Pierre Baldi

List of Publications by Year
in descending order

277 papers	32,479 citations	5261 83 h-index	4770 169 g-index
303 all docs	303 docs citations	303 times ranked	42255 citing authors

#	Article	IF	Citations
1	CircadiOmics: integrating circadian genomics, transcriptomics, proteomics and metabolomics. Nature Methods, 2012, 9, 772-773.	9.0	2,006
2	Assessing the accuracy of prediction algorithms for classification: an overview. Bioinformatics, 2000, 16, 412-424.	1.8	1,762
3	A Bayesian framework for the analysis of microarray expression data: regularized t -test and statistical inferences of gene changes. Bioinformatics, 2001, 17, 509-519.	1.8	1,526
4	Neural networks and principal component analysis: Learning from examples without local minima. Neural Networks, 1989, 2, 53-58.	3.3	960
5	Bayesian surprise attracts human attention. Vision Research, 2009, 49, 1295-1306.	0.7	850
6	SCRATCH: a protein structure and structural feature prediction server. Nucleic Acids Research, 2005, 33, W72-W76.	6.5	839
7	Highly Accurate Machine Fault Diagnosis Using Deep Transfer Learning. IEEE Transactions on Industrial Informatics, 2019, 15, 2446-2455.	7.2	829
8	Prediction of protein stability changes for single-site mutations using support vector machines. Proteins: Structure, Function and Bioinformatics, 2005, 62, 1125-1132.	1.5	784
9	Mitochondrial mutations in cancer. Oncogene, 2006, 25, 4647-4662.	2.6	730
10	Searching for exotic particles in high-energy physics with deep learning. Nature Communications, 2014, 5, 4308.	5.8	685
11	Improving the prediction of protein secondary structure in three and eight classes using recurrent neural networks and profiles. Proteins: Structure, Function and Bioinformatics, 2002, 47, 228-235.	1.5	652
12	Reprogramming of the Circadian Clock by Nutritional Challenge. Cell, 2013, 155, 1464-1478.	13.5	579
13	An enhanced MITOMAP with a global mtDNA mutational phylogeny. Nucleic Acids Research, 2007, 35, D823-D828.	6.5	528
14	Deep Learning Localizes and Identifies Polyps in Real Time With 96% Accuracy in Screening Colonoscopy. Gastroenterology, 2018, 155, 1069-1078.e8.	0.6	510
15	Exploiting the past and the future in protein secondary structure prediction. Bioinformatics, 1999, 15, 937-946.	1.8	422
16	A prospective analysis of the Ab response to *Plasmodium falciparum* before and after a malaria season by protein microarray. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6958-6963.	3.3	412
17	Deep Architectures and Deep Learning in Chemoinformatics: The Prediction of Aqueous Solubility for Drug-Like Molecules. Journal of Chemical Information and Modeling, 2013, 53, 1563-1575.	2.5	408
18	SOLpro: accurate sequence-based prediction of protein solubility. Bioinformatics, 2009, 25, 2200-2207.	1.8	400

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19	Hidden Markov models of biological primary sequence information.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 1059-1063.	3.3	396
20	Profiling the humoral immune response to infection by using proteome microarrays: High-throughput vaccine and diagnostic antigen discovery. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 547-552.	3.3	378
21	Coordination of the transcriptome and metabolome by the circadian clock. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5541-5546.	3.3	353
22	Graph kernels for chemical informatics. Neural Networks, 2005, 18, 1093-1110.	3.3	329
23	Improved Statistical Inference from DNA Microarray Data Using Analysis of Variance and A Bayesian Statistical Framework. Journal of Biological Chemistry, 2001, 276, 19937-19944.	1.6	328
24	High-throughput prediction of protein antigenicity using protein microarray data. Bioinformatics, 2010, 26, 2936-2943.	1.8	328
25	Muscle insulin sensitivity and glucose metabolism are controlled by the intrinsic muscle clock. Molecular Metabolism, 2014, 3, 29-41.	3.0	324
26	Deep-Learning Convolutional Neural Networks Accurately Classify Genetic Mutations in Gliomas. American Journal of Neuroradiology, 2018, 39, 1201-1207.	1.2	323
27	SSpro/ACCpro 5: almost perfect prediction of protein secondary structure and relative solvent accessibility using profiles, machine learning and structural similarity. Bioinformatics, 2014, 30, 2592-2597.	1.8	312
28	Partitioning Circadian Transcription by SIRT6 Leads to Segregated Control of Cellular Metabolism. Cell, 2014, 158, 659-672.	13.5	259
29	Atlas of Circadian Metabolism Reveals System-wide Coordination and Communication between Clocks. Cell, 2018, 174, 1571-1585.e11.	13.5	258
30	Global Gene Expression Profiling in Escherichia coli K12. Journal of Biological Chemistry, 2003, 278, 29837-29855.	1.6	249
31	A Principled Approach to Detecting Surprising Events in Video. , 0, , .		240
32	Deep architectures for protein contact map prediction. Bioinformatics, 2012, 28, 2449-2457.	1.8	240
33	PEPITO: improved discontinuous B-cell epitope prediction using multiple distance thresholds and half sphere exposure. Bioinformatics, 2008, 24, 1459-1460.	1.8	239
34	Guidelines for Genome-Scale Analysis of Biological Rhythms. Journal of Biological Rhythms, 2017, 32, 380-393.	1.4	237
35	Profiling humoral immune responses to **_P. falciparum_** infection with protein microarrays. Proteomics, 2008, 8, 4680-4694.	1.3	236
36	Global Gene Expression Profiling in Escherichia coli K12. Journal of Biological Chemistry, 2005, 280, 15084-15096.	1.6	235

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37	Of bits and wows: A Bayesian theory of surprise with applications to attention. Neural Networks, 2010, 23, 649-666.	3.3	223
38	Prediction of coordination number and relative solvent accessibility in proteins. Proteins: Structure, Function and Bioinformatics, 2002, 47, 142-153.	1.5	222
39	Circadian clock regulates the host response to *Salmonella*. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9897-9902.	3.3	216
40	The neuron-specific chromatin regulatory subunit BAF53b is necessary for synaptic plasticity and memory. Nature Neuroscience, 2013, 16, 552-561.	7.1	213
41	Defining the Independence of the Liver Circadian Clock. Cell, 2019, 177, 1448-1462.e14.	13.5	213
42	The dropout learning algorithm. Artificial Intelligence, 2014, 210, 78-122.	3.9	210
43	Towards a systems view of IBS. Nature Reviews Gastroenterology and Hepatology, 2015, 12, 592-605.	8.2	207
44	Sourcerer: mining and searching internet-scale software repositories. Data Mining and Knowledge Discovery, 2009, 18, 300-336.	2.4	196
45	Lung Adenocarcinoma Distally Rewires Hepatic Circadian Homeostasis. Cell, 2016, 165, 896-909.	13.5	195
46	Improved residue contact prediction using support vector machines and a large feature set. BMC Bioinformatics, 2007, 8, 113.	1.2	192
47	Accurate Prediction of Protein Disordered Regions by Mining Protein Structure Data. Data Mining and Knowledge Discovery, 2005, 11, 213-222.	2.4	187
48	Time of Exercise Specifies the Impact on Muscle Metabolic Pathways and Systemic Energy Homeostasis. Cell Metabolism, 2019, 30, 92-110.e4.	7.2	176
49	Distinct Circadian Signatures in Liver and Gut Clocks Revealed by Ketogenic Diet. Cell Metabolism, 2017, 26, 523-538.e5.	7.2	162
50	COBEpro: a novel system for predicting continuous B-cell epitopes. Protein Engineering, Design and Selection, 2009, 22, 113-120.	1.0	161
51	Detecting Cardiovascular Disease from Mammograms With Deep Learning. IEEE Transactions on Medical Imaging, 2017, 36, 1172-1181.	5.4	159
52	ChemDB: a public database of small molecules and related chemoinformatics resources. Bioinformatics, 2005, 21, 4133-4139.	1.8	155
53	MotifMap: integrative genome-wide maps of regulatory motif sites for model species. BMC Bioinformatics, 2011, 12, 495.	1.2	154
54	Learning to Predict Chemical Reactions. Journal of Chemical Information and Modeling, 2011, 51, 2209-2222.	2.5	148

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55	Kernels for small molecules and the prediction of mutagenicity, toxicity and anti-cancer activity. Bioinformatics, 2005, 21, i359-i368.	1.8	145
56	Jet substructure classification in high-energy physics with deep neural networks. Physical Review D, 2016, 93, .	1.6	144
57	Cyber-T web server: differential analysis of high-throughput data. Nucleic Acids Research, 2012, 40, W553-W559.	6.5	142
58	Deep learning for chemical reaction prediction. Molecular Systems Design and Engineering, 2018, 3, 442-452.	1.7	141
59	Parameterized neural networks for high-energy physics. European Physical Journal C, 2016, 76, 1.	1.4	140
60	A Genome-Wide Proteome Array Reveals a Limited Set of Immunogens in Natural Infections of Humans and White-Footed Mice with<i>Borrelia burgdorferi</i>. Infection and Immunity, 2008, 76, 3374-3389.	1.0	137
61	Sterile Protective Immunity to Malaria is Associated with a Panel of Novel P. falciparum Antigens. Molecular and Cellular Proteomics, 2011, 10, M111.007948.	2.5	134
62	Circadian acetylome reveals regulation of mitochondrial metabolic pathways. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3339-3344.	3.3	133
63	Adaptive Low Power Listening for Wireless Sensor Networks. IEEE Transactions on Mobile Computing, 2007, 6, 988-1004.	3.9	132
64	Prediction of contact maps by GIOHMMs and recurrent neural networks using lateral propagation from all four cardinal corners. Bioinformatics, 2002, 18, S62-S70.	1.8	128
65	Population-wide analysis of differences in disease progression patterns in men and women. Nature Communications, 2019, 10, 666.	5.8	128
66	Gut microbiota directs <scp>PPAR</scp> Î³â€‰driven reprogramming of the liver circadian clock by nutritional challenge. EMBO Reports, 2016, 17, 1292-1303.	2.0	127
67	Neural Networks for Fingerprint Recognition. Neural Computation, 1993, 5, 402-418.	1.3	126
68	ReactionPredictor: Prediction of Complex Chemical Reactions at the Mechanistic Level Using Machine Learning. Journal of Chemical Information and Modeling, 2012, 52, 2526-2540.	2.5	124
69	Enforcing Analytic Constraints in Neural Networks Emulating Physical Systems. Physical Review Letters, 2021, 126, 098302.	2.9	124
70	Global Gene Expression Profiling in Escherichia coliK12. Journal of Biological Chemistry, 2002, 277, 40309-40323.	1.6	121
71	Epigenetic regulation of the circadian gene Per1 contributes to age-related changes in hippocampal memory. Nature Communications, 2018, 9, 3323.	5.8	118
72	Large-scale prediction of disulphide bridges using kernel methods, two-dimensional recursive neural networks, and weighted graph matching. Proteins: Structure, Function and Bioinformatics, 2005, 62, 617-629.	1.5	117

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73	ChemDB update full-text search and virtual chemical space. Bioinformatics, 2007, 23, 2348-2351.	1.8	117
74	Differential analysis of DNA microarray gene expression data. Molecular Microbiology, 2003, 47, 871-877.	1.2	113
75	Cycles in spatial and temporal chromosomal organization driven by the circadian clock. Nature Structural and Molecular Biology, 2013, 20, 1206-1213.	3.6	110
76	Fasting Imparts a Switch to Alternative Daily Pathways in Liver and Muscle. Cell Reports, 2018, 25, 3299-3314.e6.	2.9	106
77	Machine Learning Methods for Protein Structure Prediction. IEEE Reviews in Biomedical Engineering, 2008, 1, 41-49.	13.1	99
78	Jet flavor classification in high-energy physics with deep neural networks. Physical Review D, 2016, 94, .	1.6	99
79	MITOMASTER: a bioinformatics tool for the analysis of mitochondrial DNA sequences. Human Mutation, 2009, 30, 1-6.	1.1	98
80	A multi-resolution approach for spinal metastasis detection using deep Siamese neural networks. Computers in Biology and Medicine, 2017, 84, 137-146.	3.9	96
81	DOMpro: Protein Domain Prediction Using Profiles, Secondary Structure, Relative Solvent Accessibility, and Recursive Neural Networks. Data Mining and Knowledge Discovery, 2006, 13, 1-10.	2.4	93
82	Identification of humoral immune responses in protein microarrays using DNA microarray data analysis techniques. Bioinformatics, 2006, 22, 1760-1766.	1.8	93
83	OSCILLATIONS AND SYNCHRONIZATIONS IN NEURAL NETWORKS: AN EXPLORATION OF THE LABELING HYPOTHESIS. International Journal of Neural Systems, 1989, 01, 103-124.	3.2	91
84	When is Chemical Similarity Significant? The Statistical Distribution of Chemical Similarity Scores and Its Extreme Values. Journal of Chemical Information and Modeling, 2010, 50, 1205-1222.	2.5	89
85	A CROC stronger than ROC: measuring, visualizing and optimizing early retrieval. Bioinformatics, 2010, 26, 1348-1356.	1.8	88
86	Smooth On-Line Learning Algorithms for Hidden Markov Models. Neural Computation, 1994, 6, 307-318.	1.3	87
87	Bounds and Algorithms for Fast Exact Searches of Chemical Fingerprints in Linear and Sublinear Time. Journal of Chemical Information and Modeling, 2007, 47, 302-317.	2.5	87
88	Data structures and compression algorithms for genomic sequence data. Bioinformatics, 2009, 25, 1731-1738.	1.8	87
89	From protein microarrays to diagnostic antigen discovery: a study of the pathogen <i>Francisella tularensis</i>. Bioinformatics, 2007, 23, i508-i518.	1.8	86
90	Atlas of exercise metabolism reveals time-dependent signatures of metabolic homeostasis. Cell Metabolism, 2022, 34, 329-345.e8.	7.2	86

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91	DNA structure in human RNA polymerase II promoters 1 1Edited by J. Karn. Journal of Molecular Biology, 1998, 281, 663-673.	2.0	81
92	Computing with Arrays of Coupled Oscillators: An Application to Preattentive Texture Discrimination. Neural Computation, 1990, 2, 458-471.	1.3	80
93	Enhanced Higgs Boson to<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"><mml:mrow><mml:msup><mml:mrow><mml:mi>Ï„</mml:mi></mml:mrow><mml:mrow><mml:mo>+</mml:mmls8o0</m with Deep Learning. Physical Review Letters, 2015, 114, 111801.	2.9	80
94	The Stability and Complexity of Antibody Responses to the Major Surface Antigen of Plasmodium falciparum Are Associated with Age in a Malaria Endemic Area. Molecular and Cellular Proteomics, 2011, 10, M111.008326.	2.5	78
95	Sherpa: Robust hyperparameter optimization for machine learning. SoftwareX, 2020, 12, 100591.	1.2	78
96	Deep Learning in Biomedical Data Science. Annual Review of Biomedical Data Science, 2018, 1, 181-205.	2.8	76
97	TMBpro: secondary structure, Î²-contact and tertiary structure prediction of transmembrane Î²-barrel proteins. Bioinformatics, 2008, 24, 513-520.	1.8	75
98	Solving the Rubikâ€™s cube with deep reinforcement learning and search. Nature Machine Intelligence, 2019, 1, 356-363.	8.3	75
99	Deep Learning Analysis of Vibrational Spectra of Bacterial Lysate for Rapid Antimicrobial Susceptibility Testing. ACS Nano, 2020, 14, 15336-15348.	7.3	75
100	Decorrelated jet substructure tagging using adversarial neural networks. Physical Review D, 2017, 96, .	1.6	74
101	Naturally Occurring Nucleosome Positioning Signals in Human Exons and Introns. Journal of Molecular Biology, 1996, 263, 503-510.	2.0	68
102	What time is it? Deep learning approaches for circadian rhythms. Bioinformatics, 2016, 32, i8-i17.	1.8	68
103	Sequence Assembly of Yarrowia lipolytica Strain W29/CLIB89 Shows Transposable Element Diversity. PLoS ONE, 2016, 11, e0162363.	1.1	68
104	Serological Profiling of a Candida albicans Protein Microarray Reveals Permanent Host-Pathogen Interplay and Stage-Specific Responses during Candidemia. PLoS Pathogens, 2010, 6, e1000827.	2.1	66
105	Neural networks, orientations of the hypercube, and algebraic threshold functions. IEEE Transactions on Information Theory, 1988, 34, 523-530.	1.5	63
106	Mathematical Correction for Fingerprint Similarity Measures to Improve Chemical Retrieval. Journal of Chemical Information and Modeling, 2007, 47, 952-964.	2.5	61
107	Comparative Circadian Metabolomics Reveal Differential Effects of Nutritional Challenge in the Serum and Liver. Journal of Biological Chemistry, 2016, 291, 2812-2828.	1.6	61
108	Modeling and optimization of UWB communication networks through a flexible cost function. IEEE Journal on Selected Areas in Communications, 2002, 20, 1733-1744.	9.7	59

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109	An Application of Latent Dirichlet Allocation to Analyzing Software Evolution. , 2008, , .		59
110	Discovery of Power-Laws in Chemical Space. Journal of Chemical Information and Modeling, 2008, 48, 1138-1151.	2.5	58
111	Metabolic changes associated with methionine stress sensitivity in MDA-MB-468 breast cancer cells. Cancer & Metabolism, 2016, 4, 9.	2.4	58
112	Beep: 3D indoor positioning using audible sound. , 0, , .		57
113	SIDEpro: A novel machine learning approach for the fast and accurate prediction of side‐chain conformations. Proteins: Structure, Function and Bioinformatics, 2012, 80, 142-153.	1.5	57
114	One- to Four-Dimensional Kernels for Virtual Screening and the Prediction of Physical, Chemical, and Biological Properties. Journal of Chemical Information and Modeling, 2007, 47, 965-974.	2.5	56
115	An automated machine learning-based model predicts postoperative mortality using readily-extractable preoperative electronic health record data. British Journal of Anaesthesia, 2019, 123, 877-886.	1.5	56
116	ClusterCAD: a computational platform for type I modular polyketide synthase design. Nucleic Acids Research, 2018, 46, D509-D515.	6.5	55
117	Assessment of predictions submitted for the CASP7 domain prediction category. Proteins: Structure, Function and Bioinformatics, 2007, 69, 137-151.	1.5	51
118	No Electron Left Behind: A Rule-Based Expert System To Predict Chemical Reactions and Reaction Mechanisms. Journal of Chemical Information and Modeling, 2009, 49, 2034-2043.	2.5	51
119	Longitudinal Monitoring of Biofilm Formation via Robust Surface-Enhanced Raman Scattering Quantification of <i>Pseudomonas aeruginosa</i>-Produced Metabolites. ACS Applied Materials & Interfaces, 2018, 10, 12364-12373.	4.0	51
120	Sequence analysis by additive scales: DNA structure for sequences and repeats of all lengths. Bioinformatics, 2000, 16, 865-889.	1.8	50
121	The circadian dynamics of the hippocampal transcriptome and proteome is altered in experimental temporal lobe epilepsy. Science Advances, 2020, 6, .	4.7	50
122	Integration of feeding behavior by the liver circadian clock reveals network dependency of metabolic rhythms. Science Advances, 2021, 7, eabi7828.	4.7	50
123	Influence Relevance Voting: An Accurate And Interpretable Virtual High Throughput Screening Method. Journal of Chemical Information and Modeling, 2009, 49, 756-766.	2.5	49
124	S-adenosyl- <scp>l</scp> -homocysteine hydrolase links methionine metabolism to the circadian clock and chromatin remodeling. Science Advances, 2020, 6, .	4.7	49
125	Mining Eclipse Developer Contributions via Author-Topic Models. , 2007, , .		48
126	Development and validation of an interpretable neural network for prediction of postoperative in-hospital mortality. Npj Digital Medicine, 2021, 4, 8.	5.7	48

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127	Lossless Compression of Chemical Fingerprints Using Integer Entropy Codes Improves Storage and Retrieval. Journal of Chemical Information and Modeling, 2007, 47, 2098-2109.	2.5	45
128	SIRT6 Suppresses Cancer Stem-like Capacity in Tumors with PI3K Activation Independently of Its Deacetylase Activity. Cell Reports, 2017, 18, 1858-1868.	2.9	45
129	Improved prediction of the number of residue contacts in proteins by recurrent neural networks. Bioinformatics, 2001, 17, S234-S242.	1.8	44
130	A theory of local learning, the learning channel, and the optimality of backpropagation. Neural Networks, 2016, 83, 51-74.	3.3	44
131	Distribution patterns of over-represented k-mers in non-coding yeast DNA. Bioinformatics, 2002, 18, 513-528.	1.8	43
132	Synergies Between Quantum Mechanics and Machine Learning in Reaction Prediction. Journal of Chemical Information and Modeling, 2016, 56, 2125-2128.	2.5	43
133	Learning in the machine: Random backpropagation and the deep learning channel. Artificial Intelligence, 2018, 260, 1-35.	3.9	43
134	Identification of Immunodominant Antigens by Probing a Whole *Chlamydia trachomatis* Open Reading Frame Proteome Microarray Using Sera from Immunized Mice. Infection and Immunity, 2011, 79, 246-257.	1.0	42
135	A WNT/p21 Circuit Directed by the C-Clamp, a Sequence-Specific DNA Binding Domain in TCFs. Molecular and Cellular Biology, 2012, 32, 3648-3662.	1.1	42
136	Data structures and compression algorithms for high-throughput sequencing technologies. BMC Bioinformatics, 2010, 11, 514.	1.2	41
137	A Fortran-Keras Deep Learning Bridge for Scientific Computing. Scientific Programming, 2020, 2020, 1-13.	0.5	41
138	SourcererDB: An aggregated repository of statically analyzed and cross-linked open source Java projects. , 2009, , .		40
139	Large Scale Immune Profiling of Infected Humans and Goats Reveals Differential Recognition of Brucella melitensis Antigens. PLoS Neglected Tropical Diseases, 2010, 4, e673.	1.3	40
140	CircadiOmics: circadian omic web portal. Nucleic Acids Research, 2018, 46, W157-W162.	6.5	39
141	The capacity of feedforward neural networks. Neural Networks, 2019, 116, 288-311.	3.3	39
142	Mitochondrial Mutations in Subjects with Psychiatric Disorders. PLoS ONE, 2015, 10, e0127280.	1.1	39
143	Contrastive Learning and Neural Oscillations. Neural Computation, 1991, 3, 526-545.	1.3	38
144	Deep Learning for Drug Discovery and Cancer Research: Automated Analysis of Vascularization Images. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1029-1035.	1.9	38

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145	Distinct metabolic adaptation of liver circadian pathways to acute and chronic patterns of alcohol intake. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25250-25259.	3.3	38
146	Development and validation of a deep neural network model to predict postoperative mortality, acute kidney injury, and reintubation using a single feature set. Npj Digital Medicine, 2020, 3, 58.	5.7	38
147	Speeding Up Chemical Database Searches Using a Proximity Filter Based on the Logical Exclusive OR. Journal of Chemical Information and Modeling, 2008, 48, 1367-1378.	2.5	37
148	Modeling user reputation in wikis. Statistical Analysis and Data Mining, 2010, 3, 126-139.	1.4	36
149	Identification of immunodominant antigens of Chlamydia trachomatis using proteome microarrays. Vaccine, 2010, 28, 3014-3024.	1.7	36
150	Complex-valued autoencoders. Neural Networks, 2012, 33, 136-147.	3.3	36
151	UWB ad-hoc networks. , 0, , .		35
152	Training and Validation of Deep Neural Networks for the Prediction of 90-Day Post-Liver Transplant Mortality Using UNOS Registry Data. Transplantation Proceedings, 2020, 52, 246-258.	0.3	35
153	The TCF C-clamp DNA binding domain expands the Wnt transcriptome via alternative target recognition. Nucleic Acids Research, 2014, 42, 13615-13632.	6.5	34
154	Combining protein secondary structure prediction models with ensemble methods of optimal complexity. Neurocomputing, 2004, 56, 305-327.	3.5	33
155	Functional Conservation of LncRNA JPX Despite Sequence and Structural Divergence. Journal of Molecular Biology, 2020, 432, 283-300.	2.0	33
156	Classifying shoulder implants in X-ray images using deep learning. Computational and Structural Biotechnology Journal, 2020, 18, 967-972.	1.9	33
157	Hybrid Modeling, HMM/NN Architectures, and Protein Applications. Neural Computation, 1996, 8, 1541-1565.	1.3	32
158	Mir-132/212 is required for maturation of binocular matching of orientation preference and depth perception. Nature Communications, 2017, 8, 15488.	5.8	31
159	Hippocampal gene expression patterns linked to late-life physical activity oppose age and AD-related transcriptional decline. Neurobiology of Aging, 2019, 78, 142-154.	1.5	31
160	Mining the coherence of GNOME bug reports with statistical topic models. , 2009, , .		29
161	Temporal Evolution of Generalization during Learning in Linear Networks. Neural Computation, 1991, 3, 589-603.	1.3	28
162	Functional Census of Mutation Sequence Spaces: The Example of p53 Cancer Rescue Mutants. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 114-125.	1.9	28

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163	Hashing Algorithms and Data Structures for Rapid Searches of Fingerprint Vectors. Journal of Chemical Information and Modeling, 2010, 50, 1358-1368.	2.5	28
164	Data-Driven High-Throughput Prediction of the 3-D Structure of Small Molecules: Review and Progress. Journal of Chemical Information and Modeling, 2011, 51, 760-776.	2.5	27
165	Reshaping circadian metabolism in the suprachiasmatic nucleus and prefrontal cortex by nutritional challenge. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29904-29913.	3.3	27
166	Software Acoustic Modems for Short Range Mote-based Underwater Sensor Networks. , 2006, , .		25
167	Learning to play Go using recursive neural networks. Neural Networks, 2008, 21, 1392-1400.	3.3	25
168	SELECTpro: effective protein model selection using a structure-based energy function resistant to BLUNDERs. BMC Structural Biology, 2008, 8, 52.	2.3	24
169	The pervasiveness and plasticity of circadian oscillations: the coupled circadian-oscillators framework. Bioinformatics, 2015, 31, 3181-3188.	1.8	24
170	Structural basis for triplet repeat disorders: a computational analysis. Bioinformatics, 1999, 15, 918-929.	1.8	23
171	Accurate and efficient target prediction using a potency-sensitive influence-relevance voter. Journal of Cheminformatics, 2015, 7, 63.	2.8	23
172	SPLASH: Learnable activation functions for improving accuracy and adversarial robustness. Neural Networks, 2021, 140, 1-12.	3.3	23
173	Mutation of neuron-specific chromatin remodeling subunit BAF53b: rescue of plasticity and memory by manipulating actin remodeling. Learning and Memory, 2017, 24, 199-209.	0.5	21
174	Gap Junction Channels of Innexins and Connexins: Relations and Computational Perspectives. International Journal of Molecular Sciences, 2019, 20, 2476.	1.8	21
175	Speeding Up Chemical Searches Using the Inverted Index: The Convergence of Chemoinformatics and Text Search Methods. Journal of Chemical Information and Modeling, 2012, 52, 891-900.	2.5	20
176	Assessing the Potential of Deep Learning for Emulating Cloud Superparameterization in Climate Models With Real€Geography Boundary Conditions. Journal of Advances in Modeling Earth Systems, 2021, 13, e2020MS002385.	1.3	20
177	Hippocampal ensembles represent sequential relationships among an extended sequence of nonspatial events. Nature Communications, 2022, 13, 787.	5.8	20
178	An Intersection Inequality Sharper than the Tanimoto Triangle Inequality for Efficiently Searching Large Databases. Journal of Chemical Information and Modeling, 2009, 49, 1866-1870.	2.5	19
179	VIRALpro: a tool to identify viral capsid and tail sequences. Bioinformatics, 2016, 32, 1405-1407.	1.8	19
180	Genome Architecture Mediates Transcriptional Control of Human Myogenic Reprogramming. IScience, 2018, 6, 232-246.	1.9	19

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181	Improved energy reconstruction in NOvA with regression convolutional neural networks. Physical Review D, 2019, 99, .	1.6	19
182	Cocaine-mediated circadian reprogramming in the striatum through dopamine D2R and PPARÎ³ activation. Nature Communications, 2020, 11, 4448.	5.8	19
183	FKBP10 Regulates Protein Translation to Sustain Lung Cancer Growth. Cell Reports, 2020, 30, 3851-3863.e6.	2.9	19
184	Patterns of cilia gene dysregulations in major psychiatric disorders. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2021, 109, 110255.	2.5	19
185	Modular DAGâ€"RNN Architectures for Assembling Coarse Protein Structures. Journal of Computational Biology, 2006, 13, 631-650.	0.8	18
186	Learning in the machine: The symmetries of the deep learning channel. Neural Networks, 2017, 95, 110-133.	3.3	18
187	An end-to-end CNN with attentional mechanism applied to raw EEG in a BCI classification task. Journal of Neural Engineering, 2021, 18, 0460e3.	1.8	18
188	On the convergence of a clustering algorithm for protein-coding regions in microbial genomes. Bioinformatics, 2000, 16, 367-371.	1.8	17
189	Function and Regulation of Cph2 in Candida albicans. Eukaryotic Cell, 2015, 14, 1114-1126.	3.4	17
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