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## 2021

R Massana, A Labarre, D López-Escardó, A Obiol, F Bucchini, **T Hackl** et al. (2021) Gene expression during bacterivorous growth of a widespread marine heterotrophic flagellate, The ISME journal, 15 (1), 154-167

D Shitrit, **T Hackl**, R Laurenceau, N Raho, MCG Carlson, G Sabehi et al. (2021) Genetic engineering of marine cyanophages reveals integration but not lysogeny in T7-like cyanophages, The ISME Journal, 1-12

K Haslinger, **T Hackl**, KLJ Prather (2021) Rapid in vitro prototyping of O-methyltransferases for pathway applications in Escherichia coli, Cell chemical biology,

**T Hackl**, F Trigodet, AM Eren, SJ Biller, JM Eppley, E Luo, A Burger et al. (2021) proovframe: frameshift-correction for long-read (meta) genomics, bioRxiv,

R Martin, H Dreßler, G Hattab, **T Hackl**, MG Fischer, D Heider (2021) MOSGA 2: Comparative genomics and validation tools, Computational and structural biotechnology journal, 19, 5504-5509

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, 30 (12), 2312-2320. e5

**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

**T Hackl**, R Laurenceau, MJ Ankenbrand, C Bliem, Z Cariani, E Thomas et al. (2020) Novel integrative elements and genomic plasticity in ocean ecosystems, ,

**T Hackl**, S Duponchel, K Barenhoff, A Weinmann, MG Fischer (2020) Endogenous virophages populate the genomes of a marine heterotrophic flagellate, bioRxiv,

R Martin, **T Hackl**, G Hattab, MG Fischer, D Heider (2020) MOSGA: Modular Open-Source Genome Annotator, Bioinformatics, 36 (22-23), 5514-5515

M Acker, SL Hogle, PM Berube, **T Hackl**, RM Stepanauskas et al. (2020) Phosphonate production by marine microbes: exploring new sources and potential function, bioRxiv,

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 (1), 1-7

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 (1), 1-11

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, Universität Würzburg,

## 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