

# Samuel Owen Purvine

## List of Publications by Year in descending order

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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	Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. <i>Frontiers in Bioinformatics</i> , 2022, 1, .	2.1	6
2	Widespread polycistronic gene expression in green algae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
3	Mechanisms of Manganese(II) Oxidation by Filamentous Ascomycete Fungi Vary With Species and Time as a Function of Secretome Composition. <i>Frontiers in Microbiology</i> , 2021, 12, 610497.	3.5	17
4	Intracellular pathways for lignin catabolism in white-rot fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	82
5	Anaerobic gut fungi are an untapped reservoir of natural products. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35
6	Decrypting bacterial polyphenol metabolism in an anoxic wetland soil. <i>Nature Communications</i> , 2021, 12, 2466.	12.8	45
7	Cell-Type-Specific Proteomics Analysis of a Small Number of Plant Cells by Integrating Laser Capture Microdissection with a Nanodroplet Sample Processing Platform. <i>Current Protocols</i> , 2021, 1, e153.	2.9	17
8	Soil metabolome response to whole-ecosystem warming at the Spruce and Peatland Responses under Changing Environments experiment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	54
9	Structure Dependent Determination of Organophosphate Targets in Mammalian Tissues Using Activity-Based Protein Profiling. <i>Chemical Research in Toxicology</i> , 2020, 33, 414-425.	3.3	7
10	Functional Genomics, Transcriptomics, and Proteomics Reveal Distinct Combat Strategies Between Lineages of Wood-Degrading Fungi With Redundant Wood Decay Mechanisms. <i>Frontiers in Microbiology</i> , 2020, 11, 1646.	3.5	13
11	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohn's Disease: A Randomized Diet Controlled Trial. <i>Nutrients</i> , 2020, 12, 3749.	4.1	62
12	Outer membrane vesicles catabolize lignin-derived aromatic compounds in <i>Pseudomonas putida</i> KT2440. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9302-9310.	7.1	82
13	The National Microbiome Data Collaborative: enabling microbiome science. <i>Nature Reviews Microbiology</i> , 2020, 18, 313-314.	28.6	42
14	Multimiomics resolution of molecular events during a day in the life of <i>Chlamydomonas</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2374-2383.	7.1	133
15	In situ transformation of ethoxylate and glycol surfactants by shale-colonizing microorganisms during hydraulic fracturing. <i>ISME Journal</i> , 2019, 13, 2690-2700.	9.8	18
16	Discovery and ecogenomic context of a global <i>Caldiserica</i> -related phylum active in thawing permafrost, <i>Candidatus Cryoserica</i> phylum nov., <i>Ca. Cryoserica</i> class nov., <i>Ca. Cryosericales</i> ord. nov., <i>Ca. Cryoseriaceae</i> fam. nov., comprising the four species <i>Cryosericum septentrionale</i> gen. nov. sp. nov., <i>Ca. C. hinesii</i> sp. nov., <i>Ca. C. odellii</i> sp. nov., <i>Ca. C. terrychapinii</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2019, 42, 54-66.	2.8	42
17	Deep-Subsurface Pressure Stimulates Metabolic Plasticity in Shale-Colonizing <i>Halanaerobium</i> spp. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	20
18	Mineral Surfaces as Agents of Environmental Proteolysis: Mechanisms and Controls. <i>Environmental Science &amp; Technology</i> , 2019, 53, 3018-3026.	10.0	11

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19	Genomes and secretomes of Ascomycota fungi reveal diverse functions in plant biomass decomposition and pathogenesis. BMC Genomics, 2019, 20, 976.	2.8	96
20	Single-throughput Complementary High-resolution Analytical Techniques for Characterizing Complex Natural Organic Matter Mixtures. Journal of Visualized Experiments, 2019, , .	0.3	10
21	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
22	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
23	Circadian Proteomic Analysis Uncovers Mechanisms of Post-Transcriptional Regulation in Metabolic Pathways. Cell Systems, 2018, 7, 613-626.e5.	6.2	93
24	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. Environmental Microbiology, 2018, 20, 4141-4156.	3.8	36
25	Individual Variability of Protein Expression in Human Tissues. Journal of Proteome Research, 2018, 17, 3914-3922.	3.7	15
26	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
27	Genome-centric view of carbon processing in thawing permafrost. Nature, 2018, 560, 49-54.	27.8	337
28	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
29	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
30	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
31	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
32	New roles in hemicellulosic sugar fermentation for the uncultivated Bacteroidetes family BS11. ISME Journal, 2017, 11, 691-703.	9.8	115
33	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
34	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in <i>Yarrowia lipolytica</i> . MBio, 2017, 8, .	4.1	38
35	A parts list for fungal cellulosomes revealed by comparative genomics. Nature Microbiology, 2017, 2, 17087.	13.3	183
36	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. Scientific Reports, 2017, 7, 44296.	3.3	71

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37	Activity-Based Probes for Isoenzyme- and Site-Specific Functional Characterization of Glutathione <i>S</i> -Transferases. <i>Journal of the American Chemical Society</i> , 2017, 139, 16032-16035.	13.7	34
38	High resolution visualization and exo-proteomics reveal the physiological role of XlnR and AraR in plant biomass colonization and degradation by <i>Aspergillus niger</i> . <i>Environmental Microbiology</i> , 2017, 19, 4587-4598.	3.8	6
39	Feathermoss and epiphytic <i>Nostoc</i> cooperate differently: expanding the spectrum of plant-cyanobacteria symbiosis. <i>ISME Journal</i> , 2017, 11, 2821-2833.	9.8	69
40	Quantitative iTRAQ-based secretome analysis reveals species-specific and temporal shifts in carbon utilization strategies among manganese(II)-oxidizing Ascomycete fungi. <i>Fungal Genetics and Biology</i> , 2017, 106, 61-75.	2.1	6
41	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	2.9	62
42	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016, 17, 267.	2.8	74
43	Simultaneous Proteomic Discovery and Targeted Monitoring using Liquid Chromatography, Ion Mobility Spectrometry, and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3694-3705.	3.8	29
44	Lignin depolymerization by fungal secretomes and a microbial sink. <i>Green Chemistry</i> , 2016, 18, 6046-6062.	9.0	84
45	Multi-omics analysis reveals regulators of the response to nitrogen limitation in <i>Yarrowia lipolytica</i> . <i>BMC Genomics</i> , 2016, 17, 138.	2.8	62
46	Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes. <i>Science</i> , 2016, 351, 1192-1195.	12.6	266
47	Integrated Omics Analysis of Pathogenic Host Responses during Pandemic H1N1 Influenza Virus Infection: The Crucial Role of Lipid Metabolism. <i>Cell Host and Microbe</i> , 2016, 19, 254-266.	11.0	75
48	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga <i>Micromonas pusilla</i> . <i>PLoS ONE</i> , 2016, 11, e0155839.	2.5	7
49	Comparative Analysis of Secretome Profiles of Manganese(II)-Oxidizing Ascomycete Fungi. <i>PLoS ONE</i> , 2016, 11, e0157844.	2.5	49
50	The Pacific Northwest National Laboratory library of bacterial and archaeal proteomic biodiversity. <i>Scientific Data</i> , 2015, 2, 150041.	5.3	14
51	MALDI-Mass Spectrometric Imaging Revealing Hypoxia-Driven Lipids and Proteins in a Breast Tumor Model. <i>Analytical Chemistry</i> , 2015, 87, 5947-5956.	6.5	61
52	Proteomic analysis reveals down-regulation of surfactant protein B in murine type II pneumocytes infected with influenza A virus. <i>Virology</i> , 2015, 483, 96-107.	2.4	7
53	Enrichment and Broad Representation of Plant Biomass-Degrading Enzymes in the Specialized Hyphal Swellings of <i>Leucoagaricus gongylophorus</i> , the Fungal Symbiont of Leaf-Cutter Ants. <i>PLoS ONE</i> , 2015, 10, e0134752.	2.5	28
54	A comprehensive collection of systems biology data characterizing the host response to viral infection. <i>Scientific Data</i> , 2014, 1, 140033.	5.3	62

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55	Proteomic identification and quantification of S-glutathionylation in mouse macrophages using resin-assisted enrichment and isobaric labeling. <i>Free Radical Biology and Medicine</i> , 2014, 67, 460-470.	2.9	91
56	Proteomics informed by transcriptomics identifies novel secreted proteins in <i>Dermacentor andersoni</i> saliva. <i>International Journal for Parasitology</i> , 2014, 44, 1029-1037.	3.1	75
57	Automated Genome Mining of Ribosomal Peptide Natural Products. <i>ACS Chemical Biology</i> , 2014, 9, 1545-1551.	3.4	133
58	Automated Data Extraction from <i>In Situ</i> Protein-Stable Isotope Probing Studies. <i>Journal of Proteome Research</i> , 2014, 13, 1200-1210.	3.7	20
59	Basophile: Accurate Fragment Charge State Prediction Improves Peptide Identification Rates. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 86-95.	6.9	1
60	Amino acid treatment enhances protein recovery from sediment and soils for metaproteomic studies. <i>Proteomics</i> , 2013, 13, 2776-2785.	2.2	18
61	<i>Leucoagaricus gongylophorus</i> Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3770-3778.	3.1	98
62	Activity-based protein profiling of secreted cellulolytic enzyme activity dynamics in <i>Trichoderma reesei</i> QM6a, NG14, and RUT-C30. <i>Molecular BioSystems</i> , 2013, 9, 2992.	2.9	12
63	Identification of Widespread Adenosine Nucleotide Binding in <i>Mycobacterium tuberculosis</i> . <i>Chemistry and Biology</i> , 2013, 20, 123-133.	6.0	45
64	A Multi-Omic View of Host-Pathogen-Commensal Interplay in <i>Salmonella</i> -Mediated Intestinal Infection. <i>PLoS ONE</i> , 2013, 8, e67155.	2.5	81
65	Comparative Omics-Driven Genome Annotation Refinement: Application across <i>Yersinia</i> . <i>PLoS ONE</i> , 2012, 7, e33903.	2.5	30
66	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. <i>Journal of Proteome Research</i> , 2012, 11, 668-677.	3.7	22
67	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. <i>ISME Journal</i> , 2012, 6, 1688-1701.	9.8	126
68	Tandem mass spectrometry identifies many mouse brain <i>O</i> -GlcNAcylated proteins including EGF domain-specific <i>O</i> -GlcNAc transferase targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7280-7285.	7.1	275
69	Identification of <i>c</i> -Type Heme-Containing Peptides Using Nonactivated Immobilized Metal Affinity Chromatography Resin Enrichment and Higher-Energy Collisional Dissociation. <i>Analytical Chemistry</i> , 2011, 83, 7260-7268.	6.5	5
70	A Statistical Method for Assessing Peptide Identification Confidence in Accurate Mass and Time Tag Proteomics. <i>Analytical Chemistry</i> , 2011, 83, 6135-6140.	6.5	46
71	Proteomics-based Compositional Analysis of Complex Cellulaseâ€“Hemicellulase Mixtures. <i>Journal of Proteome Research</i> , 2011, 10, 4365-4372.	3.7	81
72	Proteome insights into the symbiotic relationship between a captive colony of <i>Nasutitermes corniger</i> and its hindgut microbiome. <i>ISME Journal</i> , 2011, 5, 161-164.	9.8	57

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73	Experimental annotation of post-translational features and translated coding regions in the pathogen <i>Salmonella Typhimurium</i> . <i>BMC Genomics</i> , 2011, 12, 433.	2.8	29
74	Coupled transcriptome and proteome analysis of human lymphotropic tumor viruses: insights on the detection and discovery of viral genes. <i>BMC Genomics</i> , 2011, 12, 625.	2.8	50
75	Effectiveness of CID, HCD, and ETD with FT MS/MS for Degradomic-Peptidomic Analysis: Comparison of Peptide Identification Methods. <i>Journal of Proteome Research</i> , 2011, 10, 3929-3943.	3.7	76
76	Discovering Mercury Protein Modifications in Whole Proteomes Using Natural Isotope Distributions Observed in Liquid Chromatography-Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.004853.	3.8	15
77	Spatial Phosphoprotein Profiling Reveals a Compartmentalized Extracellular Signal-regulated Kinase Switch Governing Neurite Growth and Retraction. <i>Journal of Biological Chemistry</i> , 2011, 286, 18190-18201.	3.4	19
78	Strategy for Degradomic-Peptidomic Analysis of Human Blood Plasma. <i>Journal of Proteome Research</i> , 2010, 9, 2339-2346.	3.7	43
79	Establishing the Proteome of Normal Human Cerebrospinal Fluid. <i>PLoS ONE</i> , 2010, 5, e10980.	2.5	183
80	Phosphoproteomics Profiling of Human Skin Fibroblast Cells Reveals Pathways and Proteins Affected by Low Doses of Ionizing Radiation. <i>PLoS ONE</i> , 2010, 5, e14152.	2.5	21
81	DtaRefinery, a Software Tool for Elimination of Systematic Errors from Parent Ion Mass Measurements in Tandem Mass Spectra Data Sets. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 486-496.	3.8	54
82	Omic data from evolved <i>E. coli</i> are consistent with computed optimal growth from genome-scale models. <i>Molecular Systems Biology</i> , 2010, 6, 390.	7.2	615
83	Quantitative Analysis of Cell Surface Membrane Proteins Using Membrane-Impermeable Chemical Probe Coupled with <sup>18</sup> O Labeling. <i>Journal of Proteome Research</i> , 2010, 9, 2160-2169.	3.7	19
84	Integrated Post-Experiment Monoisotopic Mass Refinement: An Integrated Approach to Accurately Assign Monoisotopic Precursor Masses to Tandem Mass Spectrometric Data. <i>Analytical Chemistry</i> , 2010, 82, 8510-8518.	6.5	21
85	Identification of Disulfide Bonds in Protein Proteolytic Degradation Products Using <i>de novo</i> -Protein Unique Sequence Tags Approach. <i>Journal of Proteome Research</i> , 2010, 9, 4053-4060.	3.7	6
86	Novel Ser/Thr Protein Phosphatase 5 (PP5) Regulated Targets during DNA Damage Identified by Proteomics Analysis. <i>Journal of Proteome Research</i> , 2010, 9, 945-953.	3.7	18
87	Blood Peptidome-Degradome Profile of Breast Cancer. <i>PLoS ONE</i> , 2010, 5, e13133.	2.5	54
88	Proteomic Detection of Non-Annotated Protein-Coding Genes in <i>Pseudomonas fluorescens</i> Pf0-1. <i>PLoS ONE</i> , 2009, 4, e8455.	2.5	34
89	Statistically appraising process quality of affinity isolation experiments. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1720-1726.	1.2	0
90	Platelet Proteome Changes Associated with Diabetes and during Platelet Storage for Transfusion. <i>Journal of Proteome Research</i> , 2009, 8, 2261-2272.	3.7	54

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91	Combined Pulsed-Q Dissociation and Electron Transfer Dissociation for Identification and Quantification of iTRAQ-Labeled Phosphopeptides. <i>Analytical Chemistry</i> , 2009, 81, 4137-4143.	6.5	30
92	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
93	Improved Methods for the Enrichment and Analysis of Glycated Peptides. <i>Analytical Chemistry</i> , 2008, 80, 9822-9829.	6.5	65
94	Characterization of Strategies for Obtaining Confident Identifications in Bottom-Up Proteomics Measurements Using Hybrid FTMS Instruments. <i>Analytical Chemistry</i> , 2008, 80, 8514-8525.	6.5	24
95	Linear Discriminant Analysis-Based Estimation of the False Discovery Rate for Phosphopeptide Identifications. <i>Journal of Proteome Research</i> , 2008, 7, 2195-2203.	3.7	37
96	Mass Spectrometry Analysis of Proteome-Wide Proteolytic Post-Translational Degradation of Proteins. <i>Analytical Chemistry</i> , 2008, 80, 5819-5828.	6.5	14
97	Mixed-Effects Statistical Model for Comparative LC-MS Proteomics Studies. <i>Journal of Proteome Research</i> , 2008, 7, 1209-1217.	3.7	44
98	The Influence of Sample Preparation and Replicate Analyses on HeLa Cell Phosphoproteome Coverage. <i>Journal of Proteome Research</i> , 2008, 7, 2215-2221.	3.7	31
99	Proteome-Wide Identification of Proteins and Their Modifications with Decreased Ambiguities and Improved False Discovery Rates Using Unique Sequence Tags. <i>Analytical Chemistry</i> , 2008, 80, 1871-1882.	6.5	46
100	Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step <sup>18</sup> O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography. <i>Journal of Proteome Research</i> , 2008, 7, 4215-4224.	3.7	16
101	De Novo Sequencing of Unique Sequence Tags for Discovery of Post-Translational Modifications of Proteins. <i>Analytical Chemistry</i> , 2008, 80, 7742-7754.	6.5	36
102	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. <i>Bioinformatics</i> , 2008, 24, 1021-1023.	4.1	143
103	Proteogenomics: needs and roles to be filled by proteomics in genome annotation. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2008, 7, 50-62.	3.8	124
104	Targeted Protein Degradation by Salmonella under Phagosome-mimicking Culture Conditions Investigated Using Comparative Peptidomics. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 717-727.	3.8	26
105	Applying a Targeted Label-Free Approach Using LC-MS AMT Tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition. <i>Journal of Proteome Research</i> , 2007, 6, 4489-4497.	3.7	22
106	A Method for Selective Enrichment and Analysis of Nitrotyrosine-Containing Peptides in Complex Proteome Samples. <i>Journal of Proteome Research</i> , 2007, 6, 2257-2268.	3.7	88
107	Evaluation of Multiprotein Immunoaffinity Subtraction for Plasma Proteomics and Candidate Biomarker Discovery Using Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2167-2174.	3.8	197
108	Tertiary Structural Rearrangements upon Oxidation of Methionine145 in Calmodulin Promotes Targeted Proteasomal Degradation. <i>Biophysical Journal</i> , 2006, 91, 1480-1493.	0.5	30



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109	Analysis of the Salmonella typhimurium Proteome through Environmental Response toward Infectious Conditions. Molecular and Cellular Proteomics, 2006, 5, 1450-1461.	3.8	103
110	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. Molecular and Cellular Proteomics, 2006, 5, 1899-1913.	3.8	142
111	Proteomic Analysis of Salmonella enterica Serovar Typhimurium Isolated from RAW 264.7 Macrophages. Journal of Biological Chemistry, 2006, 281, 29131-29140.	3.4	136
112	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
113	Standard Mixtures for Proteome Studies. OMICS A Journal of Integrative Biology, 2004, 8, 79-92.	2.0	48
114	Spectral Quality Assessment for High-Throughput Tandem Mass Spectrometry Proteomics. OMICS A Journal of Integrative Biology, 2004, 8, 255-265.	2.0	51
115	In Silico Metabolic Model and Protein Expression of Haemophilus influenzae Strain Rd KW20 in Rich Medium. OMICS A Journal of Integrative Biology, 2004, 8, 25-41.	2.0	42
116	Identification and functional analysis of 'hypothetical' genes expressed in Haemophilus influenzae. Nucleic Acids Research, 2004, 32, 2353-2361.	14.5	75
117	Initial Proteome Analysis of Model Microorganism <i>Haemophilus influenzae</i> Strain Rd KW20. Journal of Bacteriology, 2003, 185, 4593-4602.	2.2	66
118	Proteomic analysis of Pseudomonas aeruginosa grown under magnesium limitation. Journal of the American Society for Mass Spectrometry, 2003, 14, 742-751.	2.8	79
119	Shotgun collision-induced dissociation of peptides using a time of flight mass analyzer. Proteomics, 2003, 3, 847-850.	2.2	158
120	The study of macromolecular complexes by quantitative proteomics. Nature Genetics, 2003, 33, 349-355.	21.4	350
121	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
122	H. influenzae Consortium: Integrative Study of H. influenzae-Human Interactions. OMICS A Journal of Integrative Biology, 2002, 6, 341-348.	2.0	4
123	Experimental Protein Mixture for Validating Tandem Mass Spectral Analysis. OMICS A Journal of Integrative Biology, 2002, 6, 207-212.	2.0	246
124	Approaching complete peroxisome characterization by gas-phase fractionation. Electrophoresis, 2002, 23, 3205-3216.	2.4	193
125	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