

Radhey S Gupta

List of Publications by Year in descending order

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193
papers

14,432
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23567

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docs citations

206
times ranked

10695
citing authors

#	ARTICLE	IF	CITATIONS
1	Conserved Signatures in Protein Sequences Reliably Demarcate Different Clades of Rodents/Glires Species and Consolidate Their Evolutionary Relationships. <i>Genes</i> , 2022, 13, 288.	2.4	2
2	Conserved Molecular Signatures in the Spike, Nucleocapsid, and Polymerase Proteins Specific for the Genus Betacoronavirus and Its Different Subgenera. <i>Genes</i> , 2022, 13, 423.	2.4	1
3	Phylogenomic and comparative genomic analyses of Leuconostocaceae species: identification of molecular signatures specific for the genera Leuconostoc, Fructobacillus and Oenococcus and proposal for a novel genus Periweissella gen. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	42
4	Phylogenomic Analyses and Molecular Signatures Elucidating the Evolutionary Relationships amongst the Chlorobia and Ignavibacteria Species: Robust Demarcation of Two Family-Level Clades within the Order Chlorobiales and Proposal for the Family Chloroherpetonaceae fam. nov. <i>Microorganisms</i> , 2022, 10, 1312.	3.6	5
5	Microbial Taxonomy: How and Why Name Changes Occur and Their Significance for (Clinical) Microbiology. <i>Clinical Chemistry</i> , 2021, 68, 134-137.	3.2	9
6	A robust phylogenetic framework for members of the order Legionellales and its main genera (<i>Legionella</i> , <i>Aquicella</i> , <i>Coxiella</i> and <i>Rickettsiella</i>) based on phylogenomic analyses and identification of molecular markers demarcating different clades. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 957-982.	1.7	20
7	The Family <i>Borreliaceae</i> (Spirochaetales), a Diverse Group in Two Genera of Tick-Borne Spirochetes of Mammals, Birds, and Reptiles. <i>Journal of Medical Entomology</i> , 2021, 58, 1513-1524.	1.8	21
8	Phylogenomic and comparative genomic analyses of species of the family Pseudomonadaceae: Proposals for the genera Halopseudomonas gen. nov. and Atopomonas gen. nov., merger of the genus Oblitimonas with the genus Thiopseudomonas, and transfer of some misclassified species of the genus Pseudomonas into other genera. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	101
9	Phylogenomics and molecular signatures support division of the order Neisseriales into emended families Neisseriaceae and Chromobacteriaceae and three new families Aquaspirillaceae fam. nov., Chitinibacteraceae fam. nov., and Leeiaceae fam. nov.. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126251.	2.8	46
10	Conserved molecular signatures in the spike protein provide evidence indicating the origin of SARS-CoV-2 and a Pangolin-CoV (MP789) by recombination(s) between specific lineages of Sarbecoviruses. <i>PeerJ</i> , 2021, 9, e12434.	2.0	5
11	Novel Sequence Feature of SecA Translocase Protein Unique to the Thermophilic Bacteria: Bioinformatics Analyses to Investigate Their Potential Roles. <i>Microorganisms</i> , 2020, 8, 59.	3.6	6
12	A phylogenomic and comparative genomic framework for resolving the polyphyly of the genus <i>Bacillus</i> : Proposal for six new genera of <i>Bacillus</i> species, <i>Peribacillus</i> gen. nov., <i>Cytobacillus</i> gen. nov., <i>Mesobacillus</i> gen. nov., <i>Neobacillus</i> gen. nov., <i>Metabacillus</i> gen. nov. and <i>Alkalihalobacillus</i> gen. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 406-438.	1.7	458
13	Reply to: "Recommended rejection of the names <i>Malacoplasma</i> gen. nov., <i>Mesomycoplasma</i> gen. nov., <i>Metamycoplasma</i> gen. nov., <i>Metamycoplasmataceae</i> fam. nov., <i>Mycoplasmoidaceae</i> fam. nov., <i>Mycoplasmoidales</i> ord. nov., <i>Mycoplasmoides</i> gen. nov., <i>Mycoplasmaopsis</i> gen. nov. [Gupta, Sawnani, Adeolu, Alnajjar and Oren 2018] and all proposed species comb. nov. placed therein"™, by M. Balish et al.		

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19	Commentary: Genome-Based Taxonomic Classification of the Phylum Actinobacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 206.	3.5	12
20	A phylogenomic and molecular markers based taxonomic framework for members of the order Entomoplasmatales: proposal for an emended order Mycoplasmatales containing the family Spiroplasmataceae and emended family Mycoplasmataceae comprised of six genera. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 561-588.	1.7	81
21	Robust Demarcation of the Family Caryophanaceae (Planococcaceae) and Its Different Genera Including Three Novel Genera Based on Phylogenomics and Highly Specific Molecular Signatures. <i>Frontiers in Microbiology</i> , 2019, 10, 2821.	3.5	160
22	Phylogenetic framework for the phylum Tenericutes based on genome sequence data: proposal for the creation of a new order Mycoplasmoidales ord. nov., containing two new families Mycoplasmoidaceae fam. nov. and Metamycoplasmataceae fam. nov. harbouring Eperythrozoon, Ureaplasma and five novel genera. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1583-1630.	1.7	488
23	Impact of Genomics on Clarifying the Evolutionary Relationships amongst Mycobacteria: Identification of Molecular Signatures Specific for the Tuberculosis-Complex of Bacteria with Potential Applications for Novel Diagnostics and Therapeutics. <i>High-Throughput</i> , 2018, 7, 31.	4.4	7
24	Robust demarcation of fourteen different species groups within the genus <i>Streptococcus</i> based on genome-based phylogenies and molecular signatures. <i>Infection, Genetics and Evolution</i> , 2018, 66, 130-151.	2.3	34
25	Phylogenomics and Comparative Genomic Studies Robustly Support Division of the Genus <i>Mycobacterium</i> into an Emended Genus <i>Mycobacterium</i> and Four Novel Genera. <i>Frontiers in Microbiology</i> , 2018, 9, 67.	3.5	878
26	Novel Sequence Features of DNA Repair Genes/Proteins from <i>Deinococcus</i> Species Implicated in Protection from Oxidatively Generated Damage. <i>Genes</i> , 2018, 9, 149.	2.4	9
27	Identification of a conserved 8 aa insert in the PIP5K protein in the <i>Saccharomycetaceae</i> family of fungi and the molecular dynamics simulations and structural analysis to investigate its potential functional role. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1454-1467.	2.6	22
28	Cover Image, Volume 85, Issue 8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C1.	2.6	0
29	Phylogenomics and comparative genomic studies delineate six main clades within the family Enterobacteriaceae and support the reclassification of several polyphyletic members of the family. <i>Infection, Genetics and Evolution</i> , 2017, 54, 108-127.	2.3	112
30	Novel insights into the origin and diversification of photosynthesis based on analyses of conserved indels in the core reaction center proteins. <i>Photosynthesis Research</i> , 2017, 131, 159-171.	2.9	14
31	Ribonucleotide Reductases from Bifidobacteria Contain Multiple Conserved Indels Distinguishing Them from All Other Organisms: In Silico Analysis of the Possible Role of a 43 aa Bifidobacteria-Specific Insert in the Class III RNR Homolog. <i>Frontiers in Microbiology</i> , 2017, 8, 1409.	3.5	9
32	Novel molecular, structural and evolutionary characteristics of the phosphoketolases from bifidobacteria and Coriobacteriales. <i>PLoS ONE</i> , 2017, 12, e0172176.	2.5	41
33	Division of the genus <i>Borrelia</i> into two genera (corresponding to Lyme disease and relapsing fever) <i>Journal of Systematics and Evolutionary Microbiology</i> , 2017, 67, 2058-2067 of these two groups of microbes (Margos et al. (2016) There is inadequate evidence to support the) <i>Journal of Systematics and Evolutionary Microbiology</i> , 2017, 67, 2058-2067	1.0	7
34	Phylogenetic analysis of the diacylglycerol kinase family of proteins and identification of multiple highly-specific conserved inserts and deletions within the catalytic domain that are distinctive characteristics of different classes of DGK homologs. <i>PLoS ONE</i> , 2017, 12, e0182758.	2.5	7
35	Diacylglycerol Kinase- μ : Properties and Biological Roles. <i>Frontiers in Cell and Developmental Biology</i> , 2016, 4, 112.	3.7	36
36	Editorial: Applications of Genome Sequences for Discovering Characteristics that Are Unique to Different Groups of Organisms and Provide Insights into Evolutionary Relationships. <i>Frontiers in Genetics</i> , 2016, 7, 27.	2.3	8

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37	Phylogenomic Analyses and Comparative Studies on Genomes of the Bifidobacteriales: Identification of Molecular Signatures Specific for the Order Bifidobacteriales and Its Different Subclades. <i>Frontiers in Microbiology</i> , 2016, 7, 978.	3.5	23
38	Identification of distinctive molecular traits that are characteristic of the phylum <i>Deinococcus-Thermus</i> and distinguish its main constituent groups. <i>Systematic and Applied Microbiology</i> , 2016, 39, 453-463.	2.8	23
39	Impact of genomics on the understanding of microbial evolution and classification: the importance of Darwin's views on classification. <i>FEMS Microbiology Reviews</i> , 2016, 40, 520-553.	8.6	73
40	A phylogenomic reappraisal of family-level divisions within the class Halobacteria: proposal to divide the order Halobacteriales into the families Halobacteriaceae, Haloarculaceae fam. nov., and Halococcaceae fam. nov., and the order Haloferacales into the families, Haloferacaceae and Halorubraceae fam. nov.. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 565-587.	1.7	127
41	Molecular signatures that are distinctive characteristics of the vertebrates and chordates and supporting a grouping of vertebrates with the tunicates. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 383-391.	2.7	15
42	Evidence for the presence of key chlorophyll-biosynthesis-related proteins in the genus <i>Rubrobacter</i> (Phylum Actinobacteria) and its implications for the evolution and origin of photosynthesis. <i>Photosynthesis Research</i> , 2016, 127, 201-218.	2.9	21
43	Genome-based phylogeny and taxonomy of the <i>Enterobacteriales</i> TM : proposal for Enterobacteriales ord. nov. divided into the families Enterobacteriaceae, Erwiniaceae fam. nov., Pectobacteriaceae fam. nov., Yersiniaceae fam. nov., Hafniaceae fam. nov., Morganellaceae fam. nov., and Budviciaceae fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5575-5599.	1.7	792
44	Phylogenomic and Molecular Demarcation of the Core Members of the Polyphyletic Pasteurellaceae Genera <i>Actinobacillus</i> , <i>Haemophilus</i> , and <i>Pasteurella</i> . <i>International Journal of Genomics</i> , 2015, 2015, 1-15.	1.6	19
45	A phylogenomic and molecular marker based taxonomic framework for the order Xanthomonadales: proposal to transfer the families Algiphilaceae and Solimonadaceae to the order Nevskiales ord. nov. and to create a new family within the order Xanthomonadales, the family Rhodanobacteraceae fam. nov., containing the genus <i>Rhodanobacter</i> and its closest relatives. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 467-485.	1.7	135
46	A phylogenomic and molecular markers based analysis of the phylum Chlamydiae: proposal to divide the class Chlamydia into two orders, Chlamydiales and Parachlamydiales ord. nov., and emended description of the class Chlamydia. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 765-781.	1.7	38
47	Phylogenomic analyses and molecular signatures for the class Halobacteria and its two major clades: a proposal for division of the class Halobacteria into an emended order Halobacteriales and two new orders, Haloferacales ord. nov. and Natribacteriales ord. nov., containing the novel families Haloferacaceae fam. nov. and Natribacteraceae fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1050-1069.	1.7	260
48	Genome-based taxonomic framework for the class Negativicutes: division of the class Negativicutes into the orders Selenomonadales emend., Acidaminococcales ord. nov. and Veillonellales ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 3203-3215.	1.7	75
49	Identification of Conserved Indels that are Useful for Classification and Evolutionary Studies. <i>Methods in Microbiology</i> , 2014, 41, 153-182.	0.8	42
50	Molecular signatures and phylogenomic analysis of the genus <i>Burkholderia</i> : proposal for division of this genus into the emended genus <i>Burkholderia</i> containing pathogenic organisms and a new genus <i>Paraburkholderia</i> gen. nov. harboring environmental species. <i>Frontiers in Genetics</i> , 2014, 5, 429.	2.3	652
51	Molecular signatures for the phylum (class) Thermotogae and a proposal for its division into three orders (Thermotogales, Kosmotogales ord. nov. and Petrotogales ord. nov.) containing four families (Thermotogaceae, Fervidobacteriaceae fam. nov., Kosmotogaceae fam. nov. and Petrotogaceae fam.) <i>Tj ETQq1 1 0:784314 rg87 /Ove</i>		
52	Conserved signature indels and signature proteins as novel tools for understanding microbial phylogeny and systematics: identification of molecular signatures that are specific for the phytopathogenic genera <i>Dickeya</i> , <i>Pectobacterium</i> and <i>Brenneria</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 366-383.	1.7	59
53	Comparative proteome analysis of <i>Acidaminococcus intestini</i> supports a relationship between outer membrane biogenesis in Negativicutes and Proteobacteria. <i>Archives of Microbiology</i> , 2014, 196, 307-310.	2.2	11
54	Phylogeny and molecular signatures for the phylum Fusobacteria and its distinct subclades. <i>Anaerobe</i> , 2014, 28, 182-198.	2.1	58

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55	Insertion/Deletion-Based Approach for the Detection of <i>Escherichia coli</i> O157:H7 in Freshwater Environments. <i>Environmental Science & Technology</i> , 2014, 48, 11462-11470.	10.0	46
56	Molecular signatures for members of the genus <i>Dehalococcoides</i> and the class <i>Dehalococcoidia</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2176-2181.	1.7	13
57	Phylogenetic analysis and molecular signatures defining a monophyletic clade of heterocystous cyanobacteria and identifying its closest relatives. <i>Photosynthesis Research</i> , 2014, 122, 171-185.	2.9	25
58	A phylogenomic and molecular marker based proposal for the division of the genus <i>Borrelia</i> into two genera: the emended genus <i>Borrelia</i> containing only the members of the relapsing fever <i>Borrelia</i> , and the genus <i>Borreliella</i> gen. nov. containing the members of the Lyme disease <i>Borrelia</i> (<i>Borrelia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 612	1.7	207
59	The Phylum <i>Thermotogae</i> . , 2014, , 989-1015.		26
60	The Phylum <i>Aquificae</i> . , 2014, , 417-445.		11
61	Molecular signatures for the phylum <i>Aquificae</i> and its different clades: proposal for division of the phylum <i>Aquificae</i> into the emended order <i>Aquificales</i> , containing the families <i>Aquificaceae</i> and <i>Hydrogenothermaceae</i> , and a new order <i>Desulfurobacteriales</i> ord. nov., containing the family <i>Desulfurobacteriaceae</i> . <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 349-368.	1.7	47
62	Adenosine Metabolism, Adenosine Kinase, and Evolution. , 2013, , 23-54.		17
63	Molecular signatures for the class <i>Coriobacteriia</i> and its different clades; proposal for division of the class <i>Coriobacteriia</i> into the emended order <i>Coriobacteriales</i> , containing the emended family <i>Coriobacteriaceae</i> and <i>Atopobiaceae</i> fam. nov., and <i>Eggerthel</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3379-3397.	1.7	119
64	Phylogenomics and molecular signatures for the order <i>Neisseriales</i> : proposal for division of the order <i>Neisseriales</i> into the emended family <i>Neisseriaceae</i> and <i>Chromobacteriaceae</i> fam. nov.. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 1-24.	1.7	81
65	Molecular signatures for <i>Bacillus</i> species: demarcation of the <i>Bacillus subtilis</i> and <i>Bacillus cereus</i> clades in molecular terms and proposal to limit the placement of new species into the genus <i>Bacillus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 2712-2726.	1.7	78
66	Molecular Markers for Photosynthetic Bacteria and Insights into the Origin and Spread of Photosynthesis. <i>Advances in Botanical Research</i> , 2013, 66, 37-66.	1.1	20
67	Phylogenetic framework and molecular signatures for the class <i>Chloroflexi</i> and its different clades; proposal for division of the class <i>Chloroflexi</i> class. nov. into the suborder <i>Chloroflexineae</i> subord. nov., consisting of the emended family <i>Oscillochloridaceae</i> and the family <i>Chloroflexaceae</i> fam. nov., and the suborder <i>Roseiflexineae</i> subord. nov., containing the family <i>Roseiflexaceae</i> fam. nov.. <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 89-118.	1.7	157
68	A phylogenomic and molecular signature based approach for characterization of the phylum <i>Spirochaetes</i> and its major clades: proposal for a taxonomic revision of the phylum. <i>Frontiers in Microbiology</i> , 2013, 4, 217.	3.5	95
69	Phylogenomics and Molecular Signatures for Species from the Plant Pathogen-Containing Order <i>Xanthomonadales</i> . <i>PLoS ONE</i> , 2013, 8, e55216.	2.5	62
70	Protein based molecular markers provide reliable means to understand prokaryotic phylogeny and support Darwinian mode of evolution. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 98.	3.9	30
71	Molecular signatures for the phylum <i>Synergistetes</i> and some of its subclades. <i>Antonie Van Leeuwenhoek</i> , 2012, 102, 517-540.	1.7	32
72	Molecular signatures for the PVC clade (<i>Planctomycetes</i> , <i>Verrucomicrobia</i> , <i>Chlamydiae</i> , and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 Td <i>Microbiology</i> , 2012, 3, 327.	3.5	49

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73	Origin and Spread of Photosynthesis Based upon Conserved Sequence Features in Key Bacteriochlorophyll Biosynthesis Proteins. <i>Molecular Biology and Evolution</i> , 2012, 29, 3397-3412.	8.9	27
74	Phylogenetic Framework and Molecular Signatures for the Main Clades of the Phylum Actinobacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2012, 76, 66-112.	6.6	244
75	Molecular signatures (conserved indels) in protein sequences that are specific for the order Pasteurellales and distinguish two of its main clades. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 105-124.	1.7	18
76	Microbial systematics in the post-genomics era. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 45-54.	1.7	51
77	Identification of a <i>Bacillus anthracis</i> specific indel in the <i>yeaC</i> gene and development of a rapid pyrosequencing assay for distinguishing <i>B. anthracis</i> from the <i>B. cereus</i> group. <i>Journal of Microbiological Methods</i> , 2011, 87, 278-285.	1.6	52
78	Molecular signatures for the Crenarchaeota and the Thaumarchaeota. <i>Antonie Van Leeuwenhoek</i> , 2011, 99, 133-157.	1.7	28
79	Phylogeny and molecular signatures for the phylum Thermotogae and its subgroups. <i>Antonie Van Leeuwenhoek</i> , 2011, 100, 1-34.	1.7	42
80	Origin of diderm (Gram-negative) bacteria: antibiotic selection pressure rather than endosymbiosis likely led to the evolution of bacterial cells with two membranes. <i>Antonie Van Leeuwenhoek</i> , 2011, 100, 171-182.	1.7	126
81	Molecular Characterization of Chinese Hamster Cells Mutants Affected in Adenosine Kinase and Showing Novel Genetic and Biochemical Characteristics. <i>BMC Biochemistry</i> , 2011, 12, 22.	4.4	10
82	Molecular signatures for the main phyla of photosynthetic bacteria and their subgroups. <i>Photosynthesis Research</i> , 2010, 104, 357-372.	2.9	35
83	Signature proteins for the major clades of Cyanobacteria. <i>BMC Evolutionary Biology</i> , 2010, 10, 24.	3.2	67
84	Structure and Protein-Protein Interaction Studies on <i>Chlamydia trachomatis</i> Protein CT670 (YscO Homolog). <i>Journal of Bacteriology</i> , 2010, 192, 2746-2756.	2.2	34
85	Phylogenomics and protein signatures elucidating the evolutionary relationships among the Gammaproteobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 234-247.	1.7	93
86	Protein signatures (molecular synapomorphies) that are distinctive characteristics of the major cyanobacterial clades. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2510-2526.	1.7	58
87	Approaches to the study of the systematics of anaerobic, Gram-negative, non-sporeforming rods: Current status and perspectives. <i>Anaerobe</i> , 2009, 15, 179-194.	2.1	54
88	Mycobacterial adenosine kinase is not a typical adenosine kinase. <i>FEBS Letters</i> , 2009, 583, 2231-2236.	2.8	8
89	Conserved inserts in the Hsp60 (GroEL) and Hsp70 (DnaK) proteins are essential for cellular growth. <i>Molecular Genetics and Genomics</i> , 2009, 281, 361-373.	2.1	78
90	Structural and phylogenetic analysis of a conserved actinobacteria-specific protein (ASP1; SCO1997) from <i>Streptomyces coelicolor</i> . <i>BMC Structural Biology</i> , 2009, 9, 40.	2.3	10

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91	Subcellular localization of adenosine kinase in mammalian cells: The long isoform of AdK is localized in the nucleus. <i>Biochemical and Biophysical Research Communications</i> , 2009, 388, 46-50.	2.1	51
92	Phylogenomic analyses of clostridia and identification of novel protein signatures that are specific to the genus <i>Clostridium sensu stricto</i> (cluster I). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 285-294.	1.7	92
93	Novel mitochondrial extensions provide evidence for a link between microtubule-directed movement and mitochondrial fission. <i>Biochemical and Biophysical Research Communications</i> , 2008, 376, 40-45.	2.1	27
94	Unusual Cellular Disposition of the Mitochondrial Molecular Chaperones Hsp60, Hsp70 and Hsp10. <i>Novartis Foundation Symposium</i> , 2008, 291, 59-73.	1.1	37
95	Phylogeny and shared conserved inserts in proteins provide evidence that Verrucomicrobia are the closest known free-living relatives of chlamydiae. <i>Microbiology (United Kingdom)</i> , 2007, 153, 2648-2654.	1.8	42
96	Identification and characterization of human ribokinase and comparison of its properties with E. coli ribokinase and human adenosine kinase. <i>FEBS Letters</i> , 2007, 581, 3211-3216.	2.8	40
97	Phylogeny and molecular signatures (conserved proteins and indels) that are specific for the Bacteroidetes and Chlorobi species. <i>BMC Evolutionary Biology</i> , 2007, 7, 71.	3.2	79
98	Phylogenomic analysis of proteins that are distinctive of Archaea and its main subgroups and the origin of methanogenesis. <i>BMC Genomics</i> , 2007, 8, 86.	2.8	65
99	Phylogenomics and signature proteins for the alpha Proteobacteria and its main groups. <i>BMC Microbiology</i> , 2007, 7, 106.	3.3	130
100	Application of the Character Compatibility Approach to Generalized Molecular Sequence Data: Branching Order of the Proteobacterial Subdivisions. <i>Journal of Molecular Evolution</i> , 2007, 64, 90-100.	1.8	32
101	Identification and Biochemical Studies on Novel Non-Nucleoside Inhibitors of the Enzyme Adenosine Kinase. <i>Protein Journal</i> , 2007, 26, 203-212.	1.6	7
102	Genomics as a means to understand bacterial phylogeny and ecological adaptation: the case of bifidobacteria. <i>Antonie Van Leeuwenhoek</i> , 2007, 91, 351-372.	1.7	95
103	Subcellular localization of fumarase in mammalian cells and tissues. <i>Histochemistry and Cell Biology</i> , 2007, 127, 335-346.	1.7	14
104	Identification of signature proteins that are distinctive of the <i>Deinococcus-Thermus</i> phylum. <i>International Microbiology</i> , 2007, 10, 201-8.	2.4	50
105	Mitochondrial import of human and yeast fumarase in live mammalian cells: Retrograde translocation of the yeast enzyme is mainly caused by its poor targeting sequence. <i>Biochemical and Biophysical Research Communications</i> , 2006, 346, 911-918.	2.1	19
106	Chlamydiae-specific proteins and indels: novel tools for studies. <i>Trends in Microbiology</i> , 2006, 14, 527-535.	7.7	41
107	Inhibition of adenosine kinase by phosphonate and bisphosphonate derivatives. <i>Molecular and Cellular Biochemistry</i> , 2006, 283, 11-21.	3.1	11
108	Signature proteins that are distinctive characteristics of Actinobacteria and their subgroups. <i>Antonie Van Leeuwenhoek</i> , 2006, 90, 69-91.	1.7	115

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109	Lateral Transfers of Serine Hydroxymethyltransferase (glyA) and UDP-N-Acetylglucosamine Enolpyruvyl Transferase (murA) Genes from Free-living Actinobacteria to the Parasitic Chlamydiae. <i>Journal of Molecular Evolution</i> , 2006, 63, 283-296.	1.8	21
110	BLAST screening of chlamydial genomes to identify signature proteins that are unique for the Chlamydiales, Chlamydiaceae, Chlamydophila and Chlamydia groups of species. <i>BMC Genomics</i> , 2006, 7, 14.	2.8	41
111	Molecular signatures (unique proteins and conserved indels) that are specific for the epsilon proteobacteria (Campylobacterales). <i>BMC Genomics</i> , 2006, 7, 167.	2.8	53
112	Molecular signatures in protein sequences that are characteristics of the phylum Aquificae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 99-107.	1.7	33
113	Signature proteins that are distinctive of alpha proteobacteria. <i>BMC Genomics</i> , 2005, 6, 94.	2.8	30
114	Induction of mitochondrial fusion by cysteine-alkylators ethacrynic acid and N-ethylmaleimide. <i>Journal of Cellular Physiology</i> , 2005, 202, 796-804.	4.1	17
115	Localization of mitochondrial DNA encoded cytochrome c oxidase subunits I and II in rat pancreatic zymogen granules and pituitary growth hormone granules. <i>Histochemistry and Cell Biology</i> , 2005, 124, 409-421.	1.7	15
116	Intracellular Disposition of Mitochondrial Molecular Chaperones: Hsp60, mHsp70, Cpn10 and TRAP-1. , 2005, , 22-42.		2
117	Conserved indels in essential proteins that are distinctive characteristics of Chlamydiales and provide novel means for their identification. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2647-2657.	1.8	39
118	Conserved indels in protein sequences that are characteristic of the phylum Actinobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 2401-2412.	1.7	110
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