Lennane Michel Espinoza-Fonseca

List of Publications by Year
in descending order

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62 papers	1,435 citations	304743 22 h-index	377865 34 g-index
64 all docs	64 docs citations	64 times ranked	1809 citing authors

#	Article	IF	Citations
1	Homologous cardiac calcium pump regulators phospholamban and sarcolipin adopt distinct oligomeric states in the membrane. Computational and Structural Biotechnology Journal, 2022, 20, 380-384.	4.1	4
2	Fluorescence lifetime imaging microscopy reveals sodium pump dimers in live cells. Journal of Biological Chemistry, 2022, 298, 101865.	3.4	12
3	Primitive Phospholamban- and Sarcolipin-like Peptides Inhibit the Sarcoplasmic Reticulum Calcium Pump SERCA. Biochemistry, 2022, 61, 1419-1430.	2.5	2
4	Structural Basis for the Function of the C-Terminal Proton Release Pathway in the Calcium Pump. International Journal of Molecular Sciences, 2021, 22, 3507.	4.1	0
5	Dwarf open reading frame (DWORF) is a direct activator of the sarcoplasmic reticulum calcium pump SERCA. ELife, 2021, 10, .	6.0	31
6	A multiscale approach for bridging the gap between potency, efficacy, and safety of small molecules directed at membrane proteins. Scientific Reports, 2021, 11, 16580.	3.3	10
7	Nothing Regular about the Regulins: Distinct Functional Properties of SERCA Transmembrane Peptide Regulatory Subunits. International Journal of Molecular Sciences, 2021, 22, 8891.	4.1	32
8	An in silico pipeline for the discovery of multitarget ligands: A case study for epi-polypharmacology based on DNMT1/HDAC2 inhibition. Artificial Intelligence in the Life Sciences, 2021, 1, 100008.	2.2	1
9	Interaction of a Sarcolipin Pentamer and Monomer with the Sarcoplasmic Reticulum Calcium Pump, SERCA. Biophysical Journal, 2020, 118, 518-531.	0.5	13
10	Atomistic Structure and Dynamics of the Ca2+-ATPase Bound to Phosphorylated Phospholamban. International Journal of Molecular Sciences, 2020, 21, 7261.	4.1	6
11	Conserved Luminal C-Terminal Domain Dynamically Controls Interdomain Communication in Sarcolipin. Journal of Chemical Information and Modeling, 2020, 60, 3985-3991.	5.4	3
12	Multiscale Simulation Reveals Passive Proton Transport Through SERCA on the Microsecond Timescale. Biophysical Journal, 2020, 119, 1033-1040.	0.5	11
13	Linking Biochemical and Structural States of SERCA: Achievements, Challenges, and New Opportunities. International Journal of Molecular Sciences, 2020, 21, 4146.	4.1	36
14	A hallmark of phospholamban functional divergence is located in the N-terminal phosphorylation domain. Computational and Structural Biotechnology Journal, 2020, 18, 705-713.	4.1	3
15	Dynamics-Driven Allostery Underlies Ca2+-Mediated Release of SERCA Inhibition by Phospholamban. Biophysical Journal, 2020, 119, 1917-1926.	0.5	10
16	The Phospholamban Pentamer Alters Function of the Sarcoplasmic Reticulum Calcium Pump SERCA. Biophysical Journal, 2019, 116, 633-647.	0.5	30
17	Probing the effects of nonannular lipid binding on the stability of the calcium pump SERCA. Scientific Reports, 2019, 9, 3349.	3.3	4
18	Structural Basis for the Limited Response to Oxidative and Thiol-Conjugating Agents by Triosephosphate Isomerase From the Photosynthetic Bacteria Synechocystis. Frontiers in Molecular Biosciences, 2018, 5, 103.	3.5	5

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19	Structural basis for relief of phospholamban-mediated inhibition of the sarcoplasmic reticulum Ca2+-ATPase at saturating Ca2+ conditions. Journal of Biological Chemistry, 2018, 293, 12405-12414.	3.4	20
20	The Ca²⁺-ATPase pump facilitates bidirectional proton transport across the sarco/endoplasmic reticulum. Molecular BioSystems, 2017, 13, 633-637.	2.9	10
21	Preexisting domain motions underlie protonation-dependent structural transitions of the P-type Ca2+-ATPase. Physical Chemistry Chemical Physics, 2017, 19, 10153-10162.	2.8	11
22	Sarcolipin Promotes Uncoupling of the SERCA Ca²⁺ Pump by Inducing a Structural Rearrangement in the Energy-Transduction Domain. Biochemistry, 2016, 55, 6083-6086.	2.5	39
23	Pathogenic mutation R959W alters recognition dynamics of dysferlin inner DysF domain. Molecular BioSystems, 2016, 12, 973-981.	2.9	6
24	Site-directed spectroscopy of cardiac myosin-binding protein C reveals effects of phosphorylation on protein structural dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3233-3238.	7.1	47
25	Structural Mechanism for Regulation of Bcl-2 protein Noxa by phosphorylation. Scientific Reports, 2015, 5, 14557.	3.3	11
26	Microsecond Molecular Simulations Reveal a Transient Proton Pathway in the Calcium Pump. Journal of the American Chemical Society, 2015, 137, 7055-7058.	13.7	18
27	Sarcolipin and phospholamban inhibit the calcium pump by populating a similar metal ion-free intermediate state. Biochemical and Biophysical Research Communications, 2015, 463, 37-41.	2.1	31
28	Sequential myosin phosphorylation activates tarantula thick filament via a disorderâ€“order transition. Molecular BioSystems, 2015, 11, 2167-2179.	2.9	15
29	Atomistic Characterization of the First Step of Calcium Pump Activation Associated with Proton Countertransport. Biochemistry, 2015, 54, 5235-5241.	2.5	9
30	Atomic-Level Mechanisms for Phospholamban Regulation of the Calcium Pump. Biophysical Journal, 2015, 108, 1697-1708.	0.5	35
31	Microsecond Molecular Dynamics Simulations of Mg2+- and K+- Bound E1 Intermediate States of the Calcium Pump. PLoS ONE, 2014, 9, e95979.	2.5	39
32	Effects of pseudophosphorylation mutants on the structural dynamics of smooth muscle myosin regulatory light chain. Molecular BioSystems, 2014, 10, 2693-2698.	2.9	15
33	Backbone conformational preferences of an intrinsically disordered protein in solution. Molecular BioSystems, 2012, 8, 1798.	2.9	24
34	Dynamic optimization of signal transductionvia intrinsic disorder. Molecular BioSystems, 2012, 8, 194-197.	2.9	4
35	Aromatic residues link binding and function of intrinsically disordered proteins. Molecular BioSystems, 2012, 8, 237-246.	2.9	31
36	Atomic-Level Characterization of the Activation Mechanism of SERCA by Calcium. PLoS ONE, 2011, 6, e26936.	2.5	50

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37	Phosphorylation-induced structural changes in smooth muscle myosin regulatory light chain. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8207-8212.	7.1	74
38	Tyr74 is essential for the formation, stability and function of Plasmodium falciparum triosephosphate isomerase dimer. Archives of Biochemistry and Biophysics, 2010, 494, 46-57.	3.0	8
39	Leucineâ€rich hydrophobic clusters promote folding of the Nâ€terminus of the intrinsically disordered transactivation domain of p53. FEBS Letters, 2009, 583, 556-560.	2.8	31
40	Thermodynamic Aspects of Coupled Binding and Folding of an Intrinsically Disordered Protein: A Computational Alanine Scanning Study. Biochemistry, 2009, 48, 11332-11334.	2.5	19
41	Reconciling binding mechanisms of intrinsically disordered proteins. Biochemical and Biophysical Research Communications, 2009, 382, 479-482.	2.1	83
42	Knowledgebase for addiction-related genes: Is it possible an extrapolation to rational multi-target drug design?. Bioorganic and Medicinal Chemistry, 2008, 16, 9346-9348.	3.0	4
43	Structure and dynamics of the full-length M1 muscarinic acetylcholine receptor studied by molecular dynamics simulations. Archives of Biochemistry and Biophysics, 2008, 469, 142-150.	3.0	10
44	Aromaticâ€“aromatic interactions in the formation of the MDM2â€“p53 complex. Biochemical and Biophysical Research Communications, 2008, 370, 547-551.	2.1	23
45	Thermodynamic and Structural Basis of Phosphorylation-Induced Disorder-to-Order Transition in the Regulatory Light Chain of Smooth Muscle Myosin. Journal of the American Chemical Society, 2008, 130, 12208-12209.	13.7	57
46	Molecular Dynamics Simulations Reveal a Disorder-to-Order Transition on Phosphorylation of Smooth Muscle Myosin. Biophysical Journal, 2007, 93, 2083-2090.	0.5	64
47	Docking and quantum mechanic studies on cholinesterases and their inhibitors. European Journal of Medicinal Chemistry, 2007, 42, 10-19.	5.5	46
48	Transient stability of the helical pattern of region F19â€“L22 of the N-terminal domain of p53: A molecular dynamics simulation study. Biochemical and Biophysical Research Communications, 2006, 343, 110-116.	2.1	15
49	The existence of a second allosteric site on the M1 muscarinic acetylcholine receptor and its implications for drug design. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 1217-1220.	2.2	20
50	Toward a rational design of selective multi-trypanosomatid inhibitors: A computational docking study. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 6288-6292.	2.2	19
51	The benefits of the multi-target approach in drug design and discovery. Bioorganic and Medicinal Chemistry, 2006, 14, 896-897.	3.0	130
52	Fully flexible docking models of the complex between Î±7 nicotinic receptor and a potent heptapeptide inhibitor of the Î²-amyloid peptide binding. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 3519-3523.	2.2	7
53	Inhibition of acetylcholinesterase by two arylderivatives: 3a-Acetoxy-5H-pyrrolo(1,2-a) (3,1)benzoxazin-1,5-(3aH)-dione andcis-N-p-Acetoxy-phenylisomaleimide. Journal of Enzyme Inhibition and Medicinal Chemistry, 2006, 21, 133-138.	5.2	15
54	pâ€“Aminobenzoic acid derivatives as acetylcholinesterase inhibitors. European Journal of Medicinal Chemistry, 2005, 40, 732-735.	5.5	35

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55	Targeting MDM2 by the small molecule RITA: towards the development of new multi-target drugs against cancer. , 2005, 2, 38.		25
56	Structural considerations for the rational design of selective anti-trypanosomal agents: The role of the aromatic clusters at the interface of triosephosphate isomerase dimer. Biochemical and Biophysical Research Communications, 2005, 328, 922-928.	2.1	22
57	Identification of multiple allosteric sites on the M1muscarinic acetylcholine receptor. FEBS Letters, 2005, 579, 6726-6732.	2.8	11
58	Exploring the possible binding sites at the interface of triosephosphate isomerase dimer as a potential target for anti-tripanosomal drug design. Bioorganic and Medicinal Chemistry Letters, 2004, 14, 3151-3154.	2.2	20
59	Base docking model of the homomeric Î±7 nicotinic receptorâ€“Î²-amyloid1â€“42 complex. Biochemical and Biophysical Research Communications, 2004, 320, 587-591.	2.1	16
60	Molecular docking of four Î²-amyloid1â€“42 fragments on the Î±7 nicotinic receptor: delineating the binding site of the Aî² peptides. Biochemical and Biophysical Research Communications, 2004, 323, 1191-1196.	2.1	10
61	Synthesis, Anticholinesterase Activity and Structureâ€”Activity Relationships of m-Aminobenzoic Acid Derivatives.. ChemInform, 2003, 34, no.	0.0	0
62	Synthesis, anticholinesterase activity and structureâ€“Activity relationships of m-Aminobenzoic acid derivatives. Bioorganic and Medicinal Chemistry Letters, 2003, 13, 1825-1827.	2.2	42