

# David Landsman

## List of Publications by Year in descending order

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113  
papers

8,809  
citations

109321

35  
h-index

46799

89  
g-index

124  
all docs

124  
docs citations

124  
times ranked

11446  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mediator dynamics during heat shock in budding yeast. <i>Genome Research</i> , 2022, 32, 111-123.	5.5	3
2	DNA methylation cues in nucleosome geometry, stability and unwrapping. <i>Nucleic Acids Research</i> , 2022, 50, 1864-1874.	14.5	25
3	Multiple epigenetic factors co-localize with HMGN proteins in A-compartment chromatin. <i>Epigenetics and Chromatin</i> , 2022, 15, .	3.9	5
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	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
10	Binding of regulatory proteins to nucleosomes is modulated by dynamic histone tails. <i>Nature Communications</i> , 2021, 12, 5280.	12.8	43
11	Data sets on human histone interaction networks. <i>Data in Brief</i> , 2020, 33, 106555.	1.0	1
12	Kin28 depletion increases association of TFIID subunits Taf1 and Taf4 with promoters in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2020, 48, 4244-4255.	14.5	9
13	BAMscale: quantification of next-generation sequencing peaks and generation of scaled coverage tracks. <i>Epigenetics and Chromatin</i> , 2020, 13, 21.	3.9	40
14	Banana ( <i>Musa acuminata</i> ) transcriptome profiling in response to rhizobacteria: <i>Bacillus amyloliquefaciens</i> Bs006 and <i>Pseudomonas fluorescens</i> Ps006. <i>BMC Genomics</i> , 2019, 20, 378.	2.8	31
15	Molecular recognition of nucleosomes by binding partners. <i>Current Opinion in Structural Biology</i> , 2019, 56, 164-170.	5.7	21
16	TPMCalculator: one-step software to quantify mRNA abundance of genomic features. <i>Bioinformatics</i> , 2019, 35, 1960-1962.	4.1	149
17	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2018, 46, D8-D13.	14.5	1,291
18	SNPDeIScore: combining multiple methods to score deleterious effects of noncoding mutations in the human genome. <i>Bioinformatics</i> , 2018, 34, 289-291.	4.1	11

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19	Binding of HMGN proteins to cell specific enhancers stabilizes cell identity. Nature Communications, 2018, 9, 5240.	12.8	32
20	Structural interpretation of DNA-protein hydroxyl-radical footprinting experiments with high resolution using HYDROID. Nature Protocols, 2018, 13, 2535-2556.	12.0	6
21	A Genome-Wide Screen Reveals a Role for the HIR Histone Chaperone Complex in Preventing Mislocalization of Budding Yeast CENP-A. Genetics, 2018, 210, 203-218.	2.9	20
22	The Mediator co-activator complex regulates Ty1 retromobility by controlling the balance between Ty1i and Ty1 promoters. PLoS Genetics, 2018, 14, e1007232.	3.5	13
23	Role of the pre-initiation complex in Mediator recruitment and dynamics. ELife, 2018, 7, .	6.0	30
24	Molecular basis of CENP-C association with the CENP-A nucleosome at yeast centromeres. Genes and Development, 2017, 31, 1958-1972.	5.9	45
25	Workflow and web application for annotating NCBI BioProject transcriptome data. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	6
26	MS_HistoneDB, a manually curated resource for proteomic analysis of human and mouse histones. Epigenetics and Chromatin, 2017, 10, 2.	3.9	40
27	Hydroxyl-radical footprinting combined with molecular modeling identifies unique features of DNA conformation and nucleosome positioning. Nucleic Acids Research, 2017, 45, 9229-9243.	14.5	18
28	Whole-Genome Sequence of Multidrug-Resistant <i>Campylobacter coli</i> Strain COL B1-266, Isolated from the Colombian Poultry Chain. Genome Announcements, 2016, 4, .	0.8	1
29	Quantifying deleterious effects of regulatory variants. Nucleic Acids Research, 2016, 45, gkw1263.	14.5	14
30	HistoneDB 2.0: a histone database with variants—an integrated resource to explore histones and their variants. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw014.	3.0	99
31	Whole-Genome Sequences of Two <i>Campylobacter coli</i> Isolates from the Antimicrobial Resistance Monitoring Program in Colombia. Genome Announcements, 2016, 4, .	0.8	1
32	Genome Sequence of the Banana Plant Growth-Promoting Rhizobacterium <i>Pseudomonas fluorescens</i> PS006. Genome Announcements, 2016, 4, .	0.8	10
33	Trajectories of microsecond molecular dynamics simulations of nucleosomes and nucleosome core particles. Data in Brief, 2016, 7, 1678-1681.	1.0	3
34	HMGN proteins modulate chromatin regulatory sites and gene expression during activation of naïve B cells. Nucleic Acids Research, 2016, 44, gkw323.	14.5	11
35	Most of the tight positional conservation of transcription factor binding sites near the transcription start site reflects their co-localization within regulatory modules. BMC Bioinformatics, 2016, 17, 479.	2.6	1
36	Coupling between Histone Conformations and DNA Geometry in Nucleosomes on a Microsecond Timescale: Atomistic Insights into Nucleosome Functions. Journal of Molecular Biology, 2016, 428, 221-237.	4.2	131

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37	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav063.	3.0	8
38	Genome-Wide Association of Mediator and RNA Polymerase II in Wild-Type and Mediator Mutant Yeast. Molecular and Cellular Biology, 2015, 35, 331-342.	2.3	48
39	Genetic diversity and population structure in <i>Physalis peruviana</i> and related taxa based on InDels and SNPs derived from COSII and IRG markers. Plant Gene, 2015, 4, 29-37.	2.3	30
40	Genome Sequence of the Banana Plant Growth-Promoting Rhizobacterium <i>Bacillus amyloliquefaciens</i> BS006. Genome Announcements, 2015, 3, .	0.8	11
41	Functional compensation among HMGN variants modulates the DNase I hypersensitive sites at enhancers. Genome Research, 2015, 25, 1295-1308.	5.5	38
42	Nucleosome adaptability conferred by sequence and structural variations in histone H2A-H2B dimers. Current Opinion in Structural Biology, 2015, 32, 48-57.	5.7	52
43	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	2.6	13
44	Genome Sequences of Multidrug-Resistant <i>Salmonella enterica</i> Serovar Paratyphi B (dT+) and Heidelberg Strains from the Colombian Poultry Chain. Genome Announcements, 2015, 3, .	0.8	7
45	Log-odds sequence logos. Bioinformatics, 2015, 31, 324-331.	4.1	14
46	Genome-wide DNA methylation patterns in LSH mutant reveals de-repression of repeat elements and redundant epigenetic silencing pathways. Genome Research, 2014, 24, 1613-1623.	5.5	83
47	HMGN1 Modulates Nucleosome Occupancy and DNase I Hypersensitivity at the CpG Island Promoters of Embryonic Stem Cells. Molecular and Cellular Biology, 2013, 33, 3377-3389.	2.3	68
48	Identification of Immunity Related Genes to Study the <i>Physalis peruviana</i> - <i>Fusarium oxysporum</i> Pathosystem. PLoS ONE, 2013, 8, e68500.	2.5	30
49	Differences in local genomic context of bound and unbound motifs. Gene, 2012, 506, 125-134.	2.2	3
50	The <i>Physalis peruviana</i> leaf transcriptome: assembly, annotation and gene model prediction. BMC Genomics, 2012, 13, 151.	2.8	52
51	A unified phylogeny-based nomenclature for histone variants. Epigenetics and Chromatin, 2012, 5, 7.	3.9	265
52	Analysis of Biological Features Associated with Meiotic Recombination Hot and Cold Spots in <i>Saccharomyces cerevisiae</i> . PLoS ONE, 2011, 6, e29711.	2.5	20
53	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	3.0	30
54	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	14.5	32

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55	Genome Sequence of the Mycobacterium colombiense Type Strain, CECT 3035. <i>Journal of Bacteriology</i> , 2011, 193, 5866-5867.	2.2	7
56	Effects of HMGN variants on the cellular transcription profile. <i>Nucleic Acids Research</i> , 2011, 39, 4076-4087.	14.5	38
57	Ten Simple Rules for Developing a Short Bioinformatics Training Course. <i>PLoS Computational Biology</i> , 2011, 7, e1002245.	3.2	29
58	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
59	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
60	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
61	Repetitive DNA elements, nucleosome binding and human gene expression. <i>Gene</i> , 2009, 436, 12-22.	2.2	32
62	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
63	Promoter Analysis: Gene Regulatory Motif Identification with A-GLAM. <i>Methods in Molecular Biology</i> , 2009, 537, 263-276.	0.9	7
64	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
65	Expression Patterns of Protein Kinases Correlate with Gene Architecture and Evolutionary Rates. <i>PLoS ONE</i> , 2008, 3, e3599.	2.5	20
66	Multiple Evolutionary Solutions to Core Histone Gene Regulation. <i>FASEB Journal</i> , 2007, 21, A1033.	0.5	0
67	Multiple independent evolutionary solutions to core histone gene regulation. <i>Genome Biology</i> , 2006, 7, R122.	9.6	47
68	Scanning sequences after Gibbs sampling to find multiple occurrences of functional elements. <i>BMC Bioinformatics</i> , 2006, 7, 408.	2.6	2
69	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
70	Alignments anchored on genomic landmarks can aid in the identification of regulatory elements. <i>Bioinformatics</i> , 2005, 21, i440-i448.	4.1	30
71	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
72	Histone structure and nucleosome stability. <i>Expert Review of Proteomics</i> , 2005, 2, 719-729.	3.0	237

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73	TLX1/HOX11-Mediated Disruption of Hematopoietic Differentiation Programs.. Blood, 2005, 106, 2997-2997.	1.4	0
74	Statistical analysis of over-represented words in human promoter sequences. Nucleic Acids Research, 2004, 32, 949-958.	14.5	108
75	High-resolution genome-wide mapping of histone modifications. Nature Biotechnology, 2004, 22, 1013-1016.	17.5	199
76	Characterization of sequence variability in nucleosome core histone folds. Proteins: Structure, Function and Bioinformatics, 2003, 52, 454-465.	2.6	18
77	Mining Core Histone Sequences from Public Protein Databases. Methods in Enzymology, 2003, 375, 3-20.	1.0	3
78	Identifying related L1 retrotransposons by analyzing 3' transduced sequences. Genome Biology, 2003, 4, R30.	9.6	34
79	Retroposed Copies of the HMG Genes: A Window to Genome Dynamics. Genome Research, 2003, 13, 800-812.	5.5	35
80	B-ZIP Proteins Encoded by the Drosophila Genome: Evaluation of Potential Dimerization Partners. Genome Research, 2002, 12, 1190-1200.	5.5	68
81	Expressed Sequence Tags (ESTs). Methods of Biochemical Analysis, 2002, 43, 283-301.	0.2	8
82	The Histone Database. Nucleic Acids Research, 2002, 30, 341-342.	14.5	58
83	Molecular archeology of L1 insertions in the human genome. Genome Biology, 2002, 3, research0052.1.	9.6	180
84	Learning about addiction from the genome. Nature, 2001, 409, 834-835.	27.8	137
85	PROSPECT improves cis-acting regulatory element prediction by integrating expression profile data with consensus pattern searches. Nucleic Acids Research, 2001, 29, 3988-3996.	14.5	24
86	HMGN4, a Newly Discovered Nucleosome-Binding Protein Encoded by an Intronless Gene. DNA and Cell Biology, 2001, 20, 256-263.	1.9	30
87	NBP-45, a Novel Nucleosomal Binding Protein with a Tissue-specific and Developmentally Regulated Expression. Journal of Biological Chemistry, 2000, 275, 6368-6374.	3.4	51
88	Histone Sequence Database: sequences, structures, post-translational modifications and genetic loci. Nucleic Acids Research, 1999, 27, 323-324.	14.5	10
89	Bioinformatics and the developing world. Biotechnology and Development Monitor, 1999, 40, 10-13.	0.0	4
90	Candidate Regulatory Sequence Elements for Cell Cycle-Dependent Transcription in <i>Saccharomyces cerevisiae</i> . Genome Research, 1999, 9, 775-792.	5.5	69

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91	A Genome-Wide Transcriptional Analysis of the Mitotic Cell Cycle. <i>Molecular Cell</i> , 1998, 2, 65-73.	9.7	1,927
92	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
93	Predictive Methods Using Protein Sequences. <i>Methods of Biochemical Analysis</i> , 1998, 39, 246-267.	0.2	0
94	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
95	Homology model building of the HMG-1 box structural domain. <i>Nucleic Acids Research</i> , 1995, 23, 1019-1029.	14.5	27
96	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
97	The HMG-1 box protein family: classification and functional relationships. <i>Nucleic Acids Research</i> , 1995, 23, 1604-1613.	14.5	209
98	A variety of DNA-binding and multimeric proteins contain the histone fold motif. <i>Nucleic Acids Research</i> , 1995, 23, 2685-2691.	14.5	195
99	A signature for the HMG-1 box DNA-binding proteins. <i>BioEssays</i> , 1993, 15, 539-546.	2.5	265
100	No HMG-1 box signature. <i>Nature</i> , 1993, 363, 590-590.	27.8	7
101	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
102	Mapping the human gene coding for chromosomal protein HMG-17. <i>Human Genetics</i> , 1990, 85, 376-8.	3.8	13
103	Mouse non-histone chromosomal protein HMG-14 cDNA sequence. <i>Nucleic Acids Research</i> , 1990, 18, 5311-5311.	14.5	8
104	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
105	Structural features of the HMG chromosomal proteins and their genes. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1990, 1049, 231-243.	2.4	440
106	Human non-histone chromosomal protein HMG-17: identification, characterization, chromosome localization and RFLPs of a functional gene from the large multigene family. <i>Nucleic Acids Research</i> , 1989, 17, 2301-2314.	14.5	29
107	Mouse non-histone chromosomal protein HMG-17 cDNA sequence. <i>Nucleic Acids Research</i> , 1988, 16, 10386-10386.	14.5	9
108	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

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109	Chicken non-histone chromosomal protein HMG-17 cDNA sequence. <i>Nucleic Acids Research</i> , 1987, 15, 6750-6750.	14.5	12
110	Retropseudogenes for human chromosomal protein HMG-17. <i>Journal of Molecular Biology</i> , 1987, 197, 405-413.	4.2	38
111	Immunofractionation of DNA sequences associated with HMG-17 in chromatin. <i>Experimental Cell Research</i> , 1986, 166, 486-496.	2.6	50
112	Exchange of proteins during immunofractionation of chromatin. <i>Experimental Cell Research</i> , 1986, 163, 95-102.	2.6	21
113	Immunofractionation of chromatin regions associated with histone H1o. <i>FEBS Journal</i> , 1986, 160, 253-260.	0.2	26