

Luis Serrano Pubull

List of Publications by Year in descending order

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414
papers

44,697
citations

1994

101
h-index

2684

193
g-index

440
all docs

440
docs citations

440
times ranked

36005
citing authors

#	ARTICLE	IF	CITATIONS
1	The FoldX web server: an online force field. Nucleic Acids Research, 2005, 33, W382-W388.	14.5	2,110
2	Predicting Changes in the Stability of Proteins and Protein Complexes: A Study of More Than 1000 Mutations. Journal of Molecular Biology, 2002, 320, 369-387.	4.2	1,609
3	Correlation of mRNA and protein in complex biological samples. FEBS Letters, 2009, 583, 3966-3973.	2.8	1,519
4	Prediction of sequence-dependent and mutational effects on the aggregation of peptides and proteins. Nature Biotechnology, 2004, 22, 1302-1306.	17.5	1,435
5	Engineering stability in gene networks by autoregulation. Nature, 2000, 405, 590-593.	27.8	1,385
6	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 771-782.	4.2	855
7	Mapping the transition state and pathway of protein folding by protein engineering. Nature, 1989, 340, 122-126.	27.8	715
8	Elucidating the folding problem of helical peptides using empirical parameters. Nature Structural and Molecular Biology, 1994, 1, 399-409.	8.2	637
9	Positive feedback in eukaryotic gene networks: cell differentiation by graded to binary response conversion. EMBO Journal, 2001, 20, 2528-2535.	7.8	614
10	Exploring the sequence determinants of amyloid structure using position-specific scoring matrices. Nature Methods, 2010, 7, 237-242.	19.0	566
11	A short linear peptide that folds into a native stable β^2 -hairpin in aqueous solution. Nature Structural and Molecular Biology, 1994, 1, 584-590.	8.2	513
12	Transient folding intermediates characterized by protein engineering. Nature, 1990, 346, 440-445.	27.8	501
13	Structure-based redesign of the dimerization interface reduces the toxicity of zinc-finger nucleases. Nature Biotechnology, 2007, 25, 786-793.	17.5	492
14	How Protein Stability and New Functions Trade Off. PLoS Computational Biology, 2008, 4, e1000002.	3.2	468
15	Proteome Organization in a Genome-Reduced Bacterium. Science, 2009, 326, 1235-1240.	12.6	440
16	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 783-804.	4.2	421
17	Development of the multiple sequence approximation within the AGADIR model of β -helix formation: Comparison with Zimm-Bragg and Lifson-Roig formalisms. Biopolymers, 1997, 41, 495-509.	2.4	418
18	Elucidating the folding problem of β -helices: local motifs, long-range electrostatics, ionic-strength dependence and prediction of NMR parameters 1 Edited by A. R. Fersht. Journal of Molecular Biology, 1998, 284, 173-191.	4.2	416

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19	Strength and co-operativity of contributions of surface salt bridges to protein stability. Journal of Molecular Biology, 1990, 216, 1031-1044.	4.2	410
20	The Stability Effects of Protein Mutations Appear to be Universally Distributed. Journal of Molecular Biology, 2007, 369, 1318-1332.	4.2	396
21	Transcriptome Complexity in a Genome-Reduced Bacterium. Science, 2009, 326, 1268-1271.	12.6	394
22	Estimating the contribution of engineered surface electrostatic interactions to protein stability by using double-mutant cycles. Biochemistry, 1990, 29, 9343-9352.	2.5	390
23	De novo designed peptide-based amyloid fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16052-16057.	7.1	381
24	Capping and α -helix stability. Nature, 1989, 342, 296-299.	27.8	378
25	Sequence determinants of amyloid fibril formation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 87-92.	7.1	376
26	Elucidating the Folding Problem of Helical Peptides using Empirical Parameters. II. Helix Macrodipole Effects and Rational Modification of the Helical Content of Natural Peptides. Journal of Molecular Biology, 1995, 245, 275-296.	4.2	371
27	Structure-Based Assembly of Protein Complexes in Yeast. Science, 2004, 303, 2026-2029.	12.6	367
28	A Comparative Study of the Relationship Between Protein Structure and β -Aggregation in Globular and Intrinsically Disordered Proteins. Journal of Molecular Biology, 2004, 342, 345-353.	4.2	353
29	α -Helix stability in proteins. Journal of Molecular Biology, 1992, 227, 544-559.	4.2	323
30	Protein aggregation and amyloidosis: confusion of the kinds?. Current Opinion in Structural Biology, 2006, 16, 118-126.	5.7	322
31	Aromatic-aromatic interactions and protein stability. Journal of Molecular Biology, 1991, 218, 465-475.	4.2	315
32	Prediction of water and metal binding sites and their affinities by using the Fold-X force field. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10147-10152.	7.1	315
33	The folding transition state between SH3 domains is conformationally restricted and evolutionarily conserved. , 1999, 6, 1010-1016.		311
34	Systematic Discovery of New Recognition Peptides Mediating Protein Interaction Networks. PLoS Biology, 2005, 3, e405.	5.6	310
35	Design of a 20-Amino Acid, Three-Stranded β -Sheet Protein. , 1998, 281, 253-256.		308
36	Control of Drosophila Gastrulation by Apical Localization of Adherens Junctions and RhoGEF2. Science, 2007, 315, 384-386.	12.6	295

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37	Thermodynamic and Kinetic Analysis of the SH3 Domain of Spectrin Shows a Two-State Folding Transition. <i>Biochemistry</i> , 1994, 33, 2142-2150.	2.5	294
38	A graphical interface for the FoldX forcefield. <i>Bioinformatics</i> , 2011, 27, 1711-1712.	4.1	288
39	Evolvability and hierarchy in rewired bacterial gene networks. <i>Nature</i> , 2008, 452, 840-845.	27.8	285
40	Intrinsic secondary structure propensities of the amino acids, using statistical Ψ^{core} - Ψ^{loop} matrices: Comparison with experimental scales. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 20, 301-311.	2.6	284
41	Controlled proteolysis of tubulin by subtilisin: localization of the site for MAP2 interaction. <i>Biochemistry</i> , 1984, 23, 4675-4681.	2.5	279
42	Principles of protein stability derived from protein engineering experiments. <i>Current Opinion in Structural Biology</i> , 1993, 3, 75-83.	5.7	277
43	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 805-818.	4.2	269
44	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. <i>Science</i> , 2009, 326, 1263-1268.	12.6	267
45	Quantification of mRNA and protein and integration with protein turnover in a bacterium. <i>Molecular Systems Biology</i> , 2011, 7, 511.	7.2	267
46	De novo design and structural analysis of a model β^2 -hairpin peptide system. <i>Nature Structural Biology</i> , 1996, 3, 604-612.	9.7	264
47	From in vivo to in silico biology and back. <i>Nature</i> , 2006, 443, 527-533.	27.8	261
48	Involvement of the carboxyl-terminal domain of tubulin in the regulation of its assembly.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1984, 81, 5989-5993.	7.1	256
49	Elucidating the Folding Problem of Helical Peptides using Empirical Parameters. III>Temperature and pH Dependence. <i>Journal of Molecular Biology</i> , 1995, 245, 297-308.	4.2	253
50	Noise in transcription negative feedback loops: simulation and experimental analysis. <i>Molecular Systems Biology</i> , 2006, 2, 41.	7.2	247
51	How Evolutionary Pressure Against Protein Aggregation Shaped Chaperone Specificity. <i>Journal of Molecular Biology</i> , 2006, 355, 1037-1047.	4.2	242
52	Detection and characterization of a folding intermediate in barnase by NMR. <i>Nature</i> , 1990, 346, 488-490.	27.8	241
53	Short amino acid stretches can mediate amyloid formation in globular proteins: The Src homology 3 (SH3) case. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7258-7263.	7.1	241
54	Obligatory steps in protein folding and the conformational diversity of the transition state. <i>Nature Structural and Molecular Biology</i> , 1998, 5, 721-729.	8.2	231

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55	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 819-835.	4.2	222
56	FoldX 5.0: working with RNA, small molecules and a new graphical interface. Bioinformatics, 2019, 35, 4168-4169.	4.1	220
57	Effect of active site residues in barnase on activity and stability. Journal of Molecular Biology, 1992, 225, 585-589.	4.2	217
58	Different folding transition states may result in the same native structure. Nature Structural and Molecular Biology, 1996, 3, 874-880.	8.2	211
59	Protein folding: Defining a "standard" set of experimental conditions and a preliminary kinetic data set of two-state proteins. Protein Science, 2005, 14, 602-616.	7.6	207
60	Effect of alanine versus glycine in α -helices on protein stability. Nature, 1992, 356, 453-455.	27.8	204
61	Step-wise Mutation of Barnase to Binase. Journal of Molecular Biology, 1993, 233, 305-312.	4.2	176
62	Engineering of Large Numbers of Highly Specific Homing Endonucleases that Induce Recombination on Novel DNA Targets. Journal of Molecular Biology, 2006, 355, 443-458.	4.2	175
63	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 847-859.	4.2	169
64	Crosstalk between phosphorylation and lysine acetylation in a genome-reduced bacterium. Molecular Systems Biology, 2012, 8, 571.	7.2	169
65	Structure of the transition state in the folding process of human procarboxypeptidase A2 activation domain. Journal of Molecular Biology, 1998, 283, 1027-1036.	4.2	165
66	Comparison between the χ^2 Distribution of the Amino Acids in the Protein Database and NMR Data Indicates that Amino Acids have Various χ^2 Propensities in the Random Coil Conformation. Journal of Molecular Biology, 1995, 254, 322-333.	4.2	163
67	Synthetic biology: promises and challenges. Molecular Systems Biology, 2007, 3, 158.	7.2	162
68	A casein kinase II-related activity is involved in phosphorylation of microtubule-associated protein MAP-1B during neuroblastoma cell differentiation.. Journal of Cell Biology, 1988, 106, 2057-2065.	5.2	159
69	Structure of the transition state for folding of the 129 aa protein CheY resembles that of a smaller protein, Cl-2. Folding & Design, 1996, 1, 43-55.	4.5	158
70	Folding of Protein G B1 Domain Studied by the Conformational Characterization of Fragments Comprising Its Secondary Structure Elements. FEBS Journal, 1995, 230, 634-649.	0.2	158
71	Predicted Effects of Missense Mutations on Native-State Stability Account for Phenotypic Outcome in Phenylketonuria, a Paradigm of Misfolding Diseases. American Journal of Human Genetics, 2007, 81, 1006-1024.	6.2	157
72	Recognizing and Defining True Ras Binding Domains I: Biochemical Analysis. Journal of Molecular Biology, 2005, 348, 741-758.	4.2	154

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73	Side-chain interactions between sulfur-containing amino acids and phenylalanine in .alpha.-helices. <i>Biochemistry</i> , 1995, 34, 8771-8779.	2.5	153
74	Formation and stability of β^2 -hairpin structures in polypeptides. <i>Current Opinion in Structural Biology</i> , 1998, 8, 107-111.	5.7	152
75	Designed tumor necrosis factor-related apoptosis-inducing ligand variants initiating apoptosis exclusively via the DR5 receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8634-8639.	7.1	151
76	Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. <i>Nature</i> , 2008, 456, 107-111.	27.8	150
77	Computational design of peptide ligands. <i>Trends in Biotechnology</i> , 2011, 29, 231-239.	9.3	146
78	The SH3-fold Family: Experimental Evidence and Prediction of Variations in the Folding Pathways. <i>Journal of Molecular Biology</i> , 2000, 304, 967-982.	4.2	142
79	Histidine residues at the N- and C-termini of .alpha.-helices: perturbed pKas and protein stability. <i>Biochemistry</i> , 1992, 31, 2253-2258.	2.5	138
80	Characterization of the Interaction of Natural Proline-Rich Peptides with Five Different SH3 Domains. <i>Biochemistry</i> , 1994, 33, 10925-10933.	2.5	137
81	SNPeffect: a database mapping molecular phenotypic effects of human non-synonymous coding SNPs. <i>Nucleic Acids Research</i> , 2004, 33, D527-D532.	14.5	136
82	Role of β^2 -turn residues in β^2 -hairpin formation and stability in designed peptides 1 Edited by A.R. Fersht. <i>Journal of Molecular Biology</i> , 1997, 273, 898-912.	4.2	134
83	Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. <i>Genome Research</i> , 2009, 19, 1905-1911.	5.5	134
84	Defining a minimal cell: essentiality of small <scp>ORF</scp> s and nc <scp>RNA</scp> s in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2015, 11, 780.	7.2	133
85	Magnesium Binding to the Bacterial Chemotaxis Protein CheY Results in Large Conformational Changes Involving its Functional Surface. <i>Journal of Molecular Biology</i> , 1994, 238, 489-495.	4.2	131
86	The design of linear peptides that fold as monomeric β^2 -sheet structures. <i>Current Opinion in Structural Biology</i> , 1999, 9, 487-493.	5.7	128
87	SmartCell, a framework to simulate cellular processes that combines stochastic approximation with diffusion and localisation: analysis of simple networks. <i>IET Systems Biology</i> , 2004, 1, 129-138.	2.0	127
88	The amyloid stretch hypothesis: Recruiting proteins toward the dark side. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16672-16677.	7.1	127
89	Rational Design of Specific High-Affinity Peptide Ligands for the Abl-SH3 Domain. <i>Biochemistry</i> , 1996, 35, 10634-10640.	2.5	126
90	The hydrophobic-staple motif and a role for loop-residues in β^2 -helix stability and protein folding. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 380-385.	8.2	125

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91	Localization of the tubulin binding site for tau protein. FEBS Journal, 1985, 153, 595-600.	0.2	124
92	Bacterial transcriptomics: what is beyond the RNA hori-zome?. Nature Reviews Microbiology, 2011, 9, 658-669.	28.6	121
93	Î²-Hairpin and Î²-sheet formation in designed linear peptides. Bioorganic and Medicinal Chemistry, 1999, 7, 93-103.	3.0	120
94	Three-dimensional crystal structure of the transcription factor PhoB receiver domain 1 Edited by R. Huber. Journal of Molecular Biology, 1999, 285, 675-687.	4.2	120
95	Tubulin phosphorylation by casein kinase II is similar to that found in vivo.. Journal of Cell Biology, 1987, 105, 1731-1739.	5.2	119
96	Bacterial antisense RNAs are mainly the product of transcriptional noise. Science Advances, 2016, 2, e1501363.	10.3	118
97	Human Epidermal Stem Cell Function Is Regulated by Circadian Oscillations. Cell Stem Cell, 2013, 13, 745-753.	11.1	117
98	The order of secondary structure elements does not determine the structure of a protein but does affect its folding kinetics. Journal of Molecular Biology, 1995, 247, 670-681.	4.2	116
99	Engineering Signal Transduction Pathways. Cell, 2010, 140, 33-47.	28.9	112
100	Self assembly of microtubule associated protein tau into filaments resembling those found in alzheimer disease. Biochemical and Biophysical Research Communications, 1986, 141, 790-796.	2.1	111
101	Engineering Gene Networks to Emulate Drosophila Embryonic Pattern Formation. PLoS Biology, 2005, 3, e64.	5.6	111
102	Specificity and Evolvability in Eukaryotic Protein Interaction Networks. PLoS Computational Biology, 2007, 3, e25.	3.2	111
103	Protein engineering as a strategy to avoid formation of amyloid fibrils. Protein Science, 2000, 9, 1700-1708.	7.6	109
104	Comprehensive Methylome Characterization of Mycoplasma genitalium and Mycoplasma pneumoniae at Single-Base Resolution. PLoS Genetics, 2013, 9, e1003191.	3.5	109
105	Phosphorylation of tubulin by a calmodulin-dependent protein kinase.. Journal of Biological Chemistry, 1986, 261, 10332-10339.	3.4	106
106	Loop length, intramolecular diffusion and protein folding. Nature Structural and Molecular Biology, 1997, 4, 939-946.	8.2	102
107	PepX: a structural database of non-redundant proteinâ€‘peptide complexes. Nucleic Acids Research, 2010, 38, D545-D551.	14.5	102
108	Crystal structure of the abl-SH3 domain complexed with a designed high-affinity peptide ligand: implications for SH3-ligand interactions. Journal of Molecular Biology, 1998, 281, 513-521.	4.2	101

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109	Recognizing and Defining True Ras Binding Domains II: In Silico Prediction Based on Homology Modelling and Energy Calculations. Journal of Molecular Biology, 2005, 348, 759-775.	4.2	101
110	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 837-845.	4.2	100
111	Conformational strain in the hydrophobic core and its implications for protein folding and design. Nature Structural Biology, 2002, 9, 485-493.	9.7	100
112	Evidence for a Two-State Transition in the Folding Process of the Activation Domain of Human Procarboxypeptidase A2. Biochemistry, 1995, 34, 15105-15110.	2.5	99
113	Strategies for protein synthetic biology. Nucleic Acids Research, 2010, 38, 2663-2675.	14.5	99
114	Unraveling the hidden universe of small proteins in bacterial genomes. Molecular Systems Biology, 2019, 15, e8290.	7.2	96
115	Tumor suppressor properties of the splicing regulatory factor RBM10. RNA Biology, 2016, 13, 466-472.	3.1	94
116	Phosphorylation of alpha-tubulin carboxyl-terminal tyrosine prevents its incorporation into microtubules.. Journal of Biological Chemistry, 1987, 262, 8268-8273.	3.4	93
117	Favourable native-like helical local interactions can accelerate protein folding. Folding & Design, 1997, 2, 23-33.	4.5	92
118	Similarities between the spectrin SH3 domain denatured state and its folding transition state ¹¹ Edited by A. R. Fersht. Journal of Molecular Biology, 2000, 297, 1217-1229.	4.2	91
119	Phosphorylation of a neuronal-specific beta-tubulin isotype.. Journal of Biological Chemistry, 1990, 265, 13949-13954.	3.4	88
120	Computer-aided design of β -sheet peptides ¹ Edited by J. Thornton. Journal of Molecular Biology, 2001, 312, 229-246.	4.2	87
121	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	14.5	87
122	Local versus nonlocal interactions in protein folding and stability “an experimentalist's point of view. Folding & Design, 1996, 1, R71-R77.	4.5	86
123	Analysis of Disease-Linked Rhodopsin Mutations Based on Structure, Function, and Protein Stability Calculations. Journal of Molecular Biology, 2011, 405, 584-606.	4.2	86
124	Analyzing Protein Interaction Networks Using Structural Information. Annual Review of Biochemistry, 2008, 77, 415-441.	11.1	85
125	Phosphorylation of tubulin by a calmodulin-dependent protein kinase. Journal of Biological Chemistry, 1986, 261, 10332-9.	3.4	85
126	Helix design, prediction and stability. Current Opinion in Biotechnology, 1995, 6, 382-386.	6.6	84

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127	Conformational Analysis of Peptides Corresponding to β^2 -Hairpins and a β^2 -Sheet that Represent the Entire Sequence of the β^2 -Spectrin SH3 Domain. <i>Journal of Molecular Biology</i> , 1996, 255, 507-521.	4.2	84
128	Energy estimation in protein design. <i>Current Opinion in Structural Biology</i> , 2002, 12, 441-446.	5.7	84
129	Sequence Dependence of Amyloid Fibril Formation: Insights from Molecular Dynamics Simulations. <i>Journal of Molecular Biology</i> , 2005, 349, 583-596.	4.2	84
130	The order of secondary structure elements does not determine the structure of a protein but does affect its folding kinetics. <i>Journal of Molecular Biology</i> , 1995, 247, 670-681.	4.2	83
131	Stabilization of proteins by rational design of β^2 -helix stability using helix/coil transition theory. <i>Folding & Design</i> , 1996, 1, 29-34.	4.5	83
132	Computer-aided design of a PDZ domain to recognize new target sequences. <i>Nature Structural Biology</i> , 2002, 9, 621-7.	9.7	83
133	A Detailed Thermodynamic Analysis of Ras/Effector Complex Interfaces. <i>Journal of Molecular Biology</i> , 2004, 340, 1039-1058.	4.2	81
134	Defined chromosome structure in the genome-reduced bacterium <i>Mycoplasma pneumoniae</i> . <i>Nature Communications</i> , 2017, 8, 14665.	12.8	81
135	Negative selection in tumor genome evolution acts on essential cellular functions and the immunopeptidome. <i>Genome Biology</i> , 2018, 19, 67.	8.8	81
136	Protein-Peptide Interactions Adopt the Same Structural Motifs as Monomeric Protein Folds. <i>Structure</i> , 2009, 17, 1128-1136.	3.3	79
137	Characterization and structural aspects of the enhanced assembly of tubulin after removal of its carboxyl-terminal domain. <i>FEBS Journal</i> , 1986, 156, 375-381.	0.2	78
138	The multiple α -specificity landscape of modular peptide recognition domains. <i>Molecular Systems Biology</i> , 2011, 7, 484.	7.2	78
139	Kinetic Characterization of the Chemotactic Protein from <i>Escherichia coli</i> , CheY. Kinetic Analysis of the Inverse Hydrophobic Effect. <i>Biochemistry</i> , 1994, 33, 5858-5866.	2.5	77
140	Phosphorylation of Microtubule Proteins in Rat Brain at Different Developmental Stages: Comparison with That Found in Neuronal Cultures. <i>Journal of Neurochemistry</i> , 1990, 54, 211-222.	3.9	76
141	Strand-specific deep sequencing of the transcriptome. <i>Genome Research</i> , 2010, 20, 989-999.	5.5	76
142	Localization of the high affinity calcium-binding site on tubulin molecule.. <i>Journal of Biological Chemistry</i> , 1986, 261, 7076-7081.	3.4	76
143	Phosphorylation of a neuronal-specific beta-tubulin isotype. <i>Journal of Biological Chemistry</i> , 1990, 265, 13949-54.	3.4	76
144	Effect of thermal treatment on physicochemical properties of Gympie messmate wood. <i>Industrial Crops and Products</i> , 2013, 45, 360-366.	5.2	74

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145	Structure-energy-based predictions and network modelling of <sc>RAS</sc>opathy and cancer missense mutations. Molecular Systems Biology, 2014, 10, 727.	7.2	74
146	Space as the final frontier in stochastic simulations of biological systems. FEBS Letters, 2005, 579, 1789-1794.	2.8	73
147	Using a structural and logics systems approach to infer bHLH-DNA binding specificity determinants. Nucleic Acids Research, 2011, 39, 4553-4563.	14.5	73
148	Position dependence of non-polar amino acid intrinsic helical propensities. Journal of Molecular Biology, 1998, 278, 279-289.	4.2	72
149	The Ubiquitin Domain Superfold: Structure-based Sequence Alignments and Characterization of Binding Epitopes. Journal of Molecular Biology, 2006, 355, 821-844.	4.2	72
150	Amyloid Toxicity Is Independent of Polypeptide Sequence, Length and Chirality. Journal of Molecular Biology, 2008, 375, 695-707.	4.2	72
151	Association of casein kinase II with microtubules. Experimental Cell Research, 1989, 181, 263-272.	2.6	71
152	Solvation in protein folding analysis: Combination of theoretical and experimental approaches. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2834-2839.	7.1	70
153	Combinatorial approaches: A new tool to search for highly structured α -hairpin peptides. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 614-619.	7.1	69
154	Towards Cellular Systems in 4D. Cell, 2005, 121, 507-509.	28.9	69
155	Dissecting the energy metabolism in <i>Mycoplasma pneumoniae</i> through genome-scale metabolic modeling. Molecular Systems Biology, 2013, 9, 653.	7.2	69
156	Unspecific hydrophobic stabilization of folding transition states. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5349-5354.	7.1	68
157	Helix Stop and Start Signals in Peptides and Proteins The Capping Box does not Necessarily Prevent Helix Elongation. Journal of Molecular Biology, 1994, 242, 487-496.	4.2	67
158	Structures in systems biology. Current Opinion in Structural Biology, 2007, 17, 378-384.	5.7	67
159	Computer modelling in combination with in vitro studies reveals similar binding affinities of Drosophila Crumbs for the PDZ domains of Stardust and DmPar-6. European Journal of Cell Biology, 2006, 85, 753-767.	3.6	66
160	Assessing the limits of restraint-based 3D modeling of genomes and genomic domains. Nucleic Acids Research, 2015, 43, 3465-3477.	14.5	66
161	Localization of the high affinity calcium-binding site on tubulin molecule. Journal of Biological Chemistry, 1986, 261, 7076-81.	3.4	66
162	Analysis of the effect of local interactions on protein stability. Folding & Design, 1996, 1, 167-178.	4.5	65

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163	Cell type-specific properties and environment shape tissue specificity of cancer genes. Scientific Reports, 2016, 6, 20707.	3.3	64
164	Cell Typeâ€“Specific Importance of Rasâ€“c-Raf Complex Association Rate Constants for MAPK Signaling. Science Signaling, 2009, 2, ra38.	3.6	63
165	Rapid and efficient cancer cell killing mediated by high-affinity death receptor homotrimerizing TRAIL variants. Cell Death and Disease, 2010, 1, e83-e83.	6.3	63
166	Molecular basis of engineered meganuclease targeting of the endogenous human RAG1 locus. Nucleic Acids Research, 2011, 39, 729-743.	14.5	63
167	Correcting for the study bias associated with proteinâ€“protein interaction measurements reveals differences between protein degree distributions from different cancer types. Frontiers in Genetics, 2015, 6, 260.	2.3	63
168	Model for stathmin/OP18 binding to tubulin. EMBO Journal, 2000, 19, 213-222.	7.8	62
169	The relationship between sequence and structure in elementary folding units. Advances in Protein Chemistry, 2000, 53, 49-85.	4.4	62
170	Engineering of weak helper interactions for high-efficiency FRET probes. Nature Methods, 2013, 10, 1021-1027.	19.0	62
171	Thermodynamic analysis of the chemotactic protein from Escherichia coli, CheY. Biochemistry, 1993, 32, 12906-12921.	2.5	61
172	Experimental Analysis of the Schellman Motif. Journal of Molecular Biology, 1995, 251, 150-160.	4.2	61
173	Folding kinetics of Che Y mutants with enhanced native α -helix propensities 1 1 Edited by A. R. Fersht. Journal of Molecular Biology, 1997, 266, 610-620.	4.2	61
174	Local water bridges and protein conformational stability. Protein Science, 1999, 8, 1982-1989.	7.6	61
175	Personalized Respiratory Medicine: Exploring the Horizon, Addressing the Issues. Summary of a BRN-AJRCCM Workshop Held in Barcelona on June 12, 2014. American Journal of Respiratory and Critical Care Medicine, 2015, 191, 391-401.	5.6	61
176	Non-native local interactions in protein folding and stability: introducing a helical tendency in the all β -sheet β -spectrin SH3 domain. Journal of Molecular Biology, 1997, 268, 760-778.	4.2	60
177	NMR and SAXS characterization of the denatured state of the chemotactic protein Che Y: Implications for protein folding initiation. Protein Science, 2001, 10, 1100-1112.	7.6	60
178	Early Kinetics of Amyloid Fibril Formation Reveals Conformational Reorganisation of Initial Aggregates. Journal of Molecular Biology, 2007, 366, 1351-1363.	4.2	60
179	Protein-Peptide Complex Prediction through Fragment Interaction Patterns. Structure, 2013, 21, 789-797.	3.3	59
180	The Vaccinia Virus 14-Kilodalton (A27L) Fusion Protein Forms a Triple Coiled-Coil Structure and Interacts with the 21-Kilodalton (A17L) Virus Membrane Protein through a C-Terminal α -Helix. Journal of Virology, 1998, 72, 10126-10137.	3.4	59

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181	C-capping and helix stability: the pro C-capping motif. <i>Journal of Molecular Biology</i> , 1997, 274, 276-288.	4.2	58
182	The Tryptophan Switch: Changing Ligand-binding Specificity from Type I to Type II in SH3 Domains. <i>Journal of Molecular Biology</i> , 2004, 335, 619-629.	4.2	56
183	DR4-selective Tumor Necrosis Factor-related Apoptosis-inducing Ligand (TRAIL) Variants Obtained by Structure-based Design. <i>Journal of Biological Chemistry</i> , 2008, 283, 20560-20568.	3.4	56
184	Thermodynamic Analysis of α -spectrin SH3 and Two of Its Circular Permutants with Different Loop Lengths: Discerning the Reasons for Rapid Folding in Proteins. <i>Biochemistry</i> , 1999, 38, 549-559.	2.5	55
185	Using protein design algorithms to understand the molecular basis of disease caused by protein-DNA interactions: the Pax6 example. <i>Nucleic Acids Research</i> , 2010, 38, 7422-7431.	14.5	55
186	Advancing Cell Biology Through Proteomics in Space and Time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , 2012, 11, O112.017731.	3.8	55
187	High populations of non-native structures in the denatured state are compatible with the formation of the native folded state. <i>Journal of Molecular Biology</i> , 1998, 284, 1153-1164.	4.2	54
188	A thermodynamic analysis of a family of small globular proteins: SH3 domains. <i>Biophysical Chemistry</i> , 1999, 77, 195-208.	2.8	54
189	Decoy receptors block TRAIL sensitivity at a supracellular level: the role of stromal cells in controlling tumour TRAIL sensitivity. <i>Oncogene</i> , 2016, 35, 1261-1270.	5.9	54
190	¹ H and ¹⁵ N NMR assignment and solution structure of the SH3 domain of spectrin: comparison of unrefined and refined structure sets with the crystal structure. <i>Journal of Biomolecular NMR</i> , 1997, 9, 347-357.	2.8	53
191	Stabilisation of α -helices by site-directed mutagenesis reveals the importance of secondary structure in the transition state for acylphosphatase folding. <i>Journal of Molecular Biology</i> , 2000, 300, 633-647.	4.2	53
192	E-Cadherin Destabilization Accounts for the Pathogenicity of Missense Mutations in Hereditary Diffuse Gastric Cancer. <i>PLoS ONE</i> , 2012, 7, e33783.	2.5	53
193	High Frequency of Germline Succinate Dehydrogenase Mutations in Sporadic Cervical Paragangliomas in Northern Spain: Mitochondrial Succinate Dehydrogenase Structure-Function Relationships and Clinical-Pathological Correlations. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2007, 92, 4853-4864.	3.6	51
194	Limited proteolysis of tubulin and the localization of the binding site for colchicine. <i>Journal of Biological Chemistry</i> , 1984, 259, 6607-6611.	3.4	51
195	Origins of Helix-Coil Switching in a Light-Sensitive Peptide. <i>Biochemistry</i> , 2004, 43, 15329-15338.	2.5	50
196	Position dependence of amino acid intrinsic helical propensities II: Non-charged polar residues: Ser, Thr, Asn, and Gln. <i>Protein Science</i> , 1999, 8, 2144-2150.	7.6	49
197	Hacking the Code of Amyloid Formation. <i>Prion</i> , 2007, 1, 9-14.	1.8	49
198	Computer design of obligate heterodimer meganucleases allows efficient cutting of custom DNA sequences. <i>Nucleic Acids Research</i> , 2008, 36, 2163-2173.	14.5	49

#	ARTICLE	IF	CITATIONS
199	BriX: a database of protein building blocks for structural analysis, modeling and design. Nucleic Acids Research, 2011, 39, D435-D442.	14.5	48
200	Integration of Protein Abundance and Structure Data Reveals Competition in the ErbB Signaling Network. Science Signaling, 2013, 6, ra109.	3.6	48
201	Rational design of a GCN4-derived mimetic of interleukin-4. Nature Structural Biology, 1999, 6, 652-656.	9.7	46
202	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
203	COSMIC analysis of the major α -helix of barnase during folding. Journal of Molecular Biology, 1991, 219, 5-9.	4.2	45
204	Structure of the transition state for folding of the 129 aa protein CheY resembles that of a smaller protein, Cl-2. Folding & Design, 1996, 1, 43-55.	4.5	45
205	Folding of Protein G B1 Domain Studied by the Conformational Characterization of Fragments Comprising Its Secondary Structure Elements. FEBS Journal, 1995, 230, 634-649.	0.2	44
206	Conformational analysis of peptides corresponding to all the secondary structure elements of protein L B1 domain: Secondary structure propensities are not conserved in proteins with the same fold. Protein Science, 1997, 6, 162-174.	7.6	44
207	Reading protein sequences backwards. Folding & Design, 1998, 3, 79-85.	4.5	44
208	Stable proline box motif at the N-terminal end of α -helices. Protein Science, 1999, 8, 1733-1742.	7.6	44
209	Comparative α -omics in Mycoplasma pneumoniae Clinical Isolates Reveals Key Virulence Factors. PLoS ONE, 2015, 10, e0137354.	2.5	44
210	Elongation of the BH8 β -hairpin peptide: Electrostatic interactions in β -hairpin formation and stability. Protein Science, 2008, 10, 1381-1392.	7.6	43
211	Infrared evidence of a β -hairpin peptide structure in solution. FEBS Letters, 1996, 384, 35-37.	2.8	42
212	Protein design based on folding models. Current Opinion in Structural Biology, 2001, 11, 101-106.	5.7	42
213	Point Mutations in Protein Globular Domains: Contributions from Function, Stability and Misfolding. Journal of Molecular Biology, 2006, 363, 422-432.	4.2	42
214	Reconstruction of Protein Backbones from the BriX Collection of Canonical Protein Fragments. PLoS Computational Biology, 2008, 4, e1000083.	3.2	42
215	Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D. Nature Communications, 2020, 11, 499.	12.8	42
216	Translational efficiency across healthy and tumor tissues is proliferation-related. Molecular Systems Biology, 2020, 16, e9275.	7.2	42

#	ARTICLE	IF	CITATIONS
217	Insights into the Mechanisms of Basal Coordination of Transcription Using a Genome-Reduced Bacterium. <i>Cell Systems</i> , 2016, 2, 391-401.	6.2	41
218	Exploring the conformational properties of the sequence space between two proteins with different folds: an experimental study 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 285, 741-753.	4.2	40
219	Insights into the Origin of the Tendency of the PI3-SH3 Domain to form Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2002, 322, 1147-1158.	4.2	40
220	H-bonding in protein hydration revisited. <i>Protein Science</i> , 2004, 13, 2120-2129.	7.6	40
221	Comparative Genomics and Disorder Prediction Identify Biologically Relevant SH3 Protein Interactions. <i>PLoS Computational Biology</i> , 2005, 1, e26.	3.2	40
222	Transcription start site associated RNAs in bacteria. <i>Molecular Systems Biology</i> , 2012, 8, 585.	7.2	40
223	Analysis of i,i+5 and i,i+8 Hydrophobic Interactions in a Helical Model Peptide Bearing the Hydrophobic Staple Motif. <i>Biochemistry</i> , 1995, 34, 15301-15306.	2.5	39
224	Amino acid intrinsic alpha-helical propensities III: Positional dependence at several positions of C terminus. <i>Protein Science</i> , 2002, 11, 766-777.	7.6	39
225	Genome-Wide Prediction of SH2 Domain Targets Using Structural Information and the FoldX Algorithm. <i>PLoS Computational Biology</i> , 2008, 4, e1000052.	3.2	39
226	Challenges ahead in signal transduction: MAPK as an example. <i>Current Opinion in Biotechnology</i> , 2012, 23, 305-314.	6.6	39
227	Limited proteolysis of tubulin and the localization of the binding site for colchicine. <i>Journal of Biological Chemistry</i> , 1984, 259, 6607-11.	3.4	39
228	Characterization of different alginate lyases for dissolving <i>Pseudomonas aeruginosa</i> biofilms. <i>Scientific Reports</i> , 2020, 10, 9390.	3.3	38
229	Computational estimation of specific side chain interaction energies in α helices. <i>Protein Science</i> , 2001, 10, 809-818.	7.6	37
230	Designing proteins from the inside out. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 1-10.	2.6	37
231	Localized transfection on arrays of magnetic beads coated with PCR products. <i>Nature Methods</i> , 2005, 2, 113-118.	19.0	36
232	Crystal structure of I-Dmol in complex with its target DNA provides new insights into meganuclease engineering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16888-16893.	7.1	36
233	ADAN: a database for prediction of protein-protein interaction of modular domains mediated by linear motifs. <i>Bioinformatics</i> , 2009, 25, 2418-2424.	4.1	36
234	The role of clonal communication and heterogeneity in breast cancer. <i>BMC Cancer</i> , 2019, 19, 666.	2.6	36

#	ARTICLE	IF	CITATIONS
235	Determination of the Gene Regulatory Network of a Genome-Reduced Bacterium Highlights Alternative Regulation Independent of Transcription Factors. <i>Cell Systems</i> , 2019, 9, 143-158.e13.	6.2	36
236	In silico mutagenesis of human ACE2 with S protein and translational efficiency explain SARS-CoV-2 infectivity in different species. <i>PLoS Computational Biology</i> , 2020, 16, e1008450.	3.2	36
237	Structural analysis of peptides encompassing all α -helices of three α / β parallel proteins: Che-Y, flavodoxin and P21-Ras: Implications for α -Helix stability and the folding of α / β parallel proteins. <i>Journal of Molecular Biology</i> , 1995, 247, 648-669.	4.2	35
238	Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. <i>Nucleic Acids Research</i> , 2016, 44, 1192-1202.	14.5	35
239	A reporter system coupled with high-throughput sequencing unveils key bacterial transcription and translation determinants. <i>Nature Communications</i> , 2017, 8, 368.	12.8	35
240	^1H - and ^{15}N -NMR assignment and solution structure of the chemotactic <i>Escherichia coli</i> Che Y protein. <i>FEBS Journal</i> , 1993, 215, 573-585.	0.2	34
241	Amide hydrogen exchange and internal dynamics the chemotactic protein CheY from <i>Escherichia coli</i> 1 Edited by A.R.Fersht. <i>Journal of Molecular Biology</i> , 1997, 271, 472-487.	4.2	34
242	Role of a nonnative interaction in the folding of the protein G B1 domain as inferred from the conformational analysis of the α -helix fragment. <i>Folding & Design</i> , 1997, 2, 123-133.	4.5	34
243	A Genome-wide Ras-Effector Interaction Network. <i>Journal of Molecular Biology</i> , 2007, 370, 1020-1032.	4.2	34
244	The yin-yang of kinase activation and unfolding explains the peculiarity of Val600 in the activation segment of BRAF. <i>ELife</i> , 2016, 5, e12814.	6.0	34
245	A Thermodynamic and Kinetic Analysis of the Folding Pathway of an SH3 Domain Entropically Stabilised by a Redesigned Hydrophobic Core. <i>Journal of Molecular Biology</i> , 2003, 328, 221-233.	4.2	33
246	A Miniprotein Scaffold Used to Assemble the Polyproline II Binding Epitope Recognized by SH3 Domains. <i>Journal of Molecular Biology</i> , 2004, 342, 355-365.	4.2	33
247	Quantifying information transfer by protein domains: Analysis of the Fyn SH2 domain structure. <i>BMC Structural Biology</i> , 2008, 8, 43.	2.3	33
248	Structure-Based Prediction of the <i>Saccharomyces cerevisiae</i> SH3-Ligand Interactions. <i>Journal of Molecular Biology</i> , 2009, 388, 902-916.	4.2	33
249	Structural and functional protein network analyses predict novel signaling functions for rhodopsin. <i>Molecular Systems Biology</i> , 2011, 7, 551.	7.2	33
250	Tissue-specific DNA methylation loss during ageing and carcinogenesis is linked to chromosome structure, replication timing and cell division rates. <i>Nucleic Acids Research</i> , 2018, 46, 7022-7039.	14.5	33
251	The interaction between subunits in the tubulin dimer. <i>Biochemical Journal</i> , 1985, 230, 551-556.	3.7	32
252	Effect of specific proteolytic cleavages on tubulin polymer formation. <i>Biochemical Journal</i> , 1988, 252, 683-691.	3.7	32

#	ARTICLE	IF	CITATIONS
253	Thermodynamic and structural characterization of Asn and Ala residues in the disallowed $\beta\beta^2$ region of the Ramachandran plot. <i>Protein Science</i> , 2000, 9, 2322-2328.	7.6	32
254	Protein design with fragment databases. <i>Current Opinion in Structural Biology</i> , 2011, 21, 452-459.	5.7	32
255	Location of the regions recognized by five commercial antibodies on the tubulin molecule. <i>Analytical Biochemistry</i> , 1986, 159, 253-259.	2.4	31
256	A tale of two secondary structure elements: when a β^2 -hairpin becomes an α -helix 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 292, 389-401.	4.2	31
257	Calculation of Mutational Free Energy Changes in Transition States for Protein Folding. <i>Biophysical Journal</i> , 2003, 85, 1207-1214.	0.5	31
258	An improved understanding of TNFL/TNFR interactions using structure-based classifications. <i>Trends in Biochemical Sciences</i> , 2012, 37, 353-363.	7.5	31
259	Identification of zinc-binding sites of proteins: Zinc binds to the amino-terminal region of tubulin. <i>Analytical Biochemistry</i> , 1988, 172, 210-218.	2.4	30
260	The Three-dimensional Structure of Two Mutants of the Signal Transduction Protein CheY Suggest its Molecular Activation Mechanism. <i>Journal of Molecular Biology</i> , 1996, 257, 116-128.	4.2	30
261	Identification of Protein Ligands in Complex Biological Samples Using Intensity-Fading MALDI-TOF Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 3385-3395.	6.5	30
262	Stabilization of TRAIL, an all- α -sheet multimeric protein, using computational redesign. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 673-680.	2.1	30
263	MyMpn: a database for the systems biology model organism <i>Mycoplasma pneumoniae</i> . <i>Nucleic Acids Research</i> , 2015, 43, D618-D623.	14.5	30
264	Enhancement of Antitumor Properties of rhTRAIL by Affinity Increase toward Its Death Receptors. <i>Biochemistry</i> , 2009, 48, 2180-2191.	2.5	29
265	Engineering Biological Approaches for Detection of Toxic Compounds: A New Microbial Biosensor Based on the <i>Pseudomonas putida</i> TtgR Repressor. <i>Molecular Biotechnology</i> , 2015, 57, 558-564.	2.4	29
266	A Comprehensive View of the β^2 -Arrestinome. <i>Frontiers in Endocrinology</i> , 2017, 8, 32.	3.5	29
267	Three-dimensional structure of chemotactic Che Y protein in aqueous solution by nuclear magnetic resonance methods. <i>Journal of Molecular Biology</i> , 1995, 247, 717-725.	4.2	29
268	Bergerac-SH3: α -frustration induced by stabilizing the folding nucleus. <i>Journal of Molecular Biology</i> , 2001, 311, 357-371.	4.2	28
269	Hydrogen-exchange stability analysis of Bergerac-Src homology 3 variants allows the characterization of a folding intermediate in equilibrium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5730-5735.	7.1	28
270	New Strategy for the Generation of Specific d-Peptide Amyloid Inhibitors. <i>Journal of Molecular Biology</i> , 2008, 377, 1372-1381.	4.2	28

#	ARTICLE	IF	CITATIONS
271	Building blocks for protein interaction devices. <i>Nucleic Acids Research</i> , 2010, 38, 2645-2662.	14.5	28
272	Protein Conservation and Variation Suggest Mechanisms of Cell Type-Specific Modulation of Signaling Pathways. <i>PLoS Computational Biology</i> , 2014, 10, e1003659.	3.2	28
273	Towards understanding a molecular switch mechanism: thermodynamic and crystallographic studies of the signal transduction protein CheY. <i>Journal of Molecular Biology</i> , 2000, 303, 213-225.	4.2	27
274	Reconstitution of Mdm2-Dependent Post-Translational Modifications of p53 in Yeast. <i>PLoS ONE</i> , 2008, 3, e1507.	2.5	27
275	Large-scale metabolome analysis and quantitative integration with genomics and proteomics data in <i>Mycoplasma pneumoniae</i> . <i>Molecular BioSystems</i> , 2013, 9, 1743.	2.9	27
276	Helix Stop and Start Signals in Peptides and Proteins. <i>Journal of Molecular Biology</i> , 1994, 242, 487-496.	4.2	26
277	Chemical modification of fast-growing eucalyptus wood. <i>Wood Science and Technology</i> , 2015, 49, 273-288.	3.2	26
278	rec-YnH enables simultaneous many-by-many detection of direct proteinâ€“protein and proteinâ€“RNA interactions. <i>Nature Communications</i> , 2018, 9, 3747.	12.8	26
279	<i>Mycoplasma pneumoniae</i> Genome Editing Based on Oligo Recombineering and Cas9-Mediated Counterselection. <i>ACS Synthetic Biology</i> , 2020, 9, 1693-1704.	3.8	26
280	Structural and functional domains of tubulin. <i>BioEssays</i> , 1985, 2, 165-169.	2.5	25
281	A more precise characterization of chaperonin substrates. <i>Bioinformatics</i> , 2010, 26, 1685-1689.	4.1	25
282	Kinetics in Signal Transduction Pathways Involving Promiscuous Oligomerizing Receptors Can Be Determined by Receptor Specificity: Apoptosis Induction by TRAIL. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013730.	3.8	25
283	Structure and Non-Structure of Centrosomal Proteins. <i>PLoS ONE</i> , 2013, 8, e62633.	2.5	25
284	Domain Swapping in p13suc1 Results in Formation of Native-like, Cytotoxic Aggregates. <i>Journal of Molecular Biology</i> , 2006, 363, 496-505.	4.2	24
285	Protein design in biological networks: from manipulating the input to modifying the output. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 537-542.	2.1	24
286	Impact of C-terminal amino acid composition on protein expression in bacteria. <i>Molecular Systems Biology</i> , 2020, 16, e9208.	7.2	24
287	Repository of proposed pathways and proteinâ€“protein interaction networks in age-related macular degeneration. <i>Npj Aging and Mechanisms of Disease</i> , 2020, 6, 2.	4.5	24
288	Protein haploinsufficiency drivers identify MYBPC3 variants that cause hypertrophic cardiomyopathy. <i>Journal of Biological Chemistry</i> , 2021, 297, 100854.	3.4	23

#	ARTICLE	IF	CITATIONS
289	Pathway and stability of protein folding. Philosophical Transactions of the Royal Society B: Biological Sciences, 1991, 332, 171-176.	4.0	22
290	Molecular dynamics as a tool to detect protein foldability. A mutant of domain B1 of protein G with non-native secondary structure propensities. Protein Science, 1999, 8, 271-282.	7.6	22
291	FoldX accurate structural protein-DNA binding prediction using PADA1 (Protein Assisted DNA) Tj ETQq1 1 0.784314 rgBT /Overl	14.5	22
292	[19] Proteolytic modification of tubulin. Methods in Enzymology, 1986, 134, 179-190.	1.0	21
293	Homology modeling of the Abl-SH3 domain. Proteins: Structure, Function and Bioinformatics, 1994, 20, 203-215.	2.6	21
294	Kinesin subfamily UNC104 contains a FHA domain: boundaries and physicochemical characterization. FEBS Letters, 2000, 486, 285-290.	2.8	21
295	Engineering a genome-reduced bacterium to eliminate <i>Staphylococcus aureus</i> biofilms <i>in vivo</i> . Molecular Systems Biology, 2021, 17, e10145.	7.2	21
296	Dissecting the Calcium-Induced Differentiation of Human Primary Keratinocytes Stem Cells by Integrative and Structural Network Analyses. PLoS Computational Biology, 2015, 11, e1004256.	3.2	20
297	Mutation bias within oncogene families is related to proliferation-specific codon usage. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30848-30856.	7.1	20
298	Protein engineering and the dissection of protein folding pathways. Current Opinion in Structural Biology, 1994, 4, 107-111.	5.7	19
299	Design of stable α -helices using global sequence optimization. Journal of Peptide Science, 2009, 15, 359-365.	1.4	19
300	Distinguishing between productive and abortive promoters using a random forest classifier in <i>Mycoplasma pneumoniae</i> . Nucleic Acids Research, 2015, 43, 3442-3453.	14.5	19
301	Unusual properties of a cold-labile fraction of Atlantic cod (<i>Gadus morhua</i>) brain microtubules. Biochemistry and Cell Biology, 1989, 67, 791-800.	2.0	18
302	The distribution of α -helix propensity along the polypeptide chain is not conserved in proteins from the same family. Protein Science, 1995, 4, 1577-1586.	7.6	18
303	Investigating the Structural Determinants of the p21-like Triphosphate and Mg ²⁺ -Binding Site. Journal of Molecular Biology, 1995, 249, 654-664.	4.2	18
304	Motional dynamics of residues in a β^2 -hairpin peptide measured by ¹³ C-NMR relaxation. Protein Science, 1998, 7, 720-729.	7.6	18
305	Conformational Exchange on the Microsecond Time Scale in α -Helix and β^2 -Hairpin Peptides Measured by ¹³ C NMR Transverse Relaxation. Biochemistry, 2001, 40, 2844-2853.	2.5	18
306	Targeting AML through DR4 with a novel variant of rhTRAIL. Journal of Cellular and Molecular Medicine, 2011, 15, 2216-2231.	3.6	18

#	ARTICLE	IF	CITATIONS
307	Alternative transcriptional regulation in genome-reduced bacteria. <i>Current Opinion in Microbiology</i> , 2017, 39, 89-95.	5.1	18
308	SynMyco transposon: engineering transposon vectors for efficient transformation of minimal genomes. <i>DNA Research</i> , 2019, 26, 327-339.	3.4	18
309	Model-driven design allows growth of <i>Mycoplasma pneumoniae</i> on serum-free media. <i>Npj Systems Biology and Applications</i> , 2020, 6, 33.	3.0	18
310	Three-dimensional structure of chemotactic che Y protein in aqueous solution by nuclear magnetic resonance methods. <i>Journal of Molecular Biology</i> , 1995, 247, 717-725.	4.2	17
311	An NMR View of the Folding Process of a CheY Mutant at the Residue Level. <i>Structure</i> , 2002, 10, 1173-1185.	3.3	17
312	Synthetic Biology: challenges ahead. <i>Bioinformatics</i> , 2006, 22, 127-128.	4.1	17
313	A Molecular Dynamics Study of the Interaction of d-Peptide Amyloid Inhibitors with Their Target Sequence Reveals a Potential Inhibitory Pharmacophore Conformation. <i>Journal of Molecular Biology</i> , 2008, 383, 266-280.	4.2	17
314	Protein quality control and regulated proteolysis in the genome-reduced organism <i>Mycoplasma pneumoniae</i> . <i>Molecular Systems Biology</i> , 2020, 16, e9530.	7.2	17
315	Stabilization of proteins by rational design of alpha-helix stability using helix/coil transition theory. <i>Folding & Design</i> , 1996, 1, 29-34.	4.5	17
316	The removal of the carboxy-terminal region of tubulin favors its vinblastine-induced aggregation into spiral-like structures. <i>Archives of Biochemistry and Biophysics</i> , 1986, 249, 611-615.	3.0	16
317	Protein secondary structure and stability determined by combining exoproteolysis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2002, 37, 974-984.	1.6	16
318	Microtubule-associated protein, MAP2, is a calcium-binding protein. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1988, 965, 195-201.	2.4	15
319	Design and NMR conformational study of a β^2 -sheet peptide based on Betanova and WW domains. <i>Protein Science</i> , 2006, 15, 2278-2289.	7.6	15
320	Effect of replacing glutamic residues upon the biological activity and stability of the circular enterocin AS-48. <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 61, 1256-1265.	3.0	15
321	Interaction Dynamics Determine Signaling and Output Pathway Responses. <i>Cell Reports</i> , 2017, 19, 136-149.	6.4	15
322	FASTQINS and ANUBIS: two bioinformatic tools to explore facts and artifacts in transposon sequencing and essentiality studies. <i>Nucleic Acids Research</i> , 2020, 48, e102-e102.	14.5	15
323	Silencing of SRRM4 suppresses microexon inclusion and promotes tumor growth across cancers. <i>PLoS Biology</i> , 2021, 19, e3001138.	5.6	15
324	Translational adaptation of human viruses to the tissues they infect. <i>Cell Reports</i> , 2021, 34, 108872.	6.4	15

#	ARTICLE	IF	CITATIONS
325	New approaches to high-throughput structure characterization of SH3 complexes: The example of Myosin-3 and Myosin-5 SH3 domains from <i>S. cerevisiae</i> . <i>Protein Science</i> , 2006, 15, 795-807.	7.6	14
326	Prediction of Protein-Protein Interaction Based on Structure. , 2006, 340, 207-234.		14
327	Association Rate Constants of Ras-Effector Interactions Are Evolutionarily Conserved. <i>PLoS Computational Biology</i> , 2008, 4, e1000245.	3.2	14
328	Structural Data in Synthetic Biology Approaches for Studying General Design Principles of Cellular Signaling Networks. <i>Structure</i> , 2012, 20, 1806-1813.	3.3	14
329	Simple and complex retinal dystrophies are associated with profoundly different disease networks. <i>Scientific Reports</i> , 2017, 7, 41835.	3.3	14
330	Pathway of protein folding. <i>Faraday Discussions</i> , 1992, 93, 183.	3.2	13
331	Molecular modeling of the interaction of polyproline-based peptides with the Abl-SH3 domain: rational modification of the interaction. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1455-1462.	2.1	13
332	Thermodynamic analysis of helix-engineered forms of the activation domain of human procarboxypeptidase A2. <i>FEBS Journal</i> , 2000, 267, 5891-5899.	0.2	13
333	Surfing on protein folding energy landscapes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15846-15848.	7.1	13
334	Mean first-passage time analysis reveals rate-limiting steps, parallel pathways and dead ends in a simple model of protein folding. <i>Europhysics Letters</i> , 2003, 61, 561-566.	2.0	13
335	Prediction of Ras-effector interactions using position energy matrices. <i>Bioinformatics</i> , 2007, 23, 2226-2230.	4.1	13
336	<i>In Situ</i> Overlap and Sequence Synthesis During DNA Assembly. <i>ACS Synthetic Biology</i> , 2013, 2, 750-755.	3.8	13
337	Phosphorylation of neuronal microtubule proteins. <i>Protoplasma</i> , 1988, 145, 82-88.	2.1	12
338	Role of the carboxy terminal region of β tubulin on microtubule dynamics through its interaction with the GTP phosphate binding region. <i>FEBS Letters</i> , 1993, 325, 173-176.	2.8	12
339	Improving the refolding yield of interleukin-4 through the optimization of local interactions. <i>Journal of Biotechnology</i> , 2000, 84, 217-230.	3.8	12
340	Conformational Stability and Activity of Circular Enterocin AS-48 Derivatives. <i>Protein and Peptide Letters</i> , 2010, 17, 708-714.	0.9	12
341	Quantification of ErbB Network Proteins in Three Cell Types Using Complementary Approaches Identifies Cell-General and Cell-Type-Specific Signaling Proteins. <i>Journal of Proteome Research</i> , 2014, 13, 300-313.	3.7	12
342	Internal motional amplitudes and correlated bond rotations in an α -helical peptide derived from ^{13}C and ^{15}N NMR relaxation. <i>Protein Science</i> , 2000, 9, 2118-2127.	7.6	11

#	ARTICLE	IF	CITATIONS
343	Plasticity in amino acid sensing of the chimeric receptor Taz. <i>Molecular Microbiology</i> , 2005, 58, 257-266.	2.5	11
344	Functional Characterization of the Cell Division Gene Cluster of the Wall-less Bacterium <i>Mycoplasma genitalium</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 695572.	3.5	11
345	A RAC-GEF network critical for early intestinal tumorigenesis. <i>Nature Communications</i> , 2021, 12, 56.	12.8	11
346	Specialization of the photoreceptor transcriptome by <i>Srrm3</i> -dependent microexons is required for outer segment maintenance and vision. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
347	Differential phosphorylation of microtubule proteins by ATP and GTP. <i>Molecular and Cellular Biochemistry</i> , 1988, 79, 73-79.	3.1	10
348	Ligand Screening by Exoproteolysis and Mass Spectrometry in Combination With Computer Modelling. <i>Journal of Molecular Biology</i> , 2003, 330, 1039-1048.	4.2	10
349	Localized transfection with magnetic beads coated with PCR products and other nucleic acids. <i>Nature Protocols</i> , 2006, 1, 526-531.	12.0	10
350	SAPIN: A framework for the structural analysis of protein interaction networks. <i>Bioinformatics</i> , 2012, 28, 2998-2999.	4.1	10
351	VarQ: A Tool for the Structural and Functional Analysis of Human Protein Variants. <i>Frontiers in Genetics</i> , 2018, 9, 620.	2.3	10
352	Protein-assisted RNA fragment docking (RnaX) for modeling RNA-protein interactions using ModelX. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24568-24573.	7.1	10
353	Inferring Active Metabolic Pathways from Proteomics and Essentiality Data. <i>Cell Reports</i> , 2020, 31, 107722.	6.4	10
354	Structure-Based DNA-Binding Prediction and Design. <i>Methods in Molecular Biology</i> , 2010, 649, 77-88.	0.9	10
355	Characterisation of the Isolated Che Y C-terminal Fragment (79-129). Exploring the Structure/Stability/Folding Relationships of the alpha/beta Parallel Protein Che Y. <i>FEBS Journal</i> , 1997, 243, 384-392.	0.2	9
356	Identification of peptides that neutralize bacterial endotoxins using beta-hairpin conformationally restricted libraries. <i>Molecular Diversity</i> , 2000, 5, 117-126.	3.9	9
357	NMR solution structure of the activation domain of human procarboxypeptidase A2. <i>Protein Science</i> , 2003, 12, 296-305.	7.6	9
358	Shaping dots and lines: Adding modularity into protein interaction networks using structural information. <i>FEBS Letters</i> , 2008, 582, 1231-1236.	2.8	9
359	DNA-Binding Specificity Prediction with FoldX. <i>Methods in Enzymology</i> , 2011, 498, 3-18.	1.0	9
360	Generation of rationally-designed nerve growth factor (NGF) variants with receptor specificity. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 700-705.	2.1	9

#	ARTICLE	IF	CITATIONS
361	LoxTnSeq: random transposon insertions combined with cre/lox recombination and counterselection to generate large random genome reductions. <i>Microbial Biotechnology</i> , 2021, 14, 2403-2419.	4.2	9
362	Structure Analysis of Two CheY Mutants: Importance of the Hydrogen-Bond Contribution to Protein Stability. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 378-385.	2.5	8
363	Folding specificity induced by loop stiffness. <i>Protein Science</i> , 2003, 12, 1473-1482.	7.6	8
364	Monitoring disappearance of monomers and generation of resistance to proteolysis during the formation of the activation domain of human procarboxypeptidase A2 (ADA2h) amyloid fibrils by matrix-assisted laser-desorption ionization–time-of-flight-MS. <i>Biochemical Journal</i> , 2003, 374, 489-495.	3.7	8
365	Systematic Bioinformatics and Experimental Validation of Yeast Complexes Reduces the Rate of Attrition during Structural Investigations. <i>Structure</i> , 2010, 18, 1075-1082.	3.3	8
366	The Design and Characterization of Receptor-selective APRIL Variants*. <i>Journal of Biological Chemistry</i> , 2012, 287, 37434-37446.	3.4	8
367	Interpretable parametric voice conversion functions based on Gaussian mixture models and constrained transformations. <i>Computer Speech and Language</i> , 2015, 30, 3-15.	4.3	8
368	Evolution of the SH3 Domain Specificity Landscape in Yeasts. <i>PLoS ONE</i> , 2015, 10, e0129229.	2.5	8
369	A network of epigenetic modifiers and DNA repair genes controls tissue-specific copy number alteration preference. <i>ELife</i> , 2016, 5, .	6.0	8
370	Folding pathway enigma. <i>Nature</i> , 1990, 343, 602-602.	27.8	7
371	Physical-organic molecular biology: pathway and stability of protein folding. <i>Pure and Applied Chemistry</i> , 1991, 63, 187-194.	1.9	7
372	Empirical correlation for the replacement of Ala by Gly: Importance of amino acid secondary intrinsic propensities. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 340-349.	2.6	7
373	The DSC data analysis for small, single-domain proteins. Application to the SH3 domain. <i>Reactive and Functional Polymers</i> , 1998, 36, 221-225.	4.1	7
374	Computer-assisted re-design of spectrin SH3 residue clusters. <i>New Biotechnology</i> , 2001, 18, 125-134.	2.7	7
375	Regulatory aspects of the colchicine interactions with tubulin. <i>Molecular and Cellular Biochemistry</i> , 1987, 73, 29-36.	3.1	6
376	Towards the design and computational characterization of a membrane protein. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 20, 219-234.	2.4	6
377	Rescuing discarded spectra: Full comprehensive analysis of a minimal proteome. <i>Proteomics</i> , 2016, 16, 554-563.	2.2	6
378	pyFoldX: enabling biomolecular analysis and engineering along structural ensembles. <i>Bioinformatics</i> , 2022, 38, 2353-2355.	4.1	6

#	ARTICLE	IF	CITATIONS
379	The combined use of limited proteolysis and differential peptide staining for protein characterization. <i>Journal of Proteomics</i> , 1986, 12, 281-287.	2.4	5
380	Atomic resolution structure of a mutant of the spectrin SH3 domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 337-340.	2.5	5
381	T-RMSD: A Fine-grained, Structure-based Classification Method and its Application to the Functional Characterization of TNF Receptors. <i>Journal of Molecular Biology</i> , 2010, 400, 605-617.	4.2	5
382	Spectroscopic Analysis of Amyloid Fibril Formation in SH3-Domains. <i>Spectroscopy</i> , 2003, 17, 647-652.	0.8	4
383	Assessing the hodgepodge of non-mapped reads in bacterial transcriptomes: real or artifactual RNA chimeras?. <i>BMC Genomics</i> , 2014, 15, 633.	2.8	4
384	Tuneable endogenous mammalian target complementation via multiplexed plasmid-based recombineering. <i>Scientific Reports</i> , 2015, 5, 17432.	3.3	4
385	Opportunities and Challenges of Whole-Cell and -Tissue Simulations of the Outer Retina in Health and Disease. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 131-152.	6.5	4
386	Systems level expression correlation of Ras GTPase regulators. <i>Cell Communication and Signaling</i> , 2018, 16, 46.	6.5	4
387	Affinity Can have Many Faces: Thermodynamic and Kinetic Properties of Ras-Effector Complex Formation. <i>Current Chemical Biology</i> , 2007, 1, 215-225.	0.5	4
388	Bacterial genomes: from regulatory complexity to engineering. <i>Current Opinion in Microbiology</i> , 2011, 14, 577-578.	5.1	3
389	Co-acting gene networks predict TRAIL responsiveness of tumour cells with high accuracy. <i>BMC Genomics</i> , 2014, 15, 1144.	2.8	3
390	Creating stable stem regions for loop elongation in Fcabs â€” Insights from combining yeast surface display, in silico loop reconstruction and molecular dynamics simulations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1530-1540.	2.3	3
391	<i>ProteinFishing</i>: a protein complex generator within the ModelX toolsuite. <i>Bioinformatics</i> , 2020, 36, 4208-4210.	4.1	3
392	Loxâ€™d in translation: contradictions in the nomenclature surrounding common lox-site mutants and their implications in experiments. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	3
393	Chapter 10. Protein Misfolding and Î²-Amyloid Formation. <i>RSC Biomolecular Sciences</i> , 2008, , 214-240.	0.4	3
394	Overexpression, purification, crystallization and preliminary X-ray diffraction analysis of the receiver domain of PhoB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1460-1463.	2.5	2
395	Affinity Can have Many Faces: Thermodynamic and Kinetic Properties of Ras-Effector Complex Formation. <i>Current Chemical Biology</i> , 2007, 1, 215-225.	0.5	2
396	TAPAS: tools to assist the targeted protein quantification of human alternative splice variants. <i>Bioinformatics</i> , 2014, 30, 2989-2990.	4.1	2

#	ARTICLE	IF	CITATIONS
397	Complexities in Quantitative Systems Analysis of Signaling Networks. , 2014, , 65-88.		2
398	A calcium binding protein from Drosophila melanogaster which activates cAMP phosphodiesterase: Comparison of this protein with porcine brain calmodulin. Archives of Biochemistry and Biophysics, 1986, 247, 147-154.	3.0	1
399	The Carboxyterminal Region of Tubulin Regulates Its Assembly into Microtubules. Annals of the New York Academy of Sciences, 1986, 466, 642-644.	3.8	1
400	Modeling protein-peptide interactions using protein fragments: fitting the pieces?. BMC Bioinformatics, 2010, 11, .	2.6	1
401	Widespread ribosome stalling in a genome-reduced bacterium and the need for translational quality control. IScience, 2021, 24, 102985.	4.1	1
402	Prediction of sequence-dependent and mutational effects on the aggregation of peptides and proteins. , 0, .		1
403	The Impact of Structural Proteomics on the Prediction of Proteinâ€ Protein Interactions. , 2008, , 251-267.		0
404	Evolvability of Chaperonin Substrate Proteins. Nature Precedings, 2009, , .	0.1	0
405	Novel determinants describe chaperonin substrate proteins. Nature Precedings, 2009, , .	0.1	0
406	13-P083 Apical localization of RhoGEF2 and adherens junctions during gastrulation in Drosophila melanogaster. Mechanisms of Development, 2009, 126, S219-S220.	1.7	0
407	Analysis of Proteinâ€ Protein Interactions in Complex Biological Samples by MALDI TOF MS. Feasibility and Use of the Intensity-Fading (IF-) Approach. Principles and Practice, 2004, , 183-202.	0.3	0
408	Reconstruction of the Regulatory Network in a Minimal Bacterium Reveals Extensive Non-Transcription Factor Dependent Regulation. SSRN Electronic Journal, 0, , .	0.4	0
409	Title is missing!. , 2020, 16, e1008450.		0
410	Title is missing!. , 2020, 16, e1008450.		0
411	Title is missing!. , 2020, 16, e1008450.		0
412	Title is missing!. , 2020, 16, e1008450.		0
413	Title is missing!. , 2020, 16, e1008450.		0
414	Title is missing!. , 2020, 16, e1008450.		0