# Vytas Svedas

List of Publications by Year
in descending order

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Version: 2024-02-01

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|---|---|---|---|
| 114 papers | 2,884 citations | 159585 30 h-index | 206112 48 g-index |
| 116 all docs | 116 docs citations | 116 times ranked | 2049 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The interaction of amino acids with o-phthaldialdehyde: A kinetic study and spectrophotometric assay of the reaction product. Analytical Biochemistry, 1980, 101, 188-195. | 2.4 | 146 |
| 2 | Guidelines for reporting of biocatalytic reactions. Trends in Biotechnology, 2010, 28, 171-180. | 9.3 | 144 |
| 3 | Biocatalytic approach to enantiomerically pure Î²-amino acids. Tetrahedron: Asymmetry, 1995, 6, 1601-1610. | 1.8 | 94 |
| 4 | Substrate specificity of penicillin amidase from E. coli. Biochimica Et Biophysica Acta - Biomembranes, 1980, 616, 283-289. | 2.6 | 90 |
| 5 | Biomimetic Transamination of Î±-Alkyl Î²-Keto Carboxylic Esters. Chemoenzymatic Approach to the Stereochemically Defined Î±-Alkyl Î²-Fluoroalkyl Î²-Amino Acids. Journal of Organic Chemistry, 1998, 63, 1878-1884. | 3.2 | 80 |
| 6 | Enzymatic synthesis of Î²-lactam antibiotics: A thermodynamic background. Enzyme and Microbial Technology, 1980, 2, 138-144. | 3.2 | 78 |
| 7 | Chemo-enzymatic approach to the synthesis of each of the four isomers of Î±-alkyl-Î²-fluoroalkyl-substituted Î²-amino acids. Tetrahedron: Asymmetry, 1994, 5, 1225-1228. | 1.8 | 77 |
| 8 | Biocatalytic resolution of Î²-fluoroalkyl-Î²-amino acids. Tetrahedron: Asymmetry, 1994, 5, 1119-1126. | 1.8 | 74 |
| 9 | Robust enzyme design: Bioinformatic tools for improved protein stability. Biotechnology Journal, 2015, 10, 344-355. | 3.5 | 65 |
| 10 | Tyrosyl-DNA Phosphodiesterase 1 Inhibitors: Usnic Acid Enamines Enhance the Cytotoxic Effect of Camptothecin. Journal of Natural Products, 2016, 79, 2961-2967. | 3.0 | 65 |
| 11 | Kinetic study of penicillin acylase from Alcaligenes faecalis. FEBS Letters, 1997, 417, 414-418. | 2.8 | 62 |
| 12 | Quantitative characterization of the nucleophile reactivity in penicillin acylase-catalyzed acyl transfer reactions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2002, 1599, 134-140. | 2.3 | 60 |
| 13 | Penicillin acylase-catalyzed resolution of amines in aqueous organic solvents. Tetrahedron: Asymmetry, 2000, 11, 4593-4600. | 1.8 | 59 |
| 14 | Penicillin acylase-catalyzed synthesis of ampicillin in â€œaqueous solutionâ€“precipitateâ€•systems. High substrate concentration and supersaturation effect. Journal of Molecular Catalysis B: Enzymatic, 2000, 10, 509-515. | 1.8 | 58 |
| 15 | Highly efficient synthesis of ampicillin in an ?aqueous solution-precipitate? system: Repetitive addition of substrates in a semicontinuous process. Biotechnology and Bioengineering, 2001, 73, 426-430. | 3.3 | 56 |
| 16 | Penicillin acylase-catalyzed synthesis of ?-lactam antibiotics in highly condensed aqueous systems: Beneficial impact of kinetic substrate supersaturation. Biotechnology and Bioengineering, 2004, 85, 323-329. | 3.3 | 54 |
| 17 | Computational Design of a pH Stable Enzyme: Understanding Molecular Mechanism of Penicillin Acylase's Adaptation to Alkaline Conditions. PLoS ONE, 2014, 9, e100643. | 2.5 | 54 |
| 18 | Preparation of optically active 1-aminoalkylphosphonic acids by stereoselective enzymatic hydrolysis of racemic N-acylated 1-aminoalkylphosphonic acids. Tetrahedron, 1991, 47, 3989-3998. | 1.9 | 49 |

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|---|---|---|---|
| 19 | Highly efficient and enantioselective enzymatic acylation of amines in aqueous medium. Tetrahedron: Asymmetry, 2001, 12, 1645-1650. | 1.8 | 49 |
| 20 | Active site titration as a tool for the evaluation of immobilization procedures of penicillin acylase. Biotechnology and Bioengineering, 2002, 79, 224-228. | 3.3 | 48 |
| 21 | Bioinformatic analysis of alpha/beta-hydrolase fold enzymes reveals subfamily-specific positions responsible for discrimination of amidase and lipase activities. Protein Engineering, Design and Selection, 2012, 25, 689-697. | 2.1 | 48 |
| 22 | Preparation and properties of penicillin amidase immobilized in polyelectrolyte complexes. Biochimica Et Biophysica Acta - Biomembranes, 1981, 660, 359-365. | 2.6 | 47 |
| 23 | Penicillin acylase-catalyzed protection and deprotection of amino groups as a promising approach in enzymatic peptide synthesis. FEBS Letters, 1991, 287, 31-33. | 2.8 | 46 |
| 24 | Quantitative characteristic of the catalytic properties and microstructure of cross-linked enzyme aggregates of penicillin acylase. Journal of Molecular Catalysis B: Enzymatic, 2009, 56, 202-207. | 1.8 | 45 |
| 25 | Penicillin acylase-catalyzed ampicillin synthesis using a pH gradient: A new approach to optimization. Biotechnology and Bioengineering, 2002, 78, 589-593. | 3.3 | 40 |
| 26 | Kinetics of the enzymatic synthesis of benzylpenicillin. Enzyme and Microbial Technology, 1980, 2, 313-317. | 3.2 | 35 |
| 27 | Enzymatic preparation of both L- and D-enantiomers of phosphonic and phosphonous analogues of alanine using penicillin acylase. Tetrahedron: Asymmetry, 1993, 4, 1965-1968. | 1.8 | 35 |
| 28 | Penicillin acylase-catalyzed peptide synthesis: a chemo-enzymatic route to stereoisomers of 3,6-diphenylpiperazine-2,5-dione. Tetrahedron: Asymmetry, 2000, 11, 1077-1083. | 1.8 | 34 |
| 29 | Saturation mutagenesis reveals the importance of residues Î±R145 and Î±F146 of penicillin acylase in the synthesis of Î²-lactam antibiotics. Journal of Biotechnology, 2008, 133, 18-26. | 3.8 | 34 |
| 30 | Zebra: a web server for bioinformatic analysis of diverse protein families. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1752-1758. | 3.5 | 34 |
| 31 | Bioinformatic analysis of the fold type I <scp>PLP</scp>â€dependent enzymes reveals determinants of reaction specificity in <scp>l</scp>â€threonine aldolase from Aeromonas jandaei. FEBS Open Bio, 2018, 8, 1013-1028. | 2.3 | 33 |
| 32 | Soluble-insoluble immobilized enzymes. Biotechnology and Bioengineering, 1982, 24, 237-240. | 3.3 | 31 |
| 33 | Mustguseal: a server for multiple structure-guided sequence alignment of protein families. Bioinformatics, 2018, 34, 1583-1585. | 4.1 | 31 |
| 34 | Bioinformatic analysis of protein families for identification of variable amino acid residues responsible for functional diversity. Journal of Biomolecular Structure and Dynamics, 2014, 32, 75-87. | 3.5 | 30 |
| 35 | A kinetic study of hog kidney aminoacylase. BBA - Proteins and Proteomics, 1982, 701, 389-394. | 2.1 | 29 |
| 36 | A green, fully enzymatic procedure for amine resolution, using a lipase and a penicillin G acylase. Green Chemistry, 2008, 10, 415. | 9.0 | 28 |

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| 37 | pocketZebra: a web-server for automated selection and classification of subfamily-specific binding sites by bioinformatic analysis of diverse protein families. Nucleic Acids Research, 2014, 42, W344-W349. | 14.5 | 28 |
| 38 | Kinetics of ampicillin synthesis catalyzed by penicillin acylase from E. coli in homogeneous and heterogeneous systems. Quantitative characterization of nucleophile reactivity and mathematical modeling of the process. , 2000, 65, 1367-1375. | | 26 |
| 39 | Acyl group transfer by proteases forming an acylenzyme intermediate: Kinetic model analysis (including hydrolysis of acylenzyme-nucleophile complex). Journal of Theoretical Biology, 1989, 140, 193-204. | 1.7 | 25 |
| 40 | Application of aminoacylase I to the enantioselective resolution of Î±-amino acid esters and amides. Tetrahedron: Asymmetry, 2004, 15, 1933-1936. | 1.8 | 25 |
| 41 | Penicillin acylase-catalyzed peptide synthesis in aqueous medium: a chemo-enzymatic route to stereoisomerically pure diketopiperazines. Tetrahedron: Asymmetry, 2003, 14, 3123-3128. | 1.8 | 24 |
| 42 | Catalytic Cycle of Penicillin Acylase from Escherichia coli: QM/MM Modeling of Chemical Transformations in the Enzyme Active Site upon Penicillin G Hydrolysis. ACS Catalysis, 2014, 4, 2521-2529. | 11.2 | 24 |
| 43 | Resolution of (RS)-phenylglycinonitrile by penicillin acylase-catalyzed acylation in aqueous medium. Tetrahedron: Asymmetry, 2003, 14, 2613-2617. | 1.8 | 23 |
| 44 | An â€˜easy-on, easy-offâ€™ protecting group for the enzymatic resolution of (Â±)-1-phenylethylamine in an aqueous medium. Tetrahedron: Asymmetry, 2004, 15, 2901-2906. | 1.8 | 22 |
| 45 | Efficient enantiomeric analysis of primary amines and amino alcohols by high-performance liquid chromatography with precolumn derivatization using novel chiral SH-reagent N-(R)-mandelyl-(S)-cysteine. Journal of Chromatography A, 2005, 1095, 89-93. | 3.7 | 21 |
| 46 | Continuous Spectrophotometric Assay of Human Lysosomal Cathepsin A/Protective Protein in Normal and Galactosialidosis Cells. Analytical Biochemistry, 1995, 230, 303-307. | 2.4 | 20 |
| 47 | Molecular Mechanisms of PARP-1 Inhibitor 7-Methylguanine. International Journal of Molecular Sciences, 2020, 21, 2159. | 4.1 | 20 |
| 48 | Penicillin Acylase-Catalyzed Solid-State Ampicillin Synthesis. Advanced Synthesis and Catalysis, 2002, 344, 894-898. | 4.3 | 19 |
| 49 | Chiral high-performance liquid chromatography analysis of Î±-amino acid mixtures using a novel SH reagentâ€”N-R-mandelyl-l-cysteine and traditional enantiomeric thiols for precolumn derivatization. Journal of Chromatography A, 2007, 1175, 89-95. | 3.7 | 19 |
| 50 | Yosshi: a web-server for disulfide engineering by bioinformatic analysis of diverse protein families. Nucleic Acids Research, 2019, 47, W308-W314. | 14.5 | 18 |
| 51 | Zebra2: advanced and easy-to-use web-server for bioinformatic analysis of subfamily-specific and conserved positions in diverse protein superfamilies. Nucleic Acids Research, 2020, 48, W65-W71. | 14.5 | 18 |
| 52 | Molecular modeling of formate dehydrogenase: the formation of the Michaelis complex. Journal of Biomolecular Structure and Dynamics, 2012, 30, 170-179. | 3.5 | 17 |
| 53 | Neuraminidase A from Streptococcus pneumoniae has a modular organization of catalytic and lectin domains separated by a flexible linker. FEBS Journal, 2018, 285, 2428-2445. | 4.7 | 17 |
| 54 | The visualCMAT: A web-server to select and interpret correlated mutations/co-evolving residues in protein families. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840005. | 0.8 | 16 |

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| 55 | Prospects of Using Biocatalysis for the Synthesis and Modification of Polymers. Molecules, 2021, 26, 2750. | 3.8 | 16 |
| 56 | The effect of ultrasound as a new method of studying conformational transitions in enzyme active sites. FEBS Letters, 1975, 49, 325-328. | 2.8 | 15 |
| 57 | Enzymatic hydrolysis of Î²-lactam antibiotics at low pH in a two-phase "aqueous solution - water-immiscible organic solvent" system. Canadian Journal of Chemistry, 2002, 80, 699-707. | 1.1 | 15 |
| 58 | Aliphatic Amidase from Rhodococcus rhodochrous M8 Is Related to the Nitrilase/Cyanide Hydratase Family. Biochemistry (Moscow), 2005, 70, 1280-1287. | 1.5 | 15 |
| 59 | Structural insights into the broad substrate specificity of carboxypeptidase T from ThermoactinomycesÂvulgaris. FEBS Journal, 2015, 282, 1214-1224. | 4.7 | 15 |
| 60 | Comparative Modeling of Substrate Binding in the S1â€˜ Subsite of Serine Carboxypeptidases from Yeast, Wheat, and Humanâ€. Biochemistry, 1996, 35, 14899-14909. | 2.5 | 14 |
| 61 | Hydrophobicity of Î²-lactam antibiotics. Journal of Chromatography A, 1991, 585, 3-34. | 3.7 | 13 |
| 62 | pH stability of penicillin acylase from Escherichia coli. Biochemistry (Moscow), 2004, 69, 1386-1390. | 1.5 | 13 |
| 63 | Molecular modeling of different substrateâ€binding modes and their role in penicillin acylase catalysis. FEBS Journal, 2013, 280, 115-126. | 4.7 | 13 |
| 64 | Parallel workflow manager for non-parallel bioinformatic applications to solve large-scale biological problems on a supercomputer. Journal of Bioinformatics and Computational Biology, 2016, 14, 1641008. | 0.8 | 13 |
| 65 | Human p38Î± mitogen-activated protein kinase in the Asp168-Phe169-Gly170-in (DFG-in) state can bind allosteric inhibitor Doramapimod. Journal of Biomolecular Structure and Dynamics, 2019, 37, 2049-2060. | 3.5 | 13 |
| 66 | Inhibitory Effect of New Semisynthetic Usnic Acid Derivatives on Human Tyrosyl-DNA Phosphodiesterase 1. Planta Medica, 2019, 85, 103-111. | 1.3 | 13 |
| 67 | Thermodynamic and kinetic stability of penicillin acylase from Escherichia coli. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 736-746. | 2.3 | 12 |
| 68 | Novel inhibitors of glyceraldehyde-3-phosphate dehydrogenase: Covalent modification of NAD-binding site by aromatic thiols. Biochemistry (Moscow), 2010, 75, 1444-1449. | 1.5 | 12 |
| 69 | 2,5-Diketopiperazines: A New Class of Poly(ADP-ribose)polymerase Inhibitors. Biochemistry (Moscow), 2018, 83, 152-158. | 1.5 | 12 |
| 70 | Inhibition of Poly(ADP-Ribose) Polymerase by Nucleic Acid Metabolite 7-Methylguanine. Acta Naturae, 2016, 8, 108-115. | 1.7 | 12 |
| 71 | The Mechanism of the alpha-Chymotrypsin and Trypsin-Catalyzed Hydrolysis of Amides. Evidence for the Participation of the Active Serine in the amidase Activity of Trypsin. FEBS Journal, 1973, 38, 529-536. | 0.2 | 11 |
| 72 | Influence of the immunization against heterologous alcohol dehydrogenase on liver alcohol dehydrogenase isozymes and alcohol abuse of rats. FEBS Journal, 1993, 212, 757-761. | 0.2 | 11 |

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| 73 | Quantum chemical studies of the catalytic mechanism of N-terminal nucleophile hydrolase. Biochemistry (Moscow), 2007, 72, 495-500. | 1.5 | 11 |
| 74 | Bioinformatic Analysis of the Nicotinamide Binding Site in Poly(ADP-Ribose) Polymerase Family Proteins. Cancers, 2021, 13, 1201. | 3.7 | 11 |
| 75 | Bioinformatic analysis of subfamily-specific regions in 3D-structures of homologs to study functional diversity and conformational plasticity in protein superfamilies. Computational and Structural Biotechnology Journal, 2021, 19, 1302-1311. | 4.1 | 11 |
| 76 | Increased nucleophile reactivity of amino acid Î²-naphthylamides in Î±-chymotrypsin-catalyzed peptide synthesis. BBA - Proteins and Proteomics, 1990, 1041, 71-78. | 2.1 | 10 |
| 77 | Design, Synthesis, and Molecular Docking Study of New Tyrosyl-DNA Phosphodiesterase 1 (TDP1) Inhibitors Combining Resin Acids and Adamantane Moieties. Pharmaceuticals, 2021, 14, 422. | 3.8 | 10 |
| 78 | Study of nucleophile binding in the penicillin acylase active center. Kinetic analysis. Biochemistry (Moscow), 2003, 68, 334-338. | 1.5 | 9 |
| 79 | EasyAmber: A comprehensive toolbox to automate the molecular dynamics simulation of proteins. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040011. | 0.8 | 9 |
| 80 | Force field parametrization for 6-aminopenicillanic acid. Computational and Theoretical Chemistry, 2003, 631, 117-125. | 1.5 | 8 |
| 81 | Totally Enzymatic Synthesis of Peptides: Penicillin Acylase-Catalyzed Protection and Deprotection of Amino Groups as Important Building Blocks of This Strategy. Annals of the New York Academy of Sciences, 1998, 864, 524-527. | 3.8 | 7 |
| 82 | Molecular modeling studies of substrate binding by penicillin acylase. Biochemistry (Moscow), 2008, 73, 56-64. | 1.5 | 7 |
| 83 | Biologically active cyclic polypeptides with fragments of Î²-amino acid derivatives isolated from marine organisms (review). Chemistry of Heterocyclic Compounds, 2011, 47, 395-417. | 1.2 | 7 |
| 84 | Structure of the carboxypeptidase B complex with N-sulfamoyl-L-phenylalanine â€“ a transition state analog of non-specific substrate. Journal of Biomolecular Structure and Dynamics, 2018, 36, 956-965. | 3.5 | 7 |
| 85 | Catalytic and lectin domains in neuraminidase A from Streptococcus pneumoniae are capable of an intermolecular assembly: Implications for biofilm formation. FEBS Journal, 2021, 288, 3217-3230. | 4.7 | 7 |
| 86 | Mustguseal and Sister Web-Methods: A Practical Guide to Bioinformatic Analysis of Protein Superfamilies. Methods in Molecular Biology, 2021, 2231, 179-200. | 0.9 | 6 |
| 87 | Comparative Bioinformatic Analysis of Active Site Structures in Evolutionarily Remote Homologues of Î±,Î²-Hydrolase Superfamily Enzymes. Acta Naturae, 2011, 3, 93-98. | 1.7 | 6 |
| 88 | Bifunctional Inhibitors of Influenza Virus Neuraminidase: Molecular Design of a Sulfonamide Linker. International Journal of Molecular Sciences, 2021, 22, 13112. | 4.1 | 6 |
| 89 | The methyl ester of Î±-aminophenylacetic acid: pH-dependence and phosphate catalysis of hydrolysis. Journal of the Chemical Society Perkin Transactions II, 1986, , 1537-1540. | 0.9 | 5 |
| 90 | Investigation of formate transport through the substrate channel of formate dehydrogenase by steered molecular dynamics simulations. Biochemistry (Moscow), 2011, 76, 172-174. | 1.5 | 5 |

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| 91 | Bioinformatic Analysis, Molecular Modeling of Role of Lys65 Residue in Catalytic Triad of D-aminopeptidase from Ochrobactrum anthropi. Acta Naturae, 2010, 2, 66-70. | 1.7 | 5 |
| 92 | Modeling of the Full-Size 3D Structure of Human Chaperone Hsp70 and Study of Its Interdomain Interactions. Acta Naturae, 2010, 2, 66-71. | 1.7 | 5 |
| 93 | Building a Full-Atom Model of L,Dtranspeptidase 2 from Mycobacterium tuberculosis for Screening New Inhibitors. Acta Naturae, 2017, 9, 44-51. | 1.7 | 5 |
| 94 | Preparative Biocatalytic Synthesis of Î±-Ketoglutaramate. International Journal of Molecular Sciences, 2021, 22, 12748. | 4.1 | 5 |
| 95 | Soft Tissue Sarcoma Study: Association of Genetic Alterations in the Apoptosis Pathways with Chemoresistance to Doxorubicin. Cancers, 2022, 14, 1796. | 3.7 | 5 |
| 96 | BESSICC, a COSMOâ€RS based tool for in silico solvent screening of biocatalyzed reactions. Biotechnology and Bioengineering, 2012, 109, 1864-1868. | 3.3 | 4 |
| 97 | Thermodynamics of phenylacetamides synthesis: Linear free energy relationship with the pK of amine. Journal of Molecular Catalysis B: Enzymatic, 2012, 74, 48-53. | 1.8 | 4 |
| 98 | The nature of the ligandâ€™s side chain interacting with the S1'-subsite of metallocarboxypeptidase T (from Thermoactinomyces vulgaris) determines the geometry of the tetrahedral transition complex. PLoS ONE, 2019, 14, e0226636. | 2.5 | 4 |
| 99 | Mutation of Residue Î²F71 of Escherichia coli Penicillin Acylase Results in Enhanced Enantioselectivity and Improved Catalytic Properties. Acta Naturae, 2009, 1, 94-98. | 1.7 | 4 |
| 100 | Penicillin Acylase-Catalyzed Effective and Stereoselective Acylation of 1-phenylethylamine in Aqueous Medium using Non-Activated Acyl Donor. Acta Naturae, 2010, 2, 94-96. | 1.7 | 4 |
| 101 | The role of Tyr102 residue in the functioning of bacterial NAD+-dependent formate dehydrogenase of Pseudomonas sp. 101. Biochemical and Biophysical Research Communications, 2022, 616, 134-139. | 2.1 | 4 |
| 102 | Use of high acyl donor concentrations leads to penicillin acylase inactivation in the course of peptide synthesis. Journal of Molecular Catalysis B: Enzymatic, 2004, 31, 63-65. | 1.8 | 3 |
| 103 | A new method for spectrophotometric assay of activity of cross-linked penicillin acylase aggregates. Biochemistry (Moscow), 2006, 71, 315-319. | 1.5 | 3 |
| 104 | Cloning of penicillin acylase from Escherichia coli: Catalytic properties of recombinant enzymes. Moscow University Chemistry Bulletin, 2008, 63, 103-107. | 0.6 | 3 |
| 105 | Crystal structures of carboxypeptidase T complexes with transition-state analogs. Journal of Biomolecular Structure and Dynamics, 2018, 36, 3958-3966. | 3.5 | 3 |
| 106 | Molecular Modeling of the Binding of the Allosteric Inhibitor Optactin at a New Binding Site in Neuraminidase A from Streptococcus pneumoniae. Moscow University Chemistry Bulletin, 2018, 73, 205-211. | 0.6 | 2 |
| 107 | Study of the Conformational Variety of the Oligosaccharide Substrates of Neuraminidases from Pathogens using Molecular Modeling. Moscow University Chemistry Bulletin, 2018, 73, 39-45. | 0.6 | 2 |
| 108 | Co-designing HPC-systems by computing capabilities and management flexibility to accommodate bioinformatic workflows at different complexity levels. Journal of Supercomputing, 0, , 1. | 3.6 | 2 |

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| 109 | The Î²D484N mutant of penicillin acylase from Escherichia coli is more resistant to inactivation by substrates and can effectively perform peptide synthesis in aqueous medium. Journal of Molecular Catalysis B: Enzymatic, 2015, 112, 66-68. | 1.8 | 1 |
| 110 | Professor Dr Roger A. Sheldonâ€"65 years on. Green Chemistry, 2008, 10, 270. | 9.0 | 0 |
| 111 | Synthesis of Schiff bases from 3-amino-3-arylpropionic acid esters in aqueous medium. Russian Journal of Organic Chemistry, 2012, 48, 860-863. | 0.8 | 0 |
| 112 | Probing the Substrate Specificity and Intersubunit Interactions of <i>Brevundimonas Diminuta</i> Glutaryl Acylase with Site-Directed Mutagenesis. American Journal of Biochemistry and Biotechnology, 2014, 10, 169-179. | 0.4 | 0 |
| 113 | Identification of New Structural Fragments for the Design of Lactate Dehydrogenase A Inhibitors. Acta Naturae, 2016, 8, 118-122. | 1.7 | 0 |
| 114 | High-Performance Hybrid Computing for Bioinformatic Analysis of Protein Superfamilies. Communications in Computer and Information Science, 2019, , 249-264. | 0.5 | 0 |