

Published online 06 November 2014

*Nucleic Acids Research, 2015, Vol. 43, Database issue D1107–D1112
doi: 10.1093/nar/gku990*

diArk – the database for eukaryotic genome and transcriptome assemblies in 2014

Martin Kollmar^{*}, Lotte Kollmar, Björn Hammesfahr and Dominic Simm

Group Systems Biology of Motor Proteins, Department of NMR-based Structural Biology, Max-Planck-Institute for Biophysical Chemistry, Göttingen, 37085, Germany

Received September 10, 2014; Accepted September 30, 2014

ABSTRACT

Eukaryotic genomes are the basis for understanding the complexity of life from populations to the molecu-

NCBI/ENA/DDBJ are the central repositories for sequence read archives (SRAs), the ‘raw data’ for generating assemblies, but publishers and funding agencies often do not require assemblies to also be stored there. Thus