Rachid C Maroun Or Rachid Maroun

List of Publications by Year
in descending order

32 papers	1,035 citations	430874 18 h-index	454955 30 g-index
34 all docs	34 docs citations	34 times ranked	1266 citing authors

#	Article	IF	Citations
1	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
2	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
3	Molecular dynamics of the histamine H3 membrane receptor reveals different mechanisms of GPCR signal transduction. Scientific Reports, 2020, 10, 16889.	3.3	4
4	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
5	Multiplex epithelium dysfunction due to CLDN10 mutation: the HELIX syndrome. Genetics in Medicine, 2018, 20, 190-201.	2.4	75
6	Why computational methods for the study of biological macromolecules and their effectors?. BoletÃn MÃ©dico Del Hospital Infantil De MÃ©xico, 2016, 73, 363-364.	0.3	0
7	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
8	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
9	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
10	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
11	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
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	Snake venom serine proteinases: sequence homology vs. substrate specificity, a paradox to be solved. Toxicon, 2005, 45, 1115-1132.	1.6	287
14	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
15	Toxicity evolution ofVipera aspis aspisvenom: identification and molecular modeling of a novel phospholipase A2heterodimer neurotoxin1. FEBS Letters, 2002, 527, 263-268.	2.8	42
16	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
17	Combining phage display and molecular modeling to map the epitope of a neutralizing antitoxin antibody. FEBS Journal, 2000, 267, 2345-2353.	0.2	20
18	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

#	Article	IF	Citations
19	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
20	Trimeresurus stejnegeri Snake Venom Plasminogen Activator. Journal of Biological Chemistry, 1997, 272, 20531-20537.	3.4	55
21	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
22	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
23	Induction of DNA bending by bifunctional intercalating agents of the 7H-pyridocarbazole family. Biophysical Chemistry, 1991, 39, 45-56.	2.8	2
24	Intercalative Binding of Ditercalinium to d(CpGpCpG)₂: A Theoretical Study. Journal of Biomolecular Structure and Dynamics, 1989, 7, 607-621.	3.5	11
25	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
26	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
27	Base sequence effects in double-helical DNA. II. Configurational statistics of rodlike chains. Biopolymers, 1988, 27, 561-584.	2.4	47
28	Base sequence effects in double-helical DNA. III. Average properties of curved dna. Biopolymers, 1988, 27, 585-603.	2.4	65
29	Triangular matrix representation of dimensionless helical hydrophobic moment ratios. International Journal of Biological Macromolecules, 1986, 8, 73-78.	7.5	1
30	Influence of l-cystinyl side-chain configurations on the melting of crosslinked Î±-tropomyosin dimers. BBA - Proteins and Proteomics, 1984, 784, 133-139.	2.1	0
31	Solution conformations of the pituitary opioid peptide dynorphin-(1â€“13). Biochemical and Biophysical Research Communications, 1981, 103, 442-446.	2.1	32
32	Electrostatic interactions in ionic homopolypeptides in solutions of moderate ionic strength. Biopolymers, 1981, 20, 2181-2194.	2.4	4