

Identification and characterization of missing proteins from human chromosome 9

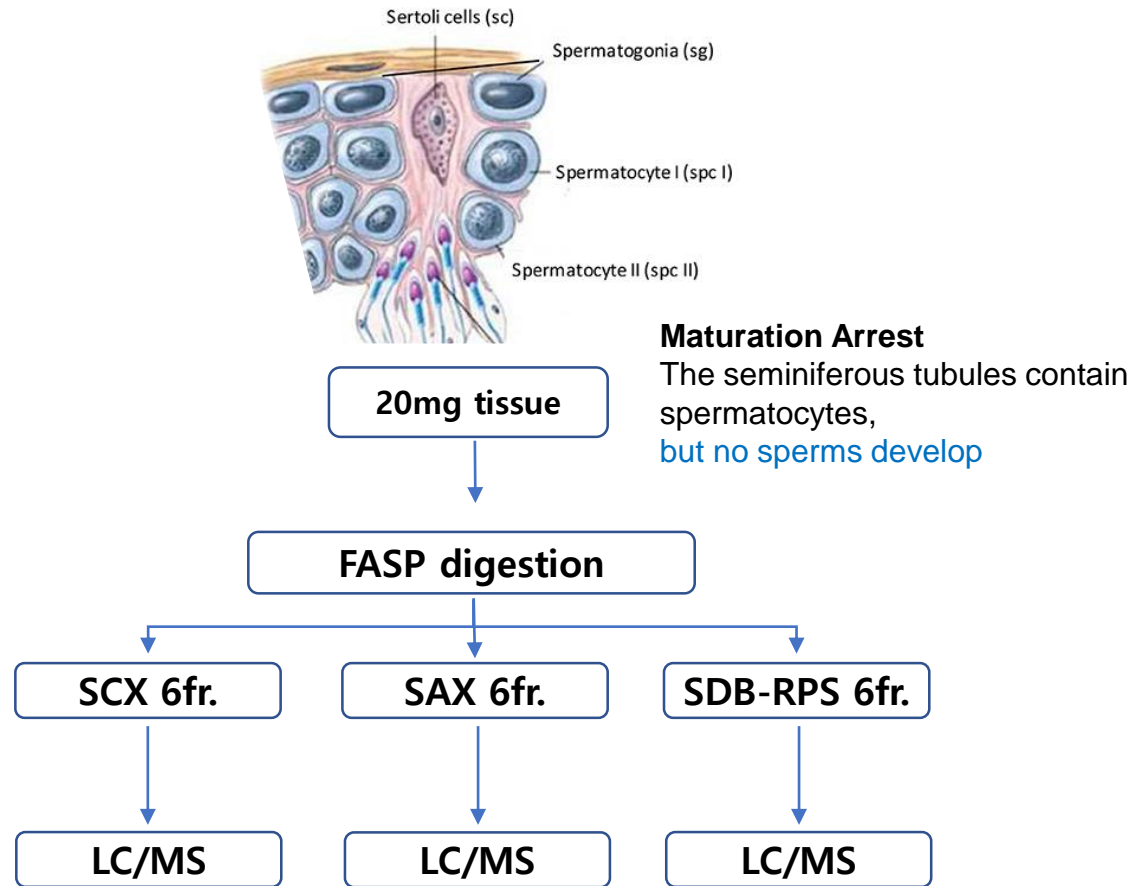
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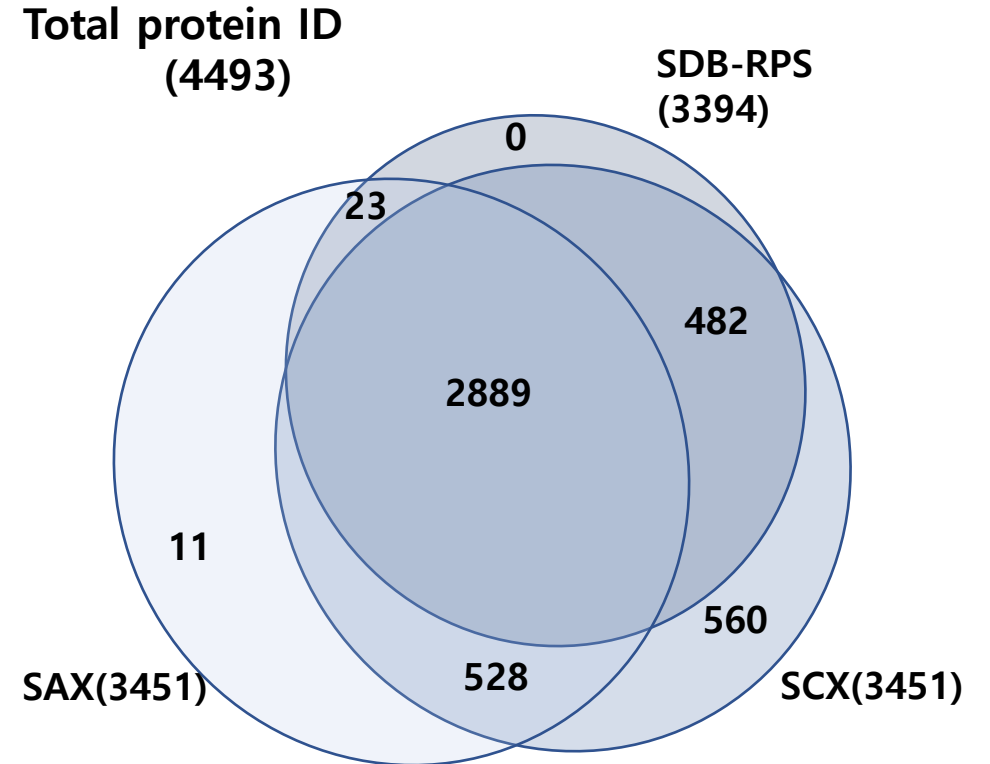
1. MP Identification Trials On Testis Disease Sample

2. Characterization of MPs on Chr.9

Testis Analysis for Identification of MPs



EASY-nLC1000 / 150mm col. / 2hr gradient
Q-Exactive
MaxQuant (Pep FDR <1%, Prot FDR <1%)



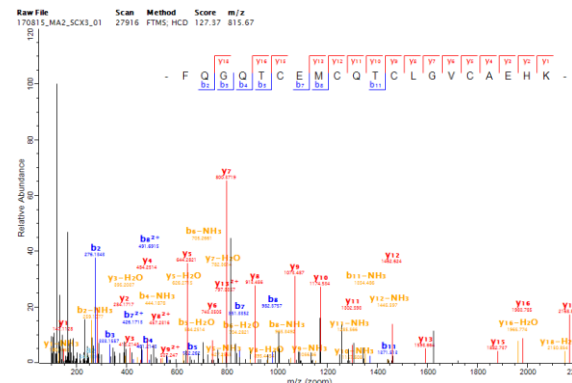
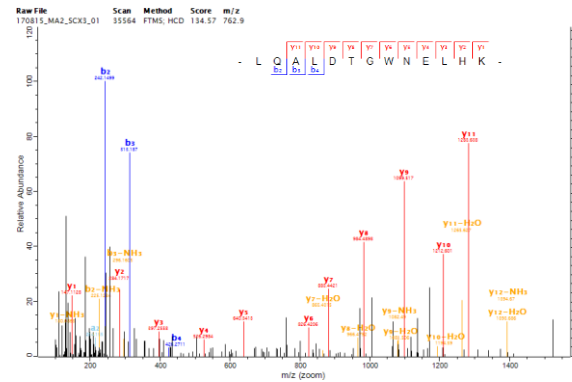
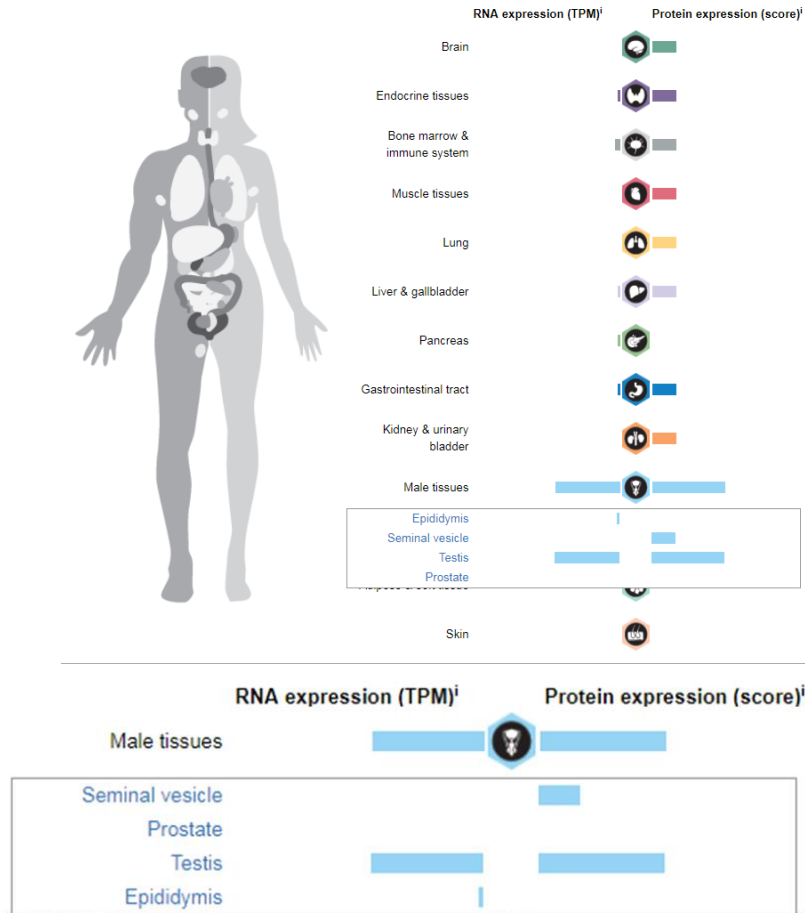
➔ **MP IDs (1)**
: DEFB123

Claimed by Wang et al., JPR, 2017 Dec

Homology on MPs of High Resemblance

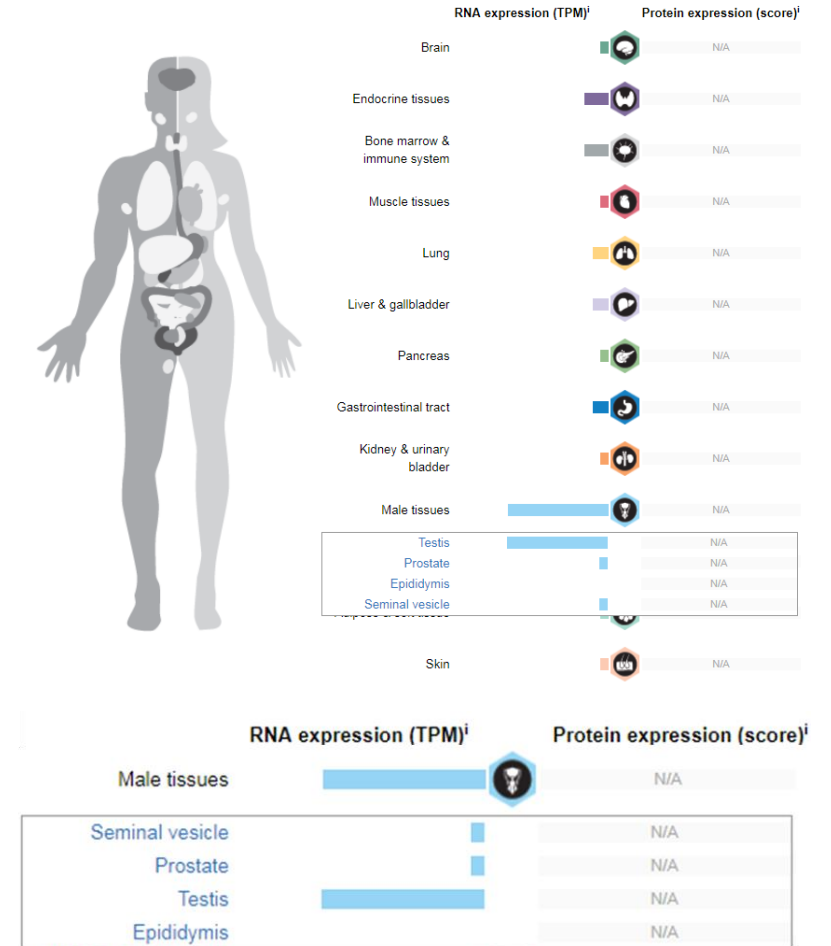
RGPD1

RANBP2-like and GRIP domain-containing protein 1



RGPD2

RANBP2-like and GRIP domain-containing protein 1



Homology on MPs of High Resemblance

RGPD1 vs RGPD2

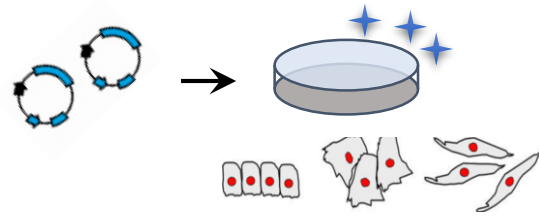
[PODJD1](#) | [RGPD2_HUMAN - RANBP2-like and GRIP domain-containing protein 2](#) | [Homo sapiens \(Human\)](#)
 E-value: 0.0
 Score: 8972
 Ident.: 99.9%
 Positives : 99.9%
 Query Length: 1748
 Match Length: 1756

PODJD0	RGPD1_HUMAN	17	KLRGFYFAKLYVEAKEYDLAKKYVCTYLSVQERDPPAHRFLGLLYELEENTEKAVECYRR	76
PODJD1	RGPD2_HUMAN	25	KLRGFYFAKLYVEAKEYDLAKKYVCTYLSVQERDPPAHRFLGLLYELEENTEKAVECYRR	84
...				
PODJD0	RGPD1_HUMAN	1277	NFSFKSALSLSKSPA ¹²⁷⁷ KL ¹²⁷⁸ NQSGTSVGTDEESDVTQE ¹²⁷⁹ EEFDGQV ¹²⁸⁰ FEPV ¹²⁸¹ WFLPDLVEVSSGEE	1336
PODJD1	RGPD2_HUMAN	1285	NFSFKSALSLSKSPA ¹²⁸⁵ KL ¹²⁸⁶ NQSGTSVGTDEESDVTQE ¹²⁸⁷ EEFDGQV ¹²⁸⁸ FEPV ¹²⁸⁹ WFLPDLVEVSSGEE	1344
PODJD0	RGPD1_HUMAN	1337	NEQWVFSH ¹³³⁷ AE ¹³³⁸ LYRYDKDV ¹³³⁹ GQW ¹³⁴⁰ KERGI ¹³⁴¹ GD ¹³⁴² IK ¹³⁴³ ILQ ¹³⁴⁴ YDNKQV ¹³⁴⁵ RI ¹³⁴⁶ YMF ¹³⁴⁷ RDQV ¹³⁴⁸ LKLCANHRI ¹³⁴⁹ T	1396
PODJD1	RGPD2_HUMAN	1345	NEQWVFSH ¹³⁴⁵ MA ¹³⁴⁶ E ¹³⁴⁷ LYRYDKDV ¹³⁴⁸ GQW ¹³⁴⁹ KERGI ¹³⁵⁰ GD ¹³⁵¹ IK ¹³⁵² ILQ ¹³⁵³ YDNKQV ¹³⁵⁴ RI ¹³⁵⁵ YMF ¹³⁵⁶ RDQV ¹³⁵⁷ LKLCANHRI ¹³⁵⁸ T	1404

These proteins have only one unique peptide.

1. MP Identification Trials On Testis Disease Sample
- 2. Characterization of MPs on Chr.9**

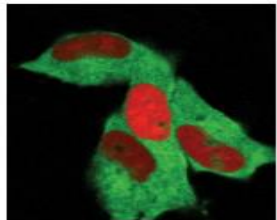
Characterization Strategy of MPs



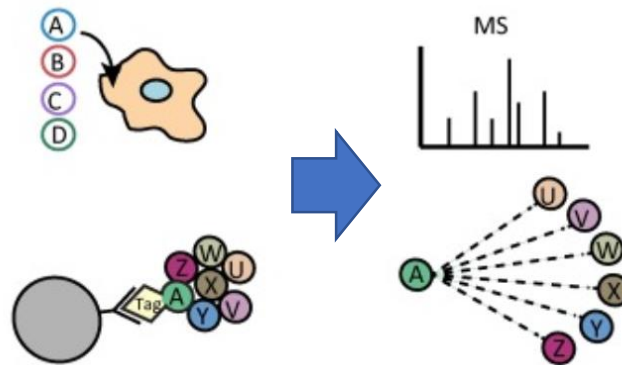
O/E in human cell line



Subcellular Localization



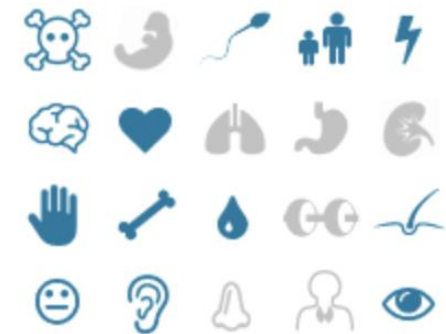
Interactome Analysis



K/O mice



In vivo Study



Priority uPE1 Selection

uPE1: 59 proteins (Chr.9,)
 → 10 proteins were selected
 → 2 proteins for this year

Priority	Acc. code	Protein name	Gene name	Chr	Years
1	NX_Q9UFN0	Protein NipSnap homolog 3A	NIPSNAP3A	9	2018
2	NX_Q5T7W7	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 2	TSTD2	9	2018
3	NX_Q7Z304	MAM domain-containing protein 2	MAMDC2	9	
4	NX_Q7L5A3	Protein FAM214B	FAM214B		
5	NX_Q5JUQ0	Protein FAM78A	FAM78A	9	
6	NX_Q2TAM9	Tumor suppressor candidate gene 1 protein	TUSC1	9	
7	NX_Q96J77	Tumor protein D55	TPD52L3		
8	NX_Q9NX38	Protein Simiate	FAM206A	9	
9	NX_Q15527	Surfeit locus protein	SURF2	9	
10	NX_Q8N5I2	Arrestin domain-containing protein 1	ARRDC1	9	

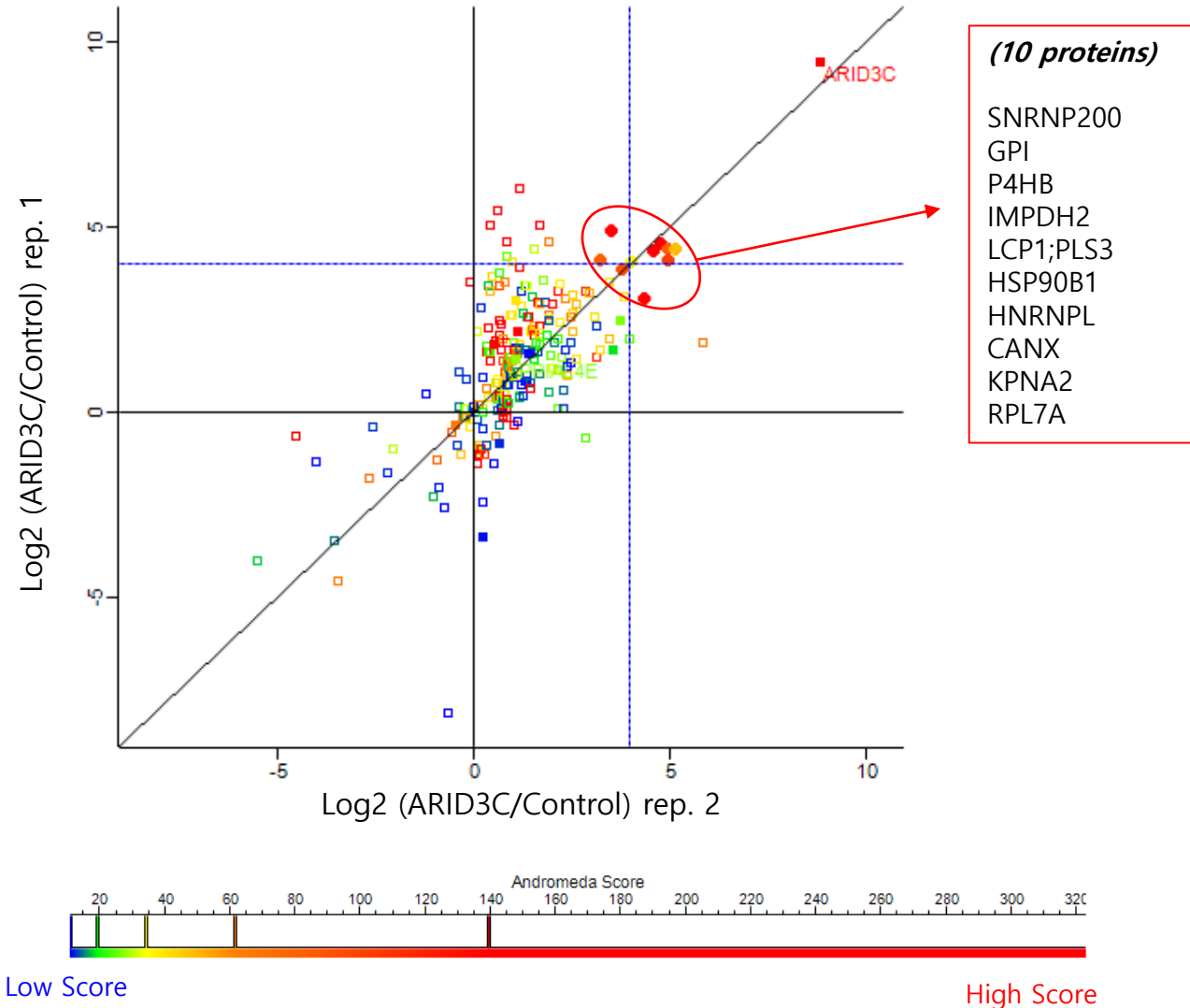
Orange: IMPC KO mice supported

Gene	Production	Phenotype	Register
Nipsnap3a	ES Cells Mice	phenotype data available	➔ Interest

ARID3C IP-MS: Interactome Selection

ARID3C

- AT-rich interactive domain-containing protein 3C
- Inferred from homology
- Molecular Function: DNA-binding
- Biological Process: Transcription, Transcription regulation
- Subcellular location: Nucleus



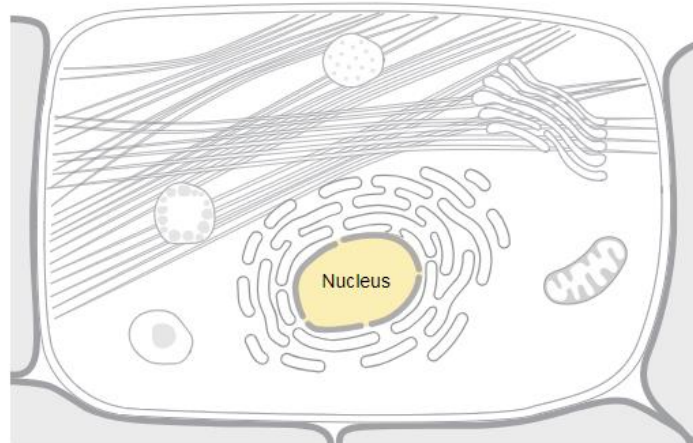
ARID3C IP-MS: Network analysis

ARID3C brief information

GO - Molecular function (DNA binding)

- chromatin binding Source: Ensembl
- RNA polymerase II regulatory region sequence-specific DNA binding Source: GO_Central
- transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific DNA binding Source: GO_Central

Subcellular localization (Nucleus)



Graphics by Christian Stolte; Source: COMPARTMENTS

Manual annotation Automatic computational assertion

Nucleus

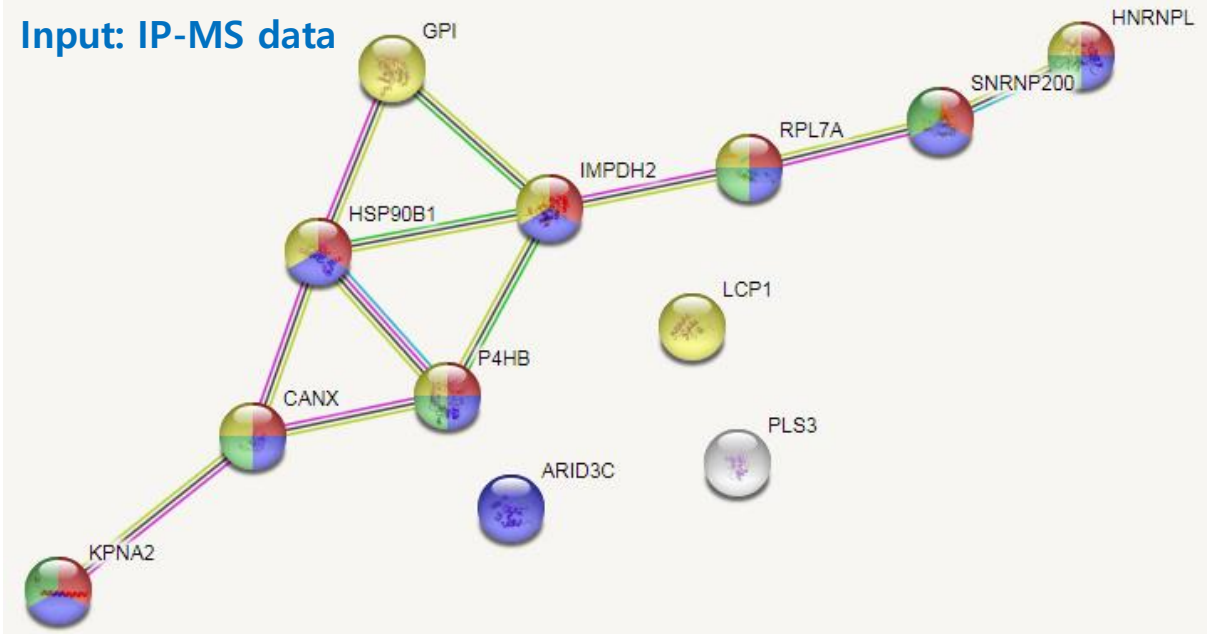
nucleus Source: GO_Central

Other locations

cytoplasm Source: Ensembl

membrane raft Source: MGI

Input: IP-MS data



Make sense

Molecular Function (GO)			
pathway ID	pathway description	count in gene set	false discovery rate
GO:0003723	RNA binding	8	0.00109
GO:0003676	nucleic acid binding	9	0.0251
GO:0044822	poly(A) RNA binding	6	0.0251

Cellular Component (GO)			
pathway ID	pathway description	count in gene set	false discovery rate
GO:0034663	endoplasmic reticulum chaperone complex	2	0.00549
GO:0042470	melanosome	3	0.00549
GO:0070062	extracellular exosome	8	0.00549
GO:0005925	focal adhesion	4	0.00706
GO:0005788	endoplasmic reticulum lumen	3	0.0175

Acknowledgements



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Dr. Dong-Wook Kim



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Yong-In Kim



Prof. Bonghee Lee



Dr. Ghasem Hosseini Salekdeh



taæl zælə'z-a w'ɫ luθθ'zʃə: ,y ʃæ khidi ɔz'ɪŋʃ, zʊŋə: ,y ʃæ mæŋæʃzɪ 'z həl'ʃa & wəl'z'æ, rəθu,læ: 'z k'zə' (hi13c-2098-030013) 'ŋ: ' ɔz'ɪŋʃ ʃa'z'ʊbə ʃæ n'ʃæ'ŋ'ɪ rələ'z-a f'ʊŋ:'ʃæ'ŋ 'z k'zə' (nrf) zʊŋə: ,y ʃæ mæŋæʃzɪ 'z sæŋə, ict & fuʃuzə pl'ɪŋŋəŋə (2014m3a9d5a01073598)