

David James Sherman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3504368/publications.pdf>

Version: 2024-02-01

41
papers

3,886
citations

331670

21
h-index

302126

39
g-index

43
all docs

43
docs citations

43
times ranked

4843
citing authors

#	ARTICLE	IF	CITATIONS
1	Many interspecific chromosomal introgressions are highly prevalent in Holarctic <i>Saccharomyces uvarum</i> strains found in human-related fermentations. <i>Yeast</i> , 2018, 35, 141-156.	1.7	30
2	Genome Sequence of the Yeast <i>Clavispora lusitaniae</i> Type Strain CBS 6936. <i>Genome Announcements</i> , 2017, 5, .	0.8	16
3	Two different <i>Oenococcus oeni</i> lineages are associated to either red or white wines in Burgundy: genomics and metabolomics insights. <i>Oeno One</i> , 2017, 51, 309.	1.4	34
4	Phylogenomic Analysis of <i>Oenococcus oeni</i> Reveals Specific Domestication of Strains to Cider and Wines. <i>Genome Biology and Evolution</i> , 2015, 7, 1506-1518.	2.5	57
5	Pantograph: A template-based method for genome-scale metabolic model reconstruction. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550006.	0.8	29
6	Mimosa: web-based semantic zooming and navigation in metabolic networks. <i>BMC Systems Biology</i> , 2015, 9, 10.	3.0	5
7	Knowledge-based generalization of metabolic networks: A practical study. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1441001.	0.8	1
8	Draft Genome Sequence of <i>Rhodospiridium toruloides</i> CECT1137, an Oleaginous Yeast of Biotechnological Interest. <i>Genome Announcements</i> , 2014, 2, .	0.8	24
9	Diversity and Variability of NOD-Like Receptors in Fungi. <i>Genome Biology and Evolution</i> , 2014, 6, 3137-3158.	2.5	83
10	Knowledge-based Generalization of Metabolic Models. <i>Journal of Computational Biology</i> , 2014, 21, 534-547.	1.6	3
11	The complete genome of <i>Blastobotrys (Arxula) adenivorans</i> LS3 - a yeast of biotechnological interest. <i>Biotechnology for Biofuels</i> , 2014, 7, 66.	6.2	57
12	A Gondwanan imprint on global diversity and domestication of wine and cider yeast <i>Saccharomyces uvarum</i> . <i>Nature Communications</i> , 2014, 5, 4044.	12.8	214
13	Modeling acclimatization by hybrid systems: Condition changes alter biological system behavior models. <i>BioSystems</i> , 2014, 121, 43-53.	2.0	3
14	QTL Dissection of Lag Phase in Wine Fermentation Reveals a New Translocation Responsible for <i>Saccharomyces cerevisiae</i> Adaptation to Sulfite. <i>PLoS ONE</i> , 2014, 9, e86298.	2.5	109
15	Implementing biological hybrid systems: Allowing composition and avoiding stiffness. <i>Applied Mathematics and Computation</i> , 2013, 223, 167-179.	2.2	7
16	<i>Pichia sorbitophila</i> , an Interspecies Yeast Hybrid, Reveals Early Steps of Genome Resolution After Polyploidization. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 299-311.	1.8	113
17	A genome-scale metabolic model of the lipid-accumulating yeast <i>Yarrowia lipolytica</i> . <i>BMC Systems Biology</i> , 2012, 6, 35.	3.0	105
18	Reusing and composing models of cell fate regulation of human bone precursor cells. <i>BioSystems</i> , 2012, 108, 63-72.	2.0	5

#	ARTICLE	IF	CITATIONS
19	Reconciling Competing Models: A Case Study of Wine Fermentation Kinetics. Lecture Notes in Computer Science, 2012, , 98-116.	1.3	0
20	The GÃ©nolevures database. Comptes Rendus - Biologies, 2011, 334, 585-589.	0.2	9
21	Minimum information about a protein affinity reagent (MIAPAR). Nature Biotechnology, 2010, 28, 650-653.	17.5	50
22	A Community Standard Format for the Representation of Protein Affinity Reagents. Molecular and Cellular Proteomics, 2010, 9, 1-10.	3.8	35
23	GÃ©nolevures: protein families and synteny among complete hemiascomycetous yeast proteomes and genomes. Nucleic Acids Research, 2009, 37, D550-D554.	14.5	117
24	Mining the Semantics of Genome Super-Blocks to Infer Ancestral Architectures. Journal of Computational Biology, 2009, 16, 1267-1284.	1.6	9
25	Unusual composition of a yeast chromosome arm is associated with its delayed replication. Genome Research, 2009, 19, 1710-1721.	5.5	43
26	Swarming along the evolutionary branches sheds light on genome rearrangement scenarios. , 2009, , .		0
27	Comparative genomics of protoploid <i>Saccharomycetaceae</i> . Genome Research, 2009, 19, 1696-1709.	5.5	207
28	Minimum information requirements: Neither bandits in the Attic nor bats in the belfry. New Biotechnology, 2009, 25, 173-174.	4.4	4
29	Extrapolation of metabolic pathways as an aid to modelling completely sequenced non- <i>Saccharomyces</i> yeasts. FEMS Yeast Research, 2008, 8, 132-139.	2.3	3
30	An efficient probabilistic population-based descent for the median genome problem. , 2008, , .		4
31	Exploratory simulation of cell ageing using hierarchical models. , 2008, , .		1
32	Fusion and Fission of Genes Define a Metric between Fungal Genomes. PLoS Computational Biology, 2008, 4, e1000200.	3.2	22
33	Family relationships: should consensus reign?—consensus clustering for protein families. Bioinformatics, 2007, 23, e71-e76.	4.1	25
34	ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. Nature Methods, 2007, 4, 13-17.	19.0	231
35	How to decide which are the most pertinent overly-represented features during gene set enrichment analysis. BMC Bioinformatics, 2007, 8, 332.	2.6	11
36	A systematic nomenclature of chromosomal elements for hemiascomycete yeasts. Yeast, 2005, 22, 337-342.	1.7	15

#	ARTICLE	IF	CITATIONS
37	New strategy for the representation and the integration of biomolecular knowledge at a cellular scale. <i>Nucleic Acids Research</i> , 2004, 32, 3581-3589.	14.5	21
38	The HUPO PSI's Molecular Interaction formatâ€”a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	17.5	581
39	Genome evolution in yeasts. <i>Nature</i> , 2004, 430, 35-44.	27.8	1,498
40	Common interchange standards for proteomics data: Public availability of tools and schemaReport on the Proteomic Standards Initiative Workshop, 2nd Annual HUPO Congress, Montreal, Canada, 8â€”11th October 2003. <i>Proteomics</i> , 2004, 4, 490-491.	2.2	100
41	Squeezing intermediate construction in equational programs. <i>Lecture Notes in Computer Science</i> , 1996, , 284-302.	1.3	3