

# Jose M Arguello

## List of Publications by Year in descending order

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81  
papers

4,271  
citations

116194

36  
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129628

63  
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86  
all docs

86  
docs citations

86  
times ranked

3328  
citing authors

#	ARTICLE	IF	CITATIONS
1	Copper Handling in the Salmonella Cell Envelope and Its Impact on Virulence. Trends in Microbiology, 2021, 29, 384-387.	3.5	8
2	<i>Medicago truncatula</i> Ferroportin2 mediates iron import into nodule symbiosomes. New Phytologist, 2020, 228, 194-209.	3.5	23
3	Fast, Simple, Student Generated Augmented Reality Approach for Protein Visualization in the Classroom and Home Study. Journal of Chemical Education, 2020, 97, 2327-2331.	1.1	13
4	The Two-Component System CopRS Maintains Subfemtomolar Levels of Free Copper in the Periplasm of <i>Pseudomonas aeruginosa</i> Using a Phosphatase-Based Mechanism. MSphere, 2020, 5, .	1.3	18
5	The interplay of the metallosensor CueR with two distinct CopZ chaperones defines copper homeostasis in <i>Pseudomonas aeruginosa</i> . Journal of Biological Chemistry, 2019, 294, 4934-4945.	1.6	27
6	Nicotianamine Synthase 2 Is Required for Symbiotic Nitrogen Fixation in <i>Medicago truncatula</i> Nodules. Frontiers in Plant Science, 2019, 10, 1780.	1.7	13
7	An important role for periplasmic storage in <i>Pseudomonas aeruginosa</i> copper homeostasis revealed by a combined experimental and computational modeling study. Molecular Microbiology, 2018, 110, 357-369.	1.2	13
8	The cytoplasmic Cu + chaperones of <i>Pseudomonas aeruginosa</i> . FASEB Journal, 2018, 32, 803.4.	0.2	0
9	Copper homeostasis networks in the bacterium <i>Pseudomonas aeruginosa</i> . Journal of Biological Chemistry, 2017, 292, 15691-15704.	1.6	100
10	The <i>Listeria monocytogenes</i> Fur-regulated virulence protein FrvA is an Fe(II) efflux P <sub>1B4</sub> -type ATPase. Molecular Microbiology, 2016, 100, 1066-1079.	1.2	48
11	Fine-tuning of Substrate Affinity Leads to Alternative Roles of <i>Mycobacterium tuberculosis</i> Fe <sup>2+</sup> -ATPases. Journal of Biological Chemistry, 2016, 291, 11529-11539.	1.6	36
12	Bacterial Cu <sup>+</sup> -ATPases: models for molecular structure-function studies. Metallomics, 2016, 8, 906-914.	1.0	24
13	Assay of Copper Transfer and Binding to P1B-ATPases. Methods in Molecular Biology, 2016, 1377, 267-277.	0.4	5
14	PfeT, a P <sub>1B4</sub> -type ATPase, effluxes ferrous iron and protects <i>Bacillus subtilis</i> against iron intoxication. Molecular Microbiology, 2015, 98, 787-803.	1.2	72
15	A Novel Antimycobacterial Compound Acts as an Intracellular Iron Chelator. Antimicrobial Agents and Chemotherapy, 2015, 59, 2256-2264.	1.4	33
16	Evolution of a plant-specific copper chaperone family for chloroplast copper homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5480-7.	3.3	57
17	Functional diversity of five homologous Cu <sup>+</sup> -ATPases present in <i>Sinorhizobium meliloti</i> . Microbiology (United Kingdom), 2014, 160, 1237-1251.	0.7	21
18	Mechanism of ATPase-mediated Cu <sup>+</sup> Export and Delivery to Periplasmic Chaperones. Journal of Biological Chemistry, 2014, 289, 20492-20501.	1.6	73

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19	Differential roles for the $\text{Co}^{2+}$ -transporting ATPases, CtpD and CtpJ, in <i>Mycobacterium tuberculosis</i> virulence. <i>Molecular Microbiology</i> , 2014, 91, 185-197.	1.2	52
20	Sinorhizobium meliloti Nia is a P1B-5-ATPase expressed in the nodule during plant symbiosis and is involved in Ni and Fe transport. <i>Metallomics</i> , 2013, 5, 1614.	1.0	39
21	Periplasmic response upon disruption of transmembrane Cu transport in <i>Pseudomonas aeruginosa</i> . <i>Metallomics</i> , 2013, 5, 144.	1.0	31
22	The Mechanism of $\text{Cu}^+$ Transport ATPases. <i>Journal of Biological Chemistry</i> , 2013, 288, 69-78.	1.6	67
23	A Novel P1B-type $\text{Mn}^{2+}$ -transporting ATPase Is Required for Secreted Protein Metallation in Mycobacteria. <i>Journal of Biological Chemistry</i> , 2013, 288, 11334-11347.	1.6	86
24	Mechanisms of copper homeostasis in bacteria. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013, 3, 73.	1.8	193
25	Mechanisms of $\text{Cu}^+$ transfer from soluble $\text{Cu}^+$ chaperones to transmembrane transport ATPases. <i>FASEB Journal</i> , 2013, 27, 1017.1.	0.2	0
26	Toward a Molecular Understanding of Metal Transport by P1B-Type ATPases. <i>Current Topics in Membranes</i> , 2012, 69, 113-136.	0.5	55
27	Conformations of the apo-, substrate-bound and phosphate-bound ATP-binding domain of the Cu(II) ATPase CopB illustrate coupling of domain movement to the catalytic cycle. <i>Bioscience Reports</i> , 2012, 32, 443-453.	1.1	10
28	Metal Transport across Biomembranes: Emerging Models for a Distinct Chemistry. <i>Journal of Biological Chemistry</i> , 2012, 287, 13510-13517.	1.6	94
29	A tetrahedral coordination of Zinc during transmembrane transport by P-type $\text{Zn}^{2+}$ -ATPases. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1374-1377.	1.4	29
30	Evolution and diversity of periplasmic proteins involved in copper homeostasis in gamma proteobacteria. <i>BMC Microbiology</i> , 2012, 12, 249.	1.3	60
31	Identifying metalloproteins through X-ray fluorescence mapping and mass spectrometry. <i>Metallomics</i> , 2012, 4, 921.	1.0	22
32	Role in metal homeostasis of CtpD, a $\text{Co}^{2+}$ transporting P <sub>1B4</sub> -ATPase of <i>Mycobacterium smegmatis</i> . <i>Molecular Microbiology</i> , 2012, 84, 1139-1149.	1.2	50
33	The Mechanism of Bacterial $\text{Cu}^+$ -ATPases. Distinct Efflux Rates Adapted to Different Function. <i>Biophysical Journal</i> , 2011, 100, 465a.	0.2	0
34	Bacterial Transition Metal P <sub>1B</sub> -ATPases: Transport Mechanism and Roles in Virulence. <i>Biochemistry</i> , 2011, 50, 9940-9949.	1.2	101
35	The transport mechanism of bacterial $\text{Cu}^+$ -ATPases: distinct efflux rates adapted to different function. <i>BioMetals</i> , 2011, 24, 467-475.	1.8	106
36	A Novel Zinc Binding System, ZevAB, Is Critical for Survival of Nontypeable <i>Haemophilus influenzae</i> in a Murine Lung Infection Model. <i>Infection and Immunity</i> , 2011, 79, 3366-3376.	1.0	44

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37	Structure and interactions of the C-terminal metal binding domain of <i>Archaeoglobus fulgidus</i> CopA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2450-2458.	1.5	18
38	Distinct functional roles of homologous Cu <sup>+</sup> efflux ATPases in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2010, 78, 1246-1258.	1.2	139
39	Reversible Unfolding of a Thermophilic Membrane Protein in Phospholipid/Detergent Mixed Micelles. <i>Journal of Molecular Biology</i> , 2010, 397, 550-559.	2.0	29
40	Chaperone-mediated Cu <sup>+</sup> Delivery to Cu <sup>+</sup> Transport ATPases. <i>Journal of Biological Chemistry</i> , 2009, 284, 20804-20811.	1.6	52
41	Mechanistic steps of metal uploading into Cu <sup>+</sup> -transporting ATPases. <i>FASEB Journal</i> , 2009, 23, 867.3.	0.2	0
42	Mechanism of Cu <sup>+</sup> -transporting ATPases: Soluble Cu <sup>+</sup> chaperones directly transfer Cu <sup>+</sup> to transmembrane transport sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5992-5997.	3.3	210
43	Cu <sup>+</sup> -ATPases Brake System. <i>Structure</i> , 2008, 16, 833-834.	1.6	12
44	Thermal stability of CopA, a polytopic membrane protein from the hyperthermophile <i>Archaeoglobus fulgidus</i> . <i>Archives of Biochemistry and Biophysics</i> , 2008, 471, 198-206.	1.4	17
45	Structure of the Two Transmembrane Cu <sup>+</sup> Transport Sites of the Cu <sup>+</sup> -ATPases*. <i>Journal of Biological Chemistry</i> , 2008, 283, 29753-29759.	1.6	90
46	Characterization and Structure of a Zn <sup>2+</sup> and [2Fe-2S]-containing Copper Chaperone from <i>Archaeoglobus fulgidus</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 25950-25959.	1.6	32
47	Activation of <i>Archaeoglobus fulgidus</i> Cu <sup>+</sup> -ATPase CopA by cysteine. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 495-501.	1.4	25
48	Novel Zn <sup>2+</sup> Coordination by the Regulatory N-Terminus Metal Binding Domain of <i>Arabidopsis thaliana</i> Zn <sup>2+</sup> -ATPase HMA2. <i>Biochemistry</i> , 2007, 46, 7754-7764.	1.2	52
49	The structure and function of heavy metal transport P1B-ATPases. <i>BioMetals</i> , 2007, 20, 233-248.	1.8	303
50	Structure of the ATP Binding Domain from the <i>Archaeoglobus fulgidus</i> Cu <sup>+</sup> -ATPase. <i>Journal of Biological Chemistry</i> , 2006, 281, 11161-11166.	1.6	84
51	Structure of the Actuator Domain from the <i>Archaeoglobus fulgidus</i> Cu <sup>+</sup> -ATPase. <i>Biochemistry</i> , 2006, 45, 9949-9955.	1.2	56
52	A Novel Regulatory Metal Binding Domain Is Present in the C Terminus of <i>Arabidopsis</i> Zn <sup>2+</sup> -ATPase HMA2*. <i>Journal of Biological Chemistry</i> , 2006, 281, 33881-33891.	1.6	58
53	<i>Arabidopsis</i> HMA2, a Divalent Heavy Metal-Transporting PIB-Type ATPase, Is Involved in Cytoplasmic Zn <sup>2+</sup> Homeostasis. <i>Plant Physiology</i> , 2004, 136, 3712-3723.	2.3	206
54	Identification of the Transmembrane Metal Binding Site in Cu <sup>+</sup> -transporting PIB-type ATPases. <i>Journal of Biological Chemistry</i> , 2004, 279, 54802-54807.	1.6	67

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55	Identification of Ion-Selectivity Determinants in Heavy-Metal Transport P 1B -type ATPases. <i>Journal of Membrane Biology</i> , 2003, 195, 93-108.	1.0	255
56	Heavy Metal Transport CPxâ€ATPases from the Thermophile <i>Archaeoglobus fulgidus</i>. <i>Annals of the New York Academy of Sciences</i> , 2003, 986, 212-218.	1.8	27
57	The Na,Kâ€ATPase S5â€H5 Helix. <i>Annals of the New York Academy of Sciences</i> , 2003, 986, 224-225.	1.8	4
58	Functional Roles of Metal Binding Domains of the <i>Archaeoglobus fulgidus</i> Cu <sup>++</sup> -ATPase CopA. <i>Biochemistry</i> , 2003, 42, 11040-11047.	1.2	97
59	<i>Archaeoglobus fulgidus</i> CopB Is a Thermophilic Cu <sup>2+</sup> -ATPase. <i>Journal of Biological Chemistry</i> , 2003, 278, 40534-40541.	1.6	102
60	Characterization of a Thermophilic P-type Ag <sup>+</sup> /Cu <sup>+</sup> -ATPase from the Extremophile <i>Archaeoglobus fulgidus</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 7201-7208.	1.6	106
61	Catalytic Phosphorylation of Na,K-ATPase Drives the Outward Movement of Its Cation-Binding H5â€H6 Hairpinâ€. <i>Biochemistry</i> , 2002, 41, 8195-8202.	1.2	9
62	Reactivity of Cysteines in the Transmembrane Region of the Na,K-ATPase Î± Subunit Probed with Hg <sup>2+</sup> . <i>Journal of Membrane Biology</i> , 2000, 177, 187-197.	1.0	11
63	Electrogenic Sodiumâ€Sodium Exchange Carried Out by Na,k -Atpase Containing the Amino Acid Substitution Glu779ala. <i>Journal of General Physiology</i> , 2000, 116, 61-74.	0.9	13
64	The Role of Na,k-Atpase Î± Subunit Serine 775 and Glutamate 779 in Determining the Extracellular K <sup>+</sup> And Membrane Potentialâ€Dependent Properties of the Na,k -Pump. <i>Journal of General Physiology</i> , 2000, 116, 47-60.	0.9	17
65	Functional role of cysteine residues in the (Na,K)-ATPase Î± subunit. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2000, 1464, 177-187.	1.4	22
66	Functional Role of Oxygen-Containing Residues in the Fifth Transmembrane Segment of the Na,K-ATPase Î± Subunit. <i>Archives of Biochemistry and Biophysics</i> , 1999, 364, 254-263.	1.4	18
67	Alanine Scanning Mutagenesis of Oxygen-Containing Amino Acids in the Transmembrane Region of the Na,K-ATPase. <i>Archives of Biochemistry and Biophysics</i> , 1999, 367, 341-347.	1.4	17
68	Evidence That Ser775 in the Î± Subunit of the Na,K-ATPase Is a Residue in the Cation Binding Pocket. <i>Journal of Biological Chemistry</i> , 1997, 272, 24987-24993.	1.6	47
69	Cation and Cardiac Glycoside Binding Sites of the Na,K-ATPase. <i>Annals of the New York Academy of Sciences</i> , 1997, 834, 194-206.	1.8	75
70	Changes to Na,K-ATPase Î±-Subunit E779 Separate the Structural Basis for VM and Ion Dependence of Na,K-Pump Current. <i>Annals of the New York Academy of Sciences</i> , 1997, 834, 339-342.	1.8	5
71	Substitution of Glutamic 779 with Alanine in the Na,K-ATPase Î± Subunit Removes Voltage Dependence of Ion Transport. <i>Journal of Biological Chemistry</i> , 1996, 271, 24610-24616.	1.6	35
72	Ouabain Interactions with the H5-H6 Hairpin of the Na,K-ATPase Reveal a Possible Inhibition Mechanism via the Cation Binding Domain. <i>Journal of Biological Chemistry</i> , 1996, 271, 14176-14182.	1.6	101

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73	Asp804 and Asp808 in the Transmembrane Domain of the Na,K-ATPase $\hat{\pm}$ Subunit Are Cation Coordinating Residues. <i>Journal of Biological Chemistry</i> , 1996, 271, 29682-29687.	1.6	86
74	Substitutions of Serine 775 in the $\hat{\pm}$ Subunit of the Na,K-ATPase Selectively Disrupt K <sup>+</sup> High Affinity Activation without Affecting Na <sup>+</sup> Interaction. <i>Journal of Biological Chemistry</i> , 1995, 270, 22764-22771.	1.6	67
75	The Stabilization of Cation Binding and its Relation to Na <sup>+</sup> /K <sup>+</sup> -ATPase Structure and Function. , 1994, , 321-331.		2
76	N-Acetylimidazole inactivates renal sodium-potassium ATPase by disrupting ATP binding to the catalytic site. <i>Biochemistry</i> , 1990, 29, 5775-5782.	1.2	13
77	Biochemical alterations in skeletal muscle induced by 2,4-dichlorophenoxyacetic butyl ester during chick embryonic development. <i>Biochemical Pharmacology</i> , 1990, 40, 2433-2440.	2.0	7
78	Ca <sup>2+</sup> Homeostasis alterations induced by 2,4-dichlorophenoxyacetic butyl ester and 2,4-dichlorophenoxyacetic acid on avian skeletal muscle. <i>Biochemical Pharmacology</i> , 1990, 40, 2441-2448.	2.0	11
79	Nucleic Acid Content and Residue Determination in Tissues of Chicks Born From 2,4-Dichlorophenoxyacetic Butyl Ester Treated Eggs. <i>Drug and Chemical Toxicology</i> , 1987, 10, 339-355.	1.2	11
80	Effect of post-rigor fish storage on ice on physicochemical properties of actomyosin. <i>Journal of the Science of Food and Agriculture</i> , 1982, 33, 1129-1134.	1.7	21
81	Unique underlying principles shaping copper homeostasis networks. <i>Journal of Biological Inorganic Chemistry</i> , 0, , .	1.1	10