

## **Abysis, an antibody database**

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Abstract:

The Abysis database links all publicly available Ig protein sequence data together. This involves three main data sources kabat, imgt and the pdb. The sequences are then numbered using the kabat numbering scheme, via a program developed by Abhinandan Raghavan and Andrew Martin. This numbering allows antibody sequences to be directly compared with each other. The three data sources have been combined into a common XML format and loaded into a postgres database.

As, well as providing numbering and other annotation, missing information such as the correct heavy and light chain pairing has been mined from available data.

The next step is to provide a facility for structural comparison of known Ig structures, with the standard numbering scheme. All of this data will be publicly available via the Internet.