

Yi-Wei Chang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46 papers	1,474 citations	21 h-index	38 g-index
63 ext. papers	1,975 ext. citations	9.9 avg, IF	4.64 L-index

#	Paper	IF	Citations
46	Parasitology meets cryo-electron tomography - exciting prospects await.. <i>Trends in Parasitology</i> , 2022 ,	6.4	1
45	Novel transient cytoplasmic rings stabilize assembling bacterial flagellar motors.. <i>EMBO Journal</i> , 2022 , e109523	13	3
44	The Cryo-EM Effect: Structural Biology of Neurodegenerative Disease Proteostasis Factors. <i>Journal of Neuropathology and Experimental Neurology</i> , 2021 , 80, 494-513	3.1	0
43	The Cryo-EM Effect: Structural Biology of Neurodegenerative Disease Aggregates. <i>Journal of Neuropathology and Experimental Neurology</i> , 2021 , 80, 514-529	3.1	4
42	Loss of the Bacterial Flagellar Motor Switch Complex upon Cell Lysis. <i>MBio</i> , 2021 , 12, e0029821	7.8	1
41	Programmed Flagellar Ejection in <i>Caulobacter crescentus</i> Leaves PL-subcomplexes. <i>Journal of Molecular Biology</i> , 2021 , 433, 167004	6.5	2
40	An Alveolata secretory machinery adapted to parasite host cell invasion. <i>Nature Microbiology</i> , 2021 , 6, 425-434	26.6	13
39	Active Learning to Classify Macromolecular Structures in situ for Less Supervision in Cryo-Electron Tomography. <i>Bioinformatics</i> , 2021 ,	7.2	4
38	In situ ultrastructures of two evolutionarily distant apicomplexan rhoptry secretion systems. <i>Nature Communications</i> , 2021 , 12, 4983	17.4	5
37	UNSUPERVISED DOMAIN ALIGNMENT BASED OPEN SET STRUCTURAL RECOGNITION OF MACROMOLECULES CAPTURED BY CRYO-ELECTRON TOMOGRAPHY.. <i>Proceedings International Conference on Image Processing</i> , 2021 , 2021, 106-110	1.6	0
36	Bacteria suit up with virus armor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 6297-6299	11.5	0
35	Bacterial flagellar motor PL-ring disassembly subcomplexes are widespread and ancient. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 8941-8947	11.5	10
34	PilY1 and minor pilins form a complex priming the type IVa pilus in <i>Myxococcus xanthus</i> . <i>Nature Communications</i> , 2020 , 11, 5054	17.4	25
33	In Situ Imaging and Structure Determination of Bacterial Toxin Delivery Systems Using Electron Cryotomography. <i>Methods in Molecular Biology</i> , 2019 , 1921, 249-265	1.4	2
32	Simulations suggest a constrictive force is required for Gram-negative bacterial cell division. <i>Nature Communications</i> , 2019 , 10, 1259	17.4	10
31	Molecular architecture, polar targeting and biogenesis of the <i>Legionella</i> Dot/Icm T4SS. <i>Nature Microbiology</i> , 2019 , 4, 1173-1182	26.6	42
30	De Novo Structural Pattern Mining in Cellular Electron Cryotomograms. <i>Structure</i> , 2019 , 27, 679-691.e14	5.2	25

29	InVivo Structures of the Helicobacter pylori cag Type IV Secretion System. <i>Cell Reports</i> , 2018 , 23, 673-681	10.6	48
28	Architecture of the Vibrio cholerae toxin-coregulated pilus machine revealed by electron cryotomography. <i>Nature Microbiology</i> , 2017 , 2, 16269	26.6	46
27	Short FtsZ filaments can drive asymmetric cell envelope constriction at the onset of bacterial cytokinesis. <i>EMBO Journal</i> , 2017 , 36, 1577-1589	13	41
26	structures of an intact type VI secretion system revealed by electron cryotomography. <i>EMBO Reports</i> , 2017 , 18, 1090-1099	6.5	48
25	Uncharacterized Bacterial Structures Revealed by Electron Cryotomography. <i>Journal of Bacteriology</i> , 2017 , 199,	3.5	29
24	structure of the Dot/Icm type IV secretion system by electron cryotomography. <i>EMBO Reports</i> , 2017 , 18, 726-732	6.5	70
23	Dynamics of the peptidoglycan biosynthetic machinery in the stalked budding bacterium Hyphomonas neptunium. <i>Molecular Microbiology</i> , 2017 , 103, 875-895	4.1	26
22	Morphology of the archaellar motor and associated cytoplasmic cone in. <i>EMBO Reports</i> , 2017 , 18, 1660-1670	16.3	28
21	Polar delivery of type IV secretion system substrates is essential for virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 8077-8082	11.5	35
20	Architecture of the type IVa pilus machine. <i>Science</i> , 2016 , 351, aad2001	33.3	233
19	A new view into prokaryotic cell biology from electron cryotomography. <i>Nature Reviews Microbiology</i> , 2016 , 14, 205-20	22.2	63
18	Architecture of the Type IVA Pilus Machine. <i>Biophysical Journal</i> , 2016 , 110, 468a-469a	2.9	2
17	Electron cryotomography. <i>Methods in Microbiology</i> , 2016 , 43, 115-139	2.8	6
16	Correlated cryogenic photoactivated localization microscopy and cryo-electron tomography. <i>Nature Methods</i> , 2014 , 11, 737-9	21.6	155
15	Structure of bacterial cytoplasmic chemoreceptor arrays and implications for chemotactic signaling. <i>ELife</i> , 2014 , 3, e02151	8.9	73
14	Structural basis of a physical blockage mechanism for the interaction of response regulator PmrA with connector protein PmrD from Klebsiella pneumoniae. <i>Journal of Biological Chemistry</i> , 2013 , 288, 25551-25561	5.4	16
13	Interaction surface and topology of Get3-Get4-Get5 protein complex, involved in targeting tail-anchored proteins to endoplasmic reticulum. <i>Journal of Biological Chemistry</i> , 2012 , 287, 4783-9	5.4	12
12	Crystal structure of DnaK protein complexed with nucleotide exchange factor GrpE in DnaK chaperone system: insight into intermolecular communication. <i>Journal of Biological Chemistry</i> , 2012 , 287, 21461-70	5.4	33

11	Crystal structure of Get4-Get5 complex and its interactions with Sgt2, Get3, and Ydj1. <i>Journal of Biological Chemistry</i> , 2010 , 285, 9962-9970	5-4	67
10	Structural fold, conservation and Fe(II) binding of the intracellular domain of prokaryote FeoB. <i>Journal of Structural Biology</i> , 2010 , 170, 501-12	3-4	24
9	Crystal structure of the N-terminal domain of Geobacillus kaustophilus HTA426 DnaD protein. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 375, 220-4	3-4	13
8	Crystal structures of the 70-kDa heat shock proteins in domain disjoining conformation. <i>Journal of Biological Chemistry</i> , 2008 , 283, 15502-11	5-4	78
7	Structure of the SARS coronavirus nucleocapsid protein RNA-binding dimerization domain suggests a mechanism for helical packaging of viral RNA. <i>Journal of Molecular Biology</i> , 2007 , 368, 1075-86	6-5	163
6	S1f2-4 Structural insights into packaging of the helical nucleocapsid from the structure of SARS coronavirus(S1-f2: "Functions and dynamics of protein systems in various aspect",Symposia,Abstract,Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , 2006 , 46, S119	0	
5	In vivo structures of an intact type VI secretion system revealed by electron cryotomography		2
4	In vivo structures of the Helicobacter pylori cag type IV secretion system		1
3	Molecular architecture of the Legionella Dot/Icm type IV secretion system		6
2	Structure of the Legionella Dot/Icm type IV secretion system in situ by electron cryotomography		1
1	Structure of the archaeellar motor and associated cytoplasmic cone in Thermococcus kodakaraensis		1