

Katsumi Imada

List of Publications by Year in descending order

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108
papers

4,835
citations

101543

36
h-index

106344

65
g-index

112
all docs

112
docs citations

112
times ranked

3080
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the bacterial flagellar protofilament and implications for a switch for supercoiling. <i>Nature</i> , 2001, 410, 331-337.	27.8	480
2	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
3	The bacterial flagellar motor and its structural diversity. <i>Trends in Microbiology</i> , 2015, 23, 267-274.	7.7	209
4	Molecular motors of the bacterial flagella. <i>Current Opinion in Structural Biology</i> , 2008, 18, 693-701.	5.7	190
5	Structure of the bacterial flagellar hook and implication for the molecular universal joint mechanism. <i>Nature</i> , 2004, 431, 1062-1068.	27.8	176
6	Mechanisms of type III protein export for bacterial flagellar assembly. <i>Molecular BioSystems</i> , 2008, 4, 1105.	2.9	171
7	Stator assembly and activation mechanism of the flagellar motor by the periplasmic region of MotB. <i>Molecular Microbiology</i> , 2009, 73, 710-718.	2.5	170
8	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
9	Structural similarity between the flagellar type III ATPase FliI and F1-ATPase subunits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 485-490.	7.1	146
10	ATP-induced hexameric ring structure of the cyanobacterial circadian clock protein KaiC. <i>Genes To Cells</i> , 2003, 8, 287-296.	1.2	125
11	Coarse-Grained Molecular Dynamics Simulations of a Rotating Bacterial Flagellum. <i>Biophysical Journal</i> , 2006, 91, 4589-4597.	0.5	93
12	Structural Insight into the Rotational Switching Mechanism of the Bacterial Flagellar Motor. <i>PLoS Biology</i> , 2011, 9, e1000616.	5.6	88
13	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
14	Interactions of bacterial flagellar chaperone-substrate complexes with <i>FlhA</i> contribute to coordinating assembly of the flagellar filament. <i>Molecular Microbiology</i> , 2013, 90, 1249-1261.	2.5	86
15	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
16	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
17	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
18	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

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19	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
20	Structural insight into the regulatory mechanisms of interactions of the flagellar type III chaperone FliT with its binding partners. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8812-8817.	7.1	73
21	Assembly and stoichiometry of the core structure of the bacterial flagellar type III export gate complex. PLoS Biology, 2017, 15, e2002281.	5.6	69
22	Ligand Specificity Determined by Differentially Arranged Common Ligand-binding Residues in Bacterial Amino Acid Chemoreceptors Tsr and Tar. Journal of Biological Chemistry, 2011, 286, 42200-42210.	3.4	68
23	Functionally Important Substructures of Circadian Clock Protein KaiB in a Unique Tetramer Complex. Journal of Biological Chemistry, 2005, 280, 43141-43149.	3.4	65
24	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. Structure, 1998, 6, 971-982.	3.3	64
25	Identification of a <i>Vibrio cholerae</i> chemoreceptor that senses taurine and amino acids as attractants. Scientific Reports, 2016, 6, 20866.	3.3	61
26	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
27	Interaction between FliJ and FlhA, Components of the Bacterial Flagellar Type III Export Apparatus. Journal of Bacteriology, 2013, 195, 466-473.	2.2	59
28	Role of the C-Terminal Cytoplasmic Domain of FlhA in Bacterial Flagellar Type III Protein Export. Journal of Bacteriology, 2010, 192, 1929-1936.	2.2	57
29	Insight into the flagella type III export revealed by the complex structure of the type III ATPase and its regulator. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3633-3638.	7.1	57
30	A partial atomic structure for the flagellar hook of <i>Salmonella typhimurium</i> . Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1023-1028.	7.1	50
31	Crystal Structure of <i>Legionella</i> DotD: Insights into the Relationship between Type IVB and Type II/III Secretion Systems. PLoS Pathogens, 2010, 6, e1001129.	4.7	50
32	Interaction between FliI ATPase and a flagellar chaperone FliT during bacterial flagellar protein export. Molecular Microbiology, 2012, 83, 168-178.	2.5	50
33	Insight into structural remodeling of the FlhA ring responsible for bacterial flagellar type III protein export. Science Advances, 2018, 4, eaao7054.	10.3	50
34	Insight into the assembly mechanism in the supramolecular rings of the sodium-driven <i>Vibrio</i> flagellar motor from the structure of FlgT. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6133-6138.	7.1	48
35	Structural differences in the bacterial flagellar motor among bacterial species. Biophysics and Physicobiology, 2017, 14, 191-198.	1.0	47
36	Dependence of fluorescent protein brightness on protein concentration in solution and enhancement of it. Scientific Reports, 2016, 6, 22342.	3.3	44

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37	Bacterial flagellar axial structure and its construction. <i>Biophysical Reviews</i> , 2018, 10, 559-570.	3.2	42
38	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
39	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
40	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
41	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
42	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
43	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
44	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
45	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
46	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
47	In Vitro Reconstitution of Functional Type III Protein Export and Insights into Flagellar Assembly. <i>MBio</i> , 2018, 9, .	4.1	32
48	Structure and Energy-Conversion Mechanism of the Bacterial Na ⁺ -Driven Flagellar Motor. <i>Trends in Microbiology</i> , 2020, 28, 719-731.	7.7	31
49	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
50	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
51	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
52	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
53	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
54	Phase-dependent generation and transmission of time information by the KaiABC circadian clock oscillator through SasA-KaiC interaction in cyanobacteria. <i>Genes To Cells</i> , 2012, 17, 398-419.	1.2	25

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55	Recombinant expression, molecular characterization and crystal structure of antitumor enzyme, L-lysine α -oxidase from <i>Trichoderma viride</i> . <i>Journal of Biochemistry</i> , 2015, 157, 549-559.	1.7	24
56	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
57	Structure and quantum chemical analysis of NAD ⁺ -dependent isocitrate dehydrogenase: Hydride transfer and co-factor specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 63-71.	2.6	22
58	Glycine Insertion Makes Yellow Fluorescent Protein Sensitive to Hydrostatic Pressure. <i>PLoS ONE</i> , 2013, 8, e73212.	2.5	22
59	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
60	<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
61	Two Distinct Conformations in 34 FlIF Subunits Generate Three Different Symmetries within the Flagellar MS-Ring. <i>MBio</i> , 2021, 12, .	4.1	20
62	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
63	Role of the N-terminal domain of Flil ATPase in bacterial flagellar protein export. <i>FEBS Letters</i> , 2009, 583, 743-748.	2.8	18
64	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
65	The FlhA linker mediates flagellar protein export switching during flagellar assembly. <i>Communications Biology</i> , 2021, 4, 646.	4.4	16
66	Architecture of the Bacterial Flagellar Distal Rod and Hook of <i>Salmonella</i> . <i>Biomolecules</i> , 2019, 9, 260.	4.0	15
67	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
68	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
69	Structural Basis of Ubiquitin Recognition by a Bacterial Ovarian Tumor Deubiquitinase LotA. <i>Journal of Bacteriology</i> , 2022, 204, JB0037621.	2.2	11
70	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
71	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
72	Crystallization and preliminary X-ray analysis of FliJ, a cytoplasmic component of the flagellar type III protein-export apparatus from <i>Salmonella</i> sp.. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 47-50.	0.7	9

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73	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
74	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
75	In Vitro Autonomous Construction of the Flagellar Axial Structure in Inverted Membrane Vesicles. <i>Biomolecules</i> , 2020, 10, 126.	4.0	9
76	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
77	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
78	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
79	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
80	Structural basis of strict substrate recognition of lysine oxidase from <i>Trichoderma viride</i> . <i>Protein Science</i> , 2020, 29, 2213-2225.	7.6	8
81	Biochemical characterization of the flagellar stator-associated inner membrane protein FlIL from <i>Vibrio alginolyticus</i> . <i>Journal of Biochemistry</i> , 2017, 161, mvw076.	1.7	8
82	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
83	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
84	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
85	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
86	Structure of the bacterial flagellar hook cap provides insights into a hook assembly mechanism. <i>Communications Biology</i> , 2021, 4, 1291.	4.4	6
87	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
88	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
89	Effects of Chain Length of an Amphipathic Polypeptide Carrying the Repeated Amino Acid Sequence (LETLAKA) _n on α -Helix and Fibrous Assembly Formation. <i>Biochemistry</i> , 2013, 52, 2810-2820.	2.5	5
90	Crystallization and preliminary X-ray analysis of the periplasmic domain of FlIP, 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

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91	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
92	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
93	A new <i>scp</i> arginine oxidase engineered from <i>scp</i> glutamate oxidase. <i>Protein Science</i> , 2021, 30, 1044-1055.	7.6	4
94	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
95	Crystallization and preliminary X-ray analysis of Salmonella Flil, the ATPase component of the type III flagellar protein-export apparatus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 973-975.	0.7	3
96	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
97	<i>Salmonella</i> Flagellum. , 2018, , .		3
98	Structural basis of enzyme activity regulation by the propeptide of l-lysine β -oxidase precursor from <i>Trichoderma viride</i> . <i>Journal of Structural Biology: X</i> , 2021, 5, 100044.	1.3	3
99	Crystallization and preliminary X-ray analysis of MotY, a stator component of the <i>Vibrio alginolyticus</i> polar flagellar motor. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 89-92.	0.7	2
100	Crystallization and preliminary X-ray analysis of the Flil 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
101	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
102	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
103	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
104	Molecular Interaction and Energy Frustration Play Essential Roles in Polymorphic Supercoiling of Bacterial Flagellar Filament. <i>Seibutsu Butsuri</i> , 2008, 48, 011-017.	0.1	0
105	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
106	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
107	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
108	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