

# Andras Szilagy

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

2,525  
citations

331670

21  
h-index

197818

49  
g-index

56  
all docs

56  
docs citations

56  
times ranked

3563  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early pathways, biomarkers, and four distinct molecular subclasses of preeclampsia: The intersection of clinical, pathological, and high-dimensional biology studies. <i>Placenta</i> , 2022, 125, 10-19.	1.5	19
2	Novel biomarkers of recurrent pregnancy loss identified by next generation proteomics of maternal plasma. <i>Placenta</i> , 2021, 112, e19.	1.5	0
3	Transcriptional co-activator TAZ controls EVT differentiation in the developing human placenta. <i>Placenta</i> , 2021, 112, e50-e51.	1.5	0
4	Epigenetic Dysregulation of Trophoblastic Gene Expression in Gestational Trophoblastic Disease. <i>Biomedicines</i> , 2021, 9, 1935.	3.2	7
5	Ligand-induced conformational rearrangements regulate the switch between membrane-proximal and distal functions of Rho kinase 2. <i>Communications Biology</i> , 2020, 3, 721.	4.4	3
6	Proteomic identification of Placental Protein 1 (PP1), PP8, and PP22 and characterization of their placental expression in healthy pregnancies and in preeclampsia. <i>Placenta</i> , 2020, 99, 197-207.	1.5	3
7	Decreased Expression of ZNF554 in Gliomas is Associated with the Activation of Tumor Pathways and Shorter Patient Survival. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5762.	4.1	5
8	Pivotal role of the transcriptional co-activator YAP in trophoblast stemness of the developing human placenta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13562-13570.	7.1	95
9	Placenta-Specific Genes, Their Regulation During Villous Trophoblast Differentiation and Dysregulation in Preterm Preeclampsia. <i>International Journal of Molecular Sciences</i> , 2020, 21, 628.	4.1	30
10	Dysregulation of Placental Functions and Immune Pathways in Complete Hydatidiform Moles. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4999.	4.1	13
11	New type of interaction between the SARAH domain of the tumour suppressor RASSF1A and its mitotic kinase Aurora A. <i>Scientific Reports</i> , 2019, 9, 5550.	3.3	4
12	Sex hormone-binding globulin provides a novel entry pathway for estradiol and influences subsequent signaling in lymphocytes via membrane receptor. <i>Scientific Reports</i> , 2019, 9, 4.	3.3	29
13	Calculation of Configurational Entropy Differences from Conformational Ensembles Using Gaussian Mixtures. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 29-41.	5.3	16
14	Segment swapping aided the evolution of enzyme function: The case of uroporphyrinogen III synthase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 46-53.	2.6	3
15	Extensive Basal Level Activation of Complement Mannose-Binding Lectin-Associated Serine Protease-3: Kinetic Modeling of Lectin Pathway Activation Provides Possible Mechanism. <i>Frontiers in Immunology</i> , 2017, 8, 1821.	4.8	20
16	Structural Determinants of Sleeping Beauty Transposase Activity. <i>Molecular Therapy</i> , 2016, 24, 1369-1377.	8.2	7
17	Placental Protein 13 (PP13) – A Placental Immunoregulatory Galectin Protecting Pregnancy. <i>Frontiers in Immunology</i> , 2014, 5, 348.	4.8	90
18	Template-based structure modeling of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2014, 24, 10-23.	5.7	149

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19	Drugs Against Mycobacterium tuberculosis 3-Isopropylmalate Dehydrogenase Can be Developed Using Homologous Enzymes as Surrogate Targets. Protein and Peptide Letters, 2014, 21, 1295-1307.	0.9	2
20	Structure Prediction and Analysis of DNA Transposon and LINE Retrotransposon Proteins. Journal of Biological Chemistry, 2013, 288, 16127-16138.	3.4	12
21	Turning gold into "junk": transposable elements utilize central proteins of cellular networks. Nucleic Acids Research, 2013, 41, 3190-3200.	14.5	22
22	Editorial (Hot Topic: From Allosteric Drugs to Allo-Network Drugs: State of the Art and Trends of) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 6	2.1	22
23	Allo-Network Drugs: Extension of the Allosteric Drug Concept to Protein- Protein Interaction and Signaling Networks. Current Topics in Medicinal Chemistry, 2013, 13, 64-77.	2.1	68
24	"Pull Moves" for Rectangular Lattice Polymer Models Are Not Fully Reversible. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1847-1849.	3.0	7
25	Intra-Chain 3D Segment Swapping Spawns the Evolution of New Multidomain Protein Architectures. Journal of Molecular Biology, 2012, 415, 221-235.	4.2	13
26	Genome-Wide Protein Structure Prediction. , 2011, , 255-279.		2
27	Improving Protein Structure Prediction Using Multiple Sequence-Based Contact Predictions. Structure, 2011, 19, 1182-1191.	3.3	62
28	PP13, Maternal ABO Blood Groups and the Risk Assessment of Pregnancy Complications. PLoS ONE, 2011, 6, e21564.	2.5	45
29	Protein Homology Analysis for Function Prediction with Parallel Sub-Graph Isomorphism. , 2011, , 129-144.		0
30	iDBPs: a web server for the identification of DNA binding proteins. Bioinformatics, 2010, 26, 692-693.	4.1	76
31	A primate subfamily of galectins expressed at the maternal-fetal interface that promote immune cell death. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9731-9736.	7.1	200
32	Two-patch model of spatial niche segregation. Evolutionary Ecology, 2009, 23, 187-205.	1.2	12
33	Identification of DNA-binding Proteins Using Structural, Electrostatic and Evolutionary Features. Journal of Molecular Biology, 2009, 387, 1040-1053.	4.2	75
34	A Link between Hinge-Bending Domain Motions and the Temperature Dependence of Catalysis in 3-Isopropylmalate Dehydrogenase. Biophysical Journal, 2009, 96, 5003-5012.	0.5	11
35	Adjustment of conformational flexibility of glyceraldehyde-3-phosphate dehydrogenase as a means of thermal adaptation and allosteric regulation. European Biophysics Journal, 2008, 37, 1139-1144.	2.2	8
36	A mathematically related singularity and the maximum size of protein domains. Proteins: Structure, Function and Bioinformatics, 2008, 71, 2086-2088.	2.6	1

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37	The Twilight Zone between Protein Order and Disorder. <i>Biophysical Journal</i> , 2008, 95, 1612-1626.	0.5	29
38	Engineering the thermostability of a TIM-barrel enzyme by rational family shuffling. <i>Biochemical and Biophysical Research Communications</i> , 2008, 374, 725-730.	2.1	16
39	Rates of Unfolding, Rather than Refolding, Determine Thermal Stabilities of Thermophilic, Mesophilic, and Psychrotrophic 3-Isopropylmalate Dehydrogenases. <i>Biochemistry</i> , 2007, 46, 11536-11549.	2.5	13
40	Protein Folding. , 2007, , 303-343.		7
41	Efficient Prediction of Nucleic Acid Binding Function from Low-resolution Protein Structures. <i>Journal of Molecular Biology</i> , 2006, 358, 922-933.	4.2	149
42	Prediction of physical protein-protein interactions. <i>Physical Biology</i> , 2005, 2, S1-S16.	1.8	97
43	On the Sequential Determinants of Calpain Cleavage. <i>Journal of Biological Chemistry</i> , 2004, 279, 20775-20785.	3.4	279
44	TOUCHSTONE: A unified approach to protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 469-479.	2.6	72
45	Homology modeling reveals the structural background of the striking difference in thermal stability between two related [NiFe]hydrogenases. <i>Journal of Molecular Modeling</i> , 2002, 8, 58-64.	1.8	11
46	Increasing the thermal stability of cellulase C using rules learned from thermophilic proteins: a pilot study. <i>Biophysical Chemistry</i> , 2002, 96, 229-241.	2.8	22
47	Structural differences between mesophilic, moderately thermophilic and extremely thermophilic protein subunits: results of a comprehensive survey. <i>Structure</i> , 2000, 8, 493-504.	3.3	588
48	Mirror image mutations reveal the significance of an intersubunit ion cluster in the stability of 3-isopropylmalate dehydrogenase. <i>FEBS Letters</i> , 2000, 468, 48-52.	2.8	15
49	Separation of nonionic surfactant according to the length of the ethylene oxide chain on alumina layers. <i>Toxicological and Environmental Chemistry</i> , 1998, 65, 95-102.	1.2	3
50	Sequence and homology model of 3-isopropylmalate dehydrogenase from the psychrotrophic bacterium <i>Vibrio</i> sp. I5 suggest reasons for thermal instability. <i>Protein Engineering, Design and Selection</i> , 1997, 10, 665-672.	2.1	43
51	Relationship between thermal stability and 3-D structure in a homology model of 3-isopropylmalate dehydrogenase from <i>Escherichia coli</i> . <i>Protein Engineering, Design and Selection</i> , 1996, 9, 663-670.	2.1	12
52	Structural basis for the extreme thermostability of D-glyceraldehyde-3-phosphate dehydrogenase from <i>Thermotoga maritima</i> : analysis based on homology modelling. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 779-789.	2.1	30
53	Protein Homology Analysis for Function Prediction with Parallel Sub-Graph Isomorphism. , 0, , 386-399.		2