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	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
2	Origins and functional impact of copy number variation in the human genome. Nature, 2010, 464, 704-712.	27.8	1,721
3	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
4	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
5	Identification of neutral tumor evolution across cancer types. Nature Genetics, 2016, 48, 238-244.	21.4	525
6	Quantification of subclonal selection in cancer from bulk sequencing data. Nature Genetics, 2018, 50, 895-903.	21.4	222
7	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
8	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
9	A robust statistical method for case-control association testing with copy number variation. Nature Genetics, 2008, 40, 1245-1252.	21.4	151
10	ABC-SysBio—approximate Bayesian computation in Python with GPU support. Bioinformatics, 2010, 26, 1797-1799.	4.1	124
11	Ptch1 and Gli regulate Shh signalling dynamics via multiple mechanisms. Nature Communications, 2015, 6, 6709.	12.8	123
12	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
13	Synthetic Biology and Engineered Live Biotherapeutics: Toward Increasing System Complexity. Cell Systems, 2018, 7, 5-16.	6.2	107
14	Modelling microbiome recovery after antibiotics using a stability landscape framework. ISME Journal, 2019, 13, 1845-1856.	9.8	98
15	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
16	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
17	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
18	GPU accelerated biochemical network simulation. Bioinformatics, 2011, 27, 874-876.	4.1	81

#	ARTICLE	IF	CITATIONS
19	Subclonal reconstruction of tumors by using machine learning and population genetics. Nature Genetics, 2020, 52, 898-907.	21.4	77
20	Computational design approaches and tools for synthetic biology. Integrative Biology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702	1.3	74
21	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
22	A theoretical framework for the regulation of Shh morphogen-controlled gene expression. Development (Cambridge), 2014, 141, 3868-3878.	2.5	70
23	Deep reinforcement learning for the control of microbial co-cultures in bioreactors. PLoS Computational Biology, 2020, 16, e1007783.	3.2	69
24	Directional Collective Cell Migration Emerges as a Property of Cell Interactions. PLoS ONE, 2014, 9, e104969.	2.5	68
25	Evolutionary dynamics of neoantigens in growing tumors. Nature Genetics, 2020, 52, 1057-1066.	21.4	68
26	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
27	Designing attractive models via automated identification of chaotic and oscillatory dynamical regimes. Nature Communications, 2011, 2, 489.	12.8	62
28	A Statistical Approach Reveals Designs for the Most Robust Stochastic Gene Oscillators. ACS Synthetic Biology, 2016, 5, 459-470.	3.8	61
29	Automated design of synthetic microbial communities. Nature Communications, 2021, 12, 672.	12.8	58
30	Robustness of MEK-ERK Dynamics and Origins of Cell-to-Cell Variability in MAPK Signaling. Cell Reports, 2016, 15, 2524-2535.	6.4	57
31	Model Selection in Systems Biology Depends on Experimental Design. PLoS Computational Biology, 2014, 10, e1003650.	3.2	54
32	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
33	Considerate approaches to constructing summary statistics for ABC model selection. Statistics and Computing, 2012, 22, 1181-1197.	1.5	45
34	Computing with biological switches and clocks. Natural Computing, 2018, 17, 761-779.	3.0	45
35	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
36	Measuring single cell divisions in human tissues from multi-region sequencing data. Nature Communications, 2020, 11, 1035.	12.8	41

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37	Single strain control of microbial consortia. Nature Communications, 2021, 12, 1977.	12.8	37
38	Reconstructing single-cell karyotype alterations in colorectal cancer identifies punctuated and gradual diversification patterns. Nature Genetics, 2021, 53, 1187-1195.	21.4	37
39	A computational method for the investigation of multistable systems and its application to genetic switches. BMC Systems Biology, 2016, 10, 130.	3.0	33
40	Measuring the distribution of fitness effects in somatic evolution by combining clonal dynamics with dN/dS ratios. ELife, 2020, 9, .	6.0	32
41	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
42	Bayesian design strategies for synthetic biology. Interface Focus, 2011, 1, 895-908.	3.0	29
43	Reduced burden of very large and rare CNVs in bipolar affective disorder. Bipolar Disorders, 2013, 15, 893-898.	1.9	28
44	Crypt fusion as a homeostatic mechanism in the human colon. Gut, 2019, 68, 1986-1993.	12.1	28
45	Reply to â€˜Neutral tumor evolution?â€™. Nature Genetics, 2018, 50, 1633-1637.	21.4	27
46	Catch my drift? Making sense of genomic intra-tumour heterogeneity. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1867, 95-100.	7.4	23
47	Fluctuating methylation clocks for cell lineage tracing at high temporal resolution in human tissues. Nature Biotechnology, 2022, 40, 720-730.	17.5	22
48	Detecting Changes in the *Caenorhabditis elegans* Intestinal Environment Using an Engineered Bacterial Biosensor. ACS Synthetic Biology, 2019, 8, 2620-2628.	3.8	21
49	From Microbial Communities to Distributed Computing Systems. Frontiers in Bioengineering and Biotechnology, 2020, 8, 834.	4.1	19
50	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
51	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
52	A Bayesian framework for the analysis of systems biology models of the brain. PLoS Computational Biology, 2019, 15, e1006631.	3.2	11
53	Engineered acetoacetateâ€inducible wholeâ€cell biosensors based on the AtoSC twoâ€component system. Biotechnology and Bioengineering, 2021, 118, 4278-4289.	3.3	10
54	Mechanistic Modelling and Bayesian Inference Elucidates the Variable Dynamics of Double-Strand Break Repair. PLoS Computational Biology, 2016, 12, e1005131.	3.2	8

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55	Reply: Uncertainties in tumor allele frequencies limit power to infer evolutionary pressures. Nature Genetics, 2017, 49, 1289-1291.	21.4	7
56	Towards an Aspect-Oriented Design and Modelling Framework for Synthetic Biology. Processes, 2018, 6, 167.	2.8	6
57	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
58	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
59	Fundamental Building Blocks of Whole-Cell Biosensor Design. , 2020, , 1-23.		4
60	Reply: Is the evolution of tumors Darwinian or non-Darwinian?. National Science Review, 2018, 5, 17-19.	9.5	3
61	Reply: Neutral tumor evolution?. , 0, , .		1
62	Fundamental Building Blocks of Whole-Cell Biosensor Design. , 2022, , 383-405.		0
63	On Industrial Strength Bio-design Automation. Communications in Computer and Information Science, 2014, , 277-299.	0.5	0