Michael Paul Snyder

List of Publications by Citations

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	RNA-Seq: a revolutionary tool for transcriptomics. *Nature Reviews Genetics*, **2009**, 10, 57-63	30.1	8302
480	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
479	Functional profiling of the Saccharomyces cerevisiae genome. *Nature*, **2002**, 418, 387-91	50.4	3278
478	Functional characterization of the S. cerevisiae genome by gene deletion and parallel analysis. *Science*, **1999**, 285, 901-6	33.3	3254
477	Global analysis of protein activities using proteome chips. *Science*, **2001**, 293, 2101-5	33.3	1899
476	The transcriptional landscape of the yeast genome defined by RNA sequencing. *Science*, **2008**, 320, 1344-9	33.3	1867
475	Annotation of functional variation in personal genomes using RegulomeDB. *Genome Research*, **2012**, 22, 1790-7	9.7	1723
474	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. *Genome Research*, **2012**, 22, 1813-31	9.7	1211
473	Single-cell chromatin accessibility reveals principles of regulatory variation. *Nature*, **2015**, 523, 486-90	50.4	1110
472	Architecture of the human regulatory network derived from ENCODE data. *Nature*, **2012**, 489, 91-100	50.4	1104
471	High-quality binary protein interaction map of the yeast interactome network. *Science*, **2008**, 322, 104-10	33.3	1100
470	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. *Nature Methods*, **2007**, 4, 651-7	21.6	1077
469	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
468	A Bayesian networks approach for predicting protein-protein interactions from genomic data. *Science*, **2003**, 302, 449-53	33.3	1007
467	CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. *Genome Research*, **2011**, 21, 974-84	9.7	944
466	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. *Nature*, **2001**, 409, 533-8	50.4	927
465	Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell*, **2012**, 148, 1293-307	56.2	921

464	Paired-end mapping reveals extensive structural variation in the human genome. *Science*, **2007**, 318, 420-6	33.3	895
463	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. *Cell*, **2012**, 148, 84-98	56.2	882
462	Global identification of human transcribed sequences with genome tiling arrays. *Science*, **2004**, 306, 2242-6	33.3	868
461	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
460	Global analysis of protein phosphorylation in yeast. *Nature*, **2005**, 438, 679-84	50.4	818
459	Protein chip technology. *Current Opinion in Chemical Biology*, **2003**, 7, 55-63	9.7	792
458	Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project. *Science*, **2010**, 330, 1775-87	33.3	744
457	Analysis of yeast protein kinases using protein chips. *Nature Genetics*, **2000**, 26, 283-9	36.3	734
456	High-throughput sequencing technologies. *Molecular Cell*, **2015**, 58, 586-97	17.6	629
455	Unlocking the secrets of the genome. *Nature*, **2009**, 459, 927-30	50.4	620
454	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. *Genome Research*, **2012**, 22, 1798-812	9.7	596
453	Topologically associating domains are stable units of replication-timing regulation. *Nature*, **2014**, 515, 402-5	50.4	563
452	Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution. *Nature Genetics*, **2016**, 48, 1193-203	36.3	555
451	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. *Cell*, **2016**, 166, 755-765	56.2	544
450	Protein analysis on a proteomic scale. *Nature*, **2003**, 422, 208-15	50.4	541
449	Linking disease associations with regulatory information in the human genome. *Genome Research*, **2012**, 22, 1748-59	9.7	538
448	Defining functional DNA elements in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6131-8	11.5	490
447	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. *Nature*, **1999**, 402, 413-8	50.4	470

446   PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. *Nature Biotechnology*, **2009**, 27, 66-75   44.5   463

445   Predicting non-small cell lung cancer prognosis by fully automated microscopic pathology image features. *Nature Communications*, **2016**, 7, 12474   17.4   452

444   Variation in transcription factor binding among humans. *Science*, **2010**, 328, 232-5   33.3   447

443   Integrative omics for health and disease. *Nature Reviews Genetics*, **2018**, 19, 299-310   30.1   402

442   Performance comparison of exome DNA sequencing technologies. *Nature Biotechnology*, **2011**, 29, 908-14   44.5   397

441   A single-molecule long-read survey of the human transcriptome. *Nature Biotechnology*, **2013**, 31, 1009-14   44.5   396

440   Landscape and variation of RNA secondary structure across the human transcriptome. *Nature*, **2014**, 505, 706-9   50.4   390

439   Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. *Genes and Development*, **2005**, 19, 2816-26   12.6   387

438   Getting connected: analysis and principles of biological networks. *Genes and Development*, **2007**, 21, 1010-24   12.6   380

437   MAPK target networks in Arabidopsis thaliana revealed using functional protein microarrays. *Genes and Development*, **2009**, 23, 80-92   12.6   370

436   New insights into Acinetobacter baumannii pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. *Genes and Development*, **2007**, 21, 601-14   12.6   361

435   Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710   50.4   360

434   Clinical interpretation and implications of whole-genome sequencing. *JAMA - Journal of the American Medical Association*, **2014**, 311, 1035-45   27.4   333

433   Protein arrays and microarrays. *Current Opinion in Chemical Biology*, **2001**, 5, 40-5   9.7   331

432   How many human proteoforms are there?. *Nature Chemical Biology*, **2018**, 14, 206-214   11.7   324

431   A proposal for validation of antibodies. *Nature Methods*, **2016**, 13, 823-7   21.6   312

430   Annotating non-coding regions of the genome. *Nature Reviews Genetics*, **2010**, 11, 559-71   30.1   303

429   The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight. *Science*, **2019**, 364,   33.3   300

428	Differential binding of calmodulin-related proteins to their targets revealed through high-density Arabidopsis protein microarrays. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 4730-5	11.5	299
427	Proteomics. *Annual Review of Biochemistry*, **2003**, 72, 783-812	29.1	295
426	Divergence of transcription factor binding sites across related yeast species. *Science*, **2007**, 317, 815-9	33.3	286
425	H3K4me3 breadth is linked to cell identity and transcriptional consistency. *Cell*, **2014**, 158, 673-88	56.2	278
424	Extensive variation in chromatin states across humans. *Science*, **2013**, 342, 750-2	33.3	276
423	Variation and genetic control of protein abundance in humans. *Nature*, **2013**, 499, 79-82	50.4	272
422	Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs. *Science Signaling*, **2010**, 3, ra12	8.8	262
421	Landscape of next-generation sequencing technologies. *Analytical Chemistry*, **2011**, 83, 4327-41	7.8	253
420	Widespread contribution of transposable elements to the innovation of gene regulatory networks. *Genome Research*, **2014**, 24, 1963-76	9.7	251
419	The human proteome project: current state and future direction. *Molecular and Cellular Proteomics*, **2011**, 10, M111.009993	7.6	249
418	Analyzing antibody specificity with whole proteome microarrays. *Nature Biotechnology*, **2003**, 21, 1509-12	14.5	248
417	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. *Nature Biotechnology*, **2012**, 30, 221-3	44.5	244
416	Performance comparison of whole-genome sequencing platforms. *Nature Biotechnology*, **2011**, 30, 78-82	44.5	241
415	Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions. *Cell*, **2015**, 162, 1051-65	56.2	240
414	Comparison of the transcriptional landscapes between human and mouse tissues. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 17224-9	11.5	239
413	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. *Cell*, **2019**, 177, 1035-1049.e19	56.2	237
412	Identification of differentially expressed proteins in ovarian cancer using high-density protein microarrays. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 17494-9	11.5	230
411	AlleleSeq: analysis of allele-specific expression and binding in a network framework. *Molecular Systems Biology*, **2011**, 7, 522	12.2	228

410	Cell polarity and morphogenesis in budding yeast. *Annual Review of Microbiology*, **1998**, 52, 687-744	17.5	223
409	Non-equivalence of Wnt and R-spondin ligands during Lgr5 intestinal stem-cell self-renewal. *Nature*, **2017**, 545, 238-242	50.4	209
408	Finding new components of the target of rapamycin (TOR) signaling network through chemical genetics and proteome chips. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 16594-9	11.5	208
407	Regulation of gene expression by a metabolic enzyme. *Science*, **2004**, 306, 482-4	33.3	206
406	Digital Health: Tracking Physiomes and Activity Using Wearable Biosensors Reveals Useful Health-Related Information. *PLoS Biology*, **2017**, 15, e2001402	9.7	204
405	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. *Genome Biology*, **2009**, 10, R23	18.3	201
404	Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae. *Genes and Development*, **2002**, 16, 3017-33	12.6	201
403	Longitudinal multi-omics of host-microbe dynamics in prediabetes. *Nature*, **2019**, 569, 663-671	50.4	197
402	Genome-wide map of regulatory interactions in the human genome. *Genome Research*, **2014**, 24, 1905-17	9.7	197
401	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. *Genome Biology*, **2012**, 13, R48	18.3	194
400	Principles of regulatory information conservation between mouse and human. *Nature*, **2014**, 515, 371-375	50.4	190
399	Recurrent somatic mutations in regulatory regions of human cancer genomes. *Nature Genetics*, **2015**, 47, 710-6	36.3	190
398	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. *Cell Metabolism*, **2018**, 27, 559-571.e5	24.6	189
397	Promise of personalized omics to precision medicine. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **2013**, 5, 73-82	6.6	188
396	Genomic analysis of mycosis fungoides and Sézary syndrome identifies recurrent alterations in TNFR2. *Nature Genetics*, **2015**, 47, 1056-60	36.3	186
395	High-throughput sequencing for biology and medicine. *Molecular Systems Biology*, **2013**, 9, 640	12.2	186
394	A longitudinal big data approach for precision health. *Nature Medicine*, **2019**, 25, 792-804	50.5	183
393	Wearables and the medical revolution. *Personalized Medicine*, **2018**, 15, 429-448	2.2	180

392	Novel mutations in PIEZO1 cause an autosomal recessive generalized lymphatic dysplasia with non-immune hydrops fetalis. *Nature Communications*, **2015**, 6, 8085	17.4	174
391	Defining a personal, allele-specific, and single-molecule long-read transcriptome. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 9869-74	11.5	168
390	Mapping of transcription factor binding regions in mammalian cells by ChIP: comparison of array- and sequencing-based technologies. *Genome Research*, **2007**, 17, 898-909	9.7	164
389	Mapping accessible chromatin regions using Sono-Seq. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 14926-31	11.5	163
388	Diverse roles and interactions of the SWI/SNF chromatin remodeling complex revealed using global approaches. *PLoS Genetics*, **2011**, 7, e1002008	6	162
387	Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analyses. *Cell*, **2010**, 143, 639-50	56.2	162
386	Macrophage de novo NAD synthesis specifies immune function in aging and inflammation. *Nature Immunology*, **2019**, 20, 50-63	19.1	160
385	Genomic binding profiles of functionally distinct RNA polymerase III transcription complexes in human cells. *Nature Structural and Molecular Biology*, **2010**, 17, 635-40	17.6	159
384	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. *Nature Genetics*, **2017**, 49, 1522-1528	36.3	158
383	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E440-9	11.5	149
382	Genome-scale measurement of off-target activity using Cas9 toxicity in high-throughput screens. *Nature Communications*, **2017**, 8, 15178	17.4	148
381	Whole-genome haplotyping using long reads and statistical methods. *Nature Biotechnology*, **2014**, 32, 261-266	44.5	146
380	Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. *Nature Biotechnology*, **2014**, 32, 562-8	44.5	146
379	Close association of RNA polymerase II and many transcription factors with Pol III genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 3639-44	11.5	143
378	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 5254-9	11.5	142
377	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. *Cell*, **2020**, 181, 236-249	56.2	140
376	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. *Molecular and Cellular Proteomics*, **2015**, 14, 1684-95	7.6	138
375	Mutations in NGLY1 cause an inherited disorder of the endoplasmic reticulum-associated degradation pathway. *Genetics in Medicine*, **2014**, 16, 751-8	8.1	138

374	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. *Molecular Cell*, **2017**, 67, 1037-1048.e6	17.6	138
373	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. *Nature Biotechnology*, **2010**, 28, 47-55	44.5	136
372	Comparative analysis of regulatory information and circuits across distant species. *Nature*, **2014**, 512, 453-6	50.4	135
371	Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events. *Nature Biotechnology*, **2015**, 33, 736-42	44.5	134
370	Genome-wide identification of binding sites defines distinct functions for Caenorhabditis elegans PHA-4/FOXA in development and environmental response. *PLoS Genetics*, **2010**, 6, e1000848	6	132
369	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
368	ChIP-chip: a genomic approach for identifying transcription factor binding sites. *Methods in Enzymology*, **2002**, 350, 469-83	1.7	131
367	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. *Nature Communications*, **2017**, 8, 59	17.4	130
366	Genetic analysis of variation in transcription factor binding in yeast. *Nature*, **2010**, 464, 1187-91	50.4	130
365	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. *Genome Research*, **2012**, 22, 1735-47	9.7	129
364	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. *BMC Genomics*, **2009**, 10, 37	4.5	129
363	Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures. *Bioinformatics*, **2014**, 30, 2808-10	7.2	122
362	Molecular mechanisms of ethanol-induced pathogenesis revealed by RNA-sequencing. *PLoS Pathogens*, **2010**, 6, e1000834	7.6	122
361	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. *Cell*, **2016**, 167, 1734-1749.e22	56.2	122
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359	Severe acute respiratory syndrome diagnostics using a coronavirus protein microarray. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 4011-6	11.5	118
358	Patient-Specific iPSC-Derived Endothelial Cells Uncover Pathways that Protect against Pulmonary Hypertension in BMPR2 Mutation Carriers. *Cell Stem Cell*, **2017**, 20, 490-504.e5	18	117
357	Charging it up: global analysis of protein phosphorylation. *Trends in Genetics*, **2006**, 22, 545-54	8.5	116

356	Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. *Genome Research*, **2015**, 25, 1610-21	9.7	115
355	Pre-symptomatic detection of COVID-19 from smartwatch data. *Nature Biomedical Engineering*, **2020**, 4, 1208-1220	19	115
354	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. *Cell Systems*, **2018**, 6, 157-170.e8	10.68	114
353	Phased whole-genome genetic risk in a family quartet using a major allele reference sequence. *PLoS Genetics*, **2011**, 7, e1002280	6	112
352	High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 4534-9	11.5	112
351	Whole-exome sequencing identifies tetratricopeptide repeat domain 7A (TTC7A) mutations for combined immunodeficiency with intestinal atresias. *Journal of Allergy and Clinical Immunology*, **2013**, 132, 656-664.e17	11.5	109
350	Dynamic trans-acting factor colocalization in human cells. *Cell*, **2013**, 155, 713-24	56.2	109
349	Gpr124 is essential for blood-brain barrier integrity in central nervous system disease. *Nature Medicine*, **2017**, 23, 450-460	50.5	108
348	Circular DNA elements of chromosomal origin are common in healthy human somatic tissue. *Nature Communications*, **2018**, 9, 1069	17.4	108
347	Physiological blood-brain transport is impaired with age by a shift in transcytosis. *Nature*, **2020**, 583, 425-430	50.4	107
346	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. *Cell Metabolism*, **2016**, 24, 172-84	24.6	105
345	Transcriptome Profiling of Patient-Specific Human iPSC-Cardiomyocytes Predicts Individual Drug Safety and Efficacy Responses In Vitro. *Cell Stem Cell*, **2016**, 19, 311-25	18	103
344	iPSC-derived cardiomyocytes reveal abnormal TGF-β signalling in left ventricular non-compaction cardiomyopathy. *Nature Cell Biology*, **2016**, 18, 1031-42	23.4	103
343	Personal genome sequencing: current approaches and challenges. *Genes and Development*, **2010**, 24, 423-31	12.6	103
342	Personal aging markers and ageotypes revealed by deep longitudinal profiling. *Nature Medicine*, **2020**, 26, 83-90	50.5	102
341	Index switching causes "spreading-of-signal" among multiplexed samples in Illumina HiSeq 4000 DNA sequencing		98
340	Molecular Choreography of Acute Exercise. *Cell*, **2020**, 181, 1112-1130.e16	56.2	96
339	Glucotypes reveal new patterns of glucose dysregulation. *PLoS Biology*, **2018**, 16, e2005143	9.7	95

338	Mango: a bias-correcting ChIA-PET analysis pipeline. *Bioinformatics*, **2015**, 31, 3092-8	7.2	91
337	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. *Cell*, **2019**, 178, 1245-1259.e14	56.2	91
336	Detecting and annotating genetic variations using the HugeSeq pipeline. *Nature Biotechnology*, **2012**, 30, 226-9	44.5	90
335	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. *Molecular Systems Biology*, **2014**, 10, 774	12.2	89
334	Genomics. Defining genes in the genomics era. *Science*, **2003**, 300, 258-60	33.3	89
333	High-resolution copy-number variation map reflects human olfactory receptor diversity and evolution. *PLoS Genetics*, **2008**, 4, e1000249	6	87
332	Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. *Cell*, **2018**, 175, 277-291.e31	56.2	86
331	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. *Nature*, **2019**, 574, 553-558	50.4	84
330	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. *Nature Methods*, **2021**, 18, 747-756	21.6	83
329	Emerging technologies in yeast genomics. *Nature Reviews Genetics*, **2001**, 2, 302-12	30.1	82
328	Regulatory analysis of the C. elegans genome with spatiotemporal resolution. *Nature*, **2014**, 512, 400-5	50.4	81
327	Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression. *Nature Communications*, **2017**, 8, 14995	17.4	80
326	Overview of high throughput sequencing technologies to elucidate molecular pathways in cardiovascular diseases. *Circulation Research*, **2013**, 112, 1613-23	15.7	77
325	Dynamic and complex transcription factor binding during an inducible response in yeast. *Genes and Development*, **2009**, 23, 1351-63	12.6	77
324	Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome. *Nature Biotechnology*, **2016**, 34, 64-9	44.5	75
323	Systematic functional regulatory assessment of disease-associated variants. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 9607-12	11.5	75
322	A global transcriptional network connecting noncoding mutations to changes in tumor gene expression. *Nature Genetics*, **2018**, 50, 613-620	36.3	74
321	A filamentous growth response mediated by the yeast mating pathway. *Genetics*, **2001**, 159, 919-28	4	73

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319	Network analyses identify liver-specific targets for treating liver diseases. *Molecular Systems Biology*, **2017**, 13, 938	12.2	71
318	Systems biology: personalized medicine for the future?. *Current Opinion in Pharmacology*, **2012**, 12, 623-8	5.1	71
317	Global analysis of the glycoproteome in Saccharomyces cerevisiae reveals new roles for protein glycosylation in eukaryotes. *Molecular Systems Biology*, **2009**, 5, 308	12.2	71
316	Tcf7 is an important regulator of the switch of self-renewal and differentiation in a multipotential hematopoietic cell line. *PLoS Genetics*, **2012**, 8, e1002565	6	71
315	The development of protein microarrays and their applications in DNA-protein and protein-protein interaction analyses of Arabidopsis transcription factors. *Molecular Plant*, **2008**, 1, 27-41	14.4	70
314	NIH working group report-using genomic information to guide weight management: From universal to precision treatment. *Obesity*, **2016**, 24, 14-22	8	70
313	Genome-Wide Temporal Profiling of Transcriptome and Open Chromatin of Early Cardiomyocyte Differentiation Derived From hiPSCs and hESCs. *Circulation Research*, **2017**, 121, 376-391	15.7	69
312	Identification of phagocytosis regulators using magnetic genome-wide CRISPR screens. *Nature Genetics*, **2018**, 50, 1716-1727	36.3	67
311	Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. *Genes and Development*, **2003**, 17, 2698-708	12.6	63
310	Omics Profiling in Precision Oncology. *Molecular and Cellular Proteomics*, **2016**, 15, 2525-36	7.6	63
309	ChIA-PET2: a versatile and flexible pipeline for ChIA-PET data analysis. *Nucleic Acids Research*, **2017**, 45, e4	20.1	61
308	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
307	Identification of significantly mutated regions across cancer types highlights a rich landscape of functional molecular alterations. *Nature Genetics*, **2016**, 48, 117-25	36.3	60
306	Matrix stiffness induces a tumorigenic phenotype in mammary epithelium through changes in chromatin accessibility. *Nature Biomedical Engineering*, **2019**, 3, 1009-1019	19	60
305	A high-stringency blueprint of the human proteome. *Nature Communications*, **2020**, 11, 5301	17.4	59
304	Windows Into Human Health Through Wearables Data Analytics. *Current Opinion in Biomedical Engineering*, **2019**, 9, 28-46	4.4	58
303	Association of Omics Features with Histopathology Patterns in Lung Adenocarcinoma. *Cell Systems*, **2017**, 5, 620-627.e3	10.6	57

302	RNA Sequencing Analysis Detection of a Novel Pathway of Endothelial Dysfunction in Pulmonary Arterial Hypertension. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 356-66	10.2	57
301	iPOP goes the world: integrated personalized Omics profiling and the road toward improved health care. *Chemistry and Biology*, **2013**, 20, 660-6		57
300	Multiomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. *Bioinformatics*, **2019**, 35, 95-103	7.2	54
299	Pharmacological rescue of diabetic skeletal stem cell niches. *Science Translational Medicine*, **2017**, 9,	17.5	53
298	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. *PLoS ONE*, **2016**, 11, e0162868	3.7	53
297	Induced Pluripotent Stem Cell Model of Pulmonary Arterial Hypertension Reveals Novel Gene Expression and Patient Specificity. *American Journal of Respiratory and Critical Care Medicine*, **2017**, 195, 930-941	10.2	52
296	Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. *Frontiers in Microbiology*, **2017**, 8, 1079	5.7	52
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292	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. *Genes and Development*, **2011**, 25, 767-78	12.6	51
291	Genome-wide mapping of copy number variation in humans: comparative analysis of high resolution array platforms. *PLoS ONE*, **2011**, 6, e27859	3.7	51
290	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. *Nature Communications*, **2019**, 10, 4063	17.4	49
289	Identification of STAT5A and STAT5B target genes in human T cells. *PLoS ONE*, **2014**, 9, e86790	3.7	49
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283	Molecular and functional resemblance of differentiated cells derived from isogenic human iPSCs and SCNT-derived ESCs. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E11111-E11120	11.5	47
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