**Open Access data and scientific articles**

**FRESHBAR** will generate the following data, which will all be published with open access and available to the Swedish EPA immediately at the end of the project period:

● New diatom reference sequences (rbcL & 18S) linked to voucher specimens

○ stored at the Herbarium Berolinense (BGBM), developed to host inter alia microalgae (AlgaTerra and SpecimenTool, GGBN, DNABank Network, Phycobank Information System, 2018)

○ incorporated into R-Syst::diatom, the envisaged curated European open access database for rbcL, and into The German Reference Library (AlgaTerra, GGBN, SpecimenTool, public access: 2019) currently the most updated for 18S

● New chironomid and oligochaete reference sequences (COI & 16S) linked to voucher specimens

○ stored at the Museum of Natural History.

● Both diatom and invertebrate sequences will also be

○ archived at NCBI’s Sequence Read Archive, a part of INSDC (International Nucleotide Sequence Database Cooperation, 2018), and at BOLD (2018)

○ linked to a national Swedish biodiversity infrastructure currently in construction (cooperation of Swedish LiveWatch, the existing database on Swedish taxa geographical distribution including Dyntaxa, and Biodiversity Atlas Sweden (BAS))

● Established live diatom clones archived in the first public collection of diatoms in Europe (BCCM/DCG Diatoms Collection in Ghent, Belgium, 2018), offering free long-term archiving, including strain maintenance and cryopreservation, coupled to a public access of the strains. (There are no Nagoya protocol issues for an exchange of DNA material between Sweden and Belgium.)

● Project metadata including community composition of the metabarcoding studies archived in the Dryad Digital Repository (2018) to ensure open access

● We plan to publish the following Scientific articles (all with full Open Access):

○ New diatom barcodes from Sweden, and implications for freshwater benthic diatom taxonomy and metabarcoding

○ Diatom metabarcoding with new technology using long sequences

○ DNA metabarcoding reveals the complex and hidden responses of chironomids and oligochaetes to multiple stressors

○ Short primer performance in discriminating Chironomidae species

○ Increasing the discriminatory power in ecological status classifications with metabarcoding using the Swedish national standard method (BQI) based on chironomids