

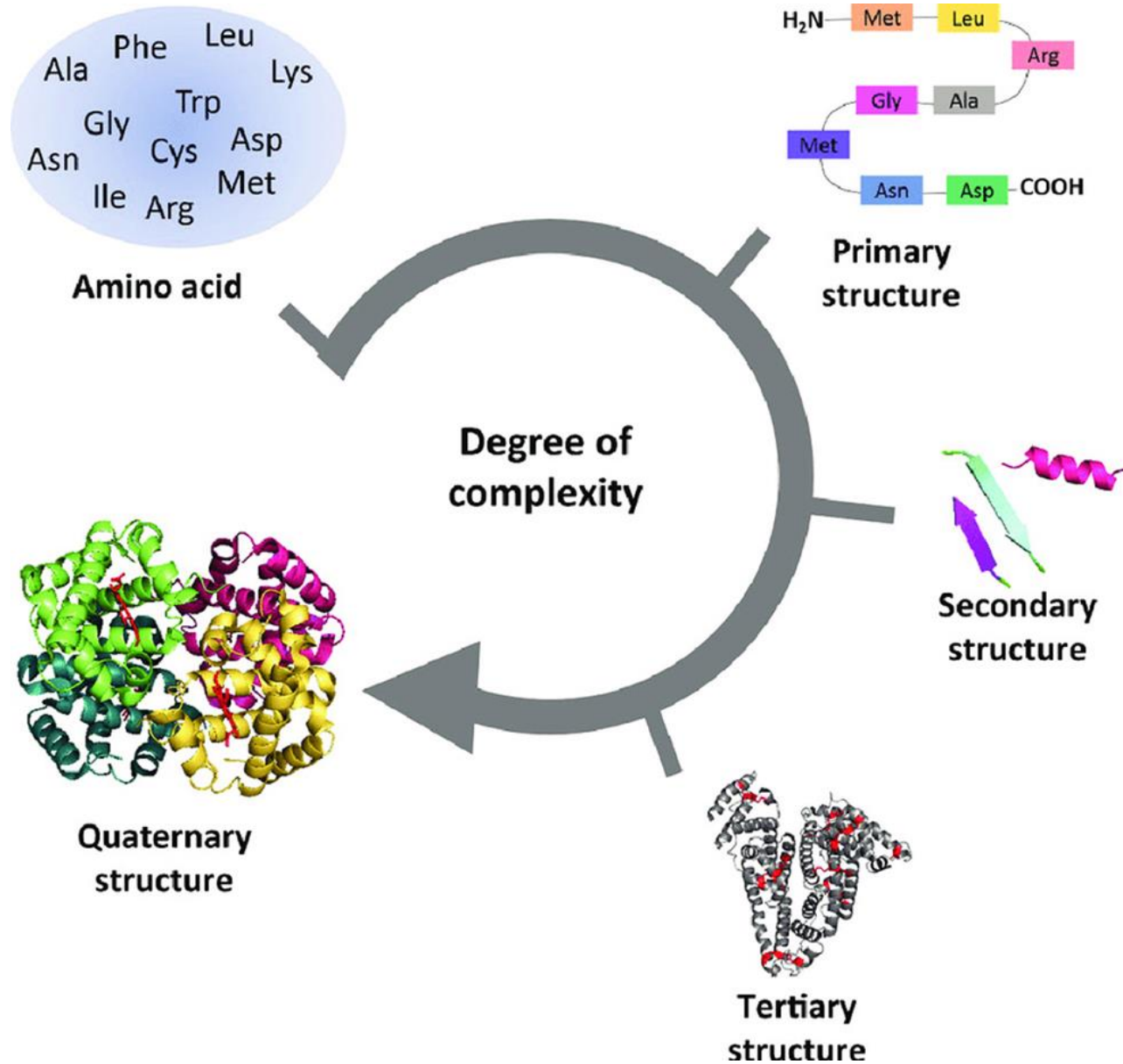
A collection of chocolate cupcakes, each decorated with a network of colorful M&M's candies (red, yellow, blue, orange, green) connected by white frosting lines, resembling a biological network. The cupcakes are arranged in a grid-like pattern on a light-colored surface.

Biological Networks

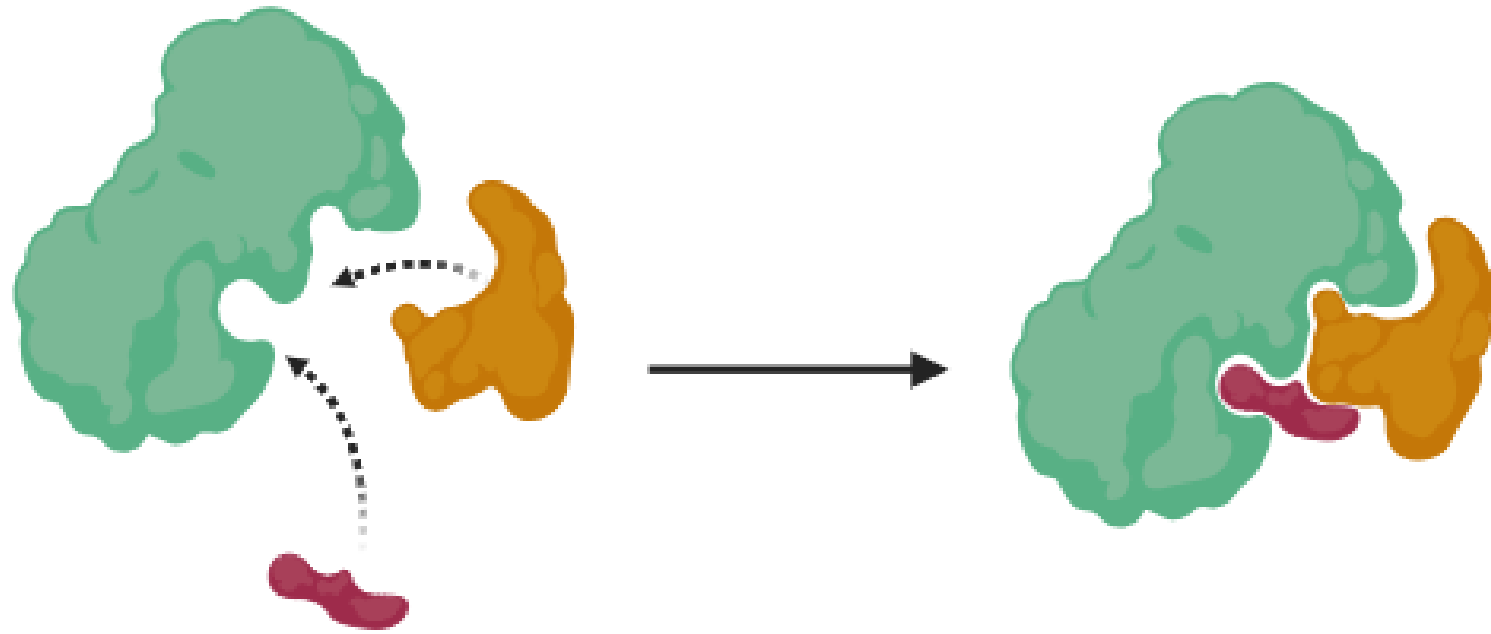
Maggie Chrostowski and
Brooke Fuerstenau

cupcake art by Ahna Skop!

What is a protein?

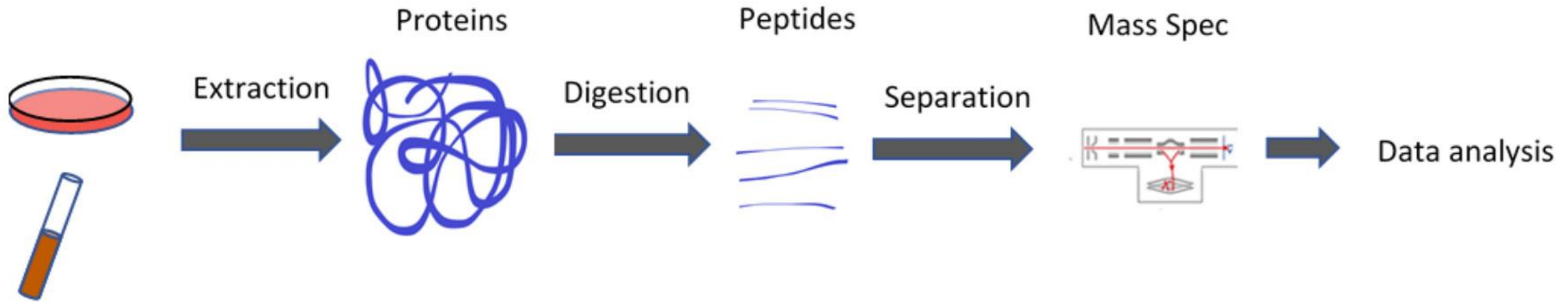


What are protein-protein interactions (PPIs)?



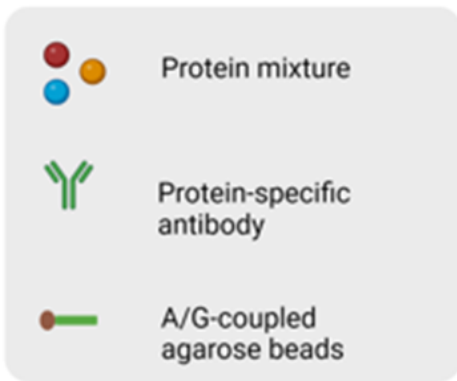
Proteins bind directly or indirectly to one another in many cellular processes.

What is proteomics?

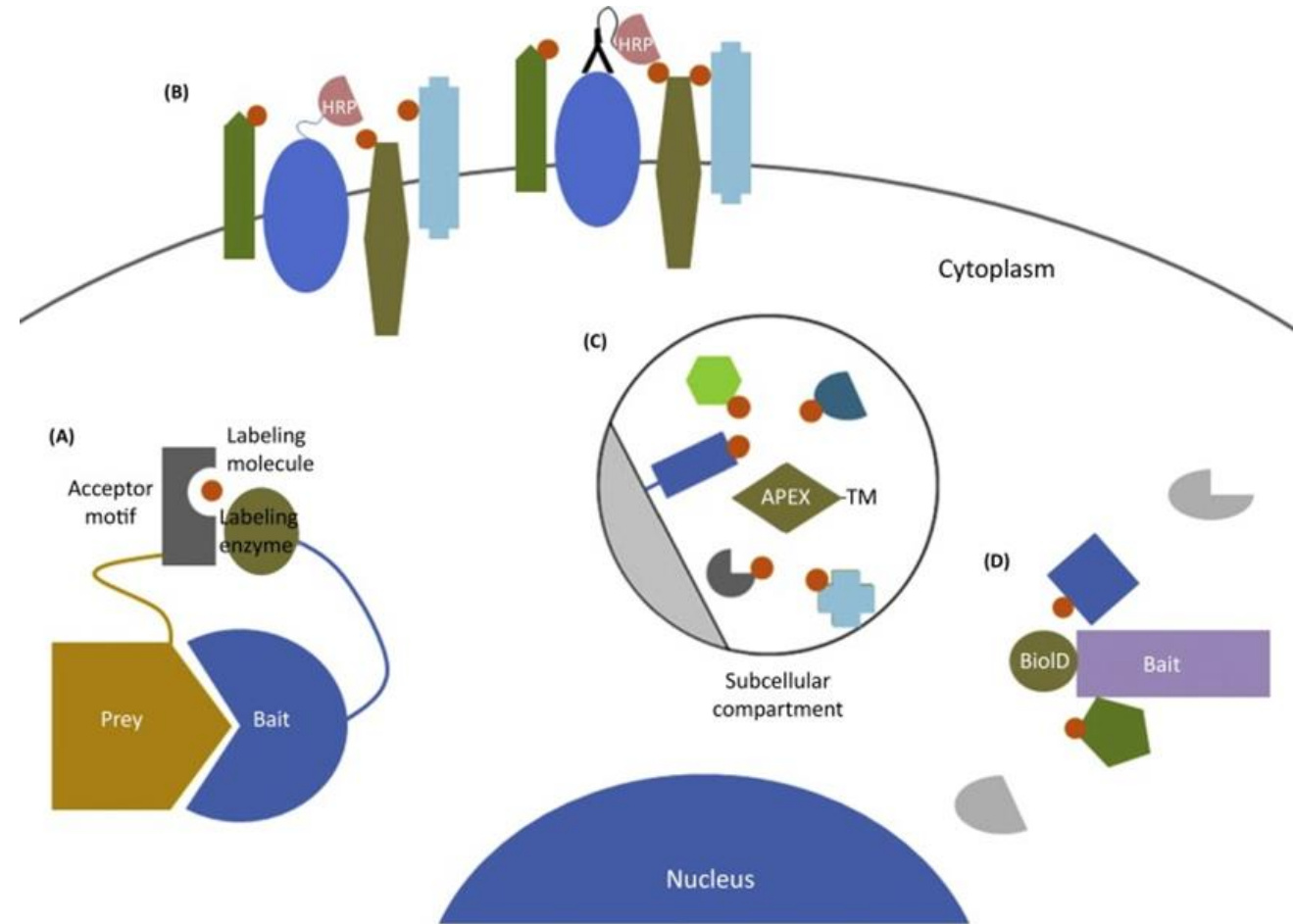


Study of isolated peptides through mass spectroscopy.

1) What are the ways to isolate proteins?



Immunoprecipitation
[Affinity Purification]

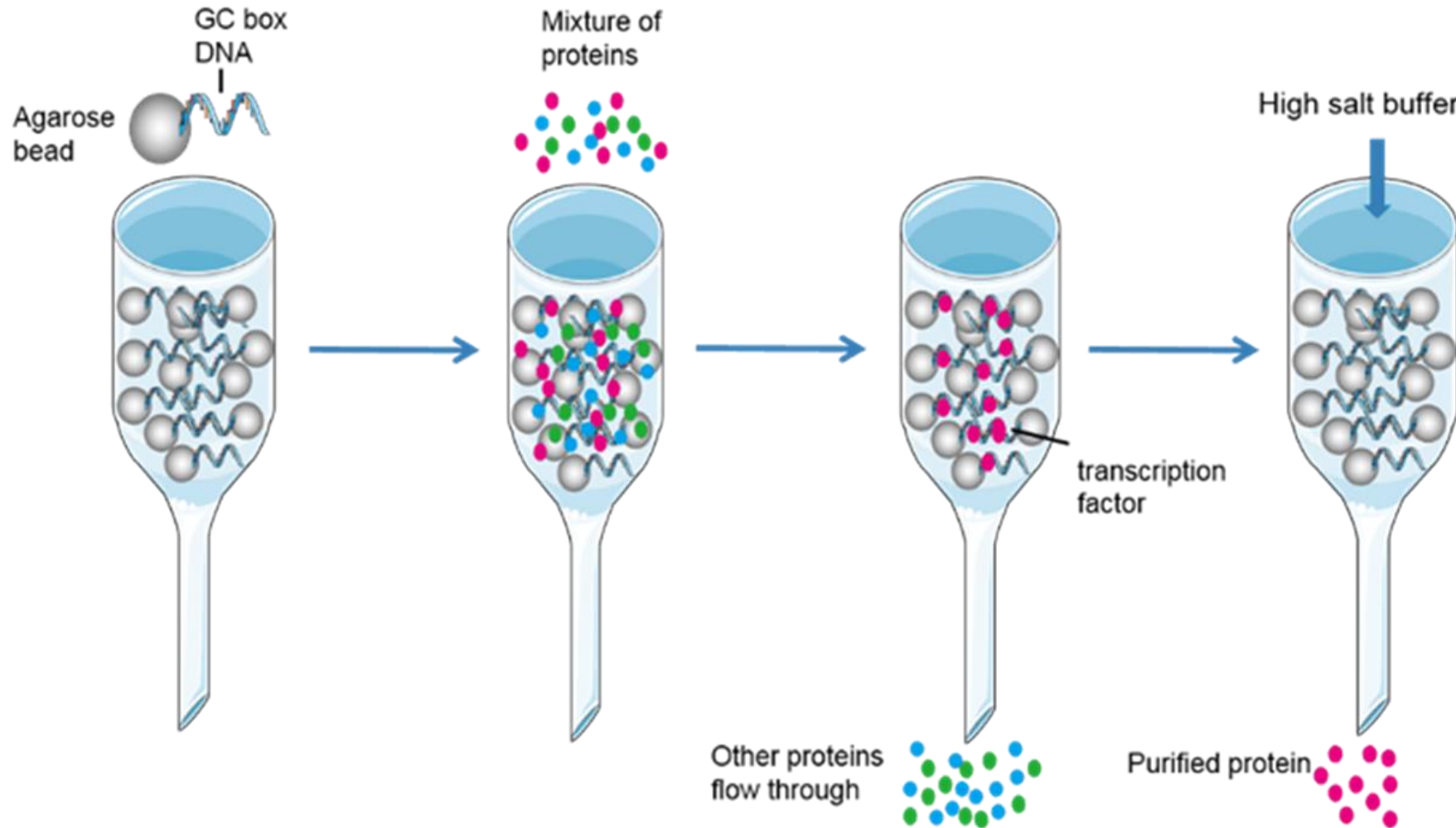


Proximity Dependent Labeling

(Fhearraigh, 2021)

(In Kim & Roux, 2016)

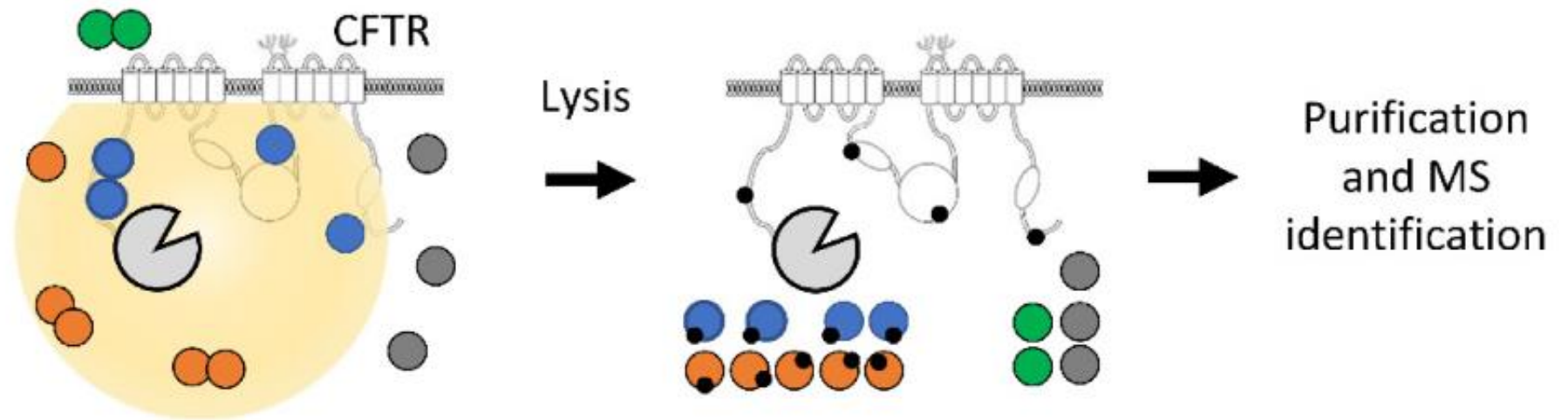
1) What is Affinity Purification (AP)?



(Creative BioMart, n. d.)

1) What is Proximity Dependent Labeling?

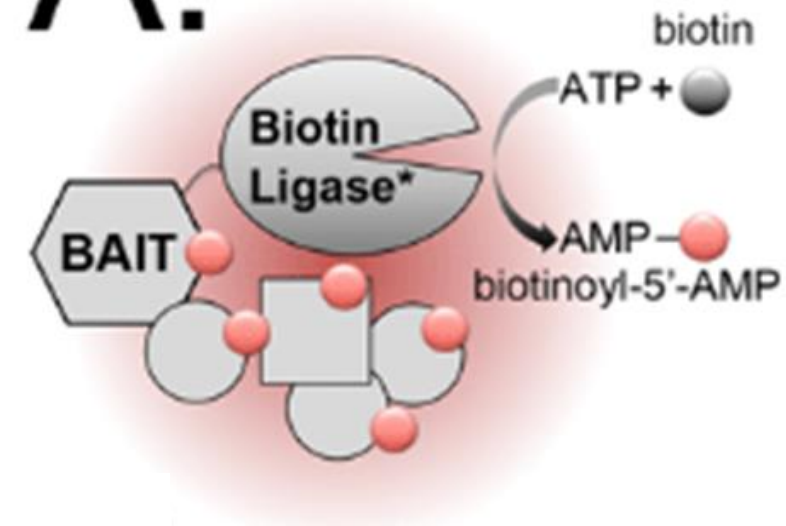
- Interacting protein
- Proximal protein
- Distal protein
- Protein in different compartment
- Covalently bound biotin



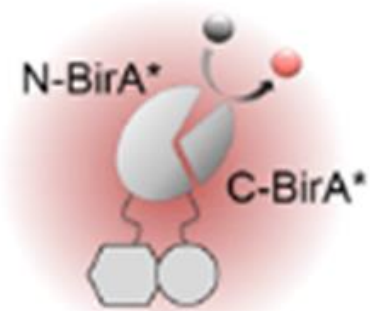
It uses enzymes that construct reactive molecules to bind and label neighboring proteins.

1) What are the standard proximity-dependent labeling methods?

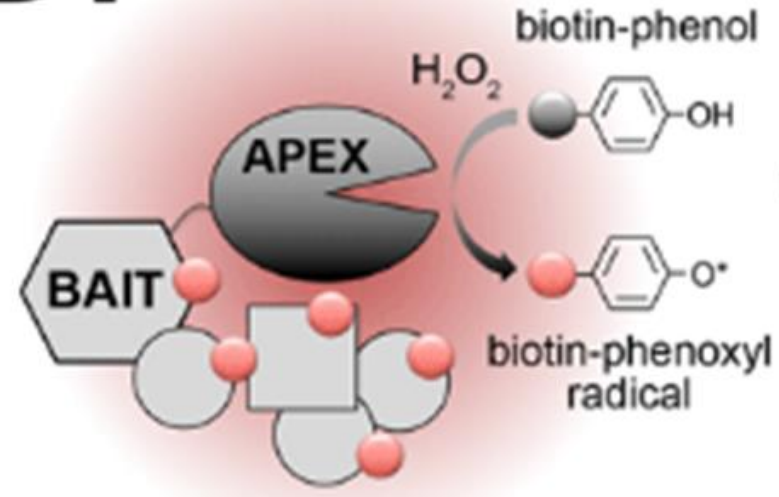
A. BioID /TurboID



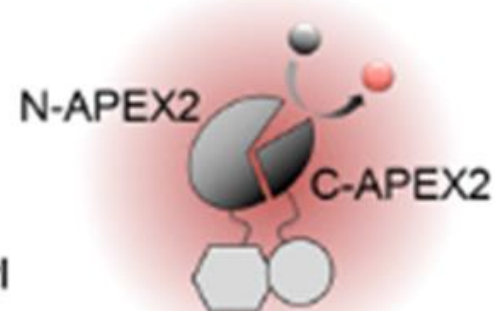
Split-BioID



B. APEX

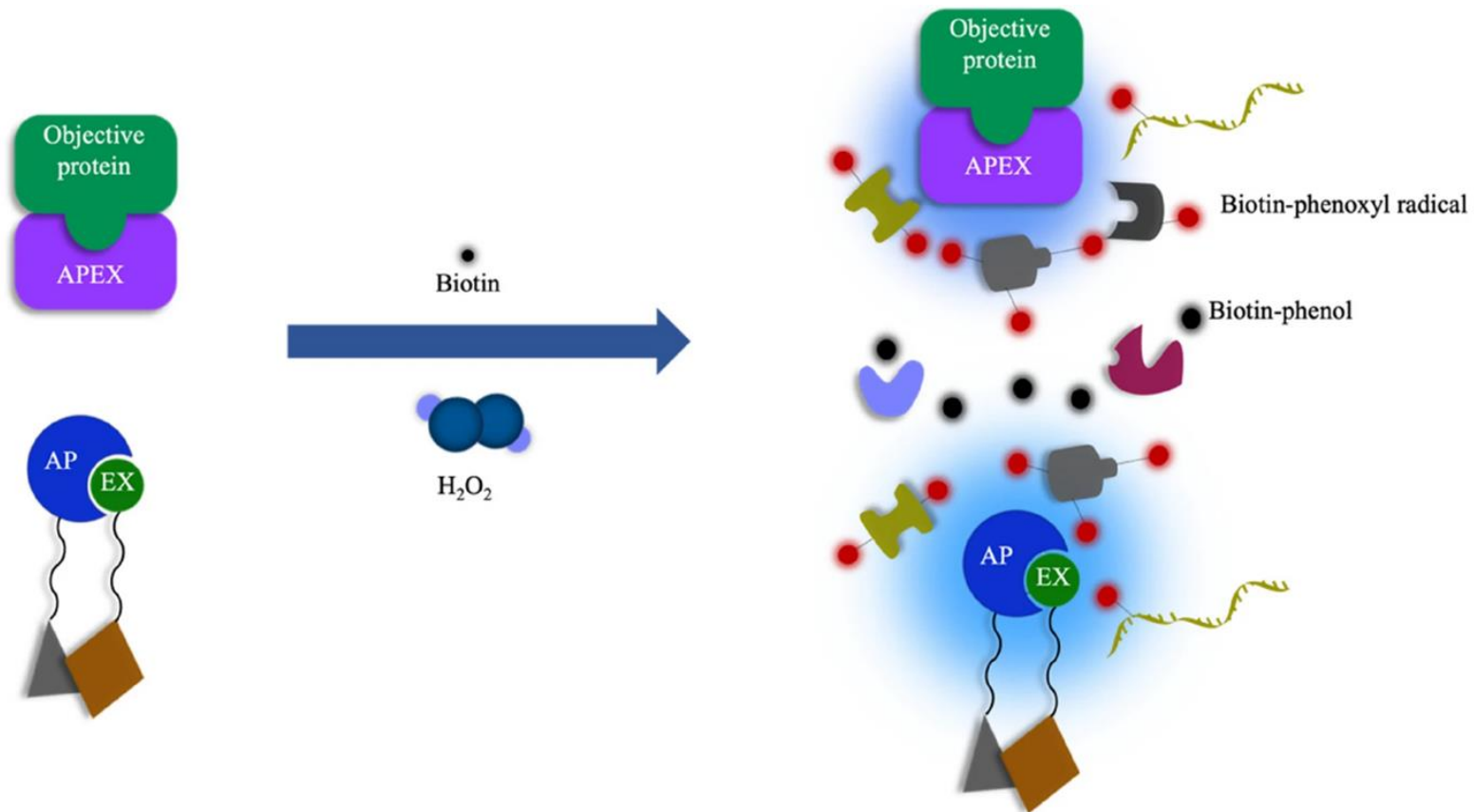


Split-APEX



1) How does APEX work?

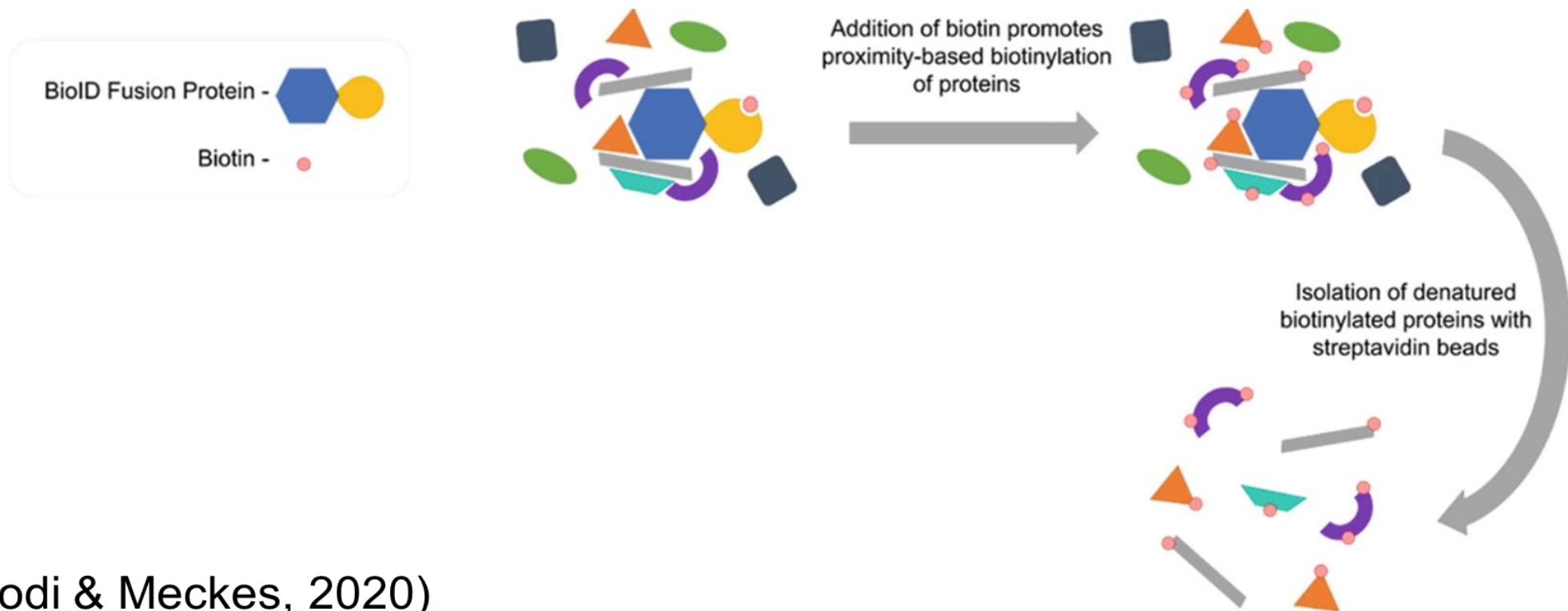
Enzyme	Type	Size (kDa)	Labelling time	Substrate	Target
APEX2	Peroxidase	28	1 min	Biotin-phenol + H ₂ O ₂	Tyr, Trp, Cys, His



(Gou et al., 2023)

1) How does BioID work?

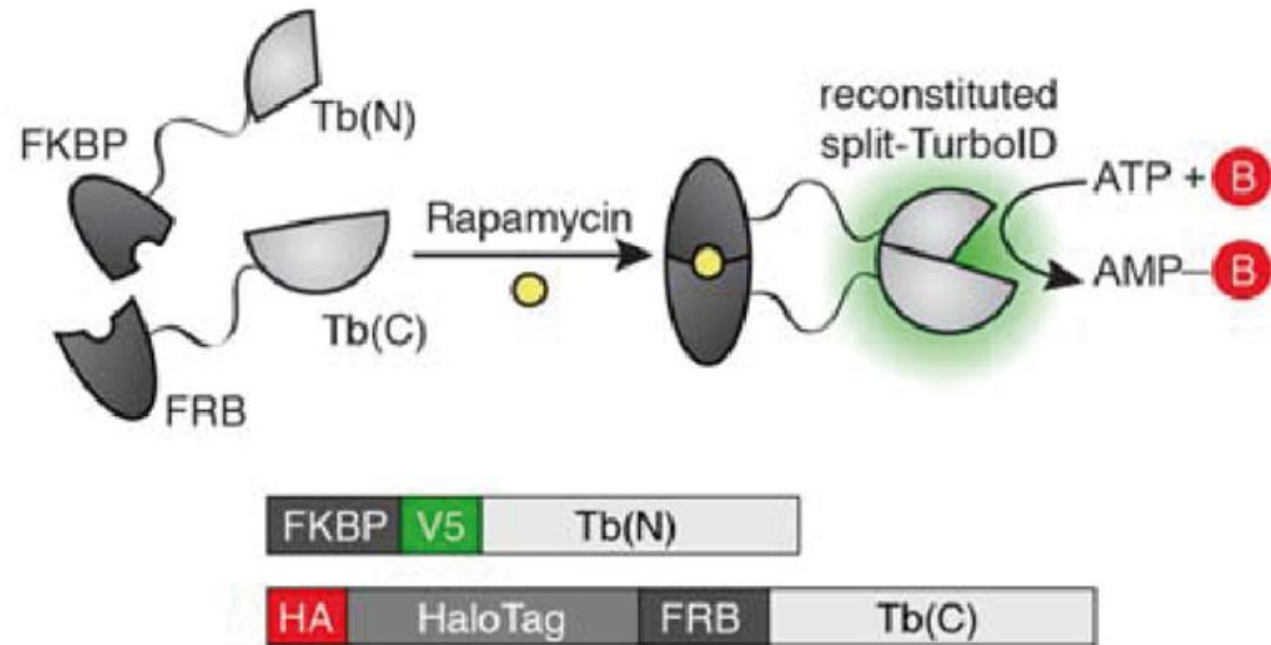
Enzyme	Type	Size (kDa)	Labelling time	Substrate	Target
BioID	Biotin ligase	35	18 h	Biotin	Lys



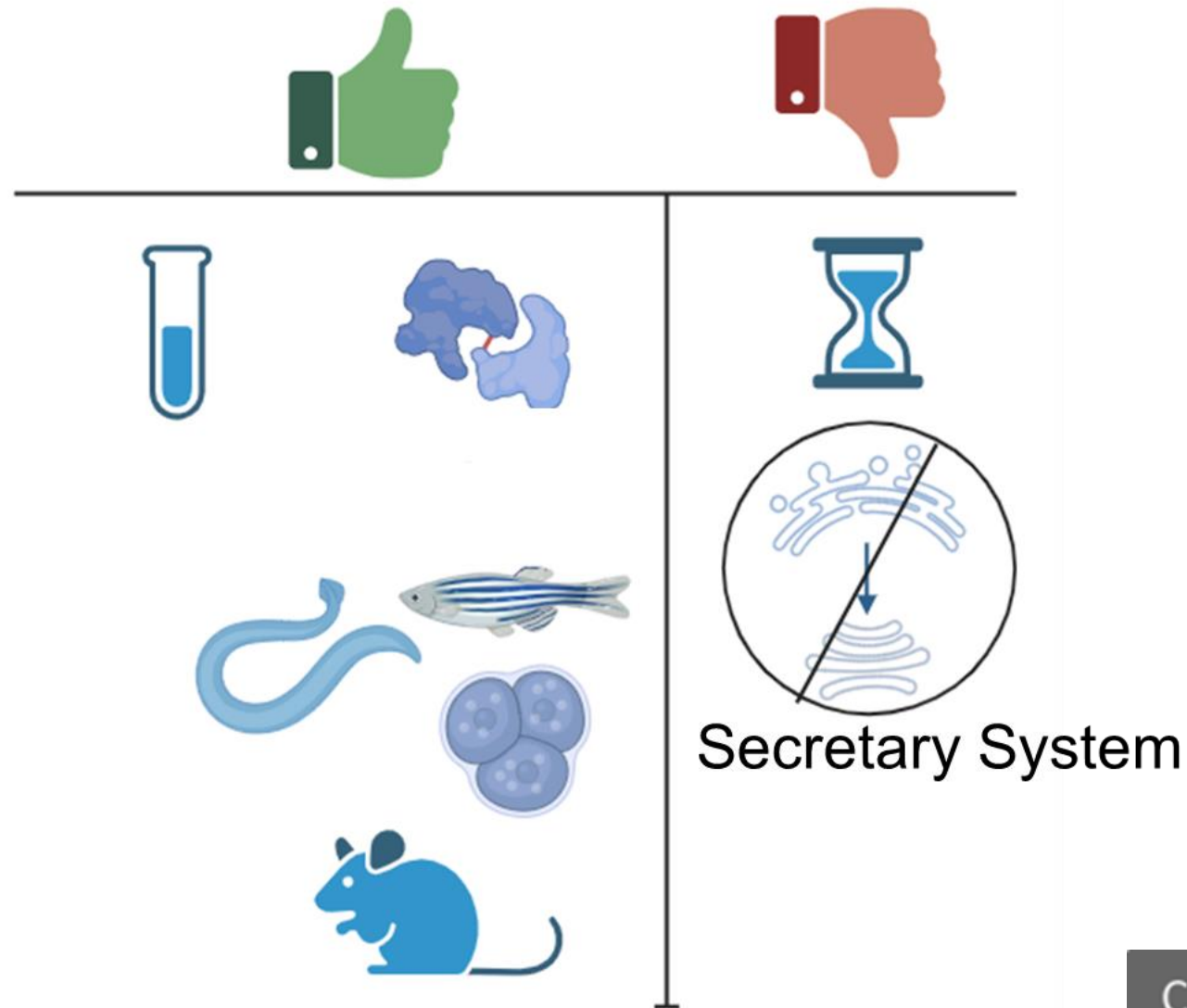
1) How does TurboID work?



Enzyme	Type	Size (kDa)	Labelling time	Substrate	Target
TurboID	Biotin ligase	35	10 min	Biotin	Lys

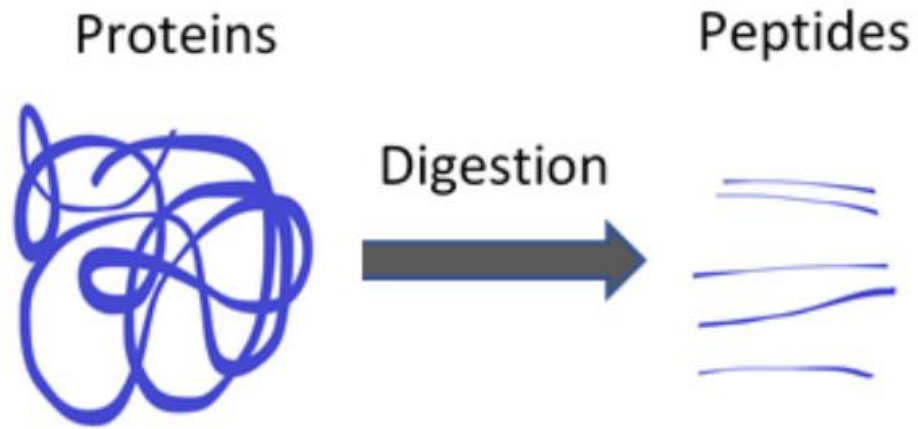


1) What are the pros and cons of using BioID and TurboID?

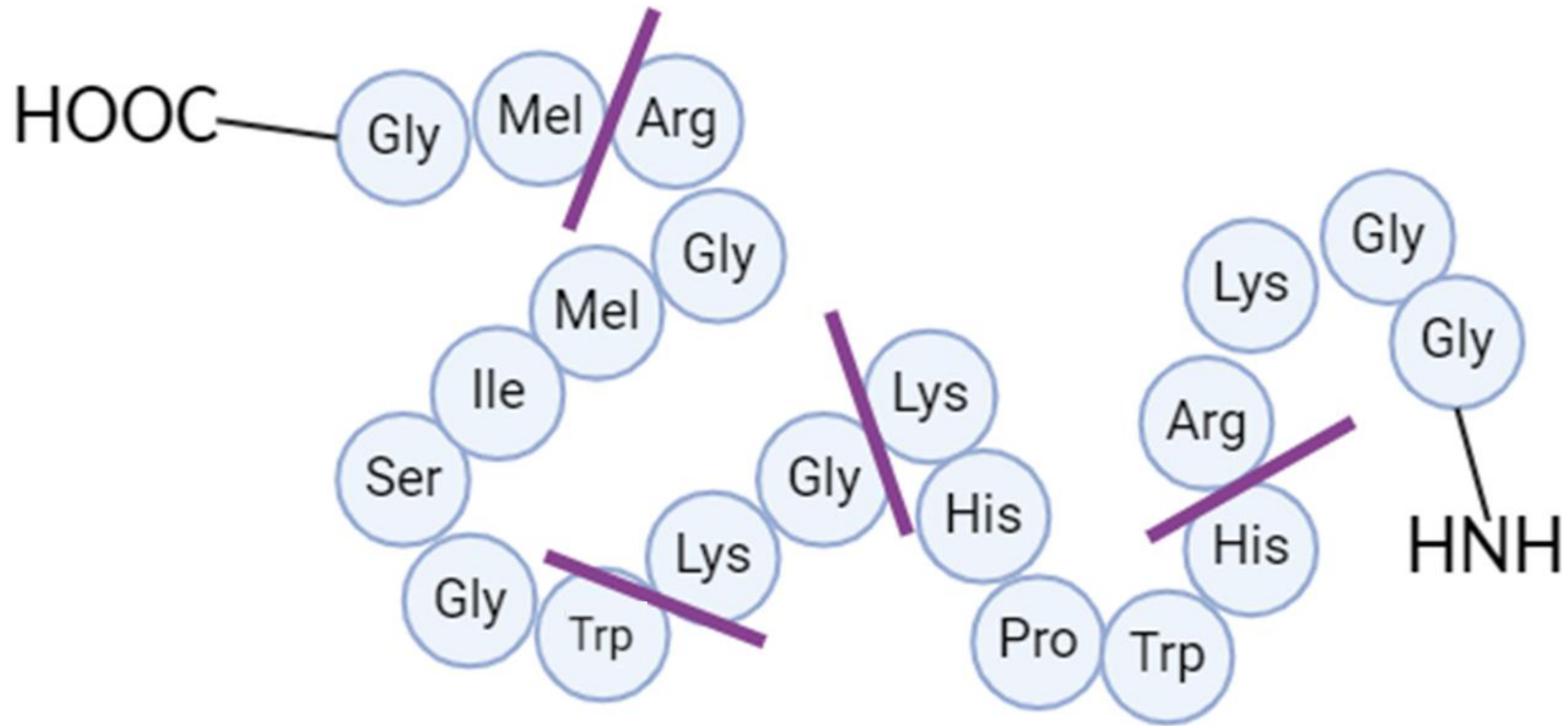


(Varnaitė & MacNeill, 2016)

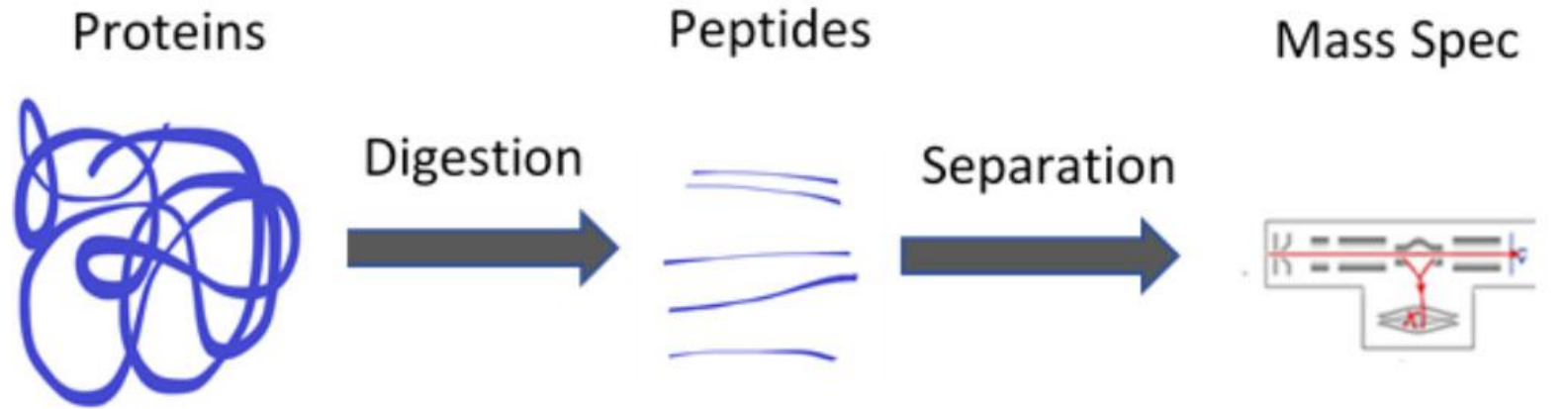
Step 2: Digestion



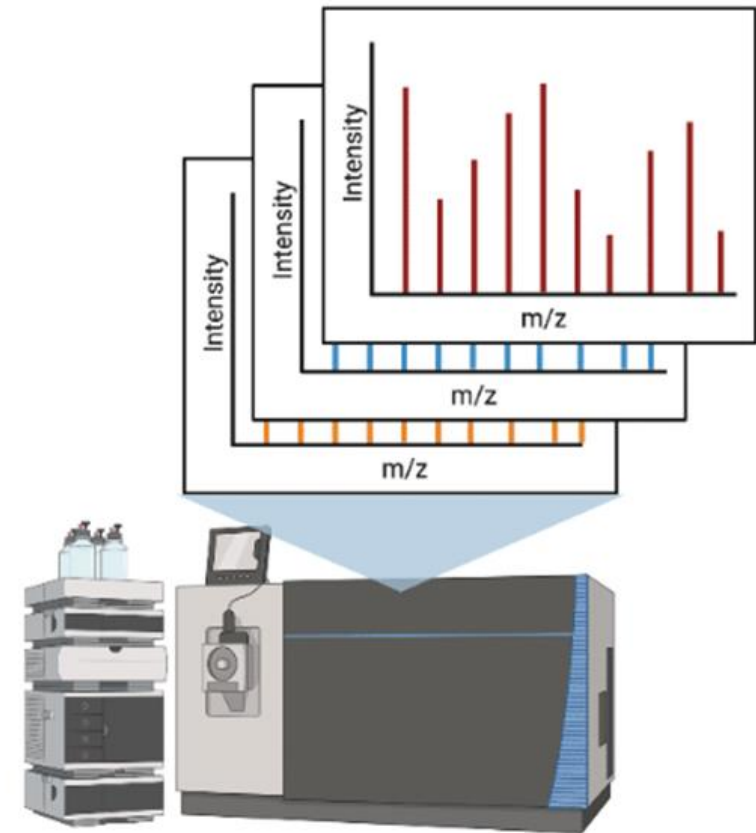
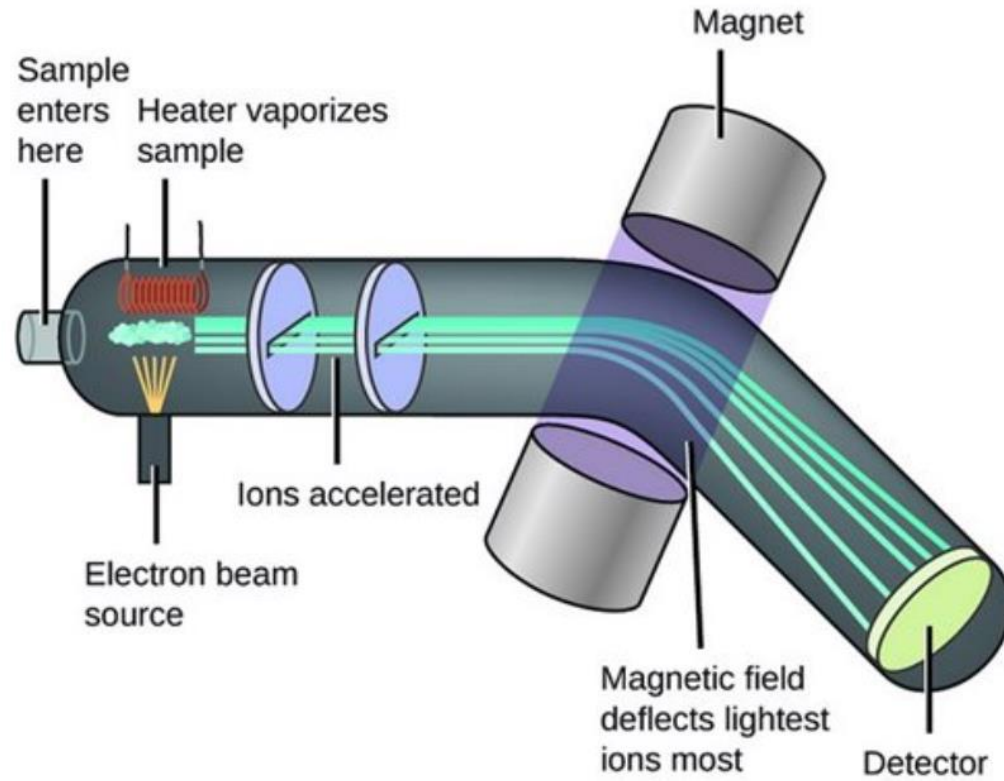
2) How does Trypsin Cut proteins?



Step 3: Mass Spec



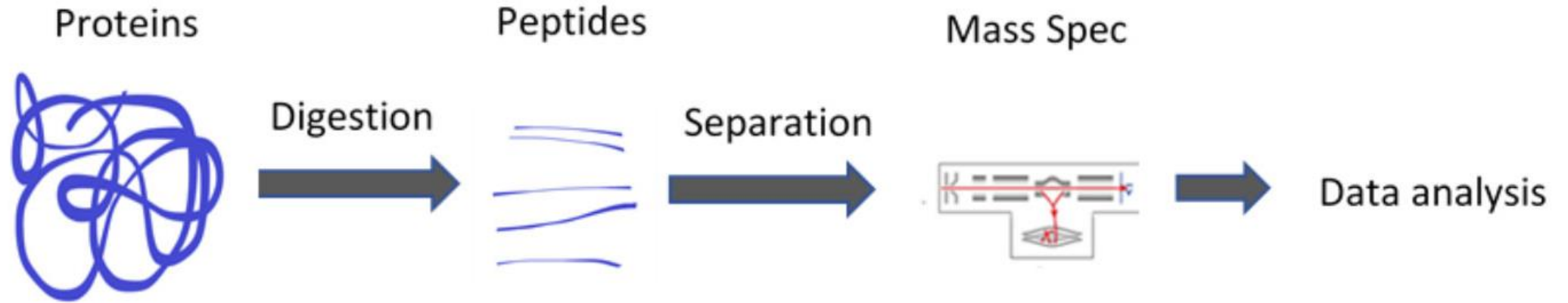
3) How do you perform a simple mass spectroscopy experiment?



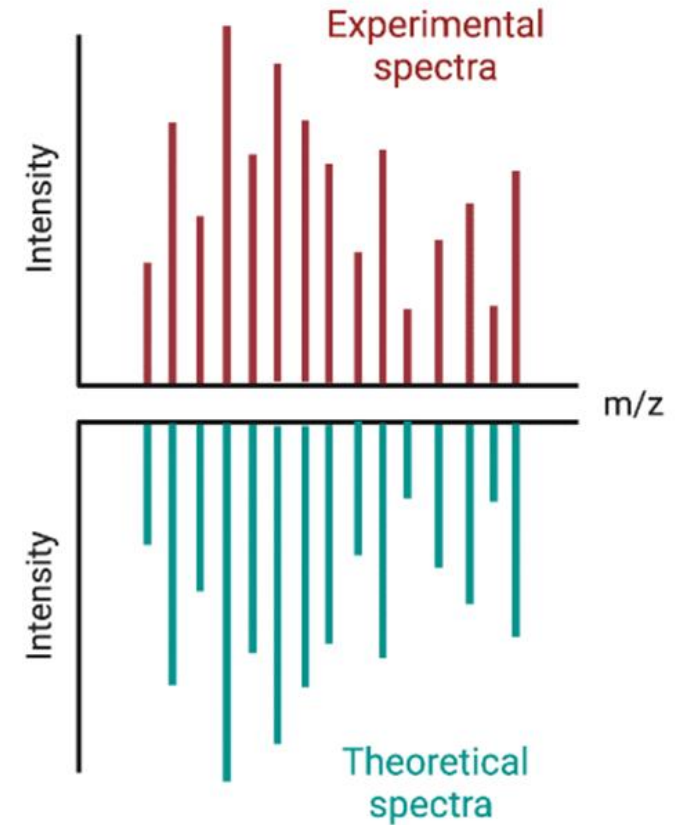
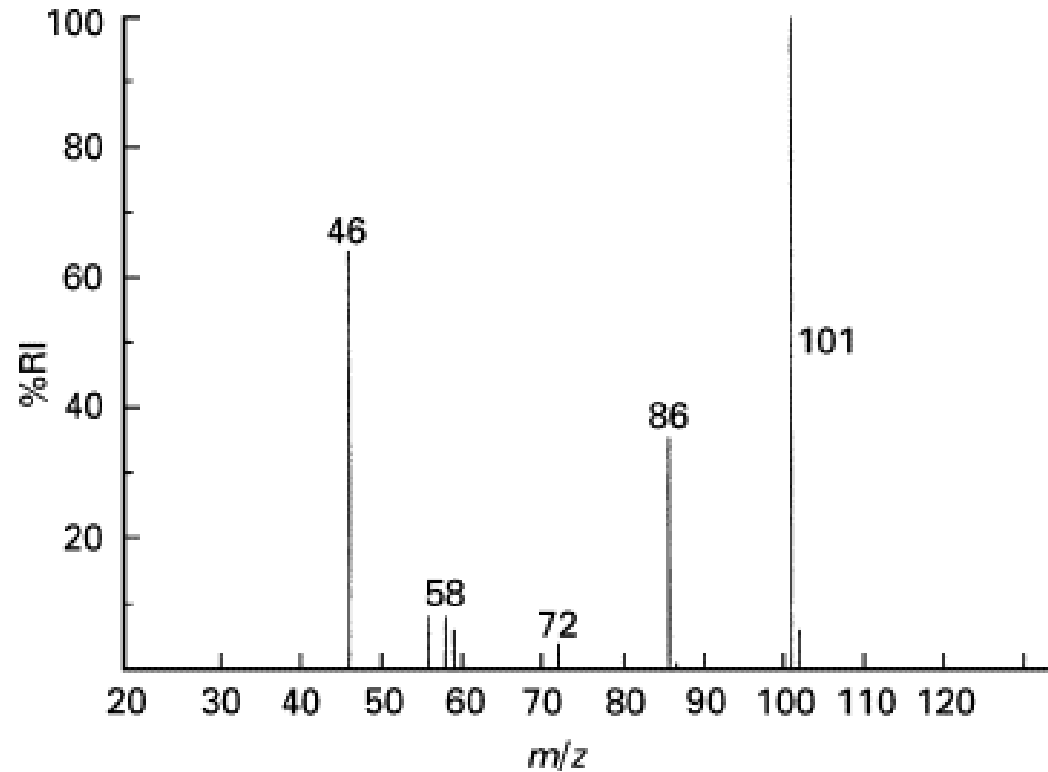
After preparing the sample, a mass spectrometer collects data to obtain separate mass/charge ratios for isolated peptides.

(Science Ready, 2021)

Step 4: Data Analysis



4) What does the mass\charge ratio mean in MS?



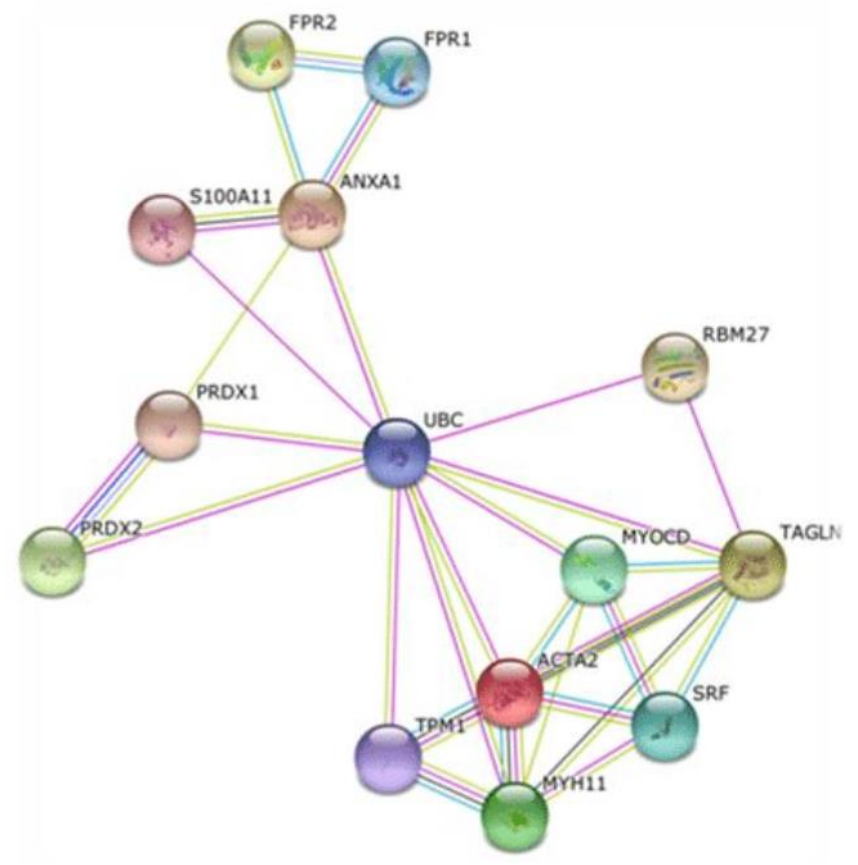
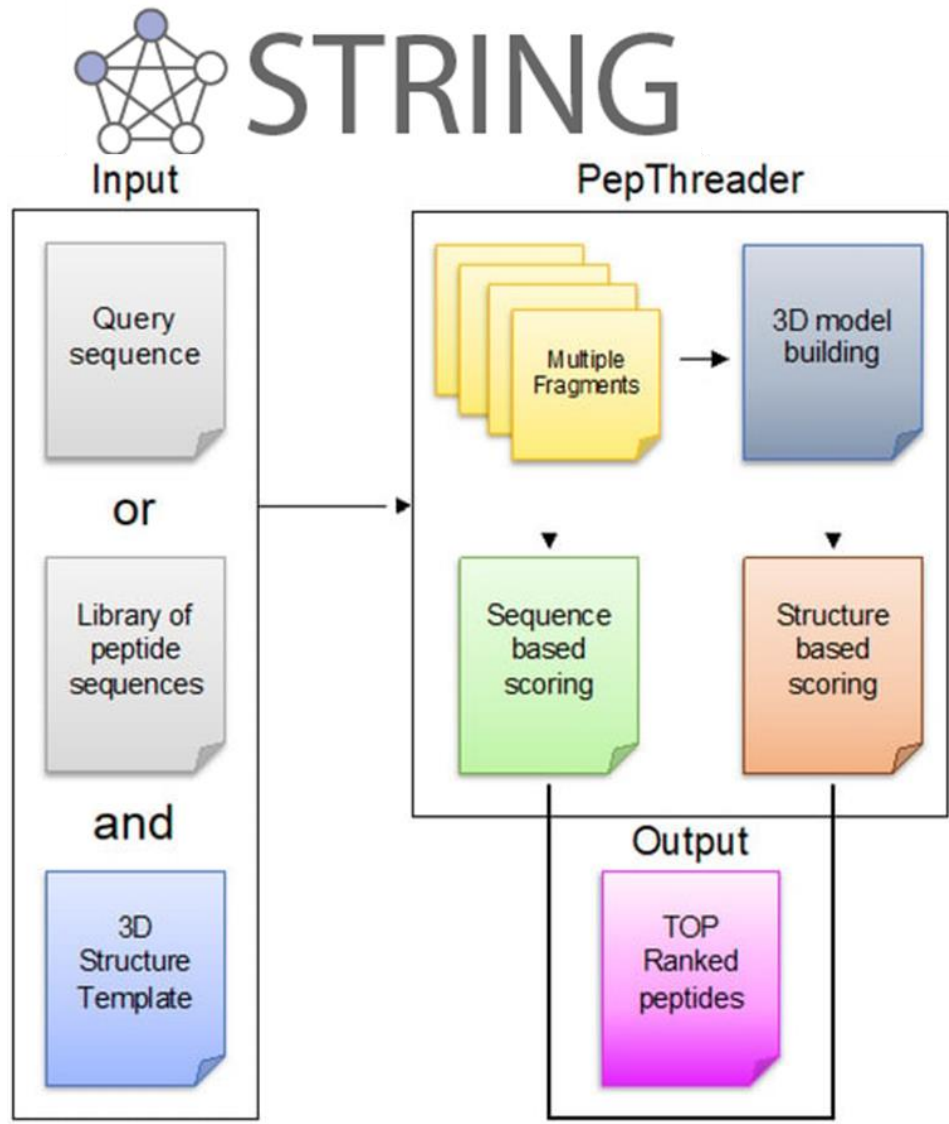
The peptide mass is divided by the charge of the protein, allowing us to identify any peptides present and cross reference with databases.

(Babele & Yadav, 2023)

4) What databases do you use to analyze data?



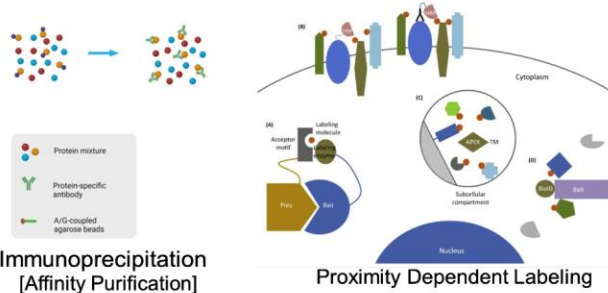
How do you build interaction models?



(Gasbarri, 2022)

Summary

1) What are the ways to isolate proteins?

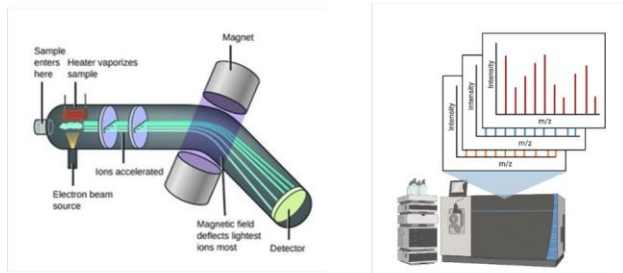


(Fhearraigh, 2021)

(In Kim & Roux, 2016)

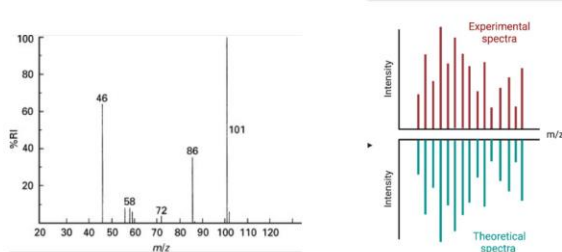
Immunoprecipitation and Proximity Dependent Labeling are two ways to isolate protein. TurboID is a biotin ligase that uses ATP to target Lysine.

3) How do you perform a simple mass spectroscopy experiment?



After preparing the sample, a mass spectrometer collects data to obtain separate mass/charge ratios for isolated peptides. (Science Ready, 2021)

4) What does the mass\charge ratio mean in MS?



The peptide mass is divided by the charge of the protein, allowing us to identify any peptides present and cross reference with databases.

(Babele & Yadav, 2023)

Mass spectroscopy takes the tagged peptides (cut-up proteins) and analyzes them through a magnetic field to get mass/charge ratio.

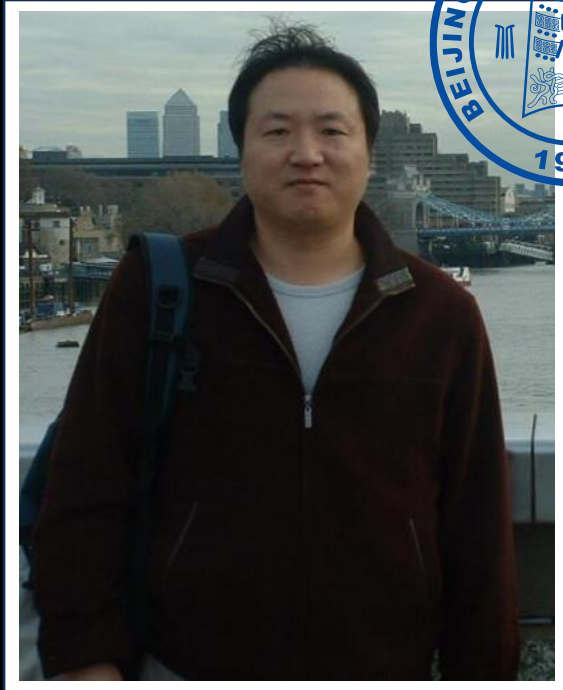
The mass/charge ratio allows you to determine the proteins present by comparing the experimental data to the theoretical data found in a database. To do this, you can use UniProt, NCBI, nextprot, or EMBL.



Questions?

“An antibody-based proximity labeling map reveals mechanisms of SARS-CoV-2 inhibition of antiviral immunity”

Authors :

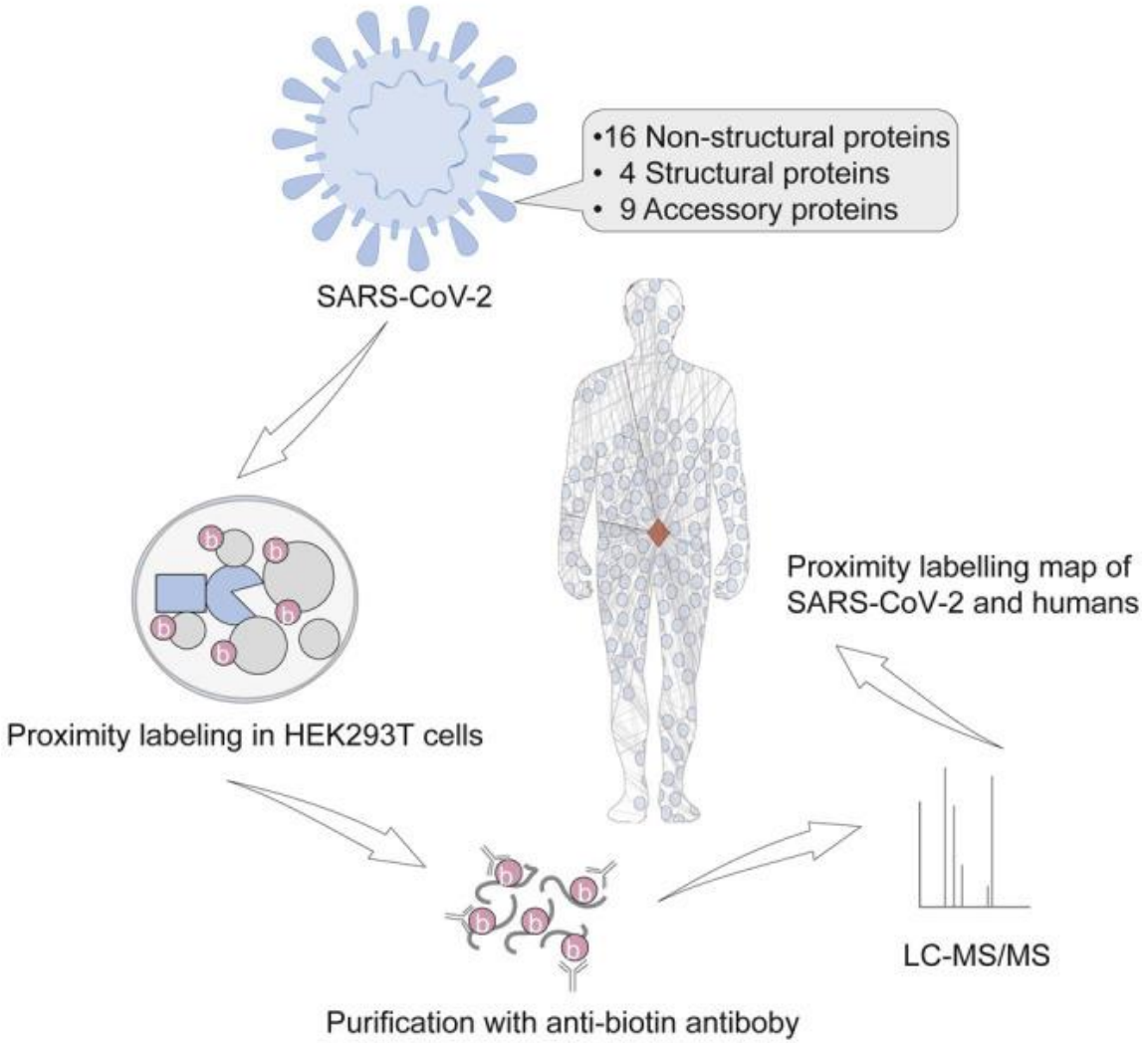


Yuehui
Zhang



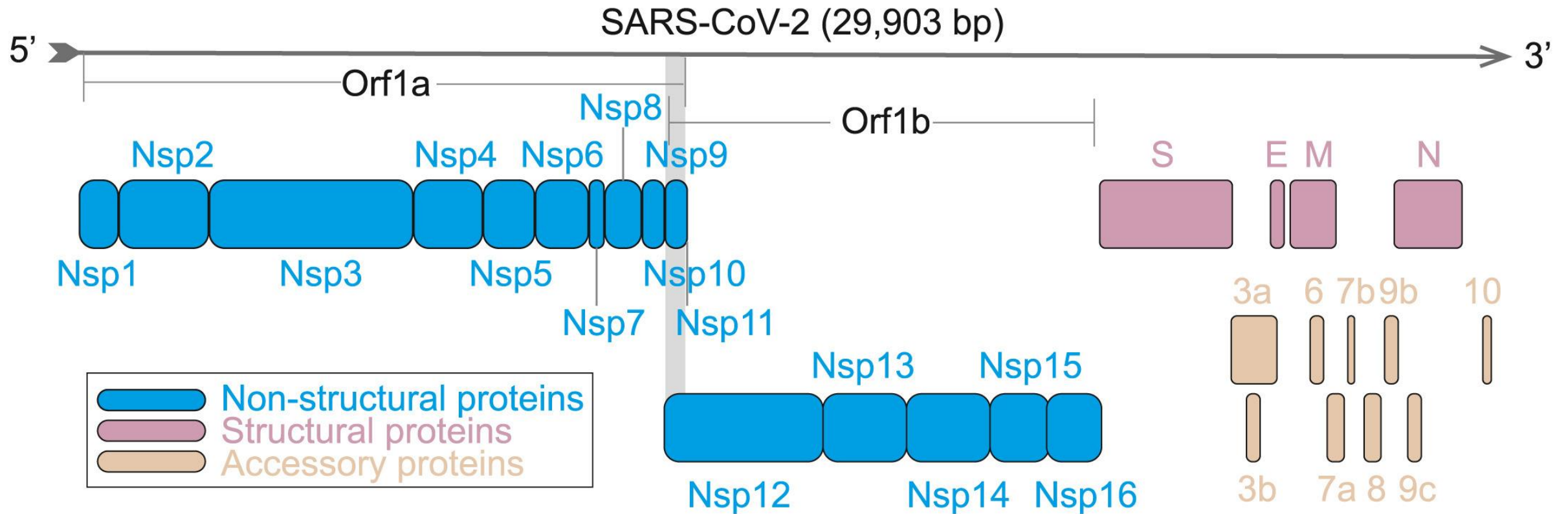
Limin Shang

How can TurboID be used in SARS-CoV-2 research?

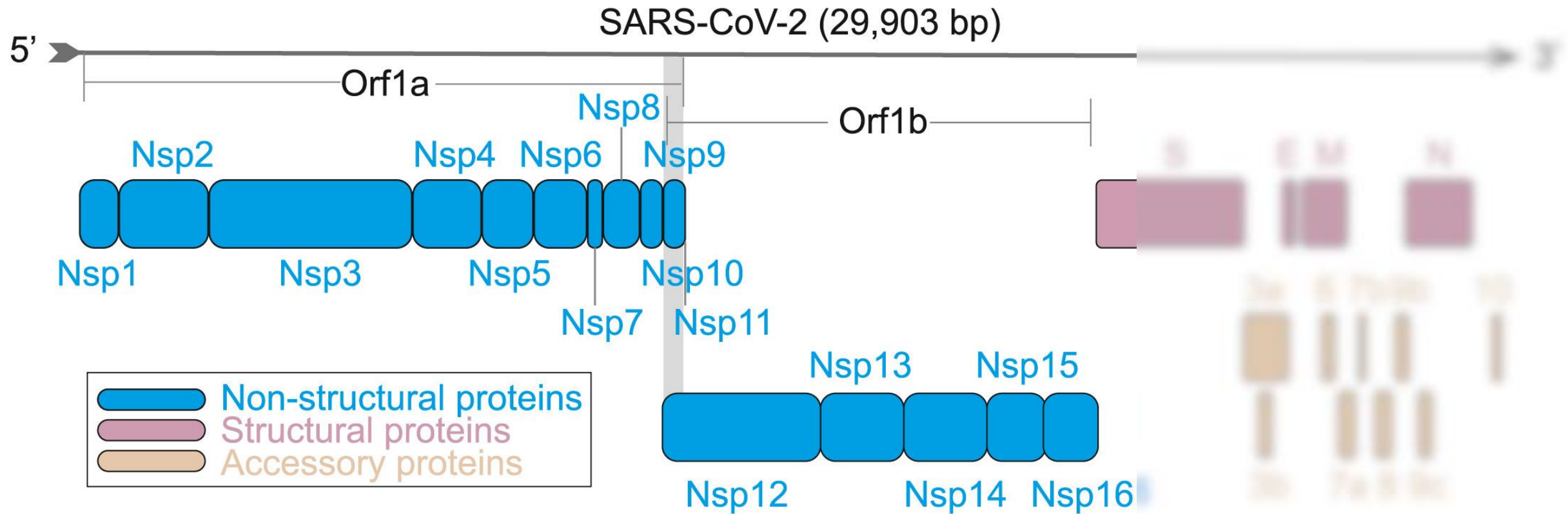


(Zhang et al., 2021)

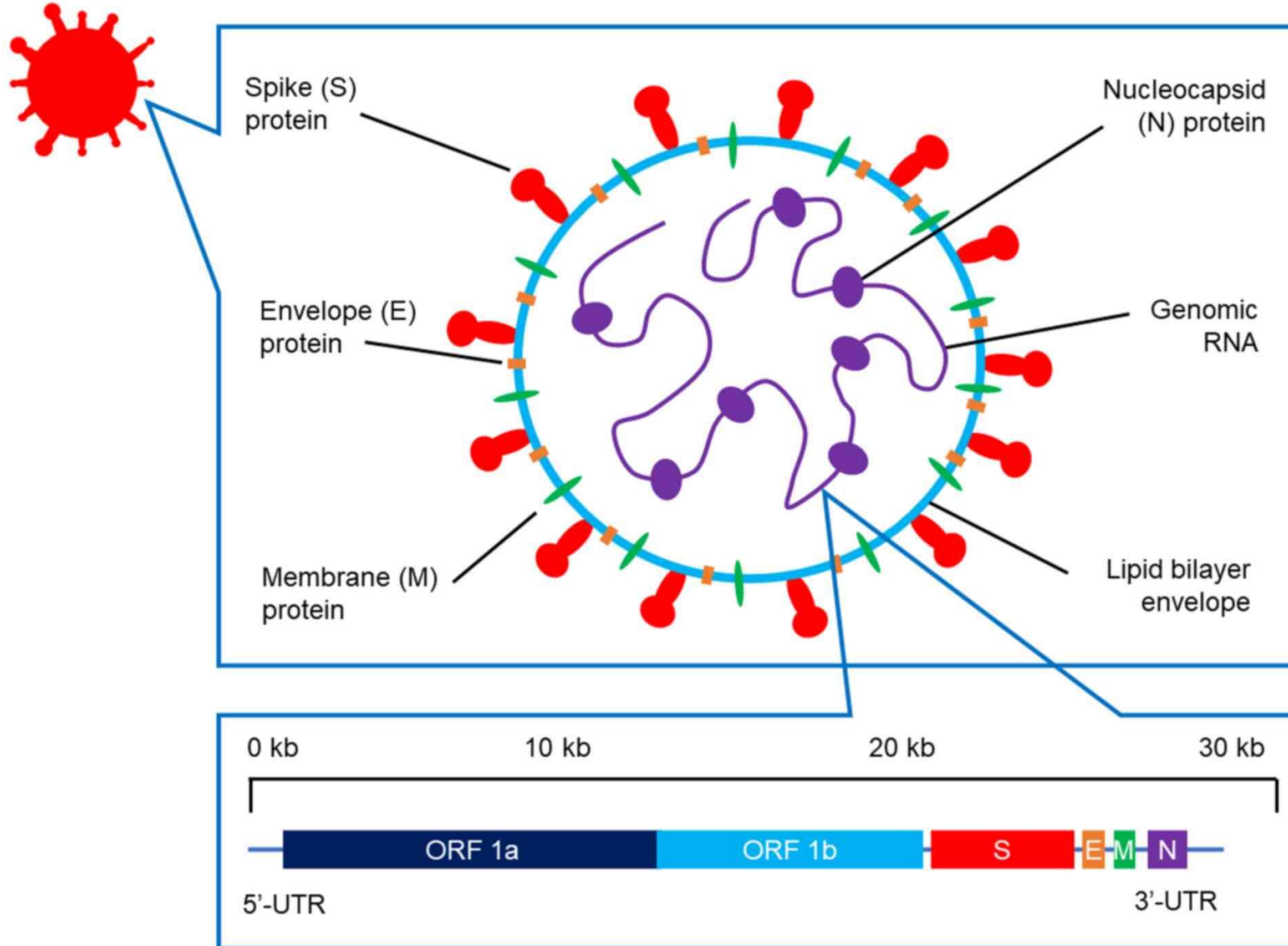
What proteins are encoded by SARS-CoV-2?



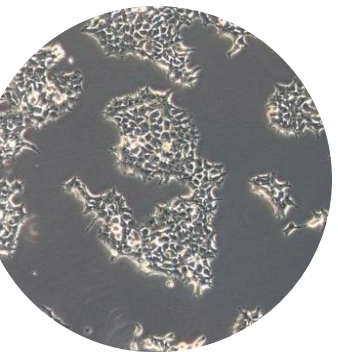
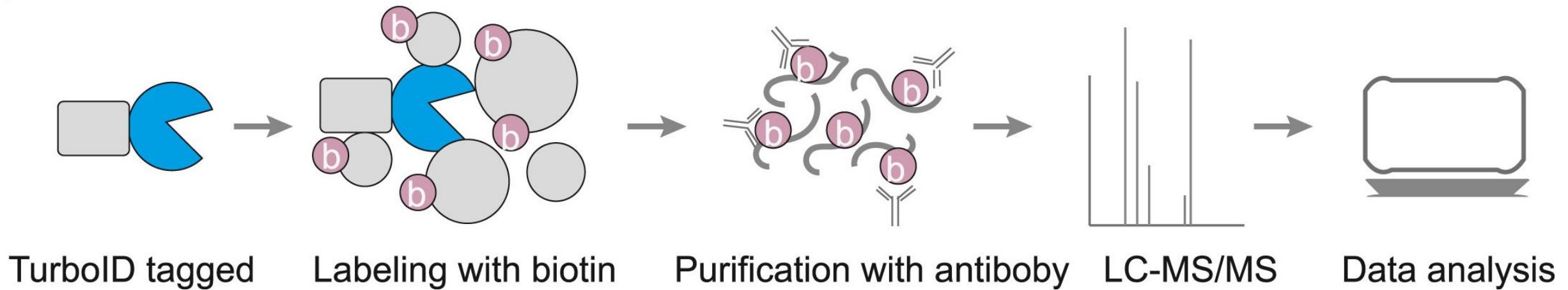
What proteins are encoded by SARS-CoV-2?



What proteins are encoded by SARS-CoV-2?

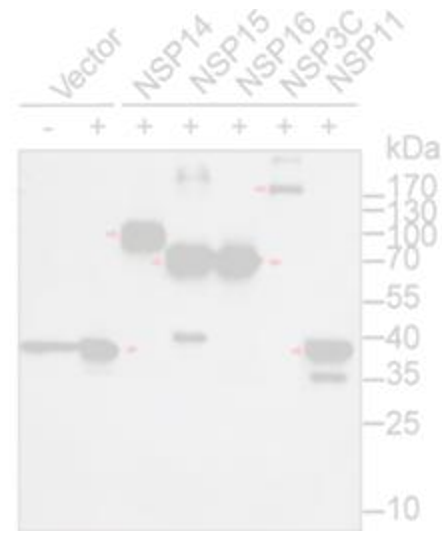
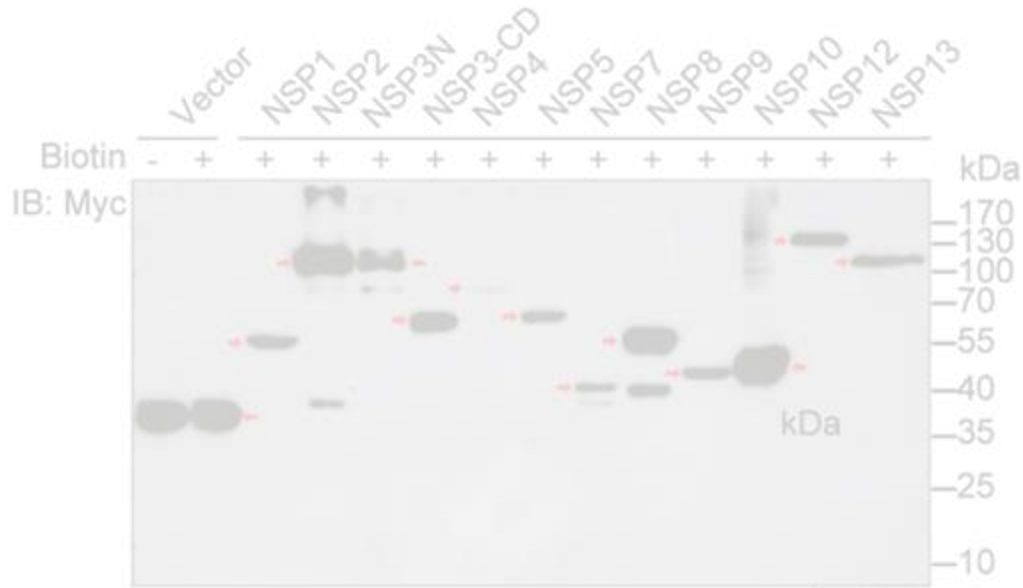
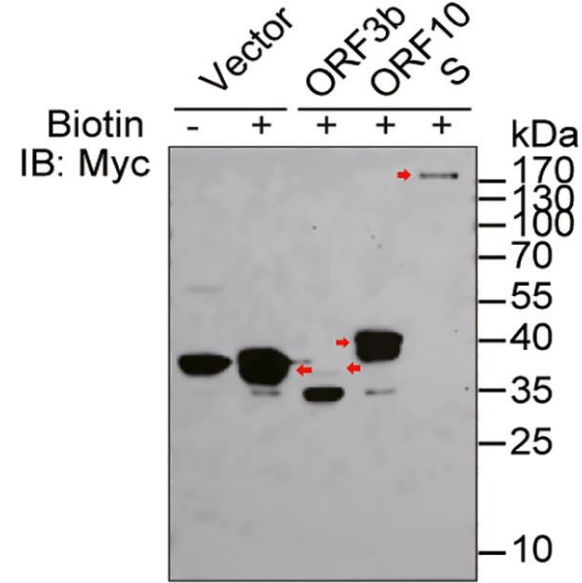
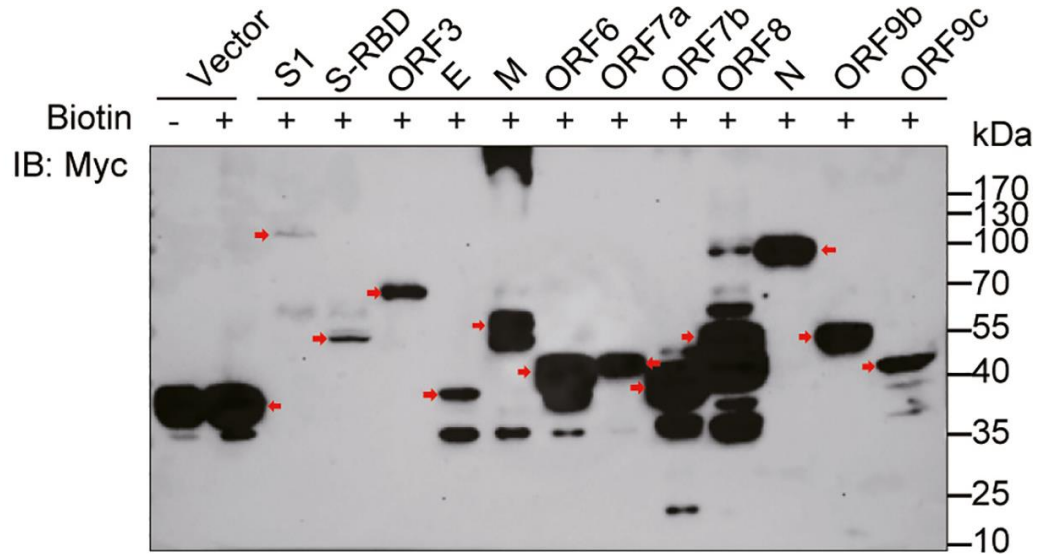


How was TurboID used to identify proximal proteins?



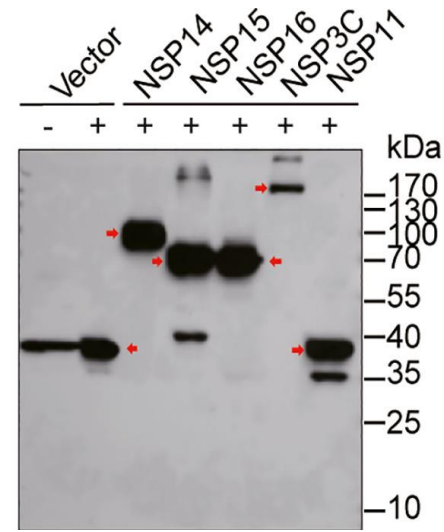
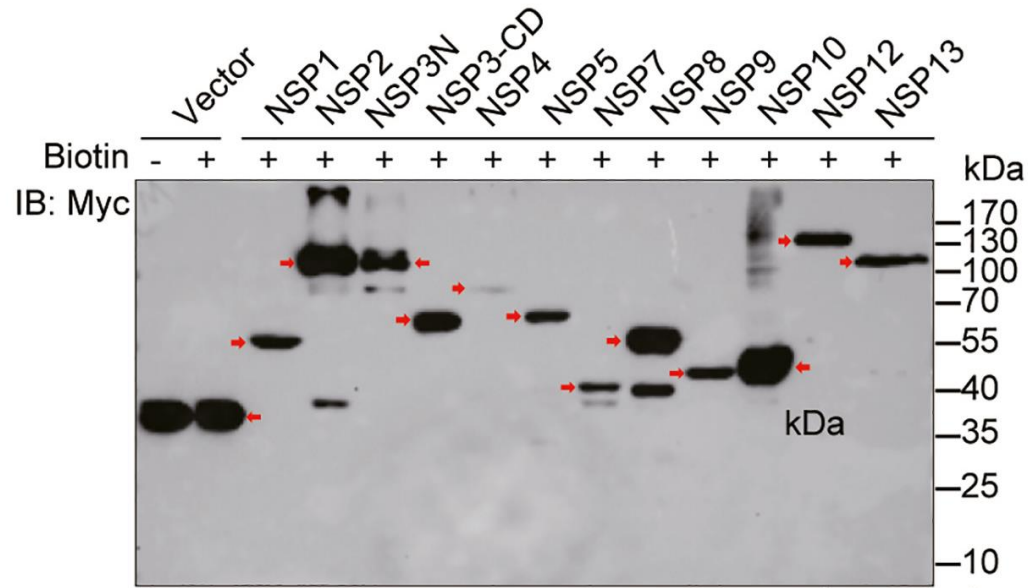
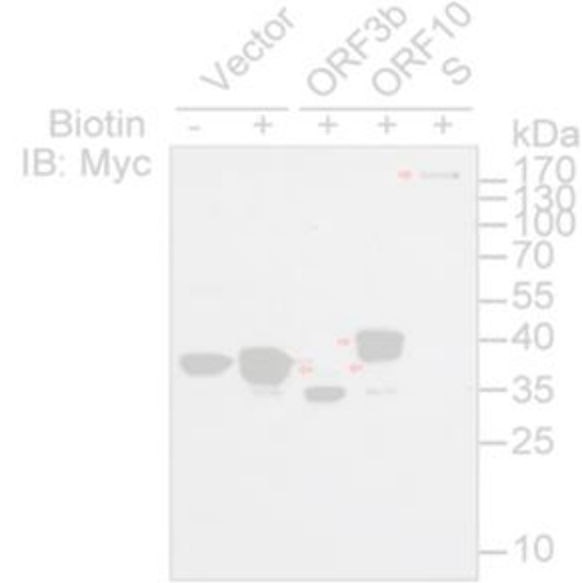
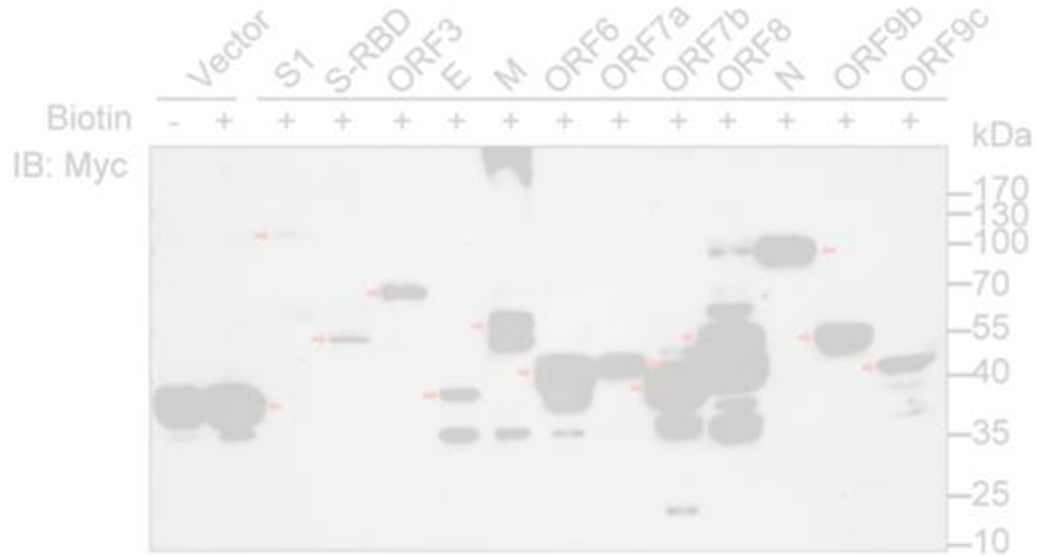
HEK293T
cells


What **protein expressions** were detected by western blot assays?



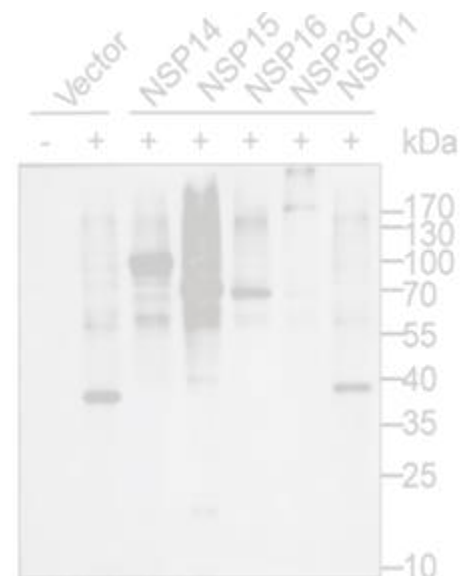
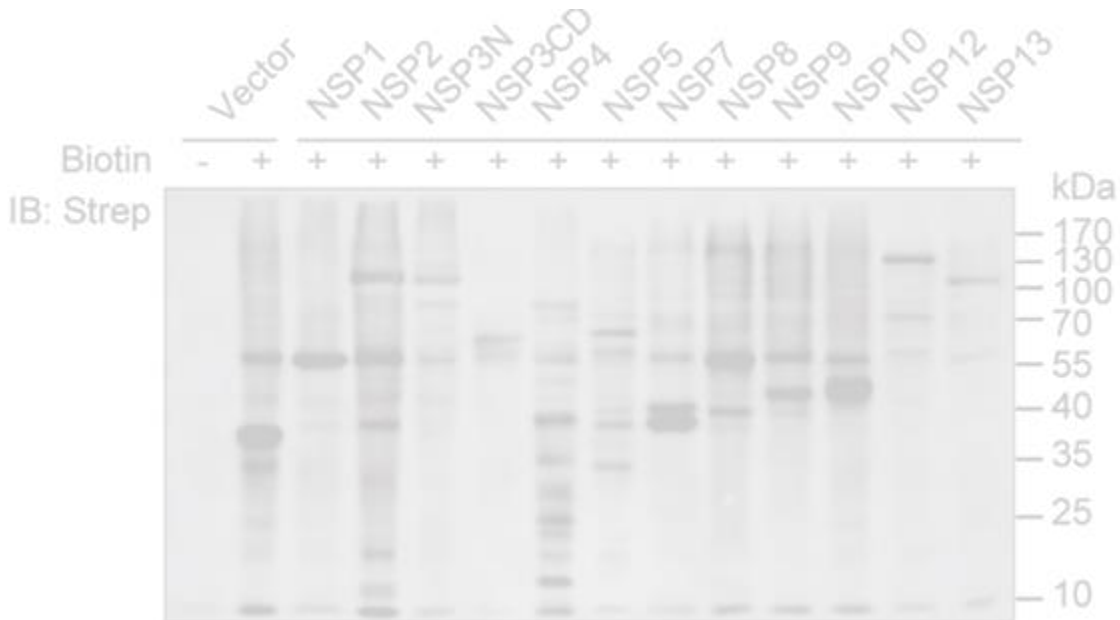
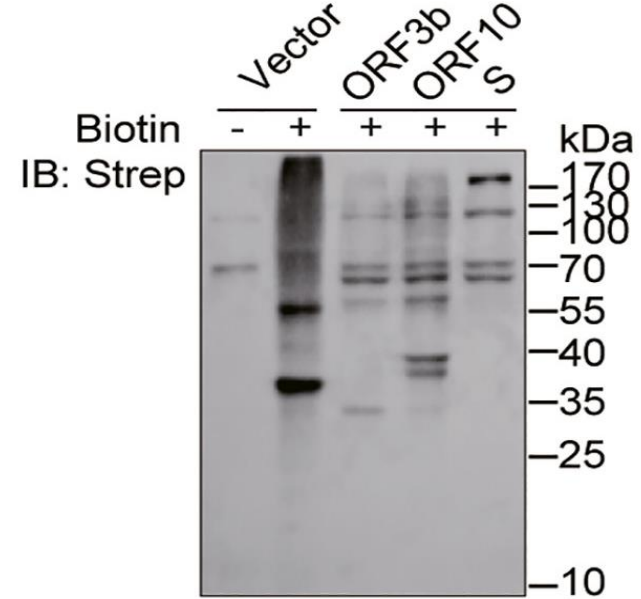
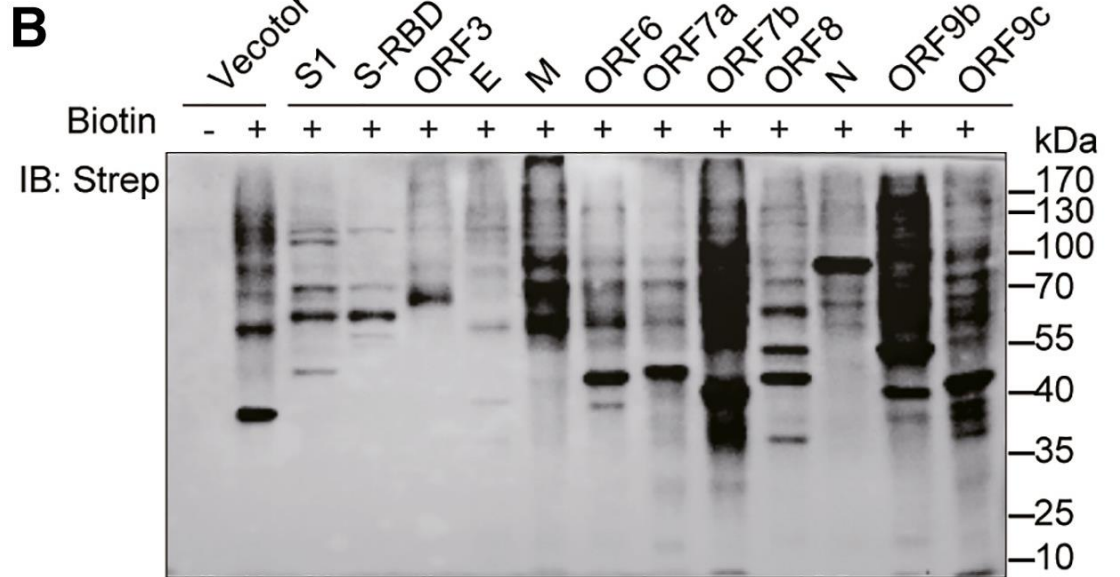
→ Indicates expression of target proteins

What **protein expressions** were detected by western blot assays?

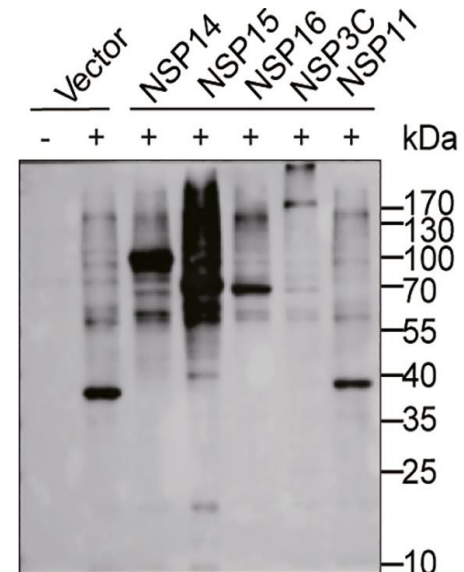
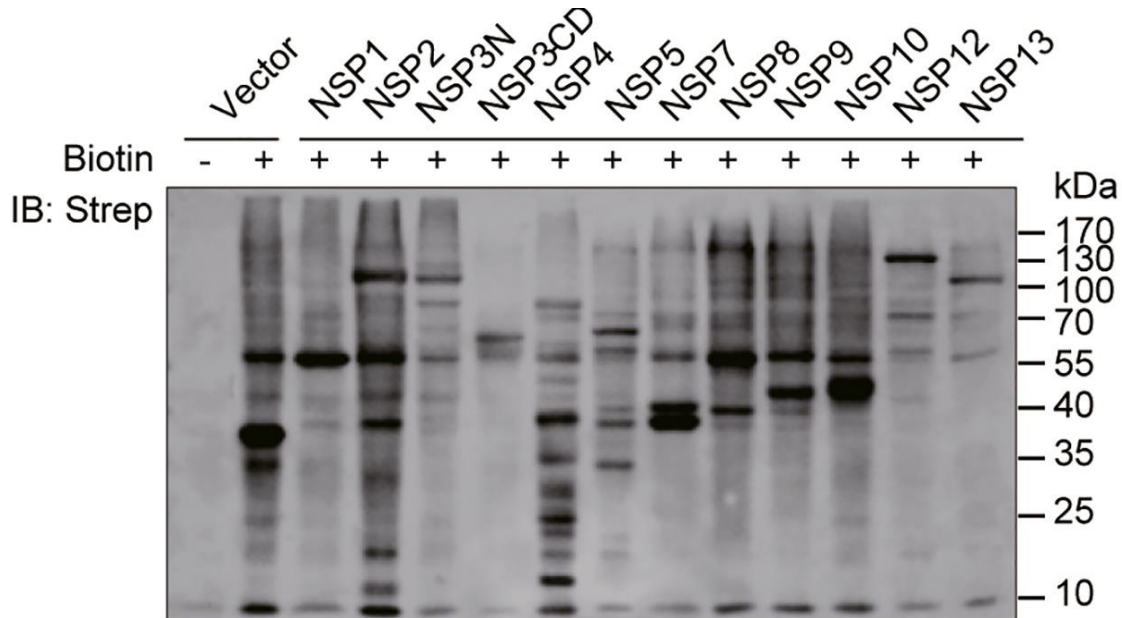
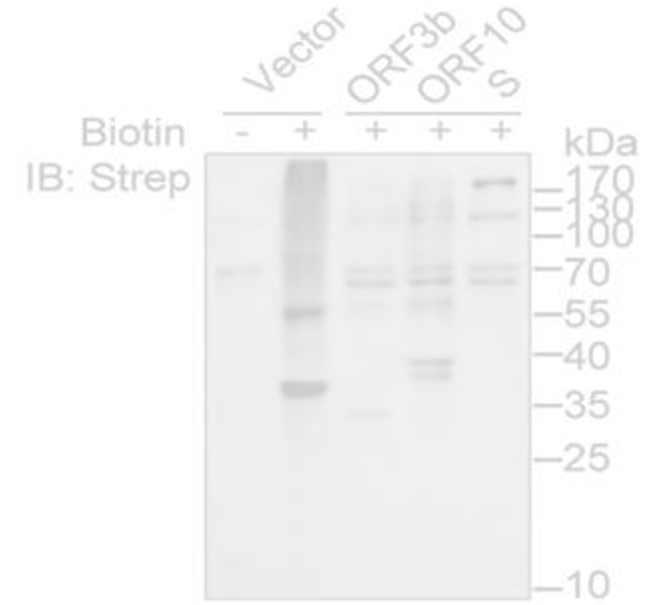
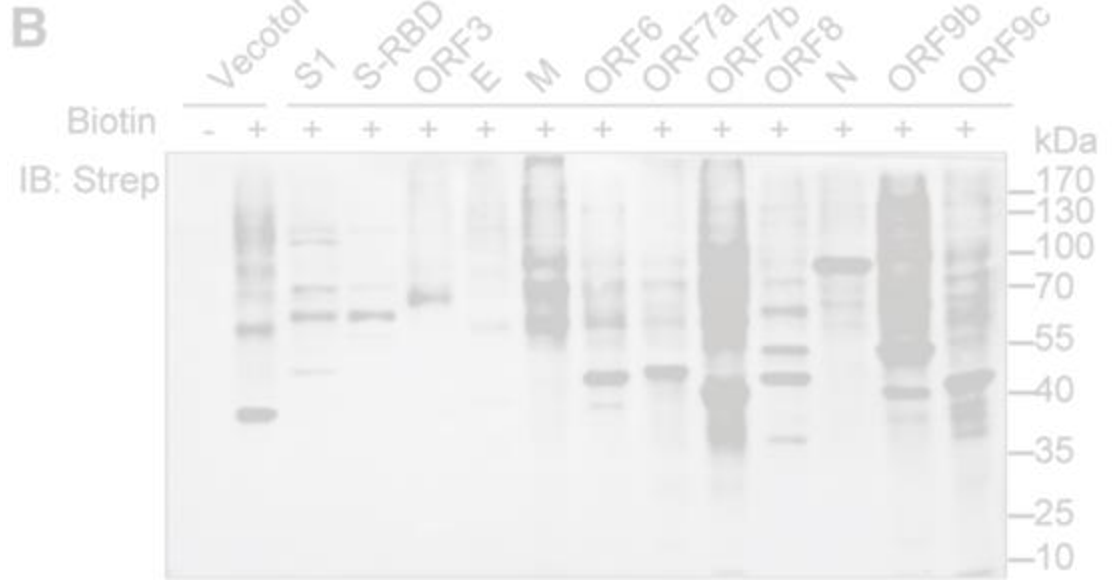


 Indicates expression of target proteins

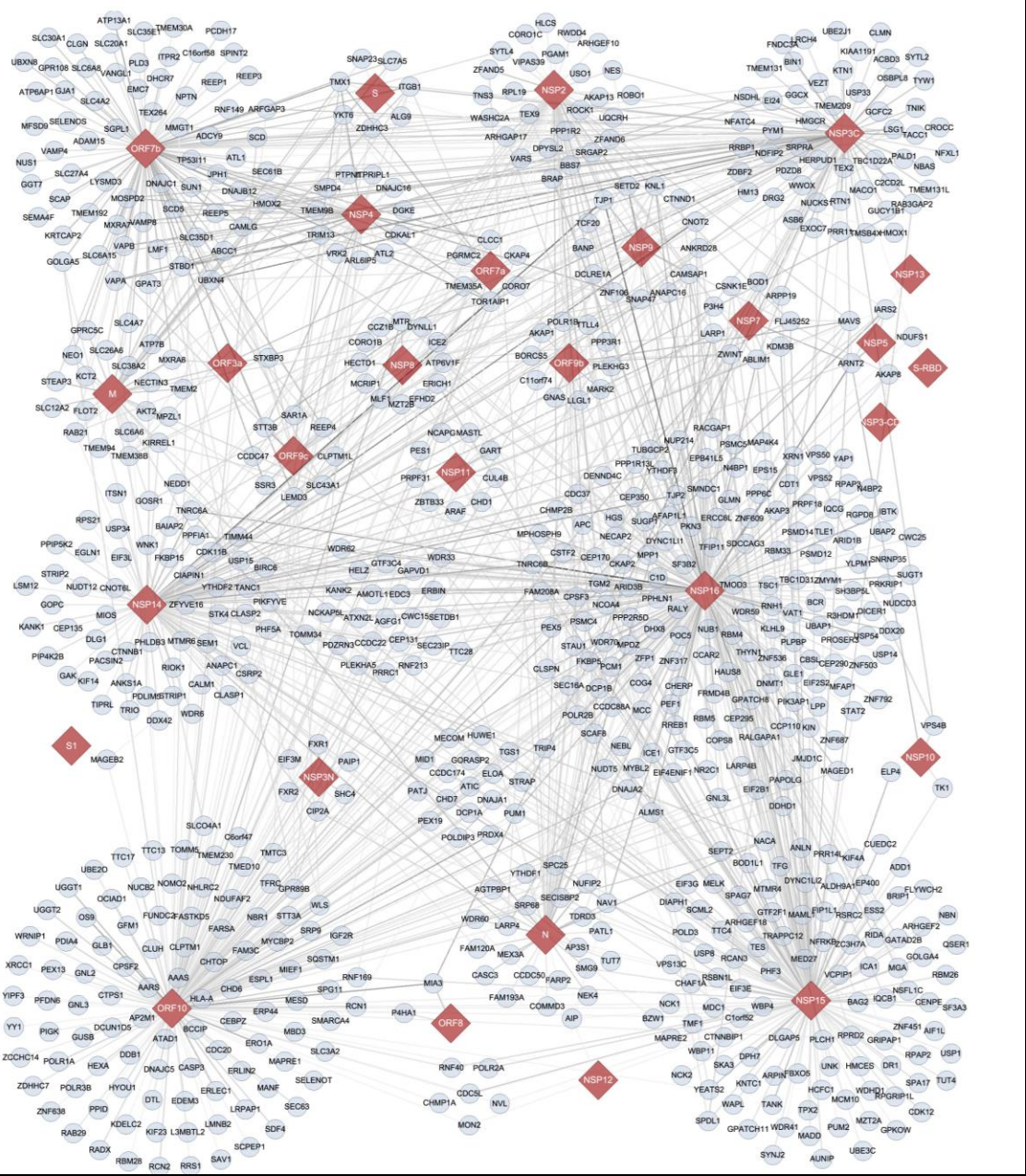
What **protein expressions** were detected by western blot assays?



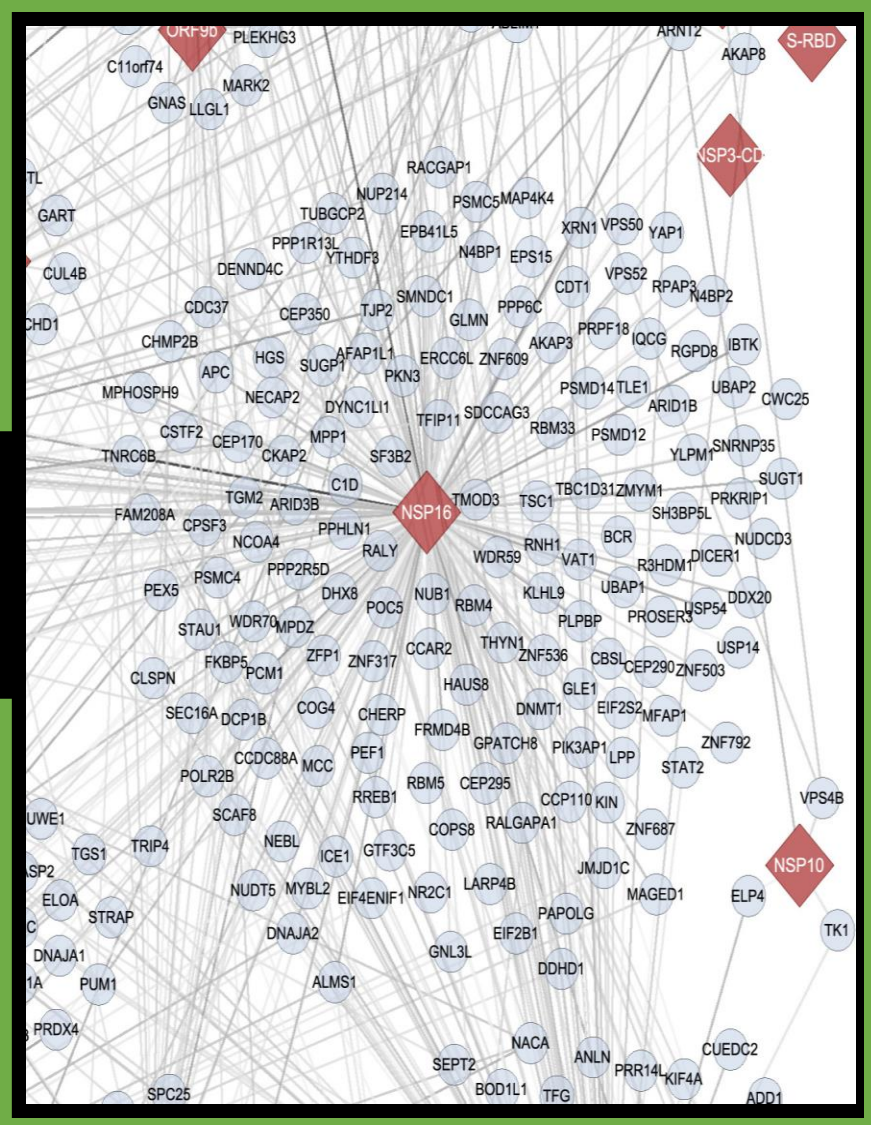
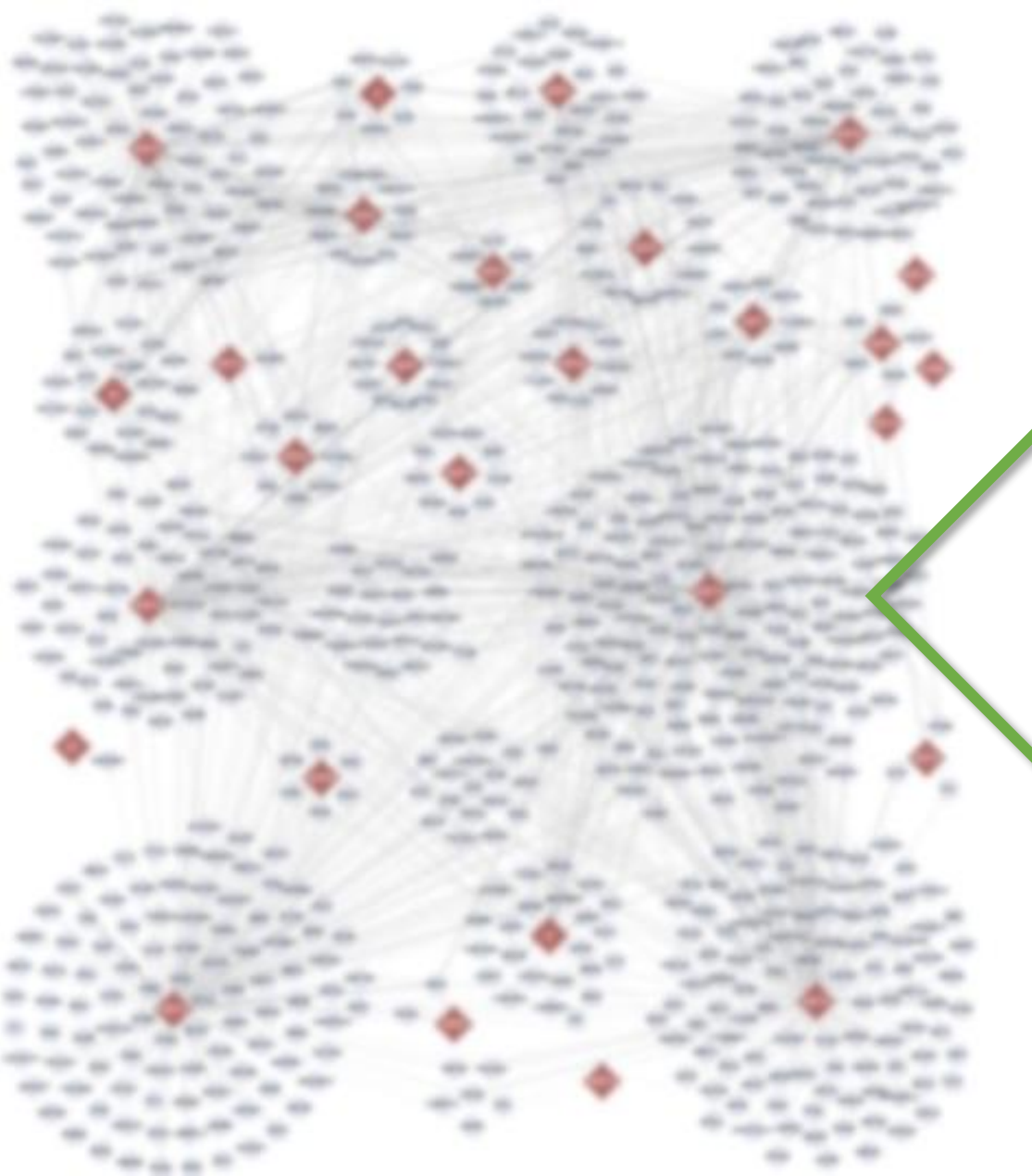
What **protein expressions** were detected by western blot assays?



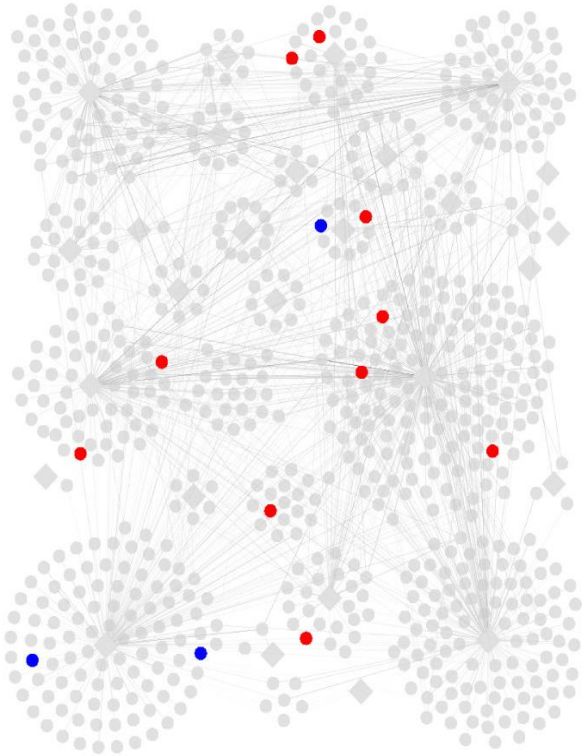
How does mass spectrometry confirm these identified protein interactions?



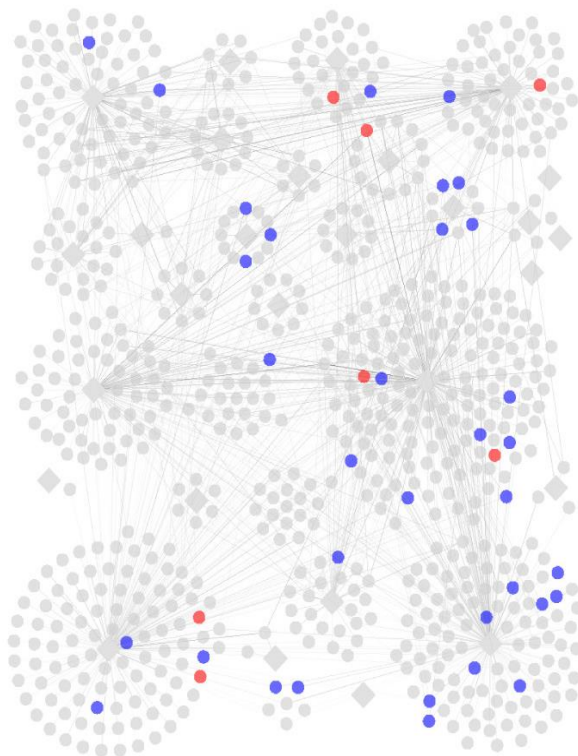
How does mass spectrometry confirm these identified **protein interactions**?



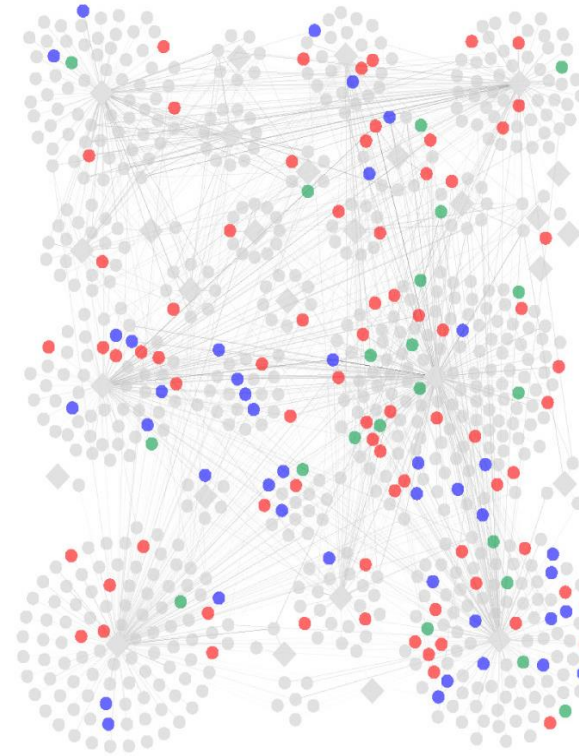
How do these proximal proteins compare to altered proteins of our genome?



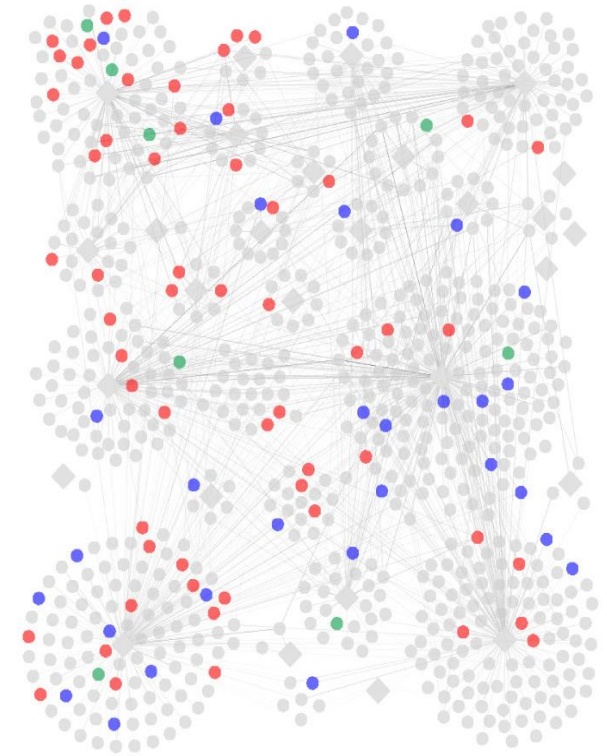
Transcriptome



Proteome




Phosphoproteome

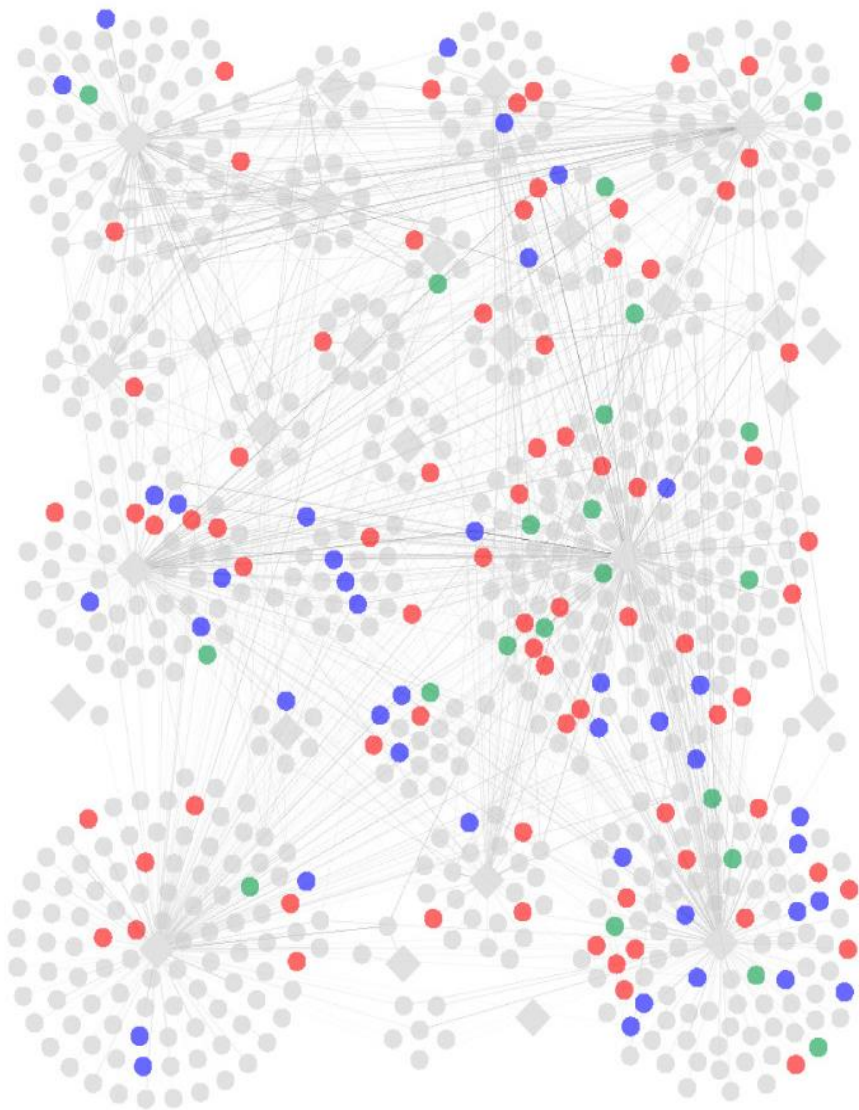


Ubiquitinome

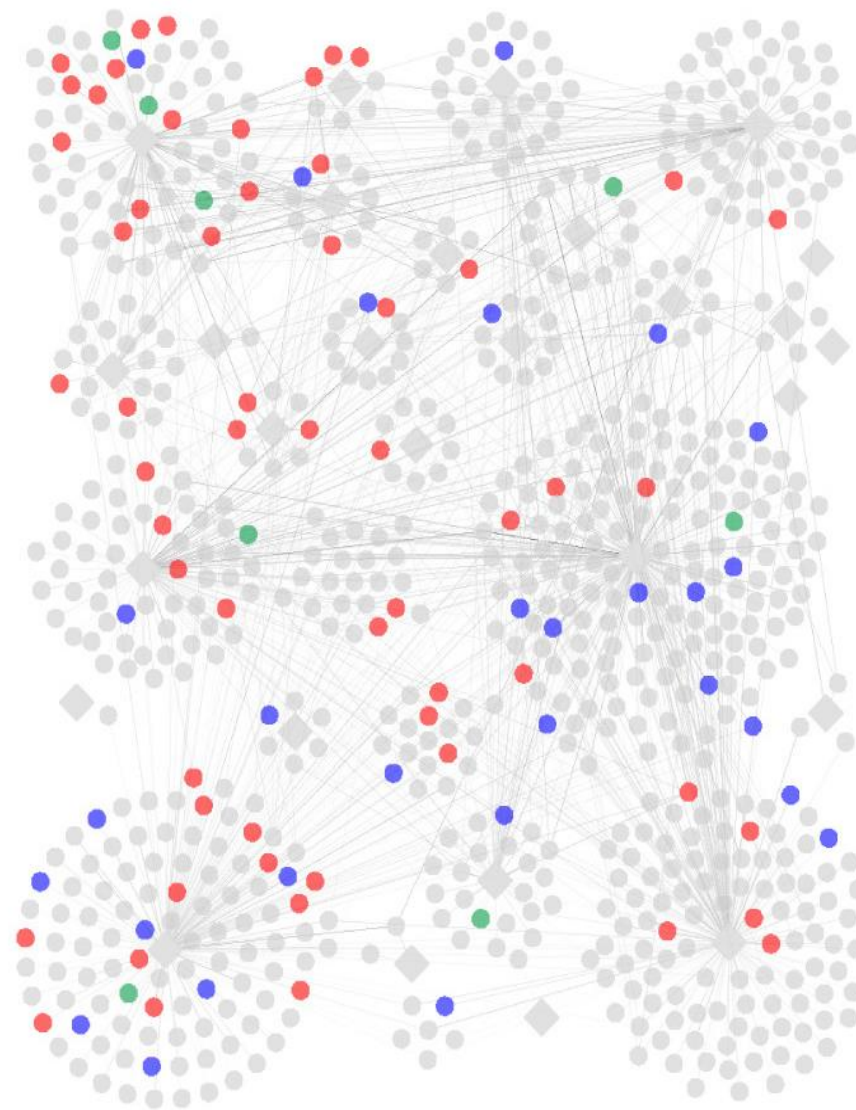
 downregulated proteins

 upregulated proteins

 dynamically regulated proteins




Phosphoproteome



Ubiquitinome

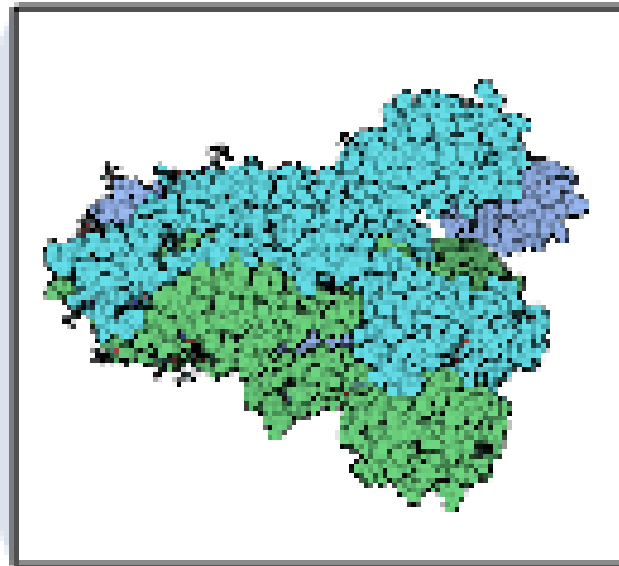
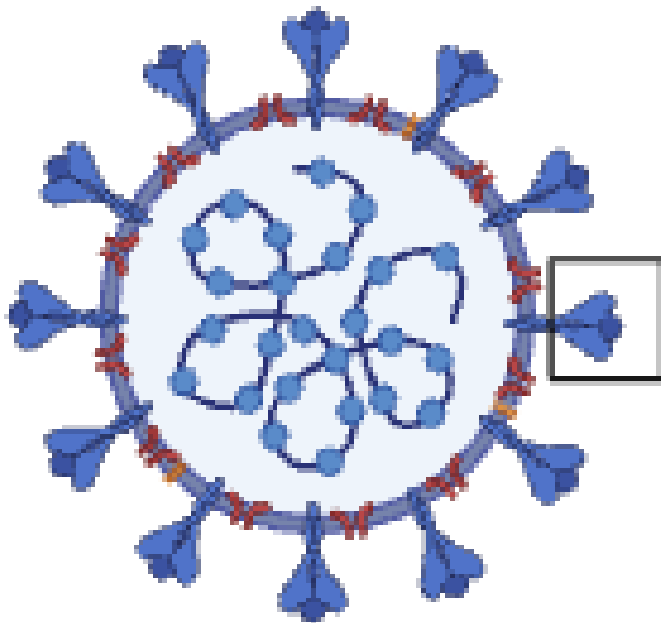
 downregulated proteins

 upregulated proteins

 dynamically regulated proteins

Interactions with S protein

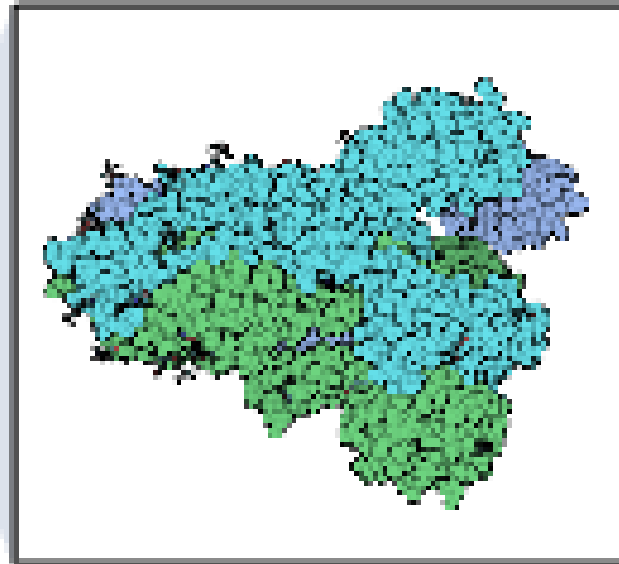
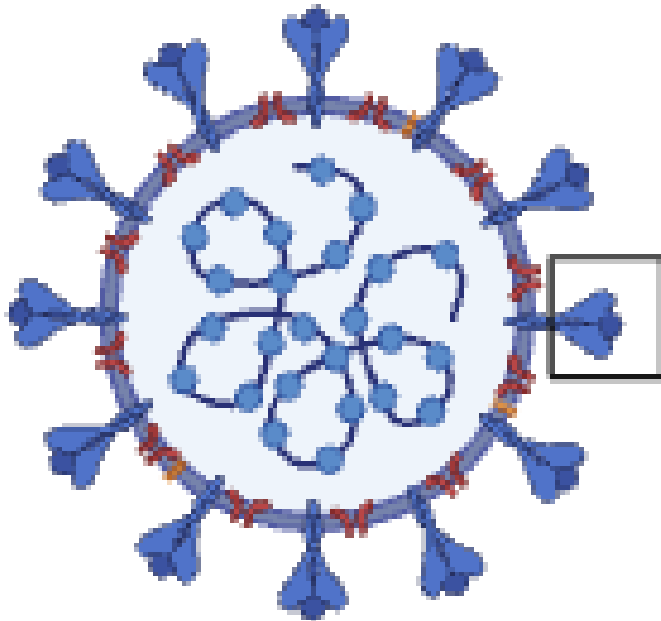
SARS-CoV-2



Prefusion spike
glycoprotein (S1)

Interactions with S protein

SARS-CoV-2

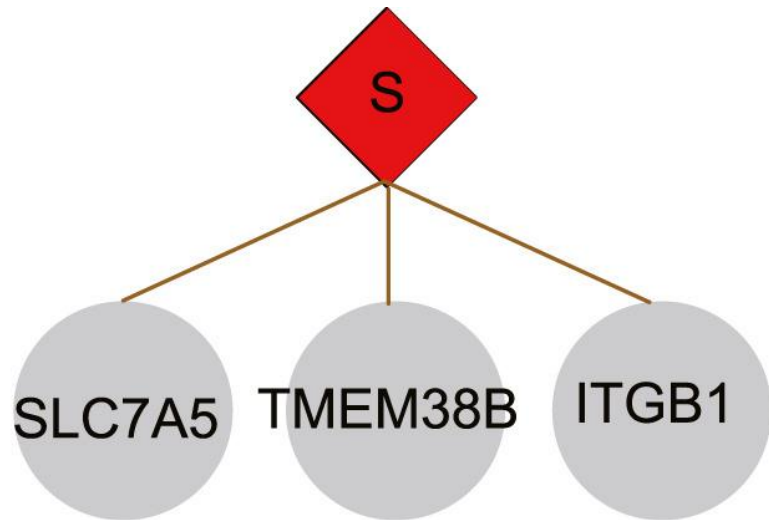


Prefusion spike
glycoprotein (S1)

Integrin subunit beta 1
(**ITGB1**)
Transmembrane protein
38B (**TMEM38B**)
Solute carrier family 7
member 5 (**SLC7A5**)

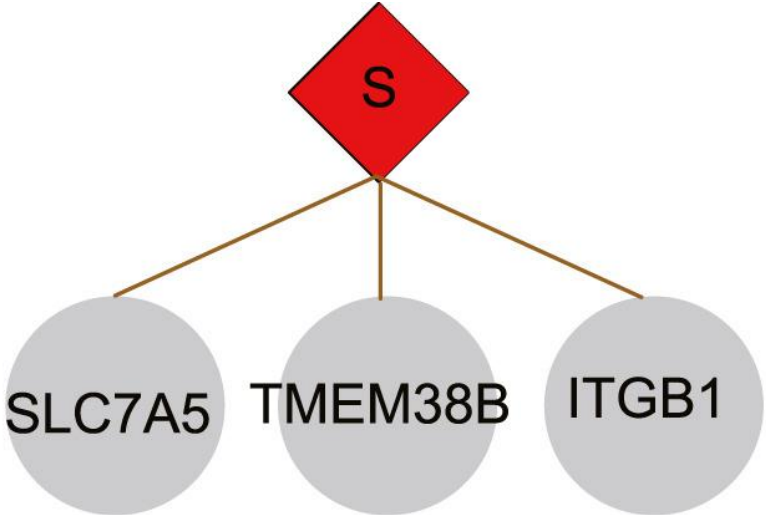
How do these membrane proteins interact with the **S protein** of SARS-CoV-2?

A

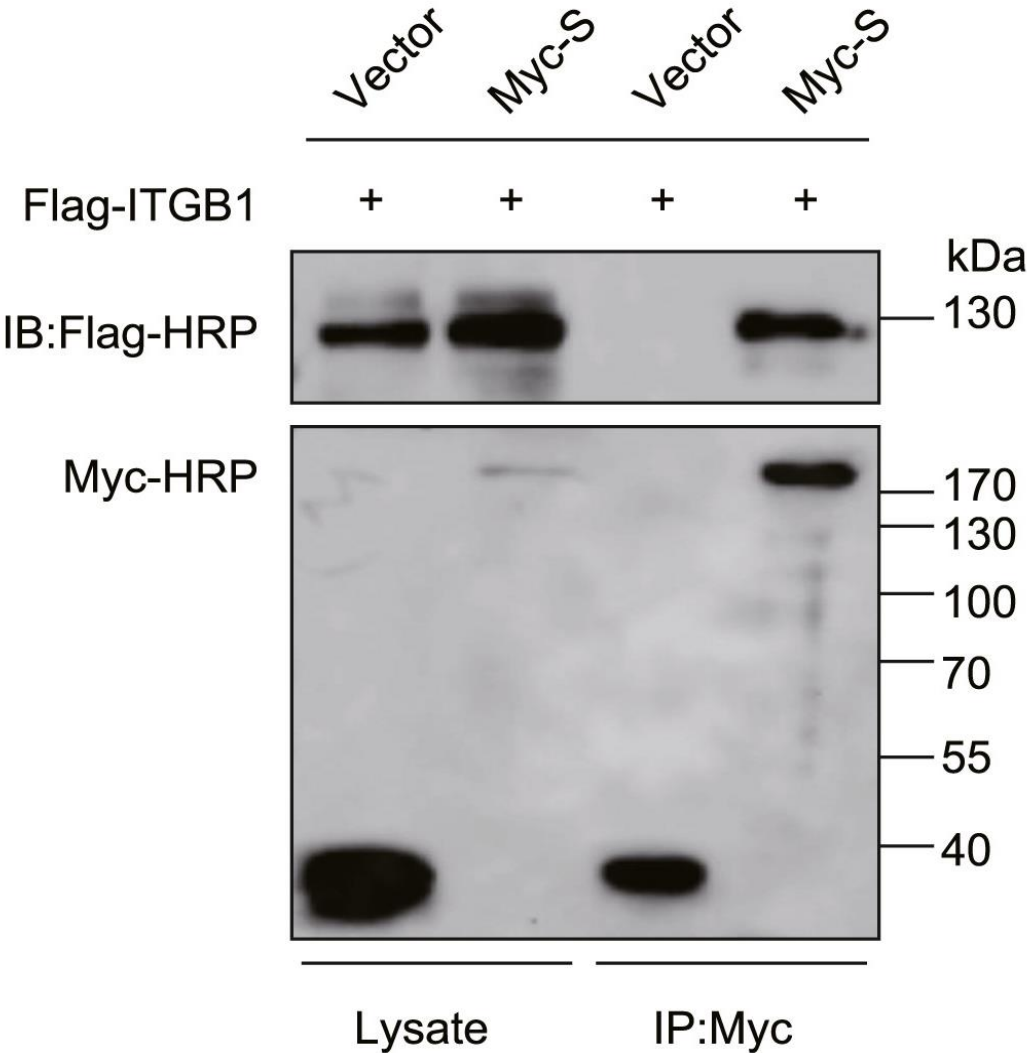


How do these membrane proteins interact with the **S protein** of SARS-CoV-2?

A

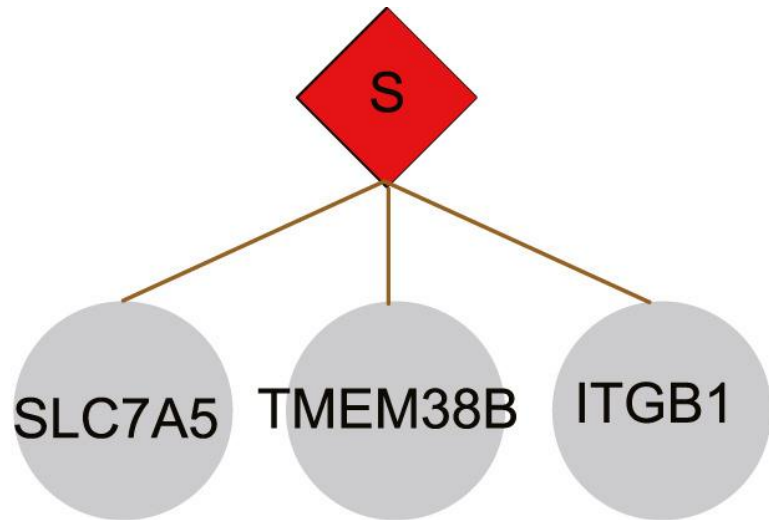


B

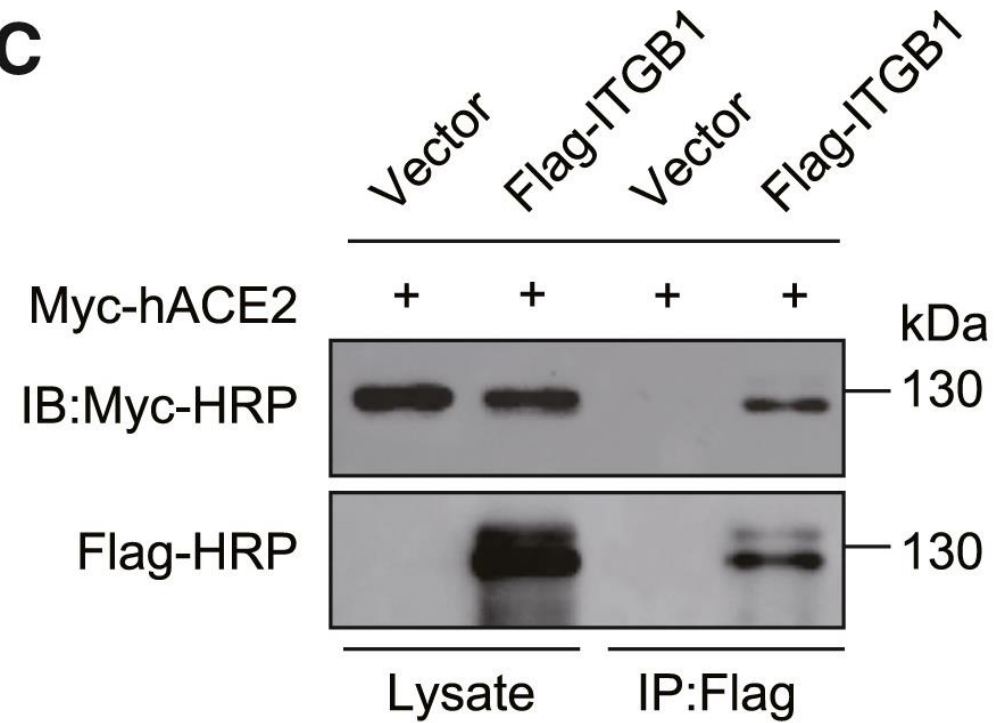


How do these membrane proteins interact with the **S protein** of SARS-CoV-2?

A

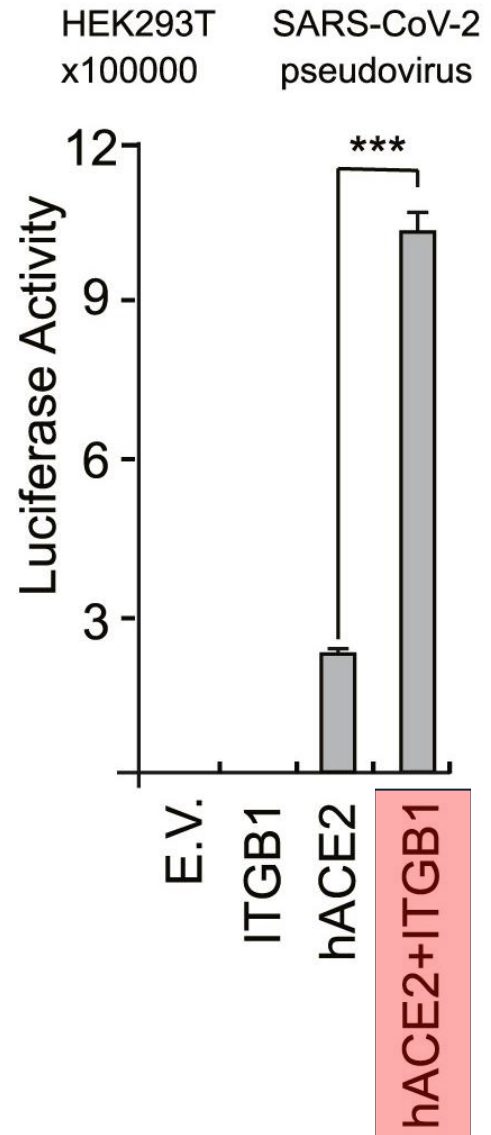


C



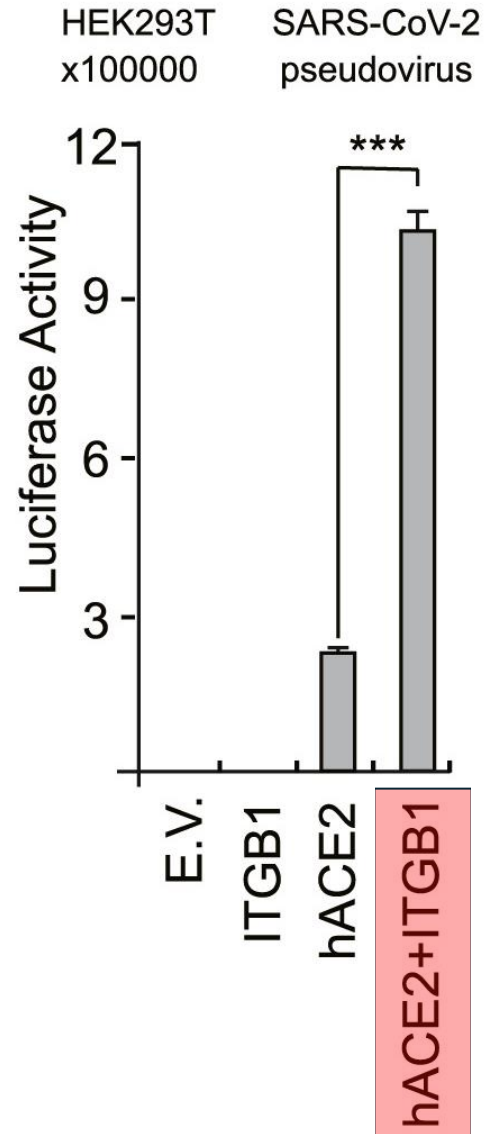
How does **ITGB1** mediate the entry of SARS-CoV-2 into HEK293T cells?

D

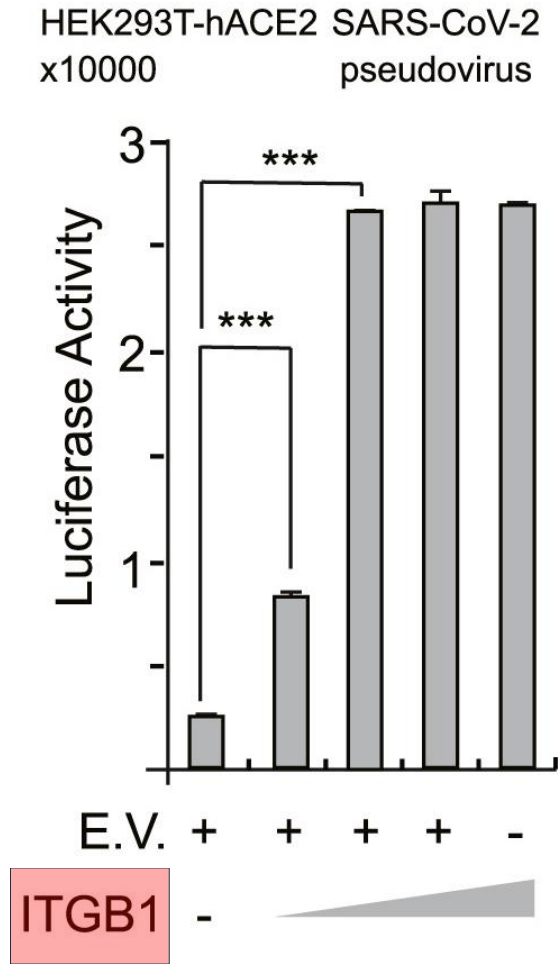


How does **ITGB1** mediate the entry of SARS-CoV-2 into HEK293T cells?

D

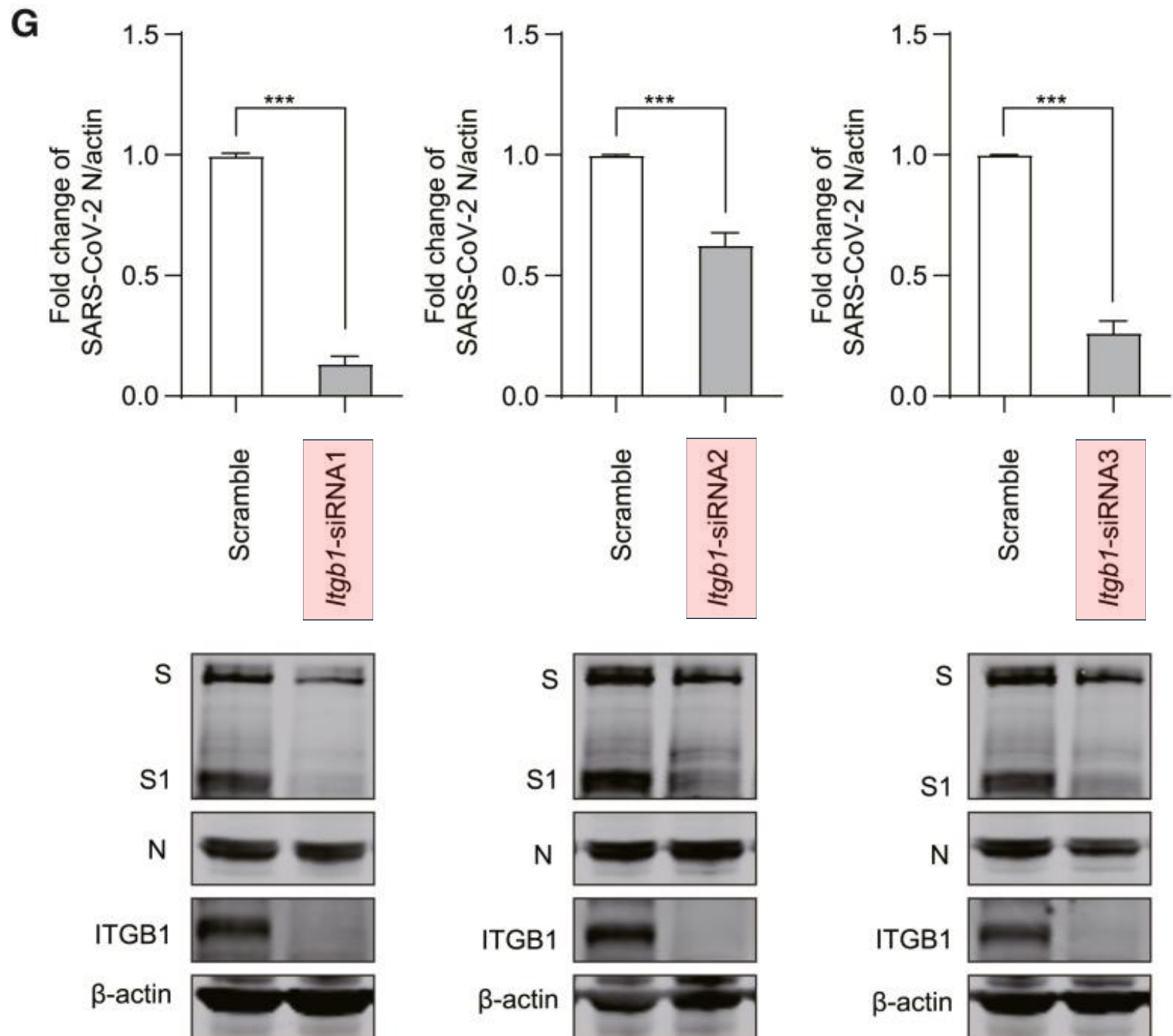


E

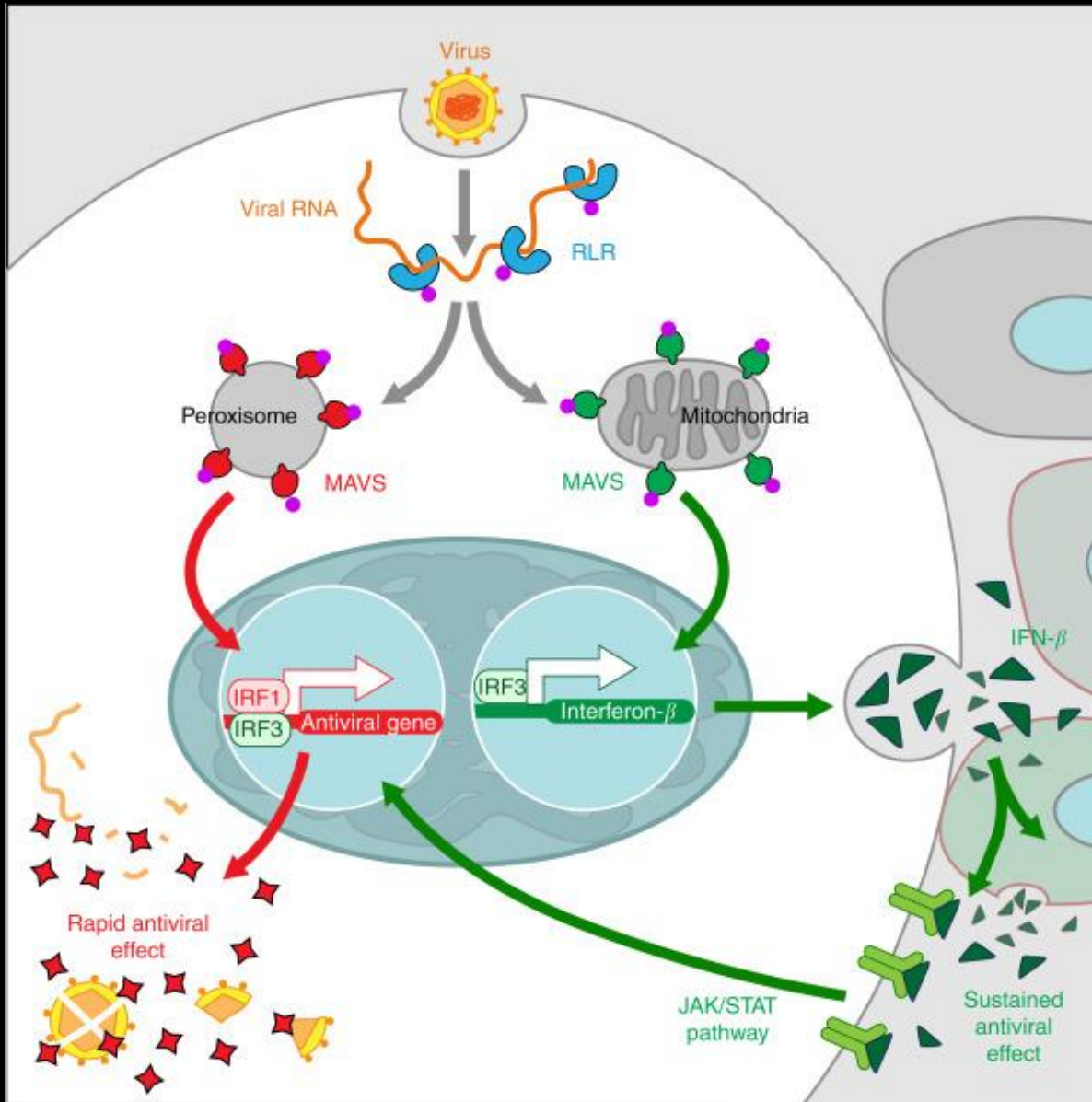


These results indicate that ITGB1 is a co-factor for SARS-CoV-2 entry.

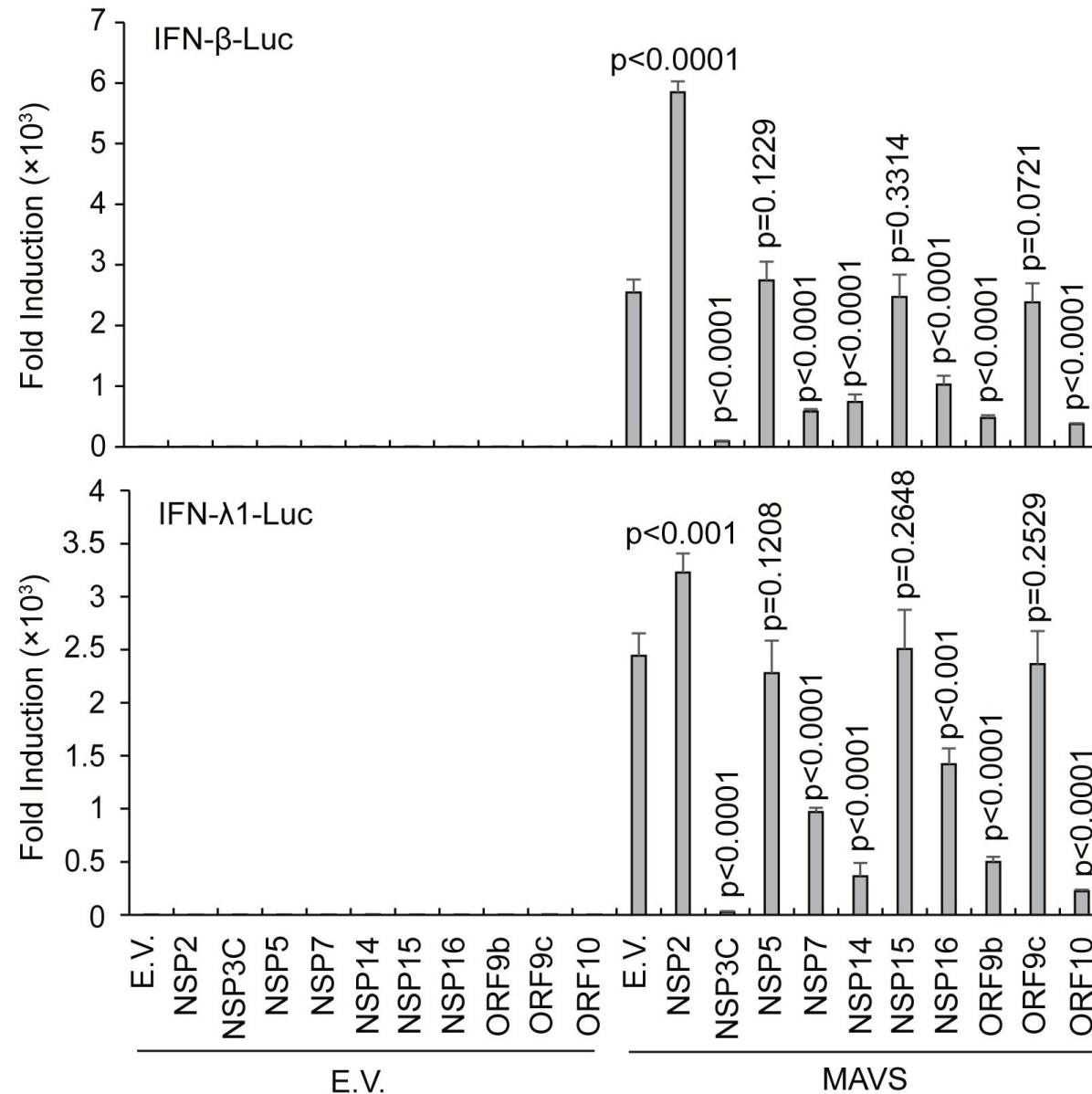
How is this proof that ITGB1 is a **co-factor** for SARS-CoV-2?



What is the MAVS signaling pathway?

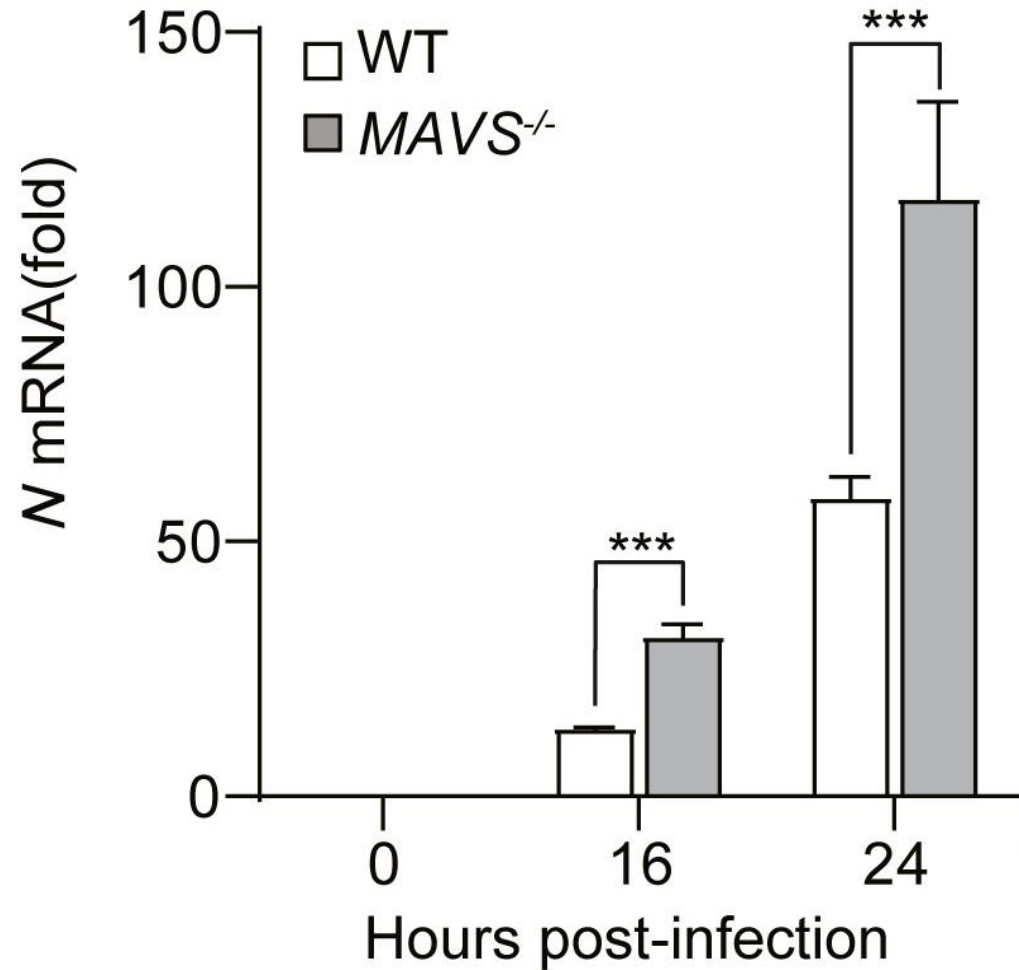


What effect do the proteins of SARS-CoV-2 have on MAVS-induced activation of IFN reporters?

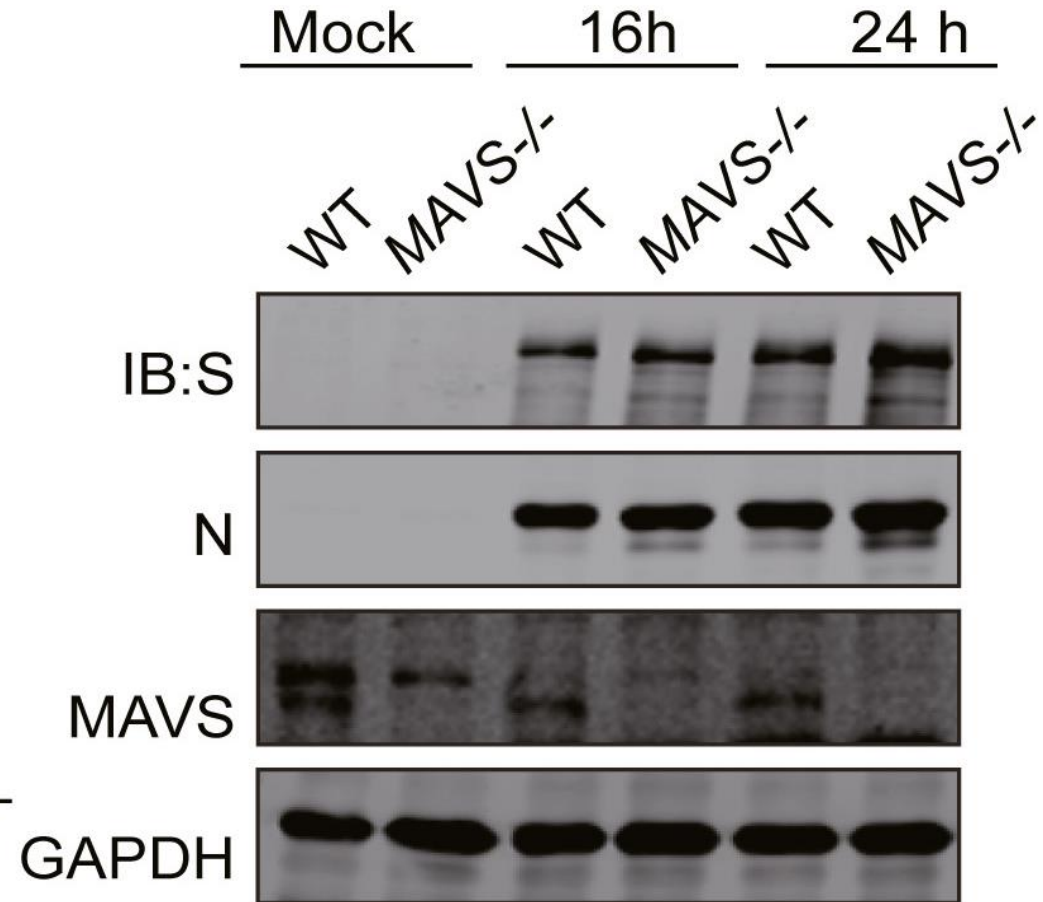


How was the role of MAVS during infection confirmed?

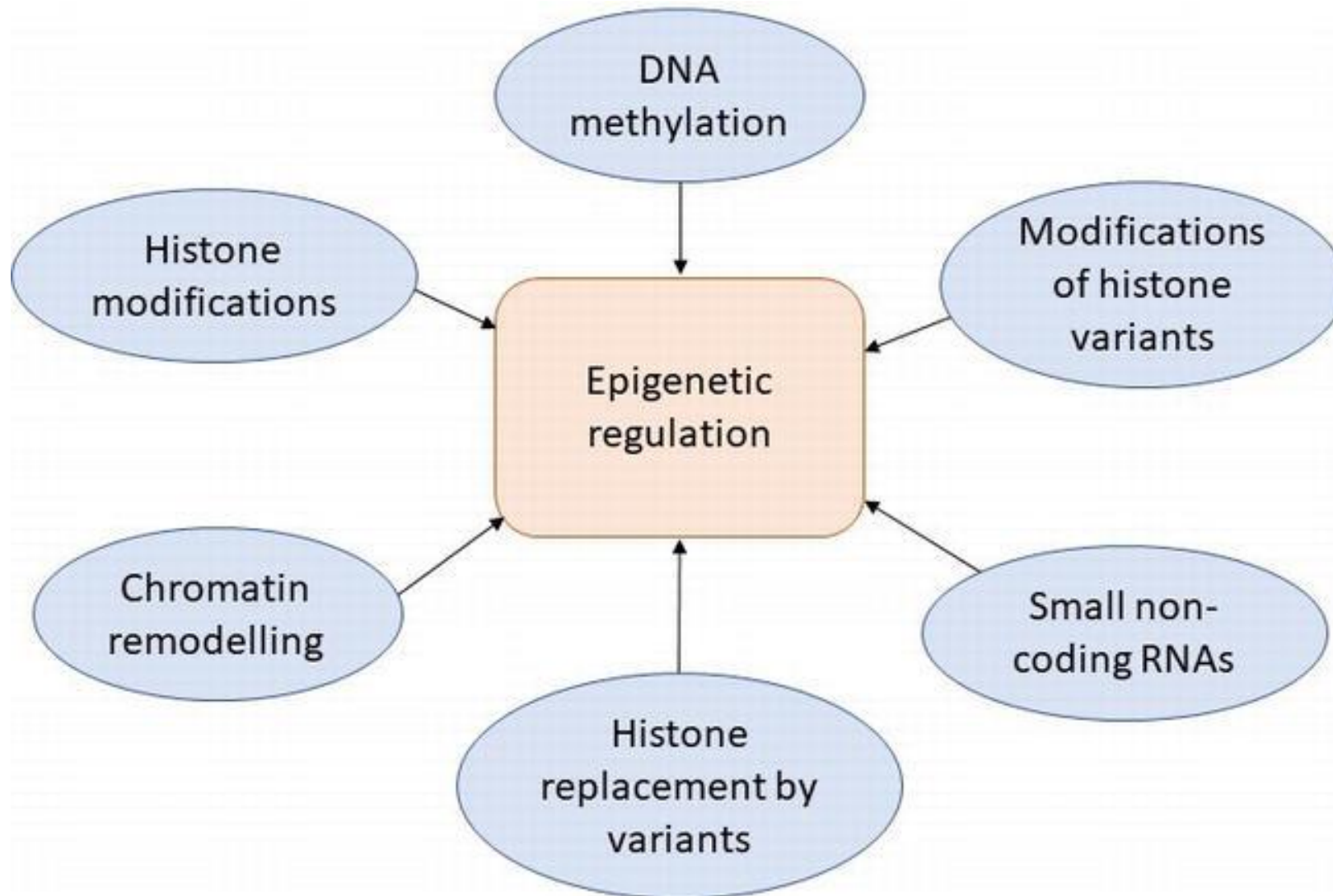
E



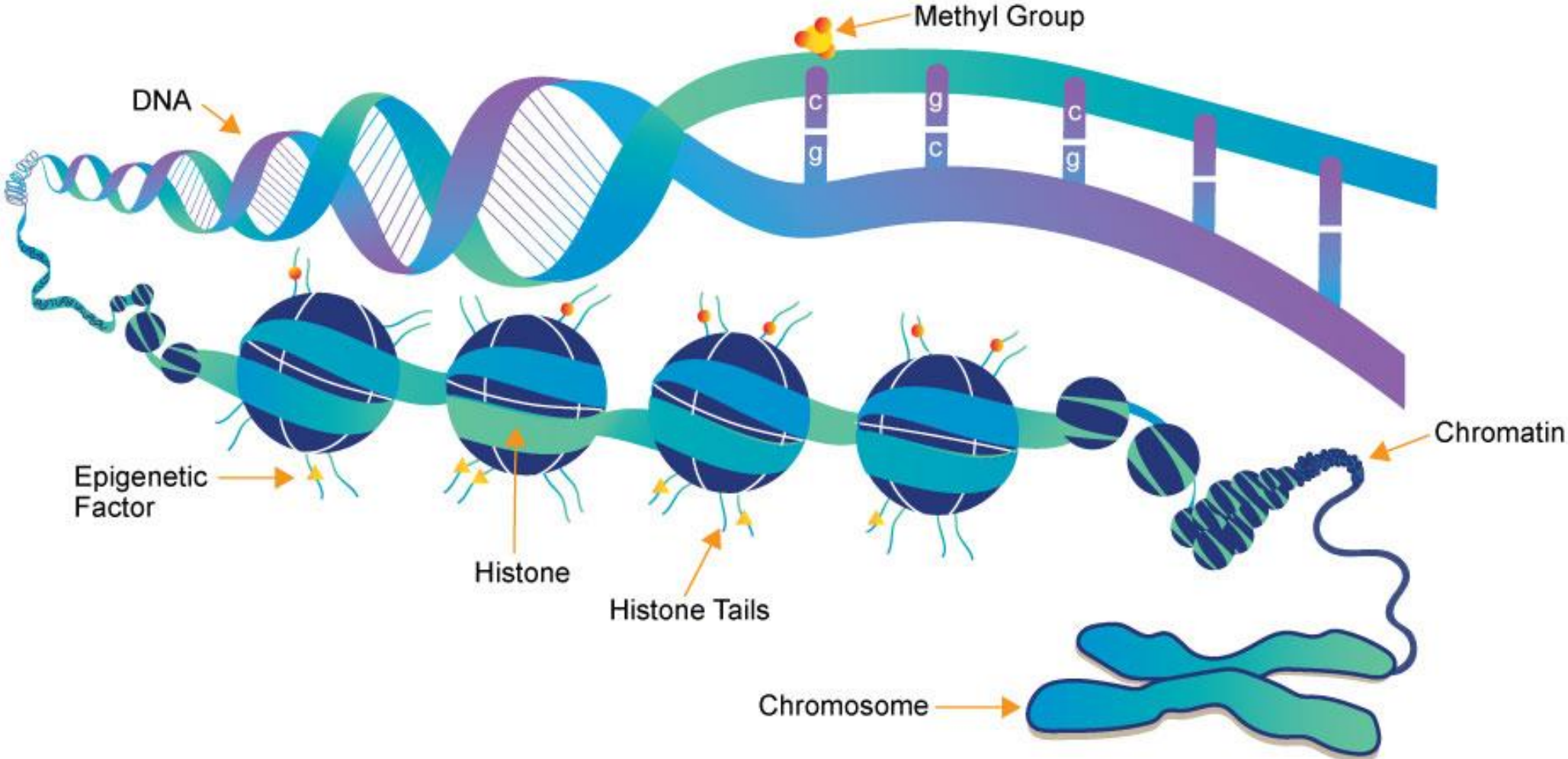
F



What are epigenetic regulators?

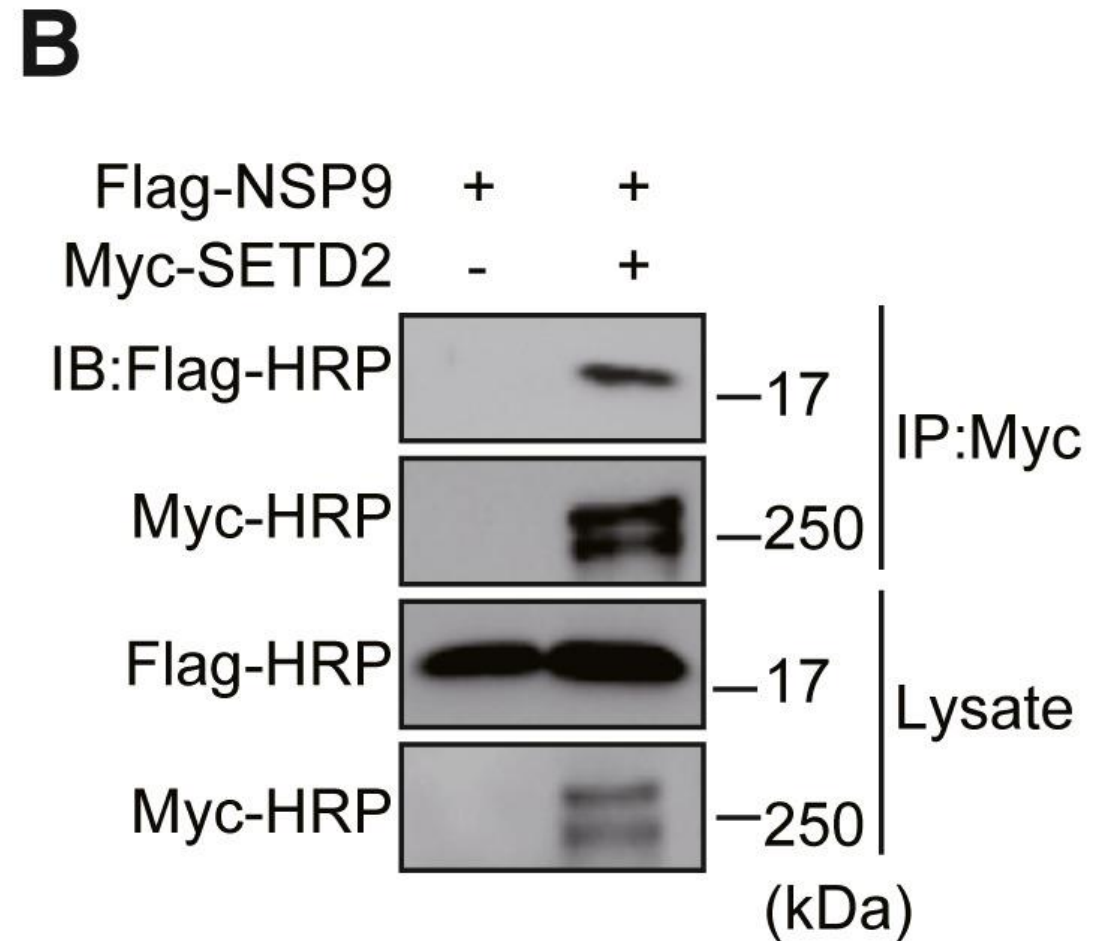
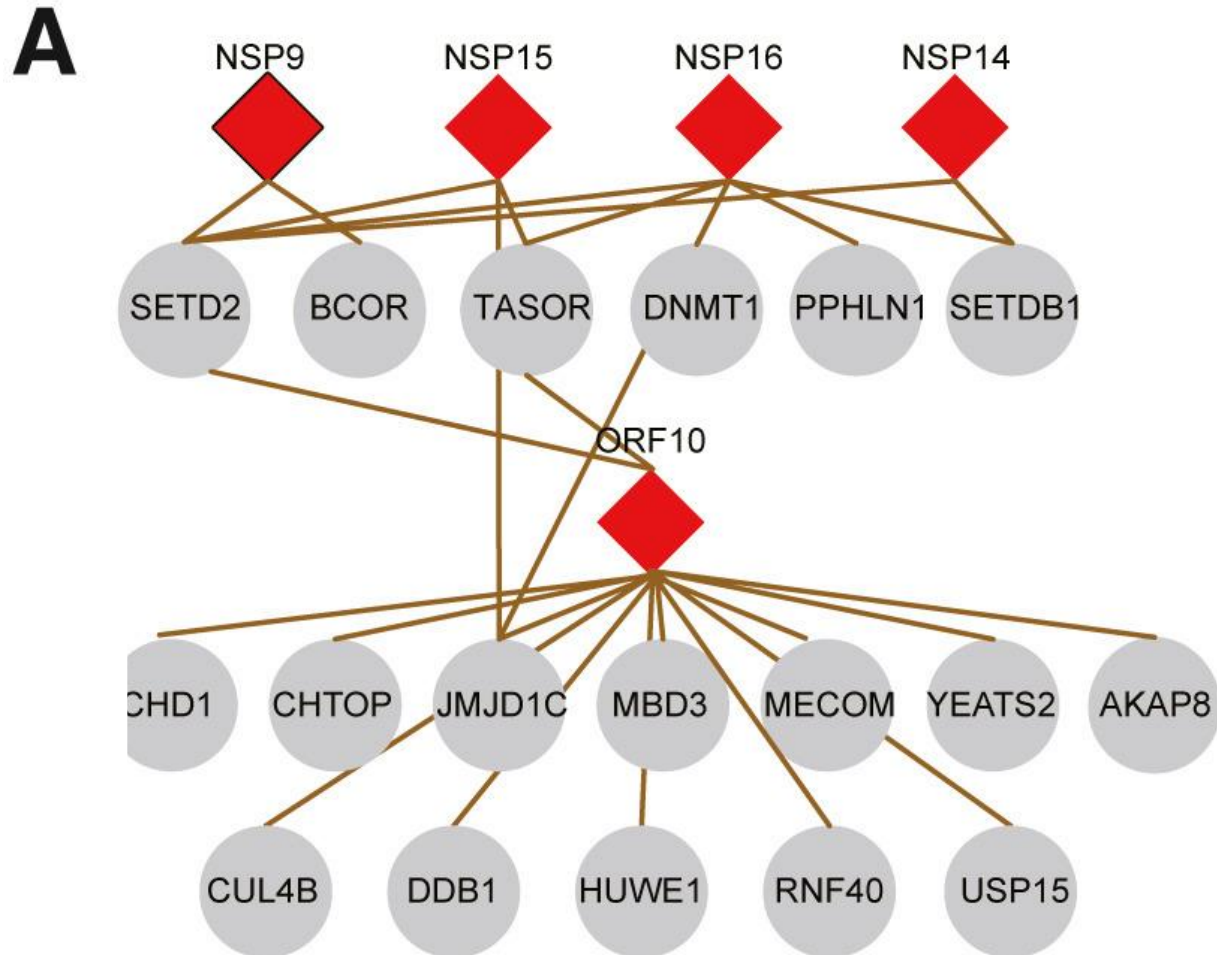


What are epigenetic regulators?



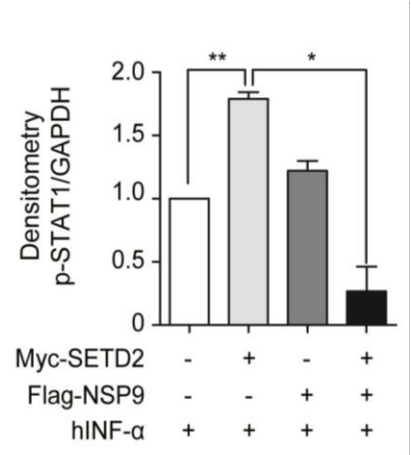
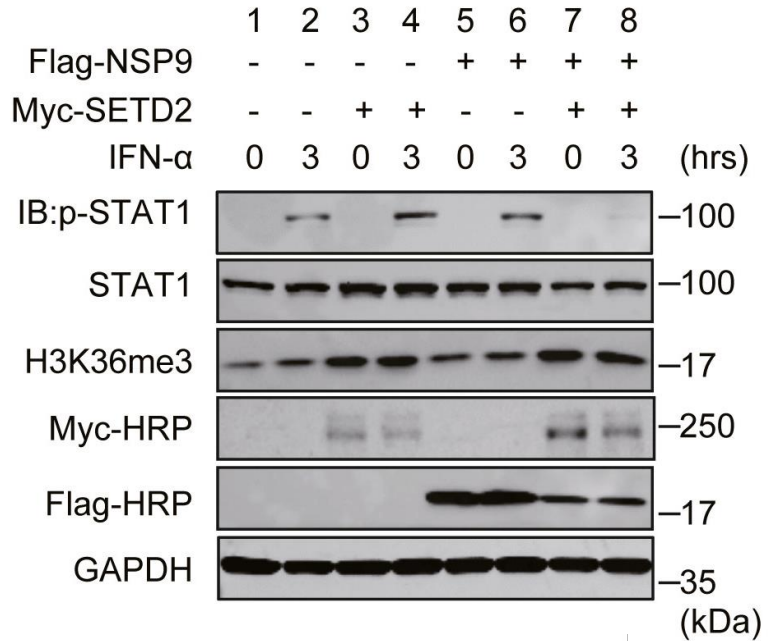
(Mammas et al., 2022)

What proteins target epigenetic regulators for viral infection?

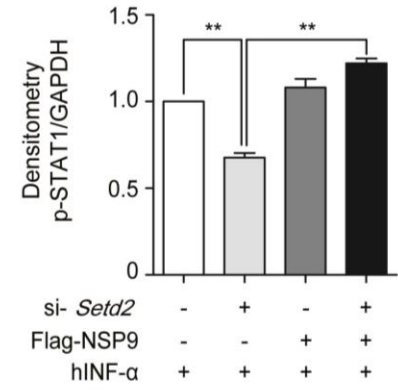
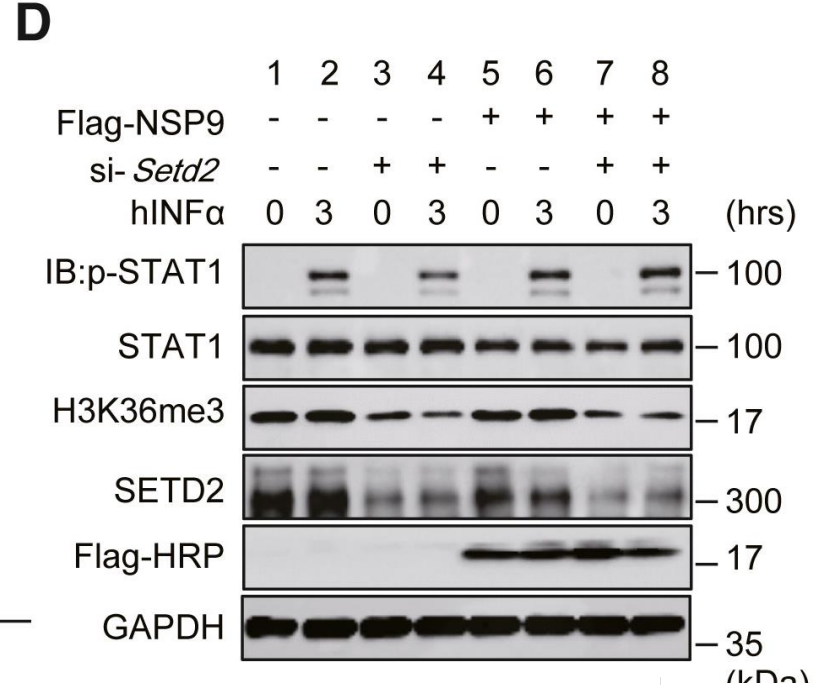
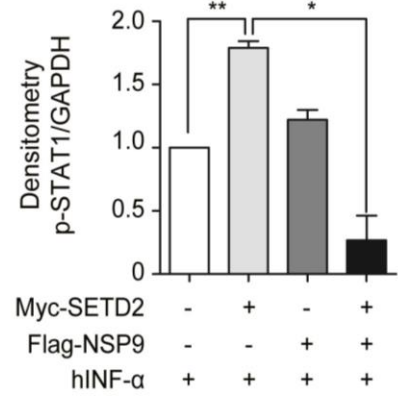
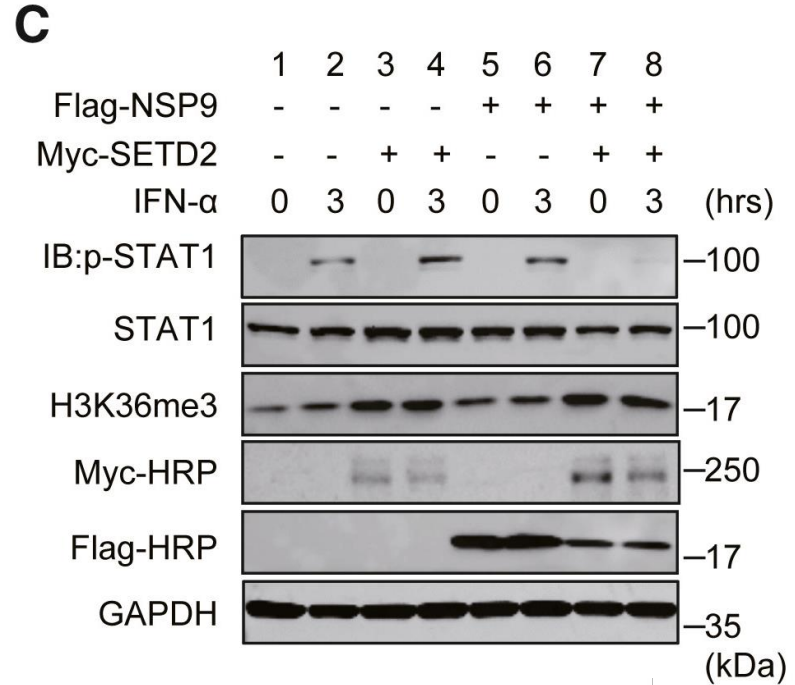


How were epigenetic regulators tested to confirm blocking of IFN signaling?

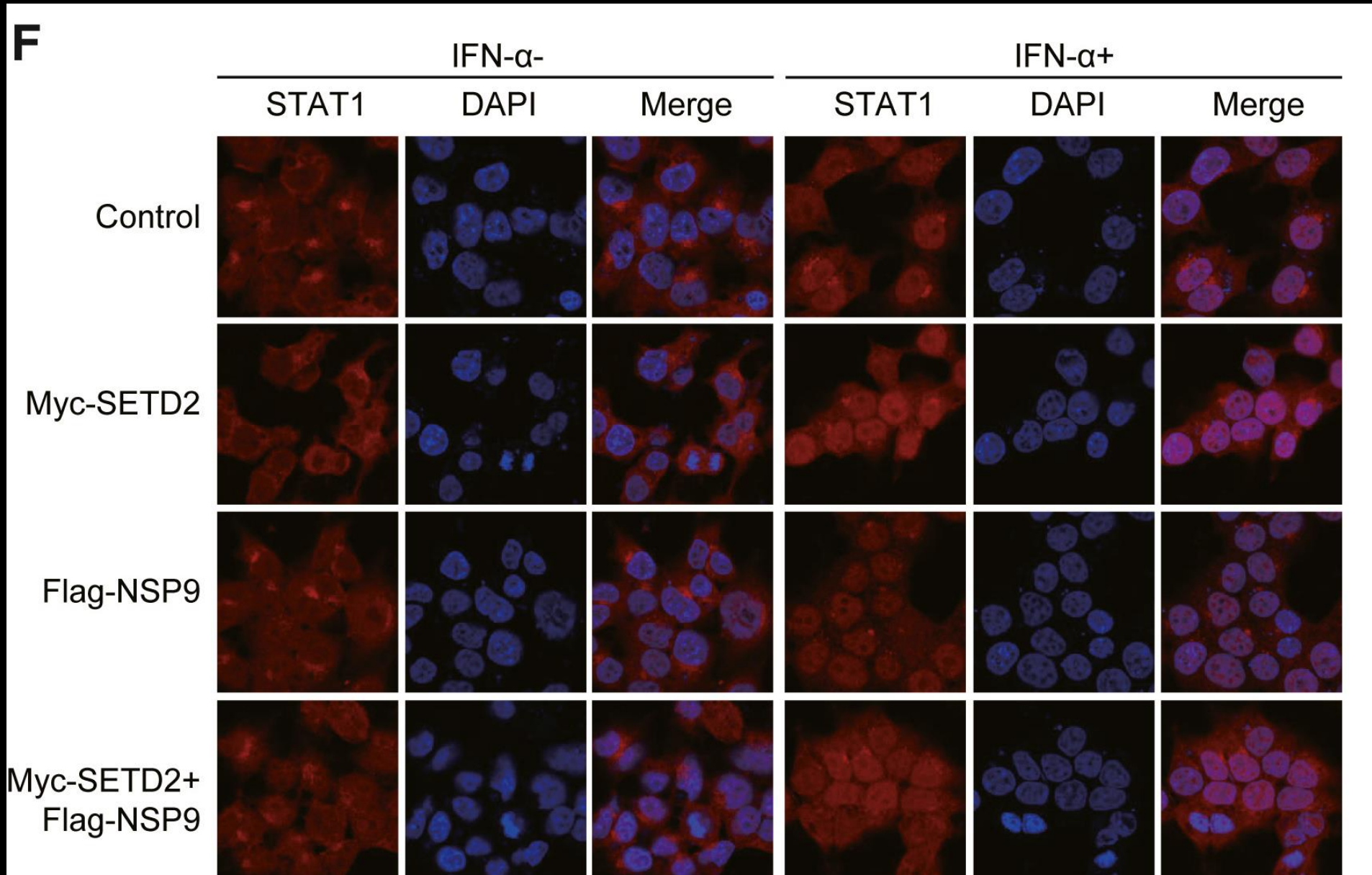
C



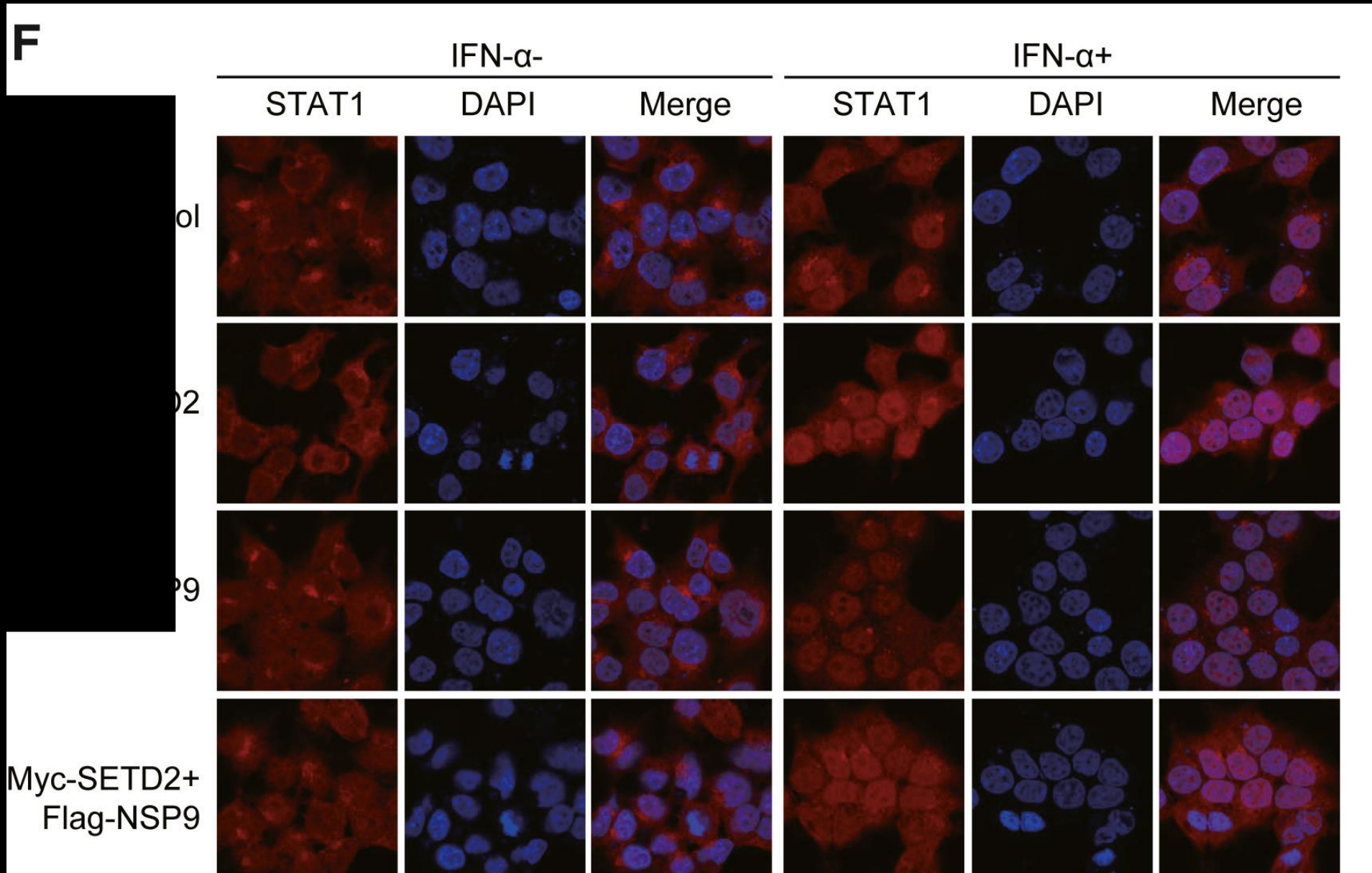
How were epigenetic regulators tested to confirm blocking of IFN signaling?



How was microscopy used to show how NSP9-SETD2 cells inhibit translocation of STAT1?

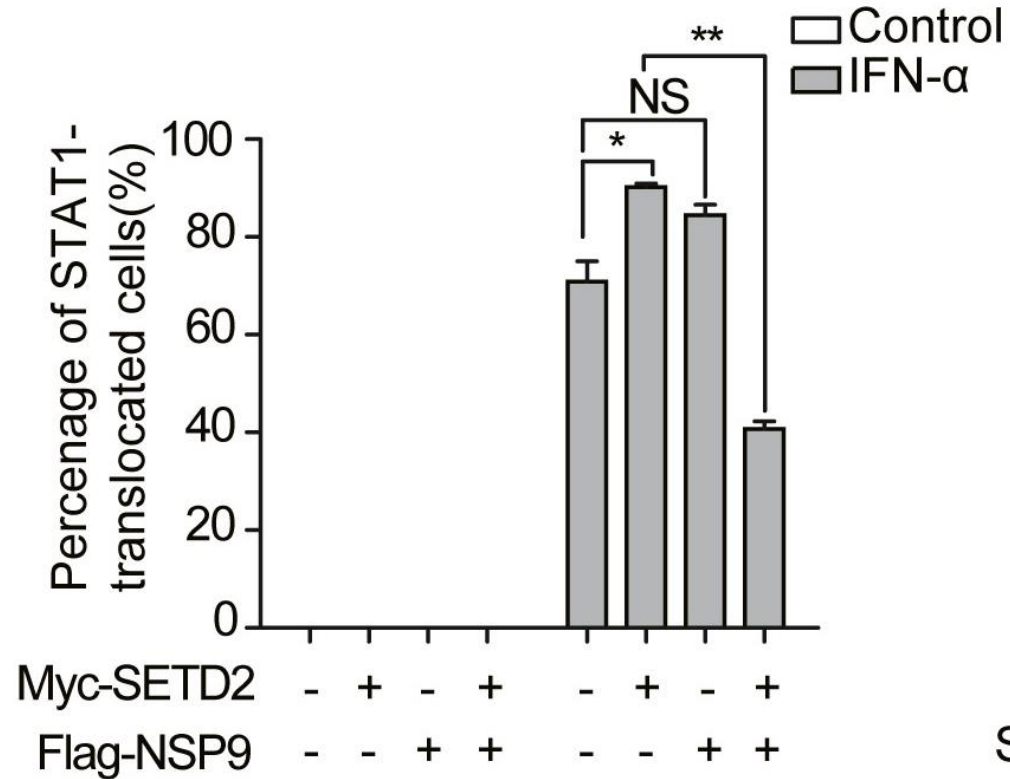


How was microscopy used to show how NSP9-SETD2 cells inhibit translocation of STAT1?

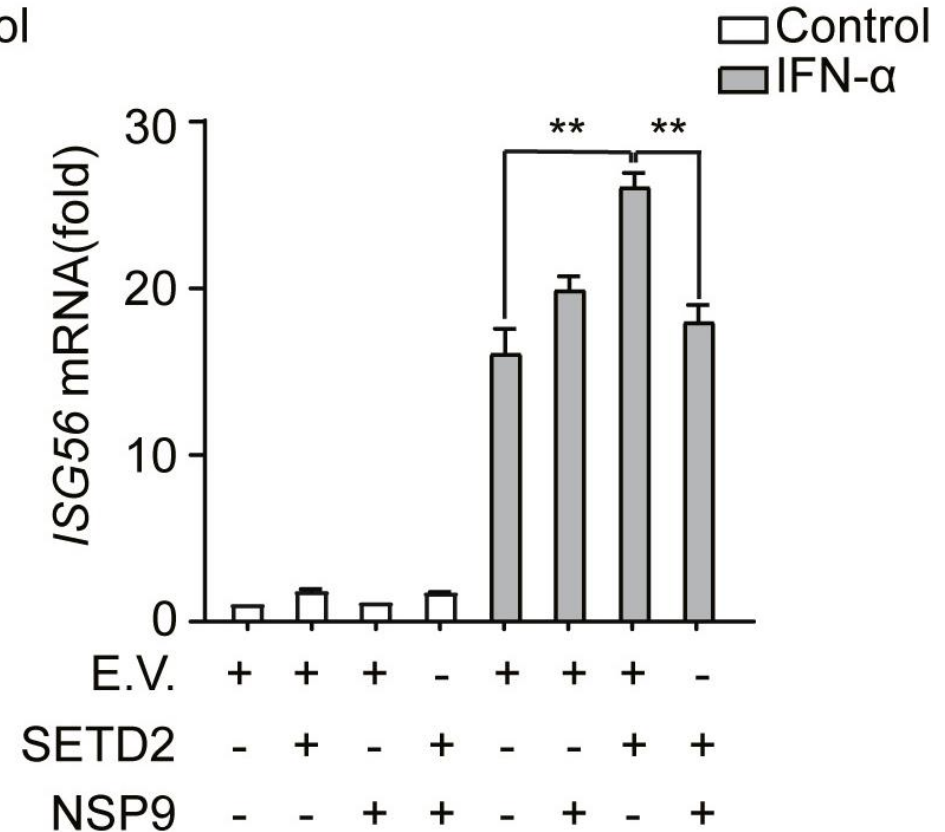


How does this show how NSP9-SETD2 cells inhibit translocation of STAT1?

G

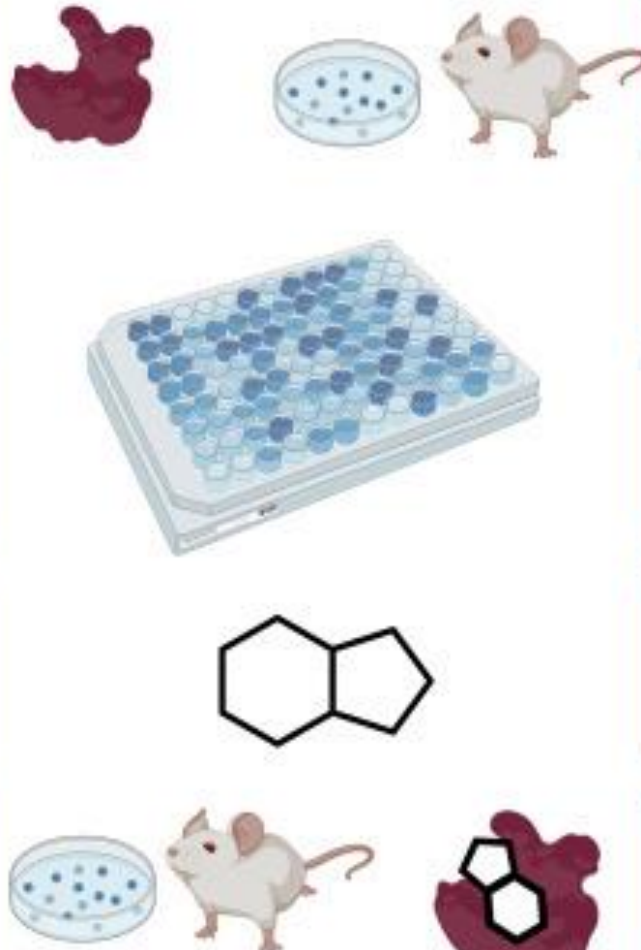


H

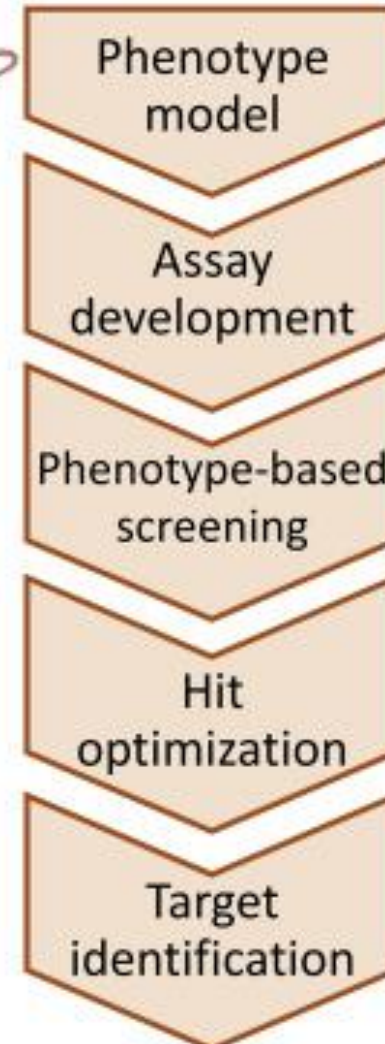


How are drugs used to target proximal proteins?

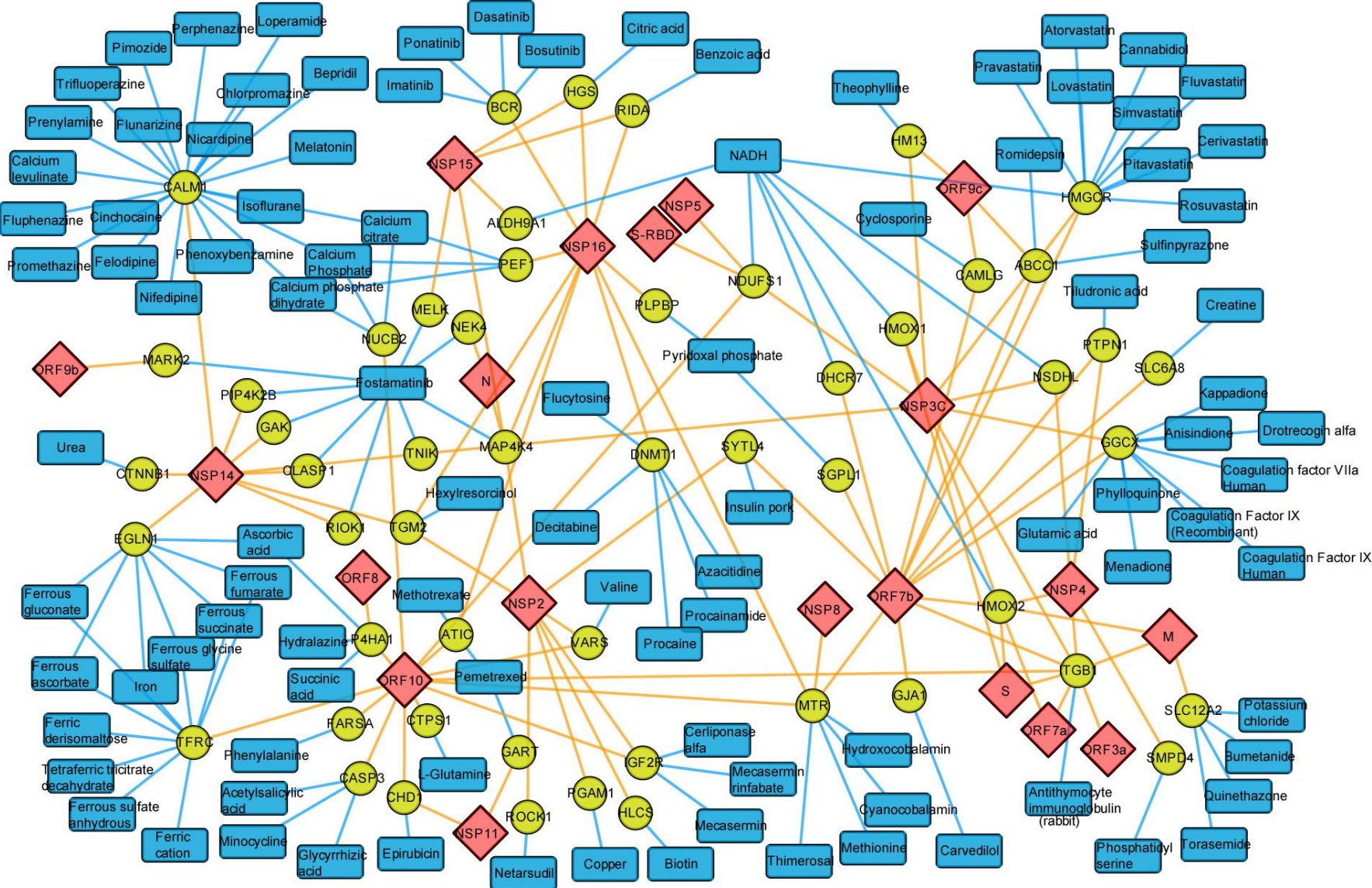
Target-based approach



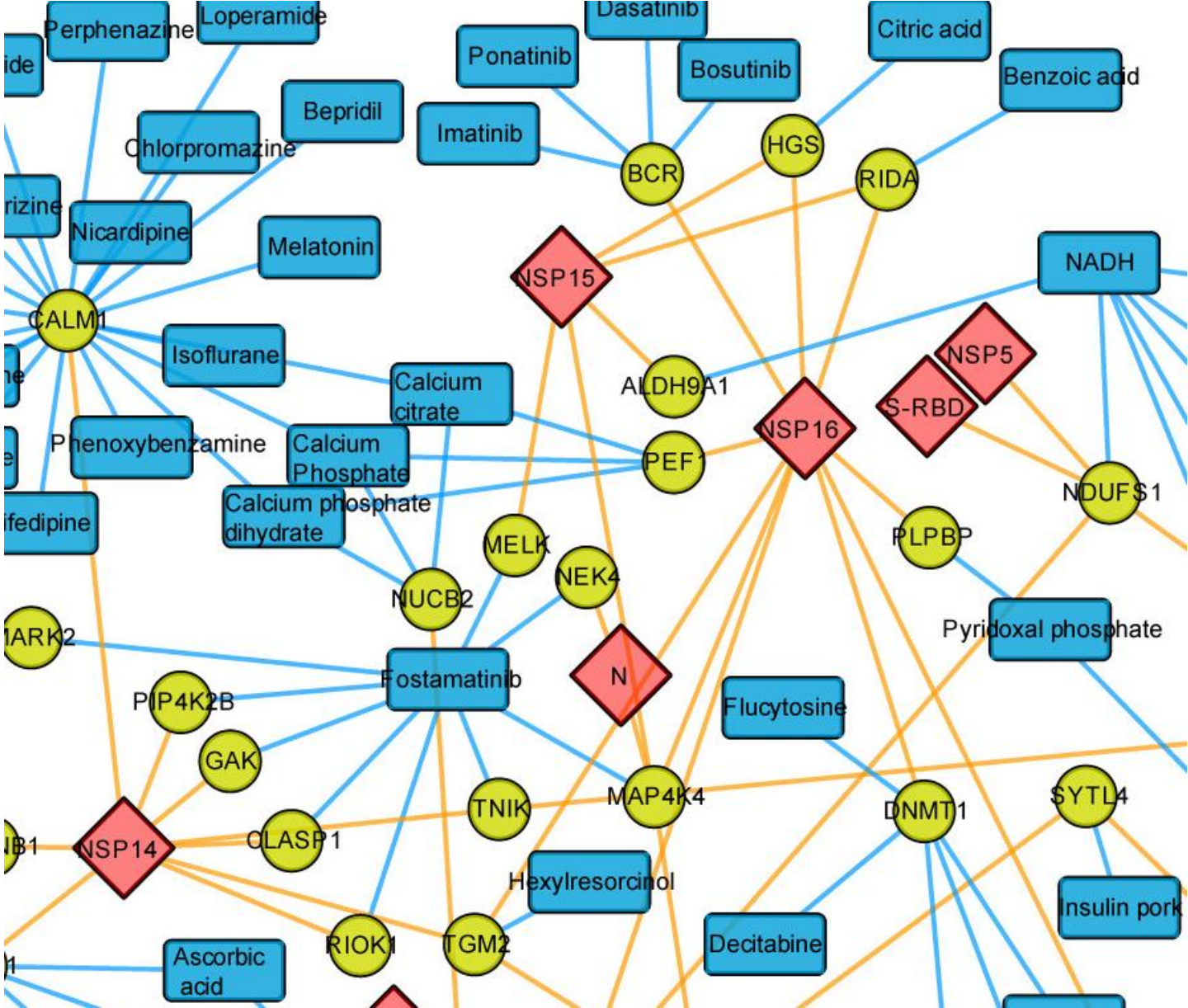
Phenotype-based approach



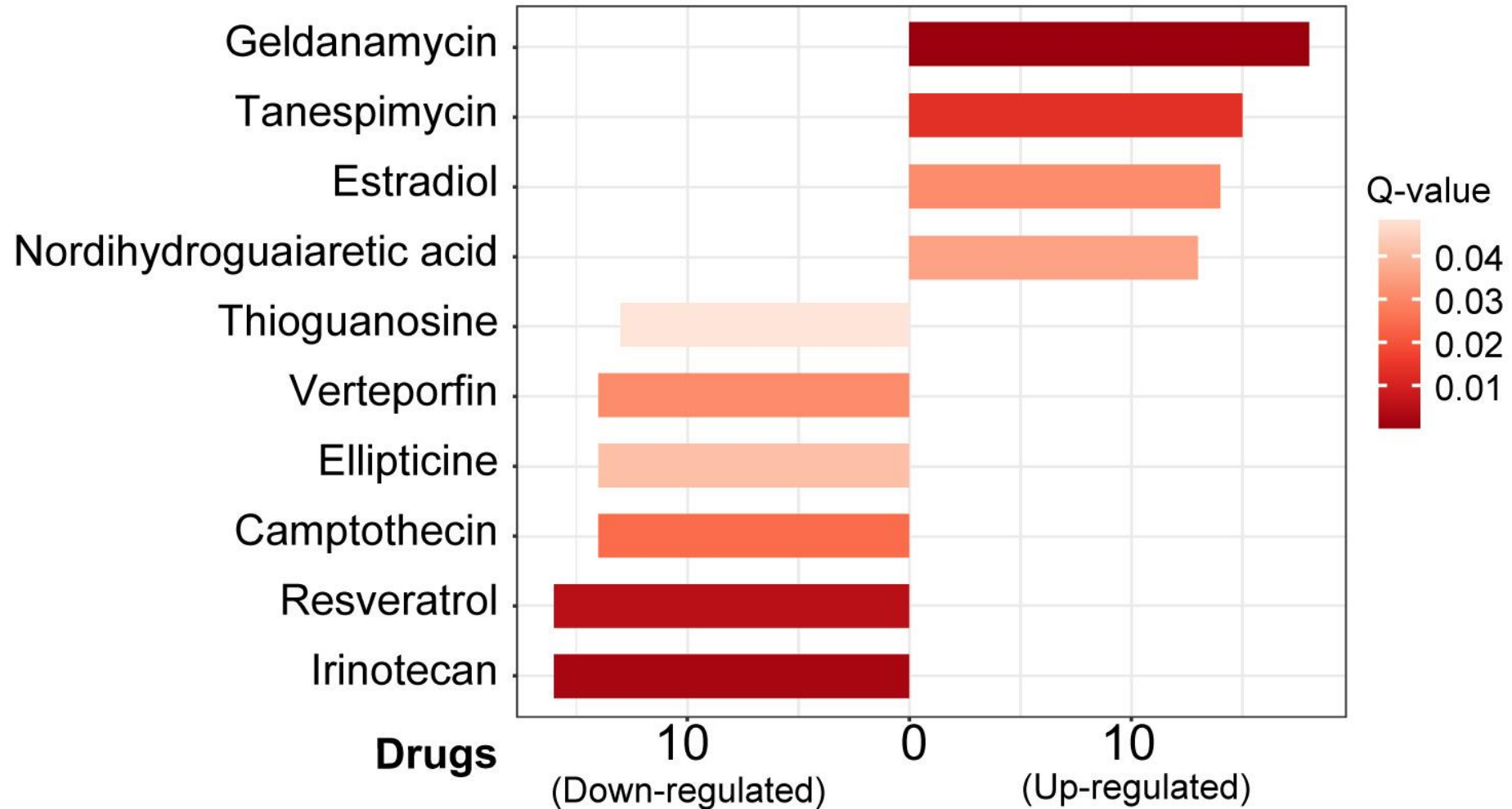
How were potential drug targets revealed by proximity labeling map?



How were potential drug targets revealed by proximity labeling map?

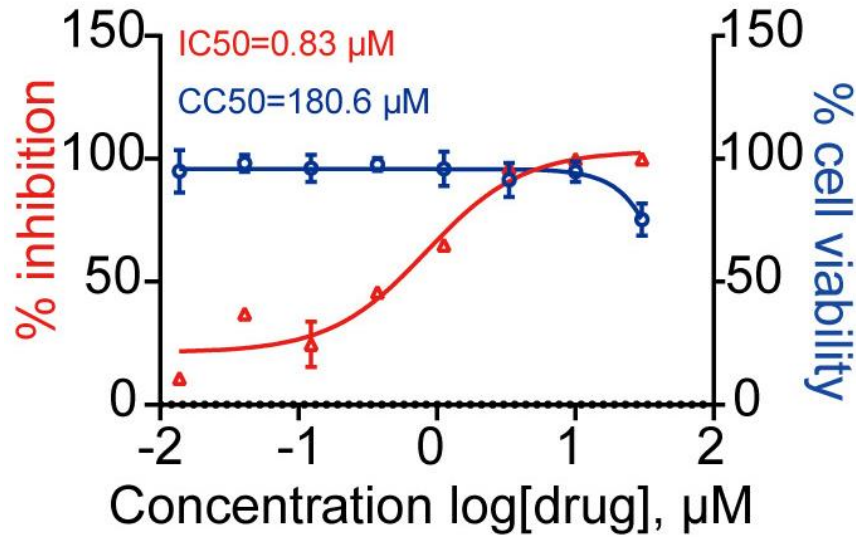


What drugs target these identified proteins?

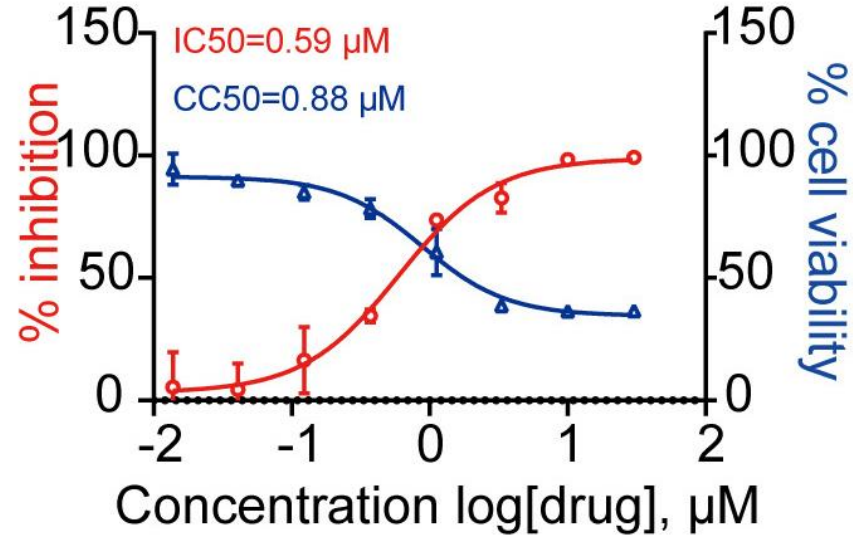


How do different drugs interact differently within our genome?

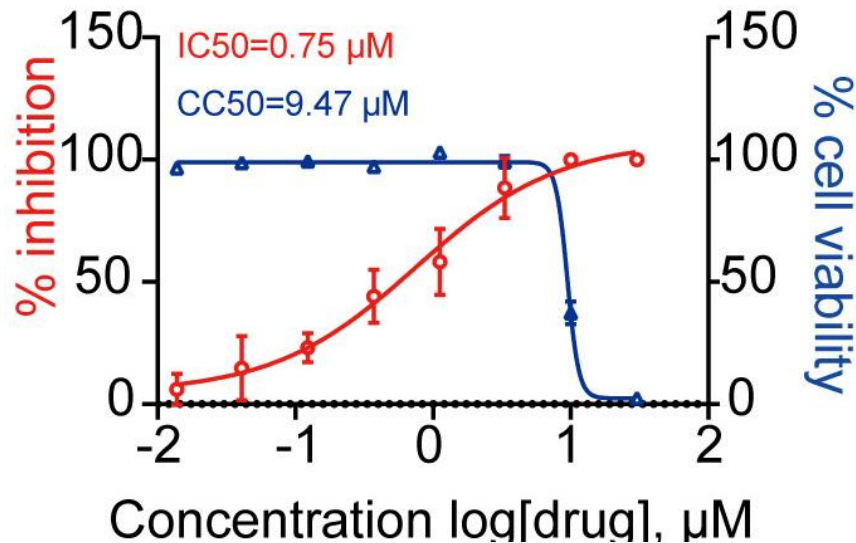
Remdesivir



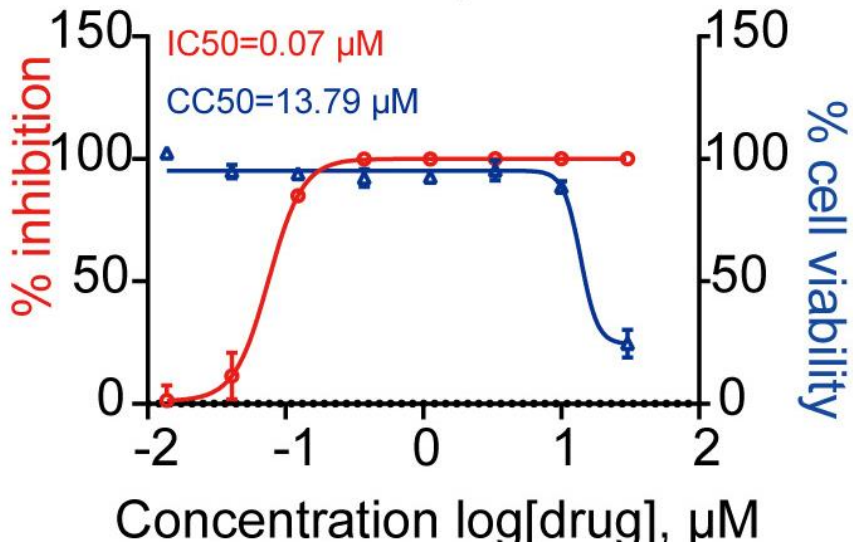
Azacitidine



Thimerosal



Verteporfin



Cell viability

Percent inhibition

Future research??

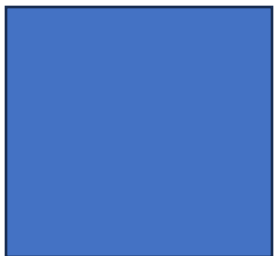
Summary



AP-MS has been used to further look into human proximal protein reactions with SARS-CoV-2, however integrating this with other data, such as **TurboID**, allows for more information to be determined regarding protein interactions



Approximately 1,388 interactions were found between proximal proteins and SARS-CoV-2, notably finding manipulations in key cellular processes regarding **antiviral and immune response**



Three compounds were identified that inhibit replication of SARS-CoV-2 : **azacitidine, thimerosal, and verteporfin**



Questions?

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