

# Ignacio E SÃ¡nchez

## List of Publications by Year in descending order

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46  
papers

1,614  
citations

331259

21  
h-index

301761

39  
g-index

50  
all docs

50  
docs citations

50  
times ranked

4076  
citing authors

#	ARTICLE	IF	CITATIONS
1	NGOME-Lite: Proteome-wide prediction of spontaneous protein deamidation highlights differences between taxa. <i>Methods</i> , 2022, 200, 15-22.	1.9	6
2	Transcription factor specificity limits the number of DNA-binding motifs. <i>PLoS ONE</i> , 2022, 17, e0263307.	1.1	3
3	Host diversification is concurrent with linear motif evolution in a Mastadenovirus hub protein. <i>Journal of Molecular Biology</i> , 2022, , 167563.	2.0	2
4	Thousands of protein linear motif classes may still be undiscovered. <i>PLoS ONE</i> , 2021, 16, e0248841.	1.1	4
5	A Thermodynamic Analysis of the Binding Specificity between Four Human PDZ Domains and Eight Host, Viral and Designed Ligands. <i>Biomolecules</i> , 2021, 11, 1071.	1.8	1
6	Developing synthetic biology in Argentina: the Latin American TECNOx community as an alternative way for growth of the field. <i>Critical Reviews in Biotechnology</i> , 2020, 40, 357-364.	5.1	5
7	Topology Dictates Evolution of Regulatory Cysteines in a Family of Viral Oncoproteins. <i>Molecular Biology and Evolution</i> , 2019, 36, 1521-1532.	3.5	6
8	Interplay between sequence, structure and linear motifs in the adenovirus E1A hub protein. <i>Virology</i> , 2018, 525, 117-131.	1.1	17
9	Degenerate cysteine patterns mediate two redox sensing mechanisms in the papillomavirus E7 oncoprotein. <i>Redox Biology</i> , 2017, 11, 38-50.	3.9	6
10	Hidden Structural Codes in Protein Intrinsic Disorder. <i>Biochemistry</i> , 2017, 56, 5560-5569.	1.2	30
11	Detailing Protein Landscapes under Pressure. <i>Biophysical Journal</i> , 2016, 111, 2339-2341.	0.2	5
12	Optimal threshold estimation for binary classifiers using game theory. <i>F1000Research</i> , 2016, 5, 2762.	0.8	3
13	Conformational Heterogeneity Determined by Folding and Oligomer Assembly Routes of the Interferon Response Inhibitor NS1 Protein, Unique to Human Respiratory Syncytial Virus. <i>Biochemistry</i> , 2015, 54, 5136-5146.	1.2	7
14	Convergent evolution and mimicry of protein linear motifs in hostâ€“pathogen interactions. <i>Current Opinion in Structural Biology</i> , 2015, 32, 91-101.	2.6	43
15	The E. coli thioredoxin folding mechanism: The key role of the C-terminal helix. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 127-137.	1.1	14
16	Prediction of Spontaneous Protein Deamidation from Sequence-Derived Secondary Structure and Intrinsic Disorder. <i>PLoS ONE</i> , 2015, 10, e0145186.	1.1	28
17	Amino Acid Metabolism Conflicts with Protein Diversity. <i>Molecular Biology and Evolution</i> , 2014, 31, 2905-2912.	3.5	41
18	The eukaryotic linear motif resource ELM: 10 years and counting. <i>Nucleic Acids Research</i> , 2014, 42, D259-D266.	6.5	260

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19	Cysteine-Rich Positions Outside the Structural Zinc Motif of Human Papillomavirus E7 Provide Conformational Modulation and Suggest Functional Redox Roles. <i>Biochemistry</i> , 2014, 53, 1680-1696.	1.2	17
20	Folding of a Cyclin Box. <i>Journal of Biological Chemistry</i> , 2013, 288, 18923-18938.	1.6	17
21	Detecting Repetitions and Periodicities in Proteins by Tiling the Structural Space. <i>Journal of Physical Chemistry B</i> , 2013, 117, 12887-12897.	1.2	35
22	Minute Time Scale Prolyl Isomerization Governs Antibody Recognition of an Intrinsically Disordered Immunodominant Epitope. <i>Journal of Biological Chemistry</i> , 2013, 288, 13110-13123.	1.6	15
23	Evolution of Linear Motifs within the Papillomavirus E7 Oncoprotein. <i>Journal of Molecular Biology</i> , 2012, 422, 336-346.	2.0	27
24	Sequence Evolution of the Intrinsically Disordered and Globular Domains of a Model Viral Oncoprotein. <i>PLoS ONE</i> , 2012, 7, e47661.	1.1	25
25	The Respiratory Syncytial Virus Transcription Antiterminator M2 <sup>1</sup> is a Highly Stable, Zinc Binding Tetramer with Strong pH-Dependent Dissociation and a Monomeric Unfolding Intermediate. <i>Biochemistry</i> , 2011, 50, 8529-8539.	1.2	10
26	Folding Kinetics of the Cooperatively Folded Subdomain of the $\beta$ -Ankyrin Repeat Domain. <i>Journal of Molecular Biology</i> , 2011, 408, 163-176.	2.0	24
27	Kinetic Recognition of the Retinoblastoma Tumor Suppressor by a Specific Protein Target. <i>Journal of Molecular Biology</i> , 2011, 412, 267-284.	2.0	38
28	Mutational analysis of kinetic partitioning in protein folding and protein-DNA binding. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 179-184.	1.0	3
29	Targeting mechanism of the retinoblastoma tumor suppressor by a prototypical viral oncoprotein. <i>FEBS Journal</i> , 2010, 277, 973-988.	2.2	52
30	Experimental snapshots of a protein-DNA binding landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7751-7756.	3.3	19
31	Thermodynamics of Cooperative DNA Recognition at a Replication Origin and Transcription Regulatory Site. <i>Biochemistry</i> , 2010, 49, 10277-10286.	1.2	8
32	A strained DNA binding helix is conserved for site recognition, folding nucleation, and conformational modulation. <i>Biopolymers</i> , 2009, 91, 432-443.	1.2	9
33	Indirect DNA Readout on the Protein Side: Coupling between Histidine Protonation, Global Structural Cooperativity, Dynamics, and DNA Binding of the Human Papillomavirus Type 16 E2C Domain. <i>Journal of Molecular Biology</i> , 2009, 388, 327-344.	2.0	14
34	Genome-Wide Prediction of SH2 Domain Targets Using Structural Information and the FoldX Algorithm. <i>PLoS Computational Biology</i> , 2008, 4, e1000052.	1.5	39
35	Comprehensive comparison of the interaction of the E2 master regulator with its cognate target DNA sites in 73 human papillomavirus types by sequence statistics. <i>Nucleic Acids Research</i> , 2008, 36, 756-769.	6.5	32
36	Transition state for protein-DNA recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10797-10802.	3.3	28

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37	Increased Stability and DNA Site Discrimination of "Single Chain" Variants of the Dimeric $\beta$ -Barrel DNA Binding Domain of the Human Papillomavirus E2 Transcriptional Regulator. <i>Biochemistry</i> , 2007, 46, 12441-12450.	1.2	11
38	Protein folding transition states probed by loop extension. <i>Protein Science</i> , 2007, 17, 183-186.	3.1	7
39	Point Mutations in Protein Globular Domains: Contributions from Function, Stability and Misfolding. <i>Journal of Molecular Biology</i> , 2006, 363, 422-432.	2.0	42
40	Formation of On- and Off-Pathway Intermediates in the Folding Kinetics of <i>Azotobacter vinelandii</i> Apoflavodoxin. <i>Biochemistry</i> , 2004, 43, 10475-10489.	1.2	68
41	Fast Folding of the Two-domain Semliki Forest Virus Capsid Protein Explains Co-translational Proteolytic Activity. <i>Journal of Molecular Biology</i> , 2004, 338, 159-167.	2.0	34
42	Origin of Unusual $\Delta G^\ddagger$ -values in Protein Folding: Evidence Against Specific Nucleation Sites. <i>Journal of Molecular Biology</i> , 2003, 334, 1077-1085.	2.0	140
43	Evidence for Sequential Barriers and Obligatory Intermediates in Apparent Two-state Protein Folding. <i>Journal of Molecular Biology</i> , 2003, 325, 367-376.	2.0	225
44	Hammond Behavior versus Ground State Effects in Protein Folding: Evidence for Narrow Free Energy Barriers and Residual Structure in Unfolded States. <i>Journal of Molecular Biology</i> , 2003, 327, 867-884.	2.0	135
45	Non-linear rate-equilibrium free energy relationships and Hammond behavior in protein folding. <i>Biophysical Chemistry</i> , 2002, 100, 397-407.	1.5	51
46	Optimal threshold estimation for binary classifiers using game theory. <i>F1000Research</i> , 0, 5, 2762.	0.8	2