

# Kevin Judd McKernan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4266869/publications.pdf>

Version: 2024-02-01

44  
papers

34,649  
citations

218677  
26  
h-index

330143  
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. Nature, 2001, 409, 860-921.	27.8	21,074
2	An integrated semiconductor device enabling non-optical genome sequencing. Nature, 2011, 475, 348-352.	27.8	1,891
3	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
4	Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. Nature, 2004, 431, 946-957.	27.8	1,801
5	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16899-16903.	7.1	1,610
6	Mapping and sequencing of structural variation from eight human genomes. Nature, 2008, 453, 56-64.	27.8	983
7	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	27.8	972
8	Stem cell transcriptome profiling via massive-scale mRNA sequencing. Nature Methods, 2008, 5, 613-619.	19.0	952
9	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. Genome Research, 2002, 12, 532-542.	5.5	573
10	A high-resolution, nucleosome position map of <i>C. elegans</i> reveals a lack of universal sequence-dictated positioning. Genome Research, 2008, 18, 1051-1063.	5.5	503
11	Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two-base encoding. Genome Research, 2009, 19, 1527-1541.	5.5	448
12	Development of Personalized Tumor Biomarkers Using Massively Parallel Sequencing. Science Translational Medicine, 2010, 2, 20ra14.	12.4	447
13	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. Genome Biology, 2011, 12, R126.	9.6	297
14	Rapid whole-genome mutational profiling using next-generation sequencing technologies. Genome Research, 2008, 18, 1638-1642.	5.5	225
15	ALLPATHS 2: small genomes assembled accurately and with high continuity from short paired reads. Genome Biology, 2009, 10, R103.	9.6	151
16	Maternal Plasma DNA Analysis with Massively Parallel Sequencing by Ligation for Noninvasive Prenatal Diagnosis of Trisomy 21. Clinical Chemistry, 2010, 56, 459-463.	3.2	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. Human Mutation, 2014, 35, n/a-n/a.	2.5	66
18	Differential binding and co-binding pattern of FOXA1 and FOXA3 and their relation to H3K4me3 in HepG2 cells revealed by ChIP-seq. Genome Biology, 2009, 10, R129.	9.6	64

#	ARTICLE	IF	CITATIONS
19	DNA SEQUENCING: A Magnetic Attraction to High-Throughput Genomics. Science, 1997, 276, 1887-1889.	12.6	55
20	Rare genetic variants in the endocannabinoid system genes CNR1 and DAGLA are associated with neurological phenotypes in humans. PLoS ONE, 2017, 12, e0187926.	2.5	55
21	Whole Methylome Analysis by Ultra-Deep Sequencing Using Two-Base Encoding. PLoS ONE, 2010, 5, e9320.	2.5	52
22	Genomic characterization of the complete terpene synthase gene family from Cannabis sativa. PLoS ONE, 2019, 14, e0222363.	2.5	47
23	Protein interaction mapping on a functional shotgun sequence of Rickettsia sibirica. Nucleic Acids Research, 2004, 32, 1059-1064.	14.5	40
24	Cannabis microbiome sequencing reveals several mycotoxic fungi native to dispensary grade Cannabis flowers. F1000Research, 2015, 4, 1422.	1.6	36
25	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.	1.6	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. F1000Research, 2015, 4, 1422.	1.6	33
28	Deep-transcriptome and ribonome sequencing redefines the molecular networks of pluripotency and the extracellular space in human embryonic stem cells. Genome Research, 2011, 21, 2014-2025.	5.5	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. Mitochondrion, 2015, 23, 64-70.	3.4	15
30	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
31	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.	1.6	11
32	Expanded Genetic Codes in Next Generation Sequencing Enable Decontamination and Mitochondrial Enrichment. PLoS ONE, 2014, 9, e96492.	2.5	11
33	DREAMing of a patent-free human genome for clinical sequencing. Nature Biotechnology, 2013, 31, 884-887.	17.5	6
34	A whole genome atlas of 81 Psilocybe genomes as a resource for psilocybin production.. F1000Research, 0, 10, 961.	1.6	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. F1000Research, 2021, 10, 624.	1.6	5
36	A draft sequence reference of the Psilocybe cubensis genome. F1000Research, 2021, 10, 281.	1.6	1

#	ARTICLE	IF	CITATIONS
37	A draft reference assembly of the <i>Psilocybe cubensis</i> genome. <i>F1000Research</i> , 2021, 10, 281.	1.6	1
38	Polymorphism discovery in high-throughput resequenced microarray-enriched human genomic loci. <i>Journal of Biomolecular Techniques</i> , 2009, 20, 253-7.	1.5	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.	1.6	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.	1.7	0
43	A whole genome atlas of 81 <i>Psilocybe</i> genomes as a resource for psilocybin production.. <i>F1000Research</i> , 0, 10, 961.	1.6	0
44	Pathogenic Enterobacteriaceae require multiple culture temperatures for detection in <i>Cannabis sativa</i> L.. <i>F1000Research</i> , 0, 11, 578.	1.6	0