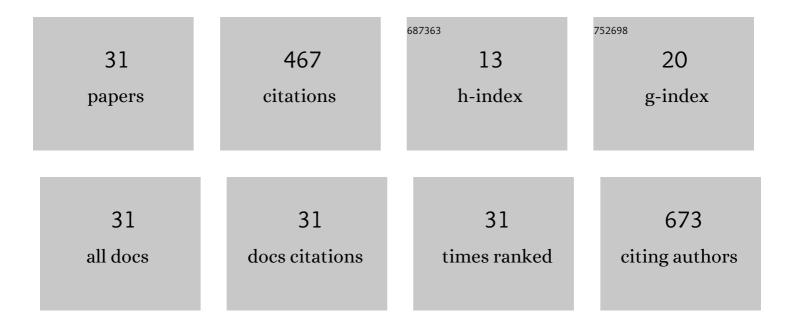
## Ricardo Cabrera

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Engineering an acetoacetyl-CoA reductase from Cupriavidus necator toward NADH preference under physiological conditions. Scientific Reports, 2022, 12, 3757.	3.3	6
2	An NADH preferring acetoacetyl-CoA reductase is engaged in poly-3-hydroxybutyrate accumulation in Escherichia coli. Journal of Biotechnology, 2021, 325, 207-216.	3.8	9
3	Comparative characterization of the hemocyanin-derived phenol oxidase activity from spiders inhabiting different thermal habitats. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2021, 253, 110548.	1.6	1
4	Deletion and Randomization of Structurally Variable Regions in B. subtilis Lipase A (BSLA) Alter Its Stability and Hydrolytic Performance Against Long Chain Fatty Acid Esters. International Journal of Molecular Sciences, 2020, 21, 1990.	4.1	6
5	Functional characterisation and in silico modelling of MdPSY2 variants and MdPSY5 phytoene synthases from Malus domestica. Journal of Plant Physiology, 2020, 249, 153166.	3.5	8
6	>Fluorescence enzymatic assay for bacterial polyphosphate kinase 1 (PPK1) as a platform for screening antivirulence molecules. Infection and Drug Resistance, 2019, Volume 12, 2237-2242.	2.7	3
7	Surfaces based on amino acid functionalized polyelectrolyte films towards active surfaces for enzyme immobilization. Materials Science and Engineering C, 2019, 104, 109938.	7.3	7
8	Studying the phosphoryl transfer mechanism of the <i>E. coli</i> phosphofructokinase-2: from X-ray structure to quantum mechanics/molecular mechanics simulations. Chemical Science, 2019, 10, 2882-2892.	7.4	15
9	Cold tolerance mechanisms of two arthropods from the Andean Range of Central Chile: Agathemera crassa (Insecta: Agathemeridae) and Euathlus condorito (Arachnida: Theraphosidae). Journal of Thermal Biology, 2018, 74, 133-139.	2.5	16
10	Understanding the impact of the cofactor swapping of isocitrate dehydrogenase over the growth phenotype of Escherichia coli on acetate by using constraint-based modeling. PLoS ONE, 2018, 13, e0196182.	2.5	12
11	Inorganic Polyphosphate, Exopolyphosphatase, and <i>Pho84</i> -Like Transporters May Be Involved in Copper Resistance in <i>Metallosphaera sedula</i> DSM 5348 <sup>T</sup> . Archaea, 2018, 2018, 1-12.	2.3	36
12	Multi-level evaluation of Escherichia coli polyphosphate related mutants using global transcriptomic, proteomic and phenomic analyses. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 871-883.	2.4	21
13	Datasets for transcriptomics, q-proteomics and phenotype microarrays of polyphosphate metabolism mutants from Escherichia coli. Data in Brief, 2017, 12, 13-17.	1.0	2
14	Dictyostelium discoideum as a surrogate host–microbe model for antivirulence screening in Pseudomonas aeruginosa PAO1. International Journal of Antimicrobial Agents, 2016, 47, 403-409.	2.5	30
15	Determinants of Cofactor Specificity for the Glucose-6-Phosphate Dehydrogenase from Escherichia coli: Simulation, Kinetics and Evolutionary Studies. PLoS ONE, 2016, 11, e0152403.	2.5	19
16	Polyol specificity of recombinant Arabidopsis thaliana sorbitol dehydrogenase studied by enzyme kinetics and in silico modeling. Frontiers in Plant Science, 2015, 6, 91.	3.6	8
17	Sorbitol dehydrogenase is a cytosolic protein required for sorbitol metabolism in Arabidopsis thaliana. Plant Science, 2013, 205-206, 63-75.	3.6	45
18	A Ribokinase Family Conserved Monovalent Cation Binding Site Enhances the MgATP-induced Inhibition in E.Âcoli Phosphofructokinase-2. Biophysical Journal, 2013, 105, 185-193.	0.5	11

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19	Modeling the Interfacial Interactions between CrtS and CrtR from Xanthophyllomyces dendrorhous, a P450 System Involved in Astaxanthin Production. Journal of Agricultural and Food Chemistry, 2012, 60, 8640-8647.	5.2	19
20	The cofactor preference of glucoseâ€6â€phosphate dehydrogenase from <i>Escherichia coli</i> – modeling the physiological production of reduced cofactors. FEBS Journal, 2012, 279, 2296-2309.	4.7	31
21	The Crystal Complex of Phosphofructokinase-2 of Escherichia coli with Fructose-6-phosphate. Journal of Biological Chemistry, 2011, 286, 5774-5783.	3.4	26
22	Ribokinase family evolution and the role of conserved residues at the active site of the PfkB subfamily representative, Pfk-2 from Escherichia coli. Archives of Biochemistry and Biophysics, 2010, 502, 23-30.	3.0	32
23	Crystallographic Structure of Phosphofructokinase-2 from Escherichia coli in Complex with Two ATP Molecules. Implications for Substrate Inhibition. Journal of Molecular Biology, 2008, 383, 588-602.	4.2	26
24	Unfolding Pathway of the Dimeric and Tetrameric Forms of Phosphofructokinase-2 from Escherichia coli. Biochemistry, 2007, 46, 6141-6148.	2.5	12
25	Evidence for a Catalytic Mg2+ Ion and Effect of Phosphate on the Activity of Escherichia coli Phosphofructokinase-2:  Regulatory Properties of a Ribokinase Family Member. Biochemistry, 2006, 45, 9291-9299.	2.5	30
26	Crystallization and preliminary crystallographic analysis of the tetrameric form of phosphofructokinase-2 fromEscherichia coli, a member of the ribokinase family. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 935-937.	0.7	2
27	Role of Cys-295 on subunit interactions and allosteric regulation of phosphofructokinase-2 fromEscherichia coli. FEBS Letters, 2005, 579, 2313-2318.	2.8	11
28	Undergraduate teaching of evolution in chile: more than natural selection. Revista Chilena De Historia Natural, 2005, 78, .	1.2	0
29	Domain Motions and Quaternary Packing of Phosphofructokinase-2 from Escherichia coli Studied by Small Angle X-ray Scattering and Homology Modeling. Journal of Biological Chemistry, 2003, 278, 12913-12919.	3.4	13
30	Ligand-dependent structural changes and limited proteolysis of Escherichia coli phosphofructokinase-2. Archives of Biochemistry and Biophysics, 2002, 406, 289-295.	3.0	8
31	Crystal structure of the 6-phosphogluconate dehydrogenase from Gluconobacter oxydans reveals tetrameric 6PGDHs as the crucial intermediate in the evolution of structure and cofactor preference in the 6PGDH family. Wellcome Open Research, 0, 6, 48.	1.8	2