

Samuel Owen Purvine

List of Publications by Year in descending order

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125
papers

9,073
citations

34493

54
h-index

53065

89
g-index

133
all docs

133
docs citations

133
times ranked

14717
citing authors

#	ARTICLE	IF	CITATIONS
1	Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. <i>Frontiers in Bioinformatics</i> , 2022, 1, .	1.0	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, .	3.3	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.	1.5	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, .	3.3	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, .	3.3	35
6	Decrypting bacterial polyphenol metabolism in an anoxic wetland soil. <i>Nature Communications</i> , 2021, 12, 2466.	5.8	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.	1.3	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, .	3.3	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.	1.7	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.	1.5	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.	1.7	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.	3.3	82
13	The National Microbiome Data Collaborative: enabling microbiome science. <i>Nature Reviews Microbiology</i> , 2020, 18, 313-314.	13.6	42
14	Multiomics 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.	3.3	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.	4.4	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.	1.2	42
17	Deep-Subsurface Pressure Stimulates Metabolic Plasticity in Shale-Colonizing <i>Halanaerobium</i> spp. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
18	Mineral Surfaces as Agents of Environmental Proteolysis: Mechanisms and Controls. <i>Environmental Science & Technology</i> , 2019, 53, 3018-3026.	4.6	11

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19	Genomes and secretomes of Ascomycota fungi reveal diverse functions in plant biomass decomposition and pathogenesis. <i>BMC Genomics</i> , 2019, 20, 976.	1.2	96
20	Single-throughput Complementary High-resolution Analytical Techniques for Characterizing Complex Natural Organic Matter Mixtures. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	10
21	MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1012-E1021.	3.3	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. <i>Plant Journal</i> , 2018, 93, 545-565.	2.8	90
23	Circadian Proteomic Analysis Uncovers Mechanisms of Post-Transcriptional Regulation in Metabolic Pathways. <i>Cell Systems</i> , 2018, 7, 613-626.e5.	2.9	93
24	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. <i>Environmental Microbiology</i> , 2018, 20, 4141-4156.	1.8	36
25	Individual Variability of Protein Expression in Human Tissues. <i>Journal of Proteome Research</i> , 2018, 17, 3914-3922.	1.8	15
26	Specialized proteomic responses and an ancient photoprotection mechanism sustain marine green algal growth during phosphate limitation. <i>Nature Microbiology</i> , 2018, 3, 781-790.	5.9	26
27	Genome-centric view of carbon processing in thawing permafrost. <i>Nature</i> , 2018, 560, 49-54.	13.7	337
28	Coupled laboratory and field investigations resolve microbial interactions that underpin persistence in hydraulically fractured shales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6585-E6594.	3.3	69
29	Addressing the challenge of soil metaproteome complexity by improving metaproteome depth of coverage through two-dimensional liquid chromatography. <i>Soil Biology and Biochemistry</i> , 2018, 125, 290-299.	4.2	37
30	Coupling Secretomics with Enzyme Activities To Compare the Temporal Processes of Wood Metabolism among White and Brown Rot Fungi. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	44
31	Multi 'omics comparison reveals metabolome biochemistry, not microbiome composition or gene expression, corresponds to elevated biogeochemical function in the hyporheic zone. <i>Science of the Total Environment</i> , 2018, 642, 742-753.	3.9	60
32	New roles in hemicellulosic sugar fermentation for the uncultivated Bacteroidetes family BS11. <i>ISME Journal</i> , 2017, 11, 691-703.	4.4	115
33	Quantitative cardiac phosphoproteomics profiling during ischemia-reperfusion in an immature swine model. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2017, 313, H125-H137.	1.5	9
34	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in <i>Yarrowia lipolytica</i> . <i>MBio</i> , 2017, 8, .	1.8	38
35	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017, 2, 17087.	5.9	183
36	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. <i>Scientific Reports</i> , 2017, 7, 44296.	1.6	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.	6.6	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.	1.8	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.	4.4	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.	0.9	6
41	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	1.3	62
42	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016, 17, 267.	1.2	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.	2.5	29
44	Lignin depolymerization by fungal secretomes and a microbial sink. <i>Green Chemistry</i> , 2016, 18, 6046-6062.	4.6	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.	1.2	62
46	Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes. <i>Science</i> , 2016, 351, 1192-1195.	6.0	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.	5.1	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.	1.1	7
49	Comparative Analysis of Secretome Profiles of Manganese(II)-Oxidizing Ascomycete Fungi. <i>PLoS ONE</i> , 2016, 11, e0157844.	1.1	49
50	The Pacific Northwest National Laboratory library of bacterial and archaeal proteomic biodiversity. <i>Scientific Data</i> , 2015, 2, 150041.	2.4	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.	3.2	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.	1.1	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.	1.1	28
54	A comprehensive collection of systems biology data characterizing the host response to viral infection. <i>Scientific Data</i> , 2014, 1, 140033.	2.4	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.	1.3	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.	1.3	75
57	Automated Genome Mining of Ribosomal Peptide Natural Products. <i>ACS Chemical Biology</i> , 2014, 9, 1545-1551.	1.6	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.	1.8	20
59	Basophile: Accurate Fragment Charge State Prediction Improves Peptide Identification Rates. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 86-95.	3.0	1
60	Amino acid treatment enhances protein recovery from sediment and soils for metaproteomic studies. <i>Proteomics</i> , 2013, 13, 2776-2785.	1.3	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.	1.4	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.	6.2	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.	1.1	81
65	Comparative Omics-Driven Genome Annotation Refinement: Application across <i>Yersinia</i> . <i>PLoS ONE</i> , 2012, 7, e33903.	1.1	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.	1.8	22
67	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. <i>ISME Journal</i> , 2012, 6, 1688-1701.	4.4	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.	3.3	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.	3.2	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.	3.2	46
71	Proteomics-based Compositional Analysis of Complex Cellulaseâ€“Hemicellulase Mixtures. <i>Journal of Proteome Research</i> , 2011, 10, 4365-4372.	1.8	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.	4.4	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.	1.2	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.	1.2	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.	1.8	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.	2.5	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.	1.6	19
78	Strategy for Degradomic-Peptidomic Analysis of Human Blood Plasma. <i>Journal of Proteome Research</i> , 2010, 9, 2339-2346.	1.8	43
79	Establishing the Proteome of Normal Human Cerebrospinal Fluid. <i>PLoS ONE</i> , 2010, 5, e10980.	1.1	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.	1.1	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.	2.5	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.	3.2	615
83	Quantitative Analysis of Cell Surface Membrane Proteins Using Membrane-Impermeable Chemical Probe Coupled with ¹⁸ O Labeling. <i>Journal of Proteome Research</i> , 2010, 9, 2160-2169.	1.8	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.	3.2	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.	1.8	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.	1.8	18
87	Blood Peptidome-Degradome Profile of Breast Cancer. <i>PLoS ONE</i> , 2010, 5, e13133.	1.1	54
88	Proteomic Detection of Non-Annotated Protein-Coding Genes in <i>Pseudomonas fluorescens</i> Pf0-1. <i>PLoS ONE</i> , 2009, 4, e8455.	1.1	34
89	Statistically appraising process quality of affinity isolation experiments. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1720-1726.	0.7	0
90	Platelet Proteome Changes Associated with Diabetes and during Platelet Storage for Transfusion. <i>Journal of Proteome Research</i> , 2009, 8, 2261-2272.	1.8	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.	3.2	30
92	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	9.4	155
93	Improved Methods for the Enrichment and Analysis of Glycated Peptides. <i>Analytical Chemistry</i> , 2008, 80, 9822-9829.	3.2	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.	3.2	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.	1.8	37
96	Mass Spectrometry Analysis of Proteome-Wide Proteolytic Post-Translational Degradation of Proteins. <i>Analytical Chemistry</i> , 2008, 80, 5819-5828.	3.2	14
97	Mixed-Effects Statistical Model for Comparative LC-MS Proteomics Studies. <i>Journal of Proteome Research</i> , 2008, 7, 1209-1217.	1.8	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.	1.8	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.	3.2	46
100	Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step ¹⁸ O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography. <i>Journal of Proteome Research</i> , 2008, 7, 4215-4224.	1.8	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.	3.2	36
102	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. <i>Bioinformatics</i> , 2008, 24, 1021-1023.	1.8	143
103	Proteogenomics: needs and roles to be filled by proteomics in genome annotation. <i>Briefings in Functional Genomics & 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.	2.5	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.	1.8	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.	1.8	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.	2.5	197
108	Tertiary Structural Rearrangements upon Oxidation of Methionine145 in Calmodulin Promotes Targeted Proteasomal Degradation. <i>Biophysical Journal</i> , 2006, 91, 1480-1493.	0.2	30

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109	Analysis of the Salmonella typhimurium Proteome through Environmental Response toward Infectious Conditions. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1450-1461.	2.5	103
110	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	2.5	142
111	Proteomic Analysis of Salmonella enterica Serovar Typhimurium Isolated from RAW 264.7 Macrophages. <i>Journal of Biological Chemistry</i> , 2006, 281, 29131-29140.	1.6	136
112	Global profiling of Shewanella oneidensis MR-1: Expression of hypothetical genes and improved functional annotations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2099-2104.	3.3	113
113	Standard Mixtures for Proteome Studies. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 79-92.	1.0	48
114	Spectral Quality Assessment for High-Throughput Tandem Mass Spectrometry Proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 255-265.	1.0	51
115	In Silico Metabolic Model and Protein Expression of Haemophilus influenzae Strain Rd KW20 in Rich Medium. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 25-41.	1.0	42
116	Identification and functional analysis of 'hypothetical' genes expressed in Haemophilus influenzae. <i>Nucleic Acids Research</i> , 2004, 32, 2353-2361.	6.5	75
117	Initial Proteome Analysis of Model Microorganism Haemophilus influenzae Strain Rd KW20. <i>Journal of Bacteriology</i> , 2003, 185, 4593-4602.	1.0	66
118	Proteomic analysis of Pseudomonas aeruginosa grown under magnesium limitation. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 742-751.	1.2	79
119	Shotgun collision-induced dissociation of peptides using a time of flight mass analyzer. <i>Proteomics</i> , 2003, 3, 847-850.	1.3	158
120	The study of macromolecular complexes by quantitative proteomics. <i>Nature Genetics</i> , 2003, 33, 349-355.	9.4	350
121	Quantitative proteomic analysis indicates increased synthesis of a quinolone by Pseudomonas aeruginosa isolates from cystic fibrosis airways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2771-2776.	3.3	137
122	H. influenzae Consortium: Integrative Study of H. influenzae-Human Interactions. <i>OMICS A Journal of Integrative Biology</i> , 2002, 6, 341-348.	1.0	4
123	Experimental Protein Mixture for Validating Tandem Mass Spectral Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2002, 6, 207-212.	1.0	246
124	Approaching complete peroxisome characterization by gas-phase fractionation. <i>Electrophoresis</i> , 2002, 23, 3205-3216.	1.3	193
125	Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1214-1221.	0.7	277