

Benjamin Chagot

List of Publications by Year in descending order

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516710

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docs citations

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times ranked

1367
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards improved understanding of intersubunit interactions in modular polyketide biosynthesis: Docking in the enacyloxin IIa polyketide synthase. <i>Journal of Structural Biology</i> , 2020, 212, 107581.	2.8	9
2	Insights into a dual function amide oxidase/macrocyclase from lankacidin biosynthesis. <i>Nature Communications</i> , 2018, 9, 3998.	12.8	17
3	Characterization of Intersubunit Communication in the Virginiamycin <i>trans</i> -Acyl Transferase Polyketide Synthase. <i>Journal of the American Chemical Society</i> , 2016, 138, 4155-4167.	13.7	42
4	Bacteriophage SPP1 Tail Tube Protein Self-assembles into β^2 -Structure-rich Tubes. <i>Journal of Biological Chemistry</i> , 2015, 290, 3836-3849.	3.4	24
5	Insights into the function of trans-acyl transferase polyketide synthases from the SAXS structure of a complete module. <i>Chemical Science</i> , 2014, 5, 3081-3095.	7.4	33
6	Function of polyketide synthases from the SAXS structure of a complete module. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C407-C407.	0.1	0
7	Inhibition of Histone Deacetylase 3 Causes Replication Stress in Cutaneous T Cell Lymphoma. <i>PLoS ONE</i> , 2013, 8, e68915.	2.5	87
8	NMR Studies of the Interaction of Calmodulin with IQ Motif Peptides. <i>Methods in Molecular Biology</i> , 2013, 963, 173-186.	0.9	6
9	Solution structure of gp17 from the <i>Siphoviridae</i> bacteriophage SPP1: Insights into its role in virion assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 319-326.	2.6	15
10	Mapping Residues that Influence Fast Inactivation Within Ca-Sensing Domains in the Nav1.5 C-Terminus. <i>Biophysical Journal</i> , 2011, 100, 423a.	0.5	1
11	Solution NMR Structure of Apo-Calmodulin in Complex with the IQ Motif of Human Cardiac Sodium Channel NaV1.5. <i>Journal of Molecular Biology</i> , 2011, 406, 106-119.	4.2	105
12	Solution NMR Structure of the C-terminal DNA Binding Domain of Mcm10 Reveals a Conserved MCM Motif. <i>Journal of Biological Chemistry</i> , 2010, 285, 22942-22949.	3.4	19
13	Structure-Function Analysis of Inositol Hexakisphosphate-induced Autoprocessing in <i>Clostridium difficile</i> Toxin A. <i>Journal of Biological Chemistry</i> , 2009, 284, 21934-21940.	3.4	99
14	Solution NMR Structure of the C-terminal EF-hand Domain of Human Cardiac Sodium Channel NaV1.5. <i>Journal of Biological Chemistry</i> , 2009, 284, 6436-6445.	3.4	65
15	Functional Interactions between Distinct Sodium Channel Cytoplasmic Domains through the Action of Calmodulin. <i>Journal of Biological Chemistry</i> , 2009, 284, 8846-8854.	3.4	76
16	Solution structure of PcFK1, a spider peptide active against <i>Plasmodium falciparum</i> . <i>Protein Science</i> , 2006, 15, 628-634.	7.6	24
17	An unusual fold for potassium channel blockers: NMR structure of three toxins from the scorpion <i>Opisthacanthus madagascariensis</i> . <i>Biochemical Journal</i> , 2005, 388, 263-271.	3.7	73
18	Solution structure of APETx2, a specific peptide inhibitor of ASIC3 proton-gated channels. <i>Protein Science</i> , 2005, 14, 2003-2010.	7.6	61

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19	Solution structure of two insect-specific spider toxins and their pharmacological interaction with the insect voltage-gated Na ⁺ channel. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 368-379.	2.6	31
20	Solution structure of APETx1 from the sea anemone <i>Anthopleura elegantissima</i> : A new fold for an HERG toxin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 380-386.	2.6	35
21	Increasing the molecular contacts between maurotoxin and Kv1.2 channel augments ligand affinity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 401-411.	2.6	10
22	Solution structure of Phrixotoxin 1, a specific peptide inhibitor of Kv4 potassium channels from the venom of the theraphosid spider <i>Phrixotrichus auratus</i> . <i>Protein Science</i> , 2004, 13, 1197-1208.	7.6	47