

# Kano Suzuki

## List of Publications by Year in descending order

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13  
papers

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citations

1040056

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1125743

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15  
docs citations

15  
times ranked

388  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural characterization of proton-pumping rhodopsin lacking a cytoplasmic proton donor residue by X-ray crystallography. <i>Journal of Biological Chemistry</i> , 2022, 298, 101722.	3.4	6
2	Discovery of ultrafast myosin, its amino acid sequence, and structural features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	12
3	Revealing a Hidden Intermediate of Rotatory Catalysis with X-ray Crystallography and Molecular Simulations. <i>ACS Central Science</i> , 2022, 8, 915-925.	11.3	3
4	Cryo-EM Structure of K <sup>+</sup> -Bound hERG Channel Complexed with the Blocker Astemizole. <i>Structure</i> , 2021, 29, 203-212.e4.	3.3	45
5	Crystal structure of an anti-podoplanin antibody bound to a disialylated O-linked glycopeptide. <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 57-63.	2.1	2
6	Metastable asymmetrical structure of a shaftless V <sub>1</sub> motor. <i>Science Advances</i> , 2019, 5, eaau8149.	10.3	13
7	Rotational Mechanism Model of the Bacterial V <sub>1</sub> Motor Based on Structural and Computational Analyses. <i>Frontiers in Physiology</i> , 2019, 10, 46.	2.8	7
8	Crystal structure and calcium-induced conformational changes of diacylglycerol kinase $\epsilon$ hand domains. <i>Protein Science</i> , 2019, 28, 694-706.	7.6	14
9	Structure and dynamics of rotary V <sub>1</sub> motor. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 1789-1802.	5.4	14
10	Crystal structures of the ATP-binding and ADP-release dwells of the V <sub>1</sub> rotary motor. <i>Nature Communications</i> , 2016, 7, 13235.	12.8	40
11	Rotational mechanism of <i>Enterococcus hirae</i> V <sub>1</sub> -ATPase by crystal-structure and single-molecule analyses. <i>Current Opinion in Structural Biology</i> , 2015, 31, 49-56.	5.7	16
12	Rotation mechanism of <i>Enterococcus hirae</i> V <sub>1</sub> -ATPase based on asymmetric crystal structures. <i>Nature</i> , 2013, 493, 703-707.	27.8	114
13	Crystal structure of the central axis DF complex of the prokaryotic V-ATPase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19955-19960.	7.1	47