

Salvador Capella-Gutierrez

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

14,297
citations

212478

28
h-index

252626

46
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53
all docs

53
docs citations

53
times ranked

24113
citing authors

#	ARTICLE	IF	CITATIONS
1	PhylomeDB V5: an expanding repository for genome-wide catalogues of annotated gene phylogenies. <i>Nucleic Acids Research</i> , 2022, 50, D1062-D1068.	6.5	30
2	The Quest for Orthologs orthology benchmark service in 2022. <i>Nucleic Acids Research</i> , 2022, 50, W623-W632.	6.5	29
3	FGFR Inhibition Overcomes Resistance to EGFR-targeted Therapy in Epithelial-like Cutaneous Carcinoma. <i>Clinical Cancer Research</i> , 2021, 27, 1491-1504.	3.2	13
4	The eTRANSafe Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. <i>Pharmaceuticals</i> , 2021, 14, 237.	1.7	17
5	Recommendations for the FAIRification of genomic track metadata. <i>F1000Research</i> , 2021, 10, 268.	0.8	7
6	DOME: recommendations for supervised machine learning validation in biology. <i>Nature Methods</i> , 2021, 18, 1122-1127.	9.0	105
7	Perspectives on automated composition of workflows in the life sciences. <i>F1000Research</i> , 2021, 10, 897.	0.8	7
8	A catalogue of 863 Rett-syndrome-causing MECP2 mutations and lessons learned from data integration. <i>Scientific Data</i> , 2021, 8, 10.	2.4	12
9	COVID-19 Flow-Maps an open geographic information system on COVID-19 and human mobility for Spain. <i>Scientific Data</i> , 2021, 8, 310.	2.4	11
10	Towards FAIR principles for research software. <i>Data Science</i> , 2020, 3, 37-59.	0.7	144
11	Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships. <i>Nature Communications</i> , 2020, 11, 2854.	5.8	20
12	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020, 48, W538-W545.	6.5	41
13	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. <i>F1000Research</i> , 2020, 9, 1229.	0.8	5
14	ECCB2020: the 19th European Conference on Computational Biology. <i>Bioinformatics</i> , 2020, 36, i569-i572.	1.8	1
15	The bio.tools registry of software tools and data resources for the life sciences. <i>Genome Biology</i> , 2019, 20, 164.	3.8	39
16	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	7.7	69
17	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
18	Ten steps to get started in Genome Assembly and Annotation. <i>F1000Research</i> , 2018, 7, 148.	0.8	85

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19	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
20	LimTox: a web tool for applied text mining of adverse event and toxicity associations of compounds, drugs and genes. <i>Nucleic Acids Research</i> , 2017, 45, W484-W489.	6.5	41
21	Genomic history of the origin and domestication of common bean unveils its closest sister species. <i>Genome Biology</i> , 2017, 18, 60.	3.8	142
22	Phylogenomics: The Evolution of Common Bean as Seen from the Perspective of All of Its Genes. <i>Compendium of Plant Genomes</i> , 2017, , 263-287.	0.3	0
23	Four simple recommendations to encourage best practices in research software. <i>F1000Research</i> , 2017, 6, 876.	0.8	88
24	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	3.8	131
25	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	198
26	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , 2016, 17, 32.	3.8	166
27	High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. <i>Developmental Cell</i> , 2016, 39, 186-197.	3.1	51
28	The <i>Solanum commersonii</i> Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. <i>Plant Cell</i> , 2015, 27, 954-968.	3.1	149
29	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. <i>Genome Research</i> , 2015, 25, 1256-1267.	2.4	46
30	From community approaches to single-cell genomics: the discovery of ubiquitous hyperhalophilic <i>Bacteroidetes</i> generalists. <i>ISME Journal</i> , 2015, 9, 16-31.	4.4	51
31	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , 2014, 12, e1002005.	2.6	221
32	Transcriptomic analysis of a psammophyte food crop, sand rice (<i>Agriophyllum squarrosum</i>) and identification of candidate genes essential for sand dune adaptation. <i>BMC Genomics</i> , 2014, 15, 872.	1.2	27
33	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254-1259.	6.0	300
34	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
35	A phylogenomics approach for selecting robust sets of phylogenetic markers. <i>Nucleic Acids Research</i> , 2014, 42, e54-e54.	6.5	45
36	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. <i>Nucleic Acids Research</i> , 2014, 42, D897-D902.	6.5	264

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37	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	13.7	569
38	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5247-5252.	3.3	307
39	Measuring guide-tree dependency of inferred gaps in progressive aligners. <i>Bioinformatics</i> , 2013, 29, 1011-1017.	1.8	26
40	Phylogenomics supports microsporidia as the earliest diverging clade of sequenced fungi. <i>BMC Biology</i> , 2012, 10, 47.	1.7	182
41	The genome of melon (<i>Cucumis melo</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11872-11877.	3.3	654
42	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
43	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
44	Lack of phylogenetic support for a supposed actinobacterial origin of peroxisomes. <i>Gene</i> , 2010, 465, 61-65.	1.0	15
45	trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. <i>Bioinformatics</i> , 2009, 25, 1972-1973.	1.8	7,974
46	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. <i>F1000Research</i> , 0, 10, 80.	0.8	8
47	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. <i>F1000Research</i> , 0, 10, 80.	0.8	0