

# John L Hartman Iv

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 | University of Alabama at Birmingham Nathan Shock Center: comparative energetics of aging. <i>GeroScience</i> , <b>2021</b> , 43, 2149-2160   | 8.9  | 0         |
| 28 | High-resolution yeast quiescence profiling in human-like media reveals complex influences of auxotrophy and nutrient availability. <i>GeroScience</i> , <b>2021</b> , 43, 941-964  | 8.9  | 3         |
| 27 | A cell-nonautonomous mechanism of yeast chronological aging regulated by caloric restriction and one-carbon metabolism. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 296, 100125   | 5.4  | 4         |
| 26 | A Humanized Yeast Phenomic Model of Deoxycytidine Kinase to Predict Genetic Buffering of Nucleoside Analog Cytotoxicity. <i>Genes</i> , <b>2019</b> , 10,  | 4.2  | 1         |
| 25 | A yeast phenomic model for the influence of Warburg metabolism on genetic buffering of doxorubicin. <i>Cancer &amp; Metabolism</i> , <b>2019</b> , 7, 9  | 5.4  | 4         |
| 24 | Slowing ribosome velocity restores folding and function of mutant CFTR. <i>Journal of Clinical Investigation</i> , <b>2019</b> , 129, 5236-5253  | 15.9 | 16        |
| 23 | Gene-nutrient interaction markedly influences yeast chronological lifespan. <i>Experimental Gerontology</i> , <b>2016</b> , 86, 113-123  | 4.5  | 17        |
| 22 | 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> , <b>2016</b> , 30, 1247-62 | 0.9  | 11        |
| 21 | Ribosomal Stalk Protein Silencing Partially Corrects the $\beta$ 508-CFTR Functional Expression Defect. <i>PLoS Biology</i> , <b>2016</b> , 14, e1002462   | 9.7  | 37        |
| 20 | Yeast Phenomics: An Experimental Approach for Modeling Gene Interaction Networks that Buffer Disease. <i>Genes</i> , <b>2015</b> , 6, 24-45  | 4.2  | 10        |
| 19 | 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> , <b>2014</b> , 289, 19942-57  | 5.4  | 15        |
| 18 | Aging and energetics <b>Wtop 40W</b> future research opportunities 2010-2013. <i>F1000Research</i> , <b>2014</b> , 3, 219  | 3.6  | 14        |
| 17 | Phenomic assessment of genetic buffering by kinetic analysis of cell arrays. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1205, 187-208   | 1.4  | 7         |
| 16 | The SWI/SNF chromatin remodeling complex influences transcription by RNA polymerase I in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , <b>2013</b> , 8, e56793   | 3.7  | 15        |
| 15 | A yeast phenomic model for the gene interaction network modulating CFTR- $\beta$ 508 protein biogenesis. <i>Genome Medicine</i> , <b>2012</b> , 4, 103   | 14.4 | 58        |
| 14 | A screen to identify small molecule inhibitors of protein-protein interactions in mycobacteria. <i>Assay and Drug Development Technologies</i> , <b>2011</b> , 9, 299-310  | 2.1  | 11        |
| 13 | Recursive expectation-maximization clustering: a method for identifying buffering mechanisms composed of phenomic modules. <i>Chaos</i> , <b>2010</b> , 20, 026103   | 3.3  | 9         |

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|----|--|------|-----|
| 12 | Genomewide analysis reveals novel pathways affecting endoplasmic reticulum homeostasis, protein modification and quality control. <i>Genetics</i> , <b>2009</b> , 182, 757-69  | 4    | 49  |
| 11 | Stringent mating-type-regulated auxotrophy increases the accuracy of systematic genetic interaction screens with <i>Saccharomyces cerevisiae</i> mutant arrays. <i>Genetics</i> , <b>2009</b> , 181, 289-300   | 4    | 13  |
| 10 | Defining genetic interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 3461-6   | 11.5 | 321 |
| 9  | High throughput drug screening for human immunodeficiency virus type 1 reactivating compounds. <i>Assay and Drug Development Technologies</i> , <b>2007</b> , 5, 181-89  | 2.1  | 17  |
| 8  | 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> , <b>2007</b> , 1, 3   | 3.5  | 34  |
| 7  | Buffering of deoxyribonucleotide pool homeostasis by threonine metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 11700-5   | 11.5 | 36  |
| 6  | Genetic and Molecular Buffering of Phenotypes <b>2006</b> , 105-134  |      | 2   |
| 5  | The case for strategic international alliances to harness nutritional genomics for public and personal health. <i>British Journal of Nutrition</i> , <b>2005</b> , 94, 623-32  | 3.6  | 112 |
| 4  | Systematic quantification of gene interactions by phenotypic array analysis. <i>Genome Biology</i> , <b>2004</b> , 5, R49  | 18.3 | 54  |
| 3  | Principles for the Buffering of Genetic Variation. <i>Science</i> , <b>2001</b> , 291, 1001-1004   | 33.3 | 101 |
| 2  | Functional reconstitution in situ of 5-hydroxytryptamine <sub>2c</sub> (5HT <sub>2c</sub> ) receptors with alphaq and inverse agonism of 5HT <sub>2c</sub> receptor antagonists. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 22591-7 | 5.4  | 78  |
| 1  | A yeast phenomic model for the influence of Warburg metabolism on genetic buffering of doxorubicin   |      | 1   |