

Nathan D Price

List of Publications by Year in descending order

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Version: 2024-02-01

222
papers

19,205
citations

17440

63
h-index

15732

125
g-index

259
all docs

259
docs citations

259
times ranked

26120
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-scale models of microbial cells: evaluating the consequences of constraints. <i>Nature Reviews Microbiology</i> , 2004, 2, 886-897.	28.6	935
2	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	17.5	920
3	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795
4	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.	21.4	783
5	Multiple early factors anticipate post-acute COVID-19 sequelae. <i>Cell</i> , 2022, 185, 881-895.e20.	28.9	605
6	Multiscale Analysis of Independent Alzheimer's Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. <i>Neuron</i> , 2018, 99, 64-82.e7.	8.1	558
7	Multi-Omics Resolves a Sharp Disease-State Shift between Mild and Moderate COVID-19. <i>Cell</i> , 2020, 183, 1479-1495.e20.	28.9	449
8	P4 medicine: how systems medicine will transform the healthcare sector and society. <i>Personalized Medicine</i> , 2013, 10, 565-576.	1.5	422
9	Probabilistic integrative modeling of genome-scale metabolic and regulatory networks in <i>Escherichia coli</i> and <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17845-17850.	7.1	378
10	Health and disease markers correlate with gut microbiome composition across thousands of people. <i>Nature Communications</i> , 2020, 11, 5206.	12.8	378
11	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.	14.3	373
12	Genome-scale microbial in silico models: the constraints-based approach. <i>Trends in Biotechnology</i> , 2003, 21, 162-169.	9.3	365
13	Human whole genome genotype and transcriptome data for Alzheimer's and other neurodegenerative diseases. <i>Scientific Data</i> , 2016, 3, 160089.	5.3	361
14	Metabolic pathways in the post-genome era. <i>Trends in Biochemical Sciences</i> , 2003, 28, 250-258.	7.5	347
15	Comparison of network-based pathway analysis methods. <i>Trends in Biotechnology</i> , 2004, 22, 400-405.	9.3	347
16	A wellness study of 108 individuals using personal, dense, dynamic data clouds. <i>Nature Biotechnology</i> , 2017, 35, 747-756.	17.5	340
17	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
18	IL-10 Alters Immunoproteostasis in APP Mice, Increasing Plaque Burden and Worsening Cognitive Behavior. <i>Neuron</i> , 2015, 85, 519-533.	8.1	292

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19	Gut microbiome pattern reflects healthy ageing and predicts survival in humans. <i>Nature Metabolism</i> , 2021, 3, 274-286.	11.9	278
20	Achievements and perspectives to overcome the poor solvent resistance in acetone and butanol-producing microorganisms. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 1697-1712.	3.6	249
21	Reconstruction of genome-scale metabolic models for 126 human tissues using mCADRE. <i>BMC Systems Biology</i> , 2012, 6, 153.	3.0	239
22	A systems approach to prion disease. <i>Molecular Systems Biology</i> , 2009, 5, 252.	7.2	230
23	Expanded Metabolic Reconstruction of <i>Helicobacter pylori</i> (i IT341 GSM/GPR): an In Silico Genome-Scale Characterization of Single- and Double-Deletion Mutants. <i>Journal of Bacteriology</i> , 2005, 187, 5818-5830.	2.2	220
24	Blood metabolome predicts gut microbiome α -diversity in humans. <i>Nature Biotechnology</i> , 2019, 37, 1217-1228.	17.5	213
25	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020, 32, 107908.	6.4	199
26	The DNA-binding network of <i>Mycobacterium tuberculosis</i> s. <i>Nature Communications</i> , 2015, 6, 5829.	12.8	192
27	Gene expression dynamics in the macrophage exhibit criticality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1897-1900.	7.1	191
28	The P4 Health Spectrum – A Predictive, Preventive, Personalized and Participatory Continuum for Promoting Healthspan. <i>Progress in Cardiovascular Diseases</i> , 2017, 59, 506-521.	3.1	178
29	A Blood-Based Proteomic Classifier for the Molecular Characterization of Pulmonary Nodules. <i>Science Translational Medicine</i> , 2013, 5, 207ra142.	12.4	165
30	Behavior-specific changes in transcriptional modules lead to distinct and predictable neurogenomic states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18020-18025.	7.1	156
31	MicroRNAs and lipid metabolism. <i>Current Opinion in Lipidology</i> , 2017, 28, 273-280.	2.7	156
32	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.	7.1	152
33	Highly accurate two-gene classifier for differentiating gastrointestinal stromal tumors and leiomyosarcomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3414-3419.	7.1	144
34	Candidate Metabolic Network States in Human Mitochondria. <i>Journal of Biological Chemistry</i> , 2005, 280, 11683-11695.	3.4	138
35	Mapping and manipulating the <i>Mycobacterium tuberculosis</i> transcriptome using a transcription factor overexpression-derived regulatory network. <i>Genome Biology</i> , 2014, 15, 502.	8.8	136
36	Uniform Sampling of Steady-State Flux Spaces: Means to Design Experiments and to Interpret Enzymopathies. <i>Biophysical Journal</i> , 2004, 87, 2172-2186.	0.5	130

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37	Extreme Pathway Lengths and Reaction Participation in Genome-Scale Metabolic Networks. <i>Genome Research</i> , 2002, 12, 1889-1900.	5.5	125
38	ITEP: An integrated toolkit for exploration of microbial pan-genomes. <i>BMC Genomics</i> , 2014, 15, 8.	2.8	123
39	Extreme Pathways and Kirchhoff's Second Law. <i>Biophysical Journal</i> , 2002, 83, 2879-2882.	0.5	122
40	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. <i>Alzheimer's and Dementia</i> , 2018, 14, 352-366.	0.8	116
41	The Genome-Scale Metabolic Extreme Pathway Structure in <i>Haemophilus influenzae</i> Shows Significant Network Redundancy. <i>Journal of Theoretical Biology</i> , 2002, 215, 67-82.	1.7	115
42	A CD133-related gene expression signature identifies an aggressive glioblastoma subtype with excessive mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1591-1596.	7.1	114
43	Relative Expression Analysis for Molecular Cancer Diagnosis and Prognosis. <i>Technology in Cancer Research and Treatment</i> , 2010, 9, 149-159.	1.9	111
44	Determination of Redundancy and Systems Properties of the Metabolic Network of <i>Helicobacter pylori</i> Using Genome-Scale Extreme Pathway Analysis. <i>Genome Research</i> , 2002, 12, 760-769.	5.5	106
45	<i>In silico</i> models of cancer. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 438-459.	6.6	103
46	Crops In Silico: Generating Virtual Crops Using an Integrative and Multi-scale Modeling Platform. <i>Frontiers in Plant Science</i> , 2017, 8, 786.	3.6	102
47	Metabolic Network Analysis Reveals Altered Bile Acid Synthesis and Metabolism in Alzheimer's Disease. <i>Cell Reports Medicine</i> , 2020, 1, 100138.	6.5	102
48	Molecular signatures from omics data: From chaos to consensus. <i>Biotechnology Journal</i> , 2012, 7, 946-957.	3.5	101
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.	11.1	99
50	Metabolic network reconstruction and genome-scale model of butanol-producing strain <i>Clostridium beijerinckii</i> NCIMB 8052. <i>BMC Systems Biology</i> , 2011, 5, 130.	3.0	95
51	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.	2.5	94
52	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.	7.1	91
53	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.	3.0	89
54	Matrix Formalism to Describe Functional States of Transcriptional Regulatory Systems. <i>PLoS Computational Biology</i> , 2006, 2, e101.	3.2	84

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55	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. <i>Molecular Cell</i> , 2020, 78, 960-974.e11.	9.7	83
56	Critical Networks Exhibit Maximal Information Diversity in Structure-Dynamics Relationships. <i>Physical Review Letters</i> , 2008, 100, 058702.	7.8	82
57	Genome-scale modeling for metabolic engineering. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 327-338.	3.0	82
58	Integrated analysis of plasma and single immune cells uncovers metabolic changes in individuals with COVID-19. <i>Nature Biotechnology</i> , 2022, 40, 110-120.	17.5	81
59	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.	12.3	81
60	Genome-Scale Metabolic Reconstruction and Hypothesis Testing in the Methanogenic Archaeon <i>Methanosarcina acetivorans</i> C2A. <i>Journal of Bacteriology</i> , 2012, 194, 855-865.	2.2	79
61	Accomplishments in genome-scale <i>in silico</i> modeling for industrial and medical biotechnology. <i>Biotechnology Journal</i> , 2009, 4, 1653-1670.	3.5	77
62	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	5.3	75
63	Analysis of Metabolic Capabilities Using Singular Value Decomposition of Extreme Pathway Matrices. <i>Biophysical Journal</i> , 2003, 84, 794-804.	0.5	73
64	Identifying Tightly Regulated and Variably Expressed Networks by Differential Rank Conservation (DIRAC). <i>PLoS Computational Biology</i> , 2010, 6, e1000792.	3.2	73
65	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.	5.7	70
66	Comparative Analysis of Yeast Metabolic Network Models Highlights Progress, Opportunities for Metabolic Reconstruction. <i>PLoS Computational Biology</i> , 2015, 11, e1004530.	3.2	70
67	Big biomedical data as the key resource for discovery science. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1126-1131.	4.4	70
68	Biochemical and statistical network models for systems biology. <i>Current Opinion in Biotechnology</i> , 2007, 18, 365-370.	6.6	68
69	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	7.2	68
70	Multi-omic biomarker identification and validation for diagnosing warzone-related post-traumatic stress disorder. <i>Molecular Psychiatry</i> , 2020, 25, 3337-3349.	7.9	68
71	Demystifying Disease, Democratizing Health Care. <i>Science Translational Medicine</i> , 2014, 6, 225ed5.	12.4	67
72	Linkage, whole genome sequence, and biological data implicate variants in RAB10 in Alzheimer's disease resilience. <i>Genome Medicine</i> , 2017, 9, 100.	8.2	67

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73	Likelihood-Based Gene Annotations for Gap Filling and Quality Assessment in Genome-Scale Metabolic Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003882.	3.2	66
74	Integrating big data and actionable health coaching to optimize wellness. <i>BMC Medicine</i> , 2015, 13, 4.	5.5	66
75	Introduction to the Special Issue on Information Theory in Molecular Biology and Neuroscience. <i>IEEE Transactions on Information Theory</i> , 2010, 56, 649-652.	2.4	65
76	Network-based analysis of metabolic regulation in the human red blood cell. <i>Journal of Theoretical Biology</i> , 2003, 225, 185-194.	1.7	64
77	Integrated Modeling of Gene Regulatory and Metabolic Networks in <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2015, 11, e1004543.	3.2	64
78	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.	7.1	61
79	Transcriptional program for nitrogen starvation-induced lipid accumulation in <i>Chlamydomonas reinhardtii</i> . <i>Biotechnology for Biofuels</i> , 2015, 8, 207.	6.2	60
80	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	5.3	59
81	Network biology methods integrating biological data for translational science. <i>Briefings in Bioinformatics</i> , 2012, 13, 446-459.	6.5	57
82	Integrated Proteomics and Genomics Analysis Reveals a Novel Mesenchymal to Epithelial Reverting Transition in Leiomyosarcoma through Regulation of Slug. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2405-2413.	3.8	56
83	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.	3.6	56
84	A comprehensive map of genome-wide gene regulation in <i>Mycobacterium tuberculosis</i> . <i>Scientific Data</i> , 2015, 2, 150010.	5.3	55
85	Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. <i>Molecular Systems Biology</i> , 2018, 14, e7435.	7.2	55
86	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.	3.1	54
87	<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.	3.8	52
88	Development of network-based pathway definitions: the need to analyze real metabolic networks. <i>Trends in Biotechnology</i> , 2003, 21, 195-198.	9.3	51
89	Genome-Scale Consequences of Cofactor Balancing in Engineered Pentose Utilization Pathways in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2011, 6, e27316.	2.5	51
90	TLR5 decoy receptor as a novel anti-amyloid therapeutic for Alzheimer's disease. <i>Journal of Experimental Medicine</i> , 2018, 215, 2247-2264.	8.5	50

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91	Data-driven integration of genome-scale regulatory and metabolic network models. <i>Frontiers in Microbiology</i> , 2015, 6, 409.	3.5	49
92	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. <i>Acta Neuropathologica</i> , 2016, 132, 197-211.	7.7	49
93	Exploring Hydrogenotrophic Methanogenesis: a Genome Scale Metabolic Reconstruction of <i>Methanococcus maripaludis</i> . <i>Journal of Bacteriology</i> , 2016, 198, 3379-3390.	2.2	48
94	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.	0.8	48
95	Genetic Predisposition Impacts Clinical Changes in a Lifestyle Coaching Program. <i>Scientific Reports</i> , 2019, 9, 6805.	3.3	48
96	Comparative analysis of gene expression in maternal peripheral blood and monocytes during spontaneous preterm labor. <i>American Journal of Obstetrics and Gynecology</i> , 2018, 218, 345.e1-345.e30.	1.3	47
97	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.	7.7	47
98	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.	7.1	47
99	Long-Range Periodic Patterns in Microbial Genomes Indicate Significant Multi-Scale Chromosomal Organization. <i>PLoS Computational Biology</i> , 2006, 2, e2.	3.2	46
100	Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005489.	3.2	46
101	Candidate States of <i>Helicobacter pylori</i> 's Genome-Scale Metabolic Network upon Application of $\Delta\epsilon$ Loop Law's Thermodynamic Constraints. <i>Biophysical Journal</i> , 2006, 90, 3919-3928.	0.5	45
102	Systems Approach to Neurodegenerative Disease Biomarker Discovery. <i>Annual Review of Pharmacology and Toxicology</i> , 2014, 54, 457-481.	9.4	45
103	Relative stability of network states in Boolean network models of gene regulation in development. <i>BioSystems</i> , 2016, 142-143, 15-24.	2.0	45
104	Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. <i>Cell Systems</i> , 2019, 8, 122-135.e7.	6.2	45
105	Metabolite coupling in genome-scale metabolic networks. <i>BMC Bioinformatics</i> , 2006, 7, 111.	2.6	43
106	Genetic Co-Occurrence Network across Sequenced Microbes. <i>PLoS Computational Biology</i> , 2011, 7, e1002340.	3.2	43
107	In Silico Metabolic Model and Protein Expression of <i>Haemophilus influenzae</i> Strain Rd KW20 in Rich Medium. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 25-41.	2.0	42
108	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

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109	Research Resource: Whole Transcriptome RNA Sequencing Detects Multiple 1 \pm ,25-Dihydroxyvitamin D3-Sensitive Metabolic Pathways in Developing Zebrafish. <i>Molecular Endocrinology</i> , 2012, 26, 1630-1642.	3.7	41
110	Genomically and biochemically accurate metabolic reconstruction of <i>Methanosarcina barkeri</i> Fusaro, iMG746. <i>Biotechnology Journal</i> , 2013, 8, 1070-1079.	3.5	41
111	OptRAM: In-silico strain design via integrative regulatory-metabolic network modeling. <i>PLoS Computational Biology</i> , 2019, 15, e1006835.	3.2	41
112	A systems approach to clinical oncology uses deep phenotyping to deliver personalized care. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 183-194.	27.6	41
113	Biological Information as Set-Based Complexity. <i>IEEE Transactions on Information Theory</i> , 2010, 56, 667-677.	2.4	39
114	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.	2.9	37
115	A Cell-Surface Membrane Protein Signature for Glioblastoma. <i>Cell Systems</i> , 2017, 4, 516-529.e7.	6.2	37
116	Ion channel expression patterns in glioblastoma stem cells with functional and therapeutic implications for malignancy. <i>PLoS ONE</i> , 2017, 12, e0172884.	2.5	37
117	iREAD: a tool for intron retention detection from RNA-seq data. <i>BMC Genomics</i> , 2020, 21, 128.	2.8	35
118	I'll take that to go: Big data bags and minimal identifiers for exchange of large, complex datasets. , 2016, , .		33
119	Network-level analysis of metabolic regulation in the human red blood cell using random sampling and singular value decomposition. <i>BMC Bioinformatics</i> , 2006, 7, 132.	2.6	32
120	The building blocks of successful translation of proteomics to the clinic. <i>Current Opinion in Biotechnology</i> , 2018, 51, 123-129.	6.6	32
121	Taking Systems Medicine to Heart. <i>Circulation Research</i> , 2018, 122, 1276-1289.	4.5	32
122	Motor neuron loss and neuroinflammation in a model of α -synuclein-induced neurodegeneration. <i>Neurobiology of Disease</i> , 2018, 120, 98-106.	4.4	32
123	Metabolic Constraint-Based Refinement of Transcriptional Regulatory Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003370.	3.2	31
124	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.	3.8	29
125	Reproducible big data science: A case study in continuous FAIRness. <i>PLoS ONE</i> , 2019, 14, e0213013.	2.5	29
126	MediaDB: A Database of Microbial Growth Conditions in Defined Media. <i>PLoS ONE</i> , 2014, 9, e103548.	2.5	28

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127	Atlas of Transcription Factor Binding Sites from ENCODE DNase Hypersensitivity Data across 27 Tissue Types. <i>Cell Reports</i> , 2020, 32, 108029.	6.4	28
128	Genome-wide pleiotropy analysis of neuropathological traits related to Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2018, 10, 22.	6.2	27
129	Targeting TWIST1 through loss of function inhibits tumorigenicity of human glioblastoma. <i>Molecular Oncology</i> , 2018, 12, 1188-1202.	4.6	25
130	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.	0.8	25
131	iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W271-W276.	14.5	25
132	The top-scoring Naïve algorithm: a generalized relative expression classification method from small numbers of biomolecules. <i>BMC Bioinformatics</i> , 2012, 13, 227.	2.6	24
133	Systems pharmacology modeling: an approach to improving drug safety. <i>Biopharmaceutics and Drug Disposition</i> , 2014, 35, 1-14.	1.9	24
134	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.	0.8	24
135	Distinct communication patterns of trophoblastic miRNA among the maternal-placental-fetal compartments. <i>Placenta</i> , 2018, 72-73, 28-35.	1.5	24
136	The Limits of De Novo DNA Motif Discovery. <i>PLoS ONE</i> , 2012, 7, e47836.	2.5	23
137	Digitizing omics profiles by divergence from a baseline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4545-4552.	7.1	23
138	Comparative transcriptomic analysis of human placentae at term and preterm delivery. <i>Biology of Reproduction</i> , 2018, 98, 89-101.	2.7	23
139	Risk factors for severe COVID-19 differ by age for hospitalized adults. <i>Scientific Reports</i> , 2022, 12, 6568.	3.3	23
140	Systems biology and cancer stem cells. <i>Journal of Cellular and Molecular Medicine</i> , 2008, 12, 97-110.	3.6	22
141	Multioomic 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.	7.1	22
142	Deep phenotyping during pregnancy for predictive and preventive medicine. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	21
143	Heterogeneity in statin responses explained by variation in the human gut microbiome. <i>Med</i> , 2022, 3, 388-405.e6.	4.4	21
144	Promoting Wellness & Demystifying Disease: The 100K Project. <i>Clinical OMICs</i> , 2014, 1, 20-23.	0.0	20

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145	Transparency in metabolic network reconstruction enables scalable biological discovery. <i>Current Opinion in Biotechnology</i> , 2015, 34, 105-109.	6.6	20
146	A Comprehensive Assessment of Associations between Prenatal Phthalate Exposure and the Placental Transcriptomic Landscape. <i>Environmental Health Perspectives</i> , 2021, 129, 97003.	6.0	20
147	Serum from calorie-restricted animals delays senescence and extends the lifespan of normal human fibroblasts in vitro. <i>Aging</i> , 2015, 7, 152-166.	3.1	20
148	Label-free Proteomics and Systems Biology Analysis of Mycobacterial Phagosomes in Dendritic Cells and Macrophages. <i>Journal of Proteome Research</i> , 2011, 10, 2425-2439.	3.7	19
149	From taxonomy to metabolic output: what factors define gut microbiome health?. <i>Gut Microbes</i> , 2021, 13, 1-20.	9.8	19
150	The geometry of clinical labs and wellness states from deeply phenotyped humans. <i>Nature Communications</i> , 2021, 12, 3578.	12.8	19
151	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.	3.8	19
152	Measuring the Effect of Inter-Study Variability on Estimating Prediction Error. <i>PLoS ONE</i> , 2014, 9, e110840.	2.5	19
153	Personalized nutrition through big data. <i>Nature Biotechnology</i> , 2016, 34, 152-154.	17.5	18
154	Mechanistic modeling of aberrant energy metabolism in human disease. <i>Frontiers in Physiology</i> , 2012, 3, 404.	2.8	17
155	MicroRNA transcriptome networks in whole blood and monocytes of women undergoing preterm labour. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 6835-6845.	3.6	17
156	Two-transcript gene expression classifiers in the diagnosis and prognosis of human diseases. <i>BMC Genomics</i> , 2009, 10, 583.	2.8	16
157	Multi-study Integration of Brain Cancer Transcriptomes Reveals Organ-Level Molecular Signatures. <i>PLoS Computational Biology</i> , 2013, 9, e1003148.	3.2	16
158	Motivational, proteostatic and transcriptional deficits precede synapse loss, gliosis and neurodegeneration in the B6.Htt ^{Q111/+} model of Huntington's disease. <i>Scientific Reports</i> , 2017, 7, 41570.	3.3	16
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