MiDAS
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**Standard 16S rRNA protocols**

Amplicon sequencing of the 16S rRNA gene now allows high throughput analyses and monitoring of the whole microbial communities of wastewater treatment systems.

However, meaningful cross study comparisons are hindered by the substantial influence of the selected DNA extraction method, PCR primers and reference taxonomy.

**MiDAS** provides protocols for DNA extraction, 16S rRNA gene amplicon library preparation and bioinformatic analysis – all optimised for application to wastewater treatment system samples.

**Distribution**

Large scale surveys of the microbial communities of wastewater treatment systems incl. >50 full-scale systems over several years.

**Linking identity with function**

The online **MiDAS field guide** provides profiles for all abundant and process important phylotypes - linking their identity to current information on their morphology, physiology and distribution. This currently includes profiles for >300 bacterial and 8 archaeal genus level taxa.

**Curated site-specific taxonomy**

Reliable function prediction for phylotypes requires taxonomic assignment to the species or genus level.

Many of the abundant activated sludge and anaerobic digester organisms have no cultured representatives and are not annotated in popular public databases applied for taxonomic assignment. i.e. the uncultured fermentative bulking filament “Ca. Promineofilum” (0092 morphotype).

**MiDAS** provides a site-specific taxonomic database curated for the organisms of wastewater treatment systems.

**MiDAS includes abundance values for influent wastewater, activated sludge and anaerobic digester (AD) – identifying abundant phylotypes and giving an insight into migration. An important example being the link between foaming episodes in anaerobic digesters and migration of “Ca. Microthrix spp.” from activated sludge.**

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