

# Michael Y Galperin

## List of Publications by Year in descending order

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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	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
2	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
3	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
4	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
5	A genomic update on clostridial phylogeny: <scp>G</scp>ramâ€negative spore formers and other misplaced clostridia. <i>Environmental Microbiology</i> , 2013, 15, 2631-2641.	1.8	771
6	Novel domains of the prokaryotic two-component signal transduction systems. <i>FEMS Microbiology Letters</i> , 2001, 203, 11-21.	0.7	597
7	C-di-GMP: the dawning of a novel bacterial signalling system. <i>Molecular Microbiology</i> , 2005, 57, 629-639.	1.2	593
8	PilZ domain is part of the bacterial c-di-GMP binding protein. <i>Bioinformatics</i> , 2006, 22, 3-6.	1.8	460
9	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
10	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021, 49, D274-D281.	6.5	441
11	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
12	Bacterial cellulose biosynthesis: diversity of operons, subunits, products, and functions. <i>Trends in Microbiology</i> , 2015, 23, 545-557.	3.5	432
13	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
14	'Conserved hypothetical' proteins: prioritization of targets for experimental study. <i>Nucleic Acids Research</i> , 2004, 32, 5452-5463.	6.5	346
15	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
16	Who's your neighbor? New computational approaches for functional genomics. <i>Nature Biotechnology</i> , 2000, 18, 609-613.	9.4	319
17	Bacterial signal transduction network in a genomic perspective+. <i>Environmental Microbiology</i> , 2004, 6, 552-567.	1.8	318
18	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

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19	Diversity of structure and function of response regulator output domains. <i>Current Opinion in Microbiology</i> , 2010, 13, 150-159.	2.3	308
20	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
21	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
22	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
23	A diverse superfamily of enzymes with ATP-dependent carboxylate-amine/thiol ligase activity. <i>Protein Science</i> , 1997, 6, 2639-2643.	3.1	248
24	Diversity of Cyclic Di-GMP-Binding Proteins and Mechanisms. <i>Journal of Bacteriology</i> , 2016, 198, 32-46.	1.0	244
25	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
26	Analogous Enzymes: Independent Inventions in Enzyme Evolution. <i>Genome Research</i> , 1998, 8, 779-790.	2.4	220
27	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
28	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> , 2008, 3, 26.	1.9	216
29	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
30	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
31	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
32	House cleaning, a part of good housekeeping. <i>Molecular Microbiology</i> , 2006, 59, 5-19.	1.2	186
33	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019, 20, 1063-1070.	3.2	186
34	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, 1012-1035.	4.4	178
35	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
36	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

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37	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
38	Beyond complete genomes: from sequence to structure and function. <i>Current Opinion in Structural Biology</i> , 1998, 8, 355-363.	2.6	153
39	Genome Diversity of Spore-Forming <i>Firmicutes</i> . <i>Microbiology Spectrum</i> , 2013, 1, .	1.2	153
40	From complete genome sequence to “complete” understanding?. <i>Trends in Biotechnology</i> , 2010, 28, 398-406.	4.9	151
41	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
42	Searching for drug targets in microbial genomes. <i>Current Opinion in Biotechnology</i> , 1999, 10, 571-578.	3.3	146
43	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , 2008, 3, 13.	1.9	144
44	The 24th annual <i>Nucleic Acids Research</i> database issue: a look back and upcoming changes. <i>Nucleic Acids Research</i> , 2017, 45, D1-D11.	6.5	144
45	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
46	Co-evolution of primordial membranes and membrane proteins. <i>Trends in Biochemical Sciences</i> , 2009, 34, 206-215.	3.7	140
47	Divergence and Convergence in Enzyme Evolution. <i>Journal of Biological Chemistry</i> , 2012, 287, 21-28.	1.6	140
48	Amidase domains from bacterial and phage autolysins define a family of $\hat{I}^3$ -d,l-glutamate-specific amidohydrolases. <i>Trends in Biochemical Sciences</i> , 2003, 28, 230-234.	3.7	138
49	Prokaryotic genomes: the emerging paradigm of genome-based microbiology. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 757-763.	1.5	136
50	Genome sequence of the deep-sea $\hat{A}$ -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
51	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
52	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
53	Nucleotide binding by the widespread high-affinity cyclic di-GMP receptor MshEN domain. <i>Nature Communications</i> , 2016, 7, 12481.	5.8	129
54	Sequence “ Evolution “ Function. , 2003, , .		124

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55	Structural Insight into the Mechanism of c-di-GMP Hydrolysis by EAL Domain Phosphodiesterases. <i>Journal of Molecular Biology</i> , 2010, 402, 524-538.	2.0	121
56	Non-homologous isofunctional enzymes: A systematic analysis of alternative solutions in enzyme evolution. <i>Biology Direct</i> , 2010, 5, 31.	1.9	119
57	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
58	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
59	<sc>GIL</sc>, 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
60	The Dx/Dx/DG Motif for Calcium Binding: Multiple Structural Contexts and Implications for Evolution. <i>Journal of Molecular Biology</i> , 2004, 343, 971-984.	2.0	117
61	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
62	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
63	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
64	The 2012 <i>Nucleic Acids Research</i> Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2012, 40, D1-D8.	6.5	104
65	<i>Nucleic Acids Research</i> annual Database Issue and the NAR online Molecular Biology Database Collection in 2009. <i>Nucleic Acids Research</i> , 2009, 37, D1-D4.	6.5	101
66	The Molecular Biology Database Collection: 2005 update. <i>Nucleic Acids Research</i> , 2004, 33, D5-D24.	6.5	99
67	The Molecular Biology Database Collection: 2008 update. <i>Nucleic Acids Research</i> , 2008, 36, D2-D4.	6.5	99
68	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
69	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
70	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
71	The 2013 <i>Nucleic Acids Research</i> Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2012, 41, D1-D7.	6.5	94
72	Globins Synthesize the Second Messenger Bis-(3'-5'-Cyclic Diguanosine Monophosphate) in Bacteria. <i>Journal of Molecular Biology</i> , 2009, 388, 262-270.	2.0	91

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73	The PA14 domain, a conserved all- $\beta^2$ domain in bacterial toxins, enzymes, adhesins and signaling molecules. Trends in Biochemical Sciences, 2004, 29, 335-339.	3.7	90
74	Interplay of heritage and habitat in the distribution of bacterial signal transduction systems. Molecular BioSystems, 2010, 6, 721.	2.9	87
75	Conserved "Hypothetical"™ Proteins: New Hints and New Puzzles. Comparative and Functional Genomics, 2001, 2, 14-18.	2.0	86
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	The Molecular Biology Database Collection: 2006 update. Nucleic Acids Research, 2006, 34, D3-D5.	6.5	83
78	The 2014 Nucleic Acids Research Database Issue and an updated NAR online Molecular Biology Database Collection. Nucleic Acids Research, 2014, 42, D1-D6.	6.5	81
79	The Molecular Biology Database Collection: 2007 update. Nucleic Acids Research, 2007, 35, D3-D4.	6.5	80
80	Using the COG database to improve gene recognition in complete genomes. Genetica, 2000, 108, 9-17.	0.5	79
81	Planctomycetes and eukaryotes: A case of analogy not homology. BioEssays, 2011, 33, 810-817.	1.2	79
82	The 2015 Nucleic Acids Research Database Issue and Molecular Biology Database Collection. Nucleic Acids Research, 2015, 43, D1-D5.	6.5	79
83	Dimeric dUTPases, HisE, and MazG belong to a New Superfamily of all- $\beta$ NTP Pyrophosphohydrolases with Potential "House-cleaning" Functions. Journal of Molecular Biology, 2005, 347, 243-255.	2.0	77
84	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
85	Phylogenomic analysis of the family Peptostreptococcaceae (Clostridium cluster XI) and proposal for reclassification of Clostridium litorale (Fendrich et al. 1991) and Eubacterium acidaminophilum (Zindel et al. 1989) as Peptoclostridium litorale gen. nov. comb. nov. and Peptoclostridium acidaminophilum comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5506-5513.	0.8	77
86	Identification and functional analysis of 'hypothetical' genes expressed in Haemophilus influenzae. Nucleic Acids Research, 2004, 32, 2353-2361.	6.5	75
87	Characterization of the N-ATPase, a distinct, laterally transferred Na <sup>+</sup> -translocating form of the bacterial F-type membrane ATPase. Bioinformatics, 2010, 26, 1473-1476.	1.8	75
88	A specialized version of the HD hydrolase domain implicated in signal transduction. Journal of Molecular Microbiology and Biotechnology, 1999, 1, 303-5.	1.0	75
89	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
90	A decade of research on the second messenger c-di-AMP. FEMS Microbiology Reviews, 2020, 44, 701-724.	3.9	74

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91	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
92	What bacteria want. <i>Environmental Microbiology</i> , 2018, 20, 4221-4229.	1.8	73
93	Functional genomics and enzyme evolution. Homologous and analogous enzymes encoded in microbial genomes. , 1999, 106, 159-170.		71
94	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
95	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
96	MASE1 and MASE2: Two Novel Integral Membrane Sensory Domains. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2003, 5, 11-16.	1.0	68
97	Phylogenomic reconstruction of archaeal fatty acid metabolism. <i>Environmental Microbiology</i> , 2014, 16, 907-918.	1.8	67
98	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
99	The Molecular Biology Database Collection: 2004 update. <i>Nucleic Acids Research</i> , 2004, 32, 3D-22.	6.5	66
100	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
101	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
102	Ancient systems of sodium/potassium homeostasis as predecessors of membrane bioenergetics. <i>Biochemistry (Moscow)</i> , 2015, 80, 495-516.	0.7	64
103	MHYT, a new integral membrane sensor domain. <i>FEMS Microbiology Letters</i> , 2001, 205, 17-23.	0.7	63
104	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
105	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
106	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	2.6	54
107	Utilization of Energy Stored in the Form of Na <sup>+</sup> and K <sup>+</sup> Ion Gradients by Bacterial Cells. <i>FEBS Journal</i> , 1983, 134, 345-349.	0.2	53
108	New Structural and Functional Contexts of the Dx[DN]xDG Linear Motif: Insights into Evolution of Calcium-Binding Proteins. <i>PLoS ONE</i> , 2011, 6, e21507.	1.1	53

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109	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
110	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
111	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	41
112	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, .	2.8	41
113	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
114	Telling Bacteria: Do Not LytTR. <i>Structure</i> , 2008, 16, 657-659.	1.6	39
115	<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
116	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
117	Ways to control harmful biofilms: prevention, inhibition, and eradication. <i>Critical Reviews in Microbiology</i> , 2021, 47, 57-78.	2.7	38
118	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
119	Eukaryotic G protein-coupled receptors as descendants of prokaryotic sodium-translocating rhodopsins. <i>Biology Direct</i> , 2015, 10, 63.	1.9	36
120	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, .	1.0	36
121	Proposal for the reclassification of obligately purine-fermenting bacteria <i>Clostridium acidurici</i> (Barker 1938) and <i>Clostridium purinilyticum</i> (D'Arre et al. 1981) as <i>Gottschalkia acidurici</i> gen. nov. comb. nov. and <i>Gottschalkia purinilytica</i> comb. nov. and of <i>Eubacterium angustum</i> (Beuscher and Tj ETQq1 1 0.784314 rgBT4 Overlo <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2711-2719.	4.3	36
122	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
123	Multiple glucan-binding proteins of <i>Streptococcus sobrinus</i> . <i>Journal of Bacteriology</i> , 1996, 178, 1572-1577.	1.0	35
124	Discovery of the Second Messenger Cyclic di-GMP. <i>Methods in Molecular Biology</i> , 2017, 1657, 1-8.	0.4	34
125	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	6.5	32
126	Sustained sensing as an emerging principle in second messenger signaling systems. <i>Current Opinion in Microbiology</i> , 2016, 34, 119-126.	2.3	32

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127	Chelating agents inhibit activity and prevent expression of streptococcal glucan-binding lectins. <i>Infection and Immunity</i> , 1992, 60, 3807-3813.	1.0	31
128	Identification of Sensory and Signal-Transducing Domains in Two-Component Signaling Systems. <i>Methods in Enzymology</i> , 2007, 422, 47-74.	0.4	30
129	Sequence analysis of GerM and SpoVS, uncharacterized bacterial $\sigma$ -sporulation™ proteins with widespread phylogenetic distribution. <i>Bioinformatics</i> , 2008, 24, 1793-1797.	1.8	30
130	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
131	New metrics for comparative genomics. <i>Current Opinion in Biotechnology</i> , 2006, 17, 440-447.	3.3	29
132	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
133	How many signal peptides are there in bacteria?. <i>Environmental Microbiology</i> , 2013, 15, 983-990.	1.8	29
134	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.	2.0	29
135	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
136	Structural diversity of calcium-binding proteins in bacteria: single-handed EF-hands?. <i>Trends in Microbiology</i> , 2003, 11, 295-297.	3.5	27
137	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
138	Experimental Verification of a Sequence-Based Prediction: F <sub>1</sub> F <sub>0</sub> -Type ATPase of <i>Vibrio cholerae</i> Transports Protons, Not Na <sup>+</sup> Ions. <i>Journal of Bacteriology</i> , 2003, 185, 674-678.	1.0	26
139	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
140	Metagenomics: from acid mine to shining sea. <i>Environmental Microbiology</i> , 2004, 6, 543-545.	1.8	25
141	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> , 2005, 280, 39637-39643.	1.6	25
142	Sentra: a database of signal transduction proteins for comparative genome analysis. <i>Nucleic Acids Research</i> , 2007, 35, D271-D273.	6.5	24
143	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
144	Structural Conservation and Diversity of PilZ-Related Domains. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	24

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145	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
146	$^2\text{H}$ is required for flagellar growth in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1982, 143, 319-322.	1.3	21
147	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
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