

Andras Fiser

List of Publications by Year in descending order

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115
papers

13,063
citations

70961

41
h-index

23472

111
g-index

176
all docs

176
docs citations

176
times ranked

18970
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Protein Structure Modeling of Genes and Genomes. Annual Review of Biophysics and Biomolecular Structure, 2000, 29, 291-325.	18.3	2,811
2	Modeling of loops in protein structures. Protein Science, 2000, 9, 1753-1773.	3.1	1,895
3	Modeller: Generation and Refinement of Homology-Based Protein Structure Models. Methods in Enzymology, 2003, 374, 461-491.	0.4	1,469
4	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
5	ModLoop: automated modeling of loops in protein structures. Bioinformatics, 2003, 19, 2500-2501.	1.8	707
6	VISTA, a novel mouse Ig superfamily ligand that negatively regulates T cell responses. Journal of Experimental Medicine, 2011, 208, 577-592.	4.2	539
7	Tools for comparative protein structure modeling and analysis. Nucleic Acids Research, 2003, 31, 3375-3380.	6.5	406
8	Insights into the mechanism of microtubule stabilization by Taxol. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10166-10173.	3.3	283
9	Template-Based Protein Structure Modeling. Methods in Molecular Biology, 2010, 673, 73-94.	0.4	165
10	Structural genomics of protein phosphatases. Journal of Structural and Functional Genomics, 2007, 8, 121-140.	1.2	148
11	Bimoclomol, a heat shock protein co-inducer, acts by the prolonged activation of heat shock factor-1. Biochemical and Biophysical Research Communications, 2003, 307, 689-695.	1.0	145
12	Stabilization centers in proteins: Identification, characterization and predictions. Journal of Molecular Biology, 1997, 272, 597-612.	2.0	144
13	ArchPRED: a template based loop structure prediction server. Nucleic Acids Research, 2006, 34, W173-W176.	6.5	142
14	Expression, Clinical Significance, and Receptor Identification of the Newest B7 Family Member HHLA2 Protein. Clinical Cancer Research, 2015, 21, 2359-2366.	3.2	125
15	PSI-2: Structural Genomics to Cover Protein Domain Family Space. Structure, 2009, 17, 869-881.	1.6	120
16	M4T: a comparative protein structure modeling server. Nucleic Acids Research, 2007, 35, W363-W368.	6.5	118
17	The Immunoglobulin Heavy Chain Constant Region Affects Kinetic and Thermodynamic Parameters of Antibody Variable Region Interactions with Antigen. Journal of Biological Chemistry, 2007, 282, 13917-13927.	1.6	116
18	Evolution and Physics in Comparative Protein Structure Modeling. Accounts of Chemical Research, 2002, 35, 413-421.	7.6	103

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19	Reliability of Assessment of Protein Structure Prediction Methods. <i>Structure</i> , 2002, 10, 435-440.	1.6	95
20	Chaos game representation of protein structures. <i>Journal of Molecular Graphics</i> , 1994, 12, 302-304.	1.7	81
21	Trends in structural coverage of the protein universe and the impact of the Protein Structure Initiative. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3733-3738.	3.3	79
22	New statistical potential for quality assessment of protein models and a survey of energy functions. <i>BMC Bioinformatics</i> , 2010, 11, 128.	1.2	78
23	Modeling mutations in protein structures. <i>Protein Science</i> , 2007, 16, 2030-2041.	3.1	77
24	Prediction of DNA binding motifs from 3D models of transcription factors; identifying TLX3 regulated genes. <i>Nucleic Acids Research</i> , 2014, 42, 13500-13512.	6.5	74
25	A supersecondary structure library and search algorithm for modeling loops in protein structures. <i>Nucleic Acids Research</i> , 2006, 34, 2085-2097.	6.5	72
26	Structural genomics is the largest contributor of novel structural leverage. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 181-191.	1.2	69
27	Effects of amino acid composition, finite size of proteins, and sparse statistics on distance-dependent statistical pair potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 559-568.	1.5	63
28	Protein structure modeling in the proteomics era. <i>Expert Review of Proteomics</i> , 2004, 1, 97-110.	1.3	61
29	Multiple mapping method: A novel approach to the sequence-to-structure alignment problem in comparative protein structure modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 644-661.	1.5	60
30	High-Throughput Computational and Experimental Techniques in Structural Genomics. <i>Genome Research</i> , 2004, 14, 2145-2154.	2.4	59
31	Hallmarks of Molecular Action of Microtubule Stabilizing Agents. <i>Journal of Biological Chemistry</i> , 2011, 286, 11765-11778.	1.6	59
32	Different sequence environments of cysteines and half cystines in proteins Application to predict disulfide forming residues. <i>FEBS Letters</i> , 1992, 302, 117-120.	1.3	58
33	The Functional Roles of the His247 and His281 Residues in Folate and Proton Translocation Mediated by the Human Proton-coupled Folate Transporter SLC46A1. <i>Journal of Biological Chemistry</i> , 2009, 284, 17846-17857.	1.6	57
34	Structural Characteristics of Novel Protein Folds. <i>PLoS Computational Biology</i> , 2010, 6, e1000750.	1.5	56
35	Post-Translational Modifications to <i>Toxoplasma gondii</i> $\hat{\alpha}$ - and $\hat{\beta}$ -Tubulins Include Novel C-Terminal Methylation. <i>Journal of Proteome Research</i> , 2010, 9, 359-372.	1.8	55
36	Control of mitochondrial function and cell growth by the atypical cadherin Fat1. <i>Nature</i> , 2016, 539, 575-578.	13.7	52

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37	A biochemical mechanism for the oncogenic potential of the p110 ^β catalytic subunit of phosphoinositide 3-kinase. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19897-19902.	3.3	51
38	New York-Structural GenomiX Research Consortium (NYSGXRC): A Large Scale Center for the Protein Structure Initiative. Journal of Structural and Functional Genomics, 2005, 6, 225-232.	1.2	48
39	Predicting disulfide bond connectivity in proteins by correlated mutations analysis. Bioinformatics, 2008, 24, 498-504.	1.8	46
40	Altered Subunit Communication in Subfamilies of Trimeric dUTPases. Biochemical and Biophysical Research Communications, 2000, 279, 534-542.	1.0	42
41	Cell wall branches, penicillin resistance and the secrets of the MurM protein. Trends in Microbiology, 2003, 11, 547-553.	3.5	42
42	Exchanging Murine and Human Immunoglobulin Constant Chains Affects the Kinetics and Thermodynamics of Antigen Binding and Chimeric Antibody Autoreactivity. PLoS ONE, 2007, 2, e1310.	1.1	40
43	Saturating representation of loop conformational fragments in structure databanks. BMC Structural Biology, 2006, 6, 15.	2.3	39
44	Identification of Linear Epitopes in Bacillus anthracis Protective Antigen Bound by Neutralizing Antibodies. Journal of Biological Chemistry, 2009, 284, 25077-25086.	1.6	39
45	A Nuclear Variant of ErbB3 Receptor Tyrosine Kinase Regulates Ezrin Distribution and Schwann Cell Myelination. Journal of Neuroscience, 2011, 31, 5106-5119.	1.7	39
46	Core Histones of the Amitochondriate Protist, Giardia lamblia. Molecular Biology and Evolution, 2000, 17, 1156-1163.	3.5	38
47	The ybeY protein from Escherichia coli is a metalloprotein. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 959-963.	0.7	38
48	Improved scoring function for comparative modeling using the M4T method. Journal of Structural and Functional Genomics, 2009, 10, 95-99.	1.2	38
49	Pathogenic NAP57 mutations decrease ribonucleoprotein assembly in dyskeratosis congenita. Human Molecular Genetics, 2009, 18, 4546-4551.	1.4	36
50	Structural Basis of Inducible Costimulator Ligand Costimulatory Function: Determination of the Cell Surface Oligomeric State and Functional Mapping of the Receptor Binding Site of the Protein. Journal of Immunology, 2006, 177, 3920-3929.	0.4	35
51	MMM: a sequence-to-structure alignment protocol. Bioinformatics, 2006, 22, 2691-2692.	1.8	33
52	Computational Analysis and Experimental Validation of Gene Predictions in Toxoplasma gondii. PLoS ONE, 2008, 3, e3899.	1.1	32
53	Transactivation of Abl by the Crk II adapter protein requires a PNAY sequence in the Crk C-terminal SH3 domain. Oncogene, 2005, 24, 8187-8199.	2.6	31
54	Toxoplasma gondii proteomics. Expert Review of Proteomics, 2009, 6, 303-313.	1.3	29

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55	Buprenorphine Decreases the CCL2-Mediated Chemotactic Response of Monocytes. <i>Journal of Immunology</i> , 2015, 194, 3246-3258.	0.4	29
56	2-(m-Azidobenzoyl)taxol binds differentially to distinct β -tubulin isoforms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11294-11299.	3.3	29
57	Assessment of chemical crosslink-assisted protein structure modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1283-1297.	1.5	27
58	Conservation of amino acids in multiple alignments: aspartic acid has unexpected conservation. <i>FEBS Letters</i> , 1996, 397, 225-229.	1.3	24
59	Protein structure based prediction of catalytic residues. <i>BMC Bioinformatics</i> , 2013, 14, 63.	1.2	23
60	Functional Classification of Immune Regulatory Proteins. <i>Structure</i> , 2013, 21, 766-776.	1.6	23
61	Crystal structure of human Karyopherin β 2 bound to the PY-NLS of <i>Saccharomyces cerevisiae</i> Nab2. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 31-35.	1.2	23
62	Functional Clustering of Immunoglobulin Superfamily Proteins with Protein-Protein Interaction Information Calibrated Hidden Markov Model Sequence Profiles. <i>Journal of Molecular Biology</i> , 2014, 426, 945-961.	2.0	23
63	HIV-Tat regulates macrophage gene expression in the context of neuroAIDS. <i>PLoS ONE</i> , 2017, 12, e0179882.	1.1	22
64	miRNA-mediated loss of m6A increases nascent translation in glioblastoma. <i>PLoS Genetics</i> , 2021, 17, e1009086.	1.5	22
65	CCL2 mobilizes ALIX to facilitate Gag-p6 mediated HIV-1 virion release. <i>ELife</i> , 2019, 8, .	2.8	22
66	Probing the specificity of a trypanosomal aromatic β -hydroxy acid dehydrogenase by site-directed mutagenesis. <i>Biochemical and Biophysical Research Communications</i> , 2002, 293, 633-639.	1.0	21
67	Acetylsalicylic acid (aspirin) reduces damage to reconstituted human tissues infected with <i>Candida</i> species by inhibiting extracellular fungal lipases. <i>Microbes and Infection</i> , 2009, 11, 1131-1139.	1.0	21
68	Genetic resistance to purine nucleoside phosphorylase inhibition in <i>Plasmodium falciparum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2114-2119.	3.3	21
69	Nonprotein Based Enrichment Method to Analyze Peptide Cross-Linking in Protein Complexes. <i>Analytical Chemistry</i> , 2009, 81, 7149-7159.	3.2	19
70	Evolutionary and biophysical relationships among the papillomavirus E2 proteins. <i>Frontiers in Bioscience - Landmark</i> , 2009, Volume, 900.	3.0	19
71	Modularity of Protein Folds as a Tool for Template-Free Modeling of Structures. <i>PLoS Computational Biology</i> , 2015, 11, e1004419.	1.5	18
72	Structure of a putative BenF-like porin from <i>Pseudomonas fluorescens</i> Pf5 at 2.6 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3056-3062.	1.5	17

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73	The Underlying Molecular and Network Level Mechanisms in the Evolution of Robustness in Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1002865.	1.5	17
74	Identification of Tyr residues that enhance folate substrate binding and constrain oscillation of the proton-coupled folate transporter (PCFT-SLC46A1). <i>American Journal of Physiology - Cell Physiology</i> , 2015, 308, C631-C641.	2.1	17
75	The choice of sequence homologs included in multiple sequence alignments has a dramatic impact on evolutionary conservation analysis. <i>Bioinformatics</i> , 2019, 35, 12-19.	1.8	17
76	Different sequence environments of amino acid residues involved and not involved in long-range interactions in proteins. <i>International Journal of Peptide and Protein Research</i> , 1994, 43, 205-208.	0.1	16
77	Hereditary folate malabsorption due to a mutation in the external gate of the proton-coupled folate transporter SLC46A1. <i>Blood Advances</i> , 2018, 2, 61-68.	2.5	16
78	Gene regulation by PAX6: structural-functional correlations of missense mutants and transcriptional control of <i>Trpm3/miR-204</i> . <i>Molecular Vision</i> , 2014, 20, 270-82.	1.1	16
79	¹ H, ¹³ C, ¹⁵ N resonance assignments and fold verification of a circular permuted variant of the potent HIV-inactivating protein cyanovirin-N. <i>Journal of Biomolecular NMR</i> , 2001, 19, 289-290.	1.6	15
80	Modeling Proteins Using a Super-Secondary Structure Library and NMR Chemical Shift Information. <i>Structure</i> , 2013, 21, 891-899.	1.6	15
81	Identification of an Extracellular Gate for the Proton-coupled Folate Transporter (PCFT-SLC46A1) by Cysteine Cross-linking. <i>Journal of Biological Chemistry</i> , 2016, 291, 8162-8172.	1.6	15
82	Predicting Redox State of Cysteines in Proteins. <i>Methods in Enzymology</i> , 2002, 353, 10-21.	0.4	13
83	Computational Redesign of PD-1 Interface for PD-L1 Ligand Selectivity. <i>Structure</i> , 2019, 27, 829-836.e3.	1.6	13
84	Redesigning HVEM Interface for Selective Binding to LIGHT, BTLA, and CD160. <i>Structure</i> , 2020, 28, 1197-1205.e2.	1.6	13
85	Servers for sequence-structure relationship analysis and prediction. <i>Nucleic Acids Research</i> , 2003, 31, 3359-3363.	6.5	12
86	Protein-protein binding supersites. <i>PLoS Computational Biology</i> , 2019, 15, e1006704.	1.5	12
87	A Modular Perspective of Protein Structures: Application to Fragment Based Loop Modeling. <i>Methods in Molecular Biology</i> , 2012, 932, 141-158.	0.4	10
88	ProtLID, a Residue-Based Pharmacophore Approach to Identify Cognate Protein Ligands in the Immunoglobulin Superfamily. <i>Structure</i> , 2016, 24, 2217-2226.	1.6	10
89	Development of a motif-based topology-independent structure comparison method to identify evolutionarily related folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1859-1874.	1.5	10
90	Residues in the eighth transmembrane domain of the proton-coupled folate transporter (SLC46A1) play an important role in defining the aqueous translocation pathway and in folate substrate binding. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 2193-2202.	1.4	10

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91	Nucâ€rB3 regulates H3K27me3 levels and HMT activity to establish epigenetic repression during peripheral myelination. <i>Glia</i> , 2016, 64, 977-992.	2.5	9
92	Noncovalent Cross-links in Context with Other Structural and Functional Elements of Proteinsâ€. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 347-351.	2.8	7
93	Identifying functionally informative evolutionary sequence profiles. <i>Bioinformatics</i> , 2018, 34, 1278-1286.	1.8	7
94	Substitutions that lock and unlock the proton-coupled folate transporter (PCFT-SLC46A1) in an inward-open conformation. <i>Journal of Biological Chemistry</i> , 2019, 294, 7245-7258.	1.6	7
95	The role of long-range interactions in defining the secondary structure of proteins is overestimated. <i>Bioinformatics</i> , 1997, 13, 297-301.	1.8	6
96	Modeling Protein Structure from its Sequence. <i>Current Protocols in Bioinformatics</i> , 2003, 3, 5.1.1.	25.8	6
97	Frozen tissue can provide reproducible proteomic results of subcellular fractionation. <i>Analytical Biochemistry</i> , 2011, 418, 78-84.	1.1	6
98	Role of the tryptophan residues in proton-coupled folate transporter (PCFT-SLC46A1) function. <i>American Journal of Physiology - Cell Physiology</i> , 2016, 311, C150-C157.	2.1	6
99	Comparative Protein Structure Modelling. , 2017, , 91-134.		6
100	Substituted-cysteine accessibility and cross-linking identify an exofacial cleft in the 7th and 8th helices of the proton-coupled folate transporter (SLC46A1). <i>American Journal of Physiology - Cell Physiology</i> , 2018, 314, C289-C296.	2.1	6
101	A proton-coupled folate transporter mutation causing hereditary folate malabsorption locks the protein in an inward-open conformation. <i>Journal of Biological Chemistry</i> , 2020, 295, 15650-15661.	1.6	5
102	Photoâ€ssisted peptide enrichment in protein complex crossâ€linking analysis of a model homodimeric protein using mass spectrometry. <i>Proteomics</i> , 2011, 11, 4109-4115.	1.3	4
103	Discovery of receptorâ€ligand interfaces in the immunoglobulin superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 135-142.	1.5	4
104	Residue-based pharmacophore approaches to study proteinâ€protein interactions. <i>Current Opinion in Structural Biology</i> , 2021, 67, 205-211.	2.6	4
105	INTERCAAT: identifying interface residues between macromolecules. <i>Bioinformatics</i> , 2022, 38, 554-555.	1.8	4
106	Subventricular zone adult mouse neural stem cells require insulin receptor for self-renewal. <i>Stem Cell Reports</i> , 2022, 17, 1411-1427.	2.3	3
107	Smotifs as structural local descriptors of supersecondary elements: classification, completeness and applications. <i>BioAlgorithms and Med-Systems</i> , 2014, 10, 195-212.	1.0	2
108	A word of caution about biological inference â€ Revisiting cysteine covalent state predictions. <i>FEBS Open Bio</i> , 2014, 4, 310-314.	1.0	2

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109	GENE-25. LOSS OF m6A RNA METHYLATION DURING GLIOMA STEM CELL DIFFERENTIATION IS REGULATED BY MIRNAS AND PROMOTES TRANSLATION EFFICIENCY. <i>Neuro-Oncology</i> , 2018, 20, vi108-vi108.	0.6	1
110	Estimating the accuracy of pharmacophore-based detection of cognate receptor-ligand pairs in the immunoglobulin superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 632-638.	1.5	1
111	Allosteric regulation of binding specificity of HVEM for CD160 and BTLA ligands upon G89F mutation. <i>Current Research in Structural Biology</i> , 2021, 3, 337-345.	1.1	1
112	Reply to Moulton et al.. <i>Structure</i> , 2002, 10, 292-293.	1.6	0
113	TMIC-40. YKL-40 AS MODULATOR OF CANCER STEM CELL PHENOTYPIC TRANSITIONS IN HUMAN GLIOBLASTOMAS. <i>Neuro-Oncology</i> , 2019, 21, vi256-vi256.	0.6	0
114	A Designer Quest for the Achilles' Heel of Influenza. <i>Structure</i> , 2020, 28, 1083-1084.	1.6	0
115	Abstract 432: The Atypical Cadherin Fat1 Suppresses Mitochondrial Function to Control Vascular Smooth Muscle Cell Growth After Vascular Injury. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, .	1.1	0