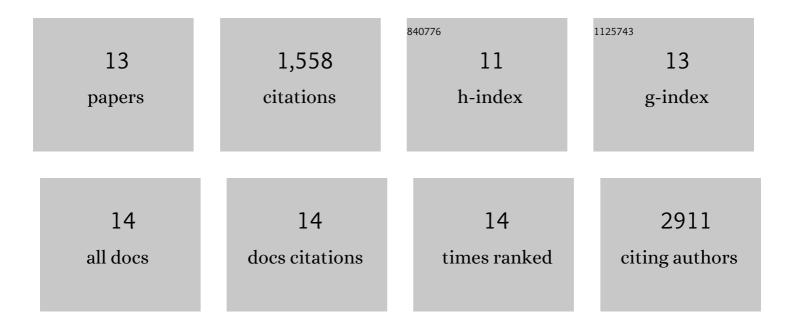
## Robert Jedrzejczak

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9672709/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A Genomic Island of Vibrio cholerae Encodes a Three-Component Cytotoxin with Monomer and Protomer Forms Structurally Similar to Alpha-Pore-Forming Toxins. Journal of Bacteriology, 2022, 204, e0055521.	2.2	3
2	Tipiracil binds to uridine site and inhibits Nsp15 endoribonuclease NendoU from SARS-CoV-2. Communications Biology, 2021, 4, 193.	4.4	85
3	Structure of papain-like protease from SARS-CoV-2 and its complexes with non-covalent inhibitors. Nature Communications, 2021, 12, 743.	12.8	297
4	<i>Mycobacterium tuberculosis</i> Phe-tRNA synthetase: structural insights into tRNA recognition and aminoacylation. Nucleic Acids Research, 2021, 49, 5351-5368.	14.5	1
5	2′-O methylation of RNA cap in SARS-CoV-2 captured by serial crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	46
6	Masitinib is a broad coronavirus 3CL inhibitor that blocks replication of SARS-CoV-2. Science, 2021, 373, 931-936.	12.6	173
7	Transient and stabilized complexes of Nsp7, Nsp8, and Nsp12 in SARS-CoV-2 replication. Biophysical Journal, 2021, 120, 3152-3165.	0.5	39
8	Structural plasticity of SARS-CoV-2 3CL Mpro active site cavity revealed by room temperature X-ray crystallography. Nature Communications, 2020, 11, 3202.	12.8	334
9	Allosteric inhibitors of <scp><i>Mycobacterium tuberculosis</i></scp> tryptophan synthase. Protein Science, 2020, 29, 779-788.	7.6	25
10	Crystal structure of Nsp15 endoribonuclease <scp>NendoU</scp> from <scp>SARSâ€CoV</scp> â€2. Protein Science, 2020, 29, 1596-1605.	7.6	294
11	Crystal structures of SARS-CoV-2 ADP-ribose phosphatase: from the apo form to ligand complexes. IUCrJ, 2020, 7, 814-824.	2.2	92
12	Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. Structure, 2019, 27, 449-463.e7.	3.3	29
13	High-throughput protein purification and quality assessment for crystallization. Methods, 2011, 55, 12-28.	3.8	138