## Enrique Rudino-Pinera

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1518969/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Experimental determination of the radiation dose limit for cryocooled protein crystals. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4912-4917.	7.1	366
2	Crystal structures of fibronectin-binding sites from <i>Staphylococcus aureus</i> FnBPA in complex with fibronectin domains. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12254-12258.	7.1	116
3	Novel transcriptome assembly and improved annotation of the whiteleg shrimp (Litopenaeus) Tj ETQq1 1 0.7843	14 rgBT /(	Dverlock 10
4	Parameters affecting the X-ray dose absorbed by macromolecular crystals. Journal of Synchrotron Radiation, 2005, 12, 268-275.	2.4	70
5	Hydropathic Complementarity Determines Interaction of Epitope 869HITDTNNK876 in Manduca sexta Bt-R1 Receptor with Loop 2 of Domain II ofBacillus thuringiensis Cry1A Toxins. Journal of Biological Chemistry, 2002, 277, 30137-30143.	3.4	64
6	Unusual Cys-Tyr Covalent Bond in a Large Catalase. Journal of Molecular Biology, 2004, 342, 971-985.	4.2	64
7	The Crystal Structure of A Ternary Complex of Betaine Aldehyde Dehydrogenase from Pseudomonas aeruginosa Provides New Insight into the Reaction Mechanism and Shows A Novel Binding Mode of the 2′-Phosphate of NADP+ and A Novel Cation Binding Site. Journal of Molecular Biology, 2009, 385, 542-557.	4.2	64
8	Selected mutations in Bacillus subtilis levansucrase semi-conserved regions affecting its biochemical properties. Protein Engineering, Design and Selection, 2008, 21, 589-595.	2.1	62
9	Structural changes caused by radiation-induced reduction and radiolysis: the effect of X-ray absorbed dose in a fungal multicopper oxidase. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 564-577.	2.5	48
10	Amino Acid Residues Critical for the Specificity for Betaine Aldehyde of the Plant ALDH10 Isoenzyme Involved in the Synthesis of Glycine Betaine  Â. Plant Physiology, 2012, 158, 1570-1582.	4.8	45
11	A Single Mutation at the Sheet Switch Region Results in Conformational Changes Favoring λ6 Light-Chain Fibrillogenesis. Journal of Molecular Biology, 2010, 396, 280-292.	4.2	43
12	The Solution and Crystal Structures of a Module Pair from the Staphylococcus aureus-Binding Site of Human Fibronectin—A Tale with a Twist. Journal of Molecular Biology, 2007, 368, 833-844.	4.2	34
13	An acceptor-substrate binding site determining glycosyl transfer emerges from mutant analysis of a plant vacuolar invertase and a fructosyltransferase. Plant Molecular Biology, 2009, 69, 47-56.	3.9	34
14	Structure–Function Relationships in Fungal Large-Subunit Catalases. Journal of Molecular Biology, 2009, 386, 218-232.	4.2	34
15	X-ray-induced catalytic active-site reduction of a multicopper oxidase: structural insights into the proton-relay mechanism and O <sub>2</sub> -reduction states. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2396-2411.	2.5	30
16	Molecular Dynamics of a Thermostable Multicopper Oxidase from Thermus thermophilus HB27: Structural Differences between the Apo and Holo Forms. PLoS ONE, 2012, 7, e40700.	2.5	29
17	Evaluation of cross-linked aggregates from purified Bacillus subtilis levansucrase mutants for transfructosylation reactions. BMC Biotechnology, 2009, 9, 68.	3.3	28
18	Molecular characterization of sucrose: sucrose 1-fructosyltransferase (1-SST) from Agave tequilana Weber var. azul Plant Science, 2007, 173, 478-486.	3.6	27

#	Article	IF	CITATIONS
19	Transcriptomic and Proteomic Analysis of the Tentacles and Mucus of Anthopleura dowii Verrill, 1869. Marine Drugs, 2019, 17, 436.	4.6	24
20	Crystal structure of shrimp arginine kinase in binary complex with arginine—a molecular view of the phosphagen precursor binding to the enzyme. Journal of Bioenergetics and Biomembranes, 2013, 45, 511-518.	2.3	22
21	On the Role of the Conformational Flexibility of the Active-site Lid on the Allosteric Kinetics of Glucosamine-6-phosphate Deaminase. Journal of Molecular Biology, 2002, 319, 183-189.	4.2	20
22	Structural flexibility, an essential component of the allosteric activation inEscherichia coliglucosamine-6-phosphate deaminase. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 10-20.	2.5	20
23	Novel Protein Crystal Growth Electrochemical Cell For Applications In X-ray Diffraction and Atomic Force Microscopy. Crystal Growth and Design, 2011, 11, 3917-3922.	3.0	20
24	Insights into ligand binding to a glutathione S-transferase from mango: Structure, thermodynamics and kinetics. Biochimie, 2017, 135, 35-45.	2.6	20
25	Novel NADPH–cysteine covalent adduct found in the active site of an aldehyde dehydrogenase. Biochemical Journal, 2011, 439, 443-455.	3.7	19
26	Structural Basis of Neutralization of the Major Toxic Component from the Scorpion Centruroides noxius Hoffmann by a Human-derived Single-chain Antibody Fragment. Journal of Biological Chemistry, 2011, 286, 20892-20900.	3.4	19
27	Optimal Neutralization of Centruroides noxius Venom Is Understood through a Structural Complex between Two Antibody Fragments and the Cn2 Toxin. Journal of Biological Chemistry, 2016, 291, 1619-1630.	3.4	19
28	Thermostable multicopper oxidase from <i>Thermus thermophilus</i> HB27: crystallization and preliminary X-ray diffraction analysis of apo and holo forms. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1595-1598.	0.7	18
29	Structural insights from a novel invertebrate triosephosphate isomerase from Litopenaeus vannamei. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1696-1706.	2.3	18
30	Evolutionary Walk between ( $\hat{l}^2/\hat{l}\pm$ )8 Barrels: Catalytic Migration from Triosephosphate Isomerase to Thiamin Phosphate Synthase. Journal of Molecular Biology, 2012, 416, 255-270.	4.2	17
31	Characterization of a Novel Functional Trimeric Catechol 1,2-Dioxygenase From a Pseudomonas stutzeri Isolated From the Gulf of Mexico. Frontiers in Microbiology, 2020, 11, 1100.	3.5	16
32	The molecular basis of the nonprocessive elongation mechanism in levansucrases. Journal of Biological Chemistry, 2021, 296, 100178.	3.4	16
33	Site-directed mutagenesis and homology modeling indicate an important role of cysteine 439 in the stability of betaine aldehyde dehydrogenase from Pseudomonas aeruginosa. Biochimie, 2005, 87, 1056-1064.	2.6	15
34	The Hcp-like protein HilE inhibits homodimerization and DNA binding of the virulence-associated transcriptional regulator HilD in Salmonella. Journal of Biological Chemistry, 2018, 293, 6578-6592.	3.4	14
35	Implications of the mutation S164A on Bacillus subtilis levansucrase product specificity and insights into protein interactions acting upon levan synthesis. International Journal of Biological Macromolecules, 2020, 161, 898-908.	7.5	13
36	Site-directed Mutagenesis Reveals Regions Implicated in the Stability and Fiber Formation of Human λ3r Light Chains. Journal of Biological Chemistry, 2015, 290, 2577-2592.	3.4	11

#	Article	IF	CITATIONS
37	ls dimerization a common feature in thioredoxins? The case of thioredoxin from <i>Litopenaeus vannamei</i> . Acta Crystallographica Section D: Structural Biology, 2017, 73, 326-339.	2.3	11
38	Crystal Structure of the Shrimp Proliferating Cell Nuclear Antigen: Structural Complementarity with WSSV DNA Polymerase PIP-Box. PLoS ONE, 2014, 9, e94369.	2.5	11
39	Crystallization and X-ray diffraction studies of arginine kinase from the white Pacific shrimpLitopenaeus vannamei. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 783-785.	0.7	10
40	Expression, purification, crystallization and X-ray crystallographic studies of different redox states of the active site of thioredoxin 1 from the whiteleg shrimp <i>Litopenaeus vannamei</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 488-493.	0.7	10
41	Simulation of the cavity-binding site of three bacterial multicopper oxidases upon complex stabilization: interactional profile and electron transference pathways. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1303-1317.	3.5	10
42	Antioxidant Capacity of Two Novel Bioactive Fe(III)-Cyclophane Complexes. Molecules, 2013, 18, 1762-1774.	3.8	9
43	Sequencing and de novo transcriptome assembly of Anthopleura dowii Verrill (1869), from Mexico. Genomics Data, 2017, 11, 92-94.	1.3	9
44	Structure, kinetics, molecular and redox properties of a cytosolic and developmentally regulated fungal catalase-peroxidase. Archives of Biochemistry and Biophysics, 2018, 640, 17-26.	3.0	8
45	Identification of a pore-forming protein from sea anemone Anthopleura dowii Verrill (1869) venom by mass spectrometry. Journal of Venomous Animals and Toxins Including Tropical Diseases, 2019, 25, e147418.	1.4	8
46	A competent catalytic active site is necessary for substrate induced dimer assembly in triosephosphate isomerase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1423-1432.	2.3	7
47	Isoelectric focusing, effect of reducing agents and inhibitors: partial characterization of proteases extracted from Bromelia karatas. Applied Biological Chemistry, 2018, 61, 459-467.	1.9	7
48	The structure of (E)-biformene synthase provides insights into the biosynthesis of bacterial bicyclic labdane-related diterpenoids. Journal of Structural Biology, 2019, 207, 29-39.	2.8	7
49	Crystal Structure of 2-Amino-5-chlorobenzophenone. Analytical Sciences, 1996, 12, 677-678.	1.6	6
50	Structures of a bi-functional Kunitz-type STI family inhibitor of serine and aspartic proteases: Could the aspartic protease inhibition have evolved from a canonical serine protease-binding loop?. Journal of Structural Biology, 2016, 195, 259-271.	2.8	6
51	De novo assembly and transcriptome characterization of the freshwater prawn Palaemonetes argentinus: Implications for a detoxification response. Marine Genomics, 2018, 37, 74-81.	1.1	6
52	X-ray driven reduction of Cpd I of Catalase-3 from N. crassa reveals differential sensitivity of active sites and formation of ferrous state. Archives of Biochemistry and Biophysics, 2019, 666, 107-115.	3.0	6
53	Crystallographic Studies Evidencing the High Energy Tolerance to Disrupting the Interface Disulfide Bond of Thioredoxin 1 from White Leg Shrimp Litopenaeus vannamei. Molecules, 2014, 19, 21113-21126.	3.8	5
54	Structure of nucleoside diphosphate kinase from pacific shrimp ( <i>Litopenaeus vannamei</i> ) in binary complexes with purine and pyrimidine nucleoside diphosphates. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1150-1154.	0.8	5

Enrique Rudino-Pinera

#	Article	IF	CITATIONS
55	Trichomonas vaginalis metalloproteinase TvMP50 is a monomeric Aminopeptidase P-like enzyme. Molecular Biotechnology, 2018, 60, 563-575.	2.4	5
56	The crystal structure of ESBL TLA-1 in complex with clavulanic acid reveals a second acylation site. Biochemical and Biophysical Research Communications, 2020, 522, 545-551.	2.1	5
57	Inductive effects in amino acids and peptides: Ionization constants and tryptophan fluorescence. Biochemistry and Biophysics Reports, 2020, 24, 100802.	1.3	5
58	Twinned or not twinned, that is the question: crystallization and preliminary crystallographic analysis of the2F13F1 module pair of human fibronectin. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1341-1345.	2.5	4
59	Crystallization and X-ray diffraction analysis of a putative bacterial class I labdane-related diterpene synthase. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1194-1199.	0.8	4
60	First attempts to crystallize a non-homogeneous sample of thioredoxin from Litopenaeus vannamei: What to do when you have diffraction data of a protein that is not the target?. Biochemistry and Biophysics Reports, 2016, 8, 284-289.	1.3	4
61	Crystal structure of 6aJL2-R24G light chain variable domain: Does crystal packing explain amyloid fibril formation?. Biochemistry and Biophysics Reports, 2019, 20, 100682.	1.3	4
62	Conformational stability and crystal packing: polymorphism inNeurospora crassaCAT-3. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 753-758.	0.7	3
63	Crystal structure of a classâ€mu glutathione Sâ€transferase from whiteleg shrimp <i>Litopenaeus vannamei</i> : structural changes in the xenobiotic binding Hâ€site may alter the spectra of molecules bound. Journal of Biochemical and Molecular Toxicology, 2017, 31, N/A.	3.0	3
64	Novel Devices for Transporting Protein Crystals to the Synchrotron Facilities and Thermal Protection of Protein Crystals. Crystals, 2018, 8, 340.	2.2	2
65	Cloning, recombinant production and crystallographic structure of Proliferating Cell Nuclear Antigen from radioresistant archaeon Thermococcus gammatolerans. Biochemistry and Biophysics Reports, 2016, 8, 200-206.	1.3	1
66	Zo-peroxidase: Crystal structure and sequence of a highly-glycosylated peroxidase resistant to high concentrations of H2O2 from Japanese radish. Biochemistry and Biophysics Reports, 2018, 13, 32-38.	1.3	1
67	PCNA from <i>Thermococcus gammatolerans</i> : A protein involved in chromosomal <scp>DNA</scp> metabolism intrinsically resistant at high levels of ionizing radiation. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1684-1698.	2.6	1
68	Crystallization and X-ray diffraction studies of crustacean proliferating cell nuclear antigen. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1367-1370.	0.7	0