









enter your email address here

antiSMASH bacterial version   Submit Bacterial Sequence  Submit Fungal Sequence  Submit Plant Sequence  Download  About  ? Help  Contact

Server status: **working**

Running jobs: **9**

Queued jobs: **0**

Jobs processed: **436578**

Nucleotide input Results for existing job

Search a genome sequence for secondary metabolite biosynthetic gene clusters Load sample input Open example output

Notification settings

Email address (optional)

Data input

Upload file Get from NCBI Browse Sequence file (GenBank / EMBL / FASTA format)

Extra features All off All on

☒ KnownClusterBlast

☒ ActiveSiteFinder

☐ ClusterBlast

☐ Cluster Pfam analysis

☒ SubClusterBlast

☐ Pfam-based GO term annotation

Submit

This is the antiSMASH 5 beta
While we feel it is pretty good already, this version might still be a bit rough at the edges. Until spring 2019, you can still run antiSMASH 4 jobs here.

Incomplete RefSeq annotations
Dear antiSMASH users, it has come to our attention that a recent RefSeq reannotation again broke NRPS/PKS ORFs. If your results look weird, try uploading the corresponding GenBank record or a FASTA file.

click this

click here to select a GenBank file

click here to submit