

Emmanuel Barillot

List of Publications by Citations

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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.

173
papers

12,357
citations

55
h-index

109
g-index

197
ext. papers

15,221
ext. citations

10.1
avg, IF

5.9
L-index

#	Paper	IF	Citations
173	Spatial partitioning of the regulatory landscape of the X-inactivation centre. <i>Nature</i> , 2012 , 485, 381-5	50.4	1894
172	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. <i>Genome Biology</i> , 2015 , 16, 259	18.3	811
171	A critical function for transforming growth factor-beta, interleukin 23 and proinflammatory cytokines in driving and modulating human T(H)-17 responses. <i>Nature Immunology</i> , 2008 , 9, 650-7	19.1	748
170	Control-FREEC: a tool for assessing copy number and allelic content using next-generation sequencing data. <i>Bioinformatics</i> , 2012 , 28, 423-5	7.2	576
169	Analysis of array CGH data: from signal ratio to gain and loss of DNA regions. <i>Bioinformatics</i> , 2004 , 20, 3413-22	7.2	429
168	Continuum of overlapping clones spanning the entire human chromosome 21q. <i>Nature</i> , 1992 , 359, 380-7	50.4	394
167	LINE-1 activity in facultative heterochromatin formation during X chromosome inactivation. <i>Cell</i> , 2010 , 141, 956-69	56.2	246
166	miR-181a and miR-630 regulate cisplatin-induced cancer cell death. <i>Cancer Research</i> , 2010 , 70, 1793-803	10.1	243
165	Control-free calling of copy number alterations in deep-sequencing data using GC-content normalization. <i>Bioinformatics</i> , 2011 , 27, 268-9	7.2	190
164	Germline BAP1 mutations predispose to renal cell carcinomas. <i>American Journal of Human Genetics</i> , 2013 , 92, 974-80	11	188
163	Heterogeneity of neuroblastoma cell identity defined by transcriptional circuitries. <i>Nature Genetics</i> , 2017 , 49, 1408-1413	36.3	174
162	Frequent PTEN genomic alterations and activated phosphatidylinositol 3-kinase pathway in basal-like breast cancer cells. <i>Breast Cancer Research</i> , 2008 , 10, R101	8.3	168
161	Mapping the whole human genome by fingerprinting yeast artificial chromosomes. <i>Cell</i> , 1992 , 70, 1059-68	56.2	154
160	Genome Alteration Print (GAP): a tool to visualize and mine complex cancer genomic profiles obtained by SNP arrays. <i>Genome Biology</i> , 2009 , 10, R128	18.3	150
159	SVDetect: a tool to identify genomic structural variations from paired-end and mate-pair sequencing data. <i>Bioinformatics</i> , 2010 , 26, 1895-6	7.2	149
158	Classification of microarray data using gene networks. <i>BMC Bioinformatics</i> , 2007 , 8, 35	3.6	149
157	Beta-catenin status in paediatric medulloblastomas: correlation of immunohistochemical expression with mutational status, genetic profiles, and clinical characteristics. <i>Journal of Pathology</i> , 2009 , 218, 86-94	9.4	141

156	Mathematical modelling of cell-fate decision in response to death receptor engagement. <i>PLoS Computational Biology</i> , 2010 , 6, e1000702	5	140
155	Independent component analysis uncovers the landscape of the bladder tumor transcriptome and reveals insights into luminal and basal subtypes. <i>Cell Reports</i> , 2014 , 9, 1235-45	10.6	131
154	Polo-like kinase 1: a potential therapeutic option in combination with conventional chemotherapy for the management of patients with triple-negative breast cancer. <i>Cancer Research</i> , 2013 , 73, 813-23	10.1	125
153	The oncogenic EWS-FLI1 protein binds in vivo GGAA microsatellite sequences with potential transcriptional activation function. <i>PLoS ONE</i> , 2009 , 4, e4932	3.7	121
152	Establishment and characterization of a panel of human uveal melanoma xenografts derived from primary and/or metastatic tumors. <i>Clinical Cancer Research</i> , 2010 , 16, 2352-62	12.9	120
151	HiTC: exploration of high-throughput χ^2 experiments. <i>Bioinformatics</i> , 2012 , 28, 2843-4	7.2	119
150	Live-cell chromosome dynamics and outcome of X chromosome pairing events during ES cell differentiation. <i>Cell</i> , 2011 , 145, 447-58	56.2	118
149	Asf1b, the necessary Asf1 isoform for proliferation, is predictive of outcome in breast cancer. <i>EMBO Journal</i> , 2011 , 30, 480-93	13	112
148	Genomic profiling and identification of high-risk uveal melanoma by array CGH analysis of primary tumors and liver metastases 2009 , 50, 2572-80		107
147	VAMP: visualization and analysis of array-CGH, transcriptome and other molecular profiles. <i>Bioinformatics</i> , 2006 , 22, 2066-73	7.2	104
146	Theoretical analysis of library screening using a N-dimensional pooling strategy. <i>Nucleic Acids Research</i> , 1991 , 19, 6241-7	20.1	103
145	Prognostic impact of vitamin B6 metabolism in lung cancer. <i>Cell Reports</i> , 2012 , 2, 257-69	10.6	100
144	A comprehensive modular map of molecular interactions in RB/E2F pathway. <i>Molecular Systems Biology</i> , 2008 , 4, 173	12.2	99
143	High PTP4A3 phosphatase expression correlates with metastatic risk in uveal melanoma patients. <i>Cancer Research</i> , 2011 , 71, 666-74	10.1	96
142	myProMS, a web server for management and validation of mass spectrometry-based proteomic data. <i>Proteomics</i> , 2007 , 7, 2553-6	4.8	95
141	TTK/hMPS1 is an attractive therapeutic target for triple-negative breast cancer. <i>PLoS ONE</i> , 2013 , 8, e63737	3.7	93
140	Atlas of Cancer Signalling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. <i>Oncogenesis</i> , 2015 , 4, e160	6.6	90
139	Developmental dynamics and disease potential of random monoallelic gene expression. <i>Developmental Cell</i> , 2014 , 28, 366-80	10.2	90

138	BAC array CGH distinguishes mutually exclusive alterations that define clinicogenetic subtypes of gliomas. <i>International Journal of Cancer</i> , 2008 , 122, 1778-86	7.5	90
137	Concomitant Notch activation and p53 deletion trigger epithelial-to-mesenchymal transition and metastasis in mouse gut. <i>Nature Communications</i> , 2014 , 5, 5005	17.4	88
136	BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. <i>Bioinformatics</i> , 2008 , 24, 876-7	7.2	87
135	Isolation of chromosome 21-specific yeast artificial chromosomes from a total human genome library. <i>Nature Genetics</i> , 1992 , 1, 222-5	36.3	87
134	Multiparametric analysis of cytokine-driven human Th17 differentiation reveals a differential regulation of IL-17 and IL-22 production. <i>Blood</i> , 2009 , 114, 3610-4	2.2	85
133	Multi-factor data normalization enables the detection of copy number aberrations in amplicon sequencing data. <i>Bioinformatics</i> , 2014 , 30, 3443-50	7.2	81
132	Maternal LSD1/KDM1A is an essential regulator of chromatin and transcription landscapes during zygotic genome activation. <i>ELife</i> , 2016 , 5,	8.9	80
131	Xist-dependent imprinted X inactivation and the early developmental consequences of its failure. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 226-233	17.6	79
130	Genome-wide redistribution of meiotic double-strand breaks in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2007 , 27, 1868-80	4.8	79
129	ncPRO-seq: a tool for annotation and profiling of ncRNAs in sRNA-seq data. <i>Bioinformatics</i> , 2012 , 28, 3147-9	7.2	78
128	Mathematical Modelling of Molecular Pathways Enabling Tumour Cell Invasion and Migration. <i>PLoS Computational Biology</i> , 2015 , 11, e1004571	5	72
127	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020 , 7, 136	8.2	71
126	Frequent genomic structural alterations at HPV insertion sites in cervical carcinoma. <i>Journal of Pathology</i> , 2010 , 221, 320-30	9.4	70
125	Continuous time Boolean modeling for biological signaling: application of Gillespie algorithm. <i>BMC Systems Biology</i> , 2012 , 6, 116	3.5	68
124	Spatial normalization of array-CGH data. <i>BMC Bioinformatics</i> , 2006 , 7, 264	3.6	67
123	Aberrant ERBB4-SRC Signaling as a Hallmark of Group 4 Medulloblastoma Revealed by Integrative Phosphoproteomic Profiling. <i>Cancer Cell</i> , 2018 , 34, 379-395.e7	24.3	62
122	Highly dynamic and sex-specific expression of microRNAs during early ES cell differentiation. <i>PLoS Genetics</i> , 2009 , 5, e1000620	6	61
121	MaBoSS 2.0: an environment for stochastic Boolean modeling. <i>Bioinformatics</i> , 2017 , 33, 2226-2228	7.2	59

120	Bioinformatics for precision medicine in oncology: principles and application to the SHIVA clinical trial. <i>Frontiers in Genetics</i> , 2014 , 5, 152	4.5	59
119	Search for a gene expression signature of breast cancer local recurrence in young women. <i>Clinical Cancer Research</i> , 2012 , 18, 1704-15	12.9	56
118	NormaCurve: a SuperCurve-based method that simultaneously quantifies and normalizes reverse phase protein array data. <i>PLoS ONE</i> , 2012 , 7, e38686	3.7	54
117	High-resolution mapping of DNA breakpoints to define true recurrences among ipsilateral breast cancers. <i>Journal of the National Cancer Institute</i> , 2008 , 100, 48-58	9.7	54
116	Streamlined ion torrent PGM-based diagnostics: BRCA1 and BRCA2 genes as a model. <i>European Journal of Human Genetics</i> , 2014 , 22, 535-41	5.3	51
115	De novo motif identification improves the accuracy of predicting transcription factor binding sites in ChIP-Seq data analysis. <i>Nucleic Acids Research</i> , 2010 , 38, e126	20.1	51
114	Systems medicine disease maps: community-driven comprehensive representation of disease mechanisms. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 21	5	47
113	ITTACA: a new database for integrated tumor transcriptome array and clinical data analysis. <i>Nucleic Acids Research</i> , 2006 , 34, D613-6	20.1	47
112	Computational Systems Biology of Cancer		47
111	Identification of microRNA clusters cooperatively acting on epithelial to mesenchymal transition in triple negative breast cancer. <i>Nucleic Acids Research</i> , 2019 , 47, 2205-2215	20.1	44
110	PhysiBoSS: a multi-scale agent-based modelling framework integrating physical dimension and cell signalling. <i>Bioinformatics</i> , 2019 , 35, 1188-1196	7.2	44
109	Characterization of rearrangements involving the ALK gene reveals a novel truncated form associated with tumor aggressiveness in neuroblastoma. <i>Cancer Research</i> , 2013 , 73, 195-204	10.1	42
108	BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. <i>BMC Systems Biology</i> , 2013 , 7, 18	3.5	40
107	Classification of arrayCGH data using fused SVM. <i>Bioinformatics</i> , 2008 , 24, i375-82	7.2	40
106	NaviCell: a web-based environment for navigation, curation and maintenance of large molecular interaction maps. <i>BMC Systems Biology</i> , 2013 , 7, 100	3.5	39
105	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. <i>Nucleic Acids Research</i> , 2013 , 41, 8853-71	20.1	39
104	Transcriptional Programs Define Intratumoral Heterogeneity of Ewing Sarcoma at Single-Cell Resolution. <i>Cell Reports</i> , 2020 , 30, 1767-1779.e6	10.6	39
103	Patient-derived xenografts recapitulate molecular features of human uveal melanomas. <i>Molecular Oncology</i> , 2013 , 7, 625-36	7.9	37

102	EMA - A R package for Easy Microarray data analysis. <i>BMC Research Notes</i> , 2010 , 3, 277	2.3	37
101	Classification of gene signatures for their information value and functional redundancy. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 2	5	34
100	Contribution of epigenetic landscapes and transcription factors to X-chromosome reactivation in the inner cell mass. <i>Nature Communications</i> , 2017 , 8, 1297	17.4	33
99	RNAi-dependent and independent control of LINE1 accumulation and mobility in mouse embryonic stem cells. <i>PLoS Genetics</i> , 2013 , 9, e1003791	6	33
98	APC inactivation associates with abnormal mitosis completion and concomitant BUB1B/MAD2L1 up-regulation. <i>Gastroenterology</i> , 2007 , 132, 2448-58	13.3	33
97	LICORN: learning cooperative regulation networks from gene expression data. <i>Bioinformatics</i> , 2007 , 23, 2407-14	7.2	33
96	Genetic and epigenetic features direct differential efficiency of Xist-mediated silencing at X-chromosomal and autosomal locations. <i>Nature Communications</i> , 2017 , 8, 690	17.4	32
95	Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	32
94	Determining the optimal number of independent components for reproducible transcriptomic data analysis. <i>BMC Genomics</i> , 2017 , 18, 712	4.5	32
93	CAPweb: a bioinformatics CGH array Analysis Platform. <i>Nucleic Acids Research</i> , 2006 , 34, W477-81	20.1	32
92	Breakpoint features of genomic rearrangements in neuroblastoma with unbalanced translocations and chromothripsis. <i>PLoS ONE</i> , 2013 , 8, e72182	3.7	32
91	Nebula--a web-server for advanced ChIP-seq data analysis. <i>Bioinformatics</i> , 2012 , 28, 2517-9	7.2	31
90	Independent transcriptional reprogramming and apoptosis induction by cisplatin. <i>Cell Cycle</i> , 2012 , 11, 3472-80	4.7	31
89	Personalization of Logical Models With Multi-Omics Data Allows Clinical Stratification of Patients. <i>Frontiers in Physiology</i> , 2018 , 9, 1965	4.6	30
88	Drug-Driven Synthetic Lethality: Bypassing Tumor Cell Genetics with a Combination of AsiDNA and PARP Inhibitors. <i>Clinical Cancer Research</i> , 2017 , 23, 1001-1011	12.9	30
87	Deep-sequencing protocols influence the results obtained in small-RNA sequencing. <i>PLoS ONE</i> , 2012 , 7, e32724	3.7	30
86	Dynamical modeling of microRNA action on the protein translation process. <i>BMC Systems Biology</i> , 2010 , 4, 13	3.5	30
85	Community-driven roadmap for integrated disease maps. <i>Briefings in Bioinformatics</i> , 2019 , 20, 659-670	13.4	30

84	Preferential occurrence of chromosome breakpoints within early replicating regions in neuroblastoma. <i>Cell Cycle</i> , 2005 , 4, 1842-6	4.7	29
83	HMCAN: a method for detecting chromatin modifications in cancer samples using CHIP-seq data. <i>Bioinformatics</i> , 2013 , 29, 2979-86	7.2	28
82	Contribution to high-resolution mapping in pigs with 101 type I markers and progress in comparative map between humans and pigs. <i>Mammalian Genome</i> , 2003 , 14, 275-88	3.2	28
81	GPIoPlante-Info (GPI): a collection of databases and bioinformatics resources for plant genomics. <i>Nucleic Acids Research</i> , 2003 , 31, 179-82	20.1	27
80	NaviCell Web Service for network-based data visualization. <i>Nucleic Acids Research</i> , 2015 , 43, W560-5	20.1	26
79	ROMA: Representation and Quantification of Module Activity from Target Expression Data. <i>Frontiers in Genetics</i> , 2016 , 7, 18	4.5	25
78	SV-Bay: structural variant detection in cancer genomes using a Bayesian approach with correction for GC-content and read mappability. <i>Bioinformatics</i> , 2016 , 32, 984-92	7.2	24
77	ITALICS: an algorithm for normalization and DNA copy number calling for Affymetrix SNP arrays. <i>Bioinformatics</i> , 2008 , 24, 768-74	7.2	24
76	The shortest path is not the one you know: application of biological network resources in precision oncology research. <i>Mutagenesis</i> , 2015 , 30, 191-204	2.8	23
75	Network-based approaches for drug response prediction and targeted therapy development in cancer. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 464, 386-91	3.4	23
74	A multiscale signalling network map of innate immune response in cancer reveals cell heterogeneity signatures. <i>Nature Communications</i> , 2019 , 10, 4808	17.4	23
73	Multiple-checkpoint inhibition of thymic stromal lymphopoietin-induced TH2 response by TH17-related cytokines. <i>Journal of Allergy and Clinical Immunology</i> , 2012 , 130, 233-40.e5	11.5	23
72	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020 , 11, 69	17.4	23
71	Comparative analyses of super-enhancers reveal conserved elements in vertebrate genomes. <i>Genome Research</i> , 2017 , 27, 259-268	9.7	21
70	OCSANA: optimal combinations of interventions from network analysis. <i>Bioinformatics</i> , 2013 , 29, 1571-37.2		21
69	Spi-1/PU.1 oncogene accelerates DNA replication fork elongation and promotes genetic instability in the absence of DNA breakage. <i>Cancer Research</i> , 2010 , 70, 6757-66	10.1	21
68	Combinatorial code governing cellular responses to complex stimuli. <i>Nature Communications</i> , 2015 , 6, 6847	17.4	20
67	Synthetic lethality between gene defects affecting a single non-essential molecular pathway with reversible steps. <i>PLoS Computational Biology</i> , 2013 , 9, e1003016	5	19

66	Spi-1/PU.1 activates transcription through clustered DNA occupancy in erythroleukemia. <i>Nucleic Acids Research</i> , 2012 , 40, 8927-41	20.1	19
65	Software package for automatic microarray image analysis (MAIA). <i>Bioinformatics</i> , 2007 , 23, 639-40	7.2	17
64	DeDaL: Cytoscape 3 app for producing and morphing data-driven and structure-driven network layouts. <i>BMC Systems Biology</i> , 2015 , 9, 46	3.5	16
63	Robust and Scalable Learning of Complex Intrinsic Dataset Geometry via ELPiGraph. <i>Entropy</i> , 2020 , 22,	2.8	16
62	Predicting genetic interactions from Boolean models of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2015 , 7, 921-9	3.7	15
61	Effective normalization for copy number variation in Hi-C data. <i>BMC Bioinformatics</i> , 2018 , 19, 313	3.6	15
60	Assessing reproducibility of matrix factorization methods in independent transcriptomes. <i>Bioinformatics</i> , 2019 , 35, 4307-4313	7.2	14
59	Selecting biomedical data sources according to user preferences. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i86-93.	7.2	13
58	Detection of miRNA regulatory effect on triple negative breast cancer transcriptome. <i>BMC Genomics</i> , 2015 , 16, S4	4.5	11
57	A comprehensive approach to the molecular determinants of lifespan using a Boolean model of geroconversion. <i>Aging Cell</i> , 2016 , 15, 1018-1026	9.9	10
56	Girafe--an R/Bioconductor package for functional exploration of aligned next-generation sequencing reads. <i>Bioinformatics</i> , 2010 , 26, 2902-3	7.2	10
55	An algorithm for automatic evaluation of the spot quality in two-color DNA microarray experiments. <i>BMC Bioinformatics</i> , 2005 , 6, 293	3.6	10
54	Personalized logical models to investigate cancer response to BRAF treatments in melanomas and colorectal cancers. <i>PLoS Computational Biology</i> , 2021 , 17, e1007900	5	10
53	NaviCom: a web application to create interactive molecular network portraits using multi-level omics data. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	9
52	Regulatory network reconstruction using an integral additive model with flexible kernel functions. <i>BMC Systems Biology</i> , 2008 , 2, 8	3.5	9
51	Advanced spot quality analysis in two-colour microarray experiments. <i>BMC Research Notes</i> , 2008 , 1, 80	2.3	9
50	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021 , 17, e10387	12.2	9
49	Conceptual and computational framework for logical modelling of biological networks deregulated in diseases. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1238-1249	13.4	9

48	Signalling maps in cancer research: construction and data analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	8
47	Antagonism pattern detection between microRNA and target expression in Ewing's sarcoma. <i>PLoS ONE</i> , 2012 , 7, e41770	3.7	7
46	From a biological hypothesis to the construction of a mathematical model. <i>Methods in Molecular Biology</i> , 2013 , 1021, 107-25	1.4	7
45	cd2sbgmml: bidirectional conversion between CellDesigner and SBGN formats. <i>Bioinformatics</i> , 2020 , 36, 2620-2622	7.2	7
44	Trajectories, bifurcations, and pseudo-time in large clinical datasets: applications to myocardial infarction and diabetes data. <i>GigaScience</i> , 2020 , 9,	7.6	7
43	Application of Atlas of Cancer Signalling Network in preclinical studies. <i>Briefings in Bioinformatics</i> , 2019 , 20, 701-716	13.4	7
42	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	6
41	Logical versus kinetic modeling of biological networks: applications in cancer research. <i>Current Opinion in Chemical Engineering</i> , 2018 , 21, 22-31	5.4	5
40	Cell death and life in cancer: mathematical modeling of cell fate decisions. <i>Advances in Experimental Medicine and Biology</i> , 2012 , 736, 261-74	3.6	5
39	Practical use of BiNoM: a biological network manager software. <i>Methods in Molecular Biology</i> , 2013 , 1021, 127-46	1.4	5
38	The GENETPIG database: a tool for comparative mapping in pig (<i>Sus scrofa</i>). <i>Nucleic Acids Research</i> , 2003 , 31, 138-41	20.1	5
37	A robust algorithm for ratio estimation in two-color microarray experiments. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 1411-28	1	5
36	Moonlight: a tool for biological interpretation and driver genes discovery		5
35	Dynamical Boolean Modeling of Immunogenic Cell Death. <i>Frontiers in Physiology</i> , 2020 , 11, 590479	4.6	5
34	A high-risk retinoblastoma subtype with stemness features, dedifferentiated cone states and neuronal/ganglion cell gene expression. <i>Nature Communications</i> , 2021 , 12, 5578	17.4	5
33	Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. <i>BMC Bioinformatics</i> , 2019 , 20, 140	3.6	4
32	Sequence profiling of the <i>Saccharomyces cerevisiae</i> genome permits deconvolution of unique and multialigned reads for variant detection. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 707-15	3.2	4
31	COVID-19 Disease Map, a computational knowledge repository of SARS-CoV-2 virus-host interaction mechanisms		4

30	Modelling of Immune Checkpoint Network Explains Synergistic Effects of Combined Immune Checkpoint Inhibitor Therapy and the Impact of Cytokines in Patient Response. <i>Cancers</i> , 2020 , 12,	6.6	4
29	Patient-specific Boolean models of signalling networks guide personalised treatments.. <i>ELife</i> , 2022 , 11,	8.9	4
28	Identification of shortened 3' untranslated regions from expression arrays. <i>Journal of Bioinformatics and Computational Biology</i> , 2012 , 10, 1241001	1	3
27	A noise-resistant algorithm for grid finding in microarray image analysis. <i>Machine Vision and Applications</i> , 2006 , 17, 337-345	2.8	3
26	Application of Independent Component Analysis to Tumor Transcriptomes Reveals Specific and Reproducible Immune-Related Signals. <i>Lecture Notes in Computer Science</i> , 2018 , 501-513	0.9	2
25	Calculating Biological Module Enrichment or Depletion and Visualizing Data on Large-scale Molecular Maps with ACSNMiner and RNavicell R packages		2
24	PhysiBoSS: a multi-scale agent based modelling framework integrating physical dimension and cell signalling		2
23	Gene- and pathway-level analyses of iCOGS variants highlight novel signaling pathways underlying familial breast cancer susceptibility. <i>International Journal of Cancer</i> , 2021 , 148, 1895-1909	7.5	2
22	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network. <i>PLoS Computational Biology</i> , 2020 , 16, e1007652	5	1
21	Stability-based comparison of class discovery methods for DNA copy number profiles. <i>PLoS ONE</i> , 2013 , 8, e81458	3.7	1
20	Stabilized Independent Component Analysis outperforms other methods in finding reproducible signals in tumoral transcriptomes		1
19	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network		1
18	How Cell Decides Between Life and Death: Mathematical Modeling of Epigenetic Landscapes of Cellular Fates. <i>Springer Proceedings in Mathematics</i> , 2013 , 191-204		1
17	UPMaBoSS: a novel framework for dynamic cell population modeling		1
16	Metabolic and signalling network map integration: application to cross-talk studies and omics data analysis in cancer		1
15	Clonal assessment of functional mutations in cancer based on a genotype-aware method for clonal reconstruction		
14	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches		1
13	Patient-specific Boolean models of signaling networks guide personalized treatments		1

12	A comparison of Sars-Cov-2 vaccine platforms: the CoviCompare project.. <i>Nature Medicine</i> , 2022 , 28, 882-884	5.8	1
11	Exact solving and sensitivity analysis of stochastic continuous time Boolean models. <i>BMC Bioinformatics</i> , 2020 , 21, 241	3.6	0
10	Model selection in the reconstruction of regulatory networks from time-series data. <i>BMC Research Notes</i> , 2009 , 2, 68	2.3	0
9	Modeling Progression of Single Cell Populations Through the Cell Cycle as a Sequence of Switches.. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 793912	5.6	0
8	WebMaBoSS: A Web Interface for Simulating Boolean Models Stochastically. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 754444	5.6	0
7	UPMaBoSS: A Novel Framework for Dynamic Cell Population Modeling.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 800152	5.6	0
6	PTP4A3, a Signal Molecule Deregulated in Uveal Melanoma Metastasis. <i>Cancer Metastasis - Biology and Treatment</i> , 2010 , 255-263		
5	Atlas of Cancer Signaling Network: A Resource of Multi-Scale Biological Maps to Study Disease Mechanisms 2021 , 490-506		
4	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network 2020 , 16, e1007652		
3	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network 2020 , 16, e1007652		
2	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network 2020 , 16, e1007652		
1	Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network 2020 , 16, e1007652		