Grzegorz M Popowicz

List of Publications by Year
in descending order

78 papers	5,003 citations	126907 33 h-index	95266 68 g-index
85 all docs	85 docs citations	85 times ranked	6376 citing authors

#	Article	IF	Citations
1	FSP1 is a glutathione-independent ferroptosis suppressor. Nature, 2019, 575, 693-698.	27.8	1,624
2	Filamins: promiscuous organizers of the cytoskeleton. Trends in Biochemical Sciences, 2006, 31, 411-419.	7.5	256
3	Structure of the Stapled p53 Peptide Bound to Mdm2. Journal of the American Chemical Society, 2012, 134, 103-106.	13.7	222
4	Structures of low molecular weight inhibitors bound to MDMX and MDM2 reveal new approaches for p53-MDMX/MDM2 antagonist drug discovery. Cell Cycle, 2010, 9, 1104-1111.	2.6	217
5	Structure of the human Mdmx protein bound to the p53 tumor suppressor transactivation domain. Cell Cycle, 2008, 7, 2441-2443.	2.6	182
6	The Structureâ€Based Design of Mdm2/Mdmxâ€“p53 Inhibitors Gets Serious. Angewandte Chemie - International Edition, 2011, 50, 2680-2688.	13.8	150
7	Structural basis for the inhibition of insulin-like growth factors by insulin-like growth factor-binding proteins. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13028-13033.	7.1	138
8	Robust Generation of Lead Compounds for Proteinâ€“Protein Interactions by Computational and MCR Chemistry: p53/Hdm2 Antagonists. Angewandte Chemie - International Edition, 2010, 49, 5352-5356.	13.8	136
9	Molecular Basis for the Inhibition of p53 by Mdmx. Cell Cycle, 2007, 6, 2386-2392.	2.6	132
10	The crystal structure of the non-liganded 14-3-3Ïƒ protein: insights into determinants of isoform specific ligand binding and dimerization. Cell Research, 2005, 15, 219-227.	12.0	103
11	Structural basis for the assembly of the Sxlâ€“Unr translation regulatory complex. Nature, 2014, 515, 287-290.	27.8	102
12	High affinity interaction of the p53 peptide-analogue with human Mdm2 and Mdmx. Cell Cycle, 2009, 8, 1176-1184.	2.6	98
13	Enabling Large-Scale Design, Synthesis and Validation of Small Molecule Protein-Protein Antagonists. PLoS ONE, 2012, 7, e32839.	2.5	90
14	Role of the ubiquitin-like protein Hub1 in splice-site usage and alternative splicing. Nature, 2011, 474, 173-178.	27.8	79
15	Structural Basis for the Regulation of Insulin-like Growth Factors by IGF Binding Proteins. Structure, 2005, 13, 155-167.	3.3	72
16	The p53-MDM2/MDMX axis â€“ A chemotype perspective. MedChemComm, 2011, 2, 246.	3.4	68
17	c-Abl Phosphorylates Hdmx and Regulates Its Interaction with p53. Journal of Biological Chemistry, 2009, 284, 4031-4039.	3.4	60
18	Inhibitors of PEX14 disrupt protein import into glycosomes and kill Trypanosoma parasites. Science, 2017, 355, 1416-1420.	12.6	59

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19	The Three-Dimensional Structures of Tick Carboxypeptidase Inhibitor in Complex with A/B Carboxypeptidases Reveal a Novel Double-headed Binding Mode. Journal of Molecular Biology, 2005, 350, 489-498.	4.2	57
20	Transient Protein States in Designing Inhibitors of the MDM2-p53 Interaction. Structure, 2013, 21, 2143-2151.	3.3	57
21	Structural Ramification for Acetyl-Lysine Recognition by the Bromodomain of Human BRG1 Protein, a Central ATPase of the SWI/SNF Remodeling Complex. ChemBioChem, 2007, 8, 1308-1316.	2.6	56
22	HuR biological function involves RRM3-mediated dimerization and RNA binding by all three RRMs. Nucleic Acids Research, 2019, 47, 1011-1029.	14.5	56
23	Targeting TRAF6 E3 ligase activity with a small-molecule inhibitor combats autoimmunity. Journal of Biological Chemistry, 2018, 293, 13191-13203.	3.4	52
24	Exhaustive Fluorine Scanning toward Potent p53â€“Mdm2 Antagonists. ChemMedChem, 2012, 7, 49-52.	3.2	50
25	Functional and Structural Characterization of Spl Proteases from Staphylococcus aureus. Journal of Molecular Biology, 2006, 358, 270-279.	4.2	47
26	Enzymatic Activity of the Staphylococcus aureus SplB Serine Protease is Induced by Substrates Containing the Sequence Trp-Glu-Leu-Gln. Journal of Molecular Biology, 2008, 379, 343-356.	4.2	43
27	Molecular Structure of the Rod Domain of Dictyostelium Filamin. Journal of Molecular Biology, 2004, 342, 1637-1646.	4.2	42
28	Structures of actin-bound Wiskott-Aldrich syndrome protein homology 2 (WH2) domains of Spire and the implication for filament nucleation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11757-11762.	7.1	42
29	Structural and Functional Analysis of the Natural JNK1 Inhibitor Quercetagetin. Journal of Molecular Biology, 2013, 425, 411-423.	4.2	40
30	Paramagnetic NMR in drug discovery. Journal of Biomolecular NMR, 2020, 74, 287-309.	2.8	40
31	Structural and functional characterization of SplA, an exclusively specific protease of Staphylococcus aureus. Biochemical Journal, 2009, 419, 555-564.	3.7	38
32	Discovery of Highly Potent p53-MDM2 Antagonists and Structural Basis for Anti-Acute Myeloid Leukemia Activities. ACS Chemical Biology, 2014, 9, 802-811.	3.4	38
33	Structure of the N-terminal Domain of the FOP (FGFR1OP) Protein and Implications for its Dimerization and Centrosomal Localization. Journal of Molecular Biology, 2006, 359, 863-875.	4.2	36
34	Characterization of 14-3-3sigma Dimerization Determinants: Requirement of Homodimerization for Inhibition of Cell Proliferation. Cell Cycle, 2006, 5, 2920-2926.	2.6	33
35	A Novel Class of Cysteine Protease Inhibitors:â€‰ Solution Structure of Staphostatin A from Staphylococcus aureus. Biochemistry, 2003, 42, 13449-13456.	2.5	30
36	The conserved ubiquitin-like protein Hub1 plays a critical role in splicing in human cells. Journal of Molecular Cell Biology, 2014, 6, 312-323.	3.3	30

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37	Deconstructing Noncovalent Kelch-like ECH-Associated Protein 1 (Keap1) Inhibitors into Fragments to Reconstruct New Potent Compounds. Journal of Medicinal Chemistry, 2021, 64, 4623-4661.	6.4	30
38	Identification of small-molecule inhibitors of USP2a. European Journal of Medicinal Chemistry, 2018, 150, 261-267.	5.5	24
39	Conversion of a Monoâ€•and Diacylglycerol Lipase into a Triacylglycerol Lipase by Protein Engineering. ChemBioChem, 2015, 16, 1431-1434.	2.6	20
40	Fragment-based de novo design of a cystathionine Î³-lyase selective inhibitor blocking hydrogen sulfide production. Scientific Reports, 2016, 6, 34398.	3.3	20
41	Lipase-Driven Epoxidation Is A Two-Stage Synergistic Process. ChemistrySelect, 2016, 1, 836-839.	1.5	20
42	NudC guides client transfer between the Hsp40/70 and Hsp90 chaperone systems. Molecular Cell, 2022, 82, 555-569.e7.	9.7	20
43	NMR Structural Characterization and Computational Predictions of the Major Intermediate in Oxidative Folding of Leech Carboxypeptidase Inhibitor. Structure, 2005, 13, 1193-1202.	3.3	18
44	Selective activators of protein phosphatase 5 target the auto-inhibitory mechanism. Bioscience Reports, 2015, 35, .	2.4	18
45	Study of a Major Intermediate in the Oxidative Folding of Leech Carboxypeptidase Inhibitor: Contribution of the Fourth Disulfide Bond. Journal of Molecular Biology, 2005, 352, 961-975.	4.2	17
46	Staphylococcal SplB Serine Protease Utilizes a Novel Molecular Mechanism of Activation. Journal of Biological Chemistry, 2014, 289, 15544-15553.	3.4	17
47	Discovery of novel dual inhibitors against Mdm2 and Mdmx proteins by in silico approaches and binding assay. Life Sciences, 2016, 145, 240-246.	4.3	17
48	NMR structural characterization of the N-terminal domain of the adenylyl cyclase-associated protein (CAP) from Dictyostelium discoideum. Journal of Biomolecular NMR, 2004, 29, 73-84.	2.8	15
49	Come, sweet death: targeting glycosomal protein import for antitrypanosomal drug development. Current Opinion in Microbiology, 2018, 46, 116-122.	5.1	14
50	Structureâ€“Activity Relationship in Pyrazolo[4,3-c]pyridines, First Inhibitors of PEX14â€“PEX5 Proteinâ€“Protein Interaction with Trypanocidal Activity. Journal of Medicinal Chemistry, 2020, 63, 847-879.	6.4	13
51	Introducing the CSP Analyzer: A novel Machine Learning-based application for automated analysis of two-dimensional NMR spectra in NMR fragment-based screening. Computational and Structural Biotechnology Journal, 2020, 18, 603-611.	4.1	13
52	NMR Screening for Lead Compounds Using Tryptophan-Mutated Proteins. Journal of Medicinal Chemistry, 2008, 51, 5035-5042.	6.4	12
53	A mechanistic study into the epoxidation of carboxylic acid and alkene in a mono, di-acylglycerol lipase. Biochemical and Biophysical Research Communications, 2015, 460, 392-396.	2.1	12
54	Development and binding characteristics of phosphonate inhibitors of SplA protease from Staphylococcus aureus. Protein Science, 2014, 23, 179-189.	7.6	11

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55	The Photocatalyzed Thiolâ€ene reaction: A New Tag to Yield Fast, Selective and reversible Paramagnetic Tagging of Proteins. ChemPhysChem, 2020, 21, 863-869.	2.1	11
56	Bis-choline tetrathiomolybdate prevents copper-induced bloodâ€“brain barrier damage. Life Science Alliance, 2022, 5, e202101164.	2.8	11
57	Double Strike Approach for Tumor Attack: Engineering T Cells Using a CD40L:CD28 Chimeric Co-Stimulatory Switch Protein for Enhanced Tumor Targeting in Adoptive Cell Therapy. Frontiers in Immunology, 2021, 12, 750478.	4.8	9
58	Structure and characterization of Aspergillus fumigatus lipase B with a unique, oversized regulatory subdomain. FEBS Journal, 2019, 286, 2366-2380.	4.7	8
59	Jetzt wird es ernst: strukturbasiertes Design von Mdm2/Mdmxâ€p53â€Inhibitoren. Angewandte Chemie, 2011, 123, 2732-2741.	2.0	7
60	Lid mobility in lipase SMG1 validated using a thiol/disulfide redox potential probe. FEBS Open Bio, 2016, 6, 477-483.	2.3	7
61	Focused Library Generator: case of Mdmx inhibitors. Journal of Computer-Aided Molecular Design, 2020, 34, 769-782.	2.9	7
62	Water envelope has a critical impact on the design of proteinâ€“protein interaction inhibitors. Chemical Communications, 2020, 56, 4360-4363.	4.1	7
63	Inhibitors of glycosomal protein import provide new leads against trypanosomiasis. Microbial Cell, 2017, 4, 229-232.	3.2	7
64	Comparison of enzymatic properties and small molecule inhibition of Î³â€“glutamyltranspeptidases from pathogenic and commensal bacteria. Biological Chemistry, 2017, 398, 341-357.	2.5	6
65	Deep learning model predicts water interaction sites on the surface of proteins using limited-resolution data. Chemical Communications, 2020, 56, 15454-15457.	4.1	6
66	Novel Trypanocidal Inhibitors that Block Glycosome Biogenesis by Targeting PEX3â€“PEX19 Interaction. Frontiers in Cell and Developmental Biology, 2021, 9, 737159.	3.7	4
67	Structures of the Arm-type Binding Domains of HPI and HAI7 Integrases. Journal of Biological Chemistry, 2009, 284, 31664-31671.	3.4	3
68	NMR fragment-based screening for development of the CD44-binding small molecules. Bioorganic Chemistry, 2019, 82, 284-289.	4.1	3
69	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
70	Letter to the Editor:1H,15N and13C NMR Resonance Assignments of Staphostatin A, a Specific Staphylococcus Aureus Cysteine Proteinase Inhibitor. Journal of Biomolecular NMR, 2004, 28, 295-296.	2.8	2
71	A realâ€time cellâ€binding assay reveals dynamic features of STxBâ€“Gb3 cointernalization and STxBâ€mediated cargo delivery into cancer cells. FEBS Letters, 2020, 594, 2406-2420.	2.8	2
72	Structure-activity relationship and cardiac safety of 2-aryl-2-(pyridin-2-yl)acetamides as a new class of broad-spectrum anticonvulsants derived from Disopyramide. Bioorganic Chemistry, 2020, 98, 103717.	4.1	2

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73	A fragment-based approach identifies an allosteric pocket that impacts malate dehydrogenase activity. Communications Biology, 2021, 4, 949.	4.4	2
74	What Features of Ligands Are Relevant to the Opening of Cryptic Pockets in Drug Targets?. Informatics, 2022, 9, 8.	3.9	2
75	How to Catch the Ball: Fullerene Binding to the Corannulene Pincer. Molecules, 2022, 27, 3838.	3.8	2
76	Crystal Structure of Kluyveromyces lactis Glucokinase (KlGlk1). International Journal of Molecular Sciences, 2019, 20, 4821.	4.1	1
77	NMR structural characterization of the N-terminal domain of the adenylyl cyclase-associated protein (CAP) from Dictyostelium discoideum. , 2004, 29, 73.		1
78	Computer-Aided Design and Synthesis of a New Class of PEX14 Inhibitors: Substituted 2,3,4,5-Tetrahydrobenzo[F][1,4]oxazepines as Potential New Trypanocidal Agents. Journal of Chemical Information and Modeling, 2021, 61, 5256-5268.	5.4	1