

## **KSR – Kinase substrate relationship**

### **DB Description**

We extracted information from the primary data source, which includes multiple database (DB), described in the study conducted by Savage et al., published in Clinical Protocols in 2020.

Furthermore, we integrated data from the most relevant and interconnected databases, as illustrated in Figures 1 and 2, namely PhosphoSitePlus, SIGNOR, PhosphoELM, SwissProt and HPRD. This integration allowed for a comprehensive analysis and synthesis of the information presented.

The following processing steps have been applied:

1. Species identification: Homo sapiens (human) data have been selected.
2. Gene name mapping with UniProt: gene names associated with Homo sapiens are mapped to their corresponding entries in the UniProt database.
3. Filtering redundant information: redundant or duplicate information is filtered out to ensure the dataset contains only unique entries.

These processing steps are crucial for refining the dataset and preparing it for further analysis or downstream applications.