

Kevin Judd McKernan

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

34,649
citations

218381

26
h-index

329751

37
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59
all docs

59
docs citations

59
times ranked

40414
citing authors

#	ARTICLE	IF	CITATIONS
1	A draft sequence reference of the <i>Psilocybe cubensis</i> genome. F1000Research, 2021, 10, 281.	0.8	1
2	A draft reference assembly of the <i>Psilocybe cubensis</i> genome. F1000Research, 2021, 10, 281.	0.8	1
3	Whole genome sequencing of colonies derived from cannabis flowers and the impact of media selection on benchmarking total yeast and mold detection tools. F1000Research, 2021, 10, 624.	0.8	5
4	Whole genome sequencing of colonies derived from cannabis flowers and the impact of media selection on benchmarking total yeast and mold detection tools. F1000Research, 2021, 10, 624.	0.8	11
5	Genomic characterization of the complete terpene synthase gene family from <i>Cannabis sativa</i> . PLoS ONE, 2019, 14, e0222363.	1.1	47
6	Contaminants of Concern in Cannabis: Microbes, Heavy Metals and Pesticides. , 2017, , 457-474.		33
7	Rare genetic variants in the endocannabinoid system genes CNR1 and DAGLA are associated with neurological phenotypes in humans. PLoS ONE, 2017, 12, e0187926.	1.1	55
8	Metagenomic analysis of medicinal Cannabis samples; pathogenic bacteria, toxigenic fungi, and beneficial microbes grow in culture-based yeast and mold tests. F1000Research, 2016, 5, 2471.	0.8	36
9	The chloroplast genome hidden in plain sight, open access publishing and anti-fragile distributed data sources. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4518-4519.	0.7	14
10	The genomic era is here – A new standard of care in epilepsy? Case examples. Epilepsy and Behavior, 2015, 46, 59.	0.9	0
11	Hurt, tired and queasy: Specific variants in the ATPase domain of the TRAP1 mitochondrial chaperone are associated with common, chronic –symptomatology including pain, fatigue and gastrointestinal dysmotility. Mitochondrion, 2015, 23, 64-70.	1.6	15
12	Cannabis microbiome sequencing reveals several mycotoxic fungi native to dispensary grade Cannabis flowers. F1000Research, 2015, 4, 1422.	0.8	36
13	Cannabis microbiome sequencing reveals several mycotoxic fungi native to dispensary grade Cannabis flowers. F1000Research, 2015, 4, 1422.	0.8	33
14	Mutation in The Nuclear-Encoded Mitochondrial Isoleucyl-tRNA Synthetase <i>IARS2</i> in Patients with Cataracts, Growth Hormone Deficiency with Short Stature, Partial Sensorineural Deafness, and Peripheral Neuropathy or with Leigh Syndrome. Human Mutation, 2014, 35, n/a-n/a.	1.1	66
15	Expanded Genetic Codes in Next Generation Sequencing Enable Decontamination and Mitochondrial Enrichment. PLoS ONE, 2014, 9, e96492.	1.1	11
16	DREAMing of a patent-free human genome for clinical sequencing. Nature Biotechnology, 2013, 31, 884-887.	9.4	6
17	An integrated semiconductor device enabling non-optical genome sequencing. Nature, 2011, 475, 348-352.	13.7	1,891
18	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. Genome Biology, 2011, 12, R126.	13.9	297

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19	Deep-transcriptome and ribonome sequencing redefines the molecular networks of pluripotency and the extracellular space in human embryonic stem cells. <i>Genome Research</i> , 2011, 21, 2014-2025.	2.4	23
20	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , 2010, 463, 184-190.	13.7	972
21	Maternal Plasma DNA Analysis with Massively Parallel Sequencing by Ligation for Noninvasive Prenatal Diagnosis of Trisomy 21. <i>Clinical Chemistry</i> , 2010, 56, 459-463.	1.5	125
22	Development of Personalized Tumor Biomarkers Using Massively Parallel Sequencing. <i>Science Translational Medicine</i> , 2010, 2, 20ra14.	5.8	447
23	Whole Methylome Analysis by Ultra-Deep Sequencing Using Two-Base Encoding. <i>PLoS ONE</i> , 2010, 5, e9320.	1.1	52
24	Differential binding and co-binding pattern of FOXA1 and FOXA3 and their relation to H3K4me3 in HepG2 cells revealed by ChIP-seq. <i>Genome Biology</i> , 2009, 10, R129.	13.9	64
25	ALLPATHS 2: small genomes assembled accurately and with high continuity from short paired reads. <i>Genome Biology</i> , 2009, 10, R103.	13.9	151
26	Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two-base encoding. <i>Genome Research</i> , 2009, 19, 1527-1541.	2.4	448
27	Polymorphism discovery in high-throughput resequenced microarray-enriched human genomic loci. <i>Journal of Biomolecular Techniques</i> , 2009, 20, 253-7.	0.8	1
28	Mapping and sequencing of structural variation from eight human genomes. <i>Nature</i> , 2008, 453, 56-64.	13.7	983
29	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , 2008, 5, 613-619.	9.0	952
30	Rapid whole-genome mutational profiling using next-generation sequencing technologies. <i>Genome Research</i> , 2008, 18, 1638-1642.	2.4	225
31	A high-resolution, nucleosome position map of <i>C. elegans</i> reveals a lack of universal sequence-dictated positioning. <i>Genome Research</i> , 2008, 18, 1051-1063.	2.4	503
32	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
33	Protein interaction mapping on a functional shotgun sequence of <i>Rickettsia sibirica</i> . <i>Nucleic Acids Research</i> , 2004, 32, 1059-1064.	6.5	40
34	Genome duplication in the teleost fish <i>Tetraodon nigroviridis</i> reveals the early vertebrate proto-karyotype. <i>Nature</i> , 2004, 431, 946-957.	13.7	1,801
35	Automation and Robotics for Genetic Analysis. <i>Current Protocols in Human Genetics</i> , 2004, 40, 16.0.1.	3.5	0
36	Sample Preparation. <i>Current Protocols in Human Genetics</i> , 2004, 40, Unit 16.1.	3.5	0

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37	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	2.4	573
38	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16899-16903.	3.3	1,610
39	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
40	DNA SEQUENCING: A Magnetic Attraction to High-Throughput Genomics. <i>Science</i> , 1997, 276, 1887-1889.	6.0	55
41	A whole genome atlas of 81 <i>Psilocybe</i> genomes as a resource for psilocybin production.. <i>F1000Research</i> , 0, 10, 961.	0.8	6
42	Bayes Lines Tool (BLT): A SQL-script for analyzing diagnostic test results with an application to SARS-CoV-2-testing. <i>F1000Research</i> , 0, 10, 369.	0.8	1
43	A whole genome atlas of 81 <i>Psilocybe</i> genomes as a resource for psilocybin production.. <i>F1000Research</i> , 0, 10, 961.	0.8	0
44	Pathogenic Enterobacteriaceae require multiple culture temperatures for detection in <i>Cannabis sativa</i> L.. <i>F1000Research</i> , 0, 11, 578.	0.8	0