

Yuichi Kodama, Satoshi Saruhashi, Eli Kaminuma, Hideaki Sugawara, Toshihisa Takagi, Kousaku Okubo and Yasukazu Nakamura

DNA Data Bank of Japan, National Institute of Genetics, Japan Contact: trace@ddbj.nig.ac.jp

Next generation sequencing platforms are producing biological sequencing data in unprecedented amounts. The DNA Data Bank of Japan (DDBJ) has established the DDBJ Sequence Read Archive (DRA) and the DDBJ Omics Archive (DOR). The DRA is intended to be a repository for data from the primary analysis phase of next-generation sequencing. The DOR is an archival database for quantitative genomics data both from microarray and high-throughput sequencing platforms. The DOR archives MIAME- and MINSEQE-compliant data with the MAGE-TAB metadata and export data to the ArrayExpress. The DOR register companion raw data to the DRA instead of submitters. These two public databases of the DDBJ work collaboratively with the National Center for Biotechnology Information (NCBI) and the European Bioinformatics Institute (EBI).

Databases and analytical services of DDBJ Analysis



DOR : Database for quantitative genomics data.

DRA: Database for data from the primary analysis phase of next generation sequencing.

DDBJ: Database for annotated sequence data.

DDBJ Read Annotation Pipeline : Analytical pipeline performs mapping, assembly, RNA-seq, SNP, structural, functional annotations and so on.

DDBJ Sequence Read Archive

DDBJ Omics Archive





The DOR archives both array-based and sequence-based quantitative genomics data. The DOR archives the MIAME- and MINSEQE-compliant data with MAGE-TAB metadata. The public DOR data are exported to ArrayExpress. DOR will integrate array-based CIBEX data.

For next-generation sequencing data, the DOR will register corresponding raw data to the DRA instead of submitters.