

Jaime Huerta-Cepas

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

40,282
citations

66234

42
h-index

133063

59
g-index

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.	6.5	12,237
2	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	6.5	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.	6.5	2,575
4	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017, 34, 2115-2122.	3.5	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.	6.5	1,937
6	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 1635-1638.	3.5	1,692
7	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
8	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	13.7	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.	3.5	1,174
10	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	2.6	913
11	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	6.5	526
12	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016, 352, 586-589.	6.0	461
13	ETE: a python Environment for Tree Exploration. <i>BMC Bioinformatics</i> , 2010, 11, 24.	1.2	366
14	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	5.8	298
15	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	13.5	268
16	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. <i>Nucleic Acids Research</i> , 2014, 42, D897-D902.	6.5	264
17	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	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.	6.5	182

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19	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016, 32, 2520-2523.	1.8	172
20	The human phylome. <i>Genome Biology</i> , 2007, 8, R109.	3.8	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.	6.5	134
22	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017, 45, D529-D534.	6.5	131
23	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017, 13, 960.	3.2	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.	6.5	114
25	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021, 374, 717-723.	6.0	111
26	From genes to functional classes in the study of biological systems. <i>BMC Bioinformatics</i> , 2007, 8, 114.	1.2	108
27	Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , 2006, 34, W486-W491.	6.5	107
28	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008, 9, 220-231.	3.2	91
29	PhylomeDB: a database for genome-wide collections of gene phylogenies. <i>Nucleic Acids Research</i> , 2007, 36, D491-D496.	6.5	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.	6.5	90
31	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	13.7	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.	4.4	81
33	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	4.4	74
34	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019, 68, 1781-1790.	6.1	73
35	GEPAS, a web-based tool for microarray data analysis and interpretation. <i>Nucleic Acids Research</i> , 2008, 36, W308-W314.	6.5	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.	3.2	67

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37	PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease. <i>Nucleic Acids Research</i> , 2007, 35, D815-D822.	6.5	65
38	Assigning duplication events to relative temporal scales in genome-wide studies. <i>Bioinformatics</i> , 2011, 27, 38-45.	1.8	65
39	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2020, 48, D621-D625.	6.5	60
40	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014, 42, 13525-13533.	6.5	55
41	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. <i>Nucleic Acids Research</i> , 2007, 35, W38-W42.	6.5	47
42	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. <i>Microbiome</i> , 2019, 7, 84.	4.9	42
43	Comparative transcriptomics of early dipteran development. <i>BMC Genomics</i> , 2013, 14, 123.	1.2	41
44	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020, 48, W538-W545.	6.5	41
45	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
46	Evidence for systems-level molecular mechanisms of tumorigenesis. <i>BMC Genomics</i> , 2007, 8, 185.	1.2	31
47	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. <i>Molecular Biology and Evolution</i> , 2017, 34, 1535-1542.	3.5	28
48	Neuroprotection elicited by P2Y13 receptors against genotoxic stress by inducing DUSP2 expression and MAPK signaling recovery. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1886-1898.	1.9	27
49	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , 2015, 7, 1988-1999.	1.1	25
50	ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw081.	1.4	22
51	Prevalence and Specificity of Chemoreceptor Profiles in Plant-Associated Bacteria. <i>MSystems</i> , 2021, 6, e0095121.	1.7	20
52	CycADS: an annotation database system to ease the development and update of BioCyc databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar008-bar008.	1.4	16
53	Metabolic anchor reactions for robust biorefining. <i>Metabolic Engineering</i> , 2017, 40, 1-4.	3.6	12
54	Prokaryotic ancestry and gene fusion of a dual localized peroxiredoxin in malaria parasites. <i>Microbial Cell</i> , 2015, 2, 5-13.	1.4	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.	6.5	9
56	PhyloCloud: an online platform for making sense of phylogenomic data. Nucleic Acids Research, 2022, , .	6.5	4
57	Automatic Prediction of the Genetic Code. Lecture Notes in Computer Science, 2009, , 1125-1129.	1.0	1