

Naglis Malys

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

2,834
citations

257101

24
h-index

205818

48
g-index

54
all docs

54
docs citations

54
times ranked

4416
citing authors

#	ARTICLE	IF	CITATIONS
1	Bioproduction of L- and D-lactic acids: advances and trends in microbial strain application and engineering. <i>Critical Reviews in Biotechnology</i> , 2022, 42, 342-360.	5.1	17
2	A sustainability assessment framework for the high street. <i>Cities</i> , 2022, 124, 103571.	2.7	8
3	Biosensor-informed engineering of <i>Cupriavidus necator</i> H16 for autotrophic D-mannitol production. <i>Metabolic Engineering</i> , 2022, 72, 24-34.	3.6	16
4	Identification and characterization of L- and D-lactate-inducible systems from <i>Escherichia coli</i> MG1655, <i>Cupriavidus necator</i> H16 and <i>Pseudomonas</i> species. <i>Scientific Reports</i> , 2022, 12, 2123.	1.6	8
5	Development and Characterization of Indole-Responsive Whole-Cell Biosensor Based on the Inducible Gene Expression System from <i>Pseudomonas putida</i> KT2440. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4649.	1.8	2
6	Decision support framework to rank and prioritise the potential land areas for comprehensive land consolidation. <i>Land Use Policy</i> , 2021, 100, 104908.	2.5	23
7	Engineering <i>Cupriavidus necator</i> H16 for the autotrophic production of (R)-1,3-butanediol. <i>Metabolic Engineering</i> , 2021, 67, 262-276.	3.6	36
8	The pMTL70000 modular, plasmid vector series for strain engineering in <i>Cupriavidus necator</i> H16. <i>Journal of Microbiological Methods</i> , 2021, 189, 106323.	0.7	10
9	Advances and Prospects of Phenolic Acids Production, Biorefinery and Analysis. <i>Biomolecules</i> , 2020, 10, 874.	1.8	62
10	A genome-wide approach for identification and characterisation of metabolite-inducible systems. <i>Nature Communications</i> , 2020, 11, 1213.	5.8	49
11	Design, cloning and characterization of transcription factor-based inducible gene expression systems. <i>Methods in Enzymology</i> , 2019, 621, 153-169.	0.4	9
12	A Transcription Factor-Based Biosensor for Detection of Itaconic Acid. <i>ACS Synthetic Biology</i> , 2018, 7, 1436-1446.	1.9	51
13	Dispersion of relative importance values contributes to the ranking uncertainty: Sensitivity analysis of Multiple Criteria Decision-Making methods. <i>Applied Soft Computing Journal</i> , 2018, 67, 286-298.	4.1	45
14	¹³ C-assisted metabolic flux analysis to investigate heterotrophic and mixotrophic metabolism in <i>Cupriavidus necator</i> H16. <i>Metabolomics</i> , 2018, 14, 9.	1.4	31
15	Functional Genetic Elements for Controlling Gene Expression in <i>Cupriavidus necator</i> H16. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	34
16	Characterisation of a 3-hydroxypropionic acid-inducible system from <i>Pseudomonas putida</i> for orthogonal gene expression control in <i>Escherichia coli</i> and <i>Cupriavidus necator</i> . <i>Scientific Reports</i> , 2017, 7, 1724.	1.6	41
17	Translation initiation events on structured eukaryotic mRNAs generate gene expression noise. <i>Nucleic Acids Research</i> , 2017, 45, 6981-6992.	6.5	18
18	Housing Stakeholder Preferences for the "Soft" Features of Sustainable and Healthy Housing Design in the UK. <i>International Journal of Environmental Research and Public Health</i> , 2016, 13, 111.	1.2	22

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19	Comparative analysis of MCDM methods for the assessment of sustainable housing affordability. <i>Omega</i> , 2016, 59, 146-156.	3.6	350
20	Symbiotic and antibiotic interactions between gut commensal microbiota and host immune system. <i>Medicina (Lithuania)</i> , 2015, 51, 69-75.	0.8	40
21	CLOSE-RANGE PHOTOGRAMMETRY ENABLES DOCUMENTATION OF ENVIRONMENT-INDUCED DEFORMATION OF ARCHITECTURAL HERITAGE. <i>Environmental Engineering and Management Journal</i> , 2015, 14, 1371-1381.	0.2	28
22	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. <i>FEBS Letters</i> , 2013, 587, 2832-2841.	1.3	113
23	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	9.4	920
24	Partition and Turnover of Glutathione Reductase from <i>Saccharomyces cerevisiae</i> : A Proteomic Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2885-2894.	1.8	85
25	Challenges and Opportunities in Developing Sustainable Communities in the North West of England. <i>Challenges</i> , 2012, 3, 133-152.	0.9	3
26	BROWNFIELD REGENERATION: WATERFRONT SITE DEVELOPMENTS IN LIVERPOOL AND COLOGNE / NAUDOTĀ ² TERITORIJĀ ² ATGAIVINĪMAS: KRANTINIĀ ² APLINKOS GERINĪMAS LIVERPULYĒ IR KELNĒ / 環境再生と都市再生の比較研究: リバプールとコロンヌのウォーターフロント地区の開発 / 環境再生と都市再生の比較研究: リバプールとコロンヌのウォーターフロント地区の開発. <i>Environmental Engineering and Landscape Management</i> , 2012, 20, 5-16.	0.2	28
27	Shine-Dalgarno sequence of bacteriophage T4: GAGG prevails in early genes. <i>Molecular Biology Reports</i> , 2012, 39, 33-39.	1.0	8
28	Characterisation of multiple substrate-specific (d)ITP/(d)XTPase and modelling of deaminated purine nucleotide metabolism. <i>BMB Reports</i> , 2012, 45, 259-264.	1.1	23
29	Towards a Full Quantitative Description of Yeast Metabolism. <i>Methods in Enzymology</i> , 2011, 500, 215-231.	0.4	3
30	Building a Kinetic Model of Trehalose Biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2011, 500, 355-370.	0.4	17
31	What is the true enzyme kinetics in the biological system? An investigation of macromolecular crowding effect upon enzyme kinetics of glucose-6-phosphate dehydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 388-392.	1.0	73
32	Protein Production in <i>Saccharomyces cerevisiae</i> for Systems Biology Studies. <i>Methods in Enzymology</i> , 2011, 500, 197-212.	0.4	6
33	Translation initiation: variations in the mechanism can be anticipated. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 991-1003.	2.4	85
34	Absolute Quantification of the Glycolytic Pathway in Yeast. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.007633.	2.5	70
35	Systematic integration of experimental data and models in systems biology. <i>BMC Bioinformatics</i> , 2010, 11, 582.	1.2	28
36	Enzyme kinetics informatics: from instrument to browser. <i>FEBS Journal</i> , 2010, 277, 3769-3779.	2.2	20

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37	COMMERCIAL LEISURE PROPERTY VALUATION: A COMPARISON OF THE CASE STUDIES IN UK AND LITHUANIA. <i>International Journal of Strategic Property Management</i> , 2010, 14, 35-48.	0.8	14
38	URBAN REGENERATION FOR SUSTAINABLE COMMUNITIES: A CASE STUDY. <i>Technological and Economic Development of Economy</i> , 2009, 15, 49-59.	2.3	77
39	High-quality housingâ€”A key issue in delivering sustainable communities. <i>Building and Environment</i> , 2009, 44, 426-430.	3.0	98
40	Nonâ€”canonical RNA arrangement in T4â€”even phages: accommodated ribosome binding site at the gene <i>25</i> intercistronic junction. <i>Molecular Microbiology</i> , 2009, 73, 1115-1127.	1.2	4
41	Chapter 22 Enzyme Kinetics and Computational Modeling for Systems Biology. <i>Methods in Enzymology</i> , 2009, 467, 583-599.	0.4	23
42	Sustainable Communities: Affordable Housing and Socio-economic Relations. <i>Local Economy</i> , 2008, 23, 267-276.	0.8	28
43	Dcs2, a Novel Stress-induced Modulator of m ⁷ GpppX Pyrophosphatase Activity that Locates to P Bodies. <i>Journal of Molecular Biology</i> , 2006, 363, 370-382.	2.0	36
44	The 'scavenger' m ⁷ GpppX pyrophosphatase activity of Dcs1 modulates nutrient-induced responses in yeast. <i>Nucleic Acids Research</i> , 2004, 32, 3590-3600.	6.5	44
45	eIF4E isoform 2 in <i>Schizosaccharomyces pombe</i> is a novel stressâ€”response factor. <i>EMBO Reports</i> , 2004, 5, 311-316.	2.0	29
46	A Bipartite Bacteriophage T4 SOC and HOC Randomized Peptide Display Library: Detection and Analysis of Phage T4 Terminase (gp17) and Late Î¶ Factor (gp55) Interaction. <i>Journal of Molecular Biology</i> , 2002, 319, 289-304.	2.0	55
47	Post-transcriptional control of bacteriophage T4 gene 25 expression: mRNA secondary structure that enhances translational initiation. <i>Journal of Molecular Biology</i> , 1999, 288, 291-304.	2.0	28
48	A rare type of overlapping genes in bacteriophage T4: gene 30.3â€”2 is completely embedded within gene 30.3 by one position downstream. <i>Gene</i> , 1997, 194, 157-162.	1.0	9