Dariusz Plewczynski

List of Publications by Year
in descending order

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	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. Cell, 2008, 133, 1106-1117.	13.5	2,279
3	An oestrogen-receptor-α-bound human chromatin interactome. Nature, 2009, 462, 58-64.	13.7	1,537
4	Three-dimensional Epigenome Statistical Model: Genome-wide Chromatin Looping Prediction. Scientific Reports, 2018, 8, 5217.	1.6	1,420
5	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	13.5	1,096
6	A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. Cell, 2006, 124, 207-219.	13.5	1,060
7	CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription. Cell, 2015, 163, 1611-1627.	13.5	881
8	Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. Nature Genetics, 2010, 42, 53-61.	9.4	652
9	CTCF-mediated functional chromatin interactome in pluripotent cells. Nature Genetics, 2011, 43, 630-638.	9.4	567
10	Evolutionarily Conserved Principles Predict 3D Chromatin Organization. Molecular Cell, 2017, 67, 837-852.e7.	4.5	458
11	Chromatin connectivity maps reveal dynamic promoter–enhancer long-range associations. Nature, 2013, 504, 306-310.	13.7	405
12	The Energetics and Physiological Impact of Cohesin Extrusion. Cell, 2018, 173, 1165-1178.e20.	13.5	399
13	Super-enhancers delineate disease-associated regulatory nodes in T cells. Nature, 2015, 520, 558-562.	13.7	323
14	Can we trust docking results? Evaluation of seven commonly used programs on PDBbind database. Journal of Computational Chemistry, 2011, 32, 742-755.	1.5	308
15	Interactome Maps of Mouse Gene Regulatory Domains Reveal Basic Principles of Transcriptional Regulation. Cell, 2013, 155, 1507-1520.	13.5	299
16	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. Genome Biology, 2010, 11, R22.	13.9	255
17	ChIP-based methods for the identification of long-range chromatin interactions. Journal of Cellular Biochemistry, 2009, 107, 30-39.	1.2	246
18	B Cell Super-Enhancers and Regulatory Clusters Recruit AID Tumorigenic Activity. Cell, 2014, 159, 1524-1537.	13.5	234

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19	Multiplex chromatin interactions with single-molecule precision. Nature, 2019, 566, 558-562.	13.7	180
20	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
21	Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. Cancer Cell, 2021, 39, 694-707.e7.	7.7	115
22	Assessing Different Classification Methods for Virtual Screening. Journal of Chemical Information and Modeling, 2006, 46, 1098-1106.	2.5	106
23	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. Cell Reports, 2012, 2, 1207-1219.	2.9	102
24	Long-read ChIA-PET for base-pair-resolution mapping of haplotype-specific chromatin interactions. Nature Protocols, 2017, 12, 899-915.	5.5	99
25	Detailed Mechanism of Squalene Epoxidase Inhibition by Terbinafine. Journal of Chemical Information and Modeling, 2011, 51, 455-462.	2.5	88
26	Fuzzy clustering of physicochemical and biochemical properties of amino Acids. Amino Acids, 2012, 43, 583-594.	1.2	86
27	ChIA-PET analysis of transcriptional chromatin interactions. Methods, 2012, 58, 289-299.	1.9	83
28	VoteDock: Consensus docking method for prediction of protein–ligand interactions. Journal of Computational Chemistry, 2011, 32, 568-581.	1.5	82
29	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. BMC Genomics, 2014, 15, S11.	1.2	75
30	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
31	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	3.2	70
32	A supervised learning framework for chromatin loop detection in genome-wide contact maps. Nature Communications, 2020, 11, 3428.	5.8	69
33	Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic β Cell Identity and Function. Cell Reports, 2019, 26, 788-801.e6.	2.9	68
34	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. Journal of Autoimmunity, 2016, 68, 62-74.	3.0	64
35	Protein-protein interaction and pathway databases, a graphical review. Briefings in Bioinformatics, 2011, 12, 702-713.	3.2	63
36	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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37	AutoMotif server: prediction of single residue post-translational modifications in proteins. Bioinformatics, 2005, 21, 2525-2527.	1.8	61
38	A new multi-objective technique for differential fuzzy clustering. Applied Soft Computing Journal, 2011, 11, 2765-2776.	4.1	60
39	Ensemble learning prediction of protein–protein interactions using proteins functional annotations. Molecular BioSystems, 2014, 10, 820.	2.9	47
40	An integrated 3-Dimensional Genome Modeling Engine for data-driven simulation of spatial genome organization. Genome Research, 2016, 26, 1697-1709.	2.4	46
41	AMS 3.0: prediction of post-translational modifications. BMC Bioinformatics, 2010, 11, 210.	1.2	43
42	AMS 4.0: consensus prediction of post-translational modifications in protein sequences. Amino Acids, 2012, 43, 573-582.	1.2	42
43	Three-dimensional organization and dynamics of the genome. Cell Biology and Toxicology, 2018, 34, 381-404.	2.4	41
44	SVMeFC: SVM Ensemble Fuzzy Clustering for Satellite Image Segmentation. IEEE Geoscience and Remote Sensing Letters, 2012, 9, 52-55.	1.4	40
45	3D-GNOME: an integrated web service for structural modeling of the 3D genome. Nucleic Acids Research, 2016, 44, W288-W293.	6.5	40
46	Graph embedding and unsupervised learning predict genomic sub-compartments from HiC chromatin interaction data. Nature Communications, 2020, 11, 1173.	5.8	40
47	Exploring 3D chromatin contacts in gene regulation: The evolution of approaches for the identification of functional enhancer-promoter interaction. Computational and Structural Biotechnology Journal, 2020, 18, 558-570.	1.9	37
48	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. EMBO Journal, 2020, 39, e103949.	3.5	37
49	The interactome: Predicting the protein-protein interactions in cells. Cellular and Molecular Biology Letters, 2009, 14, 1-22.	2.7	36
50	Novel neuro-audiological findings and further evidence for TWNK involvement in Perrault syndrome. Journal of Translational Medicine, 2017, 15, 25.	1.8	36
51	Spatial chromatin architecture alteration by structural variations in human genomes at the population scale. Genome Biology, 2019, 20, 148.	3.8	36
52	Performance of Machine Learning Methods for Ligand-Based Virtual Screening. Combinatorial Chemistry and High Throughput Screening, 2009, 12, 358-368.	0.6	35
53	Target Specific Compound Identification Using a Support Vector Machine. Combinatorial Chemistry and High Throughput Screening, 2007, 10, 189-196.	0.6	32
54	AutoMotif Server for prediction of phosphorylation sites in proteins using support vector machine: 2007 update. Journal of Molecular Modeling, 2008, 14, 69-76.	0.8	32

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55	PDB-UF: database of predicted enzymatic functions for unannotated protein structures from structural genomics. BMC Bioinformatics, 2006, 7, 53.	1.2	31
56	PSP_MCSVM: brainstorming consensus prediction of protein secondary structures using two-stage multiclass support vector machines. Journal of Molecular Modeling, 2011, 17, 2191-2201.	0.8	29
57	PRDX-1 Supports the Survival and Antitumor Activity of Primary and CAR-Modified NK Cells under Oxidative Stress. Cancer Immunology Research, 2022, 10, 228-244.	1.6	28
58	Quantitative 3-D morphometric analysis of individual dendritic spines. Scientific Reports, 2018, 8, 3545.	1.6	26
59	Ultrastructural visualization of 3D chromatin folding using volume electron microscopy and DNA in situ hybridization. Nature Communications, 2020, 11, 2120.	5.8	26
60	Landau theory of social clustering. Physica A: Statistical Mechanics and Its Applications, 1998, 261, 608-617.	1.2	25
61	2dSpAn: semiautomated 2-d segmentation, classification and analysis of hippocampal dendritic spine plasticity. Bioinformatics, 2016, 32, 2490-2498.	1.8	24
62	Meta-basic estimates the size of druggable human genome. Journal of Molecular Modeling, 2009, 15, 695-699.	0.8	23
63	One protein to rule them all: The role of CCCTC-binding factor in shaping human genome in health and disease. Seminars in Cell and Developmental Biology, 2019, 90, 114-127.	2.3	23
64	OUP accepted manuscript. Briefings in Functional Genomics, 2018, 17, 415-427.	1.3	23
65	ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. Science Advances, 2020, 6, eaay2078.	4.7	22
66	FIREcaller: Detecting frequently interacting regions from Hi-C data. Computational and Structural Biotechnology Journal, 2021, 19, 355-362.	1.9	22
67	Xenopus tropicalis Genome Re-Scaffolding and Re-Annotation Reach the Resolution Required for In Vivo ChIA-PET Analysis. PLoS ONE, 2015, 10, e0137526.	1.1	21
68	LATS kinase–mediated CTCF phosphorylation and selective loss of genomic binding. Science Advances, 2020, 6, eaaw4651.	4.7	21
69	PPIcons: identification of protein-protein interaction sites in selected organisms. Journal of Molecular Modeling, 2013, 19, 4059-4070.	0.8	20
70	Virtual High Throughput Screening Using Combined Random Forest and Flexible Docking. Combinatorial Chemistry and High Throughput Screening, 2009, 12, 484-489.	0.6	19
71	Clinical and molecular characteristics of newly reported mitochondrial disease entity caused by biallelic PARS2 mutations. Journal of Human Genetics, 2018, 63, 473-485.	1.1	19
72	Upregulation of MLK4 promotes migratory and invasive potential of breast cancer cells. Oncogene, 2019, 38, 2860-2875.	2.6	19

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73	3D-GNOME 2.0: a three-dimensional genome modeling engine for predicting structural variation-driven alterations of chromatin spatial structure in the human genome. Nucleic Acids Research, 2020, 48, W170-W176.	6.5	19
74	Nuclear pore protein NUP210 depletion suppresses metastasis through heterochromatin-mediated disruption of tumor cell mechanical response. Nature Communications, 2021, 12, 7216.	5.8	19
75	The RPSP: Web server for prediction of signal peptides. Polymer, 2007, 48, 5493-5496.	1.8	18
76	Chromatin interaction networks and higher order architectures of eukaryotic genomes. Journal of Cellular Biochemistry, 2011, 112, 2218-2221.	1.2	18
77	Improvement of new automatic differential fuzzy clustering using SVM classifier for microarray analysis. Expert Systems With Applications, 2011, 38, 15122-15133.	4.4	17
78	Intermingling of chromosome territories. Genes Chromosomes and Cancer, 2019, 58, 500-506.	1.5	17
79	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. Seminars in Cell and Developmental Biology, 2022, 121, 171-185.	2.3	17
80	Species Used for Drug Testing Reveal Different Inhibition Susceptibility for 17beta-Hydroxysteroid Dehydrogenase Type 1. PLoS ONE, 2010, 5, e10969.	1.1	17
81	Brainstorming: weighted voting prediction of inhibitors for protein targets. Journal of Molecular Modeling, 2011, 17, 2133-2141.	0.8	16
82	Identification of Breast Cancer Subtype Specific MicroRNAs Using Survival Analysis to Find Their Role in Transcriptomic Regulation. Frontiers in Genetics, 2019, 10, 1047.	1.1	16
83	Drug repurposing for identification of potential spike inhibitors for SARS-CoV-2 using molecular docking and molecular dynamics simulations. Methods, 2022, 203, 498-510.	1.9	16
84	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
85	Consensus classification of human leukocyte antigen class II proteins. Immunogenetics, 2013, 65, 97-105.	1.2	15
86	A combined systems and structural modeling approach repositions antibiotics for Mycoplasma genitalium. Computational Biology and Chemistry, 2015, 59, 91-97.	1.1	13
87	Multi-level machine learning prediction of protein–protein interactions in <i>Saccharomyces cerevisiae</i>. PeerJ, 2015, 3, e1041.	0.9	13
88	In Silico Prediction of SARS Protease Inhibitors by Virtual High Throughput Screening. Chemical Biology and Drug Design, 2007, 69, 269-279.	1.5	12
89	Three-Dimensional Segmentation and Reconstruction of Neuronal Nuclei in Confocal Microscopic Images. Frontiers in Neuroanatomy, 2019, 13, 81.	0.9	12
90	Chromatin topology reorganization and transcription repression by PML-RARÎ± in acute promyeloid leukemia. Genome Biology, 2020, 21, 110.	3.8	12

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91	COVID-DeepPredictor: Recurrent Neural Network to Predict SARS-CoV-2 and Other Pathogenic Viruses. Frontiers in Genetics, 2021, 12, 569120.	1.1	12
92	FunPred 3.0: improved protein function prediction using protein interaction network. PeerJ, 2019, 7, e6830.	0.9	12
93	Potent but transient immunosuppression of T-cells is a general feature of CD71+ erythroid cells. Communications Biology, 2021, 4, 1384.	2.0	12
94	Influence of colored noise on chaotic systems. Physical Review E, 2002, 66, 035202.	0.8	11
95	Improved differential evolution for microarray analysis. International Journal of Data Mining and Bioinformatics, 2012, 6, 86.	0.1	11
96	Information-sharing and aggregation models for interacting minds. Journal of Mathematical Psychology, 2012, 56, 417-426.	1.0	11
97	HarmonyDOCK: The Structural Analysis of Poses in Protein-Ligand Docking. Journal of Computational Biology, 2014, 21, 247-256.	0.8	11
98	Computational Approach to Dendritic Spine Taxonomy and Shape Transition Analysis. Frontiers in Computational Neuroscience, 2016, 10, 140.	1.2	11
99	Methods for comparative ChIA-PET and Hi-C data analysis. Methods, 2020, 170, 69-74.	1.9	11
100	Aggregated network centrality shows non-random structure of genomic and proteomic networks. Methods, 2020, 181-182, 5-14.	1.9	11
101	<i>In situ</i> Chromatin Interaction Analysis Using Paired‐End Tag Sequencing. Current Protocols, 2021, 1, e174.	1.3	11
102	Molecular modeling of phosphorylation sites in proteins using a database of local structure segments. Journal of Molecular Modeling, 2005, 11, 431-438.	0.8	10
103	3D-Fun: predicting enzyme function from structure. Nucleic Acids Research, 2008, 36, W303-W307.	6.5	10
104	Binding Activity Prediction of Cyclin-Dependent Inhibitors. Journal of Chemical Information and Modeling, 2015, 55, 1469-1482.	2.5	10
105	PDP-CON: prediction of domain/linker residues in protein sequences using a consensus approach. Journal of Molecular Modeling, 2016, 22, 72.	0.8	10
106	RNA structure interactions and ribonucleoprotein processes of the influenza A virus. Briefings in Functional Genomics, 2018, 17, 402-414.	1.3	10
107	QuIN: A Web Server for Querying and Visualizing Chromatin Interaction Networks. PLoS Computational Biology, 2016, 12, e1004809.	1.5	10
108	3dSpAn: An interactive software for 3D segmentation and analysis of dendritic spines. Neuroinformatics, 2022, 20, 679-698.	1.5	10

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109	3DGenBench: a web-server to benchmark computational models for 3D Genomics. Nucleic Acids Research, 2022, 50, W4-W12.	6.5	10
110	Integrated web service for improving alignment quality based on segments comparison. BMC Bioinformatics, 2004, 5, 98.	1.2	9
111	Deep Learning for Detection and Localization of Thoracic Diseases Using Chest X-Ray Imagery. Lecture Notes in Computer Science, 2019, , 271-282.	1.0	9
112	Spring Model â€" Chromatin Modeling Tool Based on OpenMM. Methods, 2020, 181-182, 62-69.	1.9	9
113	Unsupervised and Supervised Learning Approaches Together for Microarray Analysis. Fundamenta Informaticae, 2011, 106, 45-73.	0.3	8
114	3DFlu: database of sequence and structural variability of the influenza hemagglutinin at population scale. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw130.	1.4	8
115	Inhibition of protein disulfide isomerase induces differentiation of acute myeloid leukemia cells. Haematologica, 2018, 103, 1843-1852.	1.7	8
116	MIA-Sig: multiplex chromatin interaction analysis by signal processing and statistical algorithms. Genome Biology, 2019, 20, 251.	3.8	8
117	Complexity curve: a graphical measure of data complexity and classifier performance. PeerJ Computer Science, 0, 2, e76.	2.7	8
118	Novel <i>COL12A1</i> variant as a cause of mild familial extracellular matrixâ€related myopathy. Clinical Genetics, 2019, 95, 736-738.	1.0	7
119	Machine learning polymer models of three-dimensional chromatin organization in human lymphoblastoid cells. Methods, 2019, 166, 83-90.	1.9	7
120	PartSeg: a tool for quantitative feature extraction from 3D microscopy images for dummies. BMC Bioinformatics, 2021, 22, 72.	1.2	7
121	Computational inference of H3K4me3 and H3K27ac domain length. PeerJ, 2016, 4, e1750.	0.9	7
122	Role of the host genetic variability in the influenza A virus susceptibility. Acta Biochimica Polonica, 2014, 61, 403-19.	0.3	7
123	Activation-induced chromatin reorganization in neurons depends on HDAC1 activity. Cell Reports, 2022, 38, 110352.	2.9	7
124	Super-resolution visualization of chromatin loop folding in human lymphoblastoid cells using interferometric photoactivated localization microscopy. Scientific Reports, 2022, 12, .	1.6	7
125	Support-vector-machine classification of linear functional motifs in proteins. Journal of Molecular Modeling, 2006, 12, 453-461.	0.8	6
126	3gClust: Human Protein Cluster Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1-1.	1.9	6

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127	ProteinSplit: splitting of multi-domain proteins using prediction of ordered and disordered regions in protein sequences for virtual structural genomics. Journal of Physics Condensed Matter, 2007, 19, 285222.	0.7	5
128	Detecting reliable non interacting proteins (NIPs) significantly enhancing the computational prediction of proteinâ€"protein interactions using machine learning methods. Molecular BioSystems, 2016, 12, 778-785.	2.9	5
129	Oncogenes expand during evolution to withstand somatic amplification. Annals of Oncology, 2018, 29, 2254-2260.	0.6	5
130	Genome-wide analysis of 10664 SARS-CoV-2 genomes to identify virus strains in 73 countries based on single nucleotide polymorphism. Virus Research, 2021, 298, 198401.	1.1	5
131	Mean-field theory of meta-learning. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P11003.	0.9	4
132	MaER: A New Ensemble Based Multiclass Classifier for Binding Activity Prediction of HLA Class II Proteins. Lecture Notes in Computer Science, 2015, , 462-471.	1.0	4
133	Highlights from the 11th ISCB Student Council Symposium 2015. BMC Bioinformatics, 2016, 17, 95.	1.2	4
134	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
135	Social adaptation in multi-agent model of linguistic categorization is affected by network information flow. PLoS ONE, 2017, 12, e0182490.	1.1	4
136	Identification of miRNA Biomarkers for Diverse Cancer Types Using Statistical Learning Methods at the Whole-Genome Scale. Frontiers in Genetics, 2020, 11, 982.	1.1	4
137	The Mixture of Autoregressive Hidden Markov Models of Morphology for Dentritic Spines During Activation Process. Journal of Computational Biology, 2020, 27, 1471-1485.	0.8	4
138	*JUPPI*: A Multi-Level Feature Based Method for PPI Prediction and a Refined Strategy for Performance Assessment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 531-542.	1.9	4
139	TBC1D24 emerges as an important contributor to progressive postlingual dominant hearing loss. Scientific Reports, 2021, 11, 10300.	1.6	4
140	Multiobjective Differential Evolution: A Comparative Study on Benchmark Problems. Advances in Intelligent Systems and Computing, 2014, , 529-536.	0.5	4
141	Computational modelling of three-dimensional genome structure. Methods, 2020, 181-182, 1-4.	1.9	4
142	TVscreen: Trend Vector Virtual SCREENing of Large Commercial Compounds Collections. , 2008, , .		3
143	Real-coded differential crisp clustering for MRI brain image segmentation. , 2010, , .		3
144	The prolineâ€rich region of glyceraldehydeâ€3â€phosphate dehydrogenase from human sperm may bind SH3 domains, as revealed by a bioinformatic study of lowâ€complexity protein segments. Molecular Reproduction and Development, 2016, 83, 144-148.	1.0	3

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145	Chromatin Interaction Analysis Using Paired-End-Tag (ChIA-PET) Sequencing in Tadpole Tissues. Cold Spring Harbor Protocols, 2018, 2018, pdb.prot104620.	0.2	3
146	Dendritic Spines Taxonomy: The Functional and Structural Classification â€¢ Time-Dependent Probabilistic Model of Neuronal Activation. Journal of Computational Biology, 2019, 26, 322-335.	0.8	3
147	Consensus Multiobjective Differential Crisp Clustering for Categorical Data Analysis. Lecture Notes in Computer Science, 2010, , 30-39.	1.0	3
148	Multi-scale phase separation by explosive percolation with single-chromatin loop resolution. Computational and Structural Biotechnology Journal, 2022, 20, 3591-3603.	1.9	3
149	Landau Theory of Meta-learning. Lecture Notes in Computer Science, 2012, , 142-153.	1.0	2
150	An empirical Bayes approach for learning directed acyclic graph using MCMC algorithm. Statistical Analysis and Data Mining, 2019, 12, 394-403.	1.4	2
151	Learning directed acyclic graphs by determination of candidate causes for discrete variables. Journal of Statistical Computation and Simulation, 2019, 89, 1957-1970.	0.7	2
152	Identification of Epigenetic Biomarkers with the use of Gene Expression and DNA Methylation for Breast Cancer Subtypes. , 2019, , .		2
153	Free energy-based model of CTCF-mediated chromatin looping in the human genome. Methods, 2020, 181-182, 35-51.	1.9	2
154	PDP-RF: Protein Domain Boundary Prediction Using Random Forest Classifier. Lecture Notes in Computer Science, 2015, , 441-450.	1.0	2
155	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
156	Modelling of potentially promising SARS protease inhibitors. Journal of Physics Condensed Matter, 2007, 19, 285207.	0.7	1
157	kNNsim: k-Nearest neighbors similarity with genetic algorithm features optimization enhances the prediction of activity classes for small molecules. Journal of Molecular Modeling, 2009, 15, 591-596.	0.8	1
158	Application of High Quality Amino Acid Indices to AMS 3.0: A Update Note. Advances in Intelligent Systems and Computing, 2013, , 217-225.	0.5	1
159	Application of Machine Learning Method in Genomics and Proteomics. Scientific World Journal, The, 2015, 2015, 1-2.	0.8	1
160	A new evolutionary rough fuzzy integrated machine learning technique for microRNA selection using next-generation sequencing data of breast cancer. , 2019, , .		1
161	A Multivariate Negative-Binomial Model with Random Effects for Differential Gene-Expression Analysis of Correlated mRNA Sequencing Data. Journal of Computational Biology, 2019, 26, 1339-1348.	0.8	1
162	Chromatin: A Semi-Structured Polymer. , 2019, , 288-307.		1

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163	Biomolecular Clusters Identification in Linear Time Complexity for Biological Networks. Advances in Intelligent Systems and Computing, 2021, , 611-622.	0.5	1
164	A Gibbs sampler for learning DAG: a unification for discrete and Gaussian domains. Journal of Statistical Computation and Simulation, 2021, 91, 2833-2853.	0.7	1
165	Evaluation of Machine Learning Algorithms on Protein-Protein Interactions. Advances in Intelligent Systems and Computing, 2014, , 211-218.	0.5	1
166	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
167	Multi-levels 3D Chromatin Interactions Prediction Using Epigenomic Profiles. Lecture Notes in Computer Science, 2017, , 19-28.	1.0	1
168	Survival Analysis with the Integration of RNA-Seq and Clinical Data to Identify Breast Cancer Subtype Specific Genes. Lecture Notes in Computer Science, 2019, , 139-146.	1.0	1
169	Genomic Marks Associated with Chromatin Compartments in the CTCF, RNAPII Loop and Genomic Windows. International Journal of Molecular Sciences, 2021, 22, 11591.	1.8	1
170	3D–Epigenomic Regulation of Gene Transcription in Hepatocellular Carcinoma. Genetics & Genomics Next, 2022, 3, .	0.8	1
171	Multiobjective Differential Crisp Clustering for Evaluation of Clusters Dynamically. Advances in Intelligent and Soft Computing, 2011, , 307-313.	0.2	0
172	GIDMP: Good protein-protein interaction data metamining practice. Cellular and Molecular Biology Letters, 2011, 16, 258-63.	2.7	0
173	Divide and Conquer Ensemble Method for Time Series Forecasting. Lecture Notes in Computer Science, 2016, , 134-152.	1.0	0
174	Analysis of Structural Chromosome Variants by Next Generation Sequencing Methods. , 2016, , 39-61.		0
175	Emerging and threatening infectious diseases. Briefings in Functional Genomics, 2018, 17, 372-373.	1.3	0
176	The World Color Survey: Data Analysis and Simulations. , 2019, , 289-311.		0
177	The Changes of the Nuclear Landscape Upon Stimulation of Neuronal Cells are Dependent on the Histone Deacetylase HSAC1. SSRN Electronic Journal, 0, , .	0.4	0
178	PMAFC: A New Probabilistic Memetic Algorithm Based Fuzzy Clustering. Lecture Notes in Computer Science, 2011, , 602-611.	1.0	0
179	A Consensus Approach for Identification of Protein-Protein Interaction Sites in Homo Sapiens. Lecture Notes in Computer Science, 2013, , 674-679.	1.0	0
180	Soft Computing Approach for VLSI Mincut Partitioning: The State of the Arts. Advances in Intelligent Systems and Computing, 2014, , 895-903.	0.5	0

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181	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
182	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
183	Correction to: The World Color Survey: Data Analysis and Simulations. , 2019, , C1-C1.		0
184	Mixture of Forward-Directed and Backward-Directed Autoregressive Hidden Markov Models for Time series Modeling. Journal of the Iranian Statistical Society, 2019, 18, 89-112.	0.2	0
185	Genome-Wide Analysis to Identify Palindromes, Mirror and Inverted Repeats in SARS-CoV-2, MERS-CoV and SARS-CoV-1. IEEE Access, 2022, 10, 23708-23715.	2.6	0
186	Single-Hit Inactivation Drove Tumor Suppressor Genes Out of the X Chromosome during Evolution. Cancer Research, 2022, 82, 1482-1491.	0.4	0
187	Online Predictor Using Machine Learning to Predict Novel Coronavirus and Other Pathogenic Viruses. ACS Omega, 2022, 7, 23069-23074.	1.6	0