Federico M Ruiz

List of Publications by Year in descending order

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516710 434195 1,018 36 16 31 citations h-index g-index papers 39 39 39 1602 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Crystal structure of the 14-subunit RNA polymeraseÂl. Nature, 2013, 502, 644-649.	27.8	179
2	Aldose reductase structures: implications for mechanism and inhibition. Cellular and Molecular Life Sciences, 2004, 61, 750-762.	5.4	97
3	The Binding of Triclosan to SmeT, the Repressor of the Multidrug Efflux Pump SmeDEF, Induces Antibiotic Resistance in Stenotrophomonas maltophilia. PLoS Pathogens, 2011, 7, e1002103.	4.7	94
4	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. Proteins: Structure, Function and Bioinformatics, 2004, 55, 805-813.	2.6	83
5	Quantum model of catalysis based on a mobile proton revealed by subatomic x-ray and neutron diffraction studies of h-aldose reductase. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1844-1848.	7.1	74
6	Quorum sensing network in clinical strains of A. baumannii: AidA is a new quorum quenching enzyme. PLoS ONE, 2017, 12, e0174454.	2.5	54
7	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. International Journal of Biochemistry and Cell Biology, 2010, 42, 1019-1029.	2.8	47
8	Natural single amino acid polymorphism (F19Y) in human galectinâ€8: detection of structural alterations and increased growthâ€regulatory activity on tumor cells. FEBS Journal, 2014, 281, 1446-1464.	4.7	40
9	The structure of VgrG1 from <i>Pseudomonas aeruginosa</i> , the needle tip of the bacterial type VI secretion system. Acta Crystallographica Section D: Structural Biology, 2016, 72, 22-33.	2.3	37
10	Structure-Based Discovery of Novel Non-nucleosidic DNA Alkyltransferase Inhibitors: Virtual Screening and in Vitro and in Vivo Activities. Journal of Chemical Information and Modeling, 2008, 48, 844-854.	5.4	31
11	The crystallographic structure of the aldose reductase–IDD552 complex shows direct proton donation from tyrosine 48. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1347-1354.	2.5	29
12	Crystal Structure of Hcp from Acinetobacter baumannii: A Component of the Type VI Secretion System. PLoS ONE, 2015, 10, e0129691.	2.5	29
13	Solving the RNA polymerase I structural puzzle. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2570-2582.	2.5	23
14	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. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 2285-2297.	2.4	23
15	Development of a Novel Fluorescence Assay Based on the Use of the Thrombin-Binding Aptamer for the Detection of O6-Alkylguanine-DNA Alkyltransferase Activity. Journal of Nucleic Acids, 2010, 2010, 1-9.	1.2	20
16	Engineering protein assemblies with allosteric control via monomer fold-switching. Nature Communications, 2019, 10, 5703.	12.8	17
17	Combining Crystallography and Hydrogen–Deuterium Exchange to Study Galectin–Ligand Complexes. Chemistry - A European Journal, 2015, 21, 13558-13568.	3.3	16
18	Members of the Galectin Network with Deviations from the Canonical Sequence Signature.â€f1. <i>G</i> alectin- <i>R</i> elated <i>I</i> nter- <i>F</i> iber Prote <i>in</i> (GRIFIN). Trends in Glycoscience and Glycotechnology, 2018, 30, SE1-SE9.	0.1	16

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19	Nucleotideâ€induced folding of cell division protein FtsZ from <i>Staphylococcus aureus</i> . FEBS Journal, 2020, 287, 4048-4067.	4.7	15
20	The crystal structure of human XPG, the xeroderma pigmentosum group G endonuclease, provides insight into nucleotide excision DNA repair. Nucleic Acids Research, 2020, 48, 9943-9958.	14.5	14
21	Members of the Galectin Network with Deviations from the Canonical Sequence Signature. $\hat{a} \in f2$. <i>G</i>alectin-<i>R</i>elated <i>P</i>rotein (GRP). Trends in Glycoscience and Glycotechnology, 2018, 30, SE11-SE20.	0.1	12
22	Fine-tuning of prototype chicken galectins: structure of CG-2 and structure–activity correlations. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1665-1676.	2.5	11
23	Chicken GRIFIN: Structural characterization in crystals and in solution. Biochimie, 2018, 146, 127-138.	2.6	11
24	Targeting the FtsZ Allosteric Binding Site with a Novel Fluorescence Polarization Screen, Cytological and Structural Approaches for Antibacterial Discovery. Journal of Medicinal Chemistry, 2021, 64, 5730-5745.	6.4	11
25	FtsZ filament structures in different nucleotide states reveal the mechanism of assembly dynamics. PLoS Biology, 2022, 20, e3001497.	5. 6	11
26	Receptorâ€Based Virtual Screening and Biological Characterization of Human Apurinic/Apyrimidinic Endonuclease (Ape1) Inhibitors. ChemMedChem, 2012, 7, 2168-2178.	3.2	7
27	Structural Characterization of TssL from Acinetobacter baumannii: a Key Component of the Type VI Secretion System. Journal of Bacteriology, 2020, 202, .	2.2	5
28	Free Energy Perturbation Calculations on Glucosidase-Inhibitor Complexes. Medicinal Chemistry, 2005, 1, 455-460.	1.5	5
29	Preliminary X-ray crystallographic analysis of an engineered variant of human chimera-type galectin-3 with a shortened N-terminal domain. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 184-188.	0.8	3
30	ROUGHENING/WETTING TRANSITION IN A GROWTH MODEL WITH ADSORPTION AND DESORPTION. International Journal of Modern Physics B, 2001, 15, 2249-2259.	2.0	1
31	Structural Characterization of Rat Galectin-5, an N-Tailed Monomeric Proto-Type-like Galectin. Biomolecules, 2021, 11, 1854.	4.0	1
32	Inhibitor binding to aldose reductase studied at subatomic resolution. Acta Crystallographica Section A: Foundations and Advances, 2005, 61, c122-c122.	0.3	0
33	Neutron diffraction structure of fully deuterated aldose reductase: a necessary complement to X-ray ultra-high-resolution structures. Acta Crystallographica Section A: Foundations and Advances, 2004, 60, s155-s155.	0.3	0
34	Ultra high resolution X-ray and neutron diffraction studies of fully deuterated aldose reductase show a catalytic proton pathway. Acta Crystallographica Section A: Foundations and Advances, 2006, 62, s19-s19.	0.3	0
35	Rational design of inhibitors of APE1 supported by crystallographic techniques. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, C295-C295.	0.3	0
36	Crystal structure of SmeT bound to the biocide triclosan. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, C477-C478.	0.3	0