Laura L Elnitski

List of Publications by Year in Descending Order

75 papers	13,376 citations	28 h-index	84 g-index
84 ext. papers	14,891 ext. citations	9.1 avg, IF	4.93 L-index

#	Paper	IF	Citations
75	A novel role for nucleolin in splice site selection.. *RNA Biology*, **2022**, 19, 333-352	4.8	0
74	Characterization and clustering of kinase isoform expression in metastatic melanoma.. *PLoS Computational Biology*, **2022**, 18, e1010065	5	1
73	DNA methylation profiles unique to Kalahari KhoeSan individuals. *Epigenetics*, **2021**, 16, 537-553	5.7	2
72	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	4.9	5
71	Differential gene expression identifies a transcriptional regulatory network involving ER-alpha and PITX1 in invasive epithelial ovarian cancer. *BMC Cancer*, **2021**, 21, 768	4.8	1
70	Leveraging locus-specific epigenetic heterogeneity to improve the performance of blood-based DNA methylation biomarkers. *Clinical Epigenetics*, **2020**, 12, 154	7.7	1
69	CAGI experiments: Modeling sequence variant impact on gene splicing using predictions from computational tools. *Human Mutation*, **2019**, 40, 1252-1260	4.7	0
68	Identification of human silencers by correlating cross-tissue epigenetic profiles and gene expression. *Genome Research*, **2019**, 29, 657-667	9.7	22
67	Aberrant DNA methylation defines isoform usage in cancer, with functional implications. *PLoS Computational Biology*, **2019**, 15, e1007095	5	8
66	MethylToSNP: identifying SNPs in Illumina DNA methylation array data. *Epigenetics and Chromatin*, **2019**, 12, 79	5.8	10
65	Discovering Gene Regulatory Elements Using Coverage-Based Heuristics. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2018**, 15, 1290-1300	3	2
64	The hypothesis of ultraconserved enhancer dispensability overturned. *Genome Biology*, **2018**, 19, 57	18.3	2
63	SigSeeker: a peak-calling ensemble approach for constructing epigenetic signatures. *Bioinformatics*, **2017**, 33, 2615-2621	7.2	4
62	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types. *PLoS Computational Biology*, **2017**, 13, e1005840	5	21
61	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, 283-98	5.1	25
60	A Systems Biology Comparison of Ovarian Cancers Implicates Putative Somatic Driver Mutations through Protein-Protein Interaction Models. *PLoS ONE*, **2016**, 11, e0163353	3.7	3
59	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	8.4	11

58	The Emergence of Pan-Cancer CIMP and Its Elusive Interpretation. *Biomolecules*, **2016**, 6,	5.9	16
57	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	5.8	27
56	The functional relevance of somatic synonymous mutations in melanoma and other cancers. *Pigment Cell and Melanoma Research*, **2015**, 28, 673-84	4.5	36
55	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	11.5	22
54	Ascertaining regions affected by GC-biased gene conversion through weak-to-strong mutational hotspots. *Genomics*, **2014**, 103, 349-56	4.3	4
53	Orthology-driven mapping of bidirectional promoters in human and mouse genomes. *BMC Bioinformatics*, **2014**, 15 Suppl 17, S1	3.6	8
52	Defining functional DNA elements in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6131-8	11.5	490
51	Computational analysis reveals a correlation of exon-skipping events with splicing, transcription and epigenetic factors. *Nucleic Acids Research*, **2014**, 42, 2856-69	20.1	19
50	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, 13481-6	11.5	127
49	Recurrent patterns of DNA methylation in the ZNF154, CASP8, and VHL promoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. *Epigenetics*, **2013**, 8, 1355-72	5.7	40
48	Bidirectional promoters as important drivers for the emergence of species-specific transcripts. *PLoS ONE*, **2013**, 8, e57323	3.7	20
47	Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. *Journal of Cystic Fibrosis*, **2012**, 11, 511-7	4.1	14
46	Unique alterations of an ultraconserved non-coding element in the 3Ɯ TR of ZIC2 in holoprosencephaly. *PLoS ONE*, **2012**, 7, e39026	3.7	8
45	Differential analysis of ovarian and endometrial cancers identifies a methylator phenotype. *PLoS ONE*, **2012**, 7, e32941	3.7	29
44	Genome-wide detection of a TFIID localization element from an initial human disease mutation. *Nucleic Acids Research*, **2011**, 39, 2175-87	20.1	14
43	Functional analysis of a novel cis-acting regulatory region within the human ankyrin gene (ANK-1) promoter. *Molecular and Cellular Biology*, **2010**, 30, 3493-502	4.8	1
42	MultiPipMaker: a comparative alignment server for multiple DNA sequences. *Current Protocols in Bioinformatics*, **2010**, Chapter 10, Unit10.4	24.2	6
41	Genomic features defining exonic variants that modulate splicing. *Genome Biology*, **2010**, 11, R20	18.3	97

40	WordSeeker: concurrent bioinformatics software for discovering genome-wide patterns and word-based genomic signatures. *BMC Bioinformatics*, **2010**, 11 Suppl 12, S6	3.6	6
39	Tissue-specific and ubiquitous expression patterns from alternative promoters of human genes. *PLoS ONE*, **2010**, 5, e12274	3.7	25
38	Cross-species mapping of bidirectional promoters enables prediction of unannotated 5'UTRs and identification of species-specific transcripts. *BMC Genomics*, **2009**, 10, 189	4.5	23
37	Word-based characterization of promoters involved in human DNA repair pathways. *BMC Genomics*, **2009**, 10 Suppl 1, S18	4.5	6
36	The genome sequence of taurine cattle: a window to ruminant biology and evolution. *Science*, **2009**, 324, 522-8	33.3	863
35	Comparative analyses of bidirectional promoters in vertebrates. *BMC Bioinformatics*, **2008**, 9 Suppl 6, S9	3.6	27
34	Prediction-based approaches to characterize bidirectional promoters in the mammalian genome. *BMC Genomics*, **2008**, 9 Suppl 1, S2	4.5	19
33	Diversity of core promoter elements comprising human bidirectional promoters. *BMC Genomics*, **2008**, 9 Suppl 2, S3	4.5	38
32	Detection and characterization of silencers and enhancer-blockers in the greater CFTR locus. *Genome Research*, **2008**, 18, 1238-46	9.7	37
31	Finding Occurrences of Relevant Functional Elements in Genomic Signatures **2008**, 2, 599-606		2
30	PhenCode: connecting ENCODE data with mutations and phenotype. *Human Mutation*, **2007**, 28, 554-62	4.7	72
29	Comprehensive annotation of bidirectional promoters identifies co-regulation among breast and ovarian cancer genes. *PLoS Computational Biology*, **2007**, 3, e72	5	69
28	The ENCODEdb portal: simplified access to ENCODE Consortium data. *Genome Research*, **2007**, 17, 954-9	9.7	13
27	Computational prediction of cis-regulatory modules from multispecies alignments using Galaxy, Table Browser, and GALA. *Methods in Molecular Biology*, **2006**, 338, 91-103	1.4	2
26	Locating mammalian transcription factor binding sites: a survey of computational and experimental techniques. *Genome Research*, **2006**, 16, 1455-64	9.7	161
25	Clustering of gene locations. *Computational Statistics and Data Analysis*, **2006**, 50, 2920-2932	1.6	
24	Improvements to GALA and dbERGE II: databases featuring genomic sequence alignment, annotation and experimental results. *Nucleic Acids Research*, **2005**, 33, D466-70	20.1	6
23	MultiPipMaker: comparative alignment server for multiple DNA sequences. *Current Protocols in Bioinformatics*, **2005**, Chapter 10, Unit10.4	24.2	7

22	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. *Genome Research*, **2005**, 15, 1051-60	9.7	164
21	Molecular determinants of NOTCH4 transcription in vascular endothelium. *Molecular and Cellular Biology*, **2005**, 25, 1458-74	4.8	56
20	Galaxy: a platform for interactive large-scale genome analysis. *Genome Research*, **2005**, 15, 1451-5	9.7	1509
19	Regulatory potential scores from genome-wide three-way alignments of human, mouse, and rat. *Genome Research*, **2004**, 14, 700-7	9.7	84
18	Aligning multiple genomic sequences with the threaded blockset aligner. *Genome Research*, **2004**, 14, 708-15	9.7	1006
17	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **2004** , 428, 493-521	50.4	1689
16	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	4.5	30
15	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. *Genomics*, **2003**, 82, 417-32	4.3	66
14	Covariation in frequencies of substitution, deletion, transposition, and recombination during eutherian evolution. *Genome Research*, **2003**, 13, 13-26	9.7	234
13	PipMaker: a World Wide Web server for genomic sequence alignments. *Current Protocols in Bioinformatics*, **2003**, Chapter 10, Unit 10.2	24.2	15
12	MultiPipMaker and supporting tools: Alignments and analysis of multiple genomic DNA sequences. *Nucleic Acids Research*, **2003**, 31, 3518-24	20.1	174
11	Cross-species sequence comparisons: a review of methods and available resources. *Genome Research*, **2003**, 13, 1-12	9.7	170
10	GALA, a database for genomic sequence alignments and annotations. *Genome Research*, **2003**, 13, 732-41	9.7	39
9	Distinguishing regulatory DNA from neutral sites. *Genome Research*, **2003**, 13, 64-72	9.7	103
8	Initial sequencing and comparative analysis of the mouse genome. *Nature*, **2002**, 420, 520-62	50.4	5376
7	Generation and comparative analysis of approximately 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	9.7	54
6	PipTools: a computational toolkit to annotate and analyze pairwise comparisons of genomic sequences. *Genomics*, **2002**, 80, 681-90	4.3	28
5	A negative cis-element regulates the level of enhancement by hypersensitive site 2 of the beta-globin locus control region. *Journal of Biological Chemistry*, **2001**, 276, 6289-98	5.4	16

4	Efficient and reliable transfection of mouse erythroleukemia cells using cationic lipids. *Blood Cells, Molecules, and Diseases*, **1999**, 25, 299-304	2.1	11
3	Conserved E boxes function as part of the enhancer in hypersensitive site 2 of the beta-globin locus control region. Role of basic helix-loop-helix proteins. *Journal of Biological Chemistry*, **1997**, 272, 369-78	5.4	70
2	Feature Characterization and Testing of Bidirectional Promoters in the Human Genome Significance and Applications in Human Genome Research 321-338		
1	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types		2