Michael A Beer

List of Publications by Year
in descending order

66 papers	12,072 citations	81900 39 h-index	106344 65 g-index
76 all docs	76 docs citations	76 times ranked	16978 citing authors

#	Article	IF	Citations
1	Regulatory enhancer profiling of mesenchymal-type gastric cancer reveals subtype-specific epigenomic landscapes and targetable vulnerabilities. Gut, 2023, 72, 226-241.	12.1	6
2	Loop competition and extrusion model predicts CTCF interaction specificity. Nature Communications, 2021, 12, 1046.	12.8	25
3	Sequence-based correction of barcode bias in massively parallel reporter assays. Genome Research, 2021, 31, 1638-1645.	5.5	3
4	Integrative epigenomic and high-throughput functional enhancer profiling reveals determinants of enhancer heterogeneity in gastric cancer. Genome Medicine, 2021, 13, 158.	8.2	7
5	Indicators of Successful Career Transitions from Physical Sciences and Engineering to Biomedical Research. Current Genomics, 2021, 22, 301-305.	1.6	0
6	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
7	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
8	Enhancer Predictions and Genome-Wide Regulatory Circuits. Annual Review of Genomics and Human Genetics, 2020, 21, 37-54.	6.2	18
9	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. Journal of Clinical Investigation, 2020, 130, 3005-3020.	8.2	12
10	Epigenetic activation and memory at a *TGFB2* enhancer in systemic sclerosis. Science Translational Medicine, 2019, 11, .	12.4	47
11	Integration of multiple epigenomic marks improves prediction of variant impact in saturation mutagenesis reporter assay. Human Mutation, 2019, 40, 1280-1291.	2.5	46
12	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
13	Local epigenomic state cannot discriminate interacting and non-interacting enhancer–promoter pairs with high accuracy. PLoS Computational Biology, 2018, 14, e1006625.	3.2	45
14	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
15	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. Nature Genetics, 2018, 50, 1140-1150.	21.4	139
16	Predicting enhancer activity and variant impact using gkm–SVM. Human Mutation, 2017, 38, 1251-1258.	2.5	40
17	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	2.5	39
18	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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19	gkmSVM: an R package for gapped-kmer SVM. Bioinformatics, 2016, 32, 2205-2207.	4.1	155
20	Epigenomic landscapes of retinal rods and cones. ELife, 2016, 5, e11613.	6.0	106
21	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73
22	A method to predict the impact of regulatory variants from DNA sequence. Nature Genetics, 2015, 47, 955-961.	21.4	416
23	Identification of Predictive Cis-Regulatory Elements Using a Discriminative Objective Function and a Dynamic Search Space. PLoS ONE, 2015, 10, e0140557.	2.5	5
24	Enhanced Regulatory Sequence Prediction Using Gapped k-mer Features. PLoS Computational Biology, 2014, 10, e1003711.	3.2	426
25	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. Genome Research, 2014, 24, 1932-1944.	5.5	88
26	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
27	Robust k k -mer frequency estimation using gapped k k -mers. Journal of Mathematical Biology, 2014, 69, 469-500.	1.9	44
28	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
29	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
30	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
31	Group Normalization for Genomic Data. PLoS ONE, 2012, 7, e38695.	2.5	4
32	Identification 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
33	Discriminative prediction of mammalian enhancers from DNA sequence. Genome Research, 2011, 21, 2167-2180.	5.5	222
34	Lin-28B transactivation is necessary for Myc-mediated let-7 repression and proliferation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3384-3389.	7.1	355
35	Identification of miRâ€21 targets in breast cancer cells using a quantitative proteomic approach. Proteomics, 2009, 9, 1374-1384.	2.2	113
36	A common allele in RPGRIP1L is a modifier of retinal degeneration in ciliopathies. Nature Genetics, 2009, 41, 739-745.	21.4	255

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37	Metrics of sequence constraint overlook regulatory sequences in an exhaustive analysis at <i>phox2b</i>. Genome Research, 2008, 18, 252-260.	5.5	101
38	Transactivation of miR-34a by p53 BroadlyÂInfluences Gene Expression andÂPromotesÂApoptosis. Molecular Cell, 2007, 26, 745-752.	9.7	1,844
39	Functional Characterization of a Novel Ku70/80 Pause Site at the <i>H19/Igf2</i> Imprinting Control Region. Molecular and Cellular Biology, 2005, 25, 3855-3863.	2.3	16
40	Predicting Gene Expression from Sequence. Cell, 2004, 117, 185-198.	28.9	535
41	Whole-Genome Discovery of Transcription Factor Binding Sites by Network-Level Conservation. Genome Research, 2003, 14, 99-108.	5.5	86
42	Comparing simulation of plasma turbulence with experiment. Physics of Plasmas, 2002, 9, 177-184.	1.9	15
43	Comparisons and physics basis of tokamak transport models and turbulence simulations. Physics of Plasmas, 2000, 7, 969-983.	1.9	856
44	Shearing rate of time-dependent EÃ—B flow. Physics of Plasmas, 1999, 6, 922-926.	1.9	248
45	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
46	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
47	Fusion plasma experiments on TFTR: A 20 year retrospective. Physics of Plasmas, 1998, 5, 1577-1589.	1.9	91
48	TFTR DT experiments. Plasma Physics and Controlled Fusion, 1997, 39, B103-B114.	2.1	35
49	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
50	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
51	Deuteriumâ€"tritium plasmas in novel regimes in the Tokamak Fusion Test Reactor. Physics of Plasmas, 1997, 4, 1714-1724.	1.9	27
52	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
53	Unanswered questions in ion-temperature-gradient-driven turbulence. Physics Reports, 1997, 283, 121-146.	25.6	20
54	Turbulent Fluctuations in TFTR Configurations with Reversed Magnetic Shear. Physical Review Letters, 1996, 77, 3145-3148.	7.8	178

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55	Toroidal gyrofluid equations for simulations of tokamak turbulence. Physics of Plasmas, 1996, 3, 4046-4064.	1.9	178
56	Bounce averaged trapped electron fluid equations for plasma turbulence. Physics of Plasmas, 1996, 3, 4018-4022.	1.9	56
57	Recent D-T results on TFTR. Plasma Physics and Controlled Fusion, 1995, 37, A69-A85.	2.1	22
58	Field-aligned coordinates for nonlinear simulations of tokamak turbulence. Physics of Plasmas, 1995, 2, 2687-2700.	1.9	311
59	Review of deuterium–tritium results from the Tokamak Fusion Test Reactor. Physics of Plasmas, 1995, 2, 2176-2188.	1.9	89
60	Quantitative predictions of tokamak energy confinement from first-principles simulations with kinetic effects. Physics of Plasmas, 1995, 2, 2381-2389.	1.9	315
61	Overview of DT results from TFTR. Nuclear Fusion, 1995, 35, 1429-1436.	3.5	41
62	Preparations for deuterium–tritium experiments on the Tokamak Fusion Test Reactor*. Physics of Plasmas, 1994, 1, 1560-1567.	1.9	7
63	Comparisons of gyrofluid and gyrokinetic simulations*. Physics of Plasmas, 1994, 1, 1461-1468.	1.9	48
64	Developments in the gyrofluid approach to Tokamak turbulence simulations. Plasma Physics and Controlled Fusion, 1993, 35, 973-985.	2.1	236
65	Atomic physics effects on dissipative toroidal drift wave stability. Physics of Fluids B, 1992, 4, 2567-2576.	1.7	13
66	Overview of TFTR transport studies. Plasma Physics and Controlled Fusion, 1991, 33, 1509-1536.	2.1	59