

# Leonard J Foster

## List of Publications by Year in descending order

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156  
papers

9,063  
citations

53660

45  
h-index

53109

85  
g-index

186  
all docs

186  
docs citations

186  
times ranked

13157  
citing authors

#	ARTICLE	IF	CITATIONS
1	Unbiased quantitative proteomics of lipid rafts reveals high specificity for signaling factors. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5813-5818.	3.3	783
2	A Mammalian Organelle Map by Protein Correlation Profiling. Cell, 2006, 125, 187-199.	13.5	538
3	Isotopic labeling of terminal amines in complex samples identifies protein N-termini and protease cleavage products. Nature Biotechnology, 2010, 28, 281-288.	9.4	510
4	An exosome-based secretion pathway is responsible for protein export from <i>Leishmania</i> and communication with macrophages. Journal of Cell Science, 2010, 123, 842-852.	1.2	410
5	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	1.2	375
6	A high-throughput approach for measuring temporal changes in the interactome. Nature Methods, 2012, 9, 907-909.	9.0	293
7	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. Journal of Proteome Research, 2010, 9, 393-403.	1.8	237
8	Protein synthesis rate is the predominant regulator of protein expression during differentiation. Molecular Systems Biology, 2013, 9, 689.	3.2	209
9	Differential Expression Profiling of Membrane Proteins by Quantitative Proteomics in a Human Mesenchymal Stem Cell Line Undergoing Osteoblast Differentiation. Stem Cells, 2005, 23, 1367-1377.	1.4	185
10	Reduced Insulin Production Relieves Endoplasmic Reticulum Stress and Induces $\beta$ Cell Proliferation. Cell Metabolism, 2016, 23, 179-193.	7.2	160
11	Subcellular proteomics. Nature Reviews Methods Primers, 2021, 1, .	11.8	159
12	Standard methods for molecular research in <i>Apis mellifera</i> . Journal of Apicultural Research, 2013, 52, 1-54.	0.7	150
13	Quantitative Comparison of Caste Differences in Honeybee Hemolymph. Molecular and Cellular Proteomics, 2006, 5, 2252-2262.	2.5	133
14	Reduced Circulating Insulin Enhances Insulin Sensitivity in Old Mice and Extends Lifespan. Cell Reports, 2017, 20, 451-463.	2.9	112
15	The innate immune and systemic response in honey bees to a bacterial pathogen, <i>Paenibacillus larvae</i> . BMC Genomics, 2009, 10, 387.	1.2	111
16	Genetic Dissection of the Type VI Secretion System in <i>Acinetobacter</i> and Identification of a Novel Peptidoglycan Hydrolase, TagX, Required for Its Biogenesis. MBio, 2016, 7, .	1.8	110
17	Evaluating measures of association for single-cell transcriptomics. Nature Methods, 2019, 16, 381-386.	9.0	109
18	Standard methods for American foulbrood research. Journal of Apicultural Research, 2013, 52, 1-28.	0.7	108

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19	Insulin-dependent Interactions of Proteins with GLUT4 Revealed through Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)*. <i>Journal of Proteome Research</i> , 2006, 5, 64-75.	1.8	106
20	CNS-derived extracellular vesicles from superoxide dismutase 1 (SOD1)G93A ALS mice originate from astrocytes and neurons and carry misfolded SOD1. <i>Journal of Biological Chemistry</i> , 2019, 294, 3744-3759.	1.6	97
21	Cell type prioritization in single-cell data. <i>Nature Biotechnology</i> , 2021, 39, 30-34.	9.4	96
22	Polarization of the Endoplasmic Reticulum by ER-Septin Tethering. <i>Cell</i> , 2014, 158, 620-632.	13.5	92
23	<i>Acinetobacter</i> strains carry two functional oligosaccharyltransferases, one devoted exclusively to type IV pilin, and the other one dedicated to glycosylation of multiple proteins. <i>Molecular Microbiology</i> , 2015, 96, 1023-1041.	1.2	90
24	Mechanisms of stable lipid loss in a social insect. <i>Journal of Experimental Biology</i> , 2011, 214, 3808-3821.	0.8	88
25	Catabolism of the Last Two Steroid Rings in <i>Mycobacterium tuberculosis</i> and Other Bacteria. <i>MBio</i> , 2017, 8, .	1.8	77
26	Quantitative Analysis of Proteome Coverage and Recovery Rates for Upstream Fractionation Methods in Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 1902-1912.	1.8	76
27	Quantitative Proteomic Analysis of Type III Secretome of Enteropathogenic <i>Escherichia coli</i> Reveals an Expanded Effector Repertoire for Attaching/Effacing Bacterial Pathogens. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 692-709.	2.5	72
28	<i>Salmonella</i> Rapidly Regulates Membrane Permeability To Survive Oxidative Stress. <i>MBio</i> , 2016, 7, .	1.8	70
29	A death pheromone, oleic acid, triggers hygienic behavior in honey bees ( <i>Apis mellifera</i> L.). <i>Scientific Reports</i> , 2018, 8, 5719.	1.6	68
30	Sequestosome-1/p62 Is the Key Intracellular Target of Innate Defense Regulator Peptide. <i>Journal of Biological Chemistry</i> , 2009, 284, 36007-36011.	1.6	67
31	Biomarkers for Severity of Spinal Cord Injury in the Cerebrospinal Fluid of Rats. <i>PLoS ONE</i> , 2011, 6, e19247.	1.1	66
32	Correlation of proteome-wide changes with social immunity behaviors provides insight into resistance to the parasitic mite, <i>Varroa destructor</i> , in the honey bee ( <i>Apis mellifera</i> ). <i>Genome Biology</i> , 2012, 13, R81.	13.9	65
33	Diversity Within the O-linked Protein Glycosylation Systems of <i>Acinetobacter</i> Species. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2354-2370.	2.5	64
34	hnRNP K Coordinates Transcriptional Silencing by SETDB1 in Embryonic Stem Cells. <i>PLoS Genetics</i> , 2015, 11, e1004933.	1.5	64
35	Structure of human ST8SialIII sialyltransferase provides insight into cell-surface polysialylation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 627-635.	3.6	62
36	Clptm1 Limits Forward Trafficking of GABAA Receptors to Scale Inhibitory Synaptic Strength. <i>Neuron</i> , 2018, 97, 596-610.e8.	3.8	62

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37	Changes in protein expression during honey bee larval development. <i>Genome Biology</i> , 2008, 9, R156.	13.9	60
38	Honey bee protein atlas at organ-level resolution. <i>Genome Research</i> , 2013, 23, 1951-1960.	2.4	59
39	Vulnerability of honey bee queens to heat-induced loss of fertility. <i>Nature Sustainability</i> , 2020, 3, 367-376.	11.5	59
40	An atlas of protein-protein interactions across mouse tissues. <i>Cell</i> , 2021, 184, 4073-4089.e17.	13.5	59
41	The pathogenic <i>E. coli</i> type III effector EspZ interacts with host CD98 and facilitates host cell pro-survival signalling. <i>Cellular Microbiology</i> , 2010, 12, 1322-1339.	1.1	58
42	A general protein <i>O</i> -glycosylation system within the <i>Bacteroides cepacia</i> complex is involved in motility and virulence. <i>Molecular Microbiology</i> , 2014, 92, 116-137.	1.2	56
43	Quantitative site-specific ADP-ribosylation profiling of DNA-dependent PARPs. <i>DNA Repair</i> , 2015, 30, 68-79.	1.3	56
44	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). <i>BMC Bioinformatics</i> , 2017, 18, 457.	1.2	54
45	Next-generation Interactomics: Considerations for the Use of Co-elution to Measure Protein Interaction Networks. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1-10.	2.5	54
46	Profiling the <i>Escherichia coli</i> membrane protein interactome captured in Peptidisc libraries. <i>ELife</i> , 2019, 8, .	2.8	54
47	The pathogenic <i>Escherichia coli</i> type III secreted protease NleC degrades the host acetyltransferase p300. <i>Cellular Microbiology</i> , 2011, 13, 1542-1557.	1.1	53
48	Outer membrane proteins preferentially load MHC class II peptides: Implications for a <i>Chlamydia trachomatis</i> T cell vaccine. <i>Vaccine</i> , 2015, 33, 2159-2166.	1.7	53
49	Ecological Adaptation of Diverse Honey Bee ( <i>Apis mellifera</i> ) Populations. <i>PLoS ONE</i> , 2010, 5, e11096.	1.1	52
50	Phosphoproteomic Analysis of <i>Salmonella</i> -Infected Cells Identifies Key Kinase Regulators and SopB-Dependent Host Phosphorylation Events. <i>Science Signaling</i> , 2011, 4, rs9.	1.6	52
51	Interactome disassembly during apoptosis occurs independent of caspase cleavage. <i>Molecular Systems Biology</i> , 2017, 13, 906.	3.2	49
52	Identification and Characterization of Arabidopsis Seed Coat Mucilage Proteins. <i>Plant Physiology</i> , 2017, 173, 1059-1074.	2.3	48
53	Secretome profiling of <i>Cryptococcus neoformans</i> reveals regulation of a subset of virulence-associated proteins and potential biomarkers by protein kinase A. <i>BMC Microbiology</i> , 2015, 15, 206.	1.3	47
54	A search for protein biomarkers links olfactory signal transduction to social immunity. <i>BMC Genomics</i> , 2015, 16, 63.	1.2	45

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55	Conserved GTPase LepA (Elongation Factor 4) functions in biogenesis of the 30S subunit of the 70S ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 980-985.	3.3	45
56	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- $\kappa$ B Signaling. <i>Cell Systems</i> , 2017, 5, 564-577.e12.	2.9	44
57	Eukaryotic elongation factor 2 kinase regulates the synthesis of microtubule-related proteins in neurons. <i>Journal of Neurochemistry</i> , 2016, 136, 276-284.	2.1	42
58	The virion of Cafeteria roenbergensis virus (CroV) contains a complex suite of proteins for transcription and DNA repair. <i>Virology</i> , 2014, 466-467, 82-94.	1.1	41
59	The phospho-caveolin-1 scaffolding domain dampens force fluctuations in focal adhesions and promotes cancer cell migration. <i>Molecular Biology of the Cell</i> , 2017, 28, 2190-2201.	0.9	41
60	Peptide biomarkers used for the selective breeding of a complex polygenic trait in honey bees. <i>Scientific Reports</i> , 2017, 7, 8381.	1.6	41
61	tRNA Methylation Is a Global Determinant of Bacterial Multi-drug Resistance. <i>Cell Systems</i> , 2019, 8, 302-314.e8.	2.9	41
62	G3BP1-linked mRNA partitioning supports selective protein synthesis in response to oxidative stress. <i>Nucleic Acids Research</i> , 2020, 48, 6855-6873.	6.5	41
63	Meta-analysis defines principles for the design and analysis of co-fractionation mass spectrometry experiments. <i>Nature Methods</i> , 2021, 18, 806-815.	9.0	40
64	Genomics, transcriptomics and proteomics: enabling insights into social evolution and disease challenges for managed and wild bees. <i>Molecular Ecology</i> , 2017, 26, 718-739.	2.0	39
65	The Worker Honeybee Fat Body Proteome Is Extensively Remodeled Preceding a Major Life-History Transition. <i>PLoS ONE</i> , 2011, 6, e24794.	1.1	38
66	RaftProt: mammalian lipid raft proteome database. <i>Nucleic Acids Research</i> , 2015, 43, D335-D338.	6.5	38
67	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. <i>iScience</i> , 2019, 19, 1114-1132.	1.9	38
68	The 5' Untranslated Region of a Novel Infectious Molecular Clone of the Dicistrovirus Cricket Paralysis Virus Modulates Infection. <i>Journal of Virology</i> , 2015, 89, 5919-5934.	1.5	37
69	p38 MAP kinase-dependent phosphorylation of the Gp78 E3 ubiquitin ligase controls ER-mitochondria association and mitochondria motility. <i>Molecular Biology of the Cell</i> , 2015, 26, 3828-3840.	0.9	37
70	Lipid Raft Proteomics: More than Just Detergent-Resistant Membranes. , 2007, 43, 35-47.		36
71	Global Impact of Salmonella Pathogenicity Island 2-secreted Effectors on the Host Phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1632-1643.	2.5	36
72	A Varroa destructor protein atlas reveals molecular underpinnings of developmental transitions and sexual differentiation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2125-2137.	2.5	35

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73	An integrated global strategy for cell lysis, fractionation, enrichment and mass spectrometric analysis of phosphorylated peptides. <i>Molecular BioSystems</i> , 2010, 6, 822.	2.9	34
74	Genomic data integration systematically biases interactome mapping. <i>PLoS Computational Biology</i> , 2018, 14, e1006474.	1.5	33
75	Integrative Genomics Reveals the Genetics and Evolution of the Honey Bee's Social Immune System. <i>Genome Biology and Evolution</i> , 2019, 11, 937-948.	1.1	33
76	Protein O-linked glycosylation in the plant pathogen <i>Ralstonia solanacearum</i> . <i>Glycobiology</i> , 2016, 26, cwv098.	1.3	32
77	Novel Host Proteins and Signaling Pathways in Enteropathogenic <i>E. coli</i> Pathogenesis Identified by Global Phosphoproteome Analysis *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1927-1945.	2.5	32
78	Potent Human $\alpha$ -Amylase Inhibition by the $\beta$ -Defensin-like Protein Helianthamide. <i>ACS Central Science</i> , 2016, 2, 154-161.	5.3	32
79	Interconnection of post-transcriptional regulation: The RNA-binding protein Hfq is a novel target of the Lon protease in <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 26811.	1.6	31
80	Nanodiscs and SILAC-Based Mass Spectrometry to Identify a Membrane Protein Interactome. <i>Journal of Proteome Research</i> , 2012, 11, 1454-1459.	1.8	30
81	Development of a computational framework for the analysis of protein correlation profiling and spatial proteomics experiments. <i>Journal of Proteomics</i> , 2015, 118, 112-129.	1.2	30
82	A Targeted Proteomics Analysis of Cerebrospinal Fluid after Acute Human Spinal Cord Injury. <i>Journal of Neurotrauma</i> , 2017, 34, 2054-2068.	1.7	30
83	Integrated systems analysis reveals conserved gene networks underlying response to spinal cord injury. <i>ELife</i> , 2018, 7, .	2.8	29
84	Transcriptomic and proteomic host response to <i>Aspergillus fumigatus</i> conidia in an air-liquid interface model of human bronchial epithelium. <i>PLoS ONE</i> , 2018, 13, e0209652.	1.1	29
85	Systems Biology Methods Applied to Blood and Tissue for a Comprehensive Analysis of Immune Response to Hepatitis B Vaccine in Adults. <i>Frontiers in Immunology</i> , 2020, 11, 580373.	2.2	28
86	Trade-offs between sperm viability and immune protein expression in honey bee queens ( <i>Apis mellifera</i> ). <i>Communications Biology</i> , 2021, 4, 48.	2.0	28
87	A general protein O-glycosylation machinery conserved in <i>Burkholderia</i> species improves bacterial fitness and elicits glycan immunogenicity in humans. <i>Journal of Biological Chemistry</i> , 2019, 294, 13248-13268.	1.6	27
88	Tandem Bioorthogonal Labeling Uncovers Endogenous Cotranslationally $\alpha$ -GlcNAc Modified Nascent Proteins. <i>Journal of the American Chemical Society</i> , 2020, 142, 15729-15739.	6.6	27
89	Comprehensive Identification of mRNA-Binding Proteins of <i>Leishmania donovani</i> by Interactome Capture. <i>PLoS ONE</i> , 2017, 12, e0170068.	1.1	26
90	Proteomic analysis of chemosensory organs in the honey bee parasite <i>Varroa destructor</i> : A comprehensive examination of the potential carriers for semiochemicals. <i>Journal of Proteomics</i> , 2018, 181, 131-141.	1.2	26

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91	Feminizer and doublesex knock-outs cause honey bees to switch sexes. <i>PLoS Biology</i> , 2019, 17, e3000256.	2.6	26
92	Dynamic rewiring of the human interactome by interferon signaling. <i>Genome Biology</i> , 2020, 21, 140.	3.8	25
93	Contrasting effects of copper limitation on the photosynthetic apparatus in two strains of the open ocean diatom <i>Thalassiosira oceanica</i> . <i>PLoS ONE</i> , 2017, 12, e0181753.	1.1	24
94	Odorant cues linked to social immunity induce lateralized antenna stimulation in honey bees ( <i>Apis mellifera</i> ). <i>PLoS Biology</i> , 2016, 14, e1002353.	1.6	23
95	Toward an Upgraded Honey Bee ( <i>Apis mellifera</i> L.) Genome Annotation Using Proteogenomics. <i>Journal of Proteome Research</i> , 2016, 15, 411-421.	1.8	22
96	Context-specific interactions in literature-curated protein interaction databases. <i>BMC Genomics</i> , 2018, 19, 758.	1.2	22
97	Prioritization of cell types responsive to biological perturbations in single-cell data with Augur. <i>Nature Protocols</i> , 2021, 16, 3836-3873.	5.5	22
98	Multi-Omic Data Integration Allows Baseline Immune Signatures to Predict Hepatitis B Vaccine Response in a Small Cohort. <i>Frontiers in Immunology</i> , 2020, 11, 578801.	2.2	20
99	Interpretation of Data Underlying the Link Between Colony Collapse Disorder (CCD) and an Invertebrate Iridescent Virus. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006387.	2.5	19
100	A Horizontally Acquired Transcription Factor Coordinates <i>Salmonella</i> Adaptations to Host Microenvironments. <i>MBio</i> , 2014, 5, e01727-14.	1.8	19
101	Identification of MHC-Bound Peptides from Dendritic Cells Infected with <i>Salmonella enterica</i> Strain SL1344: Implications for a Nontyphoidal <i>Salmonella</i> Vaccine. <i>Journal of Proteome Research</i> , 2017, 16, 298-306.	1.8	19
102	Thermal Proteome Profiling Reveals the O-GlcNAc-Dependent Meltome. <i>Journal of the American Chemical Society</i> , 2022, 144, 3833-3842.	6.6	19
103	A Bio-Economic Case Study of Canadian Honey Bee (Hymenoptera: Apidae) Colonies: Marker-Assisted Selection (MAS) in Queen Breeding Affects Beekeeper Profits. <i>Journal of Economic Entomology</i> , 2017, 110, 816-825.	0.8	18
104	Protective Enterotoxigenic <i>Escherichia coli</i> Antigens in a Murine Intranasal Challenge Model. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003924.	1.3	18
105	Protein Correlation Profiling-SILAC to Study Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2014, 1188, 263-270.	0.4	17
106	Dynamics of protein complex components. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 81-85.	2.8	16
107	Differences in larval pesticide tolerance and esterase activity across honey bee ( <i>Apis mellifera</i> ) stocks. <i>Ecotoxicology and Environmental Safety</i> , 2020, 206, 111213.	2.9	16
108	A honey bee ( <i>Apis mellifera</i> L.) PeptideAtlas crossing castes and tissues. <i>BMC Genomics</i> , 2011, 12, 290.	1.2	15

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109	Leishmania donovani chaperonin 10 regulates parasite internalization and intracellular survival in human macrophages. <i>Medical Microbiology and Immunology</i> , 2017, 206, 235-257.	2.6	15
110	Candidate stress biomarkers for queen failure diagnostics. <i>BMC Genomics</i> , 2020, 21, 571.	1.2	15
111	Bicyclic Picomolar OGA Inhibitors Enable Chemoproteomic Mapping of Its Endogenous Post-translational Modifications. <i>Journal of the American Chemical Society</i> , 2022, 144, 832-844.	6.6	15
112	IRES-dependent ribosome repositioning directs translation of a +1 overlapping ORF that enhances viral infection. <i>Nucleic Acids Research</i> , 2018, 46, 11952-11967.	6.5	14
113	Honey Bee Queen Production: Canadian Costing Case Study and Profitability Analysis. <i>Journal of Economic Entomology</i> , 2020, 113, 1618-1627.	0.8	14
114	Proteomic Portraits Reveal Evolutionarily Conserved and Divergent Responses to Spinal Cord Injury. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100096.	2.5	14
115	The parasite <i>Schistocephalus solidus</i> secretes proteins with putative host manipulation functions. <i>Parasites and Vectors</i> , 2021, 14, 436.	1.0	14
116	High throughput strategies for probing the different organizational levels of protein interaction networks. <i>Molecular BioSystems</i> , 2013, 9, 2201.	2.9	13
117	High-Frequency Variation of Purine Biosynthesis Genes Is a Mechanism of Success in <i>Campylobacter jejuni</i> . <i>MBio</i> , 2015, 6, e00612-15.	1.8	13
118	<scp>tRNA</scp> methylation: An unexpected link to bacterial resistance and persistence to antibiotics and beyond. <i>Wiley Interdisciplinary Reviews RNA</i> , 2020, 11, e1609.	3.2	13
119	A Highly Effective Component Vaccine against Nontyphoidal <i>Salmonella enterica</i> Infections. <i>MBio</i> , 2015, 6, e01421-15.	1.8	11
120	Functional Analysis of BipA in <i>E. coli</i> Reveals the Natural Plasticity of 50S Subunit Assembly. <i>Journal of Molecular Biology</i> , 2020, 432, 5259-5272.	2.0	11
121	His-Tagged Peptidiscs Enable Affinity Purification of the Membrane Proteome for Downstream Mass Spectrometry Analysis. <i>Journal of Proteome Research</i> , 2020, 19, 2553-2562.	1.8	11
122	PrInCE: an R/Bioconductor package for protein-protein interaction network inference from co-fractionation mass spectrometry data. <i>Bioinformatics</i> , 2021, 37, 2775-2777.	1.8	11
123	Frequent Assembly of Chimeric Complexes in the Protein Interaction Network of an Interspecies Yeast Hybrid. <i>Molecular Biology and Evolution</i> , 2021, 38, 1384-1401.	3.5	11
124	Cx43-Associated Secretome and Interactome Reveal Synergistic Mechanisms for Glioma Migration and MMP3 Activation. <i>Frontiers in Neuroscience</i> , 2019, 13, 143.	1.4	10
125	Urinary epidermal growth factor is a novel biomarker for early diagnosis of antibody mediated kidney allograft rejection: A urinary proteomics analysis. <i>Journal of Proteomics</i> , 2021, 240, 104208.	1.2	10
126	Honey bee queen health is unaffected by contact exposure to pesticides commonly found in beeswax. <i>Scientific Reports</i> , 2021, 11, 15151.	1.6	10



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127	Jagn1 Is Induced in Response to ER Stress and Regulates Proinsulin Biosynthesis. <i>PLoS ONE</i> , 2016, 11, e0149177.	1.1	10
128	Drone honey bees are disproportionately sensitive to abiotic stressors despite expressing high levels of stress response proteins. <i>Communications Biology</i> , 2022, 5, 141.	2.0	10
129	Where protein structure and cell diversity meet. <i>Trends in Cell Biology</i> , 2022, 32, 996-1007.	3.6	10
130	Response of the honey bee ( <i>Apis mellifera</i> ) proteome to Israeli acute paralysis virus (IAPV) infection. <i>Canadian Journal of Zoology</i> , 2015, 93, 711-720.	0.4	9
131	Comparison of Chlamydia outer membrane complex to recombinant outer membrane proteins as vaccine. <i>Vaccine</i> , 2020, 38, 3280-3291.	1.7	9
132	Transmission of Cricket paralysis virus via exosome-like vesicles during infection of Drosophila cells. <i>Scientific Reports</i> , 2018, 8, 17353.	1.6	8
133	Identification of novel blood biomarkers of treatment response in cystic fibrosis pulmonary exacerbations by label-free quantitative proteomics. <i>Scientific Reports</i> , 2019, 9, 17126.	1.6	8
134	On the Robustness of Graph-Based Clustering to Random Network Alterations. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100002.	2.5	8
135	Caveolin-1 Y14 phosphorylation suppresses tumor growth while promoting invasion. <i>Oncotarget</i> , 2019, 10, 6668-6677.	0.8	8
136	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. <i>SSRN Electronic Journal</i> , 0, , .	0.4	8
137	Using MHC Molecules to Define a Chlamydia T Cell Vaccine. <i>Methods in Molecular Biology</i> , 2016, 1403, 419-432.	0.4	7
138	The application of forensic proteomics to identify an unknown snake venom in a deceased toddler. <i>Forensic Science International</i> , 2021, 323, 110820.	1.3	7
139	Queen honey bees exhibit variable resilience to temperature stress. <i>PLoS ONE</i> , 2021, 16, e0255381.	1.1	7
140	Development of a Method Combining Peptidiscs and Proteomics to Identify, Stabilize, and Purify a Detergent-Sensitive Membrane Protein Assembly. <i>Journal of Proteome Research</i> , 2022, 21, 1748-1758.	1.8	7
141	Proteomic analysis of metabolic pathways supports chloroplast-mitochondria cross-talk in a Cu-limited diatom. <i>Plant Direct</i> , 2022, 6, e376.	0.8	6
142	Discordance in the Epithelial Cell-Dendritic Cell Major Histocompatibility Complex Class II Immunoproteome: Implications for Chlamydia Vaccine Development. <i>Journal of Infectious Diseases</i> , 2020, 221, 841-850.	1.9	5
143	Phenomic analysis of the honey bee pathogen-web and its dynamics on colony productivity, health and social immunity behaviors. <i>PLoS ONE</i> , 2022, 17, e0263273.	1.1	5
144	Identification of protein complexes with quantitative proteomics in <i>S. cerevisiae</i> . <i>Journal of Visualized Experiments</i> , 2009, , .	0.2	3

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145	Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020, 5, .	1.7	3
146	Impacts of COVID-19 on Canadian Beekeeping: Survey Results and a Profitability Analysis. <i>Journal of Economic Entomology</i> , 2021, 114, 2245-2254.	0.8	3
147	At the Intersection of Proteomics and Big Data Science. <i>Clinical Chemistry</i> , 2017, 63, 1663-1663.	1.5	2
148	Nanodisc-Based Proteomics Identify Caj1 as an Hsp40 with Affinity for Phosphatidic Acid Lipids. <i>Journal of Proteome Research</i> , 2021, 20, 4831-4839.	1.8	2
149	The adult mouse proteome. <i>Nature Methods</i> , 2022, 19, 792-793.	9.0	2
150	Effect of Bodily Fluids from Honey Bee ( <i>Apis mellifera</i> ) Larvae on Growth and Genome-Wide Transcriptional Response of the Causal Agent of American Foulbrood Disease ( <i>Paenibacillus larvae</i> ). <i>PLoS ONE</i> , 2014, 9, e89175.	1.1	1
151	â€œControlled, cross-species dataset for exploring biases in genome annotation and modification profilesâ€. <i>Data in Brief</i> , 2015, 5, 829-833.	0.5	0
152	O16.6â€¦Basic science aids syphilis vaccine development: bloodstream spreading by the syphilis spirochete <i>treponema pallidum</i> . , 2019, , .		0
153	Characterizing the Honey Bee Interactome using Mass Spectrometryâ€Based Proteomics. <i>FASEB Journal</i> , 2021, 35, .	0.2	0
154	Whole cell and bacterial movement: The identification of the ubiquitin E2 enzyme (Ube2N) as a novel actinâ€associated protein. <i>FASEB Journal</i> , 2018, 32, 369.4.	0.2	0
155	Proteomic Profiles of <i>Staphylococcus aureus</i> Strains Associated with Subclinical Bovine Mastitis. <i>Current Microbiology</i> , 2022, 79, 101.	1.0	0
156	Heavy metal stress tolerance by <i>Serratia nematodiphila</i> sp. MB307: insights from mass spectrometry based proteomics. <i>Current Proteomics</i> , 2022, 19, .	0.1	0