Ioannis Xenarios

List of Publications by Citations

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	UniProt: a worldwide hub of protein knowledge. *Nucleic Acids Research*, **2019**, 47, D506-D515	20.1	3656
207	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. *Nature Biotechnology*, **2014**, 32, 223-6	44.5	2053
206	Expansion of the Gene Ontology knowledgebase and resources. *Nucleic Acids Research*, **2017**, 45, D331-D338	20.1	1258
205	DIP, the Database of Interacting Proteins: a research tool for studying cellular networks of protein interactions. *Nucleic Acids Research*, **2002**, 30, 303-5	20.1	1196
204	ExPASy: SIB bioinformatics resource portal. *Nucleic Acids Research*, **2012**, 40, W597-603	20.1	1185
203	Reorganizing the protein space at the Universal Protein Resource (UniProt). *Nucleic Acids Research*, **2012**, 40, D71-5	20.1	1096
202	The Universal Protein Resource (UniProt) in 2010. *Nucleic Acids Research*, **2010**, 38, D142-8	20.1	1035
201	Activities at the Universal Protein Resource (UniProt). *Nucleic Acids Research*, **2014**, 42, D191-8	20.1	1007
200	InterPro in 2017-beyond protein family and domain annotations. *Nucleic Acids Research*, **2017**, 45, D190-D199	20.1	970
199	The InterPro protein families database: the classification resource after 15 years. *Nucleic Acids Research*, **2015**, 43, D213-21	20.1	954
198	New and continuing developments at PROSITE. *Nucleic Acids Research*, **2013**, 41, D344-7	20.1	833
197	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, W13-7	20.1	692
196	DIP: the database of interacting proteins. *Nucleic Acids Research*, **2000**, 28, 289-91	20.1	675
195	Ongoing and future developments at the Universal Protein Resource. *Nucleic Acids Research*, **2011**, 39, D214-9	20.1	592
194	Protein function in the post-genomic era. *Nature*, **2000**, 405, 823-6	50.4	590
193	The HUPO PSI molecular interaction format--a community standard for the representation of protein interaction data. *Nature Biotechnology*, **2004**, 22, 177-83	44.5	504
192	Protein interactions: two methods for assessment of the reliability of high throughput observations. *Molecular and Cellular Proteomics*, **2002**, 1, 349-56	7.6	486

191	Gene Ontology annotations and resources. *Nucleic Acids Research*, **2013**, 41, D530-5	20.1	397
190	Microarray deacetylation maps determine genome-wide functions for yeast histone deacetylases. *Cell*, **2002**, 109, 437-46	56.2	390
189	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	1.4	386
188	Phytochrome interacting factors 4 and 5 control seedling growth in changing light conditions by directly controlling auxin signaling. *Plant Journal*, **2012**, 71, 699-711	6.9	383
187	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. *Nature Methods*, **2012**, 9, 345-50	21.6	375
186	Exome sequencing identifies recurrent somatic MAP2K1 and MAP2K2 mutations in melanoma. *Nature Genetics*, **2011**, 44, 133-9	36.3	313
185	Toward interoperable bioscience data. *Nature Genetics*, **2012**, 44, 121-6	36.3	286
184	The genome of the fire ant Solenopsis invicta. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 5679-84	11.5	279
183	IL-4 rapidly produced by V beta 4 V alpha 8 CD4+ T cells instructs Th2 development and susceptibility to Leishmania major in BALB/c mice. *Immunity*, **1997**, 6, 541-9	32.3	272
182	Complement facilitates early prion pathogenesis. *Nature Medicine*, **2001**, 7, 488-92	50.5	272
181	The UniProt-GO Annotation database in 2011. *Nucleic Acids Research*, **2012**, 40, D565-70	20.1	265
180	MorphoGraphX: A platform for quantifying morphogenesis in 4D. *ELife*, **2015**, 4, 05864	8.9	245
179	The minimum information required for reporting a molecular interaction experiment (MIMIx). *Nature Biotechnology*, **2007**, 25, 894-8	44.5	229
178	ViralZone: a knowledge resource to understand virus diversity. *Nucleic Acids Research*, **2011**, 39, D576-82	20.1	216
177	Three-dimensional cluster analysis identifies interfaces and functional residue clusters in proteins. *Journal of Molecular Biology*, **2001**, 307, 1487-502	6.5	206
176	Personalized cancer vaccine effectively mobilizes antitumor T cell immunity in ovarian cancer. *Science Translational Medicine*, **2018**, 10,	17.5	205
175	Broadening the horizon--level 2.5 of the HUPO-PSI format for molecular interactions. *BMC Biology*, **2007**, 5, 44	7.3	204
174	Characterization of the human ABCG1 gene: liver X receptor activates an internal promoter that produces a novel transcript encoding an alternative form of the protein. *Journal of Biological Chemistry*, **2001**, 276, 39438-47	5.4	204

173   Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. *European Heart Journal*, **2015**, 36, 353-68a   9.5   199

172   Proteomic analysis of the mouse liver mitochondrial inner membrane. *Journal of Biological Chemistry*, **2003**, 278, 41566-71   5.4   193

171   Synchronous versus asynchronous modeling of gene regulatory networks. *Bioinformatics*, **2008**, 24, 1917-25   7.7   191

170   Localizing proteins in the cell from their phylogenetic profiles. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 12115-20   11.5   184

169   Gene expression across mammalian organ development. *Nature*, **2019**, 571, 505-509   50.4   179

168   The Gene Ontology: enhancements for 2011. *Nucleic Acids Research*, **2012**, 40, D559-64   20.1   166

167   Type I interferons protect T cells against NK cell attack mediated by the activating receptor NCR1. *Immunity*, **2014**, 40, 961-73   32.3   159

166   A method for the generation of standardized qualitative dynamical systems of regulatory networks. *Theoretical Biology and Medical Modelling*, **2006**, 3, 13   2.3   155

165   DIP: The Database of Interacting Proteins: 2001 update. *Nucleic Acids Research*, **2001**, 29, 239-41   20.1   147

164   Standardized benchmarking in the quest for orthologs. *Nature Methods*, **2016**, 13, 425-30   21.6   133

163   The UniProtKB/Swiss-Prot Tox-Prot program: A central hub of integrated venom protein data. *Toxicon*, **2012**, 60, 551-7   2.8   128

162   Dynamic simulation of regulatory networks using SQUAD. *BMC Bioinformatics*, **2007**, 8, 462   3.6   112

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

160   Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. *Cell*, **2020**, 183, 818-834.e13   56.2   105

159   SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. *BMC Systems Biology*, **2013**, 7, 135   3.5   100

158   CDK9 regulates AR promoter selectivity and cell growth through serine 81 phosphorylation. *Molecular Endocrinology*, **2010**, 24, 2267-80   98

157   Neutrophils and Snail Orchestrate the Establishment of a Pro-tumor Microenvironment in Lung Cancer. *Cell Reports*, **2017**, 21, 3190-3204   10.6   96

156   The mzTab data exchange format: communicating mass-spectrometry-based proteomics and metabolomics experimental results to a wider audience. *Molecular and Cellular Proteomics*, **2014**, 13, 2765-75   7.6   96

155	HAMAP in 2015: updates to the protein family classification and annotation system. *Nucleic Acids Research*, **2015**, 43, D1064-70	20.1	93
154	Improving the sensitivity of the sequence profile method. *Protein Science*, **1994**, 3, 139-46	6.3	92
153	Soil fungal communities of grasslands are environmentally structured at a regional scale in the Alps. *Molecular Ecology*, **2014**, 23, 4274-90	5.7	85
152	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
151	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
150	FastEpistasis: a high performance computing solution for quantitative trait epistasis. *Bioinformatics*, **2010**, 26, 1468-9	7.2	80
149	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. *Nature Communications*, **2020**, 11, 1293	17.4	78
148	UniPathway: a resource for the exploration and annotation of metabolic pathways. *Nucleic Acids Research*, **2012**, 40, D761-9	20.1	76
147	Protein interaction databases. *Current Opinion in Biotechnology*, **2001**, 12, 334-9	11.4	76
146	Neighbor Detection Induces Organ-Specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-Specific Growth. *Plant Cell*, **2016**, 28, 2889-2904	11.6	76
145	Low number of fixed somatic mutations in a long-lived oak tree. *Nature Plants*, **2017**, 3, 926-929	11.5	74
144	Guidelines for reporting the use of mass spectrometry in proteomics. *Nature Biotechnology*, **2008**, 26, 860-1	44.5	72
143	Probabilistic base calling of Solexa sequencing data. *BMC Bioinformatics*, **2008**, 9, 431	3.6	72
142	The SwissLipids knowledgebase for lipid biology. *Bioinformatics*, **2015**, 31, 2860-6	7.2	66
141	SBML Level 3: an extensible format for the exchange and reuse of biological models. *Molecular Systems Biology*, **2020**, 16, e9110	12.2	65
140	Rhea--a manually curated resource of biochemical reactions. *Nucleic Acids Research*, **2012**, 40, D754-60	20.1	63
139	Differentially phased leaf growth and movements in Arabidopsis depend on coordinated circadian and light regulation. *Plant Cell*, **2014**, 26, 3911-21	11.6	62
138	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome. *Molecular and Cellular Proteomics*, **2018**, 17, 2347-2357	7.6	62

137	Cooperative development of logical modelling standards and tools with CoLoMoTo. *Bioinformatics*, **2015**, 31, 1154-9	7.2	61
136	Measuring the diurnal pattern of leaf hyponasty and growth in Arabidopsis - a novel phenotyping approach using laser scanning. *Functional Plant Biology*, **2012**, 39, 860-869	2.7	60
135	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	4.4	57
134	Functional and Evolutionary Analysis of the CASPARIAN STRIP MEMBRANE DOMAIN PROTEIN Family. *Plant Physiology*, **2014**, 165, 1709-1722	6.6	56
133	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
132	Hard-wired heterogeneity in blood stem cells revealed using a dynamic regulatory network model. *Bioinformatics*, **2013**, 29, i80-8	7.2	53
131	HAMAP in 2013, new developments in the protein family classification and annotation system. *Nucleic Acids Research*, **2013**, 41, D584-9	20.1	52
130	Molecular docking of competitive phosphodiesterase inhibitors. *Molecular Pharmacology*, **2002**, 61, 20-5	4.3	52
129	R-Coffee: a web server for accurately aligning noncoding RNA sequences. *Nucleic Acids Research*, **2008**, 36, W10-3	20.1	51
128	Reconciliation of metabolites and biochemical reactions for metabolic networks. *Briefings in Bioinformatics*, **2014**, 15, 123-35	13.4	49
127	Evolution of the ferric reductase domain (FRD) superfamily: modularity, functional diversification, and signature motifs. *PLoS ONE*, **2013**, 8, e58126	3.7	48
126	Updates in Rhea - an expert curated resource of biochemical reactions. *Nucleic Acids Research*, **2017**, 45, D415-D418	20.1	46
125	Evolutionary trajectories of primate genes involved in HIV pathogenesis. *Molecular Biology and Evolution*, **2009**, 26, 2865-75	8.3	46
124	Mutations in LONP1, a mitochondrial matrix protease, cause CODAS syndrome. *American Journal of Medical Genetics, Part A*, **2015**, 167, 1501-9	2.5	45
123	Local auxin production underlies a spatially restricted neighbor-detection response in. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 7444-7449	11.5	43
122	A robust second-generation genome-wide test for fetal aneuploidy based on shotgun sequencing cell-free DNA in maternal blood. *Prenatal Diagnosis*, **2013**, 33, 707-10	3.2	42
121	Genetic variations and diseases in UniProtKB/Swiss-Prot: the ins and outs of expert manual curation. *Human Mutation*, **2014**, 35, 927-35	4.7	40
120	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	3.7	40

119	Modeling stochasticity and robustness in gene regulatory networks. *Bioinformatics*, **2009**, 25, i101-9	7.2	39
118	Interplays between mouse mammary tumor virus and the cellular and humoral immune response. *Immunological Reviews*, **1999**, 168, 287-303	11.3	39
117	TBC1D7 mutations are associated with intellectual disability, macrocrania, patellar dislocation, and celiac disease. *Human Mutation*, **2014**, 35, 447-51	4.7	38
116	Updates in Rhea--a manually curated resource of biochemical reactions. *Nucleic Acids Research*, **2015**, 43, D459-64	20.1	37
115	ViralZone: recent updates to the virus knowledge resource. *Nucleic Acids Research*, **2013**, 41, D579-83	20.1	36
114	An Efficient Method for Dynamic Analysis of Gene Regulatory Networks and in silico Gene Perturbation Experiments **2007**, 62-76		34
113	Deciphering the Dynamic Transcriptional and Post-transcriptional Networks of Macrophages in the Healthy Heart and after Myocardial Injury. *Cell Reports*, **2018**, 23, 622-636	10.6	33
112	KIAA1109 Variants Are Associated with a Severe Disorder of Brain Development and Arthrogryposis. *American Journal of Human Genetics*, **2018**, 102, 116-132	11	32
111	A chemical proteomics approach to phosphatidylinositol 3-kinase signaling in macrophages. *Molecular and Cellular Proteomics*, **2007**, 6, 1829-41	7.6	32
110	Enzyme annotation in UniProtKB using Rhea. *Bioinformatics*, **2020**, 36, 1896-1901	7.2	32
109	Updates in Rhea: SPARQLing biochemical reaction data. *Nucleic Acids Research*, **2019**, 47, D596-D600	20.1	32
108	Describing biological protein interactions in terms of protein states and state transitions: the LiveDIP database. *Molecular and Cellular Proteomics*, **2002**, 1, 104-16	7.6	31
107	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
106	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
105	Substantial deletion overlap among divergent Arabidopsis genomes revealed by intersection of short reads and tiling arrays. *Genome Biology*, **2010**, 11, R4	18.3	30
104	A qualitative continuous model of cellular auxin and brassinosteroid signaling and their crosstalk. *Bioinformatics*, **2011**, 27, 1404-12	7.2	30
103	Automated quantitative histology reveals vascular morphodynamics during Arabidopsis hypocotyl secondary growth. *ELife*, **2014**, 3, e01567	8.9	30
102	Global mapping of highly pathogenic avian influenza H5N1 and H5Nx clade 2.3.4.4 viruses with spatial cross-validation. *ELife*, **2016**, 5,	8.9	30

101	Plant species distributions along environmental gradients: do belowground interactions with fungi matter?. *Frontiers in Plant Science*, **2013**, 4, 500	6.2	29
100	OpenFluDB, a database for human and animal influenza virus. *Database: the Journal of Biological Databases and Curation*, **2010**, 2010, baq004	5	29
99	TIE-2-expressing monocytes are lymphangiogenic and associate specifically with lymphatics of human breast cancer. *OncoImmunology*, **2016**, 5, e1073882	7.2	28
98	TIE-2 and VEGFR kinase activities drive immunosuppressive function of TIE-2-expressing monocytes in human breast tumors. *Clinical Cancer Research*, **2013**, 19, 3439-49	12.9	28
97	TIE-2 expressing monocytes in human cancers. *OncoImmunology*, **2017**, 6, e1303585	7.2	27
96	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. *Plant Physiology*, **2019**, 180, 305-322	6.6	27
95	Comparative transcriptome profiling of the injured zebrafish and mouse hearts identifies miRNA-dependent repair pathways. *Cardiovascular Research*, **2016**, 110, 73-84	9.9	27
94	Conceptual framework and pilot study to benchmark phylogenomic databases based on reference gene trees. *Briefings in Bioinformatics*, **2011**, 12, 423-35	13.4	27
93	Sleep-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	11.5	27
92	A systems genetics resource and analysis of sleep regulation in the mouse. *PLoS Biology*, **2018**, 16, e2005750	7.7	26
91	The direct effects of tacrolimus and cyclosporin A on isolated human islets: A functional, survival and gene expression study. *Islets*, **2009**, 1, 106-10	2	26
90	Toward unrestricted use of public genomic data. *Science*, **2019**, 363, 350-352	33.3	25
89	Gearing up to handle the mosaic nature of life in the quest for orthologs. *Bioinformatics*, **2018**, 34, 323-329	7.2	25
88	Fisetin protects against cardiac cell death through reduction of ROS production and caspases activity. *Scientific Reports*, **2020**, 10, 2896	4.9	23
87	Analysis of the dynamic co-expression network of heart regeneration in the zebrafish. *Scientific Reports*, **2016**, 6, 26822	4.9	23
86	Database resources for the tuberculosis community. *Tuberculosis*, **2013**, 93, 12-7	2.6	23
85	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	5	23
84	Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. *PLoS Computational Biology*, **2018**, 14, e1006390	5	21

83	Analysis of stop-gain and frameshift variants in human innate immunity genes. *PLoS Computational Biology*, **2014**, 10, e1003757	5	21
82	Boolean regulatory network reconstruction using literature based knowledge with a genetic algorithm optimization method. *BMC Bioinformatics*, **2016**, 17, 410	3.6	21
81	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
80	A Clb/Cdk1-mediated regulation of Fkh2 synchronizes expression in the budding yeast cell cycle. *Npj Systems Biology and Applications*, **2017**, 3, 7	5	20
79	Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	20
78	SourceData: a semantic platform for curating and searching figures. *Nature Methods*, **2017**, 14, 1021-1022	21.6	19
77	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. *Genome Biology and Evolution*, **2015**, 7, 1988-99	3.9	19
76	Animal Toxins: How is Complexity Represented in Databases?. *Toxins*, **2010**, 2, 262-282	4.9	18
75	Modeling of multiple valued gene regulatory networks. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, **2007**, 2007, 1398-404		18
74	Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. *Genome Medicine*, **2016**, 8, 105	14.4	16
73	Detection and identification of plasma proteins that bind GlialCAM using ProteinChip arrays, SELDI-TOF MS, and nano-LC MS/MS. *Proteomics*, **2008**, 8, 378-88	4.8	16
72	Human ERK1 induces filamentous growth and cell wall remodeling pathways in Saccharomyces cerevisiae. *Journal of Biological Chemistry*, **2000**, 275, 20638-46	5.4	16
71	Laser capture microdissection of human pancreatic islets reveals novel eQTLs associated with type 2 diabetes. *Molecular Metabolism*, **2019**, 24, 98-107	8.8	14
70	New molecular insights into modulation of platelet reactivity in aspirin-treated patients using a network-based approach. *Human Genetics*, **2016**, 135, 403-414	6.3	14
69	Qualitative modeling identifies IL-11 as a novel regulator in maintaining self-renewal in human pluripotent stem cells. *Frontiers in Physiology*, **2013**, 4, 303	4.6	14
68	Density-based hierarchical clustering of pyro-sequences on a large scale--the case of fungal ITS1. *Bioinformatics*, **2013**, 29, 1268-74	7.2	14
67	Angiogenic activity of breast cancer patientsᛣmonocytes reverted by combined use of systems modeling and experimental approaches. *PLoS Computational Biology*, **2015**, 11, e1004050	5	13
66	Application of text-mining for updating protein post-translational modification annotation in UniProtKB. *BMC Bioinformatics*, **2013**, 14, 104	3.6	13

65	MAR-Mediated transgene integration into permissive chromatin and increased expression by recombination pathway engineering. *Biotechnology and Bioengineering*, **2017**, 114, 384-396	4.9	13
64	MIMAS 3.0 is a Multiomics Information Management and Annotation System. *BMC Bioinformatics*, **2009**, 10, 151	3.6	13
63	Immune response to mouse mammary tumor virus in mice lacking the alpha/beta interferon or the gamma interferon receptor. *Journal of Virology*, **1998**, 72, 2638-46	6.6	13
62	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	2.8	12
61	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. *Nucleic Acids Research*, **2014**, 42, W436-41	20.1	12
60	An integrated ontology resource to explore and study host-virus relationships. *PLoS ONE*, **2014**, 9, e108075	3.7	12
59	Implicit methods for qualitative modeling of gene regulatory networks. *Methods in Molecular Biology*, **2012**, 786, 397-443	1.4	12
58	DynaStI: A Dynamic Retention Time Database for Steroidomics. *Metabolites*, **2019**, 9,	5.6	11
57	pfsearchV3: a code acceleration and heuristic to search PROSITE profiles. *Bioinformatics*, **2013**, 29, 1215-7	7.2	10
56	Genome-wide identification of microRNAs regulating the human prion protein. *Brain Pathology*, **2019**, 29, 232-244	6	10
55	West syndrome caused by homozygous variant in the evolutionary conserved gene encoding the mitochondrial elongation factor GUF1. *European Journal of Human Genetics*, **2016**, 24, 1001-8	5.3	9
54	HENA, heterogeneous network-based data set for Alzheimer@ disease. *Scientific Data*, **2019**, 6, 151	8.2	9
53	Integrative knowledge management to enhance pharmaceutical R&D. *Nature Reviews Drug Discovery*, **2014**, 13, 239-40	64.1	9
52	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	4.5	9
51	EuroDia: a beta-cell gene expression resource. *Database: the Journal of Biological Databases and Curation*, **2010**, 2010, baq024	5	9
50	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
49	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. *Briefings in Bioinformatics*, **2021**, 22, 1848-1859	13.4	9
48	Quantification of the spread of SARS-CoV-2 variant B.1.1.7 in Switzerland. *Epidemics*, **2021**, 37, 100480	5.1	9

47	Three-dimensional chromatin interactions remain stable upon CAG/CTG repeat expansion. *Science Advances*, **2020**, 6, eaaz4012	14.3	8
46	Analysis of S. pombe SIN protein association to the SPB reveals two genetically separable states of the SIN. *Journal of Cell Science*, **2015**, 128, 741-54	5.3	8
45	Comparison of strategies to detect epistasis from eQTL data. *PLoS ONE*, **2011**, 6, e28415	3.7	8
44	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
43	An Extended, Boolean Model of the Septation Initiation Network in S.Pombe Provides Insights into Its Regulation. *PLoS ONE*, **2015**, 10, e0134214	3.7	7
42	TRAL: tandem repeat annotation library. *Bioinformatics*, **2015**, 31, 3051-3	7.2	7
41	Efficient computation of minimal perturbation sets in gene regulatory networks. *Frontiers in Physiology*, **2013**, 4, 361	4.6	7
40	Visualization and quality assessment of de novo genome assemblies. *Bioinformatics*, **2011**, 27, 3425-6	7.2	7
39	Improving HIV proteome annotation: new features of BioAfrica HIV Proteomics Resource. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	7
38	Differential regulation of RNA polymerase III genes during liver regeneration. *Nucleic Acids Research*, **2019**, 47, 1786-1796	20.1	7
37	Multiple imputations applied to the DREAM3 phosphoproteomics challenge: a winning strategy. *PLoS ONE*, **2010**, 5, e8012	3.7	6
36	ENFIN--A European network for integrative systems biology. *Comptes Rendus - Biologies*, **2009**, 332, 1050-8	1.4	6
35	Animal Toxins: How is Complexity Represented in Databases?. *Toxins*, **2010**, 2, 262-82	4.9	6
34	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
33	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,	5	5
32	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. *Viruses*, **2020**, 12,	6.2	5
31	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	4.9	5
30	Consent insufficient for data release-Response. *Science*, **2019**, 364, 446	33.3	4

29	HAMAP as SPARQL rules-A portable annotation pipeline for genomes and proteomes. *GigaScience*, **2020**, 9,	7.6	4
28	The ins and outs of eukaryotic viruses: Knowledge base and ontology of a viral infection. *PLoS ONE*, **2017**, 12, e0171746	3.7	4
27	Differential reactivity of TCR Vbeta10 alleles to a mouse mammary tumor virus superantigen. *European Journal of Immunology*, **1998**, 28, 3075-85	6.1	4
26	Enzyme annotation in UniProtKB using Rhea		4
25	Characterization and mutagenesis of Chinese hamster ovary cells endogenous retroviruses to inactivate viral particle release. *Biotechnology and Bioengineering*, **2020**, 117, 466-485	4.9	4
24	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference - Application to H5N1 spread in the Mekong region. *Bioinformatics*, **2020**, 36, 2098-2104	7.2	4
23	A multi-omics digital research object for the genetics of sleep regulation. *Scientific Data*, **2019**, 6, 258	8.2	4
22	Unraveling modulators of platelet reactivity in cardiovascular patients using omics strategies: Towards a network biology paradigm. *Translational Proteomics*, **2013**, 1, 25-37		3
21	Extensive remodeling of DC function by rapid maturation-induced transcriptional silencing. *Nucleic Acids Research*, **2014**, 42, 9641-55	20.1	3
20	The Microbe browser for comparative genomics. *Nucleic Acids Research*, **2009**, 37, W296-9	20.1	3
19	AssociationViewer: a scalable and integrated software tool for visualization of large-scale variation data in genomic context. *Bioinformatics*, **2009**, 25, 662-3	7.2	3
18	Taxon sampling unequally affects individual nodes in a phylogenetic tree: consequences for model gene tree construction in SwissTree		3
17	Identifying biological mechanisms for favorable cancer prognosis using non-hypothesis-driven iterative survival analysis. *Npj Systems Biology and Applications*, **2016**, 2, 16037	5	3
16	Bacterial Virus Ontology; Coordinating across Databases. *Viruses*, **2017**, 9,	6.2	2
15	Strengths and Weaknesses of Selected Modeling Methods Used in Systems Biology **2011**,		2
14	PamgeneAnalyzeR: open and reproducible pipeline for kinase profiling. *Bioinformatics*, **2020**, 36, 5117-5119	7.2	2
13	Navigating in vitro bioactivity data by investigating available resources using model compounds. *Scientific Data*, **2019**, 6, 45	8.2	1
12	Toward a rational design of combination therapy in cancer. *OncoImmunology*, **2015**, 4, e1046674	7.2	1

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11	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	15.4	1
10	New genome assembly of the barn owl (). *Ecology and Evolution*, **2020**, 10, 2284-2298	2.8	1
9	Social networks help to infer causality in the tumor microenvironment. *BMC Research Notes*, **2016**, 9, 168	2.3	1
8	Simple and complex interactions between sleep-wake driven and circadian processes shape daily genome regulatory dynamics in the mouse		1
7	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome		1
6	Integrated Proteogenomic Deep Sequencing and Analytics Accurately Identify Non-Canonical Peptides in Tumor Immunopeptidomes		1
5	SourceData - a semantic platform for curating and searching figures		1
4	Unsupervised Analysis of Flow Cytometry Data in a Clinical Setting Captures Cell Diversity and Allows Population Discovery. *Frontiers in Immunology*, **2021**, 12, 633910	8.4	1
3	Blood virosphere in febrile Tanzanian children. *Emerging Microbes and Infections*, **2021**, 10, 982-993	18.9	0
2	Generation of Molecular Models and Pathways **2018**, 274-285		
1	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	6.8	