

# Jaime Huerta-Cepas

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/9189912/jaime-huerta-cepas-publications-by-year.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , <b>2021</b> ,	50.4	8
59	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , <b>2021</b> , 374, 717-723	33.3	15
58	Prevalence and Specificity of Chemoreceptor Profiles in Plant-Associated Bacteria. <i>MSystems</i> , <b>2021</b> , 6, e0095121	7.6	2
57	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 5825-5829	8.3	116
56	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W538-W545	20.1	17
55	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , <b>2020</b> , 14, 1247-1259	11.9	23
54	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D621-D625	20.1	21
53	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , <b>2019</b> , 68, 1781-1790	19.2	33
52	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. <i>Microbiome</i> , <b>2019</b> , 7, 84	16.6	15
51	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , <b>2019</b> , 10, 1014	17.4	134
50	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , <b>2019</b> , 179, 1068-1083.e21	56.2	113
49	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D607-D613	20.1	5966
48	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D309-D314	20.1	850
47	Structure and function of the global topsoil microbiome. <i>Nature</i> , <b>2018</b> , 560, 233-237	50.4	654
46	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , <b>2018</b> , 34, 323-329	32.9	25
45	Metabolic anchor reactions for robust biorefining. <i>Metabolic Engineering</i> , <b>2017</b> , 40, 1-4	9.7	12
44	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2115-2122	8.3	966

43	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 960	12.2	69
42	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 1535-1542	8.3	13
41	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D529-D534	20.1	74
40	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> , <b>2016</b> , 2016,	5	10
39	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 1635-8	8.3	898
38	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D286-93	20.1	1211
37	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , <b>2016</b> , 13, 425-30	21.6	133
36	MOCAT2: a metagenomic assembly, annotation and profiling framework. <i>Bioinformatics</i> , <b>2016</b> , 32, 2520-3	3.2	117
35	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , <b>2016</b> , 352, 586-9	33.3	326
34	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 1988-99	3.9	19
33	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D447-52	20.1	6276
32	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D494-502	20.1	67
31	Prokaryotic ancestry and gene fusion of a dual localized peroxiredoxin in malaria parasites. <i>Microbial Cell</i> , <b>2015</b> , 2, 5-13	3.9	9
30	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> , <b>2014</b> , 1843, 1886-98	4.9	19
29	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , <b>2014</b> , 346, 1320-31	33.3	1182
28	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 13525-33	20.1	40
27	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D897-902	20.1	171
26	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D2312	20.1	387

25	Comparative transcriptomics of early dipteran development. <i>BMC Genomics</i> , <b>2013</b> , 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> , <b>2011</b> , 12, 442-8	13.4	35
23	Assigning duplication events to relative temporal scales in genome-wide studies. <i>Bioinformatics</i> , <b>2011</b> , 27, 38-45	7.2	41
22	MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, e32	20.1	94
21	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W470-4	20.1	133
20	CycADS: an annotation database system to ease the development and update of BioCyc databases. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2011</b> , 2011, bar008	5	13
19	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> , <b>2011</b> , 39, D556-60	20.1	125
18	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. <i>ISME Journal</i> , <b>2010</b> , 4, 882-95	11.9	58
17	Genome sequence of the pea aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , <b>2010</b> , 8, e1000313	9.7	732
16	ETE: a python Environment for Tree Exploration. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 24	3.6	290
15	Automatic Prediction of the Genetic Code. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 1125-1129	0.9	1
14	GEPAS, a web-based tool for microarray data analysis and interpretation. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, W308-14	20.1	58
13	Interoperability with Moby 1.0--it's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , <b>2008</b> , 9, 220-31	13.4	73
12	PhylomeDB: a database for genome-wide collections of gene phylogenies. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D491-6	20.1	79
11	From genes to functional classes in the study of biological systems. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 114	3.6	103
10	Evidence for systems-level molecular mechanisms of tumorigenesis. <i>BMC Genomics</i> , <b>2007</b> , 8, 185	4.5	28
9	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W38-42	20.1	45
8	PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D815-22	20.1	63

7	The human phylome. <i>Genome Biology</i> , <b>2007</b> , 8, R109	18.3	111
6	Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W486-91	20.1	101
5	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language		1
4	Fast genome-wide functional annotation through orthology assignment by eggNOG-mapper		13
3	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution		22
2	RNA degradation analysis reveals ribosome dynamics in complex microbiome samples		2
1	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale		24