

Akimasa Miyanaga

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Structural Insight into the Reaction Mechanism of Ketosynthase-Like Decarboxylase in a Loading Module of Modular Polyketide Synthases. <i>ACS Chemical Biology</i> , 2022, 17, 198-206.	3.4	10
2	Protein-Protein Recognition Involved in the Intermodular Transacylation Reaction in Modular Polyketide Synthase in the Biosynthesis of Vicenistatin. <i>ChemBioChem</i> , 2022, 23, .	2.6	7
3	One-pot enzymatic synthesis of 2-deoxy- <i>scyllo</i> -inosose from <i>d</i> -glucose and polyphosphate. <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 108-114.	1.3	2
4	Stepwise Post-glycosylation Modification of Sugar Moieties in Kanamycin Biosynthesis. <i>ChemBioChem</i> , 2021, 22, 1668-1675.	2.6	3
5	Mutational Biosynthesis of Hitachimycin Analogs Controlled by the β -Amino Acid-Selective Adenylation Enzyme HitB. <i>ACS Chemical Biology</i> , 2021, 16, 539-547.	3.4	7
6	Substrate specificity of Chondroitinase ABC I based on analyses of biochemical reactions and crystal structures in complex with disaccharides. <i>Glycobiology</i> , 2021, 31, 1571-1581.	2.5	7
7	Complex structure of the acyltransferase VinK and the carrier protein VinL with a pantetheine cross-linking probe. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 294-302.	0.8	6
8	Generation of incednine derivatives by mutasynthesis. <i>Journal of Antibiotics</i> , 2020, 73, 794-797.	2.0	2
9	Structural Characterization of Complex of Adenylation Domain and Carrier Protein by Using Pantetheine Cross-Linking Probe. <i>ACS Chemical Biology</i> , 2020, 15, 1808-1812.	3.4	17
10	Biochemical and Structural Analysis of a Dehydrogenase, KanD2, and an Aminotransferase, KanS2, That Are Responsible for the Construction of the Kanosamine Moiety in Kanamycin Biosynthesis. <i>Biochemistry</i> , 2020, 59, 1470-1473.	2.5	5
11	Michael additions in polyketide biosynthesis. <i>Natural Product Reports</i> , 2019, 36, 531-547.	10.3	23
12	Structural Analysis of the Glycine Oxidase Homologue CmiS2 Reveals a Unique Substrate Recognition Mechanism for Formation of a β -Amino Acid Starter Unit in Cremimycin Biosynthesis. <i>Biochemistry</i> , 2019, 58, 2706-2709.	2.5	6
13	Functional and structural characterization of IdnL7, an adenylation enzyme involved in incednine biosynthesis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 299-306.	0.8	8
14	An Engineered Aryl Acid Adenylation Domain with an Enlarged Substrate Binding Pocket. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 6906-6910.	13.8	15
15	An Engineered Aryl Acid Adenylation Domain with an Enlarged Substrate Binding Pocket. <i>Angewandte Chemie</i> , 2019, 131, 6980-6984.	2.0	0
16	Identification, characterization, and structural analyses of a fungal endo- β -1,2-glucanase reveal a new glycoside hydrolase family. <i>Journal of Biological Chemistry</i> , 2019, 294, 7942-7965.	3.4	18
17	Phenolic Lipids Synthesized by Type III Polyketide Synthases. , 2019, , 139-149.		0
18	Type III Polyketide Synthases Responsible for Phenolic Lipid Synthesis. , 2019, , 435-443.		0

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19	Functional and Structural Analyses of the Split-Dehydratase Domain in the Biosynthesis of Macrolactam Polyketide Cremimycin. <i>Biochemistry</i> , 2019, 58, 4799-4803.	2.5	5
20	Stereochemistry in the Reaction of the <i>myo</i> -Inositol Phosphate Synthase Ortholog Ari2 during Aristeromycin Biosynthesis. <i>Biochemistry</i> , 2019, 58, 5112-5116.	2.5	5
21	Structural basis of the nonribosomal codes for nonproteinogenic amino acid selective adenylation enzymes in the biosynthesis of natural products. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 515-536.	3.0	44
22	Characterization and Structural Analysis of a Novel <i>exo</i> -Type Enzyme Acting on β -1,2-Glucooligosaccharides from <i>Parabacteroides distasonis</i> . <i>Biochemistry</i> , 2018, 57, 3849-3860.	2.5	14
23	Protein-protein interactions in polyketide synthase nonribosomal peptide synthetase hybrid assembly lines. <i>Natural Product Reports</i> , 2018, 35, 1185-1209.	10.3	73
24	Biochemical and Structural Analysis of FomD That Catalyzes the Hydrolysis of Cytidylyl (<i>S</i>)-2-Hydroxypropylphosphonate in Fosfomycin Biosynthesis. <i>Biochemistry</i> , 2018, 57, 4858-4866.	2.5	11
25	Structural Basis of Sequential Allosteric Transitions in Tetrameric <i>scp</i> -Lactate Dehydrogenases from Three Gram-Negative Bacteria. <i>Biochemistry</i> , 2018, 57, 5388-5406.	2.5	11
26	Structural Basis of Protein-Protein Interactions between a <i>trans</i> -Acting Acyltransferase and Acyl Carrier Protein in Polyketide Disorazole Biosynthesis. <i>Journal of the American Chemical Society</i> , 2018, 140, 7970-7978.	13.7	40
27	Biochemical and structural analyses of a bacterial endo- β -1,2-gluconase reveal a new glycoside hydrolase family. <i>Journal of Biological Chemistry</i> , 2017, 292, 7487-7506.	3.4	42
28	Mechanistic insight into the substrate specificity of 1,2- β -oligoglucan phosphorylase from <i>Lachnoclostridium phytofermentans</i> . <i>Scientific Reports</i> , 2017, 7, 42671.	3.3	36
29	Structural analysis of the dual-function thioesterase SAV606 unravels the mechanism of Michael addition of glycine to an α,β -unsaturated thioester. <i>Journal of Biological Chemistry</i> , 2017, 292, 10926-10937.	3.4	20
30	The ternary complex structure of <i>d</i> -mandelate dehydrogenase with NADH and anilino(oxo)acetate. <i>Biochemical and Biophysical Research Communications</i> , 2017, 486, 665-670.	2.1	6
31	Biochemical characterization and structural insight into aliphatic β -amino acid adenylation enzymes IdnL1 and CmiS6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1238-1247.	2.6	21
32	Structure and function of polyketide biosynthetic enzymes: various strategies for production of structurally diverse polyketides. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 2227-2236.	1.3	31
33	Substrate Recognition by a Dual-Function P450 Monooxygenase GfsF Involved in FD891 Biosynthesis. <i>ChemBioChem</i> , 2017, 18, 2179-2187.	2.6	14
34	Function and structure relationships of a β -1,2-glucooligosaccharide-degrading β -glucosidase. <i>FEBS Letters</i> , 2017, 591, 3926-3936.	2.8	26
35	Phenolic Lipids Synthesized by Type III Polyketide Synthases. , 2017, , 1-11.		2
36	Type III Polyketide Synthases Responsible for Phenolic Lipid Synthesis. , 2017, , 1-9.		1

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37	Phenolic Lipids Synthesized by Type III Polyketide Synthases. , 2017, , 1-11.		0
38	Functional and Structural Analysis of a Î ² -Glucosidase Involved in Î ² -1,2-Glucan Metabolism in <i>Listeria innocua</i> . PLoS ONE, 2016, 11, e0148870.	2.5	36
39	Mechanisms of Î ² -amino acid incorporation in polyketide macrolactam biosynthesis. Current Opinion in Chemical Biology, 2016, 35, 58-64.	6.1	33
40	Parallel Post-Polyketide Synthase Modification Mechanism Involved in FDâ€891 Biosynthesis in <i>Streptomyces graminofaciens</i> Aâ€8890. ChemBioChem, 2016, 17, 233-238.	2.6	7
41	Structure-based analysis of the molecular interactions between acyltransferase and acyl carrier protein in vicenistatin biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1802-1807.	7.1	69
42	Identification of the Fluvirucin B2 (Sch 38518) Biosynthetic Gene Cluster from <i>Actinomadura fulva</i> subsp. <i>indica</i> ATCC 53714: substrate Specificity of the Î ² -Amino Acid Selective Adenylating Enzyme FlvN. Bioscience, Biotechnology and Biochemistry, 2016, 80, 935-941.	1.3	20
43	Phenolic Lipids Synthesized by Type III Polyketide Synthases. , 2016, , 1-11.		0
44	Type III Polyketide Synthases Responsible for Phenolic Lipid Synthesis. , 2016, , 1-9.		0
45	Genome Mining of the Hitachimycin Biosynthetic Gene Cluster: Involvement of a Phenylalanine-2,3-aminomutase in Biosynthesis. ChemBioChem, 2015, 16, 909-914.	2.6	36
46	Mechanism-Based Trapping of the Quinonoid Intermediate by Using the K276R Mutant of PLP-Dependent 3-aminobenzoate Synthase PctV in the Biosynthesis of Pactamycin. ChemBioChem, 2015, 16, 2484-2490.	2.6	12
47	Diverse allosteric and catalytic functions of tetrameric d-lactate dehydrogenases from three Gram-negative bacteria. AMB Express, 2014, 4, 76.	3.0	14
48	The Core of Allosteric Motion in <i>Thermus caldophilus</i> L-Lactate Dehydrogenase. Journal of Biological Chemistry, 2014, 289, 31550-31564.	3.4	12
49	Crystallization and preliminary X-ray diffraction analysis of Lin1840, a putative Î ² -glucosidase from <i>Listeria innocua</i> . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1398-1401.	0.8	2
50	The Crystal Structure of the Adenylation Enzyme VinN Reveals a Unique Î ² -Amino Acid Recognition Mechanism. Journal of Biological Chemistry, 2014, 289, 31448-31457.	3.4	46
51	Biosynthesis of natural products containing Î ² -amino acids. Natural Product Reports, 2014, 31, 1056-1073.	10.3	188
52	The crystal structure of the amidohydrolase VinJ shows a unique hydrophobic tunnel for its interaction with polyketide substrates. FEBS Letters, 2014, 588, 995-1000.	2.8	10
53	Flavin-mediated dual oxidation controls an enzymatic Favorskii-type rearrangement. Nature, 2013, 503, 552-556.	27.8	147
54	The crystal structure of d-mandelate dehydrogenase reveals its distinct substrate and coenzyme recognition mechanisms from those of 2-ketopantoate reductase. Biochemical and Biophysical Research Communications, 2013, 439, 109-114.	2.1	9

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55	Structural Basis for Cyclization Specificity of Two Azotobacter Type III Polyketide Synthases. <i>Journal of Biological Chemistry</i> , 2013, 288, 34146-34157.	3.4	29
56	Characterization of Polyphosphate Glucokinase SCO5059 from <i>Streptomyces coelicolor</i> A3(2). <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2322-2324.	1.3	11
57	Discovery and Assembly-Line Biosynthesis of the Lymphostin Pyrroloquinoline Alkaloid Family of mTOR Inhibitors in <i>Salinispora</i> Bacteria. <i>Journal of the American Chemical Society</i> , 2011, 133, 13311-13313.	13.7	70
58	A molecular design that stabilizes active state in bacterial allosteric L-lactate dehydrogenases. <i>Journal of Biochemistry</i> , 2011, 150, 579-591.	1.7	9
59	A Stereoselective Vanadium-Dependent Chloroperoxidase in Bacterial Antibiotic Biosynthesis. <i>Journal of the American Chemical Society</i> , 2011, 133, 4268-4270.	13.7	109
60	Characterization of a chimeric enzyme comprising feruloyl esterase and family 42 carbohydrate-binding module. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 155-161.	3.6	13
61	Enzymatic synthesis of bis-5-alkylresorcinols by resorcinol-producing type III polyketide synthases. <i>Journal of Antibiotics</i> , 2009, 62, 371-376.	2.0	15
62	Direct transfer of starter substrates from type I fatty acid synthase to type III polyketide synthases in phenolic lipid synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 871-876.	7.1	80
63	Molecular Anatomy of the Alkaliphilic Xylanase from <i>Bacillus halodurans</i> C-125. <i>Journal of Biochemistry</i> , 2007, 141, 709-717.	1.7	6
64	New Structural Insights on Carbohydrate-active Enzymes. <i>Journal of Applied Glycoscience</i> (1999), 2007, 54, 95-102.	0.7	7
65	Mutational analysis of N-glycosylation recognition sites on the biochemical properties of <i>Aspergillus kawachii</i> α -L-arabinofuranosidase 54. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2006, 1760, 1458-1464.	2.4	25
66	The family 42 carbohydrate-binding module of family 54 α -L-arabinofuranosidase specifically binds the arabinofuranose side chain of hemicellulose. <i>Biochemical Journal</i> , 2006, 399, 503-511.	3.7	44
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