

Employing programmatic access to SRS to annotate biological entities

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SRS (Sequence Retrieval System) is a data integration platform that provides fast access to diverse life sciences information including genetic, protein, expression, pathway, molecular and clinical data from public and proprietary sources, regardless of data format (<http://www.biowisdom.com/solutions/srs/>).

Based on indexing technologies, SRS allows simultaneous queries to all of the integrated databases from a single access point, utilizing a common query format. EasySRS web services expose this SRS functionality and provide users with the required system information to formulate these queries, such as supported databases and query fields, and the operations to subsequently retrieve the data. Emphasis has been given on:

- * serving queries that span multiple databases or link different data sources.
- * employing the services in workflow enactment engines such as Taverna
- * generating a 3D visualization of the interconnected data

Currently EasySRS connects to the SRS server at EMBL-HD (<http://srs.embl.de>) which integrates the information of more than a 100 databases, including resources such as HMDB (Human Metabolome DataBase <http://www.hmdb.ca/>) aiming at bridging the gap between biological, clinical and chemical data.