

ValÃ©rie de CrÃ©cy-Lagard

List of Publications by Year in descending order

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158
papers

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41627

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165
all docs

165
docs citations

165
times ranked

16243
citing authors

#	ARTICLE	IF	CITATIONS
1	Dihydrouridine in the Transcriptome: New Life for This Ancient RNA Chemical Modification. ACS Chemical Biology, 2022, 17, 1638-1657.	1.6	9
2	Metabolite Damage and Damage Control in a Minimal Genome. MBio, 2022, 13, .	1.8	10
3	Functions of Bacterial tRNA Modifications: From Ubiquity to Diversity. Trends in Microbiology, 2021, 29, 41-53.	3.5	67
4	A network approach to elucidate and prioritize microbial dark matter in microbial communities. ISME Journal, 2021, 15, 228-244.	4.4	91
5	Dihydrouridine synthesis in tRNAs is under reductive evolution in Mollicutes. RNA Biology, 2021, 18, 2278-2289.	1.5	7
6	Quantitative mapping of the cellular small RNA landscape with AQRNA-seq. Nature Biotechnology, 2021, 39, 978-988.	9.4	43
7	Knowns and Unknowns of Vitamin B ₆ Metabolism in Escherichia coli. EcoSal Plus, 2021, 9, .	2.1	19
8	Pantoea Bacteriophage vB_PagS_MED16”A Siphovirus Containing a 2-Deoxy-7-amido-7-deazaguanosine-Modified DNA. International Journal of Molecular Sciences, 2021, 22, 7333.	1.8	2
9	Comparative Genomic Analysis of the DUF34 Protein Family Suggests Role as a Metal Ion Chaperone or Insertase. Biomolecules, 2021, 11, 1282.	1.8	5
10	Hypermodified DNA in Viruses of E.coli and Salmonella. EcoSal Plus, 2021, 9, eESP00282019.	2.1	24
11	Epoxyqueuosine Reductase QueH in the Biosynthetic Pathway to tRNA Queuosine Is a Unique Metalloenzyme. Biochemistry, 2021, 60, 3152-3161.	1.2	7
12	Bacterial RNA Degradosomes: Molecular Machines under Tight Control. Trends in Biochemical Sciences, 2020, 45, 42-57.	3.7	42
13	An Enzyme Containing the Conserved Domain of Unknown Function DUF62 Acts as a Stereoselective (R)-S-cysteine Adenosylmethionine Hydrolase. ChemBioChem, 2020, 21, 3495-3499.	1.3	2
14	An Unusual Route for p-Aminobenzoate Biosynthesis in Chlamydia trachomatis Involves a Probable Self-Sacrificing Diiron Oxygenase. Journal of Bacteriology, 2020, 202, .	1.0	6
15	Detection of preQ0 deazaguanine modifications in bacteriophage CAjan DNA using Nanopore sequencing reveals same hypermodification at two distinct DNA motifs. Nucleic Acids Research, 2020, 48, 10383-10396.	6.5	22
16	The DUF328 family member YaaA is a DNA-binding protein with a novel fold. Journal of Biological Chemistry, 2020, 295, 14236-14247.	1.6	6
17	Whole-Genome Sequence of Streptomyces kaniharaensis Shomura and Niida SF-557. Microbiology Resource Announcements, 2020, 9, .	0.3	4
18	Specificity in the biosynthesis of the universal tRNA nucleoside N ⁶ -threonylcarbamoyl adenosine (t ⁶ A) is the gatekeeper. Rna, 2020, 26, 1094-1103.	1.6	14

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19	Uncovering the chemistry of C-C bond formation in C-nucleoside biosynthesis: crystal structure of a C-glycoside synthase/PRPP complex. <i>Chemical Communications</i> , 2020, 56, 7617-7620.	2.2	15
20	<i>Clostridioides difficile</i> Senses and Hijacks Host Heme for Incorporation into an Oxidative Stress Defense System. <i>Cell Host and Microbe</i> , 2020, 28, 411-421.e6.	5.1	36
21	Survey and Validation of tRNA Modifications and Their Corresponding Genes in <i>Bacillus subtilis</i> sp Subtilis Strain 168. <i>Biomolecules</i> , 2020, 10, 977.	1.8	21
22	Loss of Elongator- and KEOPS-Dependent tRNA Modifications Leads to Severe Growth Phenotypes and Protein Aggregation in Yeast. <i>Biomolecules</i> , 2020, 10, 322.	1.8	20
23	Archaeosine Modification of Archaeal tRNA: Role in Structural Stabilization. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	10
24	Reductive Evolution and Diversification of C5-Uracil Methylation in the Nucleic Acids of Mollicutes. <i>Biomolecules</i> , 2020, 10, 587.	1.8	8
25	Deoxyinosine and 7-Deaza-2-Deoxyguanosine as Carriers of Genetic Information in the DNA of <i>Campylobacter</i> Viruses. <i>Journal of Virology</i> , 2019, 93, .	1.5	25
26	Discovery of novel bacterial queuine salvage enzymes and pathways in human pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19126-19135.	3.3	36
27	Matching tRNA modifications in humans to their known and predicted enzymes. <i>Nucleic Acids Research</i> , 2019, 47, 2143-2159.	6.5	116
28	tRNA Modification Profiles and Codon-Decoding Strategies in <i>Methanocaldococcus jannaschii</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	38
29	Identifying Pathogenic Islands through Genome Comparison. <i>American Biology Teacher</i> , 2019, 81, 577-581.	0.1	0
30	7-Deazaguanine modifications protect phage DNA from host restriction systems. <i>Nature Communications</i> , 2019, 10, 5442.	5.8	63
31	PMP-diketopiperazine adducts form at the active site of a PLP dependent enzyme involved in formycin biosynthesis. <i>Chemical Communications</i> , 2019, 55, 14502-14505.	2.2	7
32	Can Protein Expression Be Regulated by Modulation of tRNA Modification Profiles?. <i>Biochemistry</i> , 2019, 58, 355-362.	1.2	29
33	Essential metabolism for a minimal cell. <i>ELife</i> , 2019, 8, .	2.8	110
34	Evidence that the metabolite repair enzyme NAD(P)HX epimerase has a moonlighting function. <i>Bioscience Reports</i> , 2018, 38, .	1.1	20
35	A plastidial pantoate transporter with a potential role in pantothenate synthesis. <i>Biochemical Journal</i> , 2018, 475, 813-825.	1.7	13
36	Gene Graphics: a genomic neighborhood data visualization web application. <i>Bioinformatics</i> , 2018, 34, 1406-1408.	1.8	82

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37	MODOMICS: a database of RNA modification pathways. 2017 update. <i>Nucleic Acids Research</i> , 2018, 46, D303-D307.	6.5	1,442
38	The t ⁶ A modification acts as a positive determinant for the anticodon nuclease PrrC, and is distinctively nonessential in <i>Streptococcus mutans</i> . <i>RNA Biology</i> , 2018, 15, 508-517.	1.5	11
39	Newly-discovered enzymes that function in metabolite damage-control. <i>Current Opinion in Chemical Biology</i> , 2018, 47, 101-108.	2.8	30
40	Identification of the minimal bacterial 2-deoxy-7-amido-7-deazaguanine synthesis machinery. <i>Molecular Microbiology</i> , 2018, 110, 469-483.	1.2	16
41	Evolutionary insights into Trm112-methyltransferase holoenzymes involved in translation between archaea and eukaryotes. <i>Nucleic Acids Research</i> , 2018, 46, 8483-8499.	6.5	37
42	Succinylcysteine Breakdown – How <i>Bacillus subtilis</i> Utilizes an Inevitable Product of Metabolite Damage. <i>FASEB Journal</i> , 2018, 32, 536.5.	0.2	0
43	Identification of a Novel Epoxyqueuosine Reductase Family by Comparative Genomics. <i>ACS Chemical Biology</i> , 2017, 12, 844-851.	1.6	40
44	tRNA N ⁶ -adenosine threonylcarbamoyltransferase defect due to KAE1/TCS3 (OSGEP) mutation manifest by neurodegeneration and renal tubulopathy. <i>European Journal of Human Genetics</i> , 2017, 25, 545-551.	1.4	67
45	Deazaguanine derivatives, examples of crosstalk between RNA and DNA modification pathways. <i>RNA Biology</i> , 2017, 14, 1175-1184.	1.5	37
46	Discovery of a widespread prokaryotic 5-oxoprolinase that was hiding in plain sight. <i>Journal of Biological Chemistry</i> , 2017, 292, 16360-16367.	1.6	41
47	A strictly monofunctional bacterial hydroxymethylpyrimidine phosphate kinase precludes damaging errors in thiamin biosynthesis. <i>Biochemical Journal</i> , 2017, 474, 2887-2895.	1.7	6
48	The <i>Escherichia coli</i> COG1738 Member YhhQ Is Involved in 7-Cyanodeazaguanine (preQ0) Transport. <i>Biomolecules</i> , 2017, 7, 12.	1.8	48
49	QueF-Like, a Non-Homologous Archaeosine Synthase from the Crenarchaeota. <i>Biomolecules</i> , 2017, 7, 36.	1.8	10
50	Global translational impacts of the loss of the tRNA modification t ⁶ A in yeast. <i>Microbial Cell</i> , 2016, 3, 29-45.	1.4	101
51	Deciphering the Translation Initiation Factor 5A Modification Pathway in Halophilic Archaea. <i>Archaea</i> , 2016, 2016, 1-14.	2.3	24
52	Experimental and Metabolic Modeling Evidence for a Folate-Cleaving Side-Activity of Ketopantoate Hydroxymethyltransferase (PanB). <i>Frontiers in Microbiology</i> , 2016, 7, 431.	1.5	6
53	Functional Annotations of Paralogs: A Blessing and a Curse. <i>Life</i> , 2016, 6, 39.	1.1	45
54	Quality Annotations, a Key Frontier in the Microbial Sciences. <i>Microbe Magazine</i> , 2016, 11, 303-310.	0.4	3

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55	Mutations in PROSC Disrupt Cellular Pyridoxal Phosphate Homeostasis and Cause Vitamin-B6-Dependent Epilepsy. <i>American Journal of Human Genetics</i> , 2016, 99, 1325-1337.	2.6	118
56	Arabidopsis <i>TH2</i> Encodes the Orphan Enzyme Thiamin Monophosphate Phosphatase. <i>Plant Cell</i> , 2016, 28, 2683-2696.	3.1	42
57	Systematic identification and analysis of frequent gene fusion events in metabolic pathways. <i>BMC Genomics</i> , 2016, 17, 473.	1.2	13
58	“Nothing of chemistry disappears in biology”: the Top 30 damage-prone endogenous metabolites. <i>Biochemical Society Transactions</i> , 2016, 44, 961-971.	1.6	76
59	Assignment of function to a domain of unknown function: DUF1537 is a new kinase family in catabolic pathways for acid sugars. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4161-9.	3.3	46
60	The Response of <i>Acinetobacter baumannii</i> to Zinc Starvation. <i>Cell Host and Microbe</i> , 2016, 19, 826-836.	5.1	108
61	A family of metal-dependent phosphatases implicated in metabolite damage-control. <i>Nature Chemical Biology</i> , 2016, 12, 621-627.	3.9	48
62	Members of a Novel Kinase Family (DUF1537) Can Recycle Toxic Intermediates into an Essential Metabolite. <i>ACS Chemical Biology</i> , 2016, 11, 2304-2311.	1.6	12
63	Bacterial and plant HAD enzymes catalyse a missing phosphatase step in thiamin diphosphate biosynthesis. <i>Biochemical Journal</i> , 2016, 473, 157-166.	1.7	22
64	Novel genomic island modifies DNA with 7-deazaguanine derivatives. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1452-9.	3.3	99
65	Metabolite Damage and Metabolite Damage Control in Plants. <i>Annual Review of Plant Biology</i> , 2016, 67, 131-152.	8.6	43
66	Evidence that COG0325 proteins are involved in PLP homeostasis. <i>Microbiology (United Kingdom)</i> , 2016, 162, 694-706.	0.7	47
67	Essentiality of threonylcarbamoyladenine (t ⁶ A), a universal tRNA modification, in bacteria. <i>Molecular Microbiology</i> , 2015, 98, 1199-1221.	1.2	72
68	Systematic genome assessment of B-vitamin biosynthesis suggests co-operation among gut microbes. <i>Frontiers in Genetics</i> , 2015, 6, 148.	1.1	565
69	Proteins of unknown biochemical function - A persistent problem and a roadmap to help overcome it. <i>Plant Physiology</i> , 2015, 169, pp.00959.2015.	2.3	60
70	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 18678-18698.	1.6	70
71	A directed-overflow and damage-control N-glycosidase in riboflavin biosynthesis. <i>Biochemical Journal</i> , 2015, 466, 137-145.	1.7	38
72	The Levels of a Universally Conserved tRNA Modification Regulate Cell Growth. <i>Journal of Biological Chemistry</i> , 2015, 290, 18699-18707.	1.6	38

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73	Mannitol 1-phosphate dehydrogenases/phosphatases: a family of novel bifunctional enzymes for bacterial adaptation to osmotic stress. <i>Environmental Microbiology</i> , 2015, 17, 711-719.	1.8	21
74	The emerging role of complex modifications of tRNA ^{Lys} UUU in signaling pathways. <i>Microbial Cell</i> , 2015, 2, 1-4.	1.4	20
75	Predicting the Minimal Translation Apparatus: Lessons from the Reductive Evolution of Mollicutes. <i>PLoS Genetics</i> , 2014, 10, e1004363.	1.5	127
76	Salvage of the thiamin pyrimidine moiety by plant TenA proteins lacking an active-site cysteine. <i>Biochemical Journal</i> , 2014, 463, 145-155.	1.7	22
77	Promiscuous and Adaptable Enzymes Fill "Holes" in the Tetrahydrofolate Pathway in <i>Chlamydia</i> Species. <i>MBio</i> , 2014, 5, e01378-14.	1.8	47
78	Diversity of the biosynthesis pathway for threonylcarbamoyladenine (t ⁶ A), a universal modification of tRNA. <i>RNA Biology</i> , 2014, 11, 1529-1539.	1.5	79
79	Cross Kingdom Functional Conservation of the Core Universally Conserved Threonylcarbamoyladenine tRNA Synthesis Enzymes. <i>Eukaryotic Cell</i> , 2014, 13, 1222-1231.	3.4	32
80	Genome Sequence of <i>Candidatus</i> <i>Riesia pediculischaeffi</i> , Endosymbiont of Chimpanzee Lice, and Genomic Comparison of Recently Acquired Endosymbionts from Human and Chimpanzee Lice. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2189-2195.	0.8	30
81	Discovery of the Î ² -barrel type RNA methyltransferase responsible for N ⁶ -methylation of N ⁶ -threonylcarbamoyladenine in tRNAs. <i>Nucleic Acids Research</i> , 2014, 42, 9350-9365.	6.5	42
82	Plant, Animal, and Fungal Micronutrient Queuosine Is Salvaged by Members of the DUF2419 Protein Family. <i>ACS Chemical Biology</i> , 2014, 9, 1812-1825.	1.6	48
83	Variations in metabolic pathways create challenges for automated metabolic reconstructions: Examples from the tetrahydrofolate synthesis pathway. <i>Computational and Structural Biotechnology Journal</i> , 2014, 10, 41-50.	1.9	30
84	High-throughput comparison, functional annotation, and metabolic modeling of plant genomes using the PlantSEED resource. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9645-9650.	3.3	69
85	Integrative Data-Mining Tools to Link Gene and Function. <i>Methods in Molecular Biology</i> , 2014, 1101, 43-66.	0.4	4
86	Identification of the thiamin salvage enzyme thiazole kinase in <i>Arabidopsis</i> and maize. <i>Phytochemistry</i> , 2013, 94, 68-73.	1.4	24
87	The COMBEX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	2.6	54
88	Quinolate Salvage and Insights for Targeting NAD Biosynthesis in Group A Streptococci. <i>Journal of Bacteriology</i> , 2013, 195, 726-732.	1.0	50
89	Identification of Mitochondrial Coenzyme A Transporters from Maize and <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 162, 581-588.	2.3	31
90	The archaeal COG1901/DUF358 SPOUT-methyltransferase members, together with pseudouridine synthase Pus10, catalyze the formation of 1-methylpseudouridine at position 54 of tRNA. <i>Rna</i> , 2012, 18, 421-433.	1.6	36

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91	Structural Basis of Biological Nitrile Reduction. <i>Journal of Biological Chemistry</i> , 2012, 287, 30560-30570.	1.6	27
92	Experimental Evolution of a Facultative Thermophile from a Mesophilic Ancestor. <i>Applied and Environmental Microbiology</i> , 2012, 78, 144-155.	1.4	65
93	Identification and Characterization of the Missing Pyrimidine Reductase in the Plant Riboflavin Biosynthesis Pathway. <i>Plant Physiology</i> , 2012, 161, 48-56.	2.3	20
94	Comparative Genomics Guided Discovery of Two Missing Archaeal Enzyme Families Involved in the Biosynthesis of the Pterin Moiety of Tetrahydromethanopterin and Tetrahydrofolate. <i>ACS Chemical Biology</i> , 2012, 7, 1807-1816.	1.6	20
95	Plant B Vitamin Pathways and their Compartmentation: a Guide for the Perplexed. <i>Journal of Experimental Botany</i> , 2012, 63, 5379-5395.	2.4	78
96	Functional Promiscuity of the COG0720 Family. <i>ACS Chemical Biology</i> , 2012, 7, 197-209.	1.6	29
97	Diversity of Archaeosine Synthesis in Crenarchaeota. <i>ACS Chemical Biology</i> , 2012, 7, 300-305.	1.6	41
98	Biosynthesis of Threonylcarbamoyl Adenosine (t6A), a Universal tRNA Nucleoside. <i>Journal of Biological Chemistry</i> , 2012, 287, 13666-13673.	1.6	109
99	Biosynthesis and Function of Posttranscriptional Modifications of Transfer RNAs. <i>Annual Review of Genetics</i> , 2012, 46, 69-95.	3.2	448
100	Comparative genomic analysis of the DUF71/COG2102 family predicts roles in diphthamide biosynthesis and B12 salvage. <i>Biology Direct</i> , 2012, 7, 32.	1.9	19
101	YeiR: a metal-binding GTPase from <i>Escherichia coli</i> involved in metal homeostasis. <i>Metallomics</i> , 2012, 4, 488.	1.0	49
102	A Genetic Investigation of the KEOPS Complex in Halophilic Archaea. <i>PLoS ONE</i> , 2012, 7, e43013.	1.1	26
103	Decoding in <i>Candidatus Riesia pediculicola</i> , close to a minimal tRNA modification set?. <i>Trends in Cell & Molecular Biology</i> , 2012, 7, 11-34.	0.5	14
104	Synergistic use of plant-prokaryote comparative genomics for functional annotations. <i>BMC Genomics</i> , 2011, 12, S2.	1.2	43
105	Biosynthesis and function of tRNA modifications in Archaea. <i>Current Opinion in Microbiology</i> , 2011, 14, 335-341.	2.3	49
106	Erratum to "Towards a Systems Approach in the Genetic Analysis of Archaea: Accelerating Mutant Construction and Phenotypic Analysis in <i>Haloferax volcanii</i> ". <i>Archaea</i> , 2011, 2011, 1-1.	2.3	26
107	Role of a Zn-independent DksA in Zn homeostasis and stringent response. <i>Molecular Microbiology</i> , 2011, 79, 700-715.	1.2	68
108	A role for the universal Kae1/Qri7/YgjD (COG0533) family in tRNA modification. <i>EMBO Journal</i> , 2011, 30, 882-893.	3.5	132

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109	Mining high-throughput experimental data to link gene and function. Trends in Biotechnology, 2011, 29, 174-182.	4.9	45
110	A 5-formyltetrahydrofolate cycloligase paralog from all domains of life: comparative genomic and experimental evidence for a cryptic role in thiamin metabolism. Functional and Integrative Genomics, 2011, 11, 467-478.	1.4	21
111	Pseudouridine formation in archaeal RNAs: The case of <i>Haloferax volcanii</i> . Rna, 2011, 17, 1367-1380.	1.6	40
112	Gcn4 misregulation reveals a direct role for the evolutionary conserved EKC/KEOPS in the t6A modification of tRNAs. Nucleic Acids Research, 2011, 39, 6148-6160.	6.5	79
113	Deciphering synonymous codons in the three domains of life: Co-evolution with specific tRNA modification enzymes. FEBS Letters, 2010, 584, 252-264.	1.3	272
114	Predicting the pathway involved in post-translational modification of Elongation factor P in a subset of bacterial species. Biology Direct, 2010, 5, 3.	1.9	64
115	Towards a Systems Approach in the Genetic Analysis of Archaea: Accelerating Mutant Construction and Phenotypic Analysis in <i>Haloferax volcanii</i> . Archaea, 2010, 2010, 1-11.	2.3	32
116	Moonlighting Glutamate Formiminotransferases Can Functionally Replace 5-Formyltetrahydrofolate Cycloligase*. Journal of Biological Chemistry, 2010, 285, 41557-41566.	1.6	25
117	Biosynthesis of Wyosine Derivatives in tRNA: An Ancient and Highly Diverse Pathway in Archaea. Molecular Biology and Evolution, 2010, 27, 2062-2077.	3.5	71
118	A role for tetrahydrofolates in the metabolism of iron-sulfur clusters in all domains of life. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10412-10417.	3.3	81
119	FolX and FolM Are Essential for Tetrahydromonapterin Synthesis in Escherichia coli and Pseudomonas aeruginosa. Journal of Bacteriology, 2010, 192, 475-482.	1.0	46
120	Discovery and Characterization of an Amidinotransferase Involved in the Modification of Archaeal tRNA. Journal of Biological Chemistry, 2010, 285, 12706-12713.	1.6	35
121	“Unknown” proteins and “orphan” enzymes: the missing half of the engineering parts list “ and how to find it. Biochemical Journal, 2010, 425, 1-11.	1.7	183
122	A Gateway platform for functional genomics in <i>Haloferax volcanii</i> : deletion of three tRNA modification genes. Archaea, 2009, 2, 211-219.	2.3	20
123	A FAST AND ACCURATE ALGORITHM FOR COMPARATIVE ANALYSIS OF METABOLIC PATHWAYS. Journal of Bioinformatics and Computational Biology, 2009, 07, 389-428.	0.3	16
124	6-Pyruvoyltetrahydropterin Synthase Paralogs Replace the Folate Synthesis Enzyme Dihydroneopterin Aldolase in Diverse Bacteria. Journal of Bacteriology, 2009, 191, 4158-4165.	1.0	23
125	The universal YrdC/Sua5 family is required for the formation of threonylcarbamoyladenosine in tRNA. Nucleic Acids Research, 2009, 37, 2894-2909.	6.5	150
126	Zinc-Independent Folate Biosynthesis: Genetic, Biochemical, and Structural Investigations Reveal New Metal Dependence for GTP Cyclohydrolase IB. Journal of Bacteriology, 2009, 191, 6936-6949.	1.0	61

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127	A subset of the diverse COG0523 family of putative metal chaperones is linked to zinc homeostasis in all kingdoms of life. <i>BMC Genomics</i> , 2009, 10, 470.	1.2	141
128	RNomics and Modomics in the halophilic archaea <i>Haloferax volcanii</i> : identification of RNA modification genes. <i>BMC Genomics</i> , 2008, 9, 470.	1.2	66
129	<i>Plasmodium falciparum</i> : a paradigm for alternative folate biosynthesis in diverse microorganisms?. <i>Trends in Parasitology</i> , 2008, 24, 502-508.	1.5	21
130	Phylogenomic and Functional Analysis of Pterin-4a-Carbinolamine Dehydratase Family (COG2154) Proteins in Plants and Microorganisms. <i>Plant Physiology</i> , 2008, 146, 1515-1527.	2.3	33
131	Biosynthesis of 7-Deazaguanosine-Modified tRNA Nucleosides: a New Role for GTP Cyclohydrolase I. <i>Journal of Bacteriology</i> , 2008, 190, 7876-7884.	1.0	66
132	CONSISTENT ALIGNMENT OF METABOLIC PATHWAYS WITHOUT ABSTRACTION. , 2008, , .		10
133	Genetic Code Ambiguity Confers a Selective Advantage on <i>Acinetobacter baylyi</i> . <i>Journal of Bacteriology</i> , 2007, 189, 6494-6496.	1.0	36
134	Finding novel metabolic genes through plant-prokaryote phylogenomics. <i>Trends in Microbiology</i> , 2007, 15, 563-570.	3.5	22
135	Identification of Genes Encoding tRNA Modification Enzymes by Comparative Genomics. <i>Methods in Enzymology</i> , 2007, 425, 153-183.	0.4	22
136	Comparative genomics of bacterial and plant folate synthesis and salvage: predictions and validations. <i>BMC Genomics</i> , 2007, 8, 245.	1.2	133
137	Comparative RNomics and Modomics in Mollicutes: Prediction of Gene Function and Evolutionary Implications. <i>IUBMB Life</i> , 2007, 59, 634-658.	1.5	76
138	Development of a novel continuous culture device for experimental evolution of bacterial populations. <i>Applied Microbiology and Biotechnology</i> , 2007, 77, 489-496.	1.7	38
139	Molecular determinants of dihydrouridine synthase activity. <i>FEBS Letters</i> , 2006, 580, 5198-5202.	1.3	19
140	Rapid Evolution of Diminished Transformability in <i>Acinetobacter baylyi</i> . <i>Journal of Bacteriology</i> , 2006, 188, 8534-8542.	1.0	37
141	Discovery of a New Prokaryotic Type I GTP Cyclohydrolase Family. <i>Journal of Biological Chemistry</i> , 2006, 281, 37586-37593.	1.6	56
142	Inhibited cell growth and protein functional changes from an editing-defective tRNA synthetase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1697-1701.	3.3	71
143	Inhibition of Mutation and Combating the Evolution of Antibiotic Resistance. <i>PLoS Biology</i> , 2005, 3, e176.	2.6	456
144	Discovery of a Gene Family Critical to Wyosine Base Formation in a Subset of Phenylalanine-specific Transfer RNAs. <i>Journal of Biological Chemistry</i> , 2005, 280, 37616-37622.	1.6	44

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145	From cyclohydrolase to oxidoreductase: Discovery of nitrile reductase activity in a common fold. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4264-4269.	3.3	100
146	Major Biocontrol of Plant Tumors Targets tRNA Synthetase. Science, 2005, 309, 1533-1533.	6.0	86
147	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. Nucleic Acids Research, 2005, 33, 5691-5702.	6.5	1,806
148	Acinetobacter sp. ADP1: an ideal model organism for genetic analysis and genome engineering. Nucleic Acids Research, 2004, 32, 5780-5790.	6.5	159
149	Identification of Four Genes Necessary for Biosynthesis of the Modified Nucleoside Queuosine. Journal of Biological Chemistry, 2004, 279, 6280-6285.	1.6	129
150	Aminoacylation of the anticodon stem by a tRNA-synthetase paralog: relic of an ancient code?. Trends in Biochemical Sciences, 2004, 29, 519-522.	3.7	22
151	Incorporation of Nonnatural Amino Acids Into Proteins. Annual Review of Biochemistry, 2004, 73, 147-176.	5.0	234
152	Identification of the tRNA-Dihydrouridine Synthase Family. Journal of Biological Chemistry, 2002, 277, 25090-25095.	1.6	92
153	Complete Reconstitution of the Human Coenzyme A Biosynthetic Pathway via Comparative Genomics. Journal of Biological Chemistry, 2002, 277, 21431-21439.	1.6	193
154	Mutational Separation of Two Pathways for Editing by a Class I tRNA Synthetase. Molecular Cell, 2002, 9, 353-362.	4.5	71
155	An aminoacyl tRNA synthetase whose sequence fits into neither of the two known classes. Nature, 2001, 411, 110-114.	13.7	46
156	The ClpB ATPase of Streptomyces albus G belongs to the HspR heat shock regulon. Molecular Microbiology, 1999, 31, 521-532.	1.2	71
157	Alteration of the synthesis of the Clp ATP-dependent protease affects morphological and physiological differentiation in Streptomyces. Molecular Microbiology, 1999, 32, 505-517.	1.2	80
158	Identification of two fructose transport and phosphorylation pathways in Xanthomonas campestris pv. campestris. Molecular Genetics and Genomics, 1991, 227, 465-472.	2.4	12