Michael A Beer

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Transactivation of miR-34a by p53 BroadlyÂInfluences Gene Expression andÂPromotesÂApoptosis. Molecular Cell, 2007, 26, 745-752.	9.7	1,844
2	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
3	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
4	Comparisons and physics basis of tokamak transport models and turbulence simulations. Physics of Plasmas, 2000, 7, 969-983.	1.9	856
5	Predicting Gene Expression from Sequence. Cell, 2004, 117, 185-198.	28.9	535
6	Enhanced Regulatory Sequence Prediction Using Gapped k-mer Features. PLoS Computational Biology, 2014, 10, e1003711.	3.2	426
7	A method to predict the impact of regulatory variants from DNA sequence. Nature Genetics, 2015, 47, 955-961.	21.4	416
8	Lin-28B transactivation is necessary for Myc-mediated let-7 repression and proliferation. Proceedings of the United States of America, 2009, 106, 3384-3389.	7.1	355
9	Comparison of the transcriptional landscapes between human and mouse tissues. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17224-17229.	7.1	337
10	Quantitative predictions of tokamak energy confinement from firstâ€principles simulations with kinetic effects. Physics of Plasmas, 1995, 2, 2381-2389.	1.9	315
11	Fieldâ€aligned coordinates for nonlinear simulations of tokamak turbulence. Physics of Plasmas, 1995, 2, 2687-2700.	1.9	311
12	A common allele in RPGRIP1L is a modifier of retinal degeneration in ciliopathies. Nature Genetics, 2009, 41, 739-745.	21.4	255
13	Shearing rate of time-dependent E×B flow. Physics of Plasmas, 1999, 6, 922-926.	1.9	248
14	Developments in the gyrofluid approach to Tokamak turbulence simulations. Plasma Physics and Controlled Fusion, 1993, 35, 973-985.	2.1	236
15	Discriminative prediction of mammalian enhancers from DNA sequence. Genome Research, 2011, 21, 2167-2180.	5.5	222
16	Turbulent Fluctuations in TFTR Configurations with Reversed Magnetic Shear. Physical Review Letters, 1996, 77, 3145-3148.	7.8	178
17	Toroidal gyrofluid equations for simulations of tokamak turbulence. Physics of Plasmas, 1996, 3, 4046-4064.	1.9	178
18	Gyrofluid simulations of turbulence suppression in reversed-shear experiments on the Tokamak Fusion Test Reactor, Physics of Plasmas, 1997, 4, 1792-1799	1.9	157

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19	gkmSVM: an R package for gapped-kmer SVM. Bioinformatics, 2016, 32, 2205-2207.	4.1	155
20	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. Nature Genetics, 2018, 50, 1140-1150.	21.4	139
21	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
22	Roles of Electric Field Shear and Shafranov Shift in Sustaining High Confinement in Enhanced Reversed Shear Plasmas on the TFTR Tokamak. Physical Review Letters, 1997, 78, 2972-2975.	7.8	119
23	kmer-SVM: a web server for identifying predictive regulatory sequence features in genomic data sets. Nucleic Acids Research, 2013, 41, W544-W556.	14.5	118
24	Identification of miRâ€21 targets in breast cancer cells using a quantitative proteomic approach. Proteomics, 2009, 9, 1374-1384.	2.2	113
25	Local transport barrier formation and relaxation in reverse-shear plasmas on the Tokamak Fusion Test Reactor. Physics of Plasmas, 1997, 4, 1736-1744.	1.9	109
26	Epigenomic landscapes of retinal rods and cones. ELife, 2016, 5, e11613.	6.0	106
27	Metrics of sequence constraint overlook regulatory sequences in an exhaustive analysis at <i>phox2b</i> . Genome Research, 2008, 18, 252-260.	5.5	101
28	Fusion plasma experiments on TFTR: A 20 year retrospective. Physics of Plasmas, 1998, 5, 1577-1589.	1.9	91
29	Genome-scale screens identify JNK–JUN signaling as a barrier for pluripotency exit and endoderm differentiation. Nature Genetics, 2019, 51, 999-1010.	21.4	90
30	Review of deuterium–tritium results from the Tokamak Fusion Test Reactor. Physics of Plasmas, 1995, 2, 2176-2188.	1.9	89
31	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. Genome Research, 2014, 24, 1932-1944.	5.5	88
32	Whole-Genome Discovery of Transcription Factor Binding Sites by Network-Level Conservation. Genome Research, 2003, 14, 99-108.	5.5	86
33	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73
34	Integration of ChIP-seq and machine learning reveals enhancers and a predictive regulatory sequence vocabulary in melanocytes. Genome Research, 2012, 22, 2290-2301.	5.5	64
35	Overview of TFTR transport studies. Plasma Physics and Controlled Fusion, 1991, 33, 1509-1536.	2.1	59
36	Bounce averaged trapped electron fluid equations for plasma turbulence. Physics of Plasmas, 1996, 3, 4018-4022.	1.9	56

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37	Comparisons of gyrofluid and gyrokinetic simulations*. Physics of Plasmas, 1994, 1, 1461-1468.	1.9	48
38	Epigenetic activation and memory at a <i>TGFB2</i> enhancer in systemic sclerosis. Science Translational Medicine, 2019, 11, .	12.4	47
39	Integration of multiple epigenomic marks improves prediction of variant impact in saturation mutagenesis reporter assay. Human Mutation, 2019, 40, 1280-1291.	2.5	46
40	Local epigenomic state cannot discriminate interacting and non-interacting enhancer–promoter pairs with high accuracy. PLoS Computational Biology, 2018, 14, e1006625.	3.2	45
41	Robust \$\$k\$\$ k -mer frequency estimation using gapped \$\$k\$\$ k -mers. Journal of Mathematical Biology, 2014, 69, 469-500.	1.9	44
42	Overview of DT results from TFTR. Nuclear Fusion, 1995, 35, 1429-1436.	3.5	41
43	Predicting enhancer activity and variant impact using gkm VM. Human Mutation, 2017, 38, 1251-1258.	2.5	40
44	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	2.5	39
45	TFTR DT experiments. Plasma Physics and Controlled Fusion, 1997, 39, B103-B114.	2.1	35
46	ldentification of Novel Phosphorylation Motifs Through an Integrative Computational and Experimental Analysis of the Human Phosphoproteome. Journal of Proteomics and Bioinformatics, 2011, 04, 22-35.	0.4	31
47	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. American Journal of Human Genetics, 2018, 103, 874-892.	6.2	30
48	Comparative studies of core and edge transport barrier dynamics of DIII-D and TFTR tokamak plasmas. Nuclear Fusion, 1999, 39, 1733-1741.	3.5	29
49	Sheared rotation effects on kinetic stability in enhanced confinement tokamak plasmas, and nonlinear dynamics of fluctuations and flows in axisymmetric plasmas. Physics of Plasmas, 1998, 5, 1815-1821.	1.9	28
50	Deuterium–tritium plasmas in novel regimes in the Tokamak Fusion Test Reactor. Physics of Plasmas, 1997, 4, 1714-1724.	1.9	27
51	Loop competition and extrusion model predicts CTCF interaction specificity. Nature Communications, 2021, 12, 1046.	12.8	25
52	Recent D-T results on TFTR. Plasma Physics and Controlled Fusion, 1995, 37, A69-A85.	2.1	22
53	Unanswered questions in ion-temperature-gradient-driven turbulence. Physics Reports, 1997, 283, 121-146.	25.6	20
54	Embryonic loss of human females with partial trisomy 19 identifies region critical for the single active X. PLoS ONE, 2017, 12, e0170403.	2.5	19

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55	Enhancer Predictions and Genome-Wide Regulatory Circuits. Annual Review of Genomics and Human Genetics, 2020, 21, 37-54.	6.2	18
56	Functional Characterization of a Novel Ku70/80 Pause Site at the <i>H19/lgf2</i> Imprinting Control Region. Molecular and Cellular Biology, 2005, 25, 3855-3863.	2.3	16
57	Comparing simulation of plasma turbulence with experiment. Physics of Plasmas, 2002, 9, 177-184.	1.9	15
58	Atomic physics effects on dissipative toroidal drift wave stability. Physics of Fluids B, 1992, 4, 2567-2576.	1.7	13
59	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. Journal of Clinical Investigation, 2020, 130, 3005-3020.	8.2	12
60	Preparations for deuterium–tritium experiments on the Tokamak Fusion Test Reactor*. Physics of Plasmas, 1994, 1, 1560-1567.	1.9	7
61	Integrative epigenomic and high-throughput functional enhancer profiling reveals determinants of enhancer heterogeneity in gastric cancer. Genome Medicine, 2021, 13, 158.	8.2	7
62	Regulatory enhancer profiling of mesenchymal-type gastric cancer reveals subtype-specific epigenomic landscapes and targetable vulnerabilities. Gut, 2023, 72, 226-241.	12.1	6
63	Identification of Predictive Cis-Regulatory Elements Using a Discriminative Objective Function and a Dynamic Search Space. PLoS ONE, 2015, 10, e0140557.	2.5	5
64	Group Normalization for Genomic Data. PLoS ONE, 2012, 7, e38695.	2.5	4
65	Sequence-based correction of barcode bias in massively parallel reporter assays. Genome Research, 2021, 31, 1638-1645.	5.5	3
66	Indicators of Successful Career Transitions from Physical Sciences and Engineering to Biomedical Research. Current Genomics, 2021, 22, 301-305.	1.6	0