

Michael Y Galperin

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

223
papers

20,722
citations

73
h-index

142
g-index

306
ext. papers

24,744
ext. citations

8
avg, IF

7.29
L-index

#	Paper	IF	Citations
223	Comparative Genomics of Cyclic di-GMP Metabolism and Chemosensory Pathways in Shewanella algae Strains: Novel Bacterial Sensory Domains and Functional Insights into Lifestyle Regulation.. <i>MSystems</i> , 2022 , e0151821	7.6	0
222	Ways to control harmful biofilms: prevention, inhibition, and eradication. <i>Critical Reviews in Microbiology</i> , 2021 , 47, 57-78	7.8	9
221	Non-essential ribosomal proteins in bacteria and archaea identified using COGs. <i>Journal of Bacteriology</i> , 2021 ,	3.5	2
220	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021 , 49, D274-D281	20.1	84
219	Complete Genome Sequence and Methylome of the Type Strain of Shewanella algae. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0055921	1.3	2
218	Sequence conservation, domain architectures, and phylogenetic distribution of the HD-GYP type c-di-GMP phosphodiesterases.. <i>Journal of Bacteriology</i> , 2021 , jb0056121	3.5	2
217	A decade of research on the second messenger c-di-AMP. <i>FEMS Microbiology Reviews</i> , 2020 , 44, 701-724	15.1	32
216	Complete Genome Sequences of the Human Pathogen Paenibacillus thiaminolyticus Mbale and Type Strain P. thiaminolyticus NRRL B-4156. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	4
215	Cyclic di-GMP in Streptomyces: A New Conformation, New Binding Mode, New Receptor, and a New Mechanism to Control Cell Development. <i>Molecular Cell</i> , 2020 , 77, 443-445	17.6	3
214	Cyclic di-AMP, a second messenger of primary importance: tertiary structures and binding mechanisms. <i>Nucleic Acids Research</i> , 2020 , 48, 2807-2829	20.1	29
213	Noncanonical Cyclic di-GMP Binding Modes 2020 , 125-134		
212	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020 , 5, 126-140	26.6	85
211	infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	13
210	Structural Conservation and Diversity of PilZ-Related Domains. <i>Journal of Bacteriology</i> , 2020 , 202,	3.5	11
209	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	3.8	6
208	Two forms of phosphomannomutase in gammaproteobacteria: The overlooked membrane-bound form of AlgC is required for twitching motility of <i>Lyso bacter</i> enzymogenes. <i>Environmental Microbiology</i> , 2019 , 21, 3969-3978	5.2	0
207	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1063-1070	13.4	80

206	A bacterial coat that is not pure cotton. <i>Science</i> , 2018 , 359, 276-277	33.3	7
205	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	29
204	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in <i>Salmonella typhimurium</i> . <i>Journal of Molecular Biology</i> , 2018 , 430, 3170-3189	6.5	19
203	Evolution of cation binding in the active sites of P-loop nucleoside triphosphatases in relation to the basic catalytic mechanism. <i>ELife</i> , 2018 , 7,	8.9	21
202	Sensory Transduction in Bacteria 2018 ,		1
201	What bacteria want. <i>Environmental Microbiology</i> , 2018 , 20, 4221-4229	5.2	39
200	The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes. <i>Nucleic Acids Research</i> , 2017 , 45, D1-D11	20.1	50
199	Genome Sequence of Uric Acid-Fermenting Eubacterium angustum DSM 1989T (MK-1). <i>Genome Announcements</i> , 2017 , 5,		1
198	Emergence of cytochrome bc complexes in the context of photosynthesis. <i>Physiologia Plantarum</i> , 2017 , 161, 150-170	4.6	9
197	Discovery of the Second Messenger Cyclic di-GMP. <i>Methods in Molecular Biology</i> , 2017 , 1657, 1-8	1.4	22
196	Stand-Alone EAL Domain Proteins Form a Distinct Subclass of EAL Proteins Involved in Regulation of Cell Motility and Biofilm Formation in Enterobacteria. <i>Journal of Bacteriology</i> , 2017 , 199,	3.5	19
195	Proposed Role for KaiC-Like ATPases as Major Signal Transduction Hubs in Archaea. <i>MBio</i> , 2017 , 8,	7.8	9
194	Proposal for the reclassification of obligately purine-fermenting bacteria <i>Clostridium acidurici</i> (Barker 1938) and <i>Clostridium purinilyticum</i> (D'ère et al. 1981) as <i>Gottschalkia acidurici</i> gen. nov. comb. nov. and <i>Gottschalkiapurinilytica</i> comb. nov. and of <i>Eubacterium angustum</i> (Beuscher and Andreesen 1985) as <i>Andreesenia angusta</i> gen. nov. comb. nov. in the family Gottschalkiaceae fam.	2.2	9
193	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	3.5	70
192	Genome Diversity of Spore-Forming Firmicutes 2016 , 1-18		2
191	Nucleotide binding by the widespread high-affinity cyclic di-GMP receptor MshEN domain. <i>Nature Communications</i> , 2016 , 7, 12481	17.4	83
190	The emerging diversity of Na ⁺ -translocating ion pumps supports the evolutionary primacy of Na ⁺ -based bioenergetics. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016 , 1857, e68-e69	4.6	
189	Diversity of Cyclic Di-GMP-Binding Proteins and Mechanisms. <i>Journal of Bacteriology</i> , 2016 , 198, 32-46	3.5	159

188	The 2016 database issue of Nucleic Acids Research and an updated molecular biology database collection. <i>Nucleic Acids Research</i> , 2016 , 44, D1-6	20.1	63
187	Phylogenomic analysis of the family Peptostreptococcaceae (Clostridium 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	2.2	41
186	Sustained sensing as an emerging principle in second messenger signaling systems. <i>Current Opinion in Microbiology</i> , 2016 , 34, 119-126	7.9	17
185	Bacterial cellulose biosynthesis: diversity of operons, subunits, products, and functions. <i>Trends in Microbiology</i> , 2015 , 23, 545-57	12.4	275
184	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	7.2	11
183	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	7.6	77
182	Ancient Systems of Sodium/Potassium Homeostasis as Predecessors of Membrane Bioenergetics. <i>Biochemistry (Moscow)</i> , 2015 , 80, 495-516	2.9	35
181	The 2015 Nucleic Acids Research Database Issue and molecular biology database collection. <i>Nucleic Acids Research</i> , 2015 , 43, D1-5	20.1	55
180	Eukaryotic G protein-coupled receptors as descendants of prokaryotic sodium-translocating rhodopsins. <i>Biology Direct</i> , 2015 , 10, 63	7.2	24
179	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015 , 43, D261-9	20.1	818
178	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, 302-12	4.6	9
177	Phylogenomic reconstruction of archaeal fatty acid metabolism. <i>Environmental Microbiology</i> , 2014 , 16, 907-18	5.2	45
176	GIL, a new c-di-GMP-binding protein domain involved in regulation of cellulose synthesis in enterobacteria. <i>Molecular Microbiology</i> , 2014 , 93, 439-52	4.1	90
175	The 2014 Nucleic Acids Research Database Issue and an updated NAR online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2014 , 42, D1-6	20.1	60
174	Comparative Genomics Approaches to Identifying Functionally Related Genes. <i>Lecture Notes in Computer Science</i> , 2014 , 1-24	0.9	2
173	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, 1407-27	4.6	64
172	A genomic update on clostridial phylogeny: Gram-negative spore formers and other misplaced clostridia. <i>Environmental Microbiology</i> , 2013 , 15, 2631-41	5.2	362
171	Bacterial second messengers, cGMP and c-di-GMP, in a quest for regulatory dominance. <i>EMBO Journal</i> , 2013 , 32, 2421-3	13	21

170	A Time to Scatter Genes and a Time to Gather Them: Evolution of Photosynthesis Genes in Bacteria. <i>Advances in Botanical Research</i> , 2013 , 66, 1-35	2.2	7
169	Cyclic di-GMP: the first 25 years of a universal bacterial second messenger. <i>Microbiology and Molecular Biology Reviews</i> , 2013 , 77, 1-52	13.2	1073
168	The COMBREX project: design, methodology, and initial results. <i>PLoS Biology</i> , 2013 , 11, e1001638	9.7	47
167	How many signal peptides are there in bacteria?. <i>Environmental Microbiology</i> , 2013 , 15, 983-90	5.2	27
166	Genome Diversity of Spore-Forming Firmicutes. <i>Microbiology Spectrum</i> , 2013 , 1,	8.9	114
165	The 2013 Nucleic Acids Research Database Issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2013 , 41, D1-7	20.1	73
164	Genomic determinants of sporulation in Bacilli and Clostridia: towards the minimal set of sporulation-specific genes. <i>Environmental Microbiology</i> , 2012 , 14, 2870-90	5.2	168
163	The role of energy in the emergence of biology from chemistry. <i>Origins of Life and Evolution of Biospheres</i> , 2012 , 42, 459-68	1.5	17
162	Open questions on the origin of life at anoxic geothermal fields. <i>Origins of Life and Evolution of Biospheres</i> , 2012 , 42, 507-16	1.5	19
161	The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2012 , 40, D1-8	20.1	75
160	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	11.5	254
159	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	4.6	0
158	Divergence and convergence in enzyme evolution. <i>Journal of Biological Chemistry</i> , 2012 , 287, 21-28	5.4	115
157	Planctomycetes and eukaryotes: a case of analogy not homology. <i>BioEssays</i> , 2011 , 33, 810-7	4.1	73
156	The 2011 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2011 , 39, D1-6	20.1	60
155	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	3.7	46
154	On the abundance of zinc in the evolutionarily old protein domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, E137; author reply E138	11.5	9
153	The 2010 Nucleic Acids Research Database Issue and online Database Collection: a community of data resources. <i>Nucleic Acids Research</i> , 2010 , 38, D1-4	20.1	73

152	Characterization of the N-ATPase, a distinct, laterally transferred Na ⁺ -translocating form of the bacterial F-type membrane ATPase. <i>Bioinformatics</i> , 2010 , 26, 1473-6	7.2	55
151	Diversity of structure and function of response regulator output domains. <i>Current Opinion in Microbiology</i> , 2010 , 13, 150-9	7.9	251
150	Structural insight into the mechanism of c-di-GMP hydrolysis by EAL domain phosphodiesterases. <i>Journal of Molecular Biology</i> , 2010 , 402, 524-38	6.5	86
149	Interplay of heritage and habitat in the distribution of bacterial signal transduction systems. <i>Molecular BioSystems</i> , 2010 , 6, 721-8		76
148	From complete genome sequence to Complete Understanding?. <i>Trends in Biotechnology</i> , 2010 , 28, 398-406	10.6	126
147	Non-homologous isofunctional enzymes: a systematic analysis of alternative solutions in enzyme evolution. <i>Biology Direct</i> , 2010 , 5, 31	7.2	97
146	Evolutionary origins of membrane proteins 2010 , 1-28		6
145	Co-evolution of primordial membranes and membrane proteins. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 206-15	10.3	114
144	Microbial genomics as pursuit of happiness. <i>Microbial Biotechnology</i> , 2009 , 2, 135-6	6.3	1
143	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. <i>ISME Journal</i> , 2009 , 3, 1012-35	11.9	128
142	Globins synthesize the second messenger bis-(3',5'-cyclic diguanosine monophosphate in bacteria. <i>Journal of Molecular Biology</i> , 2009 , 388, 262-70	6.5	73
141	Single domain response regulators: molecular switches with emerging roles in cell organization and dynamics. <i>Current Opinion in Microbiology</i> , 2009 , 12, 152-60	7.9	73
140	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. <i>Biology Direct</i> , 2009 , 4, 27	7.2	55
139	Nucleic Acids Research annual Database Issue and the NAR online Molecular Biology Database Collection in 2009. <i>Nucleic Acids Research</i> , 2009 , 37, D1-4	20.1	83
138	Protein Domains Involved in Intracellular Signal Transduction 2009 , 269-288		
137	Sensory Transduction Network of <i>E. coli</i> 2009 , 133-148		2
136	Social bacteria and asocial eukaryotes. <i>Environmental Microbiology</i> , 2008 , 10, 281-8	5.2	4
135	The dawn of synthetic genomics. <i>Environmental Microbiology</i> , 2008 , 10, 821-5	5.2	3

134	Genomes of model organisms: know thy tools. <i>Environmental Microbiology</i> , 2008 , 10, 1383-91	5.2	3
133	New feel for new phyla. <i>Environmental Microbiology</i> , 2008 , 10, 1927-33	5.2	9
132	The quest for biofuels fuels genome sequencing. <i>Environmental Microbiology</i> , 2008 , 10, 2471-5	5.2	6
131	Sorting out the mix in microbial genomics. <i>Environmental Microbiology</i> , 2008 , 10, 3187-92	5.2	4
130	The past and present of sodium energetics: may the sodium-motive force be with you. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2008 , 1777, 985-92	4.6	112
129	Telling bacteria: do not LytTR. <i>Structure</i> , 2008 , 16, 657-9	5.2	35
128	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , 2008 , 3, 13	7.2	109
127	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	7.2	168
126	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium <i>Anoxybacillus flavithermus</i> WK1. <i>Genome Biology</i> , 2008 , 9, R161	18.3	58
125	Sequence analysis of GerM and SpoVS, uncharacterized bacterial spore proteins with widespread phylogenetic distribution. <i>Bioinformatics</i> , 2008 , 24, 1793-7	7.2	25
124	The Molecular Biology Database Collection: 2008 update. <i>Nucleic Acids Research</i> , 2008 , 36, D2-4	20.1	77
123	Origin and Evolution of Photosynthesis: Clues from Genome Comparison 2008 , 1169-1175		
122	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, 2003-15	2.5	24
121	Inventing the dynamo machine: the evolution of the F-type and V-type ATPases. <i>Nature Reviews Microbiology</i> , 2007 , 5, 892-9	22.2	149
120	Using archaeal genomics to fight global warming and clostridia to fight cancer. <i>Environmental Microbiology</i> , 2007 , 9, 279-86	5.2	3
119	Mycobacterial genomes for all tastes: from BCG to biodegradation of naphtalene and pyrene. <i>Environmental Microbiology</i> , 2007 , 9, 839-45	5.2	2
118	Linear chromosomes in bacteria: no straight edge advantage?. <i>Environmental Microbiology</i> , 2007 , 9, 1357-62	5.2	2
117	Genomics against flatulence. <i>Environmental Microbiology</i> , 2007 , 9, 1869-77	5.2	1

116	Dark matter in a deep-sea vent and in human mouth. <i>Environmental Microbiology</i> , 2007 , 9, 2385-91	5.2	2
115	Some bacteria degrade explosives, others prefer boiling methanol. <i>Environmental Microbiology</i> , 2007 , 9, 2905-10	5.2	8
114	The Molecular Biology Database Collection: 2007 update. <i>Nucleic Acids Research</i> , 2007 , 35, D3-4	20.1	60
113	Sentra: a database of signal transduction proteins for comparative genome analysis. <i>Nucleic Acids Research</i> , 2007 , 35, D271-3	20.1	22
112	Identification of sensory and signal-transducing domains in two-component signaling systems. <i>Methods in Enzymology</i> , 2007 , 422, 47-74	1.7	26
111	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> , 2007 , 66, 547-58	4.2	17
110	PilZ domain is part of the bacterial c-di-GMP binding protein. <i>Bioinformatics</i> , 2006 , 22, 3-6	7.2	394
109	Cyanobacterial response regulator PatA contains a conserved N-terminal domain (PATAN) with an alpha-helical insertion. <i>Bioinformatics</i> , 2006 , 22, 1297-301	7.2	27
108	The Molecular Biology Database Collection: 2006 update. <i>Nucleic Acids Research</i> , 2006 , 34, D3-5	20.1	62
107	Structural classification of bacterial response regulators: diversity of output domains and domain combinations. <i>Journal of Bacteriology</i> , 2006 , 188, 4169-82	3.5	375
106	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, 13126-31	11.5	236
105	Protecting sausages with bacteria instead of salt. <i>Environmental Microbiology</i> , 2006 , 8, 185-92	5.2	1
104	The minimal genome keeps growing. <i>Environmental Microbiology</i> , 2006 , 8, 569-73	5.2	5
103	Genomes to aid in bioremediation of dry cleaning solvents, mothballs and more. <i>Environmental Microbiology</i> , 2006 , 8, 949-55	5.2	
102	Sampling of microbial diversity by complete genomes. <i>Environmental Microbiology</i> , 2006 , 8, 1313-7	5.2	4
101	A square archaeon, the smallest eukaryote and the largest bacteria. <i>Environmental Microbiology</i> , 2006 , 8, 1683-7	5.2	1
100	The fuzzy border between a cell and an organelle. <i>Environmental Microbiology</i> , 2006 , 8, 2062-7	5.2	1
99	House cleaning, a part of good housekeeping. <i>Molecular Microbiology</i> , 2006 , 59, 5-19	4.1	160

98	New metrics for comparative genomics. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 440-7	11.4	26
97	OMICS-Related Research in South America. <i>OMICS A Journal of Integrative Biology</i> , 2005 , 9, 1-1	3.8	
96	Crystal structure of the bacterial YhcH protein indicates a role in sialic acid catabolism. <i>Journal of Bacteriology</i> , 2005 , 187, 5520-7	3.5	20
95	Dimeric dUTPases, HisE, and MazG belong to a new superfamily of all-alpha NTP pyrophosphohydrolases with potential "house-cleaning" functions. <i>Journal of Molecular Biology</i> , 2005 , 347, 243-55	6.5	69
94	The Molecular Biology Database Collection: 2005 update. <i>Nucleic Acids Research</i> , 2005 , 33, D5-24	20.1	62
93	Life is not defined just in base pairs. <i>Environmental Microbiology</i> , 2005 , 7, 149-52	5.2	3
92	On the bottom of the deep blue sea. <i>Environmental Microbiology</i> , 2005 , 7, 453-8	5.2	2
91	The vibrio that sheds light. <i>Environmental Microbiology</i> , 2005 , 7, 757-60	5.2	3
90	To finish or not to finish?. <i>Environmental Microbiology</i> , 2005 , 7, 1061-4	5.2	1
89	The secret of being cool. <i>Environmental Microbiology</i> , 2005 , 7, 1499-504	5.2	2
88	More cool news from marine bacteria. <i>Environmental Microbiology</i> , 2005 , 7, 1864-7	5.2	2
87	C-di-GMP: the dawning of a novel bacterial signalling system. <i>Molecular Microbiology</i> , 2005 , 57, 629-39	4.1	525
86	A census of membrane-bound and intracellular signal transduction proteins in bacteria: bacterial IQ, extroverts and introverts. <i>BMC Microbiology</i> , 2005 , 5, 35	4.5	345
85	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, 39637-43	5.4	18
84	OMICS-Related Research in Latin America. <i>OMICS A Journal of Integrative Biology</i> , 2005 , 9, 129-129	3.8	
83	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, 2099-104	11.5	106
82	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, 341-56	3.8	23
81	Genome sequence of the deep-sea gamma-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, 18036-41	11.5	110

80	In Silico Metabolic Model and Protein Expression of Haemophilus influenzae Strain Rd KW20 in Rich Medium. <i>OMICS A Journal of Integrative Biology</i> , 2004 , 8, 25-41	3.8	35
79	Conserved hypothetical proteins: prioritization of targets for experimental study. <i>Nucleic Acids Research</i> , 2004 , 32, 5452-63	20.1	279
78	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	0.9	17
77	All bugs, big and small. <i>Environmental Microbiology</i> , 2004 , 6, 435-7	5.2	3
76	Bacterial signal transduction network in a genomic perspective. <i>Environmental Microbiology</i> , 2004 , 6, 552-67	5.2	275
75	Metagenomics: from acid mine to shining sea. <i>Environmental Microbiology</i> , 2004 , 6, 543-5	5.2	22
74	Looking at big brothers for clues. <i>Environmental Microbiology</i> , 2004 , 6, 767-8	5.2	
73	The bugs that came in from the cold. <i>Environmental Microbiology</i> , 2004 , 6, 1001-4	5.2	1
72	Genomes back-to-back: when sequencing race is a good thing. <i>Environmental Microbiology</i> , 2004 , 6, 1205-9	5.2	1
71	The PA14 domain, a conserved all-beta domain in bacterial toxins, enzymes, adhesins and signaling molecules. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 335-9	10.3	79
70	Identification and functional analysis of hypothetical genes expressed in Haemophilus influenzae. <i>Nucleic Acids Research</i> , 2004 , 32, 2353-61	20.1	64
69	The Molecular Biology Database Collection: 2004 update. <i>Nucleic Acids Research</i> , 2004 , 32, D3-22	20.1	52
68	The crystal structure of a complex of Campylobacter jejuni dUTPase with substrate analogue sheds light on the mechanism and suggests the "basic module" for dimeric d(C/U)TPases. <i>Journal of Molecular Biology</i> , 2004 , 342, 1583-97	6.5	51
67	The Dx Dx DG motif for calcium binding: multiple structural contexts and implications for evolution. <i>Journal of Molecular Biology</i> , 2004 , 343, 971-84	6.5	100
66	Common extracellular sensory domains in transmembrane receptors for diverse signal transduction pathways in bacteria and archaea. <i>Journal of Bacteriology</i> , 2003 , 185, 285-94	3.5	112
65	Initial proteome analysis of model microorganism Haemophilus influenzae strain Rd KW20. <i>Journal of Bacteriology</i> , 2003 , 185, 4593-602	3.5	60
64	Amidase domains from bacterial and phage autolysins define a family of gamma-D,L-glutamate-specific amidohydrolases. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 230-4	10.3	129
63	Survival of the fittest before the beginning of life: selection of the first oligonucleotide-like polymers by UV light. <i>BMC Evolutionary Biology</i> , 2003 , 3, 12	3	55

62	Algorithms for computing parsimonious evolutionary scenarios for genome evolution, the last universal common ancestor and dominance of horizontal gene transfer in the evolution of prokaryotes. <i>BMC Evolutionary Biology</i> , 2003 , 3, 2	3	271
61	An extracellular calcium-binding domain in bacteria with a distant relationship to EF-hands. <i>FEMS Microbiology Letters</i> , 2003 , 221, 103-10	2.9	33
60	An integrated analysis of the genome of the hyperthermophilic archaeon <i>Pyrococcus abyssi</i> . <i>Molecular Microbiology</i> , 2003 , 47, 1495-512	4.1	158
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