

Katsumi Imada

List of Publications by Year in descending order

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108
papers

4,835
citations

101543

36
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106344

65
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112
all docs

112
docs citations

112
times ranked

3080
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Basis of Ubiquitin Recognition by a Bacterial Ovarian Tumor Deubiquitinase LotA. <i>Journal of Bacteriology</i> , 2022, 204, JB0037621.	2.2	11
2	A new α -arginine oxidase engineered from α -glutamate oxidase. <i>Protein Science</i> , 2021, 30, 1044-1055.	7.6	4
3	Two Distinct Conformations in 34 FlIF Subunits Generate Three Different Symmetries within the Flagellar MS-Ring. <i>MBio</i> , 2021, 12, .	4.1	20
4	The FlhA linker mediates flagellar protein export switching during flagellar assembly. <i>Communications Biology</i> , 2021, 4, 646.	4.4	16
5	A slight bending of an α -helix in FlIM creates a counterclockwise-locked structure of the flagellar motor in <i>Vibrio</i> . <i>Journal of Biochemistry</i> , 2021, 170, 531-538.	1.7	6
6	Native flagellar MS ring is formed by 34 subunits with 23-fold and 11-fold subsymmetries. <i>Nature Communications</i> , 2021, 12, 4223.	12.8	34
7	ZomB is essential for chemotaxis of <i>Vibrio alginolyticus</i> by the rotational direction control of the polar flagellar motor. <i>Genes To Cells</i> , 2021, 26, 927-937.	1.2	4
8	Structural basis of enzyme activity regulation by the propeptide of l-lysine α -oxidase precursor from <i>Trichoderma viride</i> . <i>Journal of Structural Biology: X</i> , 2021, 5, 100044.	1.3	3
9	Structure of the bacterial flagellar hook cap provides insights into a hook assembly mechanism. <i>Communications Biology</i> , 2021, 4, 1291.	4.4	6
10	Structural basis of the binding affinity of chemoreceptors Mlp24p and Mlp37p for various amino acids. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 233-238.	2.1	4
11	Structural basis of strict substrate recognition of α -lysine α -oxidase from <i>Trichoderma viride</i> . <i>Protein Science</i> , 2020, 29, 2213-2225.	7.6	8
12	PorA, a conserved C-terminal domain-containing protein, impacts the PorXY-SigP signaling of the type IX secretion system. <i>Scientific Reports</i> , 2020, 10, 21109.	3.3	7
13	PorM, a core component of bacterial type IX secretion system, forms a dimer with a unique kinked-rod shape. <i>Biochemical and Biophysical Research Communications</i> , 2020, 532, 114-119.	2.1	15
14	<i>In Situ</i> Structure of the <i>Vibrio</i> Polar Flagellum Reveals a Distinct Outer Membrane Complex and Its Specific Interaction with the Stator. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	21
15	In Vitro Autonomous Construction of the Flagellar Axial Structure in Inverted Membrane Vesicles. <i>Biomolecules</i> , 2020, 10, 126.	4.0	9
16	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
17	Structure and Energy-Conversion Mechanism of the Bacterial Na ⁺ -Driven Flagellar Motor. <i>Trends in Microbiology</i> , 2020, 28, 719-731.	7.7	31
18	Architecture of the Bacterial Flagellar Distal Rod and Hook of <i>Salmonella</i> . <i>Biomolecules</i> , 2019, 9, 260.	4.0	15

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19	Structural Insights into the Substrate Specificity Switch Mechanism of the Type III Protein Export Apparatus. <i>Structure</i> , 2019, 27, 965-976.e6.	3.3	39
20	Structure of the periplasmic domain of SflA involved in spatial regulation of the flagellar biogenesis of <i>Vibrio</i> reveals a TPR/SLR-like fold. <i>Journal of Biochemistry</i> , 2019, 166, 197-204.	1.7	9
21	Structure of <i>Vibrio</i> FliL, a New Stomatin-like Protein That Assists the Bacterial Flagellar Motor Function. <i>MBio</i> , 2019, 10, .	4.1	37
22	Calcium Ions Modulate Amino Acid Sensing of the Chemoreceptor Mlp24 of <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	10
23	Insight into structural remodeling of the FlhA ring responsible for bacterial flagellar type III protein export. <i>Science Advances</i> , 2018, 4, eaao7054.	10.3	50
24	Bacterial flagellar axial structure and its construction. <i>Biophysical Reviews</i> , 2018, 10, 559-570.	3.2	42
25	Insight into adaptive remodeling of the rotor ring complex of the bacterial flagellar motor. <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 12-17.	2.1	17
26	The Helix Rearrangement in the Periplasmic Domain of the Flagellar Stator B Subunit Activates Peptidoglycan Binding and Ion Influx. <i>Structure</i> , 2018, 26, 590-598.e5.	3.3	83
27	<i>Salmonella</i> Flagellum. , 2018, , .		3
28	In Vitro Reconstitution of Functional Type III Protein Export and Insights into Flagellar Assembly. <i>MBio</i> , 2018, 9, .	4.1	32
29	Novel insight into an energy transduction mechanism of the bacterial flagellar type III protein export. <i>Biophysics and Physicobiology</i> , 2018, 15, 173-178.	1.0	4
30	Design and Preparation of the Fragment Proteins of the Flagellar Components Suitable for X-Ray Crystal Structure Analysis. <i>Methods in Molecular Biology</i> , 2017, 1593, 97-103.	0.9	2
31	Structural differences in the bacterial flagellar motor among bacterial species. <i>Biophysics and Physicobiology</i> , 2017, 14, 191-198.	1.0	47
32	Molecular Basis of Ligand Recognition by the Taurine/Amino Acid Chemoreceptor of <i>Vibrio cholerae</i> . <i>Seibutsu Butsuri</i> , 2017, 57, 291-295.	0.1	0
33	Assembly and stoichiometry of the core structure of the bacterial flagellar type III export gate complex. <i>PLoS Biology</i> , 2017, 15, e2002281.	5.6	69
34	Biochemical characterization of the flagellar stator-associated inner membrane protein FliL from <i>Vibrio alginolyticus</i> . <i>Journal of Biochemistry</i> , 2017, 161, mwv076.	1.7	8
35	Rearrangements of α -helical structures of FlgN chaperone control the binding affinity for its cognate substrates during flagellar type III export. <i>Molecular Microbiology</i> , 2016, 101, 656-670.	2.5	23
36	Identification of a <i>Vibrio cholerae</i> chemoreceptor that senses taurine and amino acids as attractants. <i>Scientific Reports</i> , 2016, 6, 20866.	3.3	61

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37	Dependence of fluorescent protein brightness on protein concentration in solution and enhancement of it. <i>Scientific Reports</i> , 2016, 6, 22342.	3.3	44
38	Epistasis effects of multiple ancestral-consensus amino acid substitutions on the thermal stability of glycerol kinase from <i>Cellulomonas</i> sp. NT3060. <i>Journal of Bioscience and Bioengineering</i> , 2016, 121, 497-502.	2.2	10
39	Insight into the flagella type III export revealed by the complex structure of the type III ATPase and its regulator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3633-3638.	7.1	57
40	Molecular and structural analysis of <i>Legionella</i> DotI gives insights into an inner membrane complex essential for type IV secretion. <i>Scientific Reports</i> , 2015, 5, 10912.	3.3	36
41	Recombinant expression, molecular characterization and crystal structure of antitumor enzyme, L-lysine \bar{A} -oxidase from <i>Trichoderma viride</i> . <i>Journal of Biochemistry</i> , 2015, 157, 549-559.	1.7	24
42	The bacterial flagellar motor and its structural diversity. <i>Trends in Microbiology</i> , 2015, 23, 267-274.	7.7	209
43	Structural Basis of the Assembly and Activation Mechanism of the Bacterial Flagellar Stator Complex. <i>Nihon Kessho Gakkaishi</i> , 2015, 57, 291-296.	0.0	0
44	Conformational change in the periplasmic region of the flagellar stator coupled with the assembly around the rotor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13523-13528.	7.1	84
45	Crystallization and preliminary X-ray analysis of the periplasmic domain of FlhP, an integral membrane component of the bacterial flagellar type III protein-export apparatus. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1215-1218.	0.8	4
46	Assembly Mechanism of the Supramolecular Rings for Ultra High Speed Rotation in the Sodium-driven <i>Vibrio</i> Flagellar Motor. <i>Seibutsu Butsuri</i> , 2014, 54, 019-021.	0.1	0
47	X-ray Structure Analysis and Characterization of AFUEI, an Elastase Inhibitor from <i>Aspergillus fumigatus</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 17451-17459.	3.4	9
48	Effects of Chain Length of an Amphipathic Polypeptide Carrying the Repeated Amino Acid Sequence (LETLAKA) on \bar{I} -Helix and Fibrous Assembly Formation. <i>Biochemistry</i> , 2013, 52, 2810-2820.	2.5	5
49	Interactions of bacterial flagellar chaperone-substrate complexes with FlhA contribute to coordinating assembly of the flagellar filament. <i>Molecular Microbiology</i> , 2013, 90, 1249-1261.	2.5	86
50	Draft Genome Sequence of a Thermophilic Member of the Bacillaceae, <i>Anoxybacillus flavithermus</i> Strain Kn10, Isolated from the Kan-nawa Hot Spring in Japan. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
51	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
52	Interaction between FljI and FlhA, Components of the Bacterial Flagellar Type III Export Apparatus. <i>Journal of Bacteriology</i> , 2013, 195, 466-473.	2.2	59
53	Insight into the assembly mechanism in the supramolecular rings of the sodium-driven <i>Vibrio</i> flagellar motor from the structure of FlgT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6133-6138.	7.1	48
54	Glycine Insertion Makes Yellow Fluorescent Protein Sensitive to Hydrostatic Pressure. <i>PLoS ONE</i> , 2013, 8, e73212.	2.5	22

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55	Common Evolutionary Origin for the Rotor Domain of Rotary ATPases and Flagellar Protein Export Apparatus. <i>PLoS ONE</i> , 2013, 8, e64695.	2.5	34
56	The Roles of the Dimeric and Tetrameric Structures of the Clock Protein KaiB in the Generation of Circadian Oscillations in Cyanobacteria. <i>Journal of Biological Chemistry</i> , 2012, 287, 29506-29515.	3.4	35
57	Functional Defect and Restoration of Temperature-Sensitive Mutants of FlhA, a Subunit of the Flagellar Protein Export Apparatus. <i>Journal of Molecular Biology</i> , 2012, 415, 855-865.	4.2	11
58	Crystallization and preliminary X-ray analysis of the FliHâ€‘FliI complex responsible for bacterial flagellar type III protein export. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1311-1314.	0.7	2
59	Interaction between FliI ATPase and a flagellar chaperone FliT during bacterial flagellar protein export. <i>Molecular Microbiology</i> , 2012, 83, 168-178.	2.5	50
60	Interaction of a bacterial flagellar chaperone FlgN with FlhA is required for efficient export of its cognate substrates. <i>Molecular Microbiology</i> , 2012, 83, 775-788.	2.5	76
61	Phaseâ€‘dependent generation and transmission of time information by the KaiABC circadian clock oscillator through SasAâ€‘KaiC interaction in cyanobacteria. <i>Genes To Cells</i> , 2012, 17, 398-419.	1.2	25
62	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
63	Assembly and Activation Mechanism of the Flagellar Stator Revealed by the Crystal Structure of Its Periplasmic Region. <i>Seibutsu Butsuri</i> , 2012, 52, 018-021.	0.1	0
64	Common architecture of the flagellar type III protein export apparatus and F- and V-type ATPases. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 277-282.	8.2	161
65	Ligand Specificity Determined by Differentially Arranged Common Ligand-binding Residues in Bacterial Amino Acid Chemoreceptors Tsr and Tar. <i>Journal of Biological Chemistry</i> , 2011, 286, 42200-42210.	3.4	68
66	Genetic analysis of the bacterial hook-capping protein FlgD responsible for hook assembly. <i>Microbiology (United Kingdom)</i> , 2011, 157, 1354-1362.	1.8	28
67	Structural Insight into the Rotational Switching Mechanism of the Bacterial Flagellar Motor. <i>PLoS Biology</i> , 2011, 9, e1000616.	5.6	88
68	Structure of the Flagellar Type III Export Chaperone FliT, and Its Regulatory Mechanism of Flagellar Assembly. <i>Nihon Kessho Gakkaishi</i> , 2011, 53, 396-401.	0.0	0
69	Structure of the cytoplasmic domain of FlhA and implication for flagellar type III protein export. <i>Molecular Microbiology</i> , 2010, 76, 260-268.	2.5	80
70	The interaction dynamics of a negative feedback loop regulates flagellar number in <i>Salmonella enterica</i> serovar Typhimurium. <i>Molecular Microbiology</i> , 2010, 78, 1416-1430.	2.5	40
71	Structural insight into the regulatory mechanisms of interactions of the flagellar type III chaperone FliT with its binding partners. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8812-8817.	7.1	73
72	Role of the C-Terminal Cytoplasmic Domain of FlhA in Bacterial Flagellar Type III Protein Export. <i>Journal of Bacteriology</i> , 2010, 192, 1929-1936.	2.2	57

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73	Crystal Structure of Legionella DotD: Insights into the Relationship between Type IVB and Type II/III Secretion Systems. PLoS Pathogens, 2010, 6, e1001129.	4.7	50
74	Role of the N-terminal domain of Flil ATPase in bacterial flagellar protein export. FEBS Letters, 2009, 583, 743-748.	2.8	18
75	Crystallization and preliminary X-ray analysis of a C-terminal fragment of FlgJ, a putative flagellar rod cap protein from <i>Salmonella</i> . Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 17-20.	0.7	3
76	Crystallization and preliminary X-ray analysis of FljJ, a cytoplasmic component of the flagellar type III protein-export apparatus from <i>Salmonella</i> sp.. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 47-50.	0.7	9
77	Purification, crystallization and preliminary X-ray analysis of FliT, a bacterial flagellar substrate-specific export chaperone. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 825-828.	0.7	5
78	Stator assembly and activation mechanism of the flagellar motor by the periplasmic region of MotB. Molecular Microbiology, 2009, 73, 710-718.	2.5	170
79	Structure and quantum chemical analysis of NAD ⁺ -dependent isocitrate dehydrogenase: Hydride transfer and co-factor specificity. Proteins: Structure, Function and Bioinformatics, 2008, 70, 63-71.	2.6	22
80	Molecular motors of the bacterial flagella. Current Opinion in Structural Biology, 2008, 18, 693-701.	5.7	190
81	Mechanisms of type III protein export for bacterial flagellar assembly. Molecular BioSystems, 2008, 4, 1105.	2.9	171
82	Insights into the stator assembly of the <i>Vibrio</i> flagellar motor from the crystal structure of MotY. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7696-7701.	7.1	74
83	Molecular Interaction and Energy Frustration Play Essential Roles in Polymorphic Supercoiling of Bacterial Flagellar Filament. Seibutsu Butsuri, 2008, 48, 011-017.	0.1	0
84	Structural similarity between the flagellar type III ATPase Flil and F1-ATPase subunits. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 485-490.	7.1	146
85	Gap compression/extension mechanism of bacterial flagellar hook as the molecular universal joint. Journal of Structural Biology, 2007, 157, 481-490.	2.8	19
86	Crystallization and preliminary X-ray analysis of MotY, a stator component of the <i>Vibrio alginolyticus</i> polar flagellar motor. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 89-92.	0.7	2
87	PAX6 and SOX2-dependent regulation of the <i>Sox2</i> enhancer β involved in embryonic visual system development. Genes To Cells, 2007, 12, 1049-1061.	1.2	87
88	Coarse-Grained Molecular Dynamics Simulations of a Rotating Bacterial Flagellum. Biophysical Journal, 2006, 91, 4589-4597.	0.5	93
89	Crystallization and preliminary X-ray analysis of <i>Salmonella</i> Flil, the ATPase component of the type III flagellar protein-export apparatus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 973-975.	0.7	3
90	Switch interactions control energy frustration and multiple flagellar filament structures. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4894-4899.	7.1	60

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91	Crystallization and preliminary X-ray analysis of the C-terminal cytoplasmic domain of FlhA, a membrane-protein subunit of the bacterial flagellar type III protein-export apparatus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 599-602.	0.7	5
92	Functionally Important Substructures of Circadian Clock Protein KaiB in a Unique Tetramer Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 43141-43149.	3.4	65
93	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
94	Structure of the bacterial flagellar hook and implication for the molecular universal joint mechanism. <i>Nature</i> , 2004, 431, 1062-1068.	27.8	176
95	Crystallization and preliminary crystallographic analysis of the circadian clock protein KaiB from the thermophilic cyanobacterium <i>Thermosynechococcus elongatus</i> BP-1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 727-729.	2.5	8
96	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
97	ATP-induced hexameric ring structure of the cyanobacterial circadian clock protein KaiC. <i>Genes To Cells</i> , 2003, 8, 287-296.	1.2	125
98	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
99	Biochemical and molecular characterization of the NAD ⁺ -dependent isocitrate dehydrogenase from the chemolithotroph <i>Acidithiobacillus thiooxidans</i> . <i>FEMS Microbiology Letters</i> , 2002, 214, 127-132.	1.8	21
100	Structure of the bacterial flagellar protofilament and implications for a switch for supercoiling. <i>Nature</i> , 2001, 410, 331-337.	27.8	480
101	Crystallization of the F41 Fragment of Flagellin and Data Collection from Extremely Thin Crystals. <i>Journal of Structural Biology</i> , 2000, 132, 106-111.	2.8	34
102	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
103	Assembly characteristics of flagellar cap protein HAP2 of <i>Salmonella</i> : decamer and pentamer in the pH-sensitive equilibrium 1 Edited by M. F. Moody. <i>Journal of Molecular Biology</i> , 1998, 277, 883-891.	4.2	30
104	Plugging interactions of HAP2 pentamer into the distal end of flagellar filament revealed by electron microscopy 1 Edited by M. F. Moody. <i>Journal of Molecular Biology</i> , 1998, 277, 771-777.	4.2	28
105	Mechanism of self-association and filament capping by flagellar HAP2 1 Edited by M. F. Moody. <i>Journal of Molecular Biology</i> , 1998, 284, 1399-1416.	4.2	34
106	Crystallization and Preliminary X-Ray Studies of a <i>Bacillus subtilis</i> and <i>Thermus thermophilus</i> HB8 Chimeric 3-Isopropylmalate Dehydrogenase and Thermostable Mutants of It. <i>Journal of Biochemistry</i> , 1992, 112, 173-174.	1.7	8
107	Three-dimensional structure of a highly thermostable enzyme, 3-isopropylmalate dehydrogenase of <i>Thermus thermophilus</i> at 2.2 Å resolution. <i>Journal of Molecular Biology</i> , 1991, 222, 725-738.	4.2	215
108	Crystallization and Preliminary X-Ray Studies of a <i>Bacillus subtilis</i> and <i>Thermus thermophilus</i> HB8 Chimeric 3-Isopropylmalate Dehydrogenase. <i>Journal of Biochemistry</i> , 1991, 109, 1-2.	1.7	8