

# Michael Y Galperin

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/3480175/michael-y-galperin-publications-by-citations.pdf>

**Version:** 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	The COG database: a tool for genome-scale analysis of protein functions and evolution. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 33-6	20.1	2692
222	The COG database: new developments in phylogenetic classification of proteins from complete genomes. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 22-8	20.1	1433
221	Cyclic di-GMP: the first 25 years of a universal bacterial second messenger. <i>Microbiology and Molecular Biology Reviews</i> , <b>2013</b> , 77, 1-52	13.2	1073
220	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D261-9	20.1	818
219	Novel domains of the prokaryotic two-component signal transduction systems. <i>FEMS Microbiology Letters</i> , <b>2001</b> , 203, 11-21	2.9	550
218	C-di-GMP: the dawning of a novel bacterial signalling system. <i>Molecular Microbiology</i> , <b>2005</b> , 57, 629-39	4.1	525
217	PilZ domain is part of the bacterial c-di-GMP binding protein. <i>Bioinformatics</i> , <b>2006</b> , 22, 3-6	7.2	394
216	Genome sequence of the cyanobacterium <i>Prochlorococcus marinus</i> SS120, a nearly minimal oxyphototrophic genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 10020-5	11.5	390
215	Structural classification of bacterial response regulators: diversity of output domains and domain combinations. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 4169-82	3.5	375
214	A genomic update on clostridial phylogeny: Gram-negative spore formers and other misplaced clostridia. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 2631-41	5.2	362
213	A census of membrane-bound and intracellular signal transduction proteins in bacteria: bacterial IQ, extroverts and introverts. <i>BMC Microbiology</i> , <b>2005</b> , 5, 35	4.5	345
212	Conserved hypothetical proteins: prioritization of targets for experimental study. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 5452-63	20.1	279
211	Bacterial cellulose biosynthesis: diversity of operons, subunits, products, and functions. <i>Trends in Microbiology</i> , <b>2015</b> , 23, 545-57	12.4	275
210	Bacterial signal transduction network in a genomic perspective. <i>Environmental Microbiology</i> , <b>2004</b> , 6, 552-67	5.2	275
209	Who's your neighbor? New computational approaches for functional genomics. <i>Nature Biotechnology</i> , <b>2000</b> , 18, 609-13	44.5	275
208	Comparison of archaeal and bacterial genomes: computer analysis of protein sequences predicts novel functions and suggests a chimeric origin for the archaea. <i>Molecular Microbiology</i> , <b>1997</b> , 25, 619-37	4.1	271
207	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> , <b>2003</b> , 3, 2	3	271

206	Origin of first cells at terrestrial, anoxic geothermal fields. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E821-30	11.5	254
205	Diversity of structure and function of response regulator output domains. <i>Current Opinion in Microbiology</i> , <b>2010</b> , 13, 150-9	7.9	251
204	The catalytic domain of the P-type ATPase has the haloacid dehalogenase fold. <i>Trends in Biochemical Sciences</i> , <b>1998</b> , 23, 127-9	10.3	240
203	The cyanobacterial genome core and the origin of photosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 13126-31	11.5	236
202	A diverse superfamily of enzymes with ATP-dependent carboxylate-amine/thiol ligase activity. <i>Protein Science</i> , <b>1997</b> , 6, 2639-43	6.3	213
201	Analogous enzymes: independent inventions in enzyme evolution. <i>Genome Research</i> , <b>1998</b> , 8, 779-90	9.7	204
200	Comparative genomics of the Archaea (Euryarchaeota): evolution of conserved protein families, the stable core, and the variable shell. <i>Genome Research</i> , <b>1999</b> , 9, 608-28	9.7	189
199	Sodium ion cycle in bacterial pathogens: evidence from cross-genome comparisons. <i>Microbiology and Molecular Biology Reviews</i> , <b>2001</b> , 65, 353-70, table of contents	13.2	187
198	Genomic determinants of sporulation in Bacilli and Clostridia: towards the minimal set of sporulation-specific genes. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 2870-90	5.2	168
197	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, <i>Methylophilum infernum</i> , a representative of the bacterial phylum Verrucomicrobia. <i>Biology Direct</i> , <b>2008</b> , 3, 26	7.2	168
196	House cleaning, a part of good housekeeping. <i>Molecular Microbiology</i> , <b>2006</b> , 59, 5-19	4.1	160
195	Diversity of Cyclic Di-GMP-Binding Proteins and Mechanisms. <i>Journal of Bacteriology</i> , <b>2016</b> , 198, 32-46	3.5	159
194	An integrated analysis of the genome of the hyperthermophilic archaeon <i>Pyrococcus abyssi</i> . <i>Molecular Microbiology</i> , <b>2003</b> , 47, 1495-512	4.1	158
193	Inventing the dynamo machine: the evolution of the F-type and V-type ATPases. <i>Nature Reviews Microbiology</i> , <b>2007</b> , 5, 892-9	22.2	149
192	A novel type of conserved DNA-binding domain in the transcriptional regulators of the AlgR/AgrA/LytR family. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 2453-9	20.1	143
191	Beyond complete genomes: from sequence to structure and function. <i>Current Opinion in Structural Biology</i> , <b>1998</b> , 8, 355-63	8.1	140
190	A superfamily of metalloenzymes unifies phosphopentomutase and cofactor-independent phosphoglycerate mutase with alkaline phosphatases and sulfatases. <i>Protein Science</i> , <b>1998</b> , 7, 1829-35	6.3	134
189	Amidase domains from bacterial and phage autolysins define a family of gamma-D,L-glutamate-specific amidohydrolases. <i>Trends in Biochemical Sciences</i> , <b>2003</b> , 28, 230-4	10.3	129

188	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. <i>ISME Journal</i> , <b>2009</b> , 3, 1012-35	11.9	128
187	From complete genome sequence to Complete Understanding?. <i>Trends in Biotechnology</i> , <b>2010</b> , 28, 398-406	11.1	126
186	Searching for drug targets in microbial genomes. <i>Current Opinion in Biotechnology</i> , <b>1999</b> , 10, 571-8	11.4	125
185	Prokaryotic genomes: the emerging paradigm of genome-based microbiology. <i>Current Opinion in Genetics and Development</i> , <b>1997</b> , 7, 757-63	4.9	122
184	Comparative Genomics of the Archaea (Euryarchaeota): Evolution of Conserved Protein Families, the Stable Core, and the Variable Shell. <i>Genome Research</i> , <b>1999</b> , 9, 608-628	9.7	119
183	Divergence and convergence in enzyme evolution. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 21-28	5.4	115
182	Genome Diversity of Spore-Forming Firmicutes. <i>Microbiology Spectrum</i> , <b>2013</b> , 1,	8.9	114
181	Co-evolution of primordial membranes and membrane proteins. <i>Trends in Biochemical Sciences</i> , <b>2009</b> , 34, 206-15	10.3	114
180	Purification, cloning, and expression of an apyrase from the bed bug <i>Cimex lectularius</i> . A new type of nucleotide-binding enzyme. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 30583-90	5.4	113
179	The past and present of sodium energetics: may the sodium-motive force be with you. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>2008</b> , 1777, 985-92	4.6	112
178	Common extracellular sensory domains in transmembrane receptors for diverse signal transduction pathways in bacteria and archaea. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 285-94	3.5	112
177	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> , <b>2004</b> , 101, 18036-41	11.5	110
176	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , <b>2008</b> , 3, 13	7.2	109
175	Sources of systematic error in functional annotation of genomes: domain rearrangement, non-orthologous gene displacement and operon disruption. <i>In Silico Biology</i> , <b>1998</b> , 1, 55-67	2	107
174	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> , <b>2005</b> , 102, 2099-104	11.5	106
173	Sequence Evolution Function <b>2003</b> ,		103
172	Conserved core structure and active site residues in alkaline phosphatase superfamily enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2001</b> , 45, 318-24	4.2	103
171	The Dx Dx DG motif for calcium binding: multiple structural contexts and implications for evolution. <i>Journal of Molecular Biology</i> , <b>2004</b> , 343, 971-84	6.5	100

170	Non-homologous isofunctional enzymes: a systematic analysis of alternative solutions in enzyme evolution. <i>Biology Direct</i> , <b>2010</b> , 5, 31	7.2	97
169	GIL, a new c-di-GMP-binding protein domain involved in regulation of cellulose synthesis in enterobacteria. <i>Molecular Microbiology</i> , <b>2014</b> , 93, 439-52	4.1	90
168	Structural insight into the mechanism of c-di-GMP hydrolysis by EAL domain phosphodiesterases. <i>Journal of Molecular Biology</i> , <b>2010</b> , 402, 524-38	6.5	86
167	Acetyl-CoA synthetase from the amitochondriate eukaryote <i>Giardia lamblia</i> belongs to the newly recognized superfamily of acyl-CoA synthetases (Nucleoside diphosphate-forming). <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 5794-803	5.4	85
166	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , <b>2020</b> , 5, 126-140	26.6	85
165	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D274-D281	20.1	84
164	Nucleotide binding by the widespread high-affinity cyclic di-GMP receptor MshEN domain. <i>Nature Communications</i> , <b>2016</b> , 7, 12481	17.4	83
163	Nucleic Acids Research annual Database Issue and the NAR online Molecular Biology Database Collection in 2009. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D1-4	20.1	83
162	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1063-1070	13.4	80
161	The PA14 domain, a conserved all-beta domain in bacterial toxins, enzymes, adhesins and signaling molecules. <i>Trends in Biochemical Sciences</i> , <b>2004</b> , 29, 335-9	10.3	79
160	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> , <b>2015</b> , 11, e1005232	7.6	77
159	The Molecular Biology Database Collection: 2008 update. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D2-4	20.1	77
158	Interplay of heritage and habitat in the distribution of bacterial signal transduction systems. <i>Molecular BioSystems</i> , <b>2010</b> , 6, 721-8		76
157	The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D1-8	20.1	75
156	Towards understanding the first genome sequence of a crenarchaeon by genome annotation using clusters of orthologous groups of proteins (COGs). <i>Genome Biology</i> , <b>2000</b> , 1, RESEARCH0009	18.3	75
155	Planctomycetes and eukaryotes: a case of analogy not homology. <i>BioEssays</i> , <b>2011</b> , 33, 810-7	4.1	73
154	The 2010 Nucleic Acids Research Database Issue and online Database Collection: a community of data resources. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D1-4	20.1	73
153	The 2013 Nucleic Acids Research Database Issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D1-7	20.1	73

152	Globins synthesize the second messenger bis-(3',5'-cyclic diguanosine monophosphate in bacteria. <i>Journal of Molecular Biology</i> , <b>2009</b> , 388, 262-70	6.5	73
151	Single domain response regulators: molecular switches with emerging roles in cell organization and dynamics. <i>Current Opinion in Microbiology</i> , <b>2009</b> , 12, 152-60	7.9	73
150	A specialized version of the HD hydrolase domain implicated in signal transduction. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>1999</b> , 1, 303-5	0.9	73
149	Systematic Nomenclature for GGDEF and EAL Domain-Containing Cyclic Di-GMP Turnover Proteins of Escherichia coli. <i>Journal of Bacteriology</i> , <b>2016</b> , 198, 7-11	3.5	70
148	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> , <b>2005</b> , 347, 243-55	6.5	69
147	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> , <b>2013</b> , 1827, 1407-27	4.6	64
146	Identification and functional analysis of hypothetical genes expressed in Haemophilus influenzae. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 2353-61	20.1	64
145	The 2016 database issue of Nucleic Acids Research and an updated molecular biology database collection. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D1-6	20.1	63
144	The Molecular Biology Database Collection: 2006 update. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D3-5	20.1	62
143	The Molecular Biology Database Collection: 2005 update. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D5-24	20.1	62
142	Using the COG database to improve gene recognition in complete genomes. <i>Genetica</i> , <b>2000</b> , 108, 9-17	1.5	61
141	The 2014 Nucleic Acids Research Database Issue and an updated NAR online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D1-6	20.1	60
140	The 2011 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D1-6	20.1	60
139	The Molecular Biology Database Collection: 2007 update. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D3-4	20.1	60
138	Initial proteome analysis of model microorganism Haemophilus influenzae strain Rd KW20. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 4593-602	3.5	60
137	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium Anoxybacillus flavithermus WK1. <i>Genome Biology</i> , <b>2008</b> , 9, R161	18.3	58
136	MHYT, a new integral membrane sensor domain. <i>FEMS Microbiology Letters</i> , <b>2001</b> , 205, 17-23	2.9	56
135	The 2015 Nucleic Acids Research Database Issue and molecular biology database collection. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D1-5	20.1	55

134	Characterization of the N-ATPase, a distinct, laterally transferred Na <sup>+</sup> -translocating form of the bacterial F-type membrane ATPase. <i>Bioinformatics</i> , <b>2010</b> , 26, 1473-6	7.2	55
133	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> , <b>2009</b> , 4, 27	7.2	55
132	Survival of the fittest before the beginning of life: selection of the first oligonucleotide-like polymers by UV light. <i>BMC Evolutionary Biology</i> , <b>2003</b> , 3, 12	3	55
131	MASE1 and MASE2: two novel integral membrane sensory domains. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2003</b> , 5, 11-6	0.9	55
130	Functional genomics and enzyme evolution. Homologous and analogous enzymes encoded in microbial genomes. <i>Genetica</i> , <b>1999</b> , 106, 159-70	1.5	54
129	The Molecular Biology Database Collection: 2004 update. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D3-22	20.1	52
128	The crystal structure of a complex of <i>Campylobacter jejuni</i> 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> , <b>2004</b> , 342, 1583-97	6.5	51
127	The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D1-D11	20.1	50
126	Conserved Hypothetical Proteins: new hints and new puzzles. <i>Comparative and Functional Genomics</i> , <b>2001</b> , 2, 14-8		49
125	Utilization of energy stored in the form of Na <sup>+</sup> and K <sup>+</sup> ion gradients by bacterial cells. <i>FEBS Journal</i> , <b>1983</b> , 134, 345-9		48
124	The COMBREX project: design, methodology, and initial results. <i>PLoS Biology</i> , <b>2013</b> , 11, e1001638	9.7	47
123	New structural and functional contexts of the Dx[DN]xDG linear motif: insights into evolution of calcium-binding proteins. <i>PLoS ONE</i> , <b>2011</b> , 6, e21507	3.7	46
122	Phylogenomic reconstruction of archaeal fatty acid metabolism. <i>Environmental Microbiology</i> , <b>2014</b> , 16, 907-18	5.2	45
121	Analysis of structure and function of putative surface-exposed proteins encoded in the <i>Streptococcus pneumoniae</i> genome: a bioinformatics-based approach to vaccine and drug design. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , <b>2003</b> , 38, 143-68	8.7	44
120	Sequence conservation in the chagasin family suggests a common trend in cysteine proteinase binding by unrelated protein inhibitors. <i>Protein Science</i> , <b>2002</b> , 11, 1971-7	6.3	42
119	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> , <b>2016</b> , 66, F506-F513	2.2	41
118	What bacteria want. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 4221-4229	5.2	39
117	Ancient Systems of Sodium/Potassium Homeostasis as Predecessors of Membrane Bioenergetics. <i>Biochemistry (Moscow)</i> , <b>2015</b> , 80, 495-516	2.9	35

116	Telling bacteria: do not LytTR. <i>Structure</i> , <b>2008</b> , 16, 657-9	5.2	35
115	In Silico Metabolic Model and Protein Expression of Haemophilus influenzae Strain Rd KW20 in Rich Medium. <i>OMICS A Journal of Integrative Biology</i> , <b>2004</b> , 8, 25-41	3.8	35
114	Aldolases of the Dhna family: a possible solution to the problem of pentose and hexose biosynthesis in archaea. <i>FEMS Microbiology Letters</i> , <b>2000</b> , 183, 259-64	2.9	35
113	Sequence analysis of an exceptionally conserved operon suggests enzymes for a new link between histidine and purine biosynthesis. <i>Molecular Microbiology</i> , <b>1997</b> , 24, 443-5	4.1	34
112	An extracellular calcium-binding domain in bacteria with a distant relationship to EF-hands. <i>FEMS Microbiology Letters</i> , <b>2003</b> , 221, 103-10	2.9	33
111	A decade of research on the second messenger c-di-AMP. <i>FEMS Microbiology Reviews</i> , <b>2020</b> , 44, 701-724	15.1	32
110	Cyclic di-AMP, a second messenger of primary importance: tertiary structures and binding mechanisms. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 2807-2829	20.1	29
109	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , <b>2018</b> , 200,	3.5	29
108	Multiple glucan-binding proteins of Streptococcus sobrinus. <i>Journal of Bacteriology</i> , <b>1996</b> , 178, 1572-7	3.5	29
107	How many signal peptides are there in bacteria?. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 983-90	5.2	27
106	Cyanobacterial response regulator PatA contains a conserved N-terminal domain (PATAN) with an alpha-helical insertion. <i>Bioinformatics</i> , <b>2006</b> , 22, 1297-301	7.2	27
105	Chelating agents inhibit activity and prevent expression of streptococcal glucan-binding lectins. <i>Infection and Immunity</i> , <b>1992</b> , 60, 3807-13	3.7	27
104	Identification of sensory and signal-transducing domains in two-component signaling systems. <i>Methods in Enzymology</i> , <b>2007</b> , 422, 47-74	1.7	26
103	New metrics for comparative genomics. <i>Current Opinion in Biotechnology</i> , <b>2006</b> , 17, 440-7	11.4	26
102	Independent evolution of heavy metal-associated domains in copper chaperones and copper-transporting atpases. <i>Journal of Molecular Evolution</i> , <b>2001</b> , 53, 622-33	3.1	26
101	Sequence analysis of GerM and SpoVS, uncharacterized bacterial QporulationQproteins with widespread phylogenetic distribution. <i>Bioinformatics</i> , <b>2008</b> , 24, 1793-7	7.2	25
100	Eukaryotic G protein-coupled receptors as descendants of prokaryotic sodium-translocating rhodopsins. <i>Biology Direct</i> , <b>2015</b> , 10, 63	7.2	24
99	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> , <b>2007</b> , 4, 2003-15	2.5	24



98	Structural diversity of calcium-binding proteins in bacteria: single-handed EF-hands?. <i>Trends in Microbiology</i> , <b>2003</b> , 11, 295-7	12.4	24
97	Experimental verification of a sequence-based prediction: F(1)F(0)-type ATPase of <i>Vibrio cholerae</i> transports protons, not Na(+) ions. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 674-8	3.5	24
96	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> , <b>2004</b> , 8, 341-56	3.8	23
95	Discovery of the Second Messenger Cyclic di-GMP. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1657, 1-8	1.4	22
94	Sentra: a database of signal transduction proteins for comparative genome analysis. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D271-3	20.1	22
93	Metagenomics: from acid mine to shining sea. <i>Environmental Microbiology</i> , <b>2004</b> , 6, 543-5	5.2	22
92	The synthetase domains of cobalamin biosynthesis amidotransferases cobB and cobQ belong to a new family of ATP-dependent amidoligases, related to dethiobiotin synthetase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2000</b> , 41, 238-47	4.2	22
91	Bacterial second messengers, cGMP and c-di-GMP, in a quest for regulatory dominance. <i>EMBO Journal</i> , <b>2013</b> , 32, 2421-3	13	21
90	Evolution of cation binding in the active sites of P-loop nucleoside triphosphatases in relation to the basic catalytic mechanism. <i>ELife</i> , <b>2018</b> , 7,	8.9	21
89	Crystal structure of the bacterial YhcH protein indicates a role in sialic acid catabolism. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 5520-7	3.5	20
88	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in <i>Salmonella typhimurium</i> . <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 3170-3189	6.5	19
87	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> , <b>2017</b> , 199,	3.5	19
86	Open questions on the origin of life at anoxic geothermal fields. <i>Origins of Life and Evolution of Biospheres</i> , <b>2012</b> , 42, 507-16	1.5	19
85	Functional analysis of conserved polar residues in Vc-NhaD, Na <sup>+</sup> /H <sup>+</sup> antiporter of <i>Vibrio cholerae</i> . <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 39637-43	5.4	18
84	delta mu H <sup>+</sup> is required for flagellar growth in <i>Escherichia coli</i> . <i>FEBS Letters</i> , <b>1982</b> , 143, 319-22	3.8	18
83	The role of energy in the emergence of biology from chemistry. <i>Origins of Life and Evolution of Biospheres</i> , <b>2012</b> , 42, 459-68	1.5	17
82	Using metabolic pathway databases for functional annotation. <i>Trends in Genetics</i> , <b>1998</b> , 14, 332-3	8.5	17
81	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> , <b>2007</b> , 66, 547-58	4.2	17

80	Salt in the wound: a possible role of Na <sup>+</sup> gradient in chlamydial infection. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2004</b> , 8, 1-6	0.9	17
79	Sustained sensing as an emerging principle in second messenger signaling systems. <i>Current Opinion in Microbiology</i> , <b>2016</b> , 34, 119-126	7.9	17
78	Phylogenomic analysis of the <i>Giardia intestinalis</i> transcarboxylase reveals multiple instances of domain fusion and fission in the evolution of biotin-dependent enzymes. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2003</b> , 5, 172-89	0.9	15
77	infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. <i>Science Translational Medicine</i> , <b>2020</b> , 12,	17.5	13
76	Copper chaperones in bacteria: association with copper-transporting ATPases. <i>Trends in Biochemical Sciences</i> , <b>2000</b> , 25, 480-1	10.3	12
75	Modeling of interaction between cytochrome c and the WD domains of Apaf-1: bifurcated salt bridges underlying apoptosome assembly. <i>Biology Direct</i> , <b>2015</b> , 10, 29	7.2	11
74	Structural Conservation and Diversity of PilZ-Related Domains. <i>Journal of Bacteriology</i> , <b>2020</b> , 202,	3.5	11
73	Corrigendum to "Novel domains of the prokaryotic two-component signal transduction systems". <i>FEMS Microbiology Letters</i> , <b>2001</b> , 204, 213-214	2.9	10
72	Emergence of cytochrome bc complexes in the context of photosynthesis. <i>Physiologia Plantarum</i> , <b>2017</b> , 161, 150-170	4.6	9
71	Proposed Role for KaiC-Like ATPases as Major Signal Transduction Hubs in Archaea. <i>MBio</i> , <b>2017</b> , 8,	7.8	9
70	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> , <b>2015</b> , 118, 302-12	4.6	9
69	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> , <b>2010</b> , 107, E137; author reply E138	11.5	9
68	New feel for new phyla. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 1927-33	5.2	9
67	Ways to control harmful biofilms: prevention, inhibition, and eradication. <i>Critical Reviews in Microbiology</i> , <b>2021</b> , 47, 57-78	7.8	9
66	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
65	Some bacteria degrade explosives; others prefer boiling methanol. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 2905-10	5.2	8
64	Comparative genome analysis. <i>Methods of Biochemical Analysis</i> , <b>2001</b> , 43, 359-92		8
63	A bacterial coat that is not pure cotton. <i>Science</i> , <b>2018</b> , 359, 276-277	33.3	7

62	A Time to Scatter Genes and a Time to Gather Them: Evolution of Photosynthesis Genes in Bacteria. <i>Advances in Botanical Research</i> , <b>2013</b> , 66, 1-35	2.2	7
61	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> , <b>2019</b> , 1861, 183051	3.8	6
60	The quest for biofuels fuels genome sequencing. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 2471-5	5.2	6
59	Chemiluminescent detection of dextran bound to streptococcal glucan-binding lectin. <i>Analytical Biochemistry</i> , <b>1995</b> , 225, 185-7	3.1	6
58	Evolutionary origins of membrane proteins <b>2010</b> , 1-28		6
57	Genome Annotation and Analysis <b>2003</b> , 193-226		6
56	The minimal genome keeps growing. <i>Environmental Microbiology</i> , <b>2006</b> , 8, 569-73	5.2	5
55	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> , <b>2020</b> , 9,	1.3	4
54	Social bacteria and asocial eukaryotes. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 281-8	5.2	4
53	Sorting out the mix in microbial genomics. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 3187-92	5.2	4
52	Sampling of microbial diversity by complete genomes. <i>Environmental Microbiology</i> , <b>2006</b> , 8, 1313-7	5.2	4
51	Towards Automated Prediction of Protein Function from Microbial Genomic Sequences. <i>Methods in Microbiology</i> , <b>1999</b> , 245-263	2.8	4
50	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> , <b>2020</b> , 77, 443-445	17.6	3
49	The dawn of synthetic genomics. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 821-5	5.2	3
48	Genomes of model organisms: know thy tools. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 1383-91	5.2	3
47	Using archaeal genomics to fight global warming and clostridia to fight cancer. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 279-86	5.2	3
46	All bugs, big and small. <i>Environmental Microbiology</i> , <b>2004</b> , 6, 435-7	5.2	3
45	Life is not defined just in base pairs. <i>Environmental Microbiology</i> , <b>2005</b> , 7, 149-52	5.2	3

44	The vibrio that sheds light. <i>Environmental Microbiology</i> , <b>2005</b> , 7, 757-60	5.2	3
43	Comparing Microbial Genomes: How the Gene Set Determines the Lifestyle		3
42	Comparative analysis of active sites in P-loop nucleoside triphosphatases suggests an ancestral activation mechanism		3
41	Genome Diversity of Spore-Forming Firmicutes		2
40	Mycobacterial genomes for all tastes: from BCG to biodegradation of naphtalene and pyrene. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 839-45	5.2	2
39	Linear chromosomes in bacteria: no straight edge advantage?. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 1357-62	5.2	2
38	Dark matter in a deep-sea vent and in human mouth. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 2385-91	5.2	2
37	Evolution of Central Metabolic Pathways: The Playground of Non-orthologous Gene Displacement		2
36	On the bottom of the deep blue sea. <i>Environmental Microbiology</i> , <b>2005</b> , 7, 453-8	5.2	2
35	The secret of being cool. <i>Environmental Microbiology</i> , <b>2005</b> , 7, 1499-504	5.2	2
34	More cool news from marine bacteria. <i>Environmental Microbiology</i> , <b>2005</b> , 7, 1864-7	5.2	2
33	Moshe Benziman and the Discovery of Cyclic Di-GMP		2
32	Comparative Genomics Approaches to Identifying Functionally Related Genes. <i>Lecture Notes in Computer Science</i> , <b>2014</b> , 1-24	0.9	2
31	Non-essential ribosomal proteins in bacteria and archaea identified using COGs. <i>Journal of Bacteriology</i> , <b>2021</b> ,	3.5	2
30	Complete Genome Sequence and Methylome of the Type Strain of <i>Shewanella</i> algae. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0055921	1.3	2
29	Sensory Transduction Network of <i>E. coli</i>		2
28	Sequence conservation, domain architectures, and phylogenetic distribution of the HD-GYP type c-di-GMP phosphodiesterases.. <i>Journal of Bacteriology</i> , <b>2021</b> , jb0056121	3.5	2
27	Genome Sequence of Uric Acid-Fermenting Eubacterium angustum DSM 1989T (MK-1). <i>Genome Announcements</i> , <b>2017</b> , 5,		1

26	Microbial genomics as pursuit of happiness. <i>Microbial Biotechnology</i> , <b>2009</b> , 2, 135-6	6.3	1
25	Genomics against flatulence. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 1869-77	5.2	1
24	Protecting sausages with bacteria instead of salt. <i>Environmental Microbiology</i> , <b>2006</b> , 8, 185-92	5.2	1
23	A square archaeon, the smallest eukaryote and the largest bacteria. <i>Environmental Microbiology</i> , <b>2006</b> , 8, 1683-7	5.2	1
22	The fuzzy border between a cell and an organelle. <i>Environmental Microbiology</i> , <b>2006</b> , 8, 2062-7	5.2	1
21	The bugs that came in from the cold. <i>Environmental Microbiology</i> , <b>2004</b> , 6, 1001-4	5.2	1
20	Genomes back-to-back: when sequencing race is a good thing. <i>Environmental Microbiology</i> , <b>2004</b> , 6, 1205-9	5.2	1
19	To finish or not to finish?. <i>Environmental Microbiology</i> , <b>2005</b> , 7, 1061-4	5.2	1
18	Genome analysis using clusters of orthologous groups (COGs) <b>1998</b> ,		1
17	The Bacterial and Viral Complexity of Postinfectious Hydrocephalus in Uganda		1
16	Mycobacterial CarD defines a novel mechanism of response to starvation stress		1
15	Sensory Transduction in Bacteria <b>2018</b> ,		1
14	Subspecies-specific haemagglutination patterns of fimbriated <i>Bacillus thuringiensis</i> spores. <i>FEMS Microbiology Letters</i> , <b>1991</b> , 69, 1-4	2.9	1
13	Two forms of phosphomannomutase in gammaproteobacteria: The overlooked membrane-bound form of AlgC is required for twitching motility of <i>Lysobacter enzymogenes</i> . <i>Environmental Microbiology</i> , <b>2019</b> , 21, 3969-3978	5.2	0
12	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> , <b>2012</b> , 1817, S154	4.6	0
11	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> , <b>2022</b> , e0151821	7.6	0
10	The emerging diversity of Na <sup>+</sup> -translocating ion pumps supports the evolutionary primacy of Na <sup>+</sup> -based bioenergetics. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>2016</b> , 1857, e68-e69	4.6	
9	Protein Domains Involved in Intracellular Signal Transduction <b>2009</b> , 269-288		

- 8 OMICS-Related Research in South America. *OMICS A Journal of Integrative Biology*, **2005**, 9, 1-1 3.8
- 7 Genomes to aid in bioremediation of dry cleaning solvents, mothballs and more. *Environmental Microbiology*, **2006**, 8, 949-55 5.2
- 6 Looking at big brothers for clues. *Environmental Microbiology*, **2004**, 6, 767-8 5.2
- 5 OMICS-Related Research in Latin America. *OMICS A Journal of Integrative Biology*, **2005**, 9, 129-129 3.8
- 4 Effect of ultrasound on adhesiveness of *Escherichia coli*. *Bulletin of Experimental Biology and Medicine*, **1983**, 95, 646-649 0.8
- 3 Noncanonical Cyclic di-GMP Binding Modes **2020**, 125-134
- 2 Origin and Evolution of Photosynthesis: Clues from Genome Comparison **2008**, 1169-1175
- 1 Ubiquity of Cyclic Di-GMP Pathways: a Bioinformatic Analysis 24-36