

James E Galagan

List of Publications by Year in descending order

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93
papers

43,043
citations

28190

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95
all docs

95
docs citations

95
times ranked

44005
citing authors

#	ARTICLE	IF	CITATIONS
1	Paper-Based Progesterone Sensor Using an Allosteric Transcription Factor. ACS Omega, 2022, 7, 5804-5808.	1.6	3
2	An Allosteric Transcription Factor DNA-Binding Electrochemical Biosensor for Progesterone. ACS Sensors, 2022, 7, 1132-1137.	4.0	5
3	The quantum dot <i>vs.</i> organic dye conundrum for ratiometric FRET-based biosensors: which one would you chose?. Chemical Science, 2022, 13, 6715-6731.	3.7	5
4	RegulonDB 11.0: Comprehensive high-throughput datasets on transcriptional regulation in Escherichia coli K-12. Microbial Genomics, 2022, 8, .	1.0	32
5	Development and Clinical Validation of Iso-IMRS: A Novel Diagnostic Assay for <i>P. falciparum</i> Malaria. Analytical Chemistry, 2021, 93, 2097-2105.	3.2	7
6	Surface Immobilized Nucleic Acid-Transcription Factor Quantum Dots for Biosensing. Advanced Healthcare Materials, 2020, 9, e2000403.	3.9	10
7	Redefining fundamental concepts of transcription initiation in bacteria. Nature Reviews Genetics, 2020, 21, 699-714.	7.7	100
8	Transcription Factor Based Small-Molecule Sensing with a Rapid Cell Phone Enabled Fluorescent Bead Assay. Angewandte Chemie - International Edition, 2020, 59, 21597-21602.	7.2	15
9	Hydrogel-Embedded Quantum Dot-Transcription Factor Sensors for Quantitative Progesterone Detection. ACS Applied Materials & Interfaces, 2020, 12, 43513-43521.	4.0	27
10	Transcription Factor Based Small-Molecule Sensing with a Rapid Cell Phone Enabled Fluorescent Bead Assay. Angewandte Chemie, 2020, 132, 21781-21786.	1.6	2
11	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
12	A progesterone biosensor derived from microbial screening. Nature Communications, 2020, 11, 1276.	5.8	53
13	A Förster Resonance Energy Transfer-Based Ratiometric Sensor with the Allosteric Transcription Factor TetR. Small, 2020, 16, e1907522.	5.2	16
14	An Enzymatic Electrochemical Biosensor for Real-Time Detection of Physiologically Relevant Nicotine Concentrations. ECS Meeting Abstracts, 2020, MA2020-02, 3374-3374.	0.0	0
15	(Invited) Mining Microbes to Engineer Novel Biosensor Devices. ECS Meeting Abstracts, 2020, MA2020-02, 2839-2839.	0.0	0
16	An Allosteric Transcription Factor-Based Electrochemical Progesterone Sensor. ECS Meeting Abstracts, 2020, MA2020-02, 3318-3318.	0.0	0
17	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
18	Reply to Lee and Howden. Clinical Infectious Diseases, 2018, 66, 160-161.	2.9	1

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19	A unified resource for transcriptional regulation in <i>Escherichia coli</i> K-12 incorporating high-throughput-generated binding data into RegulonDB version 10.0. <i>BMC Biology</i> , 2018, 16, 91.	1.7	42
20	Genomic analysis of globally diverse <i>Mycobacterium tuberculosis</i> strains provides insights into the emergence and spread of multidrug resistance. <i>Nature Genetics</i> , 2017, 49, 395-402.	9.4	258
21	<i>Mycobacterium tuberculosis</i> Whole Genome Sequences From Southern India Suggest Novel Resistance Mechanisms and the Need for Region-Specific Diagnostics. <i>Clinical Infectious Diseases</i> , 2017, 64, 1494-1501.	2.9	76
22	The <i>Neurospora</i> Transcription Factor ADV-1 Transduces Light Signals and Temporal Information to Control Rhythmic Expression of Genes Involved in Cell Fusion. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 129-142.	0.8	47
23	Coordinated regulation of acid resistance in <i>Escherichia coli</i> . <i>BMC Systems Biology</i> , 2017, 11, 1.	3.0	142
24	Simulating Serial-Target Antibacterial Drug Synergies Using Flux Balance Analysis. <i>PLoS ONE</i> , 2016, 11, e0147651.	1.1	14
25	Genetic Determinants of Drug Resistance in <i>Mycobacterium tuberculosis</i> and Their Diagnostic Value. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 621-630.	2.5	131
26	Characterization of a cAMP responsive transcription factor, Cmr (Rv1675c), in TB complex mycobacteria reveals overlap with the DosR (DevR) dormancy regulon. <i>Nucleic Acids Research</i> , 2016, 44, 134-151.	6.5	25
27	Comprehensive Definition of the SigH Regulon of <i>Mycobacterium tuberculosis</i> Reveals Transcriptional Control of Diverse Stress Responses. <i>PLoS ONE</i> , 2016, 11, e0152145.	1.1	40
28	Metabolic modeling predicts metabolite changes in <i>Mycobacterium tuberculosis</i> . <i>BMC Systems Biology</i> , 2015, 9, 57.	3.0	25
29	The DNA-binding network of <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, 5829.	5.8	192
30	Role of intragenic binding of cAMP responsive protein (CRP) in regulation of the succinate dehydrogenase genes Rv0249c-Rv0247c in TB complex mycobacteria. <i>Nucleic Acids Research</i> , 2015, 43, 5377-5393.	6.5	29
31	Genome-Wide Characterization of Light-Regulated Genes in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1731-1745.	0.8	82
32	Genomic insights into tuberculosis. <i>Nature Reviews Genetics</i> , 2014, 15, 307-320.	7.7	227
33	Analysis of clock-regulated genes in <i>Neurospora</i> reveals widespread posttranscriptional control of metabolic potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16995-17002.	3.3	131
34	Decoding ChIP-seq with a double-binding signal refines binding peaks to single-nucleotides and predicts cooperative interaction. <i>Genome Research</i> , 2014, 24, 1686-1697.	2.4	21
35	Transcription Factor Binding Site Mapping Using ChIP-Seq. <i>Microbiology Spectrum</i> , 2014, 2, .	1.2	22
36	Genomic analysis identifies targets of convergent positive selection in drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 1183-1189.	9.4	393

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37	The Mycobacterium tuberculosis regulatory network and hypoxia. <i>Nature</i> , 2013, 499, 178-183.	13.7	416
38	The Role of Selection in Shaping Diversity of Natural M. tuberculosis Populations. <i>PLoS Pathogens</i> , 2013, 9, e1003543.	2.1	138
39	Reconstruction and Validation of a Genome-Scale Metabolic Model for the Filamentous Fungus <i>Neurospora crassa</i> Using FARM. <i>PLoS Computational Biology</i> , 2013, 9, e1003126.	1.5	70
40	Resource Competition May Lead to Effective Treatment of Antibiotic Resistant Infections. <i>PLoS ONE</i> , 2013, 8, e80775.	1.1	18
41	GenomeView: a next-generation genome browser. <i>Nucleic Acids Research</i> , 2012, 40, e12-e12.	6.5	126
42	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. <i>BMC Genomics</i> , 2012, 13, 120.	1.2	80
43	How accurate can genetic predictions be?. <i>BMC Genomics</i> , 2012, 13, 340.	1.2	16
44	ChIP-Seq and the Complexity of Bacterial Transcriptional Regulation. <i>Current Topics in Microbiology and Immunology</i> , 2012, 363, 43-68.	0.7	47
45	Independent Large Scale Duplications in Multiple M. tuberculosis Lineages Overlapping the Same Genomic Region. <i>PLoS ONE</i> , 2012, 7, e26038.	1.1	30
46	Whole-genome sequencing of rifampicin-resistant Mycobacterium tuberculosis strains identifies compensatory mutations in RNA polymerase genes. <i>Nature Genetics</i> , 2012, 44, 106-110.	9.4	475
47	Inferring Carbon Sources from Gene Expression Profiles Using Metabolic Flux Models. <i>PLoS ONE</i> , 2012, 7, e36947.	1.1	27
48	Use of whole genome sequencing to estimate the mutation rate of Mycobacterium tuberculosis during latent infection. <i>Nature Genetics</i> , 2011, 43, 482-486.	9.4	403
49	A Systems Biology Approach to Infectious Disease Research: Innovating the Pathogen-Host Research Paradigm. <i>MBio</i> , 2011, 2, e00325-10.	1.8	111
50	Genome Variation in <i>Cryptococcus gattii</i> , an Emerging Pathogen of Immunocompetent Hosts. <i>MBio</i> , 2011, 2, e00342-10.	1.8	182
51	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. <i>PLoS Pathogens</i> , 2011, 7, e1002137.	2.1	477
52	TB database 2010: Overview and update. <i>Tuberculosis</i> , 2010, 90, 225-235.	0.8	106
53	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
54	Human T cell epitopes of Mycobacterium tuberculosis are evolutionarily hyperconserved. <i>Nature Genetics</i> , 2010, 42, 498-503.	9.4	642

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55	Large-scale identification of genetic design strategies using local search. <i>Molecular Systems Biology</i> , 2009, 5, 296.	3.2	143
56	A High-Density Single Nucleotide Polymorphism Map for <i>Neurospora crassa</i> . <i>Genetics</i> , 2009, 181, 767-781.	1.2	54
57	Interpreting Expression Data with Metabolic Flux Models: Predicting <i>Mycobacterium tuberculosis</i> Mycolic Acid Production. <i>PLoS Computational Biology</i> , 2009, 5, e1000489.	1.5	371
58	Comparative Genomic Characterization of <i>Francisella tularensis</i> Strains Belonging to Low and High Virulence Subspecies. <i>PLoS Pathogens</i> , 2009, 5, e1000459.	2.1	112
59	Pneumococcal Capsular Polysaccharide Structure Predicts Serotype Prevalence. <i>PLoS Pathogens</i> , 2009, 5, e1000476.	2.1	264
60	Genomic Analysis of the Basal Lineage Fungus <i>Rhizopus oryzae</i> Reveals a Whole-Genome Duplication. <i>PLoS Genetics</i> , 2009, 5, e1000549.	1.5	332
61	TB database: an integrated platform for tuberculosis research. <i>Nucleic Acids Research</i> , 2009, 37, D499-D508.	6.5	201
62	Evolutionary Roles of Upstream Open Reading Frames in Mediating Gene Regulation in Fungi. <i>Annual Review of Microbiology</i> , 2009, 63, 385-409.	2.9	105
63	A blind deconvolution approach to high-resolution mapping of transcription factor binding sites from ChIP-seq data. <i>Genome Biology</i> , 2009, 10, R142.	13.9	61
64	Naturally occurring dominant resistance mutations to hepatitis C virus protease and polymerase inhibitors in treatment-naïve patients. <i>Hepatology</i> , 2008, 48, 1769-1778.	3.6	326
65	Short-term genome evolution of <i>Listeria monocytogenes</i> in a non-controlled environment. <i>BMC Genomics</i> , 2008, 9, 539.	1.2	170
66	Cross-kingdom patterns of alternative splicing and splice recognition. <i>Genome Biology</i> , 2008, 9, R50.	13.9	126
67	Mechanisms of intron gain and loss in <i>Cryptococcus</i> . <i>Genome Biology</i> , 2008, 9, R24.	13.9	75
68	Dynamics of <i>Pseudomonas aeruginosa</i> genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3100-3105.	3.3	492
69	Conserved Secondary Structures in <i>Aspergillus</i> . <i>PLoS ONE</i> , 2008, 3, e2812.	1.1	4
70	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.	0.8	191
71	Dual Modes of Natural Selection on Upstream Open Reading Frames. <i>Molecular Biology and Evolution</i> , 2007, 24, 1744-1751.	3.5	46
72	Conrad: Gene prediction using conditional random fields. <i>Genome Research</i> , 2007, 17, 1389-1398.	2.4	62

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73	Dothideomyceteâ€“Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i> . <i>Plant Cell</i> , 2007, 19, 3347-3368.	3.1	235
74	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	6.0	1,025
75	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 113-119.	9.4	320
76	Positive selection for unpreferred codon usage in eukaryotic genomes. <i>BMC Evolutionary Biology</i> , 2007, 7, 119.	3.2	22
77	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006, 444, 97-101.	13.7	1,113
78	Combo: a whole genome comparative browser. <i>Bioinformatics</i> , 2006, 22, 1782-1783.	1.8	46
79	The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nature</i> , 2005, 434, 980-986.	13.7	1,447
80	Genome sequencing and analysis of <i>Aspergillus oryzae</i> . <i>Nature</i> , 2005, 438, 1157-1161.	13.7	1,128
81	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
82	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , 2005, 438, 1105-1115.	13.7	1,250
83	Assembly of polymorphic genomes: Algorithms and application to <i>Ciona savignyi</i> . <i>Genome Research</i> , 2005, 15, 1127-1135.	2.4	170
84	Genomics of the fungal kingdom: Insights into eukaryotic biology. <i>Genome Research</i> , 2005, 15, 1620-1631.	2.4	269
85	Improving genome annotations using phylogenetic profile anomaly detection. <i>Bioinformatics</i> , 2005, 21, 464-470.	1.8	22
86	Patterns of Intron Gain and Loss in Fungi. <i>PLoS Biology</i> , 2004, 2, e422.	2.6	117
87	RIP: the evolutionary cost of genome defense. <i>Trends in Genetics</i> , 2004, 20, 417-423.	2.9	392
88	Lessons from the Genome Sequence of <i>Neurospora crassa</i> : Tracing the Path from Genomic Blueprint to Multicellular Organism. <i>Microbiology and Molecular Biology Reviews</i> , 2004, 68, 1-108.	2.9	572
89	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 2003, 422, 859-868.	13.7	1,528
90	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	2.4	573

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91	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
92	Genomic insights into tuberculosis. , 0, .		1
93	Transcription Factor Binding Site Mapping Using ChIP-Seq. , 0, , 161-181.		0