

Kenneth John McDowall

List of Publications by Year in descending order

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42
papers

2,951
citations

201385

27
h-index

276539

41
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44
all docs

44
docs citations

44
times ranked

2217
citing authors

#	ARTICLE	IF	CITATIONS
1	The regulation of the secondary metabolism of <i>Streptomyces</i> : new links and experimental advances. <i>Natural Product Reports</i> , 2011, 28, 1311.	5.2	390
2	Structure of <i>Escherichia coli</i> RNase E catalytic domain and implications for RNA turnover. <i>Nature</i> , 2005, 437, 1187-1191.	13.7	259
3	Regulation of antibiotic production in Actinobacteria: new perspectives from the post-genomic era. <i>Natural Product Reports</i> , 2018, 35, 575-604.	5.2	203
4	The N-terminal Domain of the Gene Product has RNase E Activity and is Non-overlapping with the Arginine-rich RNA-binding Site. <i>Journal of Molecular Biology</i> , 1996, 255, 349-355.	2.0	154
5	Site-specific RNase E cleavage of oligonucleotides and inhibition by stem-loops. <i>Nature</i> , 1995, 374, 287-290.	13.7	145
6	RNase E: still a wonderfully mysterious enzyme. <i>Molecular Microbiology</i> , 1997, 23, 1099-1106.	1.2	137
7	Chapter 3 Endonucleolytic Initiation of mRNA Decay in <i>Escherichia coli</i> . <i>Progress in Molecular Biology and Translational Science</i> , 2009, 85, 91-135.	0.9	137
8	The CafA Protein Required for the 5'-Maturation of 16 S rRNA Is a 5'-End-dependent Ribonuclease That Has Context-dependent Broad Sequence Specificity. <i>Journal of Biological Chemistry</i> , 2000, 275, 8726-8732.	1.6	133
9	Transcriptional activation of the pathway-specific regulator of the actinorhodin biosynthetic genes in <i>Streptomyces coelicolor</i> . <i>Molecular Microbiology</i> , 2005, 58, 131-150.	1.2	132
10	The <i>ams-1</i> and <i>rne-3071</i> temperature-sensitive mutations in the <i>ams</i> gene are in close proximity to each other and cause substitutions within a domain that resembles a product of the <i>Escherichia coli</i> <i>mre</i> locus. <i>Journal of Bacteriology</i> , 1993, 175, 4245-4249.	1.0	116
11	Direct entry by RNase E is a major pathway for the degradation and processing of RNA in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2014, 42, 11733-11751.	6.5	89
12	The permease gene <i>nagE2</i> is the key to N-acetylglucosamine sensing and utilization in <i>Streptomyces coelicolor</i> and is subject to multi-level control. <i>Molecular Microbiology</i> , 2010, 75, 1133-1144.	1.2	73
13	Characterization of an oxytetracycline-resistance gene, <i>otrA</i> , of <i>Streptomyces rimosus</i> . <i>Molecular Microbiology</i> , 1991, 5, 2923-2933.	1.2	72
14	Rapid cleavage of RNA by RNase E in the absence of 5' monophosphate stimulation. <i>Molecular Microbiology</i> , 2010, 76, 590-604.	1.2	70
15	Quaternary Structure and Catalytic Activity of the <i>Escherichia coli</i> Ribonuclease E Amino-Terminal Catalytic Domain. <i>Biochemistry</i> , 2003, 42, 13848-13855.	1.2	66
16	Alginases from <i>Azotobacter</i> species. <i>Journal of General Microbiology</i> , 1992, 138, 2465-2471.	2.3	55
17	Dietary zinc oxide affects the expression of genes associated with inflammation: Transcriptome analysis in piglets challenged with ETEC K88. <i>Veterinary Immunology and Immunopathology</i> , 2010, 137, 120-129.	0.5	55
18	Sensing of 5' monophosphate by <i>Escherichia coli</i> RNase G can significantly enhance association with RNA and stimulate the decay of functional mRNA transcripts <i>in vivo</i> . <i>Molecular Microbiology</i> , 2008, 67, 102-115.	1.2	54

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19	Enhanced cleavage of RNA mediated by an interaction between substrates and the arginine-rich domain of <i>E. coli</i> ribonuclease E 1 Edited by I. B. Holland. <i>Journal of Molecular Biology</i> , 2000, 301, 257-264.	2.0	52
20	Translational activation by the noncoding RNA DsrA involves alternative RNase III processing in the <i>rpoS</i> 5'-leader. <i>Rna</i> , 2008, 14, 454-459.	1.6	51
21	A comparison of key aspects of gene regulation in <i>Streptomyces coelicolor</i> and <i>Escherichia coli</i> using nucleotide-resolution transcription maps produced in parallel by global and differential RNA sequencing. <i>Molecular Microbiology</i> , 2014, 94, 963-987.	1.2	48
22	“Zn-Link” A Metal-Sharing Interface that Organizes the Quaternary Structure and Catalytic Site of the Endoribonuclease, RNase E. <i>Biochemistry</i> , 2005, 44, 4667-4675.	1.2	47
23	Determination of the Catalytic Parameters of the N-terminal Half of <i>Escherichia coli</i> Ribonuclease E and the Identification of Critical Functional Groups in RNA Substrates. <i>Journal of Biological Chemistry</i> , 2003, 278, 44001-44008.	1.6	44
24	Phosphate Control of Oxytetracycline Production by <i>Streptomyces rimosus</i> Is at the Level of Transcription from Promoters Overlapped by Tandem Repeats Similar to Those of the DNA-Binding Sites of the OmpR Family. <i>Journal of Bacteriology</i> , 1999, 181, 3025-3032.	1.0	43
25	Transcript analysis reveals an extended regulon and the importance of protein-protein co-operativity for the <i>Escherichia coli</i> methionine repressor. <i>Biochemical Journal</i> , 2006, 396, 227-234.	1.7	43
26	Adjacent single-stranded regions mediate processing of tRNA precursors by RNase E direct entry. <i>Nucleic Acids Research</i> , 2014, 42, 4577-4589.	6.5	32
27	Streptomycin production by <i>Streptomyces griseus</i> can be modulated by a mechanism not associated with change in the <i>adpA</i> component of the A-factor cascade. <i>Biotechnology Letters</i> , 2006, 29, 57-64.	1.1	31
28	Binding of a biosynthetic intermediate to <i>AtrA</i> modulates the production of lidamycin by <i>Streptomyces globisporus</i> . <i>Molecular Microbiology</i> , 2015, 96, 1257-1271.	1.2	28
29	The First Small-Molecule Inhibitors of Members of the Ribonuclease E Family. <i>Scientific Reports</i> , 2015, 5, 8028.	1.6	25
30	The Identification of Nucleic Acid-interacting Proteins Using a Simple Proteomics-based Approach That Directly Incorporates the Electrophoretic Mobility Shift Assay. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1697-1702.	2.5	23
31	A combination of improved differential and global RNA-seq reveals pervasive transcription initiation and events in all stages of the life-cycle of functional RNAs in <i>Propionibacterium acnes</i> , a major contributor to wide-spread human disease. <i>BMC Genomics</i> , 2013, 14, 620.	1.2	20
32	Differential expression and extent of fungal/plant and fungal/bacterial chitinases of <i>Aspergillus fumigatus</i> . <i>Archives of Microbiology</i> , 2005, 184, 78-81.	1.0	19
33	Chapter 12 Identifying and Characterizing Substrates of the RNase E/G Family of Enzymes. <i>Methods in Enzymology</i> , 2008, 447, 215-241.	0.4	18
34	A stereodivergent, two-directional synthesis of stereoisomeric C-linked disaccharide mimetics. <i>Organic and Biomolecular Chemistry</i> , 2003, 1, 338-349.	1.5	15
35	Transcriptional analysis of the cell division-related <i>ssg</i> genes in <i>Streptomyces coelicolor</i> reveals direct control of <i>ssgR</i> by <i>AtrA</i> . <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 201-213.	0.7	14
36	Molecular Genetics of Oxytetracycline Production by <i>Streptomyces rimosus</i> . , 1991, , 105-116.		12

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37	Expanding the Use of Zymography by the Chemical Linkage of Small, Defined Substrates to the Gel Matrix. <i>Genome Research</i> , 2003, 13, 1961-1965.	2.4	12
38	The sequence of sites recognised by a member of the RNase E/G family can control the maximal rate of cleavage, while a 5' monophosphorylated end appears to function cooperatively in mediating RNA binding. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 879-883.	1.0	11
39	Two-dimensional gel electrophoresis for identifying proteins that bind DNA or RNA. <i>Nature Protocols</i> , 2007, 2, 1839-1848.	5.5	9
40	An Improved Binary Vector and <i>Escherichia coli</i> Strain for <i>Agrobacterium tumefaciens</i> -Mediated Plant Transformation. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2195-2201.	0.8	7
41	Protein-conjugated microbubbles for the selective targeting of <i>S. aureus</i> biofilms. <i>Biofilm</i> , 2022, 4, 100074.	1.5	5
42	Cross Inoculation of Rumen Fluid to Improve Dry Matter Disappearance and Its Effect on Bacterial Composition Using an in vitro Batch Culture Model. <i>Frontiers in Microbiology</i> , 2020, 11, 531404.	1.5	2