

John L Hartman Iv

List of Publications by Citations

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29
papers

1,050
citations

15
h-index

32
g-index

32
ext. papers

1,216
ext. citations

7.1
avg, IF

3.86
L-index

#	Paper	IF	Citations
29	Defining genetic interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 3461-6	11.5	321
28	The case for strategic international alliances to harness nutritional genomics for public and personal health. <i>British Journal of Nutrition</i> , 2005 , 94, 623-32	3.6	112
27	Principles for the Buffering of Genetic Variation. <i>Science</i> , 2001 , 291, 1001-1004	33.3	101
26	Functional reconstitution in situ of 5-hydroxytryptamine _{2c} (5HT _{2c}) receptors with alphaq and inverse agonism of 5HT _{2c} receptor antagonists. <i>Journal of Biological Chemistry</i> , 1996 , 271, 22591-7	5.4	78
25	A yeast phenomic model for the gene interaction network modulating CFTR- β 508 protein biogenesis. <i>Genome Medicine</i> , 2012 , 4, 103	14.4	58
24	Systematic quantification of gene interactions by phenotypic array analysis. <i>Genome Biology</i> , 2004 , 5, R49	18.3	54
23	Genomewide analysis reveals novel pathways affecting endoplasmic reticulum homeostasis, protein modification and quality control. <i>Genetics</i> , 2009 , 182, 757-69	4	49
22	Ribosomal Stalk Protein Silencing Partially Corrects the β 508-CFTR Functional Expression Defect. <i>PLoS Biology</i> , 2016 , 14, e1002462	9.7	37
21	Buffering of deoxyribonucleotide pool homeostasis by threonine metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11700-5	11.5	36
20	Accurate, precise modeling of cell proliferation kinetics from time-lapse imaging and automated image analysis of agar yeast culture arrays. <i>BMC Systems Biology</i> , 2007 , 1, 3	3.5	34
19	Gene-nutrient interaction markedly influences yeast chronological lifespan. <i>Experimental Gerontology</i> , 2016 , 86, 113-123	4.5	17
18	High throughput drug screening for human immunodeficiency virus type 1 reactivating compounds. <i>Assay and Drug Development Technologies</i> , 2007 , 5, 181-89	2.1	17
17	Slowing ribosome velocity restores folding and function of mutant CFTR. <i>Journal of Clinical Investigation</i> , 2019 , 129, 5236-5253	15.9	16
16	Conserved allosteric hot spots in the transmembrane domains of cystic fibrosis transmembrane conductance regulator (CFTR) channels and multidrug resistance protein (MRP) pumps. <i>Journal of Biological Chemistry</i> , 2014 , 289, 19942-57	5.4	15
15	The SWI/SNF chromatin remodeling complex influences transcription by RNA polymerase I in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2013 , 8, e56793	3.7	15
14	Aging and energetics W Top 40 W Future research opportunities 2010-2013. <i>F1000Research</i> , 2014 , 3, 219	3.6	14
13	Stringent mating-type-regulated auxotrophy increases the accuracy of systematic genetic interaction screens with <i>Saccharomyces cerevisiae</i> mutant arrays. <i>Genetics</i> , 2009 , 181, 289-300	4	13

12	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, 1247-62	0.9	11
11	A screen to identify small molecule inhibitors of protein-protein interactions in mycobacteria. <i>Assay and Drug Development Technologies</i> , 2011 , 9, 299-310	2.1	11
10	Yeast Phenomics: An Experimental Approach for Modeling Gene Interaction Networks that Buffer Disease. <i>Genes</i> , 2015 , 6, 24-45	4.2	10
9	Recursive expectation-maximization clustering: a method for identifying buffering mechanisms composed of phenomic modules. <i>Chaos</i> , 2010 , 20, 026103	3.3	9
8	Phenomic assessment of genetic buffering by kinetic analysis of cell arrays. <i>Methods in Molecular Biology</i> , 2014 , 1205, 187-208	1.4	7
7	A yeast phenomic model for the influence of Warburg metabolism on genetic buffering of doxorubicin. <i>Cancer & Metabolism</i> , 2019 , 7, 9	5.4	4
6	A cell-nonautonomous mechanism of yeast chronological aging regulated by caloric restriction and one-carbon metabolism. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100125	5.4	4
5	High-resolution yeast quiescence profiling in human-like media reveals complex influences of auxotrophy and nutrient availability. <i>GeroScience</i> , 2021 , 43, 941-964	8.9	3
4	Genetic and Molecular Buffering of Phenotypes 2006 , 105-134		2
3	A Humanized Yeast Phenomic Model of Deoxycytidine Kinase to Predict Genetic Buffering of Nucleoside Analog Cytotoxicity. <i>Genes</i> , 2019 , 10,	4.2	1
2	A yeast phenomic model for the influence of Warburg metabolism on genetic buffering of doxorubicin		1
1	University of Alabama at Birmingham Nathan Shock Center: comparative energetics of aging. <i>GeroScience</i> , 2021 , 43, 2149-2160	8.9	0