

# Matthew R Henn

## List of Publications by Year in descending order

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51  
papers

6,613  
citations

101543

36  
h-index

182427

51  
g-index

51  
all docs

51  
docs citations

51  
times ranked

11061  
citing authors

#	ARTICLE	IF	CITATIONS
1	SER-109, an Oral Microbiome Therapy for Recurrent <i>Clostridioides difficile</i> Infection. <i>New England Journal of Medicine</i> , 2022, 386, 220-229.	27.0	205
2	SER-109, an Investigational Microbiome Drug to Reduce Recurrence After <i>Clostridioides difficile</i> Infection: Lessons Learned From a Phase 2 Trial. <i>Clinical Infectious Diseases</i> , 2021, 72, 2132-2140.	5.8	96
3	A Phase 1b Safety Study of SER-287, a Spore-Based Microbiome Therapeutic, for Active Mild to Moderate Ulcerative Colitis. <i>Gastroenterology</i> , 2021, 160, 115-127.e30.	1.3	48
4	Biofilms harbour <i>Clostridioides difficile</i> , serving as a reservoir for recurrent infection. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 16.	6.4	43
5	Fecal microbiota transplantation for the improvement of metabolism in obesity: The FMT-TRIM double-blind placebo-controlled pilot trial. <i>PLoS Medicine</i> , 2020, 17, e1003051.	8.4	177
6	Tu2019 - Engraftment of Ser-287, an Investigational Microbiome Therapeutic, is Related to Clinical Remission in a Placebo-Controlled, Double-Blind Randomized Trial (Seres-101) in Patients with Active Mild to Moderate Ulcerative Colitis (UC). <i>Gastroenterology</i> , 2018, 154, S-1371-S-1372.	1.3	4
7	Differences in the Selection Bottleneck between Modes of Sexual Transmission Influence the Genetic Composition of the HIV-1 Founder Virus. <i>PLoS Pathogens</i> , 2016, 12, e1005619.	4.7	97
8	Genome Sequencing and Analysis of Geographically Diverse Clinical Isolates of Herpes Simplex Virus 2. <i>Journal of Virology</i> , 2015, 89, 8219-8232.	3.4	68
9	Comparison of Illumina and 454 Deep Sequencing in Participants Failing Raltegravir-Based Antiretroviral Therapy. <i>PLoS ONE</i> , 2014, 9, e90485.	2.5	27
10	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	2.5	34
11	Complex dynamic of dengue virus serotypes 2 and 3 in Cambodia following series of climate disasters. <i>Infection, Genetics and Evolution</i> , 2013, 15, 77-86.	2.3	11
12	Genetic diversity and lineage dynamic of dengue virus serotype 1 (DENV-1) in Cambodia. <i>Infection, Genetics and Evolution</i> , 2013, 15, 59-68.	2.3	26
13	Ecology of uncultured <i>Prochlorococcus</i> clades revealed through single-cell genomics and biogeographic analysis. <i>ISME Journal</i> , 2013, 7, 184-198.	9.8	105
14	Complete viral RNA genome sequencing of ultra-low copy samples by sequence-independent amplification. <i>Nucleic Acids Research</i> , 2013, 41, e13-e13.	14.5	75
15	Tracking the Evolution of Dengue Virus Strains D2S10 and D2S20 by 454 Pyrosequencing. <i>PLoS ONE</i> , 2013, 8, e54220.	2.5	18
16	Highly Sensitive and Specific Detection of Rare Variants in Mixed Viral Populations from Massively Parallel Sequence Data. <i>PLoS Computational Biology</i> , 2012, 8, e1002417.	3.2	107
17	Whole Genome Deep Sequencing of HIV-1 Reveals the Impact of Early Minor Variants Upon Immune Recognition During Acute Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002529.	4.7	306
18	Rapid diversification of coevolving marine <i>Synechococcus</i> and a virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4544-4549.	7.1	178

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19	High-Resolution Analysis of Intra-host Genetic Diversity in Dengue Virus Serotype 1 Infection Identifies Mixed Infections. <i>Journal of Virology</i> , 2012, 86, 835-843.	3.4	52
20	Draft Genome Sequence of the Coccolithovirus <i>Emiliana huxleyi</i> Virus 202. <i>Journal of Virology</i> , 2012, 86, 2380-2381.	3.4	20
21	Genome-Wide Patterns of Intra-human Dengue Virus Diversity Reveal Associations with Viral Phylogenetic Clade and Inter-host Diversity. <i>Journal of Virology</i> , 2012, 86, 8546-8558.	3.4	78
22	Human leukocyte antigen B27 selects for rare escape mutations that significantly impair hepatitis C virus replication and require compensatory mutations. <i>Hepatology</i> , 2011, 54, 1157-1166.	7.3	47
23	Endurance, Refuge, and Reemergence of Dengue Virus Type 2, Puerto Rico, 1986–2007. <i>Emerging Infectious Diseases</i> , 2011, 17, 64-71.	4.3	38
24	Compensatory Mutations Restore the Replication Defects Caused by Cytotoxic T Lymphocyte Escape Mutations in Hepatitis C Virus Polymerase. <i>Journal of Virology</i> , 2011, 85, 11883-11890.	3.4	30
25	Dynamics of Dengue Disease Severity Determined by the Interplay Between Viral Genetics and Serotype-Specific Immunity. <i>Science Translational Medicine</i> , 2011, 3, 114ra128.	12.4	244
26	Draft Genome Sequence of the Coccolithovirus <i>Emiliana huxleyi</i> Virus 203. <i>Journal of Virology</i> , 2011, 85, 13468-13469.	3.4	15
27	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011, 7, e1002345.	3.5	164
28	Endemic Dengue Associated with the Co-Circulation of Multiple Viral Lineages and Localized Density-Dependent Transmission. <i>PLoS Pathogens</i> , 2011, 7, e1002064.	4.7	86
29	Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. <i>Environmental Microbiology</i> , 2010, 12, 3035-3056.	3.8	318
30	Analysis of High-Throughput Sequencing and Annotation Strategies for Phage Genomes. <i>PLoS ONE</i> , 2010, 5, e9083.	2.5	76
31	Index Cluster Study of Dengue Virus Infection in Nicaragua. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 83, 683-689.	1.4	35
32	Emergence of the Asian 1 Genotype of Dengue Virus Serotype 2 in Viet Nam: In Vivo Fitness Advantage and Lineage Replacement in South-East Asia. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e757.	3.0	131
33	The Major Genetic Determinants of HIV-1 Control Affect HLA Class I Peptide Presentation. <i>Science</i> , 2010, 330, 1551-1557.	12.6	1,054
34	Population genomic sequencing of <i>Coccidioides</i> fungi reveals recent hybridization and transposon control. <i>Genome Research</i> , 2010, 20, 938-946.	5.5	166
35	A High-Density Single Nucleotide Polymorphism Map for <i>Neurospora crassa</i> . <i>Genetics</i> , 2009, 181, 767-781.	2.9	54
36	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009, 19, 1722-1731.	5.5	295

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37	The GAAS Metagenomic Tool and Its Estimations of Viral and Microbial Average Genome Size in Four Major Biomes. <i>PLoS Computational Biology</i> , 2009, 5, e1000593.	3.2	177
38	Whole Genome Amplification and De novo Assembly of Single Bacterial Cells. <i>PLoS ONE</i> , 2009, 4, e6864.	2.5	225
39	A set of reference sequences for the hepatitis C genotypes 4d, 4f, and 4k covering the full open reading frame. <i>Journal of Medical Virology</i> , 2008, 80, 1370-1378.	5.0	10
40	Naturally occurring dominant resistance mutations to hepatitis C virus protease and polymerase inhibitors in treatment-naïve patients. <i>Hepatology</i> , 2008, 48, 1769-1778.	7.3	326
41	Hindsight in the relative abundance, metabolic potential and genome dynamics of uncultivated marine archaea from comparative metagenomic analyses of bathypelagic plankton of different oceanic regions. <i>ISME Journal</i> , 2008, 2, 865-886.	9.8	113
42	Comparative analysis of genome fragments of <i>Acidobacteria</i> from deep Mediterranean plankton. <i>Environmental Microbiology</i> , 2008, 10, 2704-2717.	3.8	48
43	Short-Term Temporal Variability in Airborne Bacterial and Fungal Populations. <i>Applied and Environmental Microbiology</i> , 2008, 74, 200-207.	3.1	250
44	Generating and Testing Molecular Hypotheses in the Dermatophytes. <i>Eukaryotic Cell</i> , 2008, 7, 1238-1245.	3.4	78
45	Enabling a Community to Dissect an Organism: Overview of the <i>Neurospora</i> Functional Genomics Project. <i>Advances in Genetics</i> , 2007, 57, 49-96.	1.8	191
46	Genomics of the fungal kingdom: Insights into eukaryotic biology. <i>Genome Research</i> , 2005, 15, 1620-1631.	5.5	269
47	Isotopic fractionation during ammonium assimilation by basidiomycete fungi and its implications for natural nitrogen isotope patterns. <i>New Phytologist</i> , 2004, 162, 771-781.	7.3	16
48	Growth-Dependent Stable Carbon Isotope Fractionation by Basidiomycete Fungi: $\delta^{13}\text{C}$ Pattern and Physiological Process. <i>Applied and Environmental Microbiology</i> , 2002, 68, 4956-4964.	3.1	39
49	Ectomycorrhizal fungi introduced with exotic pine plantations induce soil carbon depletion. <i>Soil Biology and Biochemistry</i> , 2001, 33, 1733-1740.	8.8	165
50	Ecophysiology of $^{13}\text{C}$ and $^{15}\text{N}$ isotopic fractionation in forest fungi and the roots of the saprotrophic-mycorrhizal divide. <i>Oecologia</i> , 2001, 128, 480-487.	2.0	87
51	Differential C Isotope Discrimination by Fungi during Decomposition of C <sub>3</sub> - and C <sub>4</sub> -Derived Sucrose. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4180-4186.	3.1	91