Celeste J Brown

List of Publications by Year
in descending order

64 papers	13,417 citations	81900 39 h-index	110387 64 g-index
64 all docs	64 docs citations	64 times ranked	13637 citing authors

#	Article	IF	Citations
1	Intrinsically disordered protein. Journal of Molecular Graphics and Modelling, 2001, 19, 26-59.	2.4	2,005
2	Intrinsic Disorder and Protein Function. Biochemistry, 2002, 41, 6573-6582.	2.5	1,605
3	Sequence complexity of disordered protein. Proteins: Structure, Function and Bioinformatics, 2001, 42, 38-48.	2.6	1,547
4	The importance of intrinsic disorder for protein phosphorylation. Nucleic Acids Research, 2004, 32, 1037-1049.	14.5	1,230
5	Intrinsic Disorder in Cell-signaling and Cancer-associated Proteins. Journal of Molecular Biology, 2002, 323, 573-584.	4.2	1,077
6	Differences in the composition of vaginal microbial communities found in healthy Caucasian and black women. ISME Journal, 2007, 1, 121-133.	9.8	470
7	OPTIMIZING LONG INTRINSIC DISORDER PREDICTORS WITH PROTEIN EVOLUTIONARY INFORMATION. Journal of Bioinformatics and Computational Biology, 2005, 03, 35-60.	0.8	428
8	Evolutionary Rate Heterogeneity in Proteins with Long Disordered Regions. Journal of Molecular Evolution, 2002, 55, 104-110.	1.8	398
9	TOP-IDP-Scale: A New Amino Acid Scale Measuring Propensity for Intrinsic Disorder. Protein and Peptide Letters, 2008, 15, 956-963.	0.9	361
10	Identification and functions of usefully disordered proteins. Advances in Protein Chemistry, 2002, 62, 25-49.	4.4	352
11	Flavors of protein disorder. Proteins: Structure, Function and Bioinformatics, 2003, 52, 573-584.	2.6	340
12	Protein flexibility and intrinsic disorder. Protein Science, 2004, 13, 71-80.	7.6	306
13	Molecular microbial ecology: land of the one-eyed king. Current Opinion in Microbiology, 2004, 7, 210-220.	5.1	267
14	Evolution and disorder. Current Opinion in Structural Biology, 2011, 21, 441-446.	5.7	243
15	DisProt: a database of protein disorder. Bioinformatics, 2005, 21, 137-140.	4.1	231
16	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
17	Comparing Models of Evolution for Ordered and Disordered Proteins. Molecular Biology and Evolution, 2010, 27, 609-621.	8.9	165
18	Predicting Plasmid Promiscuity Based on Genomic Signature. Journal of Bacteriology, 2010, 192, 6045-6055.	2.2	162

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19	Vision using multiple distinct rod opsins in deep-sea fishes. Science, 2019, 364, 588-592.	12.6	151
20	Effects of low dose estrogen therapy on the vaginal microbiomes of women with atrophic vaginitis. Scientific Reports, 2016, 6, 24380.	3.3	119
21	Plasticity of the Hsp90 chaperone machine in divergent eukaryotic organisms. Cell Stress and Chaperones, 2009, 14, 83-94.	2.9	111
22	Identification of intrinsic order and disorder in the DNA repair protein XPA. Protein Science, 2001, 10, 560-571.	7.6	108
23	Plasmid Donor Affects Host Range of Promiscuous IncP-1Î² Plasmid pB10 in an Activated-Sludge Microbial Community. Applied and Environmental Microbiology, 2005, 71, 5309-5317.	3.1	103
24	Genetic Diversity of the Ordinary Strain of Potato virus Y (PVY) and Origin of Recombinant PVY Strains. Phytopathology, 2011, 101, 778-785.	2.2	100
25	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
26	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
27	Comparison of Correspondence Analysis Methods for Synonymous Codon Usage in Bacteria. DNA Research, 2008, 15, 357-365.	3.4	71
28	Loss of LINE-1 Activity in the Megabats. Genetics, 2008, 178, 393-404.	2.9	70
29	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
30	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
31	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
32	Diverse Broad-Host-Range Plasmids from Freshwater Carry Few Accessory Genes. Applied and Environmental Microbiology, 2013, 79, 7684-7695.	3.1	64
33	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
34	Annotation of plasmid genes. Plasmid, 2017, 91, 61-67.	1.4	63
35	Using Mahalanobis distance to compare genomic signatures between bacterial plasmids and chromosomes. Nucleic Acids Research, 2008, 36, e147-e147.	14.5	58
36	Sequence characteristics of potato virus Y recombinants. Journal of General Virology, 2009, 90, 3033-3041.	2.9	57

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37	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
38	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
39	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
40	Initiating a watch list for Ebola virus antibody escape mutations. PeerJ, 2016, 4, e1674.	2.0	36
41	Characterization of Four Multidrug Resistance Plasmids Captured from the Sediments of an Urban Coastal Wetland. Frontiers in Microbiology, 2017, 8, 1922.	3.5	33
42	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
43	The Power to Detect Recombination Using the Coalescent. Molecular Biology and Evolution, 2001, 18, 1421-1424.	8.9	31
44	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
45	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
46	Comparative genomics of pAKD4, the prototype IncP-1Î´ plasmid with a complete backbone. Plasmid, 2010, 63, 98-107.	1.4	20
47	A TEST FOR RARE MALE MATING ADVANTAGE WITH DROSOPHILA PSEUDOOBSCURA KARYOTYPES. Genetics, 1984, 107, 577-589.	2.9	19
48	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
49	Predicting peak spectral sensitivities of vertebrate cone visual pigments using atomistic molecular simulations. PLoS Computational Biology, 2018, 14, e1005974.	3.2	15
50	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
51	Positive selection at high temperature reduces gene transcription in the bacteriophage Ï•X174. BMC Evolutionary Biology, 2010, 10, 378.	3.2	13
52	Improving sequence alignments for intrinsically disordered proteins. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2002, , 589-600.	0.7	13
53	Comparative genomics of IncP-1Îµ plasmids from water environments reveals diverse and unique accessory genetic elements. Plasmid, 2013, 70, 412-419.	1.4	12
54	Comparative genomics of Bifidobacterium species isolated from marmosets and humans. American Journal of Primatology, 2019, 81, e983.	1.7	12

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55	High Diversity of CTX-M Extended-Spectrum Î²-Lactamases in Municipal Wastewater and Urban Wetlands. Microbial Drug Resistance, 2016, 22, 312-320.	2.0	11
56	Selection Affects Genes Involved in Replication during Long-Term Evolution in Experimental Populations of the Bacteriophage Ï†X174. PLoS ONE, 2013, 8, e60401.	2.5	10
57	Adaptive regulatory substitutions affect multiple stages in the life cycle of the bacteriophage Ï•X174. BMC Evolutionary Biology, 2013, 13, 66.	3.2	9
58	Current practices in nutrition management and disease incidence of common marmosets (Callithrix jacchus). Journal of Medical Primatology, 2021, 50, 164-175.	0.6	8
59	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
60	Differential Transcription of Bacteriophage Ï†X174 Genes at 37Â°C and 42Â°C. PLoS ONE, 2012, 7, e35909.	2.5	6
61	The Impact of Spatial Structure on Viral Genomic Diversity Generated during Adaptation to Thermal Stress. PLoS ONE, 2014, 9, e88702.	2.5	6
62	New Perspectives on Ebola Virus Evolution. PLoS ONE, 2016, 11, e0160410.	2.5	6
63	Computational Study of Evolutionary Selection Pressure on Rainbow Trout Estrogen Receptors. PLoS ONE, 2010, 5, e9392.	2.5	4
64	An Analysis of Density-Dependent Viability Selection. Journal of the American Statistical Association, 1989, 84, 662-668.	3.1	2