

John L Hartman Iv

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,496
citations

567247

15
h-index

526264

27
g-index

32
all docs

32
docs citations

32
times ranked

2259
citing authors

#	ARTICLE	IF	CITATIONS
1	Defining genetic interaction. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3461-3466.	7.1	399
2	Principles for the Buffering of Genetic Variation. Science, 2001, 291, 1001-1004.	12.6	291
3	The case for strategic international alliances to harness nutritional genomics for public and personal health. British Journal of Nutrition, 2005, 94, 623-632.	2.3	137
4	Functional Reconstitution of 5-Hydroxytryptamine _{2c} (5HT _{2c}) Receptors with $\hat{\mu}$ q and Inverse Agonism of 5HT _{2c} Receptor Antagonists. Journal of Biological Chemistry, 1996, 271, 22591-22597.	3.4	83
5	A yeast phenomic model for the gene interaction network modulating CFTR- $\hat{\mu}$ F508 protein biogenesis. Genome Medicine, 2012, 4, 103.	8.2	76
6	Genomewide Analysis Reveals Novel Pathways Affecting Endoplasmic Reticulum Homeostasis, Protein Modification and Quality Control. Genetics, 2009, 182, 757-769.	2.9	62
7	Systematic quantification of gene interactions by phenotypic array analysis. Genome Biology, 2004, 5, R49.	8.8	58
8	Ribosomal Stalk Protein Silencing Partially Corrects the $\hat{\mu}$ F508-CFTR Functional Expression Defect. PLoS Biology, 2016, 14, e1002462.	5.6	49
9	Accurate, precise modeling of cell proliferation kinetics from time-lapse imaging and automated image analysis of agar yeast culture arrays. BMC Systems Biology, 2007, 1, 3.	3.0	44
10	Buffering of deoxyribonucleotide pool homeostasis by threonine metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11700-11705.	7.1	41
11	Slowing ribosome velocity restores folding and function of mutant CFTR. Journal of Clinical Investigation, 2019, 129, 5236-5253.	8.2	36
12	Gene-nutrient interaction markedly influences yeast chronological lifespan. Experimental Gerontology, 2016, 86, 113-123.	2.8	25
13	High Throughput Drug Screening for Human Immunodeficiency Virus Type 1 Reactivating Compounds. Assay and Drug Development Technologies, 2007, 5, 181-190.	1.2	20
14	Stringent Mating-Type-Regulated Auxotrophy Increases the Accuracy of Systematic Genetic Interaction Screens with Saccharomyces cerevisiae Mutant Arrays. Genetics, 2009, 181, 289-300.	2.9	20
15	Conserved Allosteric Hot Spots in the Transmembrane Domains of Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Channels and Multidrug Resistance Protein (MRP) Pumps. Journal of Biological Chemistry, 2014, 289, 19942-19957.	3.4	20
16	The SWI/SNF Chromatin Remodeling Complex Influences Transcription by RNA Polymerase I in Saccharomyces cerevisiae. PLoS ONE, 2013, 8, e56793.	2.5	17
17	Aging and energeticsâ€™™ â€™™Top 40â€™™ future research opportunities 2010-2013. F1000Research, 2014, 3, 219. 1.6		17
18	A cell-nonautonomous mechanism of yeast chronological aging regulated by caloric restriction and one-carbon metabolism. Journal of Biological Chemistry, 2021, 296, 100125.	3.4	17

#	ARTICLE	IF	CITATIONS
19	Yeast Phenomics: An Experimental Approach for Modeling Gene Interaction Networks that Buffer Disease. <i>Genes</i> , 2015, 6, 24-45.	2.4	15
20	Long-range coupling between the extracellular gates and the intracellular ATP binding domains of multidrug resistance protein pumps and cystic fibrosis transmembrane conductance regulator channels. <i>FASEB Journal</i> , 2016, 30, 1247-1262.	0.5	14
21	A Screen to Identify Small Molecule Inhibitors of Protein-Protein Interactions in Mycobacteria. <i>Assay and Drug Development Technologies</i> , 2011, 9, 299-310.	1.2	12
22	Recursive expectation-maximization clustering: A method for identifying buffering mechanisms composed of phenomic modules. <i>Chaos</i> , 2010, 20, 026103.	2.5	10
23	Phenomic Assessment of Genetic Buffering by Kinetic Analysis of Cell Arrays. <i>Methods in Molecular Biology</i> , 2014, 1205, 187-208.	0.9	9
24	A yeast phenomic model for the influence of Warburg metabolism on genetic buffering of doxorubicin. <i>Cancer & Metabolism</i> , 2019, 7, 9.	5.0	6
25	High-resolution yeast quiescence profiling in human-like media reveals complex influences of auxotrophy and nutrient availability. <i>GeroScience</i> , 2021, 43, 941-964.	4.6	5
26	Genetic and Molecular Buffering of Phenotypes. , 2006, , 105-134.		4
27	A Humanized Yeast Phenomic Model of Deoxycytidine Kinase to Predict Genetic Buffering of Nucleoside Analog Cytotoxicity. <i>Genes</i> , 2019, 10, 770.	2.4	3
28	University of Alabama at Birmingham Nathan Shock Center: comparative energetics of aging. <i>GeroScience</i> , 2021, 43, 2149-2160.	4.6	2