Laura I Furlong

List of Publications by Year
in descending order

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76 papers	6,630 citations	159585 30 h-index	88630 70 g-index
86 all docs	86 docs citations	86 times ranked	10607 citing authors

#	Article	IF	Citations
1	Exploring the Association of Cancer and Depression in Electronic Health Records: Combining Encoded Diagnosis and Mining Free-Text Clinical Notes. JMIR Cancer, 2022, 8, e39003.	2.4	1
2	Functional Genomics Analysis to Disentangle the Role of Genetic Variants in Major Depression. Genes, 2022, 13, 1259.	2.4	1
3	A system-level analysis of patient disease trajectories based on clinical, phenotypic and molecular similarities. Bioinformatics, 2021, 37, 1435-1443.	4.1	8
4	The DisGeNET cytoscape app: Exploring and visualizing disease genomics data. Computational and Structural Biotechnology Journal, 2021, 19, 2960-2967.	4.1	221
5	An ensemble learning approach for modeling the systems biology of drug-induced injury. Biology Direct, 2021, 16, 5.	4.6	11
6	The eTRANSAFE Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. Pharmaceuticals, 2021, 14, 237.	3.8	17
7	Comorbidity between Alzheimerâ€™s disease and major depression: a behavioural and transcriptomic characterization study in mice. Alzheimer's Research and Therapy, 2021, 13, 73.	6.2	18
8	The DisGeNET knowledge platform for disease genomics: 2019 update. Nucleic Acids Research, 2020, 48, D845-D855.	14.5	1,083
9	Quantitative Systems Toxicology Modeling To Address Key Safety Questions in Drug Development: A Focus of the TransQST Consortium. Chemical Research in Toxicology, 2020, 33, 7-9.	3.3	14
10	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	5.3	99
11	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
12	Evaluating Behavioral and Linguistic Changes During Drug Treatment for Depression Using Tweets in Spanish: Pairwise Comparison Study. Journal of Medical Internet Research, 2020, 22, e20920.	4.3	0
13	Comorbidity4j: a tool for interactive analysis of disease comorbidities over large patient datasets. Bioinformatics, 2019, 35, 3530-3532.	4.1	9
14	The BIOMEPOC Project: Personalized Biomarkers and Clinical Profiles in Chronic Obstructive Pulmonary Disease. Archivos De Bronconeumologia, 2019, 55, 93-99.	0.8	5
15	ResMarkerDB: a database of biomarkers of response to antibody therapy in breast and colorectal cancer. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	10
16	Genetic and Real-World Clinical Data, Combined with Empirical Validation, Nominate Jak-Stat Signaling as a Target for Alzheimerâ€™s Disease Therapeutic Development. Cells, 2019, 8, 425.	4.1	27
17	GUILDify v2.0: A Tool to Identify Molecular Networks Underlying Human Diseases, Their Comorbidities and Their Druggable Targets. Journal of Molecular Biology, 2019, 431, 2477-2484.	4.2	32
18	Pancreatic cancer and autoimmune diseases: An association sustained by computational and epidemiological caseâ€“control approaches. International Journal of Cancer, 2019, 144, 1540-1549.	5.1	11

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19	Proyecto de biomarcadores y perfiles clÃnicos personalizados en la enfermedad pulmonar obstructiva crÃ³nica (proyecto BIOMEPOC). Archivos De Bronconeumologia, 2019, 55, 93-99.	0.8	18
20	Detecting Signs of Depression in Tweets in Spanish: Behavioral and Linguistic Analysis. Journal of Medical Internet Research, 2019, 21, e14199.	4.3	66
21	comoRbidity: an R package for the systematic analysis of disease comorbidities. Bioinformatics, 2018, 34, 3228-3230.	4.1	31
22	Rcupcake: an R package for querying and analyzing biomedical data through the BD2K PIC-SURE RESTful API. Bioinformatics, 2018, 34, 1431-1432.	4.1	4
23	Identifying temporal patterns in patient disease trajectories using dynamic time warping: A population-based study. Scientific Reports, 2018, 8, 4216.	3.3	61
24	Embracing the Dark Side: Computational Approaches to Unveil the Functionality of Genes Lacking Biological Annotation in Drug-Induced Liver Injury. Frontiers in Genetics, 2018, 9, 527.	2.3	0
25	Nanopublications: A Growing Resource of Provenance-Centric Scientific Linked Data. , 2018, , .		21
26	Network, Transcriptomic and Genomic Features Differentiate Genes Relevant for Drug Response. Frontiers in Genetics, 2018, 9, 412.	2.3	18
27	In silico models in drug development: where we are. Current Opinion in Pharmacology, 2018, 42, 111-121.	3.5	30
28	Proximal Pathway Enrichment Analysis for Targeting Comorbid Diseases via Network Endopharmacology. Pharmaceuticals, 2018, 11, 61.	3.8	32
29	DisGeNET: a comprehensive platform integrating information on human disease-associated genes and variants. Nucleic Acids Research, 2017, 45, D833-D839.	14.5	1,865
30	psygenet2r: a R/Bioconductor package for the analysis of psychiatric disease genes. Bioinformatics, 2017, 33, 4004-4006.	4.1	3
31	Genetic and functional characterization of disease associations explains comorbidity. Scientific Reports, 2017, 7, 6207.	3.3	28
32	Text mining and expert curation to develop a database on psychiatric diseases and their genes. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	11
33	Reliable Granular References to Changing Linked Data. Lecture Notes in Computer Science, 2017, , 436-451.	1.3	10
34	Publishing DisGeNET as nanopublications. Semantic Web, 2016, 7, 519-528.	1.9	18
35	Uncovering disease mechanisms through network biology in the era of Next Generation Sequencing. Scientific Reports, 2016, 6, 24570.	3.3	29
36	DisGeNET-RDF: harnessing the innovative power of the Semantic Web to explore the genetic basis of diseases. Bioinformatics, 2016, 32, 2236-2238.	4.1	52

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37	Combining machine learning, crowdsourcing and expert knowledge to detect chemical-induced diseases in text. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw094.	3.0	14
38	A crowdsourcing workflow for extracting chemical-induced disease relations from free text. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw051.	3.0	9
39	CDH1/E-cadherin and solid tumors. An updated gene-disease association analysis using bioinformatics tools. Computational Biology and Chemistry, 2016, 60, 9-20.	2.3	7
40	DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav028-bav028.	3.0	847
41	Mining the Modular Structure of Protein Interaction Networks. PLoS ONE, 2015, 10, e0122477.	2.5	7
42	PsyGeNET: a knowledge platform on psychiatric disorders and their genes. Bioinformatics, 2015, 31, 3075-3077.	4.1	79
43	Personalized Respiratory Medicine: Exploring the Horizon, Addressing the Issues. Summary of a BRN-AJRCCM Workshop Held in Barcelona on June 12, 2014. American Journal of Respiratory and Critical Care Medicine, 2015, 191, 391-401.	5.6	61
44	Molecular and clinical diseasome of comorbidities in exacerbated COPD patients. European Respiratory Journal, 2015, 46, 1001-1010.	6.7	32
45	Extraction of relations between genes and diseases from text and large-scale data analysis: implications for translational research. BMC Bioinformatics, 2015, 16, 55.	2.6	170
46	Abstract 1085: A bioinformatics approach to evaluate the involvement of CDH1/E-cadherin in solid tumors and to identify breast cancer biomarkers. , 2015, , .		0
47	A Knowledge-Driven Approach to Extract Disease-Related Biomarkers from the Literature. BioMed Research International, 2014, 2014, 1-11.	1.9	42
48	The Semanticscience Integrated Ontology (SIO) for biomedical research and knowledge discovery. Journal of Biomedical Semantics, 2014, 5, 14.	1.6	138
49	Network medicine analysis of COPD multimorbidities. Respiratory Research, 2014, 15, 111.	3.6	48
50	Human diseases through the lens of network biology. Trends in Genetics, 2013, 29, 150-159.	6.7	182
51	Improving data and knowledge management to better integrate health care and research. Journal of Internal Medicine, 2013, 274, 321-328.	6.0	44
52	The EUâ€ADR Web Platform: delivering advanced pharmacovigilance tools. Pharmacoepidemiology and Drug Safety, 2013, 22, 459-467.	1.9	36
53	Drug-Induced Acute Myocardial Infarction: Identifying â€˜Prime Suspectsâ€™ from Electronic Healthcare Records-Based Surveillance System. PLoS ONE, 2013, 8, e72148.	2.5	41
54	Gathering and Exploring Scientific Knowledge in Pharmacovigilance. PLoS ONE, 2013, 8, e83016.	2.5	15

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55	Automatic Filtering and Substantiation of Drug Safety Signals. PLoS Computational Biology, 2012, 8, e1002457.	3.2	34
56	The EU-ADR corpus: Annotated drugs, diseases, targets, and their relationships. Journal of Biomedical Informatics, 2012, 45, 879-884.	4.3	99
57	Gene-Disease Network Analysis Reveals Functional Modules in Mendelian, Complex and Environmental Diseases. PLoS ONE, 2011, 6, e20284.	2.5	153
58	Assessment of NER solutions against the first and second CALBC Silver Standard Corpus. Journal of Biomedical Semantics, 2011, 2, S11.	1.6	39
59	Challenges in the association of human single nucleotide polymorphism mentions with unique database identifiers. BMC Bioinformatics, 2011, 12, S4.	2.6	33
60	DisGeNET: a Cytoscape plugin to visualize, integrate, search and analyze geneâ€“disease networks. Bioinformatics, 2010, 26, 2924-2926.	4.1	180
61	Digging for knowledge with information extraction. , 2010, , .		3
62	Anti-human proacrosin antibody inhibits the zona pellucida (ZP)â€“induced acrosome reaction of ZP-bound spermatozoa. Fertility and Sterility, 2010, 93, 2456-2459.	1.0	13
63	From SNPs to pathways: integration of functional effect of sequence variations on models of cell signalling pathways. BMC Bioinformatics, 2009, 10, S6.	2.6	24
64	Acrosin antibodies and infertility. I. Detection of antibodies towards proacrosin/acrosin in women consulting for infertility and evaluation of their effects upon the sperm protease activities. Fertility and Sterility, 2009, 91, 1245-1255.	1.0	21
65	Antiacrosin antibodies and infertility. II. Gene immunization with human proacrosin to assess the effect of immunity toward proacrosin/acrosin upon protein activities and animal fertility. Fertility and Sterility, 2009, 91, 1256-1268.	1.0	7
66	Pathway databases and tools for their exploitation: benefits, current limitations and challenges. Molecular Systems Biology, 2009, 5, 290.	7.2	173
67	Identification of Sequence Variants of Genes from Biomedical Literature. , 2009, , 289-300.		0
68	OSIRISv1.2: A named entity recognition system for sequence variants of genes in biomedical literature. BMC Bioinformatics, 2008, 9, 84.	2.6	31
69	Expression of epithelial cadherin in the human male reproductive tract and gametes and evidence of its participation in fertilization. Molecular Human Reproduction, 2008, 14, 561-571.	2.8	31
70	Knowledge environments representing molecular entities for the virtual physiological human. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3091-3110.	3.4	19
71	IDENTIFYING GENE-SPECIFIC VARIATIONS IN BIOMEDICAL TEXT. Journal of Bioinformatics and Computational Biology, 2007, 05, 1277-1296.	0.8	15
72	OSIRIS: a tool for retrieving literature about sequence variants. Bioinformatics, 2006, 22, 2567-2569.	4.1	22

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73	Binding of recombinant human proacrosin/acrosin to zona pellucida (ZP) glycoproteins. I. Studies with recombinant human ZPA, ZPB, and ZPC. Fertility and Sterility, 2005, 83, 1780-1790.	1.0	25
74	Binding of recombinant human proacrosin/acrosin to zona pellucida glycoproteins. II. Participation of mannose residues in the interaction. Fertility and Sterility, 2005, 83, 1791-1796.	1.0	8
75	Evaluation of the proacrosin/acrosin system and its mechanism of activation in human sperm extracts. Journal of Reproductive Immunology, 2002, 54, 43-63.	1.9	31
76	Expression of Human Proacrosin in Escherichia coli and Binding to Zona Pellucida1. Biology of Reproduction, 2000, 62, 606-615.	2.7	21