

Jose Manuel Sanchez Ruiz

List of Publications by Year in descending order

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131
papers

7,934
citations

41258

49
h-index

54797

84
g-index

140
all docs

140
docs citations

140
times ranked

6178
citing authors

#	ARTICLE	IF	CITATIONS
1	Theoretical analysis of Lumry-Eyring models in differential scanning calorimetry. <i>Biophysical Journal</i> , 1992, 61, 921-935.	0.2	500
2	Differential scanning calorimetry of the irreversible thermal denaturation of thermolysin. <i>Biochemistry</i> , 1988, 27, 1648-1652.	1.2	469
3	Protein kinetic stability. <i>Biophysical Chemistry</i> , 2010, 148, 1-15.	1.5	323
4	Experimental Identification of Downhill Protein Folding. <i>Science</i> , 2002, 298, 2191-2195.	6.0	290
5	Probing the chemistry of thioredoxin catalysis with force. <i>Nature</i> , 2007, 450, 124-127.	13.7	255
6	Thermal versus Guanidine-Induced Unfolding of Ubiquitin. An Analysis in Terms of the Contributions from Charge-charge Interactions to Protein Stability. <i>Biochemistry</i> , 1999, 38, 8138-8149.	1.2	243
7	Engineering a Thermostable Protein via Optimization of Charge-charge Interactions on the Protein Surface. <i>Biochemistry</i> , 1999, 38, 16419-16423.	1.2	213
8	Hyperstability and Substrate Promiscuity in Laboratory Resurrections of Precambrian β -Lactamases. <i>Journal of the American Chemical Society</i> , 2013, 135, 2899-2902.	6.6	212
9	To charge or not to charge?. <i>Trends in Biotechnology</i> , 2001, 19, 132-135.	4.9	203
10	Single-molecule paleoenzymology probes the chemistry of resurrected enzymes. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 592-596.	3.6	182
11	Protein Folding Drives Disulfide Formation. <i>Cell</i> , 2012, 151, 794-806.	13.5	158
12	Conformational dynamics and enzyme evolution. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180330.	1.5	140
13	Lower kinetic limit to protein thermal stability: A proposal regarding protein stability in vivo and its relation with misfolding diseases. , 2000, 40, 58-70.		133
14	Evolution of Conformational Dynamics Determines the Conversion of a Promiscuous Generalist into a Specialist Enzyme. <i>Molecular Biology and Evolution</i> , 2015, 32, 132-143.	3.5	125
15	Role of residual structure in the unfolded state of a thermophilic protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 11345-11349.	3.3	121
16	Conservation of Protein Structure over Four Billion Years. <i>Structure</i> , 2013, 21, 1690-1697.	1.6	115
17	Kinetic study on the irreversible thermal denaturation of yeast phosphoglycerate kinase. <i>Biochemistry</i> , 1991, 30, 2061-2066.	1.2	114
18	The molecular basis of cooperativity in protein folding. Thermodynamic dissection of interdomain interactions in phosphoglycerate kinase. <i>Biochemistry</i> , 1992, 31, 250-256.	1.2	111

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19	Analysis of differential scanning calorimetry data for proteins Criteria of validity of one-step mechanism of irreversible protein denaturation. <i>Biophysical Chemistry</i> , 1997, 69, 125-135.	1.5	110
20	The Efficiency of Different Salts to Screen Charge Interactions in Proteins: A Hofmeister Effect?. <i>Biophysical Journal</i> , 2004, 86, 2414-2429.	0.2	109
21	Exploring protein-folding ensembles: A variable-barrier model for the analysis of equilibrium unfolding experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17646-17651.	3.3	102
22	l-Phenylalanine Binding and Domain Organization in Human Phenylalanine Hydroxylase: A Differential Scanning Calorimetry Study. <i>Biochemistry</i> , 2002, 41, 7573-7585.	1.2	99
23	Diversity of chemical mechanisms in thioredoxin catalysis revealed by single-molecule force spectroscopy. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 890-896.	3.6	91
24	An osmolyte effect on the heat capacity change for protein folding. <i>Biochemistry</i> , 1995, 34, 8621-8630.	1.2	87
25	Role of Solvation Barriers in Protein Kinetic Stability. <i>Journal of Molecular Biology</i> , 2006, 360, 715-724.	2.0	86
26	Robustness of Downhill Folding: Guidelines for the Analysis of Equilibrium Folding Experiments on Small Proteins. <i>Biochemistry</i> , 2005, 44, 7435-7449.	1.2	81
27	Expanding the Realm of Ultrafast Protein Folding: gpW, a Midsize Natural Single-Domain with $\beta\alpha\beta$ Topology that Folds Downhill. <i>Journal of the American Chemical Society</i> , 2008, 130, 7489-7495.	6.6	81
28	Cooperativity and flexibility in enzyme evolution. <i>Current Opinion in Structural Biology</i> , 2018, 48, 83-92.	2.6	81
29	Energetic Evidence for Formation of a pH-dependent Hydrophobic Cluster in the Denatured State of <i>Thermus thermophilus</i> Ribonuclease H. <i>Journal of Molecular Biology</i> , 2003, 329, 731-743.	2.0	78
30	Estimating Free-Energy Barrier Heights for an Ultrafast Folding Protein from Calorimetric and Kinetic Data. <i>Journal of Physical Chemistry B</i> , 2008, 112, 5938-5949.	1.2	78
31	Human cystathionine β -synthase (CBS) contains two classes of binding sites for S-adenosylmethionine (SAM): complex regulation of CBS activity and stability by SAM. <i>Biochemical Journal</i> , 2013, 449, 109-121.	1.7	78
32	Electrostatic Interactions in Ubiquitin: Stabilization of Carboxylates by Lysine Amino Groups. <i>Biochemistry</i> , 2002, 41, 7586-7596.	1.2	77
33	Direct Measurement of Barrier Heights in Protein Folding. <i>Journal of the American Chemical Society</i> , 2005, 127, 17970-17971.	6.6	74
34	Mutational Studies on Resurrected Ancestral Proteins Reveal Conservation of Site-Specific Amino Acid Preferences throughout Evolutionary History. <i>Molecular Biology and Evolution</i> , 2015, 32, 440-455.	3.5	71
35	Cold denaturation of ubiquitin. <i>BBA - Proteins and Proteomics</i> , 1999, 1429, 384-390.	2.1	69
36	Differential Scanning Calorimetry of Proteins. <i>Sub-Cellular Biochemistry</i> , 1995, 24, 133-176.	1.0	68

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37	Large-scale modulation of thermodynamic protein folding barriers linked to electrostatics. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8625-8630.	3.3	68
38	Natural Selection for Kinetic Stability Is a Likely Origin of Correlations between Mutational Effects on Protein Energetics and Frequencies of Amino Acid Occurrences in Sequence Alignments. Journal of Molecular Biology, 2006, 362, 966-978.	2.0	65
39	Are There Equilibrium Intermediate States in the Urea-Induced Unfolding of Hen Egg-White Lysozyme?. Biochemistry, 1997, 36, 9616-9624.	1.2	60
40	De novo active sites for resurrected Precambrian enzymes. Nature Communications, 2017, 8, 16113.	5.8	60
41	Biotechnological and protein-engineering implications of ancestral protein resurrection. Current Opinion in Structural Biology, 2018, 51, 106-115.	2.6	60
42	Relation Between Protein Stability, Evolution and Structure, as Probed by Carboxylic Acid Mutations. Journal of Molecular Biology, 2004, 336, 313-318.	2.0	58
43	Effect of zinc(2+) on the thermal denaturation of carboxypeptidase B. Biochemistry, 1991, 30, 2067-2072.	1.2	57
44	Native hydrogen bonds in a molten globule: the apoflavodoxin thermal intermediate. Journal of Molecular Biology, 2001, 306, 877-888.	2.0	56
45	Phenotypic comparisons of consensus variants versus laboratory resurrections of Precambrian proteins. Proteins: Structure, Function and Bioinformatics, 2014, 82, 887-896.	1.5	56
46	A Fourier-transform infrared spectroscopic study of the phosphoserine residues in hen egg phosphovitin and ovalbumin. Biochemistry, 1988, 27, 3338-3342.	1.2	55
47	Differential scanning calorimetry of lobster haemocyanin. FEBS Journal, 1990, 188, 181-185.	0.2	55
48	A Model-Independent, Nonlinear Extrapolation Procedure for the Characterization of Protein Folding Energetics from Solvent-Denaturation Data. Biochemistry, 1996, 35, 14689-14702.	1.2	54
49	Role of low native state kinetic stability and interaction of partially unfolded states with molecular chaperones in the mitochondrial protein mistargeting associated with primary hyperoxaluria. Amino Acids, 2011, 41, 1233-1245.	1.2	54
50	Comparative calorimetric study of non-amyloidogenic and amyloidogenic variants of the homotetrameric protein transthyretin. Biophysical Chemistry, 2000, 88, 61-67.	1.5	53
51	Modern Analysis of Protein Folding by Differential Scanning Calorimetry. Methods in Enzymology, 2016, 567, 281-318.	0.4	51
52	Applications of scanning microcalorimetry in biophysics and biochemistry. Thermochemica Acta, 1997, 302, 165-180.	1.2	49
53	Ligand effects on protein thermodynamic stability. Biophysical Chemistry, 2007, 126, 43-49.	1.5	49
54	Analysis of the thermal unfolding of porcine procarboxypeptidase A and its functional pieces by differential scanning calorimetry. FEBS Journal, 1988, 176, 225-230.	0.2	47

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55	pH Corrections and Protein Ionization in Water/Guanidinium Chloride. <i>Biophysical Journal</i> , 2001, 81, 3489-3502.	0.2	47
56	Differential scanning calorimetric study of carboxypeptidase B, procarboxypeptidase B and its globular activation domain. <i>FEBS Journal</i> , 1991, 200, 663-670.	0.2	46
57	Between-Species Variation in the Kinetic Stability of TIM Proteins Linked to Solvation-Barrier Free Energies. <i>Journal of Molecular Biology</i> , 2009, 385, 924-937.	2.0	44
58	Thermodynamic and Kinetic Characterization of a Germ Line Human λ 6 Light-Chain Protein: The Relation between Unfolding and Fibrillogenesis. <i>Journal of Molecular Biology</i> , 2009, 386, 1153-1166.	2.0	43
59	Hinge-shift mechanism as a protein design principle for the evolution of β -lactamases from substrate promiscuity to specificity. <i>Nature Communications</i> , 2021, 12, 1852.	5.8	43
60	Manipulating Conformational Dynamics To Repurpose Ancient Proteins for Modern Catalytic Functions. <i>ACS Catalysis</i> , 2020, 10, 4863-4870.	5.5	42
61	Identification of the Structural Basis of Thermal Lability of a Virus Provides a Rationale for Improved Vaccines. <i>Structure</i> , 2014, 22, 1560-1570.	1.6	41
62	Do Proteins Always Benefit from a Stability Increase? Relevant and Residual Stabilisation in a Three-state Protein by Charge Optimisation. <i>Journal of Molecular Biology</i> , 2004, 344, 223-237.	2.0	40
63	Engineering proteins with tunable thermodynamic and kinetic stabilities. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 165-174.	1.5	39
64	Navigating the Downhill Protein Folding Regime via Structural Homologues. <i>Journal of the American Chemical Society</i> , 2010, 132, 11183-11190.	6.6	39
65	Dwell Time Analysis of a Single-Molecule Mechanochemical Reaction. <i>Langmuir</i> , 2008, 24, 1356-1364.	1.6	35
66	Heat capacity analysis of oxidized Escherichia coli thioredoxin fragments (1-73, 74-108) and their noncovalent complex. <i>FEBS Journal</i> , 2001, 268, 1477-1485.	0.2	34
67	A designed protein as experimental model of primordial folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4127-4132.	3.3	34
68	Thermostable and promiscuous α -recambrian proteins. <i>Environmental Microbiology</i> , 2014, 16, 1485-1489.	1.8	33
69	Modulation of Buried Ionizable Groups in Proteins with Engineered Surface Charge. <i>Journal of the American Chemical Society</i> , 2010, 132, 1218-1219.	6.6	31
70	Estimation of protein folding free energy barriers from calorimetric data by multi-model Bayesian analysis. <i>Physical Chemistry Chemical Physics</i> , 2011, 13, 17064.	1.3	31
71	Probing Free-Energy Surfaces with Differential Scanning Calorimetry. <i>Annual Review of Physical Chemistry</i> , 2011, 62, 231-255.	4.8	31
72	Genetic Algorithm to Design Stabilizing Surface-Charge Distributions in Proteins. <i>Journal of Physical Chemistry B</i> , 2002, 106, 6609-6613.	1.2	30

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73	The Long and Short Flavodoxins. <i>Journal of Biological Chemistry</i> , 2004, 279, 47184-47191.	1.6	30
74	A Stability Pattern of Protein Hydrophobic Mutations that Reflects Evolutionary Structural Optimization. <i>Biophysical Journal</i> , 2005, 89, 3320-3331.	0.2	30
75	The consensus-based approach for gene/enzyme replacement therapies and crystallization strategies: the case of human alanineâ€“glyoxylate aminotransferase. <i>Biochemical Journal</i> , 2014, 462, 453-463.	1.7	30
76	Ionization state of the coenzyme 5'-phosphate ester in cytosolic aspartate aminotransferase. A Fourier transform infrared spectroscopic study. <i>Biochemistry</i> , 1986, 25, 2915-2920.	1.2	29
77	Mechanism of Protein Kinetic Stabilization by Engineered Disulfide Crosslinks. <i>PLoS ONE</i> , 2013, 8, e70013.	1.1	29
78	Engineering ancestral protein hyperstability. <i>Biochemical Journal</i> , 2016, 473, 3611-3620.	1.7	29
79	Structural and stability effects of phosphorylation: Localized structural changes in phenylalanine hydroxylase. <i>Protein Science</i> , 2004, 13, 1219-1226.	3.1	26
80	pH Corrections in Chemical Denaturant Solutions. <i>Analytical Biochemistry</i> , 2002, 306, 158-161.	1.1	25
81	Enhancing a <i>de novo</i> enzyme activity by computationally-focused ultra-low-throughput screening. <i>Chemical Science</i> , 2020, 11, 6134-6148.	3.7	24
82	Are Protein Folding Intermediates the Evolutionary Consequence of Functional Constraints?. <i>Journal of Physical Chemistry B</i> , 2015, 119, 1323-1333.	1.2	22
83	Highly Anomalous Energetics of Protein Cold Denaturation Linked to Folding-Unfolding Kinetics. <i>PLoS ONE</i> , 2011, 6, e23050.	1.1	22
84	Consensus Design of an Evolved High-Redox Potential Laccase. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 354.	2.0	22
85	Proteolytic Scanning Calorimetry: A Novel Methodology that Probes the Fundamental Features of Protein Kinetic Stability. <i>Biophysical Journal</i> , 2010, 98, L12-L14.	0.2	21
86	Role of conservative mutations in protein multi-property adaptation. <i>Biochemical Journal</i> , 2010, 429, 243-249.	1.7	20
87	Directed -in vitro- evolution of Precambrian and extant Rubiscos. <i>Scientific Reports</i> , 2018, 8, 5532.	1.6	20
88	Heme-binding enables allosteric modulation in an ancient TIM-barrel glycosidase. <i>Nature Communications</i> , 2021, 12, 380.	5.8	20
89	Energetic and Structural Consequences of Desolvation/Solvation Barriers to Protein Folding/Unfolding Assessed from Experimental Unfolding Rates. <i>Biophysical Journal</i> , 2006, 91, L48-L50.	0.2	19
90	Hydration changes upon protein unfolding: cosolvent effect analysis. <i>New Journal of Chemistry</i> , 1998, 22, 1453-1461.	1.4	17

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91	Dissecting Structural and Electrostatic Interactions of Charged Groups in $\hat{\pm}$ -Sarcin. An NMR Study of Some Mutants Involving the Catalytic Residues. <i>Biochemistry</i> , 2003, 42, 13122-13133.	1.2	17
92	Protein-protein interactions at an enzyme-substrate interface: Characterization of transient reaction intermediates throughout a full catalytic cycle of <i>Escherichia coli</i> thioredoxin reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 36-51.	1.5	17
93	Engineering protein assemblies with allosteric control via monomer fold-switching. <i>Nature Communications</i> , 2019, 10, 5703.	5.8	17
94	Force-Clamp Spectroscopy Detects Residue Co-evolution in Enzyme Catalysis. <i>Journal of Biological Chemistry</i> , 2008, 283, 27121-27129.	1.6	16
95	Using multi-objective computational design to extend protein promiscuity. <i>Biophysical Chemistry</i> , 2010, 147, 13-19.	1.5	16
96	Non-conservation of folding rates in the thioredoxin family reveals degradation of ancestral unassisted-folding. <i>Biochemical Journal</i> , 2019, 476, 3631-3647.	1.7	16
97	Selection for Protein Kinetic Stability Connects Denaturation Temperatures to Organismal Temperatures and Provides Clues to Archaean Life. <i>PLoS ONE</i> , 2016, 11, e0156657.	1.1	16
98	A calorimetric approach to the kinetics of the irreversible thermal denaturation of proteins. <i>Thermochimica Acta</i> , 1992, 199, 147-157.	1.2	15
99	Maximum Entropy Analysis of Kinetic Processes Involving Chemical and Folding-Unfolding Changes in Proteins. <i>Analytical Biochemistry</i> , 1997, 244, 239-255.	1.1	15
100	How many ionizable groups can sit on a protein hydrophobic core?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1-7.	1.5	15
101	Different contribution of conserved amino acids to the global properties of triosephosphate isomerases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 323-335.	1.5	15
102	The Peripheral Binding of 14-3-3 $\hat{\text{I}}^3$ to Membranes Involves Isoform-Specific Histidine Residues. <i>PLoS ONE</i> , 2012, 7, e49671.	1.1	15
103	Empirical parametrization of pK values for carboxylic acids in proteins using a genetic algorithm. <i>Biophysical Chemistry</i> , 2005, 115, 263-266.	1.5	14
104	Using Resurrected Ancestral Proviral Proteins to Engineer Virus Resistance. <i>Cell Reports</i> , 2017, 19, 1247-1256.	2.9	14
105	Ancestral Resurrection and Directed Evolution of Fungal Mesozoic Laccases. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	14
106	Kinetics of the formation and hydrolysis of the schiff's base of 4-pyridinecarboxaldehyde with N-hexylamine in water-dioxan mixtures. <i>International Journal of Chemical Kinetics</i> , 1989, 21, 51-61.	1.0	13
107	The effect of charge-introduction mutations on <i>E. coli</i> thioredoxin stability. <i>Biophysical Chemistry</i> , 2005, 115, 105-107.	1.5	13
108	Probing the Mutational Interplay between Primary and Promiscuous Protein Functions: A Computational-Experimental Approach. <i>PLoS Computational Biology</i> , 2012, 8, e1002558.	1.5	13

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109	Beyond Lumry's Eyring: An unexpected pattern of operational reversibility/irreversibility in protein denaturation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 19-24.	1.5	12
110	Energetics of myo-inositol hexasulfate binding to human acidic fibroblast growth factor. <i>FEBS Journal</i> , 2000, 267, 3477-3486.	0.2	11
111	Differential Scanning Calorimetry of Proteins: an Overview and Some Recent Developments. , 2006, , 27-48.		11
112	Fast folding and slow unfolding of a resurrected Precambrian protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4122-E4123.	3.3	10
113	The ionization states of the 5'-phosphate group in the various coenzyme forms bound to mitochondrial aspartate aminotransferase. <i>Archives of Biochemistry and Biophysics</i> , 1991, 286, 38-45.	1.4	9
114	Energetics of heparin binding to human acidic fibroblast growth factor. <i>International Journal of Biological Macromolecules</i> , 2002, 31, 45-54.	3.6	9
115	Molecular Determinants of Expansivity of Native Globular Proteins: A Pressure Perturbation Calorimetry Study. <i>Journal of Physical Chemistry B</i> , 2014, 118, 6117-6122.	1.2	8
116	Resurrected Ancestral Proteins as Scaffolds for Protein Engineering. , 2017, , 229-255.		8
117	A simple tool to explore the distance distribution of correlated mutations in proteins. <i>Biophysical Chemistry</i> , 2006, 119, 240-246.	1.5	7
118	On promiscuity, changing environments and the possibility of replaying the molecular tape of life. <i>Biochemical Journal</i> , 2012, 445, e1-e3.	1.7	6
119	The sarcosine effect on protein stability: A case of nonadditivity?. <i>Protein Science</i> , 2000, 9, 820-826.	3.1	5
120	Combining Ancestral Reconstruction with Folding-Landscape Simulations to Engineer Heterologous Protein Expression. <i>Journal of Molecular Biology</i> , 2021, 433, 167321.	2.0	5
121	Self-assembly and protein stability. <i>Nature</i> , 1994, 370, 105-105.	13.7	2
122	Evidence for a role of phenotypic mutations in virus adaptation. <i>IScience</i> , 2021, 24, 102257.	1.9	2
123	Linkage between Temperature and Chemical Denaturant Effects on Protein Stability: The Interpretation of Calorimetrically-Determined m Values. , 2005, , 203-214.		1
124	A protocol to study bacteriophage adaptation to new hosts. <i>STAR Protocols</i> , 2021, 2, 100784.	0.5	1
125	The effect of gradual dehydration on the thermal stability of a protein entrapped in a polymeric network. <i>Journal of the Chemical Society Perkin Transactions II</i> , 1995, , 643-644.	0.9	0
126	Characterizing protein-cosolvent interactions coupled to protein refolding by kinetic calorimetry. <i>Progress in Biotechnology</i> , 1998, 15, 247-250.	0.2	0

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127	Energetics of the Interaction of Human Acidic Fibroblast Growth Factor with Heparin and the Functional Analogue Myo-Inositol Hexasulfate. , 2005, , 133-150.		0
128	Variable-Barrier Modeling of Equilibrium Protein Folding. AIP Conference Proceedings, 2006, , .	0.3	0
129	Fourier Transform Infrared Spectroscopic Analysis of Phosphate Bound to the Aspartate Aminotransferase Isozymes. , 1987, , 139-142.		0
130	Irreversible Protein Denaturation. , 2018, , 1-5.		0
131	Folding Free Energy Surfaces from Differential Scanning Calorimetry. Methods in Molecular Biology, 2022, 2376, 105-116.	0.4	0