

Last updated January 17, 2022– Pulled automatically from my [Google Scholar profile](#). See [this post](#) for how it works.

## 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

R Martin, **T Hackl**, G Hattab, MG Fischer, D Heider (2021) [MOSGA: modular open-source genome annotator](#), *Bioinformatics*, 36 (22-23), 5514-5515

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) [proofframe: 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*,

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