

Wim VersÃ©es

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

3,110
citations

186265

28
h-index

168389

53
g-index

72
all docs

72
docs citations

72
times ranked

4254
citing authors

#	ARTICLE	IF	CITATIONS
1	Nanobodies as allosteric modulators of Parkinsonâ€™s disease-associated LRRK2. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	15
2	Structure-Activity Relationship (SAR) Study of Spautin-1 to Entail the Discovery of Novel NEK4 Inhibitors. International Journal of Molecular Sciences, 2021, 22, 635.	4.1	3
3	Entropic pressure controls the oligomerization of the <i>Vibrio cholerae</i> ParD2 antitoxin. Acta Crystallographica Section D: Structural Biology, 2021, 77, 904-920.	2.3	5
4	Allosteric Inhibition of Parkinsonâ€™s-Linked LRRK2 by Constrained Peptides. ACS Chemical Biology, 2021, 16, 2326-2338.	3.4	15
5	Structural and kinetic characterization of Trypanosoma congolense pyruvate kinase. Molecular and Biochemical Parasitology, 2020, 236, 111263.	1.1	1
6	GTP Binding Is Necessary for the Activation of a Toxic Mutant Isoform of the Essential GTPase ObgE. International Journal of Molecular Sciences, 2020, 21, 16.	4.1	13
7	Allosteric modulation of the GTPase activity of a bacterial LRRK2 homolog by conformation-specific Nanobodies. Biochemical Journal, 2020, 477, 1203-1218.	3.7	12
8	A structure of substrate-bound Synaptojanin1 provides new insights in its mechanism and the effect of disease mutations. ELife, 2020, 9, .	6.0	11
9	TBC1D24-TLDC-related epilepsy exercise-induced dystonia: rescue by antioxidants in a disease model. Brain, 2019, 142, 2319-2335.	7.6	44
10	Biochemical determinants of ObgE-mediated persistence. Molecular Microbiology, 2019, 112, 1593-1608.	2.5	7
11	Roco Proteins: GTPases with a Baroque Structure and Mechanism. International Journal of Molecular Sciences, 2019, 20, 147.	4.1	31
12	Structure and nucleotide-induced conformational dynamics of the Chlorobium tepidum Roco protein. Biochemical Journal, 2019, 476, 51-66.	3.7	21
13	Phosphorylation decelerates conformational dynamics in bacterial translation elongation factors. Science Advances, 2018, 4, eaap9714.	10.3	37
14	Structural and biochemical analysis of the dual-specificity Trm10 enzyme from <i>Thermococcus kodakaraensis</i> prompts reconsideration of its catalytic mechanism. Rna, 2018, 24, 1080-1092.	3.5	16
15	Biochemical and kinetic properties of the complex Roco G-protein cycle. Biological Chemistry, 2018, 399, 1447-1456.	2.5	14
16	Yeast and Cancer: Common Mechanism Underlying Activation of Ras by Glycolytic Flux. FASEB Journal, 2018, 32, lb143.	0.5	0
17	Structural and biochemical analysis of Escherichia coli ObgE, a central regulator of bacterial persistence. Journal of Biological Chemistry, 2017, 292, 5871-5883.	3.4	20
18	The antibacterial prodrug activator Rv2466c is a mycothiol-dependent reductase in the oxidative stress response of Mycobacterium tuberculosis. Journal of Biological Chemistry, 2017, 292, 13097-13110.	3.4	27

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19	Structural and biochemical characterization of the nucleoside hydrolase from <i>C. elegans</i> reveals the role of two active site cysteine residues in catalysis. <i>Protein Science</i> , 2017, 26, 985-996.	7.6	5
20	Fructose-1,6-bisphosphate couples glycolytic flux to activation of Ras. <i>Nature Communications</i> , 2017, 8, 922.	12.8	161
21	A homologue of the Parkinson's disease-associated protein LRRK2 undergoes a monomer-dimer transition during GTP turnover. <i>Nature Communications</i> , 2017, 8, 1008.	12.8	53
22	The LRR-Roc-COR module of the <i>Chlorobium tepidum</i> Roco protein: crystallization and X-ray crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 520-524.	0.8	5
23	Invited review: MnmE, a GTPase that drives a complex tRNA modification reaction. <i>Biopolymers</i> , 2016, 105, 568-579.	2.4	14
24	Skywalker-TBC1D24 has a lipid-binding pocket mutated in epilepsy and required for synaptic function. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 965-973.	8.2	55
25	Substrate Recognition and Activity Regulation of the <i>Escherichia coli</i> mRNA Endonuclease MazF. <i>Journal of Biological Chemistry</i> , 2016, 291, 10950-10960.	3.4	44
26	Structural model of the dimeric Parkinson's protein LRRK2 reveals a compact architecture involving distant interdomain contacts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4357-E4366.	7.1	130
27	Structural and functional insights into tRNA binding and adenosine N1-methylation by an archaeal Trm10 homologue. <i>Nucleic Acids Research</i> , 2016, 44, 940-953.	14.5	27
28	Obg and Membrane Depolarization Are Part of a Microbial Bet-Hedging Strategy that Leads to Antibiotic Tolerance. <i>Molecular Cell</i> , 2015, 59, 9-21.	9.7	261
29	A Single-Amino-Acid Substitution in Obg Activates a New Programmed Cell Death Pathway in <i>Escherichia coli</i> . <i>MBio</i> , 2015, 6, e01935-15.	4.1	22
30	It Takes Two to Rule Translation Elongation. <i>Structure</i> , 2015, 23, 7-9.	3.3	3
31	SAXS analysis of the tRNA-modifying enzyme complex MnmE/MnmG reveals a novel interaction mode and GTP-induced oligomerization. <i>Nucleic Acids Research</i> , 2014, 42, 5978-5992.	14.5	27
32	Characterization of two homologous 2'-O-methyltransferases showing different specificities for their tRNA substrates. <i>Rna</i> , 2014, 20, 1257-1271.	3.5	69
33	A putative de-N-acetylase of the PIG-L superfamily affects fluoroquinolone tolerance in <i>Pseudomonas aeruginosa</i> . <i>Pathogens and Disease</i> , 2014, 71, 39-54.	2.0	25
34	Structure of an early native-like intermediate of β 2-microglobulin amyloidogenesis. <i>Protein Science</i> , 2013, 22, 1349-1357.	7.6	14
35	NrdH-redoxin of <i>Mycobacterium tuberculosis</i> and <i>Corynebacterium glutamicum</i> Dimerizes at High Protein Concentration and Exclusively Receives Electrons from Thioredoxin Reductase. <i>Journal of Biological Chemistry</i> , 2013, 288, 7942-7955.	3.4	14
36	Crystal structures of the tRNA:m ² G6 methyltransferase Trm14/TrmN from two domains of life. <i>Nucleic Acids Research</i> , 2012, 40, 5149-5161.	14.5	33

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37	The open reading frame TTC1157 of <i>Thermus thermophilus</i> HB27 encodes the methyltransferase forming N ² -methylguanosine at position 6 in tRNA. <i>Rna</i> , 2012, 18, 815-824.	3.5	16
38	The <i>Escherichia coli</i> GTPase ObgE modulates hydroxyl radical levels in response to DNA replication fork arrest. <i>FEBS Journal</i> , 2012, 279, 3692-3704.	4.7	9
39	ELP3 Controls Active Zone Morphology by Acetylating the ELKS Family Member Bruchpilot. <i>Neuron</i> , 2011, 72, 776-788.	8.1	94
40	Crystallization and preliminary X-ray crystallographic analysis of putative tRNA-modification enzymes from <i>Pyrococcus furiosus</i> and <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1432-1435.	0.7	3
41	The Universally Conserved Prokaryotic GTPases. <i>Microbiology and Molecular Biology Reviews</i> , 2011, 75, 507-542.	6.6	175
42	Polymeric nanoreactors for enzyme replacement therapy of MNGIE. <i>Journal of Controlled Release</i> , 2010, 148, e19-e20.	9.9	10
43	Elongator, a conserved multitasking complex?. <i>Molecular Microbiology</i> , 2010, 76, 1065-1069.	2.5	317
44	Evaluation of Nucleoside Hydrolase Inhibitors for Treatment of African Trypanosomiasis. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 1900-1908.	3.2	35
45	Structure and Mechanism of the 6-Oxopurine Nucleosidase from <i>Trypanosoma brucei brucei</i> . <i>Biochemistry</i> , 2010, 49, 8999-9010.	2.5	18
46	Assessment of stability, toxicity and immunogenicity of new polymeric nanoreactors for use in enzyme replacement therapy of MNGIE. <i>Journal of Controlled Release</i> , 2009, 137, 246-254.	9.9	75
47	Synthesis of Bicyclic N-Arylmethyl-Substituted Iminoribitol Derivatives as Selective Nucleoside Hydrolase Inhibitors. <i>ChemMedChem</i> , 2009, 4, 249-260.	3.2	15
48	Crystal structures of <i>T. vivax</i> nucleoside hydrolase in complex with new potent and specific inhibitors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 953-960.	2.3	22
49	G-Domain Dimerization Orchestrates the tRNA Wobble Modification Reaction in the MnmE/GidA Complex. <i>Journal of Molecular Biology</i> , 2009, 392, 910-922.	4.2	39
50	N-Arylmethyl substituted iminoribitol derivatives as inhibitors of a purine specific nucleoside hydrolase. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 6752-6763.	3.0	33
51	Crystal Structures of the Conserved tRNA-Modifying Enzyme GidA: Implications for Its Interaction with MnmE and Substrate. <i>Journal of Molecular Biology</i> , 2008, 380, 532-547.	4.2	46
52	A Flexible Loop as a Functional Element in the Catalytic Mechanism of Nucleoside Hydrolase from <i>Trypanosoma vivax</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 22272-22282.	3.4	19
53	Molecular Mechanism of Allosteric Substrate Activation in a Thiamine Diphosphate-dependent Decarboxylase. <i>Journal of Biological Chemistry</i> , 2007, 282, 35269-35278.	3.4	32
54	The Crystal Structure of <i>Trypanosoma cruzi</i> Glucokinase Reveals Features Determining Oligomerization and Anomer Specificity of Hexose-phosphorylating Enzymes. <i>Journal of Molecular Biology</i> , 2007, 372, 1215-1226.	4.2	29

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55	Characterization of Phenylpyruvate Decarboxylase, Involved in Auxin Production of <i>Azospirillum brasilense</i> . <i>Journal of Bacteriology</i> , 2007, 189, 7626-7633.	2.2	110
56	1,2,3-Triazolylalkylribitol derivatives as nucleoside hydrolase inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2007, 17, 2523-2526.	2.2	19
57	The crystal structure of phenylpyruvate decarboxylase from <i>Azospirillum brasilense</i> at 1.5 Å resolution. <i>FEBS Journal</i> , 2007, 274, 2363-2375.	4.7	35
58	Multiple Transients in the Pre-Steady-State of Nucleoside Hydrolase Reveal Complex Substrate Binding, Product Base Release, and Two Apparent Rates of Chemistry. <i>Biochemistry</i> , 2006, 45, 9307-9318.	2.5	13
59	New Insights into the Mechanism of Nucleoside Hydrolases from the Crystal Structure of the <i>Escherichia coli</i> YbeK Protein Bound to the Reaction Product. <i>Biochemistry</i> , 2006, 45, 773-782.	2.5	32
60	Transition-state Complex of the Purine-specific Nucleoside Hydrolase of <i>T. vivax</i> : Enzyme Conformational Changes and Implications for Catalysis. <i>Journal of Molecular Biology</i> , 2006, 359, 331-346.	4.2	39
61	Quantum chemical study of leaving group activation in <i>T. vivax</i> nucleoside hydrolase. <i>International Journal of Quantum Chemistry</i> , 2006, 106, 565-570.	2.0	7
62	Structural basis for the recognition of complex-type biantennary oligosaccharides by <i>Pterocarpus angolensis</i> lectin. <i>FEBS Journal</i> , 2006, 273, 2407-2420.	4.7	13
63	Substrate-assisted Leaving Group Activation in Enzyme-catalyzed N-Glycosidic Bond Cleavage. <i>Journal of Biological Chemistry</i> , 2005, 280, 14799-14802.	3.4	28
64	Therapeutic Nanoreactors: Combining Chemistry and Biology in a Novel Triblock Copolymer Drug Delivery System. <i>Nano Letters</i> , 2005, 5, 2220-2224.	9.1	196
65	Leaving Group Activation by Aromatic Stacking: An Alternative to General Acid Catalysis. <i>Journal of Molecular Biology</i> , 2004, 338, 1-6.	4.2	87
66	Catalysis by nucleoside hydrolases. <i>Current Opinion in Structural Biology</i> , 2003, 13, 731-738.	5.7	102
67	Cloning, preliminary characterization and crystallization of nucleoside hydrolases from <i>Caenorhabditis elegans</i> and <i>Campylobacter jejuni</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1087-1089.	2.5	14
68	Pre-Steady-State Analysis of the Nucleoside Hydrolase of <i>Trypanosoma vivax</i> . Evidence for Half-of-the-Sites Reactivity and Rate-Limiting Product Release. <i>Biochemistry</i> , 2003, 42, 12902-12908.	2.5	21
69	Enzyme-Substrate Interactions in the Purine-specific Nucleoside Hydrolase from <i>Trypanosoma vivax</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 15938-15946.	3.4	64
70	Structure and function of a novel purine specific nucleoside hydrolase from <i>Trypanosoma vivax</i> . Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 307, 1363-1379.	4.2	89