

Hideyuki Matsunami

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/389757/publications.pdf>

Version: 2024-02-01

37
papers

1,142
citations

567281

15
h-index

414414

32
g-index

39
all docs

39
docs citations

39
times ranked

1146
citing authors

#	ARTICLE	IF	CITATIONS
1	Assembly mechanism of the pleomorphic immature poxvirus scaffold. <i>Nature Communications</i> , 2022, 13, 1704.	12.8	6
2	Structure of the bacterial flagellar hook cap provides insights into a hook assembly mechanism. <i>Communications Biology</i> , 2021, 4, 1291.	4.4	6
3	Cryo-EM Structures of Centromeric Tri-nucleosomes Containing a Central CENP-A Nucleosome. <i>Structure</i> , 2020, 28, 44-53.e4.	3.3	47
4	Structure of polymerized type V pilin reveals assembly mechanism involving protease-mediated strand exchange. <i>Nature Microbiology</i> , 2020, 5, 830-837.	13.3	27
5	Architecture of the Bacterial Flagellar Distal Rod and Hook of Salmonella. <i>Biomolecules</i> , 2019, 9, 260.	4.0	15
6	Metastable asymmetrical structure of a shaftless V motor. <i>Science Advances</i> , 2019, 5, eaau8149.	10.3	13
7	Torque transmission mechanism of the curved bacterial flagellar hook revealed by cryo-EM. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 941-945.	8.2	30
8	Evidence for the hook supercoiling mechanism of the bacterial flagellum. <i>Biophysics and Physicobiology</i> , 2018, 15, 28-32.	1.0	11
9	Cryo-EM structure of the Ebola virus nucleoprotein-RNA complex at 3.6Å resolution. <i>Nature</i> , 2018, 563, 137-140.	27.8	94
10	The FlaG regulator is involved in length control of the polar flagella of <i>Campylobacter jejuni</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 740-750.	1.8	10
11	Cryo-EM Structure of <i>Campylobacter</i> Flagellar Hook. <i>Seibutsu Butsuri</i> , 2017, 57, 265-267.	0.1	0
12	Structural insights into bacterial flagellar hooks similarities and specificities. <i>Scientific Reports</i> , 2016, 6, 35552.	3.3	13
13	Structural flexibility of the periplasmic protein, FlgA, regulates flagellar P-ring assembly in <i>Salmonella enterica</i> . <i>Scientific Reports</i> , 2016, 6, 27399.	3.3	10
14	Complete structure of the bacterial flagellar hook reveals extensive set of stabilizing interactions. <i>Nature Communications</i> , 2016, 7, 13425.	12.8	49
15	Crystallization and preliminary X-ray diffraction analysis of the periplasmic domain of the <i>Escherichia coli</i> aspartate receptor Tar and its complex with aspartate. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1219-1223.	0.8	3
16	Purification, crystallization and preliminary X-ray crystallographic analysis of the flagellar accessory protein FlaH from the methanogenic archaeon <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1543-1545.	0.8	2
17	Expression, purification, crystallization and preliminary X-ray diffraction analysis of a core fragment of FlgG, a bacterial flagellar rod protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 547-550.	0.7	7
18	Inhibition of a type III secretion system by the deletion of a short loop in one of its membrane proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 812-820.	2.5	31

#	ARTICLE	IF	CITATIONS
19	Crystallization and preliminary X-ray analysis of FlgA, a periplasmic protein essential for flagellar P-ring assembly. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 310-313.	0.7	2
20	Crystal Structure and Mutational Analysis of the Periplasmic Flagellar Protein FlgA. <i>Biophysical Journal</i> , 2010, 98, 560a.	0.5	0
21	Molecular Mechanism of the Peptidoglycan Hydrolysis by FlgJ, A Putative Flagellar Rod Cap Protein From Salmonella. <i>Biophysical Journal</i> , 2010, 98, 248a-249a.	0.5	0
22	Crystallization and preliminary X-ray analysis of a C-terminal fragment of FlgJ, a putative flagellar rod cap protein from <i>Salmonella</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 17-20.	0.7	3
23	Purification, crystallization and preliminary X-ray analysis of FliT, a bacterial flagellar substrate-specific export chaperone. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 825-828.	0.7	5
24	Characterization of the Periplasmic Domain of MotB and Implications for Its Role in the Stator Assembly of the Bacterial Flagellar Motor. <i>Journal of Bacteriology</i> , 2008, 190, 3314-3322.	2.2	40
25	Gap compression/extension mechanism of bacterial flagellar hook as the molecular universal joint. <i>Journal of Structural Biology</i> , 2007, 157, 481-490.	2.8	19
26	PAX6 and SOX2-dependent regulation of the <i>Sox2</i> enhancer β involved in embryonic visual system development. <i>Genes To Cells</i> , 2007, 12, 1049-1061.	1.2	87
27	A partial atomic structure for the flagellar hook of <i>Salmonella typhimurium</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1023-1028.	7.1	50
28	Structure of the bacterial flagellar hook and implication for the molecular universal joint mechanism. <i>Nature</i> , 2004, 431, 1062-1068.	27.8	176
29	Crystallization of a core fragment of the flagellar hook protein FlgE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2078-2080.	2.5	8
30	Chemical Rescue of a Site-Specific Mutant of Bacterial Copper Amine Oxidase for Generation of the Topa Quinone Cofactor. <i>Biochemistry</i> , 2004, 43, 2178-2187.	2.5	20
31	Interactions between Bacterial Flagellar Axial Proteins in Their Monomeric State in Solution. <i>Journal of Molecular Biology</i> , 2002, 318, 889-900.	4.2	26
32	Purification and characterization of 3-isopropylmalate dehydrogenase from <i>Thiobacillus thiooxidans</i> . <i>Journal of Bioscience and Bioengineering</i> , 2000, 90, 459-461.	2.2	4
33	Purification and Characterization of 3-Isopropylmalate Dehydrogenase from <i>Thiobacillus thiooxidans</i> . <i>Journal of Bioscience and Bioengineering</i> , 2000, 90, 459-461.	2.2	0
34	Mechanism of Topa Quinone Biogenesis in Copper Amine Oxidase Studied by Site-Directed Mutagenesis and X-Ray Crystallography. , 2000, , 67-70.		0
35	Structure of 3-isopropylmalate dehydrogenase in complex with 3-isopropylmalate at 2.0 Å resolution: the role of Glu88 in the unique substrate-recognition mechanism. <i>Structure</i> , 1998, 6, 971-982.	3.3	64
36	Overproduction and Substrate Specificity of 3-Isopropylmalate Dehydrogenase from <i>Thiobacillus ferrooxidans</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 1998, 62, 372-373.	1.3	6

#	ARTICLE	IF	CITATIONS
37	Crystal Structures of the Copper-Containing Amine Oxidase from <i>Arthrobacter globiformis</i> in the Holo and Apo Forms: Implications for the Biogenesis of Topaquinone, <i>Biochemistry</i> , 1997, 36, 16116-16133.	2.5	258