

Nathan D Price

List of Publications by Year in descending order

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Version: 2024-02-01

222
papers

19,205
citations

20036

63
h-index

17891

125
g-index

259
all docs

259
docs citations

259
times ranked

29067
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated analysis of plasma and single immune cells uncovers metabolic changes in individuals with COVID-19. <i>Nature Biotechnology</i> , 2022, 40, 110-120.	9.4	81
2	Alzheimer's disease and progressive supranuclear palsy share similar transcriptomic changes in distinct brain regions. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	13
3	Multiple early factors anticipate post-acute COVID-19 sequelae. <i>Cell</i> , 2022, 185, 881-895.e20.	13.5	605
4	The effect of maternal SARS-CoV-2 infection timing on birth outcomes: a retrospective multicentre cohort study. <i>The Lancet Digital Health</i> , 2022, 4, e95-e104.	5.9	81
5	Distribution of 54 polygenic risk scores for common diseases in long lived individuals and their offspring. <i>GeroScience</i> , 2022, 44, 719-729.	2.1	3
6	Personal Dense Dynamic Data Clouds Connect Systems Biomedicine to Scientific Wellness. <i>Methods in Molecular Biology</i> , 2022, 2486, 315-334.	0.4	1
7	Manifestations of Alzheimer's disease genetic risk in the blood are evident in a multiomic analysis in healthy adults aged 18 to 90. <i>Scientific Reports</i> , 2022, 12, 6117.	1.6	12
8	Risk factors for severe COVID-19 differ by age for hospitalized adults. <i>Scientific Reports</i> , 2022, 12, 6568.	1.6	23
9	Heterogeneity in statin responses explained by variation in the human gut microbiome. <i>Med</i> , 2022, 3, 388-405.e6.	2.2	21
10	A systems biology clinical trial of a personalized multimodal lifestyle intervention for early Alzheimer's disease. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2021, 7, e12191.	1.8	10
11	From taxonomy to metabolic output: what factors define gut microbiome health?. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	19
12	Integrative functional genomic analysis of intron retention in human and mouse brain with Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2021, 17, 984-1004.	0.4	25
13	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. <i>Nature Metabolism</i> , 2021, 3, 274-286.	5.1	278
14	iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W271-W276.	6.5	25
15	Modulating innate immune activation states impacts the efficacy of specific A β immunotherapy. <i>Molecular Neurodegeneration</i> , 2021, 16, 32.	4.4	4
16	The geometry of clinical labs and wellness states from deeply phenotyped humans. <i>Nature Communications</i> , 2021, 12, 3578.	5.8	19
17	A Comprehensive Assessment of Associations between Prenatal Phthalate Exposure and the Placental Transcriptomic Landscape. <i>Environmental Health Perspectives</i> , 2021, 129, 97003.	2.8	20
18	Baseline Gut Metagenomic Functional Gene Signature Associated with Variable Weight Loss Responses following a Healthy Lifestyle Intervention in Humans. <i>MSystems</i> , 2021, 6, e0096421.	1.7	19

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19	Systems modeling of metabolic dysregulation in neurodegenerative diseases. <i>Current Opinion in Pharmacology</i> , 2021, 60, 59-65.	1.7	5
20	Identifying Personalized Metabolic Signatures in Breast Cancer. <i>Metabolites</i> , 2021, 11, 20.	1.3	7
21	Towards early risk biomarkers: serum metabolic signature in childhood predicts cardio-metabolic risk in adulthood. <i>EBioMedicine</i> , 2021, 72, 103611.	2.7	14
22	Conserved architecture of brain transcriptome changes between Alzheimer's disease and progressive supranuclear palsy in pathologically affected and unaffected regions.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e054424.	0.4	0
23	Investigating the importance of acylcarnitines in Alzheimer's disease.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e056647.	0.4	1
24	Case Study: A Precision Medicine Approach to Multifactorial Dementia and Alzheimer's Disease.. , 2021, 11, .		0
25	A systems approach to clinical oncology uses deep phenotyping to deliver personalized care. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 183-194.	12.5	41
26	Multi-omic biomarker identification and validation for diagnosing warzone-related post-traumatic stress disorder. <i>Molecular Psychiatry</i> , 2020, 25, 3337-3349.	4.1	68
27	Measurement of Organ-Specific and Acute-Phase Blood Protein Levels in Early Lyme Disease. <i>Journal of Proteome Research</i> , 2020, 19, 346-359.	1.8	14
28	Health and disease markers correlate with gut microbiome composition across thousands of people. <i>Nature Communications</i> , 2020, 11, 5206.	5.8	378
29	Atlas of Transcription Factor Binding Sites from ENCODE DNase Hypersensitivity Data across 27 Tissue Types. <i>Cell Reports</i> , 2020, 32, 108029.	2.9	28
30	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	2.4	75
31	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020, 32, 107908.	2.9	199
32	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Metabolism in Alzheimer's Disease. <i>Cell Reports Medicine</i> , 2020, 1, 100138.	3.3	102
33	Multi-Omics Resolves a Sharp Disease-State Shift between Mild and Moderate COVID-19. <i>Cell</i> , 2020, 183, 1479-1495.e20.	13.5	449
34	Multiomic blood correlates of genetic risk identify presymptomatic disease alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21813-21820.	3.3	22
35	Longitudinal analysis reveals transition barriers between dominant ecological states in the gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13839-13845.	3.3	47
36	Advancing human health in the decade ahead: pregnancy as a key window for discovery. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 223, 312-321.	0.7	13

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37	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	2.4	59
38	iREAD: a tool for intron retention detection from RNA-seq data. <i>BMC Genomics</i> , 2020, 21, 128.	1.2	35
39	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
40	Core transcriptional regulatory circuits in prion diseases. <i>Molecular Brain</i> , 2020, 13, 10.	1.3	7
41	Deep phenotyping during pregnancy for predictive and preventive medicine. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	21
42	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. <i>Molecular Cell</i> , 2020, 78, 960-974.e11.	4.5	83
43	Untargeted longitudinal analysis of a wellness cohort identifies markers of metastatic cancer years prior to diagnosis. <i>Scientific Reports</i> , 2020, 10, 16275.	1.6	12
44	Genome-scale metabolic model of the rat liver predicts effects of diet restriction. <i>Scientific Reports</i> , 2019, 9, 9807.	1.6	10
45	MicroRNAâ€transcriptome networks in whole blood and monocytes of women undergoing preterm labour. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 6835-6845.	1.6	17
46	Multi-Omic Biological Age Estimation and Its Correlation With Wellness and Disease Phenotypes: A Longitudinal Study of 3,558 Individuals. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, S52-S60.	1.7	56
47	Blood metabolome predicts gut microbiome α -diversity in humans. <i>Nature Biotechnology</i> , 2019, 37, 1217-1228.	9.4	213
48	Genetic Predisposition Impacts Clinical Changes in a Lifestyle Coaching Program. <i>Scientific Reports</i> , 2019, 9, 6805.	1.6	48
49	Single-Cell Proteomics Reveal that Quantitative Changes in Co-expressed Lineage-Specific Transcription Factors Determine Cell Fate. <i>Cell Stem Cell</i> , 2019, 24, 812-820.e5.	5.2	99
50	OptRAM: In-silico strain design via integrative regulatory-metabolic network modeling. <i>PLoS Computational Biology</i> , 2019, 15, e1006835.	1.5	41
51	Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. <i>Cell Systems</i> , 2019, 8, 122-135.e7.	2.9	45
52	Reproducible big data science: A case study in continuous FAIRness. <i>PLoS ONE</i> , 2019, 14, e0213013.	1.1	29
53	THE PROTEOMICS OF LONGEVITY. <i>Innovation in Aging</i> , 2019, 3, S209-S209.	0.0	0
54	MULTI-OMIC BIOLOGICAL AGE ESTIMATION, CORRELATION WITH WELLNESS, DISEASE PHENOTYPES: LONGITUDINAL SAMPLE OF 3558. <i>Innovation in Aging</i> , 2019, 3, S209-S209.	0.0	0

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55	Digitizing omics profiles by divergence from a baseline. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4545-4552.	3.3	23
56	The building blocks of successful translation of proteomics to the clinic. Current Opinion in Biotechnology, 2018, 51, 123-129.	3.3	32
57	Comparative transcriptomic analysis of human placentae at term and preterm delivery. Biology of Reproduction, 2018, 98, 89-101.	1.2	23
58	Comparative analysis of gene expression in maternal peripheral blood and monocytes during spontaneous preterm labor. American Journal of Obstetrics and Gynecology, 2018, 218, 345.e1-345.e30.	0.7	47
59	ProbAnnoWeb and ProbAnnoPy: probabilistic annotation and gap-filling of metabolic reconstructions. Bioinformatics, 2018, 34, 1594-1596.	1.8	9
60	Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. Molecular Systems Biology, 2018, 14, e7435.	3.2	55
61	Taking Systems Medicine to Heart. Circulation Research, 2018, 122, 1276-1289.	2.0	32
62	Reply. American Journal of Obstetrics and Gynecology, 2018, 219, 123-124.	0.7	0
63	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. Alzheimer's and Dementia, 2018, 14, 352-366.	0.4	116
64	O3a€O3a€01: MECHANISTIC AND DIRECTIONAL TRANSCRIPTIONAL REGULATORY NETWORKS IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P1014.	0.4	0
65	P2a€123: A PHENOMEa€WIDE ASSOCIATION STUDY (PHEWAS) OF BLOODa€BASED BIOLOGICAL MARKERS AND APOLIPOPROTEIN E GENOTYPE ACROSS THE ADULT LIFESPAN. Alzheimer's and Dementia, 2018, 14, P716.	0.4	0
66	Multiscale Analysis of Independent Alzheimer's Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. Neuron, 2018, 99, 64-82.e7.	3.8	558
67	Distinct communication patterns of trophoblastic miRNA among the maternal-placental-fetal compartments. Placenta, 2018, 72-73, 28-35.	0.7	24
68	Motor neuron loss and neuroinflammation in a model of Î±-synuclein-induced neurodegeneration. Neurobiology of Disease, 2018, 120, 98-106.	2.1	32
69	TLR5 decoy receptor as a novel anti-amyloid therapeutic for Alzheimer's disease. Journal of Experimental Medicine, 2018, 215, 2247-2264.	4.2	50
70	Temporal transcriptomic analysis of metabolic genes in maternal organs and placenta during murine pregnancy. Biology of Reproduction, 2018, 99, 1255-1265.	1.2	9
71	Reply to "Precision medicine in the clouds". Nature Biotechnology, 2018, 36, 680-682.	9.4	2
72	Targeting <sc>TWIST</sc>1 through loss of function inhibits tumorigenicity of human glioblastoma. Molecular Oncology, 2018, 12, 1188-1202.	2.1	25

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73	Genome-wide pleiotropy analysis of neuropathological traits related to Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2018, 10, 22.	3.0	27
74	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. <i>Acta Neuropathologica</i> , 2018, 136, 709-727.	3.9	47
75	Editorial overview: Systems biology: Data, discovery, delivery. <i>Current Opinion in Biotechnology</i> , 2018, 51, vii-viii.	3.3	0
76	IFPA meeting 2016 workshop report I: Genomic communication, bioinformatics, trophoblast biology and transport systems. <i>Placenta</i> , 2017, 60, S5-S9.	0.7	2
77	MicroRNAs and lipid metabolism. <i>Current Opinion in Lipidology</i> , 2017, 28, 273-280.	1.2	156
78	Motivational, proteostatic and transcriptional deficits precede synapse loss, gliosis and neurodegeneration in the B6.HttQ111/+ model of Huntington's disease. <i>Scientific Reports</i> , 2017, 7, 41570.	1.6	16
79	A Precision Medicine Approach to Improve Cancer Rehabilitation's Impact and Integration with Cancer Care and Optimize Patient Wellness. <i>Current Physical Medicine and Rehabilitation Reports</i> , 2017, 5, 64-73.	0.3	24
80	High resolution time-course mapping of early transcriptomic, molecular and cellular phenotypes in Huntington's disease CAG knock-in mice across multiple genetic backgrounds. <i>Human Molecular Genetics</i> , 2017, 26, 913-922.	1.4	37
81	A Cell-Surface Membrane Protein Signature for Glioblastoma. <i>Cell Systems</i> , 2017, 4, 516-529.e7.	2.9	37
82	A candidate regulatory variant at the <i>TREM</i> gene cluster associates with decreased Alzheimer's disease risk and increased <i>TREML1</i> and <i>TREM2</i> brain gene expression. <i>Alzheimer's and Dementia</i> , 2017, 13, 663-673.	0.4	48
83	Rare coding variants in <i>PLCG2</i> , <i>ABI3</i> , and <i>TREM2</i> implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017, 49, 1373-1384.	9.4	783
84	Genomic, Transcriptional, and Phenotypic Analysis of the Glucose Derepressed <i>Clostridium beijerinckii</i> Mutant Exhibiting Acid Crash Phenotype. <i>Biotechnology Journal</i> , 2017, 12, 1700182.	1.8	14
85	A wellness study of 108 individuals using personal, dense, dynamic data clouds. <i>Nature Biotechnology</i> , 2017, 35, 747-756.	9.4	340
86	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. <i>Progress in Preventive Medicine (New York, N Y)</i> , 2017, 2, e006.	0.7	6
87	The P4 Health Spectrum – A Predictive, Preventive, Personalized and Participatory Continuum for Promoting Healthspan. <i>Progress in Cardiovascular Diseases</i> , 2017, 59, 506-521.	1.6	178
88	Enhanced retinal responses in Huntington's disease patients. <i>Journal of Huntington's Disease</i> , 2017, 6, 237-247.	0.9	11
89	Crops In Silico: Generating Virtual Crops Using an Integrative and Multi-scale Modeling Platform. <i>Frontiers in Plant Science</i> , 2017, 8, 786.	1.7	102
90	Ion channel expression patterns in glioblastoma stem cells with functional and therapeutic implications for malignancy. <i>PLoS ONE</i> , 2017, 12, e0172884.	1.1	37

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91	Network reconstruction and systems analysis of plant cell wall deconstruction by <i>Neurospora crassa</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 225.	6.2	42
92	Linkage, whole genome sequence, and biological data implicate variants in RAB10 in Alzheimer's disease resilience. <i>Genome Medicine</i> , 2017, 9, 100.	3.6	67
93	The P4 Health Spectrum – A Predictive, Preventive, Personalized and Participatory Continuum for Promoting Healthspan. <i>Progress in Preventive Medicine (New York, N Y)</i> , 2017, 2, e0002.	0.7	10
94	Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005489.	1.5	46
95	Peripheral huntingtin silencing does not ameliorate central signs of disease in the B6.HttQ111/+ mouse model of Huntington's disease. <i>PLoS ONE</i> , 2017, 12, e0175968.	1.1	13
96	Patterns of biomarkers for three phenotype profiles of persisting specific learning disabilities during middle childhood and early adolescence: A preliminary study. , 2017, 1, .		2
97	B18...Transcriptome profiling of B6.HttQ111/+ hepatocytes in response to chemical perturbagens. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2016, 87, A15.2-A15.	0.9	0
98	Predictive Big Data Analytics: A Study of Parkinson's Disease Using Large, Complex, Heterogeneous, Incongruent, Multi-Source and Incomplete Observations. <i>PLoS ONE</i> , 2016, 11, e0157077.	1.1	94
99	Human whole genome genotype and transcriptome data for Alzheimer's and other neurodegenerative diseases. <i>Scientific Data</i> , 2016, 3, 160089.	2.4	361
100	I'll take that to go: Big data bags and minimal identifiers for exchange of large, complex datasets. , 2016, , .		33
101	P4027: Combing Evidence Across Multiple Cohorts for Systems-Based Target Discovery: the AMPAD Knowledge Portal. <i>Alzheimer's and Dementia</i> , 2016, 12, P1025.	0.4	0
102	P4031: Integrative Network Analysis of Multiple Alzheimer's Disease Rnaseq Studies From the Accelerating Medicine Partnership – Alzheimer's Disease Consortium. <i>Alzheimer's and Dementia</i> , 2016, 12, P1026.	0.4	1
103	F2-01-04: From Systems Level Transcriptomics to new Immune Targets for Alzheimer's Disease. , 2016, 12, P215-P216.		0
104	O21004: A Regulatory Variant at the <i>TREM</i> Gene Cluster Associates with Decreased Alzheimer's Disease Risk and Increased <i>TREML1</i> and <i>TREM2</i> Brain Gene Expression. <i>Alzheimer's and Dementia</i> , 2016, 12, P251.	0.4	0
105	Exploring Hydrogenotrophic Methanogenesis: a Genome Scale Metabolic Reconstruction of <i>Methanococcus marisaludis</i> . <i>Journal of Bacteriology</i> , 2016, 198, 3379-3390.	1.0	48
106	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. <i>Acta Neuropathologica</i> , 2016, 132, 197-211.	3.9	49
107	Personalized nutrition through big data. <i>Nature Biotechnology</i> , 2016, 34, 152-154.	9.4	18
108	Relative stability of network states in Boolean network models of gene regulation in development. <i>BioSystems</i> , 2016, 142-143, 15-24.	0.9	45

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109	Emerging Proteomic Technologies Provide Enormous and Underutilized Potential for Brain Cancer Research. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 362-367.	2.5	5
110	O1-11-03: Modulating chemokine signaling in preclinical Alzheimer's disease models. , 2015, 11, P157-P157.		0
111	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	3.2	68
112	A refined genome-scale reconstruction of <i>Chlamydomonas</i> metabolism provides a platform for systems-level analyses. <i>Plant Journal</i> , 2015, 84, 1239-1256.	2.8	70
113	Data-driven integration of genome-scale regulatory and metabolic network models. <i>Frontiers in Microbiology</i> , 2015, 6, 409.	1.5	49
114	Comparative Analysis of Yeast Metabolic Network Models Highlights Progress, Opportunities for Metabolic Reconstruction. <i>PLoS Computational Biology</i> , 2015, 11, e1004530.	1.5	70
115	A comprehensive map of genome-wide gene regulation in <i>Mycobacterium tuberculosis</i> . <i>Scientific Data</i> , 2015, 2, 150010.	2.4	55
116	Fostering synergy between cell biology and systems biology. <i>Trends in Cell Biology</i> , 2015, 25, 440-445.	3.6	2
117	Isoforms of RNA-Editing Enzyme ADAR1 Independently Control Nucleic Acid Sensor MDA5-Driven Autoimmunity and Multi-organ Development. <i>Immunity</i> , 2015, 43, 933-944.	6.6	373
118	Transcriptional program for nitrogen starvation-induced lipid accumulation in <i>Chlamydomonas reinhardtii</i> . <i>Biotechnology for Biofuels</i> , 2015, 8, 207.	6.2	60
119	SNAPR: A Bioinformatics Pipeline for Efficient and Accurate RNA-Seq Alignment and Analysis. <i>IEEE Life Sciences Letters</i> , 2015, 1, 22-25.	1.2	15
120	IL-10 Alters Immunoproteostasis in APP Mice, Increasing Plaque Burden and Worsening Cognitive Behavior. <i>Neuron</i> , 2015, 85, 519-533.	3.8	292
121	Genome-scale modeling for metabolic engineering. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 327-338.	1.4	82
122	The DNA-binding network of <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, 5829.	5.8	192
123	Transparency in metabolic network reconstruction enables scalable biological discovery. <i>Current Opinion in Biotechnology</i> , 2015, 34, 105-109.	3.3	20
124	Integrating big data and actionable health coaching to optimize wellness. <i>BMC Medicine</i> , 2015, 13, 4.	2.3	66
125	Big biomedical data as the key resource for discovery science. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1126-1131.	2.2	70
126	Rare variants in neuronal excitability genes influence risk for bipolar disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3576-3581.	3.3	152

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127	An argument for mechanism-based statistical inference in cancer. <i>Human Genetics</i> , 2015, 134, 479-495.	1.8	9
128	Integrated Modeling of Gene Regulatory and Metabolic Networks in <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2015, 11, e1004543.	1.5	64
129	Serum from calorie-restricted animals delays senescence and extends the lifespan of normal human fibroblasts in vitro. <i>Aging</i> , 2015, 7, 152-166.	1.4	20
130	MediaDB: A Database of Microbial Growth Conditions in Defined Media. <i>PLoS ONE</i> , 2014, 9, e103548.	1.1	28
131	Likelihood-Based Gene Annotations for Gap Filling and Quality Assessment in Genome-Scale Metabolic Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003882.	1.5	66
132	Promoting Wellness & Demystifying Disease: The 100K Project. <i>Clinical OMICs</i> , 2014, 1, 20-23.	0.1	20
133	<i>Halomonas sulfidaeris</i> -dominated microbial community inhabits a 1.8-km-deep subsurface Cambrian sandstone reservoir. <i>Environmental Microbiology</i> , 2014, 16, 1695-1708.	1.8	52
134	Mapping and manipulating the <i>Mycobacterium tuberculosis</i> transcriptome using a transcription factor overexpression-derived regulatory network. <i>Genome Biology</i> , 2014, 15, 502.	3.8	136
135	Demystifying Disease, Democratizing Health Care. <i>Science Translational Medicine</i> , 2014, 6, 225ed5.	5.8	67
136	ITEP: An integrated toolkit for exploration of microbial pan-genomes. <i>BMC Genomics</i> , 2014, 15, 8.	1.2	123
137	Systems Approach to Neurodegenerative Disease Biomarker Discovery. <i>Annual Review of Pharmacology and Toxicology</i> , 2014, 54, 457-481.	4.2	45
138	Systems pharmacology modeling: an approach to improving drug safety. <i>Biopharmaceutics and Drug Disposition</i> , 2014, 35, 1-14.	1.1	24
139	Quantitative Proteomic Analysis Reveals Effects of Epidermal Growth Factor Receptor (EGFR) on Invasion-promoting Proteins Secreted by Glioblastoma Cells. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2618-2631.	2.5	29
140	Detection of 1 α ,25-Dihydroxyvitamin D-Regulated miRNAs in Zebrafish by Whole Transcriptome Sequencing. <i>Zebrafish</i> , 2014, 11, 207-218.	0.5	14
141	Measuring the Effect of Inter-Study Variability on Estimating Prediction Error. <i>PLoS ONE</i> , 2014, 9, e110840.	1.1	19
142	AUREA: an open-source software system for accurate and user-friendly identification of relative expression molecular signatures. <i>BMC Bioinformatics</i> , 2013, 14, 78.	1.2	7
143	Genome-Scale Models for Microbial Factories. <i>Industrial Biotechnology</i> , 2013, 9, 177-178.	0.5	1
144	Development of a Gene Knockout System Using Mobile Group II Introns (Targetron) and Genetic Disruption of Acid Production Pathways in <i>Clostridium beijerinckii</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 5853-5863.	1.4	54

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145	A Blood-Based Proteomic Classifier for the Molecular Characterization of Pulmonary Nodules. <i>Science Translational Medicine</i> , 2013, 5, 207ra142.	5.8	165
146	<i>Systems Biology and Systems Medicine</i> . , 2013, , 60-72.		2
147	<i>Systems Medicine and the Emergence of Proactive P4 Medicine</i> . , 2013, , 445-467.		2
148	Genomically and biochemically accurate metabolic reconstruction of <i>Methanosarcina barkeri</i> Fusaro, iMG746. <i>Biotechnology Journal</i> , 2013, 8, 1070-1079.	1.8	41
149	A Guide to Integrating Transcriptional Regulatory and Metabolic Networks Using PROM (Probabilistic) Tj ETQq1 1 0,784314 rgBT /Overl	0.4	13
150	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	9.4	920
151	P4 medicine: how systems medicine will transform the healthcare sector and society. <i>Personalized Medicine</i> , 2013, 10, 565-576.	0.8	422
152	Multi-study Integration of Brain Cancer Transcriptomes Reveals Organ-Level Molecular Signatures. <i>PLoS Computational Biology</i> , 2013, 9, e1003148.	1.5	16
153	Metabolic Constraint-Based Refinement of Transcriptional Regulatory Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003370.	1.5	31
154	Heterogeneity in protein expression induces metabolic variability in a modeled <i>Escherichia coli</i> population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14006-14011.	3.3	91
155	Version 6 of the consensus yeast metabolic network refines biochemical coverage and improves model performance. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat059.	1.4	89
156	Cell type-specific genes show striking and distinct patterns of spatial expression in the mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3095-3100.	3.3	61
157	Transcriptional Analysis of Aggressiveness and Heterogeneity across Grades of Astrocytomas. <i>PLoS ONE</i> , 2013, 8, e76694.	1.1	7
158	<i>Computational Infrastructures for Data and Knowledge Management in Systems Biology</i> . , 2013, , 377-397.		2
159	<i>Biological Data Integration and Model Building</i> . , 2013, , 1-19.		0
160	Mechanistic modeling of aberrant energy metabolism in human disease. <i>Frontiers in Physiology</i> , 2012, 3, 404.	1.3	17
161	Network biology methods integrating biological data for translational science. <i>Briefings in Bioinformatics</i> , 2012, 13, 446-459.	3.2	57
162	Research Resource: Whole Transcriptome RNA Sequencing Detects Multiple $1\alpha,25$ -Dihydroxyvitamin D3-Sensitive Metabolic Pathways in Developing Zebrafish. <i>Molecular Endocrinology</i> , 2012, 26, 1630-1642.	3.7	41

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