

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
g-index

59
all docs

59
docs citations

59
times ranked

40414
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	An integrated semiconductor device enabling non-optical genome sequencing. <i>Nature</i> , 2011, 475, 348-352.	13.7	1,891
3	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
4	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
5	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
6	Mapping and sequencing of structural variation from eight human genomes. <i>Nature</i> , 2008, 453, 56-64.	13.7	983
7	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , 2010, 463, 184-190.	13.7	972
8	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , 2008, 5, 613-619.	9.0	952
9	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	2.4	573
10	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
11	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
12	Development of Personalized Tumor Biomarkers Using Massively Parallel Sequencing. <i>Science Translational Medicine</i> , 2010, 2, 20ra14.	5.8	447
13	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. <i>Genome Biology</i> , 2011, 12, R126.	13.9	297
14	Rapid whole-genome mutational profiling using next-generation sequencing technologies. <i>Genome Research</i> , 2008, 18, 1638-1642.	2.4	225
15	ALLPATHS 2: small genomes assembled accurately and with high continuity from short paired reads. <i>Genome Biology</i> , 2009, 10, R103.	13.9	151
16	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
17	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. <i>Human Mutation</i> , 2014, 35, n/a-n/a.	1.1	66
18	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

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19	DNA SEQUENCING: A Magnetic Attraction to High-Throughput Genomics. <i>Science</i> , 1997, 276, 1887-1889.	6.0	55
20	Rare genetic variants in the endocannabinoid system genes CNR1 and DAGLA are associated with neurological phenotypes in humans. <i>PLoS ONE</i> , 2017, 12, e0187926.	1.1	55
21	Whole Methylome Analysis by Ultra-Deep Sequencing Using Two-Base Encoding. <i>PLoS ONE</i> , 2010, 5, e9320.	1.1	52
22	Genomic characterization of the complete terpene synthase gene family from <i>Cannabis sativa</i> . <i>PLoS ONE</i> , 2019, 14, e0222363.	1.1	47
23	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
24	Cannabis microbiome sequencing reveals several mycotoxic fungi native to dispensary grade Cannabis flowers. <i>F1000Research</i> , 2015, 4, 1422.	0.8	36
25	Metagenomic analysis of medicinal Cannabis samples; pathogenic bacteria, toxigenic fungi, and beneficial microbes grow in culture-based yeast and mold tests. <i>F1000Research</i> , 2016, 5, 2471.	0.8	36
26	Contaminants of Concern in Cannabis: Microbes, Heavy Metals and Pesticides. , 2017, , 457-474.		33
27	Cannabis microbiome sequencing reveals several mycotoxic fungi native to dispensary grade Cannabis flowers. <i>F1000Research</i> , 2015, 4, 1422.	0.8	33
28	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
29	Hurt, tired and queasy: Specific variants in the ATPase domain of the TRAP1 mitochondrial chaperone are associated with common, chronic "dysfunctional" symptomatology including pain, fatigue and gastrointestinal dysmotility. <i>Mitochondrion</i> , 2015, 23, 64-70.	1.6	15
30	The chloroplast genome hidden in plain sight, open access publishing and anti-fragile distributed data sources. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4518-4519.	0.7	14
31	Whole genome sequencing of colonies derived from cannabis flowers and the impact of media selection on benchmarking total yeast and mold detection tools. <i>F1000Research</i> , 2021, 10, 624.	0.8	11
32	Expanded Genetic Codes in Next Generation Sequencing Enable Decontamination and Mitochondrial Enrichment. <i>PLoS ONE</i> , 2014, 9, e96492.	1.1	11
33	DREAMing of a patent-free human genome for clinical sequencing. <i>Nature Biotechnology</i> , 2013, 31, 884-887.	9.4	6
34	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
35	Whole genome sequencing of colonies derived from cannabis flowers and the impact of media selection on benchmarking total yeast and mold detection tools. <i>F1000Research</i> , 2021, 10, 624.	0.8	5
36	A draft sequence reference of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , 2021, 10, 281.	0.8	1

#	ARTICLE	IF	CITATIONS
37	A draft reference assembly of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , 2021, 10, 281.	0.8	1
38	Polymorphism discovery in high-throughput resequenced microarray-enriched human genomic loci. <i>Journal of Biomolecular Techniques</i> , 2009, 20, 253-7.	0.8	1
39	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
40	Automation and Robotics for Genetic Analysis. <i>Current Protocols in Human Genetics</i> , 2004, 40, 16.0.1.	3.5	0
41	Sample Preparation. <i>Current Protocols in Human Genetics</i> , 2004, 40, Unit 16.1.	3.5	0
42	The genomic era is here – A new standard of care in epilepsy? Case examples. <i>Epilepsy and Behavior</i> , 2015, 46, 59.	0.9	0
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