

# Pierre Baldi

## List of Publications by Citations

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277  
papers

23,697  
citations

75  
h-index

151  
g-index

303  
ext. papers

27,924  
ext. citations

8.2  
avg, IF

7.29  
L-index

#	Paper	IF	Citations
277	Assessing the accuracy of prediction algorithms for classification: an overview. <i>Bioinformatics</i> , <b>2000</b> , 16, 412-24	7.2	1447
276	A Bayesian framework for the analysis of microarray expression data: regularized t-test and statistical inferences of gene changes. <i>Bioinformatics</i> , <b>2001</b> , 17, 509-19	7.2	1360
275	CircadiOmics: integrating circadian genomics, transcriptomics, proteomics and metabolomics. <i>Nature Methods</i> , <b>2012</b> , 9, 772-3	21.6	1084
274	Neural networks and principal component analysis: Learning from examples without local minima. <i>Neural Networks</i> , <b>1989</b> , 2, 53-58	9.1	700
273	SCRATCH: a protein structure and structural feature prediction server. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W72-6	20.1	678
272	Mitochondrial mutations in cancer. <i>Oncogene</i> , <b>2006</b> , 25, 4647-62	9.2	640
271	Bayesian surprise attracts human attention. <i>Vision Research</i> , <b>2009</b> , 49, 1295-306	2.1	616
270	Improving the prediction of protein secondary structure in three and eight classes using recurrent neural networks and profiles. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 47, 228-35	4.2	561
269	Prediction of protein stability changes for single-site mutations using support vector machines. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 62, 1125-32	4.2	546
268	An enhanced MITOMAP with a global mtDNA mutational phylogeny. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D823-8	20.1	446
267	Searching for exotic particles in high-energy physics with deep learning. <i>Nature Communications</i> , <b>2014</b> , 5, 4308	17.4	444
266	Reprogramming of the circadian clock by nutritional challenge. <i>Cell</i> , <b>2013</b> , 155, 1464-78	56.2	421
265	Highly Accurate Machine Fault Diagnosis Using Deep Transfer Learning. <i>IEEE Transactions on Industrial Informatics</i> , <b>2019</b> , 15, 2446-2455	11.9	357
264	Deep Learning Localizes and Identifies Polyps in Real Time With 96% Accuracy in Screening Colonoscopy. <i>Gastroenterology</i> , <b>2018</b> , 155, 1069-1078.e8	13.3	347
263	Exploiting the past and the future in protein secondary structure prediction. <i>Bioinformatics</i> , <b>1999</b> , 15, 937-46	7.2	343
262	Profiling the humoral immune response to infection by using proteome microarrays: high-throughput vaccine and diagnostic antigen discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 547-52	11.5	338
261	A prospective analysis of the Ab response to Plasmodium falciparum before and after a malaria season by protein microarray. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 6958-63	11.5	328

260	Deep architectures and deep learning in chemoinformatics: the prediction of aqueous solubility for drug-like molecules. <i>Journal of Chemical Information and Modeling</i> , <b>2013</b> , 53, 1563-75	6.1	317
259	Coordination of the transcriptome and metabolome by the circadian clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 5541-6	11.5	307
258	Hidden Markov models of biological primary sequence information. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1994</b> , 91, 1059-63	11.5	301
257	Improved statistical inference from DNA microarray data using analysis of variance and a Bayesian statistical framework. Analysis of global gene expression in Escherichia coli K12. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 19937-44	5.4	282
256	Graph kernels for chemical informatics. <i>Neural Networks</i> , <b>2005</b> , 18, 1093-110	9.1	263
255	SSpro/ACCpro 5: almost perfect prediction of protein secondary structure and relative solvent accessibility using profiles, machine learning and structural similarity. <i>Bioinformatics</i> , <b>2014</b> , 30, 2592-7	7.2	249
254	SOLpro: accurate sequence-based prediction of protein solubility. <i>Bioinformatics</i> , <b>2009</b> , 25, 2200-7	7.2	243
253	Muscle insulin sensitivity and glucose metabolism are controlled by the intrinsic muscle clock. <i>Molecular Metabolism</i> , <b>2014</b> , 3, 29-41	8.8	242
252	Global gene expression profiling in Escherichia coli K12. The effects of oxygen availability and FNR. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 29837-55	5.4	231
251	Profiling humoral immune responses to P. falciparum infection with protein microarrays. <i>Proteomics</i> , <b>2008</b> , 8, 4680-94	4.8	213
250	Partitioning circadian transcription by SIRT6 leads to segregated control of cellular metabolism. <i>Cell</i> , <b>2014</b> , 158, 659-72	56.2	207
249	High-throughput prediction of protein antigenicity using protein microarray data. <i>Bioinformatics</i> , <b>2010</b> , 26, 2936-43	7.2	203
248	Deep-Learning Convolutional Neural Networks Accurately Classify Genetic Mutations in Gliomas. <i>American Journal of Neuroradiology</i> , <b>2018</b> , 39, 1201-1207	4.4	202
247	Deep architectures for protein contact map prediction. <i>Bioinformatics</i> , <b>2012</b> , 28, 2449-57	7.2	200
246	Prediction of coordination number and relative solvent accessibility in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 47, 142-53	4.2	199
245	A principled approach to detecting surprising events in video		176
244	Circadian clock regulates the host response to Salmonella. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 9897-902	11.5	173
243	The neuron-specific chromatin regulatory subunit BAF53b is necessary for synaptic plasticity and memory. <i>Nature Neuroscience</i> , <b>2013</b> , 16, 552-61	25.5	172

242	Of bits and wows: A Bayesian theory of surprise with applications to attention. <i>Neural Networks</i> , <b>2010</b> , 23, 649-66	9.1	166
241	PEPITO: improved discontinuous B-cell epitope prediction using multiple distance thresholds and half sphere exposure. <i>Bioinformatics</i> , <b>2008</b> , 24, 1459-60	7.2	165
240	Accurate Prediction of Protein Disordered Regions by Mining Protein Structure Data. <i>Data Mining and Knowledge Discovery</i> , <b>2005</b> , 11, 213-222	5.6	163
239	Improved residue contact prediction using support vector machines and a large feature set. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 113	3.6	162
238	Atlas of Circadian Metabolism Reveals System-wide Coordination and Communication between Clocks. <i>Cell</i> , <b>2018</b> , 174, 1571-1585.e11	56.2	157
237	Global gene expression profiling in Escherichia coli K12: effects of oxygen availability and ArcA. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 15084-96	5.4	155
236	Towards a systems view of IBS. <i>Nature Reviews Gastroenterology and Hepatology</i> , <b>2015</b> , 12, 592-605	24.2	154
235	The Dropout Learning Algorithm. <i>Artificial Intelligence</i> , <b>2014</b> , 210, 78-122	3.6	147
234	Lung Adenocarcinoma Distally Rewires Hepatic Circadian Homeostasis. <i>Cell</i> , <b>2016</b> , 165, 896-909	56.2	147
233	ChemDB: a public database of small molecules and related chemoinformatics resources. <i>Bioinformatics</i> , <b>2005</b> , 21, 4133-9	7.2	132
232	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , <b>2017</b> , 32, 380-393	3.2	127
231	Sourcerer: mining and searching internet-scale software repositories. <i>Data Mining and Knowledge Discovery</i> , <b>2009</b> , 18, 300-336	5.6	127
230	Kernels for small molecules and the prediction of mutagenicity, toxicity and anti-cancer activity. <i>Bioinformatics</i> , <b>2005</b> , 21 Suppl 1, i359-68	7.2	125
229	Cyber-T web server: differential analysis of high-throughput data. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W553-9	20.1	120
228	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> . <i>Infection and Immunity</i> , <b>2008</b> , 76, 3374-89	3.7	119
227	Circadian acetylome reveals regulation of mitochondrial metabolic pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 3339-44	11.5	118
226	COBEpro: a novel system for predicting continuous B-cell epitopes. <i>Protein Engineering, Design and Selection</i> , <b>2009</b> , 22, 113-20	1.9	117
225	Defining the Independence of the Liver Circadian Clock. <i>Cell</i> , <b>2019</b> , 177, 1448-1462.e14	56.2	116

224	Learning to predict chemical reactions. <i>Journal of Chemical Information and Modeling</i> , <b>2011</b> , 51, 2209-22	6.1	116
223	Global gene expression profiling in Escherichia coli K12. The effects of leucine-responsive regulatory protein. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 40309-23	5.4	116
222	Detecting Cardiovascular Disease from Mammograms With Deep Learning. <i>IEEE Transactions on Medical Imaging</i> , <b>2017</b> , 36, 1172-1181	11.7	113
221	MotifMap: integrative genome-wide maps of regulatory motif sites for model species. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 495	3.6	113
220	Sterile protective immunity to malaria is associated with a panel of novel P. falciparum antigens. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M1111.007948	7.6	112
219	Jet substructure classification in high-energy physics with deep neural networks. <i>Physical Review D</i> , <b>2016</b> , 93,	4.9	111
218	Prediction of contact maps by GIOHMMs and recurrent neural networks using lateral propagation from all four cardinal corners. <i>Bioinformatics</i> , <b>2002</b> , 18 Suppl 1, S62-70	7.2	110
217	Distinct Circadian Signatures in Liver and Gut Clocks Revealed by Ketogenic Diet. <i>Cell Metabolism</i> , <b>2017</b> , 26, 523-538.e5	24.6	103
216	ReactionPredictor: prediction of complex chemical reactions at the mechanistic level using machine learning. <i>Journal of Chemical Information and Modeling</i> , <b>2012</b> , 52, 2526-40	6.1	99
215	Differential analysis of DNA microarray gene expression data. <i>Molecular Microbiology</i> , <b>2003</b> , 47, 871-7	4.1	99
214	ChemDB update--full-text search and virtual chemical space. <i>Bioinformatics</i> , <b>2007</b> , 23, 2348-51	7.2	97
213	Adaptive Low Power Listening for Wireless Sensor Networks. <i>IEEE Transactions on Mobile Computing</i> , <b>2007</b> , 6, 988-1004	4.6	95
212	Deep learning for chemical reaction prediction. <i>Molecular Systems Design and Engineering</i> , <b>2018</b> , 3, 442-458	4.5	92
211	Large-scale prediction of disulphide bridges using kernel methods, two-dimensional recursive neural networks, and weighted graph matching. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 62, 617-29	4.2	90
210	Neural Networks for Fingerprint Recognition. <i>Neural Computation</i> , <b>1993</b> , 5, 402-418	2.9	90
209	Time of Exercise Specifies the Impact on Muscle Metabolic Pathways and Systemic Energy Homeostasis. <i>Cell Metabolism</i> , <b>2019</b> , 30, 92-110.e4	24.6	88
208	Gut microbiota directs PPAR $\alpha$ -driven reprogramming of the liver circadian clock by nutritional challenge. <i>EMBO Reports</i> , <b>2016</b> , 17, 1292-303	6.5	88
207	Parameterized neural networks for high-energy physics. <i>European Physical Journal C</i> , <b>2016</b> , 76, 1	4.2	87

206	Cycles in spatial and temporal chromosomal organization driven by the circadian clock. <i>Nature Structural and Molecular Biology</i> , <b>2013</b> , 20, 1206-13	17.6	86
205	MITOMASTER: a bioinformatics tool for the analysis of mitochondrial DNA sequences. <i>Human Mutation</i> , <b>2009</b> , 30, 1-6	4.7	84
204	Identification of humoral immune responses in protein microarrays using DNA microarray data analysis techniques. <i>Bioinformatics</i> , <b>2006</b> , 22, 1760-6	7.2	84
203	From protein microarrays to diagnostic antigen discovery: a study of the pathogen <i>Francisella tularensis</i> . <i>Bioinformatics</i> , <b>2007</b> , 23, i508-18	7.2	75
202	DOMpro: Protein Domain Prediction Using Profiles, Secondary Structure, Relative Solvent Accessibility, and Recursive Neural Networks. <i>Data Mining and Knowledge Discovery</i> , <b>2006</b> , 13, 1-10	5.6	75
201	Jet flavor classification in high-energy physics with deep neural networks. <i>Physical Review D</i> , <b>2016</b> , 94,	4.9	75
200	A CROC stronger than ROC: measuring, visualizing and optimizing early retrieval. <i>Bioinformatics</i> , <b>2010</b> , 26, 1348-56	7.2	74
199	Bounds and algorithms for fast exact searches of chemical fingerprints in linear and sublinear time. <i>Journal of Chemical Information and Modeling</i> , <b>2007</b> , 47, 302-17	6.1	74
198	When is chemical similarity significant? The statistical distribution of chemical similarity scores and its extreme values. <i>Journal of Chemical Information and Modeling</i> , <b>2010</b> , 50, 1205-22	6.1	73
197	DNA structure in human RNA polymerase II promoters. <i>Journal of Molecular Biology</i> , <b>1998</b> , 281, 663-73	6.5	73
196	OSCILLATIONS AND SYNCHRONIZATIONS IN NEURAL NETWORKS: AN EXPLORATION OF THE LABELING HYPOTHESIS. <i>International Journal of Neural Systems</i> , <b>1989</b> , 01, 103-124	6.2	73
195	Machine learning methods for protein structure prediction. <i>IEEE Reviews in Biomedical Engineering</i> , <b>2008</b> , 1, 41-9	6.4	70
194	Data structures and compression algorithms for genomic sequence data. <i>Bioinformatics</i> , <b>2009</b> , 25, 1731-8	8.2	69
193	Computing with Arrays of Coupled Oscillators: An Application to Preattentive Texture Discrimination. <i>Neural Computation</i> , <b>1990</b> , 2, 458-471	2.9	69
192	Enhanced Higgs boson to $(\tau)(\tau)$ search with deep learning. <i>Physical Review Letters</i> , <b>2015</b> , 114, 111801	7.4	68
191	TMBpro: secondary structure, beta-contact and tertiary structure prediction of transmembrane beta-barrel proteins. <i>Bioinformatics</i> , <b>2008</b> , 24, 513-20	7.2	67
190	Fasting Imparts a Switch to Alternative Daily Pathways in Liver and Muscle. <i>Cell Reports</i> , <b>2018</b> , 25, 3299-3314.e6	11.4	67
189	Smooth On-Line Learning Algorithms for Hidden Markov Models. <i>Neural Computation</i> , <b>1994</b> , 6, 307-318	2.9	65

188	Naturally occurring nucleosome positioning signals in human exons and introns. <i>Journal of Molecular Biology</i> , <b>1996</b> , 263, 503-10	6.5	62
187	A multi-resolution approach for spinal metastasis detection using deep Siamese neural networks. <i>Computers in Biology and Medicine</i> , <b>2017</b> , 84, 137-146	7	60
186	Epigenetic regulation of the circadian gene <i>Per1</i> contributes to age-related changes in hippocampal memory. <i>Nature Communications</i> , <b>2018</b> , 9, 3323	17.4	59
185	The stability and complexity of antibody responses to the major surface antigen of <i>Plasmodium falciparum</i> are associated with age in a malaria endemic area. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M111.008326	7.6	59
184	Population-wide analysis of differences in disease progression patterns in men and women. <i>Nature Communications</i> , <b>2019</b> , 10, 666	17.4	58
183	Decorrelated jet substructure tagging using adversarial neural networks. <i>Physical Review D</i> , <b>2017</b> , 96,	4.9	58
182	Serological profiling of a <i>Candida albicans</i> protein microarray reveals permanent host-pathogen interplay and stage-specific responses during candidemia. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1000827	7.6	58
181	Discovery of power-laws in chemical space. <i>Journal of Chemical Information and Modeling</i> , <b>2008</b> , 48, 1138651		53
180	Comparative Circadian Metabolomics Reveal Differential Effects of Nutritional Challenge in the Serum and Liver. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 2812-28	5.4	50
179	One- to four-dimensional kernels for virtual screening and the prediction of physical, chemical, and biological properties. <i>Journal of Chemical Information and Modeling</i> , <b>2007</b> , 47, 965-74	6.1	49
178	Mathematical correction for fingerprint similarity measures to improve chemical retrieval. <i>Journal of Chemical Information and Modeling</i> , <b>2007</b> , 47, 952-64	6.1	46
177	. <i>IEEE Transactions on Information Theory</i> , <b>1988</b> , 34, 523-530	2.8	46
176	ClusterCAD: a computational platform for type I modular polyketide synthase design. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D509-D515	20.1	45
175	Sequence analysis by additive scales: DNA structure for sequences and repeats of all lengths. <i>Bioinformatics</i> , <b>2000</b> , 16, 865-89	7.2	45
174	Sequence Assembly of <i>Yarrowia lipolytica</i> Strain W29/CLIB89 Shows Transposable Element Diversity. <i>PLoS ONE</i> , <b>2016</b> , 11, e0162363	3.7	45
173	Influence relevance voting: an accurate and interpretable virtual high throughput screening method. <i>Journal of Chemical Information and Modeling</i> , <b>2009</b> , 49, 756-66	6.1	43
172	No electron left behind: a rule-based expert system to predict chemical reactions and reaction mechanisms. <i>Journal of Chemical Information and Modeling</i> , <b>2009</b> , 49, 2034-43	6.1	43
171	SIDepro: a novel machine learning approach for the fast and accurate prediction of side-chain conformations. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2012</b> , 80, 142-53	4.2	42

170	Lossless compression of chemical fingerprints using integer entropy codes improves storage and retrieval. <i>Journal of Chemical Information and Modeling</i> , <b>2007</b> , 47, 2098-109	6.1	41
169	Modeling and optimization of UWB communication networks through a flexible cost function. <i>IEEE Journal on Selected Areas in Communications</i> , <b>2002</b> , 20, 1733-1744	14.2	41
168	Deep Learning in Biomedical Data Science. <i>Annual Review of Biomedical Data Science</i> , <b>2018</b> , 1, 181-205	5.6	40
167	An Application of Latent Dirichlet Allocation to Analyzing Software Evolution <b>2008</b> ,		39
166	What time is it? Deep learning approaches for circadian rhythms. <i>Bioinformatics</i> , <b>2016</b> , 32, i8-i17	7.2	38
165	Identification of immunodominant antigens by probing a whole <i>Chlamydia trachomatis</i> open reading frame proteome microarray using sera from immunized mice. <i>Infection and Immunity</i> , <b>2011</b> , 79, 246-57	3.7	38
164	Distribution patterns of over-represented k-mers in non-coding yeast DNA. <i>Bioinformatics</i> , <b>2002</b> , 18, 513-28	7.2	38
163	Metabolic changes associated with methionine stress sensitivity in MDA-MB-468 breast cancer cells. <i>Cancer &amp; Metabolism</i> , <b>2016</b> , 4, 9	5.4	38
162	SIRT6 Suppresses Cancer Stem-like Capacity in Tumors with PI3K Activation Independently of Its Deacetylase Activity. <i>Cell Reports</i> , <b>2017</b> , 18, 1858-1868	10.6	37
161	A WNT/p21 circuit directed by the C-clamp, a sequence-specific DNA binding domain in TCFs. <i>Molecular and Cellular Biology</i> , <b>2012</b> , 32, 3648-62	4.8	37
160	Mining Eclipse Developer Contributions via Author-Topic Models <b>2007</b> ,		37
159	Enforcing Analytic Constraints in Neural Networks Emulating Physical Systems. <i>Physical Review Letters</i> , <b>2021</b> , 126, 098302	7.4	37
158	Longitudinal Monitoring of Biofilm Formation via Robust Surface-Enhanced Raman Scattering Quantification of <i>Pseudomonas aeruginosa</i> -Produced Metabolites. <i>ACS Applied Materials &amp; Interfaces</i> , <b>2018</b> , 10, 12364-12373	9.5	36
157	Assessment of predictions submitted for the CASP7 domain prediction category. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69 Suppl 8, 137-51	4.2	36
156	Improved prediction of the number of residue contacts in proteins by recurrent neural networks. <i>Bioinformatics</i> , <b>2001</b> , 17 Suppl 1, S234-42	7.2	36
155	Sherpa: Robust hyperparameter optimization for machine learning. <i>SoftwareX</i> , <b>2020</b> , 12, 100591	2.7	35
154	A theory of local learning, the learning channel, and the optimality of backpropagation. <i>Neural Networks</i> , <b>2016</b> , 83, 51-74	9.1	34
153	Synergies Between Quantum Mechanics and Machine Learning in Reaction Prediction. <i>Journal of Chemical Information and Modeling</i> , <b>2016</b> , 56, 2125-2128	6.1	34



152	Identification of immunodominant antigens of Chlamydia trachomatis using proteome microarrays. <i>Vaccine</i> , <b>2010</b> , 28, 3014-24	4.1	34
151	Speeding up chemical database searches using a proximity filter based on the logical exclusive or. <i>Journal of Chemical Information and Modeling</i> , <b>2008</b> , 48, 1367-78	6.1	34
150	Contrastive Learning and Neural Oscillations. <i>Neural Computation</i> , <b>1991</b> , 3, 526-545	2.9	34
149	Large scale immune profiling of infected humans and goats reveals differential recognition of Brucella melitensis antigens. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e673	4.8	33
148	SourcererDB: An aggregated repository of statically analyzed and cross-linked open source Java projects <b>2009</b> ,		31
147	Mitochondrial mutations in subjects with psychiatric disorders. <i>PLoS ONE</i> , <b>2015</b> , 10, e0127280	3.7	31
146	Data structures and compression algorithms for high-throughput sequencing technologies. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 514	3.6	30
145	Beep: 3D indoor positioning using audible sound		30
144	Complex-valued autoencoders. <i>Neural Networks</i> , <b>2012</b> , 33, 136-47	9.1	29
143	<b>2002</b> ,		29
142	Deep Learning for Drug Discovery and Cancer Research: Automated Analysis of Vascularization Images. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2019</b> , 16, 1029-1035	3	28
141	Modeling user reputation in wikis. <i>Statistical Analysis and Data Mining</i> , <b>2010</b> , 3, 126-139	1.4	28
140	Hybrid modeling, HMM/NN architectures, and protein applications. <i>Neural Computation</i> , <b>1996</b> , 8, 1541-65.9		28
139	Deep Learning Analysis of Vibrational Spectra of Bacterial Lysate for Rapid Antimicrobial Susceptibility Testing. <i>ACS Nano</i> , <b>2020</b> , 14, 15336-15348	16.7	28
138	Solving the Rubik's cube with deep reinforcement learning and search. <i>Nature Machine Intelligence</i> , <b>2019</b> , 1, 356-363	22.5	27
137	Combining protein secondary structure prediction models with ensemble methods of optimal complexity. <i>Neurocomputing</i> , <b>2004</b> , 56, 305-327	5.4	27
136	Learning in the Machine: Random Backpropagation and the Deep Learning Channel. <i>Artificial Intelligence</i> , <b>2018</b> , 260, 1-35	3.6	26
135	The TCF C-clamp DNA binding domain expands the Wnt transcriptome via alternative target recognition. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 13615-32	20.1	26

134	Hashing algorithms and data structures for rapid searches of fingerprint vectors. <i>Journal of Chemical Information and Modeling</i> , <b>2010</b> , 50, 1358-68	6.1	26
133	Mir-132/212 is required for maturation of binocular matching of orientation preference and depth perception. <i>Nature Communications</i> , <b>2017</b> , 8, 15488	17.4	25
132	CircadiOmics: circadian omic web portal. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W157-W162	20.1	25
131	Mining the coherence of GNOME bug reports with statistical topic models <b>2009</b> ,		25
130	The circadian dynamics of the hippocampal transcriptome and proteome is altered in experimental temporal lobe epilepsy. <i>Science Advances</i> , <b>2020</b> , 6,	14.3	24
129	Structural basis for triplet repeat disorders: a computational analysis. <i>Bioinformatics</i> , <b>1999</b> , 15, 918-29	7.2	23
128	Temporal Evolution of Generalization during Learning in Linear Networks. <i>Neural Computation</i> , <b>1991</b> , 3, 589-603	2.9	23
127	A Fortran-Keras Deep Learning Bridge for Scientific Computing. <i>Scientific Programming</i> , <b>2020</b> , 2020, 1-13	1.4	23
126	Functional census of mutation sequence spaces: the example of p53 cancer rescue mutants. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2006</b> , 3, 114-25	3	22
125	Functional Conservation of LncRNA JPX Despite Sequence and Structural Divergence. <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 283-300	6.5	22
124	SELECTpro: effective protein model selection using a structure-based energy function resistant to BLUNDERS. <i>BMC Structural Biology</i> , <b>2008</b> , 8, 52	2.7	21
123	Hippocampal gene expression patterns linked to late-life physical activity oppose age and AD-related transcriptional decline. <i>Neurobiology of Aging</i> , <b>2019</b> , 78, 142-154	5.6	20
122	An automated machine learning-based model predicts postoperative mortality using readily-extractable preoperative electronic health record data. <i>British Journal of Anaesthesia</i> , <b>2019</b> , 123, 877-886	5.4	20
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