

Hans-Joachim Wieden

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

1,993
citations

361413

20
h-index

254184

43
g-index

63
all docs

63
docs citations

63
times ranked

2147
citing authors

#	ARTICLE	IF	CITATIONS
1	Construction of a highly selective and sensitive carbohydrate-detecting biosensor utilizing Computational Identification of Non-disruptive Conjugation sites (CINC) for flexible and streamlined biosensor design. <i>Biosensors and Bioelectronics</i> , 2022, 200, 113899.	10.1	2
2	Development of a Real-Time Pectic Oligosaccharide-Detecting Biosensor Using the Rapid and Flexible Computational Identification of Non-Disruptive Conjugation Sites (CINC) Biosensor Design Platform. <i>Sensors</i> , 2022, 22, 948.	3.8	0
3	Ribosomal Protein S1 Improves the Protein Yield of an <i>In Vitro</i> Reconstituted Cell-Free Translation System. <i>ACS Synthetic Biology</i> , 2022, 11, 1004-1008.	3.8	4
4	Strategies for improving antimicrobial peptide production. <i>Biotechnology Advances</i> , 2022, 59, 107968.	11.7	31
5	Through the looking glass: milestones on the road towards mirroring life. <i>Trends in Biochemical Sciences</i> , 2021, 46, 931-943.	7.5	5
6	Emerging regulatory challenges of next-generation synthetic biology. <i>Biochemistry and Cell Biology</i> , 2021, 99, 766-771.	2.0	3
7	A Quick Primer in Fluorescence-Based and Pre-steady State Methods for Determining Protein–Nucleotide Affinities. <i>Methods in Molecular Biology</i> , 2021, 2263, 273-287.	0.9	0
8	Human DDX17 Unwinds Rift Valley Fever Virus Non-Coding RNAs. <i>International Journal of Molecular Sciences</i> , 2021, 22, 54.	4.1	20
9	Knowledge Gaps in the Understanding of Antimicrobial Resistance in Canada. <i>Frontiers in Public Health</i> , 2021, 9, 726484.	2.7	26
10	Cellular roles of the human Obg-like ATPase 1 (hOLA1) and its YchF homologs. <i>Biochemistry and Cell Biology</i> , 2020, 98, 1-11.	2.0	7
11	Non-coding RNAs: what are we missing?. <i>Biochemistry and Cell Biology</i> , 2020, 98, 23-30.	2.0	16
12	Parenting researchers’ an invisible divide. <i>EMBO Reports</i> , 2020, 21, e50738.	4.5	3
13	Loss of m1acp3 ⁺ Ribosomal RNA Modification Is a Major Feature of Cancer. <i>Cell Reports</i> , 2020, 31, 107611.	6.4	64
14	Elongation factor-Tu can repetitively engage aminoacyl-tRNA within the ribosome during the proofreading stage of tRNA selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3610-3620.	7.1	31
15	Elongation Factor Tu Switch I Element is a Gate for Aminoacyl-tRNA Selection. <i>Journal of Molecular Biology</i> , 2020, 432, 3064-3077.	4.2	11
16	Rapid metagenomics analysis of EMS vehicles for monitoring pathogen load using nanopore DNA sequencing. <i>PLoS ONE</i> , 2019, 14, e0219961.	2.5	9
17	Elongation Factor Tu’s Nucleotide Binding Is Governed by a Thermodynamic Landscape Unique among Bacterial Translation Factors. <i>Journal of the American Chemical Society</i> , 2019, 141, 10236-10246.	13.7	5
18	Rapid generation of sequence-diverse terminator libraries and their parameterization using quantitative Term-Seq. <i>Synthetic Biology</i> , 2019, 4, ysz026.	2.2	11

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19	The C-terminal helix of ribosomal P stalk recognizes a hydrophobic groove of elongation factor 2 in a novel fashion. <i>Nucleic Acids Research</i> , 2018, 46, 3232-3244.	14.5	27
20	Molecular Determinants for 23S rRNA Recognition and Modification by the E. coli Pseudouridine Synthase RluE. <i>Journal of Molecular Biology</i> , 2018, 430, 1284-1294.	4.2	2
21	The Emergency Medical Service Microbiome. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	7
22	sdAb-DB: The Single Domain Antibody Database. <i>ACS Synthetic Biology</i> , 2018, 7, 2480-2484.	3.8	54
23	Viruses, IRESs, and a universal translation initiation mechanism. <i>Biotechnology and Genetic Engineering Reviews</i> , 2018, 34, 60-75.	6.2	15
24	Cellular mRNA recruits the ribosome via eIF3-PABP bridge to initiate internal translation. <i>RNA Biology</i> , 2017, 14, 553-567.	3.1	28
25	InVivo Cleavage Map Illuminates the Central Role of RNase E in Coding and Non-coding RNA Pathways. <i>Molecular Cell</i> , 2017, 65, 39-51.	9.7	250
26	A synthetic biology approach to integrative high school STEM training. <i>Nature Biotechnology</i> , 2017, 35, 591-595.	17.5	4
27	Taking a Step Back from Back-Translocation: an Integrative View of LepA/EF4's Cellular Function. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	12
28	Engineering bacterial translation initiation – Do we have all the tools we need?. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3060-3069.	2.4	11
29	Streamlined purification of fluorescently labeled Escherichia coli phosphate-binding protein (PhoS) suitable for rapid-kinetics applications. <i>Analytical Biochemistry</i> , 2017, 537, 106-113.	2.4	5
30	Characterization of Fluorescein Arsenical Hairpin (FLaSH) as a Probe for Single-Molecule Fluorescence Spectroscopy. <i>Scientific Reports</i> , 2017, 7, 13063.	3.3	10
31	Tetracycline does not directly inhibit the function of bacterial elongation factor Tu. <i>PLoS ONE</i> , 2017, 12, e0178523.	2.5	7
32	The C-terminal Helix of Pseudomonas aeruginosa Elongation Factor Ts Tunes EF-Tu Dynamics to Modulate Nucleotide Exchange. <i>Journal of Biological Chemistry</i> , 2016, 291, 23136-23148.	3.4	6
33	The conserved GTPase HflX is a ribosome splitting factor that binds to the E-site of the bacterial ribosome. <i>Nucleic Acids Research</i> , 2016, 44, 1952-1961.	14.5	41
34	Using Rapid Kinetics and Molecular Dynamics Simulations to Study Biomolecular Information Processing and Design. <i>Biomath Communications</i> , 2016, 3, .	0.5	0
35	Identification of Two Structural Elements Important for Ribosome-Dependent GTPase Activity of Elongation Factor 4 (EF4/LepA). <i>Scientific Reports</i> , 2015, 5, 8573.	3.3	12
36	A conserved P-loop anchor limits the structural dynamics that mediate nucleotide dissociation in EF-Tu. <i>Scientific Reports</i> , 2015, 5, 7677.	3.3	12

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37	Contribution of two conserved histidines to the dual activity of archaeal RNA guide-dependent and -independent pseudouridine synthase Cbf5. <i>Rna</i> , 2015, 21, 1233-1239.	3.5	3
38	Introducing a class of standardized and interchangeable parts utilizing programmed ribosomal frameshifts for synthetic biology applications. <i>Translation</i> , 2015, 3, e1112458.	2.9	2
39	Histidine 114 Is Critical for ATP Hydrolysis by the Universally Conserved ATPase YchF. <i>Journal of Biological Chemistry</i> , 2015, 290, 18650-18661.	3.4	9
40	An arginine-aspartate network in the active site of bacterial TruB is critical for catalyzing pseudouridine formation. <i>Nucleic Acids Research</i> , 2014, 42, 3857-3870.	14.5	17
41	The ABC-F protein EttA gates ribosome entry into the translation elongation cycle. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 143-151.	8.2	109
42	Substrate Binding in Protein-tyrosine Phosphatase-like Inositol Polyphosphatases*. <i>Journal of Biological Chemistry</i> , 2012, 287, 9722-9730.	3.4	11
43	The 70S ribosome modulates the ATPase activity of <i>Escherichia coli</i> YchF. <i>RNA Biology</i> , 2012, 9, 1288-1301.	3.1	22
44	The ribosome modulates the structural dynamics of the conserved GTPase HflX and triggers tight nucleotide binding. <i>Biochimie</i> , 2012, 94, 1647-1659.	2.6	19
45	Construction of a fully active Cys-less elongation factor Tu: Functional role of conserved cysteine 81. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 684-692.	2.3	14
46	A Combined Molecular Dynamics and Rapid Kinetics Approach to Identify Conserved Three-Dimensional Communication Networks in Elongation Factor Tu. <i>Biophysical Journal</i> , 2010, 99, 3735-3743.	0.5	15
47	Toward Understanding the Function of the Universally Conserved GTPase HflX from <i>Escherichia coli</i> : A Kinetic Approach. <i>Biochemistry</i> , 2009, 48, 10793-10802.	2.5	27
48	The Importance of P-loop and Domain Movements in EF-Tu for Guanine Nucleotide Exchange. <i>Journal of Biological Chemistry</i> , 2006, 281, 21139-21146.	3.4	16
49	Recognition and selection of tRNA in translation. <i>FEBS Letters</i> , 2005, 579, 938-942.	2.8	137
50	Interaction of Helix D of Elongation Factor Tu with Helices 4 and 5 of Protein L7/12 on the Ribosome. <i>Journal of Molecular Biology</i> , 2004, 336, 1011-1021.	4.2	73
51	Essential Role of Histidine 84 in Elongation Factor Tu for the Chemical Step of GTP Hydrolysis on the Ribosome. <i>Journal of Molecular Biology</i> , 2003, 332, 689-699.	4.2	137
52	Mechanism of Elongation Factor (EF)-Ts-catalyzed Nucleotide Exchange in EF-Tu. <i>Journal of Biological Chemistry</i> , 2002, 277, 6032-6036.	3.4	40
53	Inactivation of the Elongation Factor Tu by Mosquitocidal Toxin-Catalyzed Mono-ADP-Ribosylation. <i>Applied and Environmental Microbiology</i> , 2002, 68, 4894-4899.	3.1	33
54	Kinetic Mechanism of Elongation Factor Ts-Catalyzed Nucleotide Exchange in Elongation Factor Tu. <i>Biochemistry</i> , 2002, 41, 162-169.	2.5	104

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55	Ribosome interactions of aminoacyl-tRNA and elongation factor Tu in the codon-recognition complex. <i>Nature Structural Biology</i> , 2002, 9, 849-54.	9.7	108
56	A Common Structural Motif in Elongation Factor Ts and Ribosomal Protein L7/12 May Be Involved in the Interaction with Elongation Factor Tu. <i>Journal of Molecular Evolution</i> , 2001, 52, 129-136.	1.8	19
57	The Importance of Structural Transitions of the Switch II Region for the Functions of Elongation Factor Tu on the Ribosome. <i>Journal of Biological Chemistry</i> , 2001, 276, 22183-22190.	3.4	33
58	Large-Scale Movement of Elongation Factor G and Extensive Conformational Change of the Ribosome during Translocation. <i>Cell</i> , 2000, 100, 301-309.	28.9	294
59	Introduction: Dual use in life science research. <i>Biochemistry and Cell Biology</i> , 0, , .	2.0	0