

# Daniel-Adriano Silva

## List of Publications by Year in Descending Order

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**Version:** 2024-04-27

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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.

34  
papers

2,068  
citations

22  
h-index

35  
g-index

35  
ext. papers

2,745  
ext. citations

15.2  
avg, IF

4.5  
L-index

#	Paper	IF	Citations
34	An IL-2 Protein Therapeutic for Cancer that Gains Function on the Spot.. <i>Cancer Immunology Research</i> , <b>2022</b> , OF1	12.5	
33	Computational design of mechanically coupled axle-rotor protein assemblies.. <i>Science</i> , <b>2022</b> , 376, 383-390	35.3	2
32	Super-enhancer-based identification of a BATF3/IL-2R-module reveals vulnerabilities in anaplastic large cell lymphoma. <i>Nature Communications</i> , <b>2021</b> , 12, 5577	17.4	1
31	De novo design of potent and resilient hACE2 decoys to neutralize SARS-CoV-2. <i>Science</i> , <b>2020</b> , 370, 1208-1214	35.3	98
30	The advent of de novo proteins for cancer immunotherapy. <i>Current Opinion in Chemical Biology</i> , <b>2020</b> , 56, 119-128	9.7	5
29	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , <b>2020</b> , 17, 665-680	21.6	165
28	design of ACE2 protein decoys to neutralize SARS-CoV-2 <b>2020</b> ,		6
27	De novo protein design by citizen scientists. <i>Nature</i> , <b>2019</b> , 570, 390-394	50.4	63
26	De novo design of potent and selective mimics of IL-2 and IL-15. <i>Nature</i> , <b>2019</b> , 565, 186-191	50.4	184
25	Structures and disulfide cross-linking of de novo designed therapeutic mini-proteins. <i>FEBS Journal</i> , <b>2018</b> , 285, 1783-1785	5.7	6
24	Essentials of de novo protein design: Methods and applications. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , <b>2018</b> , 8, e1374	7.9	22
23	Principles for designing proteins with cavities formed by curved $\beta$ -sheets. <i>Science</i> , <b>2017</b> , 355, 201-206	33.3	82
22	De novo design of covalently constrained mesosize protein scaffolds with unique tertiary structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 10852-10857	11.5	44
21	Massively parallel de novo protein design for targeted therapeutics. <i>Nature</i> , <b>2017</b> , 550, 74-79	50.4	235
20	Comprehensive computational design of ordered peptide macrocycles. <i>Science</i> , <b>2017</b> , 358, 1461-1466	33.3	96
19	Computationally designed high specificity inhibitors delineate the roles of BCL2 family proteins in cancer. <i>ELife</i> , <b>2016</b> , 5,	8.9	52
18	Bridge helix bending promotes RNA polymerase II backtracking through a critical and conserved threonine residue. <i>Nature Communications</i> , <b>2016</b> , 7, 11244	17.4	54

17	Motif-Driven Design of Protein-Protein Interfaces. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1414, 285-304	1.4	26
16	Automatic state partitioning for multibody systems (APM): an efficient algorithm for constructing Markov state models to elucidate conformational dynamics of multibody systems. <i>Journal of Chemical Theory and Computation</i> , <b>2015</b> , 11, 17-27	6.4	29
15	Structural Model of RNA Polymerase II Elongation Complex with Complete Transcription Bubble Reveals NTP Entry Routes. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004354	5	9
14	On the molecular basis of the high affinity binding of basic amino acids to LAOBP, a periplasmic binding protein from <i>Salmonella typhimurium</i> . <i>Journal of Molecular Recognition</i> , <b>2015</b> , 28, 108-116	2.6	7
13	Dynamic protein conformations preferentially drive energy transfer along the active chain of the photosystem II reaction centre. <i>Nature Communications</i> , <b>2014</b> , 5, 4170	17.4	33
12	Quantitatively characterizing the ligand binding mechanisms of choline binding protein using Markov state model analysis. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003767	5	55
11	Millisecond dynamics of RNA polymerase II translocation at atomic resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 7665-70	11.5	90
10	Application of Markov State Models to simulate long timescale dynamics of biological macromolecules. <i>Advances in Experimental Medicine and Biology</i> , <b>2014</b> , 805, 29-66	3.6	22
9	Hierarchical Nystroth methods for constructing Markov state models for conformational dynamics. <i>Journal of Chemical Physics</i> , <b>2013</b> , 138, 174106	3.9	37
8	Monitoring and inhibition of insulin fibrillation by a small organic fluorogen with aggregation-induced emission characteristics. <i>Journal of the American Chemical Society</i> , <b>2012</b> , 134, 1680-9	16.4	293
7	Bridging the Gap Between Optical Spectroscopic Experiments and Computer Simulations for Fast Protein Folding Dynamics. <i>Current Physical Chemistry</i> , <b>2012</b> , 2, 45-58	0.5	4
6	Force field development for cofactors in the photosystem II. <i>Journal of Computational Chemistry</i> , <b>2012</b> , 33, 1969-80	3.5	40
5	Initiation complex structure and promoter proofreading. <i>Science</i> , <b>2011</b> , 333, 633-7	33.3	48
4	Simulating the T-jump-triggered unfolding dynamics of trpzip2 peptide and its time-resolved IR and two-dimensional IR signals using the Markov state model approach. <i>Journal of Physical Chemistry B</i> , <b>2011</b> , 115, 5415-24	3.4	59
3	Conformational dynamics of L-lysine, L-arginine, L-ornithine binding protein reveals ligand-dependent plasticity. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 2097-108	4.2	15
2	A role for both conformational selection and induced fit in ligand binding by the LAO protein. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002054	5	172
1	Analysis of the antimicrobial activities of a chemokine-derived peptide (CDAP-4) on <i>Pseudomonas aeruginosa</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2007</b> , 355, 352-8	3.4	13