

# Ioannis Xenarios

## List of Publications by Year in descending order

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205  
papers

41,414  
citations

9786

73  
h-index

2747

192  
g-index

223  
all docs

223  
docs citations

223  
times ranked

69683  
citing authors

#	ARTICLE	IF	CITATIONS
1	UniProt: a worldwide hub of protein knowledge. <i>Nucleic Acids Research</i> , 2019, 47, D506-D515.	14.5	6,185
2	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	17.5	2,505
3	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	14.5	1,838
4	ExPASy: SIB bioinformatics resource portal. <i>Nucleic Acids Research</i> , 2012, 40, W597-W603.	14.5	1,737
5	DIP, the Database of Interacting Proteins: a research tool for studying cellular networks of protein interactions. <i>Nucleic Acids Research</i> , 2002, 30, 303-305.	14.5	1,487
6	InterPro in 2017—beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	14.5	1,358
7	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	14.5	1,205
8	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2012, 40, D71-D75.	14.5	1,196
9	New and continuing developments at PROSITE. <i>Nucleic Acids Research</i> , 2012, 41, D344-D347.	14.5	1,190
10	Activities at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2014, 42, D191-D198.	14.5	1,162
11	The Universal Protein Resource (UniProt) in 2010. <i>Nucleic Acids Research</i> , 2010, 38, D142-D148.	14.5	1,131
12	T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension. <i>Nucleic Acids Research</i> , 2011, 39, W13-W17.	14.5	982
13	DIP: the Database of Interacting Proteins. <i>Nucleic Acids Research</i> , 2000, 28, 289-291.	14.5	900
14	Protein function in the post-genomic era. <i>Nature</i> , 2000, 405, 823-826.	27.8	690
15	Ongoing and future developments at the Universal Protein Resource. <i>Nucleic Acids Research</i> , 2011, 39, D214-D219.	14.5	649
16	UniProtKB/Swiss-Prot, the Manually Annotated Section of the UniProt KnowledgeBase: How to Use the Entry View. <i>Methods in Molecular Biology</i> , 2016, 1374, 23-54.	0.9	624
17	The HUPO PSI's Molecular Interaction format—a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	17.5	581
18	Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 349-356.	3.8	570

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19	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012, 9, 345-350.	19.0	500
20	Phytochrome interacting factors 4 and 5 control seedling growth in changing light conditions by directly controlling auxin signaling. <i>Plant Journal</i> , 2012, 71, 699-711.	5.7	498
21	Gene expression across mammalian organ development. <i>Nature</i> , 2019, 571, 505-509.	27.8	490
22	Gene Ontology Annotations and Resources. <i>Nucleic Acids Research</i> , 2012, 41, D530-D535.	14.5	456
23	Microarray Deacetylation Maps Determine Genome-Wide Functions for Yeast Histone Deacetylases. <i>Cell</i> , 2002, 109, 437-446.	28.9	422
24	MorphoGraphX: A platform for quantifying morphogenesis in 4D. <i>ELife</i> , 2015, 4, 05864.	6.0	389
25	Exome sequencing identifies recurrent somatic MAP2K1 and MAP2K2 mutations in melanoma. <i>Nature Genetics</i> , 2012, 44, 133-139.	21.4	369
26	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	21.4	362
27	The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , 2012, 40, D565-D570.	14.5	349
28	Personalized cancer vaccine effectively mobilizes antitumor T cell immunity in ovarian cancer. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	326
29	The genome of the fire ant <i>Solenopsis invicta</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5679-5684.	7.1	322
30	ViralZone: a knowledge resource to understand virus diversity. <i>Nucleic Acids Research</i> , 2011, 39, D576-D582.	14.5	312
31	Complement facilitates early prion pathogenesis. <i>Nature Medicine</i> , 2001, 7, 488-492.	30.7	301
32	IL-4 Rapidly Produced by $V\beta 24 V\beta 8$ CD4 <sup>+</sup> T Cells Instructs Th2 Development and Susceptibility to <i>Leishmania major</i> in BALB/c Mice. <i>Immunity</i> , 1997, 6, 541-549.	14.3	297
33	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. <i>Cell</i> , 2020, 183, 818-834.e13.	28.9	287
34	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	17.5	274
35	Synchronous versus asynchronous modeling of gene regulatory networks. <i>Bioinformatics</i> , 2008, 24, 1917-1925.	4.1	272
36	Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. <i>European Heart Journal</i> , 2015, 36, 353-368.	2.2	244

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37	Broadening the horizon “ level 2.5 of the HUPO-PSI format for molecular interactions. BMC Biology, 2007, 5, 44.	3.8	237
38	Three-dimensional cluster analysis identifies interfaces and functional residue clusters in proteins <sup>11</sup> Edited by J. Thornton. Journal of Molecular Biology, 2001, 307, 1487-1502.	4.2	226
39	Characterization of the Human ABCG1 Gene. Journal of Biological Chemistry, 2001, 276, 39438-39447.	3.4	226
40	Proteomic Analysis of the Mouse Liver Mitochondrial Inner Membrane. Journal of Biological Chemistry, 2003, 278, 41566-41571.	3.4	220
41	A method for the generation of standardized qualitative dynamical systems of regulatory networks. Theoretical Biology and Medical Modelling, 2006, 3, 13.	2.1	210
42	Localizing proteins in the cell from their phylogenetic profiles. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 12115-12120.	7.1	207
43	Type I Interferons Protect T Cells against NK Cell Attack Mediated by the Activating Receptor NCR1. Immunity, 2014, 40, 961-973.	14.3	199
44	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	19.0	198
45	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. Nature Communications, 2020, 11, 1293.	12.8	196
46	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	14.5	191
47	The UniProtKB/Swiss-Prot Tox-Prot program: A central hub of integrated venom protein data. Toxicon, 2012, 60, 551-557.	1.6	180
48	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
49	Plasma Dihydroceramides Are Diabetes Susceptibility Biomarker Candidates in Mice and Humans. Cell Reports, 2017, 18, 2269-2279.	6.4	168
50	Neutrophils and Snail Orchestrate the Establishment of a Pro-tumor Microenvironment in Lung Cancer. Cell Reports, 2017, 21, 3190-3204.	6.4	167
51	DIP: The Database of Interacting Proteins: 2001 update. Nucleic Acids Research, 2001, 29, 239-241.	14.5	165
52	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. BMC Systems Biology, 2013, 7, 135.	3.0	145
53	Dynamic simulation of regulatory networks using SQUAD. BMC Bioinformatics, 2007, 8, 462.	2.6	136
54	HAMAP in 2015: updates to the protein family classification and annotation system. Nucleic Acids Research, 2015, 43, D1064-D1070.	14.5	135

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55	Systems biology of the IMIDIA biobank from organ donors and pancreatectomised patients defines a novel transcriptomic signature of islets from individuals with type 2 diabetes. <i>Diabetologia</i> , 2018, 61, 641-657.	6.3	131
56	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2765-2775.	3.8	130
57	Neighbor Detection Induces Organ-Specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-Specific Growth. <i>Plant Cell</i> , 2016, 28, 2889-2904.	6.6	128
58	Soil fungal communities of grasslands are environmentally structured at a regional scale in the <scp>A</scp>ps. <i>Molecular Ecology</i> , 2014, 23, 4274-4290.	3.9	125
59	Sensitive and frequent identification of high avidity neo-epitope-specific CD8 + T cells in immunotherapy-naïve ovarian cancer. <i>Nature Communications</i> , 2018, 9, 1092.	12.8	122
60	Low number of fixed somatic mutations in a long-lived oak tree. <i>Nature Plants</i> , 2017, 3, 926-929.	9.3	120
61	CDK9 Regulates AR Promoter Selectivity and Cell Growth through Serine 81 Phosphorylation. <i>Molecular Endocrinology</i> , 2010, 24, 2267-2280.	3.7	119
62	The SwissLipids knowledgebase for lipid biology. <i>Bioinformatics</i> , 2015, 31, 2860-2866.	4.1	114
63	Improving the sensitivity of the sequence profile method. <i>Protein Science</i> , 1994, 3, 139-146.	7.6	108
64	FastEpistasis: a high performance computing solution for quantitative trait epistasis. <i>Bioinformatics</i> , 2010, 26, 1468-1469.	4.1	105
65	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome*. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2347-2357.	3.8	105
66	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , 2015, 31, 1154-1159.	4.1	98
67	Protein interaction databases. <i>Current Opinion in Biotechnology</i> , 2001, 12, 334-339.	6.6	89
68	Functional and Evolutionary Analysis of the CASPARIAN STRIP MEMBRANE DOMAIN PROTEIN Family. <i>Plant Physiology</i> , 2014, 165, 1709-1722.	4.8	86
69	Rhea—a manually curated resource of biochemical reactions. <i>Nucleic Acids Research</i> , 2012, 40, D754-D760.	14.5	84
70	UniPathway: a resource for the exploration and annotation of metabolic pathways. <i>Nucleic Acids Research</i> , 2012, 40, D761-D769.	14.5	83
71	Hard-wired heterogeneity in blood stem cells revealed using a dynamic regulatory network model. <i>Bioinformatics</i> , 2013, 29, i80-i88.	4.1	83
72	Differentially Phased Leaf Growth and Movements in <i>Arabidopsis</i> Depend on Coordinated Circadian and Light Regulation. <i>Plant Cell</i> , 2014, 26, 3911-3921.	6.6	83

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73	Guidelines for reporting the use of mass spectrometry in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 860-861.	17.5	82
74	Probabilistic base calling of Solexa sequencing data. <i>BMC Bioinformatics</i> , 2008, 9, 431.	2.6	82
75	Cell-free DNA testing of an extended range of chromosomal anomalies: clinical experience with 6,388 consecutive cases. <i>Genetics in Medicine</i> , 2017, 19, 169-175.	2.4	82
76	Microarray analysis of isolated human islet transcriptome in type 2 diabetes and the role of the ubiquitin-proteasome system in pancreatic beta cell dysfunction. <i>Molecular and Cellular Endocrinology</i> , 2013, 367, 1-10.	3.2	76
77	Measuring the diurnal pattern of leaf hyponasty and growth in <i>Arabidopsis</i> - a novel phenotyping approach using laser scanning. <i>Functional Plant Biology</i> , 2012, 39, 860.	2.1	73
78	Enzyme annotation in UniProtKB using Rhea. <i>Bioinformatics</i> , 2020, 36, 1896-1901.	4.1	72
79	Local auxin production underlies a spatially restricted neighbor-detection response in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7444-7449.	7.1	70
80	Evolution of the Ferric Reductase Domain (FRD) Superfamily: Modularity, Functional Diversification, and Signature Motifs. <i>PLoS ONE</i> , 2013, 8, e58126.	2.5	68
81	Sleep-wake-driven and circadian contributions to daily rhythms in gene expression and chromatin accessibility in the murine cortex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25773-25783.	7.1	66
82	Reconciliation of metabolites and biochemical reactions for metabolic networks. <i>Briefings in Bioinformatics</i> , 2014, 15, 123-135.	6.5	64
83	Mutations in <i>LONP1</i> , a mitochondrial matrix protease, cause CODAS syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 1501-1509.	1.2	61
84	HAMAP in 2013, new developments in the protein family classification and annotation system. <i>Nucleic Acids Research</i> , 2013, 41, D584-D589.	14.5	57
85	Updates in Rhea - an expert curated resource of biochemical reactions. <i>Nucleic Acids Research</i> , 2017, 45, D415-D418.	14.5	56
86	Deciphering the Dynamic Transcriptional and Post-transcriptional Networks of Macrophages in the Healthy Heart and after Myocardial Injury. <i>Cell Reports</i> , 2018, 23, 622-636.	6.4	56
87	Molecular Docking of Competitive Phosphodiesterase Inhibitors. <i>Molecular Pharmacology</i> , 2002, 61, 20-25.	2.3	54
88	Updates in Rhea: SPARQLing biochemical reaction data. <i>Nucleic Acids Research</i> , 2019, 47, D596-D600.	14.5	54
89	R-Coffee: a web server for accurately aligning noncoding RNA sequences. <i>Nucleic Acids Research</i> , 2008, 36, W10-W13.	14.5	53
90	<i>TBC1D7</i> Mutations are Associated with Intellectual Disability, Macrocrania, Patellar Dislocation, and Celiac Disease. <i>Human Mutation</i> , 2014, 35, 447-451.	2.5	52

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91	Network-Guided Analysis of Genes with Altered Somatic Copy Number and Gene Expression Reveals Pathways Commonly Perturbed in Metastatic Melanoma. PLoS ONE, 2011, 6, e18369.	2.5	51
92	Genetic Variations and Diseases in UniProtKB/SwissProt: The Ins and Outs of Expert Manual Curation. Human Mutation, 2014, 35, 927-935.	2.5	51
93	A systems genetics resource and analysis of sleep regulation in the mouse. PLoS Biology, 2018, 16, e2005750.	5.6	51
94	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. Molecular Biology and Evolution, 2009, 26, 2865-2875.	8.9	50
95	An Efficient Method for Dynamic Analysis of Gene Regulatory Networks and in silico Gene Perturbation Experiments. , 2007, , 62-76.		50
96	A robust second-generation genome-wide test for fetal aneuploidy based on shotgun sequencing cell-free DNA in maternal blood. Prenatal Diagnosis, 2013, 33, 707-710.	2.3	49
97	ViralZone: recent updates to the virus knowledge resource. Nucleic Acids Research, 2012, 41, D579-D583.	14.5	48
98	KIAA1109 Variants Are Associated with a Severe Disorder of Brain Development and Arthrogryposis. American Journal of Human Genetics, 2018, 102, 116-132.	6.2	46
99	Global mapping of highly pathogenic avian influenza H5N1 and H5Nx clade 2.3.4.4 viruses with spatial cross-validation. ELife, 2016, 5, .	6.0	45
100	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	12.6	45
101	A qualitative continuous model of cellular auxin and brassinosteroid signaling and their crosstalk. Bioinformatics, 2011, 27, 1404-1412.	4.1	44
102	Modeling stochasticity and robustness in gene regulatory networks. Bioinformatics, 2009, 25, i101-i109.	4.1	43
103	Interplays between mouse mammary tumor virus and the cellular and humoral immune response. Immunological Reviews, 1999, 168, 287-303.	6.0	42
104	Molecular phenotyping of multiple mouse strains under metabolic challenge uncovers a role for Elovl2 in glucose-induced insulin secretion. Molecular Metabolism, 2017, 6, 340-351.	6.5	42
105	TIE-2 expressing monocytes in human cancers. OncoImmunology, 2017, 6, e1303585.	4.6	42
106	Updates in Rhea—a manually curated resource of biochemical reactions. Nucleic Acids Research, 2015, 43, D459-D464.	14.5	41
107	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. Plant Physiology, 2019, 180, 305-322.	4.8	41
108	Drug Design Workshop: A Web-Based Educational Tool To Introduce Computer-Aided Drug Design to the General Public. Journal of Chemical Education, 2017, 94, 335-344.	2.3	39

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109	Plant species distributions along environmental gradients: do belowground interactions with fungi matter?. <i>Frontiers in Plant Science</i> , 2013, 4, 500.	3.6	38
110	OpenFluDB, a database for human and animal influenza virus. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq004-baq004.	3.0	37
111	Boolean regulatory network reconstruction using literature based knowledge with a genetic algorithm optimization method. <i>BMC Bioinformatics</i> , 2016, 17, 410.	2.6	37
112	TIE-2-expressing monocytes are lymphangiogenic and associate specifically with lymphatics of human breast cancer. <i>Oncolmmunology</i> , 2016, 5, e1073882.	4.6	37
113	Fisetin protects against cardiac cell death through reduction of ROS production and caspases activity. <i>Scientific Reports</i> , 2020, 10, 2896.	3.3	37
114	Automated quantitative histology reveals vascular morphodynamics during Arabidopsis hypocotyl secondary growth. <i>ELife</i> , 2014, 3, e01567.	6.0	37
115	Comparative transcriptome profiling of the injured zebrafish and mouse hearts identifies miRNA-dependent repair pathways. <i>Cardiovascular Research</i> , 2016, 110, 73-84.	3.8	36
116	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	4.1	36
117	Describing Biological Protein Interactions in Terms of Protein States and State Transitions. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 104-116.	3.8	35
118	A Chemical Proteomics Approach to Phosphatidylinositol 3-Kinase Signaling in Macrophages. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1829-1841.	3.8	34
119	HENA, heterogeneous network-based data set for Alzheimer's disease. <i>Scientific Data</i> , 2019, 6, 151.	5.3	34
120	Quantification of the spread of SARS-CoV-2 variant B.1.1.7 in Switzerland. <i>Epidemics</i> , 2021, 37, 100480.	3.0	34
121	The direct effects of tacrolimus and cyclosporin A on isolated human islets: A functional, survival and gene expression study. <i>Islets</i> , 2009, 1, 106-110.	1.8	33
122	Conceptual framework and pilot study to benchmark phylogenomic databases based on reference gene trees. <i>Briefings in Bioinformatics</i> , 2011, 12, 423-435.	6.5	33
123	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. <i>PLoS Computational Biology</i> , 2018, 14, e1006390.	3.2	33
124	TIE-2 and VEGFR Kinase Activities Drive Immunosuppressive Function of TIE-2-Expressing Monocytes in Human Breast Tumors. <i>Clinical Cancer Research</i> , 2013, 19, 3439-3449.	7.0	32
125	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. <i>PLoS Computational Biology</i> , 2014, 10, e1003757.	3.2	32
126	Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. <i>Scientific Reports</i> , 2016, 6, 26822.	3.3	32



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127	A Clb/Cdk1-mediated regulation of Fkh2 synchronizes CLB expression in the budding yeast cell cycle. <i>Npj Systems Biology and Applications</i> , 2017, 3, 7.	3.0	32
128	Substantial deletion overlap among divergent Arabidopsis genomes revealed by intersection of short reads and tiling arrays. <i>Genome Biology</i> , 2010, 11, R4.	9.6	31
129	Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw161.	3.0	30
130	SourceData: a semantic platform for curating and searching figures. <i>Nature Methods</i> , 2017, 14, 1021-1022.	19.0	29
131	The EMPRES-i genetic module: a novel tool linking epidemiological outbreak information and genetic characteristics of influenza viruses. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau008-bau008.	3.0	28
132	Improving the quality and workflow of bacterial genome sequencing and analysis: paving the way for a Switzerland-wide molecular epidemiological surveillance platform. <i>Swiss Medical Weekly</i> , 2018, 148, w14693.	1.6	28
133	Database resources for the tuberculosis community. <i>Tuberculosis</i> , 2013, 93, 12-17.	1.9	27
134	Laser capture microdissection of human pancreatic islets reveals novel eQTLs associated with type 2 diabetes. <i>Molecular Metabolism</i> , 2019, 24, 98-107.	6.5	26
135	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , 2015, 7, 1988-1999.	2.5	25
136	Enhanced metabolite annotation via dynamic retention time prediction: Steroidogenesis alterations as a case study. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1071, 11-18.	2.3	25
137	Setting the basis of best practices and standards for curation and annotation of logical models in biology – highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. <i>Briefings in Bioinformatics</i> , 2021, 22, 1848-1859.	6.5	25
138	MARCMediated transgene integration into permissive chromatin and increased expression by recombination pathway engineering. <i>Biotechnology and Bioengineering</i> , 2017, 114, 384-396.	3.3	23
139	Human ERK1 Induces Filamentous Growth and Cell Wall Remodeling Pathways in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 20638-20646.	3.4	22
140	Systems biology to battle vascular disease. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 1019-1022.	0.7	22
141	Genome-wide identification of microRNAs regulating the human prion protein. <i>Brain Pathology</i> , 2019, 29, 232-244.	4.1	22
142	New molecular insights into modulation of platelet reactivity in aspirin-treated patients using a network-based approach. <i>Human Genetics</i> , 2016, 135, 403-414.	3.8	21
143	Modeling of Multiple Valued Gene Regulatory Networks. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2007, 2007, 1398-404.	0.5	20
144	Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. <i>Genome Medicine</i> , 2016, 8, 105.	8.2	20

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145	Animal Toxins: How is Complexity Represented in Databases?. <i>Toxins</i> , 2010, 2, 262-282.	3.4	19
146	Density-based hierarchical clustering of pyro-sequences on a large scale—the case of fungal ITS1. <i>Bioinformatics</i> , 2013, 29, 1268-1274.	4.1	19
147	pfsearchV3: a code acceleration and heuristic to search PROSITE profiles. <i>Bioinformatics</i> , 2013, 29, 1215-1217.	4.1	18
148	Angiogenic Activity of Breast Cancer Patients's Monocytes Reverted by Combined Use of Systems Modeling and Experimental Approaches. <i>PLoS Computational Biology</i> , 2015, 11, e1004050.	3.2	18
149	DynaStI: A Dynamic Retention Time Database for Steroidomics. <i>Metabolites</i> , 2019, 9, 85.	2.9	18
150	Detection and identification of plasma proteins that bind GlialCAM using ProteinChip <sup>®</sup> , $\mu$ Arrays, SELDI-TOF MS, and nano- $\mu$ C MS/MS. <i>Proteomics</i> , 2008, 8, 378-388.	2.2	17
151	Application of text-mining for updating protein post-translational modification annotation in UniProtKB. <i>BMC Bioinformatics</i> , 2013, 14, 104.	2.6	17
152	TRAL: tandem repeat annotation library. <i>Bioinformatics</i> , 2015, 31, 3051-3053.	4.1	17
153	Three-dimensional chromatin interactions remain stable upon CAG/CTG repeat expansion. <i>Science Advances</i> , 2020, 6, eaaz4012.	10.3	16
154	MIMAS 3.0 is a Multiomics Information Management and Annotation System. <i>BMC Bioinformatics</i> , 2009, 10, 151.	2.6	15
155	Qualitative modeling identifies IL-11 as a novel regulator in maintaining self-renewal in human pluripotent stem cells. <i>Frontiers in Physiology</i> , 2013, 4, 303.	2.8	15
156	Implicit Methods for Qualitative Modeling of Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2012, 786, 397-443.	0.9	14
157	Immune Response to Mouse Mammary Tumor Virus in Mice Lacking the Alpha/Beta Interferon or the Gamma Interferon Receptor. <i>Journal of Virology</i> , 1998, 72, 2638-2646.	3.4	14
158	A 2D/3D image analysis system to track fluorescently labeled structures in rod-shaped cells: application to measure spindle pole asymmetry during mitosis. <i>Cell Division</i> , 2013, 8, 6.	2.4	13
159	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014, 42, W436-W441.	14.5	13
160	An Integrated Ontology Resource to Explore and Study Host-Virus Relationships. <i>PLoS ONE</i> , 2014, 9, e108075.	2.5	13
161	Efficient computation of minimal perturbation sets in gene regulatory networks. <i>Frontiers in Physiology</i> , 2013, 4, 361.	2.8	12
162	Analysis of <i>S. pombe</i> SIN protein SPB-association reveals two genetically separable states of the SIN. <i>Journal of Cell Science</i> , 2015, 128, 741-54.	2.0	12

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163	Integrative knowledge management to enhance pharmaceutical R&D. Nature Reviews Drug Discovery, 2014, 13, 239-240.	46.4	12
164	Identifying biological mechanisms for favorable cancer prognosis using non-hypothesis-driven iterative survival analysis. Npj Systems Biology and Applications, 2016, 2, 16037.	3.0	12
165	Differential regulation of RNA polymerase III genes during liver regeneration. Nucleic Acids Research, 2019, 47, 1786-1796.	14.5	12
166	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference – Application to H5N1 spread in the Mekong region. Bioinformatics, 2020, 36, 2098-2104.	4.1	11
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