

Paul Bertone

List of Publications by Year in Descending Order

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Version: 2024-04-04

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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.

83 papers	14,392 citations	52 h-index	91 g-index
91 ext. papers	16,667 ext. citations	16.6 avg, IF	6.4 L-index

#	Paper	IF	Citations
83	StemBond hydrogels control the mechanical microenvironment for pluripotent stem cells. <i>Nature Communications</i> , 2021 , 12, 6132	17.4	4
82	Sox2 modulation increases naïve pluripotency plasticity. <i>iScience</i> , 2021 , 24, 102153	6.1	2
81	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoediting to elicit immune evasion. <i>Cell</i> , 2021 , 184, 2454-2470.e26	56.2	35
80	The Role of BCL-2 Proteins in the Development of Castration-resistant Prostate Cancer and Emerging Therapeutic Strategies. <i>American Journal of Clinical Oncology: Cancer Clinical Trials</i> , 2021 , 44, 374-382	2.7	2
79	Distinct Molecular Trajectories Converge to Induce Naive Pluripotency. <i>Cell Stem Cell</i> , 2019 , 25, 388-406.e8	18	16
78	Integrated analysis of single-cell embryo data yields a unified transcriptome signature for the human pre-implantation epiblast. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	93
77	Single cell transcriptome analysis of human, marmoset and mouse embryos reveals common and divergent features of preimplantation development. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	81
76	Gain of CTCF-Anchored Chromatin Loops Marks the Exit from Naive Pluripotency. <i>Cell Systems</i> , 2018 , 7, 482-495.e10	10.6	37
75	The Nucleosome Remodeling and Deacetylation Complex Modulates Chromatin Structure at Sites of Active Transcription to Fine-Tune Gene Expression. <i>Molecular Cell</i> , 2018 , 71, 56-72.e4	17.6	70
74	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017 , 144, 1221-1234	6.6	150
73	Elevated FOXG1 and SOX2 in glioblastoma enforces neural stem cell identity through transcriptional control of cell cycle and epigenetic regulators. <i>Genes and Development</i> , 2017 , 31, 757-773	12.6	69
72	Epigenetic resetting of human pluripotency. <i>Development (Cambridge)</i> , 2017 , 144, 2748-2763	6.6	135
71	Nuclear Architecture Organized by Rif1 Underpins the Replication-Timing Program. <i>Molecular Cell</i> , 2016 , 61, 260-73	17.6	111
70	Myc Depletion Induces a Pluripotent Dormant State Mimicking Diapause. <i>Cell</i> , 2016 , 164, 668-80	56.2	132
69	Naive Pluripotent Stem Cells Derived Directly from Isolated Cells of the Human Inner Cell Mass. <i>Stem Cell Reports</i> , 2016 , 6, 437-446	8	220
68	EphrinB2 drives perivascular invasion and proliferation of glioblastoma stem-like cells. <i>ELife</i> , 2016 , 5,	8.9	60
67	Sall4 controls differentiation of pluripotent cells independently of the Nucleosome Remodelling and Deacetylation (NuRD) complex. <i>Development (Cambridge)</i> , 2016 , 143, 3074-84	6.6	40

66	Glioblastoma Stem Cells Respond to Differentiation Cues but Fail to Undergo Commitment and Terminal Cell-Cycle Arrest. <i>Stem Cell Reports</i> , 2015 , 5, 829-842	8	64
65	Lineage-Specific Profiling Delineates the Emergence and Progression of Naive Pluripotency in Mammalian Embryogenesis. <i>Developmental Cell</i> , 2015 , 35, 366-82	10.2	253
64	The ability of inner-cell-mass cells to self-renew as embryonic stem cells is acquired following epiblast specification. <i>Nature Cell Biology</i> , 2014 , 16, 516-28	23.4	312
63	Citrullination regulates pluripotency and histone H1 binding to chromatin. <i>Nature</i> , 2014 , 507, 104-8	50.4	264
62	Resetting transcription factor control circuitry toward ground-state pluripotency in human. <i>Cell</i> , 2014 , 158, 1254-1269	56.2	585
61	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014 , 345, 1251033	33.3	187
60	Identification of the missing pluripotency mediator downstream of leukaemia inhibitory factor. <i>EMBO Journal</i> , 2013 , 32, 2561-74	13	161
59	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013 , 10, 1177-84	21.6	477
58	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013 , 10, 1185-91	21.6	371
57	The non-coding snRNA 7SK controls transcriptional termination, poising, and bidirectionality in embryonic stem cells. <i>Genome Biology</i> , 2013 , 14, R98	18.3	33
56	Towards practical, high-capacity, low-maintenance information storage in synthesized DNA. <i>Nature</i> , 2013 , 494, 77-80	50.4	501
55	SMIM1 underlies the Vel blood group and influences red blood cell traits. <i>Nature Genetics</i> , 2013 , 45, 542-545	34.3	77
54	Widespread resetting of DNA methylation in glioblastoma-initiating cells suppresses malignant cellular behavior in a lineage-dependent manner. <i>Genes and Development</i> , 2013 , 27, 654-69	12.6	103
53	A high-content small molecule screen identifies sensitivity of glioblastoma stem cells to inhibition of polo-like kinase 1. <i>PLoS ONE</i> , 2013 , 8, e77053	3.7	44
52	NuRD suppresses pluripotency gene expression to promote transcriptional heterogeneity and lineage commitment. <i>Cell Stem Cell</i> , 2012 , 10, 583-94	18	168
51	Compound inheritance of a low-frequency regulatory SNP and a rare null mutation in exon-junction complex subunit RBM8A causes TAR syndrome. <i>Nature Genetics</i> , 2012 , 44, 435-9, S1-2	36.3	279
50	Digital transcriptome profiling of normal and glioblastoma-derived neural stem cells identifies genes associated with patient survival. <i>Genome Medicine</i> , 2012 , 4, 76	14.4	39
49	NuRD-mediated deacetylation of H3K27 facilitates recruitment of Polycomb Repressive Complex 2 to direct gene repression. <i>EMBO Journal</i> , 2012 , 31, 593-605	13	185

48	Genome-wide characterization of Foxa2 targets reveals upregulation of floor plate genes and repression of ventrolateral genes in midbrain dopaminergic progenitors. <i>Development (Cambridge)</i> , 2012 , 139, 2625-34	6.6	43
47	Exome sequencing identifies NBEAL2 as the causative gene for gray platelet syndrome. <i>Nature Genetics</i> , 2011 , 43, 735-7	36.3	224
46	Systematic comparison of microarray profiling, real-time PCR, and next-generation sequencing technologies for measuring differential microRNA expression. <i>Rna</i> , 2010 , 16, 991-1006	5.8	515
45	PeakAnalyzer: genome-wide annotation of chromatin binding and modification loci. <i>BMC Bioinformatics</i> , 2010 , 11, 415	3.6	183
44	Mapping organelle proteins and protein complexes in <i>Drosophila melanogaster</i> . <i>Journal of Proteome Research</i> , 2009 , 8, 2667-78	5.6	54
43	HTqPCR: high-throughput analysis and visualization of quantitative real-time PCR data in R. <i>Bioinformatics</i> , 2009 , 25, 3325-6	7.2	173
42	Modeling of C/EBPalpha mutant acute myeloid leukemia reveals a common expression signature of committed myeloid leukemia-initiating cells. <i>Cancer Cell</i> , 2008 , 13, 299-310	24.3	196
41	Genome-wide analysis reveals MOF as a key regulator of dosage compensation and gene expression in <i>Drosophila</i> . <i>Cell</i> , 2008 , 133, 813-28	56.2	125
40	Target hub proteins serve as master regulators of development in yeast. <i>Genes and Development</i> , 2006 , 20, 435-48	12.6	138
39	Transcriptional regulatory networks in bacteria: from input signals to output responses. <i>Current Opinion in Microbiology</i> , 2006 , 9, 511-9	7.9	84
38	Design optimization methods for genomic DNA tiling arrays. <i>Genome Research</i> , 2006 , 16, 271-81	9.7	41
37	Analysis of Genomic Tiling Microarrays for Transcript Mapping and the Identification of Transcription Factor Binding Sites. <i>Lecture Notes in Computer Science</i> , 2005 , 28-29	0.9	1
36	Advances in functional protein microarray technology. <i>FEBS Journal</i> , 2005 , 272, 5400-11	5.7	141
35	Issues in the analysis of oligonucleotide tiling microarrays for transcript mapping. <i>Trends in Genetics</i> , 2005 , 21, 466-75	8.5	88
34	Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery. <i>Chromosome Research</i> , 2005 , 13, 259-74	4.4	58
33	Multi-species microarrays reveal the effect of sequence divergence on gene expression profiles. <i>Genome Research</i> , 2005 , 15, 674-80	9.7	139
32	Prospects and challenges in proteomics. <i>Plant Physiology</i> , 2005 , 138, 560-2	6.6	17
31	Global changes in STAT target selection and transcription regulation upon interferon treatments. <i>Genes and Development</i> , 2005 , 19, 2953-68	12.6	83

30	CREB binds to multiple loci on human chromosome 22. <i>Molecular and Cellular Biology</i> , 2004 , 24, 3804-14	4.8	146
29	Fast optimal genome tiling with applications to microarray design and homology search. <i>Journal of Computational Biology</i> , 2004 , 11, 766-85	1.7	10
28	Global identification of human transcribed sequences with genome tiling arrays. <i>Science</i> , 2004 , 306, 2242-53	3.5	868
27	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004 , 306, 636-40	33.3	1692
26	Distribution of NF-kappaB-binding sites across human chromosome 22. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 12247-52	11.5	276
25	Identification of pseudogenes in the Drosophila melanogaster genome. <i>Nucleic Acids Research</i> , 2003 , 31, 1033-7	20.1	72
24	ExpressYourself: A modular platform for processing and visualizing microarray data. <i>Nucleic Acids Research</i> , 2003 , 31, 3477-82	20.1	34
23	The transcriptional activity of human Chromosome 22. <i>Genes and Development</i> , 2003 , 17, 529-40	12.6	226
22	SPINE 2: a system for collaborative structural proteomics within a federated database framework. <i>Nucleic Acids Research</i> , 2003 , 31, 2833-8	20.1	43
21	Identification of novel functional elements in the human genome. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003 , 68, 317-22	3.9	1
20	An integrated approach for finding overlooked genes in yeast. <i>Nature Biotechnology</i> , 2002 , 20, 58-63	44.5	97
19	GeneCensus: genome comparisons in terms of metabolic pathway activity and protein family sharing. <i>Nucleic Acids Research</i> , 2002 , 30, 4574-82	20.1	14
18	Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae. <i>Genes and Development</i> , 2002 , 16, 3017-33	12.6	201
17	Molecular fossils in the human genome: identification and analysis of the pseudogenes in chromosomes 21 and 22. <i>Genome Research</i> , 2002 , 12, 272-80	9.7	144
16	SNPs on human chromosomes 21 and 22 -- analysis in terms of protein features and pseudogenes. <i>Pharmacogenomics</i> , 2002 , 3, 393-402	2.6	14
15	Comprehensive analysis of amino acid and nucleotide composition in eukaryotic genomes, comparing genes and pseudogenes. <i>Nucleic Acids Research</i> , 2002 , 30, 2515-23	20.1	102
14	Fast Optimal Genome Tiling with Applications to Microarray Design and Homology Search. <i>Lecture Notes in Computer Science</i> , 2002 , 419-433	0.9	1
13	Integrative data mining: the new direction in bioinformatics. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2001 , 20, 33-40		25

12	SPINE: an integrated tracking database and data mining approach for identifying feasible targets in high-throughput structural proteomics. <i>Nucleic Acids Research</i> , 2001 , 29, 2884-98	20.1	89
11	Global analysis of protein activities using proteome chips. <i>Science</i> , 2001 , 293, 2101-5	33.3	1899
10	Analysis of yeast protein kinases using protein chips. <i>Nature Genetics</i> , 2000 , 26, 283-9	36.3	734
9	Computational Methods and Bioinformatic Tools769-904		
8	Single-cell transcriptome analysis of human, marmoset and mouse embryos reveals common and divergent features of preimplantation development		3
7	Mbd3 and deterministic reprogramming		2
6	Tracking the embryonic stem cell transition from ground state pluripotency		4
5	The Nucleosome Remodelling and Deacetylation complex restricts Mediator access to enhancers to control transcription		1
4	Epigenetic resetting of human pluripotency		1
3	Sox2 modulation increases naïve pluripotency plasticity		1
2	Comparative analysis of neutrophil and monocyte epigenomes		2
1	StemBond hydrogels optimise the mechanical microenvironment for embryonic stem cells		1