

Luis Serrano Pubull

List of Publications by Year in descending order

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414
papers

44,697
citations

2309

101
h-index

3100

193
g-index

440
all docs

440
docs citations

440
times ranked

40399
citing authors

#	ARTICLE	IF	CITATIONS
1	The FoldX web server: an online force field. <i>Nucleic Acids Research</i> , 2005, 33, W382-W388.	6.5	2,110
2	Predicting Changes in the Stability of Proteins and Protein Complexes: A Study of More Than 1000 Mutations. <i>Journal of Molecular Biology</i> , 2002, 320, 369-387.	2.0	1,609
3	Correlation of mRNA and protein in complex biological samples. <i>FEBS Letters</i> , 2009, 583, 3966-3973.	1.3	1,519
4	Prediction of sequence-dependent and mutational effects on the aggregation of peptides and proteins. <i>Nature Biotechnology</i> , 2004, 22, 1302-1306.	9.4	1,435
5	Engineering stability in gene networks by autoregulation. <i>Nature</i> , 2000, 405, 590-593.	13.7	1,385
6	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 771-782.	2.0	855
7	Mapping the transition state and pathway of protein folding by protein engineering. <i>Nature</i> , 1989, 340, 122-126.	13.7	715
8	Elucidating the folding problem of helical peptides using empirical parameters. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 399-409.	3.6	637
9	Positive feedback in eukaryotic gene networks: cell differentiation by graded to binary response conversion. <i>EMBO Journal</i> , 2001, 20, 2528-2535.	3.5	614
10	Exploring the sequence determinants of amyloid structure using position-specific scoring matrices. <i>Nature Methods</i> , 2010, 7, 237-242.	9.0	566
11	A short linear peptide that folds into a native stable β^2 -hairpin in aqueous solution. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 584-590.	3.6	513
12	Transient folding intermediates characterized by protein engineering. <i>Nature</i> , 1990, 346, 440-445.	13.7	501
13	Structure-based redesign of the dimerization interface reduces the toxicity of zinc-finger nucleases. <i>Nature Biotechnology</i> , 2007, 25, 786-793.	9.4	492
14	How Protein Stability and New Functions Trade Off. <i>PLoS Computational Biology</i> , 2008, 4, e1000002.	1.5	468
15	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	6.0	440
16	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 783-804.	2.0	421
17	Development of the multiple sequence approximation within the AGADIR model of β -helix formation: Comparison with Zimm-Bragg and Lifson-Roig formalisms. <i>Biopolymers</i> , 1997, 41, 495-509.	1.2	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. <i>Journal of Molecular Biology</i> , 1998, 284, 173-191.	2.0	416

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19	Strength and co-operativity of contributions of surface salt bridges to protein stability. <i>Journal of Molecular Biology</i> , 1990, 216, 1031-1044.	2.0	410
20	The Stability Effects of Protein Mutations Appear to be Universally Distributed. <i>Journal of Molecular Biology</i> , 2007, 369, 1318-1332.	2.0	396
21	Transcriptome Complexity in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1268-1271.	6.0	394
22	Estimating the contribution of engineered surface electrostatic interactions to protein stability by using double-mutant cycles. <i>Biochemistry</i> , 1990, 29, 9343-9352.	1.2	390
23	De novo designed peptide-based amyloid fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16052-16057.	3.3	381
24	Capping and α -helix stability. <i>Nature</i> , 1989, 342, 296-299.	13.7	378
25	Sequence determinants of amyloid fibril formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 87-92.	3.3	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. <i>Journal of Molecular Biology</i> , 1995, 245, 275-296.	2.0	371
27	Structure-Based Assembly of Protein Complexes in Yeast. <i>Science</i> , 2004, 303, 2026-2029.	6.0	367
28	A Comparative Study of the Relationship Between Protein Structure and β -Aggregation in Globular and Intrinsically Disordered Proteins. <i>Journal of Molecular Biology</i> , 2004, 342, 345-353.	2.0	353
29	α -Helix stability in proteins. <i>Journal of Molecular Biology</i> , 1992, 227, 544-559.	2.0	323
30	Protein aggregation and amyloidosis: confusion of the kinds?. <i>Current Opinion in Structural Biology</i> , 2006, 16, 118-126.	2.6	322
31	Aromatic-aromatic interactions and protein stability. <i>Journal of Molecular Biology</i> , 1991, 218, 465-475.	2.0	315
32	Prediction of water and metal binding sites and their affinities by using the Fold-X force field. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10147-10152.	3.3	315
33	The folding transition state between SH3 domains is conformationally restricted and evolutionarily conserved. <i>J Mol Biol</i> , 1999, 6, 1010-1016.		311
34	Systematic Discovery of New Recognition Peptides Mediating Protein Interaction Networks. <i>PLoS Biology</i> , 2005, 3, e405.	2.6	310
35	Design of a 20-Amino Acid, Three-Stranded β -Sheet Protein. <i>J Mol Biol</i> , 1998, 281, 253-256.		308
36	Control of <i>Drosophila</i> Gastrulation by Apical Localization of Adherens Junctions and RhoGEF2. <i>Science</i> , 2007, 315, 384-386.	6.0	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.	1.2	294
38	A graphical interface for the FoldX forcefield. <i>Bioinformatics</i> , 2011, 27, 1711-1712.	1.8	288
39	Evolvability and hierarchy in rewired bacterial gene networks. <i>Nature</i> , 2008, 452, 840-845.	13.7	285
40	Intrinsic secondary structure propensities of the amino acids, using statistical Ψ^{\dagger} - Ψ^{\ddagger} matrices: Comparison with experimental scales. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 20, 301-311.	1.5	284
41	Controlled proteolysis of tubulin by subtilisin: localization of the site for MAP2 interaction. <i>Biochemistry</i> , 1984, 23, 4675-4681.	1.2	279
42	Principles of protein stability derived from protein engineering experiments. <i>Current Opinion in Structural Biology</i> , 1993, 3, 75-83.	2.6	277
43	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 805-818.	2.0	269
44	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. <i>Science</i> , 2009, 326, 1263-1268.	6.0	267
45	Quantification of mRNA and protein and integration with protein turnover in a bacterium. <i>Molecular Systems Biology</i> , 2011, 7, 511.	3.2	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.	13.7	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.	3.3	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.	2.0	253
50	Noise in transcription negative feedback loops: simulation and experimental analysis. <i>Molecular Systems Biology</i> , 2006, 2, 41.	3.2	247
51	How Evolutionary Pressure Against Protein Aggregation Shaped Chaperone Specificity. <i>Journal of Molecular Biology</i> , 2006, 355, 1037-1047.	2.0	242
52	Detection and characterization of a folding intermediate in barnase by NMR. <i>Nature</i> , 1990, 346, 488-490.	13.7	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.	3.3	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.	3.6	231

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55	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 819-835.	2.0	222
56	FoldX 5.0: working with RNA, small molecules and a new graphical interface. <i>Bioinformatics</i> , 2019, 35, 4168-4169.	1.8	220
57	Effect of active site residues in barnase on activity and stability. <i>Journal of Molecular Biology</i> , 1992, 225, 585-589.	2.0	217
58	Different folding transition states may result in the same native structure. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 874-880.	3.6	211
59	Protein folding: Defining a "standard" set of experimental conditions and a preliminary kinetic data set of two-state proteins. <i>Protein Science</i> , 2005, 14, 602-616.	3.1	207
60	Effect of alanine versus glycine in α -helices on protein stability. <i>Nature</i> , 1992, 356, 453-455.	13.7	204
61	Step-wise Mutation of Barnase to Binase. <i>Journal of Molecular Biology</i> , 1993, 233, 305-312.	2.0	176
62	Engineering of Large Numbers of Highly Specific Homing Endonucleases that Induce Recombination on Novel DNA Targets. <i>Journal of Molecular Biology</i> , 2006, 355, 443-458.	2.0	175
63	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 847-859.	2.0	169
64	Crosstalk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012, 8, 571.	3.2	169
65	Structure of the transition state in the folding process of human procarboxypeptidase A2 activation domain. <i>Journal of Molecular Biology</i> , 1998, 283, 1027-1036.	2.0	165
66	Comparison between the β Distribution of the Amino Acids in the Protein Database and NMR Data Indicates that Amino Acids have Various β Propensities in the Random Coil Conformation. <i>Journal of Molecular Biology</i> , 1995, 254, 322-333.	2.0	163
67	Synthetic biology: promises and challenges. <i>Molecular Systems Biology</i> , 2007, 3, 158.	3.2	162
68	A casein kinase II-related activity is involved in phosphorylation of microtubule-associated protein MAP-1B during neuroblastoma cell differentiation.. <i>Journal of Cell Biology</i> , 1988, 106, 2057-2065.	2.3	159
69	Structure of the transition state for folding of the 129 aa protein CheY resembles that of a smaller protein, Cl-2. <i>Folding & Design</i> , 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. <i>FEBS Journal</i> , 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. <i>American Journal of Human Genetics</i> , 2007, 81, 1006-1024.	2.6	157
72	Recognizing and Defining True Ras Binding Domains I: Biochemical Analysis. <i>Journal of Molecular Biology</i> , 2005, 348, 741-758.	2.0	154

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73	Side-chain interactions between sulfur-containing amino acids and phenylalanine in α -helices. <i>Biochemistry</i> , 1995, 34, 8771-8779.	1.2	153
74	Formation and stability of β -hairpin structures in polypeptides. <i>Current Opinion in Structural Biology</i> , 1998, 8, 107-111.	2.6	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.	3.3	151
76	Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. <i>Nature</i> , 2008, 456, 107-111.	13.7	150
77	Computational design of peptide ligands. <i>Trends in Biotechnology</i> , 2011, 29, 231-239.	4.9	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.	2.0	142
79	Histidine residues at the N- and C-termini of α -helices: perturbed pKas and protein stability. <i>Biochemistry</i> , 1992, 31, 2253-2258.	1.2	138
80	Characterization of the Interaction of Natural Proline-Rich Peptides with Five Different SH3 Domains. <i>Biochemistry</i> , 1994, 33, 10925-10933.	1.2	137
81	SNPeffect: a database mapping molecular phenotypic effects of human non-synonymous coding SNPs. <i>Nucleic Acids Research</i> , 2004, 33, D527-D532.	6.5	136
82	Role of β -turn residues in β -hairpin formation and stability in designed peptides 1 Edited by A.R. Fersht. <i>Journal of Molecular Biology</i> , 1997, 273, 898-912.	2.0	134
83	Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. <i>Genome Research</i> , 2009, 19, 1905-1911.	2.4	134
84	Defining a minimal cell: essentiality of small $\langle scp \rangle$ s and nc $\langle scp \rangle$ RNA s in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2015, 11, 780.	3.2	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.	2.0	131
86	The design of linear peptides that fold as monomeric β -sheet structures. <i>Current Opinion in Structural Biology</i> , 1999, 9, 487-493.	2.6	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.	3.3	127
89	Rational Design of Specific High-Affinity Peptide Ligands for the Abl-SH3 Domain. <i>Biochemistry</i> , 1996, 35, 10634-10640.	1.2	126
90	The hydrophobic-staple motif and a role for loop-residues in β -helix stability and protein folding. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 380-385.	3.6	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.	13.6	121
93	Î²-Hairpin and Î²-sheet formation in designed linear peptides. Bioorganic and Medicinal Chemistry, 1999, 7, 93-103.	1.4	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.	2.0	120
95	Tubulin phosphorylation by casein kinase II is similar to that found in vivo.. Journal of Cell Biology, 1987, 105, 1731-1739.	2.3	119
96	Bacterial antisense RNAs are mainly the product of transcriptional noise. Science Advances, 2016, 2, e1501363.	4.7	118
97	Human Epidermal Stem Cell Function Is Regulated by Circadian Oscillations. Cell Stem Cell, 2013, 13, 745-753.	5.2	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.	2.0	116
99	Engineering Signal Transduction Pathways. Cell, 2010, 140, 33-47.	13.5	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.	1.0	111
101	Engineering Gene Networks to Emulate Drosophila Embryonic Pattern Formation. PLoS Biology, 2005, 3, e64.	2.6	111
102	Specificity and Evolvability in Eukaryotic Protein Interaction Networks. PLoS Computational Biology, 2007, 3, e25.	1.5	111
103	Protein engineering as a strategy to avoid formation of amyloid fibrils. Protein Science, 2000, 9, 1700-1708.	3.1	109
104	Comprehensive Methylome Characterization of Mycoplasma genitalium and Mycoplasma pneumoniae at Single-Base Resolution. PLoS Genetics, 2013, 9, e1003191.	1.5	109
105	Phosphorylation of tubulin by a calmodulin-dependent protein kinase.. Journal of Biological Chemistry, 1986, 261, 10332-10339.	1.6	106
106	Loop length, intramolecular diffusion and protein folding. Nature Structural and Molecular Biology, 1997, 4, 939-946.	3.6	102
107	PepX: a structural database of non-redundant proteinâ€“peptide complexes. Nucleic Acids Research, 2010, 38, D545-D551.	6.5	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.	2.0	101

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109	Recognizing and Defining True Ras Binding Domains II: In Silico Prediction Based on Homology Modelling and Energy Calculations. <i>Journal of Molecular Biology</i> , 2005, 348, 759-775.	2.0	101
110	The folding of an enzyme. <i>Journal of Molecular Biology</i> , 1992, 224, 837-845.	2.0	100
111	Conformational strain in the hydrophobic core and its implications for protein folding and design. <i>Nature Structural Biology</i> , 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. <i>Biochemistry</i> , 1995, 34, 15105-15110.	1.2	99
113	Strategies for protein synthetic biology. <i>Nucleic Acids Research</i> , 2010, 38, 2663-2675.	6.5	99
114	Unraveling the hidden universe of small proteins in bacterial genomes. <i>Molecular Systems Biology</i> , 2019, 15, e8290.	3.2	96
115	Tumor suppressor properties of the splicing regulatory factor RBM10. <i>RNA Biology</i> , 2016, 13, 466-472.	1.5	94
116	Phosphorylation of alpha-tubulin carboxyl-terminal tyrosine prevents its incorporation into microtubules.. <i>Journal of Biological Chemistry</i> , 1987, 262, 8268-8273.	1.6	93
117	Favourable native-like helical local interactions can accelerate protein folding. <i>Folding & Design</i> , 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. <i>Journal of Molecular Biology</i> , 2000, 297, 1217-1229.	2.0	91
119	Phosphorylation of a neuronal-specific beta-tubulin isotype.. <i>Journal of Biological Chemistry</i> , 1990, 265, 13949-13954.	1.6	88
120	Computer-aided design of β -sheet peptides 1 ¹ Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2001, 312, 229-246.	2.0	87
121	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	6.5	87
122	Local versus nonlocal interactions in protein folding and stability – an experimentalist's point of view. <i>Folding & Design</i> , 1996, 1, R71-R77.	4.5	86
123	Analysis of Disease-Linked Rhodopsin Mutations Based on Structure, Function, and Protein Stability Calculations. <i>Journal of Molecular Biology</i> , 2011, 405, 584-606.	2.0	86
124	Analyzing Protein Interaction Networks Using Structural Information. <i>Annual Review of Biochemistry</i> , 2008, 77, 415-441.	5.0	85
125	Phosphorylation of tubulin by a calmodulin-dependent protein kinase. <i>Journal of Biological Chemistry</i> , 1986, 261, 10332-9.	1.6	85
126	Helix design, prediction and stability. <i>Current Opinion in Biotechnology</i> , 1995, 6, 382-386.	3.3	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.	2.0	84
128	Energy estimation in protein design. <i>Current Opinion in Structural Biology</i> , 2002, 12, 441-446.	2.6	84
129	Sequence Dependence of Amyloid Fibril Formation: Insights from Molecular Dynamics Simulations. <i>Journal of Molecular Biology</i> , 2005, 349, 583-596.	2.0	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.	2.0	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.	2.0	81
134	Defined chromosome structure in the genome-reduced bacterium <i>Mycoplasma pneumoniae</i> . <i>Nature Communications</i> , 2017, 8, 14665.	5.8	81
135	Negative selection in tumor genome evolution acts on essential cellular functions and the immunopeptidome. <i>Genome Biology</i> , 2018, 19, 67.	3.8	81
136	Protein-Peptide Interactions Adopt the Same Structural Motifs as Monomeric Protein Folds. <i>Structure</i> , 2009, 17, 1128-1136.	1.6	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 β^2 -specificity landscape of modular peptide recognition domains. <i>Molecular Systems Biology</i> , 2011, 7, 484.	3.2	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.	1.2	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.	2.1	76
141	Strand-specific deep sequencing of the transcriptome. <i>Genome Research</i> , 2010, 20, 989-999.	2.4	76
142	Localization of the high affinity calcium-binding site on tubulin molecule.. <i>Journal of Biological Chemistry</i> , 1986, 261, 7076-7081.	1.6	76
143	Phosphorylation of a neuronal-specific beta-tubulin isotype. <i>Journal of Biological Chemistry</i> , 1990, 265, 13949-54.	1.6	76
144	Effect of thermal treatment on physicochemical properties of Gympie messmate wood. <i>Industrial Crops and Products</i> , 2013, 45, 360-366.	2.5	74

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145	Structure-energy-based predictions and network modelling of <sc>RAS</sc>opathy and cancer missense mutations. <i>Molecular Systems Biology</i> , 2014, 10, 727.	3.2	74
146	Space as the final frontier in stochastic simulations of biological systems. <i>FEBS Letters</i> , 2005, 579, 1789-1794.	1.3	73
147	Using a structural and logics systems approach to infer bHLH DNA binding specificity determinants. <i>Nucleic Acids Research</i> , 2011, 39, 4553-4563.	6.5	73
148	Position dependence of non-polar amino acid intrinsic helical propensities. <i>Journal of Molecular Biology</i> , 1998, 278, 279-289.	2.0	72
149	The Ubiquitin Domain Superfold: Structure-based Sequence Alignments and Characterization of Binding Epitopes. <i>Journal of Molecular Biology</i> , 2006, 355, 821-844.	2.0	72
150	Amyloid Toxicity Is Independent of Polypeptide Sequence, Length and Chirality. <i>Journal of Molecular Biology</i> , 2008, 375, 695-707.	2.0	72
151	Association of casein kinase II with microtubules. <i>Experimental Cell Research</i> , 1989, 181, 263-272.	1.2	71
152	Solvation in protein folding analysis: Combination of theoretical and experimental approaches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2834-2839.	3.3	70
153	Combinatorial approaches: A new tool to search for highly structured \hat{A} -hairpin peptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 614-619.	3.3	69
154	Towards Cellular Systems in 4D. <i>Cell</i> , 2005, 121, 507-509.	13.5	69
155	Dissecting the energy metabolism in <i>Mycoplasma pneumoniae</i> through genome-scale metabolic modeling. <i>Molecular Systems Biology</i> , 2013, 9, 653.	3.2	69
156	Unspecific hydrophobic stabilization of folding transition states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5349-5354.	3.3	68
157	Helix Stop and Start Signals in Peptides and Proteins The Capping Box does not Necessarily Prevent Helix Elongation. <i>Journal of Molecular Biology</i> , 1994, 242, 487-496.	2.0	67
158	Structures in systems biology. <i>Current Opinion in Structural Biology</i> , 2007, 17, 378-384.	2.6	67
159	Computer modelling in combination with in vitro studies reveals similar binding affinities of <i>Drosophila</i> Crumbs for the PDZ domains of Stardust and DmPar-6. <i>European Journal of Cell Biology</i> , 2006, 85, 753-767.	1.6	66
160	Assessing the limits of restraint-based 3D modeling of genomes and genomic domains. <i>Nucleic Acids Research</i> , 2015, 43, 3465-3477.	6.5	66
161	Localization of the high affinity calcium-binding site on tubulin molecule. <i>Journal of Biological Chemistry</i> , 1986, 261, 7076-81.	1.6	66
162	Analysis of the effect of local interactions on protein stability. <i>Folding & Design</i> , 1996, 1, 167-178.	4.5	65

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163	Cell type-specific properties and environment shape tissue specificity of cancer genes. <i>Scientific Reports</i> , 2016, 6, 20707.	1.6	64
164	Cell Type-Specific Importance of Ras-c-Raf Complex Association Rate Constants for MAPK Signaling. <i>Science Signaling</i> , 2009, 2, ra38.	1.6	63
165	Rapid and efficient cancer cell killing mediated by high-affinity death receptor homotrimerizing TRAIL variants. <i>Cell Death and Disease</i> , 2010, 1, e83-e83.	2.7	63
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