

David Landsman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1539945/publications.pdf>

Version: 2024-02-01

76
papers

7,449
citations

159585

30
h-index

79698

73
g-index

81
all docs

81
docs citations

81
times ranked

12001
citing authors

#	ARTICLE	IF	CITATIONS
1	Increasing concentration of COVID-19 by socioeconomic determinants and geography in Toronto, Canada: an observational study. <i>Annals of Epidemiology</i> , 2022, 65, 84-92.	1.9	25
2	DNA methylation cues in nucleosome geometry, stability and unwrapping. <i>Nucleic Acids Research</i> , 2022, 50, 1864-1874.	14.5	25
3	Impact of COVID-19 on Tuberculosis Prevention and Treatment in Canada: A Multicenter Analysis of 10,833 Patients. <i>Journal of Infectious Diseases</i> , 2022, 225, 1317-1320.	4.0	12
4	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021, 49, D274-D281.	14.5	441
5	Histone tails as signaling antennas of chromatin. <i>Current Opinion in Structural Biology</i> , 2021, 67, 153-160.	5.7	32
6	Human Histone Interaction Networks: An Old Concept, New Trends. <i>Journal of Molecular Biology</i> , 2021, 433, 166684.	4.2	4
7	PM4NGS, a project management framework for next-generation sequencing data analysis. <i>GigaScience</i> , 2021, 10, .	6.4	0
8	Transcriptome annotation in the cloud: complexity, best practices, and cost. <i>GigaScience</i> , 2021, 10, .	6.4	9
9	Cohort profile: St. Michael's Hospital Tuberculosis Database (SMH-TB), a retrospective cohort of electronic health record data and variables extracted using natural language processing. <i>PLoS ONE</i> , 2021, 16, e0247872.	2.5	0
10	A model of active transcription hubs that unifies the roles of active promoters and enhancers. <i>Nucleic Acids Research</i> , 2021, 49, 4493-4505.	14.5	27
11	Binding of regulatory proteins to nucleosomes is modulated by dynamic histone tails. <i>Nature Communications</i> , 2021, 12, 5280.	12.8	43
12	Heterogeneity in testing, diagnosis and outcome in SARS-CoV-2 infection across outbreak settings in the Greater Toronto Area, Canada: an observational study. <i>CMAJ Open</i> , 2020, 8, E627-E636.	2.4	27
13	Estimated surge in hospital and intensive care admission because of the coronavirus disease 2019 pandemic in the Greater Toronto Area, Canada: a mathematical modelling study. <i>CMAJ Open</i> , 2020, 8, E593-E604.	2.4	7
14	Molecular recognition of nucleosomes by binding partners. <i>Current Opinion in Structural Biology</i> , 2019, 56, 164-170.	5.7	21
15	Structural interpretation of DNA-protein hydroxyl-radical footprinting experiments with high resolution using HYDROID. <i>Nature Protocols</i> , 2018, 13, 2535-2556.	12.0	6
16	The Mediator co-activator complex regulates Ty1 retromobility by controlling the balance between Ty1i and Ty1 promoters. <i>PLoS Genetics</i> , 2018, 14, e1007232.	3.5	13
17	Role of the pre-initiation complex in Mediator recruitment and dynamics. <i>ELife</i> , 2018, 7, .	6.0	30
18	HMG1 Modulates Nucleosome Occupancy and DNase I Hypersensitivity at the CpG Island Promoters of Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2013, 33, 3377-3389.	2.3	68

#	ARTICLE	IF	CITATIONS
19	Identification of Immunity Related Genes to Study the <i>Physalis peruviana</i> "Fusarium oxysporum Pathosystem. <i>PLoS ONE</i> , 2013, 8, e68500.	2.5	30
20	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2012, 40, D13-D25.	14.5	510
21	Differences in local genomic context of bound and unbound motifs. <i>Gene</i> , 2012, 506, 125-134.	2.2	3
22	The <i>Physalis peruviana</i> leaf transcriptome: assembly, annotation and gene model prediction. <i>BMC Genomics</i> , 2012, 13, 151.	2.8	52
23	A unified phylogeny-based nomenclature for histone variants. <i>Epigenetics and Chromatin</i> , 2012, 5, 7.	3.9	265
24	In silico identification and characterization of the ion transport specificity for P-type ATPases in the <i>Mycobacterium tuberculosis</i> complex. <i>BMC Structural Biology</i> , 2012, 12, 25.	2.3	26
25	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2011, 39, D38-D51.	14.5	582
26	Analysis of Biological Features Associated with Meiotic Recombination Hot and Cold Spots in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2011, 6, e29711.	2.5	20
27	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	14.5	32
28	Genome Sequence of the <i>Mycobacterium colombiense</i> Type Strain, CECT 3035. <i>Journal of Bacteriology</i> , 2011, 193, 5866-5867.	2.2	7
29	Effects of HMGN variants on the cellular transcription profile. <i>Nucleic Acids Research</i> , 2011, 39, 4076-4087.	14.5	38
30	Ten Simple Rules for Developing a Short Bioinformatics Training Course. <i>PLoS Computational Biology</i> , 2011, 7, e1002245.	3.2	29
31	The Histone Database: an integrated resource for histones and histone fold-containing proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar048-bar048.	3.0	40
32	DATABASE: A new forum for biological databases and curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2009, bap002-bap002.	3.0	10
33	Many sequence-specific chromatin modifying protein-binding motifs show strong positional preferences for potential regulatory regions in the <i>Saccharomyces cerevisiae</i> genome. <i>Nucleic Acids Research</i> , 2010, 38, 1772-1779.	14.5	21
34	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2010, 38, D5-D16.	14.5	417
35	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2009, 37, D5-D15.	14.5	797
36	Repetitive DNA elements, nucleosome binding and human gene expression. <i>Gene</i> , 2009, 436, 12-22.	2.2	32

#	ARTICLE	IF	CITATIONS
37	Identification of cis-Regulatory Elements in Gene Co-expression Networks Using A-GLAM. <i>Methods in Molecular Biology</i> , 2009, 541, 3-22.	0.9	14
38	Promoter Analysis: Gene Regulatory Motif Identification with A-GLAM. <i>Methods in Molecular Biology</i> , 2009, 537, 263-276.	0.9	7
39	Evolutionary rates and patterns for human transcription factor binding sites derived from repetitive DNA. <i>BMC Genomics</i> , 2008, 9, 226.	2.8	62
40	The biological function of some human transcription factor binding motifs varies with position relative to the transcription start site. <i>Nucleic Acids Research</i> , 2008, 36, 2777-2786.	14.5	19
41	Expression Patterns of Protein Kinases Correlate with Gene Architecture and Evolutionary Rates. <i>PLoS ONE</i> , 2008, 3, e3599.	2.5	20
42	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2007, 36, D13-D21.	14.5	757
43	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2007, 35, D5-D12.	14.5	757
44	Multiple independent evolutionary solutions to core histone gene regulation. <i>Genome Biology</i> , 2006, 7, R122.	9.6	47
45	Scanning sequences after Gibbs sampling to find multiple occurrences of functional elements. <i>BMC Bioinformatics</i> , 2006, 7, 408.	2.6	2
46	The histone database: A comprehensive resource for histones and histone fold-containing proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 838-842.	2.6	51
47	Alignments anchored on genomic landmarks can aid in the identification of regulatory elements. <i>Bioinformatics</i> , 2005, 21, i440-i448.	4.1	30
48	Global Regulation by the Yeast Spt10 Protein Is Mediated through Chromatin Structure and the Histone Upstream Activating Sequence Elements. <i>Molecular and Cellular Biology</i> , 2005, 25, 9127-9137.	2.3	58
49	Histone structure and nucleosome stability. <i>Expert Review of Proteomics</i> , 2005, 2, 719-729.	3.0	237
50	Statistical analysis of over-represented words in human promoter sequences. <i>Nucleic Acids Research</i> , 2004, 32, 949-958.	14.5	108
51	High-resolution genome-wide mapping of histone modifications. <i>Nature Biotechnology</i> , 2004, 22, 1013-1016.	17.5	199
52	Characterization of sequence variability in nucleosome core histone folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 454-465.	2.6	18
53	Mining Core Histone Sequences from Public Protein Databases. <i>Methods in Enzymology</i> , 2003, 375, 3-20.	1.0	3
54	Identifying related L1 retrotransposons by analyzing 3' transduced sequences. <i>Genome Biology</i> , 2003, 4, R30.	9.6	34

#	ARTICLE	IF	CITATIONS
55	Retroposed Copies of the HMG Genes: A Window to Genome Dynamics. <i>Genome Research</i> , 2003, 13, 800-812.	5.5	35
56	B-ZIP Proteins Encoded by the <i>Drosophila</i> Genome: Evaluation of Potential Dimerization Partners. <i>Genome Research</i> , 2002, 12, 1190-1200.	5.5	68
57	Expressed Sequence Tags (ESTs). <i>Methods of Biochemical Analysis</i> , 2002, 43, 283-301.	0.2	8
58	Learning about addiction from the genome. <i>Nature</i> , 2001, 409, 834-835.	27.8	137
59	NBP-45, a Novel Nucleosomal Binding Protein with a Tissue-specific and Developmentally Regulated Expression. <i>Journal of Biological Chemistry</i> , 2000, 275, 6368-6374.	3.4	51
60	Histone Sequence Database: sequences, structures, post-translational modifications and genetic loci. <i>Nucleic Acids Research</i> , 1999, 27, 323-324.	14.5	10
61	The Biochemical and Phenotypic Characterization of Hho1p, the Putative Linker Histone H1 of <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 7268-7276.	3.4	132
62	Predictive Methods Using Protein Sequences. <i>Methods of Biochemical Analysis</i> , 1998, 39, 246-267.	0.2	0
63	Analysis of the functional role of conserved residues in the protein subunit of ribonuclease P from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1997, 267, 818-829.	4.2	74
64	Histone H1 in <i>Saccharomyces cerevisiae</i> : a double mystery solved?. <i>Trends in Biochemical Sciences</i> , 1996, 21, 287-288.	7.5	22
65	Common sequence and structural features in the heat-shock factor and Ets families of DNA-binding domains. <i>Trends in Biochemical Sciences</i> , 1995, 20, 225-226.	7.5	18
66	The HMG-1 box protein family: classification and functional relationships. <i>Nucleic Acids Research</i> , 1995, 23, 1604-1613.	14.5	209
67	A signature for the HMG box DNA-binding proteins. <i>BioEssays</i> , 1993, 15, 539-546.	2.5	265
68	RNP-1, an RNA-binding motif is conserved in the DNA-binding cold shock domain. <i>Nucleic Acids Research</i> , 1992, 20, 2861-2864.	14.5	128
69	Mapping the human gene coding for chromosomal protein HMG-17. <i>Human Genetics</i> , 1990, 85, 376-8.	3.8	13
70	Mouse non-histone chromosomal protein HMG-14 cDNA sequence. <i>Nucleic Acids Research</i> , 1990, 18, 5311-5311.	14.5	8
71	A single copy gene for chicken chromosomal protein HMG-14b has evolutionarily conserved features, has lost one of its introns and codes for a rapidly evolving protein. <i>Journal of Molecular Biology</i> , 1990, 211, 49-61.	4.2	24
72	Cell cycle regulated synthesis of an abundant transcript for human chromosomal protein HMG-17. <i>Nucleic Acids Research</i> , 1987, 15, 3549-3561.	14.5	23

#	ARTICLE	IF	CITATIONS
73	Chicken non-histone chromosomal protein HMG-17 cDNA sequence. Nucleic Acids Research, 1987, 15, 6750-6750.	14.5	12
74	Retropseudogenes for human chromosomal protein HMG-17. Journal of Molecular Biology, 1987, 197, 405-413.	4.2	38
75	Exchange of proteins during immunofractionation of chromatin. Experimental Cell Research, 1986, 163, 95-102.	2.6	21
76	Immunofractionation of chromatin regions associated with histone H1o. FEBS Journal, 1986, 160, 253-260.	0.2	26