Christopher Thomas Workman

List of Publications by Year
in descending order

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	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	12.0	2,275
2	Assessing computational tools for the discovery of transcription factor binding sites. Nature Biotechnology, 2005, 23, 137-144.	17.5	1,121
3	A scored human protein–protein interaction network to catalyze genomic interpretation. Nature Methods, 2017, 14, 61-64.	19.0	534
4	Synthesis, deprotection, analysis and purification of RNA and ribosomes. Nucleic Acids Research, 1995, 23, 2677-2684.	14.5	453
5	Obesity and Bariatric Surgery Drive Epigenetic Variation of Spermatozoa in Humans. Cell Metabolism, 2016, 23, 369-378.	16.2	435
6	Evolutionary dynamics of bacteria in a human host environment. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7481-7486.	7.1	327
7	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. Journal of Molecular Biology, 2002, 319, 1257-1265.	4.2	312
8	A Systems Approach to Mapping DNA Damage Response Pathways. Science, 2006, 312, 1054-1059.	12.6	248
9	The human gut Firmicute Roseburia intestinalis is a primary degrader of dietary β-mannans. Nature Communications, 2019, 10, 905.	12.8	202
10	enoLOGOS: a versatile web tool for energy normalized sequence logos. Nucleic Acids Research, 2005, 33, W389-W392.	14.5	199
11	ATAF1 transcription factor directly regulates abscisic acid biosynthetic gene <i>NCED3</i> in <i>Arabidopsis thaliana</i>. FEBS Open Bio, 2013, 3, 321-327.	2.3	182
12	No evidence that mRNAs have lower folding free energies than random sequences with the same dinucleotide distribution. Nucleic Acids Research, 1999, 27, 4816-4822.	14.5	179
13	15-year follow-up of the Second Nordic Mantle Cell Lymphoma trial (<scp>MCL</scp>2): prolonged remissions without survival plateau. British Journal of Haematology, 2016, 175, 410-418.	2.5	170
14	Enrichment of regulatory signals in conserved non-coding genomic sequence. Bioinformatics, 2001, 17, 871-877.	4.1	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. Environmental Microbiology, 2010, 12, 1643-1658.	3.8	124
16	Meta-analysis derived atopic dermatitis (MADAD) transcriptome defines a robust AD signature highlighting the involvement of atherosclerosis and lipid metabolism pathways. BMC Medical Genomics, 2015, 8, 60.	1.5	123
17	Differential Protein Pathways in 1,25-Dihydroxyvitamin D$_3$ and Dexamethasone Modulated Tolerogenic Human Dendritic Cells. Journal of Proteome Research, 2012, 11, 941-971.	3.7	112
18	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	6.4	110

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19	RNAâ€"Protein Interactions: An Overview. Methods in Molecular Biology, 2014, 1097, 491-521.	0.9	102
20	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. Nature Communications, 2010, 1, 145.	12.8	100
21	Major differences between human atopic dermatitis and murine models, as determined by using global transcriptomic profiling. Journal of Allergy and Clinical Immunology, 2017, 139, 562-571.	2.9	96
22	Robust estimation of bacterial cell count from optical density. Communications Biology, 2020, 3, 512.	4.4	86
23	A DNA-binding-site landscape and regulatory network analysis for NAC transcription factors in<i>Arabidopsis thaliana</i>. Nucleic Acids Research, 2014, 42, 7681-7693.	14.5	84
24	Integrated Assessment and Prediction of Transcription Factor Binding. PLoS Computational Biology, 2006, 2, e70.	3.2	82
25	Dissecting spatioâ€temporal protein networks driving human heart development and related disorders. Molecular Systems Biology, 2010, 6, 381.	7.2	80
26	Validation and refinement of gene-regulatory pathways on a network of physical interactions. Genome Biology, 2005, 6, R62.	9.6	76
27	Blood cell gene expression profiling in rheumatoid arthritis. Immunology Letters, 2004, 93, 217-226.	2.5	73
28	The identification and functional annotation of RNA structures conserved in vertebrates. Genome Research, 2017, 27, 1371-1383.	5.5	71
29	Crystal structures of an A-form duplex with single-adenosine bulges and a conformational basis for site-specific RNA self-cleavage. Chemistry and Biology, 1996, 3, 173-184.	6.0	70
30	Natural genetic variation impacts expression levels of coding, nonâ€coding, and antisense transcripts in fission yeast. Molecular Systems Biology, 2014, 10, 764.	7.2	65
31	Lysine deacetylase inhibition prevents diabetes by chromatin-independent immunoregulation and Î²-cell protection. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1055-1059.	7.1	58
32	Equitoxic Doses of 5-Azacytidine and 5-Aza-2â€²Deoxycytidine Induce Diverse Immediate and Overlapping Heritable Changes in the Transcriptome. PLoS ONE, 2010, 5, e12994.	2.5	57
33	RAIN: RNAâ€"protein Association and Interaction Networks. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw167.	3.0	53
34	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. Genome Biology, 2007, 8, R253.	9.6	52
35	Proteome analysis demonstrates profound alterations in human dendritic cell nature by TX527, an analogue of vitamin D. Proteomics, 2009, 9, 3752-3764.	2.2	51
36	Transcription factor control of growth rate dependent genes in Saccharomyces cerevisiae: A three factor design. BMC Genomics, 2008, 9, 341.	2.8	50

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37	DNA microarray analysis of fim mutations in Escherichia coli. Molecular Genetics and Genomics, 2002, 267, 721-729.	2.1	49
38	miR-18b overexpression identifies mantle cell lymphoma patients with poor outcome and improves the MIPI-B prognosticator. Blood, 2015, 125, 2669-2677.	1.4	44
39	Transcriptome Dynamics of Pseudomonas putida KT2440 under Water Stress. Applied and Environmental Microbiology, 2012, 78, 676-683.	3.1	40
40	Predicting functionality of protein–DNA interactions by integrating diverse evidence. Bioinformatics, 2009, 25, i137-i144.	4.1	38
41	Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. Nucleic Acids Research, 2019, 47, 1671-1691.	14.5	34
42	Synthetic Promoter Library for Modulation of Actinorhodin Production in Streptomyces coelicolor A3(2). PLoS ONE, 2014, 9, e99701.	2.5	34
43	Familial co-occurrence of congenital heart defects follows distinct patterns. European Heart Journal, 2018, 39, 1015-1022.	2.2	32
44	Morpholino-Linked Ribozymes: A Convergent Synthetic Approach. Journal of the American Chemical Society, 1996, 118, 3771-3772.	13.7	31
45	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. Genetic Epidemiology, 2011, 35, 318-332.	1.3	31
46	GenePublisher: automated analysis of DNA microarray data. Nucleic Acids Research, 2003, 31, 3471-3476.	14.5	30
47	Integrative analysis of miRNA and gene expression reveals regulatory networks in tamoxifen-resistant breast cancer. Oncotarget, 2016, 7, 57239-57253.	1.8	30
48	Skeletal muscle enhancer interactions identify genes controlling whole-body metabolism. Nature Communications, 2020, 11, 2695.	12.8	29
49	Revealing the beneficial effect of protease supplementation to high gravity beer fermentations using "-omics" techniques. Microbial Cell Factories, 2011, 10, 27.	4.0	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. Frontiers in Bioengineering and Biotechnology, 2018, 6, 63.	4.1	27
52	Minimising Immunohistochemical False Negative ER Classification Using a Complementary 23 Gene Expression Signature of ER Status. PLoS ONE, 2010, 5, e15031.	2.5	26
53	Oxidative stress response pathways: Fission yeast as archetype. Critical Reviews in Microbiology, 2015, 41, 520-535.	6.1	24
54	Novel Insights into the Global Proteome Responses of Insulin-Producing INS-1E Cells To Different Degrees of Endoplasmic Reticulum Stress. Journal of Proteome Research, 2010, 9, 5142-5152.	3.7	22

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55	DASS: efficient discovery and p-value calculation of substructures in unordered data. Bioinformatics, 2007, 23, 77-83.	4.1	21
56	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. Npj Systems Biology and Applications, 2016, 2, 16011.	3.0	21
57	Neural network predicts sequence of TP53 gene based on DNA chip. Bioinformatics, 2002, 18, 1133-1134.	4.1	18
58	Mapping Condition-Dependent Regulation of Lipid Metabolism in Saccharomyces cerevisiae. G3: Genes, Genomes, Genetics, 2013, 3, 1979-1995.	1.8	18
59	Colony morphology and transcriptome profiling of P seudomonas putida KT 2440 and its mutants deficient in alginate or all EPS synthesis under controlled matric potentials. MicrobiologyOpen, 2014, 3, 457-469.	3.0	18
60	Back to the Roots: Prediction of Biologically Active Natural Products from Ayurveda Traditional Medicine. Molecular Informatics, 2011, 30, 181-187.	2.5	17
61	Industrial antifoam agents impair ethanol fermentation and induce stress responses in yeast cells. Applied Microbiology and Biotechnology, 2017, 101, 8237-8248.	3.6	17
62	Investigating the Influence of Glycerol on the Utilization of Glucose in *Yarrowia lipolytica* Using RNA-Seq-Based Transcriptomics. G3: Genes, Genomes, Genetics, 2019, 9, 4059-4071.	1.8	17
63	Burden Imposed by Heterologous Protein Production in Two Major Industrial Yeast Cell Factories: Identifying Sources and Mitigation Strategies. Frontiers in Fungal Biology, 2022, 3, .	2.0	17
64	The rise of genomics in snake venom research: recent advances and future perspectives. GigaScience, 2022, 11, .	6.4	17
65	Gene prioritization for livestock diseases by data integration. Physiological Genomics, 2012, 44, 305-317.	2.3	16
66	Body fluid from the parasitic worm *Ascaris suum* inhibits broad€acting pro€inflammatory programs in dendritic cells. Immunology, 2020, 159, 322-334.	4.4	16
67	Fluctuations in glucose availability prevent global proteome changes and physiological transition during prolonged chemostat cultivations of Saccharomyces cerevisiae. Biotechnology and Bioengineering, 2020, 117, 2074-2088.	3.3	15
68	Bidirectional histone-gene promoters in Aspergillus: characterization and application for multi-gene expression. Fungal Biology and Biotechnology, 2019, 6, 24.	5.1	14
69	High-resolution kinetics and modeling of hydrogen peroxide degradation in live cells. Free Radical Biology and Medicine, 2016, 101, 143-153.	2.9	13
70	Characterization of glutathione proteome in CHO cells and its relationship with productivity and cholesterol synthesis. Biotechnology and Bioengineering, 2020, 117, 3448-3458.	3.3	13
71	Protein€induced changes during the maturation process of human dendritic cells: A 2€D DIGE approach. Proteomics - Clinical Applications, 2008, 2, 1349-1360.	1.6	12
72	IL-1 receptor antagonism and muscle gene expression in patients with type 2 diabetes. European Cytokine Network, 2009, 20, 81-87.	2.0	11

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73	Protease Activity Profiling of Snake Venoms Using High-Throughput Peptide Screening. Toxins, 2019, 11, 170.	3.4	11
74	Comparative analysis of three studies measuring fluorescence from engineered bacterial genetic constructs. PLoS ONE, 2021, 16, e0252263.	2.5	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. BMC Bioinformatics, 2014, 15, 315.	2.6	9
76	Lineage-specific interface proteins match up the cell cycle and differentiation in embryo stem cells. Stem Cell Research, 2014, 13, 316-328.	0.7	9
77	Reconstructing Dynamic Promoter Activity Profiles from Reporter Gene Data. ACS Synthetic Biology, 2018, 7, 832-841.	3.8	9
78	Small Intestinal Tuft Cell Activity Associates With Energy Metabolism in Diet-Induced Obesity. Frontiers in Immunology, 2021, 12, 629391.	4.8	9
79	Quantification of oxidative stress phenotypes based on high-throughput growth profiling of protein kinase and phosphatase knockouts. FEMS Yeast Research, 2016, 16, fov101.	2.3	8
80	Loss of AA13 LPMOs impairs degradation of resistant starch and reduces the growth of Aspergillus nidulans. Biotechnology for Biofuels, 2020, 13, 135.	6.2	8
81	Use of novel cystine analogs to decrease oxidative stress and control product quality. Journal of Biotechnology, 2021, 327, 1-8.	3.8	8
82	Crystallization and preliminary X-ray diffraction analysis of double-helical RNA octamers. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 1065-1070.	2.5	6
83	Emergence of Phenotypically Distinct Subpopulations Is a Factor in Adaptation of Recombinant Saccharomyces cerevisiae under Glucose-Limited Conditions. Applied and Environmental Microbiology, 2022, 88, e0230721.	3.1	5
84	Post-synthetically Ligated Ribozymes:Â An Alternative Approach to Iterative Solid-Phase Synthesis. Bioconjugate Chemistry, 1997, 8, 204-212.	3.6	4
85	Innate ILâ€23/Type 17 immune responses mediate the effect of the 17q21 locus on childhood asthma. Clinical and Experimental Allergy, 2021, 51, 892-901.	2.9	3
86	Does rapid sequence divergence preclude RNA structure conservation in vertebrates?. Nucleic Acids Research, 2022, 50, 2452-2463.	14.5	3
87	Modifiable risk factors promoting neurodegeneration is associated with two novel brain degradation markers measured in serum. Neurochemistry International, 2017, 108, 303-308.	3.8	2
88	Origin of cooperativity in the activation of dimeric transcription factors. Physical Review Research, 2020, 2, .	3.6	2
89	Amino-Linked Ribozymes: Post-Synthetic Conjugation of Half-Ribozymes. Nucleosides & Nucleotides, 1997, 16, 951-954.	0.5	1
90	Systematic inference of indirect transcriptional regulation by protein kinases and phosphatases. PLoS Computational Biology, 2022, 18, e1009414.	3.2	1