## Rachid C Maroun Or Rachid Maroun

List of Publications by Year in descending order

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## Rachid C Maroun Or Rachid

#	Article	IF	CITATIONS
1	Snake venom serine proteinases: sequence homology vs. substrate specificity, a paradox to be solved. Toxicon, 2005, 45, 1115-1132.	1.6	287
2	Multiplex epithelium dysfunction due to CLDN10 mutation: the HELIX syndrome. Genetics in Medicine, 2018, 20, 190-201.	2.4	75
3	Base sequence effects in double-helical DNA. III. Average properties of curved dna. Biopolymers, 1988, 27, 585-603.	2.4	65
4	Trimeresurus stejnegeri Snake Venom Plasminogen Activator. Journal of Biological Chemistry, 1997, 272, 20531-20537.	3.4	55
5	Deciphering the GPER/GPR30-agonist and antagonists interactions using molecular modeling studies, molecular dynamics, and docking simulations. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2161-2172.	3.5	53
6	Base sequence effects in double-helical DNA. II. Configurational statistics of rodlike chains. Biopolymers, 1988, 27, 561-584.	2.4	47
7	Characterization of a human coagulation factor Xa-binding site on Viperidae snake venom phospholipases A2 by affinity binding studies and molecular bioinformatics. BMC Structural Biology, 2007, 7, 82.	2.3	47
8	Toxicity evolution ofVipera aspis aspisvenom: identification and molecular modeling of a novel phospholipase A2heterodimer neurotoxin1. FEBS Letters, 2002, 527, 263-268.	2.8	42
9	The Contribution of Residues 192 and 193 to the Specificity of Snake Venom Serine Proteinases. Journal of Biological Chemistry, 2000, 275, 1823-1828.	3.4	37
10	Identification and molecular structural prediction analysis of a toxicity determinant in the Bacillus sphaericus crystal larvicidal toxin. FEBS Journal, 2001, 268, 2751-2760.	0.2	37
11	Solution conformations of the pituitary opioid peptide dynorphin-(1–13). Biochemical and Biophysical Research Communications, 1981, 103, 442-446.	2.1	32
12	Entamoeba histolytica: inhibition of cellular functions by overexpression of EhGEF1, a novel Rho/Rac guanine nucleotide exchange factor. Experimental Parasitology, 2005, 109, 150-162.	1.2	32
13	YB-1, an abundant core mRNA-binding protein, has the capacity to form an RNA nucleoprotein filament: a structural analysis. Nucleic Acids Research, 2019, 47, 3127-3141.	14.5	32
14	Synthesis and structure-activity studies of a series of [(hydroxybenzyl)amino]salicylates as inhibitors of EGF receptor-associated tyrosine kinase activity. Journal of Medicinal Chemistry, 1993, 36, 4094-4098.	6.4	31
15	Combining phage display and molecular modeling to map the epitope of a neutralizing antitoxin antibody. FEBS Journal, 2000, 267, 2345-2353.	0.2	20
16	Bioinformatics and Functional Analysis of an Entamoeba histolytica Mannosyltransferase Necessary for Parasite Complement Resistance and Hepatical Infection. PLoS Neglected Tropical Diseases, 2008, 2, e165.	3.0	20
17	1H and 31P nuclear magnetic resonance studies of the differences in DNA deformation induced by anti-tumoral 7H-pyrido[4,3-c]carbazole dimers. Journal of Molecular Biology, 1989, 210, 211-228.	4.2	19
18	Preferred antagonist binding state of the N-methyl-D-aspartate receptor: synthesis, pharmacology, and computer modeling of (phosphonomethyl)phenylalanine derivatives. Journal of Medicinal Chemistry, 1992, 35, 2551-2562.	6.4	19

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19	Mutations in zinc finger 407 [ZNF407] cause a unique autosomal recessive cognitive impairment syndrome. Orphanet Journal of Rare Diseases, 2014, 9, 80.	2.7	17
20	Identification of the substrate-binding exosites of two snake venom serine proteinases: molecular basis for the partition of two essential functions of thrombin. Journal of Molecular Recognition, 2004, 17, 51-61.	2.1	15
21	Lin28, a major translation reprogramming factor, gains access to YB-1-packaged mRNA through its cold-shock domain. Communications Biology, 2021, 4, 359.	4.4	13
22	Intercalative Binding of Ditercalinium to d(CpGpCpG) <sub>2</sub> : A Theoretical Study. Journal of Biomolecular Structure and Dynamics, 1989, 7, 607-621.	3.5	11
23	A theoretical investigation of the intercalative binding of 7-H pyrido[4.3C]carbazole chromophore into a d(CpG)2 minihelix. Biopolymers, 1989, 28, 835-849.	2.4	6
24	Homology modeling of the structure of acyl coA:isopenicillin N-acyltransferase (IAT) from Penicillium chrysogenum. IAT interaction studies with isopenicillin-N, combining molecular dynamics simulations and docking. Journal of Molecular Modeling, 2012, 18, 1189-1205.	1.8	5
25	Getting to know each other: PPIMem, a novel approach for predicting transmembrane protein-protein complexes. Computational and Structural Biotechnology Journal, 2021, 19, 5184-5197.	4.1	5
26	Electrostatic interactions in ionic homopolypeptides in solutions of moderate ionic strength. Biopolymers, 1981, 20, 2181-2194.	2.4	4
27	Molecular dynamics of the histamine H3 membrane receptor reveals different mechanisms of GPCR signal transduction. Scientific Reports, 2020, 10, 16889.	3.3	4
28	Induction of DNA bending by bifunctional intercalating agents of the 7H-pyridocarbazole family. Biophysical Chemistry, 1991, 39, 45-56.	2.8	2
29	Triangular matrix representation of dimensionless helical hydrophobic moment ratios. International Journal of Biological Macromolecules, 1986, 8, 73-78.	7.5	1
30	Molecular Modeling of an Active Loop Structure in Lysozyme. Sequence Effects or Crystal Packing?. Journal of Biomolecular Structure and Dynamics, 1999, 16, 873-889.	3.5	1
31	Influence of I-cystinyl side-chain configurations on the melting of crosslinked α-tropomyosin dimers. BBA - Proteins and Proteomics, 1984, 784, 133-139.	2.1	0
32	Why computational methods for the study of biological macromolecules and their effectors?. BoletÃn Médico Del Hospital Infantil De México, 2016, 73, 363-364.	0.3	0