

# Przemysław Grudnik

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

1,807  
citations

567281

15  
h-index

454955

30  
g-index

31  
all docs

31  
docs citations

31  
times ranked

2349  
citing authors

#	ARTICLE	IF	CITATIONS
1	Macrocyclic Peptide Inhibitor of PD-1/PD-L1 Immune Checkpoint. <i>Advanced Therapeutics</i> , 2021, 4, 2000195.	3.2	5
2	Human and mouse PD-L1: similar molecular structure, but different druggability profiles. <i>IScience</i> , 2021, 24, 101960.	4.1	45
3	Latency, thermal stability, and identification of an inhibitory compound of mirolysin, a secretory protease of the human periodontopathogen <i>Tannerella forsythia</i> . <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2021, 36, 1267-1281.	5.2	3
4	A single residue can modulate nanocage assembly in salt dependent ferritin. <i>Nanoscale</i> , 2021, 13, 11932-11942.	5.6	11
5	Chromosomal localization of PemK toxin-antitoxin system results in the loss of toxicity – Characterization of pemK-Sp from <i>Staphylococcus pseudintermedius</i> . <i>Microbiological Research</i> , 2020, 240, 126529.	5.3	1
6	Crystal Structure of Mannose Specific IIA Subunit of Phosphotransferase System from <i>Streptococcus pneumoniae</i> . <i>Molecules</i> , 2020, 25, 4633.	3.8	3
7	Structural Characterization of Glycerol Kinase from the Thermophilic Fungus <i>Chaetomium thermophilum</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 9570.	4.1	8
8	Half Way to Hypusine – Structural Basis for Substrate Recognition by Human Deoxyhypusine Synthase. <i>Biomolecules</i> , 2020, 10, 522.	4.0	17
9	Molecular basis for the bifunctional Uba4-Urm1 sulfur relay system in <i>scp</i> tRNA thiolation and ubiquitin-like conjugation. <i>EMBO Journal</i> , 2020, 39, e105087.	7.8	17
10	Development and characterization of a new inhibitor of heme oxygenase activity for cancer treatment. <i>Archives of Biochemistry and Biophysics</i> , 2019, 671, 130-142.	3.0	25
11	Crystal Structure of <i>Kluyveromyces lactis</i> Glucokinase (KlGk1). <i>International Journal of Molecular Sciences</i> , 2019, 20, 4821.	4.1	1
12	Development of a novel, high-affinity ssDNA trypsin inhibitor. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2019, 34, 638-643.	5.2	4
13	Crystal structure of ADP-dependent glucokinase from <i>Methanocaldococcus jannaschii</i> in complex with 5-iodotubercidin reveals phosphoryl transfer mechanism. <i>Protein Science</i> , 2018, 27, 790-797.	7.6	7
14	Crystal structure of the FAS1 domain of the hyaluronic acid receptor stabilin-2. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 695-701.	2.3	5
15	Structural basis for ADP-dependent glucokinase inhibition by 8-bromo-substituted adenosine nucleotide. <i>Journal of Biological Chemistry</i> , 2018, 293, 11088-11099.	3.4	10
16	Small-Molecule Inhibitors of the Programmed Cell Death-1/Programmed Death-Ligand 1 (PD-1/PD-L1) Interaction via Transiently Induced Protein States and Dimerization of PD-L1. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 5857-5867.	6.4	242
17	Structural analysis of PIM1 kinase complexes with ATP-competitive inhibitors. <i>Scientific Reports</i> , 2017, 7, 13399.	3.3	22
18	Bioactive Macrocyclic Inhibitors of the PD-1/PD-L1 Immune Checkpoint. <i>Angewandte Chemie</i> , 2017, 129, 13920-13923.	2.0	13

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19	Bioactive Macrocyclic Inhibitors of the PD-1/PD-L1 Immune Checkpoint. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 13732-13735.	13.8	131
20	Crystal structure of a low molecular weight activator Blm-pep with yeast 20S proteasome – insights into the enzyme activation mechanism. <i>Scientific Reports</i> , 2017, 7, 6177.	3.3	23
21	Structural Biology of the Immune Checkpoint Receptor PD-1 and Its Ligands PD-L1/PD-L2. <i>Structure</i> , 2017, 25, 1163-1174.	3.3	253
22	Small-molecule inhibitors of PD-1/PD-L1 immune checkpoint alleviate the PD-L1-induced exhaustion of T-cells. <i>Oncotarget</i> , 2017, 8, 72167-72181.	1.8	221
23	Structural basis for small molecule targeting of the programmed death ligand 1 (PD-L1). <i>Oncotarget</i> , 2016, 7, 30323-30335.	1.8	297
24	A Unique Mdm2-Binding Mode of the 3-Pyrrolin-2-one- and 2-Furanone-Based Antagonists of the p53-Mdm2 Interaction. <i>ACS Chemical Biology</i> , 2016, 11, 3310-3318.	3.4	31
25	Investigation of Serine-Proteinase-Catalyzed Peptide Splicing in Analogues of Sunflower Trypsin Inhibitor...1 (SFTI-1). <i>ChemBioChem</i> , 2015, 16, 2036-2045.	2.6	7
26	Atomic resolution crystal structure of HV-BBI protease inhibitor from amphibian skin in complex with bovine trypsin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 582-589.	2.6	5
27	Structural Basis of GD2 Ganglioside and Mimetic Peptide Recognition by 14G2a Antibody. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2577-2590.	3.8	32
28	Insights into eukaryotic Rubisco assembly – Crystal structures of RbcX chaperones from <i>Arabidopsis thaliana</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 2899-2906.	2.4	20
29	T cell Activation Is Driven by an ADP-Dependent Glucokinase Linking Enhanced Glycolysis with Mitochondrial Reactive Oxygen Species Generation. <i>Cell Reports</i> , 2012, 2, 1300-1315.	6.4	155
30	Structural basis for the molecular evolution of SRP-GTPase activation by protein. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1376-1380.	8.2	59
31	Protein targeting by the signal recognition particle. <i>Biological Chemistry</i> , 2009, 390, 775-782.	2.5	134