

Laura I Furlong

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

6,630
citations

159525

30
h-index

88593

70
g-index

86
all docs

86
docs citations

86
times ranked

10607
citing authors

#	ARTICLE	IF	CITATIONS
1	DisGeNET: a comprehensive platform integrating information on human disease-associated genes and variants. <i>Nucleic Acids Research</i> , 2017, 45, D833-D839.	6.5	1,865
2	The DisGeNET knowledge platform for disease genomics: 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D845-D855.	6.5	1,083
3	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.	1.4	847
4	The DisGeNET cytoscape app: Exploring and visualizing disease genomics data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2960-2967.	1.9	221
5	Human diseases through the lens of network biology. <i>Trends in Genetics</i> , 2013, 29, 150-159.	2.9	182
6	DisGeNET: a Cytoscape plugin to visualize, integrate, search and analyze gene-disease networks. <i>Bioinformatics</i> , 2010, 26, 2924-2926.	1.8	180
7	Pathway databases and tools for their exploitation: benefits, current limitations and challenges. <i>Molecular Systems Biology</i> , 2009, 5, 290.	3.2	173
8	Extraction of relations between genes and diseases from text and large-scale data analysis: implications for translational research. <i>BMC Bioinformatics</i> , 2015, 16, 55.	1.2	170
9	Gene-Disease Network Analysis Reveals Functional Modules in Mendelian, Complex and Environmental Diseases. <i>PLoS ONE</i> , 2011, 6, e20284.	1.1	153
10	The SemanticScience Integrated Ontology (SIO) for biomedical research and knowledge discovery. <i>Journal of Biomedical Semantics</i> , 2014, 5, 14.	0.9	138
11	The EU-ADR corpus: Annotated drugs, diseases, targets, and their relationships. <i>Journal of Biomedical Informatics</i> , 2012, 45, 879-884.	2.5	99
12	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136.	2.4	99
13	PsyGeNET: a knowledge platform on psychiatric disorders and their genes. <i>Bioinformatics</i> , 2015, 31, 3075-3077.	1.8	79
14	Detecting Signs of Depression in Tweets in Spanish: Behavioral and Linguistic Analysis. <i>Journal of Medical Internet Research</i> , 2019, 21, e14199.	2.1	66
15	Personalized Respiratory Medicine: Exploring the Horizon, Addressing the Issues. Summary of a BRN-AJRCCM Workshop Held in Barcelona on June 12, 2014. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 191, 391-401.	2.5	61
16	Identifying temporal patterns in patient disease trajectories using dynamic time warping: A population-based study. <i>Scientific Reports</i> , 2018, 8, 4216.	1.6	61
17	DisGeNET-RDF: harnessing the innovative power of the Semantic Web to explore the genetic basis of diseases. <i>Bioinformatics</i> , 2016, 32, 2236-2238.	1.8	52
18	Network medicine analysis of COPD multimorbidities. <i>Respiratory Research</i> , 2014, 15, 111.	1.4	48

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19	Improving data and knowledge management to better integrate health care and research. <i>Journal of Internal Medicine</i> , 2013, 274, 321-328.	2.7	44
20	A Knowledge-Driven Approach to Extract Disease-Related Biomarkers from the Literature. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	42
21	Drug-Induced Acute Myocardial Infarction: Identifying "Prime Suspects"™ from Electronic Healthcare Records-Based Surveillance System. <i>PLoS ONE</i> , 2013, 8, e72148.	1.1	41
22	Assessment of NER solutions against the first and second CALBC Silver Standard Corpus. <i>Journal of Biomedical Semantics</i> , 2011, 2, S11.	0.9	39
23	The EU-ADR Web Platform: delivering advanced pharmacovigilance tools. <i>Pharmacoepidemiology and Drug Safety</i> , 2013, 22, 459-467.	0.9	36
24	Automatic Filtering and Substantiation of Drug Safety Signals. <i>PLoS Computational Biology</i> , 2012, 8, e1002457.	1.5	34
25	Challenges in the association of human single nucleotide polymorphism mentions with unique database identifiers. <i>BMC Bioinformatics</i> , 2011, 12, S4.	1.2	33
26	Molecular and clinical disease of comorbidities in exacerbated COPD patients. <i>European Respiratory Journal</i> , 2015, 46, 1001-1010.	3.1	32
27	Proximal Pathway Enrichment Analysis for Targeting Comorbid Diseases via Network Endopharmacology. <i>Pharmaceuticals</i> , 2018, 11, 61.	1.7	32
28	GUILDify v2.0: A Tool to Identify Molecular Networks Underlying Human Diseases, Their Comorbidities and Their Druggable Targets. <i>Journal of Molecular Biology</i> , 2019, 431, 2477-2484.	2.0	32
29	Evaluation of the proacrosin/acrosin system and its mechanism of activation in human sperm extracts. <i>Journal of Reproductive Immunology</i> , 2002, 54, 43-63.	0.8	31
30	OSIRISv1.2: A named entity recognition system for sequence variants of genes in biomedical literature. <i>BMC Bioinformatics</i> , 2008, 9, 84.	1.2	31
31	Expression of epithelial cadherin in the human male reproductive tract and gametes and evidence of its participation in fertilization. <i>Molecular Human Reproduction</i> , 2008, 14, 561-571.	1.3	31
32	comoRbidity: an R package for the systematic analysis of disease comorbidities. <i>Bioinformatics</i> , 2018, 34, 3228-3230.	1.8	31
33	In silico models in drug development: where we are. <i>Current Opinion in Pharmacology</i> , 2018, 42, 111-121.	1.7	30
34	Uncovering disease mechanisms through network biology in the era of Next Generation Sequencing. <i>Scientific Reports</i> , 2016, 6, 24570.	1.6	29
35	Genetic and functional characterization of disease associations explains comorbidity. <i>Scientific Reports</i> , 2017, 7, 6207.	1.6	28
36	Genetic and Real-World Clinical Data, Combined with Empirical Validation, Nominate Jak-Stat Signaling as a Target for Alzheimer's Disease Therapeutic Development. <i>Cells</i> , 2019, 8, 425.	1.8	27

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37	Binding of recombinant human proacrosin/acrosin to zona pellucida (ZP) glycoproteins. I. Studies with recombinant human ZPA, ZPB, and ZPC. <i>Fertility and Sterility</i> , 2005, 83, 1780-1790.	0.5	25
38	From SNPs to pathways: integration of functional effect of sequence variations on models of cell signalling pathways. <i>BMC Bioinformatics</i> , 2009, 10, S6.	1.2	24
39	OSIRIS: a tool for retrieving literature about sequence variants. <i>Bioinformatics</i> , 2006, 22, 2567-2569.	1.8	22
40	Expression of Human Proacrosin in Escherichia coli and Binding to Zona Pellucida1. <i>Biology of Reproduction</i> , 2000, 62, 606-615.	1.2	21
41	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. <i>Fertility and Sterility</i> , 2009, 91, 1245-1255.	0.5	21
42	Nanopublications: A Growing Resource of Provenance-Centric Scientific Linked Data. , 2018, , .		21
43	Knowledge environments representing molecular entities for the virtual physiological human. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2008, 366, 3091-3110.	1.6	19
44	Publishing DisGeNET as nanopublications. <i>Semantic Web</i> , 2016, 7, 519-528.	1.1	18
45	Network, Transcriptomic and Genomic Features Differentiate Genes Relevant for Drug Response. <i>Frontiers in Genetics</i> , 2018, 9, 412.	1.1	18
46	Proyecto de biomarcadores y perfiles cl�nicos personalizados en la enfermedad pulmonar obstructiva cr�nica (proyecto BIOMEPOC). <i>Archivos De Bronconeumologia</i> , 2019, 55, 93-99.	0.4	18
47	Comorbidity between Alzheimer's disease and major depression: a behavioural and transcriptomic characterization study in mice. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 73.	3.0	18
48	The eTRANSafe Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. <i>Pharmaceuticals</i> , 2021, 14, 237.	1.7	17
49	IDENTIFYING GENE-SPECIFIC VARIATIONS IN BIOMEDICAL TEXT. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 1277-1296.	0.3	15
50	Gathering and Exploring Scientific Knowledge in Pharmacovigilance. <i>PLoS ONE</i> , 2013, 8, e83016.	1.1	15
51	Combining machine learning, crowdsourcing and expert knowledge to detect chemical-induced diseases in text. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw094.	1.4	14
52	Quantitative Systems Toxicology Modeling To Address Key Safety Questions in Drug Development: A Focus of the TransQST Consortium. <i>Chemical Research in Toxicology</i> , 2020, 33, 7-9.	1.7	14
53	Anti-human proacrosin antibody inhibits the zona pellucida (ZP)-induced acrosome reaction of ZP-bound spermatozoa. <i>Fertility and Sterility</i> , 2010, 93, 2456-2459.	0.5	13
54	Text mining and expert curation to develop a database on psychiatric diseases and their genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	11

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55	Pancreatic cancer and autoimmune diseases: An association sustained by computational and epidemiological caseâ€“control approaches. <i>International Journal of Cancer</i> , 2019, 144, 1540-1549.	2.3	11
56	An ensemble learning approach for modeling the systems biology of drug-induced injury. <i>Biology Direct</i> , 2021, 16, 5.	1.9	11
57	ResMarkerDB: a database of biomarkers of response to antibody therapy in breast and colorectal cancer. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	10
58	Reliable Granular References to Changing Linked Data. <i>Lecture Notes in Computer Science</i> , 2017, , 436-451.	1.0	10
59	A crowdsourcing workflow for extracting chemical-induced disease relations from free text. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw051.	1.4	9
60	Comorbidity4j: a tool for interactive analysis of disease comorbidities over large patient datasets. <i>Bioinformatics</i> , 2019, 35, 3530-3532.	1.8	9
61	Binding of recombinant human proacrosin/acrosin to zona pellucida glycoproteins. II. Participation of mannose residues in the interaction. <i>Fertility and Sterility</i> , 2005, 83, 1791-1796.	0.5	8
62	A system-level analysis of patient disease trajectories based on clinical, phenotypic and molecular similarities. <i>Bioinformatics</i> , 2021, 37, 1435-1443.	1.8	8
63	Anti-acrosin antibodies and infertility. II. Gene immunization with human proacrosin to assess the effect of immunity toward proacrosin/acrosin upon protein activities and animal fertility. <i>Fertility and Sterility</i> , 2009, 91, 1256-1268.	0.5	7
64	Mining the Modular Structure of Protein Interaction Networks. <i>PLoS ONE</i> , 2015, 10, e0122477.	1.1	7
65	CDH1/E-cadherin and solid tumors. An updated gene-disease association analysis using bioinformatics tools. <i>Computational Biology and Chemistry</i> , 2016, 60, 9-20.	1.1	7
66	The BIOMEPOC Project: Personalized Biomarkers and Clinical Profiles in Chronic Obstructive Pulmonary Disease. <i>Archivos De Bronconeumologia</i> , 2019, 55, 93-99.	0.4	5
67	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. <i>F1000Research</i> , 2020, 9, 1229.	0.8	5
68	Rcupcake: an R package for querying and analyzing biomedical data through the BD2K PIC-SURE RESTful API. <i>Bioinformatics</i> , 2018, 34, 1431-1432.	1.8	4
69	Digging for knowledge with information extraction. , 2010, , .		3
70	psygenet2r: a R/Bioconductor package for the analysis of psychiatric disease genes. <i>Bioinformatics</i> , 2017, 33, 4004-4006.	1.8	3
71	Exploring the Association of Cancer and Depression in Electronic Health Records: Combining Encoded Diagnosis and Mining Free-Text Clinical Notes. <i>JMIR Cancer</i> , 2022, 8, e39003.	0.9	1
72	Functional Genomics Analysis to Disentangle the Role of Genetic Variants in Major Depression. <i>Genes</i> , 2022, 13, 1259.	1.0	1

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73	Embracing the Dark Side: Computational Approaches to Unveil the Functionality of Genes Lacking Biological Annotation in Drug-Induced Liver Injury. <i>Frontiers in Genetics</i> , 2018, 9, 527.	1.1	0
74	Identification of Sequence Variants of Genes from Biomedical Literature. , 2009, , 289-300.		0
75	Abstract 1085: A bioinformatics approach to evaluate the involvement of CDH1/E-cadherin in solid tumors and to identify breast cancer biomarkers. , 2015, , .		0
76	Evaluating Behavioral and Linguistic Changes During Drug Treatment for Depression Using Tweets in Spanish: Pairwise Comparison Study. <i>Journal of Medical Internet Research</i> , 2020, 22, e20920.	2.1	0