

Jaime Huerta-Cepas

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

60
papers

22,365
citations

37
h-index

70
g-index

70
ext. papers

33,413
ext. citations

16.1
avg, IF

7.14
L-index

#	Paper	IF	Citations
60	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015 , 43, D447-52	20.1	6276
59	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	20.1	5966
58	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016 , 44, D286-93	20.1	1211
57	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
56	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2115-2122	8.3	966
55	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. <i>Molecular Biology and Evolution</i> , 2016 , 33, 1635-8	8.3	898
54	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	20.1	850
53	Genome sequence of the pea aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010 , 8, e1000313	9.7	732
52	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018 , 560, 233-237	50.4	654
51	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014 , 42, D2312-9	20.1	387
50	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016 , 352, 586-9	33.3	326
49	ETE: a python Environment for Tree Exploration. <i>BMC Bioinformatics</i> , 2010 , 11, 24	3.6	290
48	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. <i>Nucleic Acids Research</i> , 2014 , 42, D897-902	20.1	171
47	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019 , 10, 1014	17.4	134
46	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. <i>Nucleic Acids Research</i> , 2011 , 39, W470-4	20.1	133
45	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016 , 13, 425-30	21.6	133
44	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, D556-60	20.1	125

43	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , 2016 , 32, 2520-3.2	3.2	117
42	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5825-5829	8.3	116
41	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019 , 179, 1068-1083.e21	56.2	113
40	The human phylome. <i>Genome Biology</i> , 2007 , 8, R109	18.3	111
39	From genes to functional classes in the study of biological systems. <i>BMC Bioinformatics</i> , 2007 , 8, 114	3.6	103
38	Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , 2006 , 34, W486-91	20.1	101
37	MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score. <i>Nucleic Acids Research</i> , 2011 , 39, e32	20.1	94
36	PhylomeDB: a database for genome-wide collections of gene phylogenies. <i>Nucleic Acids Research</i> , 2008 , 36, D491-6	20.1	79
35	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017 , 45, D529-D534	20.1	74
34	Interoperability with Moby 1.0—it's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008 , 9, 220-31	13.4	73
33	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , 2017 , 13, 960	12.2	69
32	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. <i>Nucleic Acids Research</i> , 2015 , 43, D494-502	20.1	67
31	PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease. <i>Nucleic Acids Research</i> , 2007 , 35, D815-22	20.1	63
30	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. <i>ISME Journal</i> , 2010 , 4, 882-95	11.9	58
29	GEPAS, a web-based tool for microarray data analysis and interpretation. <i>Nucleic Acids Research</i> , 2008 , 36, W308-14	20.1	58
28	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. <i>Nucleic Acids Research</i> , 2007 , 35, W38-42	20.1	45
27	Assigning duplication events to relative temporal scales in genome-wide studies. <i>Bioinformatics</i> , 2011 , 27, 38-45	7.2	41
26	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014 , 42, 13525-33	20.1	40

25	Comparative transcriptomics of early dipteran development. <i>BMC Genomics</i> , 2013 , 14, 123	4.5	35
24	Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. <i>Briefings in Bioinformatics</i> , 2011 , 12, 442-8	13.4	35
23	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019 , 68, 1781-1790	19.2	33
22	Evidence for systems-level molecular mechanisms of tumorigenesis. <i>BMC Genomics</i> , 2007 , 8, 185	4.5	28
21	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018 , 34, 323-329	37.9	25
20	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale		24
19	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020 , 14, 1247-1259	11.9	23
18	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution		22
17	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	20.1	21
16	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , 2015 , 7, 1988-99	3.9	19
15	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, 1886-98	4.9	19
14	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, W538-W545	20.1	17
13	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. <i>Microbiome</i> , 2019 , 7, 84	16.6	15
12	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021 , 374, 717-723	33.3	15
11	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	8.3	13
10	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	5	13
9	Fast genome-wide functional annotation through orthology assignment by eggNOG-mapper		13
8	Metabolic anchor reactions for robust biorefining. <i>Metabolic Engineering</i> , 2017 , 40, 1-4	9.7	12

7	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,	5	10
6	Prokaryotic ancestry and gene fusion of a dual localized peroxiredoxin in malaria parasites. <i>Microbial Cell</i> , 2015 , 2, 5-13	3.9	9
5	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , 2021 ,	50.4	8
4	RNA degradation analysis reveals ribosome dynamics in complex microbiome samples		2
3	Prevalence and Specificity of Chemoreceptor Profiles in Plant-Associated Bacteria. <i>MSystems</i> , 2021 , 6, e0095121	7.6	2
2	Automatic Prediction of the Genetic Code. <i>Lecture Notes in Computer Science</i> , 2009 , 1125-1129	0.9	1
1	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language		1