Ines G Munoz

List of Publications by Year
in descending order

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28	1,214	430874	552781
papers	citations	18 h-index	26 g-index

28	28	28	1906
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrative structural biology of the penicillin-binding protein-1 from Staphylococcus aureus, an essential component of the divisome machinery. Computational and Structural Biotechnology Journal, 2021, 19, 5392-5405.	4.1	2
2	Structural and biochemical insights into an engineered high-redox potential laccase overproduced in Aspergillus. International Journal of Biological Macromolecules, 2019, 141, 855-867.	7.5	17
3	Molecular basis of Tousled-Like Kinase 2 activation. Nature Communications, 2018, 9, 2535.	12.8	24
4	A mechanism for cancerâ€associated inactivation of NQO1 due to P187S and its reactivation by the consensus mutation H80R. FEBS Letters, 2017, 591, 2826-2835.	2.8	21
5	Experimental and computational evidence on conformational fluctuations as a source of catalytic defects in genetic diseases. RSC Advances, 2016, 6, 58604-58612.	3.6	8
6	Structural and dynamics studies of human phenylalanine hydroxylase, a highly regulated allosteric enzyme. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s239-s239.	0.1	0
7	Purification, crystallization and preliminary X-ray diffraction analysis of the kinase domain of human tousled-like kinase 2. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 354-357.	0.8	3
8	Structural basis of PcsB-mediated cell separation in Streptococcus pneumoniae. Nature Communications, 2014, 5, 3842.	12.8	82
9	Crystal Structure of Inhibitor of Growth 4 (ING4) Dimerization Domain Reveals Functional Organization of ING Family of Chromatin-binding Proteins. Journal of Biological Chemistry, 2012, 287, 10876-10884.	3.4	22
10	Kinetics in Signal Transduction Pathways Involving Promiscuous Oligomerizing Receptors Can Be Determined by Receptor Specificity: Apoptosis Induction by TRAIL. Molecular and Cellular Proteomics, 2012, 11, M111.013730.	3.8	25
11	Crystal structure of the open conformation of the mammalian chaperonin CCT in complex with tubulin. Nature Structural and Molecular Biology, 2011, 18, 14-19.	8.2	128
12	Chaperonins: two rings for folding. Trends in Biochemical Sciences, 2011, 36, 424-432.	7.5	140
13	Molecular basis of engineered meganuclease targeting of the endogenous human RAG1 locus. Nucleic Acids Research, 2011, 39, 729-743.	14.5	63
14	Homing endonucleases: from basics to therapeutic applications. Cellular and Molecular Life Sciences, 2010, 67, 727-748.	5.4	73
15	Crystallization and preliminary X-ray diffraction analysis of the dimerization domain of the tumour suppressor ING4. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 567-570.	0.7	5
16	On the relevance of defining protein structures in cancer research. Clinical and Translational Oncology, 2008, 10, 204-212.	2.4	0
17	Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. Nature, 2008, 456, 107-111.	27.8	150
18	Activation of Nucleoplasmin, an Oligomeric Histone Chaperone, Challenges Its Stability[,]. Biochemistry, 2008, 47, 13897-13906.	2.5	22

#	Article	IF	Citations
19	Molecular Basis of Histone H3K4me3 Recognition by ING4. Journal of Biological Chemistry, 2008, 283, 15956-15964.	3.4	71
20	Crystal Structure of the Third Extracellular Domain of CD5 Reveals the Fold of a Group B Scavenger Cysteine-rich Receptor Domain. Journal of Biological Chemistry, 2007, 282, 12669-12677.	3.4	40
21	Three-dimensional Crystal Structure and Enzymic Characterization of Î²-Mannanase Man5A from Blue Mussel Mytilus edulis. Journal of Molecular Biology, 2006, 357, 1500-1510.	4.2	76
22	The crystal structure of an eukaryotic iron superoxide dismutase suggests intersubunit cooperation during catalysis. Protein Science, 2005, 14, 387-394.	7.6	46
23	Structures of Phanerochaete chrysosporium Cel7D in complex with product and inhibitors. FEBS Journal, 2005, 272, 1952-1964.	4.7	44
24	The catalytic module of Cel7D fromPhanerochaete chrysosporiumas a chiral selector: structural studies of its complex with the beta blocker (R)-propranolol. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 637-643.	2.5	11
25	Crystallization and preliminary X-ray diffraction studies of the eukaryotic iron superoxide dismutase (FeSOD) fromVigna unguiculata. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1070-1072.	2.5	8
26	Crystallization and X-ray analysis of native and selenomethionyl Î²-mannanase Man5A from blue mussel,Mytilus edulis, expressed inPichia pastoris. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 542-545.	2.5	10
27	Family 7 cellobiohydrolases from Phanerochaete chrysosporium: crystal structure of the catalytic module of Cel7D (CBH58) at 1.32 Ã... resolution and homology models of the isozymes. Journal of Molecular Biology, 2001, 314, 1097-1111.	4.2	101
28	Cellobiohydrolase 58 (P.c. Cel 7D) is complementary to the homologous CBH I (T.r. Cel 7A) in enantioseparations. Journal of Chromatography A, 2000, 898, 63-74.	3.7	22