

Michael Y Galperin

List of Publications by Year in descending order

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225
papers

27,399
citations

7551

77
h-index

6454

157
g-index

310
all docs

310
docs citations

310
times ranked

26599
citing authors

#	ARTICLE	IF	CITATIONS
1	Clp protease and antisense RNA jointly regulate the global regulator CarD to mediate mycobacterial starvation response. <i>ELife</i> , 2022, 11, .	2.8	6
2	Comparative Genomics of Cyclic di-GMP Metabolism and Chemosensory Pathways in <i>Shewanella</i> algae Strains: Novel Bacterial Sensory Domains and Functional Insights into Lifestyle Regulation. <i>MSystems</i> , 2022, 7, e0151821.	1.7	11
3	Sequence Conservation, Domain Architectures, and Phylogenetic Distribution of the HD-GYP Type c-di-GMP Phosphodiesterases. <i>Journal of Bacteriology</i> , 2022, 204, jb0056121.	1.0	15
4	Conservation and Evolution of the Sporulation Gene Set in Diverse Members of the <i>Firmicutes</i> . <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	20
5	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021, 49, D274-D281.	6.5	441
6	Nonessential Ribosomal Proteins in Bacteria and Archaea Identified Using Clusters of Orthologous Genes. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	14
7	Complete Genome Sequence and Methylome of the Type Strain of <i>Shewanella</i> algae. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055921.	0.3	3
8	Ways to control harmful biofilms: prevention, inhibition, and eradication. <i>Critical Reviews in Microbiology</i> , 2021, 47, 57-78.	2.7	38
9	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
10	<i>Paenibacillus</i> infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	39
11	A decade of research on the second messenger c-di-AMP. <i>FEMS Microbiology Reviews</i> , 2020, 44, 701-724.	3.9	74
12	Complete Genome Sequences of the Human Pathogen <i>Paenibacillus thiaminolyticus</i> Mbale and Type Strain <i>P. thiaminolyticus</i> NRRL B-4156. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	10
13	Cyclic di-GMP in <i>Streptomyces</i> : A New Conformation, New Binding Mode, New Receptor, and a New Mechanism to Control Cell Development. <i>Molecular Cell</i> , 2020, 77, 443-445.	4.5	5
14	Cyclic di-AMP, a second messenger of primary importance: tertiary structures and binding mechanisms. <i>Nucleic Acids Research</i> , 2020, 48, 2807-2829.	6.5	66
15	Structural Conservation and Diversity of PilZ-Related Domains. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	24
16	Noncanonical Cyclic di-GMP Binding Modes. , 2020, , 125-134.		0
17	G protein-coupled receptors of class A harness the energy of membrane potential to increase their sensitivity and selectivity. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 183051.	1.4	10
18	Two forms of phosphomannomutase in <i>gamma</i> proteobacteria: The overlooked membrane-bound form of AlgC is required for twitching motility of <i>Lysobacter enzymogenes</i> . <i>Environmental Microbiology</i> , 2019, 21, 3969-3978.	1.8	2

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19	Microbial genome analysis: the COG approach. Briefings in Bioinformatics, 2019, 20, 1063-1070.	3.2	186
20	A bacterial coat that is not pure cotton. Science, 2018, 359, 276-277.	6.0	8
21	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. Journal of Bacteriology, 2018, 200, .	1.0	41
22	Sensory Transduction in Bacteria. , 2018, , .		1
23	What bacteria want. Environmental Microbiology, 2018, 20, 4221-4229.	1.8	73
24	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in Salmonella typhimurium. Journal of Molecular Biology, 2018, 430, 3170-3189.	2.0	29
25	Evolution of cation binding in the active sites of P-loop nucleoside triphosphatases in relation to the basic catalytic mechanism. ELife, 2018, 7, .	2.8	41
26	The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes. Nucleic Acids Research, 2017, 45, D1-D11.	6.5	144
27	Genome Sequence of Uric Acid-Fermenting Eubacterium angustum DSM 1989 T (MK-1). Genome Announcements, 2017, 5, .	0.8	1
28	Emergence of cytochrome <i>b_c</i> complexes in the context of photosynthesis. Physiologia Plantarum, 2017, 161, 150-170.	2.6	13
29	Discovery of the Second Messenger Cyclic di-GMP. Methods in Molecular Biology, 2017, 1657, 1-8.	0.4	34
30	Stand-Alone EAL Domain Proteins Form a Distinct Subclass of EAL Proteins Involved in Regulation of Cell Motility and Biofilm Formation in Enterobacteria. Journal of Bacteriology, 2017, 199, .	1.0	36
31	Proposed Role for KaiC-Like ATPases as Major Signal Transduction Hubs in Archaea. MBio, 2017, 8, .	1.8	12
32	Proposal for the reclassification of obligately purine-fermenting bacteria <i>Clostridium acidurici</i> (Barker 1938) and <i>Clostridium purinilyticum</i> (D'Arre et al. 1981) as <i>Gottschalkia acidurici</i> gen. nov. comb. nov. and <i>Gottschalkia purinilytica</i> comb. nov. and of <i>Eubacterium angustum</i> (Beuscher and) Tj ETQq0 0 0 rg 0 1 0 Overlook 10 Tf 50		
33	International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2711-2719. Sustained sensing as an emerging principle in second messenger signaling systems. Current Opinion in Microbiology, 2016, 34, 119-126.	2.3	32
34	Nucleotide binding by the widespread high-affinity cyclic di-GMP receptor MshEN domain. Nature Communications, 2016, 7, 12481.	5.8	129
35	The emerging diversity of Na ⁺ -translocating ion pumps supports the evolutionary primacy of Na ⁺ -based bioenergetics. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, e68-e69.	0.5	0
36	Diversity of Cyclic Di-GMP-Binding Proteins and Mechanisms. Journal of Bacteriology, 2016, 198, 32-46.	1.0	244

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37	The 2016 database issue of <i>Nucleic Acids Research</i> and an updated molecular biology database collection. <i>Nucleic Acids Research</i> , 2016, 44, D1-D6.	6.5	119
38	Systematic Nomenclature for GGDEF and EAL Domain-Containing Cyclic Di-GMP Turnover Proteins of <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2016, 198, 7-11.	1.0	96
39	Phylogenomic analysis of the family Peptostreptococcaceae (<i>Clostridium</i> cluster XI) and proposal for reclassification of <i>Clostridium litorale</i> (Fendrich et al. 1991) and <i>Eubacterium acidaminophilum</i> (Zindel et al. 1989) as <i>Peptoclostridium litorale</i> gen. nov. comb. nov. and <i>Peptoclostridium acidaminophilum</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5506-5513.	0.8	77
40	Modeling of interaction between cytochrome c and the WD domains of Apaf-1: bifurcated salt bridges underlying apoptosome assembly. <i>Biology Direct</i> , 2015, 10, 29.	1.9	19
41	Systematic Identification of Cyclic-di-GMP Binding Proteins in <i>Vibrio cholerae</i> Reveals a Novel Class of Cyclic-di-GMP-Binding ATPases Associated with Type II Secretion Systems. <i>PLoS Pathogens</i> , 2015, 11, e1005232.	2.1	107
42	Ancient systems of sodium/potassium homeostasis as predecessors of membrane bioenergetics. <i>Biochemistry (Moscow)</i> , 2015, 80, 495-516.	0.7	64
43	The 2015 <i>Nucleic Acids Research</i> Database Issue and Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2015, 43, D1-D5.	6.5	79
44	Eukaryotic G protein-coupled receptors as descendants of prokaryotic sodium-translocating rhodopsins. <i>Biology Direct</i> , 2015, 10, 63.	1.9	36
45	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015, 43, D261-D269.	6.5	1,345
46	Comparative genomic analysis of evolutionarily conserved but functionally uncharacterized membrane proteins in archaea: Prediction of novel components of secretion, membrane remodeling and glycosylation systems. <i>Biochimie</i> , 2015, 118, 302-312.	1.3	11
47	Bacterial cellulose biosynthesis: diversity of operons, subunits, products, and functions. <i>Trends in Microbiology</i> , 2015, 23, 545-557.	3.5	432
48	Phylogenomic reconstruction of archaeal fatty acid metabolism. <i>Environmental Microbiology</i> , 2014, 16, 907-918.	1.8	67
49	<i>GIL</i> , a new c-di-GMP binding protein domain involved in regulation of cellulose synthesis in enterobacteria. <i>Molecular Microbiology</i> , 2014, 93, 439-452.	1.2	118
50	The 2014 <i>Nucleic Acids Research</i> Database Issue and an updated NAR online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2014, 42, D1-D6.	6.5	81
51	Comparative Genomics Approaches to Identifying Functionally Related Genes. <i>Lecture Notes in Computer Science</i> , 2014, , 1-24.	1.0	2
52	Evolution of cytochrome bc complexes: From membrane-anchored dehydrogenases of ancient bacteria to triggers of apoptosis in vertebrates. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 1407-1427.	0.5	73
53	A genomic update on clostridial phylogeny: <i>G</i> ram-negative spore formers and other misplaced clostridia. <i>Environmental Microbiology</i> , 2013, 15, 2631-2641.	1.8	771
54	Bacterial second messengers, cGMP and c-di-GMP, in a quest for regulatory dominance. <i>EMBO Journal</i> , 2013, 32, 2421-2423.	3.5	24

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55	A Time to Scatter Genes and a Time to Gather Them. <i>Advances in Botanical Research</i> , 2013, 66, 1-35.	0.5	8
56	Cyclic di-GMP: the First 25 Years of a Universal Bacterial Second Messenger. <i>Microbiology and Molecular Biology Reviews</i> , 2013, 77, 1-52.	2.9	1,479
57	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	2.6	54
58	How many signal peptides are there in bacteria?. <i>Environmental Microbiology</i> , 2013, 15, 983-990.	1.8	29
59	Genome Diversity of Spore-Forming <i>Firmicutes</i> . <i>Microbiology Spectrum</i> , 2013, 1, .	1.2	153
60	Divergence and Convergence in Enzyme Evolution. <i>Journal of Biological Chemistry</i> , 2012, 287, 21-28.	1.6	140
61	The 2013 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2012, 41, D1-D7.	6.5	94
62	Genomic determinants of sporulation in <i>Bacilli</i> and <i>Clostridia</i> : towards the minimal set of sporulation-specific genes. <i>Environmental Microbiology</i> , 2012, 14, 2870-2890.	1.8	235
63	The Role of Energy in the Emergence of Biology from Chemistry. <i>Origins of Life and Evolution of Biospheres</i> , 2012, 42, 459-468.	0.8	19
64	Open Questions on the Origin of Life at Anoxic Geothermal Fields. <i>Origins of Life and Evolution of Biospheres</i> , 2012, 42, 507-516.	0.8	22
65	The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2012, 40, D1-D8.	6.5	104
66	Origin of first cells at terrestrial, anoxic geothermal fields. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E821-30.	3.3	341
67	Comparative analysis of lipid biosynthesis in archaea, bacteria and eukaryotes: What was the structure of the first membrane lipids?. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2012, 1817, S154.	0.5	3
68	Planctomycetes and eukaryotes: A case of analogy not homology. <i>BioEssays</i> , 2011, 33, 810-817.	1.2	79
69	The 2011 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2011, 39, D1-D6.	6.5	70
70	Towards BioDBcore: a community-defined information specification for biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, baq027-baq027.	1.4	30
71	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	6.5	32
72	New Structural and Functional Contexts of the Dx[DN]xDG Linear Motif: Insights into Evolution of Calcium-Binding Proteins. <i>PLoS ONE</i> , 2011, 6, e21507.	1.1	53

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73	From complete genome sequence to “complete”™ understanding?. Trends in Biotechnology, 2010, 28, 398-406.	4.9	151
74	Non-homologous isofunctional enzymes: A systematic analysis of alternative solutions in enzyme evolution. Biology Direct, 2010, 5, 31.	1.9	119
75	On the abundance of zinc in the evolutionarily old protein domains. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, E137; author reply E138.	3.3	11
76	The 2010 Nucleic Acids Research Database Issue and online Database Collection: a community of data resources. Nucleic Acids Research, 2010, 38, D1-D4.	6.5	86
77	Characterization of the N-ATPase, a distinct, laterally transferred Na ⁺ -translocating form of the bacterial F-type membrane ATPase. Bioinformatics, 2010, 26, 1473-1476.	1.8	75
78	Diversity of structure and function of response regulator output domains. Current Opinion in Microbiology, 2010, 13, 150-159.	2.3	308
79	Structural Insight into the Mechanism of c-di-GMP Hydrolysis by EAL Domain Phosphodiesterases. Journal of Molecular Biology, 2010, 402, 524-538.	2.0	121
80	Interplay of heritage and habitat in the distribution of bacterial signal transduction systems. Molecular BioSystems, 2010, 6, 721.	2.9	87
81	Evolutionary origins of membrane proteins. , 2010, , 1-28.		7
82	Co-evolution of primordial membranes and membrane proteins. Trends in Biochemical Sciences, 2009, 34, 206-215.	3.7	140
83	Microbial genomics as pursuit of happiness. Microbial Biotechnology, 2009, 2, 135-136.	2.0	1
84	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. ISME Journal, 2009, 3, 1012-1035.	4.4	178
85	Microbial systems biology: bottom up and top down. FEMS Microbiology Reviews, 2009, 33, 1-2.	3.9	11
86	Globins Synthesize the Second Messenger Bis-(3′,5′)-Cyclic Diguanosine Monophosphate in Bacteria. Journal of Molecular Biology, 2009, 388, 262-270.	2.0	91
87	Single domain response regulators: molecular switches with emerging roles in cell organization and dynamics. Current Opinion in Microbiology, 2009, 12, 152-160.	2.3	77
88	On the origin of life in the Zinc world. 2. Validation of the hypothesis on the photosynthesizing zinc sulfide edifices as cradles of life on Earth. Biology Direct, 2009, 4, 27.	1.9	74
89	Nucleic Acids Research annual Database Issue and the NAR online Molecular Biology Database Collection in 2009. Nucleic Acids Research, 2009, 37, D1-D4.	6.5	101
90	Sensory Transduction Network of E. coli. , 2009, , 133-148.		2

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91	Social bacteria and asocial eukaryotes. <i>Environmental Microbiology</i> , 2008, 10, 281-288.	1.8	6
92	The dawn of synthetic genomics. <i>Environmental Microbiology</i> , 2008, 10, 821-825.	1.8	4
93	Genomes of model organisms: know thy tools. <i>Environmental Microbiology</i> , 2008, 10, 1383-1391.	1.8	4
94	New feel for new phyla. <i>Environmental Microbiology</i> , 2008, 10, 1927-1933.	1.8	9
95	The quest for biofuels fuels genome sequencing. <i>Environmental Microbiology</i> , 2008, 10, 2471-2475.	1.8	6
96	Sorting out the mix in microbial genomics. <i>Environmental Microbiology</i> , 2008, 10, 3187-3192.	1.8	4
97	The past and present of sodium energetics: May the sodium-motive force be with you. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2008, 1777, 985-992.	0.5	142
98	Telling Bacteria: Do Not LytTR. <i>Structure</i> , 2008, 16, 657-659.	1.6	39
99	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , 2008, 3, 13.	1.9	144
100	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, <i>Methylacidiphilum infernorum</i> , a representative of the bacterial phylum Verrucomicrobia. <i>Biology Direct</i> , 2008, 3, 26.	1.9	216
101	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium <i>Anoxybacillus flavithermus</i> WK1. <i>Genome Biology</i> , 2008, 9, R161.	13.9	71
102	Sequence analysis of GerM and SpoVS, uncharacterized bacterial "sporulation" proteins with widespread phylogenetic distribution. <i>Bioinformatics</i> , 2008, 24, 1793-1797.	1.8	30
103	The Molecular Biology Database Collection: 2008 update. <i>Nucleic Acids Research</i> , 2008, 36, D2-D4.	6.5	99
104	Origin and Evolution of Photosynthesis: Clues from Genome Comparison. , 2008, , 1169-1175.		0
105	The Molecular Biology Database Collection: 2007 update. <i>Nucleic Acids Research</i> , 2007, 35, D3-D4.	6.5	80
106	Sentra: a database of signal transduction proteins for comparative genome analysis. <i>Nucleic Acids Research</i> , 2007, 35, D271-D273.	6.5	24
107	Identification of Sensory and Signal-Transducing Domains in Two-Component Signaling Systems. <i>Methods in Enzymology</i> , 2007, 422, 47-74.	0.4	30
108	Physico-Chemical and Evolutionary Constraints for the Formation and Selection of First Biopolymers: Towards the Consensus Paradigm of the Abiogenic Origin of Life. <i>Chemistry and Biodiversity</i> , 2007, 4, 2003-2015.	1.0	29

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109	Inventing the dynamo machine: the evolution of the F-type and V-type ATPases. <i>Nature Reviews Microbiology</i> , 2007, 5, 892-899.	13.6	189
110	Using archaeal genomics to fight global warming and clostridia to fight cancer. <i>Environmental Microbiology</i> , 2007, 9, 279-286.	1.8	3
111	Mycobacterial genomes for all tastes: from BCG to biodegradation of naphthalene and pyrene. <i>Environmental Microbiology</i> , 2007, 9, 839-845.	1.8	2
112	Linear chromosomes in bacteria: no straight edge advantage?. <i>Environmental Microbiology</i> , 2007, 9, 1357-1362.	1.8	3
113	Genomics against flatulence. <i>Environmental Microbiology</i> , 2007, 9, 1869-1877.	1.8	1
114	Dark matter in a deep-sea vent and in human mouth. <i>Environmental Microbiology</i> , 2007, 9, 2385-2391.	1.8	3
115	Some bacteria degrade explosives, others prefer boiling methanol. <i>Environmental Microbiology</i> , 2007, 9, 2905-2910.	1.8	8
116	Structural Classification of Bacterial Response Regulators: Diversity of Output Domains and Domain Combinations. <i>Journal of Bacteriology</i> , 2006, 188, 4169-4182.	1.0	436
117	The cyanobacterial genome core and the origin of photosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13126-13131.	3.3	277
118	Genome-based identification and characterization of a putative mucin-binding protein from the surface of <i>Streptococcus pneumoniae</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 547-558.	1.5	21
119	Protecting sausages with bacteria instead of salt. <i>Environmental Microbiology</i> , 2006, 8, 185-192.	1.8	1
120	The minimal genome keeps growing. <i>Environmental Microbiology</i> , 2006, 8, 569-573.	1.8	6
121	Genomes to aid in bioremediation of dry cleaning solvents, mothballs and more. <i>Environmental Microbiology</i> , 2006, 8, 949-955.	1.8	0
122	Sampling of microbial diversity by complete genomes. <i>Environmental Microbiology</i> , 2006, 8, 1313-1317.	1.8	4
123	A square archaeon, the smallest eukaryote and the largest bacteria. <i>Environmental Microbiology</i> , 2006, 8, 1683-1687.	1.8	1
124	The fuzzy border between a cell and an organelle. <i>Environmental Microbiology</i> , 2006, 8, 2062-2067.	1.8	1
125	House cleaning, a part of good housekeeping. <i>Molecular Microbiology</i> , 2006, 59, 5-19.	1.2	186
126	New metrics for comparative genomics. <i>Current Opinion in Biotechnology</i> , 2006, 17, 440-447.	3.3	29

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127	PilZ domain is part of the bacterial c-di-GMP binding protein. <i>Bioinformatics</i> , 2006, 22, 3-6.	1.8	460
128	Cyanobacterial response regulator PatA contains a conserved N-terminal domain (PATAN) with an alpha-helical insertion. <i>Bioinformatics</i> , 2006, 22, 1297-1301.	1.8	35
129	The Molecular Biology Database Collection: 2006 update. <i>Nucleic Acids Research</i> , 2006, 34, D3-D5.	6.5	83
130	Life is not defined just in base pairs. <i>Environmental Microbiology</i> , 2005, 7, 149-152.	1.8	5
131	On the bottom of the deep blue sea. <i>Environmental Microbiology</i> , 2005, 7, 453-458.	1.8	2
132	The vibrio that sheds light. <i>Environmental Microbiology</i> , 2005, 7, 757-760.	1.8	3
133	To finish or not to finish?. <i>Environmental Microbiology</i> , 2005, 7, 1061-1064.	1.8	1
134	The secret of being cool. <i>Environmental Microbiology</i> , 2005, 7, 1499-1504.	1.8	2
135	More cool news from marine bacteria. <i>Environmental Microbiology</i> , 2005, 7, 1864-1867.	1.8	2
136	C-di-GMP: the dawning of a novel bacterial signalling system. <i>Molecular Microbiology</i> , 2005, 57, 629-639.	1.2	593
137	A census of membrane-bound and intracellular signal transduction proteins in bacteria: bacterial IQ, extroverts and introverts. <i>BMC Microbiology</i> , 2005, 5, 35.	1.3	398
138	Functional Analysis of Conserved Polar Residues in Vc-NhaD, Na ⁺ /H ⁺ Antiporter of <i>Vibrio cholerae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 39637-39643.	1.6	25
139	OMICS-Related Research in Latin America. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 129-129.	1.0	1
140	Global profiling of <i>Shewanella oneidensis</i> MR-1: Expression of hypothetical genes and improved functional annotations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2099-2104.	3.3	113
141	OMICS-Related Research in South America. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 1-1.	1.0	0
142	Crystal Structure of the Bacterial YhcH Protein Indicates a Role in Sialic Acid Catabolism. <i>Journal of Bacteriology</i> , 2005, 187, 5520-5527.	1.0	21
143	Dimeric dUTPases, HisE, and MazG belong to a New Superfamily of all- β NTP Pyrophosphohydrolases with Potential "House-cleaning" Functions. <i>Journal of Molecular Biology</i> , 2005, 347, 243-255.	2.0	77
144	Sequence Analysis and Characterization of a Novel Fibronectin-Binding Repeat Domain from the Surface of <i>Streptococcus pneumoniae</i> . <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 341-356.	1.0	25

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145	The Molecular Biology Database Collection: 2005 update. <i>Nucleic Acids Research</i> , 2004, 33, D5-D24.	6.5	99
146	Genome sequence of the deep-sea <i>Â</i> -proteobacterium <i>Idiomarina loihiensis</i> reveals amino acid fermentation as a source of carbon and energy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 18036-18041.	3.3	135
147	In Silico Metabolic Model and Protein Expression of <i>Haemophilus influenzae</i> Strain Rd KW20 in Rich Medium. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 25-41.	1.0	42
148	'Conserved hypothetical' proteins: prioritization of targets for experimental study. <i>Nucleic Acids Research</i> , 2004, 32, 5452-5463.	6.5	346
149	Salt in the Wound: A Possible Role of Na ⁺ Gradient in Chlamydial Infection. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 8, 1-6.	1.0	19
150	All bugs, big and small. <i>Environmental Microbiology</i> , 2004, 6, 435-437.	1.8	3
151	Bacterial signal transduction network in a genomic perspective+. <i>Environmental Microbiology</i> , 2004, 6, 552-567.	1.8	318
152	Metagenomics: from acid mine to shining sea. <i>Environmental Microbiology</i> , 2004, 6, 543-545.	1.8	25
153	Looking at big brothers for clues. <i>Environmental Microbiology</i> , 2004, 6, 767-768.	1.8	0
154	The bugs that came in from the cold. <i>Environmental Microbiology</i> , 2004, 6, 1001-1004.	1.8	1
155	Genomes back-to-back: when sequencing race is a good thing. <i>Environmental Microbiology</i> , 2004, 6, 1205-1209.	1.8	3
156	The PA14 domain, a conserved all-Î² domain in bacterial toxins, enzymes, adhesins and signaling molecules. <i>Trends in Biochemical Sciences</i> , 2004, 29, 335-339.	3.7	90
157	Identification and functional analysis of 'hypothetical' genes expressed in <i>Haemophilus influenzae</i> . <i>Nucleic Acids Research</i> , 2004, 32, 2353-2361.	6.5	75
158	Environmental biotechnology. <i>Current Opinion in Biotechnology</i> , 2004, 15, 167-169.	3.3	2
159	The Molecular Biology Database Collection: 2004 update. <i>Nucleic Acids Research</i> , 2004, 32, 3D-22.	6.5	66
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