Laura L Elnitski

List of Publications by Year
in descending order

80	16,020	147726 31	82499 72
papers	citations	h-index	g-index

84	84	84	23103
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
2	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
3	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	2.4	1,795
4	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. Genome Research, 2004, 14, 708-715.	2.4	1,290
5	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
6	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	3.3	635
7	Covariation in Frequencies of Substitution, Deletion, Transposition, and Recombination During Eutherian Evolution. Genome Research, 2003, 13, 13-26.	2.4	263
8	Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. Genome Research, 2003, 13, 1-12.	2.4	210
9	MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences. Nucleic Acids Research, 2003, 31, 3518-3524.	6.5	196
10	Locating mammalian transcription factor binding sites: A survey of computational and experimental techniques. Genome Research, 2006, 16, 1455-1464.	2.4	188
11	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. Genome Research, 2005, 15, 1051-1060.	2.4	185
12	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13481-13486.	3.3	147
13	Distinguishing Regulatory DNA From Neutral Sites. Genome Research, 2003, 13, 64-72.	2.4	118
14	Genomic features defining exonic variants that modulate splicing. Genome Biology, 2010, 11, R20.	13.9	104
15	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. Genome Research, 2004, 14, 700-707.	2.4	93
16	Comprehensive Annotation of Bidirectional Promoters Identifies Co-Regulation among Breast and Ovarian Cancer Genes. PLoS Computational Biology, 2007, 3, e72.	1.5	92
17	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. Genomics, 2003, 82, 417-432.	1.3	82
18	PhenCode: connecting ENCODE data with mutations and phenotype. Human Mutation, 2007, 28, 554-562.	1.1	79

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19	Conserved E Boxes Function as Part of the Enhancer in Hypersensitive Site 2 of the Î²-Globin Locus Control Region. Journal of Biological Chemistry, 1997, 272, 369-378.	1.6	74
20	Generation and Comparative Analysis of 3.3 Mb of Mouse Genomic Sequence Orthologous to the Region of Human Chromosome 7q11.23 Implicated in Williams Syndrome. Genome Research, 2002, 12, 3-15.	2.4	72
21	Molecular Determinants of NOTCH4 Transcription in Vascular Endothelium. Molecular and Cellular Biology, 2005, 25, 1458-1474.	1.1	70
22	Diversity of core promoter elements comprising human bidirectional promoters. BMC Genomics, 2008, 9, S3.	1.2	59
23	Identification of human silencers by correlating cross-tissue epigenetic profiles and gene expression. Genome Research, 2019, 29, 657-667.	2.4	56
24	Recurrent patterns of DNA methylation in theZNF154,CASP8, andVHLpromoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. Epigenetics, 2013, 8, 1355-1372.	1.3	52
25	The functional relevance of somatic synonymous mutations in melanoma and other cancers. Pigment Cell and Melanoma Research, 2015, 28, 673-684.	1.5	47
26	GALA, a Database for Genomic Sequence Alignments and Annotations. Genome Research, 2003, 13, 732-741.	2.4	45
27	Detection and characterization of silencers and enhancer-blockers in the greater CFTR locus. Genome Research, 2008, 18, 1238-1246.	2.4	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. Epigenetics and Chromatin, 2015, 8, 14.	1.8	42
29	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types. PLoS Computational Biology, 2017, 13, e1005840.	1.5	39
30	Multi-species sequence comparison reveals dynamic evolution of the elastin gene that has involved purifying selection and lineage-specific insertions/deletions. BMC Genomics, 2004, 5, 31.	1.2	35
31	Differential Analysis of Ovarian and Endometrial Cancers Identifies a Methylator Phenotype. PLoS ONE, 2012, 7, e32941.	1.1	35
32	Robust Detection of DNA Hypermethylation of ZNF154 as a Pan-Cancer Locus with in Silico Modeling for Blood-Based Diagnostic Development. Journal of Molecular Diagnostics, 2016, 18, 283-298.	1.2	33
33	PipTools: A Computational Toolkit to Annotate and Analyze Pairwise Comparisons of Genomic Sequences. Genomics, 2002, 80, 681-690.	1.3	32
34	Comparative analyses of bidirectional promoters in vertebrates. BMC Bioinformatics, 2008, 9, S9.	1.2	30
35	Tissue-Specific and Ubiquitous Expression Patterns from Alternative Promoters of Human Genes. PLoS ONE, 2010, 5, e12274.	1.1	30
36	Genome-wide detection of a TFIID localization element from an initial human disease mutation. Nucleic Acids Research, 2011, 39, 2175-2187.	6.5	26

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37	Computational analysis reveals a correlation of exon-skipping events with splicing, transcription and epigenetic factors. Nucleic Acids Research, 2014, 42, 2856-2869.	6.5	26
38	Cross-species mapping of bidirectional promoters enables prediction of unannotated 5' UTRs and identification of species-specific transcripts. BMC Genomics, 2009, 10, 189.	1.2	25
39	Bidirectional Promoters as Important Drivers for the Emergence of Species-Specific Transcripts. PLoS ONE, 2013, 8, e57323.	1.1	25
40	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3366.	3.3	25
41	The Emergence of Pan-Cancer CIMP and Its Elusive Interpretation. Biomolecules, 2016, 6, 45.	1.8	22
42	MethylToSNP: identifying SNPs in Illumina DNA methylation array data. Epigenetics and Chromatin, 2019, 12, 79.	1.8	21
43	Assessing ZNF154 methylation in patient plasma as a multicancer marker in liquid biopsies from colon, liver, ovarian and pancreatic cancer patients. Scientific Reports, 2021, 11, 221.	1.6	21
44	Prediction-based approaches to characterize bidirectional promoters in the mammalian genome. BMC Genomics, 2008, 9, S2.	1.2	20
45	A Negative Cis-element Regulates the Level of Enhancement by Hypersensitive Site 2 of the Î²-Globin Locus Control Region. Journal of Biological Chemistry, 2001, 276, 6289-6298.	1.6	17
46	Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. Journal of Cystic Fibrosis, 2012, 11, 511-517.	0.3	17
47	PipMaker: A World Wide Web Server for Genomic Sequence Alignments. Current Protocols in Bioinformatics, 2003, 00, Unit 10.2.	25.8	16
48	Aberrant DNA methylation defines isoform usage in cancer, with functional implications. PLoS Computational Biology, 2019, 15, e1007095.	1.5	16
49	A Case of IL-7R Deficiency Caused by a Novel Synonymous Mutation and Implications for Mutation Screening in SCID Diagnosis. Frontiers in Immunology, 2016, 7, 443.	2.2	15
50	The ENCODEdb portal: Simplified access to ENCODE Consortium data. Genome Research, 2007, 17, 954-959.	2.4	13
51	Efficient and Reliable Transfection of Mouse Erythroleukemia Cells Using Cationic Lipids. Blood Cells, Molecules, and Diseases, 1999, 25, 299-304.	0.6	12
52	Word-based characterization of promoters involved in human DNA repair pathways. BMC Genomics, 2009, 10, S18.	1.2	12
53	MultiPipMaker: A Comparative Alignment Server for Multiple DNA Sequences. Current Protocols in Bioinformatics, 2010, 30, Unit10.4.	25.8	12
54	MultiPipMaker: Comparative Alignment Server for Multiple DNA Sequences. Current Protocols in Bioinformatics, 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. Nucleic Acids Research, 2004, 33, D466-D470.	6.5	9
56	Orthology-driven mapping of bidirectional promoters in human and mouse genomes. BMC Bioinformatics, 2014, 15, S1.	1.2	9
57	CpG island methylator phenotype in adenocarcinomas from the digestive tract: Methods, conclusions, and controversies. World Journal of Gastrointestinal Oncology, 2017, 9, 105.	0.8	9
58	WordSeeker: concurrent bioinformatics software for discovering genome-wide patterns and word-based genomic signatures. BMC Bioinformatics, 2010, 11, S6.	1.2	8
59	Unique Alterations of an Ultraconserved Non-Coding Element in the 3â€²UTR of ZIC2 in Holoprosencephaly. PLoS ONE, 2012, 7, e39026.	1.1	8
60	SigSeeker: a peak-calling ensemble approach for constructing epigenetic signatures. Bioinformatics, 2017, 33, 2615-2621.	1.8	6
61	Ascertaining regions affected by GC-biased gene conversion through weak-to-strong mutational hotspots. Genomics, 2014, 103, 349-356.	1.3	5
62	Leveraging locus-specific epigenetic heterogeneity to improve the performance of blood-based DNA methylation biomarkers. Clinical Epigenetics, 2020, 12, 154.	1.8	5
63	Differential gene expression identifies a transcriptional regulatory network involving ER-alpha and PITX1 in invasive epithelial ovarian cancer. BMC Cancer, 2021, 21, 768.	1.1	5
64	A Systems Biology Comparison of Ovarian Cancers Implicates Putative Somatic Driver Mutations through Protein-Protein Interaction Models. PLoS ONE, 2016, 11, e0163353.	1.1	5
65	Characterization and clustering of kinase isoform expression in metastatic melanoma. PLoS Computational Biology, 2022, 18, e1010065.	1.5	4
66	A novel role for nucleolin in splice site selection. RNA Biology, 2022, 19, 333-352.	1.5	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. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1290-1300.	1.9	2
69	The hypothesis of ultraconserved enhancer dispensability overturned. Genome Biology, 2018, 19, 57.	3.8	2
70	CAGI experiments: Modeling sequence variant impact on gene splicing using predictions from computational tools. Human Mutation, 2019, 40, 1252-1260.	1.1	2
71	DNA methylation profiles unique to Kalahari KhoeSan individuals. Epigenetics, 2021, 16, 537-553.	1.3	2
72	Finding Occurrences of Relevant Functional Elements in Genomic Signatures. International Journal of Computational Science, 2008, 2, 599-606.	1.0	2

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73	Functional Analysis of a Novelcis-Acting Regulatory Region within the Human Ankyrin Gene (ANK-1) Promoter. Molecular and Cellular Biology, 2010, 30, 3493-3502.	1.1	1
74	Regulatory network nodes ofcheck point factorsin DNA repair pathways. , 2010, , .		1
75	Clustering of gene locations. Computational Statistics and Data Analysis, 2006, 50, 2920-2932.	0.7	0
76	IEEE 7th BIBE Keynote: Promoter studies in the human genome: one perspective on an unfinished story. , 2007, , .		0
77	Rigorous Mapping of Orthologous Bidirectional Promoters inVertebrates Defines their Evolutionary History. , 2007, , .		0
78	Feature Characterization and Testing of Bidirectional Promoters in the Human Genomeâ€"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 inVertebrates Defines their Evolutionary History. , 2007, , .		0