Takayuki Kato

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6644566/publications.pdf

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39 39 39 39 1424

39 39 39 1424 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Structure and dynamics of Odinarchaeota tubulin and the implications for eukaryotic microtubule evolution. Science Advances, 2022, 8, eabm2225.	10.3	13
2	Structural snapshots of V/A -ATPase reveal the rotary catalytic mechanism of rotary ATPases. Nature Communications, 2022, 13, 1213.	12.8	16
3	Structural insight into the activation mechanism of MrgD with heterotrimeric Gi-protein revealed by cryo-EM. Communications Biology, 2022, 5, .	4.4	8
4	Extraction of protein dynamics information from cryo-EM maps using deep learning. Nature Machine Intelligence, 2021, 3, 153-160.	16.0	57
5	Cryo-EM structure of a functional monomeric Photosystem I from Thermosynechococcus elongatus reveals red chlorophyll cluster. Communications Biology, 2021, 4, 304.	4.4	25
6	Two Distinct Conformations in 34 FliF Subunits Generate Three Different Symmetries within the Flagellar MS-Ring. MBio, 2021, 12, .	4.1	20
7	An infectivity-enhancing site on the SARS-CoV-2 spike protein targeted by antibodies. Cell, 2021, 184, 3452-3466.e18.	28.9	205
8	Structure of the molecular bushing of the bacterial flagellar motor. Nature Communications, 2021, 12, 4469.	12.8	33
9	Native flagellar MS ring is formed by 34 subunits with 23-fold and 11-fold subsymmetries. Nature Communications, 2021, 12, 4223.	12.8	34
10	Chained Structure of Dimeric F $<$ sub $>$ 1 $<$ /sub $>$ -like ATPase in Mycoplasma mobile Gliding Machinery. MBio, 2021, 12, e0141421.	4.1	15
11	Functional Analysis of the GPI Transamidase Complex by Screening for Amino Acid Mutations in Each Subunit. Molecules, 2021, 26, 5462.	3.8	5
12	Cryoâ€EM structure of the CENPâ€A nucleosome in complex with phosphorylated CENP . EMBO Journal, 2021, 40, e105671.	7.8	35
13	Immunodominant proteins P1 and P40/P90 from human pathogen Mycoplasma pneumoniae. Nature Communications, 2020, 11, 5188.	12.8	22
14	Structural and Functional Comparison of Salmonella Flagellar Filaments Composed of FljB and FliC. Biomolecules, 2020, 10, 246.	4.0	35
15	Mechanical inhibition of isolated Vo from V/A-ATPase for proton conductance. ELife, 2020, 9, .	6.0	11
16	CryoTEM with a Cold Field Emission Gun That Moves Structural Biology into a New Stage. Microscopy and Microanalysis, 2019, 25, 998-999.	0.4	45
17	Structure of Salmonella Flagellar Hook Reveals Intermolecular Domain Interactions for the Universal Joint Function. Biomolecules, 2019, 9, 462.	4.0	16
18	Novel Insights into Conformational Rearrangements of the Bacterial Flagellar Switch Complex. MBio, 2019, 10, .	4.1	23

Τακαγμκι Κατο

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19	Refined Mechanism of Mycoplasma mobile Gliding Based on Structure, ATPase Activity, and Sialic Acid Binding of Machinery. MBio, 2019, 10, .	4.1	17
20	Structure of the native supercoiled flagellar hook as a universal joint. Nature Communications, 2019, 10, 5295.	12.8	28
21	Electron Microscopy of Motor Structure and Possible Mechanisms. , 2018, , 1-8.		1
22	Identical folds used for distinct mechanical functions of the bacterial flagellar rod and hook. Nature Communications, 2017, 8, 14276.	12.8	60
23	Assembly and stoichiometry of the core structure of the bacterial flagellar type III export gate complex. PLoS Biology, 2017, 15, e2002281.	5.6	69
24	Periodicity in Attachment Organelle Revealed by Electron Cryotomography Suggests Conformational Changes in Gliding Mechanism of Mycoplasma pneumoniae. MBio, 2016, 7, e00243-16.	4.1	25
25	Common and distinct structural features of Salmonella injectisome and flagellar basal body. Scientific Reports, 2013, 3, 3369.	3.3	124
26	Role of the Dc domain of the bacterial hook protein FlgE in hook assembly and function. Biophysics (Nagoya-shi, Japan), 2013, 9, 63-72.	0.4	19
27	Specific Arrangement of α-Helical Coiled Coils in the Core Domain of the Bacterial Flagellar Hook for the Universal Joint Function. Structure, 2009, 17, 1485-1493.	3.3	73