Mitsuo Sakamoto

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4130155/publications.pdf

Version: 2024-02-01

182

papers

9,006

citations

41627

51

h-index

58552

86

g-index

184

all docs

184

docs citations

184

times ranked

10576

citing authors

#	ARTICLE	IF	CITATIONS
1	Prevotella lacticifex sp. nov., isolated from the rumen of cows. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	9
2	Genome-based, phenotypic and chemotaxonomic classification of Faecalibacterium strains: proposal of three novel species Faecalibacterium duncaniae sp. nov., Faecalibacterium hattorii sp. nov. and Faecalibacterium gallinarum sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	36
3	Complete Genome Sequence of Alistipes indistinctus Strain 2BBH45, Isolated from the Feces of a Healthy Japanese Male. Microbiology Resource Announcements, 2021, 10, .	0.3	1
4	Characterization of fructooligosaccharide metabolism and fructooligosaccharide-degrading enzymes in human commensal butyrate producers. Gut Microbes, 2021, 13, 1-20.	4.3	20
5	Fecal Microbiota Perspective for Evaluation of Prebiotic Potential of Bamboo Hemicellulose Hydrolysate in Mice: A Preliminary Study. Microorganisms, 2021, 9, 888.	1.6	3
6	Lactobacillus nasalidis sp. nov., isolated from the forestomach of a captive proboscis monkey (Nasalis) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	12
7	Validation and standardization of DNA extraction and library construction methods for metagenomics-based human fecal microbiome measurements. Microbiome, 2021, 9, 95.	4.9	37
8	Complete Genome Sequence of Longicatena caecimuris Strain 3BBH23, Isolated from Healthy Japanese Feces. Microbiology Resource Announcements, 2021, 10, .	0.3	1
9	Coprobacter secundus subsp. similis subsp. nov. and Solibaculum mannosilyticum gen. nov., sp. nov., isolated from human feces. Microbiology and Immunology, 2021, 65, 245-256.	0.7	19
10	Lactobacillus corticis sp. nov., isolated from hardwood bark. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	9
11	Taxonomic status of the species Clostridium methoxybenzovorans Mechichi et al. 1999. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
12	Clostridium zeae sp. nov., isolated from corn silage. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
13	Complete Genome Sequence of Megamonas funiformis Strain 1CBH44, Isolated from Human Feces. Microbiology Resource Announcements, 2021, 10, e0078521.	0.3	0
14	Adlercreutzia hattorii sp. nov., an equol non-producing bacterium isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
15	Lentilactobacillus fungorum sp. nov., isolated from spent mushroom substrates. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
16	Microbial interaction between the succinateâ€utilizing bacterium <i>Phascolarctobacterium faecium</i> and the gut commensal <i>Bacteroides thetaiotaomicron</i>. MicrobiologyOpen, 2020, 9, e1111.	1.2	54
17	Complete Genome Sequence of <i>Adlercreutzia</i> sp. Strain 8CFCBH1, a Potent Producer of Equol, Isolated from Healthy Japanese Feces. Microbiology Resource Announcements, 2020, 9, .	0.3	3
18	Stress Response of Mesosutterella multiformis Mediated by Nitrate Reduction. Microorganisms, 2020, 8, 2003.	1.6	3

#	ARTICLE	IF	CITATIONS
19	Complete Genome Sequence of Collinsella aerofaciens JCM 10188 ^T. Microbiology Resource Announcements, 2020, 9, .	0.3	1
20	Complete Genome Sequence of Akkermansia muciniphila JCM 30893, Isolated from Feces of a Healthy Japanese Male. Microbiology Resource Announcements, 2020, 9, .	0.3	8
21	Alistipes communis sp. nov., Alistipes dispar sp. nov. and Alistipes onderdonkii subsp. vulgaris subsp. nov., isolated from human faeces, and creation of Alistipes onderdonkii subsp. onderdonkii subsp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 473-480.	0.8	27
22	Dialister hominis sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 589-595.	0.8	18
23	Cutibacterium modestum sp. nov., isolated from meibum of human meibomian glands, and emended descriptions of Cutibacterium granulosum and Cutibacterium namnetense. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2457-2462.	0.8	20
24	Reclassification of Clostridium diolis Biebl and SprÃ¶er 2003 as a later heterotypic synonym of Clostridium beijerinckii Donker 1926 (Approved Lists 1980) emend. Keis et al. 2001. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2463-2466.	0.8	12
25	Lactobacillus buchneri subsp. silagei subsp. nov., isolated from rice grain silage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3111-3116.	0.8	17
26	Prevotella hominis sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4767-4773.	0.8	13
27	Amedibacterium intestinale gen. nov., sp. nov., isolated from human faeces, and reclassification of Eubacterium dolichum Moore et al. 1976 (Approved Lists 1980) as Amedibacillus dolichus gen. nov., comb. nov. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3656-3664.	0.8	18
28	Lactococcus insecticola sp. nov. and Lactococcus hodotermopsidis sp. nov., isolated from the gut of the wood-feeding lower termite Hodotermopsis sjostedti. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4515-4522.	0.8	10
29	Complete Genome Sequence of <i>Faecalibacillus intestinalis</i> JCM 34082, Isolated from Feces from a Healthy Japanese Female. Microbiology Resource Announcements, 2020, 9, .	0.3	1
30	Complete Genome Sequence of Blautia producta JCM 1471 T. Microbiology Resource Announcements, 2020, 9, .	0.3	1
31	Complete Genome Sequence of Megamonas funiformis JCM 14723 T. Microbiology Resource Announcements, 2020, 9, .	0.3	2
32	Complete Genome Sequence of Flavonifractor plautii JCM 32125 T. Microbiology Resource Announcements, 2020, 9, .	0.3	1
33	Draft Genome Sequence of Mesosutterella multiformis JCM 32464 T , a Member of the Family Sutterellaceae , Isolated from Human Feces. Microbiology Resource Announcements, 2019, 8, .	0.3	1
34	Complete Genome Sequence of Phascolarctobacterium faecium JCM 30894, a Succinate-Utilizing Bacterium Isolated from Human Feces. Microbiology Resource Announcements, 2019, 8, .	0.3	38
35	Reclassification of Paenibacillus thermophilus Zhou et al. 2013 as a later heterotypic synonym of Paenibacillus macerans (Schardinger 1905) Ash et al. 1994. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 417-421.	0.8	7
36	Lactobacillus salitolerans sp. nov., a novel lactic acid bacterium isolated from spent mushroom substrates. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 964-969.	0.8	14

#	ARTICLE	IF	CITATIONS
37	Proposal of new combination, Cutibacterium acnes subsp. elongatum comb. nov., and emended descriptions of the genus Cutibacterium, Cutibacterium acnes subsp. acnes and Cutibacterium acnes subsp. defendens. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1087-1092.	0.8	39
38	Comparative genomics of Parolsenella catena and Libanicoccus massiliensis: Reclassification of Libanicoccus massiliensis as Parolsenella massiliensis comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1123-1129.	0.8	11
39	Bacteria and methanogen community in the rumen fed different levels of grass-legume silages. Biodiversitas, 2019, 20, 1055-1062.	0.2	1
40	Methods for analyzing next-generation sequencing data XIII.RNA-seq analysis (Part 1). Japanese Journal of Lactic Acid Bacteria, 2019, 30, 38-45.	0.1	0
41	Draft Genome Sequence of Faecalimonas umbilicata JCM 30896 ^T , an Acetate-Producing Bacterium Isolated from Human Feces. Microbiology Resource Announcements, 2018, 7, .	0.3	8
42	Draft Genome Sequence of Lawsonibacter asaccharolyticus JCM 32166 T , a Butyrate-Producing Bacterium, Isolated from Human Feces. Genome Announcements, 2018, 6, .	0.8	7
43	Isolation and Characterization of Human Gut Bacteria Capable of Extracellular Electron Transport by Electrochemical Techniques. Frontiers in Microbiology, 2018, 9, 3267.	1.5	38
44	Lactococcus reticulitermitis sp. nov., isolated from the gut of the subterranean termite Reticulitermes speratus. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 596-601.	0.8	14
45	Parolsenella catena gen. nov., sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1165-1172.	0.8	15
46	Lactobacillus metriopterae sp. nov., a novel lactic acid bacterium isolated from the gut of grasshopper Metrioptera engelhardti. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1484-1489.	0.8	15
47	Lawsonibacter asaccharolyticus gen. nov., sp. nov., a butyrate-producing bacterium isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2074-2081.	0.8	41
48	Lactobacillus paragasseri sp. nov., a sister taxon of Lactobacillus gasseri, based on whole-genome sequence analyses. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3512-3517.	0.8	43
49	Lactococcus termiticola sp. nov., isolated from the gut of the wood-feeding higher termite Nasutitermes takasagoensis. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3832-3836.	0.8	10
50	Mesosutterella multiformis gen. nov., sp. nov., a member of the family Sutterellaceae and Sutterella megalosphaeroides sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3942-3950.	0.8	27
51	Microbial Community Profiling Using Terminal Restriction Fragment Length Polymorphism (T-RFLP) and Denaturing Gradient Gel Electrophoresis (DGGE). Methods in Molecular Biology, 2017, 1537, 139-152.	0.4	10
52	Draft Genome Sequence of <i>Lactococcus</i> sp. Strain Rs-Y01, Isolated from the Gut of the Lower Termite <i>Reticulitermes speratus</i>. Genome Announcements, 2017, 5, .	0.8	1
53	Genomic characterization reconfirms the taxonomic status of <i>Lactobacillus parakefiri</i>. Bioscience of Microbiota, Food and Health, 2017, 36, 129-134.	0.8	2
54	Faecalimonas umbilicata gen. nov., sp. nov., isolated from human faeces, and reclassification of Eubacterium contortum, Eubacterium fissicatena and Clostridium oroticum as Faecalicatena contorta gen. nov., comb. nov., Faecalicatena fissicatena comb. nov. and Faecalicatena orotica comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1219-1227.	0.8	77

#	ARTICLE	IF	CITATIONS
55	Lactobacillus silagincola sp. nov. and Lactobacillus pentosiphilus sp. nov., isolated from silage. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3639-3644.	0.8	19
56	Clostridium pabulibutyricum sp. nov., a butyric-acid-producing organism isolated from high-moisture grass silage. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4974-4978.	0.8	14
57	Methods for analyzing next-generation sequencing data X. Registration to DDBJ through Mass Submission System . Japanese Journal of Lactic Acid Bacteria, 2017, 28, 94-100.	0.1	0
58	Filobacterium rodentium gen. nov., sp. nov., a member of Filobacteriaceae fam. nov. within the phylum Bacteroidetes; includes a microaerobic filamentous bacterium isolated from specimens from diseased rodent respiratory tracts. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 150-157.	0.8	22
59	Athalassotoga saccharophila gen. nov., sp. nov., isolated from an acidic terrestrial hot spring, and proposal of Mesoaciditogales ord. nov. and Mesoaciditogaceae fam. nov. in the phylum Thermotogae. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1045-1051.	0.8	40
60	Bacteroides caecicola sp. nov. and Bacteroides gallinaceum sp. nov., isolated from the caecum of an Indonesian chicken. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1431-1437.	0.8	19
61	Enterococcus saigonensis sp. nov., isolated from retail chicken meat and liver. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3779-3785.	0.8	16
62	Paenibacillus silagei sp. nov. isolated from corn silage. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3873-3877.	0.8	12
63	Distribution and Evolution of Nitrogen Fixation Genes in the Phylum <i>Bacteroidetes</i>. Microbes and Environments, 2015, 30, 44-50.	0.7	67
64	High quality draft genome sequence of Bacteroides barnesiae type strain BL2T (DSM 18169T) from chicken caecum. Standards in Genomic Sciences, 2015, 10, 48.	1.5	4
65	Porphyromonas pasteri sp. nov., isolated from human saliva. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 2511-2515.	0.8	18
66	Prolixibacter denitrificans sp. nov., an iron-corroding, facultatively aerobic, nitrate-reducing bacterium isolated from crude oil, and emended descriptions of the genus Prolixibacter and Prolixibacter bellariivorans. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 2865-2869.	0.8	40
67	Parabacteroides faecis sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 1342-1346.	0.8	19
68	Fermentation Characteristics and Microbial Diversity of Tropical Grass-legumes Silages. Asian-Australasian Journal of Animal Sciences, 2015, 28, 511-518.	2.4	33
69	Dysgonomonas termitidis sp. nov., isolated from the gut of the subterranean termite Reticulitermes speratus. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 681-685.	0.8	73
70	Bacteroides caecigallinarum sp. nov., isolated from caecum of an Indonesian chicken. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4341-4346.	0.8	18
71	Dissecting the taxonomic heterogeneity within Propionibacterium acnes: proposal for Propionibacterium acnes subsp. acnes subsp. nov. and Propionibacterium acnes subsp. elongatum subsp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4776-4787.	0.8	64
72	Butyricimonas faecihominis sp. nov. and Butyricimonas paravirosa sp. nov., isolated from human faeces, and emended description of the genus Butyricimonas. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 2992-2997.	0.8	55

#	Article	IF	Citations
73	Methane Mitigation and Microbial Diversity of Silage Diets Containing Calliandra calothyrsus in a Rumen in Vitro Fermentation System. Media Peternakan, 2014, 37, 121-128.	0.3	2
74	Lactobacillus furfuricola sp. nov., isolated from Nukadoko, rice bran paste for Japanese pickles. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 2902-2906.	0.8	17
75	Draft Genome Sequence of Bacteroides reticulotermitis Strain JCM 10512 ^T , Isolated from the Gut of a Termite. Genome Announcements, 2014, 2, .	0.8	2
76	Draft Genome Sequences of Three Strains of Bacteroides pyogenes Isolated from a Cat and Swine. Genome Announcements, 2014, 2, .	0.8	4
77	Innate lymphoid cells regulate intestinal epithelial cell glycosylation. Science, 2014, 345, 1254009.	6.0	450
78	Draft Genome Sequence of Lactobacillus sucicola JCM 15457 T , a Motile Lactic Acid Bacterium Isolated from Oak Sap. Genome Announcements, 2014, 2, .	0.8	0
79	Draft Genome Sequence of Clostridium straminisolvens Strain JCM 21531 ^T , Isolated from a Cellulose-Degrading Bacterial Community. Genome Announcements, 2014, 2, .	0.8	1
80	The Family Porphyromonadaceae. , 2014, , 811-824.		45
81	Diversity of Microflora in Colonic Mucus from Severe Ulcerative Colitis Patients Analyzed by Terminal Restriction Fragment Length Polymorphism and Clone Libraries of Bacterial 16S rRNA Gene Sequences. Advances in Microbiology, 2014, 04, 857-870.	0.3	0
82	Porphyromonas crevioricanis is an earlier heterotypic synonym of Porphyromonas cansulci and has priority. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 454-457.	0.8	11
83	Sequencing orphan species initiative (SOS): Filling the gaps in the 16S rRNA gene sequence database for all species with validly published names. Systematic and Applied Microbiology, 2013, 36, 69-73.	1.2	98
84	Bacteroides reticulotermitis sp. nov., isolated from the gut of a subterranean termite (Reticulitermes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	29
85	Draft Genome Sequences of Porphyromonas crevioricanis JCM 15906 T and Porphyromonas cansulci JCM 13913 T Isolated from a Canine Oral Cavity. Genome Announcements, 2013, 1, .	0.8	2
86	Parabacteroides chinchillae sp. nov., isolated from chinchilla (Chincilla lanigera) faeces. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3470-3474.	0.8	18
87	Comprehensive microbiological findings in periâ€implantitis and periodontitis. Journal of Clinical Periodontology, 2013, 40, 218-226.	2.3	132
88	Bacteroides sartorii is an earlier heterotypic synonym of Bacteroides chinchillae and has priority. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 1241-1244.	0.8	13
89	Reclassification of Xylanibacter oryzae Ueki et al. 2006 as Prevotella oryzae comb. nov., with an emended description of the genus Prevotella. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 2637-2642.	0.8	40
90	Macellibacteroides fermentans gen. nov., sp. nov., a member of the family Porphyromonadaceae isolated from an upflow anaerobic filter treating abattoir wastewaters. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 2522-2527.	0.8	173

#	ARTICLE	IF	CITATIONS
91	Bacteroides stercorirosoris sp. nov. and Bacteroides faecichinchillae sp. nov., isolated from chinchilla (Chinchilla lanigera) faeces. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 1145-1150.	0.8	21
92	Covalently linked polyamines in the cell wall peptidoglycan of the anaerobes belonging to the order Selenomonadales. Journal of General and Applied Microbiology, 2012, 58, 339-347.	0.4	13
93	Lactobacillus floricola sp. nov., lactic acid bacteria isolated from mountain flowers. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 1356-1359.	0.8	31
94	Identification and classification of the genus Bacteroides by multilocus sequence analysis. Microbiology (United Kingdom), 2011, 157, 3388-3397.	0.7	28
95	Lactobacillus ozensis sp. nov., isolated from mountain flowers. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 2435-2438.	0.8	30
96	Bacteroides chinchillae sp. nov. and Bacteroides rodentium sp. nov., isolated from chinchilla (Chinchilla lanigera) faeces. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 877-881.	0.8	29
97	Slackia equolifaciens sp. nov., a human intestinal bacterium capable of producing equol. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 1721-1724.	0.8	89
98	Lactobacillus similis sp. nov., isolated from fermented cane molasses. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 187-190.	0.8	31
99	Prevotella aurantiaca sp. nov., isolated from the human oral cavity. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 500-503.	0.8	25
100	hsp60 and 16S rRNA gene sequence relationships among species of the genus Bacteroides with the finding that Bacteroides suis and Bacteroides tectus are heterotypic synonyms of Bacteroides pyogenes. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2984-2990.	0.8	53
101	Lactobacillus florum sp. nov., a fructophilic species isolated from flowers. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2478-2482.	0.8	70
102	Usefulness of the hsp60 gene for the identification and classification of Gram-negative anaerobic rods. Journal of Medical Microbiology, 2010, 59, 1293-1302.	0.7	62
103	Indigenous opportunistic bacteria inhabit mammalian gut-associated lymphoid tissues and share a mucosal antibody-mediated symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7419-7424.	3.3	197
104	Analysis of microbiota associated with peri-implantitis using 16S rRNA gene clone library. Journal of Oral Microbiology, 2010, 2, 5104.	1.2	111
105	Microbial Community Profiling Using Terminal Restriction Fragment Length Polymorphism (T-RFLP) and Denaturing Gradient Gel Electrophoresis (DGGE). Methods in Molecular Biology, 2010, 666, 71-85.	0.4	7
106	Butyricimonas synergistica gen. nov., sp. nov. and Butyricimonas virosa sp. nov., butyric acid-producing bacteria in the family 'Porphyromonadaceae' isolated from rat faeces. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 1748-1753.	0.8	135
107	Diversity of Spirochetes in Endodontic Infections. Journal of Clinical Microbiology, 2009, 47, 1352-1357.	1.8	37
108	Prevotella falsenii sp. nov., a Prevotella intermedia-like organism isolated from monkey dental plaque. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 319-322.	0.8	16

#	ARTICLE	IF	CITATIONS
109	Parabacteroides gordonii sp. nov., isolated from human blood cultures. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 2843-2847.	0.8	29
110	Change of Intestinal Microbiota with Elemental Diet and Its Impact on Therapeutic Effects in a Murine Model of Chronic Colitis. Digestive Diseases and Sciences, 2009, 54, 1892-1900.	1.1	49
111	Dynamics of fecal microbiota in hospitalized elderly fed probiotic LKM512 yogurt. Microbiology and Immunology, 2009, 53, 421-432.	0.7	33
112	Probiotic effects of orally administered <i>Lactobacillus salivarius</i> WB21â€containing tablets on periodontopathic bacteria: a doubleâ€blinded, placeboâ€controlled, randomized clinical trial. Journal of Clinical Periodontology, 2009, 36, 506-513.	2.3	158
113	Effect of ruminal protozoa on fecal microbiota in cattle using terminal restriction fragment length polymorphism. Animal Science Journal, 2008, 79, 29-34.	0.6	2
114	Molecular analysis of the root canal microbiota associated with endodontic treatment failures. Oral Microbiology and Immunology, 2008, 23, 275-281.	2.8	107
115	A novel keratinase from Clostridium sporogenes bv. pennavorans bv. nov., a thermotolerant organism isolated from solfataric muds. Microbiological Research, 2008, 163, 105-112.	2.5	40
116	Identification of bacteria from blood in febrile patients with ulcerative colitis by terminal restriction fragment length polymorphism profile analysis of 16S rRNA gene. Scandinavian Journal of Gastroenterology, 2008, 43, 423-430.	0.6	3
117	Distribution of Different Species of the <i>Bacteroides fragilis</i> Group in Individuals with Japanese Cedar Pollinosis. Applied and Environmental Microbiology, 2008, 74, 6814-6817.	1.4	24
118	Adlercreutzia equolifaciens gen. nov., sp. nov., an equol-producing bacterium isolated from human faeces, and emended description of the genus Eggerthella. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1221-1227.	0.8	253
119	Prevotella copri sp. nov. and Prevotella stercorea sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 941-946.	0.8	144
120	Characterization of skin microbiota in patients with atopic dermatitis and in normal subjects using 16S rRNA gene-based comprehensive analysis. Journal of Medical Microbiology, 2007, 56, 1675-1683.	0.7	87
121	Barnesiella viscericola gen. nov., sp. nov., a novel member of the family Porphyromonadaceae isolated from chicken caecum. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 342-346.	0.8	56
122	Influence of Bifidobacterium longum BB536 intake on faecal microbiota in individuals with Japanese cedar pollinosis during the pollen season. Journal of Medical Microbiology, 2007, 56, 1301-1308.	0.7	49
123	Prevotella pleuritidis sp. nov., isolated from pleural fluid. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 1725-1728.	0.8	25
124	Abnormal keratin expression in circumscribed palmar hypokeratosis. Journal of the American Academy of Dermatology, 2007, 57, 285-291.	0.6	55
125	Characterization of the Inhabitancy of Mouse Intestinal Bacteria (MIB) in Rodents and Humans by Realâ€Time PCR with Groupâ€Specific Primers. Microbiology and Immunology, 2007, 51, 349-357.	0.7	12
126	Parabacteroides johnsonii sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 293-296.	0.8	50

#	ARTICLE	IF	CITATIONS
127	Bacterial reduction and persistence after endodontic treatment procedures. Oral Microbiology and Immunology, 2007, 22, 19-23.	2.8	119
128	Bacteroides coprophilus sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 1323-1326.	0.8	32
129	<i>Clostridium glycyrrhizinilyticum</i> Sp. Nov., a Glycyrrhizinâ€Hydrolysing Bacterium Isolated from Human Faeces. Microbiology and Immunology, 2006, 50, 481-485.	0.7	20
130	Reclassification of Bacteroides distasonis, Bacteroides goldsteinii and Bacteroides merdae as Parabacteroides distasonis gen. nov., comb. nov., Parabacteroides goldsteinii comb. nov. and Parabacteroides merdae comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 1599-1605.	0.8	244
131	Molecular analysis of bacteria in asymptomatic and symptomatic endodontic infections. Oral Microbiology and Immunology, 2006, 21, 112-122.	2.8	191
132	Diversity of theClostridium coccoidesgroup in human fecal microbiota as determined by 16S rRNA gene library. FEMS Microbiology Letters, 2006, 257, 202-207.	0.7	50
133	Monitoring the cell number of Lactococcus lactis subsp. cremoris FC in human feces by real-time PCR with strain-specific primers designed using the RAPD technique. International Journal of Food Microbiology, 2006, 110, 69-76.	2.1	40
134	Bacteroides dorei sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 1639-1643.	0.8	86
135	Bacteroides intestinalis sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 151-154.	0.8	66
136	Increase in Terminal Restriction Fragments of Bacteroidetes-Derived 16S rRNA Genes after Administration of Short-Chain Fructooligosaccharides. Applied and Environmental Microbiology, 2006, 72, 6271-6276.	1.4	34
137	Bacteroides finegoldii sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 931-935.	0.8	52
138	Bacteroides barnesiae sp. nov., Bacteroides salanitronis sp. nov. and Bacteroides gallinarum sp. nov., isolated from chicken caecum. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2853-2859.	0.8	79
139	Characterization of the Genus <i>Bifidobacterium</i> by Automated Ribotyping and 16S rRNA Gene Sequences. Microbiology and Immunology, 2006, 50, 1-10.	0.7	27
140	Culture-independent analysis of fecal microbiota in infants, with special reference toBifidobacteriumspecies. FEMS Microbiology Letters, 2005, 243, 417-423.	0.7	73
141	Mucosa-associated bacteria in ulcerative colitis before and after antibiotic combination therapy. Alimentary Pharmacology and Therapeutics, 2005, 21, 1017-1027.	1.9	46
142	Molecular analysis of human oral microbiota. Journal of Periodontal Research, 2005, 40, 277-285.	1.4	92
143	Prevotella multiformis sp. nov., isolated from human subgingival plaque. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 815-819.	0.8	47
144	Movement and Fixation of Intestinal Microbiota after Administration of Human Feces to Germfree Mice. Applied and Environmental Microbiology, 2005, 71, 3171-3178.	1.4	46

#	Article	IF	Citations
145	Detection and Quantification of Four Species of the Genus <i>Clostridium</i> in Infant Feces. Microbiology and Immunology, 2005, 49, 987-992.	0.7	31
146	Prevotella multisaccharivorax sp. nov., isolated from human subgingival plaque. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 1839-1843.	0.8	56
147	Bacteroides plebeius sp. nov. and Bacteroides coprocola sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 2143-2147.	0.8	84
148	Detection of potentially novel bacterial components of the human skin microbiota using culture-independent molecular profiling. Journal of Medical Microbiology, 2005, 54, 1231-1238.	0.7	119
149	Culture-Independent Analysis of Fecal Microbiota in Cattle. Bioscience, Biotechnology and Biochemistry, 2005, 69, 1793-1797.	0.6	60
150	Direct cloning of genes encoding novel xylanases from the human gut. Canadian Journal of Microbiology, 2005, 51, 251-259.	0.8	46
151	Novel phylogenetic assignment database for terminal-restriction fragment length polymorphism analysis of human colonic microbiota. Journal of Microbiological Methods, 2005, 61, 305-319.	0.7	72
152	Molecular analysis of jejunal, ileal, caecal and recto-sigmoidal human colonic microbiota using 16S rRNA gene libraries and terminal restriction fragment length polymorphism. Journal of Medical Microbiology, 2005, 54, 1093-1101.	0.7	283
153	Evaluation of Three Different Forward Primers by Terminal Restriction Fragment Length Polymorphism Analysis for Determination of Fecal <i>Bifidobacterium</i> Spp. in Healthy Subjects. Microbiology and Immunology, 2004, 48, 1-6.	0.7	44
154	Changes in oral microbial profiles after periodontal treatment as determined by molecular analysis of 16S rRNA genes. Journal of Medical Microbiology, 2004, 53, 563-571.	0.7	86
155	Prevotella shahii sp. nov. and Prevotella salivae sp. nov., isolated from the human oral cavity. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 877-883.	0.8	60
156	Maturation of the murine cecal microbiota as revealed by terminal restriction fragment length polymorphism and 16S rRNA gene clone libraries. FEMS Microbiology Letters, 2004, 235, 139-146.	0.7	42
157	Monitoring the cell number and viability ofLactobacillus helveticusGCL1001 in human feces by PCR methods. FEMS Microbiology Letters, 2004, 231, 125-130.	0.7	25
158	Effects of Two Probiotic <i>Lactobacillus</i> Strains on Jejunal and Cecal Microbiota of Broiler Chicken under Acute Heat Stress Condition as Revealed by Molecular Analysis of 16S rRNA Genes. Microbiology and Immunology, 2004, 48, 917-929.	0.7	91
159	Comparison among Fecal Secondary Bile Acid Levels, Fecal Microbiota and <i>Clostridium scindens</i> Cell Numbers in Japanese. Microbiology and Immunology, 2004, 48, 367-375.	0.7	22
160	Maturation of the murine cecal microbiota as revealed by terminal restriction fragment length polymorphism and 16S rRNA gene clone libraries. FEMS Microbiology Letters, 2004, 235, 139-146.	0.7	24
161	Molecular Analysis of Fecal Microbiota in Elderly Individuals Using 16S rDNA Library and Tâ€RFLP. Microbiology and Immunology, 2003, 47, 557-570.	0.7	151
162	Application of terminal RFLP analysis to characterize oral bacterial flora in saliva of healthy subjects and patients with periodontitis. Journal of Medical Microbiology, 2003, 52, 79-89.	0.7	107

#	ARTICLE	IF	CITATIONS
163	Terminal Restriction Fragment Length Polymorphism Analysis for Human Fecal Microbiota and Its Application for Analysis of Complex Bifidobacterial Communities. Microbiology and Immunology, 2003, 47, 133-142.	0.7	89
164	Phylogenetic Analysis of Cecal Microbiota in Chicken by the Use of 16S rDNA Clone Libraries. Microbiology and Immunology, 2002, 46, 371-382.	0.7	91
165	Bacteroides ovatus as the Predominant Commensal Intestinal Microbe Causing a Systemic Antibody Response in Inflammatory Bowel Disease. Vaccine Journal, 2002, 9, 54-59.	3.2	58
166	Unification of Bifidobacterium infantis and Bifidobacterium suis as Bifidobacterium longum. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1945-1951.	0.8	88
167	Reclassification of Bacteroides forsythus (Tanner et al. 1986) as Tannerella forsythensis corrig., gen. nov., comb. nov. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 841-849.	0.8	147
168	Phylogenetic Analysis of the Human Gut Microbiota Using 16S rDNA Clone Libraries and Strictly Anaerobic Cultureâ€Based Methods. Microbiology and Immunology, 2002, 46, 535-548.	0.7	372
169	Fecal Microbial Diversity in a Strict Vegetarian as Determined by Molecular Analysis and Cultivation. Microbiology and Immunology, 2002, 46, 819-831.	0.7	130
170	Detection of novel oral phylotypes associated with periodontitis. FEMS Microbiology Letters, 2002, 217, 65-69.	0.7	35
171	Reclassification of Bacteroides forsythus (Tanner et al. 1986) as Tannerella forsythensis corrig., gen. nov., comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 841-849.	0.8	141
172	Rapid Detection and Quantification of Five Periodontopathic Bacteria by Realâ€Time PCR. Microbiology and Immunology, 2001, 45, 39-44.	0.7	128
173	Treponema socranskii, Treponema denticola,andPorphyromonas gingivalisAre Associated With Severity of Periodontal Tissue Destruction. Journal of Periodontology, 2001, 72, 1354-1363.	1.7	125
174	Characterization of the <i>Lactobacillus casei</i> Group and the <i>Lactobacillus acidophilus</i> Group by Automated Ribotyping. Microbiology and Immunology, 2001, 45, 271-275.	0.7	33
175	PCR Detection Method of <i>Clostridium scindens</i> and <i>C. hiranonis</i> in Human Fecal Samples. Microbiology and Immunology, 2001, 45, 263-266.	0.7	24
176	Comparison of the Oral Bacterial Flora in Saliva from a Healthy Subject and Two Periodontitis Patients by Sequence Analysis of 16S rDNA Libraries. Microbiology and Immunology, 2000, 44, 643-652.	0.7	105
177	Rapid identification and quantification ofCollinsella aerofaciensusing PCR. FEMS Microbiology Letters, 2000, 183, 43-47.	0.7	27
178	Phylogenetic Analysis of Saccharolytic Oral Treponemes Isolated from Human Subgingival Plaque. Microbiology and Immunology, 1999, 43, 711-716.	0.7	8
179	Detection of <i>Treponema socranskii</i> Associated with Human Periodontitis by PCR. Microbiology and Immunology, 1999, 43, 485-490.	0.7	29
180	Aerobic growth of some lactic acid bacteria enabled by the external addition of peroxidase (horseradish) to the culture medium. Journal of Bioscience and Bioengineering, 1998, 85, 627-629.	0.9	4

#	ARTICLE	IF	CITATIONS
181	Aerobic growth of and activities of NADH oxidase and NADH peroxidase in lactic acid bacteria. Journal of Bioscience and Bioengineering, 1996, 82, 210-216.	0.9	69
182	Comparison of H2O-forming NADH oxidase from Leuconostoc mesenteroides subsp. mesenteroides NRIC 1541T and H2O2-forming NADH oxidase from Sporolactobacillus inulinus NRIC 1133T. Journal of Bioscience and Bioengineering, 1996, 82, 531-537.	0.9	20