

Laura L Elnitski

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
74	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
73	Galaxy: a platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005 , 15, 1451-5	9.7	1509
72	Aligning multiple genomic sequences with the threaded blockset aligner. <i>Genome Research</i> , 2004 , 14, 708-15	9.7	1006
71	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
70	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, 6131-8	11.5	490
69	Covariation in frequencies of substitution, deletion, transposition, and recombination during eutherian evolution. <i>Genome Research</i> , 2003 , 13, 13-26	9.7	234
68	MultiPipMaker and supporting tools: Alignments and analysis of multiple genomic DNA sequences. <i>Nucleic Acids Research</i> , 2003 , 31, 3518-24	20.1	174
67	Cross-species sequence comparisons: a review of methods and available resources. <i>Genome Research</i> , 2003 , 13, 1-12	9.7	170
66	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. <i>Genome Research</i> , 2005 , 15, 1051-60	9.7	164
65	Locating mammalian transcription factor binding sites: a survey of computational and experimental techniques. <i>Genome Research</i> , 2006 , 16, 1455-64	9.7	161
64	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, 13481-6	11.5	127
63	Distinguishing regulatory DNA from neutral sites. <i>Genome Research</i> , 2003 , 13, 64-72	9.7	103
62	Genomic features defining exonic variants that modulate splicing. <i>Genome Biology</i> , 2010 , 11, R20	18.3	97
61	Regulatory potential scores from genome-wide three-way alignments of human, mouse, and rat. <i>Genome Research</i> , 2004 , 14, 700-7	9.7	84
60	PhenCode: connecting ENCODE data with mutations and phenotype. <i>Human Mutation</i> , 2007 , 28, 554-62	4.7	72
59	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. <i>Journal of Biological Chemistry</i> , 1997 , 272, 369-78	5.4	70

58	Comprehensive annotation of bidirectional promoters identifies co-regulation among breast and ovarian cancer genes. <i>PLoS Computational Biology</i> , 2007 , 3, e72	5	69
57	Multispecies comparative analysis of a mammalian-specific genomic domain encoding secretory proteins. <i>Genomics</i> , 2003 , 82, 417-32	4.3	66
56	Molecular determinants of NOTCH4 transcription in vascular endothelium. <i>Molecular and Cellular Biology</i> , 2005 , 25, 1458-74	4.8	56
55	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. <i>Genome Research</i> , 2002 , 12, 3-15	9.7	54
54	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. <i>Epigenetics</i> , 2013 , 8, 1355-72	5.7	40
53	GALA, a database for genomic sequence alignments and annotations. <i>Genome Research</i> , 2003 , 13, 732-41	5.7	39
52	Diversity of core promoter elements comprising human bidirectional promoters. <i>BMC Genomics</i> , 2008 , 9 Suppl 2, S3	4.5	38
51	Detection and characterization of silencers and enhancer-blockers in the greater CFTR locus. <i>Genome Research</i> , 2008 , 18, 1238-46	9.7	37
50	The functional relevance of somatic synonymous mutations in melanoma and other cancers. <i>Pigment Cell and Melanoma Research</i> , 2015 , 28, 673-84	4.5	36
49	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	4.5	30
48	Differential analysis of ovarian and endometrial cancers identifies a methylator phenotype. <i>PLoS ONE</i> , 2012 , 7, e32941	3.7	29
47	PipTools: a computational toolkit to annotate and analyze pairwise comparisons of genomic sequences. <i>Genomics</i> , 2002 , 80, 681-90	4.3	28
46	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	5.8	27
45	Comparative analyses of bidirectional promoters in vertebrates. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 6, S9	3.6	27
44	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, 283-98	5.1	25
43	Tissue-specific and ubiquitous expression patterns from alternative promoters of human genes. <i>PLoS ONE</i> , 2010 , 5, e12274	3.7	25
42	Cross-species mapping of bidirectional promoters enables prediction of unannotated 5UTRs and identification of species-specific transcripts. <i>BMC Genomics</i> , 2009 , 10, 189	4.5	23
41	Identification of human silencers by correlating cross-tissue epigenetic profiles and gene expression. <i>Genome Research</i> , 2019 , 29, 657-667	9.7	22

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	11.5	22
39	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types. <i>PLoS Computational Biology</i> , 2017 , 13, e1005840	5	21
38	Bidirectional promoters as important drivers for the emergence of species-specific transcripts. <i>PLoS ONE</i> , 2013 , 8, e57323	3.7	20
37	Computational analysis reveals a correlation of exon-skipping events with splicing, transcription and epigenetic factors. <i>Nucleic Acids Research</i> , 2014 , 42, 2856-69	20.1	19
36	Prediction-based approaches to characterize bidirectional promoters in the mammalian genome. <i>BMC Genomics</i> , 2008 , 9 Suppl 1, S2	4.5	19
35	A negative cis-element regulates the level of enhancement by hypersensitive site 2 of the beta-globin locus control region. <i>Journal of Biological Chemistry</i> , 2001 , 276, 6289-98	5.4	16
34	The Emergence of Pan-Cancer CIMP and Its Elusive Interpretation. <i>Biomolecules</i> , 2016 , 6,	5.9	16
33	PipMaker: a World Wide Web server for genomic sequence alignments. <i>Current Protocols in Bioinformatics</i> , 2003 , Chapter 10, Unit 10.2	24.2	15
32	Functional analysis of synonymous substitutions predicted to affect splicing of the CFTR gene. <i>Journal of Cystic Fibrosis</i> , 2012 , 11, 511-7	4.1	14
31	Genome-wide detection of a TFIID localization element from an initial human disease mutation. <i>Nucleic Acids Research</i> , 2011 , 39, 2175-87	20.1	14
30	The ENCODEdb portal: simplified access to ENCODE Consortium data. <i>Genome Research</i> , 2007 , 17, 954-9.7		13
29	Efficient and reliable transfection of mouse erythroleukemia cells using cationic lipids. <i>Blood Cells, Molecules, and Diseases</i> , 1999 , 25, 299-304	2.1	11
28	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	8.4	11
27	MethylToSNP: identifying SNPs in Illumina DNA methylation array data. <i>Epigenetics and Chromatin</i> , 2019 , 12, 79	5.8	10
26	Aberrant DNA methylation defines isoform usage in cancer, with functional implications. <i>PLoS Computational Biology</i> , 2019 , 15, e1007095	5	8
25	Orthology-driven mapping of bidirectional promoters in human and mouse genomes. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 17, S1	3.6	8
24	Unique alterations of an ultraconserved non-coding element in the 3'UTR of ZIC2 in holoprosencephaly. <i>PLoS ONE</i> , 2012 , 7, e39026	3.7	8
23	MultiPipMaker: comparative alignment server for multiple DNA sequences. <i>Current Protocols in Bioinformatics</i> , 2005 , Chapter 10, Unit10.4	24.2	7

22	MultiPipMaker: a comparative alignment server for multiple DNA sequences. <i>Current Protocols in Bioinformatics</i> , 2010 , Chapter 10, Unit10.4	24.2	6
21	Word-based characterization of promoters involved in human DNA repair pathways. <i>BMC Genomics</i> , 2009 , 10 Suppl 1, S18	4.5	6
20	WordSeeker: concurrent bioinformatics software for discovering genome-wide patterns and word-based genomic signatures. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 12, S6	3.6	6
19	Improvements to GALA and dbERGE II: databases featuring genomic sequence alignment, annotation and experimental results. <i>Nucleic Acids Research</i> , 2005 , 33, D466-70	20.1	6
18	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	4.9	5
17	SigSeeker: a peak-calling ensemble approach for constructing epigenetic signatures. <i>Bioinformatics</i> , 2017 , 33, 2615-2621	7.2	4
16	Ascertaining regions affected by GC-biased gene conversion through weak-to-strong mutational hotspots. <i>Genomics</i> , 2014 , 103, 349-56	4.3	4
15	A Systems Biology Comparison of Ovarian Cancers Implicates Putative Somatic Driver Mutations through Protein-Protein Interaction Models. <i>PLoS ONE</i> , 2016 , 11, e0163353	3.7	3
14	Discovering Gene Regulatory Elements Using Coverage-Based Heuristics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 1290-1300	3	2
13	The hypothesis of ultraconserved enhancer dispensability overturned. <i>Genome Biology</i> , 2018 , 19, 57	18.3	2
12	Computational prediction of cis-regulatory modules from multispecies alignments using Galaxy, Table Browser, and GALA. <i>Methods in Molecular Biology</i> , 2006 , 338, 91-103	1.4	2
11	Finding Occurrences of Relevant Functional Elements in Genomic Signatures 2008 , 2, 599-606		2
10	Significant associations between driver gene mutations and DNA methylation alterations across many cancer types		2
9	DNA methylation profiles unique to Kalahari KhoeSan individuals. <i>Epigenetics</i> , 2021 , 16, 537-553	5.7	2
8	Functional analysis of a novel cis-acting regulatory region within the human ankyrin gene (ANK-1) promoter. <i>Molecular and Cellular Biology</i> , 2010 , 30, 3493-502	4.8	1
7	Leveraging locus-specific epigenetic heterogeneity to improve the performance of blood-based DNA methylation biomarkers. <i>Clinical Epigenetics</i> , 2020 , 12, 154	7.7	1
6	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	4.8	1
5	Characterization and clustering of kinase isoform expression in metastatic melanoma.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010065	5	1

- 4 CAGI experiments: Modeling sequence variant impact on gene splicing using predictions from computational tools. *Human Mutation*, **2019**, 40, 1252-1260 4.7 ○
- 3 A novel role for nucleolin in splice site selection.. *RNA Biology*, **2022**, 19, 333-352 4.8 ○
- 2 Feature Characterization and Testing of Bidirectional Promoters in the Human Genome Significance and Applications in Human Genome Research 321-338
- 1 Clustering of gene locations. *Computational Statistics and Data Analysis*, **2006**, 50, 2920-2932 1.6