

# Anna Tramontano

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

195  
papers

12,303  
citations

57  
h-index

107  
g-index

214  
ext. papers

13,473  
ext. citations

7.2  
avg, IF

6.15  
L-index

#	Paper	IF	Citations
195	Assessment of model accuracy estimations in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2018</b> , 86 Suppl 1, 345-360	4.2	41
194	Critical assessment of methods of protein structure prediction (CASP)-Round XII. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2018</b> , 86 Suppl 1, 7-15	4.2	209
193	Evaluation of the template-based modeling in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2018</b> , 86 Suppl 1, 321-334	4.2	50
192	Genome-wide RNA-seq analysis indicates that the DAG1 transcription factor promotes hypocotyl elongation acting on ABA, ethylene and auxin signaling. <i>Scientific Reports</i> , <b>2018</b> , 8, 15895	4.9	8
191	Genome-wide identification of direct HBx genomic targets. <i>BMC Genomics</i> , <b>2017</b> , 18, 184	4.5	38
190	Superposition-free comparison and clustering of antibody binding sites: implications for the prediction of the nature of their antigen. <i>Scientific Reports</i> , <b>2017</b> , 7, 45053	4.9	22
189	Dynamics behind affinity maturation of an anti-HCMV antibody family influencing antigen binding. <i>FEBS Letters</i> , <b>2017</b> , 591, 2936-2950	3.8	3
188	The computational prediction of protein assemblies. <i>Current Opinion in Structural Biology</i> , <b>2017</b> , 46, 170-175	4.5	4
187	A computational approach for the functional classification of the epigenome. <i>Epigenetics and Chromatin</i> , <b>2017</b> , 10, 26	5.8	2
186	PIGSPRO: prediction of immunoglobulin structures v2. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W17-W23	20.1	39
185	Cover Image, Volume 84, Issue S1. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84, C1-C1	4.2	2
184	Cover Image, Volume 84, Issue S1. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84, C4-C4	4.2	12
183	A structural view of microRNA-target recognition. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e82	20.1	11
182	New encouraging developments in contact prediction: Assessment of the CASP11 results. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84 Suppl 1, 131-44	4.2	66
181	Prediction of the permeability of neutral drugs inferred from their solvation properties. <i>Bioinformatics</i> , <b>2016</b> , 32, 1163-9	7.2	13
180	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in CASP11. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84 Suppl 1, 349-69	4.2	53
179	Critical assessment of methods of protein structure prediction: Progress and new directions in round XI. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84 Suppl 1, 4-14	4.2	156

178	PepComposer: computational design of peptides binding to a given protein surface. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W522-8	20.1	36
177	Tabhu: tools for antibody humanization. <i>Bioinformatics</i> , <b>2015</b> , 31, 434-5	7.2	24
176	All-Atom Molecular Dynamics Simulation of Protein Translocation through an $\beta$ -Hemolysin Nanopore. <i>Journal of Physical Chemistry Letters</i> , <b>2015</b> , 6, 2963-8	6.4	36
175	Multistep current signal in protein translocation through graphene nanopores. <i>Journal of Physical Chemistry B</i> , <b>2015</b> , 119, 5815-23	3.4	30
174	LoopIng: a template-based tool for predicting the structure of protein loops. <i>Bioinformatics</i> , <b>2015</b> , 31, 3767-72	7.2	15
173	Novel long noncoding RNAs (lncRNAs) in myogenesis: a miR-31 overlapping lncRNA transcript controls myoblast differentiation. <i>Molecular and Cellular Biology</i> , <b>2015</b> , 35, 728-36	4.8	78
172	Characterization of the differences in the cyclopiazonic acid binding mode to mammalian and <i>P. Falciparum</i> Ca <sup>2+</sup> pumps: a computational study. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 564-74	4.2	11
171	RNA editing differently affects protein-coding genes in <i>D. melanogaster</i> and <i>H. sapiens</i> . <i>Scientific Reports</i> , <b>2015</b> , 5, 11550	4.9	1
170	MD and Docking Studies Reveal That the Functional Switch of CYFIP1 is Mediated by a Butterfly-like Motion. <i>Journal of Chemical Theory and Computation</i> , <b>2015</b> , 11, 3401-10	6.4	16
169	3USS: a web server for detecting alternative 3'UTRs from RNA-seq experiments. <i>Bioinformatics</i> , <b>2015</b> , 31, 1845-7	7.2	23
168	Exploiting homology information in nontemplate based prediction of protein structures. <i>Journal of Chemical Theory and Computation</i> , <b>2015</b> , 11, 5045-51	6.4	1
167	Digestive peptidase evolution in holometabolous insects led to a divergent group of enzymes in Lepidoptera. <i>Insect Biochemistry and Molecular Biology</i> , <b>2015</b> , 58, 1-11	4.5	13
166	Antibody modeling using the prediction of immunoglobulin structure (PIGS) web server [corrected]. <i>Nature Protocols</i> , <b>2014</b> , 9, 2771-83	18.8	46
165	Cancer-selective targeting of the NF- $\kappa$ B survival pathway with GADD45 $\beta$ /MKK7 inhibitors. <i>Cancer Cell</i> , <b>2014</b> , 26, 495-508	24.3	77
164	Mapping the hydrophobicity of amino acids based on their local solvation structure. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 6604-13	3.4	9
163	Exploring the Unfolding Pathway of Maltose Binding Proteins: An Integrated Computational Approach. <i>Journal of Chemical Theory and Computation</i> , <b>2014</b> , 10, 3589-97	6.4	7
162	Rapid profiling of the antigen regions recognized by serum antibodies using massively parallel sequencing of antigen-specific libraries. <i>PLoS ONE</i> , <b>2014</b> , 9, e114159	3.7	13
161	Critical assessment of methods of protein structure prediction (CASP)--round x. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82 Suppl 2, 1-6	4.2	291

160	Assessment of the assessment: evaluation of the model quality estimates in CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82 Suppl 2, 112-26	4.2	96
159	SAP97-mediated ADAM10 trafficking from Golgi outposts depends on PKC phosphorylation. <i>Cell Death and Disease</i> , <b>2014</b> , 5, e1547	9.8	43
158	Evaluation of residue-residue contact prediction in CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82 Suppl 2, 138-53	4.2	65
157	Improving the accuracy of the structure prediction of the third hypervariable loop of the heavy chains of antibodies. <i>Bioinformatics</i> , <b>2014</b> , 30, 2733-40	7.2	25
156	Assessment of protein disorder region predictions in CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82 Suppl 2, 127-37	4.2	123
155	Massive screening of copy number population-scale variation in <i>Bos taurus</i> genome. <i>BMC Genomics</i> , <b>2013</b> , 14, 124	4.5	33
154	Prediction of site-specific interactions in antibody-antigen complexes: the proABC method and server. <i>Bioinformatics</i> , <b>2013</b> , 29, 2285-91	7.2	66
153	ProCoCoA: A quantitative approach for analyzing protein core composition. <i>Computational Biology and Chemistry</i> , <b>2013</b> , 43, 29-34	3.6	7
152	TiPs: a database of therapeutic targets in pathogens and associated tools. <i>Bioinformatics</i> , <b>2013</b> , 29, 1821-2	7.2	1
151	MODexplorer: an integrated tool for exploring protein sequence, structure and function relationships. <i>Bioinformatics</i> , <b>2013</b> , 29, 953-4	7.2	13
150	IgS expressed by chronic lymphocytic leukemia B cells show limited binding-site structure variability. <i>Journal of Immunology</i> , <b>2013</b> , 190, 5771-8	5.3	18
149	FIDEA: a server for the functional interpretation of differential expression analysis. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, W84-8	20.1	33
148	The PARIGA server for real time filtering and analysis of reciprocal BLAST results. <i>PLoS ONE</i> , <b>2013</b> , 8, e62224	3.7	
147	Endocytosis of synaptic ADAM10 in neuronal plasticity and Alzheimer's disease. <i>Journal of Clinical Investigation</i> , <b>2013</b> , 123, 2523-38	15.9	74
146	Toward a better understanding of the interaction between TGF- $\beta$ family members and their ALK receptors. <i>Journal of Molecular Modeling</i> , <b>2012</b> , 18, 3617-25	2	6
145	A database of immunoglobulins with integrated tools: DIGIT. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D1230-4	20.1	35
144	Investigation of a potential mechanism for the inhibition of SmTGR by Auranofin and its implications for <i>Plasmodium falciparum</i> inhibition. <i>Biochemical and Biophysical Research Communications</i> , <b>2012</b> , 417, 576-81	3.4	24
143	A resource for benchmarking the usefulness of protein structure models. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 188	3.6	2

142	Improving your target-template alignment with MODalign. <i>Bioinformatics</i> , <b>2012</b> , 28, 1038-9	7.2	10
141	Detecting mutually exclusive interactions in protein-protein interaction maps. <i>PLoS ONE</i> , <b>2012</b> , 7, e38765	5.7	5
140	Hierarchical Clustering of B-Cell Receptor Structures in Splenic Marginal Zone Lymphoma. <i>Blood</i> , <b>2012</b> , 120, 1585-1585	2.2	
139	Evaluation of Protein Structure Prediction Methods: Issues and Strategies <b>2011</b> , 315-339		2
138	Coding potential of the products of alternative splicing in human. <i>Genome Biology</i> , <b>2011</b> , 12, R9	18.3	23
137	A long noncoding RNA controls muscle differentiation by functioning as a competing endogenous RNA. <i>Cell</i> , <b>2011</b> , 147, 358-69	56.2	1993
136	A Long Noncoding RNA Controls Muscle Differentiation by Functioning as a Competing Endogenous RNA. <i>Cell</i> , <b>2011</b> , 147, 947	56.2	37
135	Identification of the <i>Schistosoma mansoni</i> molecular target for the antimalarial drug artemether. <i>Journal of Chemical Information and Modeling</i> , <b>2011</b> , 51, 3005-16	6.1	14
134	Mutation pattern of paired immunoglobulin heavy and light variable domains in chronic lymphocytic leukemia B cells. <i>Molecular Medicine</i> , <b>2011</b> , 17, 1188-95	6.2	9
133	Exploiting publicly available biological and biochemical information for the discovery of novel short linear motifs. <i>PLoS ONE</i> , <b>2011</b> , 6, e22270	3.7	1
132	The association of heavy and light chain variable domains in antibodies: implications for antigen specificity. <i>FEBS Journal</i> , <b>2011</b> , 278, 2858-66	5.7	52
131	Simulation of urea-induced protein unfolding: a lesson from bovine lactoglobulin. <i>Journal of Molecular Graphics and Modelling</i> , <b>2011</b> , 30, 24-30	2.8	10
130	Horizontal and vertical growth of <i>S. cerevisiae</i> metabolic network. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 301	3	1
129	Molecular evolution of a gene cluster of serine proteases expressed in the <i>Anopheles gambiae</i> female reproductive tract. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 72	3	15
128	Structural repertoire of immunoglobulin light chains. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 1513-24	4.2	32
127	Evaluation of residue-residue contact predictions in CASP9. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79 Suppl 10, 119-25	4.2	41
126	Evaluation of disorder predictions in CASP9. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79 Suppl 10, 107-18	4.2	97
125	Evaluation of model quality predictions in CASP9. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79 Suppl 10, 91-106	4.2	72

124	Critical assessment of methods of protein structure prediction (CASP)--round IX. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79 Suppl 10, 1-5	4.2	175
123	Novel cinnamyl hydroxyamides and 2-aminoanilides as histone deacetylase inhibitors: apoptotic induction and cytodifferentiation activity. <i>ChemMedChem</i> , <b>2011</b> , 6, 698-712	3.7	13
122	MAISTAS: a tool for automatic structural evaluation of alternative splicing products. <i>Bioinformatics</i> , <b>2011</b> , 27, 1625-9	7.2	11
121	Phospho3D 2.0: an enhanced database of three-dimensional structures of phosphorylation sites. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D268-71	20.1	39
120	On the mechanism of chloroquine resistance in <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , <b>2010</b> , 5, e14064	3.7	53
119	PICMI: mapping point mutations on genomes. <i>Bioinformatics</i> , <b>2010</b> , 26, 2904-5	7.2	3
118	Stereotyped patterns of B-cell receptor in splenic marginal zone lymphoma. <i>Haematologica</i> , <b>2010</b> , 95, 1792-6	6.6	74
117	An automatic method for identifying surface proteins in bacteria: SLEP. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 39	3.6	16
116	Affinity purification of a difficult-sequence protein. <i>International Journal of Peptide and Protein Research</i> , <b>2009</b> , 42, 93-96		12
115	Evaluation of CASP8 model quality predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 77 Suppl 9, 157-66	4.2	65
114	Evaluation of template-based models in CASP8 with standard measures. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 77 Suppl 9, 18-28	4.2	105
113	Critical assessment of methods of protein structure prediction - Round VIII. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 77 Suppl 9, 1-4	4.2	154
112	Site-directed enzymatic PEGylation of the human granulocyte colony-stimulating factor. <i>FEBS Journal</i> , <b>2009</b> , 276, 6741-50	5.7	38
111	Protein function annotation by homology-based inference. <i>Genome Biology</i> , <b>2009</b> , 10, 207	18.3	144
110	The MoVIN server for the analysis of protein interaction networks. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 2, S11	3.6	5
109	FunClust: a web server for the identification of structural motifs in a set of non-homologous protein structures. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 2, S2	3.6	30
108	Modelling and molecular dynamics of the interaction between the E3 ubiquitin ligase Itch and the E2 UbcH7. <i>Biochemical Pharmacology</i> , <b>2008</b> , 76, 1620-7	6	13
107	Inhibition of endothelial cell migration and angiogenesis by a vascular endothelial growth factor receptor-1 derived peptide. <i>European Journal of Cancer</i> , <b>2008</b> , 44, 1914-21	7.5	19

106	Dissecting the structural determinants of the interaction between the human cytomegalovirus UL18 protein and the CD85j immune receptor. <i>Journal of Immunology</i> , <b>2008</b> , 180, 957-68	5.3	8
105	PIGS: automatic prediction of antibody structures. <i>Bioinformatics</i> , <b>2008</b> , 24, 1953-4	7.2	150
104	A proangiogenic peptide derived from vascular endothelial growth factor receptor-1 acts through alpha5beta1 integrin. <i>Blood</i> , <b>2008</b> , 111, 3479-88	2.2	25
103	Advances and pitfalls in protein structure prediction. <i>Current Protein and Peptide Science</i> , <b>2008</b> , 9, 567-77	2.8	10
102	Identification and functional characterization of the bile acid transport proteins in non-mammalian ileum and mammalian liver. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 70, 462-72	4.2	24
101	The evaluation of protein structure prediction results. <i>Molecular Biotechnology</i> , <b>2008</b> , 39, 1-8	3	11
100	The assessment of methods for protein structure prediction. <i>Methods in Molecular Biology</i> , <b>2008</b> , 413, 43-57	1.4	10
99	Yeast as a model of human mitochondrial tRNA base substitutions: investigation of the molecular basis of respiratory defects. <i>Rna</i> , <b>2008</b> , 14, 275-83	5.8	32
98	The mepsMAP server. Mapping epitopes on protein surface: mining annotated proteins. <i>IEEE Transactions on Nanobioscience</i> , <b>2007</b> , 6, 155-61	3.4	
97	Assessment of predictions in the model quality assessment category. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69 Suppl 8, 175-83	4.2	95
96	A model of the complex between the PfEMP1 malaria protein and the human ICAM-1 receptor. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69, 215-22	4.2	10
95	Critical assessment of methods of protein structure prediction-Round VII. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69 Suppl 8, 3-9	4.2	189
94	The MEPS server for identifying protein conformational epitopes. <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 1, S6	3.6	18
93	Analysis of hepatitis C virus hypervariable region 1 sequence from cryoglobulinemic patients and associated controls. <i>Journal of Virology</i> , <b>2007</b> , 81, 4564-71	6.6	15
92	Mg2+ binding and archaeosine modification stabilize the G15 C48 Levitt base pair in tRNAs. <i>Rna</i> , <b>2007</b> , 13, 1427-36	5.8	70
91	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 5495-500	11.5	177
90	Small molecule inhibitors of histone arginine methyltransferases: homology modeling, molecular docking, binding mode analysis, and biological evaluations. <i>Journal of Medicinal Chemistry</i> , <b>2007</b> , 50, 1241-53	8.3	88
89	Automatic procedure for using models of proteins in molecular replacement. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 66, 689-96	4.2	18

88	An analysis of the Sargasso Sea resource and the consequences for database composition. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 213	3.6	15
87	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. <i>Electrophoresis</i> , <b>2006</b> , 27, 1182-98	3.6	50
86	Identification of a novel putative mitogen-activated kinase cascade on human chromosome 21 by computational approaches. <i>Bioinformatics</i> , <b>2006</b> , 22, 775-8	7.2	12
85	Accurate energies of hydrogen bonded nucleic acid base pairs and triplets in tRNA tertiary interactions. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 865-79	20.1	71
84	The PMDB Protein Model Database. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D306-9	20.1	229
83	A structure-guided approach to an orthogonal estrogen-receptor-based gene switch activated by ligands suitable for in vivo studies. <i>Journal of Medicinal Chemistry</i> , <b>2006</b> , 49, 5404-7	8.3	17
82	The role of molecular modelling in biomedical research. <i>FEBS Letters</i> , <b>2006</b> , 580, 2928-34	3.8	19
81	Revisiting the prediction of protein function at CASP6. <i>FEBS Journal</i> , <b>2006</b> , 273, 2977-83	5.7	13
80	The betaI/betaIII-tubulin isoforms and their complexes with antimetabolic agents. Docking and molecular dynamics studies. <i>FEBS Journal</i> , <b>2006</b> , 273, 3301-10	5.7	54
79	Relationship between multiple sequence alignments and quality of protein comparative models. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 58, 151-7	4.2	39
78	Critical assessment of methods of protein structure prediction (CASP)--round 6. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61 Suppl 7, 3-7	4.2	148
77	The prediction of protein function at CASP6. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61 Suppl 7, 201-13	4.2	30
76	The Relationship Between Protein Sequence, Structure and Function <b>2005</b> , 15-29		1
75	Aminoacylation and conformational properties of yeast mitochondrial tRNA mutants with respiratory deficiency. <i>Rna</i> , <b>2005</b> , 11, 914-27	5.8	14
74	Evaluating the usefulness of protein structure models for molecular replacement. <i>Bioinformatics</i> , <b>2005</b> , 21 Suppl 2, ii72-6	7.2	49
73	A brighter future for protein design. <i>Angewandte Chemie - International Edition</i> , <b>2004</b> , 43, 3222-3	16.4	3
72	Eine bessere Zukunft für Proteindesigner. <i>Angewandte Chemie</i> , <b>2004</b> , 116, 3284-3285	3.6	
71	Integral and differential form of the protein folding problem. <i>Physics of Life Reviews</i> , <b>2004</b> , 1, 103-127	2.1	3



70	Remarkably similar antigen receptors among a subset of patients with chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , <b>2004</b> , 113, 1008-16	15.9	162
69	Exploring the cytochrome c folding mechanism: cytochrome c552 from thermus thermophilus folds through an on-pathway intermediate. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 41136-40	5.4	35
68	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , <b>2003</b> , 19, 717-26	7.2	58
67	Evolution of bacterial and archaeal multicomponent monooxygenases. <i>Journal of Molecular Evolution</i> , <b>2003</b> , 56, 435-45	3.1	107
66	Comparative modelling techniques: where are we?. <i>Comparative and Functional Genomics</i> , <b>2003</b> , 4, 402-5		4
65	Exploiting evolutionary relationships for predicting protein structures. <i>Biotechnology and Bioengineering</i> , <b>2003</b> , 84, 756-62	4.9	9
64	Assessment of homology-based predictions in CASP5. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53 Suppl 6, 352-68	4.2	155
63	Engineering stable cytoplasmic intrabodies with designed specificity. <i>Journal of Molecular Biology</i> , <b>2003</b> , 330, 323-32	6.5	36
62	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. <i>Journal of Virology</i> , <b>2003</b> , 77, 1856-67	6.6	140
61	The significance of performance ranking in CASP--response to Marti-Renom et al. <i>Structure</i> , <b>2002</b> , 10, 291-2; discussion 292-3	5.2	5
60	A model for recognition of polychlorinated dibenzo-p-dioxins by the aryl hydrocarbon receptor. <i>FEBS Journal</i> , <b>2002</b> , 269, 13-8		45
59	Classification of proteins based on the properties of the ligand-binding site: the case of adenine-binding proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 47, 106-15	4.2	32
58	Hepatitis C virus proteins as targets for drug development: the role of bioinformatics and modelling. <i>Current Drug Targets</i> , <b>2002</b> , 3, 281-96	3	9
57	Analysis and assessment of comparative modeling predictions in CASP4. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2001</b> , Suppl 5, 22-38	4.2	92
56	Conformational analysis of putative regulatory subunit D of the toluene/o-xylene-monooxygenase complex from <i>Pseudomonas stutzeri</i> OX1. <i>Protein Science</i> , <b>2001</b> , 10, 482-90	6.3	12
55	Genome sequences and great expectations. <i>Genome Biology</i> , <b>2001</b> , 2, INTERACTIONS0001	18.3	34
54	Structural conservation in single-domain proteins: implications for homology modeling. <i>Journal of Structural Biology</i> , <b>2001</b> , 134, 246-56	3.4	12
53	Mimotopes of the hyper variable region 1 of the hepatitis C virus induce cross-reactive antibodies directed against discontinuous epitopes. <i>Molecular Immunology</i> , <b>2001</b> , 38, 485-92	4.3	27

52	A model for the hepatitis C virus envelope glycoprotein E2. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2000</b> , 40, 355-66	4.2	177
51	DANTE: a workbench for sequence analysis. <i>Trends in Biochemical Sciences</i> , <b>2000</b> , 25, 402-3	10.3	3
50	In vivo selection of protease cleavage sites by using chimeric Sindbis virus libraries. <i>Journal of Virology</i> , <b>2000</b> , 74, 10563-70	6.6	14
49	Analysis of a cDNA sequence encoding the immunoglobulin heavy chain of the Antarctic teleost <i>Trematomus bernacchii</i> . <i>Fish and Shellfish Immunology</i> , <b>2000</b> , 10, 343-57	4.3	33
48	Bacteriophage lambda display of complex cDNA libraries: a new approach to functional genomics. <i>Journal of Molecular Biology</i> , <b>2000</b> , 296, 497-508	6.5	71
47	Antibody modeling: implications for engineering and design. <i>Methods</i> , <b>2000</b> , 20, 267-79	4.6	84
46	Selection of functional variants of the NS3-NS4A protease of hepatitis C virus by using chimeric sindbis viruses. <i>Journal of Virology</i> , <b>1999</b> , 73, 561-75	6.6	14
45	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. <i>EMBO Journal</i> , <b>1998</b> , 17, 3521-33	13	121
44	Rational design and functional expression of a constitutively active single-chain NS4A-NS3 proteinase. <i>Folding &amp; Design</i> , <b>1998</b> , 3, 433-41		14
43	GLASS: a tool to visualize protein structure prediction data in three dimensions and evaluate their consistency. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1998</b> , 30, 339-51	4.2	1
42	Conformations of the third hypervariable region in the VH domain of immunoglobulins. <i>Journal of Molecular Biology</i> , <b>1998</b> , 275, 269-94	6.5	313
41	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. <i>Journal of Molecular Biology</i> , <b>1998</b> , 284, 1717-25	6.5	26
40	Homology modeling with low sequence identity. <i>Methods</i> , <b>1998</b> , 14, 293-300	4.6	62
39	Protein structure prediction and design. <i>Biotechnology Annual Review</i> , <b>1998</b> , 4, 177-214		5
38	Substrate specificity of the hepatitis C virus serine protease NS3. <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 9204-9	5.4	97
37	Surface topology of Minibody by selective chemical modifications and mass spectrometry. <i>Protein Science</i> , <b>1997</b> , 6, 1901-9	6.3	48
36	Antibody structure, prediction and redesign. <i>Biophysical Chemistry</i> , <b>1997</b> , 68, 9-16	3.5	52
35	A zinc binding site in viral serine proteinases. <i>Biochemistry</i> , <b>1996</b> , 35, 13282-7	3.2	90

34	Protein structure prediction:playing the fold. <i>Trends in Biochemical Sciences</i> , <b>1996</b> , 21, 279-281	10.3	
33	Redesigning the substrate specificity of the hepatitis C virus NS3 protease. <i>Folding &amp; Design</i> , <b>1996</b> , 1, 35-42		25
32	Probing the tertiary structure of proteins by limited proteolysis and mass spectrometry: the case of Minibody. <i>Protein Science</i> , <b>1996</b> , 5, 802-13	6.3	60
31	The Architecture of Loops in Proteins <b>1996</b> , 239-259		1
30	Identification of biologically active peptides using random libraries displayed on phage. <i>Current Opinion in Biotechnology</i> , <b>1995</b> , 6, 73-80	11.4	102
29	Replacing the glutamate ligand in the structural zinc site of <i>Sulfolobus solfataricus</i> alcohol dehydrogenase with a cysteine decreases thermostability. <i>Protein Engineering, Design and Selection</i> , <b>1995</b> , 8, 31-7	1.9	8
28	Identifying a putative common binding site shared by substance P receptor and an anti-substance P monoclonal antibody. <i>Protein Engineering, Design and Selection</i> , <b>1995</b> , 8, 403-8	1.9	8
27	Modelling antibody-antigen interactions: ferritin as a case study. <i>Molecular Immunology</i> , <b>1995</b> , 32, 1001-103		14
26	Molecular model of the specificity pocket of the hepatitis C virus protease: implications for substrate recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1994</b> , 91, 888-92	11.5	95
25	Variability within the <i>Candida rugosa</i> lipases family. <i>Protein Engineering, Design and Selection</i> , <b>1994</b> , 7, 531-5	1.9	89
24	Cloning, characterization, and modeling of a monoclonal anti-human transferrin antibody that competes with the transferrin receptor. <i>Protein Science</i> , <b>1994</b> , 3, 1476-84	6.3	8
23	The making of the minibody: an engineered beta-protein for the display of conformationally constrained peptides. <i>Journal of Molecular Recognition</i> , <b>1994</b> , 7, 9-24	2.6	27
22	PUZZLE: a new method for automated protein docking based on surface shape complementarity. <i>Journal of Molecular Biology</i> , <b>1994</b> , 235, 1021-31	6.5	87
21	High level expression and rational mutagenesis of a designed protein, the minibody. From an insoluble to a soluble molecule. <i>Journal of Molecular Biology</i> , <b>1994</b> , 236, 649-59	6.5	53
20	A database system for handling phage library-derived sequences. <i>Gene</i> , <b>1993</b> , 128, 143-4	3.8	2
19	Cloning and analysis of <i>Candida cylindracea</i> lipase sequences. <i>Gene</i> , <b>1993</b> , 124, 45-55	3.8	118
18	Mimicking of discontinuous epitopes by phage-displayed peptides, I. Epitope mapping of human H ferritin using a phage library of constrained peptides. <i>Gene</i> , <b>1993</b> , 128, 51-7	3.8	231
17	Saturation mutagenesis of the human interleukin 6 receptor-binding site: implications for its three-dimensional structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1993</b> , 90, 4067-71	11.5	71

16	A designed metal-binding protein with a novel fold. <i>Nature</i> , <b>1993</b> , 362, 367-9	50.4	190
15	In vitroselection of peptides from molecular repertoires. <i>Rendiconti Lincei</i> , <b>1993</b> , 4, 359-366	1.7	
14	Protein design on computers. Five new proteins: Shpilka, Grendel, Fingerclasp, Leather, and Aida. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1992</b> , 12, 105-10	4.2	25
13	Common features of the conformations of antigen-binding loops in immunoglobulins and application to modeling loop conformations. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1992</b> , 13, 231-45	4.2	61
12	A method to evaluate the relative weights of structural and functional constraints on a genome. <i>Nuovo Cimento Della Societa Italiana Di Fisica D - Condensed Matter, Atomic, Molecular and Chemical Physics, Biophysics</i> , <b>1991</b> , 13, 553-563		
11	Members of the zinc finger protein gene family sharing a conserved N-terminal module. <i>Nucleic Acids Research</i> , <b>1991</b> , 19, 5661-7	20.1	74
10	VARIANT: a store and retrieval system for human haemoglobin variants. <i>Computer Methods and Programs in Biomedicine</i> , <b>1990</b> , 31, 113-4	6.9	1
9	Structural definition by antibody engineering of an idiotypic determinant. <i>Protein Engineering, Design and Selection</i> , <b>1990</b> , 3, 531-9	1.9	21
8	Framework residue 71 is a major determinant of the position and conformation of the second hypervariable region in the VH domains of immunoglobulins. <i>Journal of Molecular Biology</i> , <b>1990</b> , 215, 175-82	6.5	218
7	Structural determinants of the conformations of medium-sized loops in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1989</b> , 6, 382-94	4.2	75
6	Conformations of immunoglobulin hypervariable regions. <i>Nature</i> , <b>1989</b> , 342, 877-83	50.4	1091
5	The Computational Analysis of Protein Structures: Sources, Methods, Systems and Results. <i>Journal of Research of the National Bureau of Standards (United States)</i> , <b>1989</b> , 94, 85-92		3
4	A transportable interactive package for the statistical analysis and handling of sequence data. <i>Computers in Biology and Medicine</i> , <b>1988</b> , 18, 113-22	7	1
3	Information value and information content in the evolutionary strategy of the genetic code. <i>Nuovo Cimento Della Societa Italiana Di Fisica D - Condensed Matter, Atomic, Molecular and Chemical Physics, Biophysics</i> , <b>1988</b> , 10, 293-301		
2	Probability of coding of a DNA sequence: an algorithm to predict translated reading frames from their thermodynamic characteristics. <i>Nucleic Acids Research</i> , <b>1986</b> , 14, 127-35	20.1	20
1	Determination of the autocorrelation orders of proteins. <i>FEBS Journal</i> , <b>1985</b> , 149, 375-9		5