

# Enrique Rudino-Pinera

## List of Publications by Year in descending order

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68  
papers

1,754  
citations

361045

20  
h-index

288905

40  
g-index

70  
all docs

70  
docs citations

70  
times ranked

2827  
citing authors

#	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.	3.3	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.	3.3	116
3	Novel transcriptome assembly and improved annotation of the whiteleg shrimp ( <i>Litopenaeus</i> ) Tj ETQq1 1 0.784314 rrgBT /Overlock 10	1.6	89
4	Parameters affecting the X-ray dose absorbed by macromolecular crystals. Journal of Synchrotron Radiation, 2005, 12, 268-275.	1.0	70
5	Hydropathic Complementarity Determines Interaction of Epitope 869HITDTNKK876 in <i>Manduca sexta</i> Bt-R1 Receptor with Loop 2 of Domain II of <i>Bacillus thuringiensis</i> Cry1A Toxins. Journal of Biological Chemistry, 2002, 277, 30137-30143.	1.6	64
6	Unusual Cys-Tyr Covalent Bond in a Large Catalase. Journal of Molecular Biology, 2004, 342, 971-985.	2.0	64
7	The Crystal Structure of A Ternary Complex of Betaine Aldehyde Dehydrogenase from <i>Pseudomonas aeruginosa</i> 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.	2.0	64
8	Selected mutations in <i>Bacillus subtilis</i> levansucrase semi-conserved regions affecting its biochemical properties. Protein Engineering, Design and Selection, 2008, 21, 589-595.	1.0	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. Plant Physiology, 2012, 158, 1570-1582.	2.3	45
11	A Single Mutation at the Sheet Switch Region Results in Conformational Changes Favoring $\beta$ 6 Light-Chain Fibrillogenesis. Journal of Molecular Biology, 2010, 396, 280-292.	2.0	43
12	The Solution and Crystal Structures of a Module Pair from the <i>Staphylococcus aureus</i> -Binding Site of Human Fibronectin: A Tale with a Twist. Journal of Molecular Biology, 2007, 368, 833-844.	2.0	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.	2.0	34
14	Structure-Function Relationships in Fungal Large-Subunit Catalases. Journal of Molecular Biology, 2009, 386, 218-232.	2.0	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 <i>Thermus thermophilus</i> HB27: Structural Differences between the Apo and Holo Forms. PLoS ONE, 2012, 7, e40700.	1.1	29
17	Evaluation of cross-linked aggregates from purified <i>Bacillus subtilis</i> levansucrase mutants for transfructosylation reactions. BMC Biotechnology, 2009, 9, 68.	1.7	28
18	Molecular characterization of sucrose: sucrose 1-fructosyltransferase (1-SST) from <i>Agave tequilana</i> Weber var. azul.. Plant Science, 2007, 173, 478-486.	1.7	27

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19	Transcriptomic and Proteomic Analysis of the Tentacles and Mucus of <i>Anthopleura dowii</i> Verrill, 1869. <i>Marine Drugs</i> , 2019, 17, 436.	2.2	24
20	Crystal structure of shrimp arginine kinase in binary complex with arginine—a molecular view of the phosphagen precursor binding to the enzyme. <i>Journal of Bioenergetics and Biomembranes</i> , 2013, 45, 511-518.	1.0	22
21	On the Role of the Conformational Flexibility of the Active-site Lid on the Allosteric Kinetics of Glucosamine-6-phosphate Deaminase. <i>Journal of Molecular Biology</i> , 2002, 319, 183-189.	2.0	20
22	Structural flexibility, an essential component of the allosteric activation in <i>Escherichia coli</i> glucosamine-6-phosphate deaminase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 10-20.	2.5	20
23	Novel Protein Crystal Growth Electrochemical Cell For Applications In X-ray Diffraction and Atomic Force Microscopy. <i>Crystal Growth and Design</i> , 2011, 11, 3917-3922.	1.4	20
24	Insights into ligand binding to a glutathione S-transferase from mango: Structure, thermodynamics and kinetics. <i>Biochimie</i> , 2017, 135, 35-45.	1.3	20
25	Novel NADPH—cysteine covalent adduct found in the active site of an aldehyde dehydrogenase. <i>Biochemical Journal</i> , 2011, 439, 443-455.	1.7	19
26	Structural Basis of Neutralization of the Major Toxic Component from the Scorpion <i>Centruroides noxius</i> Hoffmann by a Human-derived Single-chain Antibody Fragment. <i>Journal of Biological Chemistry</i> , 2011, 286, 20892-20900.	1.6	19
27	Optimal Neutralization of <i>Centruroides noxius</i> Venom Is Understood through a Structural Complex between Two Antibody Fragments and the Cn2 Toxin. <i>Journal of Biological Chemistry</i> , 2016, 291, 1619-1630.	1.6	19
28	Thermostable multicopper oxidase from <i>Thermus thermophilus</i> HB27: crystallization and preliminary X-ray diffraction analysis of apo and holo forms. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1595-1598.	0.7	18
29	Structural insights from a novel invertebrate triosephosphate isomerase from <i>Litopenaeus vannamei</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1696-1706.	1.1	18
30	Evolutionary Walk between (12/1±)8 Barrels: Catalytic Migration from Triosephosphate Isomerase to Thiamin Phosphate Synthase. <i>Journal of Molecular Biology</i> , 2012, 416, 255-270.	2.0	17
31	Characterization of a Novel Functional Trimeric Catechol 1,2-Dioxygenase From a <i>Pseudomonas stutzeri</i> Isolated From the Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2020, 11, 1100.	1.5	16
32	The molecular basis of the nonprocessive elongation mechanism in levansucrases. <i>Journal of Biological Chemistry</i> , 2021, 296, 100178.	1.6	16
33	Site-directed mutagenesis and homology modeling indicate an important role of cysteine 439 in the stability of betaine aldehyde dehydrogenase from <i>Pseudomonas aeruginosa</i> . <i>Biochimie</i> , 2005, 87, 1056-1064.	1.3	15
34	The Hcp-like protein Hile inhibits homodimerization and DNA binding of the virulence-associated transcriptional regulator HilD in <i>Salmonella</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 6578-6592.	1.6	14
35	Implications of the mutation S164A on <i>Bacillus subtilis</i> levansucrase product specificity and insights into protein interactions acting upon levan synthesis. <i>International Journal of Biological Macromolecules</i> , 2020, 161, 898-908.	3.6	13
36	Site-directed Mutagenesis Reveals Regions Implicated in the Stability and Fiber Formation of Human $\lambda$ 3r Light Chains. <i>Journal of Biological Chemistry</i> , 2015, 290, 2577-2592.	1.6	11

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37	Is 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.	1.1	11
38	Crystal Structure of the Shrimp Proliferating Cell Nuclear Antigen: Structural Complementarity with WSSV DNA Polymerase PIP-Box. PLoS ONE, 2014, 9, e94369.	1.1	11
39	Crystallization and X-ray diffraction studies of arginine kinase from the white Pacific shrimp <i>Litopenaeus vannamei</i> . 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.	2.0	10
42	Antioxidant Capacity of Two Novel Bioactive Fe(III)-Cyclophane Complexes. Molecules, 2013, 18, 1762-1774.	1.7	9
43	Sequencing and de novo transcriptome assembly of <i>Anthopleura dowii</i> 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.	1.4	8
45	Identification of a pore-forming protein from sea anemone <i>Anthopleura dowii</i> Verrill (1869) venom by mass spectrometry. Journal of Venomous Animals and Toxins Including Tropical Diseases, 2019, 25, e147418.	0.8	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.	1.1	7
47	Isoelectric focusing, effect of reducing agents and inhibitors: partial characterization of proteases extracted from <i>Bromelia karatas</i> . Applied Biological Chemistry, 2018, 61, 459-467.	0.7	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.	1.3	7
49	Crystal Structure of 2-Amino-5-chlorobenzophenone. Analytical Sciences, 1996, 12, 677-678.	0.8	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.	1.3	6
51	De novo assembly and transcriptome characterization of the freshwater prawn <i>Palaemonetes argentinus</i> : Implications for a detoxification response. Marine Genomics, 2018, 37, 74-81.	0.4	6
52	X-ray driven reduction of Cpd I of Catalase-3 from <i>N. crassa</i> reveals differential sensitivity of active sites and formation of ferrous state. Archives of Biochemistry and Biophysics, 2019, 666, 107-115.	1.4	6
53	Crystallographic Studies Evidencing the High Energy Tolerance to Disrupting the Interface Disulfide Bond of Thioredoxin 1 from White Leg Shrimp <i>Litopenaeus vannamei</i> . Molecules, 2014, 19, 21113-21126.	1.7	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.	0.4	5

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55	Trichomonas vaginalis metalloproteinase TvMP50 is a monomeric Aminopeptidase P-like enzyme. Molecular Biotechnology, 2018, 60, 563-575.	1.3	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.	1.0	5
57	Inductive effects in amino acids and peptides: Ionization constants and tryptophan fluorescence. Biochemistry and Biophysics Reports, 2020, 24, 100802.	0.7	5
58	Twinned or not twinned, that is the question: crystallization and preliminary crystallographic analysis of the 2F13F1 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.	0.4	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.	0.7	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.	0.7	4
62	Conformational stability and crystal packing: polymorphism in Neurospora crassa CAT-3. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 753-758.	0.7	3
63	Crystal structure of a class $\mu$ glutathione S-transferase from whiteleg shrimp <i>Litopenaeus vannamei</i> : structural changes in the xenobiotic binding site may alter the spectra of molecules bound. Journal of Biochemical and Molecular Toxicology, 2017, 31, N/A.	1.4	3
64	Novel Devices for Transporting Protein Crystals to the Synchrotron Facilities and Thermal Protection of Protein Crystals. Crystals, 2018, 8, 340.	1.0	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.	0.7	1
66	Zo-peroxidase: Crystal structure and sequence of a highly-glycosylated peroxidase resistant to high concentrations of H <sub>2</sub> O <sub>2</sub> from Japanese radish. Biochemistry and Biophysics Reports, 2018, 13, 32-38.	0.7	1
67	PCNA from <i>Thermococcus gammatolerans</i> : A protein involved in chromosomal DNA metabolism intrinsically resistant at high levels of ionizing radiation. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1684-1698.	1.5	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