Questionnaire

Your name: [redacted]

Your email address: [redacted]

Your institution:McGill U.

Your position:

Undergraduate student	[ ]
PhD student	[ ]
Technician	[ ]
Postdoc	[ ]
Faculty member	[X]

Question 1: In a scale from 1 - 10, how important do you think it is to have quick access to the following type of information about each gene or protein?

a. Protein-protein interactions [1-10]: 9

b. General function of the gene/protein [1-10]: 9

c. Diseases a gene/protein is involved in [1-10]:9

d. Biochemical pathways a gene/protein is part of [1-10]: 9

e. Cell types/tissues where your gene/protein is expressed [1-10]: 9

f. Your protein's 3D structure (PDB) [1-10]: 9

g. Popularity of the gene/protein in **social networks (Twitter, Facebook)** [1-10]: 5

h. Knowing the **average impact factor** of the journals where a particular gene/protein is normally published [1-10]: 3

i. The **relative scientific weight (e.g. by h-index)** of the scientists that work on your gene/protein [1-10]: 6

j. How popular your gene/protein is in recently awarded grants (this is public information once a grant is awarded) [1-10]: 8

k. What other genes/proteins are discussed in the context of your protein [1-10]: 9

l. How your gene/protein is regulated at the transcriptional level [1-10]: 7

m. How your gene/protein is regulated post-translationally (phosphorylation, ubiquitination) [1-10]: 8

n. What is the **most popular type of experiment** other scientists typically do on your gene/protein [1-10]: 9

o. What **biochemical kits** are available for doing these experiments [1-10]: 9

p. Other (explain what type of information) [1-10]: - evolutionary conservation and protein domains - Inhibitors if an enzymes or small molecule interactor. – mouse (IMPC site) /other animal models KO phenotypes.

Question 2: What websites do you visit the most when analysing your list of genes/proteins? IMPC, PUBMED, UNIPRO, Cell MAP, an done of the least known but extraordinary site for future application of proteomics http://gingraslab.lunenfeld.ca/resources.php?cateName=SoftwareAC Gingras (lunenfeld Institute, U of Toronto web site.. and others….

What type of information do you expect to get from each of these websites?
A molecular structure, interactome, location, phenotype, and answers as described in the question 1

Some examples of websites include:

- Ensembl (www.ensembl.org)
- NCBI's Entrez (https://www.ncbi.nlm.nih.gov/Class/MLACourse/Original8Hour/Entrez/)
- NCBI Databases (https://www.ncbi.nlm.nih.gov/search/)
- EuPathDB.org (Eukaryotic Pathogens Database)
- Galaxy (https://usegalaxy.org/)
- PubMed (https://www.ncbi.nlm.nih.gov/pubmed/)
- UniProt (http://www.uniprot.org/)
- KEGG Pathway Database (https://www.genome.jp/kegg/pathway.html)
- Any other resource you use routinely.

Website	**Type of information sought**	**Priority in your analytical pipeline**
Example: PubMed	Find out what's been published about my gene or protein	1
http://gingraslab.lunenfeld.ca/resources.php?cateName=Software	Proteome and interactime virtual cell 3D soon to show up…	
(expand the table as needed)		

Question 3: How often do you perform these exploratory analyses on your genes or proteins:

[a] Daily [ ]

[b] Weekly [X]

[c] Monthly [X]

[d] Several times a year [ ]

[e] Other (explain) [ ]

Question 4: If you could obtain the same type of information that you seek by doing these analyses **in 5 minutes only**, how often would you now perform these analyses?

[a] Daily [X]

[b] Weekly [ ]

[c] Monthly [ ]

[d] Several times a year [ ]

[e] Other (explain) [ ]

Question 5: When you get **a list of genes/proteins** from a proteomics or a differential expression experiment, what **steps and tools** do you follow for the analysis?

1. Look for antibody, gather cDNA and CRISPR/siRNA/SHRNA vector

2. Obtain cell lines expressing the gene with a relevant phenotype

3. Obtain mouse tissue or animal with KO

4. Obtain disease information and human tissue/slides /cell lines.

5. Obtain inhibitor if available.

Question 6: Now and related to the previous question, instead of telling me what steps you follow in your analysis, if I asked you **what type of information you would like to know** about each one of your genes or proteins, what would you be interested in knowing?

Here you can include some information you would love to have **but do not know** how to obtain it.

1. postranslational modification
2. epigenetic controls

3.promoter interaction

4.cell localization

5. validated interactome

Question 7: If you have a long list of genes/proteins from a high-throughput experiment you ran in the lab, **what are the most useful factors in determining the next follow-up experiment?**

E.g. how easy the potential experiment is, how relevant the cell type, how much money this would cost, etc.

1. having a phenotype in cell , Animal , human disease

2. having great antibody for the endogenous target protein

3. tagging the protein and expression vector

4.cell lines are valuable for rapid development..

5.

Question 8: What do you think is the **most competitive advantage against other competing laboratories** when trying to decide what the next follow-up experiment would be?

1. validated Ab and interactome.

2. Cell line that have relevant penotype

3. IPSC potential function in our stem cell project.

4. generating rapid bioinformatics available database to put together a dossier on this protein. This dossier should be complete and rapidly available from molecular cellular tissue animal model and human disease and tools (vector, mutans inhibitors…) to modulate the gene and protein

5. Knowledge of labs working on this protein.

__END OF QUESTIONNAIRE__

Please return this questionnaire to d.mirandasaavedra@gmail.com