

Hans A Heus

List of Publications by Year in descending order

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77
papers

4,038
citations

147801

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118850

62
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docs citations

78
times ranked

3662
citing authors

#	ARTICLE	IF	CITATIONS
1	Improving Breast Cancer Treatment Specificity Using Aptamers Obtained by 3D Cell-SELEX. <i>Pharmaceuticals</i> , 2021, 14, 349.	3.8	16
2	Multivalent Sgc8c-aptamer decorated polymer scaffolds for leukemia targeting. <i>Chemical Communications</i> , 2021, 57, 2744-2747.	4.1	12
3	Ramified rolling circle amplification for synthesis of nucleosomal DNA sequences. <i>Analytical Biochemistry</i> , 2020, 588, 113469.	2.4	12
4	Transcription and Translation in Cytomimetic Protocells Perform Most Efficiently at Distinct Macromolecular Crowding Conditions. <i>ACS Synthetic Biology</i> , 2020, 9, 2797-2807.	3.8	39
5	Dissipative adaptation in driven self-assembly leading to self-dividing fibrils. <i>Nature Nanotechnology</i> , 2018, 13, 849-855.	31.5	160
6	Biomimetic Stress Sensitive Hydrogel Controlled by DNA Nanoswitches. <i>Biomacromolecules</i> , 2017, 18, 3310-3317.	5.4	31
7	A membrane-anchored aptamer sensor for probing IFN β secretion by single cells. <i>Chemical Communications</i> , 2017, 53, 8066-8069.	4.1	58
8	DNA-Responsive Polyisocyanopeptide Hydrogels with Stress-Stiffening Capacity. <i>Advanced Functional Materials</i> , 2016, 26, 9075-9082.	14.9	42
9	Stable isotope labeling methods for DNA. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2016, 96, 89-108.	7.5	15
10	Protein Synthesis in Coupled and Uncoupled Cell-Free Prokaryotic Gene Expression Systems. <i>ACS Synthetic Biology</i> , 2016, 5, 1433-1440.	3.8	17
11	Cell-Like Nanostructured Environments Alter Diffusion and Reaction Kinetics in Cell-Free Gene Expression. <i>ChemBioChem</i> , 2016, 17, 228-232.	2.6	18
12	Macromolecular crowding creates heterogeneous environments of gene expression in picolitre droplets. <i>Nature Nanotechnology</i> , 2016, 11, 191-197.	31.5	123
13	Macromolecular Crowding in the Cytosol: Underappreciated or Overestimated?. <i>Biophysical Journal</i> , 2015, 108, 114a.	0.5	0
14	Enzymatic preparation of multimilligram amounts of pure single-stranded DNA samples for material and analytical sciences. <i>Analytical Biochemistry</i> , 2015, 475, 68-73.	2.4	17
15	Associative Interactions in Crowded Solutions of Biopolymers Counteract Depletion Effects. <i>Journal of the American Chemical Society</i> , 2015, 137, 13041-13048.	13.7	55
16	Production of Homogeneous Recombinant RNA Using a tRNA Scaffold and Hammerhead Ribozymes. <i>Methods in Molecular Biology</i> , 2015, 1316, 33-44.	0.9	1
17	DNA-functionalized hydrogels for confined membrane-free in vitro transcription/translation. <i>Lab on A Chip</i> , 2014, 14, 2651.	6.0	44
18	Structural and thermodynamic signatures that define pseudotriple RNA hairpins. <i>Rna</i> , 2013, 19, 1833-1839.	3.5	7

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19	Enhanced transcription rates in membrane-free protocells formed by coacervation of cell lysate. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11692-11697.	7.1	282
20	Fast production of homogeneous recombinant RNA towards large-scale production of RNA. Nucleic Acids Research, 2012, 40, e102-e102.	14.5	54
21	Force spectroscopy of Rev-peptide-RRE interaction from HIV-1. Soft Matter, 2012, 8, 2103-2109.	2.7	8
22	Unusual Loop-Sequence Flexibility of the Proximal RNA Replication Element in EMCV. PLoS ONE, 2011, 6, e24818.	2.5	2
23	Atomic force microscope-based single-molecule force spectroscopy of RNA unfolding. Analytical Biochemistry, 2011, 414, 1-6.	2.4	27
24	Network theory approach for data evaluation in the dynamic force spectroscopy of biomolecular interactions. Europhysics Letters, 2010, 89, 68004.	2.0	2
25	¹ H and ¹³ C resonance assignments of a guanine sensing riboswitch™s terminator hairpin. Biomolecular NMR Assignments, 2010, 4, 89-91.	0.8	1
26	Enzymatic stereospecific preparation of fluorescent S-adenosyl-l-methionine analogs. Analytical Biochemistry, 2010, 396, 280-283.	2.4	29
27	Functional analysis of the SRV-1 RNA frameshifting pseudoknot. Nucleic Acids Research, 2010, 38, 7665-7672.	14.5	24
28	Preparation of selective and segmentally labeled single-stranded DNA for NMR by self-primed PCR and asymmetrical endonuclease double digestion. Nucleic Acids Research, 2009, 37, e114-e114.	14.5	10
29	The structure-function relationship of the enterovirus 3'-UTR. Virus Research, 2009, 139, 209-216.	2.2	59
30	Cartilage hair hypoplasia-associated mutations in the RNase MRP P3 domain affect RNA folding and ribonucleoprotein assembly. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 455-466.	4.1	25
31	Multiple segmental and selective isotope labeling of large RNA for NMR structural studies. Nucleic Acids Research, 2008, 36, e89-e89.	14.5	45
32	Breaking pseudo-twofold symmetry in the poliovirus 3'-UTR Y-stem by restoring Watson-Crick base pairs. Rna, 2007, 13, 781-792.	3.5	14
33	Ligand-induced folding of the guanine-sensing riboswitch is controlled by a combined predetermined-induced fit mechanism. Rna, 2007, 13, 2202-2212.	3.5	75
34	An RNA conformational shift in recent H5N1 influenza A viruses. Bioinformatics, 2007, 23, 272-276.	4.1	38
35	Nonspecific Protein Adsorption at the Single Molecule Level Studied by Atomic Force Microscopy. Langmuir, 2007, 23, 9921-9923.	3.5	35
36	Macroscopic Hierarchical Surface Patterning of Porphyrin Trimers via Self-Assembly and Dewetting. Science, 2006, 314, 1433-1436.	12.6	311

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37	Chemical synthesis of picornaviral protein primers of RNA replication. <i>Organic and Biomolecular Chemistry</i> , 2006, 4, 3576.	2.8	11
38	Structural and functional integrity of the coxsackievirus B3 oriR: spacing between coaxial RNA helices. <i>Journal of General Virology</i> , 2006, 87, 689-695.	2.9	15
39	A GCUA tetranucleotide loop found in the poliovirus oriL by in vivo SELEX (un)expectedly forms a YNMG-like structure: Extending the YNMG family with GYYA. <i>Rna</i> , 2006, 12, 1671-1682.	3.5	16
40	AFM Studies of β -Sheet Block Copolymers at Solid Surfaces: High-Resolution Structures and Aggregation Dynamics. <i>Australian Journal of Chemistry</i> , 2006, 59, 560.	0.9	1
41	Structures of Non-Canonical Tandem Base Pairs in RNA Helices: Review. <i>ChemInform</i> , 2004, 35, no.	0.0	0
42	Novel application of sRNA: Stimulation of ribosomal frameshifting. <i>Rna</i> , 2004, 10, 1702-1703.	3.5	30
43	Structures of Non-canonical Tandem Base Pairs in RNA Helices: Review. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2003, 22, 559-571.	1.1	14
44	Structure of the Pyrimidine-rich Internal Loop in the Poliovirus 3' UTR: The Importance of Maintaining Pseudo-2-fold Symmetry in RNA Helices Containing Two Adjacent Non-canonical Base-pairs. <i>Journal of Molecular Biology</i> , 2003, 331, 759-769.	4.2	20
45	Solution structure of the pseudoknot of SRV-1 RNA, involved in ribosomal frameshifting 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2001, 310, 1109-1123.	4.2	102
46	Title is missing!. <i>Helvetica Chimica Acta</i> , 2000, 83, 1278-1289.	1.6	14
47	Solution structure of a HNA-RNA hybrid. <i>Chemistry and Biology</i> , 2000, 7, 719-731.	6.0	66
48	Structure of the ribozyme substrate hairpin of <i>Neurospora VS RNA</i> : A close look at the cleavage site. <i>Rna</i> , 2000, 6, 1821-1832.	3.5	43
49	Title is missing!. <i>Journal of Biomolecular NMR</i> , 1998, 12, 423-433.	2.8	16
50	Structure of the 3'-hairpin of the TYMV pseudoknot: preformation in RNA folding. <i>EMBO Journal</i> , 1998, 17, 7498-7504.	7.8	11
51	New developments in structure determination of pseudoknots. <i>Biopolymers</i> , 1998, 48, 137-153.	2.4	48
52	NMR Structure of a Classical Pseudoknot: Interplay of Single- and Double-Stranded RNA. <i>Science</i> , 1998, 280, 434-438.	12.6	148
53	The detailed structure of tandem G \hat{A} A mismatched base-pair motifs in RNA duplexes is context dependent. <i>Journal of Molecular Biology</i> , 1997, 271, 147-158.	4.2	53
54	RNA aptamers. <i>Nature Structural Biology</i> , 1997, 4, 597-600.	9.7	14

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55	The structure of the isolated, central hairpin of the HDV antigenomic ribozyme: novel structural features and similarity of the loop in the ribozyme and free in solution. <i>EMBO Journal</i> , 1997, 16, 3685-3692.	7.8	24
56	Unambiguous Structure Characterization of a DNA-RNA Triple Helix by 15N- and 13C-Filtered NOESY Spectroscopy. <i>Biochemistry</i> , 1996, 35, 1733-1739.	2.5	15
57	A Network of Heterogeneous Hydrogen Bonds in GNRA Tetraloops. <i>Journal of Molecular Biology</i> , 1996, 264, 968-980.	4.2	360
58	Sequential backbone assignment of uniformly 13C-labeled RNAs by a two-dimensional P(CC)H-TOCSY triple resonance NMR experiment. <i>Journal of Biomolecular NMR</i> , 1995, 5, 82-86.	2.8	38
59	Irradiated [15N]DNA as an Internal Standard for Analysis of Base-Oxidized DNA Constituents by Isotope Dilution Mass Spectrometry. <i>Analytical Chemistry</i> , 1995, 67, 399-404.	6.5	5
60	Assignment Strategies and Analysis of Cross-Peak Patterns and Intensities in the Three-Dimensional Homonuclear TOCSY-NOESY of RNA. <i>Journal of Magnetic Resonance Series B</i> , 1994, 103, 134-141.	1.6	28
61	Sequential Backbone Assignment in 13C-Labeled RNA via Through-Bond Coherence Transfer Using Three-Dimensional Triple Resonance Spectroscopy (1H,13C,31P) and Two-Dimensional Hetero TOCSY. <i>Journal of the American Chemical Society</i> , 1994, 116, 4983-4984.	13.7	59
62	Novel proton NMR assignment procedure for RNA duplexes. <i>Journal of the American Chemical Society</i> , 1991, 113, 4360-4361.	13.7	49
63	Nuclear magnetic resonance studies of the hammerhead ribozyme domain. <i>Journal of Molecular Biology</i> , 1991, 217, 113-124.	4.2	110
64	Structural features that give rise to the unusual stability of RNA hairpins containing GNRA loops. <i>Science</i> , 1991, 253, 191-194.	12.6	649
65	Conformational and thermodynamic effects of naturally occurring base methylations in a ribosomal RNA hairpin of <i>Bacillus stearothermophilus</i> . <i>FEBS Journal</i> , 1990, 188, 275-281.	0.2	9
66	Sequence-dependent structural variations of hammerhead RNA enzymes. <i>Nucleic Acids Research</i> , 1990, 18, 1103-1108.	14.5	80
67	Is there a special function for U-G basepairs in ribosomal RNA?. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1990, 1050, 14-17.	2.4	20
68	The 3' Terminal Colicin Fragment of <i>Escherichia coli</i> 16S Ribosomal RNA. Conformational Details Revealed by Enzymic and Chemical Probing. <i>Journal of Biomolecular Structure and Dynamics</i> , 1988, 5, 951-963.	3.5	3
69	[12] Isolation and characterization of colicin fragments of bacterial 16S ribosomal RNA. <i>Methods in Enzymology</i> , 1988, 164, 188-200.	1.0	0
70	Circular dichroism and 500-MHz proton magnetic resonance studies of the interaction of <i>Escherichia coli</i> translational initiation factor 3 protein with the 16S ribosomal RNA 3' cloacin fragment. <i>Biochemistry</i> , 1986, 25, 2770-2777.	2.5	23
71	Phylogeny of the conserved 3' terminal structure of the RNA of small ribosomal subunits. <i>Nucleic Acids Research</i> , 1984, 12, 2595-2604.	14.5	97
72	High-resolution proton magnetic resonance studies of the 3'-terminal colicin fragment of 16 S ribosomal RNA from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1983, 170, 939-956.	4.2	31

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73	The Conformation of a Conserved Stem-Loop Structure in Ribosomal RNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 1983, 1, 371-381.	3.5	9
74	Calorimetric measurements of the destabilisation of a ribosomal RNA hairpin by dimethylation of two adjacent adenosines. <i>Nucleic Acids Research</i> , 1983, 11, 203-210.	14.5	21
75	16S Ribosomal RNA of <i>Escherichia coli</i> contains a N2-methylguanosine at 27 nucleotides from the 3' end. <i>Nucleic Acids Research</i> , 1981, 9, 2717-2725.	14.5	25
76	Destabilization of secondary structure in 16S ribosomal RNA by dimethylation of two adjacent adenosines. <i>Nucleic Acids Research</i> , 1981, 9, 4413-4422.	14.5	31
77	Adenosine dimethylation of 16S ribosomal RNA: effect of the methylgroups on local conformational stability as deduced from electrophoretic mobility of RNA fragments in denaturing polyacrylamide gels. <i>Nucleic Acids Research</i> , 1981, 9, 267-275.	14.5	21