

Mikiyasu Sakanaka

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,098
citations

623734

14
h-index

713466

21
g-index

25
all docs

25
docs citations

25
times ranked

965
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of milk oligosaccharides: Origin and selectivity of the ratio of milk oligosaccharides to lactose among mammals. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2022, 1866, 130012.	2.4	19
2	Ecological and molecular perspectives on responders and non-responders to probiotics and prebiotics. <i>Current Opinion in Biotechnology</i> , 2022, 73, 108-120.	6.6	15
3	Diversification of a Fucosyllactose Transporter within the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0143721.	3.1	18
4	Priority effects shape the structure of infant-type <i>Bifidobacterium</i> communities on human milk oligosaccharides. <i>ISME Journal</i> , 2022, 16, 2265-2279.	9.8	34
5	Next-generation prebiotic promotes selective growth of bifidobacteria, suppressing <i>Clostridioides difficile</i> . <i>Gut Microbes</i> , 2021, 13, 1973835.	9.8	18
6	<i>Bifidobacterium</i> response to lactulose ingestion in the gut relies on a solute-binding protein-dependent ABC transporter. <i>Communications Biology</i> , 2021, 4, 541.	4.4	11
7	<i>Bifidobacterium</i> species associated with breastfeeding produce aromatic lactic acids in the infant gut. <i>Nature Microbiology</i> , 2021, 6, 1367-1382.	13.3	176
8	Varied Pathways of Infant Gut-Associated <i>Bifidobacterium</i> to Assimilate Human Milk Oligosaccharides: Prevalence of the Gene Set and Its Correlation with <i>Bifidobacteria</i> -Rich Microbiota Formation. <i>Nutrients</i> , 2020, 12, 71.	4.1	127
9	Application of Recombinase-Based In Vivo Expression Technology to <i>Bifidobacterium longum</i> subsp. <i>longum</i> for Identification of Genes Induced in the Gastrointestinal Tract of Mice. <i>Microorganisms</i> , 2020, 8, 410.	3.6	6
10	Butyrate producing colonic Clostridiales metabolise human milk oligosaccharides and cross feed on mucin via conserved pathways. <i>Nature Communications</i> , 2020, 11, 3285.	12.8	102
11	Enzymatic Adaptation of <i>Bifidobacterium bifidum</i> to Host Glycans, Viewed from Glycoside Hydrolyases and Carbohydrate-Binding Modules. <i>Microorganisms</i> , 2020, 8, 481.	3.6	41
12	è«¸â-â>1/2âšâš<â?/4âšâšÿâ13â...ç””èª;è£1/2ç2%â13ââ@2â€2-âf•â,3â,âf«âf©â,âf^âf1/4â,1æ.»âšâ€”ââ@çš'â- çš,,èf(æ!â-âç?/4çš'â€”. Kag		
13	Evolutionary adaptation in fucosyllactose uptake systems supports bifidobacteria-infant symbiosis. <i>Science Advances</i> , 2019, 5, eaaw7696.	10.3	120
14	Sharing of human milk oligosaccharides degradants within bifidobacterial communities in faecal cultures supplemented with <i>Bifidobacterium bifidum</i> . <i>Scientific Reports</i> , 2018, 8, 13958.	3.3	121
15	A Transposon Mutagenesis System for <i>Bifidobacterium longum</i> subsp. <i>longum</i> Based on an IS 3 Family Insertion Sequence, IS Blo11. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	14
16	Molecular Insight into Evolution of Symbiosis between Breast-Fed Infants and a Member of the Human Gut Microbiome <i>Bifidobacterium longum</i> . <i>Cell Chemical Biology</i> , 2017, 24, 515-524.e5.	5.2	102
17	Use of Gifu Anaerobic Medium for culturing 32 dominant species of human gut microbes and its evaluation based on short-chain fatty acids fermentation profiles. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 2009-2017.	1.3	50
18	Isolation and transposition properties of ISBlo11, an active insertion sequence belonging to the IS3 family, from <i>Bifidobacterium longum</i> 105-A. <i>FEMS Microbiology Letters</i> , 2015, 362, .	1.8	6

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19	Complete Genome Sequence of Bifidobacterium longum 105-A, a Strain with High Transformation Efficiency. Genome Announcements, 2014, 2, .	0.8	16
20	Functional analysis of bifidobacterial promoters in Bifidobacterium longum and Escherichia coli using the β -galactosidase gene as a reporter. Journal of Bioscience and Bioengineering, 2014, 118, 489-495.	2.2	16
21	Development of a Double-Crossover Markerless Gene Deletion System in Bifidobacterium longum: Functional Analysis of the β -Galactosidase Gene for Raffinose Assimilation. Applied and Environmental Microbiology, 2012, 78, 4984-4994.	3.1	59
22	Technological Advances in Bifidobacterial Molecular Genetics: Application to Functional Genomics and Medical Treatments. Bioscience of Microbiota, Food and Health, 2012, 31, 15-25.	1.8	8