

# PeptiCKDdb - peptide- and protein-centric database for the investigation of genesis and progression of chronic kidney disease

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## OBJECTIVES

Integration of experimental results followed by an extensive data analysis and mining can lead to the discovery of novel biomarkers of chronic kidney disease (CKD). The present study aims at the development of a peptide and protein centric database integrating high-throughput peptidomics and proteomics data retrieved from other existing databases and state-of-the-art literature related to CKD. The database supports comprehensive data analysis in order to achieve a better understanding of kidney pathologies.

## METHODS

### Literature mining, data extraction

- Selection criteria:
- human case/control study (CKD specific)
  - information about differentially expressed molecules with fold-change and/or regulation

### Database mining

CKDdb [1], UPdb [2], KUPKB [3]



### Database development

- data preprocessing (cleaning, unification, integration)
- relational database structure
- Microsoft SQL Server

119 publications in total

26 peptidomics

81 proteomics

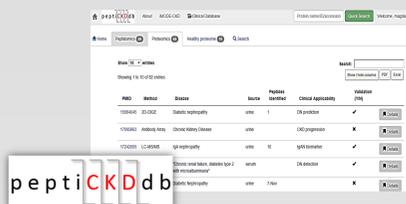
12 healthy proteome



### Website creation & deployment

- three-tier architecture (presentation, logic, data)
- HTML, CSS, JavaScript, ASP.NET Web Pages

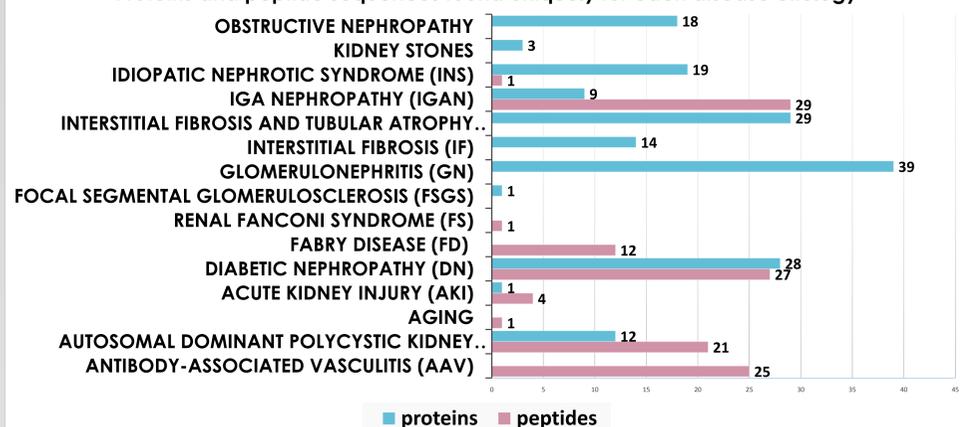
[www.peptiCKDdb.com](http://www.peptiCKDdb.com)



## SHOWCASE

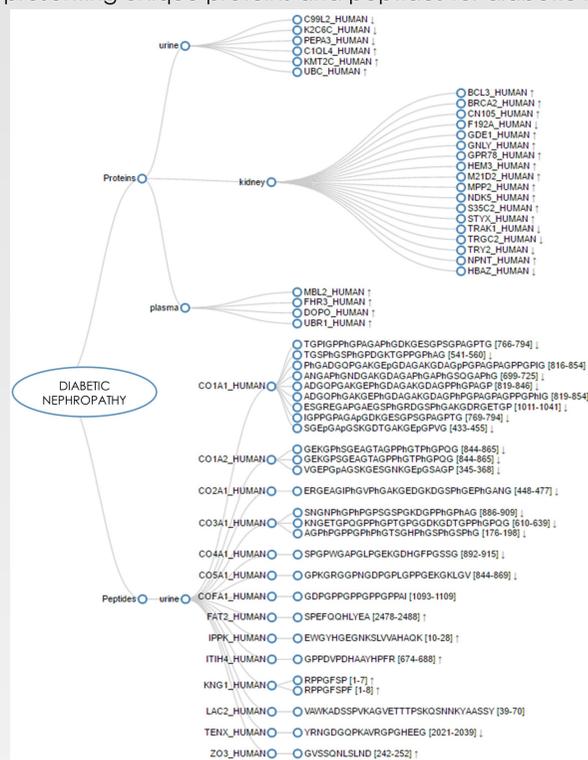
As a proof of concept, we demonstrate the usability of our platform in biomarker research. For each disease etiology, we compared proteomics and peptidomics profiles, aiming at identification of unique features associated with each disease. If not previously investigated, such features have the possibility to be disease-specific putative biomarkers.

### Proteins and peptide sequences found uniquely for each disease etiology



We explored the unique molecules found in the studies on diabetic nephropathy (DN). Based on the collected data, 28 proteins and 27 peptide sequences, originating from 14 different proteins were found uniquely associated DN. Primary functional assessment of molecules showed potential implication in characteristic processes related to kidney pathology. Thus, these proteins might be relevant in relation to diabetic nephropathy.

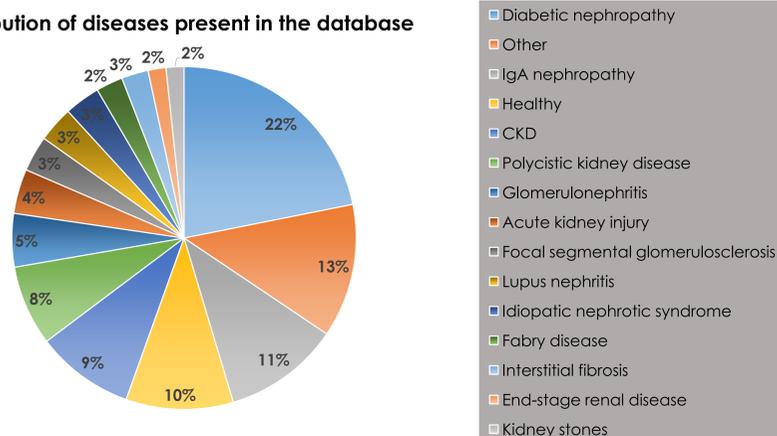
Dendrogram representing unique proteins and peptides for diabetic nephropathy (DN)



## RESULTS

Literature and database mining resulted in the identification of 119 relevant studies of body fluids and kidney tissue (26 peptidomics and 81 proteomics on human CKD, 12 healthy proteome profiling).

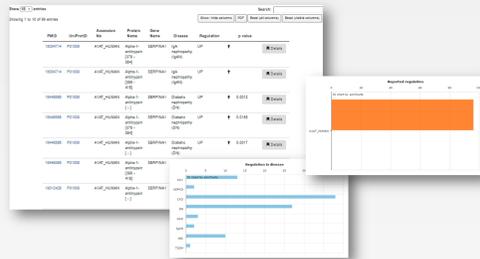
### Distribution of diseases present in the database



Dedicated web interface, equipped with multiparametric search engine to support complex user queries and data export and visualization tools, enable easy browsing of the data and comprehensive analysis.

Database search interface

Graphical representation of query results



## CONCLUSIONS

The peptiCKDdb is a repository of manually curated peptidomics and proteomics datasets extracted from scientific publications related to CKD. It can serve as a knowledge base for scientists seeking confirmation of their findings, as well as a source of data for integrative analysis supporting biomarker research in the field of renal pathology.

Database URL: [www.peptickddb.com](http://www.peptickddb.com)

## REFERENCES

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- Husi, H., Barr, J.B., Skipworth, R.J., et al. (2013) The Human Urinary Proteome Fingerprint Database UPdb. International journal of proteomics, 2013, 760208.
- Jupp, S., Klein, J., Schanstra, J., et al. (2011) Developing a kidney and urinary pathway knowledge base. Journal of biomedical semantics, 2 Suppl 2, S7.



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Chronic Kidney Disease. Pathophysiology, progression & risk factors.

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