

Jaime Huerta-Cepas

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

40,282
citations

66343

42
h-index

133252

59
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70
all docs

70
docs citations

70
times ranked

64007
citing authors

#	ARTICLE	IF	CITATIONS
1	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , 2019, 47, D607-D613.	14.5	12,237
2	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	14.5	9,029
3	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , 2019, 47, D309-D314.	14.5	2,575
4	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017, 34, 2115-2122.	8.9	2,156
5	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016, 44, D286-D293.	14.5	1,937
6	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 1635-1638.	8.9	1,692
7	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
8	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	27.8	1,370
9	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. <i>Molecular Biology and Evolution</i> , 2021, 38, 5825-5829.	8.9	1,174
10	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	5.6	913
11	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	14.5	526
12	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016, 352, 586-589.	12.6	461
13	ETE: a python Environment for Tree Exploration. <i>BMC Bioinformatics</i> , 2010, 11, 24.	2.6	366
14	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	12.8	298
15	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
16	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. <i>Nucleic Acids Research</i> , 2014, 42, D897-D902.	14.5	264
17	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	19.0	198
18	PhyloMon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. <i>Nucleic Acids Research</i> , 2011, 39, W470-W474.	14.5	182

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19	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016, 32, 2520-2523.	4.1	172
20	The human phylome. <i>Genome Biology</i> , 2007, 8, R109.	8.8	150
21	PhylomeDB v3.0: an expanding repository of genome-wide collections of trees, alignments and phylogeny-based orthology and paralogy predictions. <i>Nucleic Acids Research</i> , 2011, 39, D556-D560.	14.5	134
22	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017, 45, D529-D534.	14.5	131
23	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017, 13, 960.	7.2	115
24	MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score. <i>Nucleic Acids Research</i> , 2011, 39, e32-e32.	14.5	114
25	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021, 374, 717-723.	12.6	111
26	From genes to functional classes in the study of biological systems. <i>BMC Bioinformatics</i> , 2007, 8, 114.	2.6	108
27	Next station in microarray data analysis: CEPAS. <i>Nucleic Acids Research</i> , 2006, 34, W486-W491.	14.5	107
28	Interoperability with Moby 1.0–It's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008, 9, 220-231.	6.5	91
29	PhylomeDB: a database for genome-wide collections of gene phylogenies. <i>Nucleic Acids Research</i> , 2007, 36, D491-D496.	14.5	90
30	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. <i>Nucleic Acids Research</i> , 2015, 43, D494-D502.	14.5	90
31	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	27.8	85
32	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. <i>ISME Journal</i> , 2010, 4, 882-895.	9.8	81
33	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	9.8	74
34	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019, 68, 1781-1790.	12.1	73
35	CEPAS, a web-based tool for microarray data analysis and interpretation. <i>Nucleic Acids Research</i> , 2008, 36, W308-W314.	14.5	67
36	Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. <i>Briefings in Bioinformatics</i> , 2011, 12, 442-448.	6.5	67

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37	PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease. Nucleic Acids Research, 2007, 35, D815-D822.	14.5	65
38	Assigning duplication events to relative temporal scales in genome-wide studies. Bioinformatics, 2011, 27, 38-45.	4.1	65
39	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. Nucleic Acids Research, 2020, 48, D621-D625.	14.5	60
40	An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. Nucleic Acids Research, 2014, 42, 13525-13533.	14.5	55
41	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. Nucleic Acids Research, 2007, 35, W38-W42.	14.5	47
42	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. Microbiome, 2019, 7, 84.	11.1	42
43	Comparative transcriptomics of early dipteran development. BMC Genomics, 2013, 14, 123.	2.8	41
44	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	14.5	41
45	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	4.1	36
46	Evidence for systems-level molecular mechanisms of tumorigenesis. BMC Genomics, 2007, 8, 185.	2.8	31
47	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. Molecular Biology and Evolution, 2017, 34, 1535-1542.	8.9	28
48	Neuroprotection elicited by P2Y13 receptors against genotoxic stress by inducing DUSP2 expression and MAPK signaling recovery. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 1886-1898.	4.1	27
49	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. Genome Biology and Evolution, 2015, 7, 1988-1999.	2.5	25
50	ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw081.	3.0	22
51	Prevalence and Specificity of Chemoreceptor Profiles in Plant-Associated Bacteria. MSystems, 2021, 6, e0095121.	3.8	20
52	CycADS: an annotation database system to ease the development and update of BioCyc databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar008-bar008.	3.0	16
53	Metabolic anchor reactions for robust biorefining. Metabolic Engineering, 2017, 40, 1-4.	7.0	12
54	Prokaryotic ancestry and gene fusion of a dual localized peroxiredoxin in malaria parasites. Microbial Cell, 2015, 2, 5-13.	3.2	9

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55	GeCoViz: genomic context visualisation of prokaryotic genes from a functional and evolutionary perspective. Nucleic Acids Research, 2022, 50, W352-W357.	14.5	9
56	PhyloCloud: an online platform for making sense of phylogenomic data. Nucleic Acids Research, 2022, , .	14.5	4
57	Automatic Prediction of the Genetic Code. Lecture Notes in Computer Science, 2009, , 1125-1129.	1.3	1