Alessandro Senes

List of Publications by Year
in descending order

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	Statistical analysis of amino acid patterns in transmembrane helices: the GxxxG motif occurs frequently and in association with Î²-branched residues at neighboring positions. Journal of Molecular Biology, 2000, 296, 921-936.	4.2	567
2	Folding of helical membrane proteins: the role of polar, GxxxG-like and proline motifs. Current Opinion in Structural Biology, 2004, 14, 465-479.	5.7	402
3	Membrane protein folding: beyond the two stage model. FEBS Letters, 2003, 555, 122-125.	2.8	273
4	Inside-out Ca2+ signalling prompted by STIM1 conformational switch. Nature Communications, 2015, 6, 7826.	12.8	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. Journal of Molecular Biology, 2007, 366, 436-448.	4.2	143
6	De Novo Design and Molecular Assembly of a Transmembrane Diporphyrin-Binding Protein Complex. Journal of the American Chemical Society, 2010, 132, 15516-15518.	13.7	110
7	A frequent, GxxxG-mediated, transmembrane association motif is optimized for the formation of interhelical CÎ±â€“H hydrogen bonds. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E888-95.	7.1	94
8	The Oligomeric States of the Purified Sigma-1 Receptor Are Stabilized by Ligands. Journal of Biological Chemistry, 2014, 289, 20333-20344.	3.4	92
9	<scp>BH</scp> 3â€“groove dimerization initiates and helix 9 dimerization expands Bax pore assembly in membranes. EMBO Journal, 2016, 35, 208-236.	7.8	81
10	Consensus motif for integrin transmembrane helix association. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 703-708.	7.1	68
11	Using Î±-Helical Coiled-Coils to Design Nanostructured Metalloporphyrin Arrays. Journal of the American Chemical Society, 2008, 130, 11921-11927.	13.7	63
12	Ptc7p Dephosphorylates Select Mitochondrial Proteins to Enhance Metabolic Function. Cell Reports, 2017, 18, 307-313.	6.4	45
13	The Cytokinin Oxidase/Dehydrogenase CKX1 Is a Membrane-Bound Protein Requiring Homooligomerization in the Endoplasmic Reticulum for Its Cellular Activity. Plant Physiology, 2018, 176, 2024-2039.	4.8	40
14	Combination of CÎ±â€“H Hydrogen Bonds and van der Waals Packing Modulates the Stability of GxxxG-Mediated Dimers in Membranes. Journal of the American Chemical Society, 2017, 139, 15774-15783.	13.7	36
15	Structural Organization of FtsB, a Transmembrane Protein of the Bacterial Divisome. Biochemistry, 2013, 52, 2574-2585.	2.5	31
16	Toward high-resolution computational design of the structure and function of helical membrane proteins. Nature Structural and Molecular Biology, 2016, 23, 475-480.	8.2	30
17	The FtsLB subcomplex of the bacterial divisome is a tetramer with an uninterrupted FtsL helix linking the transmembrane and periplasmic regions. Journal of Biological Chemistry, 2018, 293, 1623-1641.	3.4	30
18	Computational design of membrane proteins. Current Opinion in Structural Biology, 2011, 21, 460-466.	5.7	29

#	Article	IF	Citations
19	Structural informatics, modeling, and design with an open-source Molecular Software Library (MSL). Journal of Computational Chemistry, 2012, 33, 1645-1661.	3.3	23
20	The Transmembrane Domains of the Bacterial Cell Division Proteins FtsB and FtsL Form a Stable High-Order Oligomer. Biochemistry, 2013, 52, 7542-7550.	2.5	23
21	A Gly-Zipper Motif Mediates Homodimerization of the Transmembrane Domain of the Mitochondrial Kinase ADCK3. Journal of the American Chemical Society, 2014, 136, 14068-14077.	13.7	17
22	An energy-based conformer library for side chain optimization: Improved prediction and adjustable sampling. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2218-2234.	2.6	14
23	Oligomerization State of Photosynthetic Core Complexes Is Correlated with the Dimerization Affinity of a Transmembrane Helix. Journal of the American Chemical Society, 2011, 133, 14071-14081.	13.7	13
24	Backbone dependency further improves side chain prediction efficiency in the Energy-based Conformer Library (bEBL). Proteins: Structure, Function and Bioinformatics, 2014, 82, 3177-3187.	2.6	12
25	Analysis of spliceosome dynamics by maximum likelihood fitting of dwell time distributions. Methods, 2019, 153, 13-21.	3.8	12
26	Fluorophores, environments, and quantification techniques in the analysis of transmembrane helix interaction using FRET. Biopolymers, 2015, 104, 247-264.	2.4	11
27	Screening for transmembrane association in divisome proteins using TOXGREEN, a high-throughput variant of the TOXCAT assay. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 2573-2583.	2.6	9
28	The coiled-coil domain of Escherichia coli FtsLB is a structurally detuned element critical for modulating its activation in bacterial cell division. Journal of Biological Chemistry, 2022, 298, 101460.	3.4	8
29	Measurement of Transmembrane Peptide Interactions in Liposomes Using Förster Resonance Energy Transfer (FRET). Methods in Molecular Biology, 2013, 1063, 19-36.	0.9	6
30	An energetics database to model protein-protein interactions. FASEB Journal, 2019, 33, 642.7.	0.5	0