

Laura I Furlong

List of Publications by Year in descending order

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Version: 2024-02-01

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 | DisGeNET: a comprehensive platform integrating information on human disease-associated genes and variants. <i>Nucleic Acids Research</i> , 2017, 45, D833-D839. | 14.5 | 1,865 |
| 2 | The DisGeNET knowledge platform for disease genomics: 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D845-D855. | 14.5 | 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. | 3.0 | 847 |
| 4 | The DisGeNET cytoscape app: Exploring and visualizing disease genomics data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2960-2967. | 4.1 | 221 |
| 5 | Human diseases through the lens of network biology. <i>Trends in Genetics</i> , 2013, 29, 150-159. | 6.7 | 182 |
| 6 | DisGeNET: a Cytoscape plugin to visualize, integrate, search and analyze gene-disease networks. <i>Bioinformatics</i> , 2010, 26, 2924-2926. | 4.1 | 180 |
| 7 | Pathway databases and tools for their exploitation: benefits, current limitations and challenges. <i>Molecular Systems Biology</i> , 2009, 5, 290. | 7.2 | 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. | 2.6 | 170 |
| 9 | Gene-Disease Network Analysis Reveals Functional Modules in Mendelian, Complex and Environmental Diseases. <i>PLoS ONE</i> , 2011, 6, e20284. | 2.5 | 153 |
| 10 | The SemanticScience Integrated Ontology (SIO) for biomedical research and knowledge discovery. <i>Journal of Biomedical Semantics</i> , 2014, 5, 14. | 1.6 | 138 |
| 11 | The EU-ADR corpus: Annotated drugs, diseases, targets, and their relationships. <i>Journal of Biomedical Informatics</i> , 2012, 45, 879-884. | 4.3 | 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. | 5.3 | 99 |
| 13 | PsyGeNET: a knowledge platform on psychiatric disorders and their genes. <i>Bioinformatics</i> , 2015, 31, 3075-3077. | 4.1 | 79 |
| 14 | Detecting Signs of Depression in Tweets in Spanish: Behavioral and Linguistic Analysis. <i>Journal of Medical Internet Research</i> , 2019, 21, e14199. | 4.3 | 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. | 5.6 | 61 |
| 16 | Identifying temporal patterns in patient disease trajectories using dynamic time warping: A population-based study. <i>Scientific Reports</i> , 2018, 8, 4216. | 3.3 | 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. | 4.1 | 52 |
| 18 | Network medicine analysis of COPD multimorbidities. <i>Respiratory Research</i> , 2014, 15, 111. | 3.6 | 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. | 6.0 | 44 |
| 20 | A Knowledge-Driven Approach to Extract Disease-Related Biomarkers from the Literature. <i>BioMed Research International</i> , 2014, 2014, 1-11. | 1.9 | 42 |
| 21 | Drug-Induced Acute Myocardial Infarction: Identifying "Prime Suspects"™ from Electronic Healthcare Records-Based Surveillance System. <i>PLoS ONE</i> , 2013, 8, e72148. | 2.5 | 41 |
| 22 | Assessment of NER solutions against the first and second CALBC Silver Standard Corpus. <i>Journal of Biomedical Semantics</i> , 2011, 2, S11. | 1.6 | 39 |
| 23 | The EU-ADR Web Platform: delivering advanced pharmacovigilance tools. <i>Pharmacoepidemiology and Drug Safety</i> , 2013, 22, 459-467. | 1.9 | 36 |
| 24 | Automatic Filtering and Substantiation of Drug Safety Signals. <i>PLoS Computational Biology</i> , 2012, 8, e1002457. | 3.2 | 34 |
| 25 | Challenges in the association of human single nucleotide polymorphism mentions with unique database identifiers. <i>BMC Bioinformatics</i> , 2011, 12, S4. | 2.6 | 33 |
| 26 | Molecular and clinical disease of comorbidities in exacerbated COPD patients. <i>European Respiratory Journal</i> , 2015, 46, 1001-1010. | 6.7 | 32 |
| 27 | Proximal Pathway Enrichment Analysis for Targeting Comorbid Diseases via Network Endopharmacology. <i>Pharmaceuticals</i> , 2018, 11, 61. | 3.8 | 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. | 4.2 | 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. | 1.9 | 31 |
| 30 | OSIRISv1.2: A named entity recognition system for sequence variants of genes in biomedical literature. <i>BMC Bioinformatics</i> , 2008, 9, 84. | 2.6 | 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. | 2.8 | 31 |
| 32 | comoRbidity: an R package for the systematic analysis of disease comorbidities. <i>Bioinformatics</i> , 2018, 34, 3228-3230. | 4.1 | 31 |
| 33 | In silico models in drug development: where we are. <i>Current Opinion in Pharmacology</i> , 2018, 42, 111-121. | 3.5 | 30 |
| 34 | Uncovering disease mechanisms through network biology in the era of Next Generation Sequencing. <i>Scientific Reports</i> , 2016, 6, 24570. | 3.3 | 29 |
| 35 | Genetic and functional characterization of disease associations explains comorbidity. <i>Scientific Reports</i> , 2017, 7, 6207. | 3.3 | 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. | 4.1 | 27 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 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. | 1.0 | 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. | 2.6 | 24 |
| 39 | OSIRIS: a tool for retrieving literature about sequence variants. <i>Bioinformatics</i> , 2006, 22, 2567-2569. | 4.1 | 22 |
| 40 | Expression of Human Proacrosin in Escherichia coli and Binding to Zona Pellucida1. <i>Biology of Reproduction</i> , 2000, 62, 606-615. | 2.7 | 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. | 1.0 | 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. | 3.4 | 19 |
| 44 | Publishing DisGeNET as nanopublications. <i>Semantic Web</i> , 2016, 7, 519-528. | 1.9 | 18 |
| 45 | Network, Transcriptomic and Genomic Features Differentiate Genes Relevant for Drug Response. <i>Frontiers in Genetics</i> , 2018, 9, 412. | 2.3 | 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. | 0.8 | 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. | 6.2 | 18 |
| 48 | The eTRANSAFE Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. <i>Pharmaceuticals</i> , 2021, 14, 237. | 3.8 | 17 |
| 49 | IDENTIFYING GENE-SPECIFIC VARIATIONS IN BIOMEDICAL TEXT. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 1277-1296. | 0.8 | 15 |
| 50 | Gathering and Exploring Scientific Knowledge in Pharmacovigilance. <i>PLoS ONE</i> , 2013, 8, e83016. | 2.5 | 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. | 3.0 | 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. | 3.3 | 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. | 1.0 | 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, . | 3.0 | 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. | 5.1 | 11 |
| 56 | An ensemble learning approach for modeling the systems biology of drug-induced injury. <i>Biology Direct</i> , 2021, 16, 5. | 4.6 | 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, . | 3.0 | 10 |
| 58 | Reliable Granular References to Changing Linked Data. <i>Lecture Notes in Computer Science</i> , 2017, , 436-451. | 1.3 | 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. | 3.0 | 9 |
| 60 | Comorbidity4j: a tool for interactive analysis of disease comorbidities over large patient datasets. <i>Bioinformatics</i> , 2019, 35, 3530-3532. | 4.1 | 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. | 1.0 | 8 |
| 62 | A system-level analysis of patient disease trajectories based on clinical, phenotypic and molecular similarities. <i>Bioinformatics</i> , 2021, 37, 1435-1443. | 4.1 | 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. | 1.0 | 7 |
| 64 | Mining the Modular Structure of Protein Interaction Networks. <i>PLoS ONE</i> , 2015, 10, e0122477. | 2.5 | 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. | 2.3 | 7 |
| 66 | The BIOMEPOC Project: Personalized Biomarkers and Clinical Profiles in Chronic Obstructive Pulmonary Disease. <i>Archivos De Bronconeumologia</i> , 2019, 55, 93-99. | 0.8 | 5 |
| 67 | The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. <i>F1000Research</i> , 2020, 9, 1229. | 1.6 | 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. | 4.1 | 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. | 4.1 | 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. | 2.4 | 1 |
| 72 | Functional Genomics Analysis to Disentangle the Role of Genetic Variants in Major Depression. <i>Genes</i> , 2022, 13, 1259. | 2.4 | 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. | 2.3 | 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. | 4.3 | 0 |