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

M Berjón-Otero, S Duponchel, **T Hackl**, MG Fischer (2020) Visualization of giant virus particles using BONCAT labeling and STED microscopy, bioRxiv,

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 referencederived 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,

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) proovread: 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