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2020

G Palfalvi, **T Hackl**, N Terhoeven, TF Shibata, T Nishiyama et al. (2020) [Genomes of the Venus Flytrap and Close Relatives Unveil the Roots of Plant Carnivory](#), *Current Biology*,

T Hackl, R Martin, K Barenhoff, S Duponchel, D Heider, MG Fischer (2020) [Four high-quality draft genome assemblies of the marine heterotrophic nanoflagellate Cafeteria roenbergensis](#), *Scientific data*, 7 (1), 1-9

E Thomas, **T Hackl**, R Laurenceau, MJ Ankenbrand, C Bliem, Z Cariani et al. (2020) [Role of Integrative Elements in Gene Transfer and Niche Adaptation in Prochlorococcus](#), *Ocean Sciences Meeting*, 2020

2018

SJ Biller, PM Berube, K Dooley, M Williams, BM Satinsky, **T Hackl** et al. (2018) [Marine microbial metagenomes sampled across space and time](#), *Scientific data*, 5, 180176

PM Berube, SJ Biller, **T Hackl**, SL Hogle, BM Satinsky, JW Becker et al. (2018) [Single cell genomes of Prochlorococcus, Synechococcus, and sympatric microbes from diverse marine environments](#), *Scientific data*, 5, 180154

MJ Ankenbrand, S Pfaff, N Terhoeven, M Qureischi, M Gündel, CL Weiß et al. (2018) [chloroExtractor: extraction and assembly of the chloroplast genome from whole genome shotgun data](#), *The Journal of Open Source Software*, 3 (21), 464

JH Grau, **T Hackl**, KP Koepfli, M Hofreiter (2018) [Improving draft genome contiguity with reference-derived in silico mate-pair libraries](#), *GigaScience*, 7 (5), giy029

N Terhoeven, J Schultz, **T Hackl** (2018) [reper: Genome-wide identification, classification and quantification of repetitive elements without an assembled genome](#), *Journal of Open Source Software*,

2017

BM Slaby, **T Hackl**, H Horn, K Bayer, U Hentschel (2017) [Metagenomic binning of a marine sponge microbiome reveals unity in defense but metabolic specialization](#), The ISME journal, 11 (11), 2465-2478

MJ Ankenbrand, S Hohlfeld, **T Hackl**, F Förster (2017) [AliTV—interactive visualization of whole genome comparisons](#), PeerJ Computer Science, 3, e116

2016

MG Fischer, **T Hackl** (2016) [Host genome integration and giant virus-induced reactivation of the virophage mavirus](#), Nature, 540 (7632), 288-291

T Hackl (2016) [A draft genome for the Venus flytrap, *Dionaea muscipula*: Evaluation of assembly strategies for a complex Genome—Development of novel approaches and bioinformatics solutions](#), ,

2014

T Hackl, R Hedrich, J Schultz, F Förster (2014) [proofread : large-scale high-accuracy PacBio correction through iterative short read consensus](#), Bioinformatics, 30 (21), 3004-3011

2012

C Koetschan, **T Hackl**, T Müller, M Wolf, F Förster, J Schultz (2012) [ITS2 database IV: interactive taxon sampling for internal transcribed spacer 2 based phylogenies](#), Molecular Phylogenetics and Evolution, 63 (3), 585-588

B Merget, C Koetschan, **T Hackl**, F Förster, T Dandekar, T Müller et al. (2012) [The ITS2 database](#), JoVE (Journal of Visualized Experiments), e, e3806