

# Gloria Saab-Rincon

## List of Publications by Year in descending order

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40  
papers

1,108  
citations

430874

18  
h-index

395702

33  
g-index

42  
all docs

42  
docs citations

42  
times ranked

1414  
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering a calcium-dependent conformational change in Calbindin D9k by secondary elements replacement. Archives of Biochemistry and Biophysics, 2021, 714, 109065.	3.0	0
2	Modulating Glycoside Hydrolase Activity between Hydrolysis and Transfer Reactions Using an Evolutionary Approach. Molecules, 2021, 26, 6586.	3.8	5
3	Thermal diffusivity monitoring during the stages of formation of core-shell structures of SiO <sub>2</sub> @Au. Applied Physics A: Materials Science and Processing, 2020, 126, 1.	2.3	4
4	Structural characterization of scorpion peptides and their bactericidal activity against clinical isolates of multidrug-resistant bacteria. PLoS ONE, 2019, 14, e0222438.	2.5	19
5	Deep Eutectic Solvents as New Reaction Media to Produce Alkyl-Glycosides Using Alpha-Amylase from <i>Thermotoga maritima</i> . International Journal of Molecular Sciences, 2019, 20, 5439.	4.1	11
6	Biochemical Characterization of a Novel $\beta$ -Hydrolase/FSH from the White Shrimp <i>Litopenaeus vannamei</i> . Biomolecules, 2019, 9, 674.	4.0	4
7	Stabilization of the Reductase Domain in the Catalytically Self-Sufficient Cytochrome P450 <sub>BM3</sub> by Consensus-Guided Mutagenesis. ChemBioChem, 2018, 19, 622-632.	2.6	19
8	Spiked Genes: A Method to Introduce Random Point Nucleotide Mutations Evenly throughout an Entire Gene Using a Complete Set of Spiked Oligonucleotides for the Assembly. ACS Omega, 2017, 2, 3183-3191.	3.5	7
9	The Unstructured N-terminal Region of Arabidopsis Group 4 Late Embryogenesis Abundant (LEA) Proteins Is Required for Folding and for Chaperone-like Activity under Water Deficit. Journal of Biological Chemistry, 2016, 291, 10893-10903.	3.4	61
10	Identification of fibrillogenic regions in human triosephosphate isomerase. PeerJ, 2016, 4, e1676.	2.0	3
11	Acceptor-induced modification of regioselectivity in CGTase-catalyzed glycosylations of p-nitrophenyl-glucopyranosides. Carbohydrate Research, 2015, 404, 46-54.	2.3	8
12	A Group 6 Late Embryogenesis Abundant Protein from Common Bean Is a Disordered Protein with Extended Helical Structure and Oligomer-forming Properties. Journal of Biological Chemistry, 2014, 289, 31995-32009.	3.4	33
13	Characteristics and safety assessment of intractable proteins in genetically modified crops. Regulatory Toxicology and Pharmacology, 2014, 69, 154-170.	2.7	44
14	Kinetics and conformational stability studies of recombinant leucine aminopeptidase. International Journal of Biological Macromolecules, 2014, 64, 306-312.	7.5	5
15	Bacillus thuringiensis Cry1Ab mutants affecting oligomer formation are non-toxic to Manduca sexta larvae.. Journal of Biological Chemistry, 2013, 288, 8560.	3.4	2
16	Alternative Splice Variants in TIM Barrel Proteins from Human Genome Correlate with the Structural and Evolutionary Modularity of this Versatile Protein Fold. PLoS ONE, 2013, 8, e70582.	2.5	7
17	Evolutionary Walk between $(\beta/\alpha)_8$ Barrels: Catalytic Migration from Triosephosphate Isomerase to Thiamin Phosphate Synthase. Journal of Molecular Biology, 2012, 416, 255-270.	4.2	17
18	Cellular and biochemical characterization of two closely related triosephosphate isomerases from <i>Trichomonas vaginalis</i> . Parasitology, 2012, 139, 1729-1738.	1.5	18

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19	The $\beta$ 21 domain of protein G can replace the chorismate mutase domain of the $\beta$ protein. FEBS Letters, 2012, 586, 466-471.	2.8	2
20	Exploring the Structure-Function Loop Adaptability of a $(\beta/\beta)_8$ -Barrel Enzyme through Loop Swapping and Hinge Variability. Journal of Molecular Biology, 2011, 411, 143-157.	4.2	37
21	Transglycosylation reactions of <i>Thermotoga maritima</i> $\beta$ -amylase. Enzyme and Microbial Technology, 2010, 46, 331-337.	3.2	17
22	Oligomerization of Cry11Aa from <i>Bacillus thuringiensis</i> Has an Important Role in Toxicity against <i>Aedes aegypti</i> . Applied and Environmental Microbiology, 2009, 75, 7548-7550.	3.1	26
23	Domain II Loop 3 of <i>Bacillus thuringiensis</i> Cry1Ab Toxin Is Involved in a "Ping Pong" Binding Mechanism with <i>Manduca sexta</i> Aminopeptidase-N and Cadherin Receptors. Journal of Biological Chemistry, 2009, 284, 32750-32757.	3.4	118
24	Protein Design through Systematic Catalytic Loop Exchange in the $(\beta/\beta)_8$ Fold. Journal of Molecular Biology, 2009, 387, 949-964.	4.2	28
25	Protein Engineering of Redox-Active Enzymes. Antioxidants and Redox Signaling, 2009, 11, 167-192.	5.4	17
26	Role of the phenylalanine 260 residue in defining product profile and alcoholic activity of the $\beta$ -amylase AmyA from <i>Thermotoga maritima</i> . Biologia (Poland), 2008, 63, 1035-1043.	1.5	1
27	Sensitive Genome-Wide Screen for Low Secondary Enzymatic Activities: The YjbQ Family Shows Thiamin Phosphate Synthase Activity. Journal of Molecular Biology, 2008, 376, 839-853.	4.2	22
28	Enhancement of the Alcoholic Activity of $\beta$ -Amylase AmyA from <i>Thermotoga maritima</i> MSB8 (DSM 3109) by Site-Directed Mutagenesis. Applied and Environmental Microbiology, 2008, 74, 5168-5177.	3.1	15
29	<i>Bacillus thuringiensis</i> Cry1Ab Mutants Affecting Oligomer Formation Are Non-toxic to <i>Manduca sexta</i> Larvae. Journal of Biological Chemistry, 2007, 282, 21222-21229.	3.4	101
30	Generation of variability by in vivo recombination of halves of a $(\beta/\beta)_8$ barrel protein. New Biotechnology, 2005, 22, 113-120.	2.7	1
31	A more Efficient Starch Degradation by the Combination of Hydrolase and Transferase Activities of $\beta$ -Amylase and Cyclomaltodextrin Glucanotransferase. Starch/Staerke, 2004, 56, 63-68.	2.1	6
32	In vivo fragment complementation of a $(\beta/\beta)_8$ barrel protein: generation of variability by recombination. FEBS Letters, 2004, 560, 167-172.	2.8	18
33	Systematic discovery of analogous enzymes in thiamin biosynthesis. Nature Biotechnology, 2003, 21, 790-795.	17.5	121
34	$\beta$ -Amylase from <i>Bacillus licheniformis</i> mutants near to the catalytic site: effects on hydrolytic and transglycosylation activity. Protein Engineering, Design and Selection, 2003, 16, 505-514.	2.1	40
35	Unfolding of Triosephosphate Isomerase from <i>Trypanosoma brucei</i> : Identification of Intermediates and Insight into the Denaturation Pathway Using Tryptophan Mutants. Archives of Biochemistry and Biophysics, 2002, 399, 117-129.	3.0	41
36	High Temperature Biocatalysis by Chemically Modified Cytochrome c. Bioconjugate Chemistry, 2002, 13, 1336-1344.	3.6	67

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37	Different strategies to recover the activity of monomeric triosephosphate isomerase by directed evolution. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 149-155.	2.1	30
38	Introducing transglycosylation activity in a liquefying $\alpha$ -amylase. <i>FEBS Letters</i> , 1999, 453, 100-106.	2.8	25
39	Mutagenic and Thermodynamic Analyses of Residual Structure in the $\alpha$ Subunit of Tryptophan Synthase. <i>Biochemistry</i> , 1996, 35, 1988-1994.	2.5	58
40	Urea-induced unfolding of the $\alpha$ subunit of tryptophan synthase: One-dimensional proton NMR evidence for residual structure near histidine-92 at high denaturant concentration. <i>Biochemistry</i> , 1993, 32, 13981-13990.	2.5	49