Martin von Bergen

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#	Paper	IF	Citations
322	Sex differences in the gut microbiome drive hormone-dependent regulation of autoimmunity. <i>Science</i> , 2013 , 339, 1084-8	33.3	1158
321	Complete nitrification by Nitrospira bacteria. <i>Nature</i> , 2015 , 528, 504-9	50.4	1148
320	Assembly of tau protein into Alzheimer paired helical filaments depends on a local sequence motif ((306)VQIVYK(311)) forming beta structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 5129-34	11.5	743
319	Mutations of tau protein in frontotemporal dementia promote aggregation of paired helical filaments by enhancing local beta-structure. <i>Journal of Biological Chemistry</i> , 2001 , 276, 48165-74	5.4	395
318	Gut microbiota disturbance during antibiotic therapy: a multi-omic approach. <i>Gut</i> , 2013 , 62, 1591-601	19.2	371
317	A nucleated assembly mechanism of Alzheimer paired helical filaments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 15712-7	11.5	292
316	Global hairpin folding of tau in solution. <i>Biochemistry</i> , 2006 , 45, 2283-93	3.2	277
315	Inducible expression of Tau repeat domain in cell models of tauopathy: aggregation is toxic to cells but can be reversed by inhibitor drugs. <i>Journal of Biological Chemistry</i> , 2006 , 281, 1205-14	5.4	255
314	Anthraquinones inhibit tau aggregation and dissolve Alzheimer's paired helical filaments in vitro and in cells. <i>Journal of Biological Chemistry</i> , 2005 , 280, 3628-35	5.4	253
313	Tau aggregation is driven by a transition from random coil to beta sheet structure. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2005 , 1739, 158-66	6.9	249
312	Functional metaproteome analysis of protein extracts from contaminated soil and groundwater. <i>ISME Journal</i> , 2007 , 1, 224-34	11.9	229
311	Sites of tau important for aggregation populate {beta}-structure and bind to microtubules and polyanions. <i>Journal of Biological Chemistry</i> , 2005 , 280, 24978-86	5.4	229
310	Dysbiotic gut microbiota causes transmissible Crohn's disease-like ileitis independent of failure in antimicrobial defence. <i>Gut</i> , 2016 , 65, 225-37	19.2	220
309	Highly populated turn conformations in natively unfolded tau protein identified from residual dipolar couplings and molecular simulation. <i>Journal of the American Chemical Society</i> , 2007 , 129, 5235-4	13 ^{16.4}	186
308	MiR-130a, miR-203 and miR-205 jointly repress key oncogenic pathways and are downregulated in prostate carcinoma. <i>Oncogene</i> , 2013 , 32, 277-85	9.2	183
307	Structural principles of tau and the paired helical filaments of Alzheimer's disease. <i>Brain Pathology</i> , 2007 , 17, 83-90	6	179
306	The natively unfolded character of tau and its aggregation to Alzheimer-like paired helical filaments. <i>Biochemistry</i> , 2008 , 47, 10526-39	3.2	177

(2010-2011)

305	combined proteomic and metabolomic profiling of serum reveals association of the complement system with obesity and identifies novel markers of body fat mass changes. <i>Journal of Proteome Research</i> , 2011 , 10, 4769-88	5.6	164
304	Cyanate as an energy source for nitrifiers. <i>Nature</i> , 2015 , 524, 105-8	50.4	160
303	Soil Fungal:Bacterial Ratios Are Linked to Altered Carbon Cycling. Frontiers in Microbiology, 2016 , 7, 124	1 7 5.7	159
302	Microbiota from the distal guts of lean and obese adolescents exhibit partial functional redundancy besides clear differences in community structure. <i>Environmental Microbiology</i> , 2013 , 15, 211-26	5.2	150
301	Membrane vesicle formation as a multiple-stress response mechanism enhances Pseudomonas putida DOT-T1E cell surface hydrophobicity and biofilm formation. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 6217-24	4.8	148
300	Maternal and newborn vitamin D status and its impact on food allergy development in the German LINA cohort study. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2013 , 68, 220-8	9.3	144
299	Diverse sulfate-reducing bacteria of the Desulfosarcina/Desulfococcus clade are the key alkane degraders at marine seeps. <i>ISME Journal</i> , 2014 , 8, 2029-44	11.9	134
298	RNAcode: robust discrimination of coding and noncoding regions in comparative sequence data. <i>Rna</i> , 2011 , 17, 578-94	5.8	131
297	The "jaws" of the tau-microtubule interaction. <i>Journal of Biological Chemistry</i> , 2007 , 282, 12230-9	5.4	131
296	Characterization of Alzheimer's-like paired helical filaments from the core domain of tau protein using solid-state NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2008 , 130, 5922-8	16.4	124
295	MicroRNA-21 targets tumor suppressor genes ANP32A and SMARCA4. <i>Oncogene</i> , 2011 , 30, 2975-85	9.2	118
294	Structure of tau protein and assembly into paired helical filaments. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2000 , 1502, 122-32	6.9	114
293	Protein-based stable isotope probing (Protein-SIP) reveals active species within anoxic mixed cultures. <i>ISME Journal</i> , 2008 , 2, 1122-33	11.9	113
292	Maternal and cord blood miR-223 expression associates with prenatal tobacco smoke exposure and low regulatory T-cell numbers. <i>Journal of Allergy and Clinical Immunology</i> , 2014 , 133, 543-50	11.5	112
291	The core of tau-paired helical filaments studied by scanning transmission electron microscopy and limited proteolysis. <i>Biochemistry</i> , 2006 , 45, 6446-57	3.2	112
290	Higher plasma levels of lysophosphatidylcholine 18:0 are related to a lower risk of common cancers in a prospective metabolomics study. <i>BMC Medicine</i> , 2016 , 14, 13	11.4	107
289	Metaproteogenomic insights beyond bacterial response to naphthalene exposure and bio-stimulation. <i>ISME Journal</i> , 2013 , 7, 122-36	11.9	92
288	Protein-based stable isotope probing. <i>Nature Protocols</i> , 2010 , 5, 1957-66	18.8	89

287	Insights from quantitative metaproteomics and protein-stable isotope probing into microbial ecology. <i>ISME Journal</i> , 2013 , 7, 1877-85	11.9	88
286	Identification of spore allergens from the indoor mould Aspergillus versicolor. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2008 , 63, 454-60	9.3	85
285	Combined genomic and proteomic approaches identify gene clusters involved in anaerobic 2-methylnaphthalene degradation in the sulfate-reducing enrichment culture N47. <i>Journal of Bacteriology</i> , 2010 , 192, 295-306	3.5	83
284	Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. <i>ISME Journal</i> , 2012 , 6, 2291-301	11.9	82
283	Reversible biological Birch reduction at an extremely low redox potential. <i>Journal of the American Chemical Society</i> , 2010 , 132, 9850-6	16.4	80
282	Incorporation of carbon and nitrogen atoms into proteins measured by protein-based stable isotope probing (Protein-SIP). <i>Rapid Communications in Mass Spectrometry</i> , 2008 , 22, 2889-97	2.2	73
281	Discrimination of different species from the genus Drosophila by intact protein profiling using matrix-assisted laser desorption ionization mass spectrometry. <i>BMC Evolutionary Biology</i> , 2010 , 10, 95	3	70
280	Screening for inhibitors of tau polymerization. <i>Current Alzheimer Research</i> , 2005 , 2, 219-26	3	70
279	Microbial minorities modulate methane consumption through niche partitioning. <i>ISME Journal</i> , 2013 , 7, 2214-28	11.9	67
278	Prospects and challenges of multi-omics data integration in toxicology. <i>Archives of Toxicology</i> , 2020 , 94, 371-388	5.8	66
277	Functional consequences of microbial shifts in the human gastrointestinal tract linked to antibiotic treatment and obesity. <i>Gut Microbes</i> , 2013 , 4, 306-15	8.8	66
276	Expression cartography of human tissues using self organizing maps. <i>BMC Bioinformatics</i> , 2011 , 12, 306	3.6	65
275	Elucidation of in situ polycyclic aromatic hydrocarbon degradation by functional metaproteomics (protein-SIP). <i>Proteomics</i> , 2013 , 13, 2910-20	4.8	63
274	Improving protein extraction and separation methods for investigating the metaproteome of anaerobic benzene communities within sediments. <i>Biodegradation</i> , 2009 , 20, 737-50	4.1	63
273	Synbiotic-driven improvement of metabolic disturbances is associated with changes in the gut microbiome in diet-induced obese mice. <i>Molecular Metabolism</i> , 2019 , 22, 96-109	8.8	62
272	Human fibroblasts support the expansion of IL-17-producing T cells via up-regulation of IL-23 production by dendritic cells. <i>Blood</i> , 2010 , 116, 1715-25	2.2	60
271	Comparative analysis of the venom proteomes of Vipera ammodytes ammodytes and Vipera ammodytes meridionalis. <i>Journal of Proteome Research</i> , 2008 , 7, 866-86	5.6	60
270	The effect of the degree of sulfation of glycosaminoglycans on osteoclast function and signaling pathways. <i>Biomaterials</i> , 2012 , 33, 8418-29	15.6	59

269	Structure, stability, and aggregation of paired helical filaments from tau protein and FTDP-17 mutants probed by tryptophan scanning mutagenesis. <i>Journal of Biological Chemistry</i> , 2002 , 277, 41390)- 40 0	58	
268	The acclimation of Phaeodactylum tricornutum to blue and red light does not influence the photosynthetic light reaction but strongly disturbs the carbon allocation pattern. <i>PLoS ONE</i> , 2014 , 9, e99727	3.7	58	
267	Adipose tissue derived bacteria are associated with inflammation in obesity and type 2 diabetes. <i>Gut</i> , 2020 , 69, 1796-1806	19.2	58	
266	Rational design of a microbial consortium of mucosal sugar utilizers reduces Clostridiodes difficile colonization. <i>Nature Communications</i> , 2020 , 11, 5104	17.4	57	
265	In situ protein-SIP highlights Burkholderiaceae as key players degrading toluene by para ring hydroxylation in a constructed wetland model. <i>Environmental Microbiology</i> , 2016 , 18, 1176-86	5.2	57	
264	Identification of a multi-protein reductive dehalogenase complex in Dehalococcoides mccartyi strain CBDB1 suggests a protein-dependent respiratory electron transport chain obviating quinone involvement. <i>Environmental Microbiology</i> , 2016 , 18, 3044-56	5.2	57	
263	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 741-753	11.5	56	
262	Protein-based stable isotope probing (protein-SIP) in functional metaproteomics. <i>Mass Spectrometry Reviews</i> , 2012 , 31, 683-97	11	55	
261	The aromatic volatile organic compounds toluene, benzene and styrene induce COX-2 and prostaglandins in human lung epithelial cells via oxidative stress and p38 MAPK activation. <i>Toxicology</i> , 2011 , 289, 28-37	4.4	55	
260	Metabolomic biomarkers correlating with hepatic lipidosis in dairy cows. <i>BMC Veterinary Research</i> , 2014 , 10, 122	2.7	54	
259	Sulfated hyaluronan containing collagen matrices enhance cell-matrix-interaction, endocytosis, and osteogenic differentiation of human mesenchymal stromal cells. <i>Journal of Proteome Research</i> , 2013 , 12, 378-89	5.6	54	
258	The venomics of Bothrops alternatus is a pool of acidic proteins with predominant hemorrhagic and coagulopathic activities. <i>Journal of Proteome Research</i> , 2010 , 9, 2422-37	5.6	54	
257	Snake venomics of the Siamese Russell's viper (Daboia russelli siamensis) relation to pharmacological activities. <i>Journal of Proteomics</i> , 2009 , 72, 256-69	3.9	54	
256	Anaerobic naphthalene degradation by sulfate-reducing Desulfobacteraceae from various anoxic aquifers. <i>FEMS Microbiology Ecology</i> , 2015 , 91,	4.3	53	
255	Relationship between sources and patterns of VOCs in indoor air. <i>Atmospheric Pollution Research</i> , 2014 , 5, 129-137	4.5	53	
254	Snake venomic of Crotalus durissus terrificuscorrelation with pharmacological activities. <i>Journal of Proteome Research</i> , 2010 , 9, 2302-16	5.6	53	
253	Effects of chronic dietary exposure of zinc oxide nanoparticles on the serum protein profile of juvenile common carp (Cyprinus carpio L.). <i>Science of the Total Environment</i> , 2017 , 579, 1504-1511	10.2	51	
252	Microbiome manipulation modifies sex-specific risk for autoimmunity. <i>Gut Microbes</i> , 2014 , 5, 485-93	8.8	51	

251	Metaproteome analysis and molecular genetics of rat intestinal microbiota reveals section and localization resolved species distribution and enzymatic functionalities. <i>Journal of Proteome Research</i> , 2012 , 11, 5406-17	5.6	51	
250	Enhancing metaproteomicsThe value of models and defined environmental microbial systems. <i>Proteomics</i> , 2016 , 16, 783-98	4.8	50	
249	Phenol degradation in the strictly anaerobic iron-reducing bacterium Geobacter metallireducens GS-15. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3912-9	4.8	49	
248	Structural and microtubule binding properties of tau mutants of frontotemporal dementias. <i>Biochemistry</i> , 2007 , 46, 2574-82	3.2	48	
247	Mechanistic insights into the global response to phenol in the phenol-biodegrading strain Pseudomonas sp. M1 revealed by quantitative proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2007 , 11, 233-51	3.8	48	
246	Identification and characterization of 2-naphthoyl-coenzyme A reductase, the prototype of a novel class of dearomatizing reductases. <i>Molecular Microbiology</i> , 2013 , 88, 1032-9	4.1	47	
245	Spectroscopic approaches to the conformation of tau protein in solution and in paired helical filaments. <i>Neurodegenerative Diseases</i> , 2006 , 3, 197-206	2.3	47	
244	Structural characterization of beta-sheeted oligomers formed on the pathway of oxidative prion protein aggregation in vitro. <i>Journal of Structural Biology</i> , 2007 , 157, 308-20	3.4	47	
243	An unusual strategy for the anoxic biodegradation of phthalate. ISME Journal, 2017, 11, 224-236	11.9	46	
242	Bacteria dominate the short-term assimilation of plant-derived N in soil. <i>Soil Biology and Biochemistry</i> , 2016 , 96, 30-38	7.5	46	
241	Elucidating MTBE degradation in a mixed consortium using a multidisciplinary approach. <i>FEMS Microbiology Ecology</i> , 2010 , 73, 370-84	4.3	46	
240	Vitellogenin cleavage products as indicators for toxic stress in zebra fish embryos: a proteomic approach. <i>Proteomics</i> , 2007 , 7, 4541-54	4.8	46	
239	MetaProSIP: automated inference of stable isotope incorporation rates in proteins for functional metaproteomics. <i>Journal of Proteome Research</i> , 2015 , 14, 619-27	5.6	45	
238	Protein-SIP in environmental studies. <i>Current Opinion in Biotechnology</i> , 2016 , 41, 26-33	11.4	45	
237	Combining metagenomics with metaproteomics and stable isotope probing reveals metabolic pathways used by a naturally occurring marine methylotroph. <i>Environmental Microbiology</i> , 2015 , 17, 40	o 7 - 1 8	45	
236	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. <i>Scientific Reports</i> , 2016 , 6, 28616	4.9	44	
235	Volatile organic compounds enhance allergic airway inflammation in an experimental mouse model. <i>PLoS ONE</i> , 2012 , 7, e39817	3.7	44	
234	Dehalococcoides mccartyi strain DCMB5 Respires a broad spectrum of chlorinated aromatic compounds. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 587-96	4.8	43	

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233	Biochemical and molecular genetic characterisation of a novel laccase produced by the aquatic ascomycete Phoma sp. UHH 5-1-03. <i>Applied Microbiology and Biotechnology</i> , 2009 , 84, 1095-105	5.7	43
232	Random Survival Forest in practice: a method for modelling complex metabolomics data in time to event analysis. <i>International Journal of Epidemiology</i> , 2016 , 45, 1406-1420	7.8	42
231	Analysis of structure, function, and activity of a benzene-degrading microbial community. <i>FEMS Microbiology Ecology</i> , 2013 , 85, 14-26	4.3	42
230	Metaproteomics and metabolomics analyses of chronically petroleum-polluted sites reveal the importance of general anaerobic processes uncoupled with degradation. <i>Proteomics</i> , 2015 , 15, 3508-20	4.8	42
229	Serum metabolites and risk of myocardial infarction and ischemic stroke: a targeted metabolomic approach in two German prospective cohorts. <i>European Journal of Epidemiology</i> , 2018 , 33, 55-66	12.1	42
228	Maternal paraben exposure triggers childhood overweight development. <i>Nature Communications</i> , 2020 , 11, 561	17.4	41
227	Mining SOM expression portraits: feature selection and integrating concepts of molecular function. <i>BioData Mining</i> , 2012 , 5, 18	4.3	41
226	Advanced tool for characterization of microbial cultures by combining cytomics and proteomics. <i>Applied Microbiology and Biotechnology</i> , 2010 , 88, 575-84	5.7	41
225	Di-(2-Ethylhexyl)-Phthalate (DEHP) Causes Impaired Adipocyte Function and Alters Serum Metabolites. <i>PLoS ONE</i> , 2015 , 10, e0143190	3.7	41
224	Interactions between bile salts, gut microbiota, and hepatic innate immunity. <i>Immunological Reviews</i> , 2017 , 279, 23-35	11.3	40
223	Fatty Acid Oxidation Compensates for Lipopolysaccharide-Induced Warburg Effect in Glucose-Deprived Monocytes. <i>Frontiers in Immunology</i> , 2017 , 8, 609	8.4	39
222	Prenatal VOC exposure and redecoration are related to wheezing in early infancy. <i>Environment International</i> , 2014 , 73, 393-401	12.9	39
221	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. <i>Proteomics</i> , 2013 , 13, 2786-804	4.8	39
220	Identification of harmless and pathogenic algae of the genus Prototheca by MALDI-MS. <i>Proteomics - Clinical Applications</i> , 2009 , 3, 774-84	3.1	39
219	Comparison of targeted peptide quantification assays for reductive dehalogenases by selective reaction monitoring (SRM) and precursor reaction monitoring (PRM). <i>Analytical and Bioanalytical Chemistry</i> , 2014 , 406, 283-91	4.4	38
218	Styrene induces an inflammatory response in human lung epithelial cells via oxidative stress and NF-kappaB activation. <i>Toxicology and Applied Pharmacology</i> , 2008 , 231, 241-7	4.6	38
217	Concentration-response concept in ecotoxicoproteomics: effects of different phenanthrene concentrations to the zebrafish (Danio rerio) embryo proteome. <i>Ecotoxicology and Environmental Safety</i> , 2012 , 76, 11-22	7	37
216	Decarboxylating and nondecarboxylating glutaryl-coenzyme A dehydrogenases in the aromatic metabolism of obligately anaerobic bacteria. <i>Journal of Bacteriology</i> , 2009 , 191, 4401-9	3.5	36

215	Optimization of parameters for coverage of low molecular weight proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2010 , 398, 2867-81	4.4	36
214	Proteomics of the organohalide-respiring Epsilonproteobacterium Sulfurospirillum multivorans adapted to tetrachloroethene and other energy substrates. <i>Scientific Reports</i> , 2015 , 5, 13794	4.9	35
213	Enzymes involved in the anaerobic degradation of meta-substituted halobenzoates. <i>Molecular Microbiology</i> , 2011 , 82, 758-69	4.1	35
212	Identification of T helper (Th)1- and Th2-associated antigens of Cryptococcus neoformans in a murine model of pulmonary infection. <i>Scientific Reports</i> , 2018 , 8, 2681	4.9	34
211	Time resolved protein-based stable isotope probing (Protein-SIP) analysis allows quantification of induced proteins in substrate shift experiments. <i>Proteomics</i> , 2011 , 11, 2265-74	4.8	34
210	A metabolomics approach to characterize phenotypes of metabolic transition from late pregnancy to early lactation in dairy cows. <i>Metabolomics</i> , 2016 , 12, 1	4.7	33
209	Tracking active groundwater microbes with D O labelling to understand their ecosystem function. <i>Environmental Microbiology</i> , 2018 , 20, 369-384	5.2	33
208	Subpopulation-proteomics in prokaryotic populations. Current Opinion in Biotechnology, 2013, 24, 79-87	11.4	32
207	Identification of new protein coding sequences and signal peptidase cleavage sites of Helicobacter pylori strain 26695 by proteogenomics. <i>Journal of Proteomics</i> , 2013 , 86, 27-42	3.9	32
206	Pseudechis australis venomics: adaptation for a defense against microbial pathogens and recruitment of body transferrin. <i>Journal of Proteome Research</i> , 2011 , 10, 2440-64	5.6	32
205	Methylamine as a nitrogen source for microorganisms from a coastal marine environment. <i>Environmental Microbiology</i> , 2017 , 19, 2246-2257	5.2	31
204	Osteoblast-released Matrix Vesicles, Regulation of Activity and Composition by Sulfated and Non-sulfated Glycosaminoglycans. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 558-72	7.6	31
203	Combined serum proteomic and metabonomic profiling after laparoscopic sleeve gastrectomy in children and adolescents. <i>Journal of Laparoendoscopic and Advanced Surgical Techniques - Part A</i> , 2012 , 22, 184-8	2.1	30
202	Insight into the modulation of intestinal proteome of juvenile common carp (Cyprinus carpio L.) after dietary exposure to ZnO nanoparticles. <i>Science of the Total Environment</i> , 2018 , 613-614, 62-71	10.2	29
201	Microbial interactions during residual oil and n-fatty acid metabolism by a methanogenic consortium. <i>Environmental Microbiology Reports</i> , 2012 , 4, 297-306	3.7	29
200	Chlorinated benzenes cause concomitantly oxidative stress and induction of apoptotic markers in lung epithelial cells (A549) at nonacute toxic concentrations. <i>Journal of Proteome Research</i> , 2011 , 10, 363-78	5.6	29
199	Impact of vitamin B12 on formation of the tetrachloroethene reductive dehalogenase in Desulfitobacterium hafniense strain Y51. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 8025-32	4.8	29
198	The LINA cohort: indoor chemical exposure, circulating eosinophil/basophil (Eo/B) progenitors and early life skin manifestations. Clinical and Experimental Allergy, 2012, 42, 1337-46	4.1	28

197	MALDI-typing of infectious algae of the genus Prototheca using SOM portraits. <i>Journal of Microbiological Methods</i> , 2012 , 88, 83-97	2.8	28	
196	Attenuation of Postoperative Acute Liver Failure by Mesenchymal Stem Cell Treatment Due to Metabolic Implications. <i>Annals of Surgery</i> , 2016 , 263, 546-56	7.8	28	
195	Structural and functional insights into the interaction of sulfated glycosaminoglycans with tissue inhibitor of metalloproteinase-3 - A possible regulatory role on extracellular matrix homeostasis. <i>Acta Biomaterialia</i> , 2016 , 45, 143-154	10.8	28	
194	Comparative performance evaluation of multi-metal resistant fungal strains for simultaneous removal of multiple hazardous metals. <i>Journal of Hazardous Materials</i> , 2016 , 318, 679-685	12.8	28	
193	Candidate Brocadiales dominates C, N and S cycling in anoxic groundwater of a pristine limestone-fracture aquifer. <i>Journal of Proteomics</i> , 2017 , 152, 153-160	3.9	27	
192	Phylogenetic and proteomic analysis of an anaerobic toluene-degrading community. <i>Journal of Applied Microbiology</i> , 2010 , 109, 1937-45	4.7	27	
191	ATP-Dependent C-F Bond Cleavage Allows the Complete Degradation of 4-Fluoroaromatics without Oxygen. <i>MBio</i> , 2016 , 7,	7.8	27	
190	Characterization of a multianalyte GC-MS/MS procedure for detecting and quantifying polycyclic aromatic hydrocarbons (PAHs) and PAH derivatives from air particulate matter for an improved risk assessment. <i>Environmental Pollution</i> , 2019 , 255, 112967	9.3	26	
189	Deforestation fosters bacterial diversity and the cyanobacterial community responsible for carbon fixation processes under semiarid climate: a metaproteomics study. <i>Applied Soil Ecology</i> , 2015 , 93, 65-6	7 ⁵	26	
188	The ABCG2 Efflux Transporter in the Mammary Gland Mediates Veterinary Drug Secretion across the Blood-Milk Barrier into Milk of Dairy Cows. <i>Drug Metabolism and Disposition</i> , 2016 , 44, 700-8	4	26	
187	Genomic, Proteomic, and Metabolite Characterization of Gemfibrozil-Degrading Organism Bacillus sp. GeD10. <i>Environmental Science & Environmental Scien</i>	10.3	26	
186	Metaproteogenomic analysis of a sulfate-reducing enrichment culture reveals genomic organization of key enzymes in the m-xylene degradation pathway and metabolic activity of proteobacteria. Systematic and Applied Microbiology, 2014, 37, 488-501	4.2	26	
185	Pathway and time-resolved benzo[a]pyrene toxicity on Hepa1c1c7 cells at toxic and subtoxic exposure. <i>Journal of Proteome Research</i> , 2015 , 14, 164-82	5.6	26	
184	Context-specific metabolic network reconstruction of a naphthalene-degrading bacterial community guided by metaproteomic data. <i>Bioinformatics</i> , 2015 , 31, 1771-9	7.2	26	
183	Proteome profile and proteogenomics of the organohalide-respiring bacterium Dehalococcoides mccartyi strain CBDB1 grown on hexachlorobenzene as electron acceptor. <i>Journal of Proteomics</i> , 2014 , 98, 59-64	3.9	26	
182	Identification and characterization of a re-citrate synthase in Dehalococcoides strain CBDB1. Journal of Bacteriology, 2011 , 193, 5171-8	3.5	26	
181	Aromatizing cyclohexa-1,5-diene-1-carbonyl-coenzyme A oxidase. Characterization and its role in anaerobic aromatic metabolism. <i>Journal of Biological Chemistry</i> , 2008 , 283, 20713-21	5.4	26	
180	Rice Paddy Nitrospirae Carry and Express Genes Related to Sulfate Respiration: Proposal of the New Genus "Candidatus Sulfobium". <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	26	

179	Biochemical Foundations of Health and Energy Conservation in Hibernating Free-ranging Subadult Brown Bear Ursus arctos. <i>Journal of Biological Chemistry</i> , 2016 , 291, 22509-22523	5.4	25
178	Comparison of methods for simultaneous identification of bacterial species and determination of metabolic activity by protein-based stable isotope probing (Protein-SIP) experiments. <i>Rapid Communications in Mass Spectrometry</i> , 2009 , 23, 1871-8	2.2	25
177	Validation of a multi-analyte HPLC-DAD method for determination of uric acid, creatinine, homovanillic acid, niacinamide, hippuric acid, indole-3-acetic acid and 2-methylhippuric acid in human urine. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life	3.2	24
176	Sciences, 2015 , 998-999, 40-4 Maximization of cell viability rather than biocatalyst activity improves whole-cell Ebxyfunctionalization performance. <i>Biotechnology and Bioengineering</i> , 2017 , 114, 874-884	4.9	24
175	Exploring the limits of robust detection of incorporation of 13C by mass spectrometry in protein-based stable isotope probing (protein-SIP). <i>Analytical and Bioanalytical Chemistry</i> , 2011 , 401, 1975-82	4.4	24
174	A patchwork pathway for oxygenase-independent degradation of side chain containing steroids. <i>Environmental Microbiology</i> , 2017 , 19, 4684-4699	5.2	23
173	Disease Development Is Accompanied by Changes in Bacterial Protein Abundance and Functions in a Refined Model of Dextran Sulfate Sodium (DSS)-Induced Colitis. <i>Journal of Proteome Research</i> , 2019 , 18, 1774-1786	5.6	23
172	An integrative overview of genomic, transcriptomic and proteomic analyses in organohalide respiration research. <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	23
171	One-megadalton metalloenzyme complex in involved in benzene ring reduction beyond the biological redox window. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 2259-2264	11.5	22
170	Optimization of metabolomics of defined in vitro gut microbial ecosystems. <i>International Journal of Medical Microbiology</i> , 2016 , 306, 280-289	3.7	22
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17	Differences in cortical contractility between healthy epithelial and cancerous mesenchymal breast cells. <i>New Journal of Physics</i> ,	2.9	1
16	The EU chemicals strategy for sustainability: an opportunity to develop new approaches for hazard and risk assessment <i>Archives of Toxicology</i> , 2022 ,	5.8	1
15	Microbial community functioning during plant litter decomposition Scientific Reports, 2022, 12, 7451	4.9	1
14	Danger signal extracellular calcium initiates differentiation of monocytes into SPP1/osteopontin-producing macrophages <i>Cell Death and Disease</i> , 2022 , 13, 53	9.8	O
13	Effects of exposure to single and multiple parabens on asthma development in an experimental mouse model and a prospective cohort study <i>Science of the Total Environment</i> , 2021 , 814, 152676	10.2	O
12	An environmental ecocorona influences the formation and evolution of the biological corona on the surface of single-walled carbon nanotubes <i>NanoImpact</i> , 2021 , 22, 100315	5.6	O
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4	Protein Stable Isotope Probing73-95		
3	PIPINO: A Software Package to Facilitate the Identification of Protein-Protein Interactions from Affinity Purification Mass Spectrometry Data. <i>BioMed Research International</i> , 2016 , 2016, 2891918	3	
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