Gabriel Moreno-Hagelsieb

List of Publications by Year
in descending order

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71	8,019	156536 32	100535 70
papers	citations	h-index	g-index
76	76	76	14067
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	The Functional Differences between the GroEL Chaperonin of Escherichia coli and the HtpB Chaperonin of Legionella pneumophila Can Be Mapped to Specific Amino Acid Residues. Biomolecules, 2022, 12, 59.	1.8	2
2	RegulonDB 11.0: Comprehensive high-throughput datasets on transcriptional regulation in Escherichia coli K-12. Microbial Genomics, 2022, 8, .	1.0	32
3	The Transporter Classification Database (TCDB): 2021 update. Nucleic Acids Research, 2021, 49, D461-D467.	6.5	192
4	PathFams: statistical detection of pathogen-associated protein domains. BMC Genomics, 2021, 22, 663.	1.2	1
5	The volatile organic compound dimethylhexadecylamine affects bacterial growth and swarming motility of bacteria. Folia Microbiologica, 2020, 65, 523-532.	1.1	18
6	Progress in quickly finding orthologs as reciprocal best hits: comparing blast, last, diamond and MMseqs2. BMC Genomics, 2020, 21, 741.	1.2	43
7	Expansion of the Transporter-Opsin-G protein-coupled receptor superfamily with five new protein families. PLoS ONE, 2020, 15, e0231085.	1.1	11
8	An assessment of genome annotation coverage across the bacterial tree of life. Microbial Genomics, 2020, 6, .	1.0	55
9	Metabolic role of aldehyde dehydrogenases in Pseudomonas putida KT2440. FASEB Journal, 2020, 34, 1-1.	0.2	1
10	The predominance of nucleotidyl activation in bacterial phosphonate biosynthesis. Nature Communications, 2019, 10, 3698.	5.8	16
11	Aldehyde dehydrogenase diversity in bacteria of the Pseudomonas genus. Chemico-Biological Interactions, 2019, 304, 83-87.	1.7	26
12	Taxonomy and diversity of aldehyde dehydrogenases in bacteria of the Pseudomonas genus. FASEB Journal, 2019, 33, lb246.	0.2	0
13	Environmentally-driven gene content convergence and the Bacillus phylogeny. BMC Evolutionary Biology, 2018, 18, 148.	3.2	23
14	Bioinformatic characterization of the Anoctamin Superfamily of Ca2+-activated ion channels and lipid scramblases. PLoS ONE, 2018, 13, e0192851.	1.1	52
15	Transplantation of fecal microbiota from patients with irritable bowel syndrome alters gut function and behavior in recipient mice. Science Translational Medicine, 2017, 9, .	5.8	366
16	Inferring Functional Relationships from Conservation of Gene Order. Methods in Molecular Biology, 2017, 1526, 41-63.	0.4	0
17	The Membrane Attack Complex/Perforin Superfamily. Journal of Molecular Microbiology and Biotechnology, 2017, 27, 252-267.	1.0	23
18	Genome Comparison of Pseudomonas fluorescens UM270 with Related Fluorescent Strains Unveils Genes Involved in Rhizosphere Competence and Colonization. Journal of Genomics, 2017, 5, 91-98.	0.6	11

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19	Association of host genome with intestinal microbial composition in a large healthy cohort. Nature Genetics, 2016, 48, 1413-1417.	9.4	388
20	Analysis of 58 Families of Holins Using a Novel Program, PhyST. Journal of Molecular Microbiology and Biotechnology, 2016, 26, 381-388.	1.0	3
21	Draft Genome Sequence of the Biocontrol and Plant Growth-Promoting Rhizobacterium Pseudomonas fluorescens strain UM270. Standards in Genomic Sciences, 2016, 11, 5.	1.5	21
22	The Transporter Classification Database (TCDB): recent advances. Nucleic Acids Research, 2016, 44, D372-D379.	6.5	711
23	Plant growth-promoting bacterial endophytes. Microbiological Research, 2016, 183, 92-99.	2.5	1,194
24	Remote homology and the functions of metagenomic dark matter. Frontiers in Genetics, 2015, 6, 234.	1.1	31
25	The functional landscape bound to the transcription factors of Escherichia coli K-12. Computational Biology and Chemistry, 2015, 58, 93-103.	1.1	16
26	Determinants of Intestinal Permeability in Healthy First-Degree Relatives of Individuals with CrohnÊ¼s Disease. Inflammatory Bowel Diseases, 2015, 21, 879-887.	0.9	49
27	The power of operon rearrangements for predicting functional associations. Computational and Structural Biotechnology Journal, 2015, 13, 402-406.	1.9	18
28	Estimating overannotation across prokaryotic genomes using BLAST+, UBLAST, LAST and BLAT. BMC Research Notes, 2014, 7, 651.	0.6	6
29	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in Escherichia coli. PLoS Genetics, 2014, 10, e1004120.	1.5	96
30	The loose evolutionary relationships between transcription factors and other gene products across prokaryotes. BMC Research Notes, 2014, 7, 928.	0.6	2
31	Evaluating Bias of Illumina-Based Bacterial 16S rRNA Gene Profiles. Applied and Environmental Microbiology, 2014, 80, 5717-5722.	1.4	250
32	Quickly Finding Orthologs as Reciprocal Best Hits with BLAT, LAST, and UBLAST: How Much Do We Miss?. PLoS ONE, 2014, 9, e101850.	1.1	133
33	Phylogenomic clustering for selecting non-redundant genomes for comparative genomics. Bioinformatics, 2013, 29, 947-949.	1.8	38
34	Meeting Report: 1st International Functional Metagenomics Workshop May 7â€“8, 2012, St. Jacobs, Ontario, Canada.. Standards in Genomic Sciences, 2013, 8, 106-111.	1.5	2
35	The evolutionary dynamics of functional modules and the extraordinary plasticity of regulons: the Escherichia coli perspective. Nucleic Acids Research, 2012, 40, 7104-7112.	6.5	12
36	Metagenomic Annotation Networks: Construction and Applications. PLoS ONE, 2012, 7, e41283.	1.1	15

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37	Genetic Interaction Maps in Escherichia coli Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. PLoS Genetics, 2011, 7, e1002377.	1.5	95
38	Open resource metagenomics: a model for sharing metagenomic libraries. Standards in Genomic Sciences, 2011, 5, 203-210.	1.5	20
39	Generation of Multimillion-Sequence 16S rRNA Gene Libraries from Complex Microbial Communities by Assembling Paired-End Illumina Reads. Applied and Environmental Microbiology, 2011, 77, 3846-3852.	1.4	697
40	Phylogenetic Distribution and Evolutionary History of Bacterial DEAD-Box Proteins. Journal of Molecular Evolution, 2011, 72, 413-431.	0.8	30
41	Network-based function prediction and interactomics: The case for metabolic enzymes. Metabolic Engineering, 2011, 13, 1-10.	3.6	43
42	Bacterial biogeography of the human digestive tract. Scientific Reports, 2011, 1, 170.	1.6	347
43	The pseudogenes of Mycobacterium leprae reveal the functional relevance of gene order within operons. Nucleic Acids Research, 2011, 39, 1732-1738.	6.5	15
44	Understanding the evolutionary relationships and major traits of Bacillus through comparative genomics. BMC Genomics, 2010, 11, 332.	1.2	143
45	Characterization of the NifA-RpoN Regulon in <i>Rhizobium etli</i> in Free Life and in Symbiosis with <i>Phaseolus vulgaris</i>. Applied and Environmental Microbiology, 2010, 76, 4510-4520.	1.4	62
46	Beyond the bounds of orthology: functional inference from metagenomic context. Molecular BioSystems, 2010, 6, 1247.	2.9	6
47	Global Functional Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins. PLoS Biology, 2009, 7, e1000096.	2.6	331
48	Probing Teichoic Acid Genetics with Bioactive Molecules Reveals New Interactions among Diverse Processes in Bacterial Cell Wall Biogenesis. Chemistry and Biology, 2009, 16, 548-556.	6.2	68
49	Operons and the effect of genome redundancy in deciphering functional relationships using phylogenetic profiles. Proteins: Structure, Function and Bioinformatics, 2008, 70, 344-352.	1.5	27
50	eSGA: E. coli synthetic genetic array analysis. Nature Methods, 2008, 5, 789-795.	9.0	231
51	Inferring Functional Relationships from Conservation of Gene Order. Methods in Molecular Biology, 2008, 453, 181-199.	0.4	2
52	Choosing BLAST options for better detection of orthologs as reciprocal best hits. Bioinformatics, 2008, 24, 319-324.	1.8	482
53	Whole-Genome Expression Profiling Defines the HrpL Regulon of Pseudomonas syringae pv. tomato DC3000, Allows de novo Reconstruction of the Hrp cis Element, and Identifies Novel Coregulated Genes. Molecular Plant-Microbe Interactions, 2006, 19, 1167-1179.	1.4	105
54	The distinctive signatures of promoter regions and operon junctions across prokaryotes. Nucleic Acids Research, 2006, 34, 3980-3987.	6.5	14

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55	Operons Across Prokaryotes: Genomic Analyses and Predictions 300+ Genomes Later. Current Genomics, 2006, 7, 163-170.	0.7	8
56	The partitioned Rhizobium etli genome: Genetic and metabolic redundancy in seven interacting replicons. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3834-3839.	3.3	365
57	Modelling Dynamics of Genetic Networks as a Multiscale Process. Lecture Notes in Computer Science, 2005, , 134-138.	1.0	2
58	Nebulon: a system for the inference of functional relationships of gene products from the rearrangement of predicted operons. Nucleic Acids Research, 2005, 33, 2521-2530.	6.5	44
59	Successful Lateral Transfer Requires Codon Usage Compatibility Between Foreign Genes and Recipient Genomes. Molecular Biology and Evolution, 2004, 21, 1884-1894.	3.5	75
60	Conservation of adjacency as evidence of paralogous operons. Nucleic Acids Research, 2004, 32, 5392-5397.	6.5	36
61	A new method of solution for the occupancy problem and its application to operon size prediction. Journal of Theoretical Biology, 2004, 227, 315-322.	0.8	1
62	The mosaic structure of the symbiotic plasmid of Rhizobium etli CFN42 and its relation to other symbiotic genome compartments. Genome Biology, 2003, 4, R36.	13.9	167
63	Conservation of DNA curvature signals in regulatory regions of prokaryotic genes. Nucleic Acids Research, 2003, 31, 6770-6777.	6.5	54
64	A powerful non-homology method for the prediction of operons in prokaryotes. Bioinformatics, 2002, 18, S329-S336.	1.8	173
65	Microbial computational genomics of gene regulation. Pure and Applied Chemistry, 2002, 74, 899-905.	0.9	3
66	Operon conservation from the point of view of Escherichia coli, and inference of functional interdependence of gene products from genome context. In Silico Biology, 2002, 2, 87-95.	0.4	15
67	VIR.II: a new interface with the antibody sequences in the Kabat database. BioSystems, 2001, 61, 125-131.	0.9	6
68	Transcription unit conservation in the three domains of life: a perspective from Escherichia coli. Trends in Genetics, 2001, 17, 175-177.	2.9	46
69	A Comparative Genomics Approach to Prediction of New Members of Regulons. Genome Research, 2001, 11, 566-584.	2.4	113
70	Operons in Escherichia coli: Genomic analyses and predictions. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 6652-6657.	3.3	314
71	Escherichia coli TEM1 Î²-lactamase in CTAB reverse micelles: exchange/diffusion-limited catalysis. FEBS Letters, 1999, 459, 111-114.	1.3	6