Jose Miguel MancheÃ±o

List of Publications by Year
in descending order

86	3,472	32	56
papers	citations	h-index	g-index
		136950	149698

86	86	86	3554
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Biochemical and structural studies of two tetrameric nucleoside 2â€²-deoxyribosyltransferases from psychrophilic and mesophilic bacteria: Insights into cold-adaptation. International Journal of Biological Macromolecules, 2021, 192, 138-150.	7.5	4
2	A structurally unique Fusobacterium nucleatum tannase provides detoxicant activity against gallotannins and pathogen resistance. Microbial Biotechnology, 2020, , .	4.2	3
3	Identification of a highly active tannase enzyme from the oral pathogen Fusobacterium nucleatum subsp. polymorphum. Microbial Cell Factories, 2018, 17, 33.	4.0	17
4	2â€²-Deoxyribosyltransferase from Bacillus psychrosaccharolyticus: A Mesophilic-Like Biocatalyst for the Synthesis of Modified Nucleosides from a Psychrotolerant Bacterium. Catalysts, 2018, 8, 8.	3.5	18
5	Enzymatic Synthesis of Therapeutic Nucleosides using a Highly Versatile Purine Nucleoside 2â€™â€Deoxyribosyl Transferase from <i>Trypanosoma brucei</i>. ChemCatChem, 2018, 10, 4406-4416.	3.7	28
6	Characterization of an atypical, thermostable, organic solvent- and acid-tolerant 2â€²-deoxyribosyltransferase from Chroococcidiopsis thermalis. Applied Microbiology and Biotechnology, 2018, 102, 6947-6957.	3.6	17
7	Structural basis of the substrate specificity and instability in solution of a glycosidase from Lactobacillus plantarum. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1227-1236.	2.3	6
8	2â€²-Deoxyribosyltransferase from Leishmania mexicana, an efficient biocatalyst for one-pot, one-step synthesis of nucleosides from poorly soluble purine bases. Applied Microbiology and Biotechnology, 2017, 101, 7187-7200.	3.6	20
9	The Lp_3561 and Lp_3562 Enzymes Support a Functional Divergence Process in the Lipase/Esterase Toolkit from Lactobacillus plantarum. Frontiers in Microbiology, 2016, 7, 1118.	3.5	22
10	Refactoring the Î» phage lytic/lysogenic decision with a synthetic regulator. MicrobiologyOpen, 2016, 5, 575-581.	3.0	12
11	Oriented Attachment of Recombinant Proteins to Agarose-Coated Magnetic Nanoparticles by Means of a Î²-Trefoil Lectin Domain. Bioconjugate Chemistry, 2016, 27, 2734-2743.	3.6	1
12	Two-Photon Fluorescence Anisotropy Imaging to Elucidate the Dynamics and the Stability of Immobilized Proteins. Journal of Physical Chemistry B, 2016, 120, 485-491.	2.6	16
13	Improving Properties of a Novel Î²-Galactosidase from Lactobacillus plantarum by Covalent Immobilization. Molecules, 2015, 20, 7874-7889.	3.8	19
14	GSE4, a Small Dyskerin- and GSE24.2-Related Peptide, Induces Telomerase Activity, Cell Proliferation and Reduces DNA Damage, Oxidative Stress and Cell Senescence in Dyskerin Mutant Cells. PLoS ONE, 2015, 10, e0142980.	2.5	16
15	Enantioselective oxidation of galactitol 1-phosphate by galactitol-1-phosphate 5-dehydrogenase from<i>Escherichia coli</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1540-1554.	2.5	6
16	Characterization of a halotolerant lipase from the lactic acid bacteria Lactobacillus plantarum useful in food fermentations. LWT - Food Science and Technology, 2015, 60, 246-252.	5.2	56
17	Personal perspectives. Arbor, 2015, 191, a223.	0.3	0
18	Esterase LpEst1 from Lactobacillus plantarum: A Novel and Atypical Member of the Î±Î² Hydrolase Superfamily of Enzymes. PLoS ONE, 2014, 9, e92257.	2.5	23

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19	Tannin Degradation by a Novel Tannase Enzyme Present in Some Lactobacillus plantarum Strains. Applied and Environmental Microbiology, 2014, 80, 2991-2997.	3.1	97
20	Characterization of a Versatile Arylesterase from <i>Lactobacillus plantarum</i> Active on Wine Esters. Journal of Agricultural and Food Chemistry, 2014, 62, 5118-5125.	5.2	19
21	Characterization of a Cold-Active Esterase from <i>Lactobacillus plantarum</i> Suitable for Food Fermentations. Journal of Agricultural and Food Chemistry, 2014, 62, 5126-5132.	5.2	36
22	Characterization of a Feruloyl Esterase from Lactobacillus plantarum. Applied and Environmental Microbiology, 2013, 79, 5130-5136.	3.1	120
23	Structure, biochemical characterization and analysis of the pleomorphism of carboxylesterase Cest-2923 from<i>LactobacillusÂplantarum</i>WCFS1. FEBS Journal, 2013, 280, 6658-6671.	4.7	32
24	Identification of a Missing Link in the Evolution of an Enzyme into a Transcriptional Regulator. PLoS ONE, 2013, 8, e57518.	2.5	13
25	The crystal structure of galactitolâ€1â€phosphate 5â€dehydrogenase from <i>Escherichia coli</i> K12 provides insights into its anomalous behavior on IMAC processes. FEBS Letters, 2012, 586, 3127-3133.	2.8	7
26	Directed, Strong, and Reversible Immobilization of Proteins Tagged with a Î²-Trefoil Lectin Domain: A Simple Method to Immobilize Biomolecules on Plain Agarose Matrixes. Bioconjugate Chemistry, 2012, 23, 565-573.	3.6	20
27	The pURI family of expression vectors: A versatile set of ligation independent cloning plasmids for producing recombinant His-fusion proteins. Protein Expression and Purification, 2011, 76, 44-53.	1.3	45
28	Preliminary X-ray analysis of twinned crystals of the Q88Y25_Lacpl esterase from<i>Lactobacillus plantarum</i>WCFS1. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1436-1439.	0.7	3
29	High-resolution structural insights on the sugar-recognition and fusion tag properties of a versatile Î²-trefoil lectin domain from the mushroom Laetiporus sulphureus. Glycobiology, 2011, 21, 1349-1361.	2.5	34
30	Gene cloning, expression, and characterization of phenolic acid decarboxylase from Lactobacillus brevis RM84. Journal of Industrial Microbiology and Biotechnology, 2010, 37, 617-624.	3.0	55
31	Crystallization and preliminary crystallographic analysis of the catalytic module of endolysin from Cp-7, a phage infecting<i>Streptococcus pneumoniae</i>. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 670-673.	0.7	7
32	A preliminary crystallographic study of recombinant NicX, an Fe²⁺-dependent 2,5-dihydroxypyridine dioxygenase from<i>Pseudomonas putida</i>KT2440. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 549-553.	0.7	4
33	<i>p</i>â€Coumaric acid decarboxylase from <i>Lactobacillus plantarum</i>: Structural insights into the active site and decarboxylation catalytic mechanism. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1662-1676.	2.6	52
34	Laetiporus sulphureus Lectin and Aerolysin Protein Family. Advances in Experimental Medicine and Biology, 2010, 677, 67-80.	1.6	28
35	Biochemical Characterization of the Transcriptional Regulator BzdR from Azoarcus sp. CIB. Journal of Biological Chemistry, 2010, 285, 35694-35705.	3.4	33
36	Food phenolics and lactic acid bacteria. International Journal of Food Microbiology, 2009, 132, 79-90.	4.7	494

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37	Sticholysins, two pore-forming toxins produced by the Caribbean Sea anemone Stichodactyla helianthus: Their interaction with membranes. Toxicon, 2009, 54, 1135-1147.	1.6	100
38	Cloning, production, purification and preliminary crystallographic analysis of a glycosidase from the food lactic acid bacterium Lactobacillus plantarum CECT 748T. Protein Expression and Purification, 2009, 68, 177-182.	1.3	22
39	Crystal Structure of the Hexameric Catabolic Ornithine Transcarbamylase from Lactobacillus hilgardii: Structural Insights into the Oligomeric Assembly and Metal Binding. Journal of Molecular Biology, 2009, 393, 425-434.	4.2	17
40	Production and Physicochemical Properties of Recombinant <i>Lactobacillus plantarum</i> Tannase. Journal of Agricultural and Food Chemistry, 2009, 57, 6224-6230.	5.2	79
41	Expression Vectors for Enzyme Restriction- and Ligation-Independent Cloning for Producing Recombinant His-Fusion Proteins. Biotechnology Progress, 2008, 23, 680-686.	2.6	23
42	Characterization of the <i>p</i>-Coumaric Acid Decarboxylase from Lactobacillus plantarum CECT 748^T. Journal of Agricultural and Food Chemistry, 2008, 56, 3068-3072.	5.2	81
43	Overexpression, purification, crystallization and preliminary structural studies ofp-coumaric acid decarboxylase fromLactobacillus plantarum. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 300-303.	0.7	8
44	Insights into the activation of brain serine racemase by the multiâ€PDZ domain glutamate receptor interacting protein, divalent cations and ATP. FEBS Journal, 2007, 274, 4561-4571.	4.7	29
45	The role of electrostatic interactions in the antitumor activity of dimeric RNases. FEBS Journal, 2006, 273, 3687-3697.	4.7	35
46	A complementary microscopy analysis of Sticholysin II crystals on lipid films: Atomic force and transmission electron characterizations. Biophysical Chemistry, 2006, 119, 219-223.	2.8	22
47	X-ray and Neutron Diffraction Approaches to the Structural Analysis of Protein-Lipid Interactions. , 2006, , 63-110.		1
48	Hydralysins, a New Category of Î²-Pore-forming Toxins in Cnidaria. Journal of Biological Chemistry, 2005, 280, 22847-22855.	3.4	75
49	BzdR, a Repressor That Controls the Anaerobic Catabolism of Benzoate in Azoarcus sp. CIB, Is the First Member of a New Subfamily of Transcriptional Regulators. Journal of Biological Chemistry, 2005, 280, 10683-10694.	3.4	77
50	Structural Analysis of the Laetiporus sulphureus Hemolytic Pore-forming Lectin in Complex with Sugars. Journal of Biological Chemistry, 2005, 280, 17251-17259.	3.4	109
51	Crystallization and preliminary crystallographic analysis of a novel haemolytic lectin from the mushroomLaetiporus sulphureus. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1139-1141.	2.5	15
52	Crystallization of a proteolyzed form of the horse pancreatic lipase-related protein 2: structural basis for the specific detergent requirement. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2107-2109.	2.5	6
53	Phenotypic selection and characterization of randomly produced non-haemolytic mutants of the toxic sea anemone protein sticholysin II. FEBS Letters, 2004, 575, 14-18.	2.8	34
54	Crystal and Electron Microscopy Structures of Sticholysin II Actinoporin Reveal Insights into the Mechanism of Membrane Pore Formation. Structure, 2003, 11, 1319-1328.	3.3	218

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55	Crystallization and preliminary X-ray diffraction studies of two different crystal forms of the lipase 2 isoform from the yeastCandida rugosa. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 499-501.	2.5	5
56	Structural Insights into the Lipase/esterase Behavior in the Candida rugosa Lipases Family: Crystal Structure of the Lipase 2 Isoenzyme at 1.97Ã… Resolution. Journal of Molecular Biology, 2003, 332, 1059-1069.	4.2	95
57	The Antifungal Protein AFP of Aspergillus giganteusIs an Oligonucleotide/Oligosaccharide Binding (OB) Fold-containing Protein That Produces Condensation of DNA. Journal of Biological Chemistry, 2002, 277, 46179-46183.	3.4	33
58	Deletion of the NH2-terminal Î²-Hairpin of the Ribotoxin Î±-Sarcin Produces a Nontoxic but Active Ribonuclease. Journal of Biological Chemistry, 2002, 277, 18632-18639.	3.4	48
59	Crystallization and preliminary X-ray diffraction studies of the water-soluble state of the pore-forming toxin sticholysin II from the sea anemoneStichodactyla helianthus. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1229-1231.	2.5	3
60	RNase U2 and Î±-Sarcin: A Study of Relationships. Methods in Enzymology, 2001, 341, 335-351.	1.0	44
61	Arginine 121 is a crucial residue for the specific cytotoxic activity of the ribotoxin Î±-sarcin. FEBS Journal, 2001, 268, 6190-6196.	0.2	24
62	Involvement of the amino-terminal Î²-hairpin of theAspergillusribotoxins on the interaction with membrances and nonspecific ribonuclease activity. Protein Science, 2001, 10, 1658-1668.	7.6	30
63	Partially folded states of the cytolytic protein sticholysin II. BBA - Proteins and Proteomics, 2001, 1545, 122-131.	2.1	25
64	Assignment of the contribution of the tryptophan residues to the spectroscopic and functional properties of the ribotoxin ?-sarcin. Proteins: Structure, Function and Bioinformatics, 2000, 41, 350-361.	2.6	29
65	Ribonuclease U2: cloning, production inPichia pastorisand affinity chromatography purification of the active recombinant protein. FEMS Microbiology Letters, 2000, 189, 165-169.	1.8	8
66	Overproduction in Escherichia coli and Purification of the Hemolytic Protein Sticholysin II from the Sea Anemone Stichodactyla helianthus. Protein Expression and Purification, 2000, 18, 71-76.	1.3	36
67	Two-Dimensional Crystallization on Lipid Monolayers and Three-Dimensional Structure of Sticholysin II, a Cytolysin from the Sea Anemone Stichodactyla helianthus. Biophysical Journal, 2000, 78, 3186-3194.	0.5	36
68	Ribonuclease U2: cloning, production in Pichia pastoris and affinity chromatography purification of the active recombinant protein. FEMS Microbiology Letters, 2000, 189, 165-169.	1.8	8
69	Role of histidine-50, glutamic acid-96, and histidine-137 in the ribonucleolytic mechanism of the ribotoxin ?-sarcin. , 1999, 37, 474-484.		47
70	Sticholysin II, a cytolysin from the sea anemoneStichodactyla helianthus, is a monomer-tetramer associating protein. FEBS Letters, 1999, 455, 27-30.	2.8	55
71	Mechanism of the leakage induced on lipid model membranes by the hemolytic protein sticholysin II from the sea anemone Stichodactyla helianthus. FEBS Journal, 1998, 252, 284-289.	0.2	102
72	The cytotoxin Î±-sarcin behaves as a cyclizing ribonuclease. FEBS Letters, 1998, 424, 46-48.	2.8	36

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73	Secretion of Recombinant Pro- and Mature Fungal Î±-Sarcin Ribotoxin by the Methylotrophic YeastPichia pastoris:The Lysâ€“Arg Motif Is Required for Maturation. Protein Expression and Purification, 1998, 12, 315-322.	1.3	32
74	Oligomerization of the cytotoxin Î±-sarcin associated with phospholipid membranes. Molecular Membrane Biology, 1998, 15, 141-144.	2.0	13
75	A peptide of nine amino acid residues from Î±â€sarcin cytotoxin is a membraneâ€perturbing structure. Chemical Biology and Drug Design, 1998, 51, 142-148.	1.1	17
76	Sequence Determination and Molecular Characterization of Gigantin, a Cytotoxic Protein Produced by the MouldAspergillus giganteusIFO 5818. Archives of Biochemistry and Biophysics, 1997, 343, 188-193.	3.0	24
77	Characterization of a natural larger form of the antifungal protein (AFP) from Aspergillus giganteus. BBA - Proteins and Proteomics, 1997, 1340, 81-87.	2.1	31
78	Release of Lipid Vesicle Contents by an Antibacterial Cecropin Aâˆ'Melittin Hybrid Peptide. Biochemistry, 1996, 35, 9892-9899.	2.5	50
79	Predictive study of the conformation of the cytotoxic protein Î±-sarcin: a structural model to explain Î±-sarcin-membrane interaction. Journal of Theoretical Biology, 1995, 172, 259-267.	1.7	33
80	Escherichia coli JA221 can suppress the UAG stop signal. Letters in Applied Microbiology, 1995, 21, 96-98.	2.2	3
81	Characterization of the Antifungal Protein Secreted by the MouldAspergillus giganteus. Archives of Biochemistry and Biophysics, 1995, 324, 273-281.	3.0	101
82	Food mustard allergen interaction with phospholipid vesicles. FEBS Journal, 1994, 225, 609-615.	0.2	47
83	Kinetic study of the aggregation and lipid mixing produced by alpha-sarcin on phosphatidylglycerol and phosphatidylserine vesicles: stopped-flow light scattering and fluorescence energy transfer measurements. Biophysical Journal, 1994, 67, 1117-1125.	0.5	27
84	Bovine Seminal Ribonuclease Destabilizes Negatively Charged Membranes. Biochemical and Biophysical Research Communications, 1994, 199, 119-124.	2.1	31
85	Overproduction and purification of biologically active native fungal Î±-sarcin in Escherichia coli. Gene, 1994, 142, 147-151.	2.2	64
86	Molecular Interactions Involved in the Passage of the Cytotoxic Protein Î±-Sarcin Across Membranes. , 1994, , 269-276.		1