# Gabriel Moreno-Hagelsieb

List of Publications by Year
in descending order

| 71 papers | 8,019 citations | 136950 32 h-index | 88630 70 g-index |
|---|---|---|---|
| 76 all docs | 76 docs citations | 76 times ranked | 12627 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Plant growth-promoting bacterial endophytes. Microbiological Research, 2016, 183, 92-99. | 5.3 | 1,194 |
| 2 | The Transporter Classification Database (TCDB): recent advances. Nucleic Acids Research, 2016, 44, D372-D379. | 14.5 | 711 |
| 3 | 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. | 3.1 | 697 |
| 4 | Choosing BLAST options for better detection of orthologs as reciprocal best hits. Bioinformatics, 2008, 24, 319-324. | 4.1 | 482 |
| 5 | Association of host genome with intestinal microbial composition in a large healthy cohort. Nature Genetics, 2016, 48, 1413-1417. | 21.4 | 388 |
| 6 | Transplantation of fecal microbiota from patients with irritable bowel syndrome alters gut function and behavior in recipient mice. Science Translational Medicine, 2017, 9, . | 12.4 | 366 |
| 7 | 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. | 7.1 | 365 |
| 8 | Bacterial biogeography of the human digestive tract. Scientific Reports, 2011, 1, 170. | 3.3 | 347 |
| 9 | Global Functional Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins. PLoS Biology, 2009, 7, e1000096. | 5.6 | 331 |
| 10 | 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. | 7.1 | 314 |
| 11 | Evaluating Bias of Illumina-Based Bacterial 16S rRNA Gene Profiles. Applied and Environmental Microbiology, 2014, 80, 5717-5722. | 3.1 | 250 |
| 12 | eSGA: E. coli synthetic genetic array analysis. Nature Methods, 2008, 5, 789-795. | 19.0 | 231 |
| 13 | The Transporter Classification Database (TCDB): 2021 update. Nucleic Acids Research, 2021, 49, D461-D467. | 14.5 | 192 |
| 14 | A powerful non-homology method for the prediction of operons in prokaryotes. Bioinformatics, 2002, 18, S329-S336. | 4.1 | 173 |
| 15 | The mosaic structure of the symbiotic plasmid of Rhizobium etliCFN42 and its relation to other symbiotic genome compartments. Genome Biology, 2003, 4, R36. | 9.6 | 167 |
| 16 | Understanding the evolutionary relationships and major traits of Bacillus through comparative genomics. BMC Genomics, 2010, 11, 332. | 2.8 | 143 |
| 17 | Quickly Finding Orthologs as Reciprocal Best Hits with BLAT, LAST, and UBLAST: How Much Do We Miss?. PLoS ONE, 2014, 9, e101850. | 2.5 | 133 |
| 18 | A Comparative Genomics Approach to Prediction of New Members of Regulons. Genome Research, 2001, 11, 566-584. | 5.5 | 113 |

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|---|---------|-----|-----------|
| 19 | 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. | 2.6 | 105 |
| 20 | Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in Escherichia coli. PLoS Genetics, 2014, 10, e1004120. | 3.5 | 96 |
| 21 | Genetic Interaction Maps in Escherichia coli Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. PLoS Genetics, 2011, 7, e1002377. | 3.5 | 95 |
| 22 | Successful Lateral Transfer Requires Codon Usage Compatibility Between Foreign Genes and Recipient Genomes. Molecular Biology and Evolution, 2004, 21, 1884-1894. | 8.9 | 75 |
| 23 | 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. | 6.0 | 68 |
| 24 | Characterization of the NifA-RpoN Regulon in *Rhizobium etli* in Free Life and in Symbiosis with *Phaseolus vulgaris*. Applied and Environmental Microbiology, 2010, 76, 4510-4520. | 3.1 | 62 |
| 25 | An assessment of genome annotation coverage across the bacterial tree of life. Microbial Genomics, 2020, 6, . | 2.0 | 55 |
| 26 | Conservation of DNA curvature signals in regulatory regions of prokaryotic genes. Nucleic Acids Research, 2003, 31, 6770-6777. | 14.5 | 54 |
| 27 | Bioinformatic characterization of the Anoctamin Superfamily of $Ca^{2+}$-activated ion channels and lipid scramblases. PLoS ONE, 2018, 13, e0192851. | 2.5 | 52 |
| 28 | Determinants of Intestinal Permeability in Healthy First-Degree Relatives of Individuals with Crohn¼s Disease. Inflammatory Bowel Diseases, 2015, 21, 879-887. | 1.9 | 49 |
| 29 | Transcription unit conservation in the three domains of life: a perspective from Escherichia coli. Trends in Genetics, 2001, 17, 175-177. | 6.7 | 46 |
| 30 | 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. | 14.5 | 44 |
| 31 | Network-based function prediction and interactomics: The case for metabolic enzymes. Metabolic Engineering, 2011, 13, 1-10. | 7.0 | 43 |
| 32 | Progress in quickly finding orthologs as reciprocal best hits: comparing blast, last, diamond and MMseqs2. BMC Genomics, 2020, 21, 741. | 2.8 | 43 |
| 33 | Phylogenomic clustering for selecting non-redundant genomes for comparative genomics. Bioinformatics, 2013, 29, 947-949. | 4.1 | 38 |
| 34 | Conservation of adjacency as evidence of paralogous operons. Nucleic Acids Research, 2004, 32, 5392-5397. | 14.5 | 36 |
| 35 | RegulonDB 11.0: Comprehensive high-throughput datasets on transcriptional regulation in Escherichia coli K-12. Microbial Genomics, 2022, 8, . | 2.0 | 32 |
| 36 | Remote homology and the functions of metagenomic dark matter. Frontiers in Genetics, 2015, 6, 234. | 2.3 | 31 |

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|---|---------|-----|-----------|
| 37 | Phylogenetic Distribution and Evolutionary History of Bacterial DEAD-Box Proteins. Journal of Molecular Evolution, 2011, 72, 413-431. | 1.8 | 30 |
| 38 | Operons and the effect of genome redundancy in deciphering functional relationships using phylogenetic profiles. Proteins: Structure, Function and Bioinformatics, 2008, 70, 344-352. | 2.6 | 27 |
| 39 | Aldehyde dehydrogenase diversity in bacteria of the Pseudomonas genus. Chemico-Biological Interactions, 2019, 304, 83-87. | 4.0 | 26 |
| 40 | The Membrane Attack Complex/Perforin Superfamily. Journal of Molecular Microbiology and Biotechnology, 2017, 27, 252-267. | 1.0 | 23 |
| 41 | Environmentally-driven gene content convergence and the Bacillus phylogeny. BMC Evolutionary Biology, 2018, 18, 148. | 3.2 | 23 |
| 42 | 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 |
| 43 | Open resource metagenomics: a model for sharing metagenomic libraries. Standards in Genomic Sciences, 2011, 5, 203-210. | 1.5 | 20 |
| 44 | The power of operon rearrangements for predicting functional associations. Computational and Structural Biotechnology Journal, 2015, 13, 402-406. | 4.1 | 18 |
| 45 | The volatile organic compound dimethylhexadecylamine affects bacterial growth and swarming motility of bacteria. Folia Microbiologica, 2020, 65, 523-532. | 2.3 | 18 |
| 46 | The functional landscape bound to the transcription factors of Escherichia coli K-12. Computational Biology and Chemistry, 2015, 58, 93-103. | 2.3 | 16 |
| 47 | The predominance of nucleotidyl activation in bacterial phosphonate biosynthesis. Nature Communications, 2019, 10, 3698. | 12.8 | 16 |
| 48 | The pseudogenes of Mycobacterium leprae reveal the functional relevance of gene order within operons. Nucleic Acids Research, 2011, 39, 1732-1738. | 14.5 | 15 |
| 49 | Metagenomic Annotation Networks: Construction and Applications. PLoS ONE, 2012, 7, e41283. | 2.5 | 15 |
| 50 | 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. | 0.9 | 15 |
| 51 | The distinctive signatures of promoter regions and operon junctions across prokaryotes. Nucleic Acids Research, 2006, 34, 3980-3987. | 14.5 | 14 |
| 52 | The evolutionary dynamics of functional modules and the extraordinary plasticity of regulons: the Escherichia coli perspective. Nucleic Acids Research, 2012, 40, 7104-7112. | 14.5 | 12 |
| 53 | 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. | 0.9 | 11 |
| 54 | Expansion of the Transporter-Opsin-G protein-coupled receptor superfamily with five new protein families. PLoS ONE, 2020, 15, e0231085. | 2.5 | 11 |

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|---|---------|----|-----------| 
| 55 | Operons Across Prokaryotes: Genomic Analyses and Predictions 300+ Genomes Later. Current Genomics, 2006, 7, 163-170. | 1.6 | 8 |
| 56 | Escherichia coli TEM1 Î²-lactamase in CTAB reverse micelles: exchange/diffusion-limited catalysis. FEBS Letters, 1999, 459, 111-114. | 2.8 | 6 |
| 57 | VIR.II: a new interface with the antibody sequences in the Kabat database. BioSystems, 2001, 61, 125-131. | 2.0 | 6 |
| 58 | Beyond the bounds of orthology: functional inference from metagenomic context. Molecular BioSystems, 2010, 6, 1247. | 2.9 | 6 |
| 59 | Estimating overannotation across prokaryotic genomes using BLAST+, UBLAST, LAST and BLAT. BMC Research Notes, 2014, 7, 651. | 1.4 | 6 |
| 60 | Microbial computational genomics of gene regulation. Pure and Applied Chemistry, 2002, 74, 899-905. | 1.9 | 3 |
| 61 | Analysis of 58 Families of Holins Using a Novel Program, PhyST. Journal of Molecular Microbiology and Biotechnology, 2016, 26, 381-388. | 1.0 | 3 |
| 62 | Modelling Dynamics of Genetic Networks as a Multiscale Process. Lecture Notes in Computer Science, 2005, , 134-138. | 1.3 | 2 |
| 63 | Inferring Functional Relationships from Conservation of Gene Order. Methods in Molecular Biology, 2008, 453, 181-199. | 0.9 | 2 |
| 64 | 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 |
| 65 | The loose evolutionary relationships between transcription factors and other gene products across prokaryotes. BMC Research Notes, 2014, 7, 928. | 1.4 | 2 |
| 66 | 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. | 4.0 | 2 |
| 67 | A new method of solution for the occupancy problem and its application to operon size prediction. Journal of Theoretical Biology, 2004, 227, 315-322. | 1.7 | 1 |
| 68 | PathFams: statistical detection of pathogen-associated protein domains. BMC Genomics, 2021, 22, 663. | 2.8 | 1 |
| 69 | Metabolic role of aldehyde dehydrogenases in Pseudomonas putida KT2440. FASEB Journal, 2020, 34, 1-1. | 0.5 | 1 |
| 70 | Inferring Functional Relationships from Conservation of Gene Order. Methods in Molecular Biology, 2017, 1526, 41-63. | 0.9 | 0 |
| 71 | Taxonomy and diversity of aldehyde dehydrogenases in bacteria of the Pseudomonas genus. FASEB Journal, 2019, 33, lb246. | 0.5 | 0 |