

# Jiřá- Zahradnř-k

## List of Publications by Year in descending order

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23  
papers

2,468  
citations

759055

12  
h-index

713332

21  
g-index

32  
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32  
docs citations

32  
times ranked

3585  
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. <i>Cell</i> , 2022, 185, 467-484.e15.	13.5	788
2	SARS-CoV-2 spike L452R variant evades cellular immunity and increases infectivity. <i>Cell Host and Microbe</i> , 2021, 29, 1124-1136.e11.	5.1	421
3	SARS-CoV-2 variant prediction and antiviral drug design are enabled by RBD in vitro evolution. <i>Nature Microbiology</i> , 2021, 6, 1188-1198.	5.9	314
4	Virological characteristics of the SARS-CoV-2 Omicron BA.2 spike. <i>Cell</i> , 2022, 185, 2103-2115.e19.	13.5	273
5	The SARS-CoV-2 Lambda variant exhibits enhanced infectivity and immune resistance. <i>Cell Reports</i> , 2022, 38, 110218.	2.9	148
6	A Protein-Engineered, Enhanced Yeast Display Platform for Rapid Evolution of Challenging Targets. <i>ACS Synthetic Biology</i> , 2021, 10, 3445-3460.	1.9	28
7	Flexible regions govern promiscuous binding of $\alpha 24$ to receptors $\alpha 20R1$ and $\alpha 22R1$ . <i>FEBS Journal</i> , 2019, 286, 3858-3873.	2.2	21
8	Interferons type II and their receptors R1 and R2 in fish species: Evolution, structure, and function. <i>Fish and Shellfish Immunology</i> , 2018, 79, 140-152.	1.6	19
9	Characterization of the catabolic pathway of diclofenac in <i>Raoultella</i> sp. KDF8. <i>International Biodeterioration and Biodegradation</i> , 2019, 137, 88-94.	1.9	19
10	<i>Agrobacterium bohemicum</i> sp. nov. isolated from poppy seed wastes in central Bohemia. <i>Systematic and Applied Microbiology</i> , 2018, 41, 184-190.	1.2	14
11	Potential of the strain <i>Raoultella</i> sp. KDF8 for removal of analgesics. <i>Folia Microbiologica</i> , 2018, 63, 273-282.	1.1	14
12	Biotransformation of codeine to 14-OH-codeine derivatives by <i>Rhizobium radiobacter</i> R89-1. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2013, 87, 1-5.	1.8	12
13	Crystal structure of human interferon- $\beta$ receptor 2 reveals the structural basis for receptor specificity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1017-1025.	1.1	12
14	Perspectives: SARS-CoV-2 Spike Convergent Evolution as a Guide to Explore Adaptive Advantage. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	12
15	Effect of the anti-inflammatory drug diclofenac on lipid composition of bacterial strain <i>Raoultella</i> sp. KDF8. <i>Folia Microbiologica</i> , 2020, 65, 763-773.	1.1	7
16	Protein Binder (ProBi) as a New Class of Structurally Robust Non-Antibody Protein Scaffold for Directed Evolution. <i>Viruses</i> , 2021, 13, 190.	1.5	7
17	In-silico driven engineering of enantioselectivity of a penicillin G acylase towards active pharmaceutical ingredients. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2016, 133, S53-S59.	1.8	6
18	Redesigning Protein Cavities as a Strategy for Increasing Affinity in Protein-Protein Interaction: Interferon- $\beta$ Receptor 1 as a Model. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	5

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19	Draft Genome Sequence of <i>Agrobacterium</i> sp. Strain R89-1, a Morphine Alkaloid-Biotransforming Bacterium. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
20	The crystal structure of XdpB, the bacterial old yellow enzyme, in an FMN-free form. <i>PLoS ONE</i> , 2018, 13, e0195299.	1.1	4
21	<i>De novo</i> developed protein binders mimicking Interferon lambda signaling. <i>FEBS Journal</i> , 2022, 289, 2672-2684.	2.2	4
22	Protein Engineering in the Design of Protein-Protein Interactions: SARS-CoV-2 Inhibitors as a Test Case. <i>Biochemistry</i> , 2021, 60, 3429-3435.	1.2	3
23	Draft Genome Sequence of <i>Pantoea agglomerans</i> JM1, a Strain Isolated from Soil Polluted by Industrial Production of Beta-Lactam Antibiotics That Exhibits Valacyclovir-Like Hydrolase Activity. <i>Genome Announcements</i> , 2017, 5, .	0.8	1