

Laura L Elnitski

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

16,020
citations

147786

31
h-index

82542

72
g-index

84
all docs

84
docs citations

84
times ranked

23103
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	27.8	6,319
2	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
3	Galaxy: A platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005, 15, 1451-1455.	5.5	1,795
4	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. <i>Genome Research</i> , 2004, 14, 708-715.	5.5	1,290
5	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
6	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138.	7.1	635
7	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. <i>Genome Research</i> , 2003, 13, 13-26.	5.5	263
8	Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. <i>Genome Research</i> , 2003, 13, 1-12.	5.5	210
9	MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3518-3524.	14.5	196
10	Locating mammalian transcription factor binding sites: A survey of computational and experimental techniques. <i>Genome Research</i> , 2006, 16, 1455-1464.	5.5	188
11	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. <i>Genome Research</i> , 2005, 15, 1051-1060.	5.5	185
12	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13481-13486.	7.1	147
13	Distinguishing Regulatory DNA From Neutral Sites. <i>Genome Research</i> , 2003, 13, 64-72.	5.5	118
14	Genomic features defining exonic variants that modulate splicing. <i>Genome Biology</i> , 2010, 11, R20.	9.6	104
15	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. <i>Genome Research</i> , 2004, 14, 700-707.	5.5	93
16	Comprehensive Annotation of Bidirectional Promoters Identifies Co-Regulation among Breast and Ovarian Cancer Genes. <i>PLoS Computational Biology</i> , 2007, 3, e72.	3.2	92
17	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. <i>Genomics</i> , 2003, 82, 417-432.	2.9	82
18	PhenCode: connecting ENCODE data with mutations and phenotype. <i>Human Mutation</i> , 2007, 28, 554-562.	2.5	79

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19	Conserved E Boxes Function as Part of the Enhancer in Hypersensitive Site 2 of the β -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 1997, 272, 369-378.	3.4	74
20	Generation and Comparative Analysis of \approx 3.3 Mb of Mouse Genomic Sequence Orthologous to the Region of Human Chromosome 7q11.23 Implicated in Williams Syndrome. <i>Genome Research</i> , 2002, 12, 3-15.	5.5	72
21	Molecular Determinants of NOTCH4 Transcription in Vascular Endothelium. <i>Molecular and Cellular Biology</i> , 2005, 25, 1458-1474.	2.3	70
22	Diversity of core promoter elements comprising human bidirectional promoters. <i>BMC Genomics</i> , 2008, 9, S3.	2.8	59
23	Identification of human silencers by correlating cross-tissue epigenetic profiles and gene expression. <i>Genome Research</i> , 2019, 29, 657-667.	5.5	56
24	Recurrent patterns of DNA methylation in the <i>ZNF154</i> , <i>CASP8</i> , and <i>VHL</i> promoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. <i>Epigenetics</i> , 2013, 8, 1355-1372.	2.7	52
25	The functional relevance of somatic synonymous mutations in melanoma and other cancers. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 673-684.	3.3	47
26	GALA, a Database for Genomic Sequence Alignments and Annotations. <i>Genome Research</i> , 2003, 13, 732-741.	5.5	45
27	Detection and characterization of silencers and enhancer-blockers in the greater <i>CFTR</i> locus. <i>Genome Research</i> , 2008, 18, 1238-1246.	5.5	45
28	Pan-cancer stratification of solid human epithelial tumors and cancer cell lines reveals commonalities and tissue-specific features of the CpG island methylator phenotype. <i>Epigenetics and Chromatin</i> , 2015, 8, 14.	3.9	42
29	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types. <i>PLoS Computational Biology</i> , 2017, 13, e1005840.	3.2	39
30	Multi-species sequence comparison reveals dynamic evolution of the elastin gene that has involved purifying selection and lineage-specific insertions/deletions. <i>BMC Genomics</i> , 2004, 5, 31.	2.8	35
31	Differential Analysis of Ovarian and Endometrial Cancers Identifies a Methylator Phenotype. <i>PLoS ONE</i> , 2012, 7, e32941.	2.5	35
32	Robust Detection of DNA Hypermethylation of ZNF154 as a Pan-Cancer Locus with in Silico Modeling for Blood-Based Diagnostic Development. <i>Journal of Molecular Diagnostics</i> , 2016, 18, 283-298.	2.8	33
33	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. <i>Genomics</i> , 2002, 80, 681-690.	2.9	32
34	Comparative analyses of bidirectional promoters in vertebrates. <i>BMC Bioinformatics</i> , 2008, 9, S9.	2.6	30
35	Tissue-Specific and Ubiquitous Expression Patterns from Alternative Promoters of Human Genes. <i>PLoS ONE</i> , 2010, 5, e12274.	2.5	30
36	Genome-wide detection of a TFIID localization element from an initial human disease mutation. <i>Nucleic Acids Research</i> , 2011, 39, 2175-2187.	14.5	26

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37	Computational analysis reveals a correlation of exon-skipping events with splicing, transcription and epigenetic factors. <i>Nucleic Acids Research</i> , 2014, 42, 2856-2869.	14.5	26
38	Cross-species mapping of bidirectional promoters enables prediction of unannotated 5' UTRs and identification of species-specific transcripts. <i>BMC Genomics</i> , 2009, 10, 189.	2.8	25
39	Bidirectional Promoters as Important Drivers for the Emergence of Species-Specific Transcripts. <i>PLoS ONE</i> , 2013, 8, e57323.	2.5	25
40	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3366.	7.1	25
41	The Emergence of Pan-Cancer CIMP and Its Elusive Interpretation. <i>Biomolecules</i> , 2016, 6, 45.	4.0	22
42	MethylToSNP: identifying SNPs in Illumina DNA methylation array data. <i>Epigenetics and Chromatin</i> , 2019, 12, 79.	3.9	21
43	Assessing ZNF154 methylation in patient plasma as a multicancer marker in liquid biopsies from colon, liver, ovarian and pancreatic cancer patients. <i>Scientific Reports</i> , 2021, 11, 221.	3.3	21
44	Prediction-based approaches to characterize bidirectional promoters in the mammalian genome. <i>BMC Genomics</i> , 2008, 9, S2.	2.8	20
45	A Negative Cis-element Regulates the Level of Enhancement by Hypersensitive Site 2 of the β -Globin Locus Control Region. <i>Journal of Biological Chemistry</i> , 2001, 276, 6289-6298.	3.4	17
46	Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. <i>Journal of Cystic Fibrosis</i> , 2012, 11, 511-517.	0.7	17
47	PipMaker: A World Wide Web Server for Genomic Sequence Alignments. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 10.2.	25.8	16
48	Aberrant DNA methylation defines isoform usage in cancer, with functional implications. <i>PLoS Computational Biology</i> , 2019, 15, e1007095.	3.2	16
49	A Case of IL-7R Deficiency Caused by a Novel Synonymous Mutation and Implications for Mutation Screening in SCID Diagnosis. <i>Frontiers in Immunology</i> , 2016, 7, 443.	4.8	15
50	The ENCODEdb portal: Simplified access to ENCODE Consortium data. <i>Genome Research</i> , 2007, 17, 954-959.	5.5	13
51	Efficient and Reliable Transfection of Mouse Erythroleukemia Cells Using Cationic Lipids. <i>Blood Cells, Molecules, and Diseases</i> , 1999, 25, 299-304.	1.4	12
52	Word-based characterization of promoters involved in human DNA repair pathways. <i>BMC Genomics</i> , 2009, 10, S18.	2.8	12
53	MultiPipMaker: A Comparative Alignment Server for Multiple DNA Sequences. <i>Current Protocols in Bioinformatics</i> , 2010, 30, Unit10.4.	25.8	12
54	MultiPipMaker: Comparative Alignment Server for Multiple DNA Sequences. <i>Current Protocols in Bioinformatics</i> , 2005, 9, Unit10.4.	25.8	11

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55	Improvements to GALA and dbERGE II: databases featuring genomic sequence alignment, annotation and experimental results. <i>Nucleic Acids Research</i> , 2004, 33, D466-D470.	14.5	9
56	Orthology-driven mapping of bidirectional promoters in human and mouse genomes. <i>BMC Bioinformatics</i> , 2014, 15, S1.	2.6	9
57	CpG island methylator phenotype in adenocarcinomas from the digestive tract: Methods, conclusions, and controversies. <i>World Journal of Gastrointestinal Oncology</i> , 2017, 9, 105.	2.0	9
58	WordSeeker: concurrent bioinformatics software for discovering genome-wide patterns and word-based genomic signatures. <i>BMC Bioinformatics</i> , 2010, 11, S6.	2.6	8
59	Unique Alterations of an Ultraconserved Non-Coding Element in the 3' UTR of ZIC2 in Holoprosencephaly. <i>PLoS ONE</i> , 2012, 7, e39026.	2.5	8
60	SigSeeker: a peak-calling ensemble approach for constructing epigenetic signatures. <i>Bioinformatics</i> , 2017, 33, 2615-2621.	4.1	6
61	Ascertaining regions affected by GC-biased gene conversion through weak-to-strong mutational hotspots. <i>Genomics</i> , 2014, 103, 349-356.	2.9	5
62	Leveraging locus-specific epigenetic heterogeneity to improve the performance of blood-based DNA methylation biomarkers. <i>Clinical Epigenetics</i> , 2020, 12, 154.	4.1	5
63	Differential gene expression identifies a transcriptional regulatory network involving ER-alpha and PITX1 in invasive epithelial ovarian cancer. <i>BMC Cancer</i> , 2021, 21, 768.	2.6	5
64	A Systems Biology Comparison of Ovarian Cancers Implicates Putative Somatic Driver Mutations through Protein-Protein Interaction Models. <i>PLoS ONE</i> , 2016, 11, e0163353.	2.5	5
65	Characterization and clustering of kinase isoform expression in metastatic melanoma. <i>PLoS Computational Biology</i> , 2022, 18, e1010065.	3.2	4
66	A novel role for nucleolin in splice site selection. <i>RNA Biology</i> , 2022, 19, 333-352.	3.1	3
67	Computational Prediction of cis-Regulatory Modules from Multispecies Alignments Using Galaxy, Table Browser, and GALA. , 2006, 338, 91-104.		2
68	Discovering Gene Regulatory Elements Using Coverage-Based Heuristics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1290-1300.	3.0	2
69	The hypothesis of ultraconserved enhancer dispensability overturned. <i>Genome Biology</i> , 2018, 19, 57.	8.8	2
70	CAGI experiments: Modeling sequence variant impact on gene splicing using predictions from computational tools. <i>Human Mutation</i> , 2019, 40, 1252-1260.	2.5	2
71	DNA methylation profiles unique to Kalahari KhoeSan individuals. <i>Epigenetics</i> , 2021, 16, 537-553.	2.7	2
72	Finding Occurrences of Relevant Functional Elements in Genomic Signatures. <i>International Journal of Computational Science</i> , 2008, 2, 599-606.	1.0	2

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73	Functional Analysis of a Novel <i>cis</i> -Acting Regulatory Region within the Human Ankyrin Gene (<i>ANK-1</i>) Promoter. <i>Molecular and Cellular Biology</i> , 2010, 30, 3493-3502.	2.3	1
74	Regulatory network nodes of check point factors in DNA repair pathways. , 2010, , .		1
75	Clustering of gene locations. <i>Computational Statistics and Data Analysis</i> , 2006, 50, 2920-2932.	1.2	0
76	IEEE &sup>th&sup>; BIBE Keynote: Promoter studies in the human genome: one perspective on an unfinished story. , 2007, , .		0
77	Rigorous Mapping of Orthologous Bidirectional Promoters in Vertebrates Defines their Evolutionary History. , 2007, , .		0
78	Feature Characterization and Testing of Bidirectional Promoters in the Human Genome—Significance and Applications in Human Genome Research. , 0, , 321-338.		0
79	Construction of Genomic Regulatory Encyclopedias: Strategies and Case Studies. , 2009, , .		0
80	Rigorous Mapping of Orthologous Bidirectional Promoters in Vertebrates Defines their Evolutionary History. , 2007, , .		0