

Andras Fiser

List of Publications by Year in descending order

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115
papers

13,063
citations

71102

41
h-index

23533

111
g-index

176
all docs

176
docs citations

176
times ranked

18970
citing authors

#	ARTICLE	IF	CITATIONS
1	INTERCAAT: identifying interface residues between macromolecules. <i>Bioinformatics</i> , 2022, 38, 554-555.	4.1	4
2	Subventricular zone adult mouse neural stem cells require insulin receptor for self-renewal. <i>Stem Cell Reports</i> , 2022, 17, 1411-1427.	4.8	3
3	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.	2.6	1
4	miRNA-mediated loss of m6A increases nascent translation in glioblastoma. <i>PLoS Genetics</i> , 2021, 17, e1009086.	3.5	22
5	Residue-based pharmacophore approaches to study protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2021, 67, 205-211.	5.7	4
6	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.	2.2	1
7	Discovery of receptor-ligand interfaces in the immunoglobulin superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 135-142.	2.6	4
8	A Designer Quest for the Achilles™ Heel of Influenza. <i>Structure</i> , 2020, 28, 1083-1084.	3.3	0
9	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.	3.4	5
10	Redesigning HVEM Interface for Selective Binding to LIGHT, BTLA, and CD160. <i>Structure</i> , 2020, 28, 1197-1205.e2.	3.3	13
11	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.	4.1	17
12	Assessment of chemical-crosslink-assisted protein structure modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1283-1297.	2.6	27
13	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.	3.4	7
14	Computational Redesign of PD-1 Interface for PD-L1 Ligand Selectivity. <i>Structure</i> , 2019, 27, 829-836.e3.	3.3	13
15	TMIC-40. YKL-40 AS MODULATOR OF CANCER STEM CELL PHENOTYPIC TRANSITIONS IN HUMAN GLIOBLASTOMAS. <i>Neuro-Oncology</i> , 2019, 21, vi256-vi256.	1.2	0
16	Protein-protein binding supersites. <i>PLoS Computational Biology</i> , 2019, 15, e1006704.	3.2	12
17	CCL2 mobilizes ALIX to facilitate Gag-p6 mediated HIV-1 virion release. <i>ELife</i> , 2019, 8, .	6.0	22
18	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.	7.1	21

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19	Identifying functionally informative evolutionary sequence profiles. <i>Bioinformatics</i> , 2018, 34, 1278-1286.	4.1	7
20	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.	1.2	1
21	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.	5.2	16
22	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.	4.6	6
23	Comparative Protein Structure Modelling. , 2017, , 91-134.		6
24	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.	2.6	10
25	HIV-Tat regulates macrophage gene expression in the context of neuroAIDS. <i>PLoS ONE</i> , 2017, 12, e0179882.	2.5	22
26	ProtLID, a Residue-Based Pharmacophore Approach to Identify Cognate Protein Ligands in the Immunoglobulin Superfamily. <i>Structure</i> , 2016, 24, 2217-2226.	3.3	10
27	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.	4.6	6
28	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.	7.1	29
29	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.	2.6	10
30	Nucâ€œErbb3 regulates H3K27me3 levels and HMT activity to establish epigenetic repression during peripheral myelination. <i>Glia</i> , 2016, 64, 977-992.	4.9	9
31	Control of mitochondrial function and cell growth by the atypical cadherin Fat1. <i>Nature</i> , 2016, 539, 575-578.	27.8	52
32	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.	3.4	15
33	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.	4.6	17
34	Buprenorphine Decreases the CCL2-Mediated Chemotactic Response of Monocytes. <i>Journal of Immunology</i> , 2015, 194, 3246-3258.	0.8	29
35	Expression, Clinical Significance, and Receptor Identification of the Newest B7 Family Member HHLA2 Protein. <i>Clinical Cancer Research</i> , 2015, 21, 2359-2366.	7.0	125
36	Modularity of Protein Folds as a Tool for Template-Free Modeling of Structures. <i>PLoS Computational Biology</i> , 2015, 11, e1004419.	3.2	18

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37	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, .	2.4	0
38	Prediction of DNA binding motifs from 3D models of transcription factors; identifying TLX3 regulated genes. <i>Nucleic Acids Research</i> , 2014, 42, 13500-13512.	14.5	74
39	Smotifs as structural local descriptors of supersecondary elements: classification, completeness and applications. <i>Bio-Algorithms and Med-Systems</i> , 2014, 10, 195-212.	2.4	2
40	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.	7.1	79
41	A word of caution about biological inference – Revisiting cysteine covalent state predictions. <i>FEBS Open Bio</i> , 2014, 4, 310-314.	2.3	2
42	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.	4.2	23
43	Gene regulation by PAX6: structural-functional correlations of missense mutants and transcriptional control of Trpm3/miR-204. <i>Molecular Vision</i> , 2014, 20, 270-82.	1.1	16
44	Protein structure based prediction of catalytic residues. <i>BMC Bioinformatics</i> , 2013, 14, 63.	2.6	23
45	Functional Classification of Immune Regulatory Proteins. <i>Structure</i> , 2013, 21, 766-776.	3.3	23
46	Crystal structure of human Karyopherin $\beta 2$ 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
47	Modeling Proteins Using a Super-Secondary Structure Library and NMR Chemical Shift Information. <i>Structure</i> , 2013, 21, 891-899.	3.3	15
48	The Underlying Molecular and Network Level Mechanisms in the Evolution of Robustness in Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1002865.	3.2	17
49	A Modular Perspective of Protein Structures: Application to Fragment Based Loop Modeling. <i>Methods in Molecular Biology</i> , 2012, 932, 141-158.	0.9	10
50	Frozen tissue can provide reproducible proteomic results of subcellular fractionation. <i>Analytical Biochemistry</i> , 2011, 418, 78-84.	2.4	6
51	Photo-assisted peptide enrichment in protein complex cross-linking analysis of a model homodimeric protein using mass spectrometry. <i>Proteomics</i> , 2011, 11, 4109-4115.	2.2	4
52	VISTA, a novel mouse Ig superfamily ligand that negatively regulates T cell responses. <i>Journal of Experimental Medicine</i> , 2011, 208, 577-592.	8.5	539
53	A Nuclear Variant of ErbB3 Receptor Tyrosine Kinase Regulates Ezrin Distribution and Schwann Cell Myelination. <i>Journal of Neuroscience</i> , 2011, 31, 5106-5119.	3.6	39
54	Hallmarks of Molecular Action of Microtubule Stabilizing Agents. <i>Journal of Biological Chemistry</i> , 2011, 286, 11765-11778.	3.4	59

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55	New statistical potential for quality assessment of protein models and a survey of energy functions. BMC Bioinformatics, 2010, 11, 128.	2.6	78
56	Structure of a putative BenFá€like porin from <i>Pseudomonas fluorescens</i> Pfá€5 at 2.6 Å... resolution. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3056-3062.	2.6	17
57	A biochemical mechanism for the oncogenic potential of the p110 ^{Î²} catalytic subunit of phosphoinositide 3-kinase. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19897-19902.	7.1	51
58	Structural Characteristics of Novel Protein Folds. PLoS Computational Biology, 2010, 6, e1000750.	3.2	56
59	Post-Translational Modifications to <i>Toxoplasma gondii</i> Î±- and Î²-Tubulins Include Novel C-Terminal Methylation. Journal of Proteome Research, 2010, 9, 359-372.	3.7	55
60	Template-Based Protein Structure Modeling. Methods in Molecular Biology, 2010, 673, 73-94.	0.9	165
61	The Functional Roles of the His247 and His281 Residues in Folate and Proton Translocation Mediated by the Human Proton-coupled Folate Transporter SLC46A1. Journal of Biological Chemistry, 2009, 284, 17846-17857.	3.4	57
62	Identification of Linear Epitopes in Bacillus anthracis Protective Antigen Bound by Neutralizing Antibodies. Journal of Biological Chemistry, 2009, 284, 25077-25086.	3.4	39
63	Pathogenic NAP57 mutations decrease ribonucleoprotein assembly in dyskeratosis congenita. Human Molecular Genetics, 2009, 18, 4546-4551.	2.9	36
64	<i>Toxoplasma gondii</i> proteomics. Expert Review of Proteomics, 2009, 6, 303-313.	3.0	29
65	PSI-2: Structural Genomics to Cover Protein Domain Family Space. Structure, 2009, 17, 869-881.	3.3	120
66	Improved scoring function for comparative modeling using the M4T method. Journal of Structural and Functional Genomics, 2009, 10, 95-99.	1.2	38
67	Structural genomics is the largest contributor of novel structural leverage. Journal of Structural and Functional Genomics, 2009, 10, 181-191.	1.2	69
68	Acetylsalicylic acid (aspirin) reduces damage to reconstituted human tissues infected with Candida species by inhibiting extracellular fungal lipases. Microbes and Infection, 2009, 11, 1131-1139.	1.9	21
69	Nonprotein Based Enrichment Method to Analyze Peptide Cross-Linking in Protein Complexes. Analytical Chemistry, 2009, 81, 7149-7159.	6.5	19
70	Evolutionary and biophysical relationships among the papillomavirus E2 proteins. Frontiers in Bioscience - Landmark, 2009, Volume, 900.	3.0	19
71	Protein production and purification. Nature Methods, 2008, 5, 135-146.	19.0	763
72	Predicting disulfide bond connectivity in proteins by correlated mutations analysis. Bioinformatics, 2008, 24, 498-504.	4.1	46

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73	Computational Analysis and Experimental Validation of Gene Predictions in <i>Toxoplasma gondii</i> . PLoS ONE, 2008, 3, e3899.	2.5	32
74	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.	3.4	116
75	M4T: a comparative protein structure modeling server. Nucleic Acids Research, 2007, 35, W363-W368.	14.5	118
76	Exchanging Murine and Human Immunoglobulin Constant Chains Affects the Kinetics and Thermodynamics of Antigen Binding and Chimeric Antibody Autoreactivity. PLoS ONE, 2007, 2, e1310.	2.5	40
77	Effects of amino acid composition, finite size of proteins, and sparse statistics on distance-dependent statistical pair potentials. Proteins: Structure, Function and Bioinformatics, 2007, 67, 559-568.	2.6	63
78	Modeling mutations in protein structures. Protein Science, 2007, 16, 2030-2041.	7.6	77
79	Structural genomics of protein phosphatases. Journal of Structural and Functional Genomics, 2007, 8, 121-140.	1.2	148
80	Saturating representation of loop conformational fragments in structure databanks. BMC Structural Biology, 2006, 6, 15.	2.3	39
81	Multiple mapping method: A novel approach to the sequence-to-structure alignment problem in comparative protein structure modeling. Proteins: Structure, Function and Bioinformatics, 2006, 63, 644-661.	2.6	60
82	A supersecondary structure library and search algorithm for modeling loops in protein structures. Nucleic Acids Research, 2006, 34, 2085-2097.	14.5	72
83	ArchPRED: a template based loop structure prediction server. Nucleic Acids Research, 2006, 34, W173-W176.	14.5	142
84	MMM: a sequence-to-structure alignment protocol. Bioinformatics, 2006, 22, 2691-2692.	4.1	33
85	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.	7.1	283
86	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.	0.8	35
87	Transactivation of Abl by the Crk II adapter protein requires a PNAV sequence in the Crk C-terminal SH3 domain. Oncogene, 2005, 24, 8187-8199.	5.9	31
88	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
89	The ybeY protein from <i>Escherichia coli</i> is a metalloprotein. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 959-963.	0.7	38
90	Protein structure modeling in the proteomics era. Expert Review of Proteomics, 2004, 1, 97-110.	3.0	61

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91	High-Throughput Computational and Experimental Techniques in Structural Genomics. <i>Genome Research</i> , 2004, 14, 2145-2154.	5.5	59
92	Noncovalent Cross-links in Context with Other Structural and Functional Elements of Proteins. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 347-351.	2.8	7
93	Modeling Protein Structure from its Sequence. <i>Current Protocols in Bioinformatics</i> , 2003, 3, 5.1.1.	25.8	6
94	Cell wall branches, penicillin resistance and the secrets of the MurM protein. <i>Trends in Microbiology</i> , 2003, 11, 547-553.	7.7	42
95	Modeller: Generation and Refinement of Homology-Based Protein Structure Models. <i>Methods in Enzymology</i> , 2003, 374, 461-491.	1.0	1,469
96	Bimoclomol, a heat shock protein co-inducer, acts by the prolonged activation of heat shock factor-1. <i>Biochemical and Biophysical Research Communications</i> , 2003, 307, 689-695.	2.1	145
97	Tools for comparative protein structure modeling and analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3375-3380.	14.5	406
98	Servers for sequence-structure relationship analysis and prediction. <i>Nucleic Acids Research</i> , 2003, 31, 3359-3363.	14.5	12
99	ModLoop: automated modeling of loops in protein structures. <i>Bioinformatics</i> , 2003, 19, 2500-2501.	4.1	707
100	Predicting Redox State of Cysteines in Proteins. <i>Methods in Enzymology</i> , 2002, 353, 10-21.	1.0	13
101	Evolution and Physics in Comparative Protein Structure Modeling. <i>Accounts of Chemical Research</i> , 2002, 35, 413-421.	15.6	103
102	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.	2.1	21
103	Reply to Moulton et al.. <i>Structure</i> , 2002, 10, 292-293.	3.3	0
104	Reliability of Assessment of Protein Structure Prediction Methods. <i>Structure</i> , 2002, 10, 435-440.	3.3	95
105	^1H , ^{13}C , ^{15}N resonance assignments and fold verification of a circularly permuted variant of the potent HIV-inactivating protein cyanovirin-N. <i>Journal of Biomolecular NMR</i> , 2001, 19, 289-290.	2.8	15
106	Modeling of loops in protein structures. <i>Protein Science</i> , 2000, 9, 1753-1773.	7.6	1,895
107	Comparative Protein Structure Modeling of Genes and Genomes. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2000, 29, 291-325.	18.3	2,811
108	Core Histones of the Amitochondriate Protist, <i>Giardia lamblia</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 1156-1163.	8.9	38

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109	Altered Subunit Communication in Subfamilies of Trimeric dUTPases. Biochemical and Biophysical Research Communications, 2000, 279, 534-542.	2.1	42
110	The role of long-range interactions in defining the secondary structure of proteins is overestimated. Bioinformatics, 1997, 13, 297-301.	4.1	6
111	Stabilization centers in proteins: Identification, characterization and predictions. Journal of Molecular Biology, 1997, 272, 597-612.	4.2	144
112	Conservation of amino acids in multiple alignments: aspartic acid has unexpected conservation. FEBS Letters, 1996, 397, 225-229.	2.8	24
113	Chaos game representation of protein structures. Journal of Molecular Graphics, 1994, 12, 302-304.	1.1	81
114	Different sequence environments of amino acid residues involved and not involved in long-range interactions in proteins. International Journal of Peptide and Protein Research, 1994, 43, 205-208.	0.1	16
115	Different sequence environments of cysteines and half cystines in proteins Application to predict disulfide forming residues. FEBS Letters, 1992, 302, 117-120.	2.8	58