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	Assessment of model accuracy estimations in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 345-360.	1.5	61
2	Critical assessment of methods of protein structure prediction (CASP)â€"Round XII. Proteins: Structure, Function and Bioinformatics, 2018, 86, 7-15.	1.5	296
3	Evaluation of the templateâ€based modeling in <scp>CASP12</scp>. Proteins: Structure, Function and Bioinformatics, 2018, 86, 321-334.	1.5	61
4	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
5	Modeling of Antibody and T-Cell Receptor Structures. , 2018, , 1-8.		0
6	Genome-wide identification of direct HBx genomic targets. BMC Genomics, 2017, 18, 184.	1.2	52
7	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
8	Dynamics behind affinity maturation of an antiâ€•HCMV antibody family influencing antigen binding. FEBS Letters, 2017, 591, 2936-2950.	1.3	11
9	The computational prediction of protein assemblies. Current Opinion in Structural Biology, 2017, 46, 170-175.	2.6	4
10	A computational approach for the functional classification of the epigenome. Epigenetics and Chromatin, 2017, 10, 26.	1.8	4
11	PIGSPro: prediction of immunoGlobulin structures v2. Nucleic Acids Research, 2017, 45, W17-W23.	6.5	52
12	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
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	PepComposer: computational design of peptides binding to a given protein surface. Nucleic Acids Research, 2016, 44, W522-W528.	6.5	52
15	Cover Image, Volume 84, Issue S1. Proteins: Structure, Function and Bioinformatics, 2016, 84, C1-C1.	1.5	2
16	Cover Image, Volume 84, Issue S1. Proteins: Structure, Function and Bioinformatics, 2016, 84, C4.	1.5	13
17	A structural view of microRNAâ€"target recognition. Nucleic Acids Research, 2016, 44, e82-e82.	6.5	13
18	New encouraging developments in contact prediction: Assessment of the <scp>CASP</scp>11 results. Proteins: Structure, Function and Bioinformatics, 2016, 84, 131-144.	1.5	81

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19	Prediction of the permeability of neutral drugs inferred from their solvation properties. Bioinformatics, 2016, 32, 1163-1169.	1.8	20
20	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
21	RNA editing differently affects protein-coding genes in D. melanogaster and H. sapiens. Scientific Reports, 2015, 5, 11550.	1.6	3
22	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
23	3USS: a web server for detecting alternative 3â€²UTRs from RNA-seq experiments. Bioinformatics, 2015, 31, 1845-1847.	1.8	40
24	Exploiting Homology Information in Nontemplate Based Prediction of Protein Structures. Journal of Chemical Theory and Computation, 2015, 11, 5045-5051.	2.3	1
25	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
26	Tabhu: tools for antibody humanization. Bioinformatics, 2015, 31, 434-435.	1.8	32
27	All-Atom Molecular Dynamics Simulation of Protein Translocation through an Î±-Hemolysin Nanopore. Journal of Physical Chemistry Letters, 2015, 6, 2963-2968.	2.1	41
28	Multistep Current Signal in Protein Translocation through Graphene Nanopores. Journal of Physical Chemistry B, 2015, 119, 5815-5823.	1.2	33
29	LoopIng: a template-based tool for predicting the structure of protein loops. Bioinformatics, 2015, 31, 3767-3772.	1.8	26
30	Novel Long Noncoding RNAs (lncRNAs) in Myogenesis: a *miR-31* Overlapping lncRNA Transcript Controls Myoblast Differentiation. Molecular and Cellular Biology, 2015, 35, 728-736.	1.1	99
31	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
32	Critical assessment of methods of protein structure prediction (CASP) â€" round x. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1-6.	1.5	366
33	Assessment of the assessment: Evaluation of the model quality estimates in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 112-126.	1.5	114
34	SAP97-mediated ADAM10 trafficking from Golgi outposts depends on PKC phosphorylation. Cell Death and Disease, 2014, 5, e1547-e1547.	2.7	56
35	Evaluation of residueâ€"residue contact prediction in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 138-153.	1.5	72
36	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

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37	All-Atoms Md Simulation of Protein Translocation through Î±-Hemolysin Nanopore: Implications for Protein Sequence/Structural Analyses. Biophysical Journal, 2014, 106, 803a.	0.2	0
38	Assessment of protein disorder region predictions in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 127-137.	1.5	140
39	Antibody modeling using the Prediction of ImmunoGlobulin Structure (PIGS) web server. Nature Protocols, 2014, 9, 2771-2783.	5.5	58
40	Cancer-Selective Targeting of the NF-κB Survival Pathway with GADD45Î²/MKK7 Inhibitors. Cancer Cell, 2014, 26, 495-508.	7.7	99
41	Mapping the Hydropathy of Amino Acids Based on Their Local Solvation Structure. Journal of Physical Chemistry B, 2014, 118, 6604-6613.	1.2	13
42	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
43	Massive screening of copy number population-scale variation in Bos taurus genome. BMC Genomics, 2013, 14, 124.	1.2	48
44	Prediction of site-specific interactions in antibody-antigen complexes: the proABC method and server. Bioinformatics, 2013, 29, 2285-2291.	1.8	91
45	ProCoCoA: A quantitative approach for analyzing protein core composition. Computational Biology and Chemistry, 2013, 43, 29-34.	1.1	8
46	TiPs: a database of therapeutic targets in pathogens and associated tools. Bioinformatics, 2013, 29, 1821-1822.	1.8	1
47	MODexplorer: an integrated tool for exploring protein sequence, structure and function relationships. Bioinformatics, 2013, 29, 953-954.	1.8	13
48	Igs Expressed by Chronic Lymphocytic Leukemia B Cells Show Limited Binding-Site Structure Variability. Journal of Immunology, 2013, 190, 5771-5778.	0.4	21
49	FIDEA: a server for the functional interpretation of differential expression analysis. Nucleic Acids Research, 2013, 41, W84-W88.	6.5	39
50	The PARIGA Server for Real Time Filtering and Analysis of Reciprocal BLAST Results. PLoS ONE, 2013, 8, e62224.	1.1	1
51	Endocytosis of synaptic ADAM10 in neuronal plasticity and Alzheimerâ€™s disease. Journal of Clinical Investigation, 2013, 123, 2523-2538.	3.9	96
52	Improving your target-template alignment with MODalign. Bioinformatics, 2012, 28, 1038-1039.	1.8	10
53	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
54	A database of immunoglobulins with integrated tools: DIGIT. Nucleic Acids Research, 2012, 40, D1230-D1234.	6.5	37

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55	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
56	A resource for benchmarking the usefulness of protein structure models. BMC Bioinformatics, 2012, 13, 188.	1.2	2
57	Detecting Mutually Exclusive Interactions in Protein-Protein Interaction Maps. PLoS ONE, 2012, 7, e38765.	1.1	8
58	Hierarchical Clustering of B-Cell Receptor Structures in Splenic Marginal Zone Lymphoma. Blood, 2012, 120, 1585-1585.	0.6	0
59	Evaluation of Protein Structure Prediction Methods: Issues and Strategies. , 2011, , 315-339.		2
60	Coding potential of the products of alternative splicing in human. Genome Biology, 2011, 12, R9.	3.8	38
61	A Long Noncoding RNA Controls Muscle Differentiation by Functioning as a Competing Endogenous RNA. Cell, 2011, 147, 358-369.	13.5	2,390
62	A Long Noncoding RNA Controls Muscle Differentiation by Functioning as a Competing Endogenous RNA. Cell, 2011, 147, 947.	13.5	39
63	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
64	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
65	Exploiting Publicly Available Biological and Biochemical Information for the Discovery of Novel Short Linear Motifs. PLoS ONE, 2011, 6, e22270.	1.1	2
66	The association of heavy and light chain variable domains in antibodies: implications for antigen specificity. FEBS Journal, 2011, 278, 2858-2866.	2.2	76
67	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
68	Horizontal and vertical growth of S. cerevisiae metabolic network. BMC Evolutionary Biology, 2011, 11, 301.	3.2	3
69	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
70	Structural repertoire of immunoglobulin λ light chains. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1513-1524.	1.5	35
71	Evaluation of residue–residue contact predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 119-125.	1.5	75
72	Evaluation of disorder predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 107-118.	1.5	102

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73	Evaluation of model quality predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 91-106.	1.5	83
74	Critical assessment of methods of protein structure prediction (CASP)â€"round IX. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1-5.	1.5	187
75	Novel Cinnamyl Hydroxyamides and 2â€Aminoanilides as Histone Deacetylase Inhibitors: Apoptotic Induction and Cytodifferentiation Activity. ChemMedChem, 2011, 6, 698-712.	1.6	17
76	MAISTAS: a tool for automatic structural evaluation of alternative splicing products. Bioinformatics, 2011, 27, 1625-1629.	1.8	12
77	Phospho3D 2.0: an enhanced database of three-dimensional structures of phosphorylation sites. Nucleic Acids Research, 2011, 39, D268-D271.	6.5	45
78	Ten Simple Rules for Developing a Short Bioinformatics Training Course. PLoS Computational Biology, 2011, 7, e1002245.	1.5	29
79	Stereotyped patterns of B-cell receptor in splenic marginal zone lymphoma. Haematologica, 2010, 95, 1792-1796.	1.7	91
80	An automatic method for identifying surface proteins in bacteria: SLEP. BMC Bioinformatics, 2010, 11, 39.	1.2	17
81	In memoriam. Proteins: Structure, Function and Bioinformatics, 2010, 78, iii-viii.	1.5	0
82	On the Mechanism of Chloroquine Resistance in Plasmodium falciparum. PLoS ONE, 2010, 5, e14064.	1.1	67
83	PICMI: mapping point mutations on genomes. Bioinformatics, 2010, 26, 2904-2905.	1.8	4
84	No protein is an island. Current Opinion in Structural Biology, 2009, 19, 310-311.	2.6	6
85	Evaluation of CASP8 model quality predictions. Proteins: Structure, Function and Bioinformatics, 2009, 77, 157-166.	1.5	76
86	Evaluation of templateâ€based models in CASP8 with standard measures. Proteins: Structure, Function and Bioinformatics, 2009, 77, 18-28.	1.5	114
87	Critical assessment of methods of protein structure predictionâ€"Round VIII. Proteins: Structure, Function and Bioinformatics, 2009, 77, 1-4.	1.5	229
88	Siteâ€directed enzymatic PEGylation of the human granulocyte colonyâ€stimulating factor. FEBS Journal, 2009, 276, 6741-6750.	2.2	42
89	Protein function annotation by homology-based inference. Genome Biology, 2009, 10, 207.	13.9	182
90	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

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91	The Evaluation of Protein Structure Prediction Results. Molecular Biotechnology, 2008, 39, 1-8.	1.3	13
92	The Assessment of Methods for Protein Structure Prediction. , 2008, 413, 43-57.		11
93	The MoVIN server for the analysis of protein interaction networks. BMC Bioinformatics, 2008, 9, S11.	1.2	7
94	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
95	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
96	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
97	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
98	Editorial. Bioinformatics, 2008, 24, i1-i1.	1.8	2
99	PIGS: automatic prediction of antibody structures. Bioinformatics, 2008, 24, 1953-1954.	1.8	186
100	A proangiogenic peptide derived from vascular endothelial growth factor receptor-1 acts through $\hat{\text{I}}\pm 5\hat{\text{I}}^2 1$ integrin. Blood, 2008, 111, 3479-3488.	0.6	30
101	Advances and Pitfalls in Protein Structure Prediction. Current Protein and Peptide Science, 2008, 9, 567-577.	0.7	11
102	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
103	Mg^{2+} binding and archaeosine modification stabilize the G15â€"C48 Levitt base pair in tRNAs. Rna, 2007, 13, 1427-1436.	1.6	79
104	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
105	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
106	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
107	The mepsMAP Server. Mapping Epitopes on Protein Surface: Mining Annotated Proteins. IEEE Transactions on Nanobioscience, 2007, 6, 155-161.	2.2	0
108	Assessment of predictions in the model quality assessment category. Proteins: Structure, Function and Bioinformatics, 2007, 69, 175-183.	1.5	122

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109	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
110	Critical assessment of methods of protein structure prediction—Round VII. Proteins: Structure, Function and Bioinformatics, 2007, 69, 3-9.	1.5	199
111	The MEPS server for identifying protein conformational epitopes. BMC Bioinformatics, 2007, 8, S6.	1.2	21
112	Sequences and topology: the completeness of biological space. Current Opinion in Structural Biology, 2007, 17, 334-336.	2.6	2
113	The PMDB Protein Model Database. Nucleic Acids Research, 2006, 34, D306-D309.	6.5	266
114	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
115	The role of molecular modelling in biomedical research. FEBS Letters, 2006, 580, 2928-2934.	1.3	25
116	Automatic procedure for using models of proteins in molecular replacement. Proteins: Structure, Function and Bioinformatics, 2006, 66, 689-696.	1.5	23
117	Revisiting the prediction of protein function at CASP6. FEBS Journal, 2006, 273, 2977-2983.	2.2	15
118	The betaI/betaIII-tubulin isoforms and their complexes with antimitotic agents.. FEBS Journal, 2006, 273, 3301-3310.	2.2	57
119	An analysis of the Sargasso Sea resource and the consequences for database composition. BMC Bioinformatics, 2006, 7, 213.	1.2	18
120	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
121	Identification of a novel putative mitogen-activated kinase cascade on human chromosome 21 by computational approaches. Bioinformatics, 2006, 22, 775-778.	1.8	13
122	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
123	QUALITY AND EFFECTIVENESS OF PROTEIN STRUCTURE COMPARATIVE MODELS. , 2006, , .		0
124	Research Networks: BioSapiens: a European network for integrated genome annotation. European Journal of Human Genetics, 2005, 13, 994-997.	1.4	8
125	Critical assessment of methods of protein structure prediction (CASP)—Round 6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 3-7.	1.5	162
126	The prediction of protein function at CASP6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 201-213.	1.5	35

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127	The Relationship Between Protein Sequence, Structure and Function. , 2005, , 15-29.		4
128	Aminoacylation and conformational properties of yeast mitochondrial tRNA mutants with respiratory deficiency. Rna, 2005, 11, 914-927.	1.6	15
129	Evaluating the usefulness of protein structure models for molecular replacement. Bioinformatics, 2005, 21, ii72-ii76.	1.8	57
130	Relationship between multiple sequence alignments and quality of protein comparative models. Proteins: Structure, Function and Bioinformatics, 2004, 58, 151-157.	1.5	46
131	A Brighter Future for Protein Design. Angewandte Chemie - International Edition, 2004, 43, 3222-3223.	7.2	4
132	A Brighter Future for Protein Design. ChemInform, 2004, 35, no.	0.1	0
133	Integral and differential form of the protein folding problem. Physics of Life Reviews, 2004, 1, 103-127.	1.5	5
134	Remarkably similar antigen receptors among a subset of patients with chronic lymphocytic leukemia. Journal of Clinical Investigation, 2004, 113, 1008-1016.	3.9	190
135	Evolution of Bacterial and Archaeal Multicomponent Monooxygenases. Journal of Molecular Evolution, 2003, 56, 435-445.	0.8	118
136	Comparative Modelling Techniques: Where are we?. Comparative and Functional Genomics, 2003, 4, 402-405.	2.0	4
137	Exploiting evolutionary relationships for predicting protein structures. Biotechnology and Bioengineering, 2003, 84, 756-762.	1.7	10
138	Assessment of homology-based predictions in CASP5. Proteins: Structure, Function and Bioinformatics, 2003, 53, 352-368.	1.5	165
139	Engineering Stable Cytoplasmic Intrabodies with Designed Specificity. Journal of Molecular Biology, 2003, 330, 323-332.	2.0	38
140	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
141	Exploring the Cytochrome c Folding Mechanism. Journal of Biological Chemistry, 2003, 278, 41136-41140.	1.6	38
142	Evaluation of annotation strategies using an entire genome sequence. Bioinformatics, 2003, 19, 717-726.	1.8	65
143	The Significance of Performance Ranking in CASPâ€"Response to Marti-Renom et al.. Structure, 2002, 10, 291-292.	1.6	5
144	A model for recognition of polychlorinated dibenzo-p -dioxins by the aryl hydrocarbon receptor. FEBS Journal, 2002, 269, 13-18.	0.2	50

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145	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
146	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
147	Structural Conservation in Single-Domain Proteins: Implications for Homology Modeling. Journal of Structural Biology, 2001, 134, 246-256.	1.3	16
148	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
149	Analysis and assessment of comparative modeling predictions in CASP4. Proteins: Structure, Function and Bioinformatics, 2001, 45, 22-38.	1.5	101
150	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
151	A model for the hepatitis C virus envelope glycoprotein E2. Proteins: Structure, Function and Bioinformatics, 2000, 40, 355-366.	1.5	191
152	DANTE: a workbench for sequence analysis. Trends in Biochemical Sciences, 2000, 25, 402-403.	3.7	3
153	In Vivo Selection of Protease Cleavage Sites by Using Chimeric Sindbis Virus Libraries. Journal of Virology, 2000, 74, 10563-10570.	1.5	15
154	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
155	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
156	Antibody Modeling: Implications for Engineering and Design. Methods, 2000, 20, 267-279.	1.9	98
157	Genome sequences and great expectations. Genome Biology, 2000, 2, interactions0001.1.	13.9	40
158	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
159	Towards a solution for hepatitis C virus hypervariability: mimotopes of the hypervariable region 1can induce antibodies cross-reacting with a large number of viral variants. EMBO Journal, 1998, 17, 3521-3533.	3.5	137
160	Rational design and functional expression of a constitutively active single-chain NS4Aâ€"NS3 proteinase. Folding & Design, 1998, 3, 433-441.	4.5	14
161	GLASS: A tool to visualize protein structure prediction data in three dimensions and evaluate their consistency. , 1998, 30, 339-351.		3
162	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

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163	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
164	Homology Modeling with Low Sequence Identity. Methods, 1998, 14, 293-300.	1.9	72
165	Protein structure prediction and design. Biotechnology Annual Review, 1998, 4, 177-214.	2.1	5
166	Substrate Specificity of the Hepatitis C Virus Serine Protease NS3. Journal of Biological Chemistry, 1997, 272, 9204-9209.	1.6	109
167	Surface topology of Minibody by selective chemical modifications and mass spectrometry. Protein Science, 1997, 6, 1901-1909.	3.1	52
168	Antibody structure, prediction and redesign. Biophysical Chemistry, 1997, 68, 9-16.	1.5	56
169	A Zinc Binding Site in Viral Serine Proteinases. Biochemistry, 1996, 35, 13282-13287.	1.2	103
170	Protein structure prediction:playing the fold. Trends in Biochemical Sciences, 1996, 21, 279-281.	3.7	1
171	Redesigning the substrate specificity of the hepatitis C virus NS3 protease. Folding & Design, 1996, 1, 35-42.	4.5	26
172	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
173	The Architecture of Loops in Proteins. , 1996, , 239-259.		1
174	Identification of biologically active peptides using random libraries displayed on phage. Current Opinion in Biotechnology, 1995, 6, 73-80.	3.3	115
175	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
176	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
177	Modelling antibody-antigen interactions: ferritin as a case study. Molecular Immunology, 1995, 32, 1001-1010.	1.0	15
178	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
179	Variability within the Candida rugosa Upases family. Protein Engineering, Design and Selection, 1994, 7, 531-535.	1.0	97
180	Cloning, characterization, and modeling of a monoclonal antiâ€human transferrin antibody that competes with the transferrin receptor. Protein Science, 1994, 3, 1476-1484.	3.1	8

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181	The making of the minibody: An engineered β-protein for the display of conformationally constrained peptides. Journal of Molecular Recognition, 1994, 7, 9-24.	1.1	29
182	PUZZLE: A New Method for Automated Protein Docking Based on Surface Shape Complementarity. Journal of Molecular Biology, 1994, 235, 1021-1031.	2.0	91
183	High Level Expression and Rational Mutagenesis of a Designed Protein, the Minibody. Journal of Molecular Biology, 1994, 236, 649-659.	2.0	61
184	A designed metal-binding protein with a novel fold. Nature, 1993, 362, 367-369.	13.7	228
185	In vitroselection of peptides from molecular repertoires. Rendiconti Lincei, 1993, 4, 359-366.	1.0	0
186	A database system for handling phage library-derived sequences. Gene, 1993, 128, 143-144.	1.0	2
187	Cloning and analysis of Candida cylindracea lipase sequences. Gene, 1993, 124, 45-55.	1.0	131
188	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
189	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
190	Affinity purification of a difficultâ€sequence protein. International Journal of Peptide and Protein Research, 1993, 42, 93-96.	0.1	12
191	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
192	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
193	A method to evaluate the relative weights of structural and functional constraints on a genome. Nuovo Cimento Della Societa Italiana Di Fisica D - Condensed Matter, Atomic, Molecular and Chemical Physics, Biophysics, 1991, 13, 553-563.	0.4	0
194	Members of the zinc finger protein gene family sharing a conserved N-terminal module. Nucleic Acids Research, 1991, 19, 5661-5667.	6.5	78
195	VARIANT: a store and retrieval system for human haemoglobin variants. Computer Methods and Programs in Biomedicine, 1990, 31, 113-114.	2.6	1
196	Structural definition by antibody engineering of an idiotypic determinant. Protein Engineering, Design and Selection, 1990, 3, 531-539.	1.0	23
197	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
198	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

#	Article	IF	Citations
199	Structural determinants of the conformations of medium-sized loops in proteins. Proteins: Structure, Function and Bioinformatics, 1989, 6, 382-394.	1.5	82
200	Conformations of immunoglobulin hypervariable regions. Nature, 1989, 342, 877-883.	13.7	1,199
201	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
202	Information value and information content in the evolutionary strategy of the genetic code. Nuovo Cimento Della Societa Italiana Di Fisica D - Condensed Matter, Atomic, Molecular and Chemical Physics, Biophysics, 1988, 10, 293-301.	0.4	0
203	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
204	Determination of the autocorrelation orders of proteins. FEBS Journal, 1985, 149, 375-379.	0.2	6