

# Dariusz Plewczynski

## List of Publications by Year in descending order

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187  
papers

29,964  
citations

76196

40  
h-index

7136

153  
g-index

226  
all docs

226  
docs citations

226  
times ranked

53158  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>JUPPI</i> : A Multi-Level Feature Based Method for PPI Prediction and a Refined Strategy for Performance Assessment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 531-542.	1.9	4
2	From DNA human sequence to the chromatin higher order organisation and its biological meaning: Using biomolecular interaction networks to understand the influence of structural variation on spatial genome organisation and its functional effect. <i>Seminars in Cell and Developmental Biology</i> , 2022, 121, 171-185.	2.3	17
3	3dSpAn: An interactive software for 3D segmentation and analysis of dendritic spines. <i>Neuroinformatics</i> , 2022, 20, 679-698.	1.5	10
4	PRDX-1 Supports the Survival and Antitumor Activity of Primary and CAR-Modified NK Cells under Oxidative Stress. <i>Cancer Immunology Research</i> , 2022, 10, 228-244.	1.6	28
5	Drug repurposing for identification of potential spike inhibitors for SARS-CoV-2 using molecular docking and molecular dynamics simulations. <i>Methods</i> , 2022, 203, 498-510.	1.9	16
6	Genome-Wide Analysis to Identify Palindromes, Mirror and Inverted Repeats in SARS-CoV-2, MERS-CoV and SARS-CoV-1. <i>IEEE Access</i> , 2022, 10, 23708-23715.	2.6	0
7	Activation-induced chromatin reorganization in neurons depends on HDAC1 activity. <i>Cell Reports</i> , 2022, 38, 110352.	2.9	7
8	Single-Hit Inactivation Drove Tumor Suppressor Genes Out of the X Chromosome during Evolution. <i>Cancer Research</i> , 2022, 82, 1482-1491.	0.4	0
9	Super-resolution visualization of chromatin loop folding in human lymphoblastoid cells using interferometric photoactivated localization microscopy. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
10	3DGenBench: a web-server to benchmark computational models for 3D Genomics. <i>Nucleic Acids Research</i> , 2022, 50, W4-W12.	6.5	10
11	Multi-scale phase separation by explosive percolation with single-chromatin loop resolution. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3591-3603.	1.9	3
12	3D $\alpha$ Epigenomic Regulation of Gene Transcription in Hepatocellular Carcinoma. <i>Genetics &amp; Genomics Next</i> , 2022, 3, .	0.8	1
13	Online Predictor Using Machine Learning to Predict Novel Coronavirus and Other Pathogenic Viruses. <i>ACS Omega</i> , 2022, 7, 23069-23074.	1.6	0
14	Biomolecular Clusters Identification in Linear Time Complexity for Biological Networks. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 611-622.	0.5	1
15	FIREcaller: Detecting frequently interacting regions from Hi-C data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 355-362.	1.9	22
16	PartSeg: a tool for quantitative feature extraction from 3D microscopy images for dummies. <i>BMC Bioinformatics</i> , 2021, 22, 72.	1.2	7
17	COVID-DeepPredictor: Recurrent Neural Network to Predict SARS-CoV-2 and Other Pathogenic Viruses. <i>Frontiers in Genetics</i> , 2021, 12, 569120.	1.1	12
18	A Gibbs sampler for learning DAG: a unification for discrete and Gaussian domains. <i>Journal of Statistical Computation and Simulation</i> , 2021, 91, 2833-2853.	0.7	1

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19	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. <i>Cancer Cell</i> , 2021, 39, 694-707.e7.	7.7	115
20	TBC1D24 emerges as an important contributor to progressive postlingual dominant hearing loss. <i>Scientific Reports</i> , 2021, 11, 10300.	1.6	4
21	Genome-wide analysis of 10664 SARS-CoV-2 genomes to identify virus strains in 73 countries based on single nucleotide polymorphism. <i>Virus Research</i> , 2021, 298, 198401.	1.1	5
22	<i>In situ</i> Chromatin Interaction Analysis Using Paired-End Tag Sequencing. <i>Current Protocols</i> , 2021, 1, e174.	1.3	11
23	Genomic Marks Associated with Chromatin Compartments in the CTCF, RNAPII Loop and Genomic Windows. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11591.	1.8	1
24	Nuclear pore protein NUP210 depletion suppresses metastasis through heterochromatin-mediated disruption of tumor cell mechanical response. <i>Nature Communications</i> , 2021, 12, 7216.	5.8	19
25	Potent but transient immunosuppression of T-cells is a general feature of CD71+ erythroid cells. <i>Communications Biology</i> , 2021, 4, 1384.	2.0	12
26	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	3.2	70
27	Methods for comparative ChIA-PET and Hi-C data analysis. <i>Methods</i> , 2020, 170, 69-74.	1.9	11
28	Aggregated network centrality shows non-random structure of genomic and proteomic networks. <i>Methods</i> , 2020, 181-182, 5-14.	1.9	11
29	Spring Model – Chromatin Modeling Tool Based on OpenMM. <i>Methods</i> , 2020, 181-182, 62-69.	1.9	9
30	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. <i>Science Advances</i> , 2020, 6, eaay2078.	4.7	22
31	Identification of miRNA Biomarkers for Diverse Cancer Types Using Statistical Learning Methods at the Whole-Genome Scale. <i>Frontiers in Genetics</i> , 2020, 11, 982.	1.1	4
32	Chromatin topology reorganization and transcription repression by PML-RAR $\alpha$ in acute promyeloid leukemia. <i>Genome Biology</i> , 2020, 21, 110.	3.8	12
33	The Mixture of Autoregressive Hidden Markov Models of Morphology for Dendritic Spines During Activation Process. <i>Journal of Computational Biology</i> , 2020, 27, 1471-1485.	0.8	4
34	Exploring 3D chromatin contacts in gene regulation: The evolution of approaches for the identification of functional enhancer-promoter interaction. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 558-570.	1.9	37
35	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. <i>EMBO Journal</i> , 2020, 39, e103949.	3.5	37
36	LATS kinase-mediated CTCF phosphorylation and selective loss of genomic binding. <i>Science Advances</i> , 2020, 6, eaaw4651.	4.7	21

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37	Graph embedding and unsupervised learning predict genomic sub-compartments from HiC chromatin interaction data. <i>Nature Communications</i> , 2020, 11, 1173.	5.8	40
38	Free energy-based model of CTCF-mediated chromatin looping in the human genome. <i>Methods</i> , 2020, 181-182, 35-51.	1.9	2
39	A supervised learning framework for chromatin loop detection in genome-wide contact maps. <i>Nature Communications</i> , 2020, 11, 3428.	5.8	69
40	Ultrastructural visualization of 3D chromatin folding using volume electron microscopy and DNA in situ hybridization. <i>Nature Communications</i> , 2020, 11, 2120.	5.8	26
41	3D-GNOME 2.0: a three-dimensional genome modeling engine for predicting structural variation-driven alterations of chromatin spatial structure in the human genome. <i>Nucleic Acids Research</i> , 2020, 48, W170-W176.	6.5	19
42	Computational modelling of three-dimensional genome structure. <i>Methods</i> , 2020, 181-182, 1-4.	1.9	4
43	3gClust: Human Protein Cluster Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1-1.	1.9	6
44	An empirical Bayes approach for learning directed acyclic graph using MCMC algorithm. <i>Statistical Analysis and Data Mining</i> , 2019, 12, 394-403.	1.4	2
45	A new evolutionary rough fuzzy integrated machine learning technique for microRNA selection using next-generation sequencing data of breast cancer. , 2019, , .		1
46	Spatial chromatin architecture alteration by structural variations in human genomes at the population scale. <i>Genome Biology</i> , 2019, 20, 148.	3.8	36
47	Three-Dimensional Segmentation and Reconstruction of Neuronal Nuclei in Confocal Microscopic Images. <i>Frontiers in Neuroanatomy</i> , 2019, 13, 81.	0.9	12
48	A Multivariate Negative-Binomial Model with Random Effects for Differential Gene-Expression Analysis of Correlated mRNA Sequencing Data. <i>Journal of Computational Biology</i> , 2019, 26, 1339-1348.	0.8	1
49	Intermingling of chromosome territories. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 500-506.	1.5	17
50	Learning directed acyclic graphs by determination of candidate causes for discrete variables. <i>Journal of Statistical Computation and Simulation</i> , 2019, 89, 1957-1970.	0.7	2
51	Deep Learning for Detection and Localization of Thoracic Diseases Using Chest X-Ray Imagery. <i>Lecture Notes in Computer Science</i> , 2019, , 271-282.	1.0	9
52	Dendritic Spines Taxonomy: The Functional and Structural Classification of Time-Dependent Probabilistic Model of Neuronal Activation. <i>Journal of Computational Biology</i> , 2019, 26, 322-335.	0.8	3
53	Novel <i>COL12A1</i> variant as a cause of mild familial extracellular matrix-related myopathy. <i>Clinical Genetics</i> , 2019, 95, 736-738.	1.0	7
54	Machine learning polymer models of three-dimensional chromatin organization in human lymphoblastoid cells. <i>Methods</i> , 2019, 166, 83-90.	1.9	7

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55	Multiplex chromatin interactions with single-molecule precision. <i>Nature</i> , 2019, 566, 558-562.	13.7	180
56	MIA-Sig: multiplex chromatin interaction analysis by signal processing and statistical algorithms. <i>Genome Biology</i> , 2019, 20, 251.	3.8	8
57	Identification of Breast Cancer Subtype Specific MicroRNAs Using Survival Analysis to Find Their Role in Transcriptomic Regulation. <i>Frontiers in Genetics</i> , 2019, 10, 1047.	1.1	16
58	Identification of Epigenetic Biomarkers with the use of Gene Expression and DNA Methylation for Breast Cancer Subtypes. , 2019, , .		2
59	Upregulation of MLK4 promotes migratory and invasive potential of breast cancer cells. <i>Oncogene</i> , 2019, 38, 2860-2875.	2.6	19
60	Chromatin: A Semi-Structured Polymer. , 2019, , 288-307.		1
61	Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic $\hat{I}^2$ Cell Identity and Function. <i>Cell Reports</i> , 2019, 26, 788-801.e6.	2.9	68
62	The World Color Survey: Data Analysis and Simulations. , 2019, , 289-311.		0
63	One protein to rule them all: The role of CCCTC-binding factor in shaping human genome in health and disease. <i>Seminars in Cell and Developmental Biology</i> , 2019, 90, 114-127.	2.3	23
64	FunPred 3.0: improved protein function prediction using protein interaction network. <i>PeerJ</i> , 2019, 7, e6830.	0.9	12
65	Correction to: The World Color Survey: Data Analysis and Simulations. , 2019, , C1-C1.		0
66	Survival Analysis with the Integration of RNA-Seq and Clinical Data to Identify Breast Cancer Subtype Specific Genes. <i>Lecture Notes in Computer Science</i> , 2019, , 139-146.	1.0	1
67	Mixture of Forward-Directed and Backward-Directed Autoregressive Hidden Markov Models for Time series Modeling. <i>Journal of the Iranian Statistical Society</i> , 2019, 18, 89-112.	0.2	0
68	RNA structure interactions and ribonucleoprotein processes of the influenza A virus. <i>Briefings in Functional Genomics</i> , 2018, 17, 402-414.	1.3	10
69	Quantitative 3-D morphometric analysis of individual dendritic spines. <i>Scientific Reports</i> , 2018, 8, 3545.	1.6	26
70	The Energetics and Physiological Impact of Cohesin Extrusion. <i>Cell</i> , 2018, 173, 1165-1178.e20.	13.5	399
71	Clinical and molecular characteristics of newly reported mitochondrial disease entity caused by biallelic PARS2 mutations. <i>Journal of Human Genetics</i> , 2018, 63, 473-485.	1.1	19
72	Three-dimensional organization and dynamics of the genome. <i>Cell Biology and Toxicology</i> , 2018, 34, 381-404.	2.4	41

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73	Emerging and threatening infectious diseases. Briefings in Functional Genomics, 2018, 17, 372-373.	1.3	0
74	Oncogenes expand during evolution to withstand somatic amplification. Annals of Oncology, 2018, 29, 2254-2260.	0.6	5
75	The Tandem Duplicator Phenotype Is a Prevalent Genome-Wide Cancer Configuration Driven by Distinct Gene Mutations. Cancer Cell, 2018, 34, 197-210.e5.	7.7	130
76	Inhibition of protein disulfide isomerase induces differentiation of acute myeloid leukemia cells. Haematologica, 2018, 103, 1843-1852.	1.7	8
77	Three-dimensional Epigenome Statistical Model: Genome-wide Chromatin Looping Prediction. Scientific Reports, 2018, 8, 5217.	1.6	1,420
78	Chromatin Interaction Analysis Using Paired-End-Tag (ChIA-PET) Sequencing in Tadpole Tissues. Cold Spring Harbor Protocols, 2018, 2018, pdb.prot104620.	0.2	3
79	OUP accepted manuscript. Briefings in Functional Genomics, 2018, 17, 415-427.	1.3	23
80	ShapeGTB: the role of local DNA shape in prioritization of functional variants in human promoters with machine learning. PeerJ, 2018, 6, e5742.	0.9	2
81	Generalized Baum-Welch and Viterbi Algorithms Based on the Direct Dependency among Observations. Journal of the Iranian Statistical Society, 2018, 17, 0-0.	0.2	0
82	Novel neuro-audiological findings and further evidence for TWNK involvement in Perrault syndrome. Journal of Translational Medicine, 2017, 15, 25.	1.8	36
83	Long-read ChIA-PET for base-pair-resolution mapping of haplotype-specific chromatin interactions. Nature Protocols, 2017, 12, 899-915.	5.5	99
84	STAT5-mediated chromatin interactions in superenhancers activate IL-2 highly inducible genes: Functional dissection of the <i>Il2ra</i> gene locus. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12111-12119.	3.3	72
85	Evolutionarily Conserved Principles Predict 3D Chromatin Organization. Molecular Cell, 2017, 67, 837-852.e7.	4.5	458
86	Predicting Post-Translational Modifications from Local Sequence Fragments Using Machine Learning Algorithms: Overview and Best Practices. Methods in Molecular Biology, 2017, 1484, 275-300.	0.4	4
87	Social adaptation in multi-agent model of linguistic categorization is affected by network information flow. PLoS ONE, 2017, 12, e0182490.	1.1	4
88	Multi-levels 3D Chromatin Interactions Prediction Using Epigenomic Profiles. Lecture Notes in Computer Science, 2017, , 19-28.	1.0	1
89	Computational Approach to Dendritic Spine Taxonomy and Shape Transition Analysis. Frontiers in Computational Neuroscience, 2016, 10, 140.	1.2	11
90	The proline-rich region of glyceraldehyde-3-phosphate dehydrogenase from human sperm may bind SH3 domains, as revealed by a bioinformatic study of low-complexity protein segments. Molecular Reproduction and Development, 2016, 83, 144-148.	1.0	3

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91	3D-GNOME: an integrated web service for structural modeling of the 3D genome. <i>Nucleic Acids Research</i> , 2016, 44, W288-W293.	6.5	40
92	2dSpAn: semiautomated 2-d segmentation, classification and analysis of hippocampal dendritic spine plasticity. <i>Bioinformatics</i> , 2016, 32, 2490-2498.	1.8	24
93	Divide and Conquer Ensemble Method for Time Series Forecasting. <i>Lecture Notes in Computer Science</i> , 2016, , 134-152.	1.0	0
94	An integrated 3-Dimensional Genome Modeling Engine for data-driven simulation of spatial genome organization. <i>Genome Research</i> , 2016, 26, 1697-1709.	2.4	46
95	3DFlu: database of sequence and structural variability of the influenza hemagglutinin at population scale. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw130.	1.4	8
96	Highlights from the 11th ISCB Student Council Symposium 2015. <i>BMC Bioinformatics</i> , 2016, 17, 95.	1.2	4
97	PDP-CON: prediction of domain/linker residues in protein sequences using a consensus approach. <i>Journal of Molecular Modeling</i> , 2016, 22, 72.	0.8	10
98	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. <i>Journal of Autoimmunity</i> , 2016, 68, 62-74.	3.0	64
99	Detecting reliable non interacting proteins (NIPs) significantly enhancing the computational prediction of protein-protein interactions using machine learning methods. <i>Molecular BioSystems</i> , 2016, 12, 778-785.	2.9	5
100	Analysis of Structural Chromosome Variants by Next Generation Sequencing Methods. , 2016, , 39-61.		0
101	QulN: A Web Server for Querying and Visualizing Chromatin Interaction Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1004809.	1.5	10
102	Computational inference of H3K4me3 and H3K27ac domain length. <i>PeerJ</i> , 2016, 4, e1750.	0.9	7
103	<i>Xenopus tropicalis</i> Genome Re-Scaffolding and Re-Annotation Reach the Resolution Required for In Vivo ChIA-PET Analysis. <i>PLoS ONE</i> , 2015, 10, e0137526.	1.1	21
104	Application of Machine Learning Method in Genomics and Proteomics. <i>Scientific World Journal</i> , The, 2015, 2015, 1-2.	0.8	1
105	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. <i>Cell</i> , 2015, 163, 1611-1627.	13.5	881
106	Super-enhancers delineate disease-associated regulatory nodes in T cells. <i>Nature</i> , 2015, 520, 558-562.	13.7	323
107	MaER: A New Ensemble Based Multiclass Classifier for Binding Activity Prediction of HLA Class II Proteins. <i>Lecture Notes in Computer Science</i> , 2015, , 462-471.	1.0	4
108	Binding Activity Prediction of Cyclin-Dependent Inhibitors. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 1469-1482.	2.5	10

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109	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
110	A combined systems and structural modeling approach repositions antibiotics for <i>Mycoplasma genitalium</i> . <i>Computational Biology and Chemistry</i> , 2015, 59, 91-97.	1.1	13
111	PDP-RF: Protein Domain Boundary Prediction Using Random Forest Classifier. <i>Lecture Notes in Computer Science</i> , 2015, , 441-450.	1.0	2
112	Multi-level machine learning prediction of proteinâ€“protein interactions in <i>Saccharomyces cerevisiae</i> . <i>PeerJ</i> , 2015, 3, e1041.	0.9	13
113	Abstract 5347: SK053, a small molecule inhibitor of enzymes involved in allosteric disulfide bonds formation, shows potent anti-leukemic effects and induces differentiation of human AML cells. , 2015, , .		0
114	B Cell Super-Enhancers and Regulatory Clusters Recruit AID Tumorigenic Activity. <i>Cell</i> , 2014, 159, 1524-1537.	13.5	234
115	Ensemble learning prediction of proteinâ€“protein interactions using proteins functional annotations. <i>Molecular BioSystems</i> , 2014, 10, 820.	2.9	47
116	HarmonyDOCK: The Structural Analysis of Poses in Protein-Ligand Docking. <i>Journal of Computational Biology</i> , 2014, 21, 247-256.	0.8	11
117	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. <i>BMC Genomics</i> , 2014, 15, S11.	1.2	75
118	Evaluation of Machine Learning Algorithms on Protein-Protein Interactions. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 211-218.	0.5	1
119	Multiobjective Differential Evolution: A Comparative Study on Benchmark Problems. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 529-536.	0.5	4
120	Soft Computing Approach for VLSI Mincut Partitioning: The State of the Arts. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 895-903.	0.5	0
121	Role of the host genetic variability in the influenza A virus susceptibility. <i>Acta Biochimica Polonica</i> , 2014, 61, 403-19.	0.3	7
122	PPIcons: identification of protein-protein interaction sites in selected organisms. <i>Journal of Molecular Modeling</i> , 2013, 19, 4059-4070.	0.8	20
123	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. <i>Cell</i> , 2013, 155, 1507-1520.	13.5	299
124	Chromatin connectivity maps reveal dynamic promoterâ€“enhancer long-range associations. <i>Nature</i> , 2013, 504, 306-310.	13.7	405
125	Application of High Quality Amino Acid Indices to AMS 3.0: A Update Note. <i>Advances in Intelligent Systems and Computing</i> , 2013, , 217-225.	0.5	1
126	Consensus classification of human leukocyte antigen class II proteins. <i>Immunogenetics</i> , 2013, 65, 97-105.	1.2	15

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127	A Consensus Approach for Identification of Protein-Protein Interaction Sites in Homo Sapiens. Lecture Notes in Computer Science, 2013, , 674-679.	1.0	0
128	Improved differential evolution for microarray analysis. International Journal of Data Mining and Bioinformatics, 2012, 6, 86.	0.1	11
129	Chromatin Interaction Analysis with Paired-End Tag Sequencing (ChIA-PET) for Mapping Chromatin Interactions and Understanding Transcription Regulation. Journal of Visualized Experiments, 2012, , .	0.2	15
130	ChIA-PET analysis of transcriptional chromatin interactions. Methods, 2012, 58, 289-299.	1.9	83
131	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. Cell Reports, 2012, 2, 1207-1219.	2.9	102
132	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	13.5	1,096
133	Information-sharing and aggregation models for interacting minds. Journal of Mathematical Psychology, 2012, 56, 417-426.	1.0	11
134	Landau Theory of Meta-learning. Lecture Notes in Computer Science, 2012, , 142-153.	1.0	2
135	Fuzzy clustering of physicochemical and biochemical properties of amino Acids. Amino Acids, 2012, 43, 583-594.	1.2	86
136	AMS 4.0: consensus prediction of post-translational modifications in protein sequences. Amino Acids, 2012, 43, 573-582.	1.2	42
137	SVMFC: SVM Ensemble Fuzzy Clustering for Satellite Image Segmentation. IEEE Geoscience and Remote Sensing Letters, 2012, 9, 52-55.	1.4	40
138	Prediction of E.coli Protein-Protein Interaction Sites Using Inter-Residue Distances and High-Quality-Index Features. Advances in Intelligent and Soft Computing, 2012, , 837-844.	0.2	1
139	Multiobjective Differential Crisp Clustering for Evaluation of Clusters Dynamically. Advances in Intelligent and Soft Computing, 2011, , 307-313.	0.2	0
140	Unsupervised and Supervised Learning Approaches Together for Microarray Analysis. Fundamenta Informaticae, 2011, 106, 45-73.	0.3	8
141	Improvement of new automatic differential fuzzy clustering using SVM classifier for microarray analysis. Expert Systems With Applications, 2011, 38, 15122-15133.	4.4	17
142	Protein-protein interaction and pathway databases, a graphical review. Briefings in Bioinformatics, 2011, 12, 702-713.	3.2	63
143	GIDMP: Good protein-protein interaction data metamining practice. Cellular and Molecular Biology Letters, 2011, 16, 258-63.	2.7	0
144	PPI_SVM: Prediction of protein-protein interactions using machine learning, domain-domain affinities and frequency tables. Cellular and Molecular Biology Letters, 2011, 16, 264-78.	2.7	63

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145	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011, 43, 630-638.	9.4	567
146	Detailed Mechanism of Squalene Epoxidase Inhibition by Terbinafine. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 455-462.	2.5	88
147	Brainstorming: weighted voting prediction of inhibitors for protein targets. <i>Journal of Molecular Modeling</i> , 2011, 17, 2133-2141.	0.8	16
148	PSP_MCSVM: brainstorming consensus prediction of protein secondary structures using two-stage multiclass support vector machines. <i>Journal of Molecular Modeling</i> , 2011, 17, 2191-2201.	0.8	29
149	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <i>Journal of Cellular Biochemistry</i> , 2011, 112, 2218-2221.	1.2	18
150	VoteDock: Consensus docking method for prediction of protein-ligand interactions. <i>Journal of Computational Chemistry</i> , 2011, 32, 568-581.	1.5	82
151	Can we trust docking results? Evaluation of seven commonly used programs on PDBbind database. <i>Journal of Computational Chemistry</i> , 2011, 32, 742-755.	1.5	308
152	A new multi-objective technique for differential fuzzy clustering. <i>Applied Soft Computing Journal</i> , 2011, 11, 2765-2776.	4.1	60
153	PMAFC: A New Probabilistic Memetic Algorithm Based Fuzzy Clustering. <i>Lecture Notes in Computer Science</i> , 2011, , 602-611.	1.0	0
154	AMS 3.0: prediction of post-translational modifications. <i>BMC Bioinformatics</i> , 2010, 11, 210.	1.2	43
155	Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. <i>Nature Genetics</i> , 2010, 42, 53-61.	9.4	652
156	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010, 11, R22.	13.9	255
157	Real-coded differential crisp clustering for MRI brain image segmentation. , 2010, , .		3
158	Species Used for Drug Testing Reveal Different Inhibition Susceptibility for 17beta-Hydroxysteroid Dehydrogenase Type 1. <i>PLoS ONE</i> , 2010, 5, e10969.	1.1	17
159	Consensus Multiobjective Differential Crisp Clustering for Categorical Data Analysis. <i>Lecture Notes in Computer Science</i> , 2010, , 30-39.	1.0	3
160	Virtual High Throughput Screening Using Combined Random Forest and Flexible Docking. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2009, 12, 484-489.	0.6	19
161	Mean-field theory of meta-learning. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009, 2009, P11003.	0.9	4
162	ChIP-based methods for the identification of long-range chromatin interactions. <i>Journal of Cellular Biochemistry</i> , 2009, 107, 30-39.	1.2	246

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163	kNNsim: k-Nearest neighbors similarity with genetic algorithm features optimization enhances the prediction of activity classes for small molecules. <i>Journal of Molecular Modeling</i> , 2009, 15, 591-596.	0.8	1
164	Meta-basic estimates the size of druggable human genome. <i>Journal of Molecular Modeling</i> , 2009, 15, 695-699.	0.8	23
165	An oestrogen-receptor-bound human chromatin interactome. <i>Nature</i> , 2009, 462, 58-64.	13.7	1,537
166	The interactome: Predicting the protein-protein interactions in cells. <i>Cellular and Molecular Biology Letters</i> , 2009, 14, 1-22.	2.7	36
167	Performance of Machine Learning Methods for Ligand-Based Virtual Screening. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2009, 12, 358-368.	0.6	35
168	AutoMotif Server for prediction of phosphorylation sites in proteins using support vector machine: 2007 update. <i>Journal of Molecular Modeling</i> , 2008, 14, 69-76.	0.8	32
169	Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. <i>Cell</i> , 2008, 133, 1106-1117.	13.5	2,279
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