# Ines G Munoz

List of Publications by Year
in descending order

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|---|---|---|---|
| 28<br>papers | 1,214<br>citations | 430874<br>18<br>h-index | 552781<br>26<br>g-index |
| 28<br>all docs | 28<br>docs citations | 28<br>times ranked | 1906<br>citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. Nature, 2008, 456, 107-111. | 27.8 | 150 |
| 2 | Chaperonins: two rings for folding. Trends in Biochemical Sciences, 2011, 36, 424-432. | 7.5 | 140 |
| 3 | 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 |
| 4 | 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 |
| 5 | Structural basis of PcsB-mediated cell separation in Streptococcus pneumoniae. Nature Communications, 2014, 5, 3842. | 12.8 | 82 |
| 6 | 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 |
| 7 | Homing endonucleases: from basics to therapeutic applications. Cellular and Molecular Life Sciences, 2010, 67, 727-748. | 5.4 | 73 |
| 8 | Molecular Basis of Histone H3K4me3 Recognition by ING4. Journal of Biological Chemistry, 2008, 283, 15956-15964. | 3.4 | 71 |
| 9 | Molecular basis of engineered meganuclease targeting of the endogenous human RAG1 locus. Nucleic Acids Research, 2011, 39, 729-743. | 14.5 | 63 |
| 10 | The crystal structure of an eukaryotic iron superoxide dismutase suggests intersubunit cooperation during catalysis. Protein Science, 2005, 14, 387-394. | 7.6 | 46 |
| 11 | Structures of Phanerochaete chrysosporium Cel7D in complex with product and inhibitors. FEBS Journal, 2005, 272, 1952-1964. | 4.7 | 44 |
| 12 | 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 |
| 13 | 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 |
| 14 | Molecular basis of Tousled-Like Kinase 2 activation. Nature Communications, 2018, 9, 2535. | 12.8 | 24 |
| 15 | 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 |
| 16 | Activation of Nucleoplasmin, an Oligomeric Histone Chaperone, Challenges Its Stability<sup>,</sup>. Biochemistry, 2008, 47, 13897-13906. | 2.5 | 22 |
| 17 | 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 |
| 18 | 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 |

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|---|---|---|---|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | On the relevance of defining protein structures in cancer research. Clinical and Translational Oncology, 2008, 10, 204-212. | 2.4 | 0 |
| 28 | 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 |