

Denis C Bauer

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

3,103
citations

257450

24
h-index

175258

52
g-index

71
all docs

71
docs citations

71
times ranked

7119
citing authors

#	ARTICLE	IF	CITATIONS
1	Isling: A Tool for Detecting Integration of Wild-Type Viruses and Clinical Vectors. <i>Journal of Molecular Biology</i> , 2022, 434, 167408.	4.2	2
2	A bioinformatic pipeline for simulating viral integration data. <i>Data in Brief</i> , 2022, 42, 108161.	1.0	1
3	Data-driven platform for identifying variants of interest in COVID-19 virus. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2942-2950.	4.1	2
4	Evidence for polygenic and oligogenic basis of Australian sporadic amyotrophic lateral sclerosis. <i>Journal of Medical Genetics</i> , 2021, 58, 87-95.	3.2	48
5	Domain-specific introduction to machine learning terminology, pitfalls and opportunities in CRISPR-based gene editing. <i>Briefings in Bioinformatics</i> , 2021, 22, 308-314.	6.5	12
6	Interoperable medical data: The missing link for understanding COVID-19. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 1753-1760.	3.0	21
7	INSIDER: alignment-free detection of foreign DNA sequences. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3810-3816.	4.1	2
8	GOANA: A Universal High-Throughput Web Service for Assessing and Comparing the Outcome and Efficiency of Genome Editing Experiments. <i>CRISPR Journal</i> , 2021, 4, 243-252.	2.9	3
9	Genetic analysis of GLT8D1 and ARPP21 in Australian familial and sporadic amyotrophic lateral sclerosis. <i>Neurobiology of Aging</i> , 2021, 101, 297.e9-297.e11.	3.1	6
10	Genetic Analysis of Tryptophan Metabolism Genes in Sporadic Amyotrophic Lateral Sclerosis. <i>Frontiers in Immunology</i> , 2021, 12, 701550.	4.8	8
11	Fast and accurate exhaustive higher-order epistasis search with BitEpi. <i>Scientific Reports</i> , 2021, 11, 15923.	3.3	11
12	Optimized nickase- and nuclease-based prime editing in human and mouse cells. <i>Nucleic Acids Research</i> , 2021, 49, 10785-10795.	14.5	47
13	A comparative study of multi-omics integration tools for cancer driver gene identification and tumour subtyping. <i>Briefings in Bioinformatics</i> , 2020, 21, 1920-1936.	6.5	51
14	VariantSpark: Cloud-based machine learning for association study of complex phenotype and large-scale genomic data. <i>GigaScience</i> , 2020, 9, .	6.4	10
15	A Navigation System for Base Editing: Are We There Yet?. <i>CRISPR Journal</i> , 2020, 3, 224-225.	2.9	0
16	Identity by descent analysis identifies founder events and links SOD1 familial and sporadic ALS cases. <i>Npj Genomic Medicine</i> , 2020, 5, 32.	3.8	20
17	Genetic and immunopathological analysis of CHCHD10 in Australian amyotrophic lateral sclerosis and frontotemporal dementia and transgenic TDP-43 mice. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2020, 91, 162-171.	1.9	8
18	Supporting pandemic response using genomics and bioinformatics: A case study on the emergent SARS-CoV-2 outbreak. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 1453-1462.	3.0	46

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19	Host Porphobilinogen Deaminase Deficiency Confers Malaria Resistance in <i>Plasmodium chabaudi</i> but Not in <i>Plasmodium berghei</i> or <i>Plasmodium falciparum</i> During Intraerythrocytic Growth. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 464.	3.9	2
20	Artificial Intelligence and Machine Learning in Bioinformatics. , 2019, , 272-286.		11
21	VARSCOT: variant-aware detection and scoring enables sensitive and personalized off-target detection for CRISPR-Cas9. <i>BMC Biotechnology</i> , 2019, 19, 40.	3.3	9
22	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. <i>Scientific Reports</i> , 2019, 9, 9511.	3.3	24
23	Monozygotic twins and triplets discordant for amyotrophic lateral sclerosis display differential methylation and gene expression. <i>Scientific Reports</i> , 2019, 9, 8254.	3.3	36
24	Unlocking HDR-mediated nucleotide editing by identifying high-efficiency target sites using machine learning. <i>Scientific Reports</i> , 2019, 9, 2788.	3.3	31
25	Evaluation of computational programs to predict HLA genotypes from genomic sequencing data. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw097.	6.5	60
26	High Activity Target-Site Identification Using Phenotypic Independent CRISPR-Cas9 Core Functionality. <i>CRISPR Journal</i> , 2018, 1, 182-190.	2.9	43
27	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. <i>Neuron</i> , 2018, 97, 1268-1283.e6.	8.1	517
28	The Current State and Future of CRISPR-Cas9 gRNA Design Tools. <i>Frontiers in Pharmacology</i> , 2018, 9, 749.	3.5	103
29	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. <i>Nature Communications</i> , 2017, 8, 14774.	12.8	114
30	Ankyrin-1 Gene Exhibits Allelic Heterogeneity in Conferring Protection Against Malaria. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3133-3144.	1.8	3
31	Genetic and Pathological Assessment of hnRNPA1, hnRNPA2/B1, and hnRNPA3 in Familial and Sporadic Amyotrophic Lateral Sclerosis. <i>Neurodegenerative Diseases</i> , 2017, 17, 304-312.	1.4	27
32	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <i>Genome Research</i> , 2016, 26, 719-731.	5.5	312
33	Adenosine monophosphate deaminase 3 activation shortens erythrocyte half-life and provides malaria resistance in mice. <i>Blood</i> , 2016, 128, 1290-1301.	1.4	32
34	A novel ENU-induced ankyrin-1 mutation impairs parasite invasion and increases erythrocyte clearance during malaria infection in mice. <i>Scientific Reports</i> , 2016, 6, 37197.	3.3	8
35	Targeted next-generation sequencing of 22 mismatch repair genes identifies Lynch syndrome families. <i>Cancer Medicine</i> , 2016, 5, 929-941.	2.8	25
36	VariantSpark: population scale clustering of genotype information. <i>BMC Genomics</i> , 2015, 16, 1052.	2.8	24

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37	Genome-wide analysis of chemically induced mutations in mouse in phenotype-driven screens. <i>BMC Genomics</i> , 2015, 16, 866.	2.8	21
38	Cpipe: a shared variant detection pipeline designed for diagnostic settings. <i>Genome Medicine</i> , 2015, 7, 68.	8.2	78
39	Early life events influence whole-of-life metabolic health via gut microflora and gut permeability. <i>Critical Reviews in Microbiology</i> , 2015, 41, 326-340.	6.1	97
40	Gut permeability, its interaction with gut microflora and effects on metabolic health are mediated by the lymphatics system, liver and bile acid. <i>Future Microbiology</i> , 2015, 10, 1339-1353.	2.0	39
41	Mutation analysis of MATR3 in Australian familial amyotrophic lateral sclerosis. <i>Neurobiology of Aging</i> , 2015, 36, 1602.e1-1602.e2.	3.1	13
42	A Comparative Study of Techniques for Differential Expression Analysis on RNA-Seq Data. <i>PLoS ONE</i> , 2014, 9, e103207.	2.5	195
43	NGSANE: a lightweight production informatics framework for high-throughput data analysis. <i>Bioinformatics</i> , 2014, 30, 1471-1472.	4.1	22
44	Genomics and personalised whole-of-life healthcare. <i>Trends in Molecular Medicine</i> , 2014, 20, 479-486.	6.7	18
45	Blue: correcting sequencing errors using consensus and context. <i>Bioinformatics</i> , 2014, 30, 2723-2732.	4.1	68
46	Triplex-Inspector: an analysis tool for triplex-mediated targeting of genomic loci. <i>Bioinformatics</i> , 2013, 29, 1895-1897.	4.1	29
47	Abstract LB-237: Human and microbial transcriptomics from lean and obese individuals with colorectal cancer: A comparison of Total and Poly A RNA sequencing from clinical samples.. , 2013, , .		0
48	Hybridization-based reconstruction of small non-coding RNA transcripts from deep sequencing data. <i>Nucleic Acids Research</i> , 2012, 40, 7633-7643.	14.5	10
49	Triplexator: Detecting nucleic acid triple helices in genomic and transcriptomic data. <i>Genome Research</i> , 2012, 22, 1372-1381.	5.5	181
50	Sorting the nuclear proteome. <i>Bioinformatics</i> , 2011, 27, i7-i14.	4.1	18
51	Predicting SUMOylation sites in developmental transcription factors of <i>Drosophila melanogaster</i> . <i>Neurocomputing</i> , 2010, 73, 2300-2307.	5.9	2
52	Dual-functioning transcription factors in the developmental gene network of <i>Drosophila melanogaster</i> . <i>BMC Bioinformatics</i> , 2010, 11, 366.	2.6	19
53	Assigning roles to DNA regulatory motifs using comparative genomics. <i>Bioinformatics</i> , 2010, 26, 860-866.	4.1	155
54	Optimizing static thermodynamic models of transcriptional regulation. <i>Bioinformatics</i> , 2009, 25, 1640-1646.	4.1	7

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55	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
56	Studying the functional conservation of cis-regulatory modules and their transcriptional output. <i>BMC Bioinformatics</i> , 2008, 9, 220.	2.6	9
57	STREAM: Static Thermodynamic REgulAtory Model of transcription. <i>Bioinformatics</i> , 2008, 24, 2544-2545.	4.1	2
58	Predicting SUMOylation Sites. <i>Lecture Notes in Computer Science</i> , 2008, , 28-40.	1.3	4
59	STAR: predicting recombination sites from amino acid sequence. <i>BMC Bioinformatics</i> , 2006, 7, 437.	2.6	6
60	Predicting Structural Disruption of Proteins Caused by Crossover. , 2005, , .		0