Jaime Huerta-Cepas

List of Publications by Year
in descending order

57 papers	40,282 citations	66315 42 h-index	133188 59 g-index
70 all docs	70 docs citations	70 times ranked	64007 citing authors

#	Article	IF	Citations
1	Towards the biogeography of prokaryotic genes. Nature, 2022, 601, 252-256.	13.7	85
2	GeCoViz: genomic context visualisation of prokaryotic genes from a functional and evolutionary perspective. Nucleic Acids Research, 2022, 50, W352-W357.	6.5	9
3	PhyloCloud: an online platform for making sense of phylogenomic data. Nucleic Acids Research, 2022, , .	6.5	4
4	Prevalence and Specificity of Chemoreceptor Profiles in Plant-Associated Bacteria. MSystems, 2021, 6, e0095121.	1.7	20
5	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. Molecular Biology and Evolution, 2021, 38, 5825-5829.	3.5	1,174
6	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. Science, 2021, 374, 717-723.	6.0	111
7	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. Nucleic Acids Research, 2020, 48, D621-D625.	6.5	60
8	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	6.5	41
9	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. ISME Journal, 2020, 14, 1247-1259.	4.4	74
10	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. Cell, 2019, 179, 1068-1083.e21.	13.5	268
11	Antibiotics-induced monodominance of a novel gut bacterial order. Gut, 2019, 68, 1781-1790.	6.1	73
12	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. Microbiome, 2019, 7, 84.	4.9	42
13	Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014.	5.8	298
14	STRING v11: protein–protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	6.5	12,237
15	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. Nucleic Acids Research, 2019, 47, D309-D314.	6.5	2,575
16	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	1.8	36
17	Structure and function of the global topsoil microbiome. Nature, 2018, 560, 233-237.	13.7	1,370
18	Metabolic anchor reactions for robust biorefining. Metabolic Engineering, 2017, 40, 1-4.	3.6	12

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19	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. Molecular Biology and Evolution, 2017, 34, 2115-2122.	3.5	2,156
20	Subspecies in the global human gut microbiome. Molecular Systems Biology, 2017, 13, 960.	3.2	115
21	A Critical Review on the Use of Support Values in Tree Viewers and Bioinformatics Toolkits. Molecular Biology and Evolution, 2017, 34, 1535-1542.	3.5	28
22	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. Nucleic Acids Research, 2017, 45, D529-D534.	6.5	131
23	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
24	MOCAT2: a metagenomic assembly, annotation and profiling framework. Bioinformatics, 2016, 32, 2520-2523.	1.8	172
25	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. Science, 2016, 352, 586-589.	6.0	461
26	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.	1.4	22
27	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. Molecular Biology and Evolution, 2016, 33, 1635-1638.	3.5	1,692
28	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. Nucleic Acids Research, 2016, 44, D286-D293.	6.5	1,937
29	STRING v10: protein–protein interaction networks, integrated over the tree of life. Nucleic Acids Research, 2015, 43, D447-D452.	6.5	9,029
30	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. Nucleic Acids Research, 2015, 43, D494-D502.	6.5	90
31	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. Genome Biology and Evolution, 2015, 7, 1988-1999.	1.1	25
32	Prokaryotic ancestry and gene fusion of a dual localized peroxiredoxin in malaria parasites. Microbial Cell, 2015, 2, 5-13.	1.4	9
33	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
34	An integrated approach for genome annotation of the eukaryotic thermophile Chaetomium thermophilum. Nucleic Acids Research, 2014, 42, 13525-13533.	6.5	55
35	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. Nucleic Acids Research, 2014, 42, D897-D902.	6.5	264
36	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526

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37	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.	1.9	27
38	Comparative transcriptomics of early dipteran development. BMC Genomics, 2013, 14, 123.	1.2	41
39	Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. Briefings in Bioinformatics, 2011, 12, 442-448.	3.2	67
40	Assigning duplication events to relative temporal scales in genome-wide studies. Bioinformatics, 2011, 27, 38-45.	1.8	65
41	MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score. Nucleic Acids Research, 2011, 39, e32-e32.	6.5	114
42	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. Nucleic Acids Research, 2011, 39, W470-W474.	6.5	182
43	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.	1.4	16
44	PhylomeDB v3.0: an expanding repository of genome-wide collections of trees, alignments and phylogeny-based orthology and paralogy predictions. Nucleic Acids Research, 2011, 39, D556-D560.	6.5	134
45	ETE: a python Environment for Tree Exploration. BMC Bioinformatics, 2010, 11, 24.	1.2	366
46	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. ISME Journal, 2010, 4, 882-895.	4.4	81
47	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	2.6	913
48	Automatic Prediction of the Genetic Code. Lecture Notes in Computer Science, 2009, , 1125-1129.	1.0	1
49	GEPAS, a web-based tool for microarray data analysis and interpretation. Nucleic Acids Research, 2008, 36, W308-W314.	6.5	67
50	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	3.2	91
51	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. Nucleic Acids Research, 2007, 35, W38-W42.	6.5	47
52	PhylomeDB: a database for genome-wide collections of gene phylogenies. Nucleic Acids Research, 2007, 36, D491-D496.	6.5	90
53	PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease. Nucleic Acids Research, 2007, 35, D815-D822.	6.5	65
54	The human phylome. Genome Biology, 2007, 8, R109.	3.8	150

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55	From genes to functional classes in the study of biological systems. BMC Bioinformatics, 2007, 8, 114.	1.2	108
56	Evidence for systems-level molecular mechanisms of tumorigenesis. BMC Genomics, 2007, 8, 185.	1.2	31
57	Next station in microarray data analysis: GEPAS. Nucleic Acids Research, 2006, 34, W486-W491.	6.5	107