Salvador Capella-Gutierrez

List of Publications by Year
in descending order

47	14,297	186209	223716
papers	citations	28	46
		h-index	g-index

53	53	53	21724
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics, 2009, 25, 1972-1973.	1.8	7,974
2	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
3	The genome of melon (*Cucumis melo* L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	3.3	654
4	The genome of the recently domesticated crop plant sugar beet (Beta vulgaris). Nature, 2014, 505, 546-549.	13.7	569
5	Genome structure and metabolic features in the red seaweed *Chondrus crispus* shed light on evolution of the Archaeplastida. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5247-5252.	3.3	307
6	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	6.0	300
7	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. Nucleic Acids Research, 2014, 42, D897-D902.	6.5	264
8	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede Strigamia maritima. PLoS Biology, 2014, 12, e1002005.	2.6	221
9	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
10	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
11	Phylogenomics supports microsporidia as the earliest diverging clade of sequenced fungi. BMC Biology, 2012, 10, 47.	1.7	182
12	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. Genome Biology, 2016, 17, 32.	3.8	166
13	The *Solanum commersonii* Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. Plant Cell, 2015, 27, 954-968.	3.1	149
14	Towards FAIR principles for research software. Data Science, 2020, 3, 37-59.	0.7	144
15	Genomic history of the origin and domestication of common bean unveils its closest sister species. Genome Biology, 2017, 18, 60.	3.8	142
16	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
17	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
18	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	9.0	105

#	Article	IF	Citations
19	Four simple recommendations to encourage best practices in research software. F1000Research, 2017, 6, 876.	0.8	88
20	Ten steps to get started in Genome Assembly and Annotation. F1000Research, 2018, 7, 148.	0.8	85
21	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
22	From community approaches to single-cell genomics: the discovery of ubiquitous hyperhalophilic *Bacteroidetes* generalists. ISME Journal, 2015, 9, 16-31.	4.4	51
23	High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. Developmental Cell, 2016, 39, 186-197.	3.1	51
24	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. Genome Research, 2015, 25, 1256-1267.	2.4	46
25	A phylogenomics approach for selecting robust sets of phylogenetic markers. Nucleic Acids Research, 2014, 42, e54-e54.	6.5	45
26	LimTox: a web tool for applied text mining of adverse event and toxicity associations of compounds, drugs and genes. Nucleic Acids Research, 2017, 45, W484-W489.	6.5	41
27	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	6.5	41
28	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	3.8	39
29	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	1.8	36
30	PhylomeDB V5: an expanding repository for genome-wide catalogues of annotated gene phylogenies. Nucleic Acids Research, 2022, 50, D1062-D1068.	6.5	30
31	The Quest for Orthologs orthology benchmark service in 2022. Nucleic Acids Research, 2022, 50, W623-W632.	6.5	29
32	Transcriptomic analysis of a psammophyte food crop, sand rice (Agriophyllum squarrosum) and identification of candidate genes essential for sand dune adaptation. BMC Genomics, 2014, 15, 872.	1.2	27
33	Measuring guide-tree dependency of inferred gaps in progressive aligners. Bioinformatics, 2013, 29, 1011-1017.	1.8	26
34	Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships. Nature Communications, 2020, 11, 2854.	5.8	20
35	The eTRANSAFE Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. Pharmaceuticals, 2021, 14, 237.	1.7	17
36	Lack of phylogenetic support for a supposed actinobacterial origin of peroxisomes. Gene, 2010, 465, 61-65.	1.0	15

#	Article	IF	Citations
37	FGFR Inhibition Overcomes Resistance to EGFR-targeted Therapy in Epithelial-like Cutaneous Carcinoma. Clinical Cancer Research, 2021, 27, 1491-1504.	3.2	13
38	A catalogue of 863 Rett-syndrome-causing MECP2 mutations and lessons learned from data integration. Scientific Data, 2021, 8, 10.	2.4	12
39	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	0.8	12
40	COVID-19 Flow-Maps an open geographic information system on COVID-19 and human mobility for Spain. Scientific Data, 2021, 8, 310.	2.4	11
41	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	0.8	8
42	Recommendations for the FAIRification of genomic track metadata. F1000Research, 2021, 10, 268.	0.8	7
43	Perspectives on automated composition of workflows in the life sciences. F1000Research, 2021, 10, 897.	0.8	7
44	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	0.8	5
45	ECCB2020: the 19th European Conference on Computational Biology. Bioinformatics, 2020, 36, i569-i572.	1.8	1
46	Phylogenomics: The Evolution of Common Bean as Seen from the Perspective of All of Its Genes. Compendium of Plant Genomes, 2017, , 263-287.	0.3	0
47	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	0.8	0