

# Orla O'Sullivan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4469899/publications.pdf>

Version: 2024-02-01

134  
papers

19,386  
citations

20817

60  
h-index

12597

132  
g-index

144  
all docs

144  
docs citations

144  
times ranked

24364  
citing authors

#	ARTICLE	IF	CITATIONS
1	More than a gut feeling: What is the role of the gastrointestinal tract in female athlete health?. European Journal of Sport Science, 2022, 22, 755-764.	2.7	16
2	Impact of nisin on <i>Clostridioides difficile</i> and microbiota composition in a faecal fermentation model of the human colon. Journal of Applied Microbiology, 2022, 132, 1397-1408.	3.1	7
3	Next-Generation Food Research: Use of Meta-Omic Approaches for Characterizing Microbial Communities Along the Food Chain. Annual Review of Food Science and Technology, 2022, 13, 361-384.	9.9	21
4	Identification of Gut Bacteria such as <i>Lactobacillus johnsonii</i> that Disseminate to Systemic Tissues of Wild Type and MyD88 <sup>-/-</sup> Mice. Gut Microbes, 2022, 14, 2007743.	9.8	1
5	A Graph-Based Molecular Communications Model Analysis of the Human Gut Bacteriome. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 3567-3577.	6.3	5
6	Best Practices for Probiotic Research in Athletic and Physically Active Populations: Guidance for Future Randomized Controlled Trials. Frontiers in Nutrition, 2022, 9, 809983.	3.7	11
7	In Vitro and In Silico Based Approaches to Identify Potential Novel Bacteriocins from the Athlete Gut Microbiome of an Elite Athlete Cohort. Microorganisms, 2022, 10, 701.	3.6	8
8	The effects of sustained fitness improvement on the gut microbiome: A longitudinal, repeated measures case study approach. Translational Sports Medicine, 2021, 4, 174-192.	1.1	14
9	The Lung Microbiome in Young Children with Cystic Fibrosis: A Prospective Cohort Study. Microorganisms, 2021, 9, 492.	3.6	12
10	In vitro "in vivo Validation of Stimulatory Effect of Oat Ingredients on Lactobacilli. Pathogens, 2021, 10, 235.	2.8	8
11	Alpha-synuclein alters the faecal viromes of rats in a gut-initiated model of Parkinson's disease. Communications Biology, 2021, 4, 1140.	4.4	6
12	Seasonality and Geography Have a Greater Influence than the Use of Chlorine-Based Cleaning Agents on the Microbiota of Bulk Tank Raw Milk. Applied and Environmental Microbiology, 2021, 87, e0108121.	3.1	8
13	Binding Process Analysis of Bacterial-based AND Logic Gates. , 2021, , .		1
14	Distinct microbiome composition and metabolome exists across subgroups of elite Irish athletes. Journal of Science and Medicine in Sport, 2020, 23, 63-68.	1.3	74
15	Infographic. Athlete health and performance: no guts no glory. British Journal of Sports Medicine, 2020, 54, 250-250.	6.7	1
16	Nigral overexpression of $\alpha$ -synuclein in a rat Parkinson's disease model indicates alterations in the enteric nervous system and the gut microbiome. Neurogastroenterology and Motility, 2020, 32, e13726.	3.0	61
17	Nisin J, a Novel Natural Nisin Variant, Is Produced by <i>Staphylococcus capitis</i> Sourced from the Human Skin Microbiota. Journal of Bacteriology, 2020, 202, .	2.2	48
18	Investigating the Role of Diet and Exercise in Gut Microbe-Host Cometabolism. MSystems, 2020, 5, .	3.8	11

#	ARTICLE	IF	CITATIONS
19	Fermented-Food Metagenomics Reveals Substrate-Associated Differences in Taxonomy and Health-Associated and Antibiotic Resistance Determinants. <i>MSystems</i> , 2020, 5, .	3.8	78
20	Evaluation of methods for the reduction of contaminating host reads when performing shotgun metagenomic sequencing of the milk microbiome. <i>Scientific Reports</i> , 2020, 10, 21665.	3.3	33
21	Enduring Behavioral Effects Induced by Birth by Caesarean Section in the Mouse. <i>Current Biology</i> , 2020, 30, 3761-3774.e6.	3.9	65
22	Instances of altered gut microbiomes among Irish cricketers over periods of travel in the lead up to the 2016 World Cup: A sequencing analysis. <i>Travel Medicine and Infectious Disease</i> , 2020, 35, 101553.	3.0	11
23	Encapsulated cyclosporine does not change the composition of the human microbiota when assessed ex vivo and in vivo. <i>Journal of Medical Microbiology</i> , 2020, 69, 854-863.	1.8	12
24	The Potential Impact of Probiotics on the Gut Microbiome of Athletes. <i>Nutrients</i> , 2019, 11, 2270.	4.1	55
25	Porcine Feed Efficiency-Associated Intestinal Microbiota and Physiological Traits: Finding Consistent Cross-Locational Biomarkers for Residual Feed Intake. <i>MSystems</i> , 2019, 4, .	3.8	45
26	Four men in a boat: Ultra-endurance exercise alters the gut microbiome. <i>Journal of Science and Medicine in Sport</i> , 2019, 22, 1059-1064.	1.3	69
27	Influence of the Intestinal Microbiota on Colonization Resistance to <i>Salmonella</i> and the Shedding Pattern of Naturally Exposed Pigs. <i>MSystems</i> , 2019, 4, .	3.8	40
28	<i>Lactobacillus gasseri</i> APC 678 Reduces Shedding of the Pathogen <i>Clostridium difficile</i> in a Murine Model. <i>Frontiers in Microbiology</i> , 2019, 10, 273.	3.5	9
29	Moderate-intensity aerobic and resistance exercise is safe and favorably influences body composition in patients with quiescent Inflammatory Bowel Disease: a randomized controlled cross-over trial. <i>BMC Gastroenterology</i> , 2019, 19, 29.	2.0	47
30	Metabolic phenotyping of the human microbiome. <i>F1000Research</i> , 2019, 8, 1956.	1.6	12
31	Draft Genome Sequence of <i>Bacillus thuringiensis</i> DPC6431, Producer of the Bacteriocin Thuricin CD. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
32	The microbiome of professional athletes differs from that of more sedentary subjects in composition and particularly at the functional metabolic level. <i>Gut</i> , 2018, 67, gutjnl-2016-313627.	12.1	333
33	A Prospective Metagenomic and Metabolomic Analysis of the Impact of Exercise and/or Whey Protein Supplementation on the Gut Microbiome of Sedentary Adults. <i>MSystems</i> , 2018, 3, .	3.8	148
34	Post-weaning social isolation of rats leads to long-term disruption of the gut microbiota-immune-brain axis. <i>Brain, Behavior, and Immunity</i> , 2018, 68, 261-273.	4.1	97
35	Early <i>Salmonella Typhimurium</i> infection in pigs disrupts Microbiome composition and functionality principally at the ileum mucosa. <i>Scientific Reports</i> , 2018, 8, 7788.	3.3	61
36	Short-chain fatty acids: microbial metabolites that alleviate stress-induced brain-gut axis alterations. <i>Journal of Physiology</i> , 2018, 596, 4923-4944.	2.9	460

#	ARTICLE	IF	CITATIONS
37	Species classifier choice is a key consideration when analysing low-complexity food microbiome data. <i>Microbiome</i> , 2018, 6, 50.	11.1	65
38	Gut Microbiology – A Relatively Unexplored Domain. , 2018, , 629-648.		0
39	Prospective case-control study describing the lower airway microbiome in pre-school children with cystic fibrosis. , 2018, , .		1
40	Gut microbiota: implications for sports and exercise medicine. <i>British Journal of Sports Medicine</i> , 2017, 51, 700-701.	6.7	31
41	“Microbes in sport” – The potential role of the gut microbiota in athlete health and performance. <i>British Journal of Sports Medicine</i> , 2017, 51, 698-699.	6.7	21
42	The altered gut microbiota in adults with cystic fibrosis. <i>BMC Microbiology</i> , 2017, 17, 58.	3.3	104
43	Strain-Level Metagenomic Analysis of the Fermented Dairy Beverage Nunu Highlights Potential Food Safety Risks. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	78
44	Exploring a Possible Link between the Intestinal Microbiota and Feed Efficiency in Pigs. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	258
45	Bacteriocin Gene-Trait matching across the complete <i>Lactobacillus</i> Pan-genome. <i>Scientific Reports</i> , 2017, 7, 3481.	3.3	75
46	A pilot study demonstrating the altered gut microbiota functionality in stable adults with Cystic Fibrosis. <i>Scientific Reports</i> , 2017, 7, 6685.	3.3	35
47	Microbiota of Raw Milk and Raw Milk Cheeses. , 2017, , 301-316.		15
48	The Fungal Frontier: A Comparative Analysis of Methods Used in the Study of the Human Gut Mycobiome. <i>Frontiers in Microbiology</i> , 2017, 8, 1432.	3.5	86
49	Comparative Genomic Analysis Reveals a Diverse Repertoire of Genes Involved in Prokaryote-Eukaryote Interactions within the <i>Pseudovibrio</i> Genus. <i>Frontiers in Microbiology</i> , 2016, 7, 387.	3.5	36
50	<i>Thermus</i> and the Pink Discoloration Defect in Cheese. <i>MSystems</i> , 2016, 1, .	3.8	70
51	The bacteriocin bactofencin A subtly modulates gut microbial populations. <i>Anaerobe</i> , 2016, 40, 41-49.	2.1	34
52	Behavioural and neurochemical consequences of chronic gut microbiota depletion during adulthood in the rat. <i>Neuroscience</i> , 2016, 339, 463-477.	2.3	196
53	Microbial Succession and Flavor Production in the Fermented Dairy Beverage Kefir. <i>MSystems</i> , 2016, 1, .	3.8	202
54	<i>Miscanthus</i> biochar promotes growth of spring barley and shifts bacterial community structures including phosphorus and sulfur mobilizing bacteria. <i>Pedobiologia</i> , 2016, 59, 195-202.	1.2	28

#	ARTICLE	IF	CITATIONS
55	Preparation of a standardised faecal slurry for ex-vivo microbiota studies which reduces inter-individual donor bias. <i>Journal of Microbiological Methods</i> , 2016, 129, 109-116.	1.6	29
56	Influence of GABA and GABA-producing <i>Lactobacillus brevis</i> DPC 6108 on the development of diabetes in a streptozotocin rat model. <i>Beneficial Microbes</i> , 2016, 7, 409-420.	2.4	46
57	FoodMicrobionet: A database for the visualisation and exploration of food bacterial communities based on network analysis. <i>International Journal of Food Microbiology</i> , 2016, 219, 28-37.	4.7	65
58	Formicin – a novel broad-spectrum two-component lantibiotic produced by <i>Bacillus paralicheniformis</i> APC 1576. <i>Microbiology (United Kingdom)</i> , 2016, 162, 1662-1671.	1.8	31
59	High-throughput DNA sequencing to survey bacterial histidine and tyrosine decarboxylases in raw milk cheeses. <i>BMC Microbiology</i> , 2015, 15, 266.	3.3	39
60	N-3 Polyunsaturated Fatty Acids (PUFAs) Reverse the Impact of Early-Life Stress on the Gut Microbiota. <i>PLoS ONE</i> , 2015, 10, e0139721.	2.5	143
61	Dietary trans-10, cis-12-conjugated linoleic acid alters fatty acid metabolism and microbiota composition in mice. <i>British Journal of Nutrition</i> , 2015, 113, 728-738.	2.3	89
62	Author response: linking lifestyle and microbes. <i>Gut</i> , 2015, 64, 520.1-520.	12.1	2
63	Spatial variation of the colonic microbiota in patients with ulcerative colitis and control volunteers. <i>Gut</i> , 2015, 64, 1553-1561.	12.1	226
64	Prenatal stress-induced alterations in major physiological systems correlate with gut microbiota composition in adulthood. <i>Psychoneuroendocrinology</i> , 2015, 60, 58-74.	2.7	224
65	Temporal and Spatial Differences in Microbial Composition during the Manufacture of a Continental-Type Cheese. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2525-2533.	3.1	62
66	Exercise and the microbiota. <i>Gut Microbes</i> , 2015, 6, 131-136.	9.8	127
67	Nisin H Is a New Nisin Variant Produced by the Gut-Derived Strain <i>Streptococcus hyointestinalis</i> DPC6484. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3953-3960.	3.1	74
68	Gut microbiota depletion from early adolescence in mice: Implications for brain and behaviour. <i>Brain, Behavior, and Immunity</i> , 2015, 48, 165-173.	4.1	572
69	Re: Gut microbiota depletion from early adolescence in mice: Implications for brain and behaviour. <i>Brain, Behavior, and Immunity</i> , 2015, 50, 335-336.	4.1	24
70	The metabolic role of the microbiota. <i>Clinical Liver Disease</i> , 2015, 5, 91-93.	2.1	2
71	Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. <i>Nature Communications</i> , 2015, 6, 8322.	12.8	488
72	Streptozotocin-induced type-1-diabetes disease onset in Sprague-Dawley rats is associated with an altered intestinal microbiota composition and decreased diversity. <i>Microbiology (United Kingdom)</i> , 2015, 161, 182-193.	1.8	70

#	ARTICLE	IF	CITATIONS
73	The Effects of Freezing on Faecal Microbiota as Determined Using MiSeq Sequencing and Culture-Based Investigations. <i>PLoS ONE</i> , 2015, 10, e0119355.	2.5	241
74	Marine <i>Pseudovibrio</i> sp. as a Novel Source of Antimicrobials. <i>Marine Drugs</i> , 2014, 12, 5916-5929.	4.6	36
75	Complete Genome Sequence of vB_EcoM_112, a T-Even-Type Bacteriophage Specific for <i>Escherichia coli</i> O157:H7. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
76	Impact of dietary fatty acids on metabolic activity and host intestinal microbiota composition in C57BL/6J mice. <i>British Journal of Nutrition</i> , 2014, 111, 1905-1917.	2.3	152
77	Sequence-based analysis of the bacterial and fungal compositions of multiple kombucha (tea fungus) samples. <i>Food Microbiology</i> , 2014, 38, 171-178.	4.2	303
78	Exopolysaccharide-Producing Probiotic Lactobacilli Reduce Serum Cholesterol and Modify Enteric Microbiota in ApoE-Deficient Mice. <i>Journal of Nutrition</i> , 2014, 144, 1956-1962.	2.9	80
79	Exercise and associated dietary extremes impact on gut microbial diversity. <i>Gut</i> , 2014, 63, 1913-1920.	12.1	987
80	Sequence-based analysis of the microbial composition of water kefir from multiple sources. <i>FEMS Microbiology Letters</i> , 2013, 348, 79-85.	1.8	70
81	Antipsychotics and the gut microbiome: olanzapine-induced metabolic dysfunction is attenuated by antibiotic administration in the rat. <i>Translational Psychiatry</i> , 2013, 3, e309-e309.	4.8	201
82	Divergent metabolic outcomes arising from targeted manipulation of the gut microbiota in diet-induced obesity. <i>Gut</i> , 2013, 62, 220-226.	12.1	235
83	The microbial content of raw and pasteurized cow milk as determined by molecular approaches. <i>Journal of Dairy Science</i> , 2013, 96, 4928-4937.	3.4	122
84	Bacterial Communities Established in Bauxite Residues with Different Restoration Histories. <i>Environmental Science &amp; Technology</i> , 2013, 47, 7110-7119.	10.0	69
85	The complex microbiota of raw milk. <i>FEMS Microbiology Reviews</i> , 2013, 37, 664-698.	8.6	591
86	Alterations in intestinal microbiota of elderly Irish subjects post-antibiotic therapy. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 214-221.	3.0	67
87	Bactofencin A, a New Type of Cationic Bacteriocin with Unusual Immunity. <i>MBio</i> , 2013, 4, e00498-13.	4.1	46
88	The individual-specific and diverse nature of the preterm infant microbiota. <i>Archives of Disease in Childhood: Fetal and Neonatal Edition</i> , 2013, 98, F334-F340.	2.8	105
89	Gut microbial diversity is reduced and is associated with colonic inflammation in a piglet model of short bowel syndrome. <i>Gut Microbes</i> , 2013, 4, 212-221.	9.8	82
90	Prevalence and characterization of <i>Clostridium perfringens</i> from the faecal microbiota of elderly Irish subjects. <i>Journal of Medical Microbiology</i> , 2013, 62, 457-466.	1.8	42

#	ARTICLE	IF	CITATIONS
91	Sequence-Based Analysis of the Intestinal Microbiota of Sows and Their Offspring Fed Genetically Modified Maize Expressing a Truncated Form of <i>Bacillus thuringiensis</i> Cry1Ab Protein (Bt Maize). <i>Applied and Environmental Microbiology</i> , 2013, 79, 7735-7744.	3.1	15
92	Targeting the Microbiota to Address Diet-Induced Obesity: A Time Dependent Challenge. <i>PLoS ONE</i> , 2013, 8, e65790.	2.5	132
93	The Effect of Dietary Supplementation with Spent Cider Yeast on the Swine Distal Gut Microbiome. <i>PLoS ONE</i> , 2013, 8, e75714.	2.5	37
94	Sequencing-Based Analysis of the Bacterial and Fungal Composition of Kefir Grains and Milks from Multiple Sources. <i>PLoS ONE</i> , 2013, 8, e69371.	2.5	169
95	High-Throughput Sequence-Based Analysis of the Intestinal Microbiota of Weanling Pigs Fed Genetically Modified MON810 Maize Expressing <i>Bacillus thuringiensis</i> Cry1Ab (Bt Maize) for 31 Days. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4217-4224.	3.1	52
96	High-Throughput Sequencing for Detection of Subpopulations of Bacteria Not Previously Associated with Artisanal Cheeses. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5717-5723.	3.1	236
97	Contrasting effects of <i>Bifidobacterium breve</i> NCIMB 702258 and <i>Bifidobacterium breve</i> DPC 6330 on the composition of murine brain fatty acids and gut microbiota. <i>American Journal of Clinical Nutrition</i> , 2012, 95, 1278-1287.	4.7	109
98	Genome sequence of the phage clP1, which infects the beer spoilage bacterium <i>Pediococcus damnosus</i> . <i>Gene</i> , 2012, 504, 53-63.	2.2	18
99	Gut microbiota composition correlates with diet and health in the elderly. <i>Nature</i> , 2012, 488, 178-184.	27.8	2,618
100	<i>Clostridium difficile</i> Carriage in Elderly Subjects and Associated Changes in the Intestinal Microbiota. <i>Journal of Clinical Microbiology</i> , 2012, 50, 867-875.	3.9	184
101	Gender-dependent consequences of chronic olanzapine in the rat: effects on body weight, inflammatory, metabolic and microbiota parameters. <i>Psychopharmacology</i> , 2012, 221, 155-169.	3.1	231
102	A comparison of methods used to extract bacterial DNA from raw milk and raw milk cheese. <i>Journal of Applied Microbiology</i> , 2012, 113, 96-105.	3.1	98
103	The Effect of Feeding Bt MON810 Maize to Pigs for 110 Days on Intestinal Microbiota. <i>PLoS ONE</i> , 2012, 7, e33668.	2.5	35
104	A new phage on the "Mozzarella" block: Bacteriophage 5093 shares a low level of homology with other <i>Streptococcus thermophilus</i> phages. <i>International Dairy Journal</i> , 2011, 21, 963-969.	3.0	45
105	Genome Mining for Radical SAM Protein Determinants Reveals Multiple Sactibiotic-Like Gene Clusters. <i>PLoS ONE</i> , 2011, 6, e20852.	2.5	68
106	Correlation of rRNA gene amplicon pyrosequencing and bacterial culture for microbial compositional analysis of faecal samples from elderly Irish subjects. <i>Journal of Applied Microbiology</i> , 2011, 111, 467-473.	3.1	21
107	High-throughput sequence-based analysis of the bacterial composition of kefir and an associated kefir grain. <i>FEMS Microbiology Letters</i> , 2011, 320, 56-62.	1.8	120
108	Fate and efficacy of lactacin 3147-producing <i>Lactococcus lactis</i> in the mammalian gastrointestinal tract. <i>FEMS Microbiology Ecology</i> , 2011, 76, 602-614.	2.7	50



#	ARTICLE	IF	CITATIONS
109	Molecular approaches to analysing the microbial composition of raw milk and raw milk cheese. <i>International Journal of Food Microbiology</i> , 2011, 150, 81-94.	4.7	205
110	Further Identification of Novel Lantibiotic Operons Using LanM-Based Genome Mining. <i>Probiotics and Antimicrobial Proteins</i> , 2011, 3, 27-40.	3.9	7
111	Myosin-cross-reactive antigen (MCRA) protein from <i>Bifidobacterium breve</i> is a FAD-dependent fatty acid hydratase which has a function in stress protection. <i>BMC Biochemistry</i> , 2011, 12, 9.	4.4	75
112	Effect of broad- and narrow-spectrum antimicrobials on <i>Clostridium difficile</i> and microbial diversity in a model of the distal colon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4639-4644.	7.1	313
113	Composition, variability, and temporal stability of the intestinal microbiota of the elderly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4586-4591.	7.1	1,418
114	In silico analysis highlights the frequency and diversity of type 1 lantibiotic gene clusters in genome sequenced bacteria. <i>BMC Genomics</i> , 2010, 11, 679.	2.8	74
115	The changing face of dairy starter culture research: From genomics to economics. <i>International Journal of Dairy Technology</i> , 2010, 63, 149-170.	2.8	50
116	Composition and energy harvesting capacity of the gut microbiota: relationship to diet, obesity and time in mouse models. <i>Gut</i> , 2010, 59, 1635-1642.	12.1	808
117	In silico analysis of Ardmore, a novel mycobacteriophage isolated from soil. <i>Gene</i> , 2010, 453, 9-23.	2.2	22
118	Genome analysis of the <i>Clostridium difficile</i> phage $\hat{1}$ CD6356, a temperate phage of the Siphoviridae family. <i>Gene</i> , 2010, 462, 34-43.	2.2	50
119	Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. <i>Nucleic Acids Research</i> , 2010, 38, e200-e200.	14.5	808
120	Comparative genomics of lactic acid bacteria reveals a niche-specific gene set. <i>BMC Microbiology</i> , 2009, 9, 50.	3.3	122
121	Antimicrobial activity of two peptides casecidin 15 and 17, found naturally in bovine colostrum. <i>Journal of Applied Microbiology</i> , 2009, 106, 233-240.	3.1	77
122	Characterisation of single nucleotide polymorphisms identified in the bovine lactoferrin gene sequences across a range of dairy cow breeds. <i>Biochimie</i> , 2009, 91, 68-75.	2.6	24
123	Genome of a virulent bacteriophage Lb338-1 that lyses the probiotic <i>Lactobacillus paracasei</i> cheese strain. <i>Gene</i> , 2009, 448, 29-39.	2.2	36
124	Comparative Analysis of Pyrosequencing and a Phylogenetic Microarray for Exploring Microbial Community Structures in the Human Distal Intestine. <i>PLoS ONE</i> , 2009, 4, e6669.	2.5	719
125	295: Causes of massive obstetric haemorrhage and outcomes of medical and surgical management strategies. <i>American Journal of Obstetrics and Gynecology</i> , 2008, 199, S93.	1.3	0
126	Genome Sequence of <i>Lactobacillus helveticus</i> , an Organism Distinguished by Selective Gene Loss and Insertion Sequence Element Expansion. <i>Journal of Bacteriology</i> , 2008, 190, 727-735.	2.2	208



#	ARTICLE	IF	CITATIONS
127	Casein Fermentate of <i>Lactobacillus animalis</i> DPC6134 Contains a Range of Novel Propeptide Angiotensin-Converting Enzyme Inhibitors. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4658-4667.	3.1	125
128	Relatedness between the two-component lantibiotics lacticin 3147 and staphylococcin C55 based on structure, genetics and biological activity. <i>BMC Microbiology</i> , 2007, 7, 24.	3.3	23
129	pEOC01: A plasmid from <i>Pediococcus acidilactici</i> which encodes an identical streptomycin resistance (aadE) gene to that found in <i>Campylobacter jejuni</i> . <i>Plasmid</i> , 2007, 58, 115-126.	1.4	25
130	M-Coffee: combining multiple sequence alignment methods with T-Coffee. <i>Nucleic Acids Research</i> , 2006, 34, 1692-1699.	14.5	533
131	Evaluation of iterative alignment algorithms for multiple alignment. <i>Bioinformatics</i> , 2005, 21, 1408-1414.	4.1	52
132	3DCoffee: Combining Protein Sequences and Structures within Multiple Sequence Alignments. <i>Journal of Molecular Biology</i> , 2004, 340, 385-395.	4.2	302
133	APDB: a novel measure for benchmarking sequence alignment methods without reference alignments. <i>Bioinformatics</i> , 2003, 19, i215-i221.	4.1	62
134	A SAT-Based Approach to Multiple Sequence Alignment. <i>Lecture Notes in Computer Science</i> , 2003, , 940-944.	1.3	3