

2021 performance:

169,000 page visits (+69%)

19,000 analyses (+52%)

2,000 newly stored type-strain genomes (+14%)

3,000 active users (+51%)

10M genome comparisons (+41%)

600 citations so far (+340)



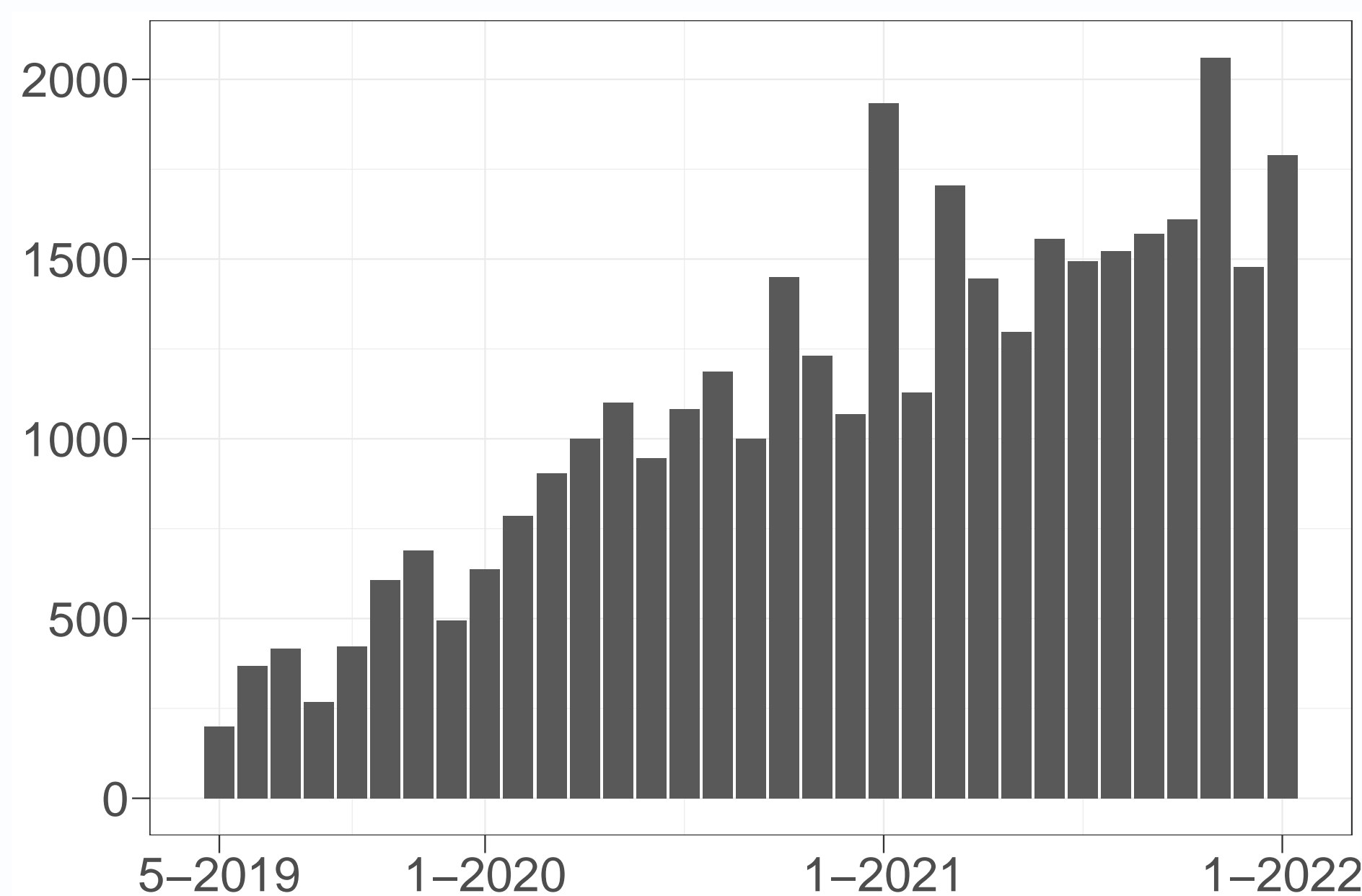
EST. 2019

TYGS 2021 Year in Review

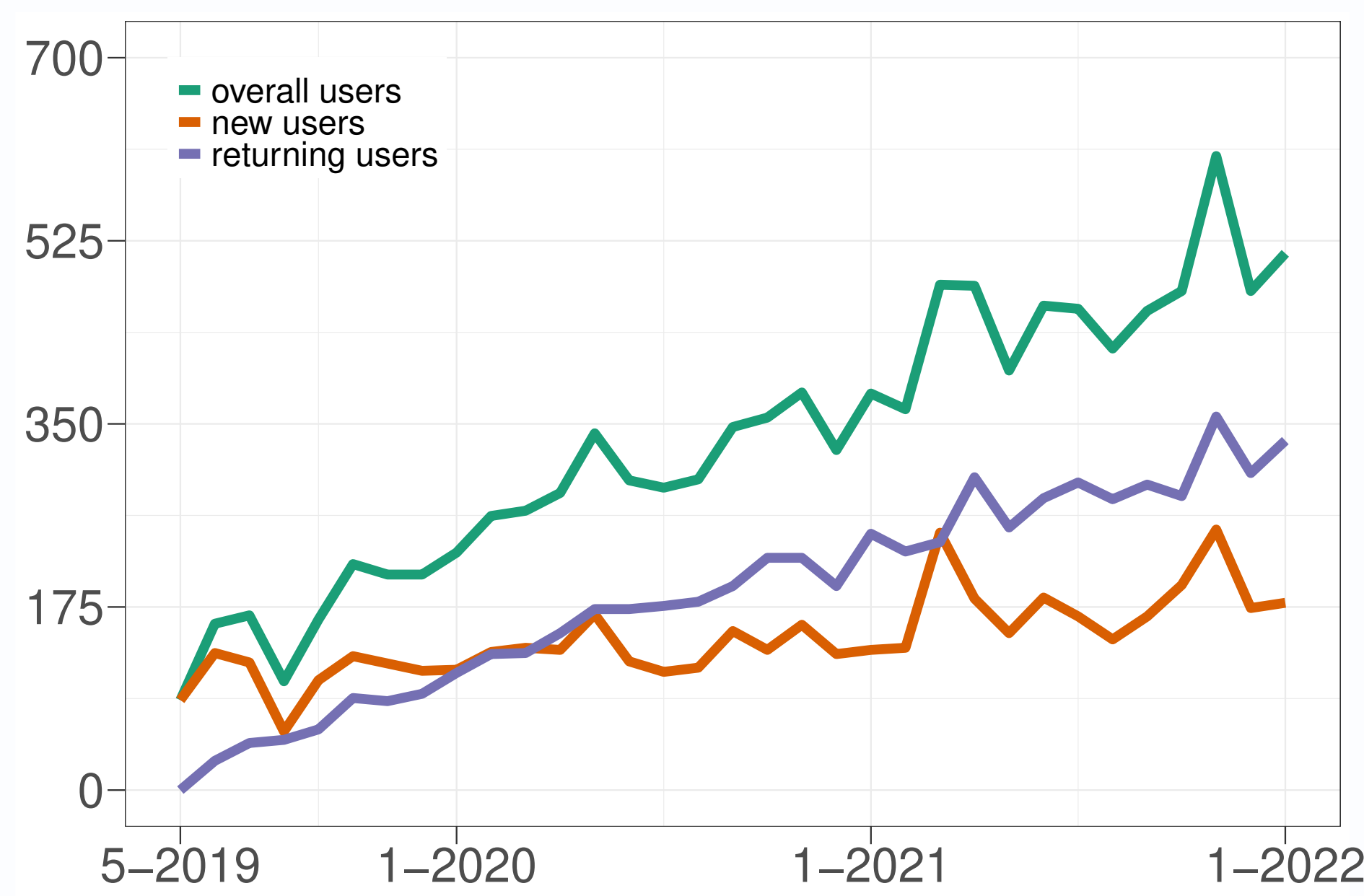
DSMZ platform for automated genome-based taxonomy in numbers

Jan Meier-Kolthoff

Monthly job submissions



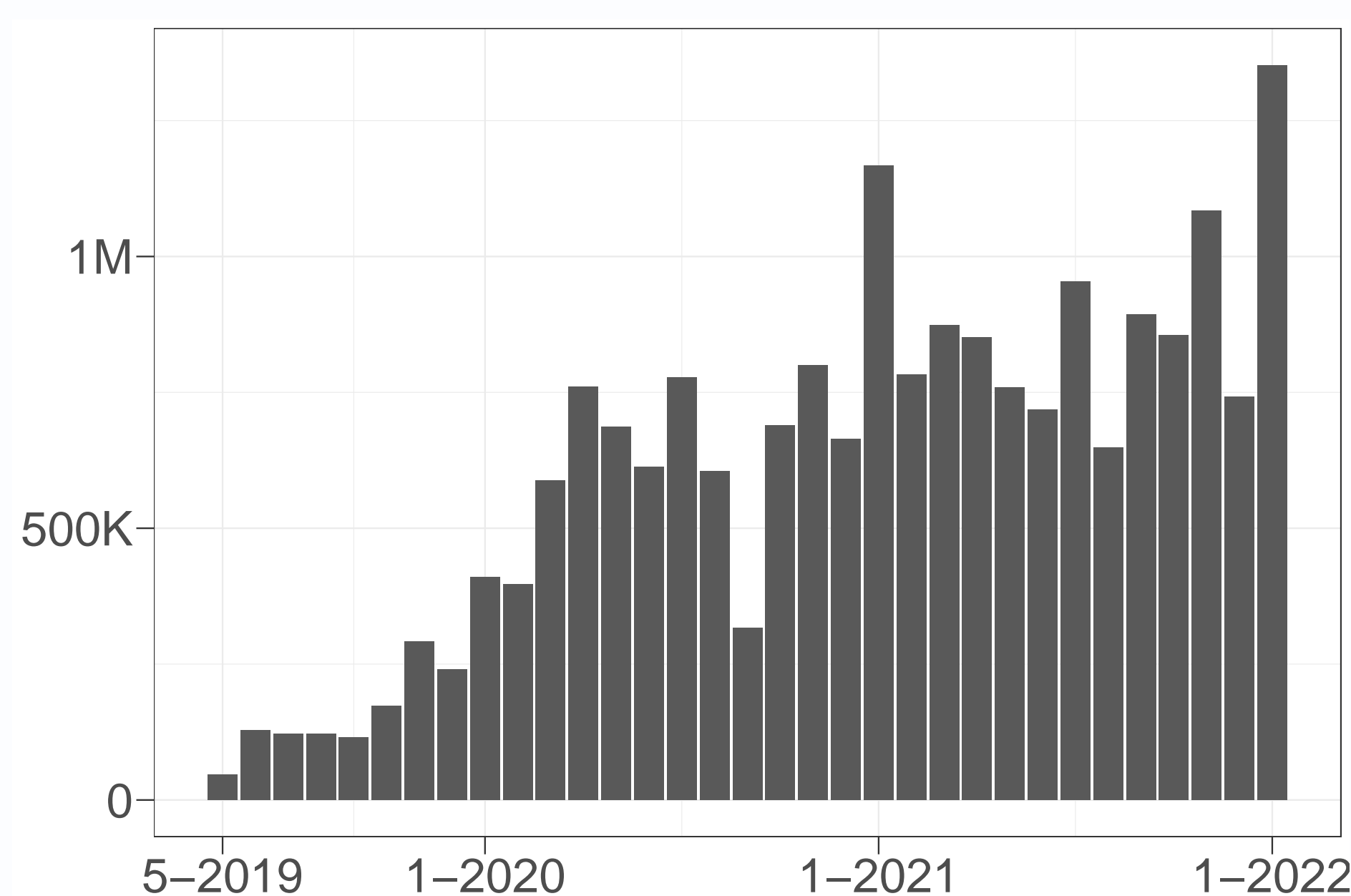
New vs. returning users



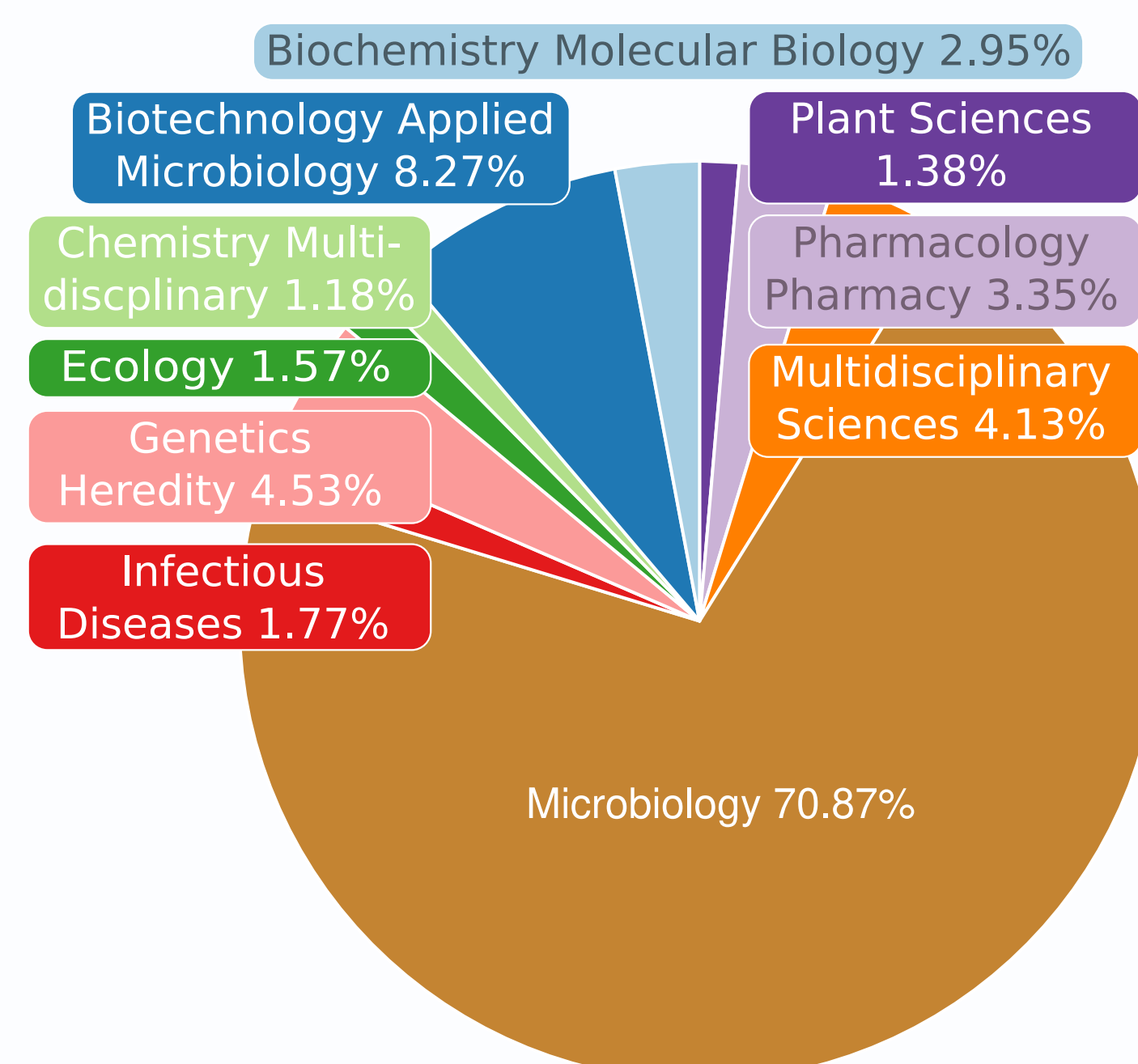
Ten most frequent locations of TYGS users



Genome comparisons



Analysis of citations



Major achievements and updates in 2021

- ⊕ The TYGS paper is still placed in the top 1% of the academic field of Microbiology based on the Web of Science (tm) 'highly cited' threshold.
- ⊕ New paper published: *TYGS and LPSN: a database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. Nucleic Acids Res. 2022;50: D801–D807.*
- ⊕ option for reconstruction of proteome-based GBDP trees
- ⊕ many non-visible technical improvements

2021 User feedback

"I want to thank you for developing TYGS, it is such a wonderful and complete tool and it makes my life as a microbiology researcher so much easier. I am involved in several ongoing taxonomic studies and for some, we will be analyzing around 150-200 genomes."

TYGS user from Ghent University, Belgium

"Thank you for your high quality service"

TYGS user from AIST, Japan

"Your service is excellent and TYGS is becoming the golden standard for bacterial identification."

TYGS user from University of Copenhagen, Denmark

"Impressive service you have generated at DSMZ."

TYGS user from Aarhus University Hospital, Denmark

"Thank you so much for the TYGS service. I am relatively new to phylogenomics, and this made the process much easier for me."

TYGS user from Bridgewater College, USA

"I must say I enjoy the TYGS workflow, so thanks a lot for providing this."

TYGS user from The Arctic University of Norway, Norway

"Fabulous website, we've tested our 20 genomes and the result was amazing!"

TYGS user from Duke University, USA

"First of all, hats off to your work. This platform is wonderful and easy to use. It basically removes the needs to do preliminary MLSA analyses to identify the closest type strains before doing GGDC analyses."

TYGS user from Agriculture and Agri-Food, Canada

"By the way, I love your site :-). It is so useful!"

TYGS user from University of Hawaii, USA

"Thanks, its highly helpful and quick service."

TYGS user from Korea Research Institute of Bioscience and Biotechnology, Korea

"I am a new convert to this very impressive service/software."

TYGS user from University of Oklahoma, USA

"I applaud what your group at DSMZ is doing to provide easy-to-use and powerful tools to sort out what can be sorted out. I can't express how valuable your part of the DSMZ has been to me and to my students."

TYGS user from Midwestern University, USA

"We would like to appreciate you for opening a very convenient site."

TYGS user from AIST, Japan



TYPE (STRAIN)
GENOME SERVER

<https://tygs.dsmz.de>
Nat. Commun. 10, 2182 (2019)

Questions? Contact us via
<https://tygs.dsmz.de/feedback/new>

