

Federico M Ruiz

List of Publications by Year in descending order

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516710

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31
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docs citations

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	FtsZ filament structures in different nucleotide states reveal the mechanism of assembly dynamics. <i>PLoS Biology</i> , 2022, 20, e3001497.	5.6	11
2	Targeting the FtsZ Allosteric Binding Site with a Novel Fluorescence Polarization Screen, Cytological and Structural Approaches for Antibacterial Discovery. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 5730-5745.	6.4	11
3	Structural Characterization of Rat Galectin-5, an N-Tailed Monomeric Proto-Type-like Galectin. <i>Biomolecules</i> , 2021, 11, 1854.	4.0	1
4	Nucleotide-induced folding of cell division protein FtsZ from <i>Staphylococcus aureus</i> . <i>FEBS Journal</i> , 2020, 287, 4048-4067.	4.7	15
5	The crystal structure of human XPG, the xeroderma pigmentosum group G endonuclease, provides insight into nucleotide excision DNA repair. <i>Nucleic Acids Research</i> , 2020, 48, 9943-9958.	14.5	14
6	Structural Characterization of TssL from <i>Acinetobacter baumannii</i> : a Key Component of the Type VI Secretion System. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	5
7	Engineering protein assemblies with allosteric control via monomer fold-switching. <i>Nature Communications</i> , 2019, 10, 5703.	12.8	17
8	Chicken GRIFIN: Structural characterization in crystals and in solution. <i>Biochimie</i> , 2018, 146, 127-138.	2.6	11
9	Members of the Galectin Network with Deviations from the Canonical Sequence Signature. <i>Trends in Glycoscience and Glycotechnology</i> , 2018, 30, SE1-SE9.	0.1	16
10	Members of the Galectin Network with Deviations from the Canonical Sequence Signature. <i>Trends in Glycoscience and Glycotechnology</i> , 2018, 30, SE11-SE20.	0.1	12
11	Quorum sensing network in clinical strains of <i>A. baumannii</i> : AidA is a new quorum quenching enzyme. <i>PLoS ONE</i> , 2017, 12, e0174454.	2.5	54
12	Galectin-related protein: An integral member of the network of chicken galectins 1. From strong sequence conservation of the gene confined to vertebrates to biochemical characteristics of the chicken protein and its crystal structure. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2285-2297.	2.4	23
13	The structure of VgrG1 from <i>Pseudomonas aeruginosa</i> , the needle tip of the bacterial type VI secretion system. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 22-33.	2.3	37
14	Combining Crystallography and Hydrogen-Deuterium Exchange to Study Galectin-Ligand Complexes. <i>Chemistry - A European Journal</i> , 2015, 21, 13558-13568.	3.3	16
15	Crystal Structure of Hcp from <i>Acinetobacter baumannii</i> : A Component of the Type VI Secretion System. <i>PLoS ONE</i> , 2015, 10, e0129691.	2.5	29
16	Preliminary X-ray crystallographic analysis of an engineered variant of human chimera-type galectin-3 with a shortened N-terminal domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 184-188.	0.8	3
17	Natural single amino acid polymorphism (F19Y) in human galectin-8: detection of structural alterations and increased growth-regulatory activity on tumor cells. <i>FEBS Journal</i> , 2014, 281, 1446-1464.	4.7	40
18	Solving the RNA polymerase I structural puzzle. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2570-2582.	2.5	23

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19	Crystal structure of the 14-subunit RNA polymerase. <i>Nature</i> , 2013, 502, 644-649.	27.8	179
20	Fine-tuning of prototype chicken galectins: structure of CG-2 and structure-activity correlations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1665-1676.	2.5	11
21	Receptor-Based Virtual Screening and Biological Characterization of Human Apurinic/Apyrimidinic Endonuclease (Ape1) Inhibitors. <i>ChemMedChem</i> , 2012, 7, 2168-2178.	3.2	7
22	The Binding of Triclosan to SmeT, the Repressor of the Multidrug Efflux Pump SmeDEF, Induces Antibiotic Resistance in <i>Stenotrophomonas maltophilia</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002103.	4.7	94
23	Rational design of inhibitors of APE1 supported by crystallographic techniques. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, C295-C295.	0.3	0
24	Crystal structure of SmeT bound to the biocide triclosan. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, C477-C478.	0.3	0
25	Development of a Novel Fluorescence Assay Based on the Use of the Thrombin-Binding Aptamer for the Detection of O6-Alkylguanine-DNA Alkyltransferase Activity. <i>Journal of Nucleic Acids</i> , 2010, 2010, 1-9.	1.2	20
26	N-domain of human adhesion/growth-regulatory galectin-9: Preference for distinct conformers and non-sialylated N-glycans and detection of ligand-induced structural changes in crystal and solution. <i>International Journal of Biochemistry and Cell Biology</i> , 2010, 42, 1019-1029.	2.8	47
27	Structure-Based Discovery of Novel Non-nucleosidic DNA Alkyltransferase Inhibitors: Virtual Screening and in Vitro and in Vivo Activities. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 844-854.	5.4	31
28	Quantum model of catalysis based on a mobile proton revealed by subatomic x-ray and neutron diffraction studies of h-aldose reductase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1844-1848.	7.1	74
29	Ultra high resolution X-ray and neutron diffraction studies of fully deuterated aldose reductase show a catalytic proton pathway. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2006, 62, s19-s19.	0.3	0
30	Inhibitor binding to aldose reductase studied at subatomic resolution. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2005, 61, c122-c122.	0.3	0
31	Free Energy Perturbation Calculations on Glucosidase-Inhibitor Complexes. <i>Medicinal Chemistry</i> , 2005, 1, 455-460.	1.5	5
32	Aldose reductase structures: implications for mechanism and inhibition. <i>Cellular and Molecular Life Sciences</i> , 2004, 61, 750-762.	5.4	97
33	Ultrahigh resolution drug design. II. Atomic resolution structures of human aldose reductase holoenzyme complexed with fidarestat and minalrestat: Implications for the binding of cyclic imide inhibitors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 805-813.	2.6	83
34	The crystallographic structure of the aldose reductase-IDD552 complex shows direct proton donation from tyrosine 48. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1347-1354.	2.5	29
35	Neutron diffraction structure of fully deuterated aldose reductase: a necessary complement to X-ray ultra-high-resolution structures. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2004, 60, s155-s155.	0.3	0
36	ROUGHENING/WETTING TRANSITION IN A GROWTH MODEL WITH ADSORPTION AND DESORPTION. <i>International Journal of Modern Physics B</i> , 2001, 15, 2249-2259.	2.0	1