Lydie Lane

List of Publications by Citations

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61 2,805 31 52 g-index

70 3,412 6.9 avg, IF 5.47 L-index

| # | Paper | IF | Citations |
|----|---|----------------|-----------|
| 61 | The Universal Protein Resource (UniProt) 2009. <i>Nucleic Acids Research</i> , 2009 , 37, D169-74 | 20.1 | 509 |
| 60 | neXtProt: a knowledge platform for human proteins. <i>Nucleic Acids Research</i> , 2012 , 40, D76-83 | 20.1 | 142 |
| 59 | Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016 , 15, 3961-3970 | 5.6 | 130 |
| 58 | The neXtProt knowledgebase on human proteins: 2017 update. <i>Nucleic Acids Research</i> , 2017 , 45, D177- | D168.2 | 123 |
| 57 | Metrics for the Human Proteome Project 2013-2014 and strategies for finding missing proteins. Journal of Proteome Research, 2014 , 13, 15-20 | 5.6 | 113 |
| 56 | neXtProt: organizing protein knowledge in the context of human proteome projects. <i>Journal of Proteome Research</i> , 2013 , 12, 293-8 | 5.6 | 110 |
| 55 | Down-regulation of ECRG4, a candidate tumor suppressor gene, in human breast cancer. <i>PLoS ONE</i> , 2011 , 6, e27656 | 3.7 | 108 |
| 54 | Proteomic analysis of podocyte exosome-enriched fraction from normal human urine. <i>Journal of Proteomics</i> , 2013 , 82, 193-229 | 3.9 | 96 |
| 53 | Protein variety and functional diversity: Swiss-Prot annotation in its biological context. <i>Comptes Rendus - Biologies</i> , 2005 , 328, 882-99 | 1.4 | 80 |
| 52 | The neXtProt knowledgebase on human proteins: current status. <i>Nucleic Acids Research</i> , 2015 , 43, D764 | 1-70 .1 | 76 |
| 51 | Metrics for the Human Proteome Project 2015: Progress on the Human Proteome and Guidelines for High-Confidence Protein Identification. <i>Journal of Proteome Research</i> , 2015 , 14, 3452-60 | 5.6 | 74 |
| 50 | The neXtProt knowledgebase in 2020: data, tools and usability improvements. <i>Nucleic Acids Research</i> , 2020 , 48, D328-D334 | 20.1 | 67 |
| 49 | The UniProtKB/Swiss-Prot knowledgebase and its Plant Proteome Annotation Program. <i>Journal of Proteomics</i> , 2009 , 72, 567-73 | 3.9 | 63 |
| 48 | Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. <i>Journal of Proteome Research</i> , 2016 , 15, 3951-3960 | 5.6 | 60 |
| 47 | A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301 | 17.4 | 59 |
| 46 | Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. <i>Journal of Proteome Research</i> , 2016 , 15, 3998-4019 | 5.6 | 55 |
| 45 | Human Spermatozoa as a Model for Detecting Missing Proteins in the Context of the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015 , 14, 3606-20 | 5.6 | 50 |

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| Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015 , 14, 3415-31 | 5.6 | 50 |
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| Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2018 , 17, 4031-4041 | 5.6 | 46 |
| Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. Journal of Proteome Research, 2017 , 16, 4281-4287 | 5.6 | 46 |
| C11orf83, a mitochondrial cardiolipin-binding protein involved in bc1 complex assembly and supercomplex stabilization. <i>Molecular and Cellular Biology</i> , 2015 , 35, 1139-56 | 4.8 | 44 |
| N-terminome analysis of the human mitochondrial proteome. <i>Proteomics</i> , 2015 , 15, 2519-24 | 4.8 | 43 |
| The SIB Swiss Institute of BioinformaticsR esources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016 , 44, D27-37 | 20.1 | 41 |
| The neXtProt peptide uniqueness checker: a tool for the proteomics community. <i>Bioinformatics</i> , 2017 , 33, 3471-3472 | 7.2 | 40 |
| Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. <i>Journal of Proteome Research</i> , 2019 , 18, 4108-4116 | 5.6 | 37 |
| Deep Dive on the Proteome of Human Cerebrospinal Fluid: A Valuable Data Resource for Biomarker Discovery and Missing Protein Identification. <i>Journal of Proteome Research</i> , 2018 , 17, 4113-4 | 126 | 36 |
| Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2019 , 18, 4098-4107 | 5.6 | 32 |
| Evidence for a molecular link between the tuberous sclerosis complex and the Crumbs complex. <i>Human Molecular Genetics</i> , 2007 , 16, 529-36 | 5.6 | 32 |
| Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. <i>Journal of Proteome Research</i> , 2015 , 14, 3621-34 | 5.6 | 31 |
| Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. <i>Genome Medicine</i> , 2017 , 9, 113 | 14.4 | 31 |
| Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. <i>Journal of Proteome Research</i> , 2018 , 17, 4042-4050 | 5.6 | 31 |
| Mitochondrial peptide BRAWNIN is essential for vertebrate respiratory complex III assembly. <i>Nature Communications</i> , 2020 , 11, 1312 | 17.4 | 26 |
| Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020 , 19, 4735-4746 | 5.6 | 25 |
| Advances in the Chromosome-Centric Human Proteome Project: looking to the future. <i>Expert Review of Proteomics</i> , 2017 , 14, 1059-1071 | 4.2 | 21 |
| DERA is the human deoxyribose phosphate aldolase and is involved in stress response. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014 , 1843, 2913-25 | 4.9 | 19 |
| | Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2018, 17, 4031-4041 Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. Journal of Proteome Research, 2017, 16, 4281-4287 C11orf83, a mitochondrial cardiolipin-binding protein involved in bc1 complex assembly and supercomplex stabilization. Molecular and Cellular Biology, 2015, 35, 1139-56 N-terminome analysis of the human mitochondrial proteome. Proteomics, 2015, 15, 2519-24 The SIB Swiss Institute of Bioinformatics/resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-37 The neXtProt peptide uniqueness checker: a tool for the proteomics community. Bioinformatics, 2017, 33, 3471-3472 Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116 Deep Dive on the Proteome of Human Cerebrospinal Fluid: A Valuable Data Resource for Biomarker Discovery and Missing Protein Identification. Journal of Proteome Research, 2018, 17, 4113-4 Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2019, 18, 4098-4107 Evidence for a molecular link between the tuberous sclerosis complex and the Crumbs complex. Human Molecular Genetics, 2007, 16, 529-36 Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. Journal of Proteome Research, 2015, 14, 3621-34 Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113 Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. Journal of Proteome Research, 2018, 17, 4042-4050 Mitochondrial peptide BRAWNIN is essential for vertebrate respiratory complex III assembly. Nature Co | Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2018, 17, 4031-4041 5.6 Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. Journal of Proteome Research, 2017, 16, 4281-4287 5.6 C11orf83, a mitochondrial cardiolipin-binding protein involved in bc1 complex assembly and supercomplex stabilization. Molecular and Cellular Biology, 2015, 35, 1139-56 4.8 N-terminome analysis of the human mitochondrial proteome. Proteomics, 2015, 15, 2519-24 4.8 The SIB Swiss Institute of BioinformaticsResources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-37 The neXtProt peptide uniqueness checker: a tool for the proteomics community. Bioinformatics, 2017, 33, 3471-3472 7.2 Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116 5.6 Deep Dive on the Proteome of Human Cerebrospinal Fluid: A Valuable Data Resource for Biomarker Discovery and Missing Protein Identification. Journal of Proteome Research, 2018, 17, 4113-4126 Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO 4.1 Evidence for a molecular link between the tuberous sclerosis complex and the Crumbs complex. Human Proteome Project. Journal of Proteome Research, 2019, 18, 4098-4107 5.6 Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. Journal of Proteome Research, 2015, 14, 3621-34 Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113 144 Launching the C-HPP neXt-C-PSO Pilot Project for Functional Characterization of Identified Proteins with No Known Function. Journal of Proteome Research, 2018, 17, 4042-4050 5.6 Mitochondrial peptide BRAWNIN is essential for vertebrate respiratory complex III assembly. Nature Co |

| 26 | Functional identification of APIP as human mtnB, a key enzyme in the methionine salvage pathway. <i>PLoS ONE</i> , 2012 , 7, e52877 | 3.7 | 19 |
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| 25 | Systems Proteomics View of the Endogenous Human Claudin Protein Family. <i>Journal of Proteome Research</i> , 2016 , 15, 339-59 | 5.6 | 17 |
| 24 | Exploring the Uncharacterized Human Proteome Using neXtProt. <i>Journal of Proteome Research</i> , 2018 , 17, 4211-4226 | 5.6 | 17 |
| 23 | Validating Missing Proteins in Human Sperm Cells by Targeted Mass-Spectrometry- and Antibody-based Methods. <i>Journal of Proteome Research</i> , 2017 , 16, 4340-4351 | 5.6 | 15 |
| 22 | C2orf62 and TTC17 are involved in actin organization and ciliogenesis in zebrafish and human. <i>PLoS ONE</i> , 2014 , 9, e86476 | 3.7 | 13 |
| 21 | Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018-2019 Additions to neXtProt and the CAFA3 Challenge. <i>Journal of Proteome Research</i> , 2019 , 18, 4154-4166 | 5.6 | 12 |
| 20 | Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014 , 42, W436-41 | 20.1 | 12 |
| 19 | Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. <i>Journal of Proteome Research</i> , 2016 , 15, 3971-3978 | 5.6 | 12 |
| 18 | Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 2019, 18, 2686 | -256 6 2 | 11 |
| 17 | Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. <i>Web Semantics</i> , 2014 , 29, 3-11 | 2.9 | 11 |
| 16 | Identification of Missing Proteins in Normal Human Cerebrospinal Fluid. <i>Journal of Proteome Research</i> , 2018 , 17, 4315-4319 | 5.6 | 10 |
| 15 | Converting neXtProt into Linked Data and nanopublications. Semantic Web, 2015, 6, 147-153 | 2.4 | 10 |
| 14 | A community proposal to integrate proteomics activities in ELIXIR. F1000Research, 2017, 6, | 3.6 | 10 |
| 13 | Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. <i>Journal of Proteome Research</i> , 2018 , 17, 4160-4170 | 5.6 | 10 |
| 12 | Collaborative annotation of genes and proteins between UniProtKB/Swiss-Prot and dictyBase. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap016 | 5 | 9 |
| 11 | Progress Identifying and Analyzing the Human Proteome: 2021[Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2021 , 20, 5227-5240 | 5.6 | 7 |
| 10 | Combining bioinformatics and MS-based proteomics: clinical implications. <i>Expert Review of Proteomics</i> , 2014 , 11, 269-84 | 4.2 | 6 |
| 9 | Worming into the Uncharacterized Human Proteome. <i>Journal of Proteome Research</i> , 2019 , 18, 4143-415 | 5 3 5.6 | 4 |

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| 8 | The Functionally Unannotated Proteome of Human Male Tissues: A Shared Resource to Uncover New Protein Functions Associated with Reproductive Biology. <i>Journal of Proteome Research</i> , 2020 , 19, 4782-4794 | 5.6 | 4 |
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| 7 | Update of the Functional Mitochondrial Human Proteome Network. <i>Journal of Proteome Research</i> , 2018 , 17, 4297-4306 | 5.6 | 4 |
| 6 | C21orf91 Regulates Oligodendroglial Precursor Cell Fate-A Switch in the Glial Lineage?. <i>Frontiers in Cellular Neuroscience</i> , 2021 , 15, 653075 | 6.1 | 3 |
| 5 | Querying NeXtProt Nanopublications and Their Value for Insights on Sequence Variants and Tissue Expression. SSRN Electronic Journal, | 1 | 2 |
| 4 | Functionathon: a manual data mining workflow to generate functional hypotheses for uncharacterized human proteins and its application by undergraduate students. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021, | 5 | 2 |
| 3 | A Preliminary Study on the Prediction of Human Protein Functions. <i>Lecture Notes in Computer Science</i> , 2011 , 334-343 | 0.9 | 1 |
| 2 | Proteomics Standards Initiative Extended FASTA Format (PEFF) | | 1 |
| 1 | UniProtKB/Swiss-Prot Manual and Automated Annotation of Complete Proteomes: The Dictyostelium discoideum Case Study 2009 , 149-168 | | |