

Leonard J Foster

List of Publications by Citations

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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.

162
papers

6,590
citations

40
h-index

77
g-index

186
ext. papers

8,032
ext. citations

8.5
avg, IF

5.9
L-index

#	Paper	IF	Citations
162	Unbiased quantitative proteomics of lipid rafts reveals high specificity for signaling factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 5813-8	11.5	743
161	A mammalian organelle map by protein correlation profiling. <i>Cell</i> , 2006 , 125, 187-99	56.2	477
160	Isotopic labeling of terminal amines in complex samples identifies protein N-termini and protease cleavage products. <i>Nature Biotechnology</i> , 2010 , 28, 281-8	44.5	403
159	An exosome-based secretion pathway is responsible for protein export from Leishmania and communication with macrophages. <i>Journal of Cell Science</i> , 2010 , 123, 842-52	5.3	321
158	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014 , 15, 86	4.5	284
157	A high-throughput approach for measuring temporal changes in the interactome. <i>Nature Methods</i> , 2012 , 9, 907-9	21.6	236
156	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 393-403	5.6	225
155	Differential expression profiling of membrane proteins by quantitative proteomics in a human mesenchymal stem cell line undergoing osteoblast differentiation. <i>Stem Cells</i> , 2005 , 23, 1367-77	5.8	175
154	Protein synthesis rate is the predominant regulator of protein expression during differentiation. <i>Molecular Systems Biology</i> , 2013 , 9, 689	12.2	150
153	Quantitative comparison of caste differences in honeybee hemolymph. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 2252-62	7.6	122
152	Reduced Insulin Production Relieves Endoplasmic Reticulum Stress and Induces β Cell Proliferation. <i>Cell Metabolism</i> , 2016 , 23, 179-93	24.6	120
151	Standard methods for molecular research in <i>Apis mellifera</i> . <i>Journal of Apicultural Research</i> , 2013 , 52, 1-54	2	113
150	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	5.6	98
149	The innate immune and systemic response in honey bees to a bacterial pathogen, <i>Paenibacillus</i> larvae. <i>BMC Genomics</i> , 2009 , 10, 387	4.5	95
148	Standard methods for American foulbrood research. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-28	2	76
147	Reduced Circulating Insulin Enhances Insulin Sensitivity in Old Mice and Extends Lifespan. <i>Cell Reports</i> , 2017 , 20, 451-463	10.6	74
146	Polarization of the endoplasmic reticulum by ER-septin tethering. <i>Cell</i> , 2014 , 158, 620-32	56.2	72

145	Mechanisms of stable lipid loss in a social insect. <i>Journal of Experimental Biology</i> , 2011 , 214, 3808-21	3	72
144	Quantitative analysis of proteome coverage and recovery rates for upstream fractionation methods in proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 1902-12	5.6	70
143	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	7.6	68
142	Genetic Dissection of the Type VI Secretion System in <i>Acinetobacter</i> and Identification of a Novel Peptidoglycan Hydrolase, TagX, Required for Its Biogenesis. <i>MBio</i> , 2016 , 7,	7.8	64
141	<i>Acinetobacter</i> strains carry two functional oligosaccharyltransferases, one devoted exclusively to type IV pilin, and the other one dedicated to O-glycosylation of multiple proteins. <i>Molecular Microbiology</i> , 2015 , 96, 1023-41	4.1	59
140	CNS-derived extracellular vesicles from superoxide dismutase 1 (SOD1) ALS mice originate from astrocytes and neurons and carry misfolded SOD1. <i>Journal of Biological Chemistry</i> , 2019 , 294, 3744-3759 ^{5.4}	5.4	59
139	Structure of human ST8SialIII sialyltransferase provides insight into cell-surface polysialylation. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 627-35	17.6	55
138	Sequestosome-1/p62 is the key intracellular target of innate defense regulator peptide. <i>Journal of Biological Chemistry</i> , 2009 , 284, 36007-36011	5.4	54
137	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	18.3	53
136	Changes in protein expression during honey bee larval development. <i>Genome Biology</i> , 2008 , 9, R156	18.3	53
135	Catabolism of the Last Two Steroid Rings in and Other Bacteria. <i>MBio</i> , 2017 , 8,	7.8	50
134	The pathogenic <i>E. coli</i> type III effector EspZ interacts with host CD98 and facilitates host cell prosurvival signalling. <i>Cellular Microbiology</i> , 2010 , 12, 1322-39	3.9	49
133	Evaluating measures of association for single-cell transcriptomics. <i>Nature Methods</i> , 2019 , 16, 381-386	21.6	46
132	Quantitative site-specific ADP-ribosylation profiling of DNA-dependent PARPs. <i>DNA Repair</i> , 2015 , 30, 68-79	4.3	46
131	The pathogenic <i>Escherichia coli</i> type III secreted protease NleC degrades the host acetyltransferase p300. <i>Cellular Microbiology</i> , 2011 , 13, 1542-57	3.9	46
130	hnRNP K coordinates transcriptional silencing by SETDB1 in embryonic stem cells. <i>PLoS Genetics</i> , 2015 , 11, e1004933	6	45
129	Outer membrane proteins preferentially load MHC class II peptides: implications for a <i>Chlamydia trachomatis</i> T cell vaccine. <i>Vaccine</i> , 2015 , 33, 2159-66	4.1	45
128	Biomarkers for severity of spinal cord injury in the cerebrospinal fluid of rats. <i>PLoS ONE</i> , 2011 , 6, e19247 ^{3.7}	3.7	45

127	Diversity within the O-linked protein glycosylation systems of acinetobacter species. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2354-70	7.6	44
126	Ecological adaptation of diverse honey bee (<i>Apis mellifera</i>) populations. <i>PLoS ONE</i> , 2010 , 5, e11096	3.7	43
125	A general protein O-glycosylation system within the Burkholderia cepacia complex is involved in motility and virulence. <i>Molecular Microbiology</i> , 2014 , 92, 116-37	4.1	42
124	Honey bee protein atlas at organ-level resolution. <i>Genome Research</i> , 2013 , 23, 1951-60	9.7	42
123	Phosphoproteomic analysis of Salmonella-infected cells identifies key kinase regulators and SopB-dependent host phosphorylation events. <i>Science Signaling</i> , 2011 , 4, rs9	8.8	42
122	A death pheromone, oleic acid, triggers hygienic behavior in honey bees (<i>Apis mellifera</i> L.). <i>Scientific Reports</i> , 2018 , 8, 5719	4.9	40
121	Salmonella Rapidly Regulates Membrane Permeability To Survive Oxidative Stress. <i>MBio</i> , 2016 , 7,	7.8	40
120	Interactome disassembly during apoptosis occurs independent of caspase cleavage. <i>Molecular Systems Biology</i> , 2017 , 13, 906	12.2	37
119	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- κ B Signaling. <i>Cell Systems</i> , 2017 , 5, 564-577.e12	10.6	37
118	Clptm1 Limits Forward Trafficking of GABA Receptors to Scale Inhibitory Synaptic Strength. <i>Neuron</i> , 2018 , 97, 596-610.e8	13.9	35
117	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). <i>BMC Bioinformatics</i> , 2017 , 18, 457	3.6	34
116	The worker honeybee fat body proteome is extensively remodeled preceding a major life-history transition. <i>PLoS ONE</i> , 2011 , 6, e24794	3.7	34
115	Identification and Characterization of Arabidopsis Seed Coat Mucilage Proteins. <i>Plant Physiology</i> , 2017 , 173, 1059-1074	6.6	33
114	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	4.5	33
113	RaftProt: mammalian lipid raft proteome database. <i>Nucleic Acids Research</i> , 2015 , 43, D335-8	20.1	32
112	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	11.5	31
111	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, 3828-40	3.5	31
110	Lipid raft proteomics: more than just detergent-resistant membranes. <i>Sub-Cellular Biochemistry</i> , 2007 , 43, 35-47	5.5	31

109	A search for protein biomarkers links olfactory signal transduction to social immunity. <i>BMC Genomics</i> , 2015 , 16, 63	4.5	30
108	Eukaryotic elongation factor 2 kinase regulates the synthesis of microtubule-related proteins in neurons. <i>Journal of Neurochemistry</i> , 2016 , 136, 276-84	6	29
107	Profiling the membrane protein interactome captured in Peptidisc libraries. <i>ELife</i> , 2019 , 8,	8.9	29
106	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	3.5	28
105	Global impact of Salmonella pathogenicity island 2-secreted effectors on the host phosphoproteome. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 1632-43	7.6	28
104	An integrated global strategy for cell lysis, fractionation, enrichment and mass spectrometric analysis of phosphorylated peptides. <i>Molecular BioSystems</i> , 2010 , 6, 822-9		28
103	Cell type prioritization in single-cell data. <i>Nature Biotechnology</i> , 2021 , 39, 30-34	44.5	27
102	Peptide biomarkers used for the selective breeding of a complex polygenic trait in honey bees. <i>Scientific Reports</i> , 2017 , 7, 8381	4.9	25
101	A protein atlas reveals molecular underpinnings of developmental transitions and sexual differentiation. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 2125-2137	7.6	25
100	Novel Host Proteins and Signaling Pathways in Enteropathogenic E. coli Pathogenesis Identified by Global Phosphoproteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1927-45	7.6	25
99	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	7.6	25
98	Development of a computational framework for the analysis of protein correlation profiling and spatial proteomics experiments. <i>Journal of Proteomics</i> , 2015 , 118, 112-29	3.9	24
97	Vulnerability of honey bee queens to heat-induced loss of fertility. <i>Nature Sustainability</i> , 2020 , 3, 367-376	62.1	24
96	Potent Human α -Amylase Inhibition by the β -Defensin-like Protein Helianthamide. <i>ACS Central Science</i> , 2016 , 2, 154-161	16.8	24
95	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	3.6	24
94	Nanodiscs and SILAC-based mass spectrometry to identify a membrane protein interactome. <i>Journal of Proteome Research</i> , 2012 , 11, 1454-9	5.6	24
93	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	3.9	24
92	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, 5919-34	6.6	22

91	Comprehensive Identification of mRNA-Binding Proteins of <i>Leishmania donovani</i> by Interactome Capture. <i>PLoS ONE</i> , 2017 , 12, e0170068	3.7	21
90	Protein O-linked glycosylation in the plant pathogen <i>Ralstonia solanacearum</i> . <i>Glycobiology</i> , 2016 , 26, 301-11	5.8	21
89	A Targeted Proteomics Analysis of Cerebrospinal Fluid after Acute Human Spinal Cord Injury. <i>Journal of Neurotrauma</i> , 2017 , 34, 2054-2068	5.4	20
88	tRNA Methylation Is a Global Determinant of Bacterial Multi-drug Resistance. <i>Cell Systems</i> , 2019 , 8, 302-314.e820	10.6	20
87	Genomic data integration systematically biases interactome mapping. <i>PLoS Computational Biology</i> , 2018 , 14, e1006474	5	20
86	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	3.7	19
85	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	7.6	18
84	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. <i>iScience</i> , 2019 , 19, 1114-1132	6.1	17
83	Protective Enterotoxigenic <i>Escherichia coli</i> Antigens in a Murine Intranasal Challenge Model. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003924	4.8	17
82	Integrated systems analysis reveals conserved gene networks underlying response to spinal cord injury. <i>ELife</i> , 2018 , 7,	8.9	17
81	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	5.7	16
80	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	3.9	16
79	A general protein glycosylation machinery conserved in species improves bacterial fitness and elicits glycan immunogenicity in humans. <i>Journal of Biological Chemistry</i> , 2019 , 294, 13248-13268	5.4	16
78	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	4.9	16
77	Toward an Upgraded Honey Bee (<i>Apis mellifera</i> L.) Genome Annotation Using Proteogenomics. <i>Journal of Proteome Research</i> , 2016 , 15, 411-21	5.6	15
76	Odorant cues linked to social immunity induce lateralized antenna stimulation in honey bees (<i>Apis mellifera</i> L.). <i>Scientific Reports</i> , 2017 , 7, 46171	4.9	15
75	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	5.6	15
74	A horizontally acquired transcription factor coordinates <i>Salmonella</i> adaptations to host microenvironments. <i>MBio</i> , 2014 , 5, e01727-14	7.8	15

73	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	3.7	15
72	Tandem Bioorthogonal Labeling Uncovers Endogenous Cotranslationally -GlcNAc Modified Nascent Proteins. <i>Journal of the American Chemical Society</i> , 2020 , 142, 15729-15739	16.4	15
71	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	2.2	14
70	G3BP1-linked mRNA partitioning supports selective protein synthesis in response to oxidative stress. <i>Nucleic Acids Research</i> , 2020 , 48, 6855-6873	20.1	14
69	Feminizer and doublesex knock-outs cause honey bees to switch sexes. <i>PLoS Biology</i> , 2019 , 17, e3000256	9.7	13
68	A honey bee (<i>Apis mellifera</i> L.) PeptideAtlas crossing castes and tissues. <i>BMC Genomics</i> , 2011 , 12, 290	4.5	13
67	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		13
66	Context-specific interactions in literature-curated protein interaction databases. <i>BMC Genomics</i> , 2018 , 19, 758	4.5	13
65	Dynamic rewiring of the human interactome by interferon signaling. <i>Genome Biology</i> , 2020 , 21, 140	18.3	12
64	<i>Leishmania donovani</i> chaperonin 10 regulates parasite internalization and intracellular survival in human macrophages. <i>Medical Microbiology and Immunology</i> , 2017 , 206, 235-257	4	11
63	Protein correlation profiling-SILAC to study protein-protein interactions. <i>Methods in Molecular Biology</i> , 2014 , 1188, 263-70	1.4	11
62	High throughput strategies for probing the different organizational levels of protein interaction networks. <i>Molecular BioSystems</i> , 2013 , 9, 2201-12		10
61	A Highly Effective Component Vaccine against Nontyphoidal <i>Salmonella enterica</i> Infections. <i>MBio</i> , 2015 , 6, e01421-15	7.8	10
60	Dynamics of protein complex components. <i>Current Opinion in Chemical Biology</i> , 2019 , 48, 81-85	9.7	10
59	Cx43-Associated Secretome and Interactome Reveal Synergistic Mechanisms for Glioma Migration and MMP3 Activation. <i>Frontiers in Neuroscience</i> , 2019 , 13, 143	5.1	9
58	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	1.5	9
57	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	8.4	9
56	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. <i>SSRN Electronic Journal</i> ,	1	8

55	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	8.4	8
54	Trade-offs between sperm viability and immune protein expression in honey bee queens (<i>Apis mellifera</i>). <i>Communications Biology</i> , 2021 , 4, 48	6.7	8
53	High-Frequency Variation of Purine Biosynthesis Genes Is a Mechanism of Success in <i>Campylobacter jejuni</i> . <i>MBio</i> , 2015 , 6, e00612-15	7.8	7
52	An atlas of protein-protein interactions across mammalian tissues		7
51	Candidate stress biomarkers for queen failure diagnostics. <i>BMC Genomics</i> , 2020 , 21, 571	4.5	7
50	Using MHC Molecules to Define a Chlamydia T Cell Vaccine. <i>Methods in Molecular Biology</i> , 2016 , 1403, 419-32	1.4	7
49	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	4.9	7
48	IRES-dependent ribosome repositioning directs translation of a +1 overlapping ORF that enhances viral infection. <i>Nucleic Acids Research</i> , 2018 , 46, 11952-11967	20.1	7
47	An atlas of protein-protein interactions across mouse tissues. <i>Cell</i> , 2021 , 184, 4073-4089.e17	56.2	7
46	Honey Bee Queen Production: Canadian Costing Case Study and Profitability Analysis. <i>Journal of Economic Entomology</i> , 2020 , 113, 1618-1627	2.2	6
45	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	6.5	6
44	Meta-analysis defines principles for the design and analysis of co-fractionation mass spectrometry experiments. <i>Nature Methods</i> , 2021 , 18, 806-815	21.6	6
43	tRNA methylation: An unexpected link to bacterial resistance and persistence to antibiotics and beyond. <i>Wiley Interdisciplinary Reviews RNA</i> , 2020 , 11, e1609	9.3	5
42	Comparison of Chlamydia outer membrane complex to recombinant outer membrane proteins as vaccine. <i>Vaccine</i> , 2020 , 38, 3280-3291	4.1	5
41	Jagn1 Is Induced in Response to ER Stress and Regulates Proinsulin Biosynthesis. <i>PLoS ONE</i> , 2016 , 11, e0149177	3.7	5
40	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	7	5
39	Caveolin-1 Y14 phosphorylation suppresses tumor growth while promoting invasion. <i>Oncotarget</i> , 2019 , 10, 6668-6677	3.3	4
38	Bicyclic Picomolar OGA Inhibitors Enable Chemoproteomic Mapping of Its Endogenous Post-translational Modifications.. <i>Journal of the American Chemical Society</i> , 2022 ,	16.4	4

37	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	8.3	4
36	Prioritization of cell types responsive to biological perturbations in single-cell data with Augur. <i>Nature Protocols</i> , 2021 , 16, 3836-3873	18.8	4
35	Proteomic Portraits Reveal Evolutionarily Conserved and Divergent Responses to Spinal Cord Injury. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100096	7.6	4
34	Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020 , 5,	7.6	3
33	Expression biomarkers used for the selective breeding of complex polygenic traits		3
32	Honey bee queen health is unaffected by contact exposure to pesticides commonly found in beeswax. <i>Scientific Reports</i> , 2021 , 11, 15151	4.9	3
31	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	7	3
30	On the Robustness of Graph-Based Clustering to Random Network Alterations. <i>Molecular and Cellular Proteomics</i> , 2020 , 20, 100002	7.6	3
29	PrInCE: an R/bioconductor package for protein-protein interaction network inference from co-fractionation mass spectrometry data. <i>Bioinformatics</i> , 2021 ,	7.2	3
28	Transmission of Cricket paralysis virus via exosome-like vesicles during infection of Drosophila cells. <i>Scientific Reports</i> , 2018 , 8, 17353	4.9	3
27	At the Intersection of Proteomics and Big Data Science. <i>Clinical Chemistry</i> , 2017 , 63, 1663	5.5	2
26	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	5.6	2
25	Identification of protein complexes with quantitative proteomics in <i>S. cerevisiae</i> . <i>Journal of Visualized Experiments</i> , 2009 ,	1.6	2
24	Cell type prioritization in single-cell data		2
23	Proteomic analysis of chemosensory organs in the honey bee parasite <i>Varroa destructor</i> : a comprehensive examination of the potential carriers for semiochemicals		2
22	Honey bee queens are vulnerable to heat-induced loss of fertility		2
21	Dynamic rewiring of the human interactome by interferon signalling		2
20	A Deep Generative Model Enables Automated Structure Elucidation of Novel Psychoactive Substances		2

19	The application of forensic proteomics to identify an unknown snake venom in a deceased toddler. <i>Forensic Science International</i> , 2021 , 323, 110820	2.6	2
18	Impacts of COVID-19 on Canadian Beekeeping: Survey Results and a Profitability Analysis. <i>Journal of Economic Entomology</i> , 2021 , 114, 2245-2254	2.2	2
17	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	3.7	1
16	The parasite <i>Schistocephalus solidus</i> secretes proteins with putative host manipulation functions		1
15	Frequent assembly of chimeric complexes in the protein interaction network of an interspecies yeast hybrid		1
14	Odorant cues linked to social immunity induce lateralized antenna stimulation in honey bees (<i>Apis mellifera</i> L.)		1
13	A rapid and accurate approach for Prediction of interactomes from co-elution data (PrInCE)		1
12	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	3.9	1
11	Queen honey bees exhibit variable resilience to temperature stress. <i>PLoS ONE</i> , 2021 , 16, e0255381	3.7	1
10	Proteomic portraits reveal evolutionarily conserved and divergent responses to spinal cord injury		1
9	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	3.7	0
8	Proteomic analysis of metabolic pathways supports chloroplast-mitochondria cross-talk in a Cu-limited diatom.. <i>Plant Direct</i> , 2022 , 6, e376	3.3	0
7	The parasite <i>Schistocephalus solidus</i> secretes proteins with putative host manipulation functions. <i>Parasites and Vectors</i> , 2021 , 14, 436	4	0
6	Nanodisc-Based Proteomics Identify Caj1 as an Hsp40 with Affinity for Phosphatidic Acid Lipids. <i>Journal of Proteome Research</i> , 2021 , 20, 4831-4839	5.6	0
5	Drone honey bees are disproportionately sensitive to abiotic stressors despite expressing high levels of stress response proteins.. <i>Communications Biology</i> , 2022 , 5, 141	6.7	0
4	"Controlled, cross-species dataset for exploring biases in genome annotation and modification profiles". <i>Data in Brief</i> , 2015 , 5, 829-33	1.2	
3	Proteomic Profiles of <i>Staphylococcus aureus</i> Strains Associated with Subclinical Bovine Mastitis.. <i>Current Microbiology</i> , 2022 , 79, 101	2.4	
2	Whole cell and bacterial movement: The identification of the ubiquitin E2 enzyme (Ube2N) as a novel actin-associated protein. <i>FASEB Journal</i> , 2018 , 32, 369.4	0.9	

1 Lipid Rafts61-70