David Kenneth Gifford

List of Publications by Year
in descending order

56 papers	6,299 citations	218677 26 h-index	197818 49 g-index
73 all docs	73 docs citations	73 times ranked	9316 citing authors

#	Article	IF	Citations
1	Transcriptional Regulatory Networks in Saccharomyces cerevisiae. Science, 2002, 298, 799-804.	12.6	2,706
2	Discovery of directional and nondirectional pioneer transcription factors by modeling DNase profile magnitude and shape. Nature Biotechnology, 2014, 32, 171-178.	17.5	415
3	Predictable and precise template-free CRISPR editing of pathogenic variants. Nature, 2018, 563, 646-651.	27.8	414
4	Convolutional neural network architectures for predicting DNAâ€“protein binding. Bioinformatics, 2016, 32, i121-i127.	4.1	386
5	High Resolution Genome Wide Binding Event Finding and Motif Discovery Reveals Transcription Factor Spatial Binding Constraints. PLoS Computational Biology, 2012, 8, e1002638.	3.2	261
6	High-throughput mapping of regulatory DNA. Nature Biotechnology, 2016, 34, 167-174.	17.5	217
7	Synergistic binding of transcription factors to cell-specific enhancers programs motor neuron identity. Nature Neuroscience, 2013, 16, 1219-1227.	14.8	195
8	Saltatory remodeling of Hox chromatin in response to rostrocaudal patterning signals. Nature Neuroscience, 2013, 16, 1191-1198.	14.8	140
9	Gene co-regulation by Fezf2 selects neurotransmitter identity and connectivity of corticospinal neurons. Nature Neuroscience, 2014, 17, 1046-1054.	14.8	121
10	A Peninsular Structure Coordinates Asynchronous Differentiation with Morphogenesis to Generate Pancreatic Islets. Cell, 2019, 176, 790-804.e13.	28.9	103
11	Wnt Signaling Separates the Progenitor and Endocrine Compartments during Pancreas Development. Cell Reports, 2019, 27, 2281-2291.e5.	6.4	100
12	MARIS: Method for Analyzing RNA following Intracellular Sorting. PLoS ONE, 2014, 9, e89459.	2.5	93
13	Antibody complementarity determining region design using high-capacity machine learning. Bioinformatics, 2020, 36, 2126-2133.	4.1	92
14	A distant trophoblast-specific enhancer controls HLA-G expression at the maternalâ€“fetal interface. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5364-5369.	7.1	90
15	Predicting the impact of non-coding variants on DNA methylation. Nucleic Acids Research, 2017, 45, e99-e99.	14.5	81
16	An Integrated Model of Multiple-Condition ChIP-Seq Data Reveals Predeterminants of Cdx2 Binding. PLoS Computational Biology, 2014, 10, e1003501.	3.2	78
17	Expression of Terminal Effector Genes in Mammalian Neurons Is Maintained by a Dynamic Relay of Transient Enhancers. Neuron, 2016, 92, 1252-1265.	8.1	70
18	Computationally Optimized SARS-CoV-2 MHC Class I and II Vaccine Formulations Predicted to Target Human Haplotype Distributions. Cell Systems, 2020, 11, 131-144.e6.	6.2	50

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19	Quantification of Uncertainty in Peptide-MHC Binding Prediction Improves High-Affinity Peptide Selection for Therapeutic Design. Cell Systems, 2019, 9, 159-166.e3.	6.2	46
20	Discovering homotypic binding events at high spatial resolution. Bioinformatics, 2010, 26, 3028-3034.	4.1	43
21	A novel k-mer set memory (KSM) motif representation improves regulatory variant prediction. Genome Research, 2018, 28, 891-900.	5.5	42
22	GERV: a statistical method for generative evaluation of regulatory variants for transcription factor binding. Bioinformatics, 2016, 32, 490-496.	4.1	40
23	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	2.5	39
24	Interactions between chromosomal and nonchromosomal elements reveal missing heritability. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7719-7722.	7.1	37
25	Predicted Cellular Immunity Population Coverage Gaps for SARS-CoV-2 Subunit Vaccines and Their Augmentation by Compact Peptide Sets. Cell Systems, 2021, 12, 102-107.e4.	6.2	35
26	Cas9 Functionally Opens Chromatin. PLoS ONE, 2016, 11, e0152683.	2.5	34
27	Identification of new branch points and unconventional introns in Saccharomyces cerevisiae. Rna, 2016, 22, 1522-1534.	3.5	32
28	DeepLigand: accurate prediction of MHC class I ligands using peptide embedding. Bioinformatics, 2019, 35, i278-i283.	4.1	32
29	Modular combinatorial binding among human trans-acting factors reveals direct and indirect factor binding. BMC Genomics, 2017, 18, 45.	2.8	27
30	Generative modeling of single-cell time series with PRESCIENT enables prediction of cell trajectories with interventions. Nature Communications, 2021, 12, 3222.	12.8	27
31	An expansion of the non-coding genome and its regulatory potential underlies vertebrate neuronal diversity. Neuron, 2022, 110, 70-85.e6.	8.1	22
32	A synergistic DNA logic predicts genome-wide chromatin accessibility. Genome Research, 2016, 26, 1430-1440.	5.5	18
33	Universal Count Correction for High-Throughput Sequencing. PLoS Computational Biology, 2014, 10, e1003494.	3.2	17
34	Identification of determinants of differential chromatin accessibility through a massively parallel genome-integrated reporter assay. Genome Research, 2020, 30, 1468-1480.	5.5	16
35	Accurate eQTL prioritization with an ensembleâ€based framework. Human Mutation, 2017, 38, 1259-1265.	2.5	15
36	Small molecule inhibition of ATM kinase increases CRISPR-Cas9 1-bp insertion frequency. Nature Communications, 2021, 12, 5111.	12.8	15

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37	Chemogenetic System Demonstrates That Cas9 Longevity Impacts Genome Editing Outcomes. ACS Central Science, 2020, 6, 2228-2237.	11.3	14
38	Comprehensive Mapping of Key Regulatory Networks that Drive Oncogene Expression. Cell Reports, 2020, 33, 108426.	6.4	14
39	Visualizing complex feature interactions and feature sharing in genomic deep neural networks. BMC Bioinformatics, 2019, 20, 401.	2.6	13
40	A Multiplexed Barcodelet Single-Cell RNA-Seq Approach Elucidates Combinatorial Signaling Pathways that Drive ESC Differentiation. Cell Stem Cell, 2020, 26, 938-950.e6.	11.1	12
41	A high-throughput yeast display approach to profile pathogen proteomes for MHC-II binding. ELife, 0, 11, .	6.0	12
42	IDR2D identifies reproducible genomic interactions. Nucleic Acids Research, 2020, 48, e31-e31.	14.5	10
43	Ranking reprogramming factors for cell differentiation. Nature Methods, 2022, 19, 812-822.	19.0	10
44	Discovering differential genome sequence activity with interpretable and efficient deep learning. PLoS Computational Biology, 2021, 17, e1009282.	3.2	9
45	High resolution discovery of chromatin interactions. Nucleic Acids Research, 2019, 47, e35-e35.	14.5	8
46	Machine learning optimization of peptides for presentation by class II MHCs. Bioinformatics, 2021, 37, 3160-3167.	4.1	8
47	Machine learning based CRISPR gRNA design for therapeutic exon skipping. PLoS Computational Biology, 2021, 17, e1008605.	3.2	7
48	Differential chromatin profiles partially determine transcription factor binding. PLoS ONE, 2017, 12, e0179411.	2.5	5
49	spatzie: an R package for identifying significant transcription factor motif co-enrichment from enhancerâ€“promoter interactions. Nucleic Acids Research, 2022, 50, e52-e52.	14.5	2
50	Detection of gene cis-regulatory element perturbations in single-cell transcriptomes. PLoS Computational Biology, 2021, 17, e1008789.	3.2	0
51	seqgra: principled selection of neural network architectures for genomics prediction tasks. Bioinformatics, 2022, 38, 2381-2388.	4.1	0
52	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
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55	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
56	Ultra high diversity factorizable libraries for efficient therapeutic discovery. Genome Research, 0, , gr.276593.122.	5.5	0