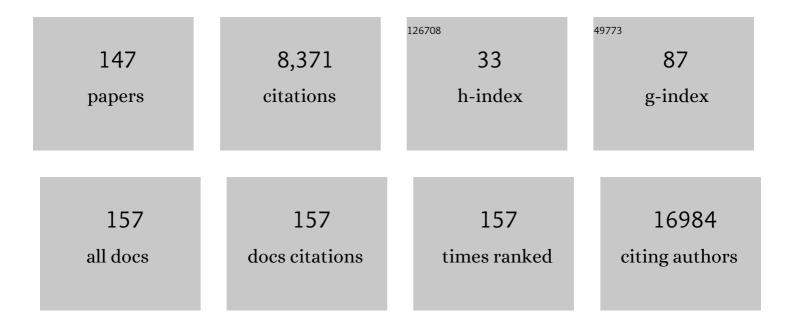
BeÃjta G Vértessy

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	4.3	4,701
2	Keeping Uracil Out of DNA: Physiological Role, Structure and Catalytic Mechanism of dUTPases. Accounts of Chemical Research, 2009, 42, 97-106.	7.6	213
3	Structural Biology and Regulation of Protein Import into the Nucleus. Journal of Molecular Biology, 2016, 428, 2060-2090.	2.0	204
4	Elasticity of the human red cell membrane skeleton. Effects of temperature and denaturants. Biophysical Journal, 1989, 55, 255-262.	0.2	105
5	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.	2.9	84
6	Aromatic stacking between nucleobase and enzyme promotes phosphate ester hydrolysis in dUTPase. Nucleic Acids Research, 2010, 38, 7179-7186.	6.5	80
7	Simultaneous Binding of Drugs with Different Chemical Structures to Ca2+-Calmodulin: Crystallographic and Spectroscopic Studies,. Biochemistry, 1998, 37, 15300-15310.	1.2	75
8	Structural Insights into the Catalytic Mechanism of Phosphate Ester Hydrolysis by dUTPase. Journal of Biological Chemistry, 2004, 279, 42907-42915.	1.6	75
9	Alternative Binding of Two Sequential Glycolytic Enzymes to Microtubules. Journal of Biological Chemistry, 1997, 272, 25542-25546.	1.6	73
10	p53 controls expression of the DNA deaminase APOBEC3B to limit its potential mutagenic activity in cancer cells. Nucleic Acids Research, 2017, 45, 11056-11069.	6.5	70
11	Uracil-Containing DNA in Drosophila: Stability, Stage-Specific Accumulation, and Developmental Involvement. PLoS Genetics, 2012, 8, e1002738.	1.5	63
12	Active site of mycobacterial dUTPase: Structural characteristics and a built-in sensor. Biochemical and Biophysical Research Communications, 2008, 373, 8-13.	1.0	60
13	Kinetic Mechanism of Human dUTPase, an Essential Nucleotide Pyrophosphatase Enzyme. Journal of Biological Chemistry, 2007, 282, 33572-33582.	1.6	58
14	Active site closure facilitates juxtaposition of reactant atoms for initiation of catalysis by human dUTPase. FEBS Letters, 2007, 581, 4783-4788.	1.3	58
15	Quantitative determination of uracil residues in Escherichia coli DNA: Contribution of ung, dug, and dut genes to uracil avoidance. DNA Repair, 2006, 5, 1407-1420.	1.3	52
16	Flexible glycine rich motif ofEscherichia coli deoxyuridine triphosphate nucleotidohydrolase is important for functional but not for structural integrity of the enzyme. , 1997, 28, 568-579.		51
17	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, 5670-5675.	3.3	46
18	Phenylalanine Ammonia‣yase atalyzed Deamination of an Acyclic Amino Acid: Enzyme Mechanistic Studies Aided by a Novel Microreactor Filled with Magnetic Nanoparticles. ChemBioChem, 2015, 16, 2283-2288.	1.3	46

#	Article	IF	CITATIONS
19	The dUTPase Enzyme Is Essential in Mycobacterium smegmatis. PLoS ONE, 2012, 7, e37461.	1.1	44
20	Immobilization of Phenylalanine Ammonia‣yase on Singleâ€Walled Carbon Nanotubes for Stereoselective Biotransformations in Batch and Continuousâ€Flow Modes. ChemCatChem, 2015, 7, 1122-1128.	1.8	43
21	Altered Subunit Communication in Subfamilies of Trimeric dUTPases. Biochemical and Biophysical Research Communications, 2000, 279, 534-542.	1.0	42
22	Altered Active Site Flexibility and a Structural Metal-binding Site in Eukaryotic dUTPase. Journal of Biological Chemistry, 2004, 279, 17932-17944.	1.6	42
23	Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. Nucleic Acids Research, 2006, 35, 495-505.	6.5	42
24	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, 2495-2505.	2.5	42
25	A simple approach to detect active-site-directed enzyme-enzyme interactions. The aldolase/glycerol-phosphate-dehydrogenase enzyme system. FEBS Journal, 1987, 164, 655-659.	0.2	41
26	The control of cell metabolism for homogeneous vs. heterogeneous enzyme systems. Journal of Theoretical Biology, 1988, 130, 407-422.	0.8	40
27	The complete triphosphate moiety of non-hydrolyzable substrate analogues is required for a conformational shift of the flexible C-terminus inE. colidUTP pyrophosphatase. FEBS Letters, 1998, 421, 83-88.	1.3	40
28	A new potent calmodulin antagonist with arylalkylamine structure: crystallographic, spectroscopic and functional studies. Journal of Molecular Biology, 2000, 297, 747-755.	2.0	40
29	Silicon carbide quantum dots for bioimaging. Journal of Materials Research, 2013, 28, 205-209.	1.2	40
30	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.	1.0	38
31	Developmental Regulation of dUTPase in Drosophila melanogaster. Journal of Biological Chemistry, 2004, 279, 22362-22370.	1.6	38
32	Preventive <scp>DNA</scp> repair by sanitizing the cellular (deoxy)nucleoside triphosphate pool. FEBS Journal, 2014, 281, 4207-4223.	2.2	38
33	Improving thermostability and catalytic activity of pyranose 2â€oxidase from <i>Trametes multicolor</i> by rational and semiâ€rational design. FEBS Journal, 2009, 276, 776-792.	2.2	37
34	Highly potent dUTPase inhibition by a bacterial repressor protein reveals a novel mechanism for gene expression control. Nucleic Acids Research, 2014, 42, 11912-11920.	6.5	36
35	A one-step method for quantitative determination of uracil in DNA by real-time PCR. Nucleic Acids Research, 2010, 38, e196-e196.	6.5	35
36	Shared developmental roles and transcriptional control of autophagy and apoptosis in <i>Caenorhabditis elegans</i> . Journal of Cell Science, 2011, 124, 1510-1518.	1.2	34

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37	Characterization of Microtubuleâ^'Phosphofructokinase Complex:Â Specific Effects of MgATP and Vinblastineâ€. Biochemistry, 1997, 36, 2051-2062.	1.2	33
38	Immobilized Whole-Cell Transaminase Biocatalysts for Continuous-Flow Kinetic Resolution of Amines. Catalysts, 2019, 9, 438.	1.6	33
39	Structural Characterization of Arginine Fingers: Identification of an Arginine Finger for the Pyrophosphatase dUTPases. Journal of the American Chemical Society, 2016, 138, 15035-15045.	6.6	32
40	Methylene substitution at the α–β bridging position within the phosphate chain of dUDP profoundly perturbs ligand accommodation into the dUTPase active site. Proteins: Structure, Function and Bioinformatics, 2008, 71, 308-319.	1.5	31
41	From "fluctuation fit―to "conformational selection― Evolution, rediscovery, and integration of a concept. BioEssays, 2011, 33, 30-34.	1.2	31
42	Enhanced Cellular Uptake of a New,in Silicoldentified Antitubercular Candidate by Peptide Conjugation. Bioconjugate Chemistry, 2012, 23, 900-907.	1.8	31
43	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.	6.5	31
44	Pyruvate Kinase as a Microtubule Destabilizing Factorin Vitro. Biochemical and Biophysical Research Communications, 1999, 254, 430-435.	1.0	30
45	A tradeoff between protein stability and conformational mobility in homotrimeric dUTPases. FEBS Letters, 2004, 566, 48-54.	1.3	30
46	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, 14437-14442.	3.3	30
47	Detection of uracil within DNA using a sensitive labeling method for <i>in vitro</i> and cellular applications. Nucleic Acids Research, 2016, 44, e28-e28.	6.5	29
48	Covalently immobilized Trp60Cys mutant of ω-transaminase from Chromobacterium violaceum for kinetic resolution of racemic amines in batch and continuous-flow modes. Biochemical Engineering Journal, 2018, 132, 270-278.	1.8	29
49	Neutron scattering studies on dUTPase complex in the presence of bioprotectant systems. Chemical Physics, 2008, 345, 250-258.	0.9	28
50	Mutations Decouple Proton Transfer from Phosphate Cleavage in the dUTPase Catalytic Reaction. ACS Catalysis, 2015, 5, 3225-3237.	5.5	28
51	Triosephosphate Isomerase Deficiency: Predictions and Facts. Journal of Theoretical Biology, 1996, 182, 437-447.	0.8	26
52	Specific characteristics of phosphofructokinase-microtubule interaction. FEBS Letters, 1996, 379, 191-195.	1.3	25
53	Identification of tyrosine as a functional residue in the active site of Escherichia coli dUTPase. BBA - Proteins and Proteomics, 1994, 1205, 146-150.	2.1	24
54	Life without dUTPase. Frontiers in Microbiology, 2016, 7, 1768.	1.5	24

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55	Expression and Properties of the Highly Alkalophilic Phenylalanine Ammonia-Lyase of Thermophilic Rubrobacter xylanophilus. PLoS ONE, 2014, 9, e85943.	1.1	24
56	Anti-calmodulin potency of indol alkaloids in in vitro systems. European Journal of Pharmacology, 1995, 291, 73-82.	2.7	23
57	Molecular shape and prominent role of βâ€strand swapping in organization of dUTPase oligomers. FEBS Letters, 2009, 583, 865-871.	1.3	23
58	Dynamics of re-constitution of the human nuclear proteome after cell division is regulated by NLS-adjacent phosphorylation. Cell Cycle, 2014, 13, 3551-3564.	1.3	23
59	A novel fruitfly protein under developmental control degrades uracil-DNA. Biochemical and Biophysical Research Communications, 2007, 355, 643-648.	1.0	22
60	Enzymatic degradation of poly-[(R)-3-hydroxybutyrate]: Mechanism, kinetics, consequences. International Journal of Biological Macromolecules, 2018, 112, 156-162.	3.6	22
61	Interaction of a new bis-indol derivative, KAR-2 with tubulin and its antimitotic activity. British Journal of Pharmacology, 1997, 121, 947-954.	2.7	21
62	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, 38803-38812.	1.6	21
63	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, 369-390.	0.4	21
64	Proteins with Complex Architecture as Potential Targets for Drug Design: A Case Study of Mycobacterium tuberculosis. PLoS Computational Biology, 2011, 7, e1002118.	1.5	21
65	Structure and enzymatic mechanism of a moonlighting dUTPase. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2298-2308.	2.5	21
66	Unshielding Multidrug Resistant Cancer through Selective Iron Depletion of P-Glycoprotein–Expressing Cells. Cancer Research, 2020, 80, 663-674.	0.4	21
67	Substrate Tunnel Engineering Aided by X-ray Crystallography and Functional Dynamics Swaps the Function of MIO-Enzymes. ACS Catalysis, 2021, 11, 4538-4549.	5.5	21
68	Investigations of homologous disaccharides by elastic incoherent neutron scattering and wavelet multiresolution analysis. Chemical Physics, 2013, 424, 56-61.	0.9	20
69	Composite Aromatic Boxes for Enzymatic Transformations of Quaternary Ammonium Substrates. Angewandte Chemie - International Edition, 2014, 53, 13471-13476.	7.2	20
70	Cross-species inhibition of dUTPase via the Staphylococcal Stl protein perturbs dNTP pool and colony formation in Mycobacterium. DNA Repair, 2015, 30, 21-27.	1.3	20
71	Assessment of Tractable Cysteines for Covalent Targeting by Screening Covalent Fragments. ChemBioChem, 2021, 22, 743-753.	1.3	19
72	Dissociation of Calmodulin-Target Peptide Complexes by the Lipid Mediator Sphingosylphosphorylcholine. Journal of Biological Chemistry, 2010, 285, 1799-1808.	1.6	18

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73	The First Enantioselective Total Synthesis of (â^')- <i>trans</i> -Dihydronarciclasine. Journal of Natural Products, 2017, 80, 1909-1917.	1.5	18
74	Differential control of dNTP biosynthesis and genome integrity maintenance by the dUTPase superfamily enzymes. Scientific Reports, 2017, 7, 6043.	1.6	18
75	Modulation of the interaction between aldolase and glycerol-phosphate dehydrogenase by fructose phosphates. BBA - Proteins and Proteomics, 1991, 1078, 236-242.	2.1	17
76	The interaction of a new anti-tumour drug, KAR-2 with calmodulin. British Journal of Pharmacology, 1997, 121, 955-962.	2.7	17
77	Direct contacts between conserved motifs of different subunits provide major contribution to active site organization in human and mycobacterial dUTPases. FEBS Letters, 2010, 584, 3047-3054.	1.3	17
78	The nucleotidohydrolases DCTPP1 and dUTPase are involved in the cellular response to decitabine. Biochemical Journal, 2016, 473, 2635-2643.	1.7	17
79	Study of solvent–protein coupling effects by neutron scattering. Journal of Biological Physics, 2010, 36, 207-220.	0.7	16
80	Evolutionary and mechanistic insights into substrate and product accommodation of <scp>CTP</scp> :phosphocholine cytidylyltransferase from <i><scp>P</scp>lasmodiumÂfalciparum</i> . FEBS Journal, 2013, 280, 3132-3148.	2.2	16
81	Evidence-Based Structural Model of the Staphylococcal Repressor Protein: Separation of Functions into Different Domains. PLoS ONE, 2015, 10, e0139086.	1.1	16
82	Identification of Extracellular Segments by Mass Spectrometry Improves Topology Prediction of Transmembrane Proteins. Scientific Reports, 2017, 7, 42610.	1.6	15
83	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. Scientific Reports, 2018, 8, 4326.	1.6	15
84	Structure-based inhibitor design of mutant RAS proteins—a paradigm shift. Cancer and Metastasis Reviews, 2020, 39, 1091-1105.	2.7	15
85	Catalytic mechanism of α-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, 10542-10555.	6.5	14
86	Molecular cloning and characterization of a thermostable esterase/lipase produced by a novel Anoxybacillus flavithermus strain. Journal of General and Applied Microbiology, 2013, 59, 119-134.	0.4	14
87	Bisepoxide Crossâ€Linked Enzyme Aggregates—New Immobilized Biocatalysts for Selective Biotransformations. ChemCatChem, 2014, 6, 1463-1469.	1.8	14
88	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.	1.6	14
89	Multidimensional NMR Identifies the Conformational Shift Essential for Catalytic Competence in the 60-kDa Drosophila melanogaster dUTPase Trimer. Journal of Biological Chemistry, 2004, 279, 17945-17950.	1.6	13
90	Nuclear localization signal-dependent and -independent movements of Drosophila melanogaster dUTPase isoforms during nuclear cleavage. Biochemical and Biophysical Research Communications, 2009, 381, 271-275.	1.0	13

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91	Molecular Mechanisms of Survival Strategies in Extreme Conditions. Life, 2012, 2, 364-376.	1.1	13
92	CRISPR/Cas9-Mediated Knock-Out of dUTPase in Mice Leads to Early Embryonic Lethality. Biomolecules, 2019, 9, 136.	1.8	13
93	Discovery of Novel MDR-Mycobacterium tuberculosis Inhibitor by New FRIGATE Computational Screen. PLoS ONE, 2011, 6, e28428.	1.1	13
94	Genome-wide alterations of uracil distribution patterns in human DNA upon chemotherapeutic treatments. ELife, 2020, 9, .	2.8	13
95	Highly Sensitive and Rapid Characterization of the Development of Synchronized Blood Stage Malaria Parasites Via Magneto-Optical Hemozoin Quantification. Biomolecules, 2019, 9, 579.	1.8	12
96	Structural insights into the tyrosine phosphorylation–mediated inhibition of SH3 domain–ligand interactions. Journal of Biological Chemistry, 2019, 294, 4608-4620.	1.6	12
97	Rapid and quantitative antimalarial drug efficacy testing via the magneto-optical detection of hemozoin. Scientific Reports, 2020, 10, 14025.	1.6	11
98	Expanding the DNA alphabet in the fruit fly. Fly, 2013, 7, 23-27.	0.9	10
99	Perturbation of genome integrity to fight pathogenic microorganisms. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3593-3612.	1.1	10
100	Molecular Mechanism for the Thermo-Sensitive Phenotype of CHO-MT58 Cell Line Harbouring a Mutant CTP:Phosphocholine Cytidylyltransferase. PLoS ONE, 2015, 10, e0129632.	1.1	10
101	Drosophila proteins involved in metabolism of uracilâ€DNA possess different types of nuclear localization signals. FEBS Journal, 2010, 277, 2142-2156.	2.2	9
102	A Methylidene Group in the Phosphonic Acid Analogue of Phenylalanine Reverses the Enantiopreference of Binding to Phenylalanine Ammonia‣yases. Advanced Synthesis and Catalysis, 2017, 359, 2109-2120.	2.1	9
103	In Vitro Analysis of Predicted DNA-Binding Sites for the Stl Repressor of the Staphylococcus aureus SaPIBov1 Pathogenicity Island. PLoS ONE, 2016, 11, e0158793.	1.1	9
104	Immobilization of the Aspartate Ammonia‣yase from <i>Pseudomonas fluorescens</i> R124 on Magnetic Nanoparticles: Characterization and Kinetics. ChemBioChem, 2022, 23, .	1.3	9
105	Structure and mechanism of calmodulin binding to a signaling sphingolipid reveal new aspects of lipidâ€protein interactions. FASEB Journal, 2010, 24, 3829-3839.	0.2	8
106	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.	1.6	8
107	Trading in cooperativity for specificity to maintain uracil-free DNA. Scientific Reports, 2016, 6, 24219.	1.6	8
108	The role of enzyme adsorption in the enzymatic degradation of an aliphatic polyester. Enzyme and Microbial Technology, 2019, 120, 110-116.	1.6	8

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109	Calpain-Catalyzed Proteolysis of Human dUTPase Specifically Removes the Nuclear Localization Signal Peptide. PLoS ONE, 2011, 6, e19546.	1.1	8
110	Crystallization and preliminary X-ray studies of dUTPase from Mason–Pfizer monkey retrovirus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 399-401.	0.7	7
111	The Stl repressor from <i>Staphylococcus aureus</i> is an efficient inhibitor of the eukaryotic fruitfly <scp>dUTP</scp> ase. FEBS Open Bio, 2018, 8, 158-167.	1.0	7
112	Uracil moieties in <i>Plasmodium falciparum</i> genomic <scp>DNA</scp> . FEBS Open Bio, 2018, 8, 1763-1772.	1.0	7
113	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, 488.	1.8	7
114	A novel phenylalanine ammonia-lyase from kangiella koreensis. Studia Universitatis Babes-Bolyai Chemia, 2017, 62, 293-308.	0.1	7
115	Association of RNA with the uracilâ€DNAâ€degrading factor has major conformational effects and is potentially involved in protein folding. FEBS Journal, 2011, 278, 295-315.	2.2	6
116	<scp>NLS</scp> copyâ€number variation governs efficiency of nuclear import – case study on d <scp>UTP</scp> ases. FEBS Journal, 2014, 281, 5463-5478.	2.2	6
117	Structural determinants of the catalytic mechanism of Plasmodium CCT, a key enzyme of malaria lipid biosynthesis. Scientific Reports, 2018, 8, 11215.	1.6	6
118	Beyond Chelation: EDTA Tightly Binds Taq DNA Polymerase, MutT and dUTPase and Directly Inhibits dNTPase Activity. Biomolecules, 2019, 9, 621.	1.8	6
119	An Acridoneâ€Based Fluorescent Chemosensor for Cationic and Anionic Species, and Its Application for Molecular Logic Operations. ChemistrySelect, 2019, 4, 11936-11943.	0.7	6
120	Detection of Genomic Uracil Patterns. International Journal of Molecular Sciences, 2021, 22, 3902.	1.8	6
121	Crystallization and preliminary diffraction analysis of Ca2+-calmodulin-drug and apocalmodulin-drug complexes. , 1997, 28, 131-134.		5
122	Physiological truncation and domain organization of a novel uracilâ€DNAâ€degrading factor. FEBS Journal, 2010, 277, 1245-1259.	2.2	5
123	The Metagenomic Telescope. PLoS ONE, 2014, 9, e101605.	1.1	5
124	Structural characterization of a complex derived from lead(II) perchlorate and acridono-18-crown-6 ether. Structural Chemistry, 2015, 26, 1467-1471.	1.0	5
125	Exploring the role of the phage-specific insert of bacteriophage Φ11 dUTPase. Structural Chemistry, 2015, 26, 1425-1432.	1.0	5
126	Secondary Structure Prediction of Protein Constructs Using Random Incremental Truncation and Vacuum-Ultraviolet CD Spectroscopy. PLoS ONE, 2016, 11, e0156238.	1.1	5

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127	Potential steps in the evolution of a fused trimeric allâ $\widehat{\mathfrak{sl}^2}$ dUTPase involve a catalytically competent fused dimeric intermediate. FEBS Journal, 2016, 283, 3268-3286.	2.2	5
128	The novel technique of vapor pressure analysis to monitor the enzymatic degradation of PHB by HPLC chromatography. Analytical Biochemistry, 2017, 521, 20-27.	1.1	5
129	Mass spectrometryâ€based analysis of macromolecular complexes of Staphylococcus aureus uracilâ€DNA glycosylase and its inhibitor reveals specific variations due to naturally occurring mutations. FEBS Open Bio, 2019, 9, 420-427.	1.0	5
130	Crystallization and preliminary crystallographic analysis of dUTPase from the ϕ11 helper phage ofStaphylococcus aureus. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1411-1413.	0.7	4
131	Exploiting a Phage-Bacterium Interaction System as a Molecular Switch to Decipher Macromolecular Interactions in the Living Cell. Viruses, 2018, 10, 168.	1.5	4
132	Evaluation of critical design parameters for RTâ€qPCRâ€based analysis of multiple dUTPase isoform genes in mice. FEBS Open Bio, 2019, 9, 1153-1170.	1.0	4
133	Identification of tyrosing as an active site residue involved in the catalytic mechanism of Escherichia coli dUTPase. Biochemical Society Transactions, 1994, 22, 233S-233S.	1.6	3
134	d <scp>UTP</scp> ase expression correlates with cell division potential in <i>DrosophilaÂmelanogaster</i> . FEBS Journal, 2015, 282, 1998-2013.	2.2	3
135	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.	1.0	3
136	The Role of a Key Amino Acid Position in Species-Specific Proteinaceous dUTPase Inhibition. Biomolecules, 2019, 9, 221.	1.8	3
137	Synthesis of New Chiral Crown Ethers Containing Phosphine or Secondary Phosphine Oxide Units. Synthesis, 2020, 52, 2870-2882.	1.2	3
138	Structural characterization of a sodium perchlorateâ~'acridino-18-crown-6 ether complex. Structural Chemistry, 2018, 29, 113-118.	1.0	2
139	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.	1.6	2
140	Viruses with U-DNA: New Avenues for Biotechnology. Viruses, 2021, 13, 875.	1.5	2
141	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.	0.6	2
142	Primary Founder Mutations in the PRKDC Gene Increase Tumor Mutation Load in Colorectal Cancer. International Journal of Molecular Sciences, 2022, 23, 633.	1.8	2
143	Functional Analysis on a Naturally Occurring Variant of the Staphylococcus Aureus Uracil DNA Glycosylase Inhibitor. Periodica Polytechnica: Chemical Engineering, 2017, , .	0.5	1
144	Flexible glycine rich motif of Escherichia coli deoxyuridine triphosphate nucleotidohydrolase is		1

important for functional but not for structural integrity of the enzyme., 1997, 28, 568.

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145	Factors influencing nucleo-cytoplasmic trafficking: which matter? Response to Alvisi & Jans' comment onPhosphorylation adjacent to the nuclear localization signal of human dUTPase abolishes nuclear import: structural and mechanistic insights. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2777-2778.	2.5	0
146	Identification of a nuclear localization signal in the Plasmodium falciparum CTP: phosphocholine cytidylyltransferase enzyme. Scientific Reports, 2020, 10, 19739.	1.6	0
147	Search and destroy: versatile proteins offer unique structural solutions against uracil in DNA. Amino Acids, Peptides and Proteins, 2019, , 1-13.	0.7	0