Christian M Zmasek

List of Publications by Year
in descending order

22	2,865	394421	642732
papers	citations	19	23
		h-index	g-index

23	23	23	5076
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	aLeaves facilitates on-demand exploration of metazoan gene family trees on MAFFT sequence alignment server with enhanced interactivity. Nucleic Acids Research, 2013, 41, W22-W28.	14.5	624
2	phyloXML: XML for evolutionary biology and comparative genomics. BMC Bioinformatics, 2009, 10, 356.	2.6	492
3	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. Genome Research, 2008, 18, 1100-1111.	5.5	456
4	ATV: display and manipulation of annotated phylogenetic trees. Bioinformatics, 2001, 17, 383-384.	4.1	251
5	RIO: analyzing proteomes by automated phylogenomics using resampled inference of orthologs. BMC Bioinformatics, 2002, 3, 14.	2.6	160
6	GreenPhylDB v2.0: comparative and functional genomics in plants. Nucleic Acids Research, 2011, 39, D1095-D1102.	14.5	106
7	Evolution of the Human Ion Channel Set. Combinatorial Chemistry and High Throughput Screening, 2009, 12, 2-23.	1.1	90
8	Strong functional patterns in the evolution of eukaryotic genomes revealed by the reconstruction of ancestral protein domain repertoires. Genome Biology, 2011, 12, R4.	9.6	84
9	Surprising complexity of the ancestral apoptosis network. Genome Biology, 2007, 8, R226.	9.6	77
10	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). OMICS A Journal of Integrative Biology, 2006, 10, 231-237.	2.0	76
11	Domain architecture evolution of pattern-recognition receptors. Immunogenetics, 2010, 62, 263-272.	2.4	68
12	TIR domain-containing adaptor SARM is a late addition to the ongoing microbeâ€"host dialog. Developmental and Comparative Immunology, 2011, 35, 461-468.	2.3	66
13	Evolution of the Animal Apoptosis Network. Cold Spring Harbor Perspectives in Biology, 2013, 5, a008649-a008649.	5.5	63
14	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. Journal of Biomedical Semantics, 2014, 5, 5.	1.6	47
15	This DÃ©jÃ Vu Feelingâ€"Analysis of Multidomain Protein Evolution in Eukaryotic Genomes. PLoS Computational Biology, 2012, 8, e1002701.	3.2	37
16	Novel genes dramatically alter regulatory network topology in amphioxus. Genome Biology, 2008, 9, R123.	9.6	33
17	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. BMC Bioinformatics, 2013, 14, 158.	2.6	33
18	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	1.6	31

#	Article	IF	Citations
19	Phylogenomic analysis of glycogen branching and debranching enzymatic duo. BMC Evolutionary Biology, 2014, 14, 183.	3.2	27
20	Genomic evolution of the Coronaviridae family. Virology, 2022, 570, 123-133.	2.4	13
21	Classification of human Herpesviridae proteins using Domain-architecture Aware Inference of Orthologs (DAIO). Virology, 2019, 529, 29-42.	2.4	12
22	Evolution of the protein domain repertoire of eukaryotes reveals strong functional patterns. Genome Biology, 2010, 11, P43.	9.6	1