Celeste J Brown

List of Publications by Year in descending order

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64 papers

13,417 citations

39 h-index 64 g-index

64 all docs

64
docs citations

64 times ranked 13637 citing authors

#	Article	IF	CITATIONS
1	Current practices in nutrition management and disease incidence of common marmosets (<i>Callithrix jacchus</i>). Journal of Medical Primatology, 2021, 50, 164-175.	0.6	8
2	Vision using multiple distinct rod opsins in deep-sea fishes. Science, 2019, 364, 588-592.	12.6	151
3	Comparative genomics of Bifidobacterium species isolated from marmosets and humans. American Journal of Primatology, 2019, 81, e983.	1.7	12
4	Genetic diversity of potato virus Y (PVY): sequence analyses reveal ten novel PVY recombinant structures. Archives of Virology, 2018, 163, 23-32.	2.1	47
5	Predicting peak spectral sensitivities of vertebrate cone visual pigments using atomistic molecular simulations. PLoS Computational Biology, 2018, 14, e1005974.	3.2	15
6	Annotation of plasmid genes. Plasmid, 2017, 91, 61-67.	1.4	63
7	Characterization of Four Multidrug Resistance Plasmids Captured from the Sediments of an Urban Coastal Wetland. Frontiers in Microbiology, 2017, 8, 1922.	3.5	33
8	The development of a specific pathogen free (SPF) barrier colony of marmosets (Callithrix jacchus) for aging research. Aging, 2017, 9, 2544-2558.	3.1	33
9	Effects of low dose estrogen therapy on the vaginal microbiomes of women with atrophic vaginitis. Scientific Reports, 2016, 6, 24380.	3.3	119
10	High Diversity of CTX-M Extended-Spectrum \hat{I}^2 -Lactamases in Municipal Wastewater and Urban Wetlands. Microbial Drug Resistance, 2016, 22, 312-320.	2.0	11
11	New Perspectives on Ebola Virus Evolution. PLoS ONE, 2016, 11, e0160410.	2.5	6
12	Initiating a watch list for Ebola virus antibody escape mutations. PeerJ, 2016, 4, e1674.	2.0	36
13	Fine-scale analysis of 16S rRNA sequences reveals a high level of taxonomic diversity among vaginal Atopobium spp Pathogens and Disease, 2015, 73, .	2.0	16
14	The Impact of Spatial Structure on Viral Genomic Diversity Generated during Adaptation to Thermal Stress. PLoS ONE, 2014, 9, e88702.	2.5	6
15	Adaptive regulatory substitutions affect multiple stages in the life cycle of the bacteriophage i-X174. BMC Evolutionary Biology, 2013, 13, 66.	3.2	9
16	Diverse Broad-Host-Range Plasmids from Freshwater Carry Few Accessory Genes. Applied and Environmental Microbiology, 2013, 79, 7684-7695.	3.1	64
17	Intrinsically disordered regions of p53 family are highly diversified in evolution. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 725-738.	2.3	68
18	Comparative genomics of IncP-1 $\hat{l}\mu$ plasmids from water environments reveals diverse and unique accessory genetic elements. Plasmid, 2013, 70, 412-419.	1.4	12

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19	Inferring the Evolutionary History of IncP-1 Plasmids Despite Incongruence among Backbone Gene Trees. Molecular Biology and Evolution, 2013, 30, 154-166.	8.9	63
20	Selection Affects Genes Involved in Replication during Long-Term Evolution in Experimental Populations of the Bacteriophage ݆X174. PLoS ONE, 2013, 8, e60401.	2.5	10
21	HCMV-Infected Cells Maintain Efficient Nucleotide Excision Repair of the Viral Genome while Abrogating Repair of the Host Genome. PLoS Pathogens, 2012, 8, e1003038.	4.7	24
22	Differential Transcription of Bacteriophage φX174 Genes at 37°C and 42°C. PLoS ONE, 2012, 7, e35909.	2.5	6
23	The complete genome sequences of four new IncN plasmids from wastewater treatment plant effluent provide new insights into IncN plasmid diversity and evolution. Plasmid, 2012, 68, 13-24.	1.4	65
24	Genetic Diversity of the Ordinary Strain of <i>Potato virus Y</i> (PVY) and Origin of Recombinant PVY Strains. Phytopathology, 2011, 101, 778-785.	2.2	100
25	Evolution and disorder. Current Opinion in Structural Biology, 2011, 21, 441-446.	5.7	243
26	Broad-Host-Range Plasmids from Agricultural Soils Have IncP-1 Backbones with Diverse Accessory Genes. Applied and Environmental Microbiology, 2011, 77, 7975-7983.	3.1	96
27	Comparative genomics of pAKD4, the prototype IncP-1δ plasmid with a complete backbone. Plasmid, 2010, 63, 98-107.	1.4	20
28	Positive selection at high temperature reduces gene transcription in the bacteriophage i-X174. BMC Evolutionary Biology, 2010, 10, 378.	3.2	13
29	The vaginal bacterial communities of Japanese women resemble those of women in other racial groups. FEMS Immunology and Medical Microbiology, 2010, 58, 169-181.	2.7	176
30	Predicting Plasmid Promiscuity Based on Genomic Signature. Journal of Bacteriology, 2010, 192, 6045-6055.	2.2	162
31	Experimental evolution of viruses: Microviridae as a model system. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 2495-2501.	4.0	53
32	Comparing Models of Evolution for Ordered and Disordered Proteins. Molecular Biology and Evolution, 2010, 27, 609-621.	8.9	165
33	Computational Study of Evolutionary Selection Pressure on Rainbow Trout Estrogen Receptors. PLoS ONE, 2010, 5, e9392.	2.5	4
34	Sequence characteristics of potato virus Y recombinants. Journal of General Virology, 2009, 90, 3033-3041.	2.9	57
35	Plasmids captured in C. metallidurans CH34: defining the PromA family of broad-host-range plasmids. Antonie Van Leeuwenhoek, 2009, 96, 193-204.	1.7	67
36	Plasticity of the Hsp90 chaperone machine in divergent eukaryotic organisms. Cell Stress and Chaperones, 2009, 14, 83-94.	2.9	111

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37	Loss of LINE-1 Activity in the Megabats. Genetics, 2008, 178, 393-404.	2.9	70
38	Comparison of Correspondence Analysis Methods for Synonymous Codon Usage in Bacteria. DNA Research, 2008, 15, 357-365.	3.4	71
39	Using Mahalanobis distance to compare genomic signatures between bacterial plasmids and chromosomes. Nucleic Acids Research, 2008, 36, e147-e147.	14.5	58
40	TOP-IDP-Scale: A New Amino Acid Scale Measuring Propensity for Intrinsic Disorder. Protein and Peptide Letters, 2008, 15, 956-963.	0.9	361
41	Preliminary characterization of the normal microbiota of the human vulva using cultivation-independent methods. Journal of Medical Microbiology, 2007, 56, 271-276.	1.8	53
42	Differences in the composition of vaginal microbial communities found in healthy Caucasian and black women. ISME Journal, 2007, $1,121-133$.	9.8	470
43	Dynamic Behavior of an Intrinsically Unstructured Linker Domain Is Conserved in the Face of Negligible Amino Acid Sequence Conservation. Journal of Molecular Evolution, 2007, 65, 277-288.	1.8	84
44	Plasmid Donor Affects Host Range of Promiscuous IncP-1Î ² Plasmid pB10 in an Activated-Sludge Microbial Community. Applied and Environmental Microbiology, 2005, 71, 5309-5317.	3.1	103
45	OPTIMIZING LONG INTRINSIC DISORDER PREDICTORS WITH PROTEIN EVOLUTIONARY INFORMATION. Journal of Bioinformatics and Computational Biology, 2005, 03, 35-60.	0.8	428
46	DisProt: a database of protein disorder. Bioinformatics, 2005, 21, 137-140.	4.1	231
47	Protein flexibility and intrinsic disorder. Protein Science, 2004, 13, 71-80.	7.6	306
48	Molecular microbial ecology: land of the one-eyed king. Current Opinion in Microbiology, 2004, 7, 210-220.	5.1	267
49	The importance of intrinsic disorder for protein phosphorylation. Nucleic Acids Research, 2004, 32, 1037-1049.	14.5	1,230
50	Flavors of protein disorder. Proteins: Structure, Function and Bioinformatics, 2003, 52, 573-584.	2.6	340
51	Intrinsic Disorder and Protein Function. Biochemistry, 2002, 41, 6573-6582.	2.5	1,605
52	Identification and functions of usefully disordered proteins. Advances in Protein Chemistry, 2002, 62, 25-49.	4.4	352
53	Intrinsic Disorder in Cell-signaling and Cancer-associated Proteins. Journal of Molecular Biology, 2002, 323, 573-584.	4.2	1,077
54	Evolutionary Rate Heterogeneity in Proteins with Long Disordered Regions. Journal of Molecular Evolution, 2002, 55, 104-110.	1.8	398

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55	Improving sequence alignments for intrinsically disordered proteins. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2002, , 589-600.	0.7	13
56	The Power to Detect Recombination Using the Coalescent. Molecular Biology and Evolution, 2001, 18, 1421-1424.	8.9	31
57	Intrinsically disordered protein. Journal of Molecular Graphics and Modelling, 2001, 19, 26-59.	2.4	2,005
58	Sequence complexity of disordered protein. Proteins: Structure, Function and Bioinformatics, 2001, 42, 38-48.	2.6	1,547
59	Identification of intrinsic order and disorder in the DNA repair protein XPA. Protein Science, 2001, 10, 560-571.	7.6	108
60	Expression of the human ADH2 gene: an unusual Sp1-binding site in the promoter of a gene expressed at high levels in liver. Gene, 1992, 121, 313-320.	2.2	25
61	An Analysis of Density-Dependent Viability Selection. Journal of the American Statistical Association, 1989, 84, 662-668.	3.1	2
62	Genetic Transition between Northern and Southern Populations of the Estuarine Isopod, Cyathura polita, and the Discovery of a New Species of Cyathura. Estuaries and Coasts, 1988, 11, 96.	1.7	6
63	A TEST FOR RARE MALE MATING ADVANTAGE WITH DROSOPHILA PSEUDOOBSCURA KARYOTYPES. Genetics, 1984, 107, 577-589.	2.9	19
64	Genetic Differences among Populations of the Black Turpentine Beetle, Dendroctonus terebrans, and an Engraver Beetle, Ips calligraphus (Coleoptera: Scolytidae). Annals of the Entomological Society of America, 1983, 76, 896-902.	2.5	13