>Scientific Reports</i> , 2022, 12, 1291. | 1.6 | 3 |
| 9 | Whole transcriptome profiling of prospective endomyocardial biopsies reveals prognostic and diagnostic signatures of cardiac allograft rejection. <i>Journal of Heart and Lung Transplantation</i> , 2022, 41, 840-848. | 0.3 | 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. <i>Nature Reviews Endocrinology</i> , 2022, 18, 273-289. | 4.3 | 268 |
| 12 | Unbiased metabolome screen leads to personalized medicine strategy for amyotrophic lateral sclerosis. <i>Brain Communications</i> , 2022, 4, fcac069. | 1.5 | 10 |
| 13 | MITI minimum information guidelines for highly multiplexed tissue images. <i>Nature Methods</i> , 2022, 19, 262-267. | 9.0 | 37 |
| 14 | Effects of an immersive psychosocial training program on depression and well-being: A randomized clinical trial. <i>Journal of Psychiatric Research</i> , 2022, 150, 292-299. | 1.5 | 1 |
| 15 | Adverse childhood experiences, diabetes and associated conditions, preventive care practices and health care access: A population-based study. <i>Preventive Medicine</i> , 2022, 160, 107044. | 1.6 | 3 |
| 16 | Patient-derived gene and protein expression signatures of NGLY1 deficiency. <i>Journal of Biochemistry</i> , 2022, 171, 187-199. | 0.9 | 9 |
| 17 | Tet enzymes are essential for early embryogenesis and completion of embryonic genome activation. <i>EMBO Reports</i> , 2022, 23, e53968. | 2.0 | 20 |
| 18 | A machine learning algorithm with subclonal sensitivity reveals widespread pan-cancer human leukocyte antigen loss of heterozygosity. <i>Nature Communications</i> , 2022, 13, 1925. | 5.8 | 8 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Exploring disease interrelationships in patients with lymphatic disorders: A single center retrospective experience. <i>Clinical and Translational Medicine</i> , 2022, 12, e760. | 1.7 | 9 |
| 20 | Global, distinctive, and personal changes in molecular and microbial profiles by specific fibers in humans. <i>Cell Host and Microbe</i> , 2022, 30, 848-862.e7. | 5.1 | 48 |
| 21 | Prediction of gestational age using urinary metabolites in term and preterm pregnancies. <i>Scientific Reports</i> , 2022, 12, 8033. | 1.6 | 4 |
| 22 | A cancer-associated RNA polymerase III identity drives robust transcription and expression of snaR-A noncoding RNA. <i>Nature Communications</i> , 2022, 13, . | 5.8 | 12 |
| 23 | Multiomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity. <i>Cell Systems</i> , 2022, 13, 598-614.e6. | 2.9 | 10 |
| 24 | Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer. <i>Nature Genetics</i> , 2022, 54, 985-995. | 9.4 | 77 |
| 25 | Precision environmental health monitoring by longitudinal exposome and multi-omics profiling. <i>Genome Research</i> , 2022, 32, 1199-1214. | 2.4 | 26 |
| 26 | Endogenous Retroviral Elements Generate Pathologic Neutrophils in Pulmonary Arterial Hypertension. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 1019-1034. | 2.5 | 10 |
| 27 | An exercise-inducible metabolite that suppresses feeding and obesity. <i>Nature</i> , 2022, 606, 785-790. | 13.7 | 96 |
| 28 | Serine biosynthesis as a novel therapeutic target for dilated cardiomyopathy. <i>European Heart Journal</i> , 2022, 43, 3477-3489. | 1.0 | 23 |
| 29 | KMT2D-NOTCH Mediates Coronary Abnormalities in Hypoplastic Left Heart Syndrome. <i>Circulation Research</i> , 2022, 131, 280-282. | 2.0 | 3 |
| 30 | Robust identification of temporal biomarkers in longitudinal omics studies. <i>Bioinformatics</i> , 2022, 38, 3802-3811. | 1.8 | 10 |
| 31 | Towards personalized medicine in maternal and child health: integrating biologic and social determinants. <i>Pediatric Research</i> , 2021, 89, 252-258. | 1.1 | 19 |
| 32 | Obesity Drives Delayed Infarct Expansion, Inflammation, and Distinct Gene Networks in a Mouse Stroke Model. <i>Translational Stroke Research</i> , 2021, 12, 331-346. | 2.3 | 7 |
| 33 | PPAR β -p53-Mediated Vasculoregenerative Program to Reverse Pulmonary Hypertension. <i>Circulation Research</i> , 2021, 128, 401-418. | 2.0 | 41 |
| 34 | RobNorm: model-based robust normalization method for labeled quantitative mass spectrometry proteomics data. <i>Bioinformatics</i> , 2021, 37, 815-821. | 1.8 | 3 |
| 35 | CTLA-4 expression by B-1a B cells is essential for immune tolerance. <i>Nature Communications</i> , 2021, 12, 525. | 5.8 | 43 |
| 36 | The gut microbiome: a key player in the complexity of amyotrophic lateral sclerosis (ALS). <i>BMC Medicine</i> , 2021, 19, 13. | 2.3 | 52 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | Decoding personal biotic and abiotic airborne exposome. <i>Nature Protocols</i> , 2021, 16, 1129-1151. | 5.5 | 21 |
| 38 | An Integrated Sequencing Approach for Updating the Pseudorabies Virus Transcriptome. <i>Pathogens</i> , 2021, 10, 242. | 1.2 | 9 |
| 39 | Benchmarking workflows to assess performance and suitability of germline variant calling pipelines in clinical diagnostic assays. <i>BMC Bioinformatics</i> , 2021, 22, 85. | 1.2 | 12 |
| 40 | Understanding how biologic and social determinants affect disparities in preterm birth and outcomes of preterm infants in the NICU. <i>Seminars in Perinatology</i> , 2021, 45, 151408. | 1.1 | 5 |
| 41 | Response to Hulman and colleagues regarding "Glucotypes reveal new patterns of glucose dysregulation". <i>PLoS Biology</i> , 2021, 19, e3001092. | 2.6 | 3 |
| 42 | AdaReg: data adaptive robust estimation in linear regression with application in GTEx gene expressions. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2021, 20, 51-71. | 0.2 | 1 |
| 43 | iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W271-W276. | 6.5 | 25 |
| 44 | A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. <i>Nature Genetics</i> , 2021, 53, 638-649. | 9.4 | 86 |
| 45 | ALDH1A3 Coordinates Metabolism With Gene Regulation in Pulmonary Arterial Hypertension. <i>Circulation</i> , 2021, 143, 2074-2090. | 1.6 | 34 |
| 46 | Swarm: A federated cloud framework for large-scale variant analysis. <i>PLoS Computational Biology</i> , 2021, 17, e1008977. | 1.5 | 2 |
| 47 | Early detection of SARS-CoV-2 and other infections in solid organ transplant recipients and household members using wearable devices. <i>Transplant International</i> , 2021, 34, 1019-1031. | 0.8 | 6 |
| 48 | Wearable sensors enable personalized predictions of clinical laboratory measurements. <i>Nature Medicine</i> , 2021, 27, 1105-1112. | 15.2 | 121 |
| 49 | Integrated trajectories of the maternal metabolome, proteome, and immunome predict labor onset. <i>Science Translational Medicine</i> , 2021, 13, . | 5.8 | 82 |
| 50 | Improvement in Glucose Regulation Using a Digital Tracker and Continuous Glucose Monitoring in Healthy Adults and Those with Type 2 Diabetes. <i>Diabetes Therapy</i> , 2021, 12, 1871-1886. | 1.2 | 21 |
| 51 | Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19. | 13.5 | 94 |
| 52 | Precision medicine in women with epilepsy: The challenge, systematic review, and future direction. <i>Epilepsy and Behavior</i> , 2021, 118, 107928. | 0.9 | 13 |
| 53 | Non-invasive wearables for remote monitoring of HbA1c and glucose variability: proof of concept. <i>BMJ Open Diabetes Research and Care</i> , 2021, 9, e002027. | 1.2 | 14 |
| 54 | Time-course transcriptome analysis of host cell response to poxvirus infection using a dual long-read sequencing approach. <i>BMC Research Notes</i> , 2021, 14, 239. | 0.6 | 5 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | AdaTiSS: a novel data-adaptive robust method for identifying tissue specificity scores. <i>Bioinformatics</i> , 2021, 37, 4469-4476. | 1.8 | 2 |
| 56 | Physical exercise is a risk factor for amyotrophic lateral sclerosis: Convergent evidence from Mendelian randomisation, transcriptomics and risk genotypes. <i>EBioMedicine</i> , 2021, 68, 103397. | 2.7 | 65 |
| 57 | Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study. <i>JAMIA Open</i> , 2021, 4, ooab054. | 1.0 | 2 |
| 58 | Combined nanopore and single-molecule real-time sequencing survey of human betaherpesvirus 5 transcriptome. <i>Scientific Reports</i> , 2021, 11, 14487. | 1.6 | 8 |
| 59 | Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756. | 9.0 | 403 |
| 60 | The Exposome in the Era of the Quantified Self. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 255-277. | 2.8 | 10 |
| 61 | The X Chromosome from Telomere to Telomere: Key Achievements and Future Opportunities. <i>Faculty Reviews</i> , 2021, 10, 63. | 1.7 | 1 |
| 62 | Longitudinal linked-read sequencing reveals ecological and evolutionary responses of a human gut microbiome during antibiotic treatment. <i>Genome Research</i> , 2021, 31, 1433-1446. | 2.4 | 55 |
| 63 | Time-Course Transcriptome Profiling of a Poxvirus Using Long-Read Full-Length Assay. <i>Pathogens</i> , 2021, 10, 919. | 1.2 | 4 |
| 64 | Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms. <i>Clinical Cancer Research</i> , 2021, 27, 4265-4276. | 3.2 | 23 |
| 65 | Structured elements drive extensive circular RNA translation. <i>Molecular Cell</i> , 2021, 81, 4300-4318.e13. | 4.5 | 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. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 1655-1665. | 2.2 | 3 |
| 67 | Divergent patterns of selection on metabolite levels and gene expression. <i>Bmc Ecology and Evolution</i> , 2021, 21, 185. | 0.7 | 4 |
| 68 | Chromatin accessibility associates with protein-RNA correlation in human cancer. <i>Nature Communications</i> , 2021, 12, 5732. | 5.8 | 18 |
| 69 | Adapting skills from genetic counseling to wearables technology research during the COVID-19 pandemic: Poised for the pivot. <i>Journal of Genetic Counseling</i> , 2021, 30, 1269-1275. | 0.9 | 0 |
| 70 | A scalable, secure, and interoperable platform for deep data-driven health management. <i>Nature Communications</i> , 2021, 12, 5757. | 5.8 | 27 |
| 71 | In-depth triacylglycerol profiling using MS3 Q-Trap mass spectrometry. <i>Analytica Chimica Acta</i> , 2021, 1184, 339023. | 2.6 | 4 |
| 72 | Precision Neoantigen Discovery Using Large-scale Immunopeptidomes and Composite Modeling of MHC Peptide Presentation. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100111. | 2.5 | 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. <i>Shock</i> , 2021, 55, 128-137. | 1.0 | 7 |
| 74 | COVID-19-Induced New-Onset Diabetes: Trends and Technologies. <i>Diabetes</i> , 2021, 70, 2733-2744. | 0.3 | 49 |
| 75 | A DMS Shotgun Lipidomics Workflow Application to Facilitate High-Throughput, Comprehensive Lipidomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2655-2663. | 1.2 | 46 |
| 76 | Altered Cardiac Energetics and Mitochondrial Dysfunction in Hypertrophic Cardiomyopathy. <i>Circulation</i> , 2021, 144, 1714-1731. | 1.6 | 90 |
| 77 | The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. <i>Nature Genetics</i> , 2021, 53, 1564-1576. | 9.4 | 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. <i>Nucleic Acids Research</i> , 2021, 49, 12196-12210. | 6.5 | 7 |
| 79 | Cross-Laboratory Standardization of Preclinical Lipidomics Using Differential Mobility Spectrometry and Multiple Reaction Monitoring. <i>Analytical Chemistry</i> , 2021, 93, 16369-16378. | 3.2 | 40 |
| 80 | Human exposome assessment platform. <i>Environmental Epidemiology</i> , 2021, 5, e182. | 1.4 | 7 |
| 81 | Predictive Signatures for Lung Adenocarcinoma Prognostic Trajectory by Multiomics Data Integration and Ensemble Learning. <i>Lecture Notes in Computer Science</i> , 2021, , 9-23. | 1.0 | 0 |
| 82 | Design and Methods of the Validating Injury to the Renal Transplant Using Urinary Signatures (VIRTUUS) Study in Children. <i>Transplantation Direct</i> , 2021, 7, e791. | 0.8 | 3 |
| 83 | Exposome-wide Association Study for Metabolic Syndrome. <i>Frontiers in Genetics</i> , 2021, 12, 783930. | 1.1 | 6 |
| 84 | Global metabolic profiling to model biological processes of aging in twins. <i>Aging Cell</i> , 2020, 19, e13073. | 3.0 | 38 |
| 85 | Quality-control mechanisms targeting translationally stalled and C-terminally extended poly(GR) associated with ALS/FTD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25104-25115. | 3.3 | 39 |
| 86 | A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301. | 5.8 | 152 |
| 87 | iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy. <i>Cell Reports</i> , 2020, 32, 108117. | 2.9 | 40 |
| 88 | Deep longitudinal multiomics profiling reveals two biological seasonal patterns in California. <i>Nature Communications</i> , 2020, 11, 4933. | 5.8 | 36 |
| 89 | Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. <i>GigaScience</i> , 2020, 9, . | 3.3 | 6 |
| 90 | Meta-analytic approach for transcriptome profiling of herpes simplex virus type 1. <i>Scientific Data</i> , 2020, 7, 223. | 2.4 | 7 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 91 | Pre-symptomatic detection of COVID-19 from smartwatch data. <i>Nature Biomedical Engineering</i> , 2020, 4, 1208-1220. | 11.6 | 304 |
| 92 | Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. <i>Cell Reports</i> , 2020, 33, 108456. | 2.9 | 24 |
| 93 | Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. <i>IScience</i> , 2020, 23, 101844. | 1.9 | 31 |
| 94 | A Customizable Analysis Flow in Integrative Multi-Omics. <i>Biomolecules</i> , 2020, 10, 1606. | 1.8 | 14 |
| 95 | Multi-faceted epigenetic dysregulation of gene expression promotes esophageal squamous cell carcinoma. <i>Nature Communications</i> , 2020, 11, 3675. | 5.8 | 63 |
| 96 | An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , 2020, 11, 3696. | 5.8 | 95 |
| 97 | Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , 2020, 583, 737-743. | 13.7 | 134 |
| 98 | Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698. | 13.7 | 123 |
| 99 | Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710. | 13.7 | 1,252 |
| 100 | A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020, 30, 1047-1059. | 2.4 | 32 |
| 101 | Long-read assays shed new light on the transcriptome complexity of a viral pathogen. <i>Scientific Reports</i> , 2020, 10, 13822. | 1.6 | 17 |
| 102 | Candidate variants in TUB are associated with familial tremor. <i>PLoS Genetics</i> , 2020, 16, e1009010. | 1.5 | 3 |
| 103 | A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19. | 13.5 | 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. <i>Journal of Proteome Research</i> , 2020, 19, 4735-4746. | 1.8 | 38 |
| 105 | A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234. | 3.8 | 68 |
| 106 | Classifying non-small cell lung cancer types and transcriptomic subtypes using convolutional neural networks. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 757-769. | 2.2 | 69 |
| 107 | Longitudinal Analysis of Serum Cytokine Levels and Gut Microbial Abundance Links IL-17/IL-22 With <i>Clostridia</i> and Insulin Sensitivity in Humans. <i>Diabetes</i> , 2020, 69, 1833-1842. | 0.3 | 10 |
| 108 | Deep Characterization of the Human Antibody Response to Natural Infection Using Longitudinal Immune Repertoire Sequencing. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 278-293. | 2.5 | 12 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 109 | Molecular Choreography of Acute Exercise. <i>Cell</i> , 2020, 181, 1112-1130.e16. | 13.5 | 261 |
| 110 | Immunologic effects of forest fire exposure show increases in IL-1 β and CRP. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2356-2358. | 2.7 | 14 |
| 111 | Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474. | 13.5 | 147 |
| 112 | Physiological blood-brain transport is impaired with age by a shift in transcytosis. <i>Nature</i> , 2020, 583, 425-430. | 13.7 | 243 |
| 113 | Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. <i>Cell</i> , 2020, 181, 1680-1692.e15. | 13.5 | 154 |
| 114 | Multiomic immune clockworks of pregnancy. <i>Seminars in Immunopathology</i> , 2020, 42, 397-412. | 2.8 | 47 |
| 115 | Systematic identification of silencers in human cells. <i>Nature Genetics</i> , 2020, 52, 254-263. | 9.4 | 119 |
| 116 | Personal aging markers and ageotypes revealed by deep longitudinal profiling. <i>Nature Medicine</i> , 2020, 26, 83-90. | 15.2 | 225 |
| 117 | The MEK5-ERK5 Kinase Axis Controls Lipid Metabolism in Small-Cell Lung Cancer. <i>Cancer Research</i> , 2020, 80, 1293-1303. | 0.4 | 49 |
| 118 | Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension. <i>Nature Communications</i> , 2020, 11, 1673. | 5.8 | 60 |
| 119 | Humans Are Selectively Exposed to <i>Pneumocystis jirovecii</i> . <i>MBio</i> , 2020, 11, . | 1.8 | 8 |
| 120 | The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249. | 13.5 | 334 |
| 121 | Multiomics Characterization of Preterm Birth in Low- and Middle-Income Countries. <i>JAMA Network Open</i> , 2020, 3, e2029655. | 2.8 | 53 |
| 122 | Systematic Identification of Regulators of Oxidative Stress Reveals Non-canonical Roles for Peroxisomal Import and the Pentose Phosphate Pathway. <i>Cell Reports</i> , 2020, 30, 1417-1433.e7. | 2.9 | 49 |
| 123 | Precision Medicine: Role of Proteomics in Changing Clinical Management and Care. <i>Journal of Proteome Research</i> , 2019, 18, 1-6. | 1.8 | 26 |
| 124 | Multiomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. <i>Bioinformatics</i> , 2019, 35, 95-103. | 1.8 | 162 |
| 125 | High Throughput Sequencing and Assessing Disease Risk. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a026849. | 2.9 | 23 |
| 126 | Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. <i>Cell</i> , 2019, 178, 1245-1259.e14. | 13.5 | 163 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 127 | Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 834. | 1.1 | 44 |
| 128 | MISTERMINATE Mechanistically Links Mitochondrial Dysfunction with Proteostasis Failure. <i>Molecular Cell</i> , 2019, 75, 835-848.e8. | 4.5 | 56 |
| 129 | Chromatin Remodeling in Response to BRCA2-Crisis. <i>Cell Reports</i> , 2019, 28, 2182-2193.e6. | 2.9 | 6 |
| 130 | Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2019, 18, 4098-4107. | 1.8 | 41 |
| 131 | Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. <i>Nature Biomedical Engineering</i> , 2019, 3, 1009-1019. | 11.6 | 135 |
| 132 | Simultaneous RNA purification and size selection using on-chip isotachopheresis with an ionic spacer. <i>Lab on A Chip</i> , 2019, 19, 2741-2749. | 3.1 | 15 |
| 133 | A machine-compiled database of genome-wide association studies. <i>Nature Communications</i> , 2019, 10, 3341. | 5.8 | 21 |
| 134 | HAT1 Coordinates Histone Production and Acetylation via H4 Promoter Binding. <i>Molecular Cell</i> , 2019, 75, 711-724.e5. | 4.5 | 55 |
| 135 | Template-switching artifacts resemble alternative polyadenylation. <i>BMC Genomics</i> , 2019, 20, 824. | 1.2 | 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. <i>Circulation</i> , 2019, 140, 1409-1425. | 1.6 | 54 |
| 137 | Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. <i>Nature Communications</i> , 2019, 10, 4063. | 5.8 | 104 |
| 138 | Systematic Identification of Host Cell Regulators of <i>Legionella pneumophila</i> Pathogenesis Using a Genome-wide CRISPR Screen. <i>Cell Host and Microbe</i> , 2019, 26, 551-563.e6. | 5.1 | 62 |
| 139 | Genome-wide effects of social status on DNA methylation in the brain of a cichlid fish, <i>Astatotilapia burtoni</i> . <i>BMC Genomics</i> , 2019, 20, 699. | 1.2 | 10 |
| 140 | Big data and health. <i>The Lancet Digital Health</i> , 2019, 1, e252-e254. | 5.9 | 28 |
| 141 | Windows into human health through wearables data analytics. <i>Current Opinion in Biomedical Engineering</i> , 2019, 9, 28-46. | 1.8 | 101 |
| 142 | Personalized Metabolomics. <i>Methods in Molecular Biology</i> , 2019, 1978, 447-456. | 0.4 | 7 |
| 143 | Engineering Genetic Predisposition in Human Neuroepithelial Stem Cells Recapitulates Medulloblastoma Tumorigenesis. <i>Cell Stem Cell</i> , 2019, 25, 433-446.e7. | 5.2 | 56 |
| 144 | High-Resolution Bisulfite-Sequencing of Peripheral Blood DNA Methylation in Early-Onset and Familial Risk Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2019, 25, 5301-5314. | 3.2 | 11 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 145 | Longitudinal multi-omics of host-microbe dynamics in prediabetes. <i>Nature</i> , 2019, 569, 663-671. | 13.7 | 391 |
| 146 | Applying circulating tumor DNA methylation in the diagnosis of lung cancer. <i>Precision Clinical Medicine</i> , 2019, 2, 45-56. | 1.3 | 18 |
| 147 | A longitudinal big data approach for precision health. <i>Nature Medicine</i> , 2019, 25, 792-804. | 15.2 | 329 |
| 148 | Analysis of the Complete Genome Sequence of a Novel, Pseudorabies Virus Strain Isolated in Southeast Europe. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2019, 2019, 1-12. | 0.7 | 7 |
| 149 | Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19. | 13.5 | 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. <i>Scientific Reports</i> , 2019, 9, 3272. | 1.6 | 63 |
| 151 | Much ado about nothing: A qualitative study of the experiences of an average-risk population receiving results of exome sequencing. <i>Journal of Genetic Counseling</i> , 2019, 28, 428-437. | 0.9 | 15 |
| 152 | Gene-Environment Interaction in the Era of Precision Medicine. <i>Cell</i> , 2019, 177, 38-44. | 13.5 | 73 |
| 153 | The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , 2019, 364, . | 6.0 | 576 |
| 154 | Long-Read Sequencing - A Powerful Tool in Viral Transcriptome Research. <i>Trends in Microbiology</i> , 2019, 27, 578-592. | 3.5 | 76 |
| 155 | Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. <i>Nature</i> , 2019, 574, 553-558. | 13.7 | 187 |
| 156 | Metformin Affects Heme Function as a Possible Mechanism of Action. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 513-522. | 0.8 | 12 |
| 157 | Understanding health disparities. <i>Journal of Perinatology</i> , 2019, 39, 354-358. | 0.9 | 14 |
| 158 | Macrophage de novo NAD+ synthesis specifies immune function in aging and inflammation. <i>Nature Immunology</i> , 2019, 20, 50-63. | 7.0 | 304 |
| 159 | Smooth Muscle Contact Drives Endothelial Regeneration by BMP2-Notch-Mediated Metabolic and Epigenetic Changes. <i>Circulation Research</i> , 2019, 124, 211-224. | 2.0 | 78 |
| 160 | Whole-exome sequencing data of suicide victims who had suffered from major depressive disorder. <i>Scientific Data</i> , 2019, 6, 190010. | 2.4 | 5 |
| 161 | Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining. <i>Journal of Proteome Research</i> , 2018, 17, 1383-1396. | 1.8 | 16 |
| 162 | Integrative omics for health and disease. <i>Nature Reviews Genetics</i> , 2018, 19, 299-310. | 7.7 | 676 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 163 | SETD7 Drives Cardiac Lineage Commitment through Stage-Specific Transcriptional Activation. <i>Cell Stem Cell</i> , 2018, 22, 428-444.e5. | 5.2 | 38 |
| 164 | Biallelic Mutations in ATP5F1D, which Encodes a Subunit of ATP Synthase, Cause a Metabolic Disorder. <i>American Journal of Human Genetics</i> , 2018, 102, 494-504. | 2.6 | 59 |
| 165 | Fast Metagenomic Binning via Hashing and Bayesian Clustering. <i>Journal of Computational Biology</i> , 2018, 25, 677-688. | 0.8 | 5 |
| 166 | Distinct transcriptomic and exomic abnormalities within myelodysplastic syndrome marrow cells. <i>Leukemia and Lymphoma</i> , 2018, 59, 2952-2962. | 0.6 | 16 |
| 167 | Comparative analysis of respiratory motion tracking using Microsoft Kinect v2 sensor. <i>Journal of Applied Clinical Medical Physics</i> , 2018, 19, 193-204. | 0.8 | 26 |
| 168 | An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. <i>Cell Metabolism</i> , 2018, 27, 559-571.e5. | 7.2 | 321 |
| 169 | How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214. | 3.9 | 580 |
| 170 | A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. <i>Scientific Reports</i> , 2018, 8, 226. | 1.6 | 37 |
| 171 | Applying genomics in heart transplantation. <i>Transplant International</i> , 2018, 31, 278-290. | 0.8 | 8 |
| 172 | Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. <i>Cell Systems</i> , 2018, 6, 157-170.e8. | 2.9 | 183 |
| 173 | Multiplatform next-generation sequencing identifies novel RNA molecules and transcript isoforms of the endogenous retrovirus isolated from cultured cells. <i>FEMS Microbiology Letters</i> , 2018, 365, . | 0.7 | 21 |
| 174 | Personal Omics for Precision Health. <i>Circulation Research</i> , 2018, 122, 1169-1171. | 2.0 | 54 |
| 175 | A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. <i>Nature Genetics</i> , 2018, 50, 613-620. | 9.4 | 116 |
| 176 | Full Genome Sequence of the Western Reserve Strain of Vaccinia Virus Determined by Third-Generation Sequencing. <i>Genome Announcements</i> , 2018, 6, . | 0.8 | 16 |
| 177 | Circular DNA elements of chromosomal origin are common in healthy human somatic tissue. <i>Nature Communications</i> , 2018, 9, 1069. | 5.8 | 232 |
| 178 | Omics AnalySIs System for PRrecision Oncology (OASISPRO): a web-based omics analysis tool for clinical phenotype prediction. <i>Bioinformatics</i> , 2018, 34, 319-320. | 1.8 | 19 |
| 179 | Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. <i>Genome Research</i> , 2018, 28, 231-242. | 2.4 | 64 |
| 180 | <i>WISP3</i> mutation associated with pseudorheumatoid dysplasia. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a001990. | 0.5 | 16 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 181 | Transcriptomic study of Herpes simplex virus type-1 using full-length sequencing techniques. <i>Scientific Data</i> , 2018, 5, 180266. | 2.4 | 27 |
| 182 | Dynamic transcriptome profiling dataset of vaccinia virus obtained from long-read sequencing techniques. <i>GigaScience</i> , 2018, 7, . | 3.3 | 38 |
| 183 | Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. <i>Nature Genetics</i> , 2018, 50, 1716-1727. | 9.4 | 135 |
| 184 | Longitudinal personal DNA methylome dynamics in a human with a chronic condition. <i>Nature Medicine</i> , 2018, 24, 1930-1939. | 15.2 | 55 |
| 185 | Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , 2018, 14, e1007755. | 1.5 | 30 |
| 186 | Cross-Platform Comparison of Untargeted and Targeted Lipidomics Approaches on Aging Mouse Plasma. <i>Scientific Reports</i> , 2018, 8, 17747. | 1.6 | 81 |
| 187 | High-frequency actionable pathogenic exome variants in an average-risk cohort. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a003178. | 0.5 | 23 |
| 188 | Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome. <i>Frontiers in Genetics</i> , 2018, 9, 432. | 1.1 | 14 |
| 189 | Evaluation of whole exome sequencing as an alternative to BeadChip and whole genome sequencing in human population genetic analysis. <i>BMC Genomics</i> , 2018, 19, 778. | 1.2 | 11 |
| 190 | Decoding the Genomics of Abdominal Aortic Aneurysm. <i>Cell</i> , 2018, 174, 1361-1372.e10. | 13.5 | 68 |
| 191 | Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. <i>Cell</i> , 2018, 175, 277-291.e31. | 13.5 | 137 |
| 192 | Disruption of mesoderm formation during cardiac differentiation due to developmental exposure to 13-cis-retinoic acid. <i>Scientific Reports</i> , 2018, 8, 12960. | 1.6 | 19 |
| 193 | Natural Selection Has Differentiated the Progesterone Receptor among Human Populations. <i>American Journal of Human Genetics</i> , 2018, 103, 45-57. | 2.6 | 30 |
| 194 | Glucotypes reveal new patterns of glucose dysregulation. <i>PLoS Biology</i> , 2018, 16, e2005143. | 2.6 | 167 |
| 195 | Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. <i>Frontiers in Microbiology</i> , 2018, 8, 2708. | 1.5 | 64 |
| 196 | Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2018, 17, 4031-4041. | 1.8 | 59 |
| 197 | A Cloud-Based Metabolite and Chemical Prioritization System for the Biology/Disease-Driven Human Proteome Project. <i>Journal of Proteome Research</i> , 2018, 17, 4345-4357. | 1.8 | 7 |
| 198 | Long-Read Sequencing Revealed an Extensive Transcript Complexity in Herpesviruses. <i>Frontiers in Genetics</i> , 2018, 9, 259. | 1.1 | 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. | 1.1 | 21 |
| 200 | An integrated global regulatory network of hematopoietic precursor cell self-renewal and differentiation. Integrative Biology (United Kingdom), 2018, 10, 390-405. | 0.6 | 4 |
| 201 | Transcriptome-wide survey of pseudorabies virus using next- and third-generation sequencing platforms. Scientific Data, 2018, 5, 180119. | 2.4 | 31 |
| 202 | Wearables and the medical revolution. Personalized Medicine, 2018, 15, 429-448. | 0.8 | 361 |
| 203 | Single cell transcriptomics reveals unanticipated features of early hematopoietic precursors. Nucleic Acids Research, 2017, 45, gkw1214. | 6.5 | 40 |
| 204 | Association of AHSG with alopecia and mental retardation (APMR) syndrome. Human Genetics, 2017, 136, 287-296. | 1.8 | 14 |
| 205 | Pharmacological rescue of diabetic skeletal stem cell niches. Science Translational Medicine, 2017, 9, . | 5.8 | 80 |
| 206 | De novo and rare mutations in the HSPA1L heat shock gene associated with inflammatory bowel disease. Genome Medicine, 2017, 9, 8. | 3.6 | 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. | 1.6 | 19 |
| 209 | Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression. Nature Communications, 2017, 8, 14995. | 5.8 | 131 |
| 210 | Non-equivalence of Wnt and R-spondin ligands during Lgr5+ intestinal stem-cell self-renewal. Nature, 2017, 545, 238-242. | 13.7 | 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. | 1.8 | 26 |
| 212 | Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. Nature Communications, 2017, 8, 15178. | 5.8 | 284 |
| 213 | Succinate and its G-protein-coupled receptor stimulates osteoclastogenesis. Nature Communications, 2017, 8, 15621. | 5.8 | 73 |
| 214 | Multi-platform analysis reveals a complex transcriptome architecture of a circovirus. Virus Research, 2017, 237, 37-46. | 1.1 | 49 |
| 215 | Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. Nucleic Acids Research, 2017, 45, gkx026. | 6.5 | 31 |
| 216 | Gpr124 is essential for blood-brain barrier integrity in central nervous system disease. Nature Medicine, 2017, 23, 450-460. | 15.2 | 177 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 217 | Characterization of the Dynamic Transcriptome of a Herpesvirus with Long-read Single Molecule Real-Time Sequencing. <i>Scientific Reports</i> , 2017, 7, 43751. | 1.6 | 76 |
| 218 | Patient-Specific iPSC-Derived Endothelial Cells Uncover Pathways that Protect against Pulmonary Hypertension in BMPR2 Mutation Carriers. <i>Cell Stem Cell</i> , 2017, 20, 490-504.e5. | 5.2 | 163 |
| 219 | A common class of transcripts with 5â€²-intron depletion, distinct early coding sequence features, and N ¹ -methyladenosine modification. <i>Rna</i> , 2017, 23, 270-283. | 1.6 | 16 |
| 220 | Transcriptomic and epigenomic differences in human induced pluripotent stem cells generated from six reprogramming methods. <i>Nature Biomedical Engineering</i> , 2017, 1, 826-837. | 11.6 | 38 |
| 221 | Cell Type-Specific Chromatin Signatures Underline Regulatory DNA Elements in Human Induced Pluripotent Stem Cells and Somatic Cells. <i>Circulation Research</i> , 2017, 121, 1237-1250. | 2.0 | 18 |
| 222 | Network analyses identify liver-specific targets for treating liver diseases. <i>Molecular Systems Biology</i> , 2017, 13, 938. | 3.2 | 112 |
| 223 | Digital Health: Tracking Physiomes and Activity Using Wearable Biosensors Reveals Useful Health-Related Information. <i>PLoS Biology</i> , 2017, 15, e2001402. | 2.6 | 319 |
| 224 | Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. <i>Molecular Cell</i> , 2017, 67, 1037-1048.e6. | 4.5 | 242 |
| 225 | Identification of a novel mutation in the APTX gene associated with ataxia-oculomotor apraxia. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a002014. | 0.5 | 3 |
| 226 | Cloud-based interactive analytics for terabytes of genomic variants data. <i>Bioinformatics</i> , 2017, 33, 3709-3715. | 1.8 | 9 |
| 227 | Isolated Congenital Anosmia and CNGA2 Mutation. <i>Scientific Reports</i> , 2017, 7, 2667. | 1.6 | 14 |
| 228 | Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis. <i>Scientific Reports</i> , 2017, 7, 5557. | 1.6 | 19 |
| 229 | High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. <i>Scientific Reports</i> , 2017, 7, 7106. | 1.6 | 56 |
| 230 | Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017, 49, 1522-1528. | 9.4 | 255 |
| 231 | Molecular and functional resemblance of differentiated cells derived from isogenic human iPSCs and SCNT-derived ESCs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11111-E11120. | 3.3 | 68 |
| 232 | Long-Read Sequencing of Human Cytomegalovirus Transcriptome Reveals RNA Isoforms Carrying Distinct Coding Potentials. <i>Scientific Reports</i> , 2017, 7, 15989. | 1.6 | 75 |
| 233 | Association of Omics Features with Histopathology Patterns in Lung Adenocarcinoma. <i>Cell Systems</i> , 2017, 5, 620-627.e3. | 2.9 | 88 |
| 234 | Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. <i>Nature Communications</i> , 2017, 8, 59. | 5.8 | 225 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 235 | Genome-Wide Temporal Profiling of Transcriptome and Open Chromatin of Early Cardiomyocyte Differentiation Derived From hiPSCs and hESCs. <i>Circulation Research</i> , 2017, 121, 376-391. | 2.0 | 118 |
| 236 | Induced Pluripotent Stem Cell Model of Pulmonary Arterial Hypertension Reveals Novel Gene Expression and Patient Specificity. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 930-941. | 2.5 | 72 |
| 237 | ChIA-PET2: a versatile and flexible pipeline for ChIA-PET data analysis. <i>Nucleic Acids Research</i> , 2017, 45, e4-e4. | 6.5 | 104 |
| 238 | Long-read sequencing of the human cytomegalovirus transcriptome with the Pacific Biosciences RSII platform. <i>Scientific Data</i> , 2017, 4, 170194. | 2.4 | 46 |
| 239 | Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. <i>Frontiers in Microbiology</i> , 2017, 8, 1079. | 1.5 | 97 |
| 240 | Fetal de novo mutations and preterm birth. <i>PLoS Genetics</i> , 2017, 13, e1006689. | 1.5 | 30 |
| 241 | Topological organization and dynamic regulation of human tRNA genes during macrophage differentiation. <i>Genome Biology</i> , 2017, 18, 180. | 3.8 | 27 |
| 242 | Evaluation of the impact of ul54 gene-deletion on the global transcription and DNA replication of pseudorabies virus. <i>Archives of Virology</i> , 2017, 162, 2679-2694. | 0.9 | 5 |
| 243 | Long-Read Sequencing Reveals a GC Pressure during the Evolution of Porcine Endogenous Retrovirus. <i>Genome Announcements</i> , 2017, 5, . | 0.8 | 4 |
| 244 | Plasma sterols and depressive symptom severity in a population-based cohort. <i>PLoS ONE</i> , 2017, 12, e0184382. | 1.1 | 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. <i>PLoS Genetics</i> , 2016, 12, e1006347. | 1.5 | 8 |
| 246 | Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. <i>PLoS ONE</i> , 2016, 11, e0162868. | 1.1 | 93 |
| 247 | Disease Variant Landscape of a Large Multiethnic Population of Moyamoya Patients by Exome Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 41-49. | 0.8 | 42 |
| 248 | Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1. <i>Scientific Reports</i> , 2016, 6, 20104. | 1.6 | 61 |
| 249 | Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. <i>Cell</i> , 2016, 167, 1734-1749.e22. | 13.5 | 195 |
| 250 | Genome assembly from synthetic long read clouds. <i>Bioinformatics</i> , 2016, 32, i216-i224. | 1.8 | 33 |
| 251 | Yeast longevity promoted by reversing aging-associated decline in heavy isotope content. <i>Npj Aging and Mechanisms of Disease</i> , 2016, 2, 16004. | 4.5 | 23 |
| 252 | Omics Profiling in Precision Oncology. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2525-2536. | 2.5 | 84 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 253 | Can Metabolic Profiles Be Used as a Phenotypic Readout of the Genome to Enhance Precision Medicine?. <i>Clinical Chemistry</i> , 2016, 62, 676-678. | 1.5 | 21 |
| 254 | Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. <i>Nature Genetics</i> , 2016, 48, 687-693. | 9.4 | 193 |
| 255 | A proposal for validation of antibodies. <i>Nature Methods</i> , 2016, 13, 823-827. | 9.0 | 473 |
| 256 | Nat1 Deficiency Is Associated with Mitochondrial Dysfunction and Exercise Intolerance in Mice. <i>Cell Reports</i> , 2016, 17, 527-540. | 2.9 | 35 |
| 257 | Simul-seq: combined DNA and RNA sequencing for whole-genome and transcriptome profiling. <i>Nature Methods</i> , 2016, 13, 953-958. | 9.0 | 34 |
| 258 | NIH working group report using genomic information to guide weight management: From universal to precision treatment. <i>Obesity</i> , 2016, 24, 14-22. | 1.5 | 96 |
| 259 | Can heavy isotopes increase lifespan? Studies of relative abundance in various organisms reveal chemical perspectives on aging. <i>BioEssays</i> , 2016, 38, 1093-1101. | 1.2 | 12 |
| 260 | Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , 2016, 48, 1193-1203. | 9.4 | 952 |
| 261 | Transcriptome Profiling of Patient-Specific Human iPSC-Cardiomyocytes Predicts Individual Drug Safety and Efficacy Responses In Vitro. <i>Cell Stem Cell</i> , 2016, 19, 311-325. | 5.2 | 131 |
| 262 | iPSC-derived cardiomyocytes reveal abnormal TGF- β signalling in left ventricular non-compaction cardiomyopathy. <i>Nature Cell Biology</i> , 2016, 18, 1031-1042. | 4.6 | 148 |
| 263 | Predicting non-small cell lung cancer prognosis by fully automated microscopic pathology image features. <i>Nature Communications</i> , 2016, 7, 12474. | 5.8 | 694 |
| 264 | Secure cloud computing for genomic data. <i>Nature Biotechnology</i> , 2016, 34, 588-591. | 9.4 | 20 |
| 265 | Predicting Ovarian Cancer Patients' Clinical Response to Platinum-Based Chemotherapy by Their Tumor Proteomic Signatures. <i>Journal of Proteome Research</i> , 2016, 15, 2455-2465. | 1.8 | 39 |
| 266 | Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016, 24, 172-184. | 7.2 | 133 |
| 267 | Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, and allele-specific binding detection. <i>BMC Bioinformatics</i> , 2016, 17, 96. | 1.2 | 6 |
| 268 | Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. <i>Proteomics</i> , 2016, 16, 465-476. | 1.3 | 8 |
| 269 | Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765. | 13.5 | 804 |
| 270 | Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome. <i>Nature Biotechnology</i> , 2016, 34, 64-69. | 9.4 | 93 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 271 | Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations. <i>Nature Genetics</i> , 2016, 48, 117-125. | 9.4 | 80 |
| 272 | Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E440-9. | 3.3 | 224 |
| 273 | <i>Genomics and Personalized Medicine.</i> , 2016, , . | | 23 |
| 274 | Effects of cellular origin on differentiation of human induced pluripotent stem cellâ€‘derived endothelial cells. <i>JCI Insight</i> , 2016, 1, . | 2.3 | 75 |
| 275 | Probing High-density Functional Protein Microarrays to Detect Protein-protein Interactions. <i>Journal of Visualized Experiments</i> , 2015, , e51872. | 0.2 | 7 |
| 276 | Impact of alleleâ€‘specific peptides in proteome quantification. <i>Proteomics - Clinical Applications</i> , 2015, 9, 432-436. | 0.8 | 4 |
| 277 | Where Next for Genetics and Genomics?. <i>PLoS Biology</i> , 2015, 13, e1002216. | 2.6 | 9 |
| 278 | Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data. <i>PLoS Genetics</i> , 2015, 11, e1005496. | 1.5 | 23 |
| 279 | Whole-Exome Enrichment with the Agilent SureSelect Human All Exon Platform. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot083659. | 0.2 | 38 |
| 280 | Whole-Exome Enrichment with the Roche NimbleGen SeqCap EZ Exome Library SR Platform. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot084855. | 0.2 | 13 |
| 281 | Whole-Exome Enrichment with the Illumina TruSeq Exome Enrichment Platform. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.prot084863. | 0.2 | 11 |
| 282 | High-Throughput Sequencing Technologies. <i>Molecular Cell</i> , 2015, 58, 586-597. | 4.5 | 968 |
| 283 | Recurrent somatic mutations in regulatory regions of human cancer genomes. <i>Nature Genetics</i> , 2015, 47, 710-716. | 9.4 | 225 |
| 284 | RNA Sequencing Analysis Detection of a Novel Pathway of Endothelial Dysfunction in Pulmonary Arterial Hypertension. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 356-366. | 2.5 | 66 |
| 285 | Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders. <i>Cell Systems</i> , 2015, 1, 361-374. | 2.9 | 42 |
| 286 | Metabolome progression during early gut microbial colonization of gnotobiotic mice. <i>Scientific Reports</i> , 2015, 5, 11589. | 1.6 | 29 |
| 287 | Mango: a bias-correcting ChIA-PET analysis pipeline. <i>Bioinformatics</i> , 2015, 31, 3092-3098. | 1.8 | 126 |
| 288 | Transcriptome Signature and Regulation in Human Somatic Cell Reprogramming. <i>Stem Cell Reports</i> , 2015, 4, 1125-1139. | 2.3 | 19 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 289 | Single-cell chromatin accessibility reveals principles of regulatory variation. <i>Nature</i> , 2015, 523, 486-490. | 13.7 | 1,798 |
| 290 | Transglutaminase 4 as a prostate autoantigen in male subfertility. <i>Science Translational Medicine</i> , 2015, 7, 292ra101. | 5.8 | 60 |
| 291 | Characterization of Novel Transcripts in Pseudorabies Virus. <i>Viruses</i> , 2015, 7, 2727-2744. | 1.5 | 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*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1684-1695. | 2.5 | 183 |
| 293 | Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events. <i>Nature Biotechnology</i> , 2015, 33, 736-742. | 9.4 | 205 |
| 294 | Reassessment of Piwi Binding to the Genome and Piwi Impact on RNA Polymerase II Distribution. <i>Developmental Cell</i> , 2015, 32, 772-774. | 3.1 | 9 |
| 295 | Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. <i>Genome Research</i> , 2015, 25, 1610-1621. | 2.4 | 157 |
| 296 | Genomic analysis of mycosis fungoides and SÃ©zary syndrome identifies recurrent alterations in TNFR2. <i>Nature Genetics</i> , 2015, 47, 1056-1060. | 9.4 | 242 |
| 297 | Evaluating Common Humoral Responses against Fungal Infections with Yeast Protein Microarrays. <i>Journal of Proteome Research</i> , 2015, 14, 3924-3931. | 1.8 | 10 |
| 298 | Integrated Proteomic and Genomic Analysis of Gastric Cancer Patient Tissues. <i>Journal of Proteome Research</i> , 2015, 14, 4995-5006. | 1.8 | 7 |
| 299 | Novel mutations in PIEZO1 cause an autosomal recessive generalized lymphatic dysplasia with non-immune hydrops fetalis. <i>Nature Communications</i> , 2015, 6, 8085. | 5.8 | 247 |
| 300 | Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , 2015, 162, 1051-1065. | 13.5 | 304 |
| 301 | Achieving high-sensitivity for clinical applications using augmented exome sequencing. <i>Genome Medicine</i> , 2015, 7, 71. | 3.6 | 46 |
| 302 | Metformin Improves Diabetic Bone Health by Re-Balancing Catabolism and Nitrogen Disposal. <i>PLoS ONE</i> , 2015, 10, e0146152. | 1.1 | 13 |
| 303 | Abstract 19076: ATAC-seq Implicates Epigenome-wide CTCF Dissociation in the Progression of Cardiac Ischemia. <i>Circulation</i> , 2015, 132, . | 1.6 | 0 |
| 304 | Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138. | 3.3 | 635 |
| 305 | Chromatin Immunoprecipitation and Multiplex Sequencing (ChIP-Seq) to Identify Global Transcription Factor Binding Sites in the Nematode <i>Caenorhabditis Elegans</i> . <i>Methods in Enzymology</i> , 2014, 539, 89-111. | 0.4 | 7 |
| 306 | Defining a personal, allele-specific, and single-molecule long-read transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9869-9874. | 3.3 | 259 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 307 | Personalized sequencing and the future of medicine: discovery, diagnosis and defeat of disease. <i>Pharmacogenomics</i> , 2014, 15, 1771-1790. | 0.6 | 66 |
| 308 | Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. <i>Molecular Systems Biology</i> , 2014, 10, 774. | 3.2 | 138 |
| 309 | Transcriptome Sequencing from Diverse Human Populations Reveals Differentiated Regulatory Architecture. <i>PLoS Genetics</i> , 2014, 10, e1004549. | 1.5 | 49 |
| 310 | Coherent Functional Modules Improve Transcription Factor Target Identification, Cooperativity Prediction, and Disease Association. <i>PLoS Genetics</i> , 2014, 10, e1004122. | 1.5 | 29 |
| 311 | Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues. <i>PLoS Genetics</i> , 2014, 10, e1004304. | 1.5 | 60 |
| 312 | Strain Kaplan of Pseudorabies Virus Genome Sequenced by PacBio Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 29 |
| 313 | Metadata Checklist for the Integrated Personal OMICS Study: Proteomics and Metabolomics Experiments. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 81-85. | 1.0 | 14 |
| 314 | Comparison of the transcriptional landscapes between human and mouse tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17224-17229. | 3.3 | 337 |
| 315 | Exome sequencing and genome-wide copy number variant mapping reveal novel associations with sensorineural hereditary hearing loss. <i>BMC Genomics</i> , 2014, 15, 1155. | 1.2 | 27 |
| 316 | Shared functions of plant and mammalian StAR-related lipid transfer (START) domains in modulating transcription factor activity. <i>BMC Biology</i> , 2014, 12, 70. | 1.7 | 62 |
| 317 | Haplotype structure and positive selection at TLR1. <i>European Journal of Human Genetics</i> , 2014, 22, 551-557. | 1.4 | 20 |
| 318 | Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. <i>American Journal of Human Genetics</i> , 2014, 94, 349-360. | 2.6 | 158 |
| 319 | Clinical Interpretation and Implications of Whole-Genome Sequencing. <i>JAMA - Journal of the American Medical Association</i> , 2014, 311, 1035. | 3.8 | 398 |
| 320 | Whole-genome haplotyping using long reads and statistical methods. <i>Nature Biotechnology</i> , 2014, 32, 261-266. | 9.4 | 170 |
| 321 | Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. <i>Nature Biotechnology</i> , 2014, 32, 562-568. | 9.4 | 202 |
| 322 | Landscape and variation of RNA secondary structure across the human transcriptome. <i>Nature</i> , 2014, 505, 706-709. | 13.7 | 519 |
| 323 | Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375. | 13.7 | 259 |
| 324 | A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364. | 13.7 | 1,444 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 325 | Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014, 515, 402-405. | 13.7 | 779 |
| 326 | Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures. <i>Bioinformatics</i> , 2014, 30, 2808-2810. | 1.8 | 182 |
| 327 | iPOP and its role in participatory medicine. <i>Genome Medicine</i> , 2014, 6, 6. | 3.6 | 7 |
| 328 | Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulum-associated degradation pathway. <i>Genetics in Medicine</i> , 2014, 16, 751-758. | 1.1 | 191 |
| 329 | Regulatory analysis of the <i>C. elegans</i> genome with spatiotemporal resolution. <i>Nature</i> , 2014, 512, 400-405. | 13.7 | 115 |
| 330 | Genome-wide map of regulatory interactions in the human genome. <i>Genome Research</i> , 2014, 24, 1905-1917. | 2.4 | 259 |
| 331 | Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456. | 13.7 | 184 |
| 332 | Widespread contribution of transposable elements to the innovation of gene regulatory networks. <i>Genome Research</i> , 2014, 24, 1963-1976. | 2.4 | 408 |
| 333 | H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. <i>Cell</i> , 2014, 158, 673-688. | 13.5 | 404 |
| 334 | STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. <i>PLoS ONE</i> , 2014, 9, e84860. | 1.1 | 25 |
| 335 | Identification of STAT5A and STAT5B Target Genes in Human T Cells. <i>PLoS ONE</i> , 2014, 9, e86790. | 1.1 | 67 |
| 336 | Genomic era diagnosis and management of hereditary and sporadic colon cancer. <i>World Journal of Clinical Oncology</i> , 2014, 5, 1036. | 0.9 | 11 |
| 337 | Transcriptomic Evaluation of CD34+ Marrow Cells from Myelodysplastic Syndrome (MDS) Patients. <i>Blood</i> , 2014, 124, 1894-1894. | 0.6 | 5 |
| 338 | Personal genomes, quantitative dynamic omics and personalized medicine. <i>Quantitative Biology</i> , 2013, 1, 71-90. | 0.3 | 29 |
| 339 | Whole-exome sequencing identifies tetratricopeptide repeat domain 7A (TTC7A) mutations for combined immunodeficiency with intestinal atresias. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 132, 656-664.e17. | 1.5 | 140 |
| 340 | Dynamic trans-Acting Factor Colocalization in Human Cells. <i>Cell</i> , 2013, 155, 713-724. | 13.5 | 142 |
| 341 | Extensive Variation in Chromatin States Across Humans. <i>Science</i> , 2013, 342, 750-752. | 6.0 | 338 |
| 342 | A single-molecule long-read survey of the human transcriptome. <i>Nature Biotechnology</i> , 2013, 31, 1009-1014. | 9.4 | 600 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 343 | Systematic investigation of protein–small molecule interactions. <i>IUBMB Life</i> , 2013, 65, 2-8. | 1.5 | 33 |
| 344 | Promise of personalized omics to precision medicine. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 73-82. | 6.6 | 245 |
| 345 | High-throughput sequencing for biology and medicine. <i>Molecular Systems Biology</i> , 2013, 9, 640. | 3.2 | 251 |
| 346 | Metabolomics as a robust tool in systems biology and personalized medicine: an open letter to the metabolomics community. <i>Metabolomics</i> , 2013, 9, 532-534. | 1.4 | 3 |
| 347 | Preparation of Recombinant Protein Spotted Arrays for Proteome-Wide Identification of Kinase Targets. <i>Current Protocols in Protein Science</i> , 2013, 72, Unit 27.4. | 2.8 | 4 |
| 348 | iPOP Goes the World: Integrated Personalized Omics Profiling and the Road toward Improved Health Care. <i>Chemistry and Biology</i> , 2013, 20, 660-666. | 6.2 | 67 |
| 349 | Multimodal Dynamic Profiling of Healthy and Diseased States for Future Personalized Health Care. <i>Clinical Pharmacology and Therapeutics</i> , 2013, 93, 29-32. | 2.3 | 7 |
| 350 | Variation and genetic control of protein abundance in humans. <i>Nature</i> , 2013, 499, 79-82. | 13.7 | 343 |
| 351 | Centromere-Like Regions in the Budding Yeast Genome. <i>PLoS Genetics</i> , 2013, 9, e1003209. | 1.5 | 38 |
| 352 | Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 387-397. | 0.8 | 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. <i>Circulation Research</i> , 2013, 112, 1613-1623. | 2.0 | 110 |
| 355 | Extensive Transcript Diversity and Novel Upstream Open Reading Frame Regulation in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 343-352. | 0.8 | 59 |
| 356 | Systematic functional regulatory assessment of disease-associated variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9607-9612. | 3.3 | 85 |
| 357 | Metadata Checklist for the Integrated Personal Omics Study: <i>Proteomics and Metabolomics Experiments</i>. <i>Big Data</i> , 2013, 1, 202-206. | 2.1 | 8 |
| 358 | Integrative Analysis of Longitudinal Metabolomics Data from a Personal Multi-Omics Profile. <i>Metabolites</i> , 2013, 3, 741-760. | 1.3 | 56 |
| 359 | Tcf7 Is an Important Regulator of the Switch of Self-Renewal and Differentiation in a Multipotential Hematopoietic Cell Line. <i>PLoS Genetics</i> , 2012, 8, e1002565. | 1.5 | 88 |
| 360 | Annotation of functional variation in personal genomes using RegulomeDB. <i>Genome Research</i> , 2012, 22, 1790-1797. | 2.4 | 2,335 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 361 | Linking disease associations with regulatory information in the human genome. <i>Genome Research</i> , 2012, 22, 1748-1759. | 2.4 | 657 |
| 362 | Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , 2012, 22, 1798-1812. | 2.4 | 762 |
| 363 | Correlation of Global MicroRNA Expression With Basal Cell Carcinoma Subtype. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 279-286. | 0.8 | 36 |
| 364 | Investigating metabolite-protein interactions: An overview of available techniques. <i>Methods</i> , 2012, 57, 459-466. | 1.9 | 40 |
| 365 | Systems biology: personalized medicine for the future?. <i>Current Opinion in Pharmacology</i> , 2012, 12, 623-628. | 1.7 | 90 |
| 366 | Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , 2012, 13, R48. | 13.9 | 233 |
| 367 | ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831. | 2.4 | 1,708 |
| 368 | Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. <i>Genome Research</i> , 2012, 22, 1735-1747. | 2.4 | 168 |
| 369 | Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98. | 13.5 | 1,096 |
| 370 | Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307. | 13.5 | 1,134 |
| 371 | Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100. | 13.7 | 1,384 |
| 372 | Detecting and annotating genetic variations using the HugeSeq pipeline. <i>Nature Biotechnology</i> , 2012, 30, 226-229. | 9.4 | 104 |
| 373 | Performance comparison of whole-genome sequencing platforms. <i>Nature Biotechnology</i> , 2012, 30, 78-82. | 9.4 | 281 |
| 374 | The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , 2012, 30, 221-223. | 9.4 | 281 |
| 375 | Whole Genome Sequence Analysis of Primary Myelofibrosis. <i>Blood</i> , 2012, 120, 2863-2863. | 0.6 | 0 |
| 376 | Interpretome: a freely available, modular, and secure personal genome interpretation engine. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 339-350. | 0.7 | 12 |
| 377 | AlleleSeq: analysis of allele-specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , 2011, 7, 522. | 3.2 | 284 |
| 378 | Dissecting phosphorylation networks: lessons learned from yeast. <i>Expert Review of Proteomics</i> , 2011, 8, 775-786. | 1.3 | 15 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 379 | Regulatory Variation Within and Between Species. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 327-346. | 2.5 | 70 |
| 380 | Diverse Roles and Interactions of the SWI/SNF Chromatin Remodeling Complex Revealed Using Global Approaches. <i>PLoS Genetics</i> , 2011, 7, e1002008. | 1.5 | 185 |
| 381 | Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65. | 13.7 | 991 |
| 382 | Landscape of Next-Generation Sequencing Technologies. <i>Analytical Chemistry</i> , 2011, 83, 4327-4341. | 3.2 | 314 |
| 383 | Performance comparison of exome DNA sequencing technologies. <i>Nature Biotechnology</i> , 2011, 29, 908-914. | 9.4 | 464 |
| 384 | The Human Proteome Project: Current State and Future Direction. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009993. | 2.5 | 294 |
| 385 | Identification of genomic indels and structural variations using split reads. <i>BMC Genomics</i> , 2011, 12, 375. | 1.2 | 57 |
| 386 | Metabolites as global regulators: A new view of protein regulation. <i>BioEssays</i> , 2011, 33, 485-489. | 1.2 | 36 |
| 387 | Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. <i>Genes and Development</i> , 2011, 25, 767-778. | 2.7 | 60 |
| 388 | Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence. <i>PLoS Genetics</i> , 2011, 7, e1002280. | 1.5 | 137 |
| 389 | CNVnator: An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. <i>Genome Research</i> , 2011, 21, 974-984. | 2.4 | 1,387 |
| 390 | Analyzing In Vivo Metabolite-Protein Interactions by Large-Scale Systematic Analyses. <i>Current Protocols in Chemical Biology</i> , 2011, 3, 181-196. | 1.7 | 5 |
| 391 | Genome-Wide Mapping of Copy Number Variation in Humans: Comparative Analysis of High Resolution Array Platforms. <i>PLoS ONE</i> , 2011, 6, e27859. | 1.1 | 59 |
| 392 | Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. <i>Science Signaling</i> , 2010, 3, ra12. | 1.6 | 341 |
| 393 | Yeast proteomics and protein microarrays. <i>Journal of Proteomics</i> , 2010, 73, 2147-2157. | 1.2 | 31 |
| 394 | Genomic binding profiles of functionally distinct RNA polymerase III transcription complexes in human cells. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 635-640. | 3.6 | 197 |
| 395 | Genetic analysis of variation in transcription factor binding in yeast. <i>Nature</i> , 2010, 464, 1187-1191. | 13.7 | 162 |
| 396 | Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. <i>Nature Biotechnology</i> , 2010, 28, 47-55. | 9.4 | 158 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 397 | Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , 2010, 11, 559-571. | 7.7 | 398 |
| 398 | Systems Biology Approaches to Disease Marker Discovery. <i>Disease Markers</i> , 2010, 28, 209-224. | 0.6 | 18 |
| 399 | Personal genome sequencing: current approaches and challenges. <i>Genes and Development</i> , 2010, 24, 423-431. | 2.7 | 119 |
| 400 | Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5254-5259. | 3.3 | 168 |
| 401 | Molecular Mechanisms of Ethanol-Induced Pathogenesis Revealed by RNA-Sequencing. <i>PLoS Pathogens</i> , 2010, 6, e1000834. | 2.1 | 142 |
| 402 | Genome-Wide Identification of Binding Sites Defines Distinct Functions for <i>Caenorhabditis elegans</i> PHA-4/FOXA in Development and Environmental Response. <i>PLoS Genetics</i> , 2010, 6, e1000848. | 1.5 | 165 |
| 403 | Close association of RNA polymerase II and many transcription factors with Pol III genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3639-3644. | 3.3 | 167 |
| 404 | Variation in Transcription Factor Binding Among Humans. <i>Science</i> , 2010, 328, 232-235. | 6.0 | 521 |
| 405 | Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787. | 6.0 | 912 |
| 406 | ChIP-seq: A Method for Global Identification of Regulatory Elements in the Genome. <i>Current Protocols in Molecular Biology</i> , 2010, 91, Unit 21.19.1-14. | 2.9 | 49 |
| 407 | Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. <i>Cell</i> , 2010, 143, 639-650. | 13.5 | 200 |
| 408 | Systems biology approaches to disease marker discovery. <i>Disease Markers</i> , 2010, 28, 209-24. | 0.6 | 9 |
| 409 | MSB: A mean-shift-based approach for the analysis of structural variation in the genome. <i>Genome Research</i> , 2009, 19, 106-117. | 2.4 | 33 |
| 410 | Personal phenotypes to go with personal genomes. <i>Molecular Systems Biology</i> , 2009, 5, 273. | 3.2 | 41 |
| 411 | Global analysis of the glycoproteome in <i>Saccharomyces cerevisiae</i> reveals new roles for protein glycosylation in eukaryotes. <i>Molecular Systems Biology</i> , 2009, 5, 308. | 3.2 | 79 |
| 412 | Integrating Sequencing Technologies in Personal Genomics: Optimal Low Cost Reconstruction of Structural Variants. <i>PLoS Computational Biology</i> , 2009, 5, e1000432. | 1.5 | 14 |
| 413 | Dynamic and complex transcription factor binding during an inducible response in yeast. <i>Genes and Development</i> , 2009, 23, 1351-1363. | 2.7 | 89 |
| 414 | Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. <i>BMC Genomics</i> , 2009, 10, 37. | 1.2 | 137 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 415 | Systems biology from a yeast omics perspective. <i>FEBS Letters</i> , 2009, 583, 3895-3899. | 1.3 | 46 |
| 416 | PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. <i>Nature Biotechnology</i> , 2009, 27, 66-75. | 9.4 | 514 |
| 417 | Unlocking the secrets of the genome. <i>Nature</i> , 2009, 459, 927-930. | 13.7 | 744 |
| 418 | Global identification of protein kinase substrates by protein microarray analysis. <i>Nature Protocols</i> , 2009, 4, 1820-1827. | 5.5 | 46 |
| 419 | RNA-Seq: a revolutionary tool for transcriptomics. <i>Nature Reviews Genetics</i> , 2009, 10, 57-63. | 7.7 | 10,529 |
| 420 | MAPK target networks in <i>Arabidopsis thaliana</i> revealed using functional protein microarrays. <i>Genes and Development</i> , 2009, 23, 80-92. | 2.7 | 438 |
| 421 | Mapping accessible chromatin regions using Sono-Seq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14926-14931. | 3.3 | 186 |
| 422 | PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. <i>Genome Biology</i> , 2009, 10, R23. | 13.9 | 223 |
| 423 | Protein Microarrays. <i>Methods in Molecular Biology</i> , 2009, 548, 209-222. | 0.4 | 18 |
| 424 | The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing. <i>Science</i> , 2008, 320, 1344-1349. | 6.0 | 2,180 |
| 425 | High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. <i>Science</i> , 2008, 322, 104-110. | 6.0 | 1,297 |
| 426 | The Development of Protein Microarrays and Their Applications in DNA-Protein and Protein-Protein Interaction Analyses of <i>Arabidopsis</i> Transcription Factors. <i>Molecular Plant</i> , 2008, 1, 27-41. | 3.9 | 78 |
| 427 | High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. <i>PLoS Genetics</i> , 2008, 4, e1000249. | 1.5 | 99 |
| 428 | Identification of differentially expressed proteins in ovarian cancer using high-density protein microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17494-17499. | 3.3 | 250 |
| 429 | Mapping of transcription factor binding regions in mammalian cells by ChIP: Comparison of array- and sequencing-based technologies. <i>Genome Research</i> , 2007, 17, 898-909. | 2.4 | 181 |
| 430 | <i>Arabidopsis</i> Protein Microarrays for the High-Throughput Identification of Protein-Protein Interactions. <i>Plant Signaling and Behavior</i> , 2007, 2, 416-420. | 1.2 | 30 |
| 431 | Divergence of Transcription Factor Binding Sites Across Related Yeast Species. <i>Science</i> , 2007, 317, 815-819. | 6.0 | 320 |
| 432 | Differential binding of calmodulin-related proteins to their targets revealed through high-density <i>Arabidopsis</i> protein microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4730-4735. | 3.3 | 369 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 433 | New insights into <i>Acinetobacter baumannii</i> pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. <i>Genes and Development</i> , 2007, 21, 601-614. | 2.7 | 455 |
| 434 | Getting connected: analysis and principles of biological networks. <i>Genes and Development</i> , 2007, 21, 1010-1024. | 2.7 | 477 |
| 435 | Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , 2007, 4, 651-657. | 9.0 | 1,254 |
| 436 | Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816. | 13.7 | 4,709 |
| 437 | Paired-End Mapping Reveals Extensive Structural Variation in the Human Genome. <i>Science</i> , 2007, 318, 420-426. | 6.0 | 1,003 |
| 438 | Proteomics for Elucidating Protein Function, Regulatory Networks and Improving Human Health. <i>FASEB Journal</i> , 2007, 21, A211. | 0.2 | 0 |
| 439 | ProCAT: a data analysis approach for protein microarrays. <i>Genome Biology</i> , 2006, 7, R110. | 13.9 | 46 |
| 440 | Yeast as a Model for Human Disease. <i>Current Protocols in Human Genetics</i> , 2006, 48, Unit 15.6. | 3.5 | 36 |
| 441 | Charging it up: global analysis of protein phosphorylation. <i>Trends in Genetics</i> , 2006, 22, 545-554. | 2.9 | 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4534-4539. | 3.3 | 125 |
| 444 | Severe acute respiratory syndrome diagnostics using a coronavirus protein microarray. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4011-4016. | 3.3 | 131 |
| 445 | Global analysis of protein phosphorylation in yeast. <i>Nature</i> , 2005, 438, 679-684. | 13.7 | 915 |
| 446 | Global analysis of protein function using protein microarrays. <i>Mechanisms of Ageing and Development</i> , 2005, 126, 171-175. | 2.2 | 35 |
| 447 | Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. <i>Genes and Development</i> , 2005, 19, 2816-2826. | 2.7 | 443 |
| 448 | Large-Scale Mutagenesis of the Yeast Genome Using a Tn7-Derived Multipurpose Transposon. <i>Genome Research</i> , 2004, 14, 1975-1986. | 2.4 | 52 |
| 449 | Finding new components of the target of rapamycin (TOR) signaling network through chemical genetics and proteome chips. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16594-16599. | 3.3 | 225 |
| 450 | Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. <i>Science</i> , 2004, 306, 2242-2246. | 6.0 | 983 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 451 | Regulation of Gene Expression by a Metabolic Enzyme. <i>Science</i> , 2004, 306, 482-484. | 6.0 | 223 |
| 452 | Protein chip technology. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 55-63. | 2.8 | 861 |
| 453 | Protein analysis on a proteomic scale. <i>Nature</i> , 2003, 422, 208-215. | 13.7 | 610 |
| 454 | Analyzing antibody specificity with whole proteome microarrays. <i>Nature Biotechnology</i> , 2003, 21, 1509-1512. | 9.4 | 270 |
| 455 | Proteomics. <i>Annual Review of Biochemistry</i> , 2003, 72, 783-812. | 5.0 | 332 |
| 456 | A Bayesian Networks Approach for Predicting Protein-Protein Interactions from Genomic Data. <i>Science</i> , 2003, 302, 449-453. | 6.0 | 1,183 |
| 457 | GENOMICS: Defining Genes in the Genomics Era. <i>Science</i> , 2003, 300, 258-260. | 6.0 | 114 |
| 458 | Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. <i>Genes and Development</i> , 2003, 17, 2698-2708. | 2.7 | 74 |
| 459 | Complex transcriptional circuitry at the G1/S transition in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2002, 16, 3017-3033. | 2.7 | 236 |
| 460 | ChIP-chip: A genomic approach for identifying transcription factor binding sites. <i>Methods in Enzymology</i> , 2002, 350, 469-483. | 0.4 | 151 |
| 461 | Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391. | 13.7 | 3,938 |
| 462 | Global Analysis of Protein Activities Using Proteome Chips. <i>Science</i> , 2001, 293, 2101-2105. | 6.0 | 2,082 |
| 463 | Protein arrays and microarrays. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 40-45. | 2.8 | 376 |
| 464 | Making drug addicts out of yeast. <i>Nature Biotechnology</i> , 2001, 19, 1022-1023. | 9.4 | 3 |
| 465 | Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , 2001, 409, 533-538. | 13.7 | 1,030 |
| 466 | Emerging technologies in yeast genomics. <i>Nature Reviews Genetics</i> , 2001, 2, 302-312. | 7.7 | 96 |
| 467 | A Filamentous Growth Response Mediated by the Yeast Mating Pathway. <i>Genetics</i> , 2001, 159, 919-928. | 1.2 | 82 |
| 468 | Analysis of yeast protein kinases using protein chips. <i>Nature Genetics</i> , 2000, 26, 283-289. | 9.4 | 810 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 469 | An integrated web interface for large-scale characterization of sequence data. Functional and Integrative Genomics, 2000, 1, 70-75. | 1.4 | 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. | 0.9 | 51 |
| 471 | Large-scale analysis of the yeast genome by transposon tagging and gene disruption. Nature, 1999, 402, 413-418. | 13.7 | 521 |
| 472 | Functional Characterization of the <i>S. cerevisiae</i> Genome by Gene Deletion and Parallel Analysis. Science, 1999, 285, 901-906. | 6.0 | 3,761 |
| 473 | CELL POLARITY AND MORPHOGENESIS IN BUDDING YEAST. Annual Review of Microbiology, 1998, 52, 687-744. | 2.9 | 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, , . | 1.6 | 0 |