

# Andras Fiser

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | 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.   | 7.6  | 1,895     |
| 3  | Modeller: Generation and Refinement of Homology-Based Protein Structure Models. Methods in Enzymology, 2003, 374, 461-491.  | 1.0  | 1,469     |
| 4  | Protein production and purification. Nature Methods, 2008, 5, 135-146.  | 19.0 | 763       |
| 5  | ModLoop: automated modeling of loops in protein structures. Bioinformatics, 2003, 19, 2500-2501.  | 4.1  | 707       |
| 6  | VISTA, a novel mouse Ig superfamily ligand that negatively regulates T cell responses. Journal of Experimental Medicine, 2011, 208, 577-592.  | 8.5  | 539       |
| 7  | Tools for comparative protein structure modeling and analysis. Nucleic Acids Research, 2003, 31, 3375-3380.   | 14.5 | 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.                                 | 7.1  | 283       |
| 9  | Template-Based Protein Structure Modeling. Methods in Molecular Biology, 2010, 673, 73-94.  | 0.9  | 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.                              | 2.1  | 145       |
| 12 | Stabilization centers in proteins: Identification, characterization and predictions. Journal of Molecular Biology, 1997, 272, 597-612.  | 4.2  | 144       |
| 13 | ArchPRED: a template based loop structure prediction server. Nucleic Acids Research, 2006, 34, W173-W176.   | 14.5 | 142       |
| 14 | Expression, Clinical Significance, and Receptor Identification of the Newest B7 Family Member HHLA2 Protein. Clinical Cancer Research, 2015, 21, 2359-2366.   | 7.0  | 125       |
| 15 | PSI-2: Structural Genomics to Cover Protein Domain Family Space. Structure, 2009, 17, 869-881.  | 3.3  | 120       |
| 16 | M4T: a comparative protein structure modeling server. Nucleic Acids Research, 2007, 35, W363-W368.  | 14.5 | 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. | 3.4  | 116       |
| 18 | Evolution and Physics in Comparative Protein Structure Modeling. Accounts of Chemical Research, 2002, 35, 413-421.  | 15.6 | 103       |

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|----|---|------|-----------|
| 19 | Reliability of Assessment of Protein Structure Prediction Methods. <i>Structure</i> , 2002, 10, 435-440.  | 3.3  | 95        |
| 20 | Chaos game representation of protein structures. <i>Journal of Molecular Graphics</i> , 1994, 12, 302-304.  | 1.1  | 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.    | 7.1  | 79        |
| 22 | New statistical potential for quality assessment of protein models and a survey of energy functions. <i>BMC Bioinformatics</i> , 2010, 11, 128.   | 2.6  | 78        |
| 23 | Modeling mutations in protein structures. <i>Protein Science</i> , 2007, 16, 2030-2041.   | 7.6  | 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.  | 14.5 | 74        |
| 25 | A supersecondary structure library and search algorithm for modeling loops in protein structures. <i>Nucleic Acids Research</i> , 2006, 34, 2085-2097.  | 14.5 | 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.           | 2.6  | 63        |
| 28 | Protein structure modeling in the proteomics era. <i>Expert Review of Proteomics</i> , 2004, 1, 97-110.   | 3.0  | 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.            | 2.6  | 60        |
| 30 | High-Throughput Computational and Experimental Techniques in Structural Genomics. <i>Genome Research</i> , 2004, 14, 2145-2154.   | 5.5  | 59        |
| 31 | Hallmarks of Molecular Action of Microtubule Stabilizing Agents. <i>Journal of Biological Chemistry</i> , 2011, 286, 11765-11778.   | 3.4  | 59        |
| 32 | Different sequence environments of cysteines and half cysteines in proteins Application to predict disulfide forming residues. <i>FEBS Letters</i> , 1992, 302, 117-120.  | 2.8  | 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. | 3.4  | 57        |
| 34 | Structural Characteristics of Novel Protein Folds. <i>PLoS Computational Biology</i> , 2010, 6, e1000750.   | 3.2  | 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.                     | 3.7  | 55        |
| 36 | Control of mitochondrial function and cell growth by the atypical cadherin Fat1. <i>Nature</i> , 2016, 539, 575-578.  | 27.8 | 52        |

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|----|---|-----|-----------|
| 37 | A biochemical mechanism for the oncogenic potential of the p110 <sup>β</sup> catalytic subunit of phosphoinositide 3-kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19897-19902.         | 7.1 | 51        |
| 38 | New York-Structural GenomiX Research Consortium (NYSGXRC): A Large Scale Center for the Protein Structure Initiative. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 225-232.  | 1.2 | 48        |
| 39 | Predicting disulfide bond connectivity in proteins by correlated mutations analysis. <i>Bioinformatics</i> , 2008, 24, 498-504.   | 4.1 | 46        |
| 40 | Altered Subunit Communication in Subfamilies of Trimeric dUTPases. <i>Biochemical and Biophysical Research Communications</i> , 2000, 279, 534-542.   | 2.1 | 42        |
| 41 | Cell wall branches, penicillin resistance and the secrets of the MurM protein. <i>Trends in Microbiology</i> , 2003, 11, 547-553.   | 7.7 | 42        |
| 42 | Exchanging Murine and Human Immunoglobulin Constant Chains Affects the Kinetics and Thermodynamics of Antigen Binding and Chimeric Antibody Autoreactivity. <i>PLoS ONE</i> , 2007, 2, e1310.   | 2.5 | 40        |
| 43 | Saturating representation of loop conformational fragments in structure databanks. <i>BMC Structural Biology</i> , 2006, 6, 15.   | 2.3 | 39        |
| 44 | Identification of Linear Epitopes in <i>Bacillus anthracis</i> Protective Antigen Bound by Neutralizing Antibodies. <i>Journal of Biological Chemistry</i> , 2009, 284, 25077-25086.  | 3.4 | 39        |
| 45 | 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        |
| 46 | Core Histones of the Amitochondriate Protist, <i>Giardia lamblia</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 1156-1163.  | 8.9 | 38        |
| 47 | The ybeY protein from <i>Escherichia coli</i> is a metalloprotein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 959-963.  | 0.7 | 38        |
| 48 | Improved scoring function for comparative modeling using the M4T method. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 95-99.  | 1.2 | 38        |
| 49 | Pathogenic NAP57 mutations decrease ribonucleoprotein assembly in dyskeratosis congenita. <i>Human Molecular Genetics</i> , 2009, 18, 4546-4551.  | 2.9 | 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. <i>Journal of Immunology</i> , 2006, 177, 3920-3929. | 0.8 | 35        |
| 51 | MMM: a sequence-to-structure alignment protocol. <i>Bioinformatics</i> , 2006, 22, 2691-2692.   | 4.1 | 33        |
| 52 | Computational Analysis and Experimental Validation of Gene Predictions in <i>Toxoplasma gondii</i> . <i>PLoS ONE</i> , 2008, 3, e3899.  | 2.5 | 32        |
| 53 | Transactivation of Abl by the Crk II adapter protein requires a PNAY sequence in the Crk C-terminal SH3 domain. <i>Oncogene</i> , 2005, 24, 8187-8199.  | 5.9 | 31        |
| 54 | <i>Toxoplasma gondii</i> proteomics. <i>Expert Review of Proteomics</i> , 2009, 6, 303-313.   | 3.0 | 29        |

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|----|---|-----|-----------|
| 55 | Buprenorphine Decreases the CCL2-Mediated Chemotactic Response of Monocytes. <i>Journal of Immunology</i> , 2015, 194, 3246-3258.   | 0.8 | 29        |
| 56 | 2-(m-Azidobenzoyl)taxol binds differentially to distinct $\beta$ -tubulin isoforms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11294-11299.                  | 7.1 | 29        |
| 57 | Assessment of chemical crosslink-assisted protein structure modeling in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1283-1297.  | 2.6 | 27        |
| 58 | Conservation of amino acids in multiple alignments: aspartic acid has unexpected conservation. <i>FEBS Letters</i> , 1996, 397, 225-229.  | 2.8 | 24        |
| 59 | Protein structure based prediction of catalytic residues. <i>BMC Bioinformatics</i> , 2013, 14, 63.   | 2.6 | 23        |
| 60 | Functional Classification of Immune Regulatory Proteins. <i>Structure</i> , 2013, 21, 766-776.  | 3.3 | 23        |
| 61 | 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        |
| 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. | 4.2 | 23        |
| 63 | HIV-Tat regulates macrophage gene expression in the context of neuroAIDS. <i>PLoS ONE</i> , 2017, 12, e0179882.   | 2.5 | 22        |
| 64 | miRNA-mediated loss of m6A increases nascent translation in glioblastoma. <i>PLoS Genetics</i> , 2021, 17, e1009086.  | 3.5 | 22        |
| 65 | CCL2 mobilizes ALIX to facilitate Gag-p6 mediated HIV-1 virion release. <i>ELife</i> , 2019, 8, .   | 6.0 | 22        |
| 66 | Probing the specificity of a trypanosomal aromatic $\beta$ -hydroxy acid dehydrogenase by site-directed mutagenesis. <i>Biochemical and Biophysical Research Communications</i> , 2002, 293, 633-639.                 | 2.1 | 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.    | 1.9 | 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.     | 7.1 | 21        |
| 69 | Nonprotein Based Enrichment Method to Analyze Peptide Cross-Linking in Protein Complexes. <i>Analytical Chemistry</i> , 2009, 81, 7149-7159.  | 6.5 | 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.   | 3.2 | 18        |
| 72 | Structure of a putative BenA-like porin from <i>Pseudomonas fluorescens</i> Pf-5 at 2.6 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3056-3062.                                  | 2.6 | 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.  | 3.2  | 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.   | 4.6  | 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.  | 4.1  | 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.  | 5.2  | 16        |
| 78 | 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        |
| 79 | <sup>1</sup> H, <sup>13</sup> C, <sup>15</sup> 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.  | 2.8  | 15        |
| 80 | Modeling Proteins Using a Super-Secondary Structure Library and NMR Chemical Shift Information. <i>Structure</i> , 2013, 21, 891-899.   | 3.3  | 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.  | 3.4  | 15        |
| 82 | Predicting Redox State of Cysteines in Proteins. <i>Methods in Enzymology</i> , 2002, 353, 10-21.   | 1.0  | 13        |
| 83 | Computational Redesign of PD-1 Interface for PD-L1 Ligand Selectivity. <i>Structure</i> , 2019, 27, 829-836.e3.   | 3.3  | 13        |
| 84 | Redesigning HVEM Interface for Selective Binding to LIGHT, BTLA, and CD160. <i>Structure</i> , 2020, 28, 1197-1205.e2.  | 3.3  | 13        |
| 85 | Servers for sequence-structure relationship analysis and prediction. <i>Nucleic Acids Research</i> , 2003, 31, 3359-3363.   | 14.5 | 12        |
| 86 | Protein-protein binding supersites. <i>PLoS Computational Biology</i> , 2019, 15, e1006704.   | 3.2  | 12        |
| 87 | A Modular Perspective of Protein Structures: Application to Fragment Based Loop Modeling. <i>Methods in Molecular Biology</i> , 2012, 932, 141-158.   | 0.9  | 10        |
| 88 | 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        |
| 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.  | 2.6  | 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. | 2.6  | 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.  | 4.9  | 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.   | 4.1  | 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.  | 3.4  | 7         |
| 95  | The role of long-range interactions in defining the secondary structure of proteins is overestimated. <i>Bioinformatics</i> , 1997, 13, 297-301.  | 4.1  | 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.   | 2.4  | 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.   | 4.6  | 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. | 4.6  | 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.   | 3.4  | 5         |
| 102 | Photoâ€ssisted peptide enrichment in protein complex crossâ€sslinking analysis of a model homodimeric protein using mass spectrometry. <i>Proteomics</i> , 2011, 11, 4109-4115.   | 2.2  | 4         |
| 103 | Discovery of receptorâ€ssligand interfaces in the immunoglobulin superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 135-142.  | 2.6  | 4         |
| 104 | Residue-based pharmacophore approaches to study proteinâ€ssprotein interactions. <i>Current Opinion in Structural Biology</i> , 2021, 67, 205-211.  | 5.7  | 4         |
| 105 | INTERCAAT: identifying interface residues between macromolecules. <i>Bioinformatics</i> , 2022, 38, 554-555.  | 4.1  | 4         |
| 106 | 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         |
| 107 | Smotifs as structural local descriptors of supersecondary elements: classification, completeness and applications. <i>BioAlgorithms and Med-Systems</i> , 2014, 10, 195-212.  | 2.4  | 2         |
| 108 | A word of caution about biological inference â€ss Revisiting cysteine covalent state predictions. <i>FEBS Open Bio</i> , 2014, 4, 310-314.  | 2.3  | 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.                                 | 1.2 | 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.               | 2.6 | 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.   | 2.2 | 1         |
| 112 | Reply to Moulton et al.. <i>Structure</i> , 2002, 10, 292-293.  | 3.3 | 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.  | 1.2 | 0         |
| 114 | A Designer Quest for the Achilles'™ Heel of Influenza. <i>Structure</i> , 2020, 28, 1083-1084.  | 3.3 | 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, . | 2.4 | 0         |