

# Ozkan Yildiz

## List of Publications by Year in descending order

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42  
papers

2,444  
citations

218381

26  
h-index

264894

42  
g-index

50  
all docs

50  
docs citations

50  
times ranked

2732  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cyclophilin anaCyp40 regulates photosystem assembly and phycobilisome association in a cyanobacterium. <i>Nature Communications</i> , 2022, 13, 1690.	5.8	2
2	A ferredoxin bridge connects the two arms of plant mitochondrial complex I. <i>Plant Cell</i> , 2021, 33, 2072-2091.	3.1	52
3	Crystal structures of phosphatidyl serine synthase PSS reveal the catalytic mechanism of CDP-DAG alcohol O-phosphatidyl transferases. <i>Nature Communications</i> , 2021, 12, 6982.	5.8	10
4	Structural properties of an engineered outer membrane protein G mutant, OmpG-16SL, investigated with infrared spectroscopy. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2104-2115.	2.0	4
5	Ion Binding and Selectivity of the Na <sup>+</sup> /H <sup>+</sup> Antiporter MjNhaP1 from Experiment and Simulation. <i>Journal of Physical Chemistry B</i> , 2020, 124, 336-344.	1.2	8
6	Reply to Desikan et al.: Micelle formation among various mechanisms of toxin pore formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5109-5110.	3.3	1
7	Membrane perforation by the pore-forming toxin pneumolysin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13352-13357.	3.3	75
8	Rotary substates of mitochondrial ATP synthase reveal the basis of flexible F <sub>1</sub> -F <sub>o</sub> coupling. <i>Science</i> , 2019, 364, .	6.0	160
9	Mechanism of the electroneutral sodium/proton antiporter PaNhaP from transition-path shooting. <i>Nature Communications</i> , 2019, 10, 1742.	5.8	32
10	CryoEM structures of membrane pore and prepore complex reveal cytolytic mechanism of Pneumolysin. <i>ELife</i> , 2017, 6, .	2.8	119
11	Structural basis of proton translocation and force generation in mitochondrial ATP synthase. <i>ELife</i> , 2017, 6, .	2.8	59
12	Electrogenic Cation Binding in the Electroneutral Na <sup>+</sup> /H <sup>+</sup> Antiporter of <i>Pyrococcus abyssi</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 26786-26793.	1.6	15
13	Crystal Structure of a Histone Deacetylase Homologue from <i>Pseudomonas aeruginosa</i> . <i>Biochemistry</i> , 2016, 55, 6858-6868.	1.2	8
14	Unraveling the Pore-Forming Steps of Pneumolysin from <i>Streptococcus pneumoniae</i> . <i>Nano Letters</i> , 2016, 16, 7915-7924.	4.5	39
15	Structure of the mycobacterial ATP synthase F <sub>o</sub> rotor ring in complex with the anti-TB drug bedaquiline. <i>Science Advances</i> , 2015, 1, e1500106.	4.7	224
16	IR-spectroscopic characterization of an elongated OmpG mutant. <i>Archives of Biochemistry and Biophysics</i> , 2015, 576, 73-79.	1.4	10
17	Purification, Refolding, and Crystallization of the Outer Membrane Protein OmpG from <i>Escherichia coli</i> . <i>Methods in Enzymology</i> , 2015, 557, 149-166.	0.4	4
18	Directly Observing the Lipid-Dependent Self-Assembly and Pore-Forming Mechanism of the Cytolytic Toxin Listeriolysin O. <i>Nano Letters</i> , 2015, 15, 6965-6973.	4.5	74

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19	Mechanism of Na <sup>+</sup> -dependent citrate transport from the structure of an asymmetrical CitS dimer. <i>ELife</i> , 2015, 4, e09375.	2.8	58
20	Crystal structure of listeriolysin O reveals molecular details of oligomerization and pore formation. <i>Nature Communications</i> , 2014, 5, 3690.	5.8	116
21	High-resolution structure and mechanism of an F/V-hybrid rotor ring in a Na <sup>+</sup> -coupled ATP synthase. <i>Nature Communications</i> , 2014, 5, 5286.	5.8	68
22	Structure and substrate ion binding in the sodium/proton antiporter PaNhaP. <i>ELife</i> , 2014, 3, e03579.	2.8	92
23	Structure and transport mechanism of the sodium/proton antiporter MjNhaP1. <i>ELife</i> , 2014, 3, e03583.	2.8	73
24	Structural evidence for functional lipid interactions in the betaine transporter BetP. <i>EMBO Journal</i> , 2013, 32, 3096-3105.	3.5	73
25	Crystallization and X-ray crystallographic analysis of the cholesterol-dependent cytolysin listeriolysin O from <i>Listeria monocytogenes</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1212-1215.	0.7	6
26	Alternating-access mechanism in conformationally asymmetric trimers of the betaine transporter BetP. <i>Nature</i> , 2012, 490, 126-130.	13.7	133
27	In situ opening/closing of OmpG from <i>E. coli</i> and the splitting of $\beta$ -sheet signals in ATR-FTIR spectroscopy. <i>Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy</i> , 2012, 91, 395-401.	2.0	13
28	Structure of the archaeal Na <sup>+</sup> /H <sup>+</sup> antiporter NhaP1 and functional role of transmembrane helix 1. <i>EMBO Journal</i> , 2011, 30, 439-449.	3.5	54
29	One $\beta$ Hairpin Follows the Other: Exploring Refolding Pathways and Kinetics of the Transmembrane $\beta$ -Barrel Protein OmpG. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 7422-7424.	7.2	32
30	Structure of Human Na <sup>+</sup> /H <sup>+</sup> Exchanger NHE1 Regulatory Region in Complex with Calmodulin and Ca <sup>2+</sup> . <i>Journal of Biological Chemistry</i> , 2011, 286, 40954-40961.	1.6	47
31	Dual energy landscape: The functional state of the $\beta$ -barrel outer membrane protein G molds its unfolding energy landscape. <i>Proteomics</i> , 2010, 10, 4151-4162.	1.3	16
32	Microscopic rotary mechanism of ion translocation in the Fo complex of ATP synthases. <i>Nature Chemical Biology</i> , 2010, 6, 891-899.	3.9	142
33	pH-Induced Conformational Change of the $\beta$ -Barrel-Forming Protein OmpG Reconstituted into Native <i>E. coli</i> Lipids. <i>Journal of Molecular Biology</i> , 2010, 396, 610-616.	2.0	48
34	pH-Dependent Interactions Guide the Folding and Gate the Transmembrane Pore of the $\beta$ -Barrel Membrane Protein OmpG. <i>Journal of Molecular Biology</i> , 2010, 397, 878-882.	2.0	37
35	Correlation between the OmpG Secondary Structure and Its pH-Dependent Alterations Monitored by FTIR. <i>Journal of Molecular Biology</i> , 2010, 401, 56-67.	2.0	28
36	One $\beta$ Hairpin after the Other: Exploring Mechanical Unfolding Pathways of the Transmembrane $\beta$ -Barrel Protein OmpG. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 8306-8308.	7.2	38

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37	Purification, crystallization and preliminary X-ray diffraction analysis of the FeoB G domain from <i>Methanococcus jannaschii</i> . Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 684-687.	0.7	6
38	High-resolution structure of the rotor ring of a proton-dependent ATP synthase. Nature Structural and Molecular Biology, 2009, 16, 1068-1073.	3.6	194
39	Structure and Function of the FeoB G-Domain from <i>Methanococcus jannaschii</i> . Journal of Molecular Biology, 2009, 392, 405-419.	2.0	27
40	The Role of Lipids for the Functional Integrity of Porin: An FTIR Study Using Lipid and Protein Reporter Groups. Biochemistry, 2008, 47, 12126-12134.	1.2	19
41	Structure of GlnK1 with bound effectors indicates regulatory mechanism for ammonia uptake. EMBO Journal, 2007, 26, 589-599.	3.5	57
42	Structure of the monomeric outer-membrane porin OmpG in the open and closed conformation. EMBO Journal, 2006, 25, 3702-3713.	3.5	151