

# Christopher Thomas Workman

## List of Publications by Year in descending order

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90  
papers

9,537  
citations

87888

38  
h-index

43889

91  
g-index

98  
all docs

98  
docs citations

98  
times ranked

17323  
citing authors

#	ARTICLE	IF	CITATIONS
1	Does rapid sequence divergence preclude RNA structure conservation in vertebrates?. <i>Nucleic Acids Research</i> , 2022, 50, 2452-2463.	14.5	3
2	Burden Imposed by Heterologous Protein Production in Two Major Industrial Yeast Cell Factories: Identifying Sources and Mitigation Strategies. <i>Frontiers in Fungal Biology</i> , 2022, 3, .	2.0	17
3	The rise of genomics in snake venom research: recent advances and future perspectives. <i>GigaScience</i> , 2022, 11, .	6.4	17
4	Emergence of Phenotypically Distinct Subpopulations Is a Factor in Adaptation of Recombinant <i>Saccharomyces cerevisiae</i> under Glucose-Limited Conditions. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0230721.	3.1	5
5	Systematic inference of indirect transcriptional regulation by protein kinases and phosphatases. <i>PLoS Computational Biology</i> , 2022, 18, e1009414.	3.2	1
6	Use of novel cystine analogs to decrease oxidative stress and control product quality. <i>Journal of Biotechnology</i> , 2021, 327, 1-8.	3.8	8
7	Innate IL-23/Type 17 immune responses mediate the effect of the 17q21 locus on childhood asthma. <i>Clinical and Experimental Allergy</i> , 2021, 51, 892-901.	2.9	3
8	Small Intestinal Tuft Cell Activity Associates With Energy Metabolism in Diet-Induced Obesity. <i>Frontiers in Immunology</i> , 2021, 12, 629391.	4.8	9
9	Comparative analysis of three studies measuring fluorescence from engineered bacterial genetic constructs. <i>PLoS ONE</i> , 2021, 16, e0252263.	2.5	11
10	Body fluid from the parasitic worm <i>Ascaris suum</i> inhibits broad-acting pro-inflammatory programs in dendritic cells. <i>Immunology</i> , 2020, 159, 322-334.	4.4	16
11	Robust estimation of bacterial cell count from optical density. <i>Communications Biology</i> , 2020, 3, 512.	4.4	86
12	Characterization of glutathione proteome in CHO cells and its relationship with productivity and cholesterol synthesis. <i>Biotechnology and Bioengineering</i> , 2020, 117, 3448-3458.	3.3	13
13	Loss of AA13 LPMOs impairs degradation of resistant starch and reduces the growth of <i>Aspergillus nidulans</i> . <i>Biotechnology for Biofuels</i> , 2020, 13, 135.	6.2	8
14	Skeletal muscle enhancer interactions identify genes controlling whole-body metabolism. <i>Nature Communications</i> , 2020, 11, 2695.	12.8	29
15	Fluctuations in glucose availability prevent global proteome changes and physiological transition during prolonged chemostat cultivations of <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2020, 117, 2074-2088.	3.3	15
16	Origin of cooperativity in the activation of dimeric transcription factors. <i>Physical Review Research</i> , 2020, 2, .	3.6	2
17	Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. <i>Nucleic Acids Research</i> , 2019, 47, 1671-1691.	14.5	34
18	Protease Activity Profiling of Snake Venoms Using High-Throughput Peptide Screening. <i>Toxins</i> , 2019, 11, 170.	3.4	11

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19	The human gut Firmicute <i>Roseburia intestinalis</i> is a primary degrader of dietary $\beta$ -mannans. <i>Nature Communications</i> , 2019, 10, 905.	12.8	202
20	Investigating the Influence of Glycerol on the Utilization of Glucose in <i>Yarrowia lipolytica</i> Using RNA-Seq-Based Transcriptomics. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 4059-4071.	1.8	17
21	Bidirectional histone-gene promoters in <i>Aspergillus</i> : characterization and application for multi-gene expression. <i>Fungal Biology and Biotechnology</i> , 2019, 6, 24.	5.1	14
22	Reconstructing Dynamic Promoter Activity Profiles from Reporter Gene Data. <i>ACS Synthetic Biology</i> , 2018, 7, 832-841.	3.8	9
23	Familial co-occurrence of congenital heart defects follows distinct patterns. <i>European Heart Journal</i> , 2018, 39, 1015-1022.	2.2	32
24	Glucose-Dependent Promoters for Dynamic Regulation of Metabolic Pathways. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 63.	4.1	27
25	The identification and functional annotation of RNA structures conserved in vertebrates. <i>Genome Research</i> , 2017, 27, 1371-1383.	5.5	71
26	Industrial antifoam agents impair ethanol fermentation and induce stress responses in yeast cells. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8237-8248.	3.6	17
27	RAIN: RNA-protein Association and Interaction Networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw167.	3.0	53
28	Major differences between human atopic dermatitis and murine models, as determined by using global transcriptomic profiling. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 562-571.	2.9	96
29	A scored human protein-protein interaction network to catalyze genomic interpretation. <i>Nature Methods</i> , 2017, 14, 61-64.	19.0	534
30	Modifiable risk factors promoting neurodegeneration is associated with two novel brain degradation markers measured in serum. <i>Neurochemistry International</i> , 2017, 108, 303-308.	3.8	2
31	Integrative analysis of miRNA and gene expression reveals regulatory networks in tamoxifen-resistant breast cancer. <i>Oncotarget</i> , 2016, 7, 57239-57253.	1.8	30
32	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16011.	3.0	21
33	15-year follow-up of the Second Nordic Mantle Cell Lymphoma trial (<sc>MCL</sc>2): prolonged remissions without survival plateau. <i>British Journal of Haematology</i> , 2016, 175, 410-418.	2.5	170
34	High-resolution kinetics and modeling of hydrogen peroxide degradation in live cells. <i>Free Radical Biology and Medicine</i> , 2016, 101, 143-153.	2.9	13
35	Obesity and Bariatric Surgery Drive Epigenetic Variation of Spermatozoa in Humans. <i>Cell Metabolism</i> , 2016, 23, 369-378.	16.2	435
36	Quantification of oxidative stress phenotypes based on high-throughput growth profiling of protein kinase and phosphatase knockouts. <i>FEMS Yeast Research</i> , 2016, 16, fov101.	2.3	8

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37	miR-18b overexpression identifies mantle cell lymphoma patients with poor outcome and improves the MIPI-B prognosticator. <i>Blood</i> , 2015, 125, 2669-2677.	1.4	44
38	Meta-analysis derived atopic dermatitis (MADAD) transcriptome defines a robust AD signature highlighting the involvement of atherosclerosis and lipid metabolism pathways. <i>BMC Medical Genomics</i> , 2015, 8, 60.	1.5	123
39	Oxidative stress response pathways: Fission yeast as archetype. <i>Critical Reviews in Microbiology</i> , 2015, 41, 520-535.	6.1	24
40	A random set scoring model for prioritization of disease candidate genes using protein complexes and data-mining of GeneRIF, OMIM and PubMed records. <i>BMC Bioinformatics</i> , 2014, 15, 315.	2.6	9
41	Colony morphology and transcriptome profiling of <i>Pseudomonas putida</i> KT 2440 and its mutants deficient in alginate or all EPS synthesis under controlled matrix potentials. <i>MicrobiologyOpen</i> , 2014, 3, 457-469.	3.0	18
42	A DNA-binding-site landscape and regulatory network analysis for NAC transcription factors in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2014, 42, 7681-7693.	14.5	84
43	Natural genetic variation impacts expression levels of coding, non-coding, and antisense transcripts in fission yeast. <i>Molecular Systems Biology</i> , 2014, 10, 764.	7.2	65
44	Lineage-specific interface proteins match up the cell cycle and differentiation in embryo stem cells. <i>Stem Cell Research</i> , 2014, 13, 316-328.	0.7	9
45	Lysine deacetylase inhibition prevents diabetes by chromatin-independent immunoregulation and $\beta$ -cell protection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1055-1059.	7.1	58
46	RNA-Protein Interactions: An Overview. <i>Methods in Molecular Biology</i> , 2014, 1097, 491-521.	0.9	102
47	Synthetic Promoter Library for Modulation of Actinorhodin Production in <i>Streptomyces coelicolor</i> A3(2). <i>PLoS ONE</i> , 2014, 9, e99701.	2.5	34
48	ATAF1 transcription factor directly regulates abscisic acid biosynthetic gene <i>NCED3</i> in <i>Arabidopsis thaliana</i> . <i>FEBS Open Bio</i> , 2013, 3, 321-327.	2.3	182
49	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	6.4	110
50	Mapping Condition-Dependent Regulation of Lipid Metabolism in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1979-1995.	1.8	18
51	MicroRNA Profiling in Ocular Adnexal Lymphoma: A Role for MYC and NFKB1 Mediated Dysregulation of MicroRNA Expression in Aggressive Disease. <i>Investigative Ophthalmology and Visual Science</i> , 2013, 54, 5169.		27
52	Gene prioritization for livestock diseases by data integration. <i>Physiological Genomics</i> , 2012, 44, 305-317.	2.3	16
53	Transcriptome Dynamics of <i>Pseudomonas putida</i> KT2440 under Water Stress. <i>Applied and Environmental Microbiology</i> , 2012, 78, 676-683.	3.1	40
54	Differential Protein Pathways in 1,25-Dihydroxyvitamin D <sub>3</sub> and Dexamethasone Modulated Tolerogenic Human Dendritic Cells. <i>Journal of Proteome Research</i> , 2012, 11, 941-971.	3.7	112

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55	Revealing the beneficial effect of protease supplementation to high gravity beer fermentations using "-omics" techniques. <i>Microbial Cell Factories</i> , 2011, 10, 27.	4.0	27
56	Back to the Roots: Prediction of Biologically Active Natural Products from Ayurveda Traditional Medicine. <i>Molecular Informatics</i> , 2011, 30, 181-187.	2.5	17
57	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. <i>Genetic Epidemiology</i> , 2011, 35, 318-332.	1.3	31
58	Evolutionary dynamics of bacteria in a human host environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7481-7486.	7.1	327
59	Dissecting spatio-temporal protein networks driving human heart development and related disorders. <i>Molecular Systems Biology</i> , 2010, 6, 381.	7.2	80
60	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010, 1, 145.	12.8	100
61	Early adaptive developments of <i>Pseudomonas aeruginosa</i> after the transition from life in the environment to persistent colonization in the airways of human cystic fibrosis hosts. <i>Environmental Microbiology</i> , 2010, 12, 1643-1658.	3.8	124
62	Equitoxic Doses of 5-Azacytidine and 5-Aza-2-Deoxycytidine Induce Diverse Immediate and Overlapping Heritable Changes in the Transcriptome. <i>PLoS ONE</i> , 2010, 5, e12994.	2.5	57
63	Novel Insights into the Global Proteome Responses of Insulin-Producing INS-1E Cells To Different Degrees of Endoplasmic Reticulum Stress. <i>Journal of Proteome Research</i> , 2010, 9, 5142-5152.	3.7	22
64	Minimising Immunohistochemical False Negative ER Classification Using a Complementary 23 Gene Expression Signature of ER Status. <i>PLoS ONE</i> , 2010, 5, e15031.	2.5	26
65	Predicting functionality of protein-DNA interactions by integrating diverse evidence. <i>Bioinformatics</i> , 2009, 25, i137-i144.	4.1	38
66	Proteome analysis demonstrates profound alterations in human dendritic cell nature by TX527, an analogue of vitamin D. <i>Proteomics</i> , 2009, 9, 3752-3764.	2.2	51
67	IL-1 receptor antagonism and muscle gene expression in patients with type 2 diabetes. <i>European Cytokine Network</i> , 2009, 20, 81-87.	2.0	11
68	Protein-induced changes during the maturation process of human dendritic cells: A DIGE approach. <i>Proteomics - Clinical Applications</i> , 2008, 2, 1349-1360.	1.6	12
69	Transcription factor control of growth rate dependent genes in <i>Saccharomyces cerevisiae</i> : A three factor design. <i>BMC Genomics</i> , 2008, 9, 341.	2.8	50
70	DASS: efficient discovery and p-value calculation of substructures in unordered data. <i>Bioinformatics</i> , 2007, 23, 77-83.	4.1	21
71	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. <i>Genome Biology</i> , 2007, 8, R253.	9.6	52
72	Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007, 2, 2366-2382.	12.0	2,275

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73	Integrated Assessment and Prediction of Transcription Factor Binding. <i>PLoS Computational Biology</i> , 2006, 2, e70.	3.2	82
74	A Systems Approach to Mapping DNA Damage Response Pathways. <i>Science</i> , 2006, 312, 1054-1059.	12.6	248
75	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	17.5	1,121
76	enoLOGOS: a versatile web tool for energy normalized sequence logos. <i>Nucleic Acids Research</i> , 2005, 33, W389-W392.	14.5	199
77	Validation and refinement of gene-regulatory pathways on a network of physical interactions. <i>Genome Biology</i> , 2005, 6, R62.	9.6	76
78	Blood cell gene expression profiling in rheumatoid arthritis. <i>Immunology Letters</i> , 2004, 93, 217-226.	2.5	73
79	GenePublisher: automated analysis of DNA microarray data. <i>Nucleic Acids Research</i> , 2003, 31, 3471-3476.	14.5	30
80	Neural network predicts sequence of TP53 gene based on DNA chip. <i>Bioinformatics</i> , 2002, 18, 1133-1134.	4.1	18
81	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. <i>Journal of Molecular Biology</i> , 2002, 319, 1257-1265.	4.2	312
82	DNA microarray analysis of fim mutations in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 2002, 267, 721-729.	2.1	49
83	Enrichment of regulatory signals in conserved non-coding genomic sequence. <i>Bioinformatics</i> , 2001, 17, 871-877.	4.1	132
84	No evidence that mRNAs have lower folding free energies than random sequences with the same dinucleotide distribution. <i>Nucleic Acids Research</i> , 1999, 27, 4816-4822.	14.5	179
85	Post-synthetically Ligated Ribozymes: An Alternative Approach to Iterative Solid-Phase Synthesis. <i>Bioconjugate Chemistry</i> , 1997, 8, 204-212.	3.6	4
86	Amino-Linked Ribozymes: Post-Synthetic Conjugation of Half-Ribozymes. <i>Nucleosides &amp; Nucleotides</i> , 1997, 16, 951-954.	0.5	1
87	Morpholino-Linked Ribozymes: A Convergent Synthetic Approach. <i>Journal of the American Chemical Society</i> , 1996, 118, 3771-3772.	13.7	31
88	Crystal structures of an A-form duplex with single-adenosine bulges and a conformational basis for site-specific RNA self-cleavage. <i>Chemistry and Biology</i> , 1996, 3, 173-184.	6.0	70
89	Crystallization and preliminary X-ray diffraction analysis of double-helical RNA octamers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 1065-1070.	2.5	6
90	Synthesis, deprotection, analysis and purification of RNA and ribosomes. <i>Nucleic Acids Research</i> , 1995, 23, 2677-2684.	14.5	453