Lydie Lane

List of Publications by Year in Descending Order

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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.

61 papers	2,805 citations	31 h-index	52 g-index
70 ext. papers	3,412 ext. citations	6.9 avg, IF	5.47 L-index

#	Paper	IF	Citations
61	Progress Identifying and Analyzing the Human Proteome: 2021 Metrics from the HUPO Human Proteome Project. *Journal of Proteome Research*, **2021**, 20, 5227-5240	5.6	7
60	C21orf91 Regulates Oligodendroglial Precursor Cell Fate-A Switch in the Glial Lineage?. *Frontiers in Cellular Neuroscience*, **2021**, 15, 653075	6.1	3
59	Functionathon: a manual data mining workflow to generate functional hypotheses for uncharacterized human proteins and its application by undergraduate students. *Database: the Journal of Biological Databases and Curation*, **2021**, 2021,	5	2
58	Mitochondrial peptide BRAWNIN is essential for vertebrate respiratory complex III assembly. *Nature Communications*, **2020**, 11, 1312	17.4	26
57	The neXtProt knowledgebase in 2020: data, tools and usability improvements. *Nucleic Acids Research*, **2020**, 48, D328-D334	20.1	67
56	The Functionally Unannotated Proteome of Human Male Tissues: A Shared Resource to Uncover New Protein Functions Associated with Reproductive Biology. *Journal of Proteome Research*, **2020**, 19, 4782-4794	5.6	4
55	A high-stringency blueprint of the human proteome. *Nature Communications*, **2020**, 11, 5301	17.4	59
54	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. *Journal of Proteome Research*, **2020**, 19, 4735-4746	5.6	25
53	Worming into the Uncharacterized Human Proteome. *Journal of Proteome Research*, **2019**, 18, 4143-4153	5.6	4
52	Proteomics Standards Initiative Extended FASTA Format. *Journal of Proteome Research*, **2019**, 18, 2686-2692	5.6	11
51	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. *Journal of Proteome Research*, **2019**, 18, 4098-4107	5.6	32
50	Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018-2019 Additions to neXtProt and the CAFA3 Challenge. *Journal of Proteome Research*, **2019** , 18, 4154-4166	5.6	12
49	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. *Journal of Proteome Research*, **2019**, 18, 4108-4116	5.6	37
48	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	46
47	Identification of Missing Proteins in Normal Human Cerebrospinal Fluid. *Journal of Proteome Research*, **2018**, 17, 4315-4319	5.6	10
46	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	5.6	36
45	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	5.6	31

44	Exploring the Uncharacterized Human Proteome Using neXtProt. *Journal of Proteome Research*, **2018**, 17, 4211-4226	5.6	17
43	Update of the Functional Mitochondrial Human Proteome Network. *Journal of Proteome Research*, **2018**, 17, 4297-4306	5.6	4
42	Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. *Journal of Proteome Research*, **2018**, 17, 4160-4170	5.6	10
41	The neXtProt peptide uniqueness checker: a tool for the proteomics community. *Bioinformatics*, **2017**, 33, 3471-3472	7.2	40
40	Advances in the Chromosome-Centric Human Proteome Project: looking to the future. *Expert Review of Proteomics*, **2017**, 14, 1059-1071	4.2	21
39	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. *Genome Medicine*, **2017**, 9, 113	14.4	31
38	The neXtProt knowledgebase on human proteins: 2017 update. *Nucleic Acids Research*, **2017**, 45, D177-D182	20.1	123
37	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
36	Validating Missing Proteins in Human Sperm Cells by Targeted Mass-Spectrometry- and Antibody-based Methods. *Journal of Proteome Research*, **2017**, 16, 4340-4351	5.6	15
35	A community proposal to integrate proteomics activities in ELIXIR. *F1000Research*, **2017**, 6,	3.6	10
34	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. *Journal of Proteome Research*, **2016**, 15, 3998-4019	5.6	55
33	Systems Proteomics View of the Endogenous Human Claudin Protein Family. *Journal of Proteome Research*, **2016**, 15, 339-59	5.6	17
32	The SIB Swiss Institute of BioinformaticsRresources: focus on curated databases. *Nucleic Acids Research*, **2016**, 44, D27-37	20.1	41
31	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. *Journal of Proteome Research*, **2016**, 15, 3961-3970	5.6	130
30	Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. *Journal of Proteome Research*, **2016**, 15, 3971-3978	5.6	12
29	Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. *Journal of Proteome Research*, **2016**, 15, 3951-3960	5.6	60
28	C11orf83, a mitochondrial cardiolipin-binding protein involved in bc1 complex assembly and supercomplex stabilization. *Molecular and Cellular Biology*, **2015**, 35, 1139-56	4.8	44
27	Human Spermatozoa as a Model for Detecting Missing Proteins in the Context of the Chromosome-Centric Human Proteome Project. *Journal of Proteome Research*, **2015**, 14, 3606-20	5.6	50

26	Metrics for the Human Proteome Project 2015: Progress on the Human Proteome and Guidelines for High-Confidence Protein Identification. *Journal of Proteome Research*, **2015**, 14, 3452-60	5.6	74
25	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. *Journal of Proteome Research*, **2015**, 14, 3415-31	5.6	50
24	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	5.6	31
23	Converting neXtProt into Linked Data and nanopublications. *Semantic Web*, **2015**, 6, 147-153	2.4	10
22	N-terminome analysis of the human mitochondrial proteome. *Proteomics*, **2015**, 15, 2519-24	4.8	43
21	The neXtProt knowledgebase on human proteins: current status. *Nucleic Acids Research*, **2015**, 43, D764-70	20.1	76
20	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
19	Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. *Web Semantics*, **2014**, 29, 3-11	2.9	11
18	DERA is the human deoxyribose phosphate aldolase and is involved in stress response. *Biochimica Et Biophysica Acta - Molecular Cell Research*, **2014**, 1843, 2913-25	4.9	19
17	C2orf62 and TTC17 are involved in actin organization and ciliogenesis in zebrafish and human. *PLoS ONE*, **2014**, 9, e86476	3.7	13
16	Combining bioinformatics and MS-based proteomics: clinical implications. *Expert Review of Proteomics*, **2014**, 11, 269-84	4.2	6
15	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. *Nucleic Acids Research*, **2014**, 42, W436-41	20.1	12
14	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine. *Journal of Proteomics*, **2013**, 82, 193-229	3.9	96
13	neXtProt: organizing protein knowledge in the context of human proteome projects. *Journal of Proteome Research*, **2013**, 12, 293-8	5.6	110
12	neXtProt: a knowledge platform for human proteins. *Nucleic Acids Research*, **2012**, 40, D76-83	20.1	142
11	Functional identification of APIP as human mtnB, a key enzyme in the methionine salvage pathway. *PLoS ONE*, **2012**, 7, e52877	3.7	19
10	Down-regulation of ECRG4, a candidate tumor suppressor gene, in human breast cancer. *PLoS ONE*, **2011**, 6, e27656	3.7	108
9	A Preliminary Study on the Prediction of Human Protein Functions. *Lecture Notes in Computer Science*, **2011**, 334-343	0.9	1

8	The Universal Protein Resource (UniProt) 2009. *Nucleic Acids Research*, **2009**, 37, D169-74	20.1	509
7	Collaborative annotation of genes and proteins between UniProtKB/Swiss-Prot and dictyBase. *Database: the Journal of Biological Databases and Curation*, **2009**, 2009, bap016	5	9
6	The UniProtKB/Swiss-Prot knowledgebase and its Plant Proteome Annotation Program. *Journal of Proteomics*, **2009**, 72, 567-73	3.9	63
5	UniProtKB/Swiss-Prot Manual and Automated Annotation of Complete Proteomes: The Dictyostelium discoideum Case Study **2009**, 149-168		
4	Evidence for a molecular link between the tuberous sclerosis complex and the Crumbs complex. *Human Molecular Genetics*, **2007**, 16, 529-36	5.6	32
3	Protein variety and functional diversity: Swiss-Prot annotation in its biological context. *Comptes Rendus - Biologies*, **2005**, 328, 882-99	1.4	80
2	Querying NeXtProt Nanopublications and Their Value for Insights on Sequence Variants and Tissue Expression. *SSRN Electronic Journal*,	1	2
1	Proteomics Standards Initiative Extended FASTA Format (PEFF)		1