

# Masahiro Fujihashi

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

301  
citations

1040056

9  
h-index

940533

16  
g-index

19  
all docs

19  
docs citations

19  
times ranked

519  
citing authors

#	ARTICLE	IF	CITATIONS
1	Insight into the mechanism of geranyl-Î²-phellandrene formation catalyzed by Class IB terpene synthases. <i>Bioscience, Biotechnology and Biochemistry</i> , 2022, , .	1.3	0
2	Altering the Phosphorylation Position of Pyrophosphate-Dependent <i>myo</i> -Inositol-1-Kinase Based on Its Crystal Structure. <i>ACS Chemical Biology</i> , 2021, 16, 794-799.	3.4	2
3	Identification and enzymatic analysis of an archaeal ATP-dependent serine kinase from the hyperthermophilic archaeon <i>Staphylothermus marinus</i> . <i>Journal of Bacteriology</i> , 2021, 203, e0002521.	2.2	5
4	Crystallographic Analysis with Anomalous Dispersion Effects of Phosphorus Atoms Using Remote and Automated Measurements. <i>Nihon Kessho Gakkaishi</i> , 2021, 63, 222-223.	0.0	0
5	Characterization of Class IB Terpene Synthase: The First Crystal Structure Bound with a Substrate Surrogate. <i>ACS Chemical Biology</i> , 2020, 15, 1517-1525.	3.4	7
6	Crystal structure and functional analysis of large-terpene synthases belonging to a newly found subclass. <i>Chemical Science</i> , 2018, 9, 3754-3758.	7.4	25
7	Identification of a pyrophosphate-dependent kinase and its donor selectivity determinants. <i>Nature Communications</i> , 2018, 9, 1765.	12.8	17
8	Structural Study on the Reaction Mechanism of a Free Serine Kinase Involved in Cysteine Biosynthesis. <i>ACS Chemical Biology</i> , 2017, 12, 1514-1523.	3.4	7
9	Mutation design of a thermophilic Rubisco based on three-dimensional structure enhances its activity at ambient temperature. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1339-1346.	2.6	11
10	Crystal Structure and Product Analysis of an Archaeal <i>myo</i> -Inositol Kinase Reveal Substrate Recognition Mode and 3-OH Phosphorylation. <i>Biochemistry</i> , 2015, 54, 3494-3503.	2.5	7
11	Orotidine Monophosphate Decarboxylase – A Fascinating Workhorse Enzyme with Therapeutic Potential. <i>Journal of Genetics and Genomics</i> , 2015, 42, 221-234.	3.9	6
12	Structural characterization of a ligand-bound form of <i>Bacillus subtilis</i> FadR involved in the regulation of fatty acid degradation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1301-1310.	2.6	23
13	Substrate Distortion Contributes to the Catalysis of Orotidine 5-Monophosphate Decarboxylase. <i>Journal of the American Chemical Society</i> , 2013, 135, 17432-17443.	13.7	27
14	An Uncharacterized Member of the Ribokinase Family in <i>Thermococcus kodakarensis</i> Exhibits <i>myo</i> -Inositol Kinase Activity. <i>Journal of Biological Chemistry</i> , 2013, 288, 20856-20867.	3.4	9
15	Atomic Resolution Structure of the Orotidine 5-Monophosphate Decarboxylase Product Complex Combined with Surface Plasmon Resonance Analysis. <i>Journal of Biological Chemistry</i> , 2013, 288, 9011-9016.	3.4	13
16	2P020 Crystal Structure of Prefoldin beta Subunits Oligomer(Proteins-structure and) Tj ETQq0 0 0 rgBT /Overlock 10, Tf 50 142 Td (stru	0.1	0
17	Crystal Structure of Archaeal Photolyase from <i>Sulfolobus tokodaii</i> with Two FAD Molecules: Implication of a Novel Light-harvesting Cofactor. <i>Journal of Molecular Biology</i> , 2007, 365, 903-910.	4.2	65
18	X-ray crystallographic characterization and phasing of a fucose-specific lectin from <i>Aleuria aurantia</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 378-380.	2.5	10

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19	Crystal Structure of Fucose-Specific Lectin from <i>Aleuria aurantia</i> Binding Ligands at Three of Its Five Sugar Recognition Sites. <i>Biochemistry</i> , 2003, 42, 11093-11099.	2.5	67