Yoshihiro Yamaguchi

List of Publications by Year
in descending order

41 papers	1,882 citations	567281 15 h-index	315739 38 g-index
43 all docs	43 docs citations	43 times ranked	2067 citing authors

#	Article	IF	Citations
1	Structureâ€“activity relationships of antifungal phenylpropanoid derivatives and their synergy with <i>n</i> â€dodecanol and fluconazole. Letters in Applied Microbiology, 2022, 74, 377-384.	2.2	2
2	Efficient bacterial capture by amino-functionalized cellulose monolith. Journal of Porous Materials, 2021, 28, 1411-1419.	2.6	3
3	Involvement of a Multidrug Efflux Pump and Alterations in Cell Surface Structure in the Synergistic Antifungal Activity of Nagilactone E and Anethole against Budding Yeast Saccharomyces cerevisiae. Antibiotics, 2021, 10, 537.	3.7	5
4	Functional Characterization of the mazEF Toxin-Antitoxin System in the Pathogenic Bacterium Agrobacterium tumefaciens. Microorganisms, 2021, 9, 1107.	3.6	3
5	Deletion of the Golgi Ca2+-ATPase<i>PMR1</i>gene potentiates antifungal effects of dodecanol that depend on intracellular Ca2+ accumulation in budding yeast. FEMS Yeast Research, 2020, 20, .	2.3	5
6	Genome-Wide Screening for Identification of Novel Toxin-Antitoxin Systems in Staphylococcus aureus. Applied and Environmental Microbiology, 2019, 85, .	3.1	11
7	Identification and first characterization of DinJ-YafQ toxin-antitoxin systems in Lactobacillus species of biotechnological interest. Scientific Reports, 2019, 9, 7645.	3.3	7
8	Curcumin potentiates the fungicidal effect of dodecanol by inhibiting drug efflux in wildâ€type budding yeast. Letters in Applied Microbiology, 2019, 68, 17-23.	2.2	6
9	Identification of MazF Homologue in <i>Legionella pneumophila</i> Which Cleaves RNA at the AACU Sequence. Journal of Molecular Microbiology and Biotechnology, 2018, 28, 269-280.	1.0	4
10	Effect of nagilactone E on cell morphology and glucan biosynthesis in budding yeast Saccharomyces cerevisiae. FÃ¬toterapÃ¬Ã¢, 2018, 128, 112-117.	2.2	9
11	Characterization of YjjJ toxin of Escherichia coli. FEMS Microbiology Letters, 2017, 364, .	1.8	11
12	Translationâ€dependent <scp>mRNA</scp> cleavage by YhaV in <i>Escherichia coli</i>. FEBS Letters, 2017, 591, 1853-1861.	2.8	14
13	Deletion of mazF increases Staphylococcus aureus biofilm formation in an ica-dependent manner. Pathogens and Disease, 2017, 75, .	2.0	16
14	Preferential use of minor codons in the translation initiation region of human genes. Human Genetics, 2017, 136, 67-74.	3.8	6
15	Anethole potentiates dodecanol's fungicidal activity by reducing PDR5 expression in budding yeast. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 477-484.	2.4	17
16	Vacuolar H+-ATPase subunit Vma1p functions as the molecular ligand in the vacuole-targeting fungicidal activity of polymyxin B. Microbiology (United Kingdom), 2017, 163, 531-540.	1.8	4
17	The fungicidal activity of amphotericin B requires autophagy-dependent targeting to the vacuole under a nutrient-starved condition in Saccharomyces cerevisiae. Microbiology (United Kingdom), 2016, 162, 848-854.	1.8	11
18	An endogenous protein inhibitor, YjhX (TopAI), for topoisomerase I from<i>Escherichia coli</i>. Nucleic Acids Research, 2015, 43, gkv1197.	14.5	11

#	Article	IF	Citations
19	Sequence Specific RNA Recognition Mechanism of MazF. Seibutsu Butsuri, 2015, 55, 011-014.	0.1	0
20	Characterization of LdrA (Long Direct Repeat A) Protein of <i>Escherichia coli</i>. Journal of Molecular Microbiology and Biotechnology, 2014, 24, 91-97.	1.0	13
21	ACAâ€specific RNA sequence recognition is acquired via the loop 2 region of MazF mRNA interferase. Proteins: Structure, Function and Bioinformatics, 2013, 81, 874-883.	2.6	8
22	Structural Basis of mRNA Recognition and Cleavage by Toxin MazF and Its Regulation by Antitoxin MazE in Bacillus subtilis. Molecular Cell, 2013, 52, 447-458.	9.7	77
23	Type II Toxin-Antitoxin Loci: The mazEF Family. , 2013, , 107-136.		2
24	Replacement of All Arginine Residues with Canavanine in MazF-bs mRNA Interferase Changes Its Specificity. Journal of Biological Chemistry, 2013, 288, 7564-7571.	3.4	16
25	Intramolecular Regulation of the Sequence-Specific mRNA Interferase Activity of MazF Fused to a MazE Fragment with a Linker Cleavable by Specific Proteases. Applied and Environmental Microbiology, 2012, 78, 3794-3799.	3.1	29
26	Inhibition of specific gene expressions by protein-mediated mRNA interference. Nature Communications, 2012, 3, 607.	12.8	45
27	Identification of the First Functional Toxin-Antitoxin System in Streptomyces. PLoS ONE, 2012, 7, e32977.	2.5	40
28	A novel membrane-bound toxin for cell division, CptA (YgfX), inhibits polymerization of cytoskeleton proteins, FtsZ and MreB, in Escherichia coli. FEMS Microbiology Letters, 2012, 328, 174-181.	1.8	57
29	Suppression of MazF toxicity by fusing a Câ€terminal segment of MazE to MazF, and its activation by sequence specific HIVâ€1 and HCV proteases. FASEB Journal, 2012, 26, 956.2.	0.5	0
30	<i>Bacillus subtilis</i> MazFâ€bs (EndoA) is a UACAUâ€specific mRNA interferase. FEBS Letters, 2011, 585, 2526-2532.	2.8	69
31	Toxin-Antitoxin Systems in Bacteria and Archaea. Annual Review of Genetics, 2011, 45, 61-79.	7.6	557
32	Regulation of growth and death in Escherichia coli by toxinâ€"antitoxin systems. Nature Reviews Microbiology, 2011, 9, 779-790.	28.6	336
33	MqsR, a Crucial Regulator for Quorum Sensing and Biofilm Formation, Is a GCU-specific mRNA Interferase in Escherichia coli. Journal of Biological Chemistry, 2009, 284, 28746-28753.	3.4	152
34	Characterization of YafO, an Escherichia coli Toxin. Journal of Biological Chemistry, 2009, 284, 25522-25531.	3.4	58
35	<i>Staphylococcus aureus</i> YoeB Homologues Inhibit Translation Initiation. Journal of Bacteriology, 2009, 191, 5868-5872.	2.2	52
36	Chapter 12 mRNA Interferases, Sequenceâ€Specific Endoribonucleases from the Toxinâ€"Antitoxin Systems. Progress in Molecular Biology and Translational Science, 2009, 85, 467-500.	1.7	118

#	ARTICLE	IF	CITATIONS
37	Two Segments in Bacterial Antizyme P22 Are Essential for Binding and Enhance Degradation of Lysine/Ornithine Decarboxylase in Selenomonas ruminantium. Journal of Bacteriology, 2008, 190, 442-446.	2.2	3
38	Occurrence of Agmatine Pathway for Putrescine Synthesis in<i>Selenomonas ruminatium</i>. Bioscience, Biotechnology and Biochemistry, 2008, 72, 445-455.	1.3	17
39	Characterization of a Counterpart to Mammalian Ornithine Decarboxylase Antizyme in Prokaryotes. Journal of Biological Chemistry, 2006, 281, 3995-4001.	3.4	14
40	Identification of a 22-kDa Protein Required for the Degradation ofSelenomonas ruminantiumLysine Decarboxylase by ATP-dependent Protease. Bioscience, Biotechnology and Biochemistry, 2002, 66, 1431-1434.	1.3	12
41	Gene Cloning and Molecular Characterization of Lysine Decarboxylase from Selenomonas ruminantiumDelineate Its Evolutionary Relationship to Ornithine Decarboxylases from Eukaryotes. Journal of Bacteriology, 2000, 182, 6732-6741.	2.2	56