Ignacio E SÃ¡nchez

List of Publications by Year
in descending order

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46	1,614	331259 21	301761 39
papers	citations	h-index	g-index

50	50	50	4076
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The eukaryotic linear motif resource ELM: 10 years and counting. Nucleic Acids Research, 2014, 42, D259-D266.	6.5	260
2	Evidence for Sequential Barriers and Obligatory Intermediates in Apparent Two-state Protein Folding. Journal of Molecular Biology, 2003, 325, 367-376.	2.0	225
3	Origin of Unusual Ï†-values in Protein Folding: Evidence Against Specific Nucleation Sites. Journal of Molecular Biology, 2003, 334, 1077-1085.	2.0	140
4	Hammond Behavior versus Ground State Effects in Protein Folding: Evidence for Narrow Free Energy Barriers and Residual Structure in Unfolded States. Journal of Molecular Biology, 2003, 327, 867-884.	2.0	135
5	Formation of On- and Off-Pathway Intermediates in the Folding Kinetics ofAzotobacter vinelandiiApoflavodoxinâ€. Biochemistry, 2004, 43, 10475-10489.	1.2	68
6	Targeting mechanism of the retinoblastoma tumor suppressor by a prototypical viral oncoprotein. FEBS Journal, 2010, 277, 973-988.	2.2	52
7	Non-linear rate-equilibrium free energy relationships and Hammond behavior in protein folding. Biophysical Chemistry, 2002, 100, 397-407.	1.5	51
8	Convergent evolution and mimicry of protein linear motifs in hostâ€“pathogen interactions. Current Opinion in Structural Biology, 2015, 32, 91-101.	2.6	43
9	Point Mutations in Protein Globular Domains: Contributions from Function, Stability and Misfolding. Journal of Molecular Biology, 2006, 363, 422-432.	2.0	42
10	Amino Acid Metabolism Conflicts with Protein Diversity. Molecular Biology and Evolution, 2014, 31, 2905-2912.	3.5	41
11	Genome-Wide Prediction of SH2 Domain Targets Using Structural Information and the FoldX Algorithm. PLoS Computational Biology, 2008, 4, e1000052.	1.5	39
12	Kinetic Recognition of the Retinoblastoma Tumor Suppressor by a Specific Protein Target. Journal of Molecular Biology, 2011, 412, 267-284.	2.0	38
13	Detecting Repetitions and Periodicities in Proteins by Tiling the Structural Space. Journal of Physical Chemistry B, 2013, 117, 12887-12897.	1.2	35
14	Fast Folding of the Two-domain Semliki Forest Virus Capsid Protein Explains Co-translational Proteolytic Activity. Journal of Molecular Biology, 2004, 338, 159-167.	2.0	34
15	Comprehensive comparison of the interaction of the E2 master regulator with its cognate target DNA sites in 73 human papillomavirus types by sequence statistics. Nucleic Acids Research, 2008, 36, 756-769.	6.5	32
16	Hidden Structural Codes in Protein Intrinsic Disorder. Biochemistry, 2017, 56, 5560-5569.	1.2	30
17	Transition state for protein-DNA recognition. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10797-10802.	3.3	28
18	Prediction of Spontaneous Protein Deamidation from Sequence-Derived Secondary Structure and Intrinsic Disorder. PLoS ONE, 2015, 10, e0145186.	1.1	28

#	Article	IF	Citations
19	Evolution of Linear Motifs within the Papillomavirus E7 Oncoprotein. Journal of Molecular Biology, 2012, 422, 336-346.	2.0	27
20	Sequence Evolution of the Intrinsically Disordered and Globular Domains of a Model Viral Oncoprotein. PLoS ONE, 2012, 7, e47661.	1.1	25
21	Folding Kinetics of the Cooperatively Folded Subdomain of the IÎºBÎ± Ankyrin Repeat Domain. Journal of Molecular Biology, 2011, 408, 163-176.	2.0	24
22	Experimental snapshots of a protein-DNA binding landscape. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7751-7756.	3.3	19
23	Folding of a Cyclin Box. Journal of Biological Chemistry, 2013, 288, 18923-18938.	1.6	17
24	Cysteine-Rich Positions Outside the Structural Zinc Motif of Human Papillomavirus E7 Provide Conformational Modulation and Suggest Functional Redox Roles. Biochemistry, 2014, 53, 1680-1696.	1.2	17
25	Interplay between sequence, structure and linear motifs in the adenovirus E1A hub protein. Virology, 2018, 525, 117-131.	1.1	17
26	Minute Time Scale Prolyl Isomerization Governs Antibody Recognition of an Intrinsically Disordered Immunodominant Epitope. Journal of Biological Chemistry, 2013, 288, 13110-13123.	1.6	15
27	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. Journal of Molecular Biology, 2009, 388, 327-344.	2.0	14
28	The E. coli thioredoxin folding mechanism: The key role of the C-terminal helix. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 127-137.	1.1	14
29	Increased Stability and DNA Site Discrimination of â€œSingle Chainâ€•Variants of the Dimeric Î²-Barrel DNA Binding Domain of the Human Papillomavirus E2 Transcriptional Regulator. Biochemistry, 2007, 46, 12441-12450.	1.2	11
30	The Respiratory Syncytial Virus Transcription Antiterminator M2â€“1Is a Highly Stable, Zinc Binding Tetramer with Strong pH-Dependent Dissociation and a Monomeric Unfolding Intermediate. Biochemistry, 2011, 50, 8529-8539.	1.2	10
31	A strained DNA binding helix is conserved for site recognition, folding nucleation, and conformational modulation. Biopolymers, 2009, 91, 432-443.	1.2	9
32	Thermodynamics of Cooperative DNA Recognition at a Replication Origin and Transcription Regulatory Site. Biochemistry, 2010, 49, 10277-10286.	1.2	8
33	Protein folding transition states probed by loop extension. Protein Science, 2007, 17, 183-186.	3.1	7
34	Conformational Heterogeneity Determined by Folding and Oligomer Assembly Routes of the Interferon Response Inhibitor NS1 Protein, Unique to Human Respiratory Syncytial Virus. Biochemistry, 2015, 54, 5136-5146.	1.2	7
35	Degenerate cysteine patterns mediate two redox sensing mechanisms in the papillomavirus E7 oncoprotein. Redox Biology, 2017, 11, 38-50.	3.9	6
36	Topology Dictates Evolution of Regulatory Cysteines in a Family of Viral Oncoproteins. Molecular Biology and Evolution, 2019, 36, 1521-1532.	3.5	6

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37	NGOME-Lite: Proteome-wide prediction of spontaneous protein deamidation highlights differences between taxa. Methods, 2022, 200, 15-22.	1.9	6
38	Detailing Protein Landscapes under Pressure. Biophysical Journal, 2016, 111, 2339-2341.	0.2	5
39	Developing synthetic biology in Argentina: the Latin American TECNOx community as an alternative way for growth of the field. Critical Reviews in Biotechnology, 2020, 40, 357-364.	5.1	5
40	Thousands of protein linear motif classes may still be undiscovered. PLoS ONE, 2021, 16, e0248841.	1.1	4
41	Mutational analysis of kinetic partitioning in protein folding and proteinâ€“DNA binding. Protein Engineering, Design and Selection, 2011, 24, 179-184.	1.0	3
42	Optimal threshold estimation for binary classifiers using game theory. F1000Research, 2016, 5, 2762.	0.8	3
43	Transcription factor specificity limits the number of DNA-binding motifs. PLoS ONE, 2022, 17, e0263307.	1.1	3
44	Optimal threshold estimation for binary classifiers using game theory. F1000Research, 0, 5, 2762.	0.8	2
45	Host diversification is concurrent with linear motif evolution in a Mastadenovirus hub protein. Journal of Molecular Biology, 2022, , 167563.	2.0	2
46	A Thermodynamic Analysis of the Binding Specificity between Four Human PDZ Domains and Eight Host, Viral and Designed Ligands. Biomolecules, 2021, 11, 1071.	1.8	1