Andreas Burkovski

List of Publications by Year
in descending order

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174	6,673	53794	79698
papers	citations	45 h-index	73 g-index

176	176	176	5056
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of l-aspartate-derived amino acids and vitamins. Journal of Biotechnology, 2003, 104, 5-25.	3.8	844
2	Ammonium Toxicity in Bacteria. Current Microbiology, 2006, 52, 400-406.	2.2	167
3	Bacterial amino acid transport proteins: occurrence, functions, and significance for biotechnological applications. Applied Microbiology and Biotechnology, 2002, 58, 265-274.	3.6	159
4	Construction and application of new Corynebacterium glutamicum vectors. Biotechnology Letters, 1999, 13, 437-441.	0.5	148
5	Towards a phosphoproteome map of Corynebacterium glutamicum. Proteomics, 2003, 3, 1637-1646.	2.2	143
6	Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine. Journal of Bacteriology, 1996, 178, 5229-5234.	2.2	113
7	Functional and Genetic Characterization of the (Methyl)ammonium Uptake Carrier of Corynebacterium glutamicum. Journal of Biological Chemistry, 1996, 271, 5398-5403.	3.4	105
8	Proteome analysis ofCorynebacterium glutamicum. Electrophoresis, 2001, 22, 1712-1723.	2.4	105
9	Corynebacterium glutamicum Is Equipped with Four Secondary Carriers for Compatible Solutes: Identification, Sequencing, and Characterization of the Proline/Ectoine Uptake System, ProP, and the Ectoine/Proline/Glycine Betaine Carrier, EctP. Journal of Bacteriology, 1998, 180, 6005-6012.	2.2	105
10	Vanillate Metabolism in Corynebacterium glutamicum. Current Microbiology, 2005, 51, 59-65.	2.2	99
11	Regulation of GlnK activity: modification, membrane sequestration and proteolysis as regulatory principles in the network of nitrogen control in Corynebacterium glutamicum. Molecular Microbiology, 2004, 54, 132-147.	2.5	94
12	AmtR, a global repressor in the nitrogen regulation system of Corynebacterium glutamicum. Molecular Microbiology, 2000, 37, 964-977.	2.5	93
13	Osmo-sensing by N- and C-terminal Extensions of the Glycine Betaine Uptake System BetP of Corynebacterium glutamicum. Journal of Biological Chemistry, 1998, 273, 2567-2574.	3.4	91
14	Sugar Transport Systems of Bifidobacterium longum NCC2705. Journal of Molecular Microbiology and Biotechnology, 2007, 12, 9-19.	1.0	89
15	The complete genome sequence of Corynebacterium pseudotuberculosis FRC41 isolated from a 12-year-old girl with necrotizing lymphadenitis reveals insights into gene-regulatory networks contributing to virulence. BMC Genomics, 2010, 11, 728.	2.8	89
16	Regulation of AmtRâ€controlled gene expression in Corynebacterium glutamicum: mechanism and characterization of the AmtR regulon. Molecular Microbiology, 2005, 58, 580-595.	2.5	88
17	Common patterns â€“ unique features: nitrogen metabolism and regulation in Gram-positive bacteria. FEMS Microbiology Reviews, 2010, 34, 588-605.	8.6	88
18	Comparative analysis of two complete Corynebacterium ulcerans genomes and detection of candidate virulence factors. BMC Genomics, 2011, 12, 383.	2.8	85

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19	Multiplicity of ammonium uptake systems in Corynebacterium glutamicum: role of Amt and AmtB. Microbiology (United Kingdom), 2001, 147, 135-143.	1.8	85
20	A Genomic View of Sugar Transport inMycobacterium smegmatisandMycobacterium tuberculosis. Journal of Bacteriology, 2007, 189, 5903-5915.	2.2	82
21	Cell Envelope of Corynebacteria: Structure and Influence on Pathogenicity. , 2013, 2013, 1-11.		82
22	Characterization of Methionine Export in Corynebacterium glutamicum. Journal of Bacteriology, 2005, 187, 3786-3794.	2.2	80
23	Comprehensive Reactive Receiver Modeling for Diffusive Molecular Communication Systems: Reversible Binding, Molecule Degradation, and Finite Number of Receptors. IEEE Transactions on Nanobioscience, 2016, 15, 713-727.	3.3	80
24	Ammonium assimilation and nitrogen control inCorynebacterium glutamicumand its relatives: an example for new regulatory mechanisms in actinomycetes. FEMS Microbiology Reviews, 2003, 27, 617-628.	8.6	79
25	Molecular Identification of the Urea Uptake System and Transcriptional Analysis of Urea Transporter- and Urease-Encoding Genes in Corynebacterium glutamicum. Journal of Bacteriology, 2004, 186, 7645-7652.	2.2	79
26	Nitrogen Control in Mycobacterium smegmatis : Nitrogen-Dependent Expression of Ammonium Transport and Assimilation Proteins Depends on the OmpR-Type Regulator GlnR. Journal of Bacteriology, 2008, 190, 7108-7116.	2.2	78
27	The Phosphate Carrier from Yeast Mitochondria. Journal of Biological Chemistry, 1998, 273, 14269-14276.	3.4	77
28	Influence of threonine exporters on threonine production in Escherichia coli. Applied Microbiology and Biotechnology, 2002, 59, 205-210.	3.6	76
29	Biochemical and Biophysical Characterization of the Cell Wall Porin of Corynebacterium glutamicum:â€‰ The Channel Is Formed by a Low Molecular Mass Polypeptide. Biochemistry, 1998, 37, 15024-15032.	2.5	72
30	Adaptation of Corynebacterium glutamicum to Ammonium Limitation: a Global Analysis Using Transcriptome and Proteome Techniques. Applied and Environmental Microbiology, 2005, 71, 2391-2402.	3.1	72
31	Protein and Proteome Phosphorylation Stoichiometry Analysis by Element Mass Spectrometry. Analytical Chemistry, 2006, 78, 1987-1994.	6.5	71
32	Corynebacterium ulcerans, an emerging human pathogen. Future Microbiology, 2016, 11, 1191-1208.	2.0	68
33	Synthesis and characterization of manganese containing mesoporous bioactive glass nanoparticles for biomedical applications. Journal of Materials Science: Materials in Medicine, 2018, 29, 64.	3.6	68
34	Corynebacterium diphtheriae invasion-associated protein (DIP1281) is involved in cell surface organization, adhesion and internalization in epithelial cells. BMC Microbiology, 2010, 10, 2.	3.3	64
35	Nitrogen regulation inCorynebacterium glutamicum: isolation of genes involved and biochemical characterization of corresponding proteins. FEMS Microbiology Letters, 1999, 173, 303-310.	1.8	63
36	Glutamine synthetases ofCorynebacterium glutamicum: transcriptional control and regulation of activity. FEMS Microbiology Letters, 2001, 201, 91-98.	1.8	63

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37	Sensing nitrogen limitation inCorynebacterium glutamicum: the role ofglnKandglnD^{â€}. Molecular Microbiology, 2001, 42, 1281-1295.	2.5	60
38	A Genomic View on Nitrogen Metabolism and Nitrogen Control in Mycobacteria. Journal of Molecular Microbiology and Biotechnology, 2009, 17, 20-29.	1.0	60
39	Glutamate synthase of Corynebacterium glutamicum is not essential for glutamate synthesis and is regulated by the nitrogen status. Microbiology (United Kingdom), 2001, 147, 2961-2970.	1.8	55
40	Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product. Archives of Microbiology, 1998, 169, 303-312.	2.2	52
41	Two-dimensional electrophoretic analysis ofCorynebacterium glutamicum membrane fraction and surface proteins. Electrophoresis, 2000, 21, 654-659.	2.4	52
42	Polyamine Transport and Role of potE in Response to Osmotic Stress in Escherichia coli. Journal of Bacteriology, 2000, 182, 6247-6249.	2.2	50
43	Identification and characterization of the main ?-alanine uptake system in Escherichia coli. Applied Microbiology and Biotechnology, 2004, 65, 576-82.	3.6	50
44	Adherence and invasive properties of Corynebacterium diphtheriae strains correlates with the predicted membrane-associated and secreted proteome. BMC Genomics, 2015, 16, 765.	2.8	47
45	Identification of an anion-specific channel in the cell wall of the Gram-positive bacterium Corynebacterium glutamicum. Molecular Microbiology, 2003, 50, 1295-1308.	2.5	46
46	DNA microarray analysis of the nitrogen starvation response of Corynebacterium glutamicum. Journal of Biotechnology, 2005, 119, 357-367.	3.8	46
47	Urea uptake and urease activity in Corynebacterium glutamicum. Archives of Microbiology, 1998, 169, 411-416.	2.2	45
48	Isolation of the Corynebacterium glutamicum glnA gene encoding glutamine synthetase I. FEMS Microbiology Letters, 2006, 154, 81-88.	1.8	44
49	A lack of genetic basis for biovar differentiation in clinically important Corynebacterium diphtheriae from whole genome sequencing. Infection, Genetics and Evolution, 2014, 21, 54-57.	2.3	43
50	I do it my way: regulation of ammonium uptake and ammonium assimilation in Corynebacterium glutamicum. Archives of Microbiology, 2003, 179, 83-88.	2.2	42
51	Strain-specific differences in pili formation and the interaction of Corynebacterium diphtheriae with host cells. BMC Microbiology, 2010, 10, 257.	3.3	41
52	Genomic analysis of endemic clones of toxigenic and non-toxigenic Corynebacterium diphtheriae in Belarus during and after the major epidemic in 1990s. BMC Genomics, 2017, 18, 873.	2.8	41
53	A combination of metabolome and transcriptome analyses reveals new targets of the Corynebacterium glutamicum nitrogen regulator AmtR. Journal of Biotechnology, 2009, 140, 68-74.	3.8	39
54	Mapping and identification ofCorynebacterium glutamicum proteins by two-dimensional gel electrophoresis and microsequencing. Electrophoresis, 1998, 19, 3217-3221.	2.4	38

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55	Nitrogen starvation-induced transcriptome alterations and influence of transcription regulator mutants in Mycobacterium smegmatis. BMC Research Notes, 2013, 6, 482.	1.4	38
56	Destabilized <scp>eYFP</scp> variants for dynamic gene expression studies in <scp>C</scp>orynebacterium glutamicum. Microbial Biotechnology, 2013, 6, 196-201.	4.2	37
57	The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Ove	1.8	36
58	PorA Represents the Major Cell Wall Channel of the Gram-Positive Bacterium Corynebacterium glutamicum. Journal of Bacteriology, 2003, 185, 4779-4786.	2.2	36
59	Impact of improved potassium accumulation on pH homeostasis, membrane potential adjustment and survival of Corynebacterium glutamicum. Biochimica Et Biophysica Acta - Bioenergetics, 2011, 1807, 444-450.	1.0	36
60	Molecular armory or niche factors: virulence determinants ofCorynebacteriumspecies. FEMS Microbiology Letters, 2015, 362, fnv185.	1.8	34
61	Response to nitrogen starvation inCorynebacterium glutamicum. FEMS Microbiology Letters, 2000, 187, 83-88.	1.8	33
62	Evaluation of invertebrate infection models for pathogenic corynebacteria. FEMS Immunology and Medical Microbiology, 2012, 65, 413-421.	2.7	33
63	Characterization of DIP0733, a multi-functional virulence factor of Corynebacterium diphtheriae. Microbiology (United Kingdom), 2015, 161, 639-647.	1.8	32
64	Ultrastructure of the Corynebacterium glutamicum cell wall. Antonie Van Leeuwenhoek, 1997, 72, 291-297.	1.7	31
65	Isolation of the putP gene of Corynebacterium glutamicum and characterization of a low-affinity uptake system for compatible solutes. Archives of Microbiology, 1997, 168, 143-151.	2.2	31
66	Toll-Like Receptor 2 and Mincle Cooperatively Sense Corynebacterial Cell Wall Glycolipids. Infection and Immunity, 2017, 85, .	2.2	31
67	A Survey of Biological Building Blocks for Synthetic Molecular Communication Systems. IEEE Communications Surveys and Tutorials, 2020, 22, 2765-2800.	39.4	31
68	CcpA forms complexes with CodY and RpoA in Bacillusâ€ƒsubtilis. FEBS Journal, 2012, 279, 2201-2214.	4.7	30
69	FarR, a putative regulator of amino acid metabolism in Corynebacterium glutamicum. Applied Microbiology and Biotechnology, 2007, 76, 625-632.	3.6	29
70	Urease ofCorynebacterium glutamicum: organization of corresponding genes and investigation of activity. FEMS Microbiology Letters, 2000, 189, 305-310.	1.8	28
71	A game with many players: Control of gdh transcription in Corynebacterium glutamicum. Journal of Biotechnology, 2009, 142, 114-122.	3.8	28
72	Differential NtcA Responsiveness to 2-Oxoglutarate Underlies the Diversity of C/N Balance Regulation in Prochlorococcus. Frontiers in Microbiology, 2017, 8, 2641.	3.5	28

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73	l-Glutamine as a nitrogen source for Corynebacterium glutamicum: derepression of the AmtR regulon and implications for nitrogen sensing. Microbiology (United Kingdom), 2010, 156, 3180-3193.	1.8	27
74	What an Escherichia coli Mutant Can Teach Us About the Antibacterial Effect of Chlorophyllin. Microorganisms, 2019, 7, 59.	3.6	27
75	Nitrogen Metabolism and Nitrogen Control in Corynebacteria: Variations of a Common Theme. Journal of Molecular Microbiology and Biotechnology, 2007, 12, 131-138.	1.0	25
76	Methionine Uptake in Corynebacterium glutamicum by MetQNI and by MetPS, a Novel Methionine and Alanine Importer of the NSS Neurotransmitter Transporter Family. Biochemistry, 2008, 47, 12698-12709.	2.5	25
77	Dissection of Ammonium Uptake Systems inCorynebacterium glutamicum: Mechanism of Action and Energetics of AmtA and AmtB. Journal of Bacteriology, 2008, 190, 2611-2614.	2.2	25
78	Proteomics of diphtheria toxoid vaccines reveals multiple proteins that are immunogenic and may contribute to protection of humans against Corynebacterium diphtheriae. Vaccine, 2019, 37, 3061-3070.	3.8	25
79	Nitrogen control in Corynebacterium glutamicum: proteins, mechanisms, signals. Journal of Microbiology and Biotechnology, 2007, 17, 187-94.	2.1	25
80	Application of global analysis techniques to Corynebacterium glutamicum: New insights into nitrogen regulation. Journal of Biotechnology, 2006, 126, 101-110.	3.8	24
81	A proteomic study of Corynebacterium glutamicum AAA+ protease FtsH. BMC Microbiology, 2007, 7, 6.	3.3	24
82	Argon Cold Plasmaâ€“A Novel Tool to Treat Therapy-resistant Corneal Infections. American Journal of Ophthalmology, 2018, 190, 150-163.	3.3	24
83	Complementation of Escherichia coli unc mutant strains by chloroplast and cyanobacterial F1-ATPase subunits. Biochimica Et Biophysica Acta - Bioenergetics, 1993, 1144, 278-284.	1.0	23
84	GltS, the sodium-coupled L-glutamate uptake system of Corynebacterium glutamicum: identification of the corresponding gene and impact on L-glutamate production. Applied Microbiology and Biotechnology, 2003, 60, 738-742.	3.6	23
85	Utilization of creatinine as an alternative nitrogen source in Corynebacterium glutamicum. Archives of Microbiology, 2004, 181, 443-450.	2.2	22
86	A Molecular Communication Testbed Based on Proton Pumping Bacteria: Methods and Data. IEEE Transactions on Molecular, Biological, and Multi-Scale Communications, 2019, 5, 56-62.	2.1	22
87	Engineering of nitrogen metabolism and its regulation in Corynebacterium glutamicum: influence on amino acid pools and production. Applied Microbiology and Biotechnology, 2011, 89, 239-248.	3.6	21
88	Mutation-induced metabolite pool alterations in Corynebacterium glutamicum: Towards the identification of nitrogen control signals. Journal of Biotechnology, 2006, 126, 440-453.	3.8	20
89	Proteomics of corynebacteria: From biotechnology workhorses to pathogens. Proteomics, 2011, 11, 3244-3255.	2.2	20
90	The role of corynomycolic acids in Corynebacterium-host interaction. Antonie Van Leeuwenhoek, 2018, 111, 717-725.	1.7	20

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91	Caenorhabditis elegans star formation and negative chemotaxis induced by infection with corynebacteria. Microbiology (United Kingdom), 2016, 162, 84-93.	1.8	20
92	Draft Genome Sequence of Corynebacterium diphtheriae Biovar Intermedius NCTC 5011. Journal of Bacteriology, 2012, 194, 4738-4738.	2.2	19
93	Contour and persistence length of Corynebacterium diphtheriae pili by atomic force microscopy. European Biophysics Journal, 2012, 41, 561-570.	2.2	19
94	Treat Me Well or Will Resist: Uptake of Mobile Genetic Elements Determine the Resistome of Corynebacterium striatum. International Journal of Molecular Sciences, 2021, 22, 7499.	4.1	18
95	Genomic analyses reveal two distinct lineages of Corynebacterium ulcerans strains. New Microbes and New Infections, 2018, 25, 7-13.	1.6	17
96	Surface and Extracellular Proteome of the Emerging Pathogen Corynebacterium ulcerans. Proteomes, 2018, 6, 18.	3.5	17
97	More than a Toxin: Protein Inventory of Clostridium tetani Toxoid Vaccines. Proteomes, 2019, 7, 15.	3.5	17
98	Adaptation of AmtR-controlled gene expression by modulation of AmtR binding activity in Corynebacterium glutamicum. Journal of Biotechnology, 2011, 154, 156-162.	3.8	16
99	The Draft Genome Sequence of Corynebacterium diphtheriae bv. mitis NCTC 3529 Reveals Significant Diversity between the Primary Disease-Causing Biovars. Journal of Bacteriology, 2012, 194, 3269-3269.	2.2	16
100	Complex formation between malate dehydrogenase and isocitrate dehydrogenase from BacillusÂsubtilis is regulated by tricarboxylic acid cycle metabolites. FEBS Journal, 2014, 281, 1132-1143.	4.7	16
101	Corynebacterium diphtheriae putative tellurite-resistance protein (CDCE8392_0813) contributes to the intracellular survival in human epithelial cells and lethality of Caenorhabditis elegans. Memorias Do Instituto Oswaldo Cruz, 2015, 110, 662-668.	1.6	16
102	Corynebacterium pseudodiphtheriticum: Putative probiotic, opportunistic infector, emerging pathogen. Virulence, 2015, 6, 673-674.	4.4	16
103	Characterisation of Roseomonas mucosa isolated from the root canal of an infected tooth. BMC Research Notes, 2017, 10, 212.	1.4	16
104	The low-molecular-mass subunit of the cell wall channel of the Gram-positive Corynebacterium glutamicum . Immunological localization, cloning and sequencing of its gene porA. FEBS Journal, 2001, 268, 462-469.	0.2	16
105	Functional characterization of the collagen-binding protein DIP2093 and its influence on hostâ€“pathogen interaction and arthritogenic potential of Corynebacterium diphtheriae. Microbiology (United Kingdom), 2017, 163, 692-701.	1.8	16
106	Analysis of Corynebacterium diphtheriae macrophage interaction: Dispensability of corynomycolic acids for inhibition of phagolysosome maturation and identification of a new gene involved in synthesis of the corynomycolic acid layer. PLoS ONE, 2017, 12, e0180105.	2.5	16
107	The killing of macrophages byCorynebacterium ulcerans. Virulence, 2016, 7, 45-55.	4.4	15
108	Electrochemical Disinfection of Experimentally Infected Teeth by Boron-Doped Diamond Electrode Treatment. Journal of Clinical Medicine, 2019, 8, 2037.	2.4	15

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109	Glutamate excretion inEscherichia coli: dependency on thereIA andspoT genotype. Archives of Microbiology, 1995, 164, 24-28.	2.2	14
110	The low-molecular-mass subunit of the cell wall channel of the Gram-positive Corynebacterium glutamicum. FEBS Journal, 2001, 268, 462-469.	0.2	14
111	DNA binding by Corynebacterium glutamicum TetR-type transcription regulator AmtR. BMC Molecular Biology, 2009, 10, 73.	3.0	14
112	Electrochemical Disinfection of Dental Implants Experimentally Contaminated with Microorganisms as a Model for Periimplantitis. Journal of Clinical Medicine, 2020, 9, 475.	2.4	14
113	Pathogenic properties of a Corynebacterium diphtheriae strain isolated from a case of osteomyelitis. Journal of Medical Microbiology, 2016, 65, 1311-1321.	1.8	14
114	Results of WICOVIR Gargle Pool PCR Testing in German Schools Based on the First 100,000 Tests. Frontiers in Pediatrics, 2021, 9, 721518.	1.9	14
115	Using Colistin as a Trojan Horse: Inactivation of Gram-Negative Bacteria with Chlorophyllin. Antibiotics, 2019, 8, 158.	3.7	13
116	Phylogenomic characterisation of a novel corynebacterial species pathogenic to animals. Antonie Van Leeuwenhoek, 2020, 113, 1225-1239.	1.7	13
117	Characterization of a secondary uptake system for l-glutamate inCorynebacterium glutamicum. FEMS Microbiology Letters, 1996, 136, 169-173.	1.8	12
118	Detection of Fluorescence Dye-Labeled Proteins in 2-D Gels Using an Arthurâ„¢ 1442 Multiwavelength Fluoroimager. BioTechniques, 2001, 31, 146-149.	1.8	12
119	Colonization of human epithelial cell lines by Corynebacterium ulcerans from human and animal sources. Microbiology (United Kingdom), 2015, 161, 1582-1591.	1.8	12
120	Beyond diphtheria toxin: cytotoxic proteins of Corynebacterium ulcerans and Corynebacterium diphtheriae. Microbiology (United Kingdom), 2019, 165, 876-890.	1.8	12
121	Nitrogen assimilation inCorynebacterium diphtheriae: pathways and regulatory cascades. FEMS Microbiology Letters, 2002, 208, 287-293.	1.8	11
122	Impact of adenylyltransferase GlnE on nitrogen starvation response in Corynebacterium glutamicum. Journal of Biotechnology, 2010, 145, 244-252.	3.8	11
123	Induction of the NFÎº-B signal transduction pathway in response to Corynebacterium diphtheriae infection. Microbiology (United Kingdom), 2013, 159, 126-135.	1.8	11
124	Elimination of bacterial contaminations by treatment of water with boron-doped diamond electrodes. World Journal of Microbiology and Biotechnology, 2019, 35, 48.	3.6	11
125	Influence of In-Situ Electrochemical Oxidation on Implant Surface and Colonizing Microorganisms Evaluated by Scanning Electron Microscopy. Materials, 2019, 12, 3977.	2.9	11
126	Complementation of Escherichia coli uncD mutant strains by a chimeric F1-Î² subunit constructed from E. coli and spinach chloroplast F1-Î². Biochimica Et Biophysica Acta - Bioenergetics, 1994, 1186, 243-246.	1.0	10

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127	Analysis of threonine uptake in Escherichia coli threonine production strains. Biotechnology Letters, 2001, 23, 401-404.	2.2	10
128	A Glucose Kinase from <i>Mycobacterium smegmatis</i>. Journal of Molecular Microbiology and Biotechnology, 2007, 12, 75-81.	1.0	10
129	Newly Isolated Animal Pathogen Corynebacterium silvaticum Is Cytotoxic to Human Epithelial Cells. International Journal of Molecular Sciences, 2021, 22, 3549.	4.1	10
130	Diphtheria and its Etiological Agents. , 2014, , 1-14.		10
131	A Proteomic Study of Clavibacter Michiganensis Subsp. Michiganensis Culture Supernatants. Proteomes, 2015, 3, 411-423.	3.5	9
132	The C-terminal coiled-coil domain of Corynebacterium diphtheriae DIP0733 is crucial for interaction with epithelial cells and pathogenicity in invertebrate animal model systems. BMC Microbiology, 2018, 18, 106.	3.3	9
133	Of mice and men: Interaction of Corynebacterium diphtheriae strains with murine and human phagocytes. Virulence, 2019, 10, 414-428.	4.4	9
134	Tellurite resistance: a putative pitfall in Corynebacterium diphtheriae diagnosis?. Antonie Van Leeuwenhoek, 2015, 108, 1275-1279.	1.7	8
135	Pilot Study on the Use of a Laser-Structured Double Diamond Electrode (DDE) for Biofilm Removal from Dental Implant Surfaces. Journal of Clinical Medicine, 2020, 9, 3036.	2.4	8
136	Cellular and Extracellular Proteome of the Animal Pathogen Corynebacterium silvaticum, a Close Relative of Zoonotic Corynebacterium ulcerans and Corynebacterium pseudotuberculosis. Proteomes, 2020, 8, 19.	3.5	8
137	Identification of a Glucose Permease from <i>Mycobacterium smegmatis</i> mc² 155. Journal of Molecular Microbiology and Biotechnology, 2009, 16, 169-175.	1.0	7
138	Crystallization and preliminary crystallographic analysis of the global nitrogen regulator AmtR fromCorynebacterium glutamicum. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1123-1127.	0.7	7
139	Toxigenic Corynebacteria: Adhesion, Invasion and Host Response. , 2014, , 143-170.		7
140	Reactive receiver modeling for diffusive molecular communication systems with molecule degradation. , 2016, , .		7
141	Detection and virulence potential of a phospholipase D-negative Corynebacterium ulcerans from a concurrent diphtheria and infectious mononucleosis case. Antonie Van Leeuwenhoek, 2019, 112, 1055-1065.	1.7	7
142	Interactions between the Re-Emerging Pathogen Corynebacterium diphtheriae and Host Cells. International Journal of Molecular Sciences, 2022, 23, 3298.	4.1	7
143	Expression of subunitIIIot the ATP synthase from spinach chloroplasts inEscherichia coli. FEBS Letters, 1990, 271, 227-230.	2.8	6
144	Hybrid Fo Complexes of the ATP Synthases of Spinach Chloroplasts and Escherichia coli. Immunoprecipitation and Mutant Analyses. FEBS Journal, 1994, 225, 1221-1228.	0.2	6

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145	Rapid detection of bacterial surface proteins using an enzyme-linked immunosorbent assay system. Journal of Proteomics, 1997, 34, 69-71.	2.4	6
146	Induction of Necrosis in Human Macrophage Cell Lines by Corynebacterium diphtheriae and Corynebacterium ulcerans Strains Isolated from Fatal Cases of Systemic Infections. International Journal of Molecular Sciences, 2019, 20, 4109.	4.1	6
147	Genome-wide transcriptome analysis of Clavibacter michiganensis subsp. michiganensis grown in xylem mimicking medium. Journal of Biotechnology, 2013, 168, 348-354.	3.8	5
148	Ion pump based bio-synthetic modulator model for diffusive molecular communications. , 2016, , .		5
149	Glutamine metabolism ofCorynebacterium glutamicum: role of the glutaminase GlsK. FEMS Microbiology Letters, 2016, 363, fnw230.	1.8	5
150	Genome sequence of a pathogenic Corynebacterium ulcerans strain isolated from a wild boar with necrotizing lymphadenitis. BMC Research Notes, 2019, 12, 692.	1.4	5
151	Insights into old and new foes: Pan-genomics of Corynebacterium diphtheriae and Corynebacterium ulcerans. , 2020, , 81-100.		5
152	Lack of evidence for the necessity of root canal obturation. Quintessence International, 2019, 50, 22-28.	0.4	5
153	Proteomics of Corynebacterium glutamicum: essential industrial bacterium. Methods of Biochemical Analysis, 2006, 49, 137-47.	0.2	5
154	Proteomics of Bordetella pertussis whole-cell and acellular vaccines. BMC Research Notes, 2019, 12, 329.	1.4	4
155	Crystal structures of adenylylated and unadenylylated P_{II}protein GlnK fromCorynebacterium glutamicum. Acta Crystallographica Section D: Structural Biology, 2021, 77, 325-335.	2.3	4
156	How to Implement Safe, Efficient and Cost-Effective SARS-CoV-2 Testing in Urban and Rural Schools within One Month. Covid, 2021, 1, 717-727.	1.5	4
157	Complete Closed Genome Sequence of Nontoxigenic Invasive Corynebacterium diphtheriae bv. mitis Strain ISS 3319. Genome Announcements, 2018, 6, .	0.8	3
158	Live cell imaging of macrophage/bacterium interaction demonstrates cell lysis induced by Corynebacterium diphtheriae and Corynebacterium ulcerans. BMC Research Notes, 2019, 12, 695.	1.4	3
159	Pan-omics focused to Crick's central dogma. , 2020, , 1-41.		3
160	Glutamine synthetases of Corynebacterium glutamicum: transcriptional control and regulation of activity. FEMS Microbiology Letters, 2001, 201, 91-98.	1.8	3
161	Preclinical Testing of Boron-Doped Diamond Electrodes for Root Canal Disinfectionâ€"A Series of Preliminary Studies. Microorganisms, 2022, 10, 782.	3.6	3
162	Modeling and simulation of nitrogen regulation in Corynebacterium glutamicum. Discrete Applied Mathematics, 2009, 157, 2232-2243.	0.9	2

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