

# István Nagy

## List of Publications by Year in descending order

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79  
papers

2,756  
citations

218677  
26  
h-index

197818  
49  
g-index

79  
all docs

79  
docs citations

79  
times ranked

3703  
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel <i>Bacteroides</i> metallo- $\beta$ -lactamase (MBL) and its gene ( <i>crxA</i> ) in <i>Bacteroides xylanisolvens</i> revealed by genomic sequencing and functional analysis. Journal of Antimicrobial Chemotherapy, 2022, 77, 1553-1556.	3.0	11
2	High-resolution structure and biophysical characterization of the nucleocapsid phosphoprotein dimerization domain from the Covid-19 severe acute respiratory syndrome coronavirus 2. Biochemical and Biophysical Research Communications, 2021, 538, 54-62.	2.1	100
3	Myopia-26, the female-limited form of early-onset high myopia, occurring in a European family. Orphanet Journal of Rare Diseases, 2021, 16, 45.	2.7	13
4	Cyclophilin D-dependent mitochondrial permeability transition amplifies inflammatory reprogramming in endotoxemia. FEBS Open Bio, 2021, 11, 684-704.	2.3	10
5	In planta test system for targeted cellular mutagenesis by injection of oligonucleotides to apical meristem of maize seedlings. Acta Physiologiae Plantarum, 2021, 43, 1.	2.1	4
6	Cellvibrio polysaccharolyticus sp. nov., a cellulolytic bacterium isolated from agricultural soil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	6
7	Bradyrhizobium diazoefficiens USDA110 Nodulation of Aeschynomene afraspera Is Associated with Atypical Terminal Bacteroid Differentiation and Suboptimal Symbiotic Efficiency. MSystems, 2021, 6, .	3.8	4
8	Cryo-EM structure of the cetacean morbillivirus nucleoprotein-RNA complex. Journal of Structural Biology, 2021, 213, 107750.	2.8	12
9	Impaired cytoplasmic domain interactions cause co-assembly defect and loss of function in the p.Glu293Lys KCNJ2 variant isolated from an Andersen-Tawil syndrome patient. Cardiovascular Research, 2020, 117, 1923-1934.	3.8	2
10	Functional Anatomical Changes in Ulcerative Colitis Patients Determine Their Gut Microbiota Composition and Consequently the Possible Treatment Outcome. Pharmaceuticals, 2020, 13, 346.	3.8	13
11	Exploring the fitness benefits of genome reduction in Escherichia coli by a selection-driven approach. Scientific Reports, 2020, 10, 7345.	3.3	27
12	Biofungicidal Potential of Neosartorya (Aspergillus) Fischeri Antifungal Protein NFAP and Novel Synthetic $\beta$ -Core Peptides. Frontiers in Microbiology, 2020, 11, 820.	3.5	19
13	The potential use of the <i>Penicillium chrysogenum</i> antifungal protein PAF, the designed variant PAF <sup>opt</sup> and its $\beta$ -core peptide P $\beta$ <sup>opt</sup> in plant protection. Microbial Biotechnology, 2020, 13, 1403-1414.	4.2	16
14	Transcriptome Based Profiling of the Immune Cell Gene Signature in Rat Experimental Colitis and Human IBD Tissue Samples. Biomolecules, 2020, 10, 974.	4.0	4
15	Melanoma-Derived Exosomes Induce PD-1 Overexpression and Tumor Progression via Mesenchymal Stem Cell Oncogenic Reprogramming. Frontiers in Immunology, 2019, 10, 2459.	4.8	39
16	Small extracellular vesicles convey the stress-induced adaptive responses of melanoma cells. Scientific Reports, 2019, 9, 15329.	3.3	57
17	CRISPR-interference-based modulation of mobile genetic elements in bacteria. Synthetic Biology, 2019, 4, ysz008.	2.2	16
18	The Role of MicroRNAs upon Epithelial-to-Mesenchymal Transition in Inflammatory Bowel Disease. Cells, 2019, 8, 1461.	4.1	13

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19	Chemical-genetic profiling reveals limited cross-resistance between antimicrobial peptides with different modes of action. <i>Nature Communications</i> , 2019, 10, 5731.	12.8	29
20	Cryo-EM structures of the archaeal PAN-proteasome reveal an around-the-ring ATPase cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 534-539.	7.1	65
21	Structures of Ebola and Reston Virus VP35 Oligomerization Domains and Comparative Biophysical Characterization in All Ebolavirus Species. <i>Structure</i> , 2019, 27, 39-54.e6.	3.3	26
22	Proteomics Analysis of <i>Thermoplasma</i> Quinone Droplets. <i>Proteomics</i> , 2019, 19, 1800317.	2.2	1
23	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. <i>FASEB Journal</i> , 2019, 33, .	0.5	0
24	Relaxed chromatin induced by histone deacetylase inhibitors improves the oligonucleotide-directed gene editing in plant cells. <i>Journal of Plant Research</i> , 2018, 131, 179-189.	2.4	10
25	<i>Arabidopsis</i> NAP-related proteins (NRPs) contribute to the coordination of plant growth, developmental rate, and age-related pathogen resistance under short days. <i>Plant Science</i> , 2018, 267, 124-134.	3.6	15
26	Draft Genome Sequence of <i>Propionibacterium acnes</i> subsp. <i>elongatum</i> Strain Asn12. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	0
27	Increased insulin-like growth factor 1 production by polyploid adipose stem cells promotes growth of breast cancer cells. <i>BMC Cancer</i> , 2018, 18, 872.	2.6	16
28	Elevated Expression of <i>AXL</i> May Contribute to the Epithelial-to-Mesenchymal Transition in Inflammatory Bowel Disease Patients. <i>Mediators of Inflammation</i> , 2018, 2018, 1-11.	3.0	9
29	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. <i>Cell Reports</i> , 2018, 24, 1301-1315.e5.	6.4	108
30	A novel "splice site" HCN4 Gene mutation, c.1737 + 1 G > T, causes familial bradycardia, reduced heart rate response, impaired chronotropic competence and increased short-term heart rate variability. <i>International Journal of Cardiology</i> , 2017, 241, 364-372.	1.7	12
31	Stressors alter intercellular communication and exosome profile of nasopharyngeal carcinoma cells. <i>Journal of Oral Pathology and Medicine</i> , 2017, 46, 259-266.	2.7	38
32	Crystal structure of the <i>Thermoplasma acidophilum</i> protein Ta1207. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 328-335.	0.8	0
33	Specific Gene- and MicroRNA-Expression Pattern Contributes to the Epithelial to Mesenchymal Transition in a Rat Model of Experimental Colitis. <i>Mediators of Inflammation</i> , 2017, 2017, 1-9.	3.0	11
34	<i>Micrococcoides hystricis</i> gen. nov., sp. nov., a novel member of the family Micrococcaceae, phylum Actinobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2758-2765.	1.7	12
35	Lipoprotein-like particles in a prokaryote: quinone droplets of <i>Thermoplasma acidophilum</i> . <i>FEMS Microbiology Letters</i> , 2016, 363, fnw169.	1.8	4
36	The expression of inflammatory cytokines, <i>TAM</i> tyrosine kinase receptors and their ligands is upregulated in venous leg ulcer patients: a novel insight into chronic wound immunity. <i>International Wound Journal</i> , 2016, 13, 554-562.	2.9	13

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37	Emergence and evolution of an international cluster of MDR <i>Bacteroides fragilis</i> isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2441-2448.	3.0	47
38	A highly precise and portable genome engineering method allows comparison of mutational effects across bacterial species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2502-2507.	7.1	190
39	Cloning, Expression and Biochemical Characterization of Endomannanases from <i>Thermobifida</i> Species Isolated from Different Niches. <i>PLoS ONE</i> , 2016, 11, e0155769.	2.5	13
40	The Absence of N-Acetyl-D-glucosamine Causes Attenuation of Virulence of <i>Candida albicans</i> upon Interaction with Vaginal Epithelial Cells <i>In Vitro</i> . <i>BioMed Research International</i> , 2015, 2015, 1-13.	1.9	2
41	Multiplex Touchdown PCR for Rapid Typing of the Opportunistic Pathogen <i>Propionibacterium acnes</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 1149-1155.	3.9	51
42	Identification and functional characterisation of a novel <i>KCNJ2</i> mutation, Val302del, causing Andersen-Tawil syndrome. <i>Canadian Journal of Physiology and Pharmacology</i> , 2015, 93, 569-575.	1.4	3
43	Enhancing recombinant protein solubility with ubiquitin-like small archeal modifying protein fusion partners. <i>Journal of Microbiological Methods</i> , 2015, 118, 113-122.	1.6	3
44	Anti-Inflammatory Effect of Recreational Exercise in TNBS-Induced Colitis in Rats: Role of NOS/HO/MPO System. <i>Oxidative Medicine and Cellular Longevity</i> , 2014, 2014, 1-11.	4.0	41
45	Crystal structure of the proteasomal deubiquitylation module Rpn8-Rpn11. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2984-2989.	7.1	120
46	Symbiotic Plant Peptides Eliminate <i>Candida albicans</i> Both <i>In Vitro</i> and in an Epithelial Infection Model and Inhibit the Proliferation of Immortalized Human Cells. <i>BioMed Research International</i> , 2014, 2014, 1-9.	1.9	31
47	Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. <i>Nature Communications</i> , 2014, 5, 4352.	12.8	195
48	Protein complex purification from <i>Thermoplasma acidophilum</i> using a phage display library. <i>Journal of Microbiological Methods</i> , 2014, 98, 15-22.	1.6	3
49	The first transformation method for the thermo-acidophilic archaeon <i>Thermoplasma acidophilum</i> . <i>Journal of Microbiological Methods</i> , 2013, 95, 145-148.	1.6	2
50	Localization of the regulatory particle subunit Sem1 in the 26S proteasome. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 250-254.	2.1	28
51	<i>De Novo</i> Genome Project of <i>Cupriavidus basilensis</i> OR16. <i>Journal of Bacteriology</i> , 2012, 194, 2109-2110.	2.2	18
52	The proteasomal subunit Rpn6 is a molecular clamp holding the core and regulatory subcomplexes together. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 149-154.	7.1	136
53	Localization of the proteasomal ubiquitin receptors Rpn10 and Rpn13 by electron cryomicroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1479-1484.	7.1	114
54	De Novo Genome Project for the Aromatic Degradar <i>Rhodococcus pyridinivorans</i> Strain AK37. <i>Journal of Bacteriology</i> , 2012, 194, 1247-1248.	2.2	16

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55	Quantitative Proteome and Transcriptome Analysis of the Archaeon <i>Thermoplasma acidophilum</i> Cultured under Aerobic and Anaerobic Conditions. <i>Journal of Proteome Research</i> , 2010, 9, 4839-4850.	3.7	42
56	Insights into the molecular architecture of the 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11943-11947.	7.1	116
57	Size distribution of native cytosolic proteins of <i>Thermoplasma acidophilum</i> . <i>Proteomics</i> , 2009, 9, 3783-3786.	2.2	9
58	Proteomics Analysis of <i>Thermoplasma acidophilum</i> with a Focus on Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 492-502.	3.8	16
59	Proteome analysis of <i>Streptomyces coelicolor</i> mutants affected in the proteasome system reveals changes in stress-responsive proteins. <i>Archives of Microbiology</i> , 2007, 188, 257-271.	2.2	37
60	Crystal Structures of the <i>Rhodococcus</i> Proteasome with and without its Pro-peptides: Implications for the Role of the Pro-peptide in Proteasome Assembly. <i>Journal of Molecular Biology</i> , 2004, 335, 233-245.	4.2	80
61	Cloning and Heterologous Expression of a $\beta$ -D-Mannosidase (EC 3.2.1.25)-Encoding Gene from <i>Thermobifida fusca</i> TM51. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1944-1952.	3.1	52
62	Characterization of a Novel Intracellular Endopeptidase of the $\beta$ -Hydrolase Family from <i>Streptomyces coelicolor</i> A3(2). <i>Journal of Bacteriology</i> , 2003, 185, 496-503.	2.2	9
63	<i>Thermobifida cellulolytica</i> sp. nov., a novel lignocellulose-decomposing actinomycete.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 1193-1199.	1.7	26
64	Sequence Analysis of the Oxidase/Reductase Genes Upstream of the <i>Rhodococcus erythropolis</i> Aldehyde Dehydrogenase Gene <i>thcA</i> Reveals a Gene Organisation Different from <i>Mycobacterium Tuberculosis</i> . <i>DNA Sequence</i> , 1999, 10, 61-66.	0.7	3
65	Proteasomes and other self-compartmentalizing proteases in prokaryotes. <i>Trends in Microbiology</i> , 1999, 7, 88-92.	7.7	154
66	A self-compartmentalizing protease in <i>Rhodococcus</i> : the 20S proteasome. <i>Antonie Van Leeuwenhoek</i> , 1998, 74, 83-87.	1.7	8
67	Applied aspects of <i>Rhodococcus</i> genetics. <i>Antonie Van Leeuwenhoek</i> , 1998, 74, 133-153.	1.7	74
68	Characterization of ARC, a divergent member of the AAA ATPase family from <i>Rhodococcus erythropolis</i> . <i>Journal of Molecular Biology</i> , 1998, 277, 13-25.	4.2	107
69	Structural analysis of the 6 kb cryptic plasmid pFAJ2600 from <i>Rhodococcus erythropolis</i> NI86/21 and construction of <i>Escherichia coli</i> - <i>Rhodococcus</i> shuttle vectors. <i>Microbiology (United Kingdom)</i> , 1997, 143, 3137-3147.	1.8	73
70	Further Sequence Analysis of the DNA Regions with the <i>Rhodococcus</i> 20S Proteasome Structural Genes Reveals Extensive Homology with <i>Mycobacterium leprae</i> . <i>DNA Sequence</i> , 1997, 7, 225-228.	0.7	14
71	Subunit topology of the <i>Rhodococcus</i> proteasome. <i>FEBS Letters</i> , 1997, 400, 83-90.	2.8	61
72	Eubacterial proteasomes. <i>Molecular Biology Reports</i> , 1997, 24, 125-131.	2.3	48

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73	Identification of a <i>Rhodococcus</i> Gene Cluster Encoding a Homolog of the 17-kDa Antigen of <i>Brucella</i> and a Putative Regulatory Protein of the AsnC-Lrp Family. <i>Current Microbiology</i> , 1996, 33, 26-30.	2.2	5
74	Characterization of the <i>Rhodococcus</i> sp. NI86/21 gene encoding alcohol: N,N <sup>2</sup> -dimethyl-4-nitrosoaniline oxidoreductase inducible by atrazine and thiocarbamate herbicides. <i>Archives of Microbiology</i> , 1995, 163, 439-446.	2.2	30
75	Characterization of the <i>Rhodococcus</i> sp. NI86/21 gene encoding alcohol: N,N <sup>2</sup> -dimethyl-4-nitrosoaniline oxidoreductase inducible by atrazine and thiocarbamate herbicides. <i>Archives of Microbiology</i> , 1995, 163, 439-446.	2.2	6
76	Sequence of the cob A gene encoding : uroporphyrinogen III methyltransferase of <i>Pseudomonas fluorescens</i> . <i>Gene</i> , 1994, 150, 199-200.	2.2	6
77	Sequences of the cobalamin biosynthetic genes cobK, cobL and cobM from <i>Rhodococcus</i> sp. NI86/21. <i>Gene</i> , 1994, 143, 91-93.	2.2	13
78	Sequence of a <i>Rhodococcus</i> gene cluster encoding the subunits of ethanolamine ammonia-lyase and an APC-like permease. <i>Canadian Journal of Microbiology</i> , 1994, 40, 403-407.	1.7	15
79	Sequence of a <i>Rhodococcus</i> gene encoding a protein with extensive homology to the mammalian propionyl-CoA carboxylase beta chain. <i>Gene</i> , 1992, 122, 199-202.	2.2	4