

# Alessandro Senes

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

2,426  
citations

393982

19  
h-index

476904

29  
g-index

33  
all docs

33  
docs citations

33  
times ranked

3052  
citing authors

#	ARTICLE	IF	CITATIONS
1	Statistical analysis of amino acid patterns in transmembrane helices: the GxxxG motif occurs frequently and in association with $\beta^2$ -branched residues at neighboring positions. <i>Journal of Molecular Biology</i> , 2000, 296, 921-936.	2.0	567
2	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.	2.6	402
3	Membrane protein folding: beyond the two stage model. <i>FEBS Letters</i> , 2003, 555, 122-125.	1.3	273
4	Inside-out Ca <sup>2+</sup> signalling prompted by STIM1 conformational switch. <i>Nature Communications</i> , 2015, 6, 7826.	5.8	144
5	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.	2.0	143
6	De Novo Design and Molecular Assembly of a Transmembrane Diporphyrin-Binding Protein Complex. <i>Journal of the American Chemical Society</i> , 2010, 132, 15516-15518.	6.6	110
7	A frequent, GxxxG-mediated, transmembrane association motif is optimized for the formation of interhelical C $\beta$ -H hydrogen bonds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E888-95.	3.3	94
8	The Oligomeric States of the Purified Sigma-1 Receptor Are Stabilized by Ligands. <i>Journal of Biological Chemistry</i> , 2014, 289, 20333-20344.	1.6	92
9	$\alpha$ 7 nAChR groove dimerization initiates and helix 9 dimerization expands Bax pore assembly in membranes. <i>EMBO Journal</i> , 2016, 35, 208-236.	3.5	81
10	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.	3.3	68
11	Using $\beta$ -Helical Coiled-Coils to Design Nanostructured Metalloporphyrin Arrays. <i>Journal of the American Chemical Society</i> , 2008, 130, 11921-11927.	6.6	63
12	Ptc7p Dephosphorylates Select Mitochondrial Proteins to Enhance Metabolic Function. <i>Cell Reports</i> , 2017, 18, 307-313.	2.9	45
13	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.	2.3	40
14	Combination of C $\beta$ -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.	6.6	36
15	Structural Organization of FtsB, a Transmembrane Protein of the Bacterial Divisome. <i>Biochemistry</i> , 2013, 52, 2574-2585.	1.2	31
16	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.	3.6	30
17	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.	1.6	30
18	Computational design of membrane proteins. <i>Current Opinion in Structural Biology</i> , 2011, 21, 460-466.	2.6	29

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19	Structural informatics, modeling, and design with an open-source Molecular Software Library (MSL). <i>Journal of Computational Chemistry</i> , 2012, 33, 1645-1661.	1.5	23
20	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.	1.2	23
21	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.	6.6	17
22	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.	1.5	14
23	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.	6.6	13
24	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.	1.5	12
25	Analysis of spliceosome dynamics by maximum likelihood fitting of dwell time distributions. <i>Methods</i> , 2019, 153, 13-21.	1.9	12
26	Fluorophores, environments, and quantification techniques in the analysis of transmembrane helix interaction using FRET. <i>Biopolymers</i> , 2015, 104, 247-264.	1.2	11
27	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.	1.4	9
28	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.	1.6	8
29	Measurement of Transmembrane Peptide Interactions in Liposomes Using Förster Resonance Energy Transfer (FRET). <i>Methods in Molecular Biology</i> , 2013, 1063, 19-36.	0.4	6
30	An energetics database to model protein-protein interactions. <i>FASEB Journal</i> , 2019, 33, 642.7.	0.2	0