Mayako Michino

List of Publications by Year
in descending order

23 papers	1,326 citations	567281 15 h-index	713466 21 g-index
23 all docs	23 docs citations	23 times ranked	1989 citing authors

#	Article	IF	Citations
1	A Chemical Strategy toward Novel Brain-Penetrant EZH2 Inhibitors. ACS Medicinal Chemistry Letters, 2022, 13, 377-387.	2.8	10
2	Whole Cell Active Inhibitors of Mycobacterial Lipoamide Dehydrogenase Afford Selectivity over the Human Enzyme through Tight Binding Interactions. ACS Infectious Diseases, 2021, 7, 435-444.	3.8	1
3	Macrocyclic Peptides that Selectively Inhibit the Mycobacterium tuberculosis Proteasome. Journal of Medicinal Chemistry, 2021, 64, 6262-6272.	6.4	9
4	Discovery of TDI-10229: A Potent and Orally Bioavailable Inhibitor of Soluble Adenylyl Cyclase (sAC,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.8	16
5	Deglycase-activity oriented screening to identify DJ-1 inhibitors. RSC Medicinal Chemistry, 2021, 12, 1232-1238.	3.9	13
6	Inhibition of 3-phosphoglycerate dehydrogenase (PHGDH) by indole amides abrogates de novo serine synthesis in cancer cells. Bioorganic and Medicinal Chemistry Letters, 2019, 29, 2503-2510.	2.2	37
7	Selective Phenylimidazole-Based Inhibitors of the Mycobacterium tuberculosis Proteasome. Journal of Medicinal Chemistry, 2019, 62, 9246-9253.	6.4	14
8	The structural determinants of the bitopic binding mode of a negative allosteric modulator of the dopamine D 2 receptor. Biochemical Pharmacology, 2018, 148, 315-328.	4.4	26
9	Antimalarial proteasome inhibitor reveals collateral sensitivity from intersubunit interactions and fitness cost of resistance. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6863-E6870.	7.1	71
10	The E2.65A mutation disrupts dynamic binding poses of SB269652 at the dopamine D2 and D3 receptors. PLoS Computational Biology, 2018, 14, e1005948.	3.2	19
11	Toward Understanding the Structural Basis of Partial Agonism at the Dopamine D₃ Receptor. Journal of Medicinal Chemistry, 2017, 60, 580-593.	6.4	49
12	Novel Analogues of (R)-5-(Methylamino)-5,6-dihydro-4H-imidazo[4,5,1-ij]quinolin-2(1H)-one (Sumanirole) Provide Clues to Dopamine D₂/D₃ Receptor Agonist Selectivity. Journal of Medicinal Chemistry, 2016, 59, 2973-2988.	6.4	33
13	Structural Basis for the Allosteric Pharmacology of SB269652 in Dopamine D2 Receptor. Biophysical Journal, 2015, 108, 416a.	0.5	0
14	Discovery of a Novel Class of Negative Allosteric Modulator of the Dopamine D₂ Receptor Through Fragmentation of a Bitopic Ligand. Journal of Medicinal Chemistry, 2015, 58, 6819-6843.	6.4	47
15	What Can Crystal Structures of Aminergic Receptors Tell Us about Designing Subtype-Selective Ligands?. Pharmacological Reviews, 2015, 67, 198-213.	16.0	99
16	A new mechanism of allostery in a G proteinâ€"coupled receptor dimer. Nature Chemical Biology, 2014, 10, 745-752.	8.0	108
17	A Single Glycine in Extracellular Loop 1 Is the Critical Determinant for Pharmacological Specificity of Dopamine D2 and D3 Receptors. Molecular Pharmacology, 2013, 84, 854-864.	2.3	58
18	Molecular Determinants of Selectivity and Efficacy at the Dopamine D3 Receptor. Journal of Medicinal Chemistry, 2012, 55, 6689-6699.	6.4	153

#	Article	IF	Citations
19	FoldGPCR: Structure prediction protocol for the transmembrane domain of G proteinâ€coupled receptors from class A. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2189-2201.	2.6	33
20	Predicting structurally conserved contacts for homologous proteins using sequence conservation filters. Proteins: Structure, Function and Bioinformatics, 2009, 77, 448-453.	2.6	11
21	Community-wide assessment of GPCR structure modelling and ligand docking: GPCR Dock 2008. Nature Reviews Drug Discovery, 2009, 8, 455-463.	46.4	260
22	Improved model building and assessment of the Calciumâ€sensing receptor transmembrane domain. Proteins: Structure, Function and Bioinformatics, 2008, 71, 215-226.	2.6	28
23	Bridging the NFAT and NF-Î°B Families. Immunity, 2001, 15, 47-58.	14.3	231