Lydie Lane

List of Publications by Year in descending order

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65

papers

3,719

citations

136740

32

h-index

133063

59

g-index

70

all docs

70

docs citations

70

times ranked

6422

citing authors

#	ARTICLE	IF	CITATIONS
1	The Universal Protein Resource (UniProt) 2009. Nucleic Acids Research, 2009, 37, D169-D174.	6.5	548
2	neXtProt: a knowledge platform for human proteins. Nucleic Acids Research, 2012, 40, D76-D83.	6.5	167
3	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970.	1.8	158
4	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	5.8	152
5	The neXtProt knowledgebase on human proteins: 2017 update. Nucleic Acids Research, 2017, 45, D177-D182.	6.5	145
6	Down-Regulation of ECRG4, a Candidate Tumor Suppressor Gene, in Human Breast Cancer. PLoS ONE, 2011, 6, e27656.	1.1	143
7	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine. Journal of Proteomics, 2013, 82, 193-229.	1.2	125
8	Metrics for the Human Proteome Project 2013â€“2014 and Strategies for Finding Missing Proteins. Journal of Proteome Research, 2014, 13, 15-20.	1.8	124
9	The neXtProt knowledgebase in 2020: data, tools and usability improvements. Nucleic Acids Research, 2020, 48, D328-D334.	6.5	121
10	neXtProt: Organizing Protein Knowledge in the Context of Human Proteome Projects. Journal of Proteome Research, 2013, 12, 293-298.	1.8	116
11	Protein variety and functional diversity: Swiss-Prot annotation in its biological context. Comptes Rendus - Biologies, 2005, 328, 882-899.	0.1	107
12	The neXtProt knowledgebase on human proteins: current status. Nucleic Acids Research, 2015, 43, D764-D770.	6.5	94
13	Mitochondrial peptide BRAWNIN is essential for vertebrate respiratory complex III assembly. Nature Communications, 2020, 11, 1312.	5.8	87
14	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, 3452-3460.	1.8	86
15	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116.	1.8	82
16	The UniProtKB/Swiss-Prot knowledgebase and its Plant Proteome Annotation Program. Journal of Proteomics, 2009, 72, 567-573.	1.2	80
17	Nâ€•terminome analysis of the human mitochondrial proteome. Proteomics, 2015, 15, 2519-2524.	1.3	74
18	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.	1.8	72

#	ARTICLE	IF	CITATIONS
19	Looking for Missing Proteins in the Proteome of Human Spermatozoa: An Update. Journal of Proteome Research, 2016, 15, 3998-4019.	1.8	66
20	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
21	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.	1.8	63
22	C11orf83, a Mitochondrial Cardiolipin-Binding Protein Involved in <i>bc</i>₁ Complex Assembly and Supercomplex Stabilization. Molecular and Cellular Biology, 2015, 35, 1139-1156.	1.1	62
23	Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2018, 17, 4031-4041.	1.8	59
24	The neXtProt peptide uniqueness checker: a tool for the proteomics community. Bioinformatics, 2017, 33, 3471-3472.	1.8	56
25	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, 3606-3620.	1.8	55
26	Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. Journal of Proteome Research, 2017, 16, 4281-4287.	1.8	55
27	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431.	1.8	53
28	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113.	3.6	47
29	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.	1.8	41
30	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2019, 18, 4098-4107.	1.8	41
31	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.	1.8	38
32	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, 3621-3634.	1.8	35
33	Evidence for a molecular link between the tuberous sclerosis complex and the Crumbs complex. Human Molecular Genetics, 2007, 16, 529-536.	1.4	34
34	Exploring the Uncharacterized Human Proteome Using neXtProt. Journal of Proteome Research, 2018, 17, 4211-4226.	1.8	32
35	Progress Identifying and Analyzing the Human Proteome: 2021ÂMetrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2021, 20, 5227-5240.	1.8	30
36	DERA is the human deoxyribose phosphate aldolase and is involved in stress response. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 2913-2925.	1.9	26

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37	Systems Proteomics View of the Endogenous Human Claudin Protein Family. Journal of Proteome Research, 2016, 15, 339-359.	1.8	26
38	Advances in the Chromosome-Centric Human Proteome Project: looking to the future. Expert Review of Proteomics, 2017, 14, 1059-1071.	1.3	25
39	Functional Identification of APIP as Human mtnB, a Key Enzyme in the Methionine Salvage Pathway. PLoS ONE, 2012, 7, e52877.	1.1	24
40	Toward Completion of the Human Proteome Parts List: Progress Uncovering Proteins That Are Missing or Have Unknown Function and Developing Analytical Methods. Journal of Proteome Research, 2018, 17, 4023-4030.	1.8	22
41	Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 2019, 18, 2686-2692.	1.8	22
42	Validating Missing Proteins in Human Sperm Cells by Targeted Mass-Spectrometry- and Antibody-based Methods. Journal of Proteome Research, 2017, 16, 4340-4351.	1.8	21
43	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.	1.8	21
44	Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018â€“2019 Additions to neXtProt and the CAFA3 Challenge. Journal of Proteome Research, 2019, 18, 4154-4166.	1.8	20
45	C2orf62 and TTC17 Are Involved in Actin Organization and Ciliogenesis in Zebrafish and Human. PLoS ONE, 2014, 9, e86476.	1.1	19
46	Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. Journal of Proteome Research, 2016, 15, 3971-3978.	1.8	15
47	Identification of Missing Proteins in Normal Human Cerebrospinal Fluid. Journal of Proteome Research, 2018, 17, 4315-4319.	1.8	15
48	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	6.5	13
49	Converting neXtProt into Linked Data and nanopublications. Semantic Web, 2015, 6, 147-153.	1.1	13
50	Update of the Functional Mitochondrial Human Proteome Network. Journal of Proteome Research, 2018, 17, 4297-4306.	1.8	13
51	A community proposal to integrate proteomics activities in ELIXIR. F1000Research, 2017, 6, 875.	0.8	13
52	Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. Web Semantics, 2014, 29, 3-11.	2.2	12
53	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.	1.8	10
54	Collaborative annotation of genes and proteins between UniProtKB/Swiss-Prot and dictyBase. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap016-bap016.	1.4	9

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55	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, .	1.4	8
56	C21orf91 Regulates Oligodendroglial Precursor Cell Fateâ€"A Switch in the Glial Lineage?. Frontiers in Cellular Neuroscience, 2021, 15, 653075.	1.8	8
57	Combining bioinformatics and MS-based proteomics: clinical implications. Expert Review of Proteomics, 2014, 11, 269-284.	1.3	7
58	Worming into the Uncharacterized Human Proteome. Journal of Proteome Research, 2019, 18, 4143-4153.	1.8	7
59	What will neXtProt help us achieve in 2020 and beyond?. Expert Review of Proteomics, 2020, 17, 95-98.	1.3	5
60	Advances in Identifying and Characterizing the Human Proteome. Journal of Proteome Research, 2019, 18, 4079-4084.	1.8	4
61	PepPSy: a web server to prioritize gene products in experimental and biocuration workflows. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw070.	1.4	2
62	Querying NeXtProt Nanopublications and Their Value for Insights on Sequence Variants and Tissue Expression. SSRN Electronic Journal, 0, , .	0.4	2
63	A Preliminary Study on the Prediction of Human Protein Functions. Lecture Notes in Computer Science, 2011, , 334-343.	1.0	1
64	UniProtKB/Swiss-Prot Manual and Automated Annotation of Complete Proteomes: The <i>Dictyostelium discoideum</i> Case Study. , 2009, , 149-168.		0
65	Protein Function Analysis. Chapman & Hall/CRC Mathematical and Computational Biology Series, 2007, , 379-424.	0.1	0