

Stephan Schmitz-Esser

List of Publications by Year in descending order

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Version: 2024-02-01

124
papers

4,591
citations

87723

38
h-index

114278

63
g-index

131
all docs

131
docs citations

131
times ranked

4905
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Sequences of Soft Rot-Causing <i>Pectobacterium</i> Isolates from Different Vegetables. <i>Microbiology Resource Announcements</i> , 2022, 11, e0106621.	0.3	2
2	The life cycle-dependent transcriptional profile of the obligate intracellular amoeba symbiont <i>Amoebophilus asiaticus</i> . <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	1
3	Quality over quantity: unraveling the contributions to cytoplasmic incompatibility caused by two coinfecting <i>Cardinium</i> symbionts. <i>Heredity</i> , 2022, , .	1.2	4
4	Metatranscriptomic Analyses Unravel Dynamic Changes in the Microbial and Metabolic Transcriptional Profiles in Artisanal Austrian Hard-Cheeses During Ripening. <i>Frontiers in Microbiology</i> , 2022, 13, 813480.	1.5	4
5	The validation of the existence of the entero-mammary pathway and the assessment of the differences of the pathway between first and third parity sows. <i>Translational Animal Science</i> , 2022, 6, .	0.4	4
6	185 The Validation of the Existence of the Entero-Mammary Pathway and the Assessment of the Differences of the Pathway Between Gilts and Sows. <i>Journal of Animal Science</i> , 2022, 100, 88-88.	0.2	0
7	Comparison of intestinal permeability, morphology, and ileal microbial communities of commercial hens housed in conventional cages and cage-free housing systems. <i>Poultry Science</i> , 2021, 100, 1178-1191.	1.5	21
8	Xylanase Supplementation Modulates the Microbiota of the Large Intestine of Pigs Fed Corn-Based Fiber by Means of a Stimbiotic Mechanism of Action. <i>Frontiers in Microbiology</i> , 2021, 12, 619970.	1.5	14
9	Rumen Epithelial Communities Share a Core Bacterial Microbiota: A Meta-Analysis of 16S rRNA Gene Illumina MiSeq Sequencing Datasets. <i>Frontiers in Microbiology</i> , 2021, 12, 625400.	1.5	23
10	Vaginal microbiome and serum metabolite differences in late gestation commercial sows at risk for pelvic organ prolapse. <i>Scientific Reports</i> , 2021, 11, 6189.	1.6	9
11	A Large-Scale Sequencing-Based Survey of Plasmids in <i>Listeria monocytogenes</i> Reveals Global Dissemination of Plasmids. <i>Frontiers in Microbiology</i> , 2021, 12, 653155.	1.5	21
12	Virulence Pattern Analysis of Three <i>Listeria monocytogenes</i> Lineage I Epidemic Strains with Distinct Outbreak Histories. <i>Microorganisms</i> , 2021, 9, 1745.	1.6	1
13	Vaginal microbiota differences associated with pelvic organ prolapse risk during late gestation in commercial sows. <i>Biology of Reproduction</i> , 2021, 105, 1545-1561.	1.2	6
14	Certain <i>Listeria monocytogenes</i> plasmids contribute to increased UVC ultraviolet light stress. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	5
15	Xylanase modulates the microbiota of ileal mucosa and digesta of pigs fed corn-based arabinoxylans likely through both a stimbiotic and prebiotic mechanism. <i>PLoS ONE</i> , 2021, 16, e0246144.	1.1	17
16	Ewe Vaginal Microbiota: Associations With Pregnancy Outcome and Changes During Gestation. <i>Frontiers in Microbiology</i> , 2021, 12, 745884.	1.5	12
17	Investigating the relationship between vaginal microbiota and host genetics and their impact on immune response and farrowing traits in commercial gilts. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 84-102.	0.8	16
18	Host immunity and the colon microbiota of mice infected with <i>Citrobacter rodentium</i> are beneficially modulated by lipid-soluble extract from late-cutting alfalfa in the early stages of infection. <i>PLoS ONE</i> , 2020, 15, e0236106.	1.1	2

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19	Virulence characterization and comparative genomics of <i>Listeria monocytogenes</i> sequence type 155 strains. <i>BMC Genomics</i> , 2020, 21, 847.	1.2	26
20	The Cobalamin-Dependent Gene Cluster of <i>Listeria monocytogenes</i> : Implications for Virulence, Stress Response, and Food Safety. <i>Frontiers in Microbiology</i> , 2020, 11, 601816.	1.5	11
21	Beef cattle that respond differently to fescue toxicosis have distinct gastrointestinal tract microbiota. <i>PLoS ONE</i> , 2020, 15, e0229192.	1.1	16
22	The transcriptome of <i>Listeria monocytogenes</i> during co-cultivation with cheese rind bacteria suggests adaptation by induction of ethanolamine and 1,2-propanediol catabolism pathway genes. <i>PLoS ONE</i> , 2020, 15, e0233945.	1.1	17
23	Dietary Supplementation with Sugar Beet Fructooligosaccharides and Garlic Residues Promotes Growth of Beneficial Bacteria and Increases Weight Gain in Neonatal Lambs. <i>Biomolecules</i> , 2020, 10, 1179.	1.8	4
24	High-Fat Diets Led to OTU-Level Shifts in Fecal Samples of Healthy Adult Dogs. <i>Frontiers in Microbiology</i> , 2020, 11, 564160.	1.5	9
25	<i>Cardinium</i> Localization During Its Parasitoid Wasp Host's Development Provides Insights Into Cytoplasmic Incompatibility. <i>Frontiers in Microbiology</i> , 2020, 11, 606399.	1.5	9
26	Austrian Raw-Milk Hard-Cheese Ripening Involves Successional Dynamics of Non-Inoculated Bacteria and Fungi. <i>Foods</i> , 2020, 9, 1851.	1.9	13
27	Beginning to offer drinking water at birth increases the species richness and the abundance of <i>Faecalibacterium</i> and <i>Bifidobacterium</i> in the gut of preweaned dairy calves. <i>Journal of Dairy Science</i> , 2020, 103, 4262-4274.	1.4	8
28	Vaginal microbiota diverges in sows with low and high reproductive performance after porcine reproductive and respiratory syndrome vaccination. <i>Scientific Reports</i> , 2020, 10, 3046.	1.6	17
29	The Rumen Epithelial Microbiota: Possible Gatekeepers of the Rumen Epithelium and Its Potential Contributions to Epithelial Barrier Function and Animal Health and Performance. <i>Meat and Muscle Biology</i> , 2020, 4, .	0.7	3
30	PSVIII-3 Can the fermentation of insoluble corn fiber be improved in the pig? An investigation into the in vivo mode of action of xylanase. <i>Journal of Animal Science</i> , 2020, 98, 207-207.	0.2	1
31	20 Vaginal microbiome composition is associated with sow longevity. <i>Journal of Animal Science</i> , 2020, 98, 23-24.	0.2	0
32	399 Towards improving pig livability: Strategies to understand and mitigate sow mortality. <i>Journal of Animal Science</i> , 2020, 98, 183-184.	0.2	0
33	Title is missing!. , 2020, 15, e0229192.		0
34	Title is missing!. , 2020, 15, e0229192.		0
35	Title is missing!. , 2020, 15, e0229192.		0
36	Title is missing!. , 2020, 15, e0229192.		0

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37	Title is missing!. , 2020, 15, e0229192.		0
38	Title is missing!. , 2020, 15, e0229192.		0
39	Title is missing!. , 2020, 15, e0236106.		0
40	Title is missing!. , 2020, 15, e0236106.		0
41	Title is missing!. , 2020, 15, e0236106.		0
42	Title is missing!. , 2020, 15, e0236106.		0
43	Title is missing!. , 2020, 15, e0233945.		0
44	Title is missing!. , 2020, 15, e0233945.		0
45	Title is missing!. , 2020, 15, e0233945.		0
46	Title is missing!. , 2020, 15, e0233945.		0
47	77 Responses to alfalfa supplementation in mice. Journal of Animal Science, 2019, 97, 45-46.	0.2	0
48	Microbiota of newborn calves and their mothers reveals possible transfer routes for newborn calves'™ gastrointestinal microbiota. PLoS ONE, 2019, 14, e0220554.	1.1	61
49	Fluoxetine-induced alteration of murine gut microbial community structure: evidence for a microbial endocrinology-based mechanism of action responsible for fluoxetine-induced side effects. PeerJ, 2019, 7, e6199.	0.9	62
50	130 Young Scholar Presentation: Can exogenous carbohydrase supplementation to higher-fiber diets improve gut function, microbiota, and growth performance of weaned pigs?. Journal of Animal Science, 2019, 97, 76-76.	0.2	0
51	Brevibacterium from Austrian hard cheese harbor a putative histamine catabolism pathway and a plasmid for adaptation to the cheese environment. Scientific Reports, 2019, 9, 6164.	1.6	35
52	Microbiota of the Gut-Lymph Node Axis: Depletion of Mucosa-Associated Segmented Filamentous Bacteria and Enrichment of Methanobrevibacter by Colistin Sulfate and Linco-Spectin in Pigs. Frontiers in Microbiology, 2019, 10, 599.	1.5	11
53	Microbial shifts in Minas artisanal cheeses from the Serra do Salitre region of Minas Gerais, Brazil throughout ripening time. Food Microbiology, 2019, 82, 349-362.	2.1	32
54	Plasmids contribute to food processing environment-associated stress survival in three Listeria monocytogenes ST121, ST8, and ST5 strains. International Journal of Food Microbiology, 2019, 299, 39-46.	2.1	52

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55	69 The ability of an artificial sweetener (Sucram [®]) to influence microbial community structure in the rumen papillae and content through the production of microbial-based neurochemicals. <i>Journal of Animal Science</i> , 2019, 97, 100-101.	0.2	0
56	219 Relationship between host-genetics and the vaginal microbiome in commercial gilts. <i>Journal of Animal Science</i> , 2019, 97, 43-44.	0.2	0
57	PSII-16 Evidence for stratification of rumen wall microbial communities revealed by 16S rRNA based amplicon sequencing. <i>Journal of Animal Science</i> , 2019, 97, 226-227.	0.2	1
58	Development of a multi-locus sequence typing system helps reveal the evolution of <i>Cardinium hertigii</i> , a reproductive manipulator symbiont of insects. <i>BMC Microbiology</i> , 2019, 19, 266.	1.3	12
59	Exogenous carbohydrases added to a starter diet reduced markers of systemic immune activation and decreased <i>Lactobacillus</i> in weaned pigs. <i>Journal of Animal Science</i> , 2019, 97, 1242-1253.	0.2	8
60	The Plastidic Sugar Transporter pSuT Influences Flowering and Affects Cold Responses. <i>Plant Physiology</i> , 2019, 179, 569-587.	2.3	77
61	Transcriptome Sequencing of <i>Listeria monocytogenes</i> Reveals Major Gene Expression Changes in Response to Lactic Acid Stress Exposure but a Less Pronounced Response to Oxidative Stress. <i>Frontiers in Microbiology</i> , 2019, 10, 3110.	1.5	31
62	385 Evidence for Stratification of Rumen Wall Microbial Communities Revealed By 16S rRNA Based Amplicon Sequencing. <i>Journal of Animal Science</i> , 2018, 96, 207-207.	0.2	0
63	Age-associated microbiome shows the giant panda lives on hemicelluloses, not on cellulose. <i>ISME Journal</i> , 2018, 12, 1319-1328.	4.4	89
64	Autochthonous facility-specific microbiota dominates washed-rind Austrian hard cheese surfaces and its production environment. <i>International Journal of Food Microbiology</i> , 2018, 267, 54-61.	2.1	31
65	Abundance and potential contribution of Gram-negative cheese rind bacteria from Austrian artisanal hard cheeses. <i>International Journal of Food Microbiology</i> , 2018, 266, 95-103.	2.1	17
66	23 Effect of Genetic Response to Endophyte-Infected Fescue on Beef Cattle Gastrointestinal Tract Microbiota. <i>Journal of Animal Science</i> , 2018, 96, 12-13.	0.2	0
67	300 Impact of Fiber-Degrading Enzymes on Microbial Composition and NSP Metabolites in Nursery Pigs Fed a Higher Fiber Diet. <i>Journal of Animal Science</i> , 2018, 96, 161-162.	0.2	0
68	27 Composition and in Situ Gene Expression of Rumen Wall Microbial Communities. <i>Journal of Animal Science</i> , 2018, 96, 14-15.	0.2	0
69	Metatranscriptome Sequencing Reveals Insights into the Gene Expression and Functional Potential of Rumen Wall Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 43.	1.5	54
70	New Aspects on <i>Listeria monocytogenes</i> ST5-ECVI Predominance in a Heavily Contaminated Cheese Processing Environment. <i>Frontiers in Microbiology</i> , 2018, 9, 64.	1.5	45
71	Biphasic Metabolism and Host Interaction of a Chlamydial Symbiont. <i>MSystems</i> , 2017, 2, .	1.7	32
72	Epimural bacterial community structure in the rumen of Holstein cows with different responses to a long-term subacute ruminal acidosis diet challenge. <i>Journal of Dairy Science</i> , 2017, 100, 1829-1844.	1.4	60

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73	Shuttling of (deoxyâ€) purine nucleotides between compartments of the diatom <i>Phaeodactylum tricornutum</i>. <i>New Phytologist</i> , 2017, 213, 193-205.	3.5	20
74	Transcriptome Sequencing Reveals Novel Candidate Genes for <i>Cardinium hertigii</i> -Caused Cytoplasmic Incompatibility and Host-Cell Interaction. <i>MSystems</i> , 2017, 2, .	1.7	35
75	Intestinal microbiota profiles associated with low and high residual feed intake in chickens across two geographical locations. <i>PLoS ONE</i> , 2017, 12, e0187766.	1.1	73
76	Comparative genomics of human and non-human <i>Listeria monocytogenes</i> sequence type 121 strains. <i>PLoS ONE</i> , 2017, 12, e0176857.	1.1	42
77	Age-Related Differences in the Luminal and Mucosa-Associated Gut Microbiome of Broiler Chickens and Shifts Associated with <i>Campylobacter jejuni</i> Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 154.	1.8	134
78	Epimural Indicator Phylotypes of Transiently-Induced Subacute Ruminal Acidosis in Dairy Cattle. <i>Frontiers in Microbiology</i> , 2016, 7, 274.	1.5	34
79	A clinical <i>Acanthamoeba</i> isolate harboring two distinct bacterial endosymbionts. <i>European Journal of Protistology</i> , 2016, 56, 21-25.	0.5	12
80	Microbial communities in dairy processing environment floor-drains are dominated by product-associated bacteria and yeasts. <i>Food Control</i> , 2016, 70, 210-215.	2.8	26
81	Bacterial diversity of floor drain biofilms and drain waters in a <i>Listeria monocytogenes</i> contaminated food processing environment. <i>International Journal of Food Microbiology</i> , 2016, 223, 33-40.	2.1	79
82	Psychrophile spoilers dominate the bacterial microbiome in musculature samples of slaughter pigs. <i>Meat Science</i> , 2016, 117, 36-40.	2.7	27
83	Exoproteome analysis reveals higher abundance of proteins linked to alkaline stress in persistent <i>Listeria monocytogenes</i> strains. <i>International Journal of Food Microbiology</i> , 2016, 218, 17-26.	2.1	30
84	Cheese and Microbes. Edited by Catherine W. Donnelly. Washington (DC): ASM Press. \$150.00. xii + 333 p.; ill.; index. ISBN: 978-1-55581-586-8 (hc); 978-1-55581-859-3 (eb). 2014.. <i>Quarterly Review of Biology</i> , 2015, 90, 346-346.	0.0	0
85	High diversity of viable bacteria isolated from lymph nodes of slaughter pigs and its possible impacts for food safety. <i>Journal of Applied Microbiology</i> , 2015, 119, 1420-1432.	1.4	20
86	Genomes of sequence type 121 <i>Listeria monocytogenes</i> strains harbor highly conserved plasmids and prophages. <i>Frontiers in Microbiology</i> , 2015, 6, 380.	1.5	87
87	The Metabolically Active Bacterial Microbiome of Tonsils and Mandibular Lymph Nodes of Slaughter Pigs. <i>Frontiers in Microbiology</i> , 2015, 6, 1362.	1.5	23
88	Complete Genome Sequence of the Persistent <i>Listeria monocytogenes</i> Strain R479a. <i>Genome Announcements</i> , 2015, 3, .	0.8	18
89	Pyrosequencing reveals shifts in the bacterial epimural community relative to dietary concentrate amount in goats. <i>Journal of Dairy Science</i> , 2015, 98, 5572-5587.	1.4	46
90	Characterization of mucosa-associated bacterial communities in abomasal ulcers by pyrosequencing. <i>Veterinary Microbiology</i> , 2015, 177, 132-141.	0.8	15

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91	Dietary calcium concentration and cereals differentially affect mineral balance and tight junction proteins expression in jejunum of weaned pigs. <i>British Journal of Nutrition</i> , 2015, 113, 1019-1031.	1.2	13
92	Adaptation of the Cecal Bacterial Microbiome of Growing Pigs in Response to Resistant Starch Type 4. <i>Applied and Environmental Microbiology</i> , 2015, 81, 8489-8499.	1.4	59
93	Mucosa-Associated Bacterial Microbiome of the Gastrointestinal Tract of Weaned Pigs and Dynamics Linked to Dietary Calcium-Phosphorus. <i>PLoS ONE</i> , 2014, 9, e86950.	1.1	106
94	Genome Sequencing of <i>Listeria monocytogenes</i> "Quargel" Listeriosis Outbreak Strains Reveals Two Different Strains with Distinct In Vitro Virulence Potential. <i>PLoS ONE</i> , 2014, 9, e89964.	1.1	55
95	Transcriptome analysis of <i>Listeria monocytogenes</i> exposed to biocide stress reveals a multi-system response involving cell wall synthesis, sugar uptake, and motility. <i>Frontiers in Microbiology</i> , 2014, 5, 68.	1.5	75
96	The <i>Listeria monocytogenes</i> transposon Tn6188 provides increased tolerance to various quaternary ammonium compounds and ethidium bromide. <i>FEMS Microbiology Letters</i> , 2014, 361, 166-173.	0.7	68
97	Pyrosequencing reveals diverse fecal microbiota in Simmental calves during early development. <i>Frontiers in Microbiology</i> , 2014, 5, 622.	1.5	78
98	Symbiont-driven sulfur crystal formation in a thiotrophic symbiosis from deep-sea hydrocarbon seeps. <i>Environmental Microbiology Reports</i> , 2014, 6, 364-372.	1.0	26
99	Microbiomes of Unreactive and Pathologically Altered Ileocecal Lymph Nodes of Slaughter Pigs. <i>Applied and Environmental Microbiology</i> , 2014, 80, 193-203.	1.4	27
100	Cultivation-independent analysis of microbial communities on Austrian raw milk hard cheese rinds. <i>International Journal of Food Microbiology</i> , 2014, 180, 88-97.	2.1	74
101	Genome Sequencing of <i>Listeria monocytogenes</i> . <i>Methods in Molecular Biology</i> , 2014, 1157, 223-232.	0.4	2
102	Changing Dietary Calcium-Phosphorus Level and Cereal Source Selectively Alters Abundance of Bacteria and Metabolites in the Upper Gastrointestinal Tracts of Weaned Pigs. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7264-7272.	1.4	64
103	Grain-rich diets differently alter ruminal and colonic abundance of microbial populations and lipopolysaccharide in goats. <i>Anaerobe</i> , 2013, 20, 65-73.	1.0	121
104	The Endosymbiont <i>Amoebophilus asiaticus</i> Encodes an S-Adenosylmethionine Carrier That Compensates for Its Missing Methylation Cycle. <i>Journal of Bacteriology</i> , 2013, 195, 3183-3192.	1.0	9
105	Tn6188 - A Novel Transposon in <i>Listeria monocytogenes</i> Responsible for Tolerance to Benzalkonium Chloride. <i>PLoS ONE</i> , 2013, 8, e76835.	1.1	167
106	Bacteriocyte-associated gammaproteobacterial symbionts of the <i>Adelges nordmannianae/piceae</i> complex (Hemiptera: Adelgidae). <i>ISME Journal</i> , 2012, 6, 384-396.	4.4	49
107	Comparative Genomics Suggests an Independent Origin of Cytoplasmic Incompatibility in <i>Cardinium hertigii</i> . <i>PLoS Genetics</i> , 2012, 8, e1003012.	1.5	135
108	The Plant Mitochondrial Carrier Family: Functional and Evolutionary Aspects. <i>Frontiers in Plant Science</i> , 2012, 3, 2.	1.7	83

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109	A bacterial genome in transition - an exceptional enrichment of IS elements but lack of evidence for recent transposition in the symbiont <i>Amoebophilus asiaticus</i> . <i>BMC Evolutionary Biology</i> , 2011, 11, 270.	3.2	22
110	Nucleotide Parasitism by <i>Simkania negevensis</i> (<i>Chlamydiae</i>). <i>Journal of Bacteriology</i> , 2011, 193, 225-235.	1.0	27
111	The genome of the amoeba symbiont " <i>Candidatus Amoebophilus asiaticus</i> " encodes an afp-like prophage possibly used for protein secretion. <i>Virulence</i> , 2010, 1, 541-545.	1.8	31
112	The Genome of the Amoeba Symbiont <i>Candidatus Amoebophilus asiaticus</i> Reveals Common Mechanisms for Host Cell Interaction among Amoeba-Associated Bacteria. <i>Journal of Bacteriology</i> , 2010, 192, 1045-1057.	1.0	138
113	Diatom plastids depend on nucleotide import from the cytosol. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3621-3626.	3.3	80
114	High genetic similarity between two geographically distinct strains of the sulfur-oxidizing symbiont <i>Candidatus Thiobios zoothamnicoli</i> . <i>FEMS Microbiology Ecology</i> , 2009, 67, 229-241.	1.3	35
115	Environmental genomics reveals a functional chlorite dismutase in the nitrite-oxidizing bacterium <i>Candidatus Nitrospira defluvii</i> . <i>Environmental Microbiology</i> , 2008, 10, 3043-3056.	1.8	102
116	<i>Lawsonia intracellularis</i> Contains a Gene Encoding a Functional Rickettsia-Like ATP/ADP Translocase for Host Exploitation. <i>Journal of Bacteriology</i> , 2008, 190, 5746-5752.	1.0	37
117	Diversity of Bacterial Endosymbionts of Environmental <i>Acanthamoeba</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5822-5831.	1.4	92
118	Tapping the nucleotide pool of the host: novel nucleotide carrier proteins of Protochlamydia amoebophila. <i>Molecular Microbiology</i> , 2006, 60, 1534-1545.	1.2	69
119	<i>Candidatus Thiobios zoothamnicoli</i> , an Ectosymbiotic Bacterium Covering the Giant Marine Ciliate <i>Zoothamnium niveum</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 2014-2021.	1.4	84
120	Recovery of an environmental chlamydia strain from activated sludge by co-cultivation with <i>Acanthamoeba</i> sp.. <i>Microbiology (United Kingdom)</i> , 2005, 151, 301-309.	0.7	73
121	ATP/ADP Translocases: a Common Feature of Obligate Intracellular Amoebal Symbionts Related to Chlamydiae and Rickettsiae. <i>Journal of Bacteriology</i> , 2004, 186, 683-691.	1.0	162
122	A candidate NAD ⁺ transporter in an intracellular bacterial symbiont related to Chlamydiae. <i>Nature</i> , 2004, 432, 622-625.	13.7	95
123	Illuminating the Evolutionary History of Chlamydiae. <i>Science</i> , 2004, 304, 728-730.	6.0	373
124	16S-23S rDNA intergenic spacer and 23S rDNA of anaerobic ammonium-oxidizing bacteria: implications for phylogeny and in situ detection. <i>Environmental Microbiology</i> , 2001, 3, 450-459.	1.8	227