Anna Tramontano

List of Publications by Year
in descending order

204 papers	14,443 citations	20797 60 h-index	20943 115 g-index
214 all docs	214 docs citations	214 times ranked	15923 citing authors

#	ARTICLE	IF	CITATIONS
1	A Long Noncoding RNA Controls Muscle Differentiation by Functioning as a Competing Endogenous RNA. Cell, 2011, 147, 358-369.	13.5	2,390
2	Conformations of immunoglobulin hypervariable regions. Nature, 1989, 342, 877-883.	13.7	1,199
3	Critical assessment of methods of protein structure prediction (CASP) â€" round x. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1-6.	1.5	366
4	Conformations of the third hypervariable region in the VH domain of immunoglobulins 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1998, 275, 269-294.	2.0	350
5	Critical assessment of methods of protein structure prediction (CASP)â€"Round XII. Proteins: Structure, Function and Bioinformatics, 2018, 86, 7-15.	1.5	296
6	The PMDB Protein Model Database. Nucleic Acids Research, 2006, 34, D306-D309.	6.5	266
7	Mimicking of discontinuous epitopes by phage-displayed peptides, I. Epitope mapping of human H ferritin using a phage library of constrained peptides. Gene, 1993, 128, 51-57.	1.0	249
8	Framework residue 71 is a major determinant of the position and conformation of the second hypervariable region in the VH domains of immunoglobulins. Journal of Molecular Biology, 1990, 215, 175-182.	2.0	238
9	Critical assessment of methods of protein structure predictionâ€"Round VIII. Proteins: Structure, Function and Bioinformatics, 2009, 77, 1-4.	1.5	229
10	A designed metal-binding protein with a novel fold. Nature, 1993, 362, 367-369.	13.7	228
11	The implications of alternative splicing in the ENCODE protein complement. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5495-5500.	3.3	206
12	Critical assessment of methods of protein structure predictionâ€"Round VII. Proteins: Structure, Function and Bioinformatics, 2007, 69, 3-9.	1.5	199
13	Critical assessment of methods of protein structure prediction: Progress and new directions in round XI. Proteins: Structure, Function and Bioinformatics, 2016, 84, 4-14.	1.5	198
14	A model for the hepatitis C virus envelope glycoprotein E2. Proteins: Structure, Function and Bioinformatics, 2000, 40, 355-366.	1.5	191
15	Remarkably similar antigen receptors among a subset of patients with chronic lymphocytic leukemia. Journal of Clinical Investigation, 2004, 113, 1008-1016.	3.9	190
16	Critical assessment of methods of protein structure prediction (CASP)â€"round IX. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1-5.	1.5	187
17	PIGS: automatic prediction of antibody structures. Bioinformatics, 2008, 24, 1953-1954.	1.8	186
18	Protein function annotation by homology-based inference. Genome Biology, 2009, 10, 207.	13.9	182

#	Article	IF	Citations
19	Assessment of homology-based predictions in CASP5. Proteins: Structure, Function and Bioinformatics, 2003, 53, 352-368.	1.5	165
20	Critical assessment of methods of protein structure prediction (CASP)â€"Round 6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 3-7.	1.5	162
21	Binding of the Hepatitis C Virus E2 Glycoprotein to CD81 Is Strain Specific and Is Modulated by a Complex Interplay between Hypervariable Regions 1 and 2. Journal of Virology, 2003, 77, 1856-1867.	1.5	150
22	Assessment of protein disorder region predictions in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 127-137.	1.5	140
23	Towards a solution for hepatitis C virus hypervariability: mimotopes of the hypervariable region 1 can induce antibodies cross-reacting with a large number of viral variants. EMBO Journal, 1998, 17, 3521-3533.	3.5	137
24	Cloning and analysis of Candida cylindracea lipase sequences. Gene, 1993, 124, 45-55.	1.0	131
25	Molecular model of the specificity pocket of the hepatitis C virus protease: implications for substrate recognition.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 888-892.	3.3	123
26	Assessment of predictions in the model quality assessment category. Proteins: Structure, Function and Bioinformatics, 2007, 69, 175-183.	1.5	122
27	Evolution of Bacterial and Archaeal Multicomponent Monooxygenases. Journal of Molecular Evolution, 2003, 56, 435-445.	0.8	118
28	Identification of biologically active peptides using random libraries displayed on phage. Current Opinion in Biotechnology, 1995, 6, 73-80.	3.3	115
29	Evaluation of templateâ€based models in CASP8 with standard measures. Proteins: Structure, Function and Bioinformatics, 2009, 77, 18-28.	1.5	114
30	Assessment of the assessment: Evaluation of the model quality estimates in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 112-126.	1.5	114
31	Substrate Specificity of the Hepatitis C Virus Serine Protease NS3. Journal of Biological Chemistry, 1997, 272, 9204-9209.	1.6	109
32	A Zinc Binding Site in Viral Serine Proteinases. Biochemistry, 1996, 35, 13282-13287.	1.2	103
33	Evaluation of disorder predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 107-118.	1.5	102
34	Analysis and assessment of comparative modeling predictions in CASP4. Proteins: Structure, Function and Bioinformatics, 2001, 45, 22-38.	1.5	101
35	Cancer-Selective Targeting of the NF-ÎºB Survival Pathway with GADD45Î²/MKK7 Inhibitors. Cancer Cell, 2014, 26, 495-508.	7.7	99
36	Novel Long Noncoding RNAs (lncRNAs) in Myogenesis: a <i>miR-31</i> Overlapping lncRNA Transcript Controls Myoblast Differentiation. Molecular and Cellular Biology, 2015, 35, 728-736.	1.1	99

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37	Antibody Modeling: Implications for Engineering and Design. Methods, 2000, 20, 267-279.	1.9	98
38	Small Molecule Inhibitors of Histone Arginine Methyltransferases:â€° Homology Modeling, Molecular Docking, Binding Mode Analysis, and Biological Evaluations. Journal of Medicinal Chemistry, 2007, 50, 1241-1253.	2.9	98
39	Variability within the Candida rugosa Lipases family. Protein Engineering, Design and Selection, 1994, 7, 531-535.	1.0	97
40	Endocytosis of synaptic ADAM10 in neuronal plasticity and Alzheimerâ€™s disease. Journal of Clinical Investigation, 2013, 123, 2523-2538.	3.9	96
41	PUZZLE: A New Method for Automated Protein Docking Based on Surface Shape Complementarity. Journal of Molecular Biology, 1994, 235, 1021-1031.	2.0	91
42	Stereotyped patterns of B-cell receptor in splenic marginal zone lymphoma. Haematologica, 2010, 95, 1792-1796.	1.7	91
43	Prediction of site-specific interactions in antibody-antigen complexes: the proABC method and server. Bioinformatics, 2013, 29, 2285-2291.	1.8	91
44	Evaluation of model quality predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 91-106.	1.5	83
45	Structural determinants of the conformations of medium-sized loops in proteins. Proteins: Structure, Function and Bioinformatics, 1989, 6, 382-394.	1.5	82
46	New encouraging developments in contact prediction: Assessment of the CASP11 results. Proteins: Structure, Function and Bioinformatics, 2016, 84, 131-144.	1.5	81
47	Accurate energies of hydrogen bonded nucleic acid base pairs and triplets in tRNA tertiary interactions. Nucleic Acids Research, 2006, 34, 865-879.	6.5	79
48	Mg^{2+} binding and archaeosine modification stabilize the G15â€"C48 Levitt base pair in tRNAs. Rna, 2007, 13, 1427-1436.	1.6	79
49	Members of the zinc finger protein gene family sharing a conserved N-terminal module. Nucleic Acids Research, 1991, 19, 5661-5667.	6.5	78
50	Saturation mutagenesis of the human interleukin 6 receptor-binding site: implications for its three-dimensional structure.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 4067-4071.	3.3	76
51	Bacteriophage lambda display of complex cDNA libraries: a new approach to functional genomics 1 1Edited by J. M. Thornton. Journal of Molecular Biology, 2000, 296, 497-508.	2.0	76
52	Evaluation of CASP8 model quality predictions. Proteins: Structure, Function and Bioinformatics, 2009, 77, 157-166.	1.5	76
53	The association of heavy and light chain variable domains in antibodies: implications for antigen specificity. FEBS Journal, 2011, 278, 2858-2866.	2.2	76
54	Evaluation of residueâ€"residue contact predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 119-125.	1.5	75

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55	Homology Modeling with Low Sequence Identity. Methods, 1998, 14, 293-300.	1.9	72
56	Evaluation of residue–residue contact prediction in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 138-153.	1.5	72
57	On the Mechanism of Chloroquine Resistance in Plasmodium falciparum. PLoS ONE, 2010, 5, e14064.	1.1	67
58	Evaluation of annotation strategies using an entire genome sequence. Bioinformatics, 2003, 19, 717-726.	1.8	65
59	Common features of the conformations of antigen-binding loops in immunoglobulins and application to modeling loop conformations. Proteins: Structure, Function and Bioinformatics, 1992, 13, 231-245.	1.5	63
60	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in <scp>CASP</scp>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 349-369.	1.5	63
61	Probing the tertiary structure of proteins by limited proteolysis and mass spectrometry: The case of minibody. Protein Science, 1996, 5, 802-813.	3.1	62
62	High Level Expression and Rational Mutagenesis of a Designed Protein, the Minibody. Journal of Molecular Biology, 1994, 236, 649-659.	2.0	61
63	Assessment of model accuracy estimations in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 345-360.	1.5	61
64	Evaluation of the template–based modeling in <scp>CASP12</scp>. Proteins: Structure, Function and Bioinformatics, 2018, 86, 321-334.	1.5	61
65	Antibody modeling using the Prediction of ImmunoGlobulin Structure (PIGS) web server. Nature Protocols, 2014, 9, 2771-2783.	5.5	58
66	Evaluating the usefulness of protein structure models for molecular replacement. Bioinformatics, 2005, 21, ii72-ii76.	1.8	57
67	The betaI/betaIII-tubulin isoforms and their complexes with antimitotic agents.. FEBS Journal, 2006, 273, 3301-3310.	2.2	57
68	Antibody structure, prediction and redesign. Biophysical Chemistry, 1997, 68, 9-16.	1.5	56
69	SAP97-mediated ADAM10 trafficking from Golgi outposts depends on PKC phosphorylation. Cell Death and Disease, 2014, 5, e1547-e1547.	2.7	56
70	Coordinated and reversible reduction of enzymes involved in terminal oxidative metabolism in skeletal muscle mitochondria from a riboflavin-responsive, multiple acyl-CoA dehydrogenase deficiency patient. Electrophoresis, 2006, 27, 1182-1198.	1.3	55
71	Surface topology of Minibody by selective chemical modifications and mass spectrometry. Protein Science, 1997, 6, 1901-1909.	3.1	52
72	PepComposer: computational design of peptides binding to a given protein surface. Nucleic Acids Research, 2016, 44, W522-W528.	6.5	52

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73	Genome-wide identification of direct HBx genomic targets. BMC Genomics, 2017, 18, 184.	1.2	52
74	PIGSPro: prediction of immunoGlobulin structures v2. Nucleic Acids Research, 2017, 45, W17-W23.	6.5	52
75	A model for recognition of polychlorinated dibenzo-p -dioxins by the aryl hydrocarbon receptor. FEBS Journal, 2002, 269, 13-18.	0.2	50
76	Massive screening of copy number population-scale variation in Bos taurus genome. BMC Genomics, 2013, 14, 124.	1.2	48
77	Relationship between multiple sequence alignments and quality of protein comparative models. Proteins: Structure, Function and Bioinformatics, 2004, 58, 151-157.	1.5	46
78	Phospho3D 2.0: an enhanced database of three-dimensional structures of phosphorylation sites. Nucleic Acids Research, 2011, 39, D268-D271.	6.5	45
79	Site‐directed enzymatic PEGylation of the human granulocyte colony‐stimulating factor. FEBS Journal, 2009, 276, 6741-6750.	2.2	42
80	All-Atom Molecular Dynamics Simulation of Protein Translocation through an α-Hemolysin Nanopore. Journal of Physical Chemistry Letters, 2015, 6, 2963-2968.	2.1	41
81	Genome sequences and great expectations. Genome Biology, 2000, 2, interactions0001.1.	13.9	40
82	3USS: a web server for detecting alternative 3′UTRs from RNA-seq experiments. Bioinformatics, 2015, 31, 1845-1847.	1.8	40
83	A Long Noncoding RNA Controls Muscle Differentiation by Functioning as a Competing Endogenous RNA. Cell, 2011, 147, 947.	13.5	39
84	FIDEA: a server for the functional interpretation of differential expression analysis. Nucleic Acids Research, 2013, 41, W84-W88.	6.5	39
85	Analysis of a cDNA sequence encoding the immunoglobulin heavy chain of the Antarctic teleost Trematomus bernacchii. Fish and Shellfish Immunology, 2000, 10, 343-357.	1.6	38
86	Engineering Stable Cytoplasmic Intrabodies with Designed Specificity. Journal of Molecular Biology, 2003, 330, 323-332.	2.0	38
87	Exploring the Cytochrome c Folding Mechanism. Journal of Biological Chemistry, 2003, 278, 41136-41140.	1.6	38
88	Coding potential of the products of alternative splicing in human. Genome Biology, 2011, 12, R9.	3.8	38
89	A database of immunoglobulins with integrated tools: DIGIT. Nucleic Acids Research, 2012, 40, D1230-D1234.	6.5	37
90	Classification of proteins based on the properties of the ligand-binding site: The case of adenine-binding proteins. Proteins: Structure, Function and Bioinformatics, 2002, 47, 106-115.	1.5	36

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91	The prediction of protein function at CASP6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 201-213.	1.5	35
92	Yeast as a model of human mitochondrial tRNA base substitutions: Investigation of the molecular basis of respiratory defects. Rna, 2007, 14, 275-283.	1.6	35
93	Structural repertoire of immunoglobulin Î» light chains. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1513-1524.	1.5	35
94	Investigation of a potential mechanism for the inhibition of SmTGR by Auranofin and its implications for Plasmodium falciparum inhibition. Biochemical and Biophysical Research Communications, 2012, 417, 576-581.	1.0	35
95	Multistep Current Signal in Protein Translocation through Graphene Nanopores. Journal of Physical Chemistry B, 2015, 119, 5815-5823.	1.2	33
96	Tabhu: tools for antibody humanization. Bioinformatics, 2015, 31, 434-435.	1.8	32
97	FunClust: a web server for the identification of structural motifs in a set of non-homologous protein structures. BMC Bioinformatics, 2008, 9, S2.	1.2	31
98	A proangiogenic peptide derived from vascular endothelial growth factor receptor-1 acts through Î±5Î²1 integrin. Blood, 2008, 111, 3479-3488.	0.6	30
99	The making of the minibody: An engineered Î²-protein for the display of conformationally constrained peptides. Journal of Molecular Recognition, 1994, 7, 9-24.	1.1	29
100	Mutations of gly to ala in human glutathione transferase P1-1 affect helix 2 (G-site) and induce positive cooperativity in the binding of glutathione 1 1Edited by R. Huber. Journal of Molecular Biology, 1998, 284, 1717-1725.	2.0	29
101	Mimotopes of the hyper variable region 1 of the hepatitis C virus induce cross-reactive antibodies directed against discontinuous epitopes. Molecular Immunology, 2001, 38, 485-492.	1.0	29
102	Ten Simple Rules for Developing a Short Bioinformatics Training Course. PLoS Computational Biology, 2011, 7, e1002245.	1.5	29
103	Improving the accuracy of the structure prediction of the third hypervariable loop of the heavy chains of antibodies. Bioinformatics, 2014, 30, 2733-2740.	1.8	29
104	Superposition-free comparison and clustering of antibody binding sites: implications for the prediction of the nature of their antigen. Scientific Reports, 2017, 7, 45053.	1.6	27
105	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	1.5	26
106	Redesigning the substrate specificity of the hepatitis C virus NS3 protease. Folding & Design, 1996, 1, 35-42.	4.5	26
107	Identification and functional characterization of the bile acid transport proteins in nonâ€mammalian ileum and mammalian liver. Proteins: Structure, Function and Bioinformatics, 2008, 70, 462-472.	1.5	26
108	LoopIng: a template-based tool for predicting the structure of protein loops. Bioinformatics, 2015, 31, 3767-3772.	1.8	26

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109	The role of molecular modelling in biomedical research. FEBS Letters, 2006, 580, 2928-2934.	1.3	25
110	MD and Docking Studies Reveal That the Functional Switch of CYFIP1 is Mediated by a Butterfly-like Motion. Journal of Chemical Theory and Computation, 2015, 11, 3401-3410.	2.3	24
111	Structural definition by antibody engineering of an idiotypic determinant. Protein Engineering, Design and Selection, 1990, 3, 531-539.	1.0	23
112	Automatic procedure for using models of proteins in molecular replacement. Proteins: Structure, Function and Bioinformatics, 2006, 66, 689-696.	1.5	23
113	Probability of coding of a DNA sequence: an algorithm to predict translated reading frames from their thermodynamic characteristics. Nucleic Acids Research, 1986, 14, 127-135.	6.5	22
114	The MEPS server for identifying protein conformational epitopes. BMC Bioinformatics, 2007, 8, S6.	1.2	21
115	Inhibition of endothelial cell migration and angiogenesis by a vascular endothelial growth factor receptor-1 derived peptide. European Journal of Cancer, 2008, 44, 1914-1921.	1.3	21
116	Molecular evolution of a gene cluster of serine proteases expressed in the Anopheles gambiae female reproductive tract. BMC Evolutionary Biology, 2011, 11, 72.	3.2	21
117	Igs Expressed by Chronic Lymphocytic Leukemia B Cells Show Limited Binding-Site Structure Variability. Journal of Immunology, 2013, 190, 5771-5778.	0.4	21
118	Prediction of the permeability of neutral drugs inferred from their solvation properties. Bioinformatics, 2016, 32, 1163-1169.	1.8	20
119	A Structure-Guided Approach to an Orthogonal Estrogen-Receptor-Based Gene Switch Activated by Ligands Suitable for in Vivo Studies. Journal of Medicinal Chemistry, 2006, 49, 5404-5407.	2.9	19
120	An analysis of the Sargasso Sea resource and the consequences for database composition. BMC Bioinformatics, 2006, 7, 213.	1.2	18
121	Modelling and molecular dynamics of the interaction between the E3 ubiquitin ligase Itch and the E2 UbcH7. Biochemical Pharmacology, 2008, 76, 1620-1627.	2.0	18
122	Digestive peptidase evolution in holometabolous insects led to a divergent group of enzymes in Lepidoptera. Insect Biochemistry and Molecular Biology, 2015, 58, 1-11.	1.2	18
123	An automatic method for identifying surface proteins in bacteria: SLEP. BMC Bioinformatics, 2010, 11, 39.	1.2	17
124	Novel Cinnamyl Hydroxyamides and 2â€Aminoanilides as Histone Deacetylase Inhibitors: Apoptotic Induction and Cytodifferentiation Activity. ChemMedChem, 2011, 6, 698-712.	1.6	17
125	Rapid Profiling of the Antigen Regions Recognized by Serum Antibodies Using Massively Parallel Sequencing of Antigen-Specific Libraries. PLoS ONE, 2014, 9, e114159.	1.1	17
126	Genome-wide RNA-seq analysis indicates that the DAG1 transcription factor promotes hypocotyl elongation acting on ABA, ethylene and auxin signaling. Scientific Reports, 2018, 8, 15895.	1.6	17

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127	Structural Conservation in Single-Domain Proteins: Implications for Homology Modeling. Journal of Structural Biology, 2001, 134, 246-256.	1.3	16
128	Analysis of Hepatitis C Virus Hypervariable Region 1 Sequence from Cryoglobulinemic Patients and Associated Controls. Journal of Virology, 2007, 81, 4564-4571.	1.5	16
129	Modelling antibody-antigen interactions: ferritin as a case study. Molecular Immunology, 1995, 32, 1001-1010.	1.0	15
130	In Vivo Selection of Protease Cleavage Sites by Using Chimeric Sindbis Virus Libraries. Journal of Virology, 2000, 74, 10563-10570.	1.5	15
131	Aminoacylation and conformational properties of yeast mitochondrial tRNA mutants with respiratory deficiency. Rna, 2005, 11, 914-927.	1.6	15
132	Revisiting the prediction of protein function at CASP6. FEBS Journal, 2006, 273, 2977-2983.	2.2	15
133	Selection of Functional Variants of the NS3-NS4A Protease of Hepatitis C Virus by Using Chimeric Sindbis Viruses. Journal of Virology, 1999, 73, 561-575.	1.5	15
134	Rational design and functional expression of a constitutively active single-chain NS4A–NS3 proteinase. Folding & Design, 1998, 3, 433-441.	4.5	14
135	Identification of the Schistosoma mansoni Molecular Target for the Antimalarial Drug Artemether. Journal of Chemical Information and Modeling, 2011, 51, 3005-3016.	2.5	14
136	Identification of a novel putative mitogen-activated kinase cascade on human chromosome 21 by computational approaches. Bioinformatics, 2006, 22, 775-778.	1.8	13
137	The Evaluation of Protein Structure Prediction Results. Molecular Biotechnology, 2008, 39, 1-8.	1.3	13
138	Simulation of urea-induced protein unfolding: A lesson from bovine β-lactoglobulin. Journal of Molecular Graphics and Modelling, 2011, 30, 24-30.	1.3	13
139	MODexplorer: an integrated tool for exploring protein sequence, structure and function relationships. Bioinformatics, 2013, 29, 953-954.	1.8	13
140	Mapping the Hydropathy of Amino Acids Based on Their Local Solvation Structure. Journal of Physical Chemistry B, 2014, 118, 6604-6613.	1.2	13
141	Characterization of the differences in the cyclopiazonic acid binding mode to mammalian and P. Falciparum Ca2+ pumps: A computational study. Proteins: Structure, Function and Bioinformatics, 2015, 83, 564-574.	1.5	13
142	Cover Image, Volume 84, Issue S1. Proteins: Structure, Function and Bioinformatics, 2016, 84, C4.	1.5	13
143	A structural view of microRNA–target recognition. Nucleic Acids Research, 2016, 44, e82-e82.	6.5	13
144	Conformational analysis of putative regulatory subunit D of the toluene/o-xylene-monooxygenase complex from Pseudomonas stutzeri OX1. Protein Science, 2001, 10, 482-490.	3.1	12

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145	A model of the complex between the PfEMP1 malaria protein and the human ICAM–1 receptor. Proteins: Structure, Function and Bioinformatics, 2007, 69, 215-222.	1.5	12
146	Affinity purification of a difficult–sequence protein. International Journal of Peptide and Protein Research, 1993, 42, 93-96.	0.1	12
147	MAISTAS: a tool for automatic structural evaluation of alternative splicing products. Bioinformatics, 2011, 27, 1625-1629.	1.8	12
148	The Assessment of Methods for Protein Structure Prediction. , 2008, 413, 43-57.		11
149	Advances and Pitfalls in Protein Structure Prediction. Current Protein and Peptide Science, 2008, 9, 567-577.	0.7	11
150	Mutation Pattern of Paired Immunoglobulin Heavy and Light Variable Domains in Chronic Lymphocytic Leukemia B Cells. Molecular Medicine, 2011, 17, 1188-1195.	1.9	11
151	Exploring the Unfolding Pathway of Maltose Binding Proteins: An Integrated Computational Approach. Journal of Chemical Theory and Computation, 2014, 10, 3589-3597.	2.3	11
152	Dynamics behind affinity maturation of an anti–HCMV antibody family influencing antigen binding. FEBS Letters, 2017, 591, 2936-2950.	1.3	11
153	Hepatitis C Virus Proteins as Targets for Drug Development: The Role of Bioinformatics and Modelling. Current Drug Targets, 2002, 3, 281-296.	1.0	11
154	Exploiting evolutionary relationships for predicting protein structures. Biotechnology and Bioengineering, 2003, 84, 756-762.	1.7	10
155	Dissecting the Structural Determinants of the Interaction between the Human Cytomegalovirus UL18 Protein and the CD85j Immune Receptor. Journal of Immunology, 2008, 180, 957-968.	0.4	10
156	Improving your target-template alignment with MODalign. Bioinformatics, 2012, 28, 1038-1039.	1.8	10
157	Identifying a putative common binding site shared by substance P receptor and an anti-substance P monoclonal antibody. Protein Engineering, Design and Selection, 1995, 8, 403-408.	1.0	9
158	Cloning, characterization, and modeling of a monoclonal anti–human transferrin antibody that competes with the transferrin receptor. Protein Science, 1994, 3, 1476-1484.	3.1	8
159	Replacing the glutamate ligand in the structural zinc site of Sulfolobus solfataricus alcohol dehydrogenase with a cysteine decreases thermostability. Protein Engineering, Design and Selection, 1995, 8, 31-37.	1.0	8
160	Research Networks: BioSapiens: a European network for integrated genome annotation. European Journal of Human Genetics, 2005, 13, 994-997.	1.4	8
161	ProCoCoA: A quantitative approach for analyzing protein core composition. Computational Biology and Chemistry, 2013, 43, 29-34.	1.1	8
162	Detecting Mutually Exclusive Interactions in Protein-Protein Interaction Maps. PLoS ONE, 2012, 7, e38765.	1.1	8

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163	The MoVIN server for the analysis of protein interaction networks. BMC Bioinformatics, 2008, 9, S11.	1.2	7
164	Toward a better understanding of the interaction between TGF-Î² family members and their ALK receptors. Journal of Molecular Modeling, 2012, 18, 3617-3625.	0.8	7
165	Determination of the autocorrelation orders of proteins. FEBS Journal, 1985, 149, 375-379.	0.2	6
166	No protein is an island. Current Opinion in Structural Biology, 2009, 19, 310-311.	2.6	6
167	Protein structure prediction and design. Biotechnology Annual Review, 1998, 4, 177-214.	2.1	5
168	The Significance of Performance Ranking in CASPâ€"Response to Marti-Renom et al.. Structure, 2002, 10, 291-292.	1.6	5
169	Integral and differential form of the protein folding problem. Physics of Life Reviews, 2004, 1, 103-127.	1.5	5
170	Comparative Modelling Techniques: Where are we?. Comparative and Functional Genomics, 2003, 4, 402-405.	2.0	4
171	A Brighter Future for Protein Design. Angewandte Chemie - International Edition, 2004, 43, 3222-3223.	7.2	4
172	The Relationship Between Protein Sequence, Structure and Function. , 2005, , 15-29.		4
173	PICMI: mapping point mutations on genomes. Bioinformatics, 2010, 26, 2904-2905.	1.8	4
174	The computational prediction of protein assemblies. Current Opinion in Structural Biology, 2017, 46, 170-175.	2.6	4
175	A computational approach for the functional classification of the epigenome. Epigenetics and Chromatin, 2017, 10, 26.	1.8	4
176	The computational analysis of protein structures: Sources, methods, systems and results. Journal of Research of the National Bureau of Standards (United States), 1989, 94, 85.	0.3	3
177	GLASS: A tool to visualize protein structure prediction data in three dimensions and evaluate their consistency. , 1998, 30, 339-351.		3
178	DANTE: a workbench for sequence analysis. Trends in Biochemical Sciences, 2000, 25, 402-403.	3.7	3
179	Horizontal and vertical growth of S. cerevisiae metabolic network. BMC Evolutionary Biology, 2011, 11, 301.	3.2	3
180	RNA editing differently affects protein-coding genes in D. melanogaster and H. sapiens. Scientific Reports, 2015, 5, 11550.	1.6	3

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181	A transportable interactive package for the statistical analysis and handling of sequence data. Computers in Biology and Medicine, 1988, 18, 113-122.	3.9	2
182	A database system for handling phage library-derived sequences. Gene, 1993, 128, 143-144.	1.0	2
183	Sequences and topology: the completeness of biological space. Current Opinion in Structural Biology, 2007, 17, 334-336.	2.6	2
184	Editorial. Bioinformatics, 2008, 24, i1-i1.	1.8	2
185	Evaluation of Protein Structure Prediction Methods: Issues and Strategies. , 2011, , 315-339.		2
186	Exploiting Publicly Available Biological and Biochemical Information for the Discovery of Novel Short Linear Motifs. PLoS ONE, 2011, 6, e22270.	1.1	2
187	A resource for benchmarking the usefulness of protein structure models. BMC Bioinformatics, 2012, 13, 188.	1.2	2
188	Cover Image, Volume 84, Issue S1. Proteins: Structure, Function and Bioinformatics, 2016, 84, C1-C1.	1.5	2
189	VARIANT: a store and retrieval system for human haemoglobin variants. Computer Methods and Programs in Biomedicine, 1990, 31, 113-114.	2.6	1
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