

Pierre Baldi

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1797961/pierre-baldi-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Quantum Mechanics and Machine Learning Synergies: Graph Attention Neural Networks to Predict Chemical Reactivity.. <i>Journal of Chemical Information and Modeling</i> , 2022 ,	6.1	3
276	Atlas of exercise metabolism reveals time-dependent signatures of metabolic homeostasis.. <i>Cell Metabolism</i> , 2022 ,	24.6	14
275	Deep Learning from Four Vectors 2022 , 59-83		
274	Hippocampal ensembles represent sequential relationships among an extended sequence of nonspatial events.. <i>Nature Communications</i> , 2022 , 13, 787	17.4	3
273	Deep Learning from Four Vectors 2022 , 59-83		
272	Real-time reconstruction of high energy, ultrafast laser pulses using deep learning.. <i>Scientific Reports</i> , 2022 , 12, 5299	4.9	0
271	Weakly Supervised Polyp Segmentation in Colonoscopy Images Using Deep Neural Networks. <i>Journal of Imaging</i> , 2022 , 8, 121	3.1	0
270	Deep Learning-Assisted Multiphoton Microscopy to Reduce Light Exposure and Expedite Imaging in Tissues With High and Low Light Sensitivity. <i>Translational Vision Science and Technology</i> , 2021 , 10, 30	3.3	2
269	Call for a Public Open Database of All Chemical Reactions. <i>Journal of Chemical Information and Modeling</i> , 2021 ,	6.1	3
268	Learning to isolate muons. <i>Journal of High Energy Physics</i> , 2021 , 2021, 1	5.4	1
267	Transcriptome Profiling of Dysregulated GPCRs Reveals Overlapping Patterns across Psychiatric Disorders and Age-Disease Interactions. <i>Cells</i> , 2021 , 10,	7.9	3
266	Enforcing Analytic Constraints in Neural Networks Emulating Physical Systems. <i>Physical Review Letters</i> , 2021 , 126, 098302	7.4	37
265	Deep Learning in Science 2021 ,		14
264	Assessing the Potential of Deep Learning for Emulating Cloud Superparameterization in Climate Models With Real-Geography Boundary Conditions. <i>Journal of Advances in Modeling Earth Systems</i> , 2021 , 13, e2020MS002385	7.1	6
263	Learning to identify electrons. <i>Physical Review D</i> , 2021 , 103,	4.9	2
262	Intergenerational trauma transmission is associated with brain metabotranscriptome remodeling and mitochondrial dysfunction. <i>Communications Biology</i> , 2021 , 4, 783	6.7	2
261	Patterns of cilia gene dysregulations in major psychiatric disorders. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021 , 109, 110255	5.5	8

260	Large-scale analysis reveals spatiotemporal circadian patterns of cilia transcriptomes in the primate brain. <i>Journal of Neuroscience Research</i> , 2021 , 99, 2610-2624	4.4	2
259	Age-Related Neurometabolomic Signature of Mouse Brain. <i>ACS Chemical Neuroscience</i> , 2021 , 12, 2887-2902	3.9	1
258	Fold recognition by scoring protein maps using the congruence coefficient. <i>Bioinformatics</i> , 2021 , 37, 506-513	7.2	
257	Combining Deep Learning With Optical Coherence Tomography Imaging to Determine Scalp Hair and Follicle Counts. <i>Lasers in Surgery and Medicine</i> , 2021 , 53, 171-178	3.6	4
256	Sparse autoregressive models for scalable generation of sparse images in particle physics. <i>Physical Review D</i> , 2021 , 103,	4.9	7
255	Methyl Cation Affinities of Canonical Organic Functional Groups. <i>Journal of Organic Chemistry</i> , 2021 , 86, 3721-3729	4.2	2
254	SPLASH: Learnable activation functions for improving accuracy and adversarial robustness. <i>Neural Networks</i> , 2021 , 140, 1-12	9.1	7
253	An end-to-end CNN with attentional mechanism applied to raw EEG in a BCI classification task. <i>Journal of Neural Engineering</i> , 2021 , 18,	5	5
252	Detecting pulmonary Coccidioidomycosis with deep convolutional neural networks. <i>Machine Learning With Applications</i> , 2021 , 5, 100040	6.5	2
251	Integration of feeding behavior by the liver circadian clock reveals network dependency of metabolic rhythms. <i>Science Advances</i> , 2021 , 7, eabi7828	14.3	2
250	Dynamic Changes of Brain Cilia Transcriptomes across the Human Lifespan. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
249	A theory of capacity and sparse neural encoding. <i>Neural Networks</i> , 2021 , 143, 12-27	9.1	0
248	Development and validation of an interpretable neural network for prediction of postoperative in-hospital mortality. <i>Npj Digital Medicine</i> , 2021 , 4, 8	15.7	5
247	Protein profiles: Biases and protocols. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 2281-2289	6.8	2
246	FKBP10 Regulates Protein Translation to Sustain Lung Cancer Growth. <i>Cell Reports</i> , 2020 , 30, 3851-3863.e6	10.6	3
245	Training and Validation of Deep Neural Networks for the Prediction of 90-Day Post-Liver Transplant Mortality Using UNOS Registry Data. <i>Transplantation Proceedings</i> , 2020 , 52, 246-258	1.1	11
244	Development and validation of a deep neural network model to predict postoperative mortality, acute kidney injury, and reintubation using a single feature set. <i>Npj Digital Medicine</i> , 2020 , 3, 58	15.7	12
243	Classifying shoulder implants in X-ray images using deep learning. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 967-972	6.8	13

242	MiR-29 coordinates age-dependent plasticity brakes in the adult visual cortex. <i>EMBO Reports</i> , 2020 , 21, e50431	6.5	7
241	A Fortran-Keras Deep Learning Bridge for Scientific Computing. <i>Scientific Programming</i> , 2020 , 2020, 1-13	1.4	23
240	Sherpa: Robust hyperparameter optimization for machine learning. <i>SoftwareX</i> , 2020 , 12, 100591	2.7	35
239	The circadian dynamics of the hippocampal transcriptome and proteome is altered in experimental temporal lobe epilepsy. <i>Science Advances</i> , 2020 , 6,	14.3	24
238	Methyl Anion Affinities of the Canonical Organic Functional Groups. <i>Journal of Organic Chemistry</i> , 2020 , 85, 4096-4102	4.2	9
237	Reshaping circadian metabolism in the suprachiasmatic nucleus and prefrontal cortex by nutritional challenge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 29904-29913	11.5	9
236	Metabolomic and transcriptomic signatures of prenatal excessive methionine support nature rather than nurture in schizophrenia pathogenesis. <i>Communications Biology</i> , 2020 , 3, 409	6.7	8
235	A non-pharmacological therapeutic approach in the gut triggers distal metabolic rewiring capable of ameliorating diet-induced dysfunctions encompassed by metabolic syndrome. <i>Scientific Reports</i> , 2020 , 10, 12915	4.9	2
234	Deep Learning Analysis of Vibrational Spectra of Bacterial Lysate for Rapid Antimicrobial Susceptibility Testing. <i>ACS Nano</i> , 2020 , 14, 15336-15348	16.7	28
233	Cocaine-mediated circadian reprogramming in the striatum through dopamine D2R and PPAR α activation. <i>Nature Communications</i> , 2020 , 11, 4448	17.4	11
232	S-adenosyl-L-homocysteine hydrolase links methionine metabolism to the circadian clock and chromatin remodeling. <i>Science Advances</i> , 2020 , 6,	14.3	20
231	Structure, self-assembly, and properties of a truncated reflectin variant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 ,	11.5	4
230	Functional Conservation of LncRNA JPX Despite Sequence and Structural Divergence. <i>Journal of Molecular Biology</i> , 2020 , 432, 283-300	6.5	22
229	Bayesian Causality. <i>American Statistician</i> , 2020 , 74, 249-257	5	1
228	Learning in the machine: To share or not to share?. <i>Neural Networks</i> , 2020 , 126, 235-249	9.1	4
227	Improved energy reconstruction in NOVA with regression convolutional neural networks. <i>Physical Review D</i> , 2019 , 99,	4.9	11
226	Defining the Independence of the Liver Circadian Clock. <i>Cell</i> , 2019 , 177, 1448-1462.e14	56.2	116
225	Light Entrain Diurnal Changes in Insulin Sensitivity of Skeletal Muscle via Ventromedial Hypothalamic Neurons. <i>Cell Reports</i> , 2019 , 27, 2385-2398.e3	10.6	10

224	Gap Junction Channels of Innexins and Connexins: Relations and Computational Perspectives. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	11
223	Time of Exercise Specifies the Impact on Muscle Metabolic Pathways and Systemic Energy Homeostasis. <i>Cell Metabolism</i> , 2019 , 30, 92-110.e4	24.6	88
222	The capacity of feedforward neural networks. <i>Neural Networks</i> , 2019 , 116, 288-311	9.1	19
221	Hippocampal gene expression patterns linked to late-life physical activity oppose age and AD-related transcriptional decline. <i>Neurobiology of Aging</i> , 2019 , 78, 142-154	5.6	20
220	Population-wide analysis of differences in disease progression patterns in men and women. <i>Nature Communications</i> , 2019 , 10, 666	17.4	58
219	Deep Learning for Drug Discovery and Cancer Research: Automated Analysis of Vascularization Images. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1029-1035	3	28
218	Highly Accurate Machine Fault Diagnosis Using Deep Transfer Learning. <i>IEEE Transactions on Industrial Informatics</i> , 2019 , 15, 2446-2455	11.9	357
217	Mitochondrial Akt Signaling Modulated Reprogramming of Somatic Cells. <i>Scientific Reports</i> , 2019 , 9, 9912	4.9	12
216	Solving the Rubik's cube with deep reinforcement learning and search. <i>Nature Machine Intelligence</i> , 2019 , 1, 356-363	22.5	27
215	Local features determine Ty3 targeting frequency at RNA polymerase III transcription start sites. <i>Genome Research</i> , 2019 , 29, 1298-1309	9.7	6
214	An automated machine learning-based model predicts postoperative mortality using readily-extractable preoperative electronic health record data. <i>British Journal of Anaesthesia</i> , 2019 , 123, 877-886	5.4	20
213	Polynomial Threshold Functions, Hyperplane Arrangements, and Random Tensors. <i>SIAM Journal on Mathematics of Data Science</i> , 2019 , 1, 699-729	3.1	6
212	On neuronal capacity. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2019 , 2019, 124012	1.9	
211	Machine learning of physiological waveforms and electronic health record data to predict, diagnose and treat haemodynamic instability in surgical patients: protocol for a retrospective study. <i>BMJ Open</i> , 2019 , 9, e031988	3	5
210	Distinct metabolic adaptation of liver circadian pathways to acute and chronic patterns of alcohol intake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 25250-25259	11.5	17
209	Neural network gradient Hamiltonian Monte Carlo. <i>Computational Statistics</i> , 2019 , 34, 281-299	1	2
208	Learning in the Machine: Random Backpropagation and the Deep Learning Channel. <i>Artificial Intelligence</i> , 2018 , 260, 1-35	3.6	26
207	Inner and Outer Recursive Neural Networks for Chemoinformatics Applications. <i>Journal of Chemical Information and Modeling</i> , 2018 , 58, 207-211	6.1	10

206	Deep Learning in Biomedical Data Science. <i>Annual Review of Biomedical Data Science</i> , 2018 , 1, 181-205	5.6	40
205	Longitudinal Monitoring of Biofilm Formation via Robust Surface-Enhanced Raman Scattering Quantification of <i>Pseudomonas aeruginosa</i> -Produced Metabolites. <i>ACS Applied Materials & Interfaces</i> , 2018 , 10, 12364-12373	9.5	36
204	ClusterCAD: a computational platform for type I modular polyketide synthase design. <i>Nucleic Acids Research</i> , 2018 , 46, D509-D515	20.1	45
203	Deep-Learning Convolutional Neural Networks Accurately Classify Genetic Mutations in Gliomas. <i>American Journal of Neuroradiology</i> , 2018 , 39, 1201-1207	4.4	202
202	Epigenetic regulation of the circadian gene <i>Per1</i> contributes to age-related changes in hippocampal memory. <i>Nature Communications</i> , 2018 , 9, 3323	17.4	59
201	CircadiOmics: circadian omic web portal. <i>Nucleic Acids Research</i> , 2018 , 46, W157-W162	20.1	25
200	Deep learning for chemical reaction prediction. <i>Molecular Systems Design and Engineering</i> , 2018 , 3, 442-452	4.5	92
199	The inner and outer approaches to the design of recursive neural architectures. <i>Data Mining and Knowledge Discovery</i> , 2018 , 32, 218-230	5.6	6
198	Fasting Imparts a Switch to Alternative Daily Pathways in Liver and Muscle. <i>Cell Reports</i> , 2018 , 25, 3299-3314.e67	33.4	67
197	Learning in the machine: Recirculation is random backpropagation. <i>Neural Networks</i> , 2018 , 108, 479-494	9.1	3
196	Atlas of Circadian Metabolism Reveals System-wide Coordination and Communication between Clocks. <i>Cell</i> , 2018 , 174, 1571-1585.e11	56.2	157
195	Deep Learning Localizes and Identifies Polyps in Real Time With 96% Accuracy in Screening Colonoscopy. <i>Gastroenterology</i> , 2018 , 155, 1069-1078.e8	13.3	347
194	Genome Architecture Mediates Transcriptional Control of Human Myogenic Reprogramming. <i>iScience</i> , 2018 , 6, 232-246	6.1	12
193	Deep Learning in the Natural Sciences: Applications to Physics. <i>Lecture Notes in Computer Science</i> , 2018 , 269-297	0.9	4
192	Detecting Cardiovascular Disease from Mammograms With Deep Learning. <i>IEEE Transactions on Medical Imaging</i> , 2017 , 36, 1172-1181	11.7	113
191	SIRT6 Suppresses Cancer Stem-like Capacity in Tumors with PI3K Activation Independently of Its Deacetylase Activity. <i>Cell Reports</i> , 2017 , 18, 1858-1868	10.6	37
190	Mutation of neuron-specific chromatin remodeling subunit BAF53b: rescue of plasticity and memory by manipulating actin remodeling. <i>Learning and Memory</i> , 2017 , 24, 199-209	2.8	18
189	Mir-132/212 is required for maturation of binocular matching of orientation preference and depth perception. <i>Nature Communications</i> , 2017 , 8, 15488	17.4	25

188	A multi-resolution approach for spinal metastasis detection using deep Siamese neural networks. <i>Computers in Biology and Medicine</i> , 2017 , 84, 137-146	7	60
187	Distinct Circadian Signatures in Liver and Gut Clocks Revealed by Ketogenic Diet. <i>Cell Metabolism</i> , 2017 , 26, 523-538.e5	24.6	103
186	Learning in the machine: The symmetries of the deep learning channel. <i>Neural Networks</i> , 2017 , 95, 110-133	14	
185	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017 , 32, 380-393	3.2	127
184	Decorrelated jet substructure tagging using adversarial neural networks. <i>Physical Review D</i> , 2017 , 96,	4.9	58
183	Efficient antihydrogen detection in antimatter physics by deep learning. <i>Journal of Physics Communications</i> , 2017 , 1, 025001	1.2	6
182	A theory of local learning, the learning channel, and the optimality of backpropagation. <i>Neural Networks</i> , 2016 , 83, 51-74	9.1	34
181	Jet substructure classification in high-energy physics with deep neural networks. <i>Physical Review D</i> , 2016 , 93,	4.9	111
180	Synergies Between Quantum Mechanics and Machine Learning in Reaction Prediction. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 2125-2128	6.1	34
179	What time is it? Deep learning approaches for circadian rhythms. <i>Bioinformatics</i> , 2016 , 32, i8-i17	7.2	38
178	Parameterized neural networks for high-energy physics. <i>European Physical Journal C</i> , 2016 , 76, 1	4.2	87
177	Comparative Circadian Metabolomics Reveal Differential Effects of Nutritional Challenge in the Serum and Liver. <i>Journal of Biological Chemistry</i> , 2016 , 291, 2812-28	5.4	50
176	VIRALpro: a tool to identify viral capsid and tail sequences. <i>Bioinformatics</i> , 2016 , 32, 1405-7	7.2	12
175	Sequence Assembly of <i>Yarrowia lipolytica</i> Strain W29/CLIB89 Shows Transposable Element Diversity. <i>PLoS ONE</i> , 2016 , 11, e0162363	3.7	45
174	Jet flavor classification in high-energy physics with deep neural networks. <i>Physical Review D</i> , 2016 , 94,	4.9	75
173	Metabolic changes associated with methionine stress sensitivity in MDA-MB-468 breast cancer cells. <i>Cancer & Metabolism</i> , 2016 , 4, 9	5.4	38
172	Lung Adenocarcinoma Distally Rewires Hepatic Circadian Homeostasis. <i>Cell</i> , 2016 , 165, 896-909	56.2	147
171	Gut microbiota directs PPAR β -driven reprogramming of the liver circadian clock by nutritional challenge. <i>EMBO Reports</i> , 2016 , 17, 1292-303	6.5	88

170	Towards a systems view of IBS. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2015 , 12, 592-605	24.2	154
169	Function and Regulation of Cph2 in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , 2015 , 14, 1114-26		10
168	Accurate and efficient target prediction using a potency-sensitive influence-relevance voter. <i>Journal of Cheminformatics</i> , 2015 , 7, 63	8.6	19
167	Enhanced Higgs boson to $(\tau^+)(\tau^-)$ search with deep learning. <i>Physical Review Letters</i> , 2015 , 114, 111801	7.4	68
166	The pervasiveness and plasticity of circadian oscillations: the coupled circadian-oscillators framework. <i>Bioinformatics</i> , 2015 , 31, 3181-8	7.2	20
165	Mitochondrial mutations in subjects with psychiatric disorders. <i>PLoS ONE</i> , 2015 , 10, e0127280	3.7	31
164	How pervasive are circadian oscillations?. <i>Trends in Cell Biology</i> , 2014 , 24, 329-31	18.3	13
163	SSpro/ACCpro 5: almost perfect prediction of protein secondary structure and relative solvent accessibility using profiles, machine learning and structural similarity. <i>Bioinformatics</i> , 2014 , 30, 2592-7	7.2	249
162	Partitioning circadian transcription by SIRT6 leads to segregated control of cellular metabolism. <i>Cell</i> , 2014 , 158, 659-72	56.2	207
161	Searching for exotic particles in high-energy physics with deep learning. <i>Nature Communications</i> , 2014 , 5, 4308	17.4	444
160	The Dropout Learning Algorithm. <i>Artificial Intelligence</i> , 2014 , 210, 78-122	3.6	147
159	Muscle insulin sensitivity and glucose metabolism are controlled by the intrinsic muscle clock. <i>Molecular Metabolism</i> , 2014 , 3, 29-41	8.8	242
158	Incorporating post-translational modifications and unnatural amino acids into high-throughput modeling of protein structures. <i>Bioinformatics</i> , 2014 , 30, 1681-9	7.2	6
157	A Genomic Analysis Pipeline and Its Application to Pediatric Cancers. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 826-39	3	2
156	The TCF C-clamp DNA binding domain expands the Wnt transcriptome via alternative target recognition. <i>Nucleic Acids Research</i> , 2014 , 42, 13615-32	20.1	26
155	An Adaptive Reference Point Approach to Efficiently Search Large Chemical Databases. <i>Smart Innovation, Systems and Technologies</i> , 2014 , 63-74	0.5	2
154	Deep architectures and deep learning in chemoinformatics: the prediction of aqueous solubility for drug-like molecules. <i>Journal of Chemical Information and Modeling</i> , 2013 , 53, 1563-75	6.1	317
153	Reprogramming of the circadian clock by nutritional challenge. <i>Cell</i> , 2013 , 155, 1464-78	56.2	421

152	Cycles in spatial and temporal chromosomal organization driven by the circadian clock. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1206-13	17.6	86
151	Circadian acetylome reveals regulation of mitochondrial metabolic pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 3339-44	11.5	118
150	The neuron-specific chromatin regulatory subunit BAF53b is necessary for synaptic plasticity and memory. <i>Nature Neuroscience</i> , 2013 , 16, 552-61	25.5	172
149	Circadian clock regulates the host response to Salmonella. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 9897-902	11.5	173
148	A unifying kinetic framework for modeling oxidoreductase-catalyzed reactions. <i>Bioinformatics</i> , 2013 , 29, 1299-307	7.2	2
147	Complex-valued autoencoders. <i>Neural Networks</i> , 2012 , 33, 136-47	9.1	29
146	Boolean autoencoders and hypercube clustering complexity. <i>Designs, Codes, and Cryptography</i> , 2012 , 65, 383-403	1.2	6
145	Speeding up chemical searches using the inverted index: the convergence of chemoinformatics and text search methods. <i>Journal of Chemical Information and Modeling</i> , 2012 , 52, 891-900	6.1	18
144	ReactionPredictor: prediction of complex chemical reactions at the mechanistic level using machine learning. <i>Journal of Chemical Information and Modeling</i> , 2012 , 52, 2526-40	6.1	99
143	SIDEpro: a novel machine learning approach for the fast and accurate prediction of side-chain conformations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 142-53	4.2	42
142	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> , 2012 , 109, 5541-6	11.5	307
141	A WNT/p21 circuit directed by the C-clamp, a sequence-specific DNA binding domain in TCFs. <i>Molecular and Cellular Biology</i> , 2012 , 32, 3648-62	4.8	37
140	CircadiOmics: integrating circadian genomics, transcriptomics, proteomics and metabolomics. <i>Nature Methods</i> , 2012 , 9, 772-3	21.6	1084
139	Cyber-T web server: differential analysis of high-throughput data. <i>Nucleic Acids Research</i> , 2012 , 40, W553-9	20.1	120
138	Deep architectures for protein contact map prediction. <i>Bioinformatics</i> , 2012 , 28, 2449-57	7.2	200
137	Learning to predict chemical reactions. <i>Journal of Chemical Information and Modeling</i> , 2011 , 51, 2209-22	6.1	116
136	Data-driven high-throughput prediction of the 3-D structure of small molecules: review and progress. <i>Journal of Chemical Information and Modeling</i> , 2011 , 51, 760-76	6.1	19
135	Modeling of mitochondria bioenergetics using a composable chemiosmotic energy transduction rate law: theory and experimental validation. <i>PLoS ONE</i> , 2011 , 6, e14820	3.7	7

134	MotifMap: integrative genome-wide maps of regulatory motif sites for model species. <i>BMC Bioinformatics</i> , 2011 , 12, 495	3.6	113
133	Tree and Hashing Data Structures to Speed up Chemical Searches: Analysis and Experiments. <i>Molecular Informatics</i> , 2011 , 30, 791-800	3.8	6
132	Sterile protective immunity to malaria is associated with a panel of novel <i>P. falciparum</i> antigens. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.007948	7.6	112
131	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> , 2011 , 79, 246-57	3.7	38
130	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> , 2011 , 10, M111.008326	7.6	59
129	A CROC stronger than ROC: measuring, visualizing and optimizing early retrieval. <i>Bioinformatics</i> , 2010 , 26, 1348-56	7.2	74
128	High-throughput prediction of protein antigenicity using protein microarray data. <i>Bioinformatics</i> , 2010 , 26, 2936-43	7.2	203
127	A prospective analysis of the Ab response to <i>Plasmodium falciparum</i> before and after a malaria season by protein microarray. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6958-63	11.5	328
126	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> , 2010 , 6, e1000827	7.6	58
125	Large scale immune profiling of infected humans and goats reveals differential recognition of <i>Brucella melitensis</i> antigens. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e673	4.8	33
124	Hashing algorithms and data structures for rapid searches of fingerprint vectors. <i>Journal of Chemical Information and Modeling</i> , 2010 , 50, 1358-68	6.1	26
123	When is chemical similarity significant? The statistical distribution of chemical similarity scores and its extreme values. <i>Journal of Chemical Information and Modeling</i> , 2010 , 50, 1205-22	6.1	73
122	Identification of immunodominant antigens of <i>Chlamydia trachomatis</i> using proteome microarrays. <i>Vaccine</i> , 2010 , 28, 3014-24	4.1	34
121	Reaction Explorer: Towards a Knowledge Map of Organic Chemistry To Support Dynamic Assessment and Personalized Instruction. <i>ACS Symposium Series</i> , 2010 , 191-209	0.4	
120	Data structures and compression algorithms for high-throughput sequencing technologies. <i>BMC Bioinformatics</i> , 2010 , 11, 514	3.6	30
119	Of bits and wows: A Bayesian theory of surprise with applications to attention. <i>Neural Networks</i> , 2010 , 23, 649-66	9.1	166
118	Modeling user reputation in wikis. <i>Statistical Analysis and Data Mining</i> , 2010 , 3, 126-139	1.4	28
117	Transmembrane beta-barrel protein structure prediction 2010 , 83-102		

116	Exploring Java software vocabulary: A search and mining perspective 2009 ,		2
115	Data structures and compression algorithms for genomic sequence data. <i>Bioinformatics</i> , 2009 , 25, 1731-8.2		69
114	COBEpro: a novel system for predicting continuous B-cell epitopes. <i>Protein Engineering, Design and Selection</i> , 2009 , 22, 113-20	1.9	117
113	Bayesian surprise attracts human attention. <i>Vision Research</i> , 2009 , 49, 1295-306	2.1	616
112	MITOMASTER: a bioinformatics tool for the analysis of mitochondrial DNA sequences. <i>Human Mutation</i> , 2009 , 30, 1-6	4.7	84
111	Sourcerer: mining and searching internet-scale software repositories. <i>Data Mining and Knowledge Discovery</i> , 2009 , 18, 300-336	5.6	127
110	Influence relevance voting: an accurate and interpretable virtual high throughput screening method. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 756-66	6.1	43
109	An intersection inequality sharper than the tanimoto triangle inequality for efficiently searching large databases. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 1866-70	6.1	17
108	SOLpro: accurate sequence-based prediction of protein solubility. <i>Bioinformatics</i> , 2009 , 25, 2200-7	7.2	243
107	SourcererDB: An aggregated repository of statically analyzed and cross-linked open source Java projects 2009 ,		31
106	No electron left behind: a rule-based expert system to predict chemical reactions and reaction mechanisms. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 2034-43	6.1	43
105	Mining the coherence of GNOME bug reports with statistical topic models 2009 ,		25
104	Machine learning methods for protein structure prediction. <i>IEEE Reviews in Biomedical Engineering</i> , 2008 , 1, 41-9	6.4	70
103	Discovery of power-laws in chemical space. <i>Journal of Chemical Information and Modeling</i> , 2008 , 48, 1138-51		53
102	Speeding up chemical database searches using a proximity filter based on the logical exclusive or. <i>Journal of Chemical Information and Modeling</i> , 2008 , 48, 1367-78	6.1	34
101	BLASTing small molecules--statistics and extreme statistics of chemical similarity scores. <i>Bioinformatics</i> , 2008 , 24, i357-65	7.2	11
100	PEPITO: improved discontinuous B-cell epitope prediction using multiple distance thresholds and half sphere exposure. <i>Bioinformatics</i> , 2008 , 24, 1459-60	7.2	165
99	TMBpro: secondary structure, beta-contact and tertiary structure prediction of transmembrane beta-barrel proteins. <i>Bioinformatics</i> , 2008 , 24, 513-20	7.2	67

98	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> , 2008 , 76, 3374-89	3.7	119
97	An Application of Latent Dirichlet Allocation to Analyzing Software Evolution 2008 ,		39
96	SELECTpro: effective protein model selection using a structure-based energy function resistant to BLUNDERS. <i>BMC Structural Biology</i> , 2008 , 8, 52	2.7	21
95	Profiling humoral immune responses to <i>P. falciparum</i> infection with protein microarrays. <i>Proteomics</i> , 2008 , 8, 4680-94	4.8	213
94	Learning to play Go using recursive neural networks. <i>Neural Networks</i> , 2008 , 21, 1392-400	9.1	20
93	Mining Eclipse Developer Contributions via Author-Topic Models 2007 ,		37
92	Mathematical correction for fingerprint similarity measures to improve chemical retrieval. <i>Journal of Chemical Information and Modeling</i> , 2007 , 47, 952-64	6.1	46
91	Bounds and algorithms for fast exact searches of chemical fingerprints in linear and sublinear time. <i>Journal of Chemical Information and Modeling</i> , 2007 , 47, 302-17	6.1	74
90	Assessment of predictions submitted for the CASP7 domain prediction category. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69 Suppl 8, 137-51	4.2	36
89	Improved residue contact prediction using support vector machines and a large feature set. <i>BMC Bioinformatics</i> , 2007 , 8, 113	3.6	162
88	An enhanced MITOMAP with a global mtDNA mutational phylogeny. <i>Nucleic Acids Research</i> , 2007 , 35, D823-8	20.1	446
87	Minimizing the overlap problem in protein NMR: a computational framework for precision amino acid labeling. <i>Bioinformatics</i> , 2007 , 23, 2829-35	7.2	6
86	From protein microarrays to diagnostic antigen discovery: a study of the pathogen <i>Francisella tularensis</i> . <i>Bioinformatics</i> , 2007 , 23, i508-18	7.2	75
85	ChemDB update--full-text search and virtual chemical space. <i>Bioinformatics</i> , 2007 , 23, 2348-51	7.2	97
84	Lossless compression of chemical fingerprints using integer entropy codes improves storage and retrieval. <i>Journal of Chemical Information and Modeling</i> , 2007 , 47, 2098-109	6.1	41
83	Adaptive Low Power Listening for Wireless Sensor Networks. <i>IEEE Transactions on Mobile Computing</i> , 2007 , 6, 988-1004	4.6	95
82	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> , 2007 , 47, 965-74	6.1	49
81	Identification of humoral immune responses in protein microarrays using DNA microarray data analysis techniques. <i>Bioinformatics</i> , 2006 , 22, 1760-6	7.2	84

80	Functional census of mutation sequence spaces: the example of p53 cancer rescue mutants. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006 , 3, 114-25	3	22
79	Modular DAG-RNN architectures for assembling coarse protein structures. <i>Journal of Computational Biology</i> , 2006 , 13, 631-50	1.7	15
78	Software Acoustic Modems for Short Range Mote-based Underwater Sensor Networks 2006 ,		20
77	Mitochondrial mutations in cancer. <i>Oncogene</i> , 2006 , 25, 4647-62	9.2	640
76	DOMpro: Protein Domain Prediction Using Profiles, Secondary Structure, Relative Solvent Accessibility, and Recursive Neural Networks. <i>Data Mining and Knowledge Discovery</i> , 2006 , 13, 1-10	5.6	75
75	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> , 2006 , 62, 617-29	4.2	90
74	Prediction of protein stability changes for single-site mutations using support vector machines. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 1125-32	4.2	546
73	ChemDB: a public database of small molecules and related cheminformatics resources. <i>Bioinformatics</i> , 2005 , 21, 4133-9	7.2	132
72	SCRATCH: a protein structure and structural feature prediction server. <i>Nucleic Acids Research</i> , 2005 , 33, W72-6	20.1	678
71	How noisy and replicable are DNA microarray data?. <i>International Journal of Bioinformatics Research and Applications</i> , 2005 , 1, 31-50	0.9	1
70	On the relationship between deterministic and probabilistic directed Graphical models: from Bayesian networks to recursive neural networks. <i>Neural Networks</i> , 2005 , 18, 1080-6	9.1	13
69	Graph kernels for chemical informatics. <i>Neural Networks</i> , 2005 , 18, 1093-110	9.1	263
68	Accurate Prediction of Protein Disordered Regions by Mining Protein Structure Data. <i>Data Mining and Knowledge Discovery</i> , 2005 , 11, 213-222	5.6	163
67	Kernels for small molecules and the prediction of mutagenicity, toxicity and anti-cancer activity. <i>Bioinformatics</i> , 2005 , 21 Suppl 1, i359-68	7.2	125
66	Global gene expression profiling in Escherichia coli K12: effects of oxygen availability and ArcA. <i>Journal of Biological Chemistry</i> , 2005 , 280, 15084-96	5.4	155
65	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> , 2005 , 102, 547-52	11.5	338
64	Cheminformatics, drug design, and systems biology. <i>Genome Informatics</i> , 2005 , 16, 281-5		2
63	Combining protein secondary structure prediction models with ensemble methods of optimal complexity. <i>Neurocomputing</i> , 2004 , 56, 305-327	5.4	27

62	Structural proteomics of the poxvirus family. <i>Artificial Intelligence in Medicine</i> , 2004 , 31, 105-15	7.4	7
61	Appendix A: Mathematical Complements 2003 , 235-251		
60	Appendix B: List of Main Symbols and Abbreviations 2003 , 253-256		
59	Bounds on variances of estimators for multinomial processing tree models. <i>Journal of Mathematical Psychology</i> , 2003 , 47, 467-470	1.2	4
58	Differential analysis of DNA microarray gene expression data. <i>Molecular Microbiology</i> , 2003 , 47, 871-7	4.1	99
57	Global gene expression profiling in Escherichia coli K12. The effects of oxygen availability and FNR. <i>Journal of Biological Chemistry</i> , 2003 , 278, 29837-55	5.4	231
56	CyberT: An online program for the statistical analysis of DNA array data 2002 , 199-206		
55	2002 ,		29
54	Statistical analysis of array data: Inferring changes 2002 , 53-72		
53	Systems biology 2002 , 135-176		1
52	The design, analysis, and interpretation of gene expression profiling experiments 2002 , 97-134		
51	Prediction of coordination number and relative solvent accessibility in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 47, 142-53	4.2	199
50	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> , 2002 , 47, 228-35	4.2	561
49	Global gene expression profiling in Escherichia coli K12. The effects of leucine-responsive regulatory protein. <i>Journal of Biological Chemistry</i> , 2002 , 277, 40309-23	5.4	116
48	Distribution patterns of over-represented k-mers in non-coding yeast DNA. <i>Bioinformatics</i> , 2002 , 18, 513-28	7.2	38
47	Prediction of contact maps by GIOHMMs and recurrent neural networks using lateral propagation from all four cardinal corners. <i>Bioinformatics</i> , 2002 , 18 Suppl 1, S62-70	7.2	110
46	Statistical analysis of array data: Dimensionality reduction, clustering, and regulatory regions 2002 , 73-96		2
45	Modeling and optimization of UWB communication networks through a flexible cost function. <i>IEEE Journal on Selected Areas in Communications</i> , 2002 , 20, 1733-1744	14.2	41

44	A machine learning strategy for protein analysis. <i>IEEE Intelligent Systems</i> , 2002 , 17, 28-35	4.2	8
43	Flexibility of the genetic code with respect to DNA structure. <i>Bioinformatics</i> , 2001 , 17, 237-48	7.2	11
42	Improved prediction of the number of residue contacts in proteins by recurrent neural networks. <i>Bioinformatics</i> , 2001 , 17 Suppl 1, S234-42	7.2	36
41	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> , 2001 , 276, 19937-44	5.4	282
40	A Bayesian framework for the analysis of microarray expression data: regularized t-test and statistical inferences of gene changes. <i>Bioinformatics</i> , 2001 , 17, 509-19	7.2	1360
39	Assessing the accuracy of prediction algorithms for classification: an overview. <i>Bioinformatics</i> , 2000 , 16, 412-24	7.2	1447
38	Sequence analysis by additive scales: DNA structure for sequences and repeats of all lengths. <i>Bioinformatics</i> , 2000 , 16, 865-89	7.2	45
37	On the convergence of a clustering algorithm for protein-coding regions in microbial genomes. <i>Bioinformatics</i> , 2000 , 16, 367-71	7.2	16
36	Matching protein beta-sheet partners by feedforward and recurrent neural networks 2000 , 8, 25-36		8
35	Structural basis for triplet repeat disorders: a computational analysis. <i>Bioinformatics</i> , 1999 , 15, 918-29	7.2	23
34	Exploiting the past and the future in protein secondary structure prediction. <i>Bioinformatics</i> , 1999 , 15, 937-46	7.2	343
33	DNA structure in human RNA polymerase II promoters. <i>Journal of Molecular Biology</i> , 1998 , 281, 663-73	6.5	73
32	Hybrid modeling, HMM/NN architectures, and protein applications. <i>Neural Computation</i> , 1996 , 8, 1541-65.9		28
31	Naturally occurring nucleosome positioning signals in human exons and introns. <i>Journal of Molecular Biology</i> , 1996 , 263, 503-10	6.5	62
30	Periodic sequence patterns in human exons 1995 , 3, 30-8		3
29	Hidden Markov models of biological primary sequence information. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994 , 91, 1059-63	11.5	301
28	Smooth On-Line Learning Algorithms for Hidden Markov Models. <i>Neural Computation</i> , 1994 , 6, 307-318	2.9	65
27	Neural Networks for Fingerprint Recognition. <i>Neural Computation</i> , 1993 , 5, 402-418	2.9	90

26	Temporal Evolution of Generalization during Learning in Linear Networks. <i>Neural Computation</i> , 1991 , 3, 589-603	2.9	23
25	Contrastive Learning and Neural Oscillations. <i>Neural Computation</i> , 1991 , 3, 526-545	2.9	34
24	Computing with Arrays of Coupled Oscillators: An Application to Preattentive Texture Discrimination. <i>Neural Computation</i> , 1990 , 2, 458-471	2.9	69
23	OSCILLATIONS AND SYNCHRONIZATIONS IN NEURAL NETWORKS: AN EXPLORATION OF THE LABELING HYPOTHESIS. <i>International Journal of Neural Systems</i> , 1989 , 01, 103-124	6.2	73
22	Neural networks and principal component analysis: Learning from examples without local minima. <i>Neural Networks</i> , 1989 , 2, 53-58	9.1	700
21	. <i>IEEE Transactions on Information Theory</i> , 1988 , 34, 523-530	2.8	46
20	Group actions and learning for a family of automata. <i>Journal of Computer and System Sciences</i> , 1988 , 36, 1-15	1	4
19	Symmetries and learning in neural network models. <i>Physical Review Letters</i> , 1987 , 59, 1976-1978	7.4	8
18	A principled approach to detecting surprising events in video		176
17	Attention: Bits versus Wows		4
16	A Comparative Analysis and Experimental Study on Wireless Aerial and Underwater Acoustic Communications		7
15	An acoustic identification scheme for location systems		3
14	Beep: 3D indoor positioning using audible sound		30
13	UWB ad-hoc networks		16
12	Link Analysis125-147		
11	Advanced Crawling Techniques149-170		
10	Modeling and Understanding Human Behavior on the Web171-209		
9	Text Analysis77-123		

8	Basic WWW Technologies29-50		
7	Web Graphs51-76		
6	Hippocampal ensembles represent sequential relationships among discrete nonspatial events		1
5	The circadian hippocampus and its reprogramming in epilepsy: impact for chronotherapeutics		2
4	Epigenetic regulation of the circadian genePer1in the hippocampus mediates age-related changes in memory and synaptic plasticity		1
3	Intergenerational Stress Transmission is Associated with Brain Metabotranscriptome Remodeling and Mitochondrial Dysfunction		1
2	Reproducible Hyperparameter Optimization. <i>Journal of Computational and Graphical Statistics</i> ,1-16	1.4	4
1	Commerce on the Web: Models and Applications211-234		2