James E Galagan

List of Publications by Year
in descending order

93 papers	**43,043** citations	28190 **55** h-index	46693 **89** g-index
95 all docs	**95** docs citations	**95** times ranked	**44005** citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
2	The genome sequence of the filamentous fungus Neurospora crassa. Nature, 2003, 422, 859-868.	13.7	1,528
3	The genome sequence of the rice blast fungus Magnaporthe grisea. Nature, 2005, 434, 980-986.	13.7	1,447
4	Comparative genomics reveals mobile pathogenicity chromosomes in Fusarium. Nature, 2010, 464, 367-373.	13.7	1,442
5	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	13.7	1,272
6	Sequencing of Aspergillus nidulans and comparative analysis with A. fumigatus and A. oryzae. Nature, 2005, 438, 1105-1115.	13.7	1,250
7	Genome sequencing and analysis of Aspergillus oryzae. Nature, 2005, 438, 1157-1161.	13.7	1,128
8	Insights from the genome of the biotrophic fungal plant pathogen Ustilago maydis. Nature, 2006, 444, 97-101.	13.7	1,113
9	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	6.0	1,025
10	Human T cell epitopes of Mycobacterium tuberculosis are evolutionarily hyperconserved. Nature Genetics, 2010, 42, 498-503.	9.4	642
11	The Genome of M. acetivorans Reveals Extensive Metabolic and Physiological Diversity. Genome Research, 2002, 12, 532-542.	2.4	573
12	Lessons from the Genome Sequence of Neurospora crassa : Tracing the Path from Genomic Blueprint to Multicellular Organism. Microbiology and Molecular Biology Reviews, 2004, 68, 1-108.	2.9	572
13	Dynamics of Pseudomonas aeruginosa genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3100-3105.	3.3	492
14	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. PLoS Pathogens, 2011, 7, e1002137.	2.1	477
15	Whole-genome sequencing of rifampicin-resistant Mycobacterium tuberculosis strains identifies compensatory mutations in RNA polymerase genes. Nature Genetics, 2012, 44, 106-110.	9.4	475
16	The Mycobacterium tuberculosis regulatory network and hypoxia. Nature, 2013, 499, 178-183.	13.7	416
17	Use of whole genome sequencing to estimate the mutation rate of Mycobacterium tuberculosis during latent infection. Nature Genetics, 2011, 43, 482-486.	9.4	403
18	Genomic analysis identifies targets of convergent positive selection in drug-resistant Mycobacterium tuberculosis. Nature Genetics, 2013, 45, 1183-1189.	9.4	393

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19	RIP: the evolutionary cost of genome defense. Trends in Genetics, 2004, 20, 417-423.	2.9	392
20	Interpreting Expression Data with Metabolic Flux Models: Predicting Mycobacterium tuberculosis Mycolic Acid Production. PLoS Computational Biology, 2009, 5, e1000489.	1.5	371
21	Genomic Analysis of the Basal Lineage Fungus Rhizopus oryzae Reveals a Whole-Genome Duplication. PLoS Genetics, 2009, 5, e1000549.	1.5	332
22	Naturally occurring dominant resistance mutations to hepatitis C virus protease and polymerase inhibitors in treatment-naÃ¯ve patients. Hepatology, 2008, 48, 1769-1778.	3.6	326
23	RegulonDB v 10.5: tackling challenges to unify classic and high throughput knowledge of gene regulation in<i>E. coli</i>K-12. Nucleic Acids Research, 2019, 47, D212-D220.	6.5	322
24	A genome-wide map of diversity in Plasmodium falciparum. Nature Genetics, 2007, 39, 113-119.	9.4	320
25	Genomics of the fungal kingdom: Insights into eukaryotic biology. Genome Research, 2005, 15, 1620-1631.	2.4	269
26	Pneumococcal Capsular Polysaccharide Structure Predicts Serotype Prevalence. PLoS Pathogens, 2009, 5, e1000476.	2.1	264
27	Genomic analysis of globally diverse Mycobacterium tuberculosis strains provides insights into the emergence and spread of multidrug resistance. Nature Genetics, 2017, 49, 395-402.	9.4	258
28	Dothideomyceteâ€"Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i>. Plant Cell, 2007, 19, 3347-3368.	3.1	235
29	Genomic insights into tuberculosis. Nature Reviews Genetics, 2014, 15, 307-320.	7.7	227
30	TB database: an integrated platform for tuberculosis research. Nucleic Acids Research, 2009, 37, D499-D508.	6.5	201
31	The DNA-binding network of Mycobacterium tuberculosi s. Nature Communications, 2015, 6, 5829.	5.8	192
32	Enabling a Community to Dissect an Organism: Overview of the Neurospora Functional Genomics Project. Advances in Genetics, 2007, 57, 49-96.	0.8	191
33	Genome Variation in Cryptococcus gattii, an Emerging Pathogen of Immunocompetent Hosts. MBio, 2011, 2, e00342-10.	1.8	182
34	Assembly of polymorphic genomes: Algorithms and application to Ciona savignyi. Genome Research, 2005, 15, 1127-1135.	2.4	170
35	Short-term genome evolution of Listeria monocytogenes in a non-controlled environment. BMC Genomics, 2008, 9, 539.	1.2	170
36	Largeâ€scale identification of genetic design strategies using local search. Molecular Systems Biology, 2009, 5, 296.	3.2	143

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37	Coordinated regulation of acid resistance in Escherichia coli. BMC Systems Biology, 2017, 11, 1.	3.0	142
38	The Role of Selection in Shaping Diversity of Natural M. tuberculosis Populations. PLoS Pathogens, 2013, 9, e1003543.	2.1	138
39	Analysis of clock-regulated genes in <i>Neurospora</i> reveals widespread posttranscriptional control of metabolic potential. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16995-17002.	3.3	131
40	Genetic Determinants of Drug Resistance in <i>Mycobacterium tuberculosis</i> and Their Diagnostic Value. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 621-630.	2.5	131
41	Cross-kingdom patterns of alternative splicing and splice recognition. Genome Biology, 2008, 9, R50.	13.9	126
42	GenomeView: a next-generation genome browser. Nucleic Acids Research, 2012, 40, e12-e12.	6.5	126
43	Patterns of Intron Gain and Loss in Fungi. PLoS Biology, 2004, 2, e422.	2.6	117
44	Comparative Genomic Characterization of Francisella tularensis Strains Belonging to Low and High Virulence Subspecies. PLoS Pathogens, 2009, 5, e1000459.	2.1	112
45	A Systems Biology Approach to Infectious Disease Research: Innovating the Pathogen-Host Research Paradigm. MBio, 2011, 2, e00325-10.	1.8	111
46	TB database 2010: Overview and update. Tuberculosis, 2010, 90, 225-235.	0.8	106
47	Evolutionary Roles of Upstream Open Reading Frames in Mediating Gene Regulation in Fungi. Annual Review of Microbiology, 2009, 63, 385-409.	2.9	105
48	Redefining fundamental concepts of transcription initiation in bacteria. Nature Reviews Genetics, 2020, 21, 699-714.	7.7	100
49	Genome-Wide Characterization of Light-Regulated Genes in<i>Neurospora crassa</i>. G3: Genes, Genomes, Genetics, 2014, 4, 1731-1745.	0.8	82
50	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. BMC Genomics, 2012, 13, 120.	1.2	80
51	Mycobacterium tuberculosis Whole Genome Sequences From Southern India Suggest Novel Resistance Mechanisms and the Need for Region-Specific Diagnostics. Clinical Infectious Diseases, 2017, 64, 1494-1501.	2.9	76
52	Mechanisms of intron gain and loss in Cryptococcus. Genome Biology, 2008, 9, R24.	13.9	75
53	Reconstruction and Validation of a Genome-Scale Metabolic Model for the Filamentous Fungus Neurospora crassa Using FARM. PLoS Computational Biology, 2013, 9, e1003126.	1.5	70
54	Conrad: Gene prediction using conditional random fields. Genome Research, 2007, 17, 1389-1398.	2.4	62

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55	A blind deconvolution approach to high-resolution mapping of transcription factor binding sites from ChIP-seq data. Genome Biology, 2009, 10, R142.	13.9	61
56	A High-Density Single Nucleotide Polymorphism Map for *Neurospora crassa*. Genetics, 2009, 181, 767-781.	1.2	54
57	A progesterone biosensor derived from microbial screening. Nature Communications, 2020, 11, 1276.	5.8	53
58	ChIP-Seq and the Complexity of Bacterial Transcriptional Regulation. Current Topics in Microbiology and Immunology, 2012, 363, 43-68.	0.7	47
59	The Neurospora Transcription Factor ADV-1 Transduces Light Signals and Temporal Information to Control Rhythmic Expression of Genes Involved in Cell Fusion. G3: Genes, Genomes, Genetics, 2017, 7, 129-142.	0.8	47
60	Combo: a whole genome comparative browser. Bioinformatics, 2006, 22, 1782-1783.	1.8	46
61	Dual Modes of Natural Selection on Upstream Open Reading Frames. Molecular Biology and Evolution, 2007, 24, 1744-1751.	3.5	46
62	A unified resource for transcriptional regulation in Escherichia coli K-12 incorporating high-throughput-generated binding data into RegulonDB version 10.0. BMC Biology, 2018, 16, 91.	1.7	42
63	Comprehensive Definition of the SigH Regulon of Mycobacterium tuberculosis Reveals Transcriptional Control of Diverse Stress Responses. PLoS ONE, 2016, 11, e0152145.	1.1	40
64	RegulonDB 11.0: Comprehensive high-throughput datasets on transcriptional regulation in Escherichia coli K-12. Microbial Genomics, 2022, 8, .	1.0	32
65	Independent Large Scale Duplications in Multiple M. tuberculosis Lineages Overlapping the Same Genomic Region. PLoS ONE, 2012, 7, e26038.	1.1	30
66	Role of intragenic binding of cAMP responsive protein (CRP) in regulation of the succinate dehydrogenase genes Rv0249c-Rv0247c in TB complex mycobacteria. Nucleic Acids Research, 2015, 43, 5377-5393.	6.5	29
67	Hydrogel-Embedded Quantum Dotâ€"Transcription Factor Sensors for Quantitative Progesterone Detection. ACS Applied Materials & Interfaces, 2020, 12, 43513-43521.	4.0	27
68	Inferring Carbon Sources from Gene Expression Profiles Using Metabolic Flux Models. PLoS ONE, 2012, 7, e36947.	1.1	27
69	Metabolic modeling predicts metabolite changes in Mycobacterium tuberculosis. BMC Systems Biology, 2015, 9, 57.	3.0	25
70	Characterization of a cAMP responsive transcription factor, Cmr (Rv1675c), in TB complex mycobacteria reveals overlap with the DosR (DevR) dormancy regulon. Nucleic Acids Research, 2016, 44, 134-151.	6.5	25
71	Epigenetic competition reveals density-dependent regulation and target site plasticity of phosphorothioate epigenetics in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14322-14330.	3.3	25
72	Improving genome annotations using phylogenetic profile anomaly detection. Bioinformatics, 2005, 21, 464-470.	1.8	22

#	ARTICLE	IF	CITATIONS
73	Positive selection for unpreferred codon usage in eukaryotic genomes. BMC Evolutionary Biology, 2007, 7, 119.	3.2	22
74	Transcription Factor Binding Site Mapping Using ChIP-Seq. Microbiology Spectrum, 2014, 2, .	1.2	22
75	Decoding ChIP-seq with a double-binding signal refines binding peaks to single-nucleotides and predicts cooperative interaction. Genome Research, 2014, 24, 1686-1697.	2.4	21
76	Resource Competition May Lead to Effective Treatment of Antibiotic Resistant Infections. PLoS ONE, 2013, 8, e80775.	1.1	18
77	How accurate can genetic predictions be?. BMC Genomics, 2012, 13, 340.	1.2	16
78	A FÃ¶rster Resonance Energy Transferâ€Based Ratiometric Sensor with the Allosteric Transcription Factor TetR. Small, 2020, 16, e1907522.	5.2	16
79	Transcription Factor Based Smallâ€Molecule Sensing with a Rapid Cell Phone Enabled Fluorescent Bead Assay. Angewandte Chemie - International Edition, 2020, 59, 21597-21602.	7.2	15
80	Simulating Serial-Target Antibacterial Drug Synergies Using Flux Balance Analysis. PLoS ONE, 2016, 11, e0147651.	1.1	14
81	Surface Immobilized Nucleic Acidâ€"Transcription Factor Quantum Dots for Biosensing. Advanced Healthcare Materials, 2020, 9, e2000403.	3.9	10
82	Development and Clinical Validation of Iso-IMRS: A Novel Diagnostic Assay for *P. falciparum* Malaria. Analytical Chemistry, 2021, 93, 2097-2105.	3.2	7
83	An Allosteric Transcription Factor DNA-Binding Electrochemical Biosensor for Progesterone. ACS Sensors, 2022, 7, 1132-1137.	4.0	5
84	The quantum dot *vs.* organic dye conundrum for ratiometric FRET-based biosensors: which one would you chose?. Chemical Science, 2022, 13, 6715-6731.	3.7	5
85	Conserved Secondary Structures in Aspergillus. PLoS ONE, 2008, 3, e2812.	1.1	4
86	Paper-Based Progesterone Sensor Using an Allosteric Transcription Factor. ACS Omega, 2022, 7, 5804-5808.	1.6	3
87	Transcription Factor Based Smallâ€Molecule Sensing with a Rapid Cell Phone Enabled Fluorescent Bead Assay. Angewandte Chemie, 2020, 132, 21781-21786.	1.6	2
88	Reply to Lee and Howden. Clinical Infectious Diseases, 2018, 66, 160-161.	2.9	1
89	Genomic insights into tuberculosis. , 0, .		1
90	Transcription Factor Binding Site Mapping Using ChIP-Seq. , 0, , 161-181.		0

#	Article	IF	Citations
91	An Enzymatic Electrochemical Biosensor for Real-Time Detection of Physiologically Relevant Nicotine Concentrations. ECS Meeting Abstracts, 2020, MA2020-02, 3374-3374.	0.0	0
92	(Invited) Mining Microbes to Engineer Novel Biosensor Devices. ECS Meeting Abstracts, 2020, MA2020-02, 2839-2839.	0.0	0
93	An Allosteric Transcription Factor-Based Electrochemical Progesterone Sensor. ECS Meeting Abstracts, 2020, MA2020-02, 3318-3318.	0.0	0