

Christian M Zmasek

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6191846/publications.pdf>

Version: 2024-02-01

22
papers

2,865
citations

394421

19
h-index

642732

23
g-index

23
all docs

23
docs citations

23
times ranked

5076
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic evolution of the Coronaviridae family. <i>Virology</i> , 2022, 570, 123-133.	2.4	13
2	Classification of human Herpesviridae proteins using Domain-architecture Aware Inference of Orthologs (DAIO). <i>Virology</i> , 2019, 529, 29-42.	2.4	12
3	Phylogenomic analysis of glycogen branching and debranching enzymatic duo. <i>BMC Evolutionary Biology</i> , 2014, 14, 183.	3.2	27
4	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , 2014, 5, 5.	1.6	47
5	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. <i>BMC Bioinformatics</i> , 2013, 14, 158.	2.6	33
6	Evolution of the Animal Apoptosis Network. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a008649-a008649.	5.5	63
7	aLeaves facilitates on-demand exploration of metazoan gene family trees on MAFFT sequence alignment server with enhanced interactivity. <i>Nucleic Acids Research</i> , 2013, 41, W22-W28.	14.5	624
8	This DÃ©jÃ Vu Feelingâ€”Analysis of Multidomain Protein Evolution in Eukaryotic Genomes. <i>PLoS Computational Biology</i> , 2012, 8, e1002701.	3.2	37
9	Strong functional patterns in the evolution of eukaryotic genomes revealed by the reconstruction of ancestral protein domain repertoires. <i>Genome Biology</i> , 2011, 12, R4.	9.6	84
10	TIR domain-containing adaptor SARM is a late addition to the ongoing microbeâ€”host dialog. <i>Developmental and Comparative Immunology</i> , 2011, 35, 461-468.	2.3	66
11	GreenPhylDB v2.0: comparative and functional genomics in plants. <i>Nucleic Acids Research</i> , 2011, 39, D1095-D1102.	14.5	106
12	Domain architecture evolution of pattern-recognition receptors. <i>Immunogenetics</i> , 2010, 62, 263-272.	2.4	68
13	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. <i>Journal of Biomedical Semantics</i> , 2010, 1, 8.	1.6	31
14	Evolution of the protein domain repertoire of eukaryotes reveals strong functional patterns. <i>Genome Biology</i> , 2010, 11, P43.	9.6	1
15	phyloXML: XML for evolutionary biology and comparative genomics. <i>BMC Bioinformatics</i> , 2009, 10, 356.	2.6	492
16	Evolution of the Human Ion Channel Set. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2009, 12, 2-23.	1.1	90
17	Novel genes dramatically alter regulatory network topology in amphioxus. <i>Genome Biology</i> , 2008, 9, R123.	9.6	33
18	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111.	5.5	456

#	ARTICLE	IF	CITATIONS
19	Surprising complexity of the ancestral apoptosis network. <i>Genome Biology</i> , 2007, 8, R226.	9.6	77
20	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 231-237.	2.0	76
21	RIO: analyzing proteomes by automated phylogenomics using resampled inference of orthologs. <i>BMC Bioinformatics</i> , 2002, 3, 14.	2.6	160
22	ATV: display and manipulation of annotated phylogenetic trees. <i>Bioinformatics</i> , 2001, 17, 383-384.	4.1	251