# Denis C Bauer

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. Neuron, 2018, 97, 1268-1283.e6. | 8.1 | 517 |
| 2 | The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562. | 21.4 | 408 |
| 3 | Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. Genome Research, 2016, 26, 719-731. | 5.5 | 312 |
| 4 | A Comparative Study of Techniques for Differential Expression Analysis on RNA-Seq Data. PLoS ONE, 2014, 9, e103207. | 2.5 | 195 |
| 5 | Triplexator: Detecting nucleic acid triple helices in genomic and transcriptomic data. Genome Research, 2012, 22, 1372-1381. | 5.5 | 181 |
| 6 | Assigning roles to DNA regulatory motifs using comparative genomics. Bioinformatics, 2010, 26, 860-866. | 4.1 | 155 |
| 7 | Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. Nature Communications, 2017, 8, 14774. | 12.8 | 114 |
| 8 | The Current State and Future of CRISPR-Cas9 gRNA Design Tools. Frontiers in Pharmacology, 2018, 9, 749. | 3.5 | 103 |
| 9 | Early life events influence whole-of-life metabolic health via gut microflora and gut permeability. Critical Reviews in Microbiology, 2015, 41, 326-340. | 6.1 | 97 |
| 10 | Cpipe: a shared variant detection pipeline designed for diagnostic settings. Genome Medicine, 2015, 7, 68. | 8.2 | 78 |
| 11 | Blue: correcting sequencing errors using consensus and context. Bioinformatics, 2014, 30, 2723-2732. | 4.1 | 68 |
| 12 | Evaluation of computational programs to predict HLA genotypes from genomic sequencing data. Briefings in Bioinformatics, 2018, 19, bbw097. | 6.5 | 60 |
| 13 | A comparative study of multi-omics integration tools for cancer driver gene identification and tumour subtyping. Briefings in Bioinformatics, 2020, 21, 1920-1936. | 6.5 | 51 |
| 14 | Evidence for polygenic and oligogenic basis of Australian sporadic amyotrophic lateral sclerosis. Journal of Medical Genetics, 2021, 58, 87-95. | 3.2 | 48 |
| 15 | Optimized nickase- and nuclease-based prime editing in human and mouse cells. Nucleic Acids Research, 2021, 49, 10785-10795. | 14.5 | 47 |
| 16 | Supporting pandemic response using genomics and bioinformatics: A case study on the emergent SARSâ€CoVâ€2 outbreak. Transboundary and Emerging Diseases, 2020, 67, 1453-1462. | 3.0 | 46 |
| 17 | High Activity Target-Site Identification Using Phenotypic Independent CRISPR-Cas9 Core Functionality. CRISPR Journal, 2018, 1, 182-190. | 2.9 | 43 |
| 18 | Gut permeability, its interaction with gut microflora and effects on metabolic health are mediated by the lymphatics system, liver and bile acid. Future Microbiology, 2015, 10, 1339-1353. | 2.0 | 39 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Monozygotic twins and triplets discordant for amyotrophic lateral sclerosis display differential methylation and gene expression. Scientific Reports, 2019, 9, 8254. | 3.3 | 36 |
| 20 | Adenosine monophosphate deaminase 3 activation shortens erythrocyte half-life and provides malaria resistance in mice. Blood, 2016, 128, 1290-1301. | 1.4 | 32 |
| 21 | Unlocking HDR-mediated nucleotide editing by identifying high-efficiency target sites using machine learning. Scientific Reports, 2019, 9, 2788. | 3.3 | 31 |
| 22 | Triplex-Inspector: an analysis tool for triplex-mediated targeting of genomic loci. Bioinformatics, 2013, 29, 1895-1897. | 4.1 | 29 |
| 23 | Genetic and Pathological Assessment of hnRNPA1, hnRNPA2/B1, and hnRNPA3 in Familial and Sporadic Amyotrophic Lateral Sclerosis. Neurodegenerative Diseases, 2017, 17, 304-312. | 1.4 | 27 |
| 24 | Targeted nextâ€generation sequencing of 22 mismatch repair genes identifies Lynch syndrome families. Cancer Medicine, 2016, 5, 929-941. | 2.8 | 25 |
| 25 | VariantSpark: population scale clustering of genotype information. BMC Genomics, 2015, 16, 1052. | 2.8 | 24 |
| 26 | Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. Scientific Reports, 2019, 9, 9511. | 3.3 | 24 |
| 27 | NGSANE: a lightweight production informatics framework for high-throughput data analysis. Bioinformatics, 2014, 30, 1471-1472. | 4.1 | 22 |
| 28 | Genome-wide analysis of chemically induced mutations in mouse in phenotype-driven screens. BMC Genomics, 2015, 16, 866. | 2.8 | 21 |
| 29 | Interoperable medical data: The missing link for understanding COVIDâ€19. Transboundary and Emerging Diseases, 2021, 68, 1753-1760. | 3.0 | 21 |
| 30 | Identity by descent analysis identifies founder events and links SOD1 familial and sporadic ALS cases. Npj Genomic Medicine, 2020, 5, 32. | 3.8 | 20 |
| 31 | Dual-functioning transcription factors in the developmental gene network of Drosophila melanogaster. BMC Bioinformatics, 2010, 11, 366. | 2.6 | 19 |
| 32 | Sorting the nuclear proteome. Bioinformatics, 2011, 27, i7-i14. | 4.1 | 18 |
| 33 | Genomics and personalised whole-of-life healthcare. Trends in Molecular Medicine, 2014, 20, 479-486. | 6.7 | 18 |
| 34 | Mutation analysis of MATR3 in Australian familial amyotrophic lateral sclerosis. Neurobiology of Aging, 2015, 36, 1602.e1-1602.e2. | 3.1 | 13 |
| 35 | Domain-specific introduction to machine learning terminology, pitfalls and opportunities in CRISPR-based gene editing. Briefings in Bioinformatics, 2021, 22, 308-314. | 6.5 | 12 |
| 36 | Artificial Intelligence and Machine Learning in Bioinformatics. , 2019, , 272-286. | | 11 |

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|---|---|---|---|
| 37 | Fast and accurate exhaustive higher-order epistasis search with BitEpi. Scientific Reports, 2021, 11, 15923. | 3.3 | 11 |
| 38 | Hybridization-based reconstruction of small non-coding RNA transcripts from deep sequencing data. Nucleic Acids Research, 2012, 40, 7633-7643. | 14.5 | 10 |
| 39 | VariantSpark: Cloud-based machine learning for association study of complex phenotype and large-scale genomic data. GigaScience, 2020, 9, . | 6.4 | 10 |
| 40 | Studying the functional conservation of cis-regulatory modules and their transcriptional output. BMC Bioinformatics, 2008, 9, 220. | 2.6 | 9 |
| 41 | VARSCOT: variant-aware detection and scoring enables sensitive and personalized off-target detection for CRISPR-Cas9. BMC Biotechnology, 2019, 19, 40. | 3.3 | 9 |
| 42 | A novel ENU-induced ankyrin-1 mutation impairs parasite invasion and increases erythrocyte clearance during malaria infection in mice. Scientific Reports, 2016, 6, 37197. | 3.3 | 8 |
| 43 | Genetic and immunopathological analysis of CHCHD10 in Australian amyotrophic lateral sclerosis and frontotemporal dementia and transgenic TDP-43 mice. Journal of Neurology, Neurosurgery and Psychiatry, 2020, 91, 162-171. | 1.9 | 8 |
| 44 | Genetic Analysis of Tryptophan Metabolism Genes in Sporadic Amyotrophic Lateral Sclerosis. Frontiers in Immunology, 2021, 12, 701550. | 4.8 | 8 |
| 45 | Optimizing static thermodynamic models of transcriptional regulation. Bioinformatics, 2009, 25, 1640-1646. | 4.1 | 7 |
| 46 | STAR: predicting recombination sites from amino acid sequence. BMC Bioinformatics, 2006, 7, 437. | 2.6 | 6 |
| 47 | Genetic analysis of GLT8D1 and ARPP21 in Australian familial and sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2021, 101, 297.e9-297.e11. | 3.1 | 6 |
| 48 | Predicting SUMOylation Sites. Lecture Notes in Computer Science, 2008, , 28-40. | 1.3 | 4 |
| 49 | Ankyrin-1 Gene Exhibits Allelic Heterogeneity in Conferring Protection Against Malaria. G3: Genes, Genomes, Genetics, 2017, 7, 3133-3144. | 1.8 | 3 |
| 50 | GOANA: A Universal High-Throughput Web Service for Assessing and Comparing the Outcome and Efficiency of Genome Editing Experiments. CRISPR Journal, 2021, 4, 243-252. | 2.9 | 3 |
| 51 | STREAM: Static Thermodynamic REgulAtory Model of transcription. Bioinformatics, 2008, 24, 2544-2545. | 4.1 | 2 |
| 52 | Predicting SUMOylation sites in developmental transcription factors of Drosophila melanogaster. Neurocomputing, 2010, 73, 2300-2307. | 5.9 | 2 |
| 53 | INSIDER: alignment-free detection of foreign DNA sequences. Computational and Structural Biotechnology Journal, 2021, 19, 3810-3816. | 4.1 | 2 |
| 54 | Host Porphobilinogen Deaminase Deficiency Confers Malaria Resistance in Plasmodium chabaudi but Not in Plasmodium berghei or Plasmodium falciparum During Intraerythrocytic Growth. Frontiers in Cellular and Infection Microbiology, 2020, 10, 464. | 3.9 | 2 |

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|---|---|---|---|
| 55 | Isling: A Tool for Detecting Integration of Wild-Type Viruses and Clinical Vectors. Journal of Molecular Biology, 2022, 434, 167408. | 4.2 | 2 |
| 56 | Data-driven platform for identifying variants of interest in COVID-19 virus. Computational and Structural Biotechnology Journal, 2022, 20, 2942-2950. | 4.1 | 2 |
| 57 | A bioinformatic pipeline for simulating viral integration data. Data in Brief, 2022, 42, 108161. | 1.0 | 1 |
| 58 | Predicting Structural Disruption of Proteins Caused by Crossover. , 2005, , . | | 0 |
| 59 | A Navigation System for Base Editing: Are We There Yet?. CRISPR Journal, 2020, 3, 224-225. | 2.9 | 0 |
| 60 | 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 |