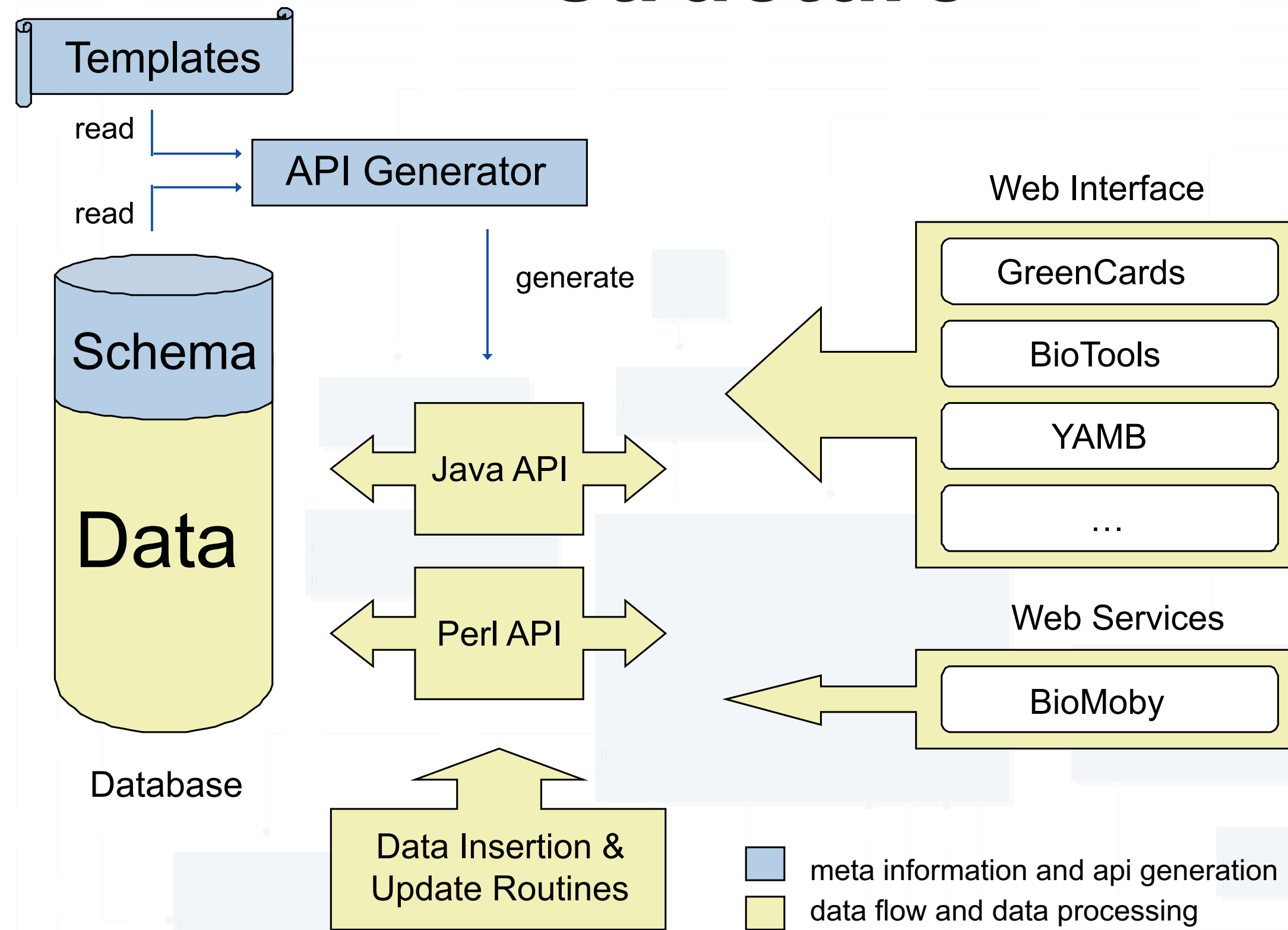


Diego Mauricio Riaño-Pachón, Axel Nagel, Robert Wagner, Jost Neigenfind, Elke Weber, Svenja Diehl, Birgit Kersten

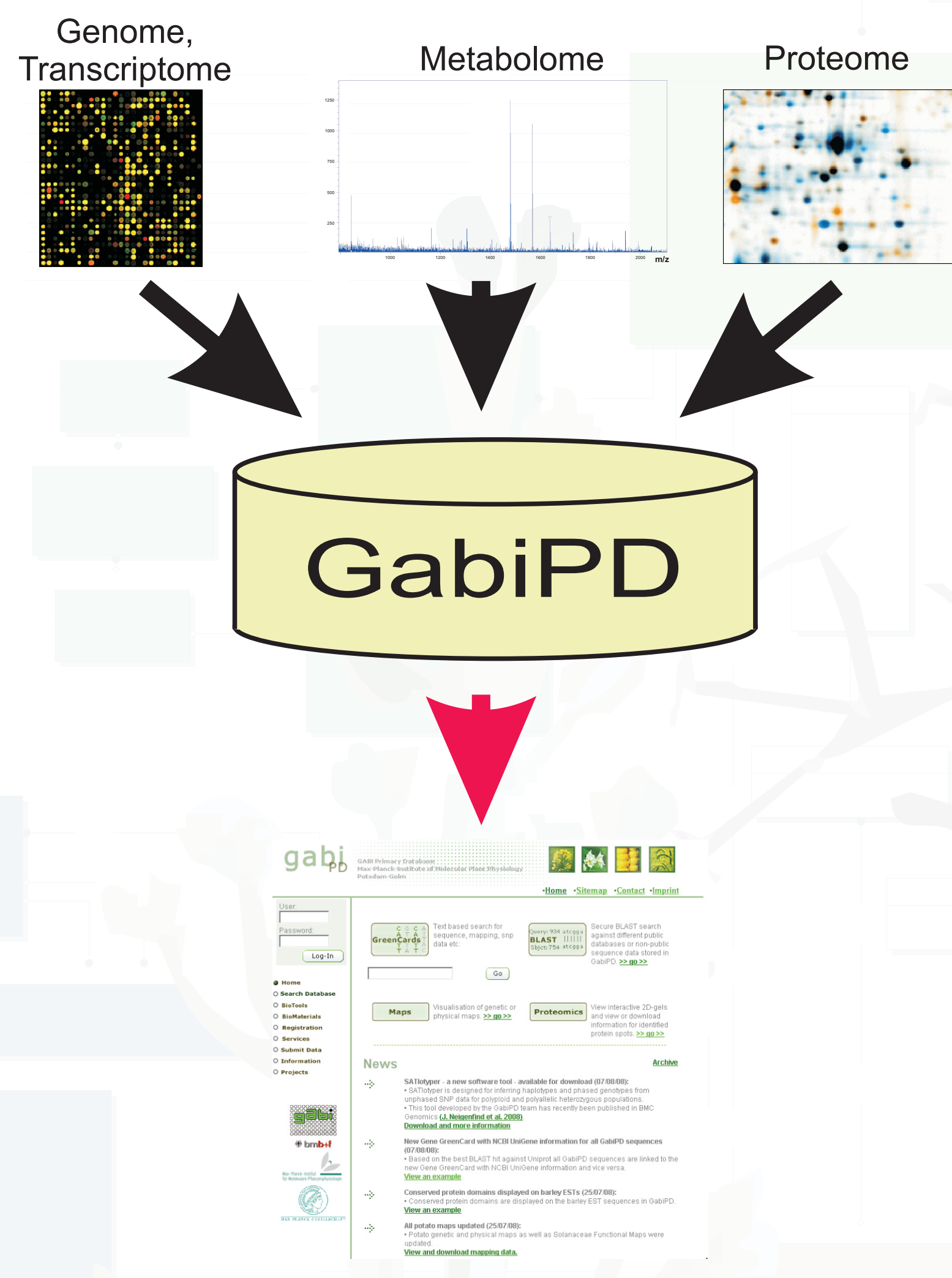
GabiPD team, Bioinformatics group, Max Planck Institute of Molecular Plant Physiology, Wissenschaftspark Golm, Am Mühlenberg 1, 14476 Potsdam - Golm, Germany

1. GabiPD application structure



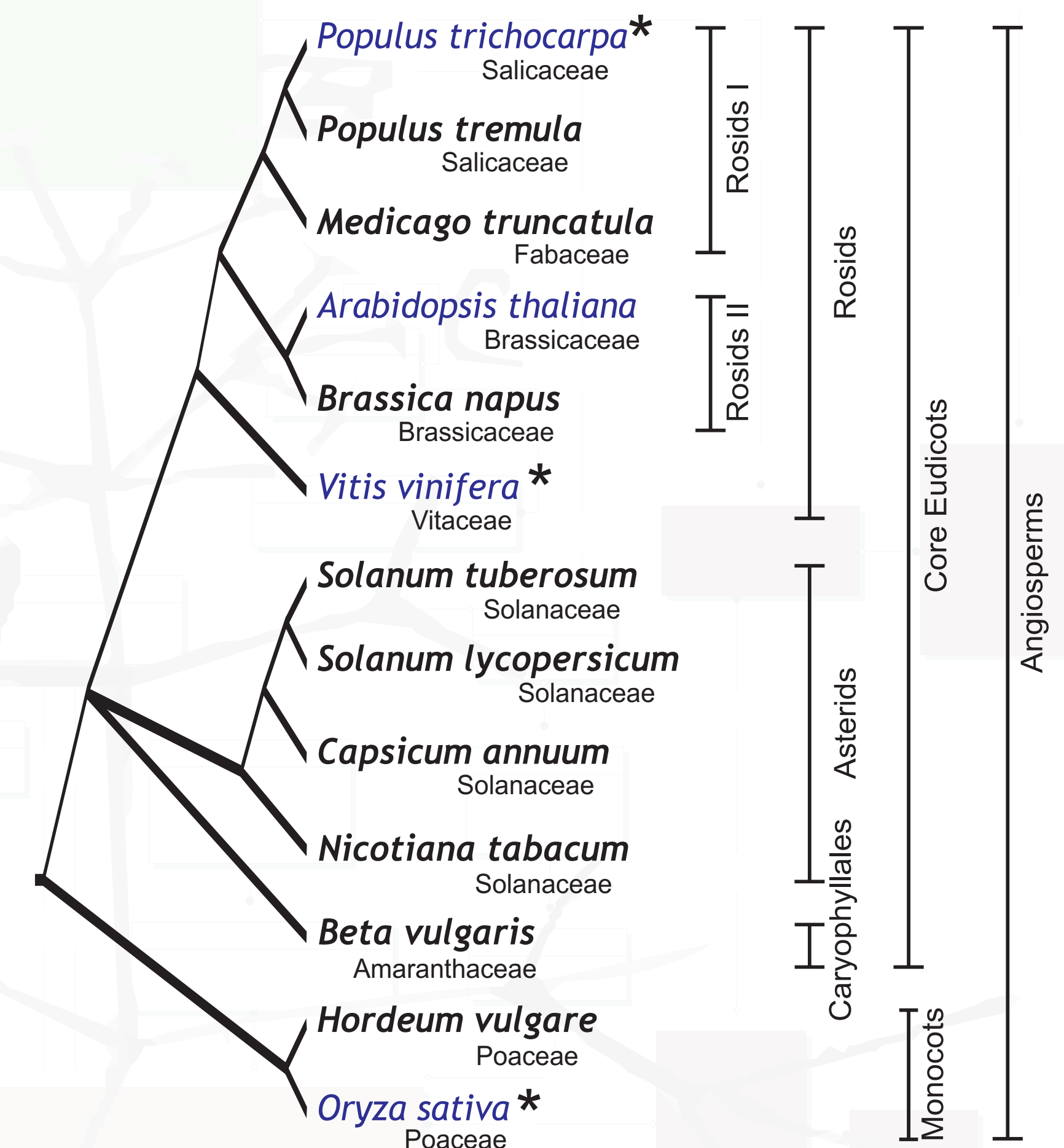
Schematic overview of the GabiPD application structure. The 'API generator' translates the 'Templates' using the database meta-information (shown in blue), generating the database application interface (Java and Perl API). The application logic (shown in yellow), i.e., Web Interface, WebServices and data manipulation routines, interacts with the 'Database' through the database application interface.

2. 'omics' data



GabiPD allows a seamless integration of varied 'omics' data types obtained from plant systems and follows the MIAME and MIAMET standards for storing gene expression and metabolic profiling data, respectively.

3. Species represented in GabiPD



Phylogenetic tree depicting the evolutionary relationships among the species represented in GabiPD. Species for which whole-genome sequences and annotations are available are shown in blue. *Species that will soon be integrated in GabiPD. Species not shown: *Solanum bulbocastanum*, *S. demissum*, *S. phureja*, *S. spegazzinii*.

4. Gene-centric view

Example of a keyword search using GreenCards. (A) The user had performed a search for the keywords 'FLOWERING LOCUS T', which retrieves links to the GreenCards of Genes (genome annotation projects), Clones (ESTs) and Plants (mutant plant lines). (B) Display of the Gene GreenCard, corresponding to the Arabidopsis annotated gene AT1G65480.1. Here the users find high confidence matching EST sequences displayed in the 'Related with' section. Sequence features and the sequences themselves are displayed as well. The selected gene has a matching EST (Clone: MPMGp2011E01215), this Clone GreenCard is shown in (C) and links back to the Gene GreenCard and to the original EST trace file, displayed by JTrev (D). A protein spot in rapeseed (*Brassica napus*) has been identified by 2-DE/MS as the protein encoded by the retrieved gene, and a link directs the user to the 2DE-gel with the identified protein spot highlighted with blue cross-hair (E). The spot identified links to a description of the protein (F) that provides links to the original Gene GreenCard.

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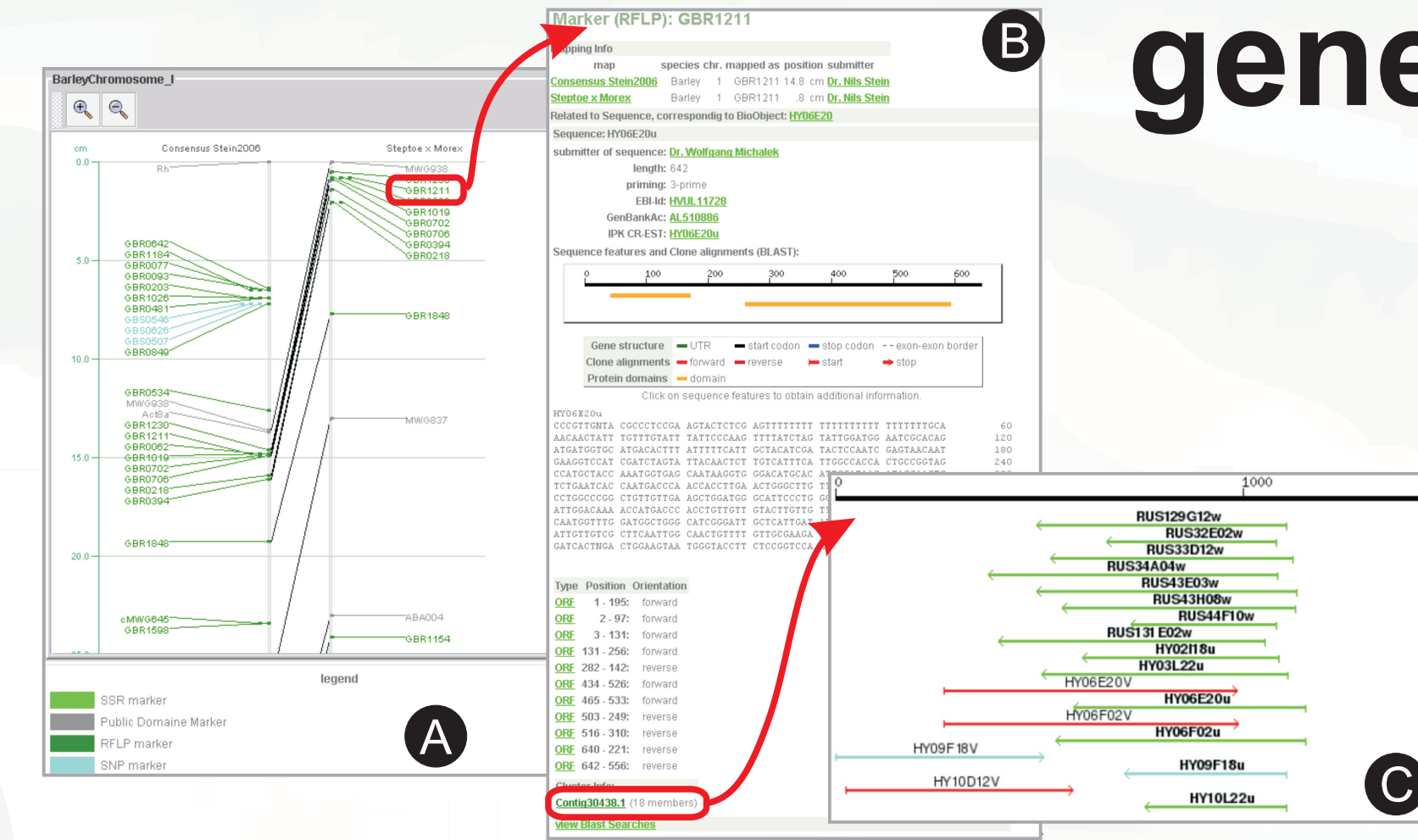
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5. Visualising expression data

Visualisation of expression profile data in MapManWeb. (A) The Affymetrix® NASC Array experiment on programmed cell death in Arabidopsis is displayed (NASCArrays reference number: 30). MapManWeb allows the visualisation of expressed genes in different biological processes; here only probesets (i.e., genes) involved in transcription regulation are shown. (B) Details for a strongly down-regulated probeset, with links to the related Gene GreenCard in *A. thaliana*. (C) The Gene GreenCard for the selected gene (ANAC79) links back to the probeset of the Affymetrix® ATH1 array.

6. Barley and Solanaceae genetic maps



Visualisation of the genetic maps published by Stein *et al.* 2007. (A) The region between 0cM and 25cM of barley chromosome I is shown. A selected marker is displayed in red, and links to the Marker GreenCard (B), which contains information on a related EST sequence therewith connecting genomic with transcriptomic information. With the EST description, cluster information is included (Contig30438.1) that links to the schematic representation of all ClusterContig members displayed onto the related consensus sequence (C). EST sequences that were selected from this ClusterContig as representatives for the new 27K barley unigene set are shown in turquoise.