Microbial secondary metabolism constitutes a rich source of antibiotics, chemotherapeutics, insecticides and other high-value chemicals. Genome mining of gene clusters that encode the biosynthetic pathways for these metabolites has become a key methodology for novel compound discovery. In 2011, we introduced antiSMASH, a web server and standalone tool for the automatic genomic identification and analysis of biosynthetic gene clusters, available at http://antismash.secondarymetabolites.org. Here, we present version 3.0 of antiSMASH, which has undergone major improvements. A full integration of the recently published ClusterFinder algorithm now allows using this probabilistic algorithm to detect putative gene clusters of unknown types. Also, a new dereplication variant of the ClusterBlast module now identifies similarities of identified clusters to any of 1172 clusters with known end products. At the enzyme level, active sites of key biosynthetic enzymes are now pinpointed through a curated pattern-matching procedure and Enzyme Commission numbers are assigned to functionally classify all enzyme-coding genes. Additionally, chemical structure prediction has been improved by incorporating polyketide reduction states. Finally, in order for users to be able to organize and analyze multiple antiSMASH outputs in a private setting, a new XML output module allows offline editing of antiSMASH annotations within the Geneious software.

General information
State: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability, New Bioactive Compounds, Saarland University, Congenomics, LLC, University of California, University of Tübingen
Number of pages: 7
Pages: W237-W243
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: Nucleic Acids Research
Volume: 43
Issue number: W1
ISSN (Print): 0305-1048
Ratings:
BFI (2019): BFI-level 2
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 10.84 SJR 9.025 SNIP 3.028
Web of Science (2017): Impact factor 11.561
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 9.28 SJR 7.883 SNIP 2.744
Web of Science (2016): Impact factor 10.162
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 9.48 SJR 7.358 SNIP 2.631
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 8.74 SJR 6.64 SNIP 2.552
Web of Science (2014): Impact factor 9.112
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 8.46 SJR 6.801 SNIP 2.284
Web of Science (2013): Impact factor 8.808
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes