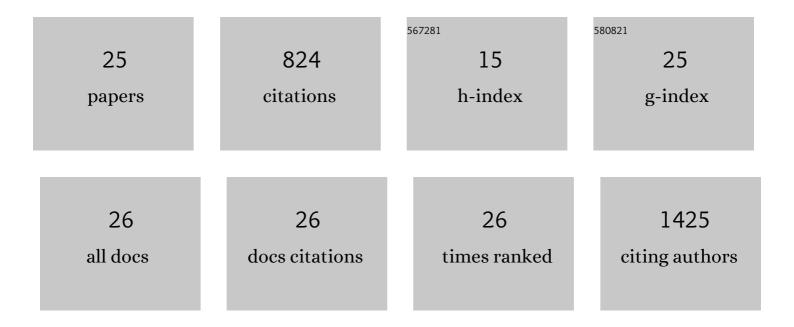
Hugh-G Patterton

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8402018/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The Biochemical and Phenotypic Characterization of Hho1p, the Putative Linker Histone H1 of Saccharomyces cerevisiae. Journal of Biological Chemistry, 1998, 273, 7268-7276.	3.4	132
2	H3ABioNet, a sustainable pan-African bioinformatics network for human heredity and health in Africa. Genome Research, 2016, 26, 271-277.	5.5	94
3	Over-expression and properties of a purified recombinant Bacillus licheniformis lipase: a comparative report on Bacillus lipases. Enzyme and Microbial Technology, 2001, 28, 705-712.	3.2	85
4	Bioinformatics EducationPerspectives and Challenges out of Africa. Briefings in Bioinformatics, 2015, 16, 355-364.	6.5	61
5	Saccharomyces cerevisiae Set1p is a methyltransferase specific for lysine 4 of histone H3 and is required for efficient gene expression. Yeast, 2003, 20, 827-835.	1.7	56
6	The <i>Saccharomyces cerevisiae</i> linker histone Hho1p is essential for chromatin compaction in stationary phase and is displaced by transcription. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14838-14843.	7.1	45
7	RNA-seq based transcriptional analysis of Saccharomyces cerevisiae and Lachancea thermotolerans in mixed-culture fermentations under anaerobic conditions. BMC Genomics, 2019, 20, 145.	2.8	38
8	Bioinformatics tools for the structural elucidation of multi-subunit protein complexes by mass spectrometric analysis of protein-protein cross-links. Briefings in Bioinformatics, 2011, 12, 660-671.	6.5	36
9	Negative Supercoiling and Nucleosome Cores. Journal of Molecular Biology, 1993, 229, 623-636.	4.2	33
10	Nucleosome Positioning and Transcription. Cold Spring Harbor Symposia on Quantitative Biology, 1993, 58, 237-245.	1.1	30
11	The epigenome of Trypanosoma brucei: A regulatory interface to an unconventional transcriptional machine. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 743-750.	1.9	29
12	Calculating the statistical significance of physical clusters of co-regulated genes in the genome: the role of chromatin in domain-wide gene regulation. Nucleic Acids Research, 2004, 32, 1798-1807.	14.5	27
13	Secondary Structures of the Core Histone N-terminal Tails: Their Role in Regulating Chromatin Structure. Sub-Cellular Biochemistry, 2013, 61, 37-55.	2.4	20
14	An LC-MS/MS based survey of contaminants of emerging concern in drinking water in South Africa. South African Journal of Science, 2015, 111, 6.	0.7	20
15	The human transketolase-like proteins TKTL1 and TKTL2 are bona fide transketolases. BMC Structural Biology, 2019, 19, 2.	2.3	16
16	Negative Supercoiling and Nucleosome Cores. Journal of Molecular Biology, 1993, 229, 637-655.	4.2	15
17	Characterization of casein and alpha lactalbumin of African elephant (Loxodonta africana) milk. Journal of Dairy Science, 2015, 98, 8308-8318.	3.4	15
18	How Does Inflammationâ€Induced Hyperglycemia Cause Mitochondrial Dysfunction in Immune Cells?. BioEssays, 2019, 41, e1800260.	2.5	15

HUGH-G PATTERTON

#	Article	IF	CITATIONS
19	Well-positioned nucleosomes punctuate polycistronic pol II transcription units and flank silent VSG gene arrays in Trypanosoma brucei. Epigenetics and Chromatin, 2017, 10, 14.	3.9	14
20	Modified curved DNA that could allow local DNA underwinding at the nucleosomal pseudodyad fails to position a nucleosomein vivo. Nucleic Acids Research, 1995, 23, 4170-4179.	14.5	10
21	Histone Octamer Helical Tubes Suggest that an Internucleosomal Four-Helix Bundle Stabilizes the Chromatin Fiber. Biophysical Journal, 2009, 96, 3363-3371.	0.5	9
22	The effect of epigenetic modifications on the secondary structures and possible binding positions of the N-terminal tail of histone H3 in the nucleosome: a computational study. Journal of Molecular Modeling, 2017, 23, 137.	1.8	8
23	The translational placement of nucleosome cores in vitro determines the access of the transacting factor suGF1 to DNA. Nucleic Acids Research, 1996, 24, 4349-4355.	14.5	7
24	Strategies and opportunities for promoting bioinformatics in Zimbabwe. PLoS Computational Biology, 2018, 14, e1006480.	3.2	6
25	AnchorMS: a bioinformatics tool to derive structural information from the mass spectra of cross-linked protein complexes. Bioinformatics, 2014, 30, 125-126.	4.1	3