PrzemysÅ‚aw Grudnik

List of Publications by Year
in descending order

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	Structural basis for small molecule targeting of the programmed death ligand 1 (PD-L1). Oncotarget, 2016, 7, 30323-30335.	1.8	297
2	Structural Biology of the Immune Checkpoint Receptor PD-1 and Its Ligands PD-L1/PD-L2. Structure, 2017, 25, 1163-1174.	3.3	253
3	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. Journal of Medicinal Chemistry, 2017, 60, 5857-5867.	6.4	242
4	Small-molecule inhibitors of PD-1/PD-L1 immune checkpoint alleviate the PD-L1-induced exhaustion of T-cells. Oncotarget, 2017, 8, 72167-72181.	1.8	221
5	T cell Activation Is Driven by an ADP-Dependent Glucokinase Linking Enhanced Glycolysis with Mitochondrial Reactive Oxygen Species Generation. Cell Reports, 2012, 2, 1300-1315.	6.4	155
6	Protein targeting by the signal recognition particle. Biological Chemistry, 2009, 390, 775-782.	2.5	134
7	Bioactive Macrocyclic Inhibitors of the PDâ€1/PDâ€L1 Immune Checkpoint. Angewandte Chemie - International Edition, 2017, 56, 13732-13735.	13.8	131
8	Structural basis for the molecular evolution of SRP-GTPase activation by protein. Nature Structural and Molecular Biology, 2011, 18, 1376-1380.	8.2	59
9	Human and mouse PD-L1: similar molecular structure, but different druggability profiles. IScience, 2021, 24, 101960.	4.1	45
10	Structural Basis of GD2 Ganglioside and Mimetic Peptide Recognition by 14G2a Antibody. Molecular and Cellular Proteomics, 2015, 14, 2577-2590.	3.8	32
11	A Unique Mdm2-Binding Mode of the 3-Pyrrolin-2-one- and 2-Furanone-Based Antagonists of the p53-Mdm2 Interaction. ACS Chemical Biology, 2016, 11, 3310-3318.	3.4	31
12	Development and characterization of a new inhibitor of heme oxygenase activity for cancer treatment. Archives of Biochemistry and Biophysics, 2019, 671, 130-142.	3.0	25
13	Crystal structure of a low molecular weight activator Blm-pep with yeast 20S proteasome â€“ insights into the enzyme activation mechanism. Scientific Reports, 2017, 7, 6177.	3.3	23
14	Structural analysis of PIM1 kinase complexes with ATP-competitive inhibitors. Scientific Reports, 2017, 7, 13399.	3.3	22
15	Insights into eukaryotic Rubisco assembly â€" Crystal structures of RbcX chaperones from Arabidopsis thaliana. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 2899-2906.	2.4	20
16	Half Way to Hypusineâ€"Structural Basis for Substrate Recognition by Human Deoxyhypusine Synthase. Biomolecules, 2020, 10, 522.	4.0	17
17	Molecular basis for the bifunctional Uba4â€"Urm1 sulfurâ€relay system in <scp>tRNA</scp> thiolation and ubiquitinâ€like conjugation. EMBO Journal, 2020, 39, e105087.	7.8	17
18	Bioactive Macrocyclic Inhibitors of the PDâ€1/PDâ€L1 Immune Checkpoint. Angewandte Chemie, 2017, 129, 13920-13923.	2.0	13

#	ARTICLE	IF	CITATIONS
19	A single residue can modulate nanocage assembly in salt dependent ferritin. Nanoscale, 2021, 13, 11932-11942.	5.6	11
20	Structural basis for ADP-dependent glucokinase inhibition by 8-bromoâ€“substituted adenosine nucleotide. Journal of Biological Chemistry, 2018, 293, 11088-11099.	3.4	10
21	Structural Characterization of Glycerol Kinase from the Thermophilic Fungus Chaetomium thermophilum. International Journal of Molecular Sciences, 2020, 21, 9570.	4.1	8
22	Investigation of Serineâ€Proteinaseâ€Catalyzed Peptide Splicing in Analogues of Sunflower Trypsin Inhibitorâ€…1 (SFTIâ€1). ChemBioChem, 2015, 16, 2036-2045.	2.6	7
23	Crystal structure of ADPâ€dependent glucokinase from Methanocaldococcus jannaschii in complex with 5â€iodotubercidin reveals phosphoryl transfer mechanism. Protein Science, 2018, 27, 790-797.	7.6	7
24	Atomic resolution crystal structure of HV-BBI protease inhibitor from amphibian skin in complex with bovine trypsin. Proteins: Structure, Function and Bioinformatics, 2015, 83, 582-589.	2.6	5
25	Crystal structure of the FAS1 domain of the hyaluronic acid receptor stabilin-2. Acta Crystallographica Section D: Structural Biology, 2018, 74, 695-701.	2.3	5
26	Macrocyclic Peptide Inhibitor of PDâ€1/PDâ€L1 Immune Checkpoint. Advanced Therapeutics, 2021, 4, 2000195.	3.2	5
27	Development of a novel, high-affinity ssDNA trypsin inhibitor. Journal of Enzyme Inhibition and Medicinal Chemistry, 2019, 34, 638-643.	5.2	4
28	Crystal Structure of Mannose Specific IIA Subunit of Phosphotransferase System from Streptococcus pneumoniae. Molecules, 2020, 25, 4633.	3.8	3
29	Latency, thermal stability, and identification of an inhibitory compound of mirolysin, a secretory protease of the human periodontopathogen Tannerella forsythia. Journal of Enzyme Inhibition and Medicinal Chemistry, 2021, 36, 1267-1281.	5.2	3
30	Crystal Structure of Kluyveromyces lactis Glucokinase (KlGlk1). International Journal of Molecular Sciences, 2019, 20, 4821.	4.1	1
31	Chromosomal localization of PemIK toxin-antitoxin system results in the loss of toxicity â€“ Characterization of pemIK-Sp from Staphylococcus pseudintermedius. Microbiological Research, 2020, 240, 126529.	5.3	1