

# miREC: A database of miRNAs involved in endometrial cancer

Benjamin Ulfenborg<sup>1,\*</sup>, Sanja Jurcevic<sup>2,\*</sup>, Angelica Lindlöf<sup>1</sup>, Karin Klinga-Levan<sup>2</sup> and Björn Olsson<sup>1</sup>

<sup>1</sup>Systems Biology Research Centre – Bioinformatics, University of Skövde, Box 408, 541 28 Skövde, Sweden

<sup>2</sup>Systems Biology Research Centre – Tumor Biology, University of Skövde, Box 408, 54128 Skövde, Sweden

\*These authors contributed equally to this work.

The miREC database is an organized collection of information about miRNAs and their target genes that have been shown to be differentially expressed in endometrial cancer.

## INTRODUCTION

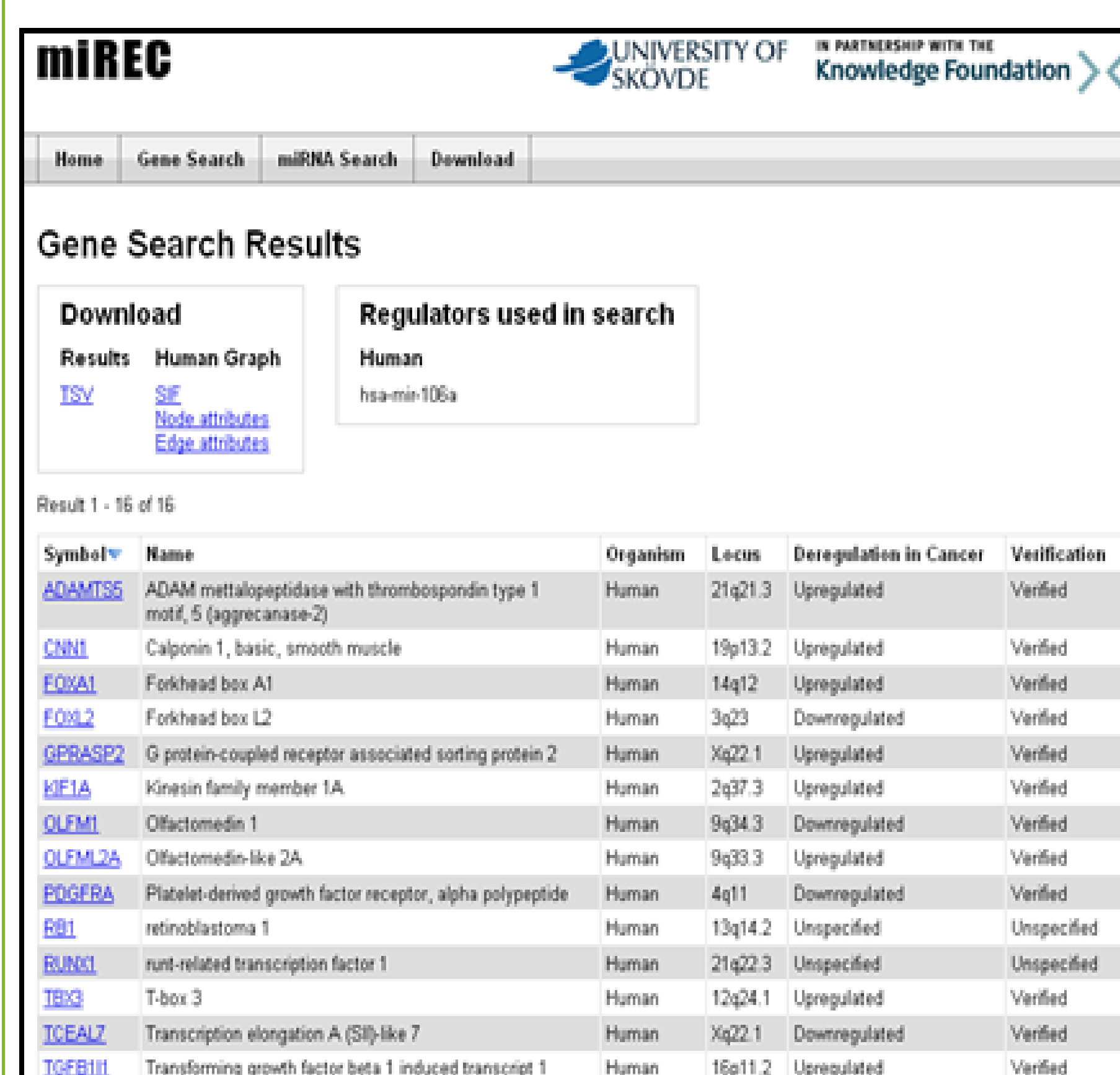
Endometrial cancer is the most frequently diagnosed gynecological malignancy in the western world, with approximately 142 000 new cases each year.

MicroRNAs (miRNAs) are small non-protein coding RNA molecules that regulate gene expression by inhibition of protein translation or by degradation of their target mRNAs. The miRNAs play a key role in the regulation of essential biological processes, including development, differentiation, cell proliferation, apoptosis and stress response. Since miRNAs play a key regulatory role in cells, their deregulation can contribute to human diseases, such as cancer.

We have established the database miREC (miRNAs involved in Endometrial Cancer) containing information about miRNAs that have been experimentally shown to be differentially expressed in EAC, as well as their target genes, thereby providing a resource contributing to a better understanding of the impact of aberrant miRNAs in EAC development (Figure 1). Available at [www.mirecdb.org/](http://www.mirecdb.org/).



Figure 1: miREC database main page



Symbol	Name	Organism	Locus	Deregulation in Cancer	Verification
ADAMTS5	ADAM metalloproteinase with thrombospondin type 1 motif, 5 (aggrecanase-2)	Human	21q21.3	Upregulated	Verified
CNN1	Calponin 1, basic, smooth muscle	Human	19p13.2	Upregulated	Verified
FOXO1	Forkhead box A1	Human	14q12	Downregulated	Verified
FOXO2	Forkhead box L2	Human	3q23	Downregulated	Verified
GPBASP2	G protein-coupled receptor associated sorting protein 2	Human	Xq22.1	Upregulated	Verified
KIF1A	Kinesin family member 1A	Human	2q37.3	Upregulated	Verified
OLEMI1	Olfactomedin 1	Human	9q34.3	Downregulated	Verified
OLEML2	Olfactomedin-like 2A	Human	9q33.3	Upregulated	Verified
PDGFRA	Platelet-derived growth factor receptor, alpha polypeptide	Human	4q11	Downregulated	Verified
RBI1	retinoblastoma 1	Human	13q14.2	Unspecified	Unspecified
RUNX1	runx-related transcription factor 1	Human	21q22.3	Unspecified	Unspecified
TBX3	T-box 3	Human	12q24.1	Downregulated	Verified
TCEAL7	Transcription elongation A (SII)-like 7	Human	Xq22.1	Upregulated	Verified
TGFBI3L	Transforming growth factor beta 1 induced transcript 1	Human	16p11.2	Upregulated	Verified

Figure 2: Results from a search for genes with hsa-mir-106a as miRNA regulator.

## METHODS

The relational database miREC holds information, extracted from literature, about miRNAs that have been shown to be aberrantly expressed in EAC and regulator-target relationships between these miRNAs and their target genes. While all miRNA deregulations have been experimentally confirmed, most of the miRNA-target connections were inferred by target prediction software.

The information from the literature was complemented by information from miRBase, TarBase, miRecords, Ensemble and the Human Genome Nomenclature Committee's database HGNC. The miRNAs and genes in miREC have been localized to chromosomes using mirBase, Ensembl and HGNC. The naming scheme follows the HGNC nomenclature.

## WEB INTERFACE AND UTILITY

Search forms at the web interface allow the user to search for genes or miRNAs. The main page presents a quick search option, while advanced search options can be found through a menu.

The result of a search is displayed as a table in the web browser. It is also possible to download all the hits in a text file. Figure 2 shows an example gene search result table and a Figure 3 shows a network generated from the same results.

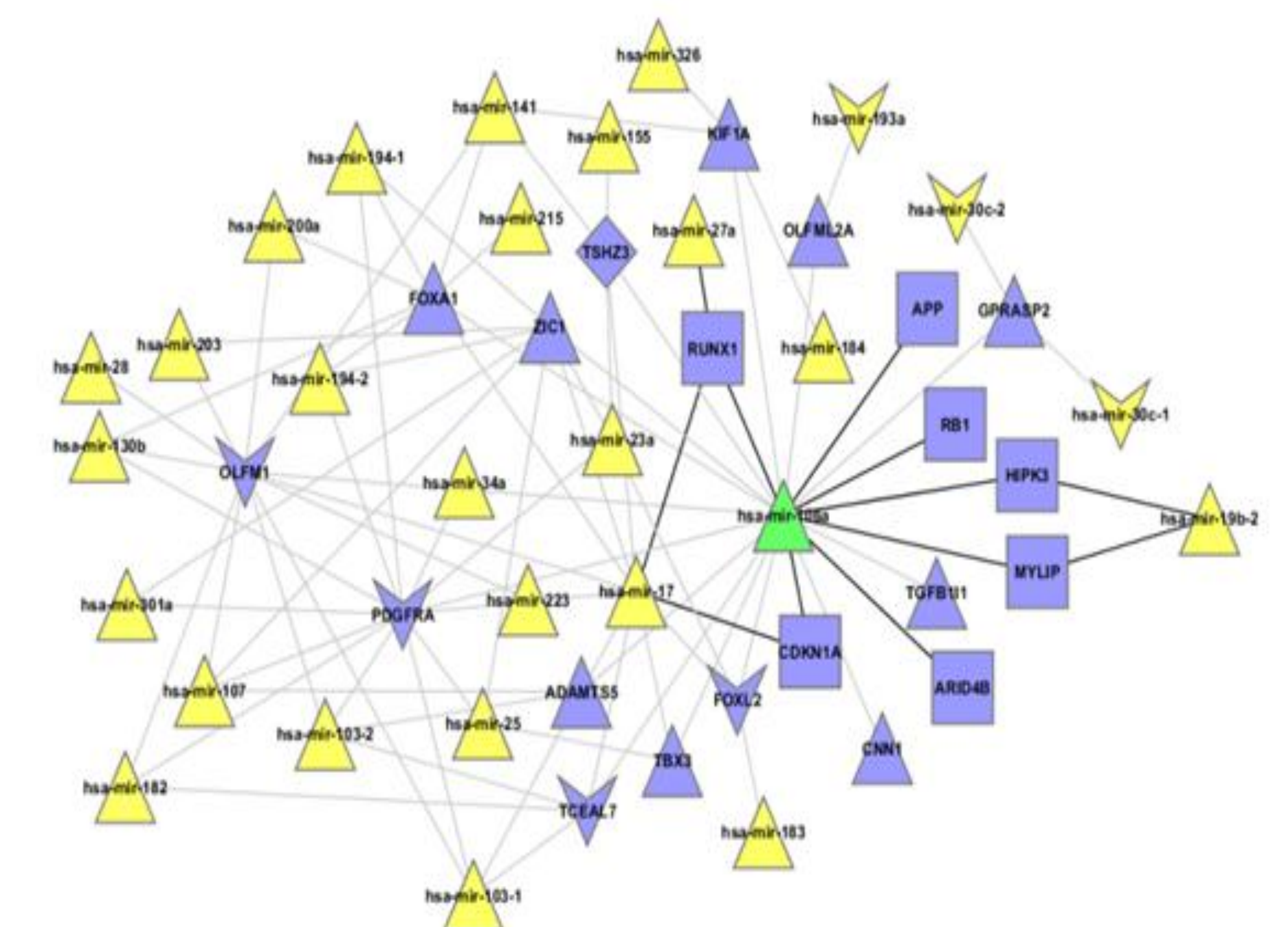


Figure 3: Network generated from the same search, showing hsa-mir-106a, its target genes and other miRNAs regulating these genes.

## CONCLUSION

The database can be used to map connections between miRNAs and their target genes in order to identify specific miRNAs that are potentially important for the development of EAC.

Sanja Jurcevic  
sanja.jurcevic@his.se



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