Christoph G Dehio

List of Publications by Year in descending order

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133 papers 9,053 citations

52 h-index 89 g-index

179 all docs

179 docs citations

179 times ranked

8663 citing authors

#	Article	IF	CITATIONS
1	Adaptive immune defense prevents Bartonella persistence upon trans-placental transmission. PLoS Pathogens, 2022, 18, e1010489.	4.7	4
2	Identification of the <i>Bartonella</i> autotransporter CFA as a protective antigen and hypervariable target of neutralizing antibodies in mice. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	5
3	Bartonella effector protein C mediates actin stress fiber formation via recruitment of GEF-H1 to the plasma membrane. PLoS Pathogens, 2021, 17, e1008548.	4.7	10
4	Structural basis for selective AMPylation of Rac-subfamily GTPases by <i>Bartonella</i> effector protein 1 (Bep1). Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	7
5	Evolutionary Diversification of Host-Targeted Bartonella Effectors Proteins Derived from a Conserved FicTA Toxin-Antitoxin Module. Microorganisms, 2021, 9, 1645.	3.6	5
6	The Impact of Bartonella VirB/VirD4 Type IV Secretion System Effectors on Eukaryotic Host Cells. Frontiers in Microbiology, 2021, 12, 762582.	3.5	5
7	A Bartonella Effector Acts as Signaling Hub for Intrinsic STAT3 Activation to Trigger Anti-inflammatory Responses. Cell Host and Microbe, 2020, 27, 476-485.e7.	11.0	22
8	A Role for the VPS Retromer in $\mbox{\ensuremath{\mbox{\ensuremath{\mbox{\sc reening.}}}}}$ MSphere, 2019, 4, .	2.9	11
9	<i>Bartonella</i> gene transfer agent: Evolution, function, and proposed role in host adaptation. Cellular Microbiology, 2019, 21, e13068.	2.1	21
10	Versatility of the BID Domain: Conserved Function as Type-IV-Secretion-Signal and Secondarily Evolved Effector Functions Within Bartonella-Infected Host Cells. Frontiers in Microbiology, 2019, 10, 921.	3.5	16
11	Quantitative contribution of efflux to multi-drug resistance of clinical Escherichia coli and Pseudomonas aeruginosa strains. EBioMedicine, 2019, 41, 479-487.	6.1	37
12	Definitions and guidelines for research on antibiotic persistence. Nature Reviews Microbiology, 2019, 17, 441-448.	28.6	748
13	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. Nature Biotechnology, 2019, 37, 314-322.	17.5	254
14	PyBDA: a command line tool for automated analysis of big biological data sets. BMC Bioinformatics, 2019, 20, 564.	2.6	3
15	Role of distinct typeâ€IVâ€secretion systems and secreted effector sets in host adaptation by pathogenic <i>Bartonella</i> species. Cellular Microbiology, 2019, 21, e13004.	2.1	37
16	3D correlative electron microscopy reveals continuity of $\langle i \rangle$ Brucella $\langle i \rangle$ -containing vacuoles with the endoplasmic reticulum. Journal of Cell Science, 2018, 131, .	2.0	40
17	Mitochondrial fragmentation affects neither the sensitivity to TNFα-induced apoptosis of Brucella-infected cells nor the intracellular replication of the bacteria. Scientific Reports, 2018, 8, 5173.	3.3	17
18	Growth-restricting effects of siRNA transfections: a largely deterministic combination of off-target binding and hybridization-independent competition. Nucleic Acids Research, 2018, 46, 9309-9320.	14.5	7

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19	Improved pathway reconstruction from RNA interference screens by exploiting off-target effects. Bioinformatics, 2018, 34, i519-i527.	4.1	8
20	The Conjugative Relaxase TrwC Promotes Integration of Foreign DNA in the Human Genome. Applied and Environmental Microbiology, 2017, 83, .	3.1	9
21	Gene Transfer Agent Promotes Evolvability within the Fittest Subpopulation of a Bacterial Pathogen. Cell Systems, 2017, 4, 611-621.e6.	6.2	47
22	Explicit Modeling of siRNA-Dependent On- and Off-Target Repression Improves the Interpretation of Screening Results. Cell Systems, 2017, 4, 182-193.e4.	6.2	22
23	Systems-level interference strategies to decipher host factors involved in bacterial pathogen interaction: from RNAi to CRISPRi. Current Opinion in Microbiology, 2017, 39, 34-41.	5.1	10
24	Editorial overview: Bacterial systems biology. Current Opinion in Microbiology, 2017, 39, viii-xi.	5.1	1
25	An integrative strategy to identify the entire protein coding potential of prokaryotic genomes by proteogenomics. Genome Research, 2017, 27, 2083-2095.	5.5	112
26	The BID Domain of Type IV Secretion Substrates Forms a Conserved Four-Helix Bundle Topped with a Hook. Structure, 2017, 25, 203-211.	3.3	15
27	Evolutionary Dynamics of Pathoadaptation Revealed by Three Independent Acquisitions of the VirB/D4 Type IV Secretion System in Bartonella. Genome Biology and Evolution, 2017, 9, 761-776.	2.5	50
28	Type IV Effector Secretion and Subversion of Host Functions by Bartonella and Brucella Species. Current Topics in Microbiology and Immunology, 2017, 413, 269-295.	1.1	20
29	A bacterial toxin-antitoxin module is the origin of inter-bacterial and inter-kingdom effectors of Bartonella. PLoS Genetics, 2017, 13, e1007077.	3.5	55
30	Crystal Structure of the Escherichia coli Fic Toxin-Like Protein in Complex with Its Cognate Antitoxin. PLoS ONE, 2016, 11, e0163654.	2.5	6
31	Biological Diversity and Molecular Plasticity of FIC Domain Proteins. Annual Review of Microbiology, 2016, 70, 341-360.	7.3	37
32	Microscopy-based Assays for High-throughput Screening of Host Factors Involved in Brucella Infection of Hela Cells. Journal of Visualized Experiments, 2016, , .	0.3	6
33	Intrinsic regulation of FIC-domain AMP-transferases by oligomerization and automodification. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E529-37.	7.1	27
34	A Genome-Wide siRNA Screen Implicates Spire 1/2 in SipA-Driven Salmonella Typhimurium Host Cell Invasion. PLoS ONE, 2016, 11, e0161965.	2.5	16
35	gespeR: a statistical model for deconvoluting off-target-confounded RNA interference screens. Genome Biology, 2015, 16, 220.	8.8	35
36	Genome-Wide siRNA Screen Identifies Complementary Signaling Pathways Involved in <i>Listeria</i> Infection and Reveals Different Actin Nucleation Mechanisms during <i>Listeria</i> Cell Invasion and Actin Comet Tail Formation. MBio, 2015, 6, e00598-15.	4.1	61

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37	NEMix: Single-cell Nested Effects Models for Probabilistic Pathway Stimulation. PLoS Computational Biology, 2015, 11, e1004078.	3.2	17
38	Adenylylation of Gyrase and Topo IV by FicT Toxins Disrupts Bacterial DNA Topology. Cell Reports, 2015, 12, 1497-1507.	6.4	92
39	Autophagy Proteins Promote Repair of Endosomal Membranes Damaged by the Salmonella Type Three Secretion System 1. Cell Host and Microbe, 2015, 18, 527-537.	11.0	116
40	New insights into the role of Bartonella effector proteins in pathogenesis. Current Opinion in Microbiology, 2015, 23, 80-85.	5.1	53
41	Structure of the N-Terminal Gyrase B Fragment in Complex with ADPâ«Pi Reveals Rigid-Body Motion Induced by ATP Hydrolysis. PLoS ONE, 2014, 9, e107289.	2.5	46
42	A Translocated Effector Required for Bartonella Dissemination from Derma to Blood Safeguards Migratory Host Cells from Damage by Co-translocated Effectors. PLoS Pathogens, 2014, 10, e1004187.	4.7	29
43	Simultaneous analysis of large-scale RNAi screens for pathogen entry. BMC Genomics, 2014, 15, 1162.	2.8	38
44	Specific inhibition of diverse pathogens in human cells by synthetic microRNA-like oligonucleotides inferred from RNAi screens. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4548-4553.	7.1	60
45	Proteome-wide identification of predominant subcellular protein localizations in a bacterial model organism. Journal of Proteomics, 2014, 99, 123-137.	2.4	55
46	An experimental strategy for the identification of <scp>AMP</scp> ylation targets from complex protein samples. Proteomics, 2014, 14, 1048-1052.	2.2	26
47	Multi-scale Gaussian representation and outline-learning based cell image segmentation. BMC Bioinformatics, 2013, 14, S6.	2.6	5
48	Dual input control: activation of the <i><scp>B</scp>artonella henselae</i> â€ <scp>VirB</scp> / <scp>D</scp> 4 type <scp>IV</scp> secretion system by the stringent sigma factor <scp>RpoH</scp> 1 and the <scp>BatR</scp> / <scp>BatS</scp> twoâ€component system. Molecular Microbiology, 2013, 90, 756-775.	2.5	17
49	Systems-level analysis of host–pathogen interaction using RNA interference. New Biotechnology, 2013, 30, 308-313.	4.4	O
50	<i>Bartonella henselae</i> trimeric autotransporter adhesin BadA expression interferes with effector translocation by the VirB/D4 type IV secretion system. Cellular Microbiology, 2013, 15, 759-778.	2.1	43
51	Partial Disruption of Translational and Posttranslational Machinery Reshapes Growth Rates of Bartonella birtlesii. MBio, 2013, 4, e00115-13.	4.1	8
52	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. Genome Research, 2013, 23, 1916-1927.	5 . 5	91
53	Imaging InIC Secretion to Investigate Cellular Infection by the Bacterial Pathogen Listeria monocytogenes . Journal of Visualized Experiments, 2013, , e51043.	0.3	6
54	A Translocation Motif in Relaxase TrwC Specifically Affects Recruitment by Its Conjugative Type IV Secretion System. Journal of Bacteriology, 2013, 195, 4999-5006.	2.2	36

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55	Bartonella and Brucella-Weapons and Strategies for Stealth Attack. Cold Spring Harbor Perspectives in Medicine, 2013, 3, a010231-a010231.	6.2	34
56	Graph cut and image intensity-based splitting improves nuclei segmentation in high-content screening, , 2013, , .		0
57	Conserved Inhibitory Mechanism and Competent ATP Binding Mode for Adenylyltransferases with Fic Fold. PLoS ONE, 2013, 8, e64901.	2.5	32
58	Manipulation of host cell signaling by bacterial FIC proteins. FASEB Journal, 2013, 27, 554.3.	0.5	1
59	Intruders below the Radar: Molecular Pathogenesis of Bartonella spp. Clinical Microbiology Reviews, 2012, 25, 42-78.	13.6	210
60	Bacterial effector binds host cell adenylyl cyclase to potentiate Gαs-dependent cAMP production. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9581-9586.	7.1	35
61	New perspectives into bacterial DNA transfer to human cells. Trends in Microbiology, 2012, 20, 355-359.	7.7	33
62	Persistent intracellular pathogens. FEMS Microbiology Reviews, 2012, 36, 513-513.	8.6	9
63	Adenylylation control by intra- or intermolecular active-site obstruction in Fic proteins. Nature, 2012, 482, 107-110.	27.8	149
64	Persistence of <i>Bartonella </i> spp. stealth pathogens: from subclinical infections to vasoproliferative tumor formation. FEMS Microbiology Reviews, 2012, 36, 563-599.	8.6	85
65	<i><scp>B</scp>artonella</i> entry mechanisms into mammalian host cells. Cellular Microbiology, 2012, 14, 1166-1173.	2.1	66
66	Bartonelloses. , 2011, , 265-270.		2
67	<i>Bartonella henselae</i> engages inside-out and outside-in signaling by integrin \hat{l}^21 and talin1 during invasome-mediated bacterial uptake. Journal of Cell Science, 2011, 124, 3591-3602.	2.0	22
68	Combined action of the type IV secretion effector proteins BepC and BepF promotes invasome formation of Bartonella henselae on endothelial and epithelial cells. Cellular Microbiology, 2011, 13, 284-299.	2.1	48
69	The Bartonella henselae VirB/Bep system interferes with vascular endothelial growth factor (VEGF) signalling in human vascular endothelial cells. Cellular Microbiology, 2011, 13, 419-431.	2.1	11
70	Fic domainâ€eatalyzed adenylylation: Insight provided by the structural analysis of the type IV secretion system effector BepA. Protein Science, 2011, 20, 492-499.	7.6	50
71	Transfer of R388 Derivatives by a Pathogenesis-Associated Type IV Secretion System into both Bacteria and Human Cells. Journal of Bacteriology, 2011, 193, 6257-6265.	2.2	35
72	Conjugative DNA transfer into human cells by the VirB/VirD4 type IV secretion system of the bacterial pathogen <i>Bartonella henselae</i> Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14643-14648.	7.1	79

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73	Parallel Evolution of a Type IV Secretion System in Radiating Lineages of the Host-Restricted Bacterial Pathogen Bartonella. PLoS Genetics, 2011, 7, e1001296.	3.5	92
74	BID-F1 and BID-F2 Domains of Bartonella henselae Effector Protein BepF Trigger Together with BepC the Formation of Invasome Structures. PLoS ONE, 2011, 6, e25106.	2.5	19
75	Functional Dissection of the Conjugative Coupling Protein TrwB. Journal of Bacteriology, 2010, 192, 2655-2669.	2.2	47
76	The BatR/BatS Two-Component Regulatory System Controls the Adaptive Response of i>Bartonella henselae i>during Human Endothelial Cell Infection. Journal of Bacteriology, 2010, 192, 3352-3367.	2.2	57
77	The Trw Type IV Secretion System of Bartonella Mediates Host-Specific Adhesion to Erythrocytes. PLoS Pathogens, 2010, 6, e1000946.	4.7	98
78	Bacterial type IV secretion systems in human disease. Molecular Microbiology, 2009, 73, 141-151.	2.5	58
79	A translocated protein of <i>Bartonella henselae</i> interferes with endocytic uptake of individual bacteria and triggers uptake of large bacterial aggregates via the invasome. Cellular Microbiology, 2009, 11, 927-945.	2.1	53
80	Bartonella henselae: Subversion of vascular endothelial cell functions by translocated bacterial effector proteins. International Journal of Biochemistry and Cell Biology, 2009, 41, 507-510.	2.8	28
81	Host Cell Interactome of Tyrosine-Phosphorylated Bacterial Proteins. Cell Host and Microbe, 2009, 5, 397-403.	11.0	175
82	Ecological fitness and strategies of adaptation of <i>Bartonella </i> Veterinary Research, 2009, 40, 29.	3.0	213
83	Infection-associated type IV secretion systems of (i>Bartonella (i>and their diverse roles in host cell interaction. Cellular Microbiology, 2008, 10, 1591-1598.	2.1	86
84	Genomic analysis of Bartonella identifies type IV secretion systems as host adaptability factors. Nature Genetics, 2007, 39, 1469-1476.	21.4	120
85	A Translocated Bacterial Protein Protects Vascular Endothelial Cells from Apoptosis. PLoS Pathogens, 2006, 2, e115.	4.7	112
86	Characterization of Genes Involved in Long-Term Bacteremia in Mice by Bartonella birtlesii. Annals of the New York Academy of Sciences, 2005, 1063, 312-314.	3.8	10
87	Characterization of the Genome Composition of Bartonella koehlerae by Microarray Comparative Genomic Hybridization Profiling. Journal of Bacteriology, 2005, 187, 6155-6165.	2.2	32
88	A bipartite signal mediates the transfer of type IV secretion substrates of Bartonella henselae into human cells. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 856-861.	7.1	205
89	Signature-tagged mutagenesis: technical advances in a negative selection method for virulence gene identification. Current Opinion in Microbiology, 2005, 8, 612-619.	5.1	65
90	VEGF-A and PIGF-1 stimulate chemotactic migration of human mesenchymal progenitor cells. Biochemical and Biophysical Research Communications, 2005, 334, 561-568.	2.1	176

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91	Virulence-associated type IV secretion systems of Bartonella. Trends in Microbiology, 2005, 13, 336-342.	7.7	34
92	Bartonella–host-cell interactions and vascular tumour formation. Nature Reviews Microbiology, 2005, 3, 621-631.	28.6	144
93	Functional interactions between type IV secretion systems involved in DNA transfer and virulence. Microbiology (United Kingdom), 2005, 151, 3505-3516.	1.8	46
94	Isolation of Bartonella schoenbuchensis from Lipoptena cervi , a Blood-Sucking Arthropod Causing Deer Ked Dermatitis. Journal of Clinical Microbiology, 2004, 42, 5320-5323.	3.9	125
95	Structure and Biological Activity of the Short-chain Lipopolysaccharide from Bartonella henselae ATCC 49882T. Journal of Biological Chemistry, 2004, 279, 21046-21054.	3.4	76
96	Coordinated activation of VEGFR-1 and VEGFR-2 is a potent arteriogenic stimulus leading to enhancement of regional perfusion. Cardiovascular Research, 2004, 61, 789-795.	3.8	53
97	Genome-wide analysis of transcriptional hierarchy and feedback regulation in the flagellar system of Helicobacter pylori. Molecular Microbiology, 2004, 52, 947-961.	2.5	165
98	The VirB type IV secretion system of <i>Bartonella henselae</i> mediates invasion, proinflammatory activation and antiapoptotic protection of endothelial cells. Molecular Microbiology, 2004, 52, 81-92.	2.5	152
99	Proteomic analysis of the sarcosine-insoluble outer membrane fraction of the bacterial pathogenBartonella henselae. Proteomics, 2004, 4, 3021-3033.	2.2	47
100	Molecular and Cellular Basis of Bartonella Pathogenesis. Annual Review of Microbiology, 2004, 58, 365-390.	7.3	183
101	An Engineered Heparin-Binding Form of VEGF-E (hbVEGF-E). Biological effects in vitro and mobilizatiion of precursor cells. Angiogenesis, 2003, 6, 201-211.	7.2	17
102	Characterization of the cryptic plasmid pBGR1 from Bartonella grahamii and construction of a versatile Escherichia coli–Bartonella spp. shuttle cloning vector. Plasmid, 2003, 49, 44-52.	1.4	19
103	A bacterial conjugation machinery recruited for pathogenesis. Molecular Microbiology, 2003, 49, 1253-1266.	2.5	112
104	Role of PIGF in the intra- and intermolecular cross talk between the VEGF receptors Flt1 and Flk1. Nature Medicine, 2003, 9, 936-943.	30.7	699
105	Recent progress in understanding Bartonella-induced vascular proliferation. Current Opinion in Microbiology, 2003, 6, 61-65.	5.1	82
106	Bartonella bovis Bermond et al. sp. nov. and Bartonella capreoli sp. nov., isolated from European ruminants International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 383-390.	1.7	101
107	The VirB/VirD4 type IV secretion system of <i>Bartonella</i> is essential for establishing intraerythrocytic infection. Molecular Microbiology, 2002, 46, 1053-1067.	2.5	132
108	Bacterial persistence within erythrocytes: A unique pathogenic strategy of Bartonella spp International Journal of Medical Microbiology, 2001, 291, 555-560.	3.6	57

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109	Bartonella interactions with endothelial cells and erythrocytes. Trends in Microbiology, 2001, 9, 279-285.	7.7	143
110	The interactions of Bartonella with endothelial cells and erythrocytes. Trends in Microbiology, 2001, 9, 531-532.	7.7	1
111	Bartonella henselae Induces NF-κB-Dependent Upregulation of Adhesion Molecules in Cultured Human Endothelial Cells: Possible Role of Outer Membrane Proteins as Pathogenic Factors. Infection and Immunity, 2001, 69, 5088-5097.	2.2	71
112	Cutting Edge: Antibody-Mediated Cessation of Hemotropic Infection by the Intraerythrocytic Mouse Pathogen <i>Bartonella grahamii</i> Iournal of Immunology, 2001, 167, 11-14.	0.8	66
113	Invasion and Persistent Intracellular Colonization of Erythrocytes. Journal of Experimental Medicine, 2001, 193, 1077-1086.	8.5	152
114	Neisseria., 2001,, 559-618.		3
115	Syndecan-1 and syndecan-4 can mediate the invasion of OpaHSPG-expressing Neisseria gonorrhoeae into epithelial cells. Cellular Microbiology, 2000, 2, 69-82.	2.1	92
116	Carcinoembryonic Antigen Family Receptor Specificity of Neisseria meningitidis Opa Variants Influences Adherence to and Invasion of Proinflammatory Cytokine-Activated Endothelial Cells. Infection and Immunity, 2000, 68, 3601-3607.	2.2	97
117	Rickettsia prowazekii and Bartonella henselae: Differences in the intracellular life styles revisited. International Journal of Medical Microbiology, 2000, 290, 135-141.	3.6	14
118	Host Cell Invasion by Pathogenic Neisseriae. Sub-Cellular Biochemistry, 2000, 33, 61-96.	2.4	42
119	Characterization of <i>Bartonella clarridgeiae</i> Flagellin (FlaA) and Detection of Antiflagellin Antibodies in Patients with Lymphadenopathy. Journal of Clinical Microbiology, 2000, 38, 2943-2948.	3.9	43
120	Bartonella alsatica sp. nov., a new Bartonella species isolated from the blood of wild rabbits. International Journal of Systematic and Evolutionary Microbiology, 1999, 49, 283-288.	1.7	79
121	Molecular analysis of neisserial Opa protein interactions with the CEA family of receptors: identification of determinants contributing to the differential specificities of binding. Cellular Microbiology, 1999, 1, 169-181.	2.1	62
122	Interactions of Bartonella henselae with vascular endothelial cells. Current Opinion in Microbiology, 1999, 2, 78-82.	5.1	40
123	Parapoxviruses: potential alternative vectors for directing the immune response in permissive and non-permissive hosts. Journal of Biotechnology, 1999, 73, 235-242.	3.8	32
124	Opa binding to cellular CD66 receptors mediates the transcellular traversal of Neisseria gonorrhoeae across polarized T84 epithelial cell monolayers. Molecular Microbiology, 1998, 30, 657-671.	2.5	106
125	Construction of versatile high-level expression vectors for Bartonella henselae and the use of green fluorescent protein as a new expression marker. Gene, 1998, 215, 223-229.	2.2	68
126	Vitronectin-dependent invasion of epithelial cells byNeisseria gonorrhoeaeinvolves αvintegrin receptors. FEBS Letters, 1998, 424, 84-88.	2.8	90

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127	Ligation of Cell Surface Heparan Sulfate Proteoglycans by Antibody-Coated Beads Stimulates Phagocytic Uptake into Epithelial Cells: A Model for Cellular Invasion byNeisseria gonorrhoeae. Experimental Cell Research, 1998, 242, 528-539.	2.6	51
128	Differential Opa specificities for CD66 receptors influence tissue interactions and cellular response to Neisseria gonorrhoeae. Molecular Microbiology, 1997, 26, 971-980.	2.5	146
129	Stable expression of a single-copy rolA gene in transgenic Arabidopsis thaliana plants allows an exhaustive mutagenic analysis of the transgene-associated phenotype. Molecular Genetics and Genomics, 1993, 241-241, 359-366.	2.4	22
130	Phenotype and hormonal status of transgenic tobacco plants overexpressing the rolA gene of Agrobacterium rhizogenes T-DNA. Plant Molecular Biology, 1993, 23, 1199-1210.	3.9	76
131	The early nodulin gene SrEnod2 from Sesbania rostrata is inducible by cytokinin Plant Journal, 1992, 2, 117-128.	5.7	93
132	Proteomic analysis of the sarcosine-insoluble outer membrane fraction of the bacterial pathogenBartonella henselae., 0,, 203-224.		0
133	Bartonella taylorii: A Model Organism for Studying Bartonella Infection in vitro and in vivo. Frontiers in Microbiology, 0, 13, .	3.5	1