

Inokentijs Josts

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

725
citations

516710

16
h-index

580821

25
g-index

29
all docs

29
docs citations

29
times ranked

1203
citing authors

#	ARTICLE	IF	CITATIONS
1	High-throughput stability screening for detergent-solubilized membrane proteins. <i>Scientific Reports</i> , 2019, 9, 10379.	3.3	79
2	Conformational States of ABC Transporter MsbA in a Lipid Environment Investigated by Small-Angle Scattering Using Stealth Carrier Nanodiscs. <i>Structure</i> , 2018, 26, 1072-1079.e4.	3.3	58
3	Lectin-Like Bacteriocins from <i>Pseudomonas</i> spp. Utilise D-Rhamnose Containing Lipopolysaccharide as a Cellular Receptor. <i>PLoS Pathogens</i> , 2014, 10, e1003898.	4.7	56
4	Ternary structure of the outer membrane transporter FoxA with resolved signalling domain provides insights into TonB-mediated siderophore uptake. <i>ELife</i> , 2019, 8, .	6.0	48
5	Discovery, characterization and <i>in vivo</i> activity of pyocin SD2, a protein antibiotic from <i>Pseudomonas aeruginosa</i> . <i>Biochemical Journal</i> , 2016, 473, 2345-2358.	3.7	42
6	The Potassium Binding Protein Kbp Is a Cytoplasmic Potassium Sensor. <i>Structure</i> , 2016, 24, 741-749.	3.3	38
7	A microfluidic flow-focusing device for low sample consumption serial synchrotron crystallography experiments in liquid flow. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 406-412.	2.4	37
8	Computational models in the service of X-ray and cryo-electron microscopy structure determination. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1633-1646.	2.6	37
9	The Structure of a Conserved Domain of TamB Reveals a Hydrophobic β^2 Taco Fold. <i>Structure</i> , 2017, 25, 1898-1906.e5.	3.3	33
10	Structural basis for activation of plasma-membrane Ca ²⁺ -ATPase by calmodulin. <i>Communications Biology</i> , 2018, 1, 206.	4.4	30
11	Structural Kinetics of MsbA Investigated by Stopped-Flow Time-Resolved Small-Angle X-Ray Scattering. <i>Structure</i> , 2020, 28, 348-354.e3.	3.3	28
12	Nocardamine-Dependent Iron Uptake in <i>Pseudomonas aeruginosa</i> : Exclusive Involvement of the FoxA Outer Membrane Transporter. <i>ACS Chemical Biology</i> , 2020, 15, 2741-2751.	3.4	27
13	Structure of the bacterial plant-ferredoxin receptor FusA. <i>Nature Communications</i> , 2016, 7, 13308.	12.8	26
14	Structures of the Ultra-High-Affinity Protein-Protein Complexes of Pyocins S2 and AP41 and Their Cognate Immunity Proteins from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2015, 427, 2852-2866.	4.2	25
15	Photocage-initiated time-resolved solution X-ray scattering investigation of protein dimerization. <i>IUCr</i> , 2018, 5, 667-672.	2.2	25
16	Structure of the atypical bacteriocin pectocin M ₂ implies a novel mechanism of protein uptake. <i>Molecular Microbiology</i> , 2014, 93, 234-246.	2.5	23
17	Structural insights into a novel family of integral membrane siderophore reductases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	21
18	Comparison of lipidic carrier systems for integral membrane proteins – MsbA as case study. <i>Biological Chemistry</i> , 2019, 400, 1509-1518.	2.5	15

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19	Structural and biophysical analysis of nuclease protein antibiotics. <i>Biochemical Journal</i> , 2016, 473, 2799-2812.	3.7	12
20	Cryo-EM structure of MsbA in saposin-lipid nanoparticles (Salipro) provides insights into nucleotide coordination. <i>FEBS Journal</i> , 2022, 289, 2959-2970.	4.7	12
21	Structure of protease-cleaved <i>Escherichia coli</i> α -2-macroglobulin reveals a putative mechanism of conformational activation for protease entrapment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1478-1486.	2.5	11
22	Lipid-like Peptides can Stabilize Integral Membrane Proteins for Biophysical and Structural Studies. <i>ChemBioChem</i> , 2017, 18, 1735-1742.	2.6	11
23	Conformation-specific detection of calmodulin binding using the unnatural amino acid p-azido-phenylalanine (AzF) as an IR-sensor. <i>Structural Dynamics</i> , 2018, 5, 064701.	2.3	10
24	Crystal Structure of a Group I Energy Coupling Factor Vitamin Transporter S Component in Complex with Its Cognate Substrate. <i>Cell Chemical Biology</i> , 2016, 23, 827-836.	5.2	9
25	Structure and stability of the Human respiratory syncytial virus M2 RNA-binding core domain reveals a compact and cooperative folding unit. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 23-30.	0.8	5
26	Recombinant expression, purification, crystallization and preliminary X-ray diffraction analysis of the C-terminal DUF4909631138 domain of TamB from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1272-1275.	0.8	4