

Orsolya Barabas

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

1,330
citations

331259

21
h-index

377514

34
g-index

46
all docs

46
docs citations

46
times ranked

1659
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanism of IS200/IS605 Family DNA Transposases: Activation and Transposon-Directed Target Site Selection. <i>Cell</i> , 2008, 132, 208-220.	13.5	120
2	<i>Helicobacter Pylori</i> 's Plasticity Zones Are Novel Transposable Elements. <i>PLoS ONE</i> , 2009, 4, e6859.	1.1	90
3	Structural Insights into the Catalytic Mechanism of Phosphate Ester Hydrolysis by dUTPase. <i>Journal of Biological Chemistry</i> , 2004, 279, 42907-42915.	1.6	75
4	In Vitro Reconstitution of a Single-Stranded Transposition Mechanism of IS608. <i>Molecular Cell</i> , 2008, 29, 302-312.	4.5	65
5	A highly soluble Sleeping Beauty transposase improves control of gene insertion. <i>Nature Biotechnology</i> , 2019, 37, 1502-1512.	9.4	63
6	Active site of mycobacterial dUTPase: Structural characteristics and a built-in sensor. <i>Biochemical and Biophysical Research Communications</i> , 2008, 373, 8-13.	1.0	60
7	Active site closure facilitates juxtaposition of reactant atoms for initiation of catalysis by human dUTPase. <i>FEBS Letters</i> , 2007, 581, 4783-4788.	1.3	58
8	Crystal structure of the primary piRNA biogenesis factor Zucchini reveals similarity to the bacterial PLD endonuclease Nuc. <i>Rna</i> , 2012, 18, 2128-2134.	1.6	55
9	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <i>Nucleic Acids Research</i> , 2014, 42, 13525-13533.	6.5	55
10	Sleeping Beauty transposase structure allows rational design of hyperactive variants for genetic engineering. <i>Nature Communications</i> , 2016, 7, 11126.	5.8	51
11	Transposase-DNA Complex Structures Reveal Mechanisms for Conjugative Transposition of Antibiotic Resistance. <i>Cell</i> , 2018, 173, 208-220.e20.	13.5	51
12	Altered Active Site Flexibility and a Structural Metal-binding Site in Eukaryotic dUTPase. <i>Journal of Biological Chemistry</i> , 2004, 279, 17932-17944.	1.6	42
13	Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. <i>Nucleic Acids Research</i> , 2006, 35, 495-505.	6.5	42
14	Revisiting the mechanism of the autoactivation of the complement protease C1r in the C1 complex: Structure of the active catalytic region of C1r. <i>Molecular Immunology</i> , 2008, 45, 1752-1760.	1.0	41
15	DNA recognition and the precleavage state during single-stranded DNA transposition in <i>D. radiodurans</i> . <i>EMBO Journal</i> , 2010, 29, 3840-3852.	3.5	41
16	The USTC co-opts an ancient machinery to drive piRNA transcription in <i>C. elegans</i> . <i>Genes and Development</i> , 2019, 33, 90-102.	2.7	34
17	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2022, 50, 3155-3168.	6.5	34
18	Sequence analysis of tyrosine recombinases allows annotation of mobile genetic elements in prokaryotic genomes. <i>Molecular Systems Biology</i> , 2021, 17, e9880.	3.2	33

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19	Acquisition of an Archaea-like ribonuclease H domain by plant L1 retrotransposons supports modular evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20140-20145.	3.3	32
20	Methylene substitution at the β bridging position within the phosphate chain of dUDP profoundly perturbs ligand accommodation into the dUTPase active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 308-319.	1.5	31
21	Resetting the Site: Redirecting Integration of an Insertion Sequence in a Predictable Way. <i>Molecular Cell</i> , 2009, 34, 612-619.	4.5	31
22	Molecular shape and prominent role of β strand swapping in organization of dUTPase oligomers. <i>FEBS Letters</i> , 2009, 583, 865-871.	1.3	23
23	dUTPase and Nucleocapsid Polypeptides of the Mason-Pfizer Monkey Virus Form a Fusion Protein in the Virion with Homotrimeric Organization and Low Catalytic Efficiency. <i>Journal of Biological Chemistry</i> , 2003, 278, 38803-38812.	1.6	21
24	Structural snapshots of Xer recombination reveal activation by synaptic complex remodeling and DNA bending. <i>ELife</i> , 2016, 5, .	2.8	15
25	Catalytic mechanism of β -phosphate attack in dUTPase is revealed by X-ray crystallographic snapshots of distinct intermediates, 31P-NMR spectroscopy and reaction path modelling. <i>Nucleic Acids Research</i> , 2013, 41, 10542-10555.	6.5	14
26	Intermolecular base stacking mediates RNA-RNA interaction in a crystal structure of the RNA chaperone Hfq. <i>Scientific Reports</i> , 2017, 7, 9903.	1.6	14
27	Theoretical and experimental studies on ring closure reactions of 4(5)-chloro-5(4)-hydroxyalkylamino-6-nitro-3(2 H)-pyridazinones. <i>Computational and Theoretical Chemistry</i> , 2001, 545, 75-96.	1.5	12
28	Targeting IS608 transposon integration to highly specific sequences by structure-based transposon engineering. <i>Nucleic Acids Research</i> , 2018, 46, 4152-4163.	6.5	12
29	Jump ahead with a twist: DNA acrobatics drive transposition forward. <i>Current Opinion in Structural Biology</i> , 2019, 59, 168-177.	2.6	12
30	Novel ring transformations of condensed [1,2,4]triazolo[4,3-b]pyridazine-6(5H)-one-3(2H)-thiones effected by dialkyl-acetylenedicarboxylates. <i>Tetrahedron</i> , 2001, 57, 7191-7198.	1.0	11
31	Effects of stably incorporated iron on protein phosphatase ϵ 1 structure and activity. <i>FEBS Letters</i> , 2018, 592, 4028-4038.	1.3	11
32	A single amino acid switch converts the Sleeping Beauty transposase into an efficient unidirectional excisionase with utility in stem cell reprogramming. <i>Nucleic Acids Research</i> , 2020, 48, 316-331.	6.5	11
33	Towards Dissecting the Mechanism of Protein Phosphatase ϵ 1 Inhibition by Its C-terminal Phosphorylation. <i>ChemBioChem</i> , 2021, 22, 834-838.	1.3	11
34	Synthesis and stereochemistry of dispiro substituted pyridazines: Application of ellipticity-absorbance ratio spectra for proving enantiomeric relationship by HPLC-CD/UV detection. <i>Chirality</i> , 2002, 14, 365-371.	1.3	10
35	Engineered <i>Sleeping Beauty</i> transposase redirects transposon integration away from genes. <i>Nucleic Acids Research</i> , 2022, 50, 2807-2825.	6.5	9
36	Structure of an <i>Escherichia coli</i> Hfq:RNA complex at 0.97Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1492-1497.	0.4	8

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37	Crystallization and preliminary X-ray studies of dUTPase from Masonâ€“Pfizer monkey retrovirus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 399-401.	0.7	7
38	Structural Determinants of Sleeping Beauty Transposase Activity. Molecular Therapy, 2016, 24, 1369-1377.	3.7	7
39	Conjugative transposition of the vancomycin resistance carrying Tn<i>1549</i>: enzymatic requirements and target site preferences. Molecular Microbiology, 2018, 107, 639-658.	1.2	7
40	Structural basis of solid solution formation during chiral resolution. Tetrahedron: Asymmetry, 2000, 11, 4061-4070.	1.8	5
41	Snapshots of a genetic cut-and-paste. Nature, 2019, 575, 447-448.	13.7	2
42	Structure and function of DNA transposition assemblies involved in antibiotic resistance spreading. FASEB Journal, 2022, 36, .	0.2	0