

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

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times ranked

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#	ARTICLE	IF	CITATIONS
1	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
2	Genome-based phylogeny and taxonomy of the "Enterobacteriales" TM : proposal for Enterobacterales 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
3	Robust demarcation of 17 distinct <i>Bacillus</i> species clades, proposed as novel <i>Bacillaceae</i> genera, by phylogenomics and comparative genomic analyses: description of <i>Robertmurraya kyonggiensis</i> sp. nov. and proposal for an emended genus <i>Bacillus</i> limiting it only to the members of the <i>Subtilis</i> and <i>Cereus</i> clades of species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5753-5798.	1.7	659
4	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
5	Protein Phylogenies and Signature Sequences: A Reappraisal of Evolutionary Relationships among Archaeobacteria, Eubacteria, and Eukaryotes. <i>Microbiology and Molecular Biology Reviews</i> , 1998, 62, 1435-1491.	6.6	527
6	Phylogenetic framework for the phylum Tenericutes based on genome sequence data: proposal for the creation of a new order Mycoplasmodales ord. nov., containing two new families Mycoplasmodaceae 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
7	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
8	Evolution of the chaperonin families (HSP60, HSP 10 and TCP-1) of proteins and the origin of eukaryotic cells. <i>Molecular Microbiology</i> , 1995, 15, 1-11.	2.5	293
9	The phylogeny of proteobacteria: relationships to other eubacterial phyla and eukaryotes. <i>FEMS Microbiology Reviews</i> , 2000, 24, 367-402.	8.6	267
10	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 Natribales ord. nov., containing the novel families Haloferacaceae fam. nov. and Natribaceae fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1050-1069.	1.7	260
11	Immunoelectron Microscopic Localization of the 60-kDa Heat Shock Chaperonin Protein (Hsp60) in Mammalian Cells. <i>Experimental Cell Research</i> , 1996, 222, 16-27.	2.6	248
12	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
13	The origin of the eukaryotic cell. <i>Trends in Biochemical Sciences</i> , 1996, 21, 166-171.	7.5	223
14	Phylogenetic analysis of 70 kD heat shock protein sequences suggests a chimeric origin for the eukaryotic cell nucleus. <i>Current Biology</i> , 1994, 4, 1104-1114.	3.9	217
15	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>Borrelia</i> gen. nov. containing the members of the Lyme disease <i>Borrelia</i> (<i>Borrelia</i>) Tj ETQq1 1 0.7843147rgBT /Overlock 10	1.7	207
16	CELL SURFACE LOCALIZATION OF THE 60 kDa HEAT SHOCK CHAPERONIN PROTEIN (hsp60) IN MAMMALIAN CELLS. <i>Cell Biology International</i> , 1997, 21, 315-320.	3.0	178
17	Mitochondrial-matrix proteins at unexpected locations: are they exported?. <i>Trends in Biochemical Sciences</i> , 1999, 24, 174-177.	7.5	160
18	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

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19	Phylogenetic framework and molecular signatures for the class Chloroflexi and its different clades; proposal for division of the class Chloroflexi class. nov. into the suborder Chloroflexineae subord. nov., consisting of the emended family Oscillochloridaceae and the family Chloroflexaceae fam. nov., and the suborder Roseiflexineae subord. nov., containing the family Roseiflexaceae fam. nov.. Antonie Van Leeuwenhoek, 2013, 103, 99-119.	1.7	157
20	Critical Issues in Bacterial Phylogeny. Theoretical Population Biology, 2002, 61, 423-434.	1.1	143
21	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 Rhodanobacter and its closest relatives. Antonie Van Leeuwenhoek, 2015,	1.7	135
22	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.) Tj ETQq0 0 0 rgt /Overlock 10 Tf		
23	Leeuwenhoek, 2014, 105, 143-168. Phylogenomics and signature proteins for the alpha Proteobacteria and its main groups. BMC Microbiology, 2007, 7, 106.	3.3	130
24	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.. Antonie Van Leeuwenhoek, 2016, 109, 565-587.	1.7	127
25	Origin of diderm (Gram-negative) bacteria: antibiotic selection pressure rather than endosymbiosis likely led to the evolution of bacterial cells with two membranes. Antonie Van Leeuwenhoek, 2011, 100, 171-182.	1.7	126
26	Molecular signatures for the class Coriobacteriia and its different clades; proposal for division of the class Coriobacteriia into the emended order Coriobacteriales , containing the emended family Coriobacteriaceae and Atopobiaceae fam. nov., and Eggerthel. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3379-3397.	1.7	119
27	Localization of P32 protein (gC1q-R) in mitochondria and at specific extramitochondrial locations in normal tissues. Histochemistry and Cell Biology, 2000, 114, 245-255.	1.7	117
28	Cellular basis for the species differences in sensitivity to cardiac glycosides (digitalis). Journal of Cellular Physiology, 1986, 127, 197-206.	4.1	116
29	Signature proteins that are distinctive characteristics of Actinobacteria and their subgroups. Antonie Van Leeuwenhoek, 2006, 90, 69-91.	1.7	115
30	Phylogenomics and comparative genomic studies delineate six main clades within the family Enterobacteriaceae and support the reclassification of several polyphyletic members of the family. Infection, Genetics and Evolution, 2017, 54, 108-127.	2.3	112
31	Conserved indels in protein sequences that are characteristic of the phylum Actinobacteria. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 2401-2412.	1.7	110
32	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. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	101
33	What are archaeobacteria: life's third domain or monoderm prokaryotes related to Gramâ€positive bacteria? A new proposal for the classification of prokaryotic organisms. Molecular Microbiology, 1998, 29, 695-707.	2.5	99
34	The Phylogeny and Signature Sequences Characteristics of Fibrobacteres, Chlorobi, and Bacteroidetes. Critical Reviews in Microbiology, 2004, 30, 123-143.	6.1	99
35	The Natural Evolutionary Relationships among Prokaryotes. Critical Reviews in Microbiology, 2000, 26, 111-131.	6.1	96
36	Genomics as a means to understand bacterial phylogeny and ecological adaptation: the case of bifidobacteria. Antonie Van Leeuwenhoek, 2007, 91, 351-372.	1.7	95

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37	A phylogenomic and molecular signature based approach for characterization of the phylum Spirochaetes and its major clades: proposal for a taxonomic revision of the phylum. <i>Frontiers in Microbiology</i> , 2013, 4, 217.	3.5	95
38	Immunoelectron Microscopy Provides Evidence That Tumor Necrosis Factor Receptor-Associated Protein 1 (TRAP-1) Is a Mitochondrial Protein Which also Localizes at Specific Extramitochondrial Sites. <i>Experimental Cell Research</i> , 2000, 260, 30-39.	2.6	94
39	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
40	The branching order and phylogenetic placement of species from completed bacterial genomes, based on conserved indels found in various proteins. <i>International Microbiology</i> , 2001, 4, 187-202.	2.4	92
41	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
42	Mitochondrial Proteins at Unexpected Cellular Locations: Export of Proteins from Mitochondria from an Evolutionary Perspective. <i>International Review of Cytology</i> , 1999, 194, 133-196.	6.2	90
43	Evolutionary relationships among photosynthetic prokaryotes (<i>Heliobacterium chlorum</i> ,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 regarding the origin of photosynthesis. <i>Molecular Microbiology</i> , 1999, 32, 893-906.	2.5	88
44	Localization of Mitochondrial 60-kD Heat Shock Chaperonin Protein (Hsp60) in Pituitary Growth Hormone Secretory Granules and Pancreatic Zymogen Granules. <i>Journal of Histochemistry and Cytochemistry</i> , 2000, 48, 45-56.	2.5	84
45	Phylogenomics and molecular signatures for the order Neisseriales: proposal for division of the order Neisseriales into the emended family Neisseriaceae and Chromobacteriaceae fam. nov.. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 1-24.	1.7	81
46	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
47	Interrelationships of endoplasmic reticulum, mitochondria, intermediate filaments, and microtubules—a quadruple fluorescence labeling study. <i>Biochemistry and Cell Biology</i> , 1992, 70, 1174-1186.	2.0	79
48	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
49	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
50	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
51	Genetic and biochemical studies with the adenosine analogs toyocamycin and tubercidin: Mutation at the adenosine kinase locus in Chinese hamster cells. <i>Somatic Cell Genetics</i> , 1978, 4, 715-735.	2.7	76
52	Evidence for functional hemizygoty at the Emtr locus in CHO cells through segregation analysis. <i>Cell</i> , 1978, 14, 1007-1013.	28.9	76
53	Evolutionary relationships among photosynthetic bacteria. <i>Photosynthesis Research</i> , 2003, 76, 173-183.	2.9	75
54	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

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55	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
56	Division of the genus <i>Borrelia</i> into two genera (corresponding to Lyme disease and relapsing fever) of these two groups of microbes (Margos et al. (2016) There is inadequate evidence to support the) <i>Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2058-2067.	8.6	73
57	Cloning and characterization of multiple groEL chaperonin-encoding genes in <i>Rhizobium meliloti</i> . <i>Gene</i> , 1993, 126, 67-75.	2.2	69
58	Cloning and Some Novel Characteristics of Mitochondrial Hsp70 from Chinese Hamster Cells. <i>Experimental Cell Research</i> , 1997, 234, 205-216.	2.6	69
59	Signature proteins for the major clades of Cyanobacteria. <i>BMC Evolutionary Biology</i> , 2010, 10, 24.	3.2	67
60	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
61	Distinction between <i>Borrelia</i> and <i>Borreliella</i> is more robustly supported by molecular and phenotypic characteristics than all other neighbouring prokaryotic genera: Response to Margos' et al. "The genus <i>Borrelia</i> reloaded" (<i>PLoS ONE</i> 13(12): e0208432). <i>PLoS ONE</i> , 2019, 14, e0221397.	2.5	64
62	Phylogenomics and Molecular Signatures for Species from the Plant Pathogen-Containing Order Xanthomonadales. <i>PLoS ONE</i> , 2013, 8, e55216.	2.5	62
63	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
64	Activation of Synovial Fluid T Lymphocytes by 60-Kd Heat-Shock Proteins in Patients with Inflammatory synovitis. <i>Arthritis and Rheumatism</i> , 1992, 35, 43-48.	6.7	58
65	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
66	Phylogeny and molecular signatures for the phylum Fusobacteria and its distinct subclades. <i>Anaerobe</i> , 2014, 28, 182-198.	2.1	58
67	Expression of Human 60-kD Heat Shock Protein (HSP60 or P1) in <i>Escherichia coli</i> and the Development and Characterization of Corresponding Monoclonal Antibodies. <i>DNA and Cell Biology</i> , 1992, 11, 489-496.	1.9	55
68	Immunoelectron microscopy provides evidence for the presence of mitochondrial heat shock 10-kDa protein (chaperonin β 10) in red blood cells and a variety of secretory granules. <i>Histochemistry and Cell Biology</i> , 2001, 116, 507-517.	1.7	55
69	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
70	Signature sequences in diverse proteins provide evidence for the late divergence of the Order Aquificales. <i>International Microbiology</i> , 2004, 7, 41-52.	2.4	54
71	Nucleotide Sequences and Novel Structural Features of Human and Chinese Hamster hsp60 (Chaperonin) Gene Families. <i>DNA and Cell Biology</i> , 1990, 9, 545-552.	1.9	53
72	Molecular signatures (unique proteins and conserved indels) that are specific for the epsilon proteobacteria (Campylobacteriales). <i>BMC Genomics</i> , 2006, 7, 167.	2.8	53

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73	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
74	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
75	Microbial systematics in the post-genomics era. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 45-54.	1.7	51
76	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
77	Protein Signatures Distinctive of Alpha Proteobacteria and Its Subgroups and a Model for Its Proteobacterial Evolution. <i>Critical Reviews in Microbiology</i> , 2005, 31, 101-135.	6.1	49
78	Molecular signatures for the PVC clade (<i>Planctomycetes</i> , <i>Verrucomicrobia</i> , <i>Chlamydiae</i> , and) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 T Microbiology</i> , 2012, 3, 327.	3.5	49
79	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
80	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
81	Phylogenomics and molecular signatures support division of the order <i>Neisseriales</i> into emended families <i>Neisseriaceae</i> and <i>Chromobacteriaceae</i> and three new families <i>Aquaspirillaceae</i> fam. nov., <i>Chitinibacteraceae</i> fam. nov., and <i>Leeiaceae</i> fam. nov.. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126251.	2.8	46
82	Pentavalent Ions Dependency Is a Conserved Property of Adenosine Kinase from Diverse Sources: Identification of a Novel Motif Implicated in Phosphate and Magnesium Ion Binding and Substrate Inhibition. <i>Biochemistry</i> , 2002, 41, 4059-4069.	2.5	45
83	Phylogeny and shared conserved inserts in proteins provide evidence that <i>Verrucomicrobia</i> are the closest known free-living relatives of <i>chlamydiae</i> . <i>Microbiology (United Kingdom)</i> , 2007, 153, 2648-2654.	1.8	42
84	Phylogeny and molecular signatures for the phylum <i>Thermotogae</i> and its subgroups. <i>Antonie Van Leeuwenhoek</i> , 2011, 100, 1-34.	1.7	42
85	Identification of Conserved Indels that are Useful for Classification and Evolutionary Studies. <i>Methods in Microbiology</i> , 2014, 41, 153-182.	0.8	42
86	Phylogenomic and comparative genomic analyses of <i>Leuconostocaceae</i> species: identification of molecular signatures specific for the genera <i>Leuconostoc</i> , <i>Fructobacillus</i> and <i>Oenococcus</i> and proposal for a novel genus <i>Periweissella</i> gen. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	42
87	<i>Mycobacteria</i> and human heat shock protein-specific cytotoxic t lymphocytes in rheumatoid synovial inflammation. <i>Arthritis and Rheumatism</i> , 1992, 35, 270-281.	6.7	41
88	<i>Chlamydiae</i> -specific proteins and indels: novel tools for studies. <i>Trends in Microbiology</i> , 2006, 14, 527-535.	7.7	41
89	BLAST screening of <i>chlamydial</i> genomes to identify signature proteins that are unique for the <i>Chlamydiales</i> , <i>Chlamydiaceae</i> , <i>Chlamydophila</i> and <i>Chlamydia</i> groups of species. <i>BMC Genomics</i> , 2006, 7, 14.	2.8	41
90	Novel molecular, structural and evolutionary characteristics of the phosphoketolases from <i>bifidobacteria</i> and <i>Coriobacteriales</i> . <i>PLoS ONE</i> , 2017, 12, e0172176.	2.5	41

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91	The use of signature sequences in different proteins to determine the relative branching order of bacterial divisions: evidence that Fibrobacter diverged at a similar time to Chlamydia and the Cytophaga "Flavobacterium" Bacteroides division The GenBank accession numbers for the sequences reported in this paper are AY017380, AY017381, AY017382 and AY017383.. Microbiology (United Kingdom), 2001, 147, 2611-2622.	1.8	41
92	Taxol resistant mutants of Chinese hamster ovary cells: Genetic biochemical, and cross-resistance studies. Journal of Cellular Physiology, 1983, 114, 137-144.	4.1	40
93	Signature Sequences in Diverse Proteins Provide Evidence of a Close Evolutionary Relationship Between the Deinococcus-Thermus Group and Cyanobacteria. Journal of Molecular Evolution, 1998, 46, 716-720.	1.8	40
94	Identification and characterization of human ribokinase and comparison of its properties with E. coli ribokinase and human adenosine kinase. FEBS Letters, 2007, 581, 3211-3216.	2.8	40
95	The sequences of heat shock protein 40 (DnaJ) homologs provide evidence for a close evolutionary relationship between the Deinococcus-Thermus group and cyanobacteria. Journal of Molecular Evolution, 1997, 45, 193-205.	1.8	39
96	Conserved indels in essential proteins that are distinctive characteristics of Chlamydiales and provide novel means for their identification. Microbiology (United Kingdom), 2005, 151, 2647-2657.	1.8	39
97	Cloning of HSP70 (dnaK) gene from Clostridium perfringens using a general polymerase chain reaction based approach. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1992, 1130, 203-208.	2.4	38
98	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. Antonie Van Leeuwenhoek, 2015, 108, 765-781.	1.7	38
99	Life's Third Domain (Archaea): An Established Fact or an Endangered Paradigm?. Theoretical Population Biology, 1998, 54, 91-104.	1.1	37
100	Unusual Cellular Disposition of the Mitochondrial Molecular Chaperones Hsp60, Hsp70 and Hsp10. Novartis Foundation Symposium, 2008, 291, 59-73.	1.1	37
101	Protein signatures distinctive of chlamydial species: horizontal transfers of cell wall biosynthesis genes glmU from archaea to chlamydiae and murA between chlamydiae and Streptomyces a The GenBank accession numbers for the sequences reported in this paper are indicated in the text.. Microbiology (United Kingdom), 2002, 148, 2541-2549.	1.8	37
102	Diacylglycerol Kinase- μ : Properties and Biological Roles. Frontiers in Cell and Developmental Biology, 2016, 4, 112.	3.7	36
103	Molecular signatures for the main phyla of photosynthetic bacteria and their subgroups. Photosynthesis Research, 2010, 104, 357-372.	2.9	35
104	Structure and Protein-Protein Interaction Studies on <i>Chlamydia trachomatis</i> Protein CT670 (YscO Homolog). Journal of Bacteriology, 2010, 192, 2746-2756.	2.2	34
105	Robust demarcation of fourteen different species groups within the genus Streptococcus based on genome-based phylogenies and molecular signatures. Infection, Genetics and Evolution, 2018, 66, 130-151.	2.3	34
106	Molecular signatures in protein sequences that are characteristic of cyanobacteria and plastid homologues. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 1833-1842.	1.7	33
107	Molecular signatures in protein sequences that are characteristics of the phylum Aquificae. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 99-107.	1.7	33
108	The development of monoclonal antibodies to the human mitochondrial 60-kd heat-shock protein, and their use in studying the expression of the protein in rheumatoid arthritis. Arthritis and Rheumatism, 1992, 35, 1427-1433.	6.7	32

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109	Distinctive Protein Signatures Provide Molecular Markers and Evidence for the Monophyletic Nature of the Deinococcus-Thermus Phylum. <i>Journal of Bacteriology</i> , 2004, 186, 3097-3107.	2.2	32
110	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
111	Molecular signatures for the phylum Synergistetes and some of its subclades. <i>Antonie Van Leeuwenhoek</i> , 2012, 102, 517-540.	1.7	32
112	Signature proteins that are distinctive of alpha proteobacteria. <i>BMC Genomics</i> , 2005, 6, 94.	2.8	30
113	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
114	Cloning and Characterization of cDNA for Adenosine Kinase from Mammalian (Chinese Hamster,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	0.2	30
115	Changes in mitochondrial shape and distribution induced by ethacrynic acid and the transient formation of a mitochondrial reticulum. <i>Journal of Cellular Physiology</i> , 1994, 159, 281-294.	4.1	29
116	Immunoelectron Microscopy of Giardia lamblia Cytoskeleton Using Antibody to Acetylated α -Tubulin. <i>Journal of Eukaryotic Microbiology</i> , 1994, 41, 625-632.	1.7	29
117	Comparison of the mutagenic responses of 12 anticancer drugs at the hypoxanthine-guanine phosphoribosyl transferase and adenosine kinase loci in chinese hamster ovary cells. <i>Environmental Mutagenesis</i> , 1983, 5, 871-880.	1.4	28
118	Molecular signatures for the Crenarchaeota and the Thaumarchaeota. <i>Antonie Van Leeuwenhoek</i> , 2011, 99, 133-157.	1.7	28
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