Jure BoriÅ¡ek

List of Publications by Year
in descending order

26 papers	418 citations	758635 12 h-index	794141 19 g-index
27 all docs	27 docs citations	27 times ranked	482 citing authors

#	Article	IF	Citations
1	Molecular basis for functional diversity among microbial Nep1-like proteins. PLoS Pathogens, 2019, 15, e1007951.	2.1	39
2	Decrypting the Information Exchange Pathways across the Spliceosome Machinery. Journal of the American Chemical Society, 2020, 142, 8403-8411.	6.6	35
3	Allosteric Cross-Talk among Spike's Receptor-Binding Domain Mutations of the SARS-CoV-2 South African Variant Triggers an Effective Hijacking of Human Cell Receptor. Journal of Physical Chemistry Letters, 2021, 12, 5987-5993.	2.1	33
4	The CWB2 Cell Wall-Anchoring Module Is Revealed by the Crystal Structures of the Clostridium difficile Cell Wall Proteins Cwp8 and Cwp6. Structure, 2017, 25, 514-521.	1.6	29
5	Senescent cells as promising targets to tackle age-related diseases. Ageing Research Reviews, 2021, 66, 101251.	5.0	28
6	All-Atom Simulations Decrypt the Molecular Terms of RNA Catalysis in the Exon-Ligation Step of the Spliceosome. ACS Catalysis, 2020, 10, 5328-5334.	5.5	26
7	Development of *N*-(Functionalized benzoyl)-homocycloleucyl-glycinonitriles as Potent Cathepsin K Inhibitors. Journal of Medicinal Chemistry, 2015, 58, 6928-6937.	2.9	24
8	Exploiting Cryo-EM Structural Information and All-Atom Simulations To Decrypt the Molecular Mechanism of Splicing Modulators. Journal of Chemical Information and Modeling, 2020, 60, 2510-2521.	2.5	24
9	Peptide Inhibitors of Bacterial Protein Synthesis with Broad Spectrum and SbmA-Independent Bactericidal Activity against Clinical Pathogens. Journal of Medicinal Chemistry, 2020, 63, 9590-9602.	2.9	24
10	Disclosing the Impact of Carcinogenic SF3b Mutations on Pre-mRNA Recognition Via All-Atom Simulations. Biomolecules, 2019, 9, 633.	1.8	23
11	Atomic-Level Mechanism of Pre-mRNA Splicing in Health and Disease. Accounts of Chemical Research, 2021, 54, 144-154.	7.6	23
12	A Water-Assisted Catalytic Mechanism in Glycoside Hydrolases Demonstrated on the *Staphylococcus aureus* Autolysin E. ACS Catalysis, 2018, 8, 4334-4345.	5.5	13
13	Computing Metal–Binding Proteins for Therapeutic Benefit. ChemMedChem, 2021, 16, 2034-2049.	1.6	12
14	An oomycete NLP cytolysin forms transient small pores in lipid membranes. Science Advances, 2022, 8, eabj9406.	4.7	11
15	Mechanistic interpretation of artificial neural network–based QSAR model for prediction of cathepsin K inhibition potency. Journal of Chemometrics, 2014, 28, 272-281.	0.7	10
16	Nep1-like proteins as a target for plant pathogen control. PLoS Pathogens, 2021, 17, e1009477.	2.1	9
17	Investigating the Molecular Mechanism of H3B-8800: A Splicing Modulator Inducing Preferential Lethality in Spliceosome-Mutant Cancers. International Journal of Molecular Sciences, 2021, 22, 11222.	1.8	9
18	The Comparison of Docking Search Algorithms and Scoring Functions. Advances in Medical Technologies and Clinical Practice Book Series, 2016, , 99-127.	0.3	8

#	ARTICLE	IF	CITATIONS
19	Comparison of *in silico* tools for binding site prediction applied for structure-based design of autolysin inhibitors. SAR and QSAR in Environmental Research, 2016, 27, 573-587.	1.0	7
20	Domain sliding of two Staphylococcus aureus N-acetylglucosaminidases enables their substrate-binding prior to its catalysis. Communications Biology, 2020, 3, 178.	2.0	7
21	Molecular Basis of SARS-CoV-2 Nsp1-Induced Immune Translational Shutdown as Revealed by All-Atom Simulations. Journal of Physical Chemistry Letters, 2021, 12, 11745-11750.	2.1	7
22	An Expanded Two-Zn^{2+}-Ion Motif Orchestrates Pre-mRNA Maturation in the 3â€²-End Processing Endonuclease Machinery. ACS Catalysis, 2021, 11, 4319-4326.	5.5	6
23	Discovery of (phenylureido)piperidinyl benzamides as prospective inhibitors of bacterial autolysin E from *Staphylococcus aureus*. Journal of Enzyme Inhibition and Medicinal Chemistry, 2018, 33, 1239-1247.	2.5	4
24	All-Atom Simulations Reveal a Key Interaction Network in the HLA-E/NKG2A/CD94 Immune Complex Fine-Tuned by the Nonameric Peptide. Journal of Chemical Information and Modeling, 2021, 61, 3593-3603.	2.5	4
25	Nonameric Peptide Orchestrates Signal Transduction in the Activating HLA-E/NKG2C/CD94 Immune Complex as Revealed by All-Atom Simulations. International Journal of Molecular Sciences, 2021, 22, 6670.	1.8	3
26	The Comparison of Docking Search Algorithms and Scoring Functions. , 2017, , 820-849.		0