Samuel Owen Purvine

List of Publications by Year
in descending order

125 papers	9,073 citations	30070 54 h-index	46799 89 g-index
133 all docs	133 docs citations	133 times ranked	13088 citing authors

#	Article	IF	Citations
1	Omic data from evolved *E. coli* are consistent with computed optimal growth from genome-scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
2	The study of macromolecular complexes by quantitative proteomics. Nature Genetics, 2003, 33, 349-355.	21.4	350
3	Genome-centric view of carbon processing in thawing permafrost. Nature, 2018, 560, 49-54.	27.8	337
4	Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. Rapid Communications in Mass Spectrometry, 2001, 15, 1214-1221.	1.5	277
5	Tandem mass spectrometry identifies many mouse brain *O*-GlcNAcylated proteins including EGF domain-specific *O*-GlcNAc transferase targets. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7280-7285.	7.1	275
6	Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes. Science, 2016, 351, 1192-1195.	12.6	266
7	Experimental Protein Mixture for Validating Tandem Mass Spectral Analysis. OMICS A Journal of Integrative Biology, 2002, 6, 207-212.	2.0	246
8	Evaluation of Multiprotein Immunoaffinity Subtraction for Plasma Proteomics and Candidate Biomarker Discovery Using Mass Spectrometry. Molecular and Cellular Proteomics, 2006, 5, 2167-2174.	3.8	197
9	Approaching complete peroxisome characterization by gas-phase fractionation. Electrophoresis, 2002, 23, 3205-3216.	2.4	193
10	Establishing the Proteome of Normal Human Cerebrospinal Fluid. PLoS ONE, 2010, 5, e10980.	2.5	183
11	A parts list for fungal cellulosomes revealed by comparative genomics. Nature Microbiology, 2017, 2, 17087.	13.3	183
12	Shotgun collision-induced dissociation of peptides using a time of flight mass analyzer. Proteomics, 2003, 3, 847-850.	2.2	158
13	Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008, 26, 164-167.	17.5	155
14	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. Bioinformatics, 2008, 24, 1021-1023.	4.1	143
15	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. Molecular and Cellular Proteomics, 2006, 5, 1899-1913.	3.8	142
16	MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1012-E1021.	7.1	142
17	Quantitative proteomic analysis indicates increased synthesis of a quinolone by Pseudomonas aeruginosa isolates from cystic fibrosis airways. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2771-2776.	7.1	137
18	Proteomic Analysis of Salmonella enterica Serovar Typhimurium Isolated from RAW 264.7 Macrophages. Journal of Biological Chemistry, 2006, 281, 29131-29140.	3.4	136

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19	Automated Genome Mining of Ribosomal Peptide Natural Products. ACS Chemical Biology, 2014, 9, 1545-1551.	3.4	133
20	Multiomics resolution of molecular events during a day in the life of Chlamydomonas. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2374-2383.	7.1	133
21	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. ISME Journal, 2012, 6, 1688-1701.	9.8	126
22	Proteogenomics: needs and roles to be filled by proteomics in genome annotation. Briefings in Functional Genomics & Proteomics, 2008, 7, 50-62.	3.8	124
23	New roles in hemicellulosic sugar fermentation for the uncultivated Bacteroidetes family BS11. ISME Journal, 2017, 11, 691-703.	9.8	115
24	Global profiling of Shewanella oneidensis MR-1: Expression of hypothetical genes and improved functional annotations. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2099-2104.	7.1	113
25	Analysis of the Salmonella typhimurium Proteome through Environmental Response toward Infectious Conditions. Molecular and Cellular Proteomics, 2006, 5, 1450-1461.	3.8	103
26	Leucoagaricus gongylophorus Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. Applied and Environmental Microbiology, 2013, 79, 3770-3778.	3.1	98
27	Genomes and secretomes of Ascomycota fungi reveal diverse functions in plant biomass decomposition and pathogenesis. BMC Genomics, 2019, 20, 976.	2.8	96
28	Circadian Proteomic Analysis Uncovers Mechanisms of Post-Transcriptional Regulation in Metabolic Pathways. Cell Systems, 2018, 7, 613-626.e5.	6.2	93
29	Proteomic identification and quantification of S-glutathionylation in mouse macrophages using resin-assisted enrichment and isobaric labeling. Free Radical Biology and Medicine, 2014, 67, 460-470.	2.9	91
30	High‐throughput sequencing of the chloroplast and mitochondrion of <i>Chlamydomonas reinhardtii</i> to generate improved <i>de novo</i> assemblies, analyze expression patterns and transcript speciation, and evaluate diversity among laboratory strains and wild isolates. Plant Journal, 2018, 93, 545-565.	5.7	90
31	A Method for Selective Enrichment and Analysis of Nitrotyrosine-Containing Peptides in Complex Proteome Samples. Journal of Proteome Research, 2007, 6, 2257-2268.	3.7	88
32	Lignin depolymerization by fungal secretomes and a microbial sink. Green Chemistry, 2016, 18, 6046-6062.	9.0	84
33	Outer membrane vesicles catabolize lignin-derived aromatic compounds in <i>Pseudomonas putida</i> KT2440. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9302-9310.	7.1	82
34	Intracellular pathways for lignin catabolism in white-rot fungi. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	82
35	Proteomics-based Compositional Analysis of Complex Cellulase‐Hemicellulase Mixtures. Journal of Proteome Research, 2011, 10, 4365-4372.	3.7	81
36	A Multi-Omic View of Host-Pathogen-Commensal Interplay in Salmonella-Mediated Intestinal Infection. PLoS ONE, 2013, 8, e67155.	2.5	81

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37	Proteomic analysis of Pseudomonas aeruginosa grown under magnesium limitation. Journal of the American Society for Mass Spectrometry, 2003, 14, 742-751.	2.8	79
38	Effectiveness of CID, HCD, and ETD with FT MS/MS for Degradomic-Peptidomic Analysis: Comparison of Peptide Identification Methods. Journal of Proteome Research, 2011, 10, 3929-3943.	3.7	76
39	Identification and functional analysis of 'hypothetical' genes expressed in Haemophilus influenzae. Nucleic Acids Research, 2004, 32, 2353-2361.	14.5	75
40	Proteomics informed by transcriptomics identifies novel secreted proteins in Dermacentor andersoni saliva. International Journal for Parasitology, 2014, 44, 1029-1037.	3.1	75
41	Integrated Omics Analysis of Pathogenic Host Responses during Pandemic H1N1 Influenza Virus Infection: The Crucial Role of Lipid Metabolism. Cell Host and Microbe, 2016, 19, 254-266.	11.0	75
42	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. BMC Genomics, 2016, 17, 267.	2.8	74
43	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. Scientific Reports, 2017, 7, 44296.	3.3	71
44	Feathermoss and epiphytic *Nostoc* cooperate differently: expanding the spectrum of plantâ€"cyanobacteria symbiosis. ISME Journal, 2017, 11, 2821-2833.	9.8	69
45	Coupled laboratory and field investigations resolve microbial interactions that underpin persistence in hydraulically fractured shales. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6585-E6594.	7.1	69
46	Initial Proteome Analysis of Model Microorganism *Haemophilus influenzae* Strain Rd KW20. Journal of Bacteriology, 2003, 185, 4593-4602.	2.2	66
47	Improved Methods for the Enrichment and Analysis of Glycated Peptides. Analytical Chemistry, 2008, 80, 9822-9829.	6.5	65
48	A comprehensive collection of systems biology data characterizing the host response to viral infection. Scientific Data, 2014, 1, 140033.	5.3	62
49	Multi-omics analysis reveals regulators of the response to nitrogen limitation in Yarrowia lipolytica. BMC Genomics, 2016, 17, 138.	2.8	62
50	Sulfide Generation by Dominant *Halanaerobium* Microorganisms in Hydraulically Fractured Shales. MSphere, 2017, 2, .	2.9	62
51	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohnâ€™s Disease: A Randomized Diet Controlled Trial. Nutrients, 2020, 12, 3749.	4.1	62
52	MALDI-Mass Spectrometric Imaging Revealing Hypoxia-Driven Lipids and Proteins in a Breast Tumor Model. Analytical Chemistry, 2015, 87, 5947-5956.	6.5	61
53	Multi 'omics comparison reveals metabolome biochemistry, not microbiome composition or gene expression, corresponds to elevated biogeochemical function in the hyporheic zone. Science of the Total Environment, 2018, 642, 742-753.	8.0	60
54	Proteome insights into the symbiotic relationship between a captive colony of *Nasutitermes corniger* and its hindgut microbiome. ISME Journal, 2011, 5, 161-164.	9.8	57

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55	Platelet Proteome Changes Associated with Diabetes and during Platelet Storage for Transfusion. Journal of Proteome Research, 2009, 8, 2261-2272.	3.7	54
56	DtaRefinery, a Software Tool for Elimination of Systematic Errors from Parent Ion Mass Measurements in Tandem Mass Spectra Data Sets. Molecular and Cellular Proteomics, 2010, 9, 486-496.	3.8	54
57	Soil metabolome response to whole-ecosystem warming at the Spruce and Peatland Responses under Changing Environments experiment. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	54
58	Blood Peptidome-Degradome Profile of Breast Cancer. PLoS ONE, 2010, 5, e13133.	2.5	54
59	Spectral Quality Assessment for High-Throughput Tandem Mass Spectrometry Proteomics. OMICS A Journal of Integrative Biology, 2004, 8, 255-265.	2.0	51
60	Coupled transcriptome and proteome analysis of human lymphotropic tumor viruses: insights on the detection and discovery of viral genes. BMC Genomics, 2011, 12, 625.	2.8	50
61	Comparative Analysis of Secretome Profiles of Manganese(II)-Oxidizing Ascomycete Fungi. PLoS ONE, 2016, 11, e0157844.	2.5	49
62	Standard Mixtures for Proteome Studies. OMICS A Journal of Integrative Biology, 2004, 8, 79-92.	2.0	48
63	Proteome-Wide Identification of Proteins and Their Modifications with Decreased Ambiguities and Improved False Discovery Rates Using Unique Sequence Tags. Analytical Chemistry, 2008, 80, 1871-1882.	6.5	46
64	A Statistical Method for Assessing Peptide Identification Confidence in Accurate Mass and Time Tag Proteomics. Analytical Chemistry, 2011, 83, 6135-6140.	6.5	46
65	Identification of Widespread Adenosine Nucleotide Binding in Mycobacterium tuberculosis. Chemistry and Biology, 2013, 20, 123-133.	6.0	45
66	Decrypting bacterial polyphenol metabolism in an anoxic wetland soil. Nature Communications, 2021, 12, 2466.	12.8	45
67	Mixed-Effects Statistical Model for Comparative LCâˆ'MS Proteomics Studies. Journal of Proteome Research, 2008, 7, 1209-1217.	3.7	44
68	Coupling Secretomics with Enzyme Activities To Compare the Temporal Processes of Wood Metabolism among White and Brown Rot Fungi. Applied and Environmental Microbiology, 2018, 84, .	3.1	44
69	Strategy for Degradomic-Peptidomic Analysis of Human Blood Plasma. Journal of Proteome Research, 2010, 9, 2339-2346.	3.7	43
70	In SilicoMetabolic Model and Protein Expression ofHaemophilus influenzaeStrain Rd KW20 in Rich Medium. OMICS A Journal of Integrative Biology, 2004, 8, 25-41.	2.0	42
71	Discovery and ecogenomic context of a global Caldiserica-related phylum active in thawing permafrost, Candidatus Cryosericota phylum nov., Ca. Cryosericia class nov., Ca. Cryosericales ord. nov., Ca. Cryosericaceae fam. nov., comprising the four species Cryosericum septentrionale gen. nov. sp. nov., Ca. C. hinesii sp. nov., Ca. C. odellii sp. nov., Ca. C. terrychapinii sp. nov.. Systematic and Applied Microbiology, 2019, 42, 54-66.	2.8	42
72	The National Microbiome Data Collaborative: enabling microbiome science. Nature Reviews Microbiology, 2020, 18, 313-314.	28.6	42

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73	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in *Yarrowia lipolytica*. MBio, 2017, 8, .	4.1	38
74	Linear Discriminant Analysis-Based Estimation of the False Discovery Rate for Phosphopeptide Identifications. Journal of Proteome Research, 2008, 7, 2195-2203.	3.7	37
75	Addressing the challenge of soil metaproteome complexity by improving metaproteome depth of coverage through two-dimensional liquid chromatography. Soil Biology and Biochemistry, 2018, 125, 290-299.	8.8	37
76	De Novo Sequencing of Unique Sequence Tags for Discovery of Post-Translational Modifications of Proteins. Analytical Chemistry, 2008, 80, 7742-7754.	6.5	36
77	*Dichomitus squalens* partially tailors its molecular responses to the composition of solid wood. Environmental Microbiology, 2018, 20, 4141-4156.	3.8	36
78	Anaerobic gut fungi are an untapped reservoir of natural products. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	35
79	Proteomic Detection of Non-Annotated Protein-Coding Genes in Pseudomonas fluorescens Pf0-1. PLoS ONE, 2009, 4, e8455.	2.5	34
80	Activity-Based Probes for Isoenzyme- and Site-Specific Functional Characterization of Glutathione *S*-Transferases. Journal of the American Chemical Society, 2017, 139, 16032-16035.	13.7	34
81	The Influence of Sample Preparation and Replicate Analyses on HeLa Cell Phosphoproteome Coverage. Journal of Proteome Research, 2008, 7, 2215-2221.	3.7	31
82	Tertiary Structural Rearrangements upon Oxidation of Methionine145 in Calmodulin Promotes Targeted Proteasomal Degradation. Biophysical Journal, 2006, 91, 1480-1493.	0.5	30
83	Combined Pulsed-Q Dissociation and Electron Transfer Dissociation for Identification and Quantification of iTRAQ-Labeled Phosphopeptides. Analytical Chemistry, 2009, 81, 4137-4143.	6.5	30
84	Comparative Omics-Driven Genome Annotation Refinement: Application across Yersiniae. PLoS ONE, 2012, 7, e33903.	2.5	30
85	Widespread polycistronic gene expression in green algae. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	30
86	Experimental annotation of post-translational features and translated coding regions in the pathogen Salmonella Typhimurium. BMC Genomics, 2011, 12, 433.	2.8	29
87	Simultaneous Proteomic Discovery and Targeted Monitoring using Liquid Chromatography, Ion Mobility Spectrometry, and Mass Spectrometry. Molecular and Cellular Proteomics, 2016, 15, 3694-3705.	3.8	29
88	Enrichment and Broad Representation of Plant Biomass-Degrading Enzymes in the Specialized Hyphal Swellings of Leucoagaricus gongylophorus, the Fungal Symbiont of Leaf-Cutter Ants. PLoS ONE, 2015, 10, e0134752.	2.5	28
89	Targeted Protein Degradation by Salmonella under Phagosome-mimicking Culture Conditions Investigated Using Comparative Peptidomics. Molecular and Cellular Proteomics, 2007, 6, 717-727.	3.8	26
90	Specialized proteomic responses and an ancient photoprotection mechanism sustain marine green algal growth during phosphate limitation. Nature Microbiology, 2018, 3, 781-790.	13.3	26

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91	Characterization of Strategies for Obtaining Confident Identifications in Bottom-Up Proteomics Measurements Using Hybrid FTMS Instruments. Analytical Chemistry, 2008, 80, 8514-8525.	6.5	24
92	Applying a Targeted Label-Free Approach Using LCâ'MS AMT Tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition. Journal of Proteome Research, 2007, 6, 4489-4497.	3.7	22
93	Improving Collision Induced Dissociation (CID), High Energy Collision Dissociation (HCD), and Electron Transfer Dissociation (ETD) Fourier Transform MS/MS Degradomeâ€"Peptidome Identifications Using High Accuracy Mass Information. Journal of Proteome Research, 2012, 11, 668-677.	3.7	22
94	Phosphoproteomics Profiling of Human Skin Fibroblast Cells Reveals Pathways and Proteins Affected by Low Doses of Ionizing Radiation. PLoS ONE, 2010, 5, e14152.	2.5	21
95	Integrated Post-Experiment Monoisotopic Mass Refinement: An Integrated Approach to Accurately Assign Monoisotopic Precursor Masses to Tandem Mass Spectrometric Data. Analytical Chemistry, 2010, 82, 8510-8518.	6.5	21
96	Automated Data Extraction from <i>In Situ</i> Protein-Stable Isotope Probing Studies. Journal of Proteome Research, 2014, 13, 1200-1210.	3.7	20
97	Deep-Subsurface Pressure Stimulates Metabolic Plasticity in Shale-Colonizing <i>Halanaerobium</i> spp. Applied and Environmental Microbiology, 2019, 85, .	3.1	20
98	Quantitative Analysis of Cell Surface Membrane Proteins Using Membrane-Impermeable Chemical Probe Coupled with ^{18}O Labeling. Journal of Proteome Research, 2010, 9, 2160-2169.	3.7	19
99	Spatial Phosphoprotein Profiling Reveals a Compartmentalized Extracellular Signal-regulated Kinase Switch Governing Neurite Growth and Retraction. Journal of Biological Chemistry, 2011, 286, 18190-18201.	3.4	19
100	Novel Ser/Thr Protein Phosphatase 5 (PP5) Regulated Targets during DNA Damage Identified by Proteomics Analysis. Journal of Proteome Research, 2010, 9, 945-953.	3.7	18
101	Amino acid treatment enhances protein recovery from sediment and soils for metaproteomic studies. Proteomics, 2013, 13, 2776-2785.	2.2	18
102	In situ transformation of ethoxylate and glycol surfactants by shale-colonizing microorganisms during hydraulic fracturing. ISME Journal, 2019, 13, 2690-2700.	9.8	18
103	Mechanisms of Manganese(II) Oxidation by Filamentous Ascomycete Fungi Vary With Species and Time as a Function of Secretome Composition. Frontiers in Microbiology, 2021, 12, 610497.	3.5	17
104	Cellâ€Typeâ€Specific Proteomics Analysis of a Small Number of Plant Cells by Integrating Laser Capture Microdissection with a Nanodroplet Sample Processing Platform. Current Protocols, 2021, 1, e153.	2.9	17
105	Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step ^{18}O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography. Journal of Proteome Research, 2008, 7, 4215-4224.	3.7	16
106	Discovering Mercury Protein Modifications in Whole Proteomes Using Natural Isotope Distributions Observed in Liquid Chromatography-Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2011, 10, M110.004853.	3.8	15
107	Individual Variability of Protein Expression in Human Tissues. Journal of Proteome Research, 2018, 17, 3914-3922.	3.7	15
108	Mass Spectrometry Analysis of Proteome-Wide Proteolytic Post-Translational Degradation of Proteins. Analytical Chemistry, 2008, 80, 5819-5828.	6.5	14

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109	The Pacific Northwest National Laboratory library of bacterial and archaeal proteomic biodiversity. Scientific Data, 2015, 2, 150041.	5.3	14
110	Functional Genomics, Transcriptomics, and Proteomics Reveal Distinct Combat Strategies Between Lineages of Wood-Degrading Fungi With Redundant Wood Decay Mechanisms. Frontiers in Microbiology, 2020, 11, 1646.	3.5	13
111	Activity-based protein profiling of secreted cellulolytic enzyme activity dynamics in Trichoderma reesei QM6a, NG14, and RUT-C30. Molecular BioSystems, 2013, 9, 2992.	2.9	12
112	Mineral Surfaces as Agents of Environmental Proteolysis: Mechanisms and Controls. Environmental Science & Technology, 2019, 53, 3018-3026.	10.0	11
113	Single-throughput Complementary High-resolution Analytical Techniques for Characterizing Complex Natural Organic Matter Mixtures. Journal of Visualized Experiments, 2019, , .	0.3	10
114	Quantitative cardiac phosphoproteomics profiling during ischemia-reperfusion in an immature swine model. American Journal of Physiology - Heart and Circulatory Physiology, 2017, 313, H125-H137.	3.2	9
115	Proteomic analysis reveals down-regulation of surfactant protein B in murine type II pneumocytes infected with influenza A virus. Virology, 2015, 483, 96-107.	2.4	7
116	Structure Dependent Determination of Organophosphate Targets in Mammalian Tissues Using Activity-Based Protein Profiling. Chemical Research in Toxicology, 2020, 33, 414-425.	3.3	7
117	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga Micromonas pusilla. PLoS ONE, 2016, 11, e0155839.	2.5	7
118	Identification of Disulfide Bonds in Protein Proteolytic Degradation Products Using <i>de novo</i>-Protein Unique Sequence Tags Approach. Journal of Proteome Research, 2010, 9, 4053-4060.	3.7	6
119	High resolution visualization and exoâ€proteomics reveal the physiological role of XlnR and AraR in plant biomass colonization and degradation by <i>Aspergillus niger</i>. Environmental Microbiology, 2017, 19, 4587-4598.	3.8	6
120	Quantitative iTRAQ-based secretome analysis reveals species-specific and temporal shifts in carbon utilization strategies among manganese(II)-oxidizing Ascomycete fungi. Fungal Genetics and Biology, 2017, 106, 61-75.	2.1	6
121	Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. Frontiers in Bioinformatics, 2022, 1, .	2.1	6
122	Identification of <i>c</i>-Type Heme-Containing Peptides Using Nonactivated Immobilized Metal Affinity Chromatography Resin Enrichment and Higher-Energy Collisional Dissociation. Analytical Chemistry, 2011, 83, 7260-7268.	6.5	5
123	H. influenzae Consortium: Integrative Study of H. influenzae-Human Interactions. OMICS A Journal of Integrative Biology, 2002, 6, 341-348.	2.0	4
124	Basophile: Accurate Fragment Charge State Prediction Improves Peptide Identification Rates. Genomics, Proteomics and Bioinformatics, 2013, 11, 86-95.	6.9	1
125	Statistically appraising process quality of affinity isolation experiments. Computational Statistics and Data Analysis, 2009, 53, 1720-1726.	1.2	0