

Jose Manuel Sanchez Ruiz

List of Publications by Year in Descending Order

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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.

130
papers

6,883
citations

47
h-index

80
g-index

140
ext. papers

7,497
ext. citations

7.2
avg, IF

5.96
L-index

#	Paper	IF	Citations
130	Folding Free Energy Surfaces from Differential Scanning Calorimetry. <i>Methods in Molecular Biology</i> , 2022 , 2376, 105-116	1.4	0
129	Combining Ancestral Reconstruction with Folding-Landscape Simulations to Engineer Heterologous Protein Expression. <i>Journal of Molecular Biology</i> , 2021 , 433, 167321	6.5	0
128	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	17.4	8
127	Evidence for a role of phenotypic mutations in virus adaptation. <i>iScience</i> , 2021 , 24, 102257	6.1	1
126	Heme-binding enables allosteric modulation in an ancient TIM-barrel glycosidase. <i>Nature Communications</i> , 2021 , 12, 380	17.4	8
125	A protocol to study bacteriophage adaptation to new hosts. <i>STAR Protocols</i> , 2021 , 2, 100784	1.4	0
124	Ancestral Resurrection and Directed Evolution of Fungal Mesozoic Laccases. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	4
123	Enhancing a enzyme activity by computationally-focused ultra-low-throughput screening. <i>Chemical Science</i> , 2020 , 11, 6134-6148	9.4	11
122	Manipulating Conformational Dynamics To Repurpose Ancient Proteins for Modern Catalytic Functions. <i>ACS Catalysis</i> , 2020 , 10, 4863-4870	13.1	25
121	Consensus Design of an Evolved High-Redox Potential Laccase. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 354	5.8	12
120	Non-conservation of folding rates in the thioredoxin family reveals degradation of ancestral unassisted-folding. <i>Biochemical Journal</i> , 2019 , 476, 3631-3647	3.8	10
119	Engineering protein assemblies with allosteric control via monomer fold-switching. <i>Nature Communications</i> , 2019 , 10, 5703	17.4	13
118	Directed -in vitro- evolution of Precambrian and extant Rubiscos. <i>Scientific Reports</i> , 2018 , 8, 5532	4.9	14
117	Biotechnological and protein-engineering implications of ancestral protein resurrection. <i>Current Opinion in Structural Biology</i> , 2018 , 51, 106-115	8.1	32
116	Conformational dynamics and enzyme evolution. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	83
115	Cooperativity and flexibility in enzyme evolution. <i>Current Opinion in Structural Biology</i> , 2018 , 48, 83-92	8.1	51
114	Using Resurrected Ancestral Proviral Proteins to Engineer Virus Resistance. <i>Cell Reports</i> , 2017 , 19, 1247-1256	12.56	8

113	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	11.5	6
112	De novo active sites for resurrected Precambrian enzymes. <i>Nature Communications</i> , 2017 , 8, 16113	17.4	36
111	Resurrected Ancestral Proteins as Scaffolds for Protein Engineering 2017 , 229-255		7
110	Modern Analysis of Protein Folding by Differential Scanning Calorimetry. <i>Methods in Enzymology</i> , 2016 , 567, 281-318	1.7	38
109	Selection for Protein Kinetic Stability Connects Denaturation Temperatures to Organismal Temperatures and Provides Clues to Archaean Life. <i>PLoS ONE</i> , 2016 , 11, e0156657	3.7	16
108	Engineering ancestral protein hyperstability. <i>Biochemical Journal</i> , 2016 , 473, 3611-3620	3.8	20
107	Are protein folding intermediates the evolutionary consequence of functional constraints?. <i>Journal of Physical Chemistry B</i> , 2015 , 119, 1323-33	3.4	16
106	Evolution of conformational dynamics determines the conversion of a promiscuous generalist into a specialist enzyme. <i>Molecular Biology and Evolution</i> , 2015 , 32, 132-43	8.3	87
105	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, 440-55	8.3	60
104	Different contribution of conserved amino acids to the global properties of triosephosphate isomerases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 323-35	4.2	13
103	Identification of the structural basis of thermal lability of a virus provides a rationale for improved vaccines. <i>Structure</i> , 2014 , 22, 1560-70	5.2	36
102	Molecular determinants of expansivity of native globular proteins: a pressure perturbation calorimetry study. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 6117-22	3.4	7
101	Phenotypic comparisons of consensus variants versus laboratory resurrections of Precambrian proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 887-96	4.2	46
100	Thermostable and promiscuous Precambrian proteins. <i>Environmental Microbiology</i> , 2014 , 16, 1485-9	5.2	24
99	The consensus-based approach for gene/enzyme replacement therapies and crystallization strategies: the case of human alanine-glyoxylate aminotransferase. <i>Biochemical Journal</i> , 2014 , 462, 453-63	3.8	24
98	Conservation of protein structure over four billion years. <i>Structure</i> , 2013 , 21, 1690-7	5.2	84
97	Hyperstability and substrate promiscuity in laboratory resurrections of Precambrian β -lactamases. <i>Journal of the American Chemical Society</i> , 2013 , 135, 2899-902	16.4	167
96	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, 109-21	3.8	68

95	Mechanism of protein kinetic stabilization by engineered disulfide crosslinks. <i>PLoS ONE</i> , 2013 , 8, e70013;7	22
94	Protein folding drives disulfide formation. <i>Cell</i> , 2012 , 151, 794-806	56.2 125
93	How many ionizable groups can sit on a protein hydrophobic core?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 1-7	4.2 11
92	On promiscuity, changing environments and the possibility of replaying the molecular tape of life. <i>Biochemical Journal</i> , 2012 , 445, e1-3	3.8 6
91	Probing the mutational interplay between primary and promiscuous protein functions: a computational-experimental approach. <i>PLoS Computational Biology</i> , 2012 , 8, e1002558	5 9
90	The peripheral binding of 14-3-3 ζ to membranes involves isoform-specific histidine residues. <i>PLoS ONE</i> , 2012 , 7, e49671	3.7 14
89	Probing free-energy surfaces with differential scanning calorimetry. <i>Annual Review of Physical Chemistry</i> , 2011 , 62, 231-55	15.7 27
88	Single-molecule paleoenzymology probes the chemistry of resurrected enzymes. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 592-6	17.6 149
87	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. <i>Amino Acids</i> , 2011 , 41, 1233-45	3.5 45
86	Estimation of protein folding free energy barriers from calorimetric data by multi-model Bayesian analysis. <i>Physical Chemistry Chemical Physics</i> , 2011 , 13, 17064-76	3.6 30
85	Highly anomalous energetics of protein cold denaturation linked to folding-unfolding kinetics. <i>PLoS ONE</i> , 2011 , 6, e23050	3.7 15
84	Proteolytic scanning calorimetry: a novel methodology that probes the fundamental features of protein kinetic stability. <i>Biophysical Journal</i> , 2010 , 98, L12-4	2.9 19
83	Modulation of buried ionizable groups in proteins with engineered surface charge. <i>Journal of the American Chemical Society</i> , 2010 , 132, 1218-9	16.4 28
82	Navigating the downhill protein folding regime via structural homologues. <i>Journal of the American Chemical Society</i> , 2010 , 132, 11183-90	16.4 37
81	Role of conservative mutations in protein multi-property adaptation. <i>Biochemical Journal</i> , 2010 , 429, 243-9	3.8 16
80	Using multi-objective computational design to extend protein promiscuity. <i>Biophysical Chemistry</i> , 2010 , 147, 13-9	3.5 15
79	Protein kinetic stability. <i>Biophysical Chemistry</i> , 2010 , 148, 1-15	3.5 272
78	Protein-protein interactions at an enzyme-substrate interface: characterization of transient reaction intermediates throughout a full catalytic cycle of Escherichia coli thioredoxin reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 36-51	4.2 14

77	Diversity of chemical mechanisms in thioredoxin catalysis revealed by single-molecule force spectroscopy. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 890-6	17.6	71
76	Between-species variation in the kinetic stability of TIM proteins linked to solvation-barrier free energies. <i>Journal of Molecular Biology</i> , 2009 , 385, 924-37	6.5	42
75	Thermodynamic and kinetic characterization of a germ line human lambda6 light-chain protein: the relation between unfolding and fibrillogenesis. <i>Journal of Molecular Biology</i> , 2009 , 386, 1153-66	6.5	37
74	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, 4127-32	11.5	31
73	Estimating free-energy barrier heights for an ultrafast folding protein from calorimetric and kinetic data. <i>Journal of Physical Chemistry B</i> , 2008 , 112, 5938-49	3.4	73
72	Expanding the realm of ultrafast protein folding: gpW, a midsize natural single-domain with alpha+beta topology that folds downhill. <i>Journal of the American Chemical Society</i> , 2008 , 130, 7489-95	16.4	74
71	Dwell time analysis of a single-molecule mechanochemical reaction. <i>Langmuir</i> , 2008 , 24, 1356-64	4	34
70	Large-scale modulation of thermodynamic protein folding barriers linked to electrostatics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 8625-30	11.5	62
69	Force-clamp spectroscopy detects residue co-evolution in enzyme catalysis. <i>Journal of Biological Chemistry</i> , 2008 , 283, 27121-9	5.4	13
68	Beyond Lumry-Eyring: an unexpected pattern of operational reversibility/irreversibility in protein denaturation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 19-24	4.2	12
67	Engineering proteins with tunable thermodynamic and kinetic stabilities. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 165-74	4.2	36
66	Probing the chemistry of thioredoxin catalysis with force. <i>Nature</i> , 2007 , 450, 124-7	50.4	224
65	Ligand effects on protein thermodynamic stability. <i>Biophysical Chemistry</i> , 2007 , 126, 43-9	3.5	47
64	Differential Scanning Calorimetry of Proteins: an Overview and Some Recent Developments 2006 , 27-48		11
63	Energetic and structural consequences of desolvation/solvation barriers to protein folding/unfolding assessed from experimental unfolding rates. <i>Biophysical Journal</i> , 2006 , 91, L48-50	2.9	18
62	Role of solvation barriers in protein kinetic stability. <i>Journal of Molecular Biology</i> , 2006 , 360, 715-24	6.5	78
61	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. <i>Journal of Molecular Biology</i> , 2006 , 362, 966-78	6.5	56
60	A simple tool to explore the distance distribution of correlated mutations in proteins. <i>Biophysical Chemistry</i> , 2006 , 119, 240-6	3.5	7

59	Robustness of downhill folding: guidelines for the analysis of equilibrium folding experiments on small proteins. <i>Biochemistry</i> , 2005 , 44, 7435-49	3.2	78
58	Direct measurement of barrier heights in protein folding. <i>Journal of the American Chemical Society</i> , 2005 , 127, 17970-1	16.4	68
57	Energetics of the Interaction of Human Acidic Fibroblast Growth Factor with Heparin and the Functional Analogue Myo-Inositol Hexasulfate 2005 , 133-150		
56	Linkage between Temperature and Chemical Denaturant Effects on Protein Stability: The Interpretation of Calorimetrically-Determined m Values 2005 , 203-214		1
55	The effect of charge-introduction mutations on E. coli thioredoxin stability. <i>Biophysical Chemistry</i> , 2005 , 115, 105-7	3.5	13
54	Empirical parametrization of pK values for carboxylic acids in proteins using a genetic algorithm. <i>Biophysical Chemistry</i> , 2005 , 115, 263-6	3.5	11
53	A stability pattern of protein hydrophobic mutations that reflects evolutionary structural optimization. <i>Biophysical Journal</i> , 2005 , 89, 3320-31	2.9	27
52	The long and short flavodoxins: II. The role of the differentiating loop in apoflavodoxin stability and folding mechanism. <i>Journal of Biological Chemistry</i> , 2004 , 279, 47184-91	5.4	27
51	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, 17646-51	11.5	95
50	Structural and stability effects of phosphorylation: Localized structural changes in phenylalanine hydroxylase. <i>Protein Science</i> , 2004 , 13, 1219-26	6.3	22
49	Relation between protein stability, evolution and structure, as probed by carboxylic acid mutations. <i>Journal of Molecular Biology</i> , 2004 , 336, 313-8	6.5	50
48	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, 223-37	6.5	36
47	The efficiency of different salts to screen charge interactions in proteins: a Hofmeister effect?. <i>Biophysical Journal</i> , 2004 , 86, 2414-29	2.9	106
46	Dissecting structural and electrostatic interactions of charged groups in alpha-sarcin. An NMR study of some mutants involving the catalytic residues. <i>Biochemistry</i> , 2003 , 42, 13122-33	3.2	16
45	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, 731-43	6.5	72
44	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, 11345-9	11.5	113
43	pH corrections in chemical denaturant solutions. <i>Analytical Biochemistry</i> , 2002 , 306, 158-61	3.1	23
42	Experimental identification of downhill protein folding. <i>Science</i> , 2002 , 298, 2191-5	33.3	270

41	Electrostatic interactions in ubiquitin: stabilization of carboxylates by lysine amino groups. <i>Biochemistry</i> , 2002 , 41, 7586-96	3.2	71
40	L-phenylalanine binding and domain organization in human phenylalanine hydroxylase: a differential scanning calorimetry study. <i>Biochemistry</i> , 2002 , 41, 7573-85	3.2	94
39	Genetic Algorithm to Design Stabilizing Surface-Charge Distributions in Proteins. <i>Journal of Physical Chemistry B</i> , 2002 , 106, 6609-6613	3.4	29
38	Energetics of heparin binding to human acidic fibroblast growth factor. <i>International Journal of Biological Macromolecules</i> , 2002 , 31, 45-54	7.9	9
37	Heat capacity analysis of oxidized Escherichia coli thioredoxin fragments (1--73, 74--108) and their noncovalent complex. Evidence for the burial of apolar surface in protein unfolded states. <i>FEBS Journal</i> , 2001 , 268, 1477-85		33
36	To charge or not to charge?. <i>Trends in Biotechnology</i> , 2001 , 19, 132-5	15.1	185
35	Native hydrogen bonds in a molten globule: the apoflavodoxin thermal intermediate. <i>Journal of Molecular Biology</i> , 2001 , 306, 877-88	6.5	52
34	pH corrections and protein ionization in water/guanidinium chloride. <i>Biophysical Journal</i> , 2001 , 81, 3489-502		44
33	The sarcosine effect on protein stability: a case of nonadditivity?. <i>Protein Science</i> , 2000 , 9, 820-6	6.3	5
32	Lower kinetic limit to protein thermal stability: a proposal regarding protein stability in vivo and its relation with misfolding diseases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 40, 58-70	4.2	121
31	Energetics of myo-inositol hexasulfate binding to human acidic fibroblast growth factor effect of ionic strength and temperature. <i>FEBS Journal</i> , 2000 , 267, 3477-86		9
30	Comparative calorimetric study of non-amyloidogenic and amyloidogenic variants of the homotetrameric protein transthyretin. <i>Biophysical Chemistry</i> , 2000 , 88, 61-7	3.5	48
29	Cold denaturation of ubiquitin. <i>BBA - Proteins and Proteomics</i> , 1999 , 1429, 384-90		66
28	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, 8138-49	3.2	222
27	Engineering a thermostable protein via optimization of charge-charge interactions on the protein surface. <i>Biochemistry</i> , 1999 , 38, 16419-23	3.2	206
26	Hydration changes upon protein unfolding: cosolvent effect analysis. <i>New Journal of Chemistry</i> , 1998 , 22, 1453-1461	3.6	17
25	Characterizing protein-cosolvent interactions coupled to protein refolding by kinetic calorimetry. <i>Progress in Biotechnology</i> , 1998 , 15, 247-250		
24	Are there equilibrium intermediate states in the urea-induced unfolding of hen egg-white lysozyme?. <i>Biochemistry</i> , 1997 , 36, 9616-24	3.2	56

23	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, 125-35	3.5	104
22	Applications of scanning microcalorimetry in biophysics and biochemistry. <i>Thermochimica Acta</i> , 1997 , 302, 165-180	2.9	40
21	Maximum entropy, analysis of kinetic processes involving chemical and folding-unfolding changes in proteins. <i>Analytical Biochemistry</i> , 1997 , 244, 239-55	3.1	13
20	A model-independent, nonlinear extrapolation procedure for the characterization of protein folding energetics from solvent-denaturation data. <i>Biochemistry</i> , 1996 , 35, 14689-702	3.2	48
19	Differential scanning calorimetry of proteins. <i>Sub-Cellular Biochemistry</i> , 1995 , 24, 133-76	5.5	51
18	An osmolyte effect on the heat capacity change for protein folding. <i>Biochemistry</i> , 1995 , 34, 8621-30	3.2	82
17	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		
16	Self-assembly and protein stability. <i>Nature</i> , 1994 , 370, 105-105	50.4	2
15	The molecular basis of cooperativity in protein folding. Thermodynamic dissection of interdomain interactions in phosphoglycerate kinase. <i>Biochemistry</i> , 1992 , 31, 250-6	3.2	102
14	Theoretical analysis of Lumry-Eyring models in differential scanning calorimetry. <i>Biophysical Journal</i> , 1992 , 61, 921-35	2.9	466
13	A calorimetric approach to the kinetics of the irreversible thermal denaturation of proteins. <i>Thermochimica Acta</i> , 1992 , 199, 147-157	2.9	14
12	Differential scanning calorimetric study of carboxypeptidase B, procarboxypeptidase B and its globular activation domain. <i>FEBS Journal</i> , 1991 , 200, 663-70		43
11	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	4.1	9
10	Kinetic study on the irreversible thermal denaturation of yeast phosphoglycerate kinase. <i>Biochemistry</i> , 1991 , 30, 2061-6	3.2	109
9	Effect of Zn ²⁺ on the thermal denaturation of carboxypeptidase B. <i>Biochemistry</i> , 1991 , 30, 2067-72	3.2	53
8	Differential scanning calorimetry of lobster haemocyanin. <i>FEBS Journal</i> , 1990 , 188, 181-5		53
7	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	1.4	12
6	Analysis of the thermal unfolding of porcine procarboxypeptidase A and its functional pieces by differential scanning calorimetry. <i>FEBS Journal</i> , 1988 , 176, 225-30		42

- 5 A Fourier-transform infrared spectroscopic study of the phosphoserine residues in hen egg phosvitin and ovalbumin. *Biochemistry*, **1988**, 27, 3338-42 3.2 49
- 4 Differential scanning calorimetry of the irreversible thermal denaturation of thermolysin. *Biochemistry*, **1988**, 27, 1648-52 3.2 449
- 3 Fourier Transform Infrared Spectroscopic Analysis of Phosphate Bound to the Aspartate Aminotransferase Isozymes **1987**, 139-142
- 2 Ionization state of the coenzyme 5Tphosphate ester in cytosolic aspartate aminotransferase. A Fourier transform infrared spectroscopic study. *Biochemistry*, **1986**, 25, 2915-20 3.2 29
- 1 Enzyme Evolution1-9