

# Alessandro Senes

## List of Publications by Year in descending order

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30  
papers

2,426  
citations

394421

19  
h-index

477307

29  
g-index

33  
all docs

33  
docs citations

33  
times ranked

3052  
citing authors

#	ARTICLE	IF	CITATIONS
1	The coiled-coil domain of Escherichia coli FtsLB is a structurally detuned element critical for modulating its activation in bacterial cell division. <i>Journal of Biological Chemistry</i> , 2022, 298, 101460.	3.4	8
2	Analysis of spliceosome dynamics by maximum likelihood fitting of dwell time distributions. <i>Methods</i> , 2019, 153, 13-21.	3.8	12
3	An energetics database to model protein-protein interactions. <i>FASEB Journal</i> , 2019, 33, 642.7.	0.5	0
4	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.	3.4	30
5	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.	4.8	40
6	Ptc7p Dephosphorylates Select Mitochondrial Proteins to Enhance Metabolic Function. <i>Cell Reports</i> , 2017, 18, 307-313.	6.4	45
7	Combination of C $\pi$ -H 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.	13.7	36
8	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.	2.6	9
9	<sc>B</sc> 3-groove dimerization initiates and helix 9 dimerization expands Bax pore assembly in membranes. <i>EMBO Journal</i> , 2016, 35, 208-236.	7.8	81
10	Toward high-resolution computational design of the structure and function of helical membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 475-480.	8.2	30
11	Fluorophores, environments, and quantification techniques in the analysis of transmembrane helix interaction using FRET. <i>Biopolymers</i> , 2015, 104, 247-264.	2.4	11
12	Inside-out Ca <sup>2+</sup> signalling prompted by STIM1 conformational switch. <i>Nature Communications</i> , 2015, 6, 7826.	12.8	144
13	The Oligomeric States of the Purified Sigma-1 Receptor Are Stabilized by Ligands. <i>Journal of Biological Chemistry</i> , 2014, 289, 20333-20344.	3.4	92
14	Backbone dependency further improves side chain prediction efficiency in the Energy-based Conformer Library (bEBL). <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3177-3187.	2.6	12
15	A frequent, GxxxG-mediated, transmembrane association motif is optimized for the formation of interhelical C $\pi$ -H hydrogen bonds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E888-95.	7.1	94
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, 14068-14077.	13.7	17
17	Measurement of Transmembrane Peptide Interactions in Liposomes Using Förster Resonance Energy Transfer (FRET). <i>Methods in Molecular Biology</i> , 2013, 1063, 19-36.	0.9	6
18	Structural Organization of FtsB, a Transmembrane Protein of the Bacterial Divisome. <i>Biochemistry</i> , 2013, 52, 2574-2585.	2.5	31

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19	The Transmembrane Domains of the Bacterial Cell Division Proteins FtsB and FtsL Form a Stable High-Order Oligomer. <i>Biochemistry</i> , 2013, 52, 7542-7550.	2.5	23
20	An energy-based conformer library for side chain optimization: Improved prediction and adjustable sampling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2218-2234.	2.6	14
21	Structural informatics, modeling, and design with an open-source Molecular Software Library (MSL). <i>Journal of Computational Chemistry</i> , 2012, 33, 1645-1661.	3.3	23
22	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, 14071-14081.	13.7	13
23	Computational design of membrane proteins. <i>Current Opinion in Structural Biology</i> , 2011, 21, 460-466.	5.7	29
24	Consensus motif for integrin transmembrane helix association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 703-708.	7.1	68
25	De Novo Design and Molecular Assembly of a Transmembrane Diporphyrin-Binding Protein Complex. <i>Journal of the American Chemical Society</i> , 2010, 132, 15516-15518.	13.7	110
26	Using $\alpha$ -Helical Coiled-Coils to Design Nanostructured Metalloporphyrin Arrays. <i>Journal of the American Chemical Society</i> , 2008, 130, 11921-11927.	13.7	63
27	Ez, 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, 436-448.	4.2	143
28	Folding of helical membrane proteins: the role of polar, GxxxG-like and proline motifs. <i>Current Opinion in Structural Biology</i> , 2004, 14, 465-479.	5.7	402
29	Membrane protein folding: beyond the two stage model. <i>FEBS Letters</i> , 2003, 555, 122-125.	2.8	273
30	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, 921-936.	4.2	567