

Alessandro Senes

List of Publications by Year in Descending Order

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Version: 2024-04-24

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

30
papers

2,097
citations

18
h-index

33
g-index

33
ext. papers

2,314
ext. citations

8.1
avg, IF

4.6
L-index

#	Paper	IF	Citations
30	The coiled-coil domain of E. coli FtsLB is a structurally detuned element critical for modulating its activation in bacterial cell division. <i>Journal of Biological Chemistry</i> , 2021 , 101460	5.4	0
29	An energetics database to model protein-protein interactions. <i>FASEB Journal</i> , 2019 , 33, 642.7	0.9	
28	Analysis of spliceosome dynamics by maximum likelihood fitting of dwell time distributions. <i>Methods</i> , 2019 , 153, 13-21	4.6	5
27	The FtsLB subcomplex of the bacterial divisome is a tetramer with an uninterrupted FtsL helix linking the transmembrane and periplasmic regions. <i>Journal of Biological Chemistry</i> , 2018 , 293, 1623-1641	5.4	11
26	The Cytokinin Oxidase/Dehydrogenase CKX1 Is a Membrane-Bound Protein Requiring Homooligomerization in the Endoplasmic Reticulum for Its Cellular Activity. <i>Plant Physiology</i> , 2018 , 176, 2024-2039	6.6	29
25	Ptc7p Dephosphorylates Select Mitochondrial Proteins to Enhance Metabolic Function. <i>Cell Reports</i> , 2017 , 18, 307-313	10.6	28
24	Combination of CEH Hydrogen Bonds and van der Waals Packing Modulates the Stability of GxxxG-Mediated Dimers in Membranes. <i>Journal of the American Chemical Society</i> , 2017 , 139, 15774-15783	16.4	24
23	BH3-in-groove dimerization initiates and helix 9 dimerization expands Bax pore assembly in membranes. <i>EMBO Journal</i> , 2016 , 35, 208-36	13	69
22	Toward high-resolution computational design of the structure and function of helical membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 475-80	17.6	21
21	Screening for transmembrane association in divisome proteins using TOXGREEN, a high-throughput variant of the TOXCAT assay. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 2573-2583	3.8	6
20	Fluorophores, environments, and quantification techniques in the analysis of transmembrane helix interaction using FRET. <i>Biopolymers</i> , 2015 , 104, 247-64	2.2	9
19	Inside-out Ca(2+) signalling prompted by STIM1 conformational switch. <i>Nature Communications</i> , 2015 , 6, 7826	17.4	119
18	Backbone dependency further improves side chain prediction efficiency in the Energy-based Conformer Library (bEBL). <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 3177-87	4.2	11
17	A frequent, GxxxG-mediated, transmembrane association motif is optimized for the formation of interhelical CEH hydrogen bonds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E888-95	11.5	73
16	A Gly-zipper motif mediates homodimerization of the transmembrane domain of the mitochondrial kinase ADCK3. <i>Journal of the American Chemical Society</i> , 2014 , 136, 14068-77	16.4	16
15	The oligomeric states of the purified sigma-1 receptor are stabilized by ligands. <i>Journal of Biological Chemistry</i> , 2014 , 289, 20333-44	5.4	72
14	Measurement of transmembrane peptide interactions in liposomes using Förster resonance energy transfer (FRET). <i>Methods in Molecular Biology</i> , 2013 , 1063, 19-36	1.4	6

13	Structural organization of FtsB, a transmembrane protein of the bacterial divisome. <i>Biochemistry</i> , 2013 , 52, 2574-85	3.2	23
12	The transmembrane domains of the bacterial cell division proteins FtsB and FtsL form a stable high-order oligomer. <i>Biochemistry</i> , 2013 , 52, 7542-50	3.2	13
11	An energy-based conformer library for side chain optimization: improved prediction and adjustable sampling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 2218-34	4.2	14
10	Structural informatics, modeling, and design with an open-source Molecular Software Library (MSL). <i>Journal of Computational Chemistry</i> , 2012 , 33, 1645-61	3.5	22
9	Computational design of membrane proteins. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 460-6	8.1	26
8	Oligomerization state of photosynthetic core complexes is correlated with the dimerization affinity of a transmembrane helix. <i>Journal of the American Chemical Society</i> , 2011 , 133, 14071-81	16.4	13
7	Consensus motif for integrin transmembrane helix association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 703-8	11.5	65
6	De novo design and molecular assembly of a transmembrane diporphyrin-binding protein complex. <i>Journal of the American Chemical Society</i> , 2010 , 132, 15516-8	16.4	99
5	Using alpha-helical coiled-coils to design nanostructured metalloporphyrin arrays. <i>Journal of the American Chemical Society</i> , 2008 , 130, 11921-7	16.4	52
4	E(z), a depth-dependent potential for assessing the energies of insertion of amino acid side-chains into membranes: derivation and applications to determining the orientation of transmembrane and interfacial helices. <i>Journal of Molecular Biology</i> , 2007 , 366, 436-48	6.5	130
3	Folding of helical membrane proteins: the role of polar, GxxxG-like and proline motifs. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 465-79	8.1	368
2	Membrane protein folding: beyond the two stage model. <i>FEBS Letters</i> , 2003 , 555, 122-5	3.8	244
1	Statistical analysis of amino acid patterns in transmembrane helices: the GxxxG motif occurs frequently and in association with beta-branched residues at neighboring positions. <i>Journal of Molecular Biology</i> , 2000 , 296, 921-36	6.5	529