

Dominique Douguet

List of Publications by Year in descending order

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43
papers

3,589
citations

218381

26
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253896

43
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46
all docs

46
docs citations

46
times ranked

5728
citing authors

#	ARTICLE	IF	CITATIONS
1	HELIQUEST: a web server to screen sequences with specific α -helical properties. <i>Bioinformatics</i> , 2008, 24, 2101-2102.	1.8	928
2	Black mamba venom peptides target acid-sensing ion channels to abolish pain. <i>Nature</i> , 2012, 490, 552-555.	13.7	344
3	Osh4p exchanges sterols for phosphatidylinositol 4-phosphate between lipid bilayers. <i>Journal of Cell Biology</i> , 2011, 195, 965-978.	2.3	343
4	Host Cell Invasion by Apicomplexan Parasites: Insights from the Co-Structure of AMA1 with a RON2 Peptide. <i>Science</i> , 2011, 333, 463-467.	6.0	168
5	LEA3D: A Computer-Aided Ligand Design for Structure-Based Drug Design. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 2457-2468.	2.9	145
6	A genetic algorithm for the automated generation of small organic molecules: drug design using an evolutionary algorithm. <i>Journal of Computer-Aided Molecular Design</i> , 2000, 14, 449-466.	1.3	128
7	Computational analysis of calculated physicochemical and ADMET properties of protein-protein interaction inhibitors. <i>Scientific Reports</i> , 2017, 7, 46277.	1.6	128
8	Extracellular acidification exerts opposite actions on TREK1 and TREK2 potassium channels via a single conserved histidine residue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14628-14633.	3.3	122
9	e-LEA3D: a computational-aided drug design web server. <i>Nucleic Acids Research</i> , 2010, 38, W615-W621.	6.5	107
10	e-Drug3D: 3D structure collections dedicated to drug repurposing and fragment-based drug design. <i>Bioinformatics</i> , 2012, 28, 1540-1541.	1.8	102
11	TWIK1, a unique background channel with variable ion selectivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5499-5504.	3.3	85
12	Substituted benzyl-pyrimidines targeting thymidine monophosphate kinase of <i>Mycobacterium tuberculosis</i> : Synthesis and in vitro anti-mycobacterial activity. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 6075-6085.	1.4	79
13	Inhibition of Adrenocortical Carcinoma Cell Proliferation by Steroidogenic Factor-1 Inverse Agonists. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2009, 94, 2178-2183.	1.8	77
14	DOCKGROUND resource for studying protein-protein interfaces. <i>Bioinformatics</i> , 2006, 22, 2612-2618.	1.8	76
15	Diacylglyceride kinases, sphingosine kinases and NAD kinases: distant relatives of 6-phosphofructokinases. <i>Trends in Biochemical Sciences</i> , 2002, 27, 273-275.	3.7	74
16	Fragment-based discovery of a new family of non-peptidic small-molecule cyclophilin inhibitors with potent antiviral activities. <i>Nature Communications</i> , 2016, 7, 12777.	5.8	67
17	DOCKGROUND system of databases for protein recognition studies: Unbound structures for docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 845-851.	1.5	65
18	Functional characterization of the AFF (AF4/FMR2) family of RNA-binding proteins: insights into the molecular pathology of FRAXE intellectual disability. <i>Human Molecular Genetics</i> , 2011, 20, 1873-1885.	1.4	63

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19	Binding Site and Inhibitory Mechanism of the Mambalgin-2 Pain-relieving Peptide on Acid-sensing Ion Channel 1a. <i>Journal of Biological Chemistry</i> , 2014, 289, 13363-13373.	1.6	50
20	Mambalgin-1 Pain-relieving Peptide, Stepwise Solid-phase Synthesis, Crystal Structure, and Functional Domain for Acid-sensing Ion Channel 1a Inhibition. <i>Journal of Biological Chemistry</i> , 2016, 291, 2616-2629.	1.6	41
21	Data Sets Representative of the Structures and Experimental Properties of FDA-Approved Drugs. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 204-209.	1.3	40
22	Structure and function of polycystins: insights into polycystic kidney disease. <i>Nature Reviews Nephrology</i> , 2019, 15, 412-422.	4.1	38
23	Exploring Acyclic Nucleoside Analogues as Inhibitors of <i>Mycobacterium tuberculosis</i> Thymidylate Kinase. <i>ChemMedChem</i> , 2008, 3, 1083-1093.	1.6	33
24	Group X Secreted Phospholipase A2 Proenzyme Is Matured by a Furin-like Proprotein Convertase and Releases Arachidonic Acid inside of Human HEK293 Cells. <i>Journal of Biological Chemistry</i> , 2011, 286, 36509-36521.	1.6	32
25	Nucleoside Analogues as Inhibitors of Thymidylate Kinases: Possible Therapeutic Applications. <i>ChemBioChem</i> , 2002, 3, 108-110.	1.3	31
26	The Adsorption of Argon and Nitrogen in Silicalite-1 Zeolite: A Grand Canonical Monte-Carlo study. <i>Molecular Simulation</i> , 1996, 17, 255-288.	0.9	30
27	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. <i>Journal of Biological Chemistry</i> , 2013, 288, 35081-35092.	1.6	25
28	Ligand-Based Approaches in Virtual Screening. <i>Current Computer-Aided Drug Design</i> , 2008, 4, 180-190.	0.8	22
29	The Pleckstrin Homology Domain of Phospholipase C β Transmits Enzymatic Activation through Modulation of the Membrane Domain Orientation. <i>Biochemistry</i> , 2006, 45, 5712-5724.	1.2	20
30	Comparative modelling and immunochemical reactivity of Escherichia coli UMP kinase. <i>Biochemical and Biophysical Research Communications</i> , 2002, 294, 173-179.	1.0	17
31	Stability of the Plasmodium falciparum AMA1-RON2 Complex Is Governed by the Domain II (DII) Loop. <i>PLoS ONE</i> , 2016, 11, e0144764.	1.1	17
32	Computational and biophysical approaches to protein-protein interaction inhibition of Plasmodium falciparum AMA1/RON2 complex. <i>Journal of Computer-Aided Molecular Design</i> , 2015, 29, 525-539.	1.3	16
33	<i>Plasmodium falciparum</i> CTP:phosphocholine cytidyltransferase possesses two functional catalytic domains and is inhibited by a CDP-choline analog selected from a virtual screening. <i>FEBS Letters</i> , 2015, 589, 992-1000.	1.3	13
34	Identification of Tazarotenic Acid as the First Xenobiotic Substrate of Human Retinoic Acid Hydroxylase CYP26A1 and CYP26B1. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2016, 357, 281-292.	1.3	11
35	Biochemical characterization of <i>Plasmodium falciparum</i> CTP:phosphoethanolamine cytidyltransferase shows that only one of the two cytidyltransferase domains is active. <i>Biochemical Journal</i> , 2013, 450, 159-167.	1.7	10
36	Mambalgin-1 pain-relieving peptide locks the hinge between α 4 and α 5 helices to inhibit rat acid-sensing ion channel 1a. <i>Neuropharmacology</i> , 2021, 185, 108453.	2.0	10

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37	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. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2016, 31, 148-161.	2.5	9
38	LARGE-SCALE STRUCTURAL MODELING OF PROTEIN COMPLEXES AT LOW RESOLUTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 789-810.	0.3	6
39	Quantitative structure-activity relationship studies of RAR $\hat{1}$, $\hat{2}$, $\hat{3}$ retinoid agonists. <i>QSAR and Combinatorial Science</i> , 1999, 18, 107-123.	1.4	5
40	From sequence to structure to function: a case study. <i>Enzyme and Microbial Technology</i> , 2002, 30, 289-294.	1.6	4
41	<scp>sensaas</scp>: Shape-based Alignment by Registration of Colored Point-based Surfaces. <i>Molecular Informatics</i> , 2020, 39, e2000081.	1.4	3
42	From Molecular Modeling to Drug Design. <i>Nucleic Acids and Molecular Biology</i> , 2008, , 35-71.	0.2	3
43	Kinetics and Thermodynamics of Apicomplexa AMA1-RON2Sp Interaction. <i>Biophysical Journal</i> , 2015, 108, 344a.	0.2	0