

Dr. Rob Finn heads the Genome Assembly and Annotation Section and is the lead of the Microbiome Informatics team at EMBL's European Bioinformatics Institute (EMBL-EBI). This team produces MGnify, a world leading resource for the functional and taxonomic analysis and archiving of microbiome derived sequence data. In addition to making large numbers of datasets available that have been processed in a systematic way, the resource allows scientists to upload their own data, either privately or publicly, and assemble and analyse their data. The MGnify resource contains one of the largest public collections of assembled metagenomes, which have been used to derive billions of proteins. In the past year, MGnify has also started to produce biome-specific catalogues of metagenome assembled genomes, derived from the aforementioned assemblies and community contributions. Collectively, these are providing new insights into the microbial diversity found in a range of environments, or associated with different hosts, such as humans.

Previously, Dr Rob Finn led a range of different data resources at EMBL-EBI, namely InterPro, Pfam, Rfam and RNACentral, which all build on his background of using probabilistic models for biological sequence analysis and genomic annotation. Rob joined EMBL-EBI from the Janelia Research Campus in the US, where he led a group that designed fast, web-based, interactive protein-sequence searches and annotations. Between 2001 and 2010, he was the project leader for Pfam at the Wellcome Trust Sanger Institute in the UK. Rob's academic background is in microbiology and he holds a PhD in biochemistry from Imperial College, London.