## Nathan D Price

List of Publications by Year in descending order

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ΝΑΤΗΛΝ Ο ΡΡΙΟΕ

#	Article	IF	CITATIONS
1	Integrated analysis of plasma and single immune cells uncovers metabolic changes in individuals with COVID-19. Nature Biotechnology, 2022, 40, 110-120.	17.5	81
2	Alzheimer's disease and progressive supranuclear palsy share similar transcriptomic changes in distinct brain regions. Journal of Clinical Investigation, 2022, 132, .	8.2	13
3	Multiple early factors anticipate post-acute COVID-19 sequelae. Cell, 2022, 185, 881-895.e20.	28.9	605
4	The effect of maternal SARS-CoV-2 infection timing on birth outcomes: a retrospective multicentre cohort study. The Lancet Digital Health, 2022, 4, e95-e104.	12.3	81
5	Distribution of 54 polygenic risk scores for common diseases in long lived individuals and their offspring. GeroScience, 2022, 44, 719-729.	4.6	3
6	Personal Dense Dynamic Data Clouds Connect Systems Biomedicine to Scientific Wellness. Methods in Molecular Biology, 2022, 2486, 315-334.	0.9	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. Scientific Reports, 2022, 12, 6117.	3.3	12
8	Risk factors for severe COVID-19 differ by age for hospitalized adults. Scientific Reports, 2022, 12, 6568.	3.3	23
9	Heterogeneity in statin responses explained by variation in the human gut microbiome. Med, 2022, 3, 388-405.e6.	4.4	21
10	A systemsâ€biology clinical trial of a personalized multimodal lifestyle intervention for early Alzheimer's disease. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2021, 7, e12191.	3.7	10
11	From taxonomy to metabolic output: what factors define gut microbiome health?. Gut Microbes, 2021, 13, 1-20.	9.8	19
12	Integrative functional genomic analysis of intron retention in human and mouse brain with Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, 984-1004.	0.8	25
13	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. Nature Metabolism, 2021, 3, 274-286.	11.9	278
14	iNetModels 2.0: an interactive visualization and database of multi-omics data. Nucleic Acids Research, 2021, 49, W271-W276.	14.5	25
15	Modulating innate immune activation states impacts the efficacy of specific AÎ <sup>2</sup> immunotherapy. Molecular Neurodegeneration, 2021, 16, 32.	10.8	4
16	The geometry of clinical labs and wellness states from deeply phenotyped humans. Nature Communications, 2021, 12, 3578.	12.8	19
17	A Comprehensive Assessment of Associations between Prenatal Phthalate Exposure and the Placental Transcriptomic Landscape. Environmental Health Perspectives, 2021, 129, 97003.	6.0	20
18	Baseline Gut Metagenomic Functional Gene Signature Associated with Variable Weight Loss Responses following a Healthy Lifestyle Intervention in Humans. MSystems, 2021, 6, e0096421.	3.8	19

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19	Systems modeling of metabolic dysregulation in neurodegenerative diseases. Current Opinion in Pharmacology, 2021, 60, 59-65.	3.5	5
20	Identifying Personalized Metabolic Signatures in Breast Cancer. Metabolites, 2021, 11, 20.	2.9	7
21	Towards early risk biomarkers: serum metabolic signature in childhood predicts cardio-metabolic risk in adulthood. EBioMedicine, 2021, 72, 103611.	6.1	14
22	Conserved architecture of brain transcriptome changes between Alzheimer's disease and progressive supranuclear palsy in pathologically affected and unaffected regions Alzheimer's and Dementia, 2021, 17 Suppl 3, e054424.	0.8	0
23	Investigating the importance of acylcarnitines in Alzheimer's disease Alzheimer's and Dementia, 2021, 17 Suppl 3, e056647.	0.8	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. Nature Reviews Clinical Oncology, 2020, 17, 183-194.	27.6	41
26	Multi-omic biomarker identification and validation for diagnosing warzone-related post-traumatic stress disorder. Molecular Psychiatry, 2020, 25, 3337-3349.	7.9	68
27	Measurement of Organ-Specific and Acute-Phase Blood Protein Levels in Early Lyme Disease. Journal of Proteome Research, 2020, 19, 346-359.	3.7	14
28	Health and disease markers correlate with gut microbiome composition across thousands of people. Nature Communications, 2020, 11, 5206.	12.8	378
29	Atlas of Transcription Factor Binding Sites from ENCODE DNase Hypersensitivity Data across 27 Tissue Types. Cell Reports, 2020, 32, 108029.	6.4	28
30	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	5.3	75
31	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	6.4	199
32	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Metabolism in Alzheimer's Disease. Cell Reports Medicine, 2020, 1, 100138.	6.5	102
33	Multi-Omics Resolves a Sharp Disease-State Shift between Mild and Moderate COVID-19. Cell, 2020, 183, 1479-1495.e20.	28.9	449
34	Multiomic blood correlates of genetic risk identify presymptomatic disease alterations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21813-21820.	7.1	22
35	Longitudinal analysis reveals transition barriers between dominant ecological states in the gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13839-13845.	7.1	47
36	Advancing human health in the decade ahead: pregnancy as a key window for discovery. American Journal of Obstetrics and Gynecology, 2020, 223, 312-321.	1.3	13

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37	A synthesis of bacterial and archaeal phenotypic trait data. Scientific Data, 2020, 7, 170.	5.3	59
38	iREAD: a tool for intron retention detection from RNA-seq data. BMC Genomics, 2020, 21, 128.	2.8	35
39	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
40	Core transcriptional regulatory circuits in prion diseases. Molecular Brain, 2020, 13, 10.	2.6	7
41	Deep phenotyping during pregnancy for predictive and preventive medicine. Science Translational Medicine, 2020, 12, .	12.4	21
42	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. Molecular Cell, 2020, 78, 960-974.e11.	9.7	83
43	Untargeted longitudinal analysis of a wellness cohort identifies markers of metastatic cancer years prior to diagnosis. Scientific Reports, 2020, 10, 16275.	3.3	12
44	Genome-scale metabolic model of the rat liver predicts effects of diet restriction. Scientific Reports, 2019, 9, 9807.	3.3	10
45	MicroRNAâ€ŧranscriptome networks in whole blood and monocytes of women undergoing preterm labour. Journal of Cellular and Molecular Medicine, 2019, 23, 6835-6845.	3.6	17
46	Multi-Omic Biological Age Estimation and Its Correlation With Wellness and Disease Phenotypes: A Longitudinal Study of 3,558 Individuals. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, S52-S60.	3.6	56
47	Blood metabolome predicts gut microbiome α-diversity in humans. Nature Biotechnology, 2019, 37, 1217-1228.	17.5	213
48	Genetic Predisposition Impacts Clinical Changes in a Lifestyle Coaching Program. Scientific Reports, 2019, 9, 6805.	3.3	48
49	Single-Cell Proteomics Reveal that Quantitative Changes in Co-expressed Lineage-Specific Transcription Factors Determine Cell Fate. Cell Stem Cell, 2019, 24, 812-820.e5.	11.1	99
50	OptRAM: In-silico strain design via integrative regulatory-metabolic network modeling. PLoS Computational Biology, 2019, 15, e1006835.	3.2	41
51	Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. Cell Systems, 2019, 8, 122-135.e7.	6.2	45
52	Reproducible big data science: A case study in continuous FAIRness. PLoS ONE, 2019, 14, e0213013.	2.5	29
53	THE PROTEOMICS OF LONGEVITY. Innovation in Aging, 2019, 3, S209-S209.	0.1	0
54	MULTI-OMIC BIOLOGICAL AGE ESTIMATION, CORRELATION WITH WELLNESS, DISEASE PHENOTYPES: LONGITUDINAL SAMPLE OF 3558. Innovation in Aging, 2019, 3, S209-S209.	0.1	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.	7.1	23
56	The building blocks of successful translation of proteomics to the clinic. Current Opinion in Biotechnology, 2018, 51, 123-129.	6.6	32
57	Comparative transcriptomic analysis of human placentae at term and preterm deliveryâ€. Biology of Reproduction, 2018, 98, 89-101.	2.7	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.	1.3	47
59	ProbAnnoWeb and ProbAnnoPy: probabilistic annotation and gap-filling of metabolic reconstructions. Bioinformatics, 2018, 34, 1594-1596.	4.1	9
60	Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. Molecular Systems Biology, 2018, 14, e7435.	7.2	55
61	Taking Systems Medicine to Heart. Circulation Research, 2018, 122, 1276-1289.	4.5	32
62	Reply. American Journal of Obstetrics and Gynecology, 2018, 219, 123-124.	1.3	0
63	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. Alzheimer's and Dementia, 2018, 14, 352-366.	0.8	116
64	O3â€03â€01: MECHANISTIC AND DIRECTIONAL TRANSCRIPTIONAL REGULATORY NETWORKS IN ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P1014.	0.8	0
65	P2â€∎23: A PHENOMEâ€WIDE ASSOCIATION STUDY (PHEWAS) OF BLOODâ€BASED BIOLOGICAL MARKERS AND APOLIPOPROTEIN E GENOTYPE ACROSS THE ADULT LIFESPAN. Alzheimer's and Dementia, 2018, 14, P716.	0.8	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.	8.1	558
67	Distinct communication patterns of trophoblastic miRNA among the maternal-placental-fetal compartments. Placenta, 2018, 72-73, 28-35.	1.5	24
68	Motor neuron loss and neuroinflammation in a model of α-synuclein-induced neurodegeneration. Neurobiology of Disease, 2018, 120, 98-106.	4.4	32
69	TLR5 decoy receptor as a novel anti-amyloid therapeutic for Alzheimer's disease. Journal of Experimental Medicine, 2018, 215, 2247-2264.	8.5	50
70	Temporal transcriptomic analysis of metabolic genes in maternal organs and placenta during murine pregnancyâ€. Biology of Reproduction, 2018, 99, 1255-1265.	2.7	9
71	Reply to "Precision medicine in the clouds". Nature Biotechnology, 2018, 36, 680-682.	17.5	2
72	Targeting <scp>TWIST</scp> 1 through loss of function inhibits tumorigenicity of human glioblastoma. Molecular Oncology, 2018, 12, 1188-1202.	4.6	25

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73	Genome-wide pleiotropy analysis of neuropathological traits related to Alzheimer's disease. Alzheimer's Research and Therapy, 2018, 10, 22.	6.2	27
74	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. Acta Neuropathologica, 2018, 136, 709-727.	7.7	47
75	Editorial overview: Systems biology: Data, discovery, delivery. Current Opinion in Biotechnology, 2018, 51, vii-viii.	6.6	0
76	IFPA meeting 2016 workshop report I: Genomic communication, bioinformatics, trophoblast biology and transport systems. Placenta, 2017, 60, S5-S9.	1.5	2
77	MicroRNAs and lipid metabolism. Current Opinion in Lipidology, 2017, 28, 273-280.	2.7	156
78	Motivational, proteostatic and transcriptional deficits precede synapse loss, gliosis and neurodegeneration in the B6.HttQ111/+ model of Huntington's disease. Scientific Reports, 2017, 7, 41570.	3.3	16
79	A Precision Medicine Approach to Improve Cancer Rehabilitation's Impact and Integration with Cancer Care and Optimize Patient Wellness. Current Physical Medicine and Rehabilitation Reports, 2017, 5, 64-73.	0.8	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. Human Molecular Genetics, 2017, 26, 913-922.	2.9	37
81	A Cell-Surface Membrane Protein Signature for Glioblastoma. Cell Systems, 2017, 4, 516-529.e7.	6.2	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. Alzheimer's and Dementia, 2017, 13, 663-673.	0.8	48
83	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
84	Genomic, Transcriptional, and Phenotypic Analysis of the Glucose Derepressed <i>Clostridium beijerinckii</i> Mutant Exhibiting Acid Crash Phenotype. Biotechnology Journal, 2017, 12, 1700182.	3.5	14
85	A wellness study of 108 individuals using personal, dense, dynamic data clouds. Nature Biotechnology, 2017, 35, 747-756.	17.5	340
86	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. Progress in Preventive Medicine (New York, N Y ), 2017, 2, e006.	0.7	6
87	The P4 Health Spectrum – A Predictive, Preventive, Personalized and Participatory Continuum for Promoting Healthspan. Progress in Cardiovascular Diseases, 2017, 59, 506-521.	3.1	178
88	Enhanced retinal responses in Huntington's disease patients. Journal of Huntington's Disease, 2017, 6, 237-247.	1.9	11
89	Crops In Silico: Generating Virtual Crops Using an Integrative and Multi-scale Modeling Platform. Frontiers in Plant Science, 2017, 8, 786.	3.6	102
90	Ion channel expression patterns in glioblastoma stem cells with functional and therapeutic implications for malignancy. PLoS ONE, 2017, 12, e0172884.	2.5	37

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91	Network reconstruction and systems analysis of plant cell wall deconstruction by Neurospora crassa. Biotechnology for Biofuels, 2017, 10, 225.	6.2	42
92	Linkage, whole genome sequence, and biological data implicate variants in RAB10 in Alzheimer's disease resilience. Genome Medicine, 2017, 9, 100.	8.2	67
93	The P4 Health Spectrum – A Predictive, Preventive, Personalized and Participatory Continuum for Promoting Healthspan. Progress in Preventive Medicine (New York, N Y ), 2017, 2, e0002.	0.7	10
94	Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. PLoS Computational Biology, 2017, 13, e1005489.	3.2	46
95	Peripheral huntingtin silencing does not ameliorate central signs of disease in the B6.HttQ111/+ mouse model of Huntington's disease. PLoS ONE, 2017, 12, e0175968.	2.5	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	B18â€Transcriptome profiling of B6.HttQ111/+ hepatocytes in response to chemical perturbagens. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A15.2-A15.	1.9	0
98	Predictive Big Data Analytics: A Study of Parkinson's Disease Using Large, Complex, Heterogeneous, Incongruent, Multi-Source and Incomplete Observations. PLoS ONE, 2016, 11, e0157077.	2.5	94
99	Human whole genome genotype and transcriptome data for Alzheimer's and other neurodegenerative diseases. Scientific Data, 2016, 3, 160089.	5.3	361
100	I'll take that to go: Big data bags and minimal identifiers for exchange of large, complex datasets. , 2016, , .		33
101	P4â€027: Combing Evidence Across Multiple Cohorts for Systemsâ€Based Target Discovery: the AMPâ€AD Knowledge Portal. Alzheimer's and Dementia, 2016, 12, P1025.	0.8	0
102	P4â€031: Integrative Network Analysis of Multiple Alzheimer's Disease Rnaseq Studies From the Accelerating Medicine Partnershipâ€Alzheimer's Disease Consortium. Alzheimer's and Dementia, 2016, 12, P1026.	0.8	1
103	F2-01-04: From Systems Level Transcriptomics to new Immune Targets for Alzheimer's Disease. , 2016, 12, P215-P216.		0
104	O2â€10â€04: 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. Alzheimer's and Dementia, 2016, 12, P251.	0.8	0
105	Exploring Hydrogenotrophic Methanogenesis: a Genome Scale Metabolic Reconstruction of Methanococcus maripaludis. Journal of Bacteriology, 2016, 198, 3379-3390.	2.2	48
106	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. Acta Neuropathologica, 2016, 132, 197-211.	7.7	49
107	Personalized nutrition through big data. Nature Biotechnology, 2016, 34, 152-154.	17.5	18
108	Relative stability of network states in Boolean network models of gene regulation in development. BioSystems, 2016, 142-143, 15-24.	2.0	45

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109	Emerging Proteomic Technologies Provide Enormous and Underutilized Potential for Brain Cancer Research. Molecular and Cellular Proteomics, 2016, 15, 362-367.	3.8	5
110	O1-11-03: Modulating chemokine signaling in preclinical Alzheimer's disease models. , 2015, 11, P157-P157.		0
111	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
112	A refined genomeâ€scale reconstruction of <i>Chlamydomonas</i> metabolism provides a platform for systemsâ€level analyses. Plant Journal, 2015, 84, 1239-1256.	5.7	70
113	Data-driven integration of genome-scale regulatory and metabolic network models. Frontiers in Microbiology, 2015, 6, 409.	3.5	49
114	Comparative Analysis of Yeast Metabolic Network Models Highlights Progress, Opportunities for Metabolic Reconstruction. PLoS Computational Biology, 2015, 11, e1004530.	3.2	70
115	A comprehensive map of genome-wide gene regulation in Mycobacterium tuberculosis. Scientific Data, 2015, 2, 150010.	5.3	55
116	Fostering synergy between cell biology and systems biology. Trends in Cell Biology, 2015, 25, 440-445.	7.9	2
117	Isoforms of RNA-Editing Enzyme ADAR1 Independently Control Nucleic Acid Sensor MDA5-Driven Autoimmunity and Multi-organ Development. Immunity, 2015, 43, 933-944.	14.3	373
118	Transcriptional program for nitrogen starvation-induced lipid accumulation in Chlamydomonas reinhardtii. Biotechnology for Biofuels, 2015, 8, 207.	6.2	60
119	SNAPR: A Bioinformatics Pipeline for Efficient and Accurate RNA-Seq Alignment and Analysis. IEEE Life Sciences Letters, 2015, 1, 22-25.	1.2	15
120	IL-10 Alters Immunoproteostasis in APP Mice, Increasing Plaque Burden and Worsening Cognitive Behavior. Neuron, 2015, 85, 519-533.	8.1	292
121	Genome-scale modeling for metabolic engineering. Journal of Industrial Microbiology and Biotechnology, 2015, 42, 327-338.	3.0	82
122	The DNA-binding network of Mycobacterium tuberculosi s. Nature Communications, 2015, 6, 5829.	12.8	192
123	Transparency in metabolic network reconstruction enables scalable biological discovery. Current Opinion in Biotechnology, 2015, 34, 105-109.	6.6	20
124	Integrating big data and actionable health coaching to optimize wellness. BMC Medicine, 2015, 13, 4.	5.5	66
125	Big biomedical data as the key resource for discovery science. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1126-1131.	4.4	70
126	Rare variants in neuronal excitability genes influence risk for bipolar disorder. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3576-3581.	7.1	152

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127	An argument for mechanism-based statistical inference in cancer. Human Genetics, 2015, 134, 479-495.	3.8	9
128	Integrated Modeling of Gene Regulatory and Metabolic Networks in Mycobacterium tuberculosis. PLoS Computational Biology, 2015, 11, e1004543.	3.2	64
129	Serum from calorie-restricted animals delays senescence and extends the lifespan of normal human fibroblasts in vitro. Aging, 2015, 7, 152-166.	3.1	20
130	MediaDB: A Database of Microbial Growth Conditions in Defined Media. PLoS ONE, 2014, 9, e103548.	2.5	28
131	Likelihood-Based Gene Annotations for Gap Filling and Quality Assessment in Genome-Scale Metabolic Models. PLoS Computational Biology, 2014, 10, e1003882.	3.2	66
132	<i>Promoting Wellness &amp; amp; Demystifying Disease:</i> The 100K Project. Clinical OMICs, 2014, 1, 20-23.	0.0	20
133	<scp><i>H</i></scp> <i>alomonas sulfidaeris</i> â€dominated microbial community inhabits a 1.8 kmâ€deep subsurface <scp>C</scp> ambrian <scp>S</scp> andstone reservoir. Environmental Microbiology, 2014, 16, 1695-1708.	3.8	52
134	Mapping and manipulating the Mycobacterium tuberculosis transcriptome using a transcription factor overexpression-derived regulatory network. Genome Biology, 2014, 15, 502.	8.8	136
135	Demystifying Disease, Democratizing Health Care. Science Translational Medicine, 2014, 6, 225ed5.	12.4	67
136	ITEP: An integrated toolkit for exploration of microbial pan-genomes. BMC Genomics, 2014, 15, 8.	2.8	123
137	Systems Approach to Neurodegenerative Disease Biomarker Discovery. Annual Review of Pharmacology and Toxicology, 2014, 54, 457-481.	9.4	45
138	Systems pharmacology modeling: an approach to improving drug safety. Biopharmaceutics and Drug Disposition, 2014, 35, 1-14.	1.9	24
139	Quantitative Proteomic Analysis Reveals Effects of Epidermal Growth Factor Receptor (EGFR) on Invasion-promoting Proteins Secreted by Glioblastoma Cells. Molecular and Cellular Proteomics, 2014, 13, 2618-2631.	3.8	29
140	Detection of 1α,25-Dihydroxyvitamin D-Regulated miRNAs in Zebrafish by Whole Transcriptome Sequencing. Zebrafish, 2014, 11, 207-218.	1.1	14
141	Measuring the Effect of Inter-Study Variability on Estimating Prediction Error. PLoS ONE, 2014, 9, e110840.	2.5	19
142	AUREA: an open-source software system for accurate and user-friendly identification of relative expression molecular signatures. BMC Bioinformatics, 2013, 14, 78.	2.6	7
143	Genome-Scale Models for Microbial Factories. Industrial Biotechnology, 2013, 9, 177-178.	0.8	1
144	Development of a Gene Knockout System Using Mobile Group II Introns (Targetron) and Genetic Disruption of Acid Production Pathways in Clostridium beijerinckii. Applied and Environmental Microbiology, 2013, 79, 5853-5863.	3.1	54

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145	A Blood-Based Proteomic Classifier for the Molecular Characterization of Pulmonary Nodules. Science Translational Medicine, 2013, 5, 207ra142.	12.4	165
146	Systems Biology and Systems Medicine. , 2013, , 60-72.		2
147	Systems Medicine and the Emergence of Proactive P4 Medicine. , 2013, , 445-467.		2
148	Genomically and biochemically accurate metabolic reconstruction of <i>Methanosarcina barkeri</i> Fusaro, iMG746. Biotechnology Journal, 2013, 8, 1070-1079.	3.5	41
149	A Guide to Integrating Transcriptional Regulatory and Metabolic Networks Using PROM (Probabilistic) Tj ETQq1 1	0,784314	1 rgBT /Overl
150	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	17.5	920
151	P4 medicine: how systems medicine will transform the healthcare sector and society. Personalized Medicine, 2013, 10, 565-576.	1.5	422
152	Multi-study Integration of Brain Cancer Transcriptomes Reveals Organ-Level Molecular Signatures. PLoS Computational Biology, 2013, 9, e1003148.	3.2	16
153	Metabolic Constraint-Based Refinement of Transcriptional Regulatory Networks. PLoS Computational Biology, 2013, 9, e1003370.	3.2	31
154	Heterogeneity in protein expression induces metabolic variability in a modeled <i>Escherichia coli</i> population. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14006-14011.	7.1	91
155	Version 6 of the consensus yeast metabolic network refines biochemical coverage and improves model performance. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat059.	3.0	89
156	Cell type-specific genes show striking and distinct patterns of spatial expression in the mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3095-3100.	7.1	61
157	Transcriptional Analysis of Aggressiveness and Heterogeneity across Grades of Astrocytomas. PLoS ONE, 2013, 8, e76694.	2.5	7
158	Computational Infrastructures for Data and Knowledge Management in Systems Biology. , 2013, , 377-397.		2
159	Biological Data Integration and Model Building. , 2013, , 1-19.		0
160	Mechanistic modeling of aberrant energy metabolism in human disease. Frontiers in Physiology, 2012, 3, 404.	2.8	17
161	Network biology methods integrating biological data for translational science. Briefings in Bioinformatics, 2012, 13, 446-459.	6.5	57
162	Research Resource: Whole Transcriptome RNA Sequencing Detects Multiple 1α,25-Dihydroxyvitamin D3-Sensitive Metabolic Pathways in Developing Zebrafish. Molecular Endocrinology, 2012, 26, 1630-1642.	3.7	41

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163	Genome-Scale Metabolic Reconstruction and Hypothesis Testing in the Methanogenic Archaeon Methanosarcina acetivorans C2A. Journal of Bacteriology, 2012, 194, 855-865.	2.2	79
164	The Limits of De Novo DNA Motif Discovery. PLoS ONE, 2012, 7, e47836.	2.5	23
165	The top-scoring â€~N' algorithm: a generalized relative expression classification method from small numbers of biomolecules. BMC Bioinformatics, 2012, 13, 227.	2.6	24
166	Reconstruction of genome-scale metabolic models for 126 human tissues using mCADRE. BMC Systems Biology, 2012, 6, 153.	3.0	239
167	Molecular signatures from omics data: From chaos to consensus. Biotechnology Journal, 2012, 7, 946-957.	3.5	101
168	Label-free Proteomics and Systems Biology Analysis of Mycobacterial Phagosomes in Dendritic Cells and Macrophages. Journal of Proteome Research, 2011, 10, 2425-2439.	3.7	19
169	Genome-Scale Consequences of Cofactor Balancing in Engineered Pentose Utilization Pathways in Saccharomyces cerevisiae. PLoS ONE, 2011, 6, e27316.	2.5	51
170	Metabolic network reconstruction and genome-scale model of butanol-producing strain Clostridium beijerinckii NCIMB 8052. BMC Systems Biology, 2011, 5, 130.	3.0	95
171	Behavior-specific changes in transcriptional modules lead to distinct and predictable neurogenomic states. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18020-18025.	7.1	156
172	A CD133-related gene expression signature identifies an aggressive glioblastoma subtype with excessive mutations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1591-1596.	7.1	114
173	Genetic Co-Occurrence Network across Sequenced Microbes. PLoS Computational Biology, 2011, 7, e1002340.	3.2	43
174	Graphics processing unit implementations of relative expression analysis algorithms enable dramatic computational speedup. Bioinformatics, 2011, 27, 872-873.	4.1	11
175	Achievements and perspectives to overcome the poor solvent resistance in acetone and butanol-producing microorganisms. Applied Microbiology and Biotechnology, 2010, 85, 1697-1712.	3.6	249
176	Introduction to the Special Issue on Information Theory in Molecular Biology and Neuroscience. IEEE Transactions on Information Theory, 2010, 56, 649-652.	2.4	65
177	Biological Information as Set-Based Complexity. IEEE Transactions on Information Theory, 2010, 56, 667-677.	2.4	39
178	<i>In silico</i> models of cancer. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 438-459.	6.6	103
179	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
180	Relative Expression Analysis for Molecular Cancer Diagnosis and Prognosis. Technology in Cancer Research and Treatment, 2010, 9, 149-159.	1.9	111

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181	Probabilistic integrative modeling of genome-scale metabolic and regulatory networks in <i>Escherichia coli</i> and <i>Mycobacterium tuberculosis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17845-17850.	7.1	378
182	Macroscopic Kinetic Effect of Cell-to-Cell Variation in Biochemical Reactions. Physical Review Letters, 2010, 104, 148103.	7.8	11
183	Identifying Tightly Regulated and Variably Expressed Networks by Differential Rank Conservation (DIRAC). PLoS Computational Biology, 2010, 6, e1000792.	3.2	73
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