List of Publications by Year in descending order

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MODCAN REERV

#	Article	IF	CITATIONS
1	Adaptation of the periplasm to maintain spatial constraints essential for cell envelope processes and cell viability. ELife, 2022, 11, .	6.0	17
2	Novel transient cytoplasmic rings stabilize assembling bacterial flagellar motors. EMBO Journal, 2022, 41, e109523.	7.8	10
3	CryoEM of bacterial secretion systems: A primer for microbiologists. Molecular Microbiology, 2021, 115, 366-382.	2.5	10
4	The "Jack-of-all-Trades―Flagellum From Salmonella and E. coli Was Horizontally Acquired From an Ancestral β-Proteobacterium. Frontiers in Microbiology, 2021, 12, 643180.	3.5	6
5	Structure of the cytoplasmic domain of SctV (SsaV) from the Salmonella SPI-2 injectisome and implications for a pH sensing mechanism. Journal of Structural Biology, 2021, 213, 107729.	2.8	13
6	Loss of the Bacterial Flagellar Motor Switch Complex upon Cell Lysis. MBio, 2021, 12, e0029821.	4.1	6
7	Lpp positions peptidoglycan at the AcrA-TolC interface in the AcrAB-TolC multidrug efflux pump. Biophysical Journal, 2021, 120, 3973-3982.	0.5	13
8	In situ imaging of bacterial outer membrane projections and associated protein complexes using electron cryo-tomography. ELife, 2021, 10, .	6.0	16
9	Evolution of Archaellum Rotation Involved Invention of a Stator Complex by Duplicating and Modifying a Core Component. Frontiers in Microbiology, 2021, 12, 773386.	3.5	3
10	How Did the Archaellum Get Its Rotation?. Frontiers in Microbiology, 2021, 12, 803720.	3.5	3
11	The structure of the periplasmic FlaG–FlaF complex and its essential role for archaellar swimming motility. Nature Microbiology, 2020, 5, 216-225.	13.3	32
12	Adenita: interactive 3D modelling and visualization of DNA nanostructures. Nucleic Acids Research, 2020, 48, 8269-8275.	14.5	33
13	An ATP-dependent partner switch links flagellar C-ring assembly with gene expression. Proceedings of the United States of America, 2020, 117, 20826-20835.	7.1	17
14	Toward Organism-scale Structural Biology: S-layer Reined in by Bacterial LPS. Trends in Biochemical Sciences, 2020, 45, 549-551.	7.5	3
15	The Brownian and Flowâ€Driven Rotational Dynamics of a Multicomponent DNA Origamiâ€Based Rotor. Small, 2020, 16, e2001855.	10.0	20
16	Propulsive nanomachines: the convergent evolution of archaella, flagella and cilia. FEMS Microbiology Reviews, 2020, 44, 253-304.	8.6	60
17	Bacterial flagellar motor PL-ring disassembly subcomplexes are widespread and ancient. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8941-8947.	7.1	23
18	Campylobacter jejuni motility integrates specialized cell shape, flagellar filament, and motor, to coordinate action of its opposed flagella. PLoS Pathogens, 2020, 16, e1008620.	4.7	40

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19	Trichinella spiralis secretes abundant unencapsulated small RNAs with potential effects on host gene expression. International Journal for Parasitology, 2020, 50, 697-705.	3.1	10
20	Diversification of Campylobacter jejuni Flagellar C-Ring Composition Impacts Its Structure and Function in Motility, Flagellar Assembly, and Cellular Processes. MBio, 2020, 11, .	4.1	23
21	Analysis of Cell–Cell Bridges in Haloferax volcanii Using Electron Cryo-Tomography Reveal a Continuous Cytoplasm and S-Layer. Frontiers in Microbiology, 2020, 11, 612239.	3.5	13
22	In situ structure of the <i>Caulobacter crescentus</i> flagellar motor and visualization of binding of a CheYâ€homolog. Molecular Microbiology, 2020, 114, 443-453.	2.5	22
23	Inter-membrane association of the Sec and BAM translocons for bacterial outer-membrane biogenesis. ELife, 2020, 9, .	6.0	39
24	Title is missing!. , 2020, 16, e1008620.		0
25	Title is missing!. , 2020, 16, e1008620.		0
26	Title is missing!. , 2020, 16, e1008620.		0
27	Title is missing!. , 2020, 16, e1008620.		0
28	Title is missing!. , 2020, 16, e1008620.		0
29	Title is missing!. , 2020, 16, e1008620.		0
30	Evolution of a family of molecular Rube Goldberg contraptions. PLoS Biology, 2019, 17, e3000405.	5.6	5
31	Simulations suggest a constrictive force is required for Gram-negative bacterial cell division. Nature Communications, 2019, 10, 1259.	12.8	12
32	Î <sup>3</sup> -proteobacteria eject their polar flagella under nutrient depletion, retaining flagellar motor relic structures. PLoS Biology, 2019, 17, e3000165.	5.6	72
33	High-Throughput Electron Cryo-tomography of Protein Complexes and Their Assembly. Methods in Molecular Biology, 2018, 1764, 29-44.	0.9	4
34	Electron Cryo-Tomography. Biological and Medical Physics Series, 2018, , 61-94.	0.4	2
35	Evolution of higher torque in Campylobacter-type bacterial flagellar motors. Scientific Reports, 2018, 8, 97.	3.3	70
36	Bacterial Flagellins: Does Size Matter?. Trends in Microbiology, 2018, 26, 575-581.	7.7	13

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37	Giant flagellins form thick flagellar filaments in two species of marine γ-proteobacteria. PLoS ONE, 2018, 13, e0206544.	2.5	10
38	Insights into the evolution of bacterial flagellar motors from high-throughput <i>in situ</i> electron cryotomography and subtomogram averaging. Acta Crystallographica Section D: Structural Biology, 2018, 74, 585-594.	2.3	30
39	Expanding the archaellum regulatory network - the eukaryotic protein kinases ArnC and ArnD influence motility of <i>Sulfolobus acidocaldarius</i> . MicrobiologyOpen, 2017, 6, e00414.	3.0	45
40	Nanoscale-length control of the flagellar driveshaft requires hitting the tethered outer membrane. Science, 2017, 356, 197-200.	12.6	86
41	Short FtsZ filaments can drive asymmetric cell envelope constriction at the onset of bacterial cytokinesis. EMBO Journal, 2017, 36, 1577-1589.	7.8	55
42	<scp>A</scp> rn <scp>S</scp> , a kinase involved in starvationâ€induced archaellum expression. Molecular Microbiology, 2017, 103, 181-194.	2.5	29
43	Communication across the bacterial cell envelope depends on the size of the periplasm. PLoS Biology, 2017, 15, e2004303.	5.6	108
44	Diverse high-torque bacterial flagellar motors assemble wider stator rings using a conserved protein scaffold. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1917-26.	7.1	170
45	Molecular Models for the Core Components of the Flagellar Type-III Secretion Complex. PLoS ONE, 2016, 11, e0164047.	2.5	14
46	Coarse-grained simulations of bacterial cell wall growth reveal that local coordination alone can be sufficient to maintain rod shape. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3689-98.	7.1	50
47	Motility in the epsilon-proteobacteria. Current Opinion in Microbiology, 2015, 28, 115-121.	5.1	40
48	The flagellum in bacterial pathogens: For motility and a whole lot more. Seminars in Cell and Developmental Biology, 2015, 46, 91-103.	5.0	275
49	Escherichia coli Peptidoglycan Structure and Mechanics as Predicted by Atomic-Scale Simulations. PLoS Computational Biology, 2014, 10, e1003475.	3.2	92
50	Ultrastructure and complex polar architecture of the human pathogen Campylobacter jejuni. MicrobiologyOpen, 2014, 3, 702-710.	3.0	25
51	Architecture of the major component of the type III secretion system export apparatus. Nature Structural and Molecular Biology, 2013, 20, 99-104.	8.2	200
52	Architecture and assembly of the <scp>G</scp> ramâ€positive cell wall. Molecular Microbiology, 2013, 88, 664-672.	2.5	116
53	Growth and Localization of Polyhydroxybutyrate Granules in Ralstonia eutropha. Journal of Bacteriology, 2012, 194, 1092-1099.	2.2	65
54	Activated chemoreceptor arrays remain intact and hexagonally packed. Molecular Microbiology, 2011, 82, 748-757.	2.5	38

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55	Structural diversity of bacterial flagellar motors. EMBO Journal, 2011, 30, 2972-2981.	7.8	281
56	Electron Cryotomography of Bacterial Cells. Journal of Visualized Experiments, 2010, , .	0.3	13
57	Exploiting genomic patterns to discover new supramolecular protein assemblies. Protein Science, 2009, 18, 69-79.	7.6	31
58	Advances in Mycobacterium tuberculosis Structural Genomics: Investigating Potential Chinks in the Armor of a Deadly Pathogen. Infectious Disorders - Drug Targets, 2009, 9, 475-492.	0.8	8
59	Proteins in a Small World. Science, 2006, 314, 1882-1883.	12.6	12
60	The Genomics of Disulfide Bonding and Protein Stabilization in Thermophiles. PLoS Biology, 2005, 3, e309.	5.6	180
61	Protein Structures Forming the Shell of Primitive Bacterial Organelles. Science, 2005, 309, 936-938.	12.6	420
62	Visualization and interpretation of protein networks in Mycobacterium tuberculosis based on hierarchical clustering of genome-wide functional linkage maps. Nucleic Acids Research, 2003, 31, 7099-7109.	14.5	55
63	Crystal Structure of 3-Amino-5-hydroxybenzoic Acid (AHBA) Synthaseâ€,‡. Biochemistry, 1999, 38, 9840-9849.	2.5	291