

Thomas Brettin

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

7,100
citations

126708

33
h-index

64668

79
g-index

83
all docs

83
docs citations

83
times ranked

9460
citing authors

#	ARTICLE	IF	CITATIONS
1	RASTtk: A modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. <i>Scientific Reports</i> , 2015, 5, 8365.	1.6	2,080
2	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017, 45, D535-D542.	6.5	1,445
3	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020, 48, D606-D612.	6.5	552
4	Antimicrobial Resistance Prediction in PATRIC and RAST. <i>Scientific Reports</i> , 2016, 6, 27930.	1.6	179
5	Whole-Genome Sequencing of Human Clinical <i>Klebsiella pneumoniae</i> Isolates Reveals Misidentification and Misunderstandings of <i>Klebsiella pneumoniae</i> , <i>Klebsiella variicola</i> , and <i>Klebsiella quasipneumoniae</i> . <i>MSphere</i> , 2017, 2, .	1.3	139
6	Developing an in silico minimum inhibitory concentration panel test for <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2018, 8, 421.	1.6	136
7	Population Genomic Analysis of 1,777 Extended-Spectrum Beta-Lactamase-Producing <i>Klebsiella pneumoniae</i> Isolates, Houston, Texas: Unexpected Abundance of Clonal Group 307. <i>MBio</i> , 2017, 8, .	1.8	124
8	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21T). <i>Standards in Genomic Sciences</i> , 2011, 5, 97-111.	1.5	115
9	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
10	PATRIC as a unique resource for studying antimicrobial resistance. <i>Briefings in Bioinformatics</i> , 2019, 20, 1094-1102.	3.2	93
11	Predicting tumor cell line response to drug pairs with deep learning. <i>BMC Bioinformatics</i> , 2018, 19, 486.	1.2	84
12	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	1.0	81
13	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034T). <i>Standards in Genomic Sciences</i> , 2010, 2, 87-95.	1.5	74
14	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2T). <i>Standards in Genomic Sciences</i> , 2010, 2, 96-106.	1.5	70
15	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20T). <i>Standards in Genomic Sciences</i> , 2010, 2, 158-167.	1.5	56
16	High-Throughput Virtual Screening and Validation of a SARS-CoV-2 Main Protease Noncovalent Inhibitor. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 116-128.	2.5	54
17	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1325, an effective microsymbiont of annual Mediterranean clovers.. <i>Standards in Genomic Sciences</i> , 2010, 2, 347-356.	1.5	53
18	Converting tabular data into images for deep learning with convolutional neural networks. <i>Scientific Reports</i> , 2021, 11, 11325.	1.6	52

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19	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95T). <i>Standards in Genomic Sciences</i> , 2011, 5, 356-370.	1.5	47
20	Whole-Genome Sequencing of a Human Clinical Isolate of the Novel Species <i>Klebsiella quasivariicola</i> sp. nov. <i>Genome Announcements</i> , 2017, 5, .	0.8	46
21	Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 283-290.	1.5	45
22	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
23	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 293-302.	1.5	44
24	CANDLE/Supervisor: a workflow framework for machine learning applied to cancer research. <i>BMC Bioinformatics</i> , 2018, 19, 491.	1.2	44
25	Ensemble transfer learning for the prediction of anti-cancer drug response. <i>Scientific Reports</i> , 2020, 10, 18040.	1.6	44
26	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 176-184.	1.5	40
27	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 46-53.	1.5	38
28	Complete genome sequence of <i>Eggerthella lenta</i> type strain (VPI 0255T). <i>Standards in Genomic Sciences</i> , 2009, 1, 174-182.	1.5	37
29	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10T). <i>Standards in Genomic Sciences</i> , 2010, 3, 194-202.	1.5	37
30	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (XT). <i>Standards in Genomic Sciences</i> , 2009, 1, 29-37.	1.5	36
31	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575T). <i>Standards in Genomic Sciences</i> , 2009, 1, 242-253.	1.5	35
32	Complete genome sequence of <i>Nakamurella multipartita</i> type strain (Y-104T). <i>Standards in Genomic Sciences</i> , 2010, 2, 168-175.	1.5	35
33	The Genome Sequence of <i>Methanohalophilus mahii</i> SLP ^T Reveals Differences in the Energy Metabolism among Members of the <i>Methanosarcinaceae</i> Inhabiting Freshwater and Saline Environments. <i>Archaea</i> , 2010, 2010, 1-16.	2.3	35
34	Complete genome sequence of the halophilic and highly halotolerant <i>Chromohalobacter salexigens</i> type strain (1H11T). <i>Standards in Genomic Sciences</i> , 2011, 5, 379-388.	1.5	35
35	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9T). <i>Standards in Genomic Sciences</i> , 2011, 4, 13-22.	1.5	35
36	Complete genome sequence of <i>Sebaldella termitidis</i> type strain (NCTC 11300T). <i>Standards in Genomic Sciences</i> , 2010, 2, 220-227.	1.5	34

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37	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4kT). Standards in Genomic Sciences, 2010, 2, 107-116.	1.5	32
38	Complete genome sequence of <i>Ferroglobus placidus</i> AEDII12DO. Standards in Genomic Sciences, 2011, 5, 50-60.	1.5	32
39	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2T). Standards in Genomic Sciences, 2009, 1, 270-277.	1.5	31
40	Complete genome sequence of <i>Acidaminococcus fermentans</i> type strain (VR4T). Standards in Genomic Sciences, 2010, 3, 1-14.	1.5	31
41	Complete genome sequence of <i>Atopobium parvulum</i> type strain (IPP 1246T). Standards in Genomic Sciences, 2009, 1, 166-173.	1.5	30
42	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175T). Standards in Genomic Sciences, 2010, 2, 149-157.	1.5	29
43	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125T). Standards in Genomic Sciences, 2009, 1, 226-233.	1.5	28
44	Complete genome sequence of <i>Coralimargarita akajimensis</i> type strain (04OKA010-24T). Standards in Genomic Sciences, 2010, 2, 290-299.	1.5	28
45	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022T). Standards in Genomic Sciences, 2010, 2, 49-56.	1.5	27
46	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100T). Standards in Genomic Sciences, 2010, 2, 29-37.	1.5	27
47	Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18T). Standards in Genomic Sciences, 2010, 2, 327-346.	1.5	26
48	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). Standards in Genomic Sciences, 2010, 2, 19-28.	1.5	26
49	Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1T). Standards in Genomic Sciences, 2009, 1, 159-165.	1.5	25
50	Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). Standards in Genomic Sciences, 2009, 1, 133-140.	1.5	25
51	Complete genome sequence of <i>Catenulispora acidiphila</i> type strain (ID 139908T). Standards in Genomic Sciences, 2009, 1, 119-125.	1.5	24
52	Complete genome sequence of <i>Leptotrichia buccalis</i> type strain (C-1013-bT). Standards in Genomic Sciences, 2009, 1, 126-132.	1.5	24
53	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101T). Standards in Genomic Sciences, 2009, 1, 141-149.	1.5	24
54	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577T). Standards in Genomic Sciences, 2010, 2, 212-219.	1.5	24

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55	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IAT). Standards in Genomic Sciences, 2010, 2, 9-18.	1.5	24
56	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883T). Standards in Genomic Sciences, 2009, 1, 254-261.	1.5	23
57	Complete genome sequence of <i>Thermobispora bispora</i> type strain (R51T). Standards in Genomic Sciences, 2010, 2, 318-326.	1.5	23
58	AI Meets Exascale Computing: Advancing Cancer Research With Large-Scale High Performance Computing. Frontiers in Oncology, 2019, 9, 984.	1.3	23
59	Complete genome sequence of <i>Halorhabdus utahensis</i> type strain (AX-2T). Standards in Genomic Sciences, 2009, 1, 218-225.	1.5	22
60	Complete genome sequence of <i>Desulfohalobium retbaense</i> type strain (HR100T). Standards in Genomic Sciences, 2010, 2, 38-48.	1.5	22
61	Complete genome sequence of <i>Streptobacillus moniliformis</i> type strain (9901T). Standards in Genomic Sciences, 2009, 1, 300-307.	1.5	21
62	Complete genome sequence of <i>Slackia heliotrinireducens</i> type strain (RHS 1T). Standards in Genomic Sciences, 2009, 1, 234-241.	1.5	20
63	Cystic Fibrosis Rapid Response: Translating Multi-omics Data into Clinically Relevant Information. MBio, 2019, 10, .	1.8	20
64	Complete genome sequence of <i>Cryptobacterium curtum</i> type strain (12-3T). Standards in Genomic Sciences, 2009, 1, 93-100.	1.5	17
65	Complete genome sequence of <i>Sanguibacter keddiei</i> type strain (ST-74T). Standards in Genomic Sciences, 2009, 1, 110-118.	1.5	16
66	Complete genome sequence of <i>Denitrovibrio acetiphilus</i> type strain (N2460T). Standards in Genomic Sciences, 2010, 2, 270-279.	1.5	16
67	Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1T). Standards in Genomic Sciences, 2010, 3, 66-75.	1.5	15
68	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. Briefings in Bioinformatics, 2021, 22, .	3.2	15
69	Learning curves for drug response prediction in cancer cell lines. BMC Bioinformatics, 2021, 22, 252.	1.2	15
70	Complete genome sequence of <i>Jonesia denitrificans</i> type strain (Prevot 55134T). Standards in Genomic Sciences, 2009, 1, 262-269.	1.5	14
71	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PATT). Standards in Genomic Sciences, 2010, 3, 174-182.	1.5	14
72	Complete genome sequence of <i>Thermosphaera aggregans</i> type strain (M11TLT). Standards in Genomic Sciences, 2010, 2, 245-259.	1.5	14

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73	Complete genome sequence of <i>Beutenbergia cavernae</i> type strain (HKI 0122T). <i>Standards in Genomic Sciences</i> , 2009, 1, 21-28.	1.5	12
74	Complete genome sequence of <i>Kribbella flavida</i> type strain (IFO 14399T). <i>Standards in Genomic Sciences</i> , 2010, 2, 185-192.	1.5	11
75	Complete genome sequence of <i>Thermobaculum terrenum</i> ™ type strain (YNP1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 153-162.	1.5	11
76	Complete genome sequence of <i>Segniliparus rotundus</i> type strain (CDC 1076T). <i>Standards in Genomic Sciences</i> , 2010, 2, 203-211.	1.5	10
77	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33T). <i>Standards in Genomic Sciences</i> , 2011, 4, 342-351.	1.5	10
78	Enhanced Co-Expression Extrapolation (COXEN) Gene Selection Method for Building Anti-Cancer Drug Response Prediction Models. <i>Genes</i> , 2020, 11, 1070.	1.0	8
79	Complete genome sequence of <i>Tolomonas auensis</i> type strain (TA 4T). <i>Standards in Genomic Sciences</i> , 2011, 5, 112-120.	1.5	6
80	Portable and Reusable Deep Learning Infrastructure with Containers to Accelerate Cancer Studies. , 2018, , .		2