# Beta G Vrtessy

## List of Publications by Year in Descending Order



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| 144 papers | 6,726 citations | 32 h-index | 80 g-index |
| 157 ext. papers | 7,683 ext. citations | 5.7 avg, IF | 4.97 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 144 | Substrate Tunnel Engineering Aided by X-ray Crystallography and Functional Dynamics Swaps the Function of MIO-Enzymes. *ACS Catalysis*, **2021**, 11, 4538-4549 | 13.1 | 7 |
| 143 | Viruses with U-DNA: New Avenues for Biotechnology. *Viruses*, **2021**, 13, | 6.2 | 1 |
| 142 | What's in a name? From "fluctuation fit" to "conformational selection": rediscovery of a concept. *History and Philosophy of the Life Sciences*, **2021**, 43, 88 | 1 | 1 |
| 141 | Assessment of Tractable Cysteines for Covalent Targeting by Screening Covalent Fragments. *ChemBioChem*, **2021**, 22, 743-753 | 3.8 | 10 |
| 140 | Identification of new reference genes with stable expression patterns for gene expression studies using human cancer and normal cell lines. *Scientific Reports*, **2021**, 11, 19459 | 4.9 | 0 |
| 139 | Synthesis of New Chiral Crown Ethers Containing Phosphine or Secondary Phosphine Oxide Units. *Synthesis*, **2020**, 52, 2870-2882 | 2.9 | 2 |
| 138 | Unshielding Multidrug Resistant Cancer through Selective Iron Depletion of P-Glycoprotein-Expressing Cells. *Cancer Research*, **2020**, 80, 663-674 | 10.1 | 8 |
| 137 | Genome-wide alterations of uracil distribution patterns in human DNA upon chemotherapeutic treatments. *ELife*, **2020**, 9, | 8.9 | 5 |
| 136 | Identification of a nuclear localization signal in the Plasmodium falciparum CTP: phosphocholine cytidylyltransferase enzyme. *Scientific Reports*, **2020**, 10, 19739 | 4.9 | |
| 135 | Structure-based inhibitor design of mutant RAS proteins-a paradigm shift. *Cancer and Metastasis Reviews*, **2020**, 39, 1091-1105 | 9.6 | 6 |
| 134 | Rapid and quantitative antimalarial drug efficacy testing via the magneto-optical detection of hemozoin. *Scientific Reports*, **2020**, 10, 14025 | 4.9 | 4 |
| 133 | Highly Sensitive and Rapid Characterization of the Development of Synchronized Blood Stage Malaria Parasites Via Magneto-Optical Hemozoin Quantification. *Biomolecules*, **2019**, 9, | 5.9 | 7 |
| 132 | HDX and Native Mass Spectrometry Reveals the Different Structural Basis for Interaction of the Staphylococcal Pathogenicity Island Repressor Stl with Dimeric and Trimeric Phage dUTPases. *Biomolecules*, **2019**, 9, | 5.9 | 2 |
| 131 | Structural insights into the tyrosine phosphorylation-mediated inhibition of SH3 domain-ligand interactions. *Journal of Biological Chemistry*, **2019**, 294, 4608-4620 | 5.4 | 5 |
| 130 | The Role of a Key Amino Acid Position in Species-Specific Proteinaceous dUTPase Inhibition. *Biomolecules*, **2019**, 9, | 5.9 | 2 |
| 129 | Immobilized Whole-Cell Transaminase Biocatalysts for Continuous-Flow Kinetic Resolution of Amines. *Catalysts*, **2019**, 9, 438 | 4 | 20 |
| 128 | Evaluation of critical design parameters for RT-qPCR-based analysis of multiple dUTPase isoform genes in mice. *FEBS Open Bio*, **2019**, 9, 1153-1170 | 2.7 | 2 |

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| 127 | Mass spectrometry-based analysis of macromolecular complexes of uracil-DNA glycosylase and its inhibitor reveals specific variations due to naturally occurring mutations. *FEBS Open Bio*, **2019**, 9, 420-427 | 2.7 | 5 |
| 126 | CRISPR/Cas9-Mediated Knock-Out of dUTPase in Mice Leads to Early Embryonic Lethality. *Biomolecules*, **2019**, 9, | 5.9 | 3 |
| 125 | Beyond Chelation: EDTA Tightly Binds Taq DNA Polymerase, MutT and dUTPase and Directly Inhibits dNTPase Activity. *Biomolecules*, **2019**, 9, | 5.9 | 5 |
| 124 | An Acridone-Based Fluorescent Chemosensor for Cationic and Anionic Species, and Its Application for Molecular Logic Operations. *ChemistrySelect*, **2019**, 4, 11936-11943 | 1.8 | 5 |
| 123 | The role of enzyme adsorption in the enzymatic degradation of an aliphatic polyester. *Enzyme and Microbial Technology*, **2019**, 120, 110-116 | 3.8 | 5 |
| 122 | The Stl repressor from is an efficient inhibitor of the eukaryotic fruitfly dUTPase. *FEBS Open Bio*, **2018**, 8, 158-167 | 2.7 | 5 |
| 121 | Covalently immobilized Trp60Cys mutant of □-transaminase from Chromobacterium violaceum for kinetic resolution of racemic amines in batch and continuous-flow modes. *Biochemical Engineering Journal*, **2018**, 132, 270-278 | 4.2 | 24 |
| 120 | Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. *Scientific Reports*, **2018**, 8, 4326 | 4.9 | 9 |
| 119 | Enzymatic degradation of poly-[(R)-3-hydroxybutyrate]: Mechanism, kinetics, consequences. *International Journal of Biological Macromolecules*, **2018**, 112, 156-162 | 7.9 | 12 |
| 118 | Structural characterization of a sodium perchlorate□cridino-18-crown-6 ether complex. *Structural Chemistry*, **2018**, 29, 113-118 | 1.8 | 2 |
| 117 | Structural determinants of the catalytic mechanism of Plasmodium CCT, a key enzyme of malaria lipid biosynthesis. *Scientific Reports*, **2018**, 8, 11215 | 4.9 | 5 |
| 116 | Uracil moieties in genomic DNA. *FEBS Open Bio*, **2018**, 8, 1763-1772 | 2.7 | 5 |
| 115 | Exploiting a Phage-Bacterium Interaction System as a Molecular Switch to Decipher Macromolecular Interactions in the Living Cell. *Viruses*, **2018**, 10, | 6.2 | 2 |
| 114 | Heterologous expression of CTP:phosphocholine cytidylyltransferase from Plasmodium falciparum rescues Chinese Hamster Ovary cells deficient in the Kennedy phosphatidylcholine biosynthesis pathway. *Scientific Reports*, **2018**, 8, 8932 | 4.9 | 2 |
| 113 | Perturbation of genome integrity to fight pathogenic microorganisms. *Biochimica Et Biophysica Acta - General Subjects*, **2017**, 1861, 3593-3612 | 4 | 8 |
| 112 | The novel technique of vapor pressure analysis to monitor the enzymatic degradation of PHB by HPLC chromatography. *Analytical Biochemistry*, **2017**, 521, 20-27 | 3.1 | 5 |
| 111 | Identification of Extracellular Segments by Mass Spectrometry Improves Topology Prediction of Transmembrane Proteins. *Scientific Reports*, **2017**, 7, 42610 | 4.9 | 8 |
| 110 | A viral suppressor of RNA silencing inhibits ARGONAUTE 1 function by precluding target RNA binding to pre-assembled RISC. *Nucleic Acids Research*, **2017**, 45, 7736-7750 | 20.1 | 21 |

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|---|---|---|---|
| 109 | A Methylidene Group in the Phosphonic Acid Analogue of Phenylalanine Reverses the Enantiopreference of Binding to Phenylalanine Ammonia-Lyases. *Advanced Synthesis and Catalysis*, **2017**, 359, 2109-2120 | 5.6 | 8 |
| 108 | The First Enantioselective Total Synthesis of (-)-trans-Dihydronarciclasine. *Journal of Natural Products*, **2017**, 80, 1909-1917 | 4.9 | 13 |
| 107 | Elevated APOBEC3B expression drives a kataegic-like mutation signature and replication stress-related therapeutic vulnerabilities in p53-defective cells. *British Journal of Cancer*, **2017**, 117, 113-123 | 8.7 | 59 |
| 106 | Functional Analysis on a Naturally Occurring Variant of the Staphylococcus Aureus Uracil DNA Glycosylase Inhibitor. *Periodica Polytechnica: Chemical Engineering*, **2017**, | 1.3 | 1 |
| 105 | Differential control of dNTP biosynthesis and genome integrity maintenance by the dUTPase superfamily enzymes. *Scientific Reports*, **2017**, 7, 6043 | 4.9 | 13 |
| 104 | p53 controls expression of the DNA deaminase APOBEC3B to limit its potential mutagenic activity in cancer cells. *Nucleic Acids Research*, **2017**, 45, 11056-11069 | 20.1 | 41 |
| 103 | Structural characterization of the crystalline diastereomeric complexes of enantiopure dimethylacridino-18-crown-6 ether and the enantiomers of 1-(1-naphthyl)ethylamine hydrogen perchlorate. *Structural Chemistry*, **2017**, 28, 289-296 | 1.8 | 3 |
| 102 | A novel phenylalanine ammonia-lyase from kangiella koreensis. *Studia Universitatis Babes-Bolyai Chemia*, **2017**, 62, 293-308 | 1 | 4 |
| 101 | Structural Characterization of Arginine Fingers: Identification of an Arginine Finger for the Pyrophosphatase dUTPases. *Journal of the American Chemical Society*, **2016**, 138, 15035-15045 | 16.4 | 20 |
| 100 | Trading in cooperativity for specificity to maintain uracil-free DNA. *Scientific Reports*, **2016**, 6, 24219 | 4.9 | 8 |
| 99 | Detection of uracil within DNA using a sensitive labeling method for in vitro and cellular applications. *Nucleic Acids Research*, **2016**, 44, e28 | 20.1 | 20 |
| 98 | Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). *Autophagy*, **2016**, 12, 1-222 | 10.2 | 3838 |
| 97 | Structural Biology and Regulation of Protein Import into the Nucleus. *Journal of Molecular Biology*, **2016**, 428, 2060-90 | 6.5 | 140 |
| 96 | In Vitro Analysis of Predicted DNA-Binding Sites for the Stl Repressor of the Staphylococcus aureus SaPIBov1 Pathogenicity Island. *PLoS ONE*, **2016**, 11, e0158793 | 3.7 | 8 |
| 95 | Life without dUTPase. *Frontiers in Microbiology*, **2016**, 7, 1768 | 5.7 | 14 |
| 94 | Secondary Structure Prediction of Protein Constructs Using Random Incremental Truncation and Vacuum-Ultraviolet CD Spectroscopy. *PLoS ONE*, **2016**, 11, e0156238 | 3.7 | 5 |
| 93 | A Hidden Active Site in the Potential Drug Target Mycobacterium tuberculosis dUTPase Is Accessible through Small Amplitude Protein Conformational Changes. *Journal of Biological Chemistry*, **2016**, 291, 26320-26331 | 5.4 | 5 |
| 92 | The nucleotidohydrolases DCTPP1 and dUTPase are involved in the cellular response to decitabine. *Biochemical Journal*, **2016**, 473, 2635-43 | 3.8 | 17 |

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| 91 | Immobilization of Phenylalanine Ammonia-Lyase on Single-Walled Carbon Nanotubes for Stereoselective Biotransformations in Batch and Continuous-Flow Modes. *ChemCatChem*, **2015**, 7, 1122-1128 | 5.2 | 36 |
| 90 | Cross-species inhibition of dUTPase via the Staphylococcal Stl protein perturbs dNTP pool and colony formation in Mycobacterium. *DNA Repair*, **2015**, 30, 21-7 | 4.3 | 16 |
| 89 | dUTPase expression correlates with cell division potential in Drosophila melanogaster. *FEBS Journal*, **2015**, 282, 1998-2013 | 5.7 | 1 |
| 88 | Exploring the role of the phage-specific insert of bacteriophage 11 dUTPase. *Structural Chemistry*, **2015**, 26, 1425-1432 | 1.8 | 5 |
| 87 | Phenylalanine Ammonia-Lyase-Catalyzed Deamination of an Acyclic Amino Acid: Enzyme Mechanistic Studies Aided by a Novel Microreactor Filled with Magnetic Nanoparticles. *ChemBioChem*, **2015**, 16, 2283-8 | 3.8 | 34 |
| 86 | Evidence-Based Structural Model of the Staphylococcal Repressor Protein: Separation of Functions into Different Domains. *PLoS ONE*, **2015**, 10, e0139086 | 3.7 | 13 |
| 85 | Mutations Decouple Proton Transfer from Phosphate Cleavage in the dUTPase Catalytic Reaction. *ACS Catalysis*, **2015**, 5, 3225-3237 | 13.1 | 22 |
| 84 | Structural characterization of a complex derived from lead(II) perchlorate and acridono-18-crown-6 ether. *Structural Chemistry*, **2015**, 26, 1467-1471 | 1.8 | 5 |
| 83 | Molecular Mechanism for the Thermo-Sensitive Phenotype of CHO-MT58 Cell Line Harbouring a Mutant CTP:Phosphocholine Cytidylyltransferase. *PLoS ONE*, **2015**, 10, e0129632 | 3.7 | 8 |
| 82 | Bisepoxide Cross-Linked Enzyme AggregatesNew Immobilized Biocatalysts for Selective Biotransformations. *ChemCatChem*, **2014**, 6, n/a-n/a | 5.2 | 3 |
| 81 | Composite aromatic boxes for enzymatic transformations of quaternary ammonium substrates. *Angewandte Chemie - International Edition*, **2014**, 53, 13471-6 | 16.4 | 19 |
| 80 | The metagenomic telescope. *PLoS ONE*, **2014**, 9, e101605 | 3.7 | 4 |
| 79 | Dynamics of re-constitution of the human nuclear proteome after cell division is regulated by NLS-adjacent phosphorylation. *Cell Cycle*, **2014**, 13, 3551-64 | 4.7 | 19 |
| 78 | Highly potent dUTPase inhibition by a bacterial repressor protein reveals a novel mechanism for gene expression control. *Nucleic Acids Research*, **2014**, 42, 11912-20 | 20.1 | 31 |
| 77 | Preventive DNA repair by sanitizing the cellular (deoxy)nucleoside triphosphate pool. *FEBS Journal*, **2014**, 281, 4207-23 | 5.7 | 24 |
| 76 | NLS copy-number variation governs efficiency of nuclear import--case study on dUTPases. *FEBS Journal*, **2014**, 281, 5463-78 | 5.7 | 5 |
| 75 | Composite Aromatic Boxes for Enzymatic Transformations of Quaternary Ammonium Substrates. *Angewandte Chemie*, **2014**, 126, 13689-13694 | 3.6 | 1 |
| 74 | Factors influencing nucleo-cytoplasmic trafficking: which matter? Response to Alvisi & JansP comment on Phosphorylation adjacent to the nuclear localization signal of human dUTPase abolishes nuclear import: structural and mechanistic insights. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 2777-8 | | |

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| 73 | Expression and properties of the highly alkalophilic phenylalanine ammonia-lyase of thermophilic Rubrobacter xylanophilus. *PLoS ONE*, **2014**, 9, e85943 | 3.7 | 16 |
| 72 | Investigations of homologous disaccharides by elastic incoherent neutron scattering and wavelet multiresolution analysis. *Chemical Physics*, **2013**, 424, 56-61 | 2.3 | 17 |
| 71 | Evolutionary and mechanistic insights into substrate and product accommodation of CTP:phosphocholine cytidylyltransferase from Plasmodium falciparum. *FEBS Journal*, **2013**, 280, 3132-48 | 5.7 | 15 |
| 70 | Expanding the DNA alphabet in the fruit fly: uracil enrichment in genomic DNA. *Fly*, **2013**, 7, 23-7 | 1.3 | 8 |
| 69 | Phosphorylation adjacent to the nuclear localization signal of human dUTPase abolishes nuclear import: structural and mechanistic insights. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2495-505 | | 26 |
| 68 | Structure and enzymatic mechanism of a moonlighting dUTPase. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2298-308 | | 20 |
| 67 | Silicon carbide quantum dots for bioimaging. *Journal of Materials Research*, **2013**, 28, 205-209 | 2.5 | 33 |
| 66 | Catalytic mechanism of phosphate attack in dUTPase is revealed by X-ray crystallographic snapshots of distinct intermediates, 31P-NMR spectroscopy and reaction path modelling. *Nucleic Acids Research*, **2013**, 41, 10542-55 | 20.1 | 12 |
| 65 | Molecular cloning and characterization of a thermostable esterase/lipase produced by a novel Anoxybacillus flavithermus strain. *Journal of General and Applied Microbiology*, **2013**, 59, 119-34 | 1.5 | 9 |
| 64 | Enhanced cellular uptake of a new, in silico identified antitubercular candidate by peptide conjugation. *Bioconjugate Chemistry*, **2012**, 23, 900-7 | 6.3 | 24 |
| 63 | Molecular mechanisms of survival strategies in extreme conditions. *Life*, **2012**, 2, 364-76 | 3 | 12 |
| 62 | Uracil-containing DNA in Drosophila: stability, stage-specific accumulation, and developmental involvement. *PLoS Genetics*, **2012**, 8, e1002738 | 6 | 49 |
| 61 | The dUTPase enzyme is essential in Mycobacterium smegmatis. *PLoS ONE*, **2012**, 7, e37461 | 3.7 | 38 |
| 60 | Shared developmental roles and transcriptional control of autophagy and apoptosis in Caenorhabditis elegans. *Journal of Cell Science*, **2011**, 124, 1510-8 | 5.3 | 30 |
| 59 | Association of RNA with the uracil-DNA-degrading factor has major conformational effects and is potentially involved in protein folding. *FEBS Journal*, **2011**, 278, 295-315 | 5.7 | 6 |
| 58 | Cellular response to efficient dUTPase RNAi silencing in stable HeLa cell lines perturbs expression levels of genes involved in thymidylate metabolism. *Nucleosides, Nucleotides and Nucleic Acids*, **2011**, 30, 369-90 | 1.4 | 17 |
| 57 | Crystallization and preliminary crystallographic analysis of dUTPase from the 11 helper phage of Staphylococcus aureus. *Acta Crystallographica Section F: Structural Biology Communications*, **2011**, 67, 1411-3 | | 4 |
| 56 | From "fluctuation fit" to "conformational selection": evolution, rediscovery, and integration of a concept. *BioEssays*, **2011**, 33, 30-4 | 4.1 | 27 |

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| 55 | Nucleotide pyrophosphatase employs a P-loop-like motif to enhance catalytic power and NDP/NTP discrimination. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 14437-42 | 11.5 | 27 |
| 54 | Proteins with complex architecture as potential targets for drug design: a case study of Mycobacterium tuberculosis. *PLoS Computational Biology*, **2011**, 7, e1002118 | 5 | 17 |
| 53 | Calpain-catalyzed proteolysis of human dUTPase specifically removes the nuclear localization signal peptide. *PLoS ONE*, **2011**, 6, e19546 | 3.7 | 6 |
| 52 | Discovery of novel MDR-Mycobacterium tuberculosis inhibitor by new FRIGATE computational screen. *PLoS ONE*, **2011**, 6, e28428 | 3.7 | 10 |
| 51 | Physiological truncation and domain organization of a novel uracil-DNA-degrading factor. *FEBS Journal*, **2010**, 277, 1245-59 | 5.7 | 5 |
| 50 | Drosophila proteins involved in metabolism of uracil-DNA possess different types of nuclear localization signals. *FEBS Journal*, **2010**, 277, 2142-56 | 5.7 | 8 |
| 49 | Aromatic stacking between nucleobase and enzyme promotes phosphate ester hydrolysis in dUTPase. *Nucleic Acids Research*, **2010**, 38, 7179-86 | 20.1 | 48 |
| 48 | A one-step method for quantitative determination of uracil in DNA by real-time PCR. *Nucleic Acids Research*, **2010**, 38, e196 | 20.1 | 30 |
| 47 | Structure and mechanism of calmodulin binding to a signaling sphingolipid reveal new aspects of lipid-protein interactions. *FASEB Journal*, **2010**, 24, 3829-39 | 0.9 | 7 |
| 46 | Dissociation of calmodulin-target peptide complexes by the lipid mediator sphingosylphosphorylcholine: implications in calcium signaling. *Journal of Biological Chemistry*, **2010**, 285, 1799-808 | 5.4 | 12 |
| 45 | Study of solvent-protein coupling effects by neutron scattering. *Journal of Biological Physics*, **2010**, 36, 207-20 | 1.6 | 13 |
| 44 | Direct contacts between conserved motifs of different subunits provide major contribution to active site organization in human and mycobacterial dUTPases. *FEBS Letters*, **2010**, 584, 3047-54 | 3.8 | 12 |
| 43 | Molecular shape and prominent role of beta-strand swapping in organization of dUTPase oligomers. *FEBS Letters*, **2009**, 583, 865-71 | 3.8 | 21 |
| 42 | Improving thermostability and catalytic activity of pyranose 2-oxidase from Trametes multicolor by rational and semi-rational design. *FEBS Journal*, **2009**, 276, 776-92 | 5.7 | 33 |
| 41 | Keeping uracil out of DNA: physiological role, structure and catalytic mechanism of dUTPases. *Accounts of Chemical Research*, **2009**, 42, 97-106 | 24.3 | 174 |
| 40 | Nuclear localization signal-dependent and -independent movements of Drosophila melanogaster dUTPase isoforms during nuclear cleavage. *Biochemical and Biophysical Research Communications*, **2009**, 381, 271-5 | 3.4 | 10 |
| 39 | Active site of mycobacterial dUTPase: structural characteristics and a built-in sensor. *Biochemical and Biophysical Research Communications*, **2008**, 373, 8-13 | 3.4 | 55 |
| 38 | Methylene substitution at the alpha-beta bridging position within the phosphate chain of dUDP profoundly perturbs ligand accommodation into the dUTPase active site. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 308-19 | 4.2 | 27 |

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| 37 | Neutron scattering studies on dUTPase complex in the presence of bioprotectant systems. *Chemical Physics*, **2008**, 345, 250-258 | 2.3 | 26 |
| 36 | Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. *Nucleic Acids Research*, **2007**, 35, 495-505 | 20.1 | 40 |
| 35 | Kinetic mechanism of human dUTPase, an essential nucleotide pyrophosphatase enzyme. *Journal of Biological Chemistry*, **2007**, 282, 33572-33582 | 5.4 | 50 |
| 34 | A novel fruitfly protein under developmental control degrades uracil-DNA. *Biochemical and Biophysical Research Communications*, **2007**, 355, 643-8 | 3.4 | 18 |
| 33 | Active site closure facilitates juxtaposition of reactant atoms for initiation of catalysis by human dUTPase. *FEBS Letters*, **2007**, 581, 4783-8 | 3.8 | 48 |
| 32 | Quantitative determination of uracil residues in Escherichia coli DNA: Contribution of ung, dug, and dut genes to uracil avoidance. *DNA Repair*, **2006**, 5, 1407-20 | 4.3 | 46 |
| 31 | Crystallization and preliminary X-ray studies of dUTPase from Mason-Pfizer monkey retrovirus. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 399-401 | | 6 |
| 30 | Developmental regulation of dUTPase in Drosophila melanogaster. *Journal of Biological Chemistry*, **2004**, 279, 22362-70 | 5.4 | 32 |
| 29 | Altered active site flexibility and a structural metal-binding site in eukaryotic dUTPase: kinetic characterization, folding, and crystallographic studies of the homotrimeric Drosophila enzyme. *Journal of Biological Chemistry*, **2004**, 279, 17932-44 | 5.4 | 36 |
| 28 | Structural insights into the catalytic mechanism of phosphate ester hydrolysis by dUTPase. *Journal of Biological Chemistry*, **2004**, 279, 42907-15 | 5.4 | 66 |
| 27 | Multidimensional NMR identifies the conformational shift essential for catalytic competence in the 60-kDa Drosophila melanogaster dUTPase trimer. *Journal of Biological Chemistry*, **2004**, 279, 17945-50 | 5.4 | 13 |
| 26 | A tradeoff between protein stability and conformational mobility in homotrimeric dUTPases. *FEBS Letters*, **2004**, 566, 48-54 | 3.8 | 27 |
| 25 | Catalytic and structural role of the metal ion in dUTP pyrophosphatase. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 5670-5 | 11.5 | 41 |
| 24 | dUTPase and nucleocapsid polypeptides of the Mason-Pfizer monkey virus form a fusion protein in the virion with homotrimeric organization and low catalytic efficiency. *Journal of Biological Chemistry*, **2003**, 278, 38803-12 | 5.4 | 18 |
| 23 | Altered subunit communication in subfamilies of trimeric dUTPases. *Biochemical and Biophysical Research Communications*, **2000**, 279, 534-42 | 3.4 | 39 |
| 22 | A new potent calmodulin antagonist with arylalkylamine structure: crystallographic, spectroscopic and functional studies. *Journal of Molecular Biology*, **2000**, 297, 747-55 | 6.5 | 36 |
| 21 | Pyruvate kinase as a microtubule destabilizing factor in vitro. *Biochemical and Biophysical Research Communications*, **1999**, 254, 430-5 | 3.4 | 28 |
| 20 | The complete triphosphate moiety of non-hydrolyzable substrate analogues is required for a conformational shift of the flexible C-terminus in E. coli dUTP pyrophosphatase. *FEBS Letters*, **1998**, 421, 83-8 | 3.8 | 35 |

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| 19 | Simultaneous binding of drugs with different chemical structures to Ca2+-calmodulin: crystallographic and spectroscopic studies. *Biochemistry*, **1998**, 37, 15300-10 | 3.2 | 63 |
| 18 | Alternative binding of two sequential glycolytic enzymes to microtubules. Molecular studies in the phosphofructokinase/aldolase/microtubule system. *Journal of Biological Chemistry*, **1997**, 272, 25542-6 | 5.4 | 61 |
| 17 | Characterization of microtubule-phosphofructokinase complex: specific effects of MgATP and vinblastine. *Biochemistry*, **1997**, 36, 2051-62 | 3.2 | 32 |
| 16 | Interaction of a new bis-indol derivative, KAR-2 with tubulin and its antimitotic activity. *British Journal of Pharmacology*, **1997**, 121, 947-54 | 8.6 | 21 |
| 15 | The interaction of a new anti-tumour drug, KAR-2 with calmodulin. *British Journal of Pharmacology*, **1997**, 121, 955-62 | 8.6 | 14 |
| 14 | Crystallization and preliminary diffraction analysis of Ca(2+)-calmodulin-drug and apocalmodulin-drug complexes. *Proteins: Structure, Function and Bioinformatics*, **1997**, 28, 131-4 | 4.2 | 4 |
| 13 | Flexible glycine rich motif of Escherichia coli deoxyuridine triphosphate nucleotidohydrolase is important for functional but not for structural integrity of the enzyme **1997**, 28, 568-579 | | 47 |
| 12 | Flexible glycine rich motif of Escherichia coli deoxyuridine triphosphate nucleotidohydrolase is important for functional but not for structural integrity of the enzyme **1997**, 28, 568 | | 1 |
| 11 | Specific characteristics of phosphofructokinase-microtubule interaction. *FEBS Letters*, **1996**, 379, 191-5 | 3.8 | 21 |
| 10 | Specific derivatization of the active site tyrosine in dUTPase perturbs ligand binding to the active site. *Biochemical and Biophysical Research Communications*, **1996**, 219, 294-300 | 3.4 | 34 |
| 9 | Triosephosphate isomerase deficiency: predictions and facts. *Journal of Theoretical Biology*, **1996**, 182, 437-47 | 2.3 | 24 |
| 8 | Anti-calmodulin potency of indol alkaloids in in vitro systems. *European Journal of Pharmacology*, **1995**, 291, 73-82 | | 22 |
| 7 | Identification of tyrosine as a functional residue in the active site of Escherichia coli dUTPase. *BBA - Proteins and Proteomics*, **1994**, 1205, 146-50 | | 21 |
| 6 | Identification of tyrosine as an active site residue involved in the catalytic mechanism of Escherichia coli dUTPase. *Biochemical Society Transactions*, **1994**, 22, 233S | 5.1 | 2 |
| 5 | Modulation of the interaction between aldolase and glycerol-phosphate dehydrogenase by fructose phosphates. *BBA - Proteins and Proteomics*, **1991**, 1078, 236-42 | | 17 |
| 4 | Elasticity of the human red cell membrane skeleton. Effects of temperature and denaturants. *Biophysical Journal*, **1989**, 55, 255-62 | 2.9 | 92 |
| 3 | The control of cell metabolism for homogeneous vs. heterogeneous enzyme systems. *Journal of Theoretical Biology*, **1988**, 130, 407-22 | 2.3 | 39 |
| 2 | A simple approach to detect active-site-directed enzyme-enzyme interactions. The aldolase/glycerol-phosphate-dehydrogenase enzyme system. *FEBS Journal*, **1987**, 164, 655-9 | | 40 |