

Michael Y Galperin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3480175/publications.pdf>

Version: 2024-02-01

225
papers

27,399
citations

8755

77
h-index

7427

157
g-index

310
all docs

310
docs citations

310
times ranked

29641
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 gammaproteobacteria: 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

#	ARTICLE	IF	CITATIONS
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

#	ARTICLE	IF	CITATIONS
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

#	ARTICLE	IF	CITATIONS
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

#	ARTICLE	IF	CITATIONS
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 inferorum</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

#	ARTICLE	IF	CITATIONS
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

#	ARTICLE	IF	CITATIONS
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- α 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

#	ARTICLE	IF	CITATIONS
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
160	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> , 2004, 342, 1583-1597.	2.0	57
161	The Dx ₂ Dx ₂ DC Motif for Calcium Binding: Multiple Structural Contexts and Implications for Evolution. <i>Journal of Molecular Biology</i> , 2004, 343, 971-984.	2.0	117
162	Initial Proteome Analysis of Model Microorganism <i>Haemophilus influenzae</i> Strain Rd KW20. <i>Journal of Bacteriology</i> , 2003, 185, 4593-4602.	1.0	66

#	ARTICLE	IF	CITATIONS
163	Amidase domains from bacterial and phage autolysins define a family of $\hat{1}^3$ -d,l-glutamate-specific amidohydrolases. <i>Trends in Biochemical Sciences</i> , 2003, 28, 230-234.	3.7	138
164	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.	3.2	64
165	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.	3.2	316
166	An extracellular calcium-binding domain in bacteria with a distant relationship to EF-hands. <i>FEMS Microbiology Letters</i> , 2003, 221, 103-110.	0.7	36
167	An integrated analysis of the genome of the hyperthermophilic archaeon <i>Pyrococcus abyssi</i> . <i>Molecular Microbiology</i> , 2003, 47, 1495-1512.	1.2	165
168	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> , 2003, 38, 143-168.	2.3	54
169	Structural diversity of calcium-binding proteins in bacteria: single-handed EF-hands?. <i>Trends in Microbiology</i> , 2003, 11, 295-297.	3.5	27
170	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> , 2003, 100, 10020-10025.	3.3	442
171	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> , 2003, 185, 674-678.	1.0	26
172	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> , 2003, 5, 172-189.	1.0	15
173	Sequence Evolution Function. , 2003, , .		124
174	Evolution of Central Metabolic Pathways: The Playground of Non-orthologous Gene Displacement. , 2003, , 295-355.		3
175	MASE1 and MASE2: Two Novel Integral Membrane Sensory Domains. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2003, 5, 11-16.	1.0	68
176	Common Extracellular Sensory Domains in Transmembrane Receptors for Diverse Signal Transduction Pathways in Bacteria and Archaea. <i>Journal of Bacteriology</i> , 2003, 185, 285-294.	1.0	129
177	Genome Annotation and Analysis. , 2003, , 193-226.		11
178	A novel type of conserved DNA-binding domain in the transcriptional regulators of the AlgR/AgrA/LytR family. <i>Nucleic Acids Research</i> , 2002, 30, 2453-2459.	6.5	167
179	Comparative Genome Analysis. <i>Methods of Biochemical Analysis</i> , 2002, 43, 359-392.	0.2	13
180	Sequence conservation in the chagasin family suggests a common trend in cysteine proteinase binding by unrelated protein inhibitors. <i>Protein Science</i> , 2002, 11, 1971-1977.	3.1	47

#	ARTICLE	IF	CITATIONS
181	Sodium Ion Cycle in Bacterial Pathogens: Evidence from Cross-Genome Comparisons. <i>Microbiology and Molecular Biology Reviews</i> , 2001, 65, 353-370.	2.9	206
182	Independent Evolution of Heavy Metal-Associated Domains in Copper Chaperones and Copper-Transporting ATPases. <i>Journal of Molecular Evolution</i> , 2001, 53, 622-633.	0.8	27
183	Conserved core structure and active site residues in alkaline phosphatase superfamily enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 318-324.	1.5	118
184	Conserved "Hypothetical" Proteins: New Hints and New Puzzles. <i>Comparative and Functional Genomics</i> , 2001, 2, 14-18.	2.0	86
185	Novel domains of the prokaryotic two-component signal transduction systems. <i>FEMS Microbiology Letters</i> , 2001, 203, 11-21.	0.7	597
186	Corrigendum to "Novel domains of the prokaryotic two-component signal transduction systems" <i>FEMS Microbiology Letters</i> , 2001, 204, 213-214.	0.7	11
187	MHYT, a new integral membrane sensor domain. <i>FEMS Microbiology Letters</i> , 2001, 205, 17-23.	0.7	63
188	The COG database: new developments in phylogenetic classification of proteins from complete genomes. <i>Nucleic Acids Research</i> , 2001, 29, 22-28.	6.5	1,733
189	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> , 2000, 41, 238-247.	1.5	26
190	Who's your neighbor? New computational approaches for functional genomics. <i>Nature Biotechnology</i> , 2000, 18, 609-613.	9.4	319
191	Aldolases of the DhnA family: a possible solution to the problem of pentose and hexose biosynthesis in archaea. <i>FEMS Microbiology Letters</i> , 2000, 183, 259-264.	0.7	39
192	Copper chaperones in bacteria: association with copper-transporting ATPases. <i>Trends in Biochemical Sciences</i> , 2000, 25, 480-481.	3.7	13
193	Towards understanding the first genome sequence of a crenarchaeon by genome annotation using clusters of orthologous groups of proteins (COGs). <i>Genome Biology</i> , 2000, 1, research0009.1.	13.9	96
194	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> , 2000, 275, 5794-5803.	1.6	98
195	The COG database: a tool for genome-scale analysis of protein functions and evolution. <i>Nucleic Acids Research</i> , 2000, 28, 33-36.	6.5	3,734
196	Using the COG database to improve gene recognition in complete genomes. <i>Genetica</i> , 2000, 108, 9-17.	0.5	79
197	Searching for drug targets in microbial genomes. <i>Current Opinion in Biotechnology</i> , 1999, 10, 571-578.	3.3	146
198	Functional genomics and enzyme evolution. Homologous and analogous enzymes encoded in microbial genomes. , 1999, 106, 159-170.		71

#	ARTICLE	IF	CITATIONS
199	Towards Automated Prediction of Protein Function from Microbial Genomic Sequences. <i>Methods in Microbiology</i> , 1999, , 245-263.	0.4	4
200	A specialized version of the HD hydrolase domain implicated in signal transduction. <i>Journal of Molecular Microbiology and Biotechnology</i> , 1999, 1, 303-5.	1.0	75
201	Comparative Genomics of the Archaea (Euryarchaeota): Evolution of Conserved Protein Families, the Stable Core, and the Variable Shell. <i>Genome Research</i> , 1999, 9, 608-628.	2.4	219
202	Comparative genomics of the Archaea (Euryarchaeota): evolution of conserved protein families, the stable core, and the variable shell. <i>Genome Research</i> , 1999, 9, 608-28.	2.4	202
203	Using metabolic pathway databases for functional annotation. <i>Trends in Genetics</i> , 1998, 14, 332-333.	2.9	19
204	The catalytic domain of the P-type ATPase has the haloacid dehalogenase fold. <i>Trends in Biochemical Sciences</i> , 1998, 23, 127-129.	3.7	263
205	A superfamily of metalloenzymes unifies phosphopentomutase and cofactor-independent phosphoglycerate mutase with alkaline phosphatases and sulfatases. <i>Protein Science</i> , 1998, 7, 1829-1835.	3.1	148
206	Beyond complete genomes: from sequence to structure and function. <i>Current Opinion in Structural Biology</i> , 1998, 8, 355-363.	2.6	153
207	Purification, Cloning, and Expression of an Apyrase from the Bed Bug <i>Cimex lectularius</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 30583-30590.	1.6	130
208	Analogous Enzymes: Independent Inventions in Enzyme Evolution. <i>Genome Research</i> , 1998, 8, 779-790.	2.4	220
209	Genome analysis using clusters of orthologous groups (COGs). , 1998, , .		3
210	Sources of systematic error in functional annotation of genomes: domain rearrangement, non-orthologous gene displacement and operon disruption. <i>In Silico Biology</i> , 1998, 1, 55-67.	0.4	116
211	Prokaryotic genomes: the emerging paradigm of genome-based microbiology. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 757-763.	1.5	136
212	Sequence analysis of an exceptionally conserved operon suggests enzymes for a new link between histidine and purine biosynthesis. <i>Molecular Microbiology</i> , 1997, 24, 443-445.	1.2	38
213	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> , 1997, 25, 619-637.	1.2	302
214	A diverse superfamily of enzymes with ATP-dependent carboxylate-amine/thiol ligase activity. <i>Protein Science</i> , 1997, 6, 2639-2643.	3.1	248
215	Multiple glucan-binding proteins of <i>Streptococcus sobrinus</i> . <i>Journal of Bacteriology</i> , 1996, 178, 1572-1577.	1.0	35
216	Chemiluminescent Detection of Dextran Bound to Streptococcal Glucan-Binding Lectin. <i>Analytical Biochemistry</i> , 1995, 225, 185-187.	1.1	6

#	ARTICLE	IF	CITATIONS
217	Chelating agents inhibit activity and prevent expression of streptococcal glucan-binding lectins. <i>Infection and Immunity</i> , 1992, 60, 3807-3813.	1.0	31
218	Subspecies-specific haemagglutination patterns of fimbriated <i>Bacillus thuringiensis</i> spores. <i>FEMS Microbiology Letters</i> , 1991, 69, 1-4.	0.7	1
219	Utilization of Energy Stored in the Form of Na ⁺ and K ⁺ Ion Gradients by Bacterial Cells. <i>FEBS Journal</i> , 1983, 134, 345-349.	0.2	53
220	Effect of ultrasound on adhesiveness of <i>Escherichia coli</i> . <i>Bulletin of Experimental Biology and Medicine</i> , 1983, 95, 646-649.	0.3	1
221	³ H is required for flagellar growth in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1982, 143, 319-322.	1.3	21
222	Genome Diversity of Spore-Forming <i>Firmicutes</i> . , 0, , 1-18.		6
223	Moshe Benziman and the Discovery of Cyclic Di-GMP. , 0, , 9-23.		2
224	Comparing Microbial Genomes: How the Gene Set Determines the Lifestyle. , 0, , 91-108.		7
225	Ubiquity of Cyclic Di-GMP Pathways: a Bioinformatic Analysis. , 0, , 24-36.		0