

# A Linked Data Approach to Help Identify Therapeutic Targets for Cancer

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## Objective

To integrate data derived from biological experimental results with public biomedical data sources such as Disasome, DrugBank and KEGG.

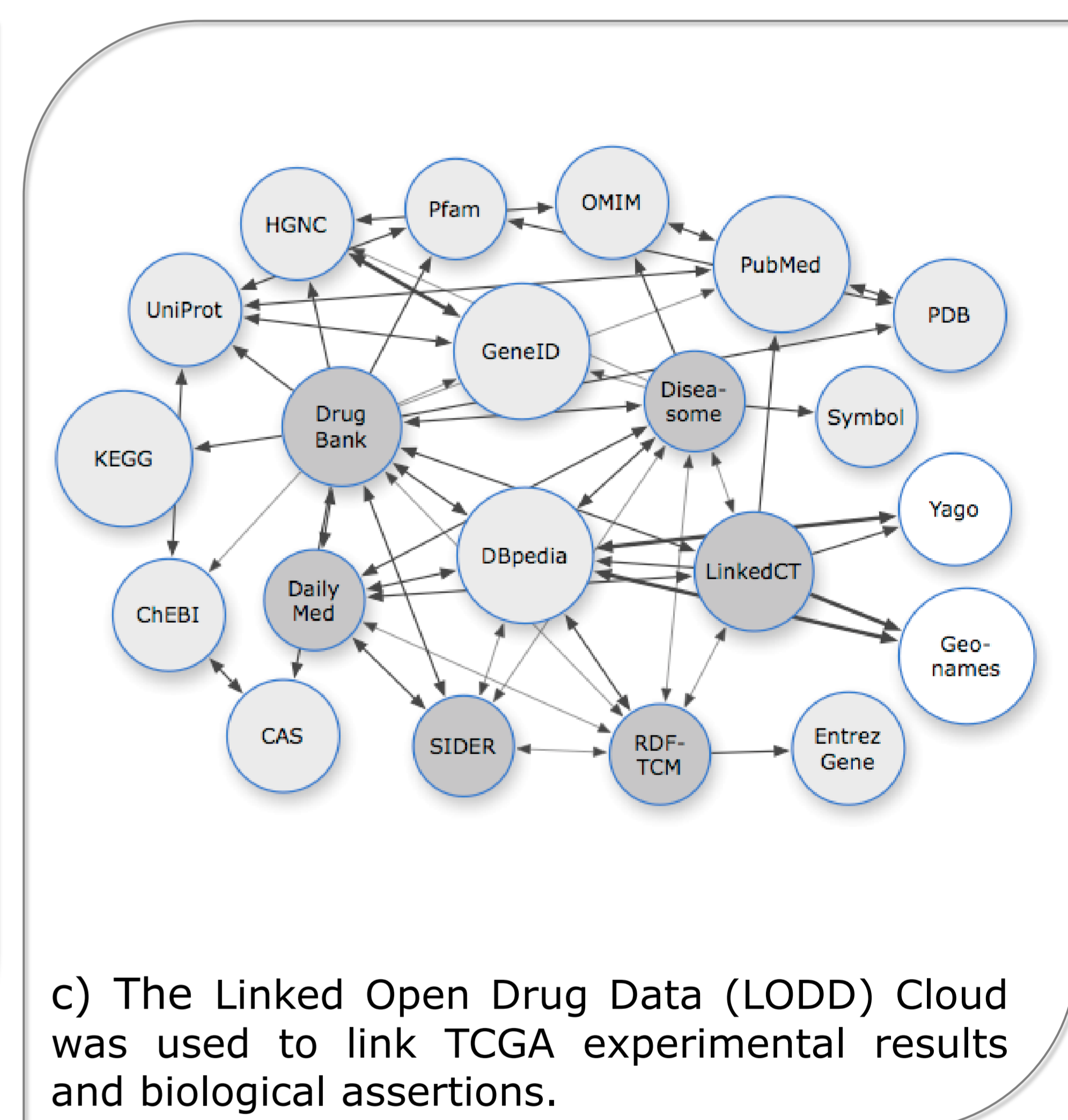
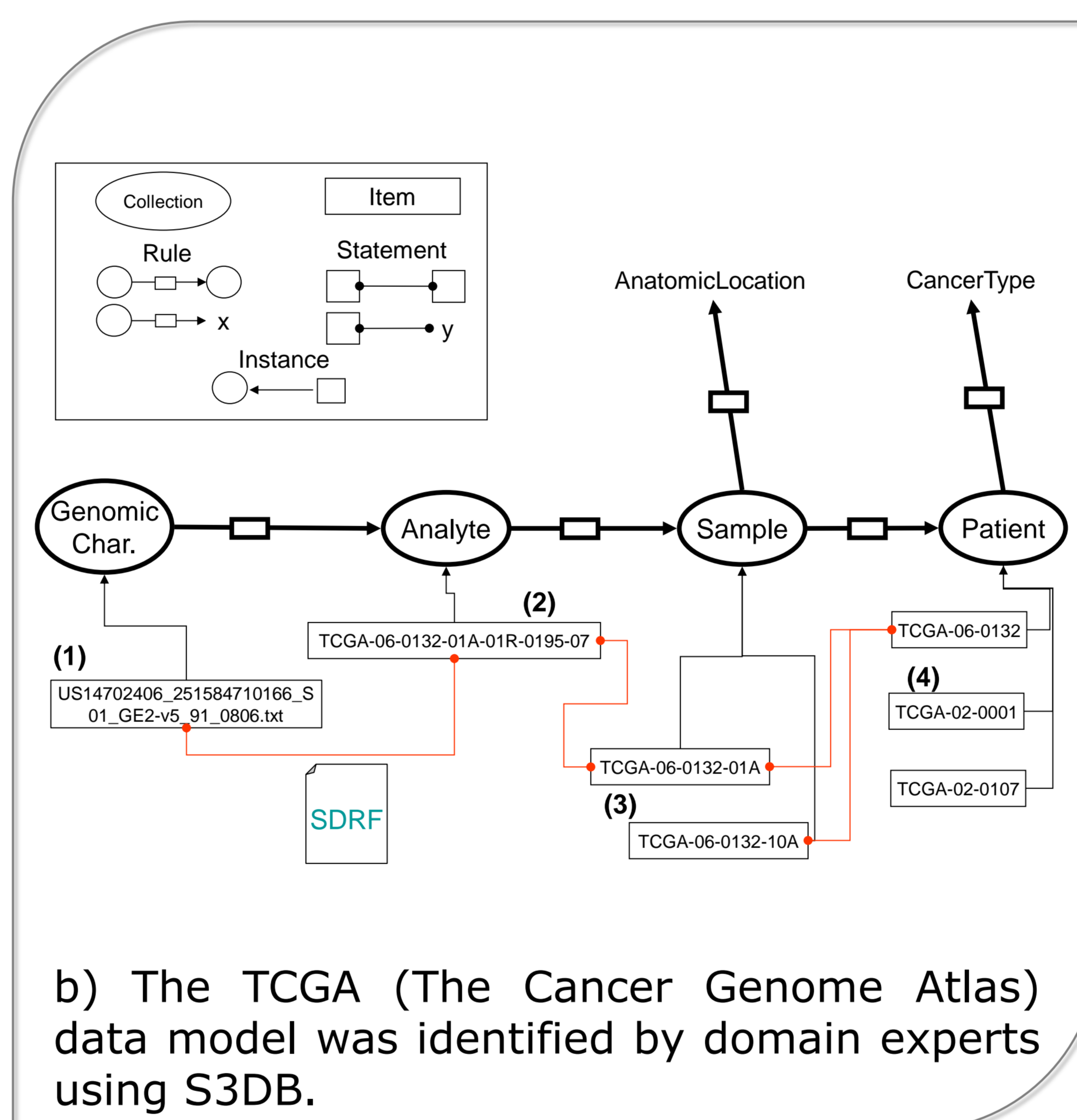
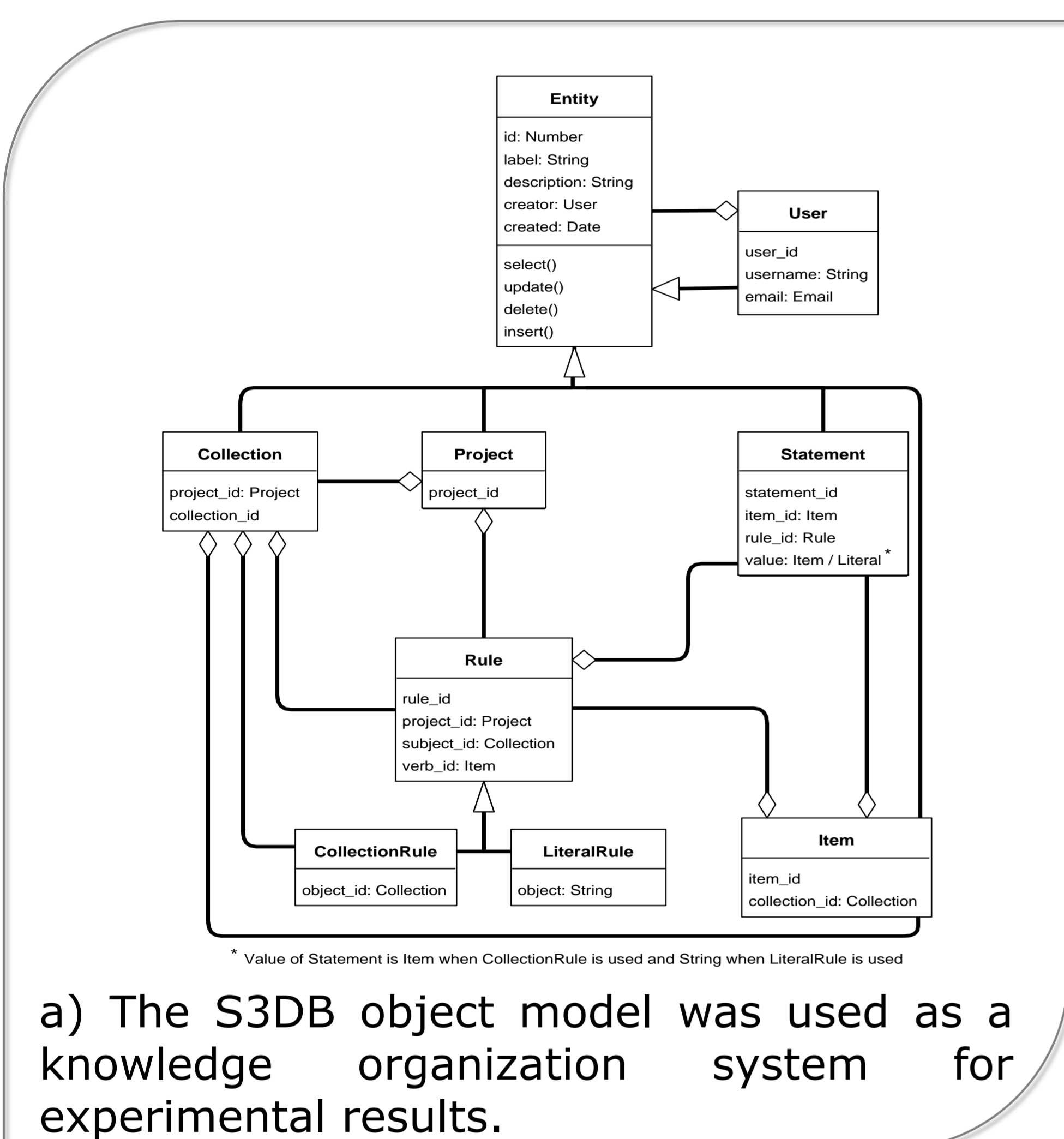
## Challenges

Integrating the biological knowledge needed to identify cancer “driver” mutations remains a challenge due to:

- 1) **Heterogeneous experimental data**
- 2) **Distributed biomedical data sources**
- 3) **Controlled access clinical information**

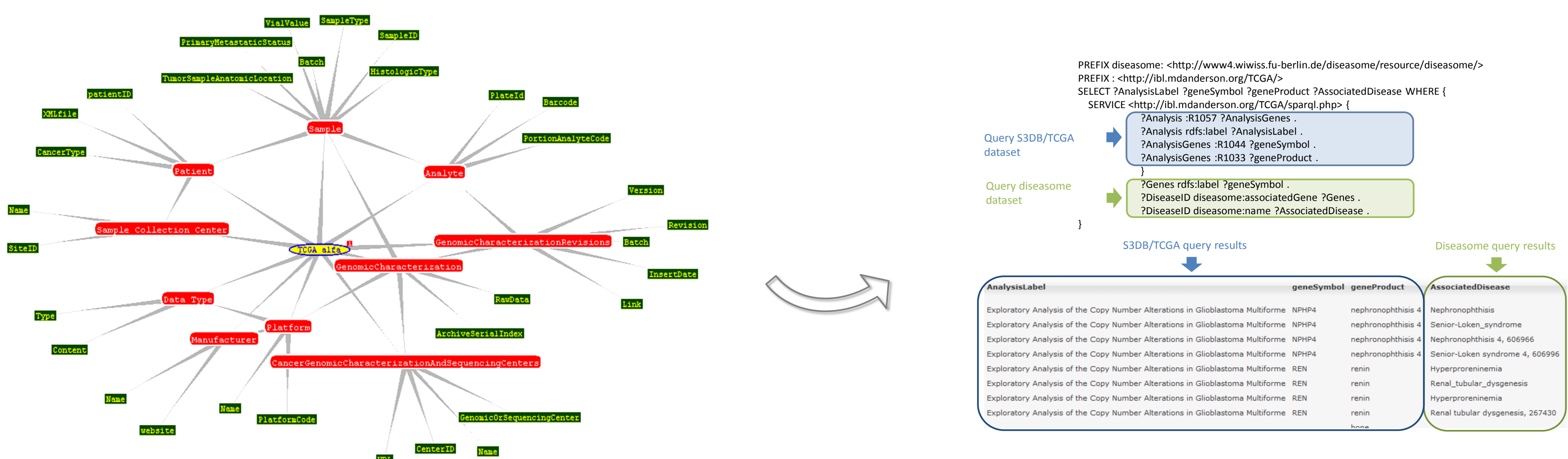
## Methods

Our approach to help identify therapeutic targets for cancer required the interoperation between three components:



## Results

Linking experimental results with biological knowledge in the LODD cloud enabled biological domain experts to easily identify relevant cancer “driver” mutations.



S3DB Model published in Public Library of Science (PLoS) One, BMC Bioinformatics and Nature Biotechnology  
TCGA Ontology published in Journal of Biomedical Informatics