Leonard J Foster

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.

162
papers6,590
citations40
h-index77
g-index186
ext. papers8,032
ext. citations8.5
avg, IF5.9
L-index

#	Paper	IF	Citations
162	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	Ο
161	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
160	Proteomic Profiles of Staphylococcus aureus Strains Associated with Subclinical Bovine Mastitis <i>Current Microbiology</i> , 2022 , 79, 101	2.4	
159	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
158	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	O
157	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
156	Subcellular proteomics. Nature Reviews Methods Primers, 2021, 1,		13
155	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
154	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
153	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
152	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
151	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
150	Cell type prioritization in single-cell data. <i>Nature Biotechnology</i> , 2021 , 39, 30-34	44.5	27
149	PrInCE: an R/bioconductor package for protein-protein interaction network inference from co-fractionation mass spectrometry data. <i>Bioinformatics</i> , 2021 ,	7.2	3
148	Proteomic Portraits Reveal Evolutionarily Conserved and Divergent Responses to Spinal Cord Injury. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100096	7.6	4
147	Trade-offs between sperm viability and immune protein expression in honey bee queens (Apis mellifera). <i>Communications Biology</i> , 2021 , 4, 48	6.7	8
146	An atlas of protein-protein interactions across mouse tissues. <i>Cell</i> , 2021 , 184, 4073-4089.e17	56.2	7

145	Queen honey bees exhibit variable resilience to temperature stress. PLoS ONE, 2021, 16, e0255381	3.7	1
144	The parasite Schistocephalus solidus secretes proteins with putative host manipulation functions. <i>Parasites and Vectors</i> , 2021 , 14, 436	4	O
143	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
142	Nanodisc-Based Proteomics Identify Caj1 as an Hsp40 with Affinity for Phosphatidic Acid Lipids. Journal of Proteome Research, 2021 , 20, 4831-4839	5.6	О
141	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
140	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
139	Dynamic rewiring of the human interactome by interferon signaling. <i>Genome Biology</i> , 2020 , 21, 140	18.3	12
138	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
137	Honey Bee Queen Production: Canadian Costing Case Study and Profitability Analysis. <i>Journal of Economic Entomology</i> , 2020 , 113, 1618-1627	2.2	6
136	Vulnerability of honey bee queens to heat-induced loss of fertility. <i>Nature Sustainability</i> , 2020 , 3, 367-3	76 2.1	24
136	Vulnerability of honey bee queens to heat-induced loss of fertility. <i>Nature Sustainability</i> , 2020 , 3, 367-3 Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020 , 5,	76 2.1	3
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135	Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020 , 5, Next-generation Interactomics: Considerations for the Use of Co-elution to Measure Protein	7.6	3
135	Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020 , 5, 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 Comparison of Chlamydia outer membrane complex to recombinant outer membrane proteins as	7.6 7.6	3 25
135 134 133	Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020 , 5, 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 Comparison of Chlamydia outer membrane complex to recombinant outer membrane proteins as vaccine. <i>Vaccine</i> , 2020 , 38, 3280-3291 Differences in larval pesticide tolerance and esterase activity across honey bee (Apis mellifera)	7.6 7.6 4.1	3 25 5
135 134 133	Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020 , 5, 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 Comparison of Chlamydia outer membrane complex to recombinant outer membrane proteins as vaccine. <i>Vaccine</i> , 2020 , 38, 3280-3291 Differences in larval pesticide tolerance and esterase activity across honey bee (Apis mellifera) stocks. <i>Ecotoxicology and Environmental Safety</i> , 2020 , 206, 111213 Systems Biology Methods Applied to Blood and Tissue for a Comprehensive Analysis of Immune	7.6 7.6 4.1	3 25 5
135 134 133 132	Master Sculptor at Work: Enteropathogenic Escherichia coli Infection Uniquely Modifies Mitochondrial Proteolysis during Its Control of Human Cell Death. <i>MSystems</i> , 2020 , 5, 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 Comparison of Chlamydia outer membrane complex to recombinant outer membrane proteins as vaccine. <i>Vaccine</i> , 2020 , 38, 3280-3291 Differences in larval pesticide tolerance and esterase activity across honey bee (Apis mellifera) stocks. <i>Ecotoxicology and Environmental Safety</i> , 2020 , 206, 111213 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 Functional Analysis of BipA in E. coli Reveals the Natural Plasticity of 50S Subunit Assembly. <i>Journal</i>	7.6 7.6 4.1 7	3 25 5 5 8

127	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
126	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
125	On the Robustness of Graph-Based Clustering to Random Network Alterations. <i>Molecular and Cellular Proteomics</i> , 2020 , 20, 100002	7.6	3
124	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
123	Feminizer and doublesex knock-outs cause honey bees to switch sexes. <i>PLoS Biology</i> , 2019 , 17, e300025	5 6 .7	13
122	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
121	Evaluating measures of association for single-cell transcriptomics. <i>Nature Methods</i> , 2019 , 16, 381-386	21.6	46
120	tRNA Methylation Is a Global Determinant of Bacterial Multi-drug Resistance. <i>Cell Systems</i> , 2019 , 8, 302	- 3 046e	820
119	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
118	Caveolin-1 Y14 phosphorylation suppresses tumor growth while promoting invasion. <i>Oncotarget</i> , 2019 , 10, 6668-6677	3.3	4
117	Profiling the membrane protein interactome captured in Peptidisc libraries. <i>ELife</i> , 2019 , 8,	8.9	29
116	Integrative Genomics Reveals the Genetics and Evolution of the Honey Beeß Social Immune System. <i>Genome Biology and Evolution</i> , 2019 , 11, 937-948	3.9	24
115	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
114	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, 3744-375	95.4	59
113	Dynamics of protein complex components. <i>Current Opinion in Chemical Biology</i> , 2019 , 48, 81-85	9.7	10
112	A death pheromone, oleic acid, triggers hygienic behavior in honey bees (Apis mellifera L.). <i>Scientific Reports</i> , 2018 , 8, 5719	4.9	40
111	Proteomic analysis of chemosensory organs in the honey bee parasite Varroa destructor: A comprehensive examination of the potential carriers for semiochemicals. <i>Journal of Proteomics</i> , 2018 , 181, 131-141	3.9	16
110	Clptm1 Limits Forward Trafficking of GABA Receptors to Scale Inhibitory Synaptic Strength. <i>Neuron</i> , 2018 , 97, 596-610.e8	13.9	35

(2017-2018)

109	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	
108	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
107	Context-specific interactions in literature-curated protein interaction databases. <i>BMC Genomics</i> , 2018 , 19, 758	4.5	13
106	Integrated systems analysis reveals conserved gene networks underlying response to spinal cord injury. <i>ELife</i> , 2018 , 7,	8.9	17
105	Transmission of Cricket paralysis virus via exosome-like vesicles during infection of Drosophila cells. <i>Scientific Reports</i> , 2018 , 8, 17353	4.9	3
104	Transcriptomic and proteomic host response to Aspergillus fumigatus conidia in an air-liquid interface model of human bronchial epithelium. <i>PLoS ONE</i> , 2018 , 13, e0209652	3.7	19
103	Genomic data integration systematically biases interactome mapping. <i>PLoS Computational Biology</i> , 2018 , 14, e1006474	5	20
102	Interactome disassembly during apoptosis occurs independent of caspase cleavage. <i>Molecular Systems Biology</i> , 2017 , 13, 906	12.2	37
101	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
100	Identification and Characterization of Arabidopsis Seed Coat Mucilage Proteins. <i>Plant Physiology</i> , 2017 , 173, 1059-1074	6.6	33
99	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
98	Leishmania donovani chaperonin 10 regulates parasite internalization and intracellular survival in human macrophages. <i>Medical Microbiology and Immunology</i> , 2017 , 206, 235-257	4	11
97	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
96	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
95	Catabolism of the Last Two Steroid Rings in and Other Bacteria. MBio, 2017, 8,	7.8	50
94	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
93	At the Intersection of Proteomics and Big Data Science. Clinical Chemistry, 2017, 63, 1663	5.5	2
92	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

91	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
90	Comprehensive Identification of mRNA-Binding Proteins of Leishmania donovani by Interactome Capture. <i>PLoS ONE</i> , 2017 , 12, e0170068	3.7	21
89	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). <i>BMC Bioinformatics</i> , 2017 , 18, 457	3.6	34
88	Odorant cues linked to social immunity induce lateralized antenna stimulation in honey bees (Apis mellifera L.). <i>Scientific Reports</i> , 2017 , 7, 46171	4.9	15
87	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- B Signaling. <i>Cell Systems</i> , 2017 , 5, 564-577.e12	10.6	37
86	Reduced Circulating Insulin Enhances Insulin Sensitivity in Old Mice and Extends Lifespan. <i>Cell Reports</i> , 2017 , 20, 451-463	10.6	74
85	Identification of MHC-Bound Peptides from Dendritic Cells Infected with Salmonella enterica Strain SL1344: Implications for a Nontyphoidal Salmonella Vaccine. <i>Journal of Proteome Research</i> , 2017 , 16, 298-306	5.6	15
84	Contrasting effects of copper limitation on the photosynthetic apparatus in two strains of the open ocean diatom Thalassiosira oceanica. <i>PLoS ONE</i> , 2017 , 12, e0181753	3.7	15
83	Salmonella Rapidly Regulates Membrane Permeability To Survive Oxidative Stress. <i>MBio</i> , 2016 , 7,	7.8	40
82	Genetic Dissection of the Type VI Secretion System in Acinetobacter and Identification of a Novel Peptidoglycan Hydrolase, TagX, Required for Its Biogenesis. <i>MBio</i> , 2016 , 7,	7.8	64
81	Potent Human EAmylase Inhibition by the EDefensin-like Protein Helianthamide. <i>ACS Central Science</i> , 2016 , 2, 154-161	16.8	24
80	Toward an Upgraded Honey Bee (Apis mellifera L.) Genome Annotation Using Proteogenomics. Journal of Proteome Research, 2016 , 15, 411-21	5.6	15
79	Reduced Insulin Production Relieves Endoplasmic Reticulum Stress and Induces © Ell Proliferation. <i>Cell Metabolism</i> , 2016 , 23, 179-93	24.6	120
78	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
77	Protein O-linked glycosylation in the plant pathogen Ralstonia solanacearum. <i>Glycobiology</i> , 2016 , 26, 301-11	5.8	21
76	Jagn1 Is Induced in Response to ER Stress and Regulates Proinsulin Biosynthesis. <i>PLoS ONE</i> , 2016 , 11, e0149177	3.7	5
75	Interconnection of post-transcriptional regulation: The RNA-binding protein Hfq is a novel target of the Lon protease in Pseudomonas aeruginosa. <i>Scientific Reports</i> , 2016 , 6, 26811	4.9	16
74	Using MHC Molecules to Define a Chlamydia T Cell Vaccine. <i>Methods in Molecular Biology</i> , 2016 , 1403, 419-32	1.4	7

(2014-2015)

73	A search for protein biomarkers links olfactory signal transduction to social immunity. <i>BMC Genomics</i> , 2015 , 16, 63	4.5	30
72	Structure of human ST8SiaIII sialyltransferase provides insight into cell-surface polysialylation. Nature Structural and Molecular Biology, 2015 , 22, 627-35	17.6	55
71	hnRNP K coordinates transcriptional silencing by SETDB1 in embryonic stem cells. <i>PLoS Genetics</i> , 2015 , 11, e1004933	6	45
70	Outer membrane proteins preferentially load MHC class II peptides: implications for a Chlamydia trachomatis T cell vaccine. <i>Vaccine</i> , 2015 , 33, 2159-66	4.1	45
69	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
68	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
67	Quantitative site-specific ADP-ribosylation profiling of DNA-dependent PARPs. <i>DNA Repair</i> , 2015 , 30, 68-79	4.3	46
66	The 5Runtranslated 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
65	Response of the honey bee (Apis mellifera) proteome to Israeli acute paralysis virus (IAPV) infection. <i>Canadian Journal of Zoology</i> , 2015 , 93, 711-720	1.5	9
64	High-Frequency Variation of Purine Biosynthesis Genes Is a Mechanism of Success in Campylobacter jejuni. <i>MBio</i> , 2015 , 6, e00612-15	7.8	7
63	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
62	RaftProt: mammalian lipid raft proteome database. <i>Nucleic Acids Research</i> , 2015 , 43, D335-8	20.1	32
61	"Controlled, cross-species dataset for exploring biases in genome annotation and modification profiles". <i>Data in Brief</i> , 2015 , 5, 829-33	1.2	
60	Secretome profiling of Cryptococcus neoformans 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
59	A Highly Effective Component Vaccine against Nontyphoidal Salmonella enterica Infections. <i>MBio</i> , 2015 , 6, e01421-15	7.8	10
58	Acinetobacter 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
57	Protective Enterotoxigenic Escherichia coli Antigens in a Murine Intranasal Challenge Model. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003924	4.8	17
56	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014 , 15, 86	4.5	284

55	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
54	Diversity within the O-linked protein glycosylation systems of acinetobacter species. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2354-70	7.6	44
53	Polarization of the endoplasmic reticulum by ER-septin tethering. <i>Cell</i> , 2014 , 158, 620-32	56.2	72
52	Effect of bodily fluids from honey bee (Apis mellifera) larvae on growth and genome-wide transcriptional response of the causal agent of American Foulbrood disease (Paenibacillus larvae). <i>PLoS ONE</i> , 2014 , 9, e89175	3.7	1
51	A horizontally acquired transcription factor coordinates Salmonella adaptations to host microenvironments. <i>MBio</i> , 2014 , 5, e01727-14	7.8	15
50	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
49	Protein correlation profiling-SILAC to study protein-protein interactions. <i>Methods in Molecular Biology</i> , 2014 , 1188, 263-70	1.4	11
48	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
47	Honey bee protein atlas at organ-level resolution. <i>Genome Research</i> , 2013 , 23, 1951-60	9.7	42
46	High throughput strategies for probing the different organizational levels of protein interaction networks. <i>Molecular BioSystems</i> , 2013 , 9, 2201-12		10
46 45		2	10
	networks. <i>Molecular BioSystems</i> , 2013 , 9, 2201-12 Standard methods for molecular research in Apis mellifera. <i>Journal of Apicultural Research</i> , 2013 ,	2	
45	networks. <i>Molecular BioSystems</i> , 2013 , 9, 2201-12 Standard methods for molecular research in Apis mellifera. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-54		113
45 44	networks. <i>Molecular BioSystems</i> , 2013 , 9, 2201-12 Standard methods for molecular research in Apis mellifera. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-54 Standard methods for American foulbrood research. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-28 Protein synthesis rate is the predominant regulator of protein expression during differentiation.	2	113 76
45 44 43	Standard methods for molecular research in Apis mellifera. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-54 Standard methods for American foulbrood research. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-28 Protein synthesis rate is the predominant regulator of protein expression during differentiation. <i>Molecular Systems Biology</i> , 2013 , 9, 689 A high-throughput approach for measuring temporal changes in the interactome. <i>Nature Methods</i> ,	2	113 76 150
45 44 43 42	Standard methods for molecular research in Apis mellifera. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-54 Standard methods for American foulbrood research. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-28 Protein synthesis rate is the predominant regulator of protein expression during differentiation. <i>Molecular Systems Biology</i> , 2013 , 9, 689 A high-throughput approach for measuring temporal changes in the interactome. <i>Nature Methods</i> , 2012 , 9, 907-9 Correlation of proteome-wide changes with social immunity behaviors provides insight into resistance to the parasitic mite, Varroa destructor, in the honey bee (Apis mellifera). <i>Genome</i>	2 12.2 21.6	113 76 150 236
45 44 43 42 41	Standard methods for molecular research in Apis mellifera. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-54 Standard methods for American foulbrood research. <i>Journal of Apicultural Research</i> , 2013 , 52, 1-28 Protein synthesis rate is the predominant regulator of protein expression during differentiation. <i>Molecular Systems Biology</i> , 2013 , 9, 689 A high-throughput approach for measuring temporal changes in the interactome. <i>Nature Methods</i> , 2012 , 9, 907-9 Correlation of proteome-wide changes with social immunity behaviors provides insight into resistance to the parasitic mite, Varroa destructor, in the honey bee (Apis mellifera). <i>Genome Biology</i> , 2012 , 13, R81 Nanodiscs and SILAC-based mass spectrometry to identify a membrane protein interactome.	2 12.2 21.6 18.3	113 76 150 236

(2007-2011)

37	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
36	The pathogenic Escherichia coli type III secreted protease NleC degrades the host acetyltransferase p300. <i>Cellular Microbiology</i> , 2011 , 13, 1542-57	3.9	46
35	A honey bee (Apis mellifera L.) PeptideAtlas crossing castes and tissues. <i>BMC Genomics</i> , 2011 , 12, 290	4.5	13
34	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
33	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
32	Biomarkers for severity of spinal cord injury in the cerebrospinal fluid of rats. <i>PLoS ONE</i> , 2011 , 6, e1924	73.7	45
31	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
30	The pathogenic E. coli 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
29	Ecological adaptation of diverse honey bee (Apis mellifera) populations. <i>PLoS ONE</i> , 2010 , 5, e11096	3.7	43
28	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 393-403	5.6	225
27	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
26	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
25	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
24	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
23	The innate immune and systemic response in honey bees to a bacterial pathogen, Paenibacillus larvae. <i>BMC Genomics</i> , 2009 , 10, 387	4.5	95
22	Identification of protein complexes with quantitative proteomics in S. cerevisiae. <i>Journal of Visualized Experiments</i> , 2009 ,	1.6	2
21	Changes in protein expression during honey bee larval development. <i>Genome Biology</i> , 2008 , 9, R156	18.3	53
20	Lipid raft proteomics: more than just detergent-resistant membranes. <i>Sub-Cellular Biochemistry</i> , 2007 , 43, 35-47	5.5	31

19	Quantitative comparison of caste differences in honeybee hemolymph. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 2252-62	7.6	122
18	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
17	A mammalian organelle map by protein correlation profiling. <i>Cell</i> , 2006 , 125, 187-99	56.2	477
16	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
15	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
14	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. SSRN Electronic Journal,	1	8
13	Cell type prioritization in single-cell data		2
12	Expression biomarkers used for the selective breeding of complex polygenic traits		3
11	The parasite Schistocephalus solidus secretes proteins with putative host manipulation functions		1
10	Frequent assembly of chimeric complexes in the protein interaction network of an interspecies yeast hybrid		1
9	Proteomic analysis of chemosensory organs in the honey bee parasite Varroa destructor: a comprehensive examination of the potential carriers for semiochemicals		2
8	An atlas of protein-protein interactions across mammalian tissues		7
7	Honey bee queens are vulnerable to heat-induced loss of fertility		2
6	Dynamic rewiring of the human interactome by interferon signalling		2
5	Odorant cues linked to social immunity induce lateralized antenna stimulation in honey bees (Apis mellifera L.)		1
4	A rapid and accurate approach for Prediction of interactomes from co-elution data (PrInCE)		1
3	Lipid Rafts61-70		
2	A Deep Generative Model Enables Automated Structure Elucidation of Novel Psychoactive Substances	5	2

Proteomic portraits reveal evolutionarily conserved and divergent responses to spinal cord injury

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