

Christopher Thomas Workman

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

9,537
citations

87843

38
h-index

43868

91
g-index

98
all docs

98
docs citations

98
times ranked

17323
citing authors

#	ARTICLE	IF	CITATIONS
1	Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007, 2, 2366-2382.	5.5	2,275
2	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	9.4	1,121
3	A scored human protein-protein interaction network to catalyze genomic interpretation. <i>Nature Methods</i> , 2017, 14, 61-64.	9.0	534
4	Synthesis, deprotection, analysis and purification of RNA and ribosomes. <i>Nucleic Acids Research</i> , 1995, 23, 2677-2684.	6.5	453
5	Obesity and Bariatric Surgery Drive Epigenetic Variation of Spermatozoa in Humans. <i>Cell Metabolism</i> , 2016, 23, 369-378.	7.2	435
6	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.	3.3	327
7	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. <i>Journal of Molecular Biology</i> , 2002, 319, 1257-1265.	2.0	312
8	A Systems Approach to Mapping DNA Damage Response Pathways. <i>Science</i> , 2006, 312, 1054-1059.	6.0	248
9	The human gut Firmicute <i>Roseburia intestinalis</i> is a primary degrader of dietary β -mannans. <i>Nature Communications</i> , 2019, 10, 905.	5.8	202
10	enoLOGOS: a versatile web tool for energy normalized sequence logos. <i>Nucleic Acids Research</i> , 2005, 33, W389-W392.	6.5	199
11	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.	1.0	182
12	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.	6.5	179
13	15-year follow-up of the Second Nordic Mantle Cell Lymphoma trial (MCL2): prolonged remissions without survival plateau. <i>British Journal of Haematology</i> , 2016, 175, 410-418.	1.2	170
14	Enrichment of regulatory signals in conserved non-coding genomic sequence. <i>Bioinformatics</i> , 2001, 17, 871-877.	1.8	132
15	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.	1.8	124
16	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.	0.7	123
17	Differential Protein Pathways in 1,25-Dihydroxyvitamin D ₃ and Dexamethasone Modulated Tolerogenic Human Dendritic Cells. <i>Journal of Proteome Research</i> , 2012, 11, 941-971.	1.8	112
18	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	2.9	110

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19	RNA-Protein Interactions: An Overview. <i>Methods in Molecular Biology</i> , 2014, 1097, 491-521.	0.4	102
20	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010, 1, 145.	5.8	100
21	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.	1.5	96
22	Robust estimation of bacterial cell count from optical density. <i>Communications Biology</i> , 2020, 3, 512.	2.0	86
23	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.	6.5	84
24	Integrated Assessment and Prediction of Transcription Factor Binding. <i>PLoS Computational Biology</i> , 2006, 2, e70.	1.5	82
25	Dissecting spatio-temporal protein networks driving human heart development and related disorders. <i>Molecular Systems Biology</i> , 2010, 6, 381.	3.2	80
26	Validation and refinement of gene-regulatory pathways on a network of physical interactions. <i>Genome Biology</i> , 2005, 6, R62.	13.9	76
27	Blood cell gene expression profiling in rheumatoid arthritis. <i>Immunology Letters</i> , 2004, 93, 217-226.	1.1	73
28	The identification and functional annotation of RNA structures conserved in vertebrates. <i>Genome Research</i> , 2017, 27, 1371-1383.	2.4	71
29	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.	6.2	70
30	Natural genetic variation impacts expression levels of coding, non-coding, and antisense transcripts in fission yeast. <i>Molecular Systems Biology</i> , 2014, 10, 764.	3.2	65
31	Lysine deacetylase inhibition prevents diabetes by chromatin-independent immunoregulation and β -cell protection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1055-1059.	3.3	58
32	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.	1.1	57
33	RAIN: RNA-protein Association and Interaction Networks. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw167.	1.4	53
34	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. <i>Genome Biology</i> , 2007, 8, R253.	13.9	52
35	Proteome analysis demonstrates profound alterations in human dendritic cell nature by TX527, an analogue of vitamin D. <i>Proteomics</i> , 2009, 9, 3752-3764.	1.3	51
36	Transcription factor control of growth rate dependent genes in <i>Saccharomyces cerevisiae</i> : A three factor design. <i>BMC Genomics</i> , 2008, 9, 341.	1.2	50

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37	DNA microarray analysis of fim mutations in Escherichia coli. <i>Molecular Genetics and Genomics</i> , 2002, 267, 721-729.	1.0	49
38	miR-18b overexpression identifies mantle cell lymphoma patients with poor outcome and improves the MIPI-B prognosticator. <i>Blood</i> , 2015, 125, 2669-2677.	0.6	44
39	Transcriptome Dynamics of <i>Pseudomonas putida</i> KT2440 under Water Stress. <i>Applied and Environmental Microbiology</i> , 2012, 78, 676-683.	1.4	40
40	Predicting functionality of protein-DNA interactions by integrating diverse evidence. <i>Bioinformatics</i> , 2009, 25, i137-i144.	1.8	38
41	Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. <i>Nucleic Acids Research</i> , 2019, 47, 1671-1691.	6.5	34
42	Synthetic Promoter Library for Modulation of Actinorhodin Production in <i>Streptomyces coelicolor</i> A3(2). <i>PLoS ONE</i> , 2014, 9, e99701.	1.1	34
43	Familial co-occurrence of congenital heart defects follows distinct patterns. <i>European Heart Journal</i> , 2018, 39, 1015-1022.	1.0	32
44	Morpholino-Linked Ribozymes: A Convergent Synthetic Approach. <i>Journal of the American Chemical Society</i> , 1996, 118, 3771-3772.	6.6	31
45	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. <i>Genetic Epidemiology</i> , 2011, 35, 318-332.	0.6	31
46	GenePublisher: automated analysis of DNA microarray data. <i>Nucleic Acids Research</i> , 2003, 31, 3471-3476.	6.5	30
47	Integrative analysis of miRNA and gene expression reveals regulatory networks in tamoxifen-resistant breast cancer. <i>Oncotarget</i> , 2016, 7, 57239-57253.	0.8	30
48	Skeletal muscle enhancer interactions identify genes controlling whole-body metabolism. <i>Nature Communications</i> , 2020, 11, 2695.	5.8	29
49	Revealing the beneficial effect of protease supplementation to high gravity beer fermentations using "-omics" techniques. <i>Microbial Cell Factories</i> , 2011, 10, 27.	1.9	27
50	MicroRNA Profiling in Ocular Adnexal Lymphoma: A Role for MYC and NFKB1 Mediated Dysregulation of MicroRNA Expression in Aggressive Disease. , 2013, 54, 5169.		27
51	Glucose-Dependent Promoters for Dynamic Regulation of Metabolic Pathways. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 63.	2.0	27
52	Minimising Immunohistochemical False Negative ER Classification Using a Complementary 23 Gene Expression Signature of ER Status. <i>PLoS ONE</i> , 2010, 5, e15031.	1.1	26
53	Oxidative stress response pathways: Fission yeast as archetype. <i>Critical Reviews in Microbiology</i> , 2015, 41, 520-535.	2.7	24
54	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.	1.8	22

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55	DASS: efficient discovery and p-value calculation of substructures in unordered data. <i>Bioinformatics</i> , 2007, 23, 77-83.	1.8	21
56	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16011.	1.4	21
57	Neural network predicts sequence of TP53 gene based on DNA chip. <i>Bioinformatics</i> , 2002, 18, 1133-1134.	1.8	18
58	Mapping Condition-Dependent Regulation of Lipid Metabolism in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1979-1995.	0.8	18
59	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.	1.2	18
60	Back to the Roots: Prediction of Biologically Active Natural Products from Ayurveda Traditional Medicine. <i>Molecular Informatics</i> , 2011, 30, 181-187.	1.4	17
61	Industrial antifoam agents impair ethanol fermentation and induce stress responses in yeast cells. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8237-8248.	1.7	17
62	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.	0.8	17
63	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, .	0.9	17
64	The rise of genomics in snake venom research: recent advances and future perspectives. <i>GigaScience</i> , 2022, 11, .	3.3	17
65	Gene prioritization for livestock diseases by data integration. <i>Physiological Genomics</i> , 2012, 44, 305-317.	1.0	16
66	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.	2.0	16
67	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.	1.7	15
68	Bidirectional histone-gene promoters in <i>Aspergillus</i> : characterization and application for multi-gene expression. <i>Fungal Biology and Biotechnology</i> , 2019, 6, 24.	2.5	14
69	High-resolution kinetics and modeling of hydrogen peroxide degradation in live cells. <i>Free Radical Biology and Medicine</i> , 2016, 101, 143-153.	1.3	13
70	Characterization of glutathione proteome in CHO cells and its relationship with productivity and cholesterol synthesis. <i>Biotechnology and Bioengineering</i> , 2020, 117, 3448-3458.	1.7	13
71	Protein-induced changes during the maturation process of human dendritic cells: A 2D DIGE approach. <i>Proteomics - Clinical Applications</i> , 2008, 2, 1349-1360.	0.8	12
72	IL-1 receptor antagonism and muscle gene expression in patients with type 2 diabetes. <i>European Cytokine Network</i> , 2009, 20, 81-87.	1.1	11

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73	Protease Activity Profiling of Snake Venoms Using High-Throughput Peptide Screening. <i>Toxins</i> , 2019, 11, 170.	1.5	11
74	Comparative analysis of three studies measuring fluorescence from engineered bacterial genetic constructs. <i>PLoS ONE</i> , 2021, 16, e0252263.	1.1	11
75	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.	1.2	9
76	Lineage-specific interface proteins match up the cell cycle and differentiation in embryo stem cells. <i>Stem Cell Research</i> , 2014, 13, 316-328.	0.3	9
77	Reconstructing Dynamic Promoter Activity Profiles from Reporter Gene Data. <i>ACS Synthetic Biology</i> , 2018, 7, 832-841.	1.9	9
78	Small Intestinal Tuft Cell Activity Associates With Energy Metabolism in Diet-Induced Obesity. <i>Frontiers in Immunology</i> , 2021, 12, 629391.	2.2	9
79	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.	1.1	8
80	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
81	Use of novel cystine analogs to decrease oxidative stress and control product quality. <i>Journal of Biotechnology</i> , 2021, 327, 1-8.	1.9	8
82	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
83	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.	1.4	5
84	Post-synthetically Ligated Ribozymes: An Alternative Approach to Iterative Solid-Phase Synthesis. <i>Bioconjugate Chemistry</i> , 1997, 8, 204-212.	1.8	4
85	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.	1.4	3
86	Does rapid sequence divergence preclude RNA structure conservation in vertebrates?. <i>Nucleic Acids Research</i> , 2022, 50, 2452-2463.	6.5	3
87	Modifiable risk factors promoting neurodegeneration is associated with two novel brain degradation markers measured in serum. <i>Neurochemistry International</i> , 2017, 108, 303-308.	1.9	2
88	Origin of cooperativity in the activation of dimeric transcription factors. <i>Physical Review Research</i> , 2020, 2, .	1.3	2
89	Amino-Linked Ribozymes: Post-Synthetic Conjugation of Half-Ribozymes. <i>Nucleosides & Nucleotides</i> , 1997, 16, 951-954.	0.5	1
90	Systematic inference of indirect transcriptional regulation by protein kinases and phosphatases. <i>PLoS Computational Biology</i> , 2022, 18, e1009414.	1.5	1