

David Kenneth Gifford

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7999211/publications.pdf>

Version: 2024-02-01

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	An expansion of the non-coding genome and its regulatory potential underlies vertebrate neuronal diversity. <i>Neuron</i> , 2022, 110, 70-85.e6.	8.1	22
2	spatzie: an R package for identifying significant transcription factor motif co-enrichment from enhancerâ€“promoter interactions. <i>Nucleic Acids Research</i> , 2022, 50, e52-e52.	14.5	2
3	seqgra: principled selection of neural network architectures for genomics prediction tasks. <i>Bioinformatics</i> , 2022, 38, 2381-2388.	4.1	0
4	Ranking reprogramming factors for cell differentiation. <i>Nature Methods</i> , 2022, 19, 812-822.	19.0	10
5	Predicted Cellular Immunity Population Coverage Gaps for SARS-CoV-2 Subunit Vaccines and Their Augmentation by Compact Peptide Sets. <i>Cell Systems</i> , 2021, 12, 102-107.e4.	6.2	35
6	Machine learning based CRISPR gRNA design for therapeutic exon skipping. <i>PLoS Computational Biology</i> , 2021, 17, e1008605.	3.2	7
7	Detection of gene cis-regulatory element perturbations in single-cell transcriptomes. <i>PLoS Computational Biology</i> , 2021, 17, e1008789.	3.2	0
8	Machine learning optimization of peptides for presentation by class II MHCs. <i>Bioinformatics</i> , 2021, 37, 3160-3167.	4.1	8
9	Generative modeling of single-cell time series with PRESCIENT enables prediction of cell trajectories with interventions. <i>Nature Communications</i> , 2021, 12, 3222.	12.8	27
10	Discovering differential genome sequence activity with interpretable and efficient deep learning. <i>PLoS Computational Biology</i> , 2021, 17, e1009282.	3.2	9
11	Small molecule inhibition of ATM kinase increases CRISPR-Cas9 1-bp insertion frequency. <i>Nature Communications</i> , 2021, 12, 5111.	12.8	15
12	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
13	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
14	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
15	Machine learning based CRISPR gRNA design for therapeutic exon skipping. , 2021, 17, e1008605.		0
16	Antibody complementarity determining region design using high-capacity machine learning. <i>Bioinformatics</i> , 2020, 36, 2126-2133.	4.1	92
17	Identification of determinants of differential chromatin accessibility through a massively parallel genome-integrated reporter assay. <i>Genome Research</i> , 2020, 30, 1468-1480.	5.5	16
18	Chemogenetic System Demonstrates That Cas9 Longevity Impacts Genome Editing Outcomes. <i>ACS Central Science</i> , 2020, 6, 2228-2237.	11.3	14

#	ARTICLE	IF	CITATIONS
19	Comprehensive Mapping of Key Regulatory Networks that Drive Oncogene Expression. <i>Cell Reports</i> , 2020, 33, 108426.	6.4	14
20	Computationally Optimized SARS-CoV-2 MHC Class I and II Vaccine Formulations Predicted to Target Human Haplotype Distributions. <i>Cell Systems</i> , 2020, 11, 131-144.e6.	6.2	50
21	A Multiplexed Barcodelet Single-Cell RNA-Seq Approach Elucidates Combinatorial Signaling Pathways that Drive ESC Differentiation. <i>Cell Stem Cell</i> , 2020, 26, 938-950.e6.	11.1	12
22	IDR2D identifies reproducible genomic interactions. <i>Nucleic Acids Research</i> , 2020, 48, e31-e31.	14.5	10
23	DeepLigand: accurate prediction of MHC class I ligands using peptide embedding. <i>Bioinformatics</i> , 2019, 35, i278-i283.	4.1	32
24	Visualizing complex feature interactions and feature sharing in genomic deep neural networks. <i>BMC Bioinformatics</i> , 2019, 20, 401.	2.6	13
25	Quantification of Uncertainty in Peptide-MHC Binding Prediction Improves High-Affinity Peptide Selection for Therapeutic Design. <i>Cell Systems</i> , 2019, 9, 159-166.e3.	6.2	46
26	Wnt Signaling Separates the Progenitor and Endocrine Compartments during Pancreas Development. <i>Cell Reports</i> , 2019, 27, 2281-2291.e5.	6.4	100
27	High resolution discovery of chromatin interactions. <i>Nucleic Acids Research</i> , 2019, 47, e35-e35.	14.5	8
28	A Peninsular Structure Coordinates Asynchronous Differentiation with Morphogenesis to Generate Pancreatic Islets. <i>Cell</i> , 2019, 176, 790-804.e13.	28.9	103
29	A novel <i>k</i> -mer set memory (KSM) motif representation improves regulatory variant prediction. <i>Genome Research</i> , 2018, 28, 891-900.	5.5	42
30	Predictable and precise template-free CRISPR editing of pathogenic variants. <i>Nature</i> , 2018, 563, 646-651.	27.8	414
31	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	2.5	39
32	Accurate eQTL prioritization with an ensemble-based framework. <i>Human Mutation</i> , 2017, 38, 1259-1265.	2.5	15
33	Predicting the impact of non-coding variants on DNA methylation. <i>Nucleic Acids Research</i> , 2017, 45, e99-e99.	14.5	81
34	Modular combinatorial binding among human trans-acting factors reveals direct and indirect factor binding. <i>BMC Genomics</i> , 2017, 18, 45.	2.8	27
35	Differential chromatin profiles partially determine transcription factor binding. <i>PLoS ONE</i> , 2017, 12, e0179411.	2.5	5
36	Cas9 Functionally Opens Chromatin. <i>PLoS ONE</i> , 2016, 11, e0152683.	2.5	34

#	ARTICLE	IF	CITATIONS
37	Expression of Terminal Effector Genes in Mammalian Neurons Is Maintained by a Dynamic Relay of Transient Enhancers. <i>Neuron</i> , 2016, 92, 1252-1265.	8.1	70
38	A distant trophoblast-specific enhancer controls HLA-G expression at the maternal-fetal interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5364-5369.	7.1	90
39	Identification of new branch points and unconventional introns in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2016, 22, 1522-1534.	3.5	32
40	A synergistic DNA logic predicts genome-wide chromatin accessibility. <i>Genome Research</i> , 2016, 26, 1430-1440.	5.5	18
41	Convolutional neural network architectures for predicting DNA-protein binding. <i>Bioinformatics</i> , 2016, 32, i121-i127.	4.1	386
42	High-throughput mapping of regulatory DNA. <i>Nature Biotechnology</i> , 2016, 34, 167-174.	17.5	217
43	GERV: a statistical method for generative evaluation of regulatory variants for transcription factor binding. <i>Bioinformatics</i> , 2016, 32, 490-496.	4.1	40
44	MARIS: Method for Analyzing RNA following Intracellular Sorting. <i>PLoS ONE</i> , 2014, 9, e89459.	2.5	93
45	An Integrated Model of Multiple-Condition ChIP-Seq Data Reveals Predeterminants of Cdx2 Binding. <i>PLoS Computational Biology</i> , 2014, 10, e1003501.	3.2	78
46	Universal Count Correction for High-Throughput Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003494.	3.2	17
47	Gene co-regulation by Fezf2 selects neurotransmitter identity and connectivity of corticospinal neurons. <i>Nature Neuroscience</i> , 2014, 17, 1046-1054.	14.8	121
48	Discovery of directional and nondirectional pioneer transcription factors by modeling DNase profile magnitude and shape. <i>Nature Biotechnology</i> , 2014, 32, 171-178.	17.5	415
49	Interactions between chromosomal and nonchromosomal elements reveal missing heritability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7719-7722.	7.1	37
50	Synergistic binding of transcription factors to cell-specific enhancers programs motor neuron identity. <i>Nature Neuroscience</i> , 2013, 16, 1219-1227.	14.8	195
51	Saltatory remodeling of Hox chromatin in response to rostrocaudal patterning signals. <i>Nature Neuroscience</i> , 2013, 16, 1191-1198.	14.8	140
52	High Resolution Genome Wide Binding Event Finding and Motif Discovery Reveals Transcription Factor Spatial Binding Constraints. <i>PLoS Computational Biology</i> , 2012, 8, e1002638.	3.2	261
53	Discovering homotypic binding events at high spatial resolution. <i>Bioinformatics</i> , 2010, 26, 3028-3034.	4.1	43
54	Transcriptional Regulatory Networks in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002, 298, 799-804.	12.6	2,706

#	ARTICLE	IF	CITATIONS
55	Ultra high diversity factorizable libraries for efficient therapeutic discovery. Genome Research, 0, , gr.276593.122.	5.5	0
56	A high-throughput yeast display approach to profile pathogen proteomes for MHC-II binding. ELife, 0, 11, .	6.0	12