

Valerie Wood

List of Publications by Year in descending order

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63
papers

25,000
citations

116194

36
h-index

129628

63
g-index

74
all docs

74
docs citations

74
times ranked

45663
citing authors

#	ARTICLE	IF	CITATIONS
1	Making biological knowledge useful for humans and machines. <i>Genetics</i> , 2022, 220, .	1.2	13
2	PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions. <i>Nucleic Acids Research</i> , 2022, 50, D837-D847.	6.5	53
3	JaponicusDB: rapid deployment of a model organism database for an emerging model species. <i>Genetics</i> , 2022, 220, .	1.2	21
4	Fission stories: using PomBase to understand <i>Schizosaccharomyces pombe</i> biology. <i>Genetics</i> , 2022, 220, .	1.2	60
5	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	6.5	2,416
6	PHI-base: the pathogen-host interactions database. <i>Nucleic Acids Research</i> , 2020, 48, D613-D620.	6.5	145
7	Community curation in PomBase: enabling fission yeast experts to provide detailed, standardized, sharable annotation from research publications. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	19
8	Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. <i>Open Biology</i> , 2020, 10, 200149.	1.5	7
9	PomBase 2018: user-driven reimplementaion of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. <i>Nucleic Acids Research</i> , 2019, 47, D821-D827.	6.5	157
10	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. <i>Open Biology</i> , 2019, 9, 180241.	1.5	80
11	Annotation of gene product function from high-throughput studies using the Gene Ontology. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	21
12	Transcriptional regulation of the genes involved in protein metabolism and processing in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	1
13	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153
14	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	6.5	3,474
15	PomBase: The Scientific Resource for Fission Yeast. <i>Methods in Molecular Biology</i> , 2018, 1757, 49-68.	0.4	32
16	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	6.5	1,838
17	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	6.5	174
18	Model organism databases: essential resources that need the support of both funders and users. <i>BMC Biology</i> , 2016, 14, 49.	1.7	46

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19	Guidelines for the functional annotation of microRNAs using the Gene Ontology. <i>Rna</i> , 2016, 22, 667-676.	1.6	35
20	AnGeLi: A Tool for the Analysis of Gene Lists from Fission Yeast. <i>Frontiers in Genetics</i> , 2015, 6, 330.	1.1	65
21	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015, 43, D656-D661.	6.5	95
22	An Ancient Yeast for Young Geneticists: A Primer on the <i>Schizosaccharomyces pombe</i> Model System. <i>Genetics</i> , 2015, 201, 403-423.	1.2	180
23	Gene Ontology Consortium: going forward. <i>Nucleic Acids Research</i> , 2015, 43, D1049-D1056.	6.5	2,743
24	Canto: an online tool for community literature curation. <i>Bioinformatics</i> , 2014, 30, 1791-1792.	1.8	41
25	Improving functional annotation for industrial microbes: a case study with <i>Pichia pastoris</i> . <i>Trends in Biotechnology</i> , 2014, 32, 396-399.	4.9	23
26	A method for increasing expressivity of Gene Ontology annotations using a compositional approach. <i>BMC Bioinformatics</i> , 2014, 15, 155.	1.2	78
27	FYPO: the fission yeast phenotype ontology. <i>Bioinformatics</i> , 2013, 29, 1671-1678.	1.8	53
28	A genome-wide resource of cell cycle and cell shape genes of fission yeast. <i>Open Biology</i> , 2013, 3, 130053.	1.5	147
29	On the Use of Gene Ontology Annotations to Assess Functional Similarity among Orthologs and Paralogs: A Short Report. <i>PLoS Computational Biology</i> , 2012, 8, e1002386.	1.5	91
30	The Gene Ontology: enhancements for 2011. <i>Nucleic Acids Research</i> , 2012, 40, D559-D564.	6.5	191
31	Gene Ontology Annotations and Resources. <i>Nucleic Acids Research</i> , 2012, 41, D530-D535.	6.5	456
32	PomBase: a comprehensive online resource for fission yeast. <i>Nucleic Acids Research</i> , 2012, 40, D695-D699.	6.5	288
33	Augmented Annotation of the <i>Schizosaccharomyces pombe</i> Genome Reveals Additional Genes Required for Growth and Viability. <i>Genetics</i> , 2011, 187, 1207-1217.	1.2	26
34	Analysis of a genome-wide set of gene deletions in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Nature Biotechnology</i> , 2010, 28, 617-623.	9.4	649
35	AmiGO: online access to ontology and annotation data. <i>Bioinformatics</i> , 2009, 25, 288-289.	1.8	1,647
36	The Gene Ontology's Reference Genome Project: A Unified Framework for Functional Annotation across Species. <i>PLoS Computational Biology</i> , 2009, 5, e1000431.	1.5	148

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37	Dynamic repertoire of a eukaryotic transcriptome surveyed at single-nucleotide resolution. <i>Nature</i> , 2008, 453, 1239-1243.	13.7	888
38	Use and misuse of the gene ontology annotations. <i>Nature Reviews Genetics</i> , 2008, 9, 509-515.	7.7	518
39	The Gene Ontology project in 2008. <i>Nucleic Acids Research</i> , 2008, 36, D440-D444.	6.5	699
40	The BioGRID Interaction Database: 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D637-D640.	6.5	610
41	How to get the most from fission yeast genome data: a report from the 2006 European Fission Yeast Meeting computing workshop. <i>Yeast</i> , 2006, 23, 905-912.	0.8	3
42	Gene Ontology annotation status of the fission yeast genome: preliminary coverage approaches 100%. <i>Yeast</i> , 2006, 23, 913-919.	0.8	47
43	Tools and resources for <i>S. pombe</i> : a report from the 2006 European Fission Yeast Meeting. <i>Yeast</i> , 2006, 23, 901-903.	0.8	6
44	The Gene Ontology (GO) project in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D322-D326.	6.5	923
45	YOGY: a web-based, integrated database to retrieve protein orthologs and associated Gene Ontology terms. <i>Nucleic Acids Research</i> , 2006, 34, W330-W334.	6.5	44
46	Integration of tools and resources for display and analysis of genomic data for protozoan parasites. <i>International Journal for Parasitology</i> , 2005, 35, 481-493.	1.3	8
47	The Gene Ontology (GO) database and informatics resource. <i>Nucleic Acids Research</i> , 2004, 32, 258D-261.	6.5	3,462
48	GeneDB: a resource for prokaryotic and eukaryotic organisms. <i>Nucleic Acids Research</i> , 2004, 32, 339D-343.	6.5	199
49	The Genome and Beyond. , 2004, , 13-25.		4
50	Retrotransposons and Their Recognition of pol II Promoters: A Comprehensive Survey of the Transposable Elements From the Complete Genome Sequence of <i>Schizosaccharomyces pombe</i> . <i>Genome Research</i> , 2003, 13, 1984-1997.	2.4	144
51	Website Review: How to Get the Best From Fission Yeast Genome Data. <i>Comparative and Functional Genomics</i> , 2002, 3, 282-288.	2.0	10
52	Themei3 region of the <i>Schizosaccharomyces pombe</i> genome. <i>Yeast</i> , 2002, 19, 521-527.	0.8	1
53	The genome sequence of <i>Schizosaccharomyces pombe</i> . <i>Nature</i> , 2002, 415, 871-880.	13.7	1,508
54	Analysis of 41â€%kb of the DNA sequence from the right arm of chromosome II of <i>Schizosaccharomyces pombe</i> . <i>Yeast</i> , 2001, 18, 1111-1116.	0.8	4

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55	A Re-Annotation of the <i>Saccharomyces cerevisiae</i> Genome. <i>Comparative and Functional Genomics</i> , 2001, 2, 143-154.	2.0	72
56	Subtelomeric sequence from the right arm of <i>Schizosaccharomyces pombe</i> chromosome I contains seven permease genes. <i>Yeast</i> , 2001, 18, 355-361.	0.8	9
57	The mating-type region of <i>Schizosaccharomyces pombe</i> h ⁺ S 972: sequencing and analysis of 69 kb including the expressed <i>mat1</i> locus. <i>Yeast</i> , 2000, 16, 1061-1067.	0.8	1
58	Analysis of 114 kb of DNA sequence from fission yeast chromosome 2 immediately centromere-distal to <i>his5</i> . <i>Yeast</i> , 2000, 16, 1405-1411.	0.8	6
59	Sequence analysis of two cosmids from <i>Schizosaccharomyces pombe</i> chromosome III. <i>Yeast</i> , 2000, 16, 1519-1526.	0.8	3
60	<i>Plasmodium falciparum</i> Genome Update. <i>Parasitology Today</i> , 2000, 16, 94.	3.1	0
61	Functional Websites for Parasite Genome Projects. <i>Parasitology Today</i> , 2000, 16, 93-94.	3.1	3
62	DNA sequencing and analysis of a 67.4 kb region from the right arm of <i>Schizosaccharomyces pombe</i> chromosome II reveals 28 open reading frames including the genes <i>his5</i> , <i>pol5</i> , <i>ppa2</i> , <i>rip1</i> , <i>rpb8</i> and <i>skb1</i> . , 1999, 15, 893-901.		5
63	<i>Schizosaccharomyces pombe</i> comparative genomics; from sequence to systems. , 0, , 233-285.		21