Dominique Douguet

List of Publications by Year
in descending order

43 papers	3,589 citations	218592 26 h-index	254106 43 g-index
46 all docs	46 docs citations	46 times ranked	5728 citing authors

#	Article	IF	Citations
1	Mambalgin-1 pain-relieving peptide locks the hinge between Î±4 and Î±5 helices to inhibit rat acid-sensing ion channel 1a. Neuropharmacology, 2021, 185, 108453.	2.0	10
2	<scp>sensaas</scp>: Shapeâ€based Alignment by Registration of Colored Pointâ€based Surfaces. Molecular Informatics, 2020, 39, e2000081.	1.4	3
3	Structure and function of polycystins: insights into polycystic kidney disease. Nature Reviews Nephrology, 2019, 15, 412-422.	4.1	38
4	Data Sets Representative of the Structures and Experimental Properties of FDA-Approved Drugs. ACS Medicinal Chemistry Letters, 2018, 9, 204-209.	1.3	40
5	Computational analysis of calculated physicochemical and ADMET properties of protein-protein interaction inhibitors. Scientific Reports, 2017, 7, 46277.	1.6	128
6	Stability of the Plasmodium falciparum AMA1-RON2 Complex Is Governed by the Domain II (DII) Loop. PLoS ONE, 2016, 11, e0144764.	1.1	17
7	Comparison of the ligand binding site of CYP2C8 with CYP26A1 and CYP26B1: a structural basis for the identification of new inhibitors of the retinoic acid hydroxylases. Journal of Enzyme Inhibition and Medicinal Chemistry, 2016, 31, 148-161.	2.5	9
8	Fragment-based discovery of a new family of non-peptidic small-molecule cyclophilin inhibitors with potent antiviral activities. Nature Communications, 2016, 7, 12777.	5.8	67
9	Mambalgin-1 Pain-relieving Peptide, Stepwise Solid-phase Synthesis, Crystal Structure, and Functional Domain for Acid-sensing Ion Channel 1a Inhibition. Journal of Biological Chemistry, 2016, 291, 2616-2629.	1.6	41
10	Identification of Tazarotenic Acid as the First Xenobiotic Substrate of Human Retinoic Acid Hydroxylase CYP26A1 and CYP26B1. Journal of Pharmacology and Experimental Therapeutics, 2016, 357, 281-292.	1.3	11
11	Kinetics and Thermodynamics of Apicomplexa AMA1-RON2Sp Interaction. Biophysical Journal, 2015, 108, 344a.	0.2	0
12	Plasmodium falciparum CTP:phosphocholine cytidylyltransferase possesses two functional catalytic domains and is inhibited by a CDPâ€choline analog selected from a virtual screening. FEBS Letters, 2015, 589, 992-1000.	1.3	13
13	Computational and biophysical approaches to proteinâ€“protein interaction inhibition of Plasmodium falciparum AMA1/RON2 complex. Journal of Computer-Aided Molecular Design, 2015, 29, 525-539.	1.3	16
14	Binding Site and Inhibitory Mechanism of the Mambalgin-2 Pain-relieving Peptide on Acid-sensing Ion Channel 1a. Journal of Biological Chemistry, 2014, 289, 13363-13373.	1.6	50
15	Biochemical characterization of Plasmodium falciparum CTP:phosphoethanolamine cytidylyltransferase shows that only one of the two cytidylyltransferase domains is active. Biochemical Journal, 2013, 450, 159-167.	1.7	10
16	Silencing of the Tandem Pore Domain Halothane-inhibited K+ Channel 2 (THIK2) Relies on Combined Intracellular Retention and Low Intrinsic Activity at the Plasma Membrane. Journal of Biological Chemistry, 2013, 288, 35081-35092.	1.6	25
17	TWIK1, a unique background channel with variable ion selectivity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5499-5504.	3.3	85
18	e-Drug3D: 3D structure collections dedicated to drug repurposing and fragment-based drug design. Bioinformatics, 2012, 28, 1540-1541.	1.8	102

#	Article	IF	Citations
19	Black mamba venom peptides target acid-sensing ion channels to abolish pain. Nature, 2012, 490, 552-555.	13.7	344
20	Host Cell Invasion by Apicomplexan Parasites: Insights from the Co-Structure of AMA1 with a RON2 Peptide. Science, 2011, 333, 463-467.	6.0	168
21	Osh4p exchanges sterols for phosphatidylinositol 4-phosphate between lipid bilayers. Journal of Cell Biology, 2011, 195, 965-978.	2.3	343
22	Group X Secreted Phospholipase A2 Proenzyme Is Matured by a Furin-like Proprotease and Releases Arachidonic Acid inside of Human HEK293 Cells. Journal of Biological Chemistry, 2011, 286, 36509-36521.	1.6	32
23	Functional characterization of the AFF (AF4/FMR2) family of RNA-binding proteins: insights into the molecular pathology of FRAXE intellectual disability. Human Molecular Genetics, 2011, 20, 1873-1885.	1.4	63
24	e-LEA3D: a computational-aided drug design web server. Nucleic Acids Research, 2010, 38, W615-W621.	6.5	107
25	Inhibition of Adrenocortical Carcinoma Cell Proliferation by Steroidogenic Factor-1 Inverse Agonists. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 2178-2183.	1.8	77
26	Extracellular acidification exerts opposite actions on TREK1 and TREK2 potassium channels via a single conserved histidine residue. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14628-14633.	3.3	122
27	Exploring Acyclic Nucleoside Analogues as Inhibitors of Mycobacterium tuberculosis Thymidylate Kinase. ChemMedChem, 2008, 3, 1083-1093.	1.6	33
28	Substituted benzyl-pyrimidines targeting thymidine monophosphate kinase of Mycobacterium tuberculosis: Synthesis and in vitro anti-mycobacterial activity. Bioorganic and Medicinal Chemistry, 2008, 16, 6075-6085.	1.4	79
29	HELIQUEST: a web server to screen sequences with specific Î±-helical properties. Bioinformatics, 2008, 24, 2101-2102.	1.8	928
30	LARGE-SCALE STRUCTURAL MODELING OF PROTEIN COMPLEXES AT LOW RESOLUTION. Journal of Bioinformatics and Computational Biology, 2008, 06, 789-810.	0.3	6
31	From Molecular Modeling to Drug Design. Nucleic Acids and Molecular Biology, 2008, , 35-71.	0.2	3
32	Ligand-Based Approaches in Virtual Screening. Current Computer-Aided Drug Design, 2008, 4, 180-190.	0.8	22
33	D<scp>OCKGROUND</scp> system of databases for protein recognition studies: Unbound structures for docking. Proteins: Structure, Function and Bioinformatics, 2007, 69, 845-851.	1.5	65
34	The Pleckstrin Homology Domain of Phospholipase CÎ² Transmits Enzymatic Activation through Modulation of the Membraneâ˜Domain Orientation. Biochemistry, 2006, 45, 5712-5724.	1.2	20
35	DOCKGROUND resource for studying protein-protein interfaces. Bioinformatics, 2006, 22, 2612-2618.	1.8	76
36	LEA3D: A Computer-Aided Ligand Design for Structure-Based Drug Design. Journal of Medicinal Chemistry, 2005, 48, 2457-2468.	2.9	145

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37	Comparative modelling and immunochemical reactivity of Escherichia coli UMP kinase. Biochemical and Biophysical Research Communications, 2002, 294, 173-179.	1.0	17
38	Diacylglyceride kinases, sphingosine kinases and NAD kinases: distant relatives of 6-phosphofructokinases. Trends in Biochemical Sciences, 2002, 27, 273-275.	3.7	74
39	Nucleoside Analogues as Inhibitors of Thymidylate Kinases: Possible Therapeutic Applications. ChemBioChem, 2002, 3, 108-110.	1.3	31
40	From sequence to structure to function: a case study. Enzyme and Microbial Technology, 2002, 30, 289-294.	1.6	4
41	A genetic algorithm for the automated generation of small organic molecules: drug design using an evolutionary algorithm. Journal of Computer-Aided Molecular Design, 2000, 14, 449-466.	1.3	128
42	Quantitative structure-activity relationship studies of RAR Î±, Î²2, Î³3 retinoid agonists. QSAR and Combinatorial Science, 1999, 18, 107-123.	1.4	5
43	The Adsorption of Argon and Nitrogen in Silicalite-1 Zeolite: A Grand Canonical Monte-Carlo study. Molecular Simulation, 1996, 17, 255-288.	0.9	30