Ioannis Xenarios

List of Publications by Year
in descending order

205 papers	41,414 citations	11235 73 h-index	3171 192 g-index
223 all docs	223 docs citations	223 times ranked	77068 citing authors

#	Article	IF	Citations
1	Setting the basis of best practices and standards for curation and annotation of logical models in biologyâ€"highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. Briefings in Bioinformatics, 2021, 22, 1848-1859.	3.2	25
2	Blood virosphere in febrile Tanzanian children. Emerging Microbes and Infections, 2021, 10, 982-993.	3.0	9
3	Unsupervised Analysis of Flow Cytometry Data in a Clinical Setting Captures Cell Diversity and Allows Population Discovery. Frontiers in Immunology, 2021, 12, 633910.	2.2	8
4	Quantification of the spread of SARS-CoV-2 variant B.1.1.7 in Switzerland. Epidemics, 2021, 37, 100480.	1.5	34
5	Enzyme annotation in UniProtKB using Rhea. Bioinformatics, 2020, 36, 1896-1901.	1.8	72
6	Characterization and mutagenesis of Chinese hamster ovary cells endogenous retroviruses to inactivate viral particle release. Biotechnology and Bioengineering, 2020, 117, 466-485.	1.7	8
7	PamgeneAnalyzeR: open and reproducible pipeline for kinase profiling. Bioinformatics, 2020, 36, 5117-5119.	1.8	3
8	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference â€" Application to H5N1 spread in the Mekong region. Bioinformatics, 2020, 36, 2098-2104.	1.8	11
9	Predicting combinations of immunomodulators to enhance dendritic cell-based vaccination based on a hybrid experimental and computational platform. Computational and Structural Biotechnology Journal, 2020, 18, 2217-2227.	1.9	0
10	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. Cell, 2020, 183, 818-834.e13.	13.5	287
11	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. Viruses, 2020, 12, 1248.	1.5	9
12	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. Nature Communications, 2020, 11, 1293.	5.8	196
13	HAMAP as SPARQL rulesâ€"A portable annotation pipeline for genomes and proteomes. GigaScience, 2020, 9, .	3.3	6
14	Three-dimensional chromatin interactions remain stable upon CAG/CTG repeat expansion. Science Advances, 2020, 6, eaaz4012.	4.7	16
15	Contribution of exome sequencing to the identification of genes involved in the response to clopidogrel in cardiovascular patients. Journal of Thrombosis and Haemostasis, 2020, 18, 1425-1434.	1.9	2
16	New genome assembly of the barn owl (*Tyto alba alba*). Ecology and Evolution, 2020, 10, 2284-2298.	0.8	11
17	Fisetin protects against cardiac cell death through reduction of ROS production and caspases activity. Scientific Reports, 2020, 10, 2896.	1.6	37
18	Front Cover Image, Volume 117, Number 2, February 2020. Biotechnology and Bioengineering, 2020, 117, i.	1.7	0

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19	\<scp\>SBML\</scp\> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
20	Abstract P6-10-22: miR363-3p mediates maintenance of breast cancer stem cells (BCSCs) and predicts resistance to neoadjuvant chemotherapy and disease recurrence. , 2020, , .		0
21	HENA, heterogeneous network-based data set for Alzheimerâ€™s disease. Scientific Data, 2019, 6, 151.	2.4	34
22	Navigating in vitro bioactivity data by investigating available resources using model compounds. Scientific Data, 2019, 6, 45.	2.4	1
23	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	6.0	45
24	Gene expression across mammalian organ development. Nature, 2019, 571, 505-509.	13.7	490
25	DynaStI: A Dynamic Retention Time Database for Steroidomics. Metabolites, 2019, 9, 85.	1.3	18
26	Consent insufficient for data releaseâ€"Response. Science, 2019, 364, 446-446.	6.0	5
27	Laser capture microdissection of human pancreatic islets reveals novel eQTLs associated with type 2 diabetes. Molecular Metabolism, 2019, 24, 98-107.	3.0	26
28	An enhanced workflow for variant interpretation in UniProtKB/Swiss-Prot improves consistency and reuse in ClinVar. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	7
29	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. Plant Physiology, 2019, 180, 305-322.	2.3	41
30	Sleepâ€"wake-driven and circadian contributions to daily rhythms in gene expression and chromatin accessibility in the murine cortex. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25773-25783.	3.3	66
31	A multi-omics digital research object for the genetics of sleep regulation. Scientific Data, 2019, 6, 258.	2.4	8
32	Differential regulation of RNA polymerase III genes during liver regeneration. Nucleic Acids Research, 2019, 47, 1786-1796.	6.5	12
33	UniProt: a worldwide hub of protein knowledge. Nucleic Acids Research, 2019, 47, D506-D515.	6.5	6,185
34	Genomeâ€wide identification of microRNAs regulating the human prion protein. Brain Pathology, 2019, 29, 232-244.	2.1	22
35	Updates in Rhea: SPARQLing biochemical reaction data. Nucleic Acids Research, 2019, 47, D596-D600.	6.5	54
36	Deciphering the Dynamic Transcriptional and Post-transcriptional Networks of Macrophages in the Healthy Heart and after Myocardial Injury. Cell Reports, 2018, 23, 622-636.	2.9	56

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37	Personalized cancer vaccine effectively mobilizes antitumor T cell immunity in ovarian cancer. Science Translational Medicine, 2018, 10, .	5.8	326
38	KIAA1109 Variants Are Associated with a Severe Disorder of Brain Development and Arthrogryposis. American Journal of Human Genetics, 2018, 102, 116-132.	2.6	46
39	Sensitive and frequent identification of high avidity neo-epitopeÂspecific CD8 + T cells in immunotherapy-naive ovarian cancer. Nature Communications, 2018, 9, 1092.	5.8	122
40	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. Diabetologia, 2018, 61, 641-657.	2.9	131
41	Expert curation for building network-based dynamical models: a case study on atherosclerotic plaque formation. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	6
42	Towards in the Field Fast Pathogens Detection Using FPGAs. , 2018, , .		0
43	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	1.8	36
44	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome*. Molecular and Cellular Proteomics, 2018, 17, 2347-2357.	2.5	105
45	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. PLoS Computational Biology, 2018, 14, e1006390.	1.5	33
46	A systems genetics resource and analysis of sleep regulation in the mouse. PLoS Biology, 2018, 16, e2005750.	2.6	51
47	Improving the quality and workflow of bacterial genome sequencing and analysis: paving the way for a Switzerland-wide molecular epidemiological surveillance platform. Swiss Medical Weekly, 2018, 148, w14693.	0.8	28
48	Cell-free DNA testing of an extended range of chromosomal anomalies: clinical experience with 6,388 consecutive cases. Genetics in Medicine, 2017, 19, 169-175.	1.1	82
49	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	6.5	1,838
50	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.	1.1	39
51	Plasma Dihydroceramides Are Diabetes Susceptibility Biomarker Candidates in Mice and Humans. Cell Reports, 2017, 18, 2269-2279.	2.9	168
52	Enhanced metabolite annotation via dynamic retention time prediction: Steroidogenesis alterations as a case study. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2017, 1071, 11-18.	1.2	25
53	MsViz: A Graphical Software Tool for In-Depth Manual Validation and Quantitation of Post-translational Modifications. Journal of Proteome Research, 2017, 16, 3092-3101.	1.8	9
54	InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	6.5	1,358

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55	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.	3.0	42
56	TIE-2 expressing monocytes in human cancers. OncoImmunology, 2017, 6, e1303585.	2.1	42
57	SourceData: a semantic platform for curating and searching figures. Nature Methods, 2017, 14, 1021-1022.	9.0	29
58	A Clb/Cdk1-mediated regulation of Fkh2 synchronizes CLB expression in the budding yeast cell cycle. Npj Systems Biology and Applications, 2017, 3, 7.	1.4	32
59	Neutrophils and Snail Orchestrate the Establishment of a Pro-tumor Microenvironment in Lung Cancer. Cell Reports, 2017, 21, 3190-3204.	2.9	167
60	Low number of fixed somatic mutations in a long-lived oak tree. Nature Plants, 2017, 3, 926-929.	4.7	120
61	Local auxin production underlies a spatially restricted neighbor-detection response in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7444-7449.	3.3	70
62	MAR-Mediated transgene integration into permissive chromatin and increased expression by recombination pathway engineering. Biotechnology and Bioengineering, 2017, 114, 384-396.	1.7	23
63	Bacterial Virus Ontology; Coordinating across Databases. Viruses, 2017, 9, 126.	1.5	3
64	Updates in Rhea â€" an expert curated resource of biochemical reactions. Nucleic Acids Research, 2017, 45, D415-D418.	6.5	56
65	The ins and outs of eukaryotic viruses: Knowledge base and ontology of a viral infection. PLoS ONE, 2017, 12, e0171746.	1.1	7
66	Global mapping of highly pathogenic avian influenza H5N1 and H5Nx clade 2.3.4.4 viruses with spatial cross-validation. ELife, 2016, 5, .	2.8	45
67	Boolean regulatory network reconstruction using literature based knowledge with a genetic algorithm optimization method. BMC Bioinformatics, 2016, 17, 410.	1.2	37
68	Improving HIV proteome annotation: new features of BioAfrica HIV Proteomics Resource. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw045.	1.4	8
69	Neighbor Detection Induces Organ-Specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-Specific Growth. Plant Cell, 2016, 28, 2889-2904.	3.1	128
70	Identifying biological mechanisms for favorable cancer prognosis using non-hypothesis-driven iterative survival analysis. Npj Systems Biology and Applications, 2016, 2, 16037.	1.4	12
71	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
72	Clade-level Spatial Modelling of HPAI H5N1 Dynamics in the Mekong Region Reveals New Patterns and Associations with Agro-Ecological Factors. Scientific Reports, 2016, 6, 30316.	1.6	6

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73	Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. Genome Medicine, 2016, 8, 105.	3.6	20
74	Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. Scientific Reports, 2016, 6, 26822.	1.6	32
75	New molecular insights into modulation of platelet reactivity in aspirin-treated patients using a network-based approach. Human Genetics, 2016, 135, 403-414.	1.8	21
76	Social networks help to infer causality in the tumor microenvironment. BMC Research Notes, 2016, 9, 168.	0.6	1
77	Comparative transcriptome profiling of the injured zebrafish and mouse hearts identifies miRNA-dependent repair pathways. Cardiovascular Research, 2016, 110, 73-84.	1.8	36
78	UniProtKB/Swiss-Prot, the Manually Annotated Section of the UniProt KnowledgeBase: How to Use the Entry View. Methods in Molecular Biology, 2016, 1374, 23-54.	0.4	624
79	TIE-2-expressing monocytes are lymphangiogenic and associate specifically with lymphatics of human breast cancer. OncoImmunology, 2016, 5, e1073882.	2.1	37
80	West syndrome caused by homozygous variant in the evolutionary conserved gene encoding the mitochondrial elongation factor GUF1. European Journal of Human Genetics, 2016, 24, 1001-1008.	1.4	10
81	Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw161.	1.4	30
82	Analysis of *S. pombe* SIN protein SPB-association reveals two genetically separable states of the SIN. Journal of Cell Science, 2015, 128, 741-54.	1.2	12
83	Mutations in *LONP1*, a mitochondrial matrix protease, cause CODAS syndrome. American Journal of Medical Genetics, Part A, 2015, 167, 1501-1509.	0.7	61
84	An Extended, Boolean Model of the Septation Initiation Network in S.Pombe Provides Insights into Its Regulation. PLoS ONE, 2015, 10, e0134214.	1.1	8
85	MorphoGraphX: A platform for quantifying morphogenesis in 4D. ELife, 2015, 4, 05864.	2.8	389
86	TRAL: tandem repeat annotation library. Bioinformatics, 2015, 31, 3051-3053.	1.8	17
87	Updates in Rhea—a manually curated resource of biochemical reactions. Nucleic Acids Research, 2015, 43, D459-D464.	6.5	41
88	Cooperative development of logical modelling standards and tools with CoLoMoTo. Bioinformatics, 2015, 31, 1154-1159.	1.8	98
89	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	6.5	1,205
90	Angiogenic Activity of Breast Cancer Patients' Monocytes Reverted by Combined Use of Systems Modeling and Experimental Approaches. PLoS Computational Biology, 2015, 11, e1004050.	1.5	18

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91	HAMAP in 2015: updates to the protein family classification and annotation system. Nucleic Acids Research, 2015, 43, D1064-D1070.	6.5	135
92	The SwissLipids knowledgebase for lipid biology. Bioinformatics, 2015, 31, 2860-2866.	1.8	114
93	Toward a rational design of combination therapy in cancer. OncoImmunology, 2015, 4, e1046674.	2.1	1
94	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. Genome Biology and Evolution, 2015, 7, 1988-1999.	1.1	25
95	Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. European Heart Journal, 2015, 36, 353-368.	1.0	244
96	Transcriptional response to cardiac injury in the zebrafish: systematic identification of genes with highly concordant activity across in vivo models. BMC Genomics, 2014, 15, 852.	1.2	10
97	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. PLoS Computational Biology, 2014, 10, e1003757.	1.5	32
98	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	6.5	13
99	Functional and Evolutionary Analysis of the CASPARIAN STRIP MEMBRANE DOMAIN PROTEIN Family Â. Plant Physiology, 2014, 165, 1709-1722.	2.3	86
100	Genetic Variations and Diseases in UniProtKB/Swissâ€Prot: The Ins and Outs of Expert Manual Curation. Human Mutation, 2014, 35, 927-935.	1.1	51
101	<i>TBC1D7</i>Mutations are Associated with Intellectual Disability, Macrocrania, Patellar Dislocation, and Celiac Disease. Human Mutation, 2014, 35, 447-451.	1.1	52
102	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. Molecular and Cellular Proteomics, 2014, 13, 2765-2775.	2.5	130
103	Extensive remodeling of DC function by rapid maturation-induced transcriptional silencing. Nucleic Acids Research, 2014, 42, 9641-9655.	6.5	5
104	The EMPRES-i genetic module: a novel tool linking epidemiological outbreak information and genetic characteristics of influenza viruses. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau008-bau008.	1.4	28
105	Reconciliation of metabolites and biochemical reactions for metabolic networks. Briefings in Bioinformatics, 2014, 15, 123-135.	3.2	64
106	Integrative knowledge management to enhance pharmaceutical R&D. Nature Reviews Drug Discovery, 2014, 13, 239-240.	21.5	12
107	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	9.4	2,505
108	Soil fungal communities of grasslands are environmentally structured at a regional scale in the <scp>A</scp>lps. Molecular Ecology, 2014, 23, 4274-4290.	2.0	125

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109	Activities at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2014, 42, D191-D198.	6.5	1,162
110	Differentially Phased Leaf Growth and Movements in <i>Arabidopsis</i> Depend on Coordinated Circadian and Light Regulation. Plant Cell, 2014, 26, 3911-3921.	3.1	83
111	Type I Interferons Protect T Cells against NK Cell Attack Mediated by the Activating Receptor NCR1. Immunity, 2014, 40, 961-973.	6.6	199
112	An Integrated Ontology Resource to Explore and Study Host-Virus Relationships. PLoS ONE, 2014, 9, e108075.	1.1	13
113	Automated quantitative histology reveals vascular morphodynamics during Arabidopsis hypocotyl secondary growth. ELife, 2014, 3, e01567.	2.8	37
114	A 2D/3D image analysis system to track fluorescently labeled structures in rod-shaped cells: application to measure spindle pole asymmetry during mitosis. Cell Division, 2013, 8, 6.	1.1	13
115	Application of text-mining for updating protein post-translational modification annotation in UniProtKB. BMC Bioinformatics, 2013, 14, 104.	1.2	17
116	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
117	Unraveling modulators of platelet reactivity in cardiovascular patients using omics strategies: Towards a network biology paradigm. Translational Proteomics, 2013, 1, 25-37.	1.2	5
118	Database resources for the tuberculosis community. Tuberculosis, 2013, 93, 12-17.	0.8	27
119	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.	1.1	49
120	Microarray analysis of isolated human islet transcriptome in type 2 diabetes and the role of the ubiquitin-proteasome system in pancreatic beta cell dysfunction. Molecular and Cellular Endocrinology, 2013, 367, 1-10.	1.6	76
121	pfsearchV3: a code acceleration and heuristic to search PROSITE profiles. Bioinformatics, 2013, 29, 1215-1217.	1.8	18
122	Plant species distributions along environmental gradients: do belowground interactions with fungi matter?. Frontiers in Plant Science, 2013, 4, 500.	1.7	38
123	Efficient computation of minimal perturbation sets in gene regulatory networks. Frontiers in Physiology, 2013, 4, 361.	1.3	12
124	Qualitative modeling identifies IL-11 as a novel regulator in maintaining self-renewal in human pluripotent stem cells. Frontiers in Physiology, 2013, 4, 303.	1.3	15
125	Density-based hierarchical clustering of pyro-sequences on a large scale—the case of fungal ITS1. Bioinformatics, 2013, 29, 1268-1274.	1.8	19
126	Hard-wired heterogeneity in blood stem cells revealed using a dynamic regulatory network model. Bioinformatics, 2013, 29, i80-i88.	1.8	83

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127	HAMAP in 2013, new developments in the protein family classification and annotation system. Nucleic Acids Research, 2013, 41, D584-D589.	6.5	57
128	TIE-2 and VEGFR Kinase Activities Drive Immunosuppressive Function of TIE-2â€"Expressing Monocytes in Human Breast Tumors. Clinical Cancer Research, 2013, 19, 3439-3449.	3.2	32
129	Evolution of the Ferric Reductase Domain (FRD) Superfamily: Modularity, Functional Diversification, and Signature Motifs. PLoS ONE, 2013, 8, e58126.	1.1	68
130	ExPASy: SIB bioinformatics resource portal. Nucleic Acids Research, 2012, 40, W597-W603.	6.5	1,737
131	Reorganizing the protein space at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2012, 40, D71-D75.	6.5	1,196
132	ViralZone: recent updates to the virus knowledge resource. Nucleic Acids Research, 2012, 41, D579-D583.	6.5	48
133	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	6.5	191
134	UniPathway: a resource for the exploration and annotation of metabolic pathways. Nucleic Acids Research, 2012, 40, D761-D769.	6.5	83
135	New and continuing developments at PROSITE. Nucleic Acids Research, 2012, 41, D344-D347.	6.5	1,190
136	Rheaâ€"a manually curated resource of biochemical reactions. Nucleic Acids Research, 2012, 40, D754-D760.	6.5	84
137	Gene Ontology Annotations and Resources. Nucleic Acids Research, 2012, 41, D530-D535.	6.5	456
138	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	9.0	500
139	Toward interoperable bioscience data. Nature Genetics, 2012, 44, 121-126.	9.4	362
140	The UniProt-GO Annotation database in 2011. Nucleic Acids Research, 2012, 40, D565-D570.	6.5	349
141	Measuring the diurnal pattern of leaf hyponasty and growth in Arabidopsis - a novel phenotyping approach using laser scanning. Functional Plant Biology, 2012, 39, 860.	1.1	73
142	Exome sequencing identifies recurrent somatic MAP2K1 and MAP2K2 mutations in melanoma. Nature Genetics, 2012, 44, 133-139.	9.4	369
143	The UniProtKB/Swiss-Prot Tox-Prot program: A central hub of integrated venom protein data. Toxicon, 2012, 60, 551-557.	0.8	180
144	Phytochrome interacting factors 4 and 5 control seedling growth in changing light conditions by directly controlling auxin signaling. Plant Journal, 2012, 71, 699-711.	2.8	498

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145	Implicit Methods for Qualitative Modeling of Gene Regulatory Networks. Methods in Molecular Biology, 2012, 786, 397-443.	0.4	14
146	T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension. Nucleic Acids Research, 2011, 39, W13-W17.	6.5	982
147	Strengths and Weaknesses of Selected Modeling Methods Used in Systems Biology. , 2011, , .		2
148	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.	1.1	51
149	Conceptual framework and pilot study to benchmark phylogenomic databases based on reference gene trees. Briefings in Bioinformatics, 2011, 12, 423-435.	3.2	33
150	ViralZone: a knowledge resource to understand virus diversity. Nucleic Acids Research, 2011, 39, D576-D582.	6.5	312
151	A qualitative continuous model of cellular auxin and brassinosteroid signaling and their crosstalk. Bioinformatics, 2011, 27, 1404-1412.	1.8	44
152	Ongoing and future developments at the Universal Protein Resource. Nucleic Acids Research, 2011, 39, D214-D219.	6.5	649
153	The genome of the fire ant *Solenopsis invicta*. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5679-5684.	3.3	322
154	Visualization and quality assessment of de novo genome assemblies. Bioinformatics, 2011, 27, 3425-3426.	1.8	9
155	Comparison of Strategies to Detect Epistasis from eQTL Data. PLoS ONE, 2011, 6, e28415.	1.1	8
156	Systems biology to battle vascular disease. Nephrology Dialysis Transplantation, 2010, 25, 1019-1022.	0.4	22
157	Animal Toxins: How is Complexity Represented in Databases?. Toxins, 2010, 2, 262-282.	1.5	19
158	Multiple Imputations Applied to the DREAM3 Phosphoproteomics Challenge: A Winning Strategy. PLoS ONE, 2010, 5, e8012.	1.1	6
159	FastEpistasis: a high performance computing solution for quantitative trait epistasis. Bioinformatics, 2010, 26, 1468-1469.	1.8	105
160	EuroDia: a beta-cell gene expression resource. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq024-baq024.	1.4	9
161	OpenFluDB, a database for human and animal influenza virus. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq004-baq004.	1.4	37
162	The Universal Protein Resource (UniProt) in 2010. Nucleic Acids Research, 2010, 38, D142-D148.	6.5	1,131

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163	CDK9 Regulates AR Promoter Selectivity and Cell Growth through Serine 81 Phosphorylation. Molecular Endocrinology, 2010, 24, 2267-2280.	3.7	119
164	Substantial deletion overlap among divergent Arabidopsis genomes revealed by intersection of short reads and tiling arrays. Genome Biology, 2010, 11, R4.	13.9	31
165	Animal Toxins: How is Complexity Represented in Databases?. Toxins, 2010, 2, 262-82.	1.5	7
166	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. Molecular Biology and Evolution, 2009, 26, 2865-2875.	3.5	50
167	The Microbe browser for comparative genomics. Nucleic Acids Research, 2009, 37, W296-W299.	6.5	3
168	The direct effects of tacrolimus and cyclosporin A on isolated human islets: A functional, survival and gene expression study. Islets, 2009, 1, 106-110.	0.9	33
169	AssociationViewer: a scalable and integrated software tool for visualization of large-scale variation data in genomic context. Bioinformatics, 2009, 25, 662-663.	1.8	3
170	MIMAS 3.0 is a Multiomics Information Management and Annotation System. BMC Bioinformatics, 2009, 10, 151.	1.2	15
171	Modeling stochasticity and robustness in gene regulatory networks. Bioinformatics, 2009, 25, i101-i109.	1.8	43
172	ENFIN â€" A European network for integrative systems biology. Comptes Rendus - Biologies, 2009, 332, 1050-1058.	0.1	6
173	Detection and identification of plasma proteins that bind GlialCAM using ProteinChipâ„¢ Arrays, SELDIâ€"TOF MS, and nanoâ€"LC MS/MS. Proteomics, 2008, 8, 378-388.	1.3	17
174	Guidelines for reporting the use of mass spectrometry in proteomics. Nature Biotechnology, 2008, 26, 860-861.	9.4	82
175	Probabilistic base calling of Solexa sequencing data. BMC Bioinformatics, 2008, 9, 431.	1.2	82
176	R-Coffee: a web server for accurately aligning noncoding RNA sequences. Nucleic Acids Research, 2008, 36, W10-W13.	6.5	53
177	Synchronous versus asynchronous modeling of gene regulatory networks. Bioinformatics, 2008, 24, 1917-1925.	1.8	272
178	Modeling of Multiple Valued Gene Regulatory Networks. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 1398-404.	0.5	20
179	A Chemical Proteomics Approach to Phosphatidylinositol 3-Kinase Signaling in Macrophages. Molecular and Cellular Proteomics, 2007, 6, 1829-1841.	2.5	34
180	Broadening the horizon â€" level 2.5 of the HUPO-PSI format for molecular interactions. BMC Biology, 2007, 5, 44.	1.7	237

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181	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	9.4	274
182	Dynamic simulation of regulatory networks using SQUAD. BMC Bioinformatics, 2007, 8, 462.	1.2	136
183	An Efficient Method for Dynamic Analysis of Gene Regulatory Networks and inÂsilico Gene Perturbation Experiments. , 2007, , 62-76.		50
184	A method for the generation of standardized qualitative dynamical systems of regulatory networks. Theoretical Biology and Medical Modelling, 2006, 3, 13.	2.1	210
185	The HUPO PSI's Molecular Interaction formatâ€"a community standard for the representation of protein interaction data. Nature Biotechnology, 2004, 22, 177-183.	9.4	581
186	Proteomic Analysis of the Mouse Liver Mitochondrial Inner Membrane. Journal of Biological Chemistry, 2003, 278, 41566-41571.	1.6	220
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