

# Michael Paul Snyder

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

481 papers	76,435 citations	122 h-index	273 g-index
537 ext. papers	93,074 ext. citations	16 avg, IF	7.88 L-index

#	Paper	IF	Citations
481	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis.. <i>Neuron</i> , <b>2022</b> ,	13.9	8
480	Dual isoform sequencing reveals complex transcriptomic and epitranscriptomic landscapes of a prototype baculovirus.. <i>Scientific Reports</i> , <b>2022</b> , 12, 1291	4.9	0
479	Elucidating Diversity in Obesity-Related Phenotypes Using Longitudinal and Multi-omic Approaches <b>2022</b> , 63-75		
478	Exerkines in health, resilience and disease.. <i>Nature Reviews Endocrinology</i> , <b>2022</b> ,	15.2	17
477	Unbiased metabolome screen leads to personalized medicine strategy for amyotrophic lateral sclerosis.. <i>Brain Communications</i> , <b>2022</b> , 4, fcac069	4.5	1
476	MITI minimum information guidelines for highly multiplexed tissue images.. <i>Nature Methods</i> , <b>2022</b> , 19, 262-267	21.6	2
475	Effects of an immersive psychosocial training program on depression and well-being: A randomized clinical trial.. <i>Journal of Psychiatric Research</i> , <b>2022</b> , 150, 292-299	5.2	
474	Adverse childhood experiences, diabetes and associated conditions, preventive care practices and healthcare access: A population-based study.. <i>Preventive Medicine</i> , <b>2022</b> , 107044	4.3	1
473	A machine learning algorithm with subclonal sensitivity reveals widespread pan-cancer human leukocyte antigen loss of heterozygosity.. <i>Nature Communications</i> , <b>2022</b> , 13, 1925	17.4	0
472	Exploring disease interrelationships in patients with lymphatic disorders: A single center retrospective experience.. <i>Clinical and Translational Medicine</i> , <b>2022</b> , 12, e760	5.7	2
471	Global, distinctive, and personal changes in molecular and microbial profiles by specific fibers in humans.. <i>Cell Host and Microbe</i> , <b>2022</b> ,	23.4	4
470	Prediction of gestational age using urinary metabolites in term and preterm pregnancies.. <i>Scientific Reports</i> , <b>2022</b> , 12, 8033	4.9	0
469	Network biology bridges the gaps between quantitative genetics and multi-omics to map complex diseases. <i>Current Opinion in Chemical Biology</i> , <b>2021</b> , 66, 102101	9.7	0
468	A review of Mendelian randomization in amyotrophic lateral sclerosis. <i>Brain</i> , <b>2021</b> ,	11.2	7
467	Heterogeneity of Diabetes: ECells, 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> , <b>2021</b> ,	14.6	1
466	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> , <b>2021</b> , 49, 12196-12210	20.1	1
465	Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging. <i>Nature Methods</i> , <b>2021</b> ,	21.6	6

464	Real-time alerting system for COVID-19 and other stress events using wearable data. <i>Nature Medicine</i> , <b>2021</b> ,	50.5	8
463	Cross-Laboratory Standardization of Preclinical Lipidomics Using Differential Mobility Spectrometry and Multiple Reaction Monitoring. <i>Analytical Chemistry</i> , <b>2021</b> ,	7.8	8
462	Human exposome assessment platform.. <i>Environmental Epidemiology</i> , <b>2021</b> , 5, e182	0.2	1
461	Predictive Signatures for Lung Adenocarcinoma Prognostic Trajectory by Multiomics Data Integration and Ensemble Learning. <i>Lecture Notes in Computer Science</i> , <b>2021</b> , 9-23	0.9	
460	COVID-19-Induced New-Onset Diabetes: Trends and Technologies. <i>Diabetes</i> , <b>2021</b> , 70, 2733-2744	0.9	9
459	A DMS Shotgun Lipidomics Workflow Application to Facilitate High-Throughput, Comprehensive Lipidomics. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2021</b> , 32, 2655-2663	3.5	4
458	Altered Cardiac Energetics and Mitochondrial Dysfunction in Hypertrophic Cardiomyopathy. <i>Circulation</i> , <b>2021</b> , 144, 1714-1731	16.7	11
457	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation. <i>Nature Genetics</i> , <b>2021</b> , 53, 1564-1576	36.3	3
456	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> , <b>2021</b> , 55, 128-137	3.4	3
455	Understanding how biologic and social determinants affect disparities in preterm birth and outcomes of preterm infants in the NICU. <i>Seminars in Perinatology</i> , <b>2021</b> , 45, 151408	3.3	1
454	Response to Hulman and colleagues regarding "Glucotypes reveal new patterns of glucose dysregulation". <i>PLoS Biology</i> , <b>2021</b> , 19, e3001092	9.7	0
453	AdaReg: data adaptive robust estimation in linear regression with application in GTEx gene expressions. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2021</b> , 20, 51-71	1.2	1
452	iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W271-W276	20.1	8
451	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. <i>Nature Genetics</i> , <b>2021</b> , 53, 638-649	36.3	20
450	ALDH1A3 Coordinates Metabolism With Gene Regulation in Pulmonary Arterial Hypertension. <i>Circulation</i> , <b>2021</b> , 143, 2074-2090	16.7	4
449	Swarm: A federated cloud framework for large-scale variant analysis. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1008977	5	1
448	Early detection of SARS-CoV-2 and other infections in solid organ transplant recipients and household members using wearable devices. <i>Transplant International</i> , <b>2021</b> , 34, 1019-1031	3	2
447	Wearable sensors enable personalized predictions of clinical laboratory measurements. <i>Nature Medicine</i> , <b>2021</b> , 27, 1105-1112	50.5	30

446	Integrated trajectories of the maternal metabolome, proteome, and immunome predict labor onset. <i>Science Translational Medicine</i> , <b>2021</b> , 13,	17.5	17
445	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> , <b>2021</b> , 12, 1871-1886	3.6	0
444	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , <b>2021</b> , 184, 2633-2648.e19	56.2	20
443	Precision medicine in women with epilepsy: The challenge, systematic review, and future direction. <i>Epilepsy and Behavior</i> , <b>2021</b> , 118, 107928	3.2	6
442	Non-invasive wearables for remote monitoring of HbA1c and glucose variability: proof of concept. <i>BMJ Open Diabetes Research and Care</i> , <b>2021</b> , 9, e002027	4.5	1
441	Common and rare variant analyses combined with single-cell multiomics reveal cell-type-specific molecular mechanisms of COVID-19 severity <b>2021</b> ,		1
440	Time-course transcriptome analysis of host cell response to poxvirus infection using a dual long-read sequencing approach. <i>BMC Research Notes</i> , <b>2021</b> , 14, 239	2.3	1
439	AdaTiSS: A Novel Data-Adaptive Robust Method for Identifying Tissue Specificity Scores. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
438	Physical exercise is a risk factor for amyotrophic lateral sclerosis: Convergent evidence from Mendelian randomisation, transcriptomics and risk genotypes. <i>EBioMedicine</i> , <b>2021</b> , 68, 103397	8.8	19
437	Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study. <i>JAMIA Open</i> , <b>2021</b> , 4, ooab054	2.9	1
436	Combined nanopore and single-molecule real-time sequencing survey of human betaherpesvirus 5 transcriptome. <i>Scientific Reports</i> , <b>2021</b> , 11, 14487	4.9	4
435	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , <b>2021</b> , 18, 747-756	21.6	83
434	The Exposome in the Era of the Quantified Self. <i>Annual Review of Biomedical Data Science</i> , <b>2021</b> , 4, 255-278	5.7	2
433	Towards personalized medicine in maternal and child health: integrating biologic and social determinants. <i>Pediatric Research</i> , <b>2021</b> , 89, 252-258	3.2	5
432	Obesity Drives Delayed Infarct Expansion, Inflammation, and Distinct Gene Networks in a Mouse Stroke Model. <i>Translational Stroke Research</i> , <b>2021</b> , 12, 331-346	7.8	2
431	PPAR $\epsilon$ -Mediated Vasculoregenerative Program to Reverse Pulmonary Hypertension. <i>Circulation Research</i> , <b>2021</b> , 128, 401-418	15.7	13
430	RobNorm: model-based robust normalization method for labeled quantitative mass spectrometry proteomics data. <i>Bioinformatics</i> , <b>2021</b> , 37, 815-821	7.2	1
429	CTLA-4 expression by B-1a B cells is essential for immune tolerance. <i>Nature Communications</i> , <b>2021</b> , 12, 525	17.4	11

428	The gut microbiome: a key player in the complexity of amyotrophic lateral sclerosis (ALS). <i>BMC Medicine</i> , <b>2021</b> , 19, 13	11.4	16
427	Decoding personal biotic and abiotic airborne exposome. <i>Nature Protocols</i> , <b>2021</b> , 16, 1129-1151	18.8	8
426	An Integrated Sequencing Approach for Updating the Pseudorabies Virus Transcriptome. <i>Pathogens</i> , <b>2021</b> , 10,	4.5	1
425	Benchmarking workflows to assess performance and suitability of germline variant calling pipelines in clinical diagnostic assays. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 85	3.6	2
424	The X chromosome from telomere to telomere: key achievements and future opportunities.. <i>Faculty Reviews</i> , <b>2021</b> , 10, 63	1.2	1
423	Longitudinal linked-read sequencing reveals ecological and evolutionary responses of a human gut microbiome during antibiotic treatment. <i>Genome Research</i> , <b>2021</b> , 31, 1433-1446	9.7	7
422	Prediction of Immunotherapy Response in Melanoma through Combined Modeling of Neoantigen Burden and Immune-Related Resistance Mechanisms. <i>Clinical Cancer Research</i> , <b>2021</b> , 27, 4265-4276	12.9	4
421	Structured elements drive extensive circular RNA translation. <i>Molecular Cell</i> , <b>2021</b> , 81, 4300-4318.e13	17.6	13
420	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> , <b>2021</b> , 114, 1655-1665	7	0
419	Divergent patterns of selection on metabolite levels and gene expression. <i>Bmc Ecology and Evolution</i> , <b>2021</b> , 21, 185	21	0
418	Chromatin accessibility associates with protein-RNA correlation in human cancer. <i>Nature Communications</i> , <b>2021</b> , 12, 5732	17.4	2
417	Adapting skills from genetic counseling to wearables technology research during the COVID-19 pandemic: Poised for the pivot. <i>Journal of Genetic Counseling</i> , <b>2021</b> , 30, 1269-1275	2.5	
416	A scalable, secure, and interoperable platform for deep data-driven health management. <i>Nature Communications</i> , <b>2021</b> , 12, 5757	17.4	10
415	In-depth triacylglycerol profiling using MS Q-Trap mass spectrometry. <i>Analytica Chimica Acta</i> , <b>2021</b> , 1184, 339023	6.6	2
414	Precision Neoantigen Discovery Using Large-scale Immunoepitidomes and Composite Modeling of MHC Peptide Presentation. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 20, 100111	7.6	6
413	Design and Methods of the Validating Injury to the Renal Transplant Using Urinary Signatures (VIRTUUS) Study in Children. <i>Transplantation Direct</i> , <b>2021</b> , 7, e791	2.3	0
412	Patient-derived gene and protein expression signatures of NGLY1 deficiency. <i>Journal of Biochemistry</i> , <b>2021</b> ,	3.1	1
411	Tet enzymes are essential for early embryogenesis and completion of embryonic genome activation. <i>EMBO Reports</i> , <b>2021</b> , e53968	6.5	1

410	Exposome-wide Association Study for Metabolic Syndrome.. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 783930	4.5	0
409	Classifying non-small cell lung cancer types and transcriptomic subtypes using convolutional neural networks. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2020</b> , 27, 757-769	8.6	25
408	Longitudinal Analysis of Serum Cytokine Levels and Gut Microbial Abundance Links IL-17/IL-22 With and Insulin Sensitivity in Humans. <i>Diabetes</i> , <b>2020</b> , 69, 1833-1842	0.9	4
407	Deep Characterization of the Human Antibody Response to Natural Infection Using Longitudinal Immune Repertoire Sequencing. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 19, 278-293	7.6	5
406	Molecular Choreography of Acute Exercise. <i>Cell</i> , <b>2020</b> , 181, 1112-1130.e16	56.2	96
405	Immunologic effects of forest fire exposure show increases in IL-1 $\beta$ and CRP. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2020</b> , 75, 2356-2358	9.3	6
404	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , <b>2020</b> , 181, 1464-1474	56.2	51
403	Physiological blood-brain transport is impaired with age by a shift in transcytosis. <i>Nature</i> , <b>2020</b> , 583, 425-430	50.4	107
402	Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. <i>Cell</i> , <b>2020</b> , 181, 1680-1692.e15	56.2	47
401	Multiomic immune clockworks of pregnancy. <i>Seminars in Immunopathology</i> , <b>2020</b> , 42, 397-412	12	24
400	Systematic identification of silencers in human cells. <i>Nature Genetics</i> , <b>2020</b> , 52, 254-263	36.3	40
399	Personal aging markers and ageotypes revealed by deep longitudinal profiling. <i>Nature Medicine</i> , <b>2020</b> , 26, 83-90	50.5	102
398	The MEK5-ERK5 Kinase Axis Controls Lipid Metabolism in Small-Cell Lung Cancer. <i>Cancer Research</i> , <b>2020</b> , 80, 1293-1303	10.1	22
397	Remodeling of active endothelial enhancers is associated with aberrant gene-regulatory networks in pulmonary arterial hypertension. <i>Nature Communications</i> , <b>2020</b> , 11, 1673	17.4	25
396	Humans Are Selectively Exposed to <i>Pneumocystis jirovecii</i> . <i>MBio</i> , <b>2020</b> , 11,	7.8	5
395	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , <b>2020</b> , 181, 236-249	56.2	140
394	Systematic Identification of Regulators of Oxidative Stress Reveals Non-canonical Roles for Peroxisomal Import and the Pentose Phosphate Pathway. <i>Cell Reports</i> , <b>2020</b> , 30, 1417-1433.e7	10.6	29
393	Global metabolic profiling to model biological processes of aging in twins. <i>Aging Cell</i> , <b>2020</b> , 19, e13073	9.9	21

392	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> , <b>2020</b> , 117, 25104-25115	11.5	13
391	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , <b>2020</b> , 11, 5301	17.4	59
390	iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy. <i>Cell Reports</i> , <b>2020</b> , 32, 108117	10.6	13
389	Deep longitudinal multiomics profiling reveals two biological seasonal patterns in California. <i>Nature Communications</i> , <b>2020</b> , 11, 4933	17.4	12
388	Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	2
387	Meta-analytic approach for transcriptome profiling of herpes simplex virus type 1. <i>Scientific Data</i> , <b>2020</b> , 7, 223	8.2	3
386	Pre-symptomatic detection of COVID-19 from smartwatch data. <i>Nature Biomedical Engineering</i> , <b>2020</b> , 4, 1208-1220	19	115
385	Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. <i>Cell Reports</i> , <b>2020</b> , 33, 108456	10.6	6
384	Cell-free DNA (cfDNA) and Exosome Profiling from a Year-Long Human Spaceflight Reveals Circulating Biomarkers. <i>IScience</i> , <b>2020</b> , 23, 101844	6.1	13
383	A Customizable Analysis Flow in Integrative Multi-Omics. <i>Biomolecules</i> , <b>2020</b> , 10,	5.9	5
382	Multi-faceted epigenetic dysregulation of gene expression promotes esophageal squamous cell carcinoma. <i>Nature Communications</i> , <b>2020</b> , 11, 3675	17.4	19
381	An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , <b>2020</b> , 11, 3696	17.4	28
380	Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , <b>2020</b> , 583, 737-743	50.4	37
379	Perspectives on ENCODE. <i>Nature</i> , <b>2020</b> , 583, 693-698	50.4	61
378	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , <b>2020</b> , 583, 699-710	50.4	360
377	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , <b>2020</b> , 30, 1047-1059	9.7	15
376	Long-read assays shed new light on the transcriptome complexity of a viral pathogen. <i>Scientific Reports</i> , <b>2020</b> , 10, 13822	4.9	6
375	Candidate variants in TUB are associated with familial tremor. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1009010	6	1



374	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , <b>2020</b> , 183, 269-283.e19	56.2	73
373	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> , <b>2020</b> , 19, 4735-4746	5.6	25
372	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , <b>2020</b> , 21, 234	18.3	18
371	Multimomics Characterization of Preterm Birth in Low- and Middle-Income Countries. <i>JAMA Network Open</i> , <b>2020</b> , 3, e2029655	10.4	13
370	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> , <b>2019</b> , 140, 1409-1425	16.7	41
369	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. <i>Nature Communications</i> , <b>2019</b> , 10, 4063	17.4	49
368	Systematic Identification of Host Cell Regulators of Legionella pneumophila Pathogenesis Using a Genome-wide CRISPR Screen. <i>Cell Host and Microbe</i> , <b>2019</b> , 26, 551-563.e6	23.4	26
367	Genome-wide effects of social status on DNA methylation in the brain of a cichlid fish, <i>Astatotilapia burtoni</i> . <i>BMC Genomics</i> , <b>2019</b> , 20, 699	4.5	3
366	Big data and health. <i>The Lancet Digital Health</i> , <b>2019</b> , 1, e252-e254	14.4	10
365	Windows Into Human Health Through Wearables Data Analytics. <i>Current Opinion in Biomedical Engineering</i> , <b>2019</b> , 9, 28-46	4.4	58
364	Personalized Metabolomics. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1978, 447-456	1.4	4
363	Engineering Genetic Predisposition in Human Neuroepithelial Stem Cells Recapitulates Medulloblastoma Tumorigenesis. <i>Cell Stem Cell</i> , <b>2019</b> , 25, 433-446.e7	18	31
362	High-Resolution Bisulfite-Sequencing of Peripheral Blood DNA Methylation in Early-Onset and Familial Risk Breast Cancer Patients. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 5301-5314	12.9	5
361	Longitudinal multi-omics of host-microbe dynamics in prediabetes. <i>Nature</i> , <b>2019</b> , 569, 663-671	50.4	197
360	Applying circulating tumor DNA methylation in the diagnosis of lung cancer. <i>Precision Clinical Medicine</i> , <b>2019</b> , 2, 45-56	6.7	7
359	A longitudinal big data approach for precision health. <i>Nature Medicine</i> , <b>2019</b> , 25, 792-804	50.5	183
358	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> , <b>2019</b> , 2019, 1806842	2.6	2
357	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , <b>2019</b> , 177, 1035-1049.e19	56.2	237



356	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> , <b>2019</b> , 9, 3272	4.9	31
355	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> , <b>2019</b> , 28, 428-437	2.5	8
354	Gene-Environment Interaction in the Era of Precision Medicine. <i>Cell</i> , <b>2019</b> , 177, 38-44	56.2	39
353	The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. <i>Science</i> , <b>2019</b> , 364,	33.3	300
352	Multimomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. <i>Bioinformatics</i> , <b>2019</b> , 35, 95-103	7.2	54
351	High Throughput Sequencing and Assessing Disease Risk. <i>Cold Spring Harbor Perspectives in Medicine</i> , <b>2019</b> , 9,	5.4	11
350	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. <i>Cell</i> , <b>2019</b> , 178, 1245-1259.e14	56.2	91
349	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 834	4.5	22
348	MISTERMINATE Mechanistically Links Mitochondrial Dysfunction with Proteostasis Failure. <i>Molecular Cell</i> , <b>2019</b> , 75, 835-848.e8	17.6	30
347	Chromatin Remodeling in Response to BRCA2-Crisis. <i>Cell Reports</i> , <b>2019</b> , 28, 2182-2193.e6	10.6	1
346	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 4098-4107	5.6	32
345	Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. <i>Nature Biomedical Engineering</i> , <b>2019</b> , 3, 1009-1019	19	60
344	Simultaneous RNA purification and size selection using on-chip isotachopheresis with an ionic spacer. <i>Lab on A Chip</i> , <b>2019</b> , 19, 2741-2749	7.2	5
343	A machine-compiled database of genome-wide association studies. <i>Nature Communications</i> , <b>2019</b> , 10, 3341	17.4	11
342	HAT1 Coordinates Histone Production and Acetylation via H4 Promoter Binding. <i>Molecular Cell</i> , <b>2019</b> , 75, 711-724.e5	17.6	24
341	Template-switching artifacts resemble alternative polyadenylation. <i>BMC Genomics</i> , <b>2019</b> , 20, 824	4.5	13
340	Whole-exome sequencing data of suicide victims who had suffered from major depressive disorder. <i>Scientific Data</i> , <b>2019</b> , 6, 190010	8.2	2
339	Long-Read Sequencing - A Powerful Tool in Viral Transcriptome Research. <i>Trends in Microbiology</i> , <b>2019</b> , 27, 578-592	12.4	38

338	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. <i>Nature</i> , <b>2019</b> , 574, 553-558	50.4	84
337	Metformin Affects Heme Function as a Possible Mechanism of Action. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 513-522	3.2	7
336	Understanding health disparities. <i>Journal of Perinatology</i> , <b>2019</b> , 39, 354-358	3.1	12
335	Macrophage de novo NAD synthesis specifies immune function in aging and inflammation. <i>Nature Immunology</i> , <b>2019</b> , 20, 50-63	19.1	160
334	Smooth Muscle Contact Drives Endothelial Regeneration by BMP2-Notch1-Mediated Metabolic and Epigenetic Changes. <i>Circulation Research</i> , <b>2019</b> , 124, 211-224	15.7	46
333	Precision Medicine: Role of Proteomics in Changing Clinical Management and Care. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 1-6	5.6	15
332	Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 1383-1396	5.6	13
331	Integrative omics for health and disease. <i>Nature Reviews Genetics</i> , <b>2018</b> , 19, 299-310	30.1	402
330	SETD7 Drives Cardiac Lineage Commitment through Stage-Specific Transcriptional Activation. <i>Cell Stem Cell</i> , <b>2018</b> , 22, 428-444.e5	18	20
329	Biallelic Mutations in ATP5F1D, which Encodes a Subunit of ATP Synthase, Cause a Metabolic Disorder. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 494-504	11	44
328	Fast Metagenomic Binning via Hashing and Bayesian Clustering. <i>Journal of Computational Biology</i> , <b>2018</b> , 25, 677-688	1.7	2
327	Distinct transcriptomic and exomic abnormalities within myelodysplastic syndrome marrow cells. <i>Leukemia and Lymphoma</i> , <b>2018</b> , 59, 2952-2962	1.9	5
326	Comparative analysis of respiratory motion tracking using Microsoft Kinect v2 sensor. <i>Journal of Applied Clinical Medical Physics</i> , <b>2018</b> , 19, 193-204	2.3	16
325	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. <i>Cell Metabolism</i> , <b>2018</b> , 27, 559-571.e5	24.6	189
324	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , <b>2018</b> , 14, 206-214	11.7	324
323	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. <i>Scientific Reports</i> , <b>2018</b> , 8, 226	4.9	21
322	Applying genomics in heart transplantation. <i>Transplant International</i> , <b>2018</b> , 31, 278-290	3	5
321	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. <i>Cell Systems</i> , <b>2018</b> , 6, 157-170.e8	10.8	114

320	Multiplatform next-generation sequencing identifies novel RNA molecules and transcript isoforms of the endogenous retrovirus isolated from cultured cells. <i>FEMS Microbiology Letters</i> , <b>2018</b> , 365,	2.9	7
319	Personal Omics for Precision Health. <i>Circulation Research</i> , <b>2018</b> , 122, 1169-1171	15.7	28
318	A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. <i>Nature Genetics</i> , <b>2018</b> , 50, 613-620	36.3	74
317	Full Genome Sequence of the Western Reserve Strain of Vaccinia Virus Determined by Third-Generation Sequencing. <i>Genome Announcements</i> , <b>2018</b> , 6,		8
316	Circular DNA elements of chromosomal origin are common in healthy human somatic tissue. <i>Nature Communications</i> , <b>2018</b> , 9, 1069	17.4	108
315	Omics AnalySIs System for PRrecision Oncology (OASISPRO): a web-based omics analysis tool for clinical phenotype prediction. <i>Bioinformatics</i> , <b>2018</b> , 34, 319-320	7.2	14
314	Natural Selection Has Differentiated the Progesterone Receptor among Human Populations. <i>American Journal of Human Genetics</i> , <b>2018</b> , 103, 45-57	11	19
313	Glucotypes reveal new patterns of glucose dysregulation. <i>PLoS Biology</i> , <b>2018</b> , 16, e2005143	9.7	95
312	Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4031-4041	5.6	46
311	A Cloud-Based Metabolite and Chemical Prioritization System for the Biology/Disease-Driven Human Proteome Project. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4345-4357	5.6	5
310	Long-Read Sequencing Revealed an Extensive Transcript Complexity in Herpesviruses. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 259	4.5	13
309	NF90/ILF3 is a transcription factor that promotes proliferation over differentiation by hierarchical regulation in K562 erythroleukemia cells. <i>PLoS ONE</i> , <b>2018</b> , 13, e0193126	3.7	14
308	An integrated global regulatory network of hematopoietic precursor cell self-renewal and differentiation. <i>Integrative Biology (United Kingdom)</i> , <b>2018</b> , 10, 390-405	3.7	1
307	Transcriptome-wide survey of pseudorabies virus using next- and third-generation sequencing platforms. <i>Scientific Data</i> , <b>2018</b> , 5, 180119	8.2	13
306	Wearables and the medical revolution. <i>Personalized Medicine</i> , <b>2018</b> , 15, 429-448	2.2	180
305	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. <i>Genome Research</i> , <b>2018</b> , 28, 231-242	9.7	38
304	mutation associated with pseudorheumatoid dysplasia. <i>Journal of Physical Education and Sports Management</i> , <b>2018</b> , 4,	2.8	10
303	Transcriptomic study of Herpes simplex virus type-1 using full-length sequencing techniques. <i>Scientific Data</i> , <b>2018</b> , 5, 180266	8.2	10

302	Dynamic transcriptome profiling dataset of vaccinia virus obtained from long-read sequencing techniques. <i>GigaScience</i> , <b>2018</b> , 7,	7.6	19
301	Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. <i>Nature Genetics</i> , <b>2018</b> , 50, 1716-1727	36.3	67
300	Longitudinal personal DNA methylome dynamics in a human with a chronic condition. <i>Nature Medicine</i> , <b>2018</b> , 24, 1930-1939	50.5	33
299	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007755	6	15
298	Cross-Platform Comparison of Untargeted and Targeted Lipidomics Approaches on Aging Mouse Plasma. <i>Scientific Reports</i> , <b>2018</b> , 8, 17747	4.9	47
297	High-frequency actionable pathogenic exome variants in an average-risk cohort. <i>Journal of Physical Education and Sports Management</i> , <b>2018</b> , 4,	2.8	15
296	Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 432	4.5	10
295	Evaluation of whole exome sequencing as an alternative to BeadChip and whole genome sequencing in human population genetic analysis. <i>BMC Genomics</i> , <b>2018</b> , 19, 778	4.5	7
294	Decoding the Genomics of Abdominal Aortic Aneurysm. <i>Cell</i> , <b>2018</b> , 174, 1361-1372.e10	56.2	34
293	Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. <i>Cell</i> , <b>2018</b> , 175, 277-291.e31	56.2	86
292	Disruption of mesoderm formation during cardiac differentiation due to developmental exposure to 13-cis-retinoic acid. <i>Scientific Reports</i> , <b>2018</b> , 8, 12960	4.9	11
291	Association of AHSR with alopecia and mental retardation (APMR) syndrome. <i>Human Genetics</i> , <b>2017</b> , 136, 287-296	6.3	8
290	Pharmacological rescue of diabetic skeletal stem cell niches. <i>Science Translational Medicine</i> , <b>2017</b> , 9,	17.5	53
289	De novo and rare mutations in the HSPA1L heat shock gene associated with inflammatory bowel disease. <i>Genome Medicine</i> , <b>2017</b> , 9, 8	14.4	22
288	Genetic Adaptation of Porcine Circovirus Type 1 to Cultured Porcine Kidney Cells Revealed by Single-Molecule Long-Read Sequencing Technology. <i>Genome Announcements</i> , <b>2017</b> , 5,		1
287	Implementation of facial recognition with Microsoft Kinect v2 sensor for patient verification. <i>Medical Physics</i> , <b>2017</b> , 44, 2391-2399	4.4	11
286	Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression. <i>Nature Communications</i> , <b>2017</b> , 8, 14995	17.4	80
285	Non-equivalence of Wnt and R-spondin ligands during Lgr5 intestinal stem-cell self-renewal. <i>Nature</i> , <b>2017</b> , 545, 238-242	50.4	209

284	A Case Report of Hypoglycemia and Hypogammaglobulinemia: DAVID Syndrome in a Patient With a Novel NFKB2 Mutation. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2017</b> , 102, 2127-2130	5.6	13
283	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. <i>Nature Communications</i> , <b>2017</b> , 8, 15178	17.4	148
282	Succinate and its G-protein-coupled receptor stimulates osteoclastogenesis. <i>Nature Communications</i> , <b>2017</b> , 8, 15621	17.4	43
281	Multi-platform analysis reveals a complex transcriptome architecture of a circovirus. <i>Virus Research</i> , <b>2017</b> , 237, 37-46	6.4	23
280	Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e77	20.1	24
279	Gpr124 is essential for blood-brain barrier integrity in central nervous system disease. <i>Nature Medicine</i> , <b>2017</b> , 23, 450-460	50.5	108
278	Characterization of the Dynamic Transcriptome of a Herpesvirus with Long-read Single Molecule Real-Time Sequencing. <i>Scientific Reports</i> , <b>2017</b> , 7, 43751	4.9	35
277	Patient-Specific iPSC-Derived Endothelial Cells Uncover Pathways that Protect against Pulmonary Hypertension in BMPR2 Mutation Carriers. <i>Cell Stem Cell</i> , <b>2017</b> , 20, 490-504.e5	18	117
276	A common class of transcripts with 5'-intron depletion, distinct early coding sequence features, and -methyadenosine modification. <i>Rna</i> , <b>2017</b> , 23, 270-283	5.8	13
275	Transcriptomic and epigenomic differences in human induced pluripotent stem cells generated from six reprogramming methods. <i>Nature Biomedical Engineering</i> , <b>2017</b> , 1, 826-837	19	24
274	Cell Type-Specific Chromatin Signatures Underline Regulatory DNA Elements in Human Induced Pluripotent Stem Cells and Somatic Cells. <i>Circulation Research</i> , <b>2017</b> , 121, 1237-1250	15.7	11
273	Fetal de novo mutations and preterm birth. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006689	6	22
272	Topological organization and dynamic regulation of human tRNA genes during macrophage differentiation. <i>Genome Biology</i> , <b>2017</b> , 18, 180	18.3	20
271	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2708	5.7	41
270	Network analyses identify liver-specific targets for treating liver diseases. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 938	12.2	71
269	Digital Health: Tracking Physiomes and Activity Using Wearable Biosensors Reveals Useful Health-Related Information. <i>PLoS Biology</i> , <b>2017</b> , 15, e2001402	9.7	204
268	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. <i>Molecular Cell</i> , <b>2017</b> , 67, 1037-1048.e6	17.6	138
267	Identification of a novel mutation in the gene associated with ataxia-oculomotor apraxia. <i>Journal of Physical Education and Sports Management</i> , <b>2017</b> , 3,	2.8	1

266	Cloud-based interactive analytics for terabytes of genomic variants data. <i>Bioinformatics</i> , <b>2017</b> , 33, 3709-3715	7	7
265	Isolated Congenital Anosmia and CNGA2 Mutation. <i>Scientific Reports</i> , <b>2017</b> , 7, 2667	4.9	8
264	Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis. <i>Scientific Reports</i> , <b>2017</b> , 7, 5557	4.9	7
263	High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. <i>Scientific Reports</i> , <b>2017</b> , 7, 7106	4.9	40
262	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , <b>2017</b> , 49, 1522-1528	36.3	158
261	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> , <b>2017</b> , 114, E11111-E11120	11.5	47
260	Long-Read Sequencing of Human Cytomegalovirus Transcriptome Reveals RNA Isoforms Carrying Distinct Coding Potentials. <i>Scientific Reports</i> , <b>2017</b> , 7, 15989	4.9	43
259	Association of Omics Features with Histopathology Patterns in Lung Adenocarcinoma. <i>Cell Systems</i> , <b>2017</b> , 5, 620-627.e3	10.6	57
258	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. <i>Nature Communications</i> , <b>2017</b> , 8, 59	17.4	130
257	Genome-Wide Temporal Profiling of Transcriptome and Open Chromatin of Early Cardiomyocyte Differentiation Derived From hiPSCs and hESCs. <i>Circulation Research</i> , <b>2017</b> , 121, 376-391	15.7	69
256	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> , <b>2017</b> , 195, 930-941	10.2	52
255	ChIA-PET2: a versatile and flexible pipeline for ChIA-PET data analysis. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e4	20.1	61
254	Long-read sequencing of the human cytomegalovirus transcriptome with the Pacific Biosciences RSII platform. <i>Scientific Data</i> , <b>2017</b> , 4, 170194	8.2	19
253	Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1079	5.7	52
252	Long-Read Sequencing Reveals a GC Pressure during the Evolution of Porcine Endogenous Retrovirus. <i>Genome Announcements</i> , <b>2017</b> , 5,		2
251	Plasma sterols and depressive symptom severity in a population-based cohort. <i>PLoS ONE</i> , <b>2017</b> , 12, e0184382	3.7	9
250	Evaluation of the impact of ul54 gene-deletion on the global transcription and DNA replication of pseudorabies virus. <i>Archives of Virology</i> , <b>2017</b> , 162, 2679-2694	2.6	3
249	Single cell transcriptomics reveals unanticipated features of early hematopoietic precursors. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 1281-1296	20.1	31



248	Can heavy isotopes increase lifespan? Studies of relative abundance in various organisms reveal chemical perspectives on aging. <i>BioEssays</i> , <b>2016</b> , 38, 1093-1101	4.1	7
247	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. <i>Nature Genetics</i> , <b>2016</b> , 48, 1193-203	36.3	555
246	Transcriptome Profiling of Patient-Specific Human iPSC-Cardiomyocytes Predicts Individual Drug Safety and Efficacy Responses In Vitro. <i>Cell Stem Cell</i> , <b>2016</b> , 19, 311-25	18	103
245	iPSC-derived cardiomyocytes reveal abnormal TGF- $\beta$ signalling in left ventricular non-compaction cardiomyopathy. <i>Nature Cell Biology</i> , <b>2016</b> , 18, 1031-42	23.4	103
244	Predicting non-small cell lung cancer prognosis by fully automated microscopic pathology image features. <i>Nature Communications</i> , <b>2016</b> , 7, 12474	17.4	452
243	Secure cloud computing for genomic data. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 588-91	44.5	14
242	Predicting Ovarian Cancer Patients' Clinical Response to Platinum-Based Chemotherapy by Their Tumor Proteomic Signatures. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 2455-65	5.6	28
241	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , <b>2016</b> , 24, 172-84	24.6	105
240	Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, and allele-specific binding detection. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 96	3.6	4
239	Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. <i>Proteomics</i> , <b>2016</b> , 16, 465-76	4.8	7
238	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , <b>2016</b> , 166, 755-765	56.2	544
237	Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 64-9	44.5	75
236	Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations. <i>Nature Genetics</i> , <b>2016</b> , 48, 117-25	36.3	60
235	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> , <b>2016</b> , 113, E440-9	11.5	149
234	Effects of cellular origin on differentiation of human induced pluripotent stem cell-derived endothelial cells. <i>JCI Insight</i> , <b>2016</b> , 1,	9.9	48
233	Genomics and Personalized Medicine <b>2016</b> ,		16
232	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> , <b>2016</b> , 12, e1006347	6	4
231	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. <i>PLoS ONE</i> , <b>2016</b> , 11, e0162868	3.7	53



230	Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1. <i>Scientific Reports</i> , <b>2016</b> , 6, 20104	4.9	46
229	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. <i>Cell</i> , <b>2016</b> , 167, 1734-1749.e22	56.2	122
228	Genome assembly from synthetic long read clouds. <i>Bioinformatics</i> , <b>2016</b> , 32, i216-i224	7.2	20
227	Yeast longevity promoted by reversing aging-associated decline in heavy isotope content. <i>Npj Aging and Mechanisms of Disease</i> , <b>2016</b> , 2, 16004	5.5	16
226	Omics Profiling in Precision Oncology. <i>Molecular and Cellular Proteomics</i> , <b>2016</b> , 15, 2525-36	7.6	63
225	Can Metabolic Profiles Be Used as a Phenotypic Readout of the Genome to Enhance Precision Medicine?. <i>Clinical Chemistry</i> , <b>2016</b> , 62, 676-8	5.5	12
224	Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. <i>Nature Genetics</i> , <b>2016</b> , 48, 687-93	36.3	122
223	A proposal for validation of antibodies. <i>Nature Methods</i> , <b>2016</b> , 13, 823-7	21.6	312
222	Nat1 Deficiency Is Associated with Mitochondrial Dysfunction and Exercise Intolerance in Mice. <i>Cell Reports</i> , <b>2016</b> , 17, 527-540	10.6	24
221	Simul-seq: combined DNA and RNA sequencing for whole-genome and transcriptome profiling. <i>Nature Methods</i> , <b>2016</b> , 13, 953-958	21.6	20
220	NIH working group report-using genomic information to guide weight management: From universal to precision treatment. <i>Obesity</i> , <b>2016</b> , 24, 14-22	8	70
219	Metabolome progression during early gut microbial colonization of gnotobiotic mice. <i>Scientific Reports</i> , <b>2015</b> , 5, 11589	4.9	24
218	Mango: a bias-correcting ChIA-PET analysis pipeline. <i>Bioinformatics</i> , <b>2015</b> , 31, 3092-8	7.2	91
217	Transcriptome Signature and Regulation in Human Somatic Cell Reprogramming. <i>Stem Cell Reports</i> , <b>2015</b> , 4, 1125-39	8	13
216	Single-cell chromatin accessibility reveals principles of regulatory variation. <i>Nature</i> , <b>2015</b> , 523, 486-90	50.4	1110
215	Transglutaminase 4 as a prostate autoantigen in male subfertility. <i>Science Translational Medicine</i> , <b>2015</b> , 7, 292ra101	17.5	47
214	Characterization of novel transcripts in pseudorabies virus. <i>Viruses</i> , <b>2015</b> , 7, 2727-44	6.2	22
213	Optimized Analytical Procedures for the Untargeted Metabolomic Profiling of Human Urine and Plasma by Combining Hydrophilic Interaction (HILIC) and Reverse-Phase Liquid Chromatography (RPLC)-Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 1684-95	7.6	138

212	Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 736-42	44.5	134
211	Reassessment of Piwi binding to the genome and Piwi impact on RNA polymerase II distribution. <i>Developmental Cell</i> , <b>2015</b> , 32, 772-4	10.2	7
210	Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. <i>Genome Research</i> , <b>2015</b> , 25, 1610-21	9.7	115
209	Genomic analysis of mycosis fungoides and S <sub>h</sub> ary syndrome identifies recurrent alterations in TNFR2. <i>Nature Genetics</i> , <b>2015</b> , 47, 1056-60	36.3	186
208	Evaluating Common Humoral Responses against Fungal Infections with Yeast Protein Microarrays. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 3924-31	5.6	7
207	Integrated Proteomic and Genomic Analysis of Gastric Cancer Patient Tissues. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 4995-5006	5.6	6
206	Novel mutations in PIEZO1 cause an autosomal recessive generalized lymphatic dysplasia with non-immune hydrops fetalis. <i>Nature Communications</i> , <b>2015</b> , 6, 8085	17.4	174
205	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. <i>Cell</i> , <b>2015</b> , 162, 1051-65	56.2	240
204	Achieving high-sensitivity for clinical applications using augmented exome sequencing. <i>Genome Medicine</i> , <b>2015</b> , 7, 71	14.4	41
203	Probing High-density Functional Protein Microarrays to Detect Protein-protein Interactions. <i>Journal of Visualized Experiments</i> , <b>2015</b> , e51872	1.6	5
202	Impact of allele-specific peptides in proteome quantification. <i>Proteomics - Clinical Applications</i> , <b>2015</b> , 9, 432-6	3.1	1
201	Where Next for Genetics and Genomics?. <i>PLoS Biology</i> , <b>2015</b> , 13, e1002216	9.7	8
200	Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005496	6	18
199	Whole-Exome Enrichment with the Agilent SureSelect Human All Exon Platform. <i>Cold Spring Harbor Protocols</i> , <b>2015</b> , 2015, 626-33	1.2	29
198	Whole-Exome Enrichment with the Roche NimbleGen SeqCap EZ Exome Library SR Platform. <i>Cold Spring Harbor Protocols</i> , <b>2015</b> , 2015, 634-41	1.2	7
197	Whole-Exome Enrichment with the Illumina TruSeq Exome Enrichment Platform. <i>Cold Spring Harbor Protocols</i> , <b>2015</b> , 2015, 642-8	1.2	9
196	High-throughput sequencing technologies. <i>Molecular Cell</i> , <b>2015</b> , 58, 586-97	17.6	629
195	Recurrent somatic mutations in regulatory regions of human cancer genomes. <i>Nature Genetics</i> , <b>2015</b> , 47, 710-6	36.3	190

194	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> , <b>2015</b> , 192, 356-66	10.2	57
193	Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders. <i>Cell Systems</i> , <b>2015</b> , 1, 361-374	10.6	29
192	Metformin Improves Diabetic Bone Health by Re-Balancing Catabolism and Nitrogen Disposal. <i>PLoS ONE</i> , <b>2015</b> , 10, e0146152	3.7	11
191	Disease Variant Landscape of a Large Multiethnic Population of Moyamoya Patients by Exome Sequencing. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 6, 41-9	3.2	32
190	Clinical interpretation and implications of whole-genome sequencing. <i>JAMA - Journal of the American Medical Association</i> , <b>2014</b> , 311, 1035-45	27.4	333
189	Whole-genome haplotyping using long reads and statistical methods. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 261-266	44.5	146
188	Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 562-8	44.5	146
187	Landscape and variation of RNA secondary structure across the human transcriptome. <i>Nature</i> , <b>2014</b> , 505, 706-9	50.4	390
186	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , <b>2014</b> , 515, 371-375	50.4	190
185	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , <b>2014</b> , 515, 355-64	50.4	1026
184	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , <b>2014</b> , 515, 402-5	50.4	563
183	Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures. <i>Bioinformatics</i> , <b>2014</b> , 30, 2808-10	7.2	122
182	iPOP and its role in participatory medicine. <i>Genome Medicine</i> , <b>2014</b> , 6, 6	14.4	6
181	Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulum-associated degradation pathway. <i>Genetics in Medicine</i> , <b>2014</b> , 16, 751-8	8.1	138
180	Regulatory analysis of the C. elegans genome with spatiotemporal resolution. <i>Nature</i> , <b>2014</b> , 512, 400-5	50.4	81
179	Genome-wide map of regulatory interactions in the human genome. <i>Genome Research</i> , <b>2014</b> , 24, 1905-17	19.7	197
178	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , <b>2014</b> , 512, 453-6	50.4	135
177	Widespread contribution of transposable elements to the innovation of gene regulatory networks. <i>Genome Research</i> , <b>2014</b> , 24, 1963-76	9.7	251

176	H3K4me3 breadth is linked to cell identity and transcriptional consistency. <i>Cell</i> , <b>2014</b> , 158, 673-88	56.2	278
175	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 6131-8	11.5	490
174	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> , <b>2014</b> , 539, 89-111	1.7	6
173	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> , <b>2014</b> , 111, 9869-74	11.5	168
172	Personalized sequencing and the future of medicine: discovery, diagnosis and defeat of disease. <i>Pharmacogenomics</i> , <b>2014</b> , 15, 1771-1790	2.6	44
171	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 774	12.2	89
170	Transcriptome sequencing from diverse human populations reveals differentiated regulatory architecture. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004549	6	35
169	Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004122	6	26
168	Allelic expression of deleterious protein-coding variants across human tissues. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004304	6	43
167	Strain Kaplan of Pseudorabies Virus Genome Sequenced by PacBio Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , <b>2014</b> , 2,		22
166	Metadata checklist for the integrated personal OMICS study: proteomics and metabolomics experiments. <i>OMICS A Journal of Integrative Biology</i> , <b>2014</b> , 18, 81-5	3.8	13
165	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> , <b>2014</b> , 111, 17224-9	11.5	239
164	Exome sequencing and genome-wide copy number variant mapping reveal novel associations with sensorineural hereditary hearing loss. <i>BMC Genomics</i> , <b>2014</b> , 15, 1155	4.5	17
163	Shared functions of plant and mammalian StAR-related lipid transfer (START) domains in modulating transcription factor activity. <i>BMC Biology</i> , <b>2014</b> , 12, 70	7.3	48
162	Haplotype structure and positive selection at TLR1. <i>European Journal of Human Genetics</i> , <b>2014</b> , 22, 551-75.3		17
161	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 349-60	11	131
160	STORMSeq: an open-source, user-friendly pipeline for processing personal genomics data in the cloud. <i>PLoS ONE</i> , <b>2014</b> , 9, e84860	3.7	21
159	Identification of STAT5A and STAT5B target genes in human T cells. <i>PLoS ONE</i> , <b>2014</b> , 9, e86790	3.7	49

158	Genomic era diagnosis and management of hereditary and sporadic colon cancer. <i>World Journal of Clinical Oncology</i> , <b>2014</b> , 5, 1036-47	2.5	10
157	Transcriptomic Evaluation of CD34+ Marrow Cells from Myelodysplastic Syndrome (MDS) Patients. <i>Blood</i> , <b>2014</b> , 124, 1894-1894	2.2	
156	Personal genomes, quantitative dynamic omics and personalized medicine. <i>Quantitative Biology</i> , <b>2013</b> , 1, 71-90	3.9	26
155	Whole-exome sequencing identifies tetratricopeptide repeat domain 7A (TTC7A) mutations for combined immunodeficiency with intestinal atresias. <i>Journal of Allergy and Clinical Immunology</i> , <b>2013</b> , 132, 656-664.e17	11.5	109
154	Dynamic trans-acting factor colocalization in human cells. <i>Cell</i> , <b>2013</b> , 155, 713-24	56.2	109
153	Extensive variation in chromatin states across humans. <i>Science</i> , <b>2013</b> , 342, 750-2	33.3	276
152	A single-molecule long-read survey of the human transcriptome. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 1009-14	44.5	396
151	Systematic investigation of protein-small molecule interactions. <i>IUBMB Life</i> , <b>2013</b> , 65, 2-8	4.7	24
150	Promise of personalized omics to precision medicine. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2013</b> , 5, 73-82	6.6	188
149	High-throughput sequencing for biology and medicine. <i>Molecular Systems Biology</i> , <b>2013</b> , 9, 640	12.2	186
148	Metabolomics as a robust tool in systems biology and personalized medicine: an open letter to the metabolomics community. <i>Metabolomics</i> , <b>2013</b> , 9, 532-534	4.7	3
147	Preparation of recombinant protein spotted arrays for proteome-wide identification of kinase targets. <i>Current Protocols in Protein Science</i> , <b>2013</b> , Chapter 27, Unit 27.4	3.1	3
146	iPOP goes the world: integrated personalized Omics profiling and the road toward improved health care. <i>Chemistry and Biology</i> , <b>2013</b> , 20, 660-6		57
145	Multimodal dynamic profiling of healthy and diseased states for future personalized health care. <i>Clinical Pharmacology and Therapeutics</i> , <b>2013</b> , 93, 29-32	6.1	4
144	Variation and genetic control of protein abundance in humans. <i>Nature</i> , <b>2013</b> , 499, 79-82	50.4	272
143	Centromere-like regions in the budding yeast genome. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003209	6	30
142	Accurate identification and analysis of human mRNA isoforms using deep long read sequencing. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 387-97	3.2	47
141	PATH-SCAN: A REPORTING TOOL FOR IDENTIFYING CLINICALLY ACTIONABLE VARIANTS <b>2013</b> ,		1

140	Overview of high throughput sequencing technologies to elucidate molecular pathways in cardiovascular diseases. <i>Circulation Research</i> , <b>2013</b> , 112, 1613-23	15.7	77
139	Extensive transcript diversity and novel upstream open reading frame regulation in yeast. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 343-52	3.2	44
138	Systematic functional regulatory assessment of disease-associated variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 9607-12	11.5	75
137	Metadata Checklist for the Integrated Personal Omics Study: Proteomics and Metabolomics Experiments. <i>Big Data</i> , <b>2013</b> , 1, 202-6	3.1	6
136	Integrative analysis of longitudinal metabolomics data from a personal multi-omics profile. <i>Metabolites</i> , <b>2013</b> , 3, 741-60	5.6	46
135	Investigating metabolite-protein interactions: an overview of available techniques. <i>Methods</i> , <b>2012</b> , 57, 459-66	4.6	33
134	Systems biology: personalized medicine for the future?. <i>Current Opinion in Pharmacology</i> , <b>2012</b> , 12, 623-8	8.1	71
133	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , <b>2012</b> , 13, R48	18.3	194
132	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , <b>2012</b> , 22, 1813-31	9.7	1211
131	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. <i>Genome Research</i> , <b>2012</b> , 22, 1735-47	9.7	129
130	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , <b>2012</b> , 148, 84-98	56.2	882
129	Personal omics profiling reveals dynamic molecular and medical phenotypes. <i>Cell</i> , <b>2012</b> , 148, 1293-307	56.2	921
128	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , <b>2012</b> , 489, 91-100	50.4	1104
127	Detecting and annotating genetic variations using the HugeSeq pipeline. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 226-9	44.5	90
126	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 221-3	44.5	244
125	Tcf7 is an important regulator of the switch of self-renewal and differentiation in a multipotential hematopoietic cell line. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002565	6	71
124	Annotation of functional variation in personal genomes using RegulomeDB. <i>Genome Research</i> , <b>2012</b> , 22, 1790-7	9.7	1723
123	Linking disease associations with regulatory information in the human genome. <i>Genome Research</i> , <b>2012</b> , 22, 1748-59	9.7	538

122	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , <b>2012</b> , 22, 1798-812	9.7	596
121	Correlation of Global MicroRNA Expression With Basal Cell Carcinoma Subtype. <i>G3: Genes, Genomes, Genetics</i> , <b>2012</b> , 2, 279-86	3.2	28
120	Interpretome: a freely available, modular, and secure personal genome interpretation engine. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2012</b> , 339-350	1.3	12
119	Whole Genome Sequence Analysis of Primary Myelofibrosis.. <i>Blood</i> , <b>2012</b> , 120, 2863-2863	2.2	
118	Performance comparison of whole-genome sequencing platforms. <i>Nature Biotechnology</i> , <b>2011</b> , 30, 78-82	4.5	241
117	Dissecting phosphorylation networks: lessons learned from yeast. <i>Expert Review of Proteomics</i> , <b>2011</b> , 8, 775-86	4.2	15
116	Regulatory variation within and between species. <i>Annual Review of Genomics and Human Genetics</i> , <b>2011</b> , 12, 327-46	9.7	52
115	Deciphering DNA Sequence Information <b>2011</b> , 1-20		
114	Diverse roles and interactions of the SWI/SNF chromatin remodeling complex revealed using global approaches. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002008	6	162
113	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , <b>2011</b> , 470, 59-65	50.4	833
112	Landscape of next-generation sequencing technologies. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 4327-41	7.8	253
111	Performance comparison of exome DNA sequencing technologies. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 908-14	4.5	397
110	The human proteome project: current state and future direction. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M111.009993	7.6	249
109	Identification of genomic indels and structural variations using split reads. <i>BMC Genomics</i> , <b>2011</b> , 12, 375	4.5	52
108	Metabolites as global regulators: a new view of protein regulation: systematic investigation of metabolite-protein interactions may help bridge the gap between genome-wide association studies and small molecule screening studies. <i>BioEssays</i> , <b>2011</b> , 33, 485-9	4.1	28
107	AlleleSeq: analysis of allele-specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 522	12.2	228
106	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. <i>Genes and Development</i> , <b>2011</b> , 25, 767-78	12.6	51
105	Phased whole-genome genetic risk in a family quartet using a major allele reference sequence. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002280	6	112



104	CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. <i>Genome Research</i> , <b>2011</b> , 21, 974-84	9.7	944
103	Analyzing In Vivo Metabolite-Protein Interactions By Large-Scale Systematic Analyses. <i>Current Protocols in Chemical Biology</i> , <b>2011</b> , 3, 181-196	1.8	5
102	Genome-wide mapping of copy number variation in humans: comparative analysis of high resolution array platforms. <i>PLoS ONE</i> , <b>2011</b> , 6, e27859	3.7	51
101	Genomic binding profiles of functionally distinct RNA polymerase III transcription complexes in human cells. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 635-40	17.6	159
100	Genetic analysis of variation in transcription factor binding in yeast. <i>Nature</i> , <b>2010</b> , 464, 1187-91	50.4	130
99	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 47-55	44.5	136
98	Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , <b>2010</b> , 11, 559-71	30.1	303
97	Systems Biology Approaches to Disease Marker Discovery. <i>Disease Markers</i> , <b>2010</b> , 28, 209-224	3.2	17
96	Personal genome sequencing: current approaches and challenges. <i>Genes and Development</i> , <b>2010</b> , 24, 423-31	12.6	103
95	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> , <b>2010</b> , 107, 5254-9	11.5	142
94	Molecular mechanisms of ethanol-induced pathogenesis revealed by RNA-sequencing. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1000834	7.6	122
93	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> , <b>2010</b> , 6, e1000848	6	132
92	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> , <b>2010</b> , 107, 3639-44	11.5	143
91	Variation in transcription factor binding among humans. <i>Science</i> , <b>2010</b> , 328, 232-5	33.3	447
90	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , <b>2010</b> , 330, 1775-87	33.3	744
89	ChIP-Seq: a method for global identification of regulatory elements in the genome. <i>Current Protocols in Molecular Biology</i> , <b>2010</b> , Chapter 21, Unit 21.19.1-14	2.9	39
88	Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analyses. <i>Cell</i> , <b>2010</b> , 143, 639-50	56.2	162
87	Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs. <i>Science Signaling</i> , <b>2010</b> , 3, ra12	8.8	262

86	Yeast proteomics and protein microarrays. <i>Journal of Proteomics</i> , <b>2010</b> , 73, 2147-57	3.9	28
85	Systems biology approaches to disease marker discovery. <i>Disease Markers</i> , <b>2010</b> , 28, 209-24	3.2	9
84	Global analysis of the glycoproteome in <i>Saccharomyces cerevisiae</i> reveals new roles for protein glycosylation in eukaryotes. <i>Molecular Systems Biology</i> , <b>2009</b> , 5, 308	12.2	71
83	Integrating sequencing technologies in personal genomics: optimal low cost reconstruction of structural variants. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000432	5	13
82	Dynamic and complex transcription factor binding during an inducible response in yeast. <i>Genes and Development</i> , <b>2009</b> , 23, 1351-63	12.6	77
81	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. <i>BMC Genomics</i> , <b>2009</b> , 10, 37	4.5	129
80	Systems biology from a yeast omics perspective. <i>FEBS Letters</i> , <b>2009</b> , 583, 3895-9	3.8	39
79	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. <i>Nature Biotechnology</i> , <b>2009</b> , 27, 66-75	44.5	463
78	Unlocking the secrets of the genome. <i>Nature</i> , <b>2009</b> , 459, 927-30	50.4	620
77	Global identification of protein kinase substrates by protein microarray analysis. <i>Nature Protocols</i> , <b>2009</b> , 4, 1820-7	18.8	37
76	RNA-Seq: a revolutionary tool for transcriptomics. <i>Nature Reviews Genetics</i> , <b>2009</b> , 10, 57-63	30.1	8302
75	MAPK target networks in <i>Arabidopsis thaliana</i> revealed using functional protein microarrays. <i>Genes and Development</i> , <b>2009</b> , 23, 80-92	12.6	370
74	Mapping accessible chromatin regions using Sono-Seq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 14926-31	11.5	163
73	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. <i>Genome Biology</i> , <b>2009</b> , 10, R23	18.3	201
72	MSB: a mean-shift-based approach for the analysis of structural variation in the genome. <i>Genome Research</i> , <b>2009</b> , 19, 106-17	9.7	29
71	Protein microarrays. <i>Methods in Molecular Biology</i> , <b>2009</b> , 548, 209-22	1.4	17
70	The transcriptional landscape of the yeast genome defined by RNA sequencing. <i>Science</i> , <b>2008</b> , 320, 1344-9	39.3	1867
69	High-quality binary protein interaction map of the yeast interactome network. <i>Science</i> , <b>2008</b> , 322, 104-10	33.3	1100

68	The development of protein microarrays and their applications in DNA-protein and protein-protein interaction analyses of Arabidopsis transcription factors. <i>Molecular Plant</i> , <b>2008</b> , 1, 27-41	14.4	70
67	High-resolution copy-number variation map reflects human olfactory receptor diversity and evolution. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000249	6	87
66	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , <b>2007</b> , 4, 651-7	21.6	1077
65	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , <b>2007</b> , 447, 799-816	50.4	4121
64	Paired-end mapping reveals extensive structural variation in the human genome. <i>Science</i> , <b>2007</b> , 318, 420-6	33.3	895
63	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> , <b>2007</b> , 104, 17494-9	11.5	230
62	Mapping of transcription factor binding regions in mammalian cells by ChIP: comparison of array- and sequencing-based technologies. <i>Genome Research</i> , <b>2007</b> , 17, 898-909	9.7	164
61	Arabidopsis protein microarrays for the high-throughput identification of protein-protein interactions. <i>Plant Signaling and Behavior</i> , <b>2007</b> , 2, 416-20	2.5	25
60	Divergence of transcription factor binding sites across related yeast species. <i>Science</i> , <b>2007</b> , 317, 815-9	33.3	286
59	Differential binding of calmodulin-related proteins to their targets revealed through high-density Arabidopsis protein microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 4730-5	11.5	299
58	New insights into <i>Acinetobacter baumannii</i> pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. <i>Genes and Development</i> , <b>2007</b> , 21, 601-14	12.6	361
57	Getting connected: analysis and principles of biological networks. <i>Genes and Development</i> , <b>2007</b> , 21, 1010-24	12.6	380
56	Proteomics for Elucidating Protein Function, Regulatory Networks and Improving Human Health. <i>FASEB Journal</i> , <b>2007</b> , 21, A211	0.9	
55	Charging it up: global analysis of protein phosphorylation. <i>Trends in Genetics</i> , <b>2006</b> , 22, 545-54	8.5	116
54	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> , <b>2006</b> , 103, 4534-9	11.5	112
53	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> , <b>2006</b> , 103, 4011-6	11.5	118
52	ProCAT: a data analysis approach for protein microarrays. <i>Genome Biology</i> , <b>2006</b> , 7, R110	18.3	43
51	Yeast as a model for human disease. <i>Current Protocols in Human Genetics</i> , <b>2006</b> , Chapter 15, Unit 15.6	3.2	27

50	Global analysis of protein phosphorylation in yeast. <i>Nature</i> , <b>2005</b> , 438, 679-84	50.4	818
49	Global analysis of protein function using protein microarrays. <i>Mechanisms of Ageing and Development</i> , <b>2005</b> , 126, 171-5	5.6	34
48	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. <i>Genes and Development</i> , <b>2005</b> , 19, 2816-26	12.6	387
47	Large-scale mutagenesis of the yeast genome using a Tn7-derived multipurpose transposon. <i>Genome Research</i> , <b>2004</b> , 14, 1975-86	9.7	43
46	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> , <b>2004</b> , 101, 16594-9	11.5	208
45	Global identification of human transcribed sequences with genome tiling arrays. <i>Science</i> , <b>2004</b> , 306, 2242-6	33.3	868
44	Regulation of gene expression by a metabolic enzyme. <i>Science</i> , <b>2004</b> , 306, 482-4	33.3	206
43	Genomics. Defining genes in the genomics era. <i>Science</i> , <b>2003</b> , 300, 258-60	33.3	89
42	Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. <i>Genes and Development</i> , <b>2003</b> , 17, 2698-708	12.6	63
41	Protein chip technology. <i>Current Opinion in Chemical Biology</i> , <b>2003</b> , 7, 55-63	9.7	792
40	Protein analysis on a proteomic scale. <i>Nature</i> , <b>2003</b> , 422, 208-15	50.4	541
39	Analyzing antibody specificity with whole proteome microarrays. <i>Nature Biotechnology</i> , <b>2003</b> , 21, 1509-12	14.5	248
38	Proteomics. <i>Annual Review of Biochemistry</i> , <b>2003</b> , 72, 783-812	29.1	295
37	A Bayesian networks approach for predicting protein-protein interactions from genomic data. <i>Science</i> , <b>2003</b> , 302, 449-53	33.3	1007
36	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , <b>2002</b> , 418, 387-91	50.4	3278
35	Complex transcriptional circuitry at the G1/S transition in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , <b>2002</b> , 16, 3017-33	12.6	201
34	ChIP-chip: a genomic approach for identifying transcription factor binding sites. <i>Methods in Enzymology</i> , <b>2002</b> , 350, 469-83	1.7	131
33	Protein arrays and microarrays. <i>Current Opinion in Chemical Biology</i> , <b>2001</b> , 5, 40-5	9.7	331

32	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , <b>2001</b> , 409, 533-8	50.4	927
31	Emerging technologies in yeast genomics. <i>Nature Reviews Genetics</i> , <b>2001</b> , 2, 302-12	30.1	82
30	Global analysis of protein activities using proteome chips. <i>Science</i> , <b>2001</b> , 293, 2101-5	33.3	1899
29	A filamentous growth response mediated by the yeast mating pathway. <i>Genetics</i> , <b>2001</b> , 159, 919-28	4	73
28	Analysis of yeast protein kinases using protein chips. <i>Nature Genetics</i> , <b>2000</b> , 26, 283-9	36.3	734
27	An integrated web interface for large-scale characterization of sequence data. <i>Functional and Integrative Genomics</i> , <b>2000</b> , 1, 70-5	3.8	1
26	The Kar3p kinesin-related protein forms a novel heterodimeric structure with its associated protein Cik1p. <i>Molecular Biology of the Cell</i> , <b>2000</b> , 11, 2373-85	3.5	48
25	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. <i>Nature</i> , <b>1999</b> , 402, 413-8	50.4	470
24	Functional characterization of the <i>S. cerevisiae</i> genome by gene deletion and parallel analysis. <i>Science</i> , <b>1999</b> , 285, 901-6	33.3	3254
23	Cell polarity and morphogenesis in budding yeast. <i>Annual Review of Microbiology</i> , <b>1998</b> , 52, 687-744	17.5	223
22	Computational Methods and Bioinformatic Tools	769-904	
21	KLF4 Recruits SWI/SNF to Increase Chromatin Accessibility and Reprogram the Endothelial Enhancer Landscape under Laminar Shear Stress		2
20	The dynamic, combinatorial cis-regulatory lexicon of epidermal differentiation		3
19	Gut microbiota analyses of Saudi populations for type 2 diabetes-related phenotypes reveals significant association		1
18	Index switching causes spreading-of-signals among multiplexed samples in Illumina HiSeq 4000 DNA sequencing		98
17	Static and dynamic DNA loops form AP-1 bound activation hubs during macrophage development		2
16	Longitudinal linked read sequencing reveals ecological and evolutionary responses of a human gut microbiome during antibiotic treatment		9
15	Early Detection Of COVID-19 Using A Smartwatch		21

14	Genome-wide Identification of the Genetic Basis of Amyotrophic Lateral Sclerosis	2
13	Classifying Non-Small Cell Lung Cancer Histopathology Types and Transcriptomic Subtypes using Convolutional Neural Networks	2
12	Cross-species blastocyst chimerism between nonhuman primates using iPSCs	3
11	iNetModels 2.0: an interactive visualization and database of multi-omics data	1
10	Atlas of transcriptionally active transposable elements in human adult tissues	3
9	A Quantitative Proteome Map of the Human Body	3
8	A genome-wide almanac of co-essential modules assigns function to uncharacterized genes	9
7	A limited set of transcriptional programs define major cell types	3
6	metID: A R package for automatable compound annotation for LCMS-based data	1
5	Integration and comparison of multi-omics profiles of NGLY1 deficiency plasma and cellular models to identify clinically relevant molecular phenotypes	1
4	Precision environmental health monitoring by longitudinal exposome and multi-omics profiling	1
3	Deep learning-based detection of COVID-19 using wearables data	8
2	Endogenous Retroviral Elements Generate Pathologic Neutrophils and Elastase Rich Exosomes in Pulmonary Arterial Hypertension	2
1	Transcriptome variation in human tissues revealed by long-read sequencing	6