# Mining for Medical Relations in Research Articles

Identification of Proteins

By Anna Palmqvist Sjövall and Eric Holmström

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Results



lssues Improvements

Biology Background

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# Lysosomal Cell Death

Eukaryotic cells Apoptosis, Necrosis... Alzheimer's and Parkinson's disease



# Genes and Proteins

Genes: blueprints for proteins. Not all genes code for proteins.

Background

# Cell death articles/year

1770 1820 1870 1920 1970 2020

Over 800 000 articles in total.



Introduction

Investigate the role of protein/genes in relation to lysosomal cell death in order to induce/inhibit diseases..

Introduction

5



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#### PubMed

Database for life sciences and biomedical literature. ~20 000 000 abstracts.

UniProt	
BLAST Align	Retrieve/ID map
UniPro	otKB - C
Protein names <sup>4</sup>	Recommended m LeucinetRN Alternative name • Leucyl-tRNA • Short name:
Gene names <sup>1</sup>	Name:leuS 🔗 U Ordered Locus N
Örganism <sup>i</sup>	Escherichia coli C
Taxonomic identifier <sup>1</sup>	83334 [NCBI]



A manually annotated protein database. ~560 000 names of genes/proteins. One protein = multiple names.

S NCBI Resource	es 🕑 How To 🖂	
SNCBI Vational Center for Biotechnology Information	All Database	
NCBI Home		
<u>Resource List (A-Z)</u>		
All Resources	1	
Chemicals & Bioassa	iys	
Data & Software		
DNA & RNA		
Domains & Stru		
Genes & Expres		رکم
Genetics & Mec		$\langle \rangle$
Genomes & Ma		
Homology	G	enetaa
Literature		
Proteins	Contains 2	20 000 se
Sequence Anal	tagged w	ith gene/J
Taxonomy	names. Us	ed as vali
Training & Tutor	set for	text mini
Variation		

20 000 sentences with gene/protein Jsed as validation text mining.

as well as prevention and treatment pn



Podocyte apoptosis is considered as the important element that promotes the development and progress of membranous nephropathy (MN). Unfortunately, the underlying mechanism of podocytes apoptosis in MN remains elusive. We compared the renal expressions of miR-130a-5p and M-type phospholipase A2 receptor (PLA2R) between MN patients (n = 30) and 30 controls by gRT-PCR and western blot, respectively. The podocyte damage model in vitro was established by angiotensin II (Ang II, 100 nmol/L) exposure for 24 h. Interaction between miR-130a-5p and PLA2R was determined using dual-luciferase reporter gene assay. MN mice were induced by intravenous injection of cBSA. In this study, miR-130a-5p expression was significantly decreased both in the renal biopsy specimens from MN patients and podocyte cell line AB8/13 following stimulation of Ang II. Overexpressed miR-130a-5p in AB8/13 cells significantly attenuated the Ang II induced-apoptosis in vitro. In contrast, down-regulated miR-130a-5p induced podocyte apoptosis. PLA2R was identified as the target of miR-130a-5p in AB8/13 cells. And up-regulated or down-regulated PLA2R could obviously attenuate the effect of miR-130a-5p overexpression or knockdown on the apoptosis of AB8/13 cells. Furthermore, it was also observed that overexpressed miR-13Oa-5p by miR-13Oa-5p agomir could obviously alleviate renal injury in MN mice. In conclusion, decreased miR-130a-5p was contributed to the pathological mechanism of MN through increasing PLA2R expression, which induced podocyte apoptosis.

Layers				<b>y</b>			
ysomatches N=6							
protmatches N=13 Perms N=624	#	term	text	type			
	#0	'Podocyte'	span(main[0:8]) = 'Podocyte'	'WORD_TITLE_CASE'			
	#1	'apoptosis'	span(main[9:18]) = 'apoptosis'	'WORD'			
	#2	'is'	span(main[19:21]) = 'is'	'WORD'			
	#3	'considered'	span(main[22:32]) = 'considered'	'WORD'			
	#4	'as'	span(main[33:35]) = 'as'	'WORD'			
			· · · ·				
	#621	'podocyte'	span(main[1520:1528]) = 'podocyte'	'WORD'			
	#622	'apoptosis'	span(main[1529:1538]) = 'apoptosis'	'WORD'			
	#623	11	span(main[1538:1539]) = '.'	'PERIOD'			

Method:

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#### Layer: protmatches

		1.0					Mathed
#	id	terms	text				Dictionary
#0	703295	[Node <terms#311>]</terms#311>	span(main[279:292]) = 'phospholipase'				10
#1	15984	[Node <terms#311>]</terms#311>	span(main[293:295]) = 'A2'				
#2	<mark>462220</mark>	[Node <terms#311>]</terms#311>	span(main[306:311]) = 'PLA2R'				
#3	469720	[Node <terms#311>]</terms#311>	span(main[365:368]) = 'PCR'				
#4	7 <mark>13</mark> 206	[2 nodes from layer: terms]	span(main[455:469]) = 'angiotensin	Iľ			
#5	33667	[2 nodes from layer: terms]	span(main[471:477]) = 'Ang II'				
#6	<mark>462220</mark>	[Node <terms#311>]</terms#311>	span(main[546:551]) = 'PLA2R'				
#7	705614	[3 nodes from layer: terms]	span(main[578:602]) = 'luciferase re	eporte	er gei	ne' I	
#8	33667	[2 nodes from layer: terms]	span(main[838:844]) = 'Ang II'				
#9	33667	[2 nodes from layer: terms]	span(main[917:923]) = 'Ang II'			Layer	: lysomatches
#10	462220	[Node <terms#311>]</terms#311>	span(main[1020:1025]) = 'PLA2R'	#	id	terms	text
<mark>#11</mark>	<mark>462220</mark>	[Node <terms#311>]</terms#311>	span(main[1122:1127]) = 'PLA2R'	#0	0	[Node <terms#623>]</terms#623>	span(main[9:18]) = 'apoptosis'
#13	462220	[Node <terms#311>]</terms#311>	span(main[1488:1493]) = 'PLA2R'	#1	0	[Node <terms#623>]</terms#623>	span(main[186:195]) = 'apoptosis'
				#2	0	[Node <terms#623>]</terms#623>	span(main[932:941]) = 'apoptosis'

#3 0 [Node<terms#623>] span(main[1009:1018]) = 'apoptosis'

#4 0 [Node<terms#623>] span(main[1215:1224]) = 'apoptosis'

#5 0 [Node<terms#623>] span(main[1529:1538]) = 'apoptosis'

#### Stopwords

the, and, in, i, me, my, he, yourself, she, it, its..

#### **Dominant right**

11S globulin seed storage protein G3

11S globulin seed storage protein G3 acidic chain

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<b>Statistics</b> Evaluation with Genetag		Actual		ርስን	Recall	ີ (ໃນ ການ Precision
		Positive	Negative	15% TPR = TP/(TP+F	N)	
Predicted	Positive	™ <b>2680</b>	<sup>FP</sup> ≈ 5025		Fl-score	
	Negative	<sup>FN</sup> <b>15553</b>	TN 🔗 📮	F1 = 2*PP∨*TPF	R/(PPV+TPR)	21%

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Statistics		Actual			
Comparison for 10 abstracts		Positive	Negative		
Predicted	Positive	™ ✓ <b>119</b>	<sup>FP</sup> <b>23</b>		
	Negative	FN 13	TN & =		







## Observations

- TNF-α vs. TNF-alpha
- IL1-13 = IL1, IL2, IL3, ... IL13
- dual-luciferase reporter gene assay

#### 💥 Issues

- Unicode characters
- Abbreviation ambiguities
- Ignoring context
- Family names





# Future Improvements

- Machine Learning-model
- Species recognition (e.g. HUMAN & RAT)
- GUI
- More extensive evaluation

## Benefits

- Includes context  $\rightarrow$  higher accuracy
- Visualize results, easier to use



# Thanks

Does anyone have any questions?

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