Chris P Barnes

List of Publications by Year
in descending order

63 papers	9,389 citations	117625 34 h-index	133252 59 g-index
84 all docs	84 docs citations	84 times ranked	18611 citing authors

#	Article	IF	Citations
1	Fundamental Building Blocks of Whole-Cell Biosensor Design. , 2022, , 383-405.		0
2	Fluctuating methylation clocks for cell lineage tracing at high temporal resolution in human tissues. Nature Biotechnology, 2022, 40, 720-730.	17.5	22
3	Automated design of synthetic microbial communities. Nature Communications, 2021, 12, 672.	12.8	58
4	Single strain control of microbial consortia. Nature Communications, 2021, 12, 1977.	12.8	37
5	Reconstructing single-cell karyotype alterations in colorectal cancer identifies punctuated and gradual diversification patterns. Nature Genetics, 2021, 53, 1187-1195.	21.4	37
6	Engineered acetoacetateâ€inducible wholeâ€cell biosensors based on the AtoSC twoâ€component system. Biotechnology and Bioengineering, 2021, 118, 4278-4289.	3.3	10
7	From Microbial Communities to Distributed Computing Systems. Frontiers in Bioengineering and Biotechnology, 2020, 8, 834.	4.1	19
8	Subclonal reconstruction of tumors by using machine learning and population genetics. Nature Genetics, 2020, 52, 898-907.	21.4	77
9	FlopR: An Open Source Software Package for Calibration and Normalization of Plate Reader and Flow Cytometry Data. ACS Synthetic Biology, 2020, 9, 2258-2266.	3.8	17
10	Evolutionary dynamics of neoantigens in growing tumors. Nature Genetics, 2020, 52, 1057-1066.	21.4	68
11	Measuring single cell divisions in human tissues from multi-region sequencing data. Nature Communications, 2020, 11, 1035.	12.8	41
12	Deep reinforcement learning for the control of microbial co-cultures in bioreactors. PLoS Computational Biology, 2020, 16, e1007783.	3.2	69
13	Fundamental Building Blocks of Whole-Cell Biosensor Design. , 2020, , 1-23.		4
14	Measuring the distribution of fitness effects in somatic evolution by combining clonal dynamics with dN/dS ratios. ELife, 2020, 9, .	6.0	32
15	Detecting Changes in the Caenorhabditis elegans Intestinal Environment Using an Engineered Bacterial Biosensor. ACS Synthetic Biology, 2019, 8, 2620-2628.	3.8	21
16	A Bayesian framework for the analysis of systems biology models of the brain. PLoS Computational Biology, 2019, 15, e1006631.	3.2	11
17	Modelling microbiome recovery after antibiotics using a stability landscape framework. ISME Journal, 2019, 13, 1845-1856.	9.8	98
18	Crypt fusion as a homeostatic mechanism in the human colon. Gut, 2019, 68, 1986-1993.	12.1	28

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19	Two New Plasmid Post-segregational Killing Mechanisms for the Implementation of Synthetic Gene Networks in Escherichia coli. IScience, 2019, 14, 323-334.	4.1	41
20	Combining a Toggle Switch and a Repressilator within the AC-DC Circuit Generates Distinct Dynamical Behaviors. Cell Systems, 2018, 6, 521-530.e3.	6.2	96
21	Reply to â€˜Revisiting signatures of neutral tumor evolution in the light of complexity of cancer genomic dataâ€™. Nature Genetics, 2018, 50, 1628-1630.	21.4	5
22	Towards an Aspect-Oriented Design and Modelling Framework for Synthetic Biology. Processes, 2018, 6, 167.	2.8	6
23	Reply to â€˜Currently available bulk sequencing data do not necessarily support a model of neutral tumor evolutionâ€™. Nature Genetics, 2018, 50, 1624-1626.	21.4	11
24	Reply to â€˜Neutral tumor evolution?â€™. Nature Genetics, 2018, 50, 1633-1637.	21.4	27
25	Quantification of subclonal selection in cancer from bulk sequencing data. Nature Genetics, 2018, 50, 895-903.	21.4	222
26	Synthetic Biology and Engineered Live Biotherapeutics: Toward Increasing System Complexity. Cell Systems, 2018, 7, 5-16.	6.2	107
27	Reply: Is the evolution of tumors Darwinian or non-Darwinian?. National Science Review, 2018, 5, 17-19.	9.5	3
28	Computing with biological switches and clocks. Natural Computing, 2018, 17, 761-779.	3.0	45
29	Catch my drift? Making sense of genomic intra-tumour heterogeneity. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1867, 95-100.	7.4	23
30	Reply: Uncertainties in tumor allele frequencies limit power to infer evolutionary pressures. Nature Genetics, 2017, 49, 1289-1291.	21.4	7
31	A computational method for the investigation of multistable systems and its application to genetic switches. BMC Systems Biology, 2016, 10, 130.	3.0	33
32	Robustness of MEK-ERK Dynamics and Origins of Cell-to-Cell Variability in MAPK Signaling. Cell Reports, 2016, 15, 2524-2535.	6.4	57
33	Identification of neutral tumor evolution across cancer types. Nature Genetics, 2016, 48, 238-244.	21.4	525
34	A Statistical Approach Reveals Designs for the Most Robust Stochastic Gene Oscillators. ACS Synthetic Biology, 2016, 5, 459-470.	3.8	61
35	Mechanistic Modelling and Bayesian Inference Elucidates the Variable Dynamics of Double-Strand Break Repair. PLoS Computational Biology, 2016, 12, e1005131.	3.2	8
36	Ptch1 and Gli regulate Shh signalling dynamics via multiple mechanisms. Nature Communications, 2015, 6, 6709.	12.8	123

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37	Directional Collective Cell Migration Emerges as a Property of Cell Interactions. PLoS ONE, 2014, 9, e104969.	2.5	68
38	Model Selection in Systems Biology Depends on Experimental Design. PLoS Computational Biology, 2014, 10, e1003650.	3.2	54
39	A theoretical framework for the regulation of Shh morphogen-controlled gene expression. Development (Cambridge), 2014, 141, 3868-3878.	2.5	70
40	Reciprocal Duplication of the Williams-Beuren Syndrome Deletion on Chromosome 7q11.23 Is Associated with Schizophrenia. Biological Psychiatry, 2014, 75, 371-377.	1.3	66
41	A framework for parameter estimation and model selection from experimental data in systems biology using approximate Bayesian computation. Nature Protocols, 2014, 9, 439-456.	12.0	185
42	On Industrial Strength Bio-design Automation. Communications in Computer and Information Science, 2014, , 277-299.	0.5	0
43	Clinical drug resistance linked to interconvertible phenotypic and functional states of tumor-propagating cells in multiple myeloma. Blood, 2013, 121, 318-328.	1.4	112
44	On optimality of kernels for approximate Bayesian computation using sequential Monte Carlo. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 87-107.	0.6	86
45	Reduced burden of very large and rare CNVs in bipolar affective disorder. Bipolar Disorders, 2013, 15, 893-898.	1.9	28
46	Considerate approaches to constructing summary statistics for ABC model selection. Statistics and Computing, 2012, 22, 1181-1197.	1.5	45
47	Calibrating spatio-temporal models of leukocyte dynamics against in vivo live-imaging data using approximate Bayesian computation. Integrative Biology (United Kingdom), 2012, 4, 335.	1.3	31
48	Independent estimation of the frequency of rare CNVs in the UK population confirms their role in schizophrenia. Schizophrenia Research, 2012, 135, 1-7.	2.0	73
49	Genome-Wide Screen for Metabolic Syndrome Susceptibility Loci Reveals Strong Lipid Gene Contribution But No Evidence for Common Genetic Basis for Clustering of Metabolic Syndrome Traits. Circulation: Cardiovascular Genetics, 2012, 5, 242-249.	5.1	182
50	Clinical Drug Resistance Linked to Inter-Convertible Phenotypic and Functional States of Tumor-Propagating Cells in Multiple Myeloma.. Blood, 2012, 120, 2909-2909.	1.4	6
51	Computational design approaches and tools for synthetic biology. Integrative Biology (United) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.3	74
52	Bayesian design strategies for synthetic biology. Interface Focus, 2011, 1, 895-908.	3.0	29
53	GPU accelerated biochemical network simulation. Bioinformatics, 2011, 27, 874-876.	4.1	81
54	Designing attractive models via automated identification of chaotic and oscillatory dynamical regimes. Nature Communications, 2011, 2, 489.	12.8	62

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55	Bayesian design of synthetic biological systems. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15190-15195.	7.1	82
56	Origins and functional impact of copy number variation in the human genome. Nature, 2010, 464, 704-712.	27.8	1,721
57	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
58	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
59	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. Genome Research, 2010, 20, 1344-1351.	5.5	52
60	ABC-SysBioâ€"approximate Bayesian computation in Python with GPU support. Bioinformatics, 2010, 26, 1797-1799.	4.1	124
61	A Genome-Wide Association Study Confirms VKORC1, CYP2C9, and CYP4F2 as Principal Genetic Determinants of Warfarin Dose. PLoS Genetics, 2009, 5, e1000433.	3.5	554
62	A robust statistical method for case-control association testing with copy number variation. Nature Genetics, 2008, 40, 1245-1252.	21.4	151
63	Reply: Neutral tumor evolution?. , 0, , .		1