

# Ioannis Xenarios

## List of Publications by Year in Descending Order

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

208  
papers

30,478  
citations

66  
h-index

174  
g-index

223  
ext. papers

37,515  
ext. citations

11.8  
avg, IF

8.6  
L-index

#	Paper	IF	Citations
208	Unsupervised Analysis of Flow Cytometry Data in a Clinical Setting Captures Cell Diversity and Allows Population Discovery. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 633910	8.4	1
207	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> , <b>2021</b> , 22, 1848-1859	13.4	9
206	Blood virosphere in febrile Tanzanian children. <i>Emerging Microbes and Infections</i> , <b>2021</b> , 10, 982-993	18.9	0
205	Quantification of the spread of SARS-CoV-2 variant B.1.1.7 in Switzerland. <i>Epidemics</i> , <b>2021</b> , 37, 100480	5.1	9
204	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. <i>Viruses</i> , <b>2020</b> , 12,	6.2	5
203	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. <i>Nature Communications</i> , <b>2020</b> , 11, 1293	17.4	78
202	HAMAP as SPARQL rules-A portable annotation pipeline for genomes and proteomes. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	4
201	Three-dimensional chromatin interactions remain stable upon CAG/CTG repeat expansion. <i>Science Advances</i> , <b>2020</b> , 6, eaaz4012	14.3	8
200	Contribution of exome sequencing to the identification of genes involved in the response to clopidogrel in cardiovascular patients. <i>Journal of Thrombosis and Haemostasis</i> , <b>2020</b> , 18, 1425-1434	15.4	1
199	New genome assembly of the barn owl (). <i>Ecology and Evolution</i> , <b>2020</b> , 10, 2284-2298	2.8	1
198	Fisetin protects against cardiac cell death through reduction of ROS production and caspases activity. <i>Scientific Reports</i> , <b>2020</b> , 10, 2896	4.9	23
197	SBML Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9110	12.2	65
196	Characterization and mutagenesis of Chinese hamster ovary cells endogenous retroviruses to inactivate viral particle release. <i>Biotechnology and Bioengineering</i> , <b>2020</b> , 117, 466-485	4.9	4
195	PamgeneAnalyzerR: open and reproducible pipeline for kinase profiling. <i>Bioinformatics</i> , <b>2020</b> , 36, 5117-5119	11.9	2
194	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference - Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , <b>2020</b> , 36, 2098-2104	7.2	4
193	Predicting combinations of immunomodulators to enhance dendritic cell-based vaccination based on a hybrid experimental and computational platform. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 2217-2227	6.8	
192	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. <i>Cell</i> , <b>2020</b> , 183, 818-834.e13	56.2	105

191	Enzyme annotation in UniProtKB using Rhea. <i>Bioinformatics</i> , <b>2020</b> , 36, 1896-1901	7.2	32
190	Navigating in vitro bioactivity data by investigating available resources using model compounds. <i>Scientific Data</i> , <b>2019</b> , 6, 45	8.2	1
189	Toward unrestricted use of public genomic data. <i>Science</i> , <b>2019</b> , 363, 350-352	33.3	25
188	Gene expression across mammalian organ development. <i>Nature</i> , <b>2019</b> , 571, 505-509	50.4	179
187	DynaStI: A Dynamic Retention Time Database for Steroidomics. <i>Metabolites</i> , <b>2019</b> , 9,	5.6	11
186	Consent insufficient for data release-Response. <i>Science</i> , <b>2019</b> , 364, 446	33.3	4
185	Laser capture microdissection of human pancreatic islets reveals novel eQTLs associated with type 2 diabetes. <i>Molecular Metabolism</i> , <b>2019</b> , 24, 98-107	8.8	14
184	An enhanced workflow for variant interpretation in UniProtKB/Swiss-Prot improves consistency and reuse in ClinVar. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2019</b> , 2019,	5	5
183	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. <i>Plant Physiology</i> , <b>2019</b> , 180, 305-322	6.6	27
182	HENA, heterogeneous network-based data set for AlzheimerQ disease. <i>Scientific Data</i> , <b>2019</b> , 6, 151	8.2	9
181	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> , <b>2019</b> , 116, 25773-25783	11.5	27
180	A multi-omics digital research object for the genetics of sleep regulation. <i>Scientific Data</i> , <b>2019</b> , 6, 258	8.2	4
179	Differential regulation of RNA polymerase III genes during liver regeneration. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 1786-1796	20.1	7
178	UniProt: a worldwide hub of protein knowledge. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D506-D515	20.1	3656
177	Genome-wide identification of microRNAs regulating the human prion protein. <i>Brain Pathology</i> , <b>2019</b> , 29, 232-244	6	10
176	Updates in Rhea: SPARQLing biochemical reaction data. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D596-D600	20.1	32
175	Deciphering the Dynamic Transcriptional and Post-transcriptional Networks of Macrophages in the Healthy Heart and after Myocardial Injury. <i>Cell Reports</i> , <b>2018</b> , 23, 622-636	10.6	33
174	Personalized cancer vaccine effectively mobilizes antitumor T cell immunity in ovarian cancer. <i>Science Translational Medicine</i> , <b>2018</b> , 10,	17.5	205

173 Generation of Molecular Models and Pathways **2018**, 274-285

172 KIAA1109 Variants Are Associated with a Severe Disorder of Brain Development and Arthrogryposis. *American Journal of Human Genetics*, **2018**, 102, 116-132 11 32

171 Sensitive and frequent identification of high avidity neo-epitope-specific CD8 T cells in immunotherapy-naive ovarian cancer. *Nature Communications*, **2018**, 9, 1092 17.4 82

170 Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. *PLoS Computational Biology*, **2018**, 14, e1006390 5 21

169 A systems genetics resource and analysis of sleep regulation in the mouse. *PLoS Biology*, **2018**, 16, e2005750 26

168 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 3.1 9

167 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 10.3 84

166 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, 5 6

165 Gearing up to handle the mosaic nature of life in the quest for orthologs. *Bioinformatics*, **2018**, 34, 323-329 25

164 Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome. *Molecular and Cellular Proteomics*, **2018**, 17, 2347-2357 7.6 62

163 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 8.1 54

162 Expansion of the Gene Ontology knowledgebase and resources. *Nucleic Acids Research*, **2017**, 45, D331-D338 1258

161 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 2.4 30

160 Plasma Dihydroceramides Are Diabetes Susceptibility Biomarker Candidates in Mice and Humans. *Cell Reports*, **2017**, 18, 2269-2279 10.6 108

159 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 3.2 20

158 MsViz: A Graphical Software Tool for In-Depth Manual Validation and Quantitation of Post-translational Modifications. *Journal of Proteome Research*, **2017**, 16, 3092-3101 5.6 7

157 InterPro in 2017-beyond protein family and domain annotations. *Nucleic Acids Research*, **2017**, 45, D190-D199 970

156 Molecular phenotyping of multiple mouse strains under metabolic challenge uncovers a role for in glucose-induced insulin secretion. *Molecular Metabolism*, **2017**, 6, 340-351 8.8 30

155	TIE-2 expressing monocytes in human cancers. <i>Oncolmmunology</i> , <b>2017</b> , 6, e1303585	7.2	27
154	SourceData: a semantic platform for curating and searching figures. <i>Nature Methods</i> , <b>2017</b> , 14, 1021-1022	1.6	19
153	The ins and outs of eukaryotic viruses: Knowledge base and ontology of a viral infection. <i>PLoS ONE</i> , <b>2017</b> , 12, e0171746	3.7	4
152	A Clb/Cdk1-mediated regulation of Fkh2 synchronizes expression in the budding yeast cell cycle. <i>Npj Systems Biology and Applications</i> , <b>2017</b> , 3, 7	5	20
151	Neutrophils and Snail Orchestrate the Establishment of a Pro-tumor Microenvironment in Lung Cancer. <i>Cell Reports</i> , <b>2017</b> , 21, 3190-3204	10.6	96
150	Low number of fixed somatic mutations in a long-lived oak tree. <i>Nature Plants</i> , <b>2017</b> , 3, 926-929	11.5	74
149	Local auxin production underlies a spatially restricted neighbor-detection response in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 7444-7449	11.5	43
148	MAR-Mediated transgene integration into permissive chromatin and increased expression by recombination pathway engineering. <i>Biotechnology and Bioengineering</i> , <b>2017</b> , 114, 384-396	4.9	13
147	Bacterial Virus Ontology; Coordinating across Databases. <i>Viruses</i> , <b>2017</b> , 9,	6.2	2
146	Updates in Rhea - an expert curated resource of biochemical reactions. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D415-D418	20.1	46
145	West syndrome caused by homozygous variant in the evolutionary conserved gene encoding the mitochondrial elongation factor GUF1. <i>European Journal of Human Genetics</i> , <b>2016</b> , 24, 1001-8	5.3	9
144	Clade-level Spatial Modelling of HPAI H5N1 Dynamics in the Mekong Region Reveals New Patterns and Associations with Agro-Ecological Factors. <i>Scientific Reports</i> , <b>2016</b> , 6, 30316	4.9	5
143	Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. <i>Genome Medicine</i> , <b>2016</b> , 8, 105	14.4	16
142	Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. <i>Scientific Reports</i> , <b>2016</b> , 6, 26822	4.9	23
141	New molecular insights into modulation of platelet reactivity in aspirin-treated patients using a network-based approach. <i>Human Genetics</i> , <b>2016</b> , 135, 403-414	6.3	14
140	Social networks help to infer causality in the tumor microenvironment. <i>BMC Research Notes</i> , <b>2016</b> , 9, 168	2.3	1
139	Comparative transcriptome profiling of the injured zebrafish and mouse hearts identifies miRNA-dependent repair pathways. <i>Cardiovascular Research</i> , <b>2016</b> , 110, 73-84	9.9	27
138	UniProtKB/Swiss-Prot, the Manually Annotated Section of the UniProt KnowledgeBase: How to Use the Entry View. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1374, 23-54	1.4	386

137	TIE-2-expressing monocytes are lymphangiogenic and associate specifically with lymphatics of human breast cancer. <i>Oncolmmunology</i> , <b>2016</b> , 5, e1073882	7.2	28
136	Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	20
135	Global mapping of highly pathogenic avian influenza H5N1 and H5Nx clade 2.3.4.4 viruses with spatial cross-validation. <i>ELife</i> , <b>2016</b> , 5,	8.9	30
134	Boolean regulatory network reconstruction using literature based knowledge with a genetic algorithm optimization method. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 410	3.6	21
133	Improving HIV proteome annotation: new features of BioAfrica HIV Proteomics Resource. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	7
132	Neighbor Detection Induces Organ-Specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-Specific Growth. <i>Plant Cell</i> , <b>2016</b> , 28, 2889-2904	11.6	76
131	Identifying biological mechanisms for favorable cancer prognosis using non-hypothesis-driven iterative survival analysis. <i>Npj Systems Biology and Applications</i> , <b>2016</b> , 2, 16037	5	3
130	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , <b>2016</b> , 13, 425-30	21.6	133
129	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D213-21	20.1	954
128	Angiogenic activity of breast cancer patients monocytes reverted by combined use of systems modeling and experimental approaches. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004050	5	13
127	HAMAP in 2015: updates to the protein family classification and annotation system. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D1064-70	20.1	93
126	The SwissLipids knowledgebase for lipid biology. <i>Bioinformatics</i> , <b>2015</b> , 31, 2860-6	7.2	66
125	Toward a rational design of combination therapy in cancer. <i>Oncolmmunology</i> , <b>2015</b> , 4, e1046674	7.2	1
124	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 1988-99	3.9	19
123	Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. <i>European Heart Journal</i> , <b>2015</b> , 36, 353-68a	9.5	199
122	Mutations in LONP1, a mitochondrial matrix protease, cause CODAS syndrome. <i>American Journal of Medical Genetics, Part A</i> , <b>2015</b> , 167, 1501-9	2.5	45
121	An Extended, Boolean Model of the Septation Initiation Network in S.Pombe Provides Insights into Its Regulation. <i>PLoS ONE</i> , <b>2015</b> , 10, e0134214	3.7	7
120	MorphoGraphX: A platform for quantifying morphogenesis in 4D. <i>ELife</i> , <b>2015</b> , 4, 05864	8.9	245

119	TRAL: tandem repeat annotation library. <i>Bioinformatics</i> , <b>2015</b> , 31, 3051-3	7.2	7
118	Updates in Rhea--a manually curated resource of biochemical reactions. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D459-64	20.1	37
117	Cooperative development of logical modelling standards and tools with CoLoMoTo. <i>Bioinformatics</i> , <b>2015</b> , 31, 1154-9	7.2	61
116	Analysis of <i>S. pombe</i> SIN protein association to the SPB reveals two genetically separable states of the SIN. <i>Journal of Cell Science</i> , <b>2015</b> , 128, 741-54	5.3	8
115	Integrative knowledge management to enhance pharmaceutical R&D. <i>Nature Reviews Drug Discovery</i> , <b>2014</b> , 13, 239-40	64.1	9
114	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 223-6	44.5	2053
113	Soil fungal communities of grasslands are environmentally structured at a regional scale in the Alps. <i>Molecular Ecology</i> , <b>2014</b> , 23, 4274-90	5.7	85
112	Activities at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D191-8	20.1	1007
111	Differentially phased leaf growth and movements in <i>Arabidopsis</i> depend on coordinated circadian and light regulation. <i>Plant Cell</i> , <b>2014</b> , 26, 3911-21	11.6	62
110	Type I interferons protect T cells against NK cell attack mediated by the activating receptor NCR1. <i>Immunity</i> , <b>2014</b> , 40, 961-73	32.3	159
109	Transcriptional response to cardiac injury in the zebrafish: systematic identification of genes with highly concordant activity across in vivo models. <i>BMC Genomics</i> , <b>2014</b> , 15, 852	4.5	9
108	Analysis of stop-gain and frameshift variants in human innate immunity genes. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003757	5	21
107	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W436-41	20.1	12
106	Functional and Evolutionary Analysis of the CASPARIAN STRIP MEMBRANE DOMAIN PROTEIN Family. <i>Plant Physiology</i> , <b>2014</b> , 165, 1709-1722	6.6	56
105	Genetic variations and diseases in UniProtKB/Swiss-Prot: the ins and outs of expert manual curation. <i>Human Mutation</i> , <b>2014</b> , 35, 927-35	4.7	40
104	TBC1D7 mutations are associated with intellectual disability, macrocrania, patellar dislocation, and celiac disease. <i>Human Mutation</i> , <b>2014</b> , 35, 447-51	4.7	38
103	The mzTab data exchange format: communicating mass-spectrometry-based proteomics and metabolomics experimental results to a wider audience. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2765-75	7.6	96
102	Extensive remodeling of DC function by rapid maturation-induced transcriptional silencing. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 9641-55	20.1	3



101	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> , <b>2014</b> , 2014, bau008	5	23
100	Reconciliation of metabolites and biochemical reactions for metabolic networks. <i>Briefings in Bioinformatics</i> , <b>2014</b> , 15, 123-35	13.4	49
99	An integrated ontology resource to explore and study host-virus relationships. <i>PLoS ONE</i> , <b>2014</b> , 9, e108075	9.7	12
98	Automated quantitative histology reveals vascular morphodynamics during Arabidopsis hypocotyl secondary growth. <i>ELife</i> , <b>2014</b> , 3, e01567	8.9	30
97	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> , <b>2013</b> , 8, 6	2.8	12
96	Application of text-mining for updating protein post-translational modification annotation in UniProtKB. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 104	3.6	13
95	SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. <i>BMC Systems Biology</i> , <b>2013</b> , 7, 135	3.5	100
94	Unraveling modulators of platelet reactivity in cardiovascular patients using omics strategies: Towards a network biology paradigm. <i>Translational Proteomics</i> , <b>2013</b> , 1, 25-37		3
93	Database resources for the tuberculosis community. <i>Tuberculosis</i> , <b>2013</b> , 93, 12-7	2.6	23
92	A robust second-generation genome-wide test for fetal aneuploidy based on shotgun sequencing cell-free DNA in maternal blood. <i>Prenatal Diagnosis</i> , <b>2013</b> , 33, 707-10	3.2	42
91	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> , <b>2013</b> , 367, 1-10	4.4	57
90	pfsearchV3: a code acceleration and heuristic to search PROSITE profiles. <i>Bioinformatics</i> , <b>2013</b> , 29, 1215-7	7.2	10
89	Plant species distributions along environmental gradients: do belowground interactions with fungi matter?. <i>Frontiers in Plant Science</i> , <b>2013</b> , 4, 500	6.2	29
88	Efficient computation of minimal perturbation sets in gene regulatory networks. <i>Frontiers in Physiology</i> , <b>2013</b> , 4, 361	4.6	7
87	Qualitative modeling identifies IL-11 as a novel regulator in maintaining self-renewal in human pluripotent stem cells. <i>Frontiers in Physiology</i> , <b>2013</b> , 4, 303	4.6	14
86	Density-based hierarchical clustering of pyro-sequences on a large scale--the case of fungal ITS1. <i>Bioinformatics</i> , <b>2013</b> , 29, 1268-74	7.2	14
85	Hard-wired heterogeneity in blood stem cells revealed using a dynamic regulatory network model. <i>Bioinformatics</i> , <b>2013</b> , 29, i80-8	7.2	53
84	HAMAP in 2013, new developments in the protein family classification and annotation system. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D584-9	20.1	52



83	TIE-2 and VEGFR kinase activities drive immunosuppressive function of TIE-2-expressing monocytes in human breast tumors. <i>Clinical Cancer Research</i> , <b>2013</b> , 19, 3439-49	12.9	28
82	Evolution of the ferric reductase domain (FRD) superfamily: modularity, functional diversification, and signature motifs. <i>PLoS ONE</i> , <b>2013</b> , 8, e58126	3.7	48
81	ViralZone: recent updates to the virus knowledge resource. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D579-83	20.1	36
80	New and continuing developments at PROSITE. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D344-7	20.1	833
79	Gene Ontology annotations and resources. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D530-5	20.1	397
78	The UniProtKB/Swiss-Prot Tox-Prot program: A central hub of integrated venom protein data. <i>Toxicon</i> , <b>2012</b> , 60, 551-7	2.8	128
77	Phytochrome interacting factors 4 and 5 control seedling growth in changing light conditions by directly controlling auxin signaling. <i>Plant Journal</i> , <b>2012</b> , 71, 699-711	6.9	383
76	ExpASY: SIB bioinformatics resource portal. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W597-603	20.1	1185
75	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D71-5	20.1	1096
74	The Gene Ontology: enhancements for 2011. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D559-64	20.1	166
73	UniPathway: a resource for the exploration and annotation of metabolic pathways. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D761-9	20.1	76
72	Rhea—a manually curated resource of biochemical reactions. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D754-60	20.1	63
71	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , <b>2012</b> , 9, 345-50	21.6	375
70	Toward interoperable bioscience data. <i>Nature Genetics</i> , <b>2012</b> , 44, 121-6	36.3	286
69	The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D565-70	20.1	265
68	Measuring the diurnal pattern of leaf hyponasty and growth in Arabidopsis - a novel phenotyping approach using laser scanning. <i>Functional Plant Biology</i> , <b>2012</b> , 39, 860-869	2.7	60
67	Implicit methods for qualitative modeling of gene regulatory networks. <i>Methods in Molecular Biology</i> , <b>2012</b> , 786, 397-443	1.4	12
66	Exome sequencing identifies recurrent somatic MAP2K1 and MAP2K2 mutations in melanoma. <i>Nature Genetics</i> , <b>2011</b> , 44, 133-9	36.3	313

65	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> , <b>2011</b> , 39, W13-7	20.1	692
64	Strengths and Weaknesses of Selected Modeling Methods Used in Systems Biology <b>2011</b> ,		2
63	Network-guided analysis of genes with altered somatic copy number and gene expression reveals pathways commonly perturbed in metastatic melanoma. <i>PLoS ONE</i> , <b>2011</b> , 6, e18369	3.7	40
62	Conceptual framework and pilot study to benchmark phylogenomic databases based on reference gene trees. <i>Briefings in Bioinformatics</i> , <b>2011</b> , 12, 423-35	13.4	27
61	ViralZone: a knowledge resource to understand virus diversity. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D576-82	20.1	216
60	A qualitative continuous model of cellular auxin and brassinosteroid signaling and their crosstalk. <i>Bioinformatics</i> , <b>2011</b> , 27, 1404-12	7.2	30
59	Ongoing and future developments at the Universal Protein Resource. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D214-9	20.1	592
58	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> , <b>2011</b> , 108, 5679-84	11.5	279
57	Visualization and quality assessment of de novo genome assemblies. <i>Bioinformatics</i> , <b>2011</b> , 27, 3425-6	7.2	7
56	Comparison of strategies to detect epistasis from eQTL data. <i>PLoS ONE</i> , <b>2011</b> , 6, e28415	3.7	8
55	Animal Toxins: How is Complexity Represented in Databases?. <i>Toxins</i> , <b>2010</b> , 2, 262-282	4.9	18
54	Multiple imputations applied to the DREAM3 phosphoproteomics challenge: a winning strategy. <i>PLoS ONE</i> , <b>2010</b> , 5, e8012	3.7	6
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3	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome		1
2	Integrated Proteogenomic Deep Sequencing and Analytics Accurately Identify Non-Canonical Peptides in Tumor Immunopeptidomes		1
1	SourceData - a semantic platform for curating and searching figures		1