Stephane Betzi

List of Publications by Year
in descending order

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35	1,522	331670	395702
papers	citations	21 h-index	33 g-index

39	39	39	2746
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Revisiting the Molecular Interactions between the Tumor Protein TCTP and the Drugs Sertraline/Thioridazine. ChemMedChem, 2022, 17, .	3.2	4
2	CRCM5484: A BET-BDII Selective Compound with Differential Anti-leukemic Drug Modulation. Journal of Medicinal Chemistry, 2022, 65, 5660-5674.	6.4	2
3	Discovery of Small-Molecule Inhibitors of the PTK7/Î²-Catenin Interaction Targeting the Wnt Signaling Pathway in Colorectal Cancer. ACS Chemical Biology, 2022, 17, 1061-1072.	3.4	1
4	In silico molecular target prediction unveils mebendazole as a potent MAPK14 inhibitor. Molecular Oncology, 2020, 14, 3083-3099.	4.6	17
5	Pharmacological inhibition of syntenin PDZ2 domain impairs breast cancer cell activities and exosome loading with syndecan and EpCAM cargo. Journal of Extracellular Vesicles, 2020, 10, e12039.	12.2	27
6	Integrated Strategy for Lead Optimization Based on Fragment Growing: The Diversity-Oriented-Target-Focused-Synthesis Approach. Journal of Medicinal Chemistry, 2018, 61, 5719-5732.	6.4	51
7	Dual protein kinase and nucleoside kinase modulators for rationally designed polypharmacology. Nature Communications, 2017, 8, 1420.	12.8	18
8	Genetic, structural, and chemical insights into the dual function of GRASP55 in germ cell Golgi remodeling and JAM-C polarized localization during spermatogenesis. PLoS Genetics, 2017, 13, e1006803.	3.5	28
9	Mutational phospho-mimicry reveals a regulatory role for the XRCC4 and XLF C-terminal tails in modulating DNA bridging during classical non-homologous end joining. ELife, 2017, 6, .	6.0	35
10	Proteinâ€“Protein Interaction Inhibition (2P2I)-Oriented Chemical Library Accelerates Hit Discovery. ACS Chemical Biology, 2016, 11, 2140-2148.	3.4	33
11	2P2Idb v2: update of a structural database dedicated to orthosteric modulation of proteinâ€“protein interactions. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw007.	3.0	61
12	Exploring Selective Inhibition of the First Bromodomain of the Human Bromodomain and Extra-terminal Domain (BET) Proteins. Journal of Medicinal Chemistry, 2016, 59, 1634-1641.	6.4	79
13	Stability of the Human Hsp90-p50Cdc37 Chaperone Complex against Nucleotides and Hsp90 Inhibitors, and the Influence of Phosphorylation by Casein Kinase 2. Molecules, 2015, 20, 1643-1660.	3.8	12
14	Pre-B cell receptor binding to galectin-1 modifies galectin-1/carbohydrate affinity to modulate specific galectin-1/glycan lattice interactions. Nature Communications, 2015, 6, 6194.	12.8	47
15	Structural and Biochemical Characterization of the Cop9 Signalosome CSN5/CSN6 Heterodimer. PLoS ONE, 2014, 9, e105688.	2.5	27
16	Crystal Structure of the Vaccinia Virus DNA Polymerase Holoenzyme Subunit D4 in Complex with the A20 N-Terminal Domain. PLoS Pathogens, 2014, 10, e1003978.	4.7	27
17	Coronavirus Nsp10, a Critical Co-factor for Activation of Multiple Replicative Enzymes. Journal of Biological Chemistry, 2014, 289, 25783-25796.	3.4	178
18	Focused chemical libraries â€“ design and enrichment: an example of proteinâ€“protein interaction chemical space. Future Medicinal Chemistry, 2014, 6, 1291-1307.	2.3	32

#	Article	IF	Citations
19	Stereoselective synthesis of original spirolactams displaying promising folded structures. Organic and Biomolecular Chemistry, 2013, 11, 4719.	2.8	15
20	Development of Highly Potent and Selective Diaminothiazole Inhibitors of Cyclin-Dependent Kinases. Journal of Medicinal Chemistry, 2013, 56, 3768-3782.	6.4	73
21	Prevalence, Specificity and Determinants of Lipid-Interacting PDZ Domains from an In-Cell Screen and In Vitro Binding Experiments. PLoS ONE, 2013, 8, e54581.	2.5	23
22	Functional Consequence of Covalent Reaction of Phosphoenolpyruvate with UDP-N-acetylglucosamine 1-Carboxyvinyltransferase (MurA). Journal of Biological Chemistry, 2012, 287, 12657-12667.	3.4	50
23	2P2Idb: a structural database dedicated to orthosteric modulation of proteinâ€“protein interactions. Nucleic Acids Research, 2012, 41, D824-D827.	14.5	133
24	A Novel Approach to the Discovery of Smallâ€Molecule Ligands of CDK2. ChemBioChem, 2012, 13, 2128-2136.	2.6	65
25	Structural recognition mechanisms between human Src homology domain 3 (SH3) and ALGâ€2â€interacting protein X (Alix). FEBS Letters, 2012, 586, 1759-1764.	2.8	9
26	Discovery of a Potential Allosteric Ligand Binding Site in CDK2. ACS Chemical Biology, 2011, 6, 492-501.	3.4	151
27	Abstract 3252: Potent Aurora kinase inhibitors based on a pyrimidine scaffold: Synthesis, SAR and X-ray crystallography studies. , 2011, , .		0
28	Abstract 3253: Novel oxindole inhibitors of Aurora A kinase: Structure based hit-to-lead approach. , 2011, , .		0
29	An integrative in silico methodology for the identification of modulators of macrophage migration inhibitory factor (MIF) tautomerase activity. Bioorganic and Medicinal Chemistry, 2010, 18, 5425-5440.	3.0	19
30	Molecular Mapping of the RNA Cap 2â€²-O-Methyltransferase Activation Interface between Severe Acute Respiratory Syndrome Coronavirus nsp10 and nsp16*. Journal of Biological Chemistry, 2010, 285, 33230-33241.	3.4	56
31	The Fungal Product Terreic Acid Is a Covalent Inhibitor of the Bacterial Cell Wall Biosynthetic Enzyme UDP-N-Acetylglucosamine 1-Carboxyvinyltransferase (MurA),. Biochemistry, 2010, 49, 4276-4282.	2.5	50
32	Identification of allosteric inhibitors blocking the hepatitis C virus polymerase NS5B in the RNA synthesis initiation step. Antiviral Research, 2009, 84, 48-59.	4.1	19
33	Protein-Protein Interaction Inhibition (2P2I): Fewer and Fewer Undruggable Targets. Combinatorial Chemistry and High Throughput Screening, 2009, 12, 968-983.	1.1	11
34	Proteinâ€“protein interaction inhibition (2P2I) combining high throughput and virtual screening: Application to the HIV-1 Nef protein. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19256-19261.	7.1	116
35	GFscore:Â A General Nonlinear Consensus Scoring Function for High-Throughput Docking. Journal of Chemical Information and Modeling, 2006, 46, 1704-1712.	5.4	52