Anna Tramontano

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195	12,303	57	107
papers	citations	h-index	g-index
214	13,473	7.2	6.15
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
195	A long noncoding RNA controls muscle differentiation by functioning as a competing endogenous RNA. *Cell*, **2011**, 147, 358-69	56.2	1993
194	Conformations of immunoglobulin hypervariable regions. *Nature*, **1989**, 342, 877-83	50.4	1091
193	Conformations of the third hypervariable region in the VH domain of immunoglobulins. *Journal of Molecular Biology*, **1998**, 275, 269-94	6.5	313
192	Critical assessment of methods of protein structure prediction (CASP)--round x. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82 Suppl 2, 1-6	4.2	291
191	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, 51-7	3.8	231
190	The PMDB Protein Model Database. *Nucleic Acids Research*, **2006**, 34, D306-9	20.1	229
189	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, 175-82	6.5	218
188	Critical assessment of methods of protein structure prediction (CASP)-Round XII. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 7-15	4.2	209
187	A designed metal-binding protein with a novel fold. *Nature*, **1993**, 362, 367-9	50.4	190
186	Critical assessment of methods of protein structure prediction-Round VII. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69 Suppl 8, 3-9	4.2	189
185	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, 5495-500	11.5	177
184	A model for the hepatitis C virus envelope glycoprotein E2. *Proteins: Structure, Function and Bioinformatics*, **2000**, 40, 355-66	4.2	177
183	Critical assessment of methods of protein structure prediction (CASP)--round IX. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79 Suppl 10, 1-5	4.2	175
182	Remarkably similar antigen receptors among a subset of patients with chronic lymphocytic leukemia. *Journal of Clinical Investigation*, **2004**, 113, 1008-16	15.9	162
181	Critical assessment of methods of protein structure prediction: Progress and new directions in round XI. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 4-14	4.2	156
180	Assessment of homology-based predictions in CASP5. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53 Suppl 6, 352-68	4.2	155
179	Critical assessment of methods of protein structure prediction - Round VIII. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 1-4	4.2	154

178	PIGS: automatic prediction of antibody structures. *Bioinformatics*, **2008**, 24, 1953-4	7.2	150
177	Critical assessment of methods of protein structure prediction (CASP)--round 6. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61 Suppl 7, 3-7	4.2	148
176	Protein function annotation by homology-based inference. *Genome Biology*, **2009**, 10, 207	18.3	144
175	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, 1856-67	6.6	140
174	Assessment of protein disorder region predictions in CASP10. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82 Suppl 2, 127-37	4.2	123
173	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, 3521-33	13	121
172	Cloning and analysis of Candida cylindracea lipase sequences. *Gene*, **1993**, 124, 45-55	3.8	118
171	Evolution of bacterial and archaeal multicomponent monooxygenases. *Journal of Molecular Evolution*, **2003**, 56, 435-45	3.1	107
170	Evaluation of template-based models in CASP8 with standard measures. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 18-28	4.2	105
169	Identification of biologically active peptides using random libraries displayed on phage. *Current Opinion in Biotechnology*, **1995**, 6, 73-80	11.4	102
168	Evaluation of disorder predictions in CASP9. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79 Suppl 10, 107-18	4.2	97
167	Substrate specificity of the hepatitis C virus serine protease NS3. *Journal of Biological Chemistry*, **1997**, 272, 9204-9	5.4	97
166	Assessment of the assessment: evaluation of the model quality estimates in CASP10. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82 Suppl 2, 112-26	4.2	96
165	Assessment of predictions in the model quality assessment category. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69 Suppl 8, 175-83	4.2	95
164	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, 888-92	11.5	95
163	Analysis and assessment of comparative modeling predictions in CASP4. *Proteins: Structure, Function and Bioinformatics*, **2001**, Suppl 5, 22-38	4.2	92
162	A zinc binding site in viral serine proteinases. *Biochemistry*, **1996**, 35, 13282-7	3.2	90
161	Variability within the Candida rugosa lipases family. *Protein Engineering, Design and Selection*, **1994**, 7, 531-5	1.9	89

160	Small molecule inhibitors of histone arginine methyltransferases: homology modeling, molecular docking, binding mode analysis, and biological evaluations. *Journal of Medicinal Chemistry*, **2007**, 50, 1241-53	8.3	88
159	PUZZLE: a new method for automated protein docking based on surface shape complementarity. *Journal of Molecular Biology*, **1994**, 235, 1021-31	6.5	87
158	Antibody modeling: implications for engineering and design. *Methods*, **2000**, 20, 267-79	4.6	84
157	Novel long noncoding RNAs (lncRNAs) in myogenesis: a miR-31 overlapping lncRNA transcript controls myoblast differentiation. *Molecular and Cellular Biology*, **2015**, 35, 728-36	4.8	78
156	Cancer-selective targeting of the NF-B survival pathway with GADD45/MKK7 inhibitors. *Cancer Cell*, **2014**, 26, 495-508	24.3	77
155	Structural determinants of the conformations of medium-sized loops in proteins. *Proteins: Structure, Function and Bioinformatics*, **1989**, 6, 382-94	4.2	75
154	Stereotyped patterns of B-cell receptor in splenic marginal zone lymphoma. *Haematologica*, **2010**, 95, 1792-6	6.6	74
153	Members of the zinc finger protein gene family sharing a conserved N-terminal module. *Nucleic Acids Research*, **1991**, 19, 5661-7	20.1	74
152	Endocytosis of synaptic ADAM10 in neuronal plasticity and AlzheimerSs disease. *Journal of Clinical Investigation*, **2013**, 123, 2523-38	15.9	74
151	Evaluation of model quality predictions in CASP9. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79 Suppl 10, 91-106	4.2	72
150	Accurate energies of hydrogen bonded nucleic acid base pairs and triplets in tRNA tertiary interactions. *Nucleic Acids Research*, **2006**, 34, 865-79	20.1	71
149	Bacteriophage lambda display of complex cDNA libraries: a new approach to functional genomics. *Journal of Molecular Biology*, **2000**, 296, 497-508	6.5	71
148	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, 4067-71	11.5	71
147	Mg2+ binding and archaeosine modification stabilize the G15 C48 Levitt base pair in tRNAs. *Rna*, **2007**, 13, 1427-36	5.8	70
146	New encouraging developments in contact prediction: Assessment of the CASP11 results. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 131-44	4.2	66
145	Prediction of site-specific interactions in antibody-antigen complexes: the proABC method and server. *Bioinformatics*, **2013**, 29, 2285-91	7.2	66
144	Evaluation of residue-residue contact prediction in CASP10. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82 Suppl 2, 138-53	4.2	65
143	Evaluation of CASP8 model quality predictions. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 157-66	4.2	65

142	Homology modeling with low sequence identity. *Methods*, **1998**, 14, 293-300	4.6	62
141	Common features of the conformations of antigen-binding loops in immunoglobulins and application to modeling loop conformations. *Proteins: Structure, Function and Bioinformatics*, **1992**, 13, 231-45	4.2	61
140	Probing the tertiary structure of proteins by limited proteolysis and mass spectrometry: the case of Minibody. *Protein Science*, **1996**, 5, 802-13	6.3	60
139	Evaluation of annotation strategies using an entire genome sequence. *Bioinformatics*, **2003**, 19, 717-26	7.2	58
138	The betaI/betaIII-tubulin isoforms and their complexes with antimitotic agents. Docking and molecular dynamics studies. *FEBS Journal*, **2006**, 273, 3301-10	5.7	54
137	On the mechanism of chloroquine resistance in Plasmodium falciparum. *PLoS ONE*, **2010**, 5, e14064	3.7	53
136	High level expression and rational mutagenesis of a designed protein, the minibody. From an insoluble to a soluble molecule. *Journal of Molecular Biology*, **1994**, 236, 649-59	6.5	53
135	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in CASP11. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 349-69	4.2	53
134	The association of heavy and light chain variable domains in antibodies: implications for antigen specificity. *FEBS Journal*, **2011**, 278, 2858-66	5.7	52
133	Antibody structure, prediction and redesign. *Biophysical Chemistry*, **1997**, 68, 9-16	3.5	52
132	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, 1182-98	3.6	50
131	Evaluation of the template-based modeling in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 321-334	4.2	50
130	Evaluating the usefulness of protein structure models for molecular replacement. *Bioinformatics*, **2005**, 21 Suppl 2, ii72-6	7.2	49
129	Surface topology of Minibody by selective chemical modifications and mass spectrometry. *Protein Science*, **1997**, 6, 1901-9	6.3	48
128	Antibody modeling using the prediction of immunoglobulin structure (PIGS) web server [corrected]. *Nature Protocols*, **2014**, 9, 2771-83	18.8	46
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125	Assessment of model accuracy estimations in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 345-360	4.2	41

124	Evaluation of residue-residue contact predictions in CASP9. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79 Suppl 10, 119-25	4.2	41
123	PIGSPro: prediction of immunoGlobulin structures v2. *Nucleic Acids Research*, **2017**, 45, W17-W23	20.1	39
122	Phospho3D 2.0: an enhanced database of three-dimensional structures of phosphorylation sites. *Nucleic Acids Research*, **2011**, 39, D268-71	20.1	39
121	Relationship between multiple sequence alignments and quality of protein comparative models. *Proteins: Structure, Function and Bioinformatics*, **2005**, 58, 151-7	4.2	39
120	Genome-wide identification of direct HBx genomic targets. *BMC Genomics*, **2017**, 18, 184	4.5	38
119	Site-directed enzymatic PEGylation of the human granulocyte colony-stimulating factor. *FEBS Journal*, **2009**, 276, 6741-50	5.7	38
118	A Long Noncoding RNA Controls Muscle Differentiation by Functioning as a Competing Endogenous RNA. *Cell*, **2011**, 147, 947	56.2	37
117	All-Atom Molecular Dynamics Simulation of Protein Translocation through an □Hemolysin Nanopore. *Journal of Physical Chemistry Letters*, **2015**, 6, 2963-8	6.4	36
116	Engineering stable cytoplasmic intrabodies with designed specificity. *Journal of Molecular Biology*, **2003**, 330, 323-32	6.5	36
115	PepComposer: computational design of peptides binding to a given protein surface. *Nucleic Acids Research*, **2016**, 44, W522-8	20.1	36
114	A database of immunoglobulins with integrated tools: DIGIT. *Nucleic Acids Research*, **2012**, 40, D1230-4	20.1	35
113	Exploring the cytochrome c folding mechanism: cytochrome c552 from thermus thermophilus folds through an on-pathway intermediate. *Journal of Biological Chemistry*, **2003**, 278, 41136-40	5.4	35
112	Genome sequences and great expectations. *Genome Biology*, **2001**, 2, INTERACTIONS0001	18.3	34
111	Massive screening of copy number population-scale variation in Bos taurus genome. *BMC Genomics*, **2013**, 14, 124	4.5	33
110	FIDEA: a server for the functional interpretation of differential expression analysis. *Nucleic Acids Research*, **2013**, 41, W84-8	20.1	33
109	Analysis of a cDNA sequence encoding the immunoglobulin heavy chain of the Antarctic teleost Trematomus bernacchii. *Fish and Shellfish Immunology*, **2000**, 10, 343-57	4.3	33
108	Structural repertoire of immunoglobulin □ight chains. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 1513-24	4.2	32
107	Yeast as a model of human mitochondrial tRNA base substitutions: investigation of the molecular basis of respiratory defects. *Rna*, **2008**, 14, 275-83	5.8	32

106	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, 106-15	4.2	32
105	Multistep current signal in protein translocation through graphene nanopores. *Journal of Physical Chemistry B*, **2015**, 119, 5815-23	3.4	30
104	FunClust: a web server for the identification of structural motifs in a set of non-homologous protein structures. *BMC Bioinformatics*, **2008**, 9 Suppl 2, S2	3.6	30
103	The prediction of protein function at CASP6. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61 Suppl 7, 201-13	4.2	30
102	Mimotopes of the hyper variable region 1 of the hepatitis C virus induce cross-reactive antibodies directed against discontinuous epitopes. *Molecular Immunology*, **2001**, 38, 485-92	4.3	27
101	The making of the minibody: an engineered beta-protein for the display of conformationally constrained peptides. *Journal of Molecular Recognition*, **1994**, 7, 9-24	2.6	27
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. *Journal of Molecular Biology*, **1998**, 284, 1717-25	6.5	26
99	Improving the accuracy of the structure prediction of the third hypervariable loop of the heavy chains of antibodies. *Bioinformatics*, **2014**, 30, 2733-40	7.2	25
98	A proangiogenic peptide derived from vascular endothelial growth factor receptor-1 acts through alpha5beta1 integrin. *Blood*, **2008**, 111, 3479-88	2.2	25
97	Redesigning the substrate specificity of the hepatitis C virus NS3 protease. *Folding & Design*, **1996**, 1, 35-42		25
96	Protein design on computers. Five new proteins: Shpilka, Grendel, Fingerclasp, Leather, and Aida. *Proteins: Structure, Function and Bioinformatics*, **1992**, 12, 105-10	4.2	25
95	Tabhu: tools for antibody humanization. *Bioinformatics*, **2015**, 31, 434-5	7.2	24
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, 576-81	3.4	24
93	Identification and functional characterization of the bile acid transport proteins in non-mammalian ileum and mammalian liver. *Proteins: Structure, Function and Bioinformatics*, **2008**, 70, 462-72	4.2	24
92	3USS: a web server for detecting alternative 3SUTRs from RNA-seq experiments. *Bioinformatics*, **2015**, 31, 1845-7	7.2	23
91	Coding potential of the products of alternative splicing in human. *Genome Biology*, **2011**, 12, R9	18.3	23
90	Superposition-free comparison and clustering of antibody binding sites: implications for the prediction of the nature of their antigen. *Scientific Reports*, **2017**, 7, 45053	4.9	22
89	Structural definition by antibody engineering of an idiotypic determinant. *Protein Engineering, Design and Selection*, **1990**, 3, 531-9	1.9	21

88	Probability of coding of a DNA sequence: an algorithm to predict translated reading frames from their thermodynamic characteristics. *Nucleic Acids Research*, **1986**, 14, 127-35	20.1	20
87	Inhibition of endothelial cell migration and angiogenesis by a vascular endothelial growth factor receptor-1 derived peptide. *European Journal of Cancer*, **2008**, 44, 1914-21	7.5	19
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85	Igs expressed by chronic lymphocytic leukemia B cells show limited binding-site structure variability. *Journal of Immunology*, **2013**, 190, 5771-8	5.3	18
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83	Automatic procedure for using models of proteins in molecular replacement. *Proteins: Structure, Function and Bioinformatics*, **2007**, 66, 689-96	4.2	18
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81	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, 3401-10	6.4	16
80	An automatic method for identifying surface proteins in bacteria: SLEP. *BMC Bioinformatics*, **2010**, 11, 39	3.6	16
79	LoopIng: a template-based tool for predicting the structure of protein loops. *Bioinformatics*, **2015**, 31, 3767-72	7.2	15
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77	An analysis of the Sargasso Sea resource and the consequences for database composition. *BMC Bioinformatics*, **2006**, 7, 213	3.6	15
76	Analysis of hepatitis C virus hypervariable region 1 sequence from cryoglobulinemic patients and associated controls. *Journal of Virology*, **2007**, 81, 4564-71	6.6	15
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74	Rational design and functional expression of a constitutively active single-chain NS4A-NS3 proteinase. *Folding & Design*, **1998**, 3, 433-41		14
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70	Selection of functional variants of the NS3-NS4A protease of hepatitis C virus by using chimeric sindbis viruses. *Journal of Virology*, **1999**, 73, 561-75	6.6	14
69	Prediction of the permeability of neutral drugs inferred from their solvation properties. *Bioinformatics*, **2016**, 32, 1163-9	7.2	13
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63	Revisiting the prediction of protein function at CASP6. *FEBS Journal*, **2006**, 273, 2977-83	5.7	13
62	Cover Image, Volume 84, Issue S1. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84, C4-C4	4.2	12
61	Affinity purification of a difficult-sequence protein. *International Journal of Peptide and Protein Research*, **2009**, 42, 93-96		12
60	Identification of a novel putative mitogen-activated kinase cascade on human chromosome 21 by computational approaches. *Bioinformatics*, **2006**, 22, 775-8	7.2	12
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57	A structural view of microRNA-target recognition. *Nucleic Acids Research*, **2016**, 44, e82	20.1	11
56	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, 564-74	4.2	11
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53	Simulation of urea-induced protein unfolding: a lesson from bovine βlactoglobulin. *Journal of Molecular Graphics and Modelling*, **2011**, 30, 24-30	2.8	10

52	Improving your target-template alignment with MODalign. *Bioinformatics*, **2012**, 28, 1038-9	7.2	10
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44	Dissecting the structural determinants of the interaction between the human cytomegalovirus UL18 protein and the CD85j immune receptor. *Journal of Immunology*, **2008**, 180, 957-68	5.3	8
43	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, 31-7	1.9	8
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31	The computational prediction of protein assemblies. *Current Opinion in Structural Biology*, **2017**, 46, 170-175	8.1	4
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25	DANTE: a workbench for sequence analysis. *Trends in Biochemical Sciences*, **2000**, 25, 402-3	10.3	3
24	The Computational Analysis of Protein Structures: Sources, Methods, Systems and Results. *Journal of Research of the National Bureau of Standards (United States)*, **1989**, 94, 85-92		3
23	Cover Image, Volume 84, Issue S1. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84, C1-C1	4.2	2
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21	A resource for benchmarking the usefulness of protein structure models. *BMC Bioinformatics*, **2012**, 13, 188	3.6	2
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