Javier Sancho

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.

141 papers	4,807 citations	39 h-index	62 g-index
149 ext. papers	5,349 ext. citations	5.4 avg, IF	5.43 L-index

#	Paper	IF	Citations
141	Design, synthesis and structure-activity evaluation of novel 2-pyridone-based inhibitors of -synuclein aggregation with potentially improved BBB permeability. *Bioorganic Chemistry*, **2021**, 117, 105472	5.1	0
140	Molecular dynamics simulations for genetic interpretation in protein coding regions: where we are, where to go and when. *Briefings in Bioinformatics*, **2021**, 22, 3-19	13.4	5
139	Protein haploinsufficiency drivers identify MYBPC3 variants that cause hypertrophic cardiomyopathy. *Journal of Biological Chemistry*, **2021**, 297, 100854	5.4	5
138	Flavodoxins as Novel Therapeutic Targets against and Other Gastric Pathogens. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	8
137	Small Molecule Inhibitors of the Response Regulator ArsR Exhibit Bactericidal Activity against. *Microorganisms*, **2020**, 8,	4.9	7
136	New variant (Val597Ile) in transmembrane region of the TSH receptor with human chorionic gonadotropin hypersensitivity in familial gestational hyperthyroidism. *Clinical Endocrinology*, **2020**, 93, 339-345	3.4	3
135	Insights into immune evasion of human metapneumovirus: novel 180- and 111-nucleotide duplications within viral G gene throughout 2014-2017 seasons in Barcelona, Spain. *Journal of Clinical Virology*, **2020**, 132, 104590	14.5	3
134	Inhibition of -Synuclein Aggregation and Mature Fibril Disassembling With a Minimalistic Compound, ZPDm. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 588947	5.8	5
133	Accurate Calculation of Barnase and SNase Folding Energetics Using Short Molecular Dynamics Simulations and an Atomistic Model of the Unfolded Ensemble: Evaluation of Force Fields and Water Models. *Journal of Chemical Information and Modeling*, **2019**, 59, 4350-4360	6.1	6
132	Design, Synthesis, and Efficacy Testing of Nitroethylene- and 7-Nitrobenzoxadiazol-Based Flavodoxin Inhibitors against Drug-Resistant Clinical Strains and in -Infected Mice. *Journal of Medicinal Chemistry*, **2019**, 62, 6102-6115	8.3	14
131	Stereoselective synthesis and biological evaluation as inhibitors of hepatitis C virus RNA polymerase of GSK3082 analogues with structural diversity at the 5-position. *European Journal of Medicinal Chemistry*, **2019**, 171, 401-419	6.8	5
130	Identifying potential novel drugs against Helicobacter pylori by targeting the essential response regulator HsrA. *Scientific Reports*, **2019**, 9, 11294	4.9	20
129	Repurposing Dihydropyridines for Treatment of Infection. *Pharmaceutics*, **2019**, 11,	6.4	8
128	ZPD-2, a Small Compound That Inhibits -Synuclein Amyloid Aggregation and Its Seeded Polymerization. *Frontiers in Molecular Neuroscience*, **2019**, 12, 306	6.1	17
127	A pyrene-inhibitor fluorescent probe with large Stokes shift for the staining of A-synuclein, and amylin amyloid fibrils as well as amyloid-containing Staphylococcus aureus biofilms. *Analytical and Bioanalytical Chemistry*, **2019**, 411, 251-265	4.4	2
126	Redox- and Ligand Binding-Dependent Conformational Ensembles in the Human Apoptosis-Inducing Factor Regulate Its Pro-Life and Cell Death Functions. *Antioxidants and Redox Signaling*, **2019**, 30, 2013-2029	8.4	9
125	Small molecule inhibits -synuclein aggregation, disrupts amyloid fibrils, and prevents degeneration of dopaminergic neurons. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 10481-10486	11.5	99

124	Identification of Inhibitors Targeting Ferredoxin-NADP+ Reductase from the Xanthomonas citri subsp. citri Phytopathogenic Bacteria. *Molecules*, **2017**, 23,	4.8	3
123	Direct examination of the relevance for folding, binding and electron transfer of a conserved protein folding intermediate. *Physical Chemistry Chemical Physics*, **2017**, 19, 19021-19031	3.6	1
122	High-Throughput Screening Methodology to Identify Alpha-Synuclein Aggregation Inhibitors. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	41
121	Exploring the complete mutational space of the LDL receptor LA5 domain using molecular dynamics: linking SNPs with disease phenotypes in familial hypercholesterolemia. *Human Molecular Genetics*, **2016**, 25, 1233-46	5.6	7
120	Inhibition of Pig Phosphoenolpyruvate Carboxykinase Isoenzymes by 3-Mercaptopicolinic Acid and Novel Inhibitors. *PLoS ONE*, **2016**, 11, e0159002	3.7	7
119	Streptococcus pneumoniae TIGR4 Flavodoxin: Structural and Biophysical Characterization of a Novel Drug Target. *PLoS ONE*, **2016**, 11, e0161020	3.7	9
118	Biophysical Screening for Identifying Pharmacological Chaperones and Inhibitors Against Conformational and Infectious Diseases. *Current Drug Targets*, **2016**, 17, 1492-505	3	10
117	Benzbromarone, Quercetin, and Folic Acid Inhibit Amylin Aggregation. *International Journal of Molecular Sciences*, **2016**, 17,	6.3	28
116	Thermal denaturation of α-chymotrypsinogen A in presence of polyols at pH 2.0 and pH 3.0. *Journal of Thermal Analysis and Calorimetry*, **2015**, 120, 489-499	4.1	8
115	In vivo reconstitution of a homodimeric cytochrome b559 like structure: The role of the N-terminus α-subunit from Synechocystis sp. PCC 6803. *Journal of Photochemistry and Photobiology B: Biology*, **2015**, 152, 308-17	6.7	
114	Rational stabilization of complex proteins: a divide and combine approach. *Scientific Reports*, **2015**, 5, 9129	4.9	14
113	Predicting stabilizing mutations in proteins using Poisson-Boltzmann based models: study of unfolded state ensemble models and development of a successful binary classifier based on residue interaction energies. *Physical Chemistry Chemical Physics*, **2015**, 17, 31044-54	3.6	1
112	The mechanism of water/ion exchange at a protein surface: a weakly bound chloride in Helicobacter pylori apoflavodoxin. *Physical Chemistry Chemical Physics*, **2015**, 17, 28635-46	3.6	4
111	DMSO affects Aβ1-40 conformation and interactions with aggregation inhibitors as revealed by NMR. *RSC Advances*, **2015**, 5, 69761-69764	3.7	6
110	The closed conformation of the LDL receptor is destabilized by the low Ca(++) concentration but favored by the high Mg(++) concentration in the endosome. *FEBS Letters*, **2015**, 589, 3534-40	3.8	4
109	Intradomain Confinement of Disulfides in the Folding of Two Consecutive Modules of the LDL Receptor. *PLoS ONE*, **2015**, 10, e0132141	3.7	3
108	PrionScan: an online database of predicted prion domains in complete proteomes. *BMC Genomics*, **2014**, 15, 102	4.5	20
107	LDL receptor/lipoprotein recognition: endosomal weakening of ApoB and ApoE binding to the convex face of the LR5 repeat. *FEBS Journal*, **2014**, 281, 1534-46	5.7	20

106	Low-density lipoprotein receptor is a calcium/magnesium sensor - role of LR4 and LR5 ion interaction kinetics in low-density lipoprotein release in the endosome. *FEBS Journal*, **2014**, 281, 2638-58	5.7	9
105	The FurA regulon in Anabaena sp. PCC 7120: in silico prediction and experimental validation of novel target genes. *Nucleic Acids Research*, **2014**, 42, 4833-46	20.1	34
104	Discovering putative prion sequences in complete proteomes using probabilistic representations of Q/N-rich domains. *BMC Genomics*, **2013**, 14, 316	4.5	50
103	Improved flavodoxin inhibitors with potential therapeutic effects against Helicobacter pylori infection. *Journal of Medicinal Chemistry*, **2013**, 56, 6248-58	8.3	20
102	The stability of 2-state, 3-state and more-state proteins from simple spectroscopic techniques... plus the structure of the equilibrium intermediates at the same time. *Archives of Biochemistry and Biophysics*, **2013**, 531, 4-13	4.1	43
101	Antimicrobial susceptibility and resistance patterns among Helicobacter pylori strains from The Gambia, West Africa. *Antimicrobial Agents and Chemotherapy*, **2013**, 57, 1231-7	5.9	35
100	Allosteric inhibitors of the NS3 protease from the hepatitis C virus. *PLoS ONE*, **2013**, 8, e69773	3.7	23
99	Discovery of novel inhibitors of amyloid β-peptide 1-42 aggregation. *Journal of Medicinal Chemistry*, **2012**, 55, 9521-30	8.3	39
98	Structure of RdxA--an oxygen-insensitive nitroreductase essential for metronidazole activation in Helicobacter pylori. *FEBS Journal*, **2012**, 279, 4306-17	5.7	34
97	Defining the nature of thermal intermediate in 3 state folding proteins: apoflavodoxin, a study case. *PLoS Computational Biology*, **2012**, 8, e1002647	5	9
96	Protein dynamics governed by interfaces of high polarity and low packing density. *PLoS ONE*, **2012**, 7, e48212	3.7	8
95	Structural and mechanistic basis of the interaction between a pharmacological chaperone and human phenylalanine hydroxylase. *ChemBioChem*, **2012**, 13, 1266-9	3.8	11
94	Identification of specific pluripotent stem cell death--inducing small molecules by chemical screening. *Stem Cell Reviews and Reports*, **2012**, 8, 116-27	6.4	15
93	Contribution of disulfide bonds to stability, folding, and amyloid fibril formation: the PI3-SH3 domain case. *Antioxidants and Redox Signaling*, **2012**, 16, 1-15	8.4	25
92	Therapeutic strategies for Gaucher disease: miglustat (NB-DNJ) as a pharmacological chaperone for glucocerebrosidase and the different thermostability of velaglucerase alfa and imiglucerase. *Molecular Pharmaceutics*, **2011**, 8, 2390-7	5.6	39
91	Structural analysis of an equilibrium folding intermediate in the apoflavodoxin native ensemble by small-angle X-ray scattering. *Journal of Molecular Biology*, **2011**, 406, 604-19	6.5	23
90	Protein-cation interactions: structural and thermodynamic aspects. *Current Protein and Peptide Science*, **2011**, 12, 325-38	2.8	16
89	Influence of calcium on the thermal stabilization of bovine α-lactalbumin by selected polyols. *Journal of Thermal Analysis and Calorimetry*, **2011**, 104, 37-44	4.1	1

88	Mechanism of FMN Binding to the Apoflavodoxin from Helicobacter pylori. *Biochemistry*, **2011**, 50, 8703-11	3.1	6
87	Distant and new mutations in CTX-M-1 beta-lactamase affect cefotaxime hydrolysis. *Antimicrobial Agents and Chemotherapy*, **2011**, 55, 4361-8	5.9	22
86	Underexposed polar residues and protein stabilization. *Protein Engineering, Design and Selection*, **2011**, 24, 171-7	1.9	9
85	FtsH cleavage of non-native conformations of proteins. *Journal of Structural Biology*, **2010**, 171, 117-24	3.4	9
84	Design and structure of an equilibrium protein folding intermediate: a hint into dynamical regions of proteins. *Journal of Molecular Biology*, **2010**, 400, 922-34	6.5	18
83	Rescue of misfolded proteins and stabilization by small molecules. *Methods in Molecular Biology*, **2010**, 648, 313-24	1.4	10
82	Helix propensities of conformationally restricted amino acids. Non-natural substitutes for helix breaking proline and helix forming alanine. *Organic and Biomolecular Chemistry*, **2010**, 8, 788-92	3.9	14
81	Comparison of DNA binding across protein superfamilies. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 52-62	4.2	11
80	Thermodynamics of protein-cation interaction: Ca(+2) and Mg(+2) binding to the fifth binding module of the LDL receptor. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 950-61	4.2	16
79	ProtSA: a web application for calculating sequence specific protein solvent accessibilities in the unfolded ensemble. *BMC Bioinformatics*, **2009**, 10, 104	3.6	58
78	VSDMIP: virtual screening data management on an integrated platform. *Journal of Computer-Aided Molecular Design*, **2009**, 23, 171-84	4.2	19
77	Thermodynamic study of the influence of polyols and glucose on the thermal stability of holo-bovine □actalbumin. *Journal of Thermal Analysis and Calorimetry*, **2009**, 98, 165-171	4.1	14
76	Discovery of specific flavodoxin inhibitors as potential therapeutic agents against Helicobacter pylori infection. *ACS Chemical Biology*, **2009**, 4, 928-38	4.9	39
75	Molten globule and native state ensemble of Helicobacter pylori flavodoxin: can crowding, osmolytes or cofactors stabilize the native conformation relative to the molten globule?. *Biophysical Journal*, **2008**, 95, 1913-27	2.9	17
74	The flavodoxin from Helicobacter pylori: structural determinants of thermostability and FMN cofactor binding. *Biochemistry*, **2008**, 47, 627-39	3.2	28
73	The Mycobacterium tuberculosis phoPR operon is positively autoregulated in the virulent strain H37Rv. *Journal of Bacteriology*, **2008**, 190, 7068-78	3.5	40
72	Conformational stability of Helicobacter pylori flavodoxin: fit to function at pH 5. *Journal of Biological Chemistry*, **2008**, 283, 2883-95	5.4	12
71	Mechanism of low density lipoprotein (LDL) release in the endosome: implications of the stability and Ca2+ affinity of the fifth binding module of the LDL receptor. *Journal of Biological Chemistry*, **2008**, 283, 22670-9	5.4	39

70	Scrambled isomers as key intermediates in the oxidative folding of ligand binding module 5 of the low density lipoprotein receptor. *Journal of Biological Chemistry*, **2008**, 283, 13627-37	5.4	20
69	Identification of pharmacological chaperones as potential therapeutic agents to treat phenylketonuria. *Journal of Clinical Investigation*, **2008**, 118, 2858-67	15.9	119
68	Common conformational changes in flavodoxins induced by FMN and anion binding: the structure of Helicobacter pylori apoflavodoxin. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 581-94	4.2	22
67	SIMPLE estimate of the free energy change due to aliphatic mutations: superior predictions based on first principles. *Proteins: Structure, Function and Bioinformatics*, **2007**, 68, 850-62	4.2	12
66	Flavodoxin:quinone reductase (FqrB): a redox partner of pyruvate:ferredoxin oxidoreductase that reversibly couples pyruvate oxidation to NADPH production in Helicobacter pylori and Campylobacter jejuni. *Journal of Bacteriology*, **2007**, 189, 4764-73	3.5	52
65	Thermal stability of beta-lactoglobulin in the presence of aqueous solution of alcohols and polyols. *International Journal of Biological Macromolecules*, **2007**, 40, 423-8	7.9	26
64	Computational diagnosis of protein conformational diseases: short molecular dynamics simulations reveal a fast unfolding of r-LDL mutants that cause familial hypercholesterolemia. *Proteins: Structure, Function and Bioinformatics*, **2007**, 66, 87-95	4.2	12
63	Flavodoxins: sequence, folding, binding, function and beyond. *Cellular and Molecular Life Sciences*, **2006**, 63, 855-64	10.3	150
62	The native-state ensemble of proteins provides clues for folding, misfolding and function. *Trends in Biochemical Sciences*, **2006**, 31, 494-6	10.3	29
61	Sequence-specific solvent accessibilities of protein residues in unfolded protein ensembles. *Biophysical Journal*, **2006**, 91, 4536-43	2.9	39
60	Equilibrium phi-analysis of a molten globule: the 1-149 apoflavodoxin fragment. *Journal of Molecular Biology*, **2006**, 356, 354-66	6.5	14
59	Filling small, empty protein cavities: structural and energetic consequences. *Journal of Molecular Biology*, **2006**, 358, 701-12	6.5	21
58	Do proteins with similar folds have similar transition state structures? A diffuse transition state of the 169 residue apoflavodoxin. *Journal of Molecular Biology*, **2006**, 359, 813-24	6.5	19
57	Native-specific stabilization of flavodoxin by the FMN cofactor: structural and thermodynamical explanation. *Proteins: Structure, Function and Bioinformatics*, **2006**, 63, 581-94	4.2	21
56	Alpha-helix stabilization by alanine relative to glycine: roles of polar and apolar solvent exposures and of backbone entropy. *Proteins: Structure, Function and Bioinformatics*, **2006**, 64, 769-78	4.2	40
55	Energetics of aliphatic deletions in protein cores. *Protein Science*, **2006**, 15, 1858-72	6.3	14
54	Miglustat (NB-DNJ) works as a chaperone for mutated acid beta-glucosidase in cells transfected with several Gaucher disease mutations. *Blood Cells, Molecules, and Diseases*, **2005**, 35, 268-76	2.1	105
53	A double-deletion method to quantifying incremental binding energies in proteins from experiment: example of a destabilizing hydrogen bonding pair. *Biophysical Journal*, **2005**, 88, 1311-21	2.9	19

52	An extensive thermodynamic characterization of the dimerization domain of the HIV-1 capsid protein. *Protein Science*, **2005**, 14, 2387-404	6.3	21
51	Towards a new therapeutic target: Helicobacter pylori flavodoxin. *Biophysical Chemistry*, **2005**, 115, 267-76	3.5	37
50	Design of ligand binding to an engineered protein cavity using virtual screening and thermal up-shift evaluation. *Journal of Computer-Aided Molecular Design*, **2005**, 19, 421-43	4.2	1
49	The long and short flavodoxins: II. The role of the differentiating loop in apoflavodoxin stability and folding mechanism. *Journal of Biological Chemistry*, **2004**, 279, 47184-91	5.4	27
48	The long and short flavodoxins: I. The role of the differentiating loop in apoflavodoxin structure and FMN binding. *Journal of Biological Chemistry*, **2004**, 279, 47177-83	5.4	32
47	Role of neighboring FMN side chains in the modulation of flavin reduction potentials and in the energetics of the FMN:apoprotein interaction in Anabaena flavodoxin. *Biochemistry*, **2004**, 43, 15111-21	3.2	25
46	Structure of stable protein folding intermediates by equilibrium phi-analysis: the apoflavodoxin thermal intermediate. *Journal of Molecular Biology*, **2004**, 344, 239-55	6.5	46
45	Do proteins always benefit from a stability increase? Relevant and residual stabilisation in a three-state protein by charge optimisation. *Journal of Molecular Biology*, **2004**, 344, 223-37	6.5	36
44	How FMN binds to anabaena apoflavodoxin: a hydrophobic encounter at an open binding site. *Journal of Biological Chemistry*, **2003**, 278, 24053-61	5.4	30
43	Purification of colored photosynthetic proteins for understanding protein isolation principles. *Biochemistry and Molecular Biology Education*, **2003**, 31, 119-122	1.3	4
42	The active site of pepsin is formed in the intermediate conformation dominant at mildly acidic pH. *FEBS Letters*, **2003**, 538, 89-95	3.8	67
41	An intragenic suppressor in the cytochrome c oxidase I gene of mouse mitochondrial DNA. *Human Molecular Genetics*, **2003**, 12, 329-39	5.6	62
40	The RelevantRstability of proteins with equilibrium intermediates. *Scientific World Journal, The*, **2002**, 2, 1209-15	2.2	11
39	Anabaena sp. PCC 7119 flavodoxin as electron carrier from photosystem I to ferredoxin-NADP+ reductase. Role of Trp(57) and Tyr(94). *Journal of Biological Chemistry*, **2002**, 277, 22338-44	5.4	27
38	Predicting the structure of protein cavities created by mutation. *Protein Engineering, Design and Selection*, **2002**, 15, 669-75	1.9	11
37	Salt-induced stabilization of apoflavodoxin at neutral pH is mediated through cation-specific effects. *Protein Science*, **2002**, 11, 1260-73	6.3	23
36	Four-state equilibrium unfolding of an scFv antibody fragment. *Biochemistry*, **2002**, 41, 9873-84	3.2	25
35	Theoretical Analysis of the Electron Spin Density Distribution of the Flavin Semiquinone Isoalloxazine Ring within Model Protein Environments. *Journal of Physical Chemistry A*, **2002**, 106, 4729-4735	2.8	36

34	Anabaena apoflavodoxin hydrogen exchange: on the stable exchange core of the alpha/beta(21345) flavodoxin-like family. *Proteins: Structure, Function and Bioinformatics*, **2001**, 43, 476-88	4.2	24
33	A comparative study of the thermal stability of plastocyanin, cytochrome c(6) and Photosystem I in thermophilic and mesophilic cyanobacteria. *Photosynthesis Research*, **2001**, 70, 281-9	3.7	12
32	Native hydrogen bonds in a molten globule: the apoflavodoxin thermal intermediate. *Journal of Molecular Biology*, **2001**, 306, 877-88	6.5	52
31	Apoflavodoxin folding mechanism: an alpha/beta protein with an essentially off-pathway intermediate. *Biochemistry*, **2001**, 40, 15234-45	3.2	47
30	Stabilization of apoflavodoxin by replacing hydrogen-bonded charged Asp or Glu residues by the neutral isosteric Asn or Gln. *Protein Engineering, Design and Selection*, **2001**, 14, 173-81	1.9	28
29	Dissecting the energetics of the apoflavodoxin-FMN complex. *Journal of Biological Chemistry*, **2000**, 275, 9518-26	5.4	61
28	Electron-nuclear double resonance and hyperfine sublevel correlation spectroscopic studies of flavodoxin mutants from Anabaena sp. PCC 7119. *Biophysical Journal*, **1999**, 77, 1712-20	2.9	23
27	Energetics of a hydrogen bond (charged and neutral) and of a cation-pi interaction in apoflavodoxin. *Journal of Molecular Biology*, **1999**, 290, 319-30	6.5	67
26	Apoflavodoxin: structure, stability, and FMN binding. *Biochimie*, **1998**, 80, 813-20	4.6	17
25	Intrahelical side chain interactions in alpha-helices: poor correlation between energetics and frequency. *FEBS Letters*, **1998**, 429, 99-103	3.8	12
24	Cooperative stabilization of a molten globule apoflavodoxin fragment. *Biochemistry*, **1998**, 37, 10589-96	3.2	33
23	Differential stabilization of the three FMN redox forms by tyrosine 94 and tryptophan 57 in flavodoxin from Anabaena and its influence on the redox potentials. *Biochemistry*, **1997**, 36, 14334-44	3.2	85
22	The tryptophan/histidine interaction in alpha-helices. *Journal of Molecular Biology*, **1997**, 267, 184-97	6.5	94
21	Conformational stability of apoflavodoxin. *Protein Science*, **1996**, 5, 1376-88	6.3	72
20	Closure of a tyrosine/tryptophan aromatic gate leads to a compact fold in apo flavodoxin. *Nature Structural and Molecular Biology*, **1996**, 3, 329-32	17.6	81
19	Folding of barnase in parts. *Biochemistry*, **1994**, 33, 3778-86	3.2	80
18	Long-range surface charge-charge interactions in proteins. Comparison of experimental results with calculations from a theoretical method. *Journal of Molecular Biology*, **1993**, 232, 574-83	6.5	80
17	Circular dichroism studies of barnase and its mutants: characterization of the contribution of aromatic side chains. *Biochemistry*, **1993**, 32, 10303-13	3.2	157

16	Energy transfer and specific fluorescence quenching effects in barnase, studied via multifrequency phase-fluorometry of tryptophan mutants **1992**, 1640, 729		
15	Pathway of protein folding. *Faraday Discussions*, **1992**, 183-93	3.6	10
14	Determination of the excited-state lifetimes of the tryptophan residues in barnase, via multifrequency phase fluorometry of tryptophan mutants. *Biochemistry*, **1992**, 31, 711-6	3.2	50
13	Histidine residues at the N- and C-termini of alpha-helices: perturbed pKas and protein stability. *Biochemistry*, **1992**, 31, 2253-8	3.2	129
12	Histidine-aromatic interactions in barnase. Elevation of histidine pKa and contribution to protein stability. *Journal of Molecular Biology*, **1992**, 224, 759-70	6.5	191
11	Dissection of an enzyme by protein engineering. The N and C-terminal fragments of barnase form a native-like complex with restored enzymic activity. *Journal of Molecular Biology*, **1992**, 224, 741-7	6.5	74
10	An N-terminal fragment of barnase has residual helical structure similar to that in a refolding intermediate. *Journal of Molecular Biology*, **1992**, 224, 749-58	6.5	83
9	Alpha-helix stability in proteins. I. Empirical correlations concerning substitution of side-chains at the N and C-caps and the replacement of alanine by glycine or serine at solvent-exposed surfaces. *Journal of Molecular Biology*, **1992**, 227, 544-59	6.5	184
8	Effect of alanine versus glycine in alpha-helices on protein stability. *Nature*, **1992**, 356, 453-5	50.4	176
7	Fluorescence spectrum of barnase: contributions of three tryptophan residues and a histidine-related pH dependence. *Biochemistry*, **1991**, 30, 6775-9	3.2	135
6	Interaction of ferredoxin-NADP+ reductase from Anabaena with its substrates. *Archives of Biochemistry and Biophysics*, **1991**, 288, 231-8	4.1	44
5	Mapping transition states of protein unfolding by protein engineering of ligand-binding sites. *Journal of Molecular Biology*, **1991**, 221, 1007-14	6.5	48
4	Arginyl groups involved in the binding of Anabaena ferredoxin--NADP+ reductase to NADP+ and to ferredoxin. *FEBS Journal*, **1990**, 187, 39-48		24
3	Preparation and properties of a cross-linked complex between ferredoxin--NADP+ reductase and flavodoxin. *FEBS Journal*, **1989**, 183, 539-44		16
2	Purification and properties of ferredoxin-NADP+ oxidoreductase from the nitrogen-fixing cyanobacteria Anabaena variabilis. *Archives of Biochemistry and Biophysics*, **1988**, 260, 200-7	4.1	65
1	Protein haploinsufficiency drivers identify MYBPC3 mutations that cause hypertrophic cardiomyopathy		2