



Decoding the signaling pathways modulated by phosphatases of intracellular pathogens.

Gwenaëlle André-Leroux

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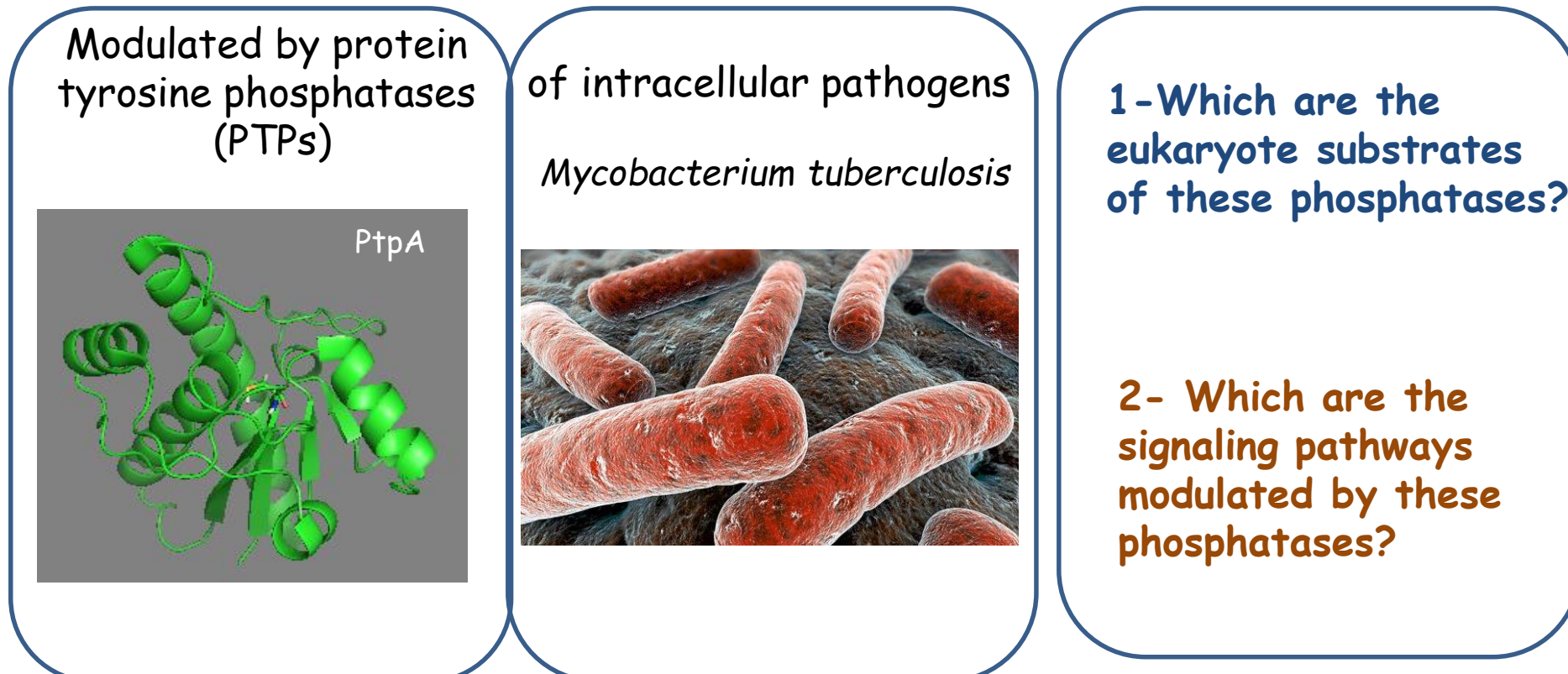
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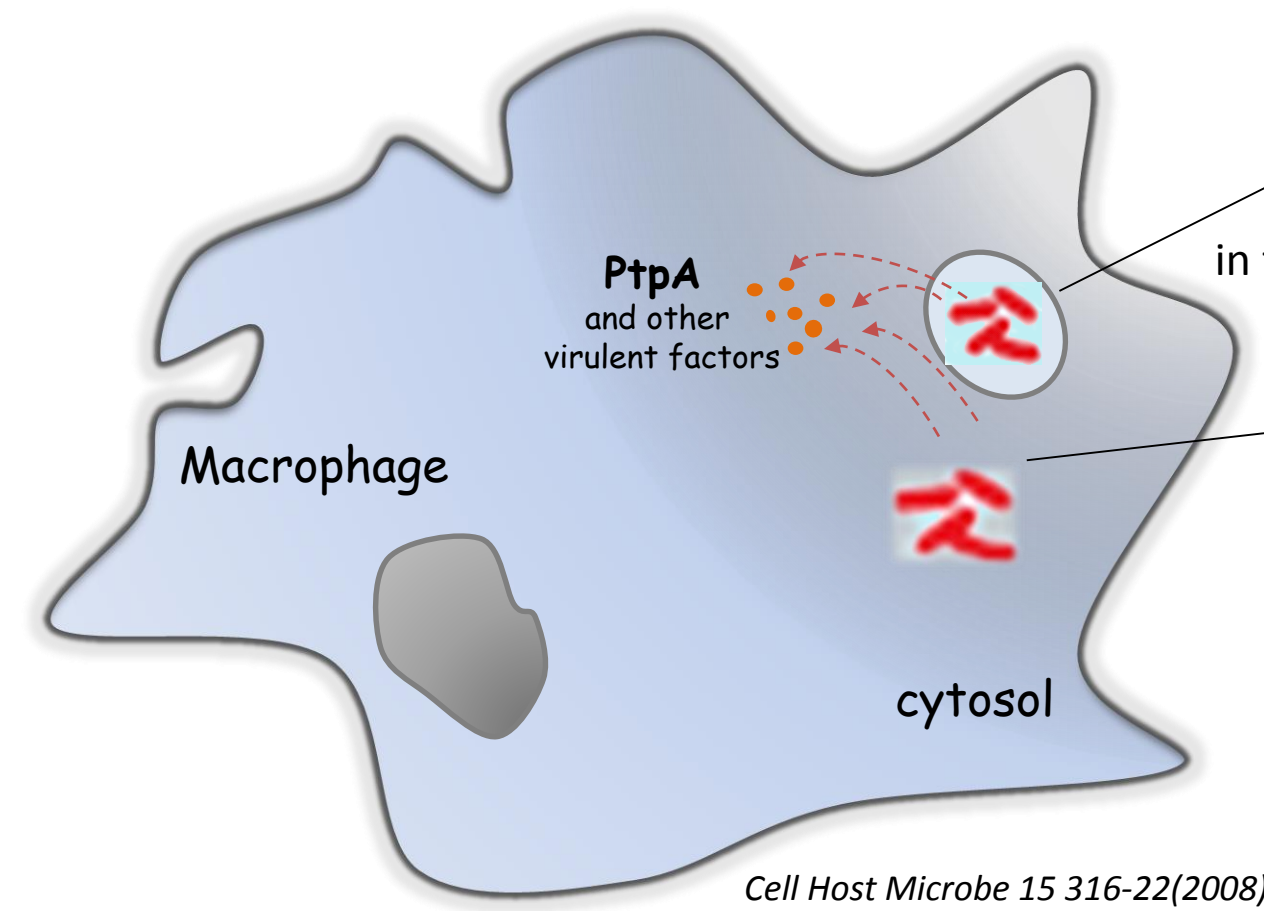
Decoding the signaling pathways modulated by phosphatases of intracellular pathogens.

Mariana Margenat, Danilo Segovia, Dario Porley, Vivian Irving, Ana Ramón, Gwénaëlle André-Leroux, Ana María Ferreira, Mabel Berois, **Andrea Villarino**.

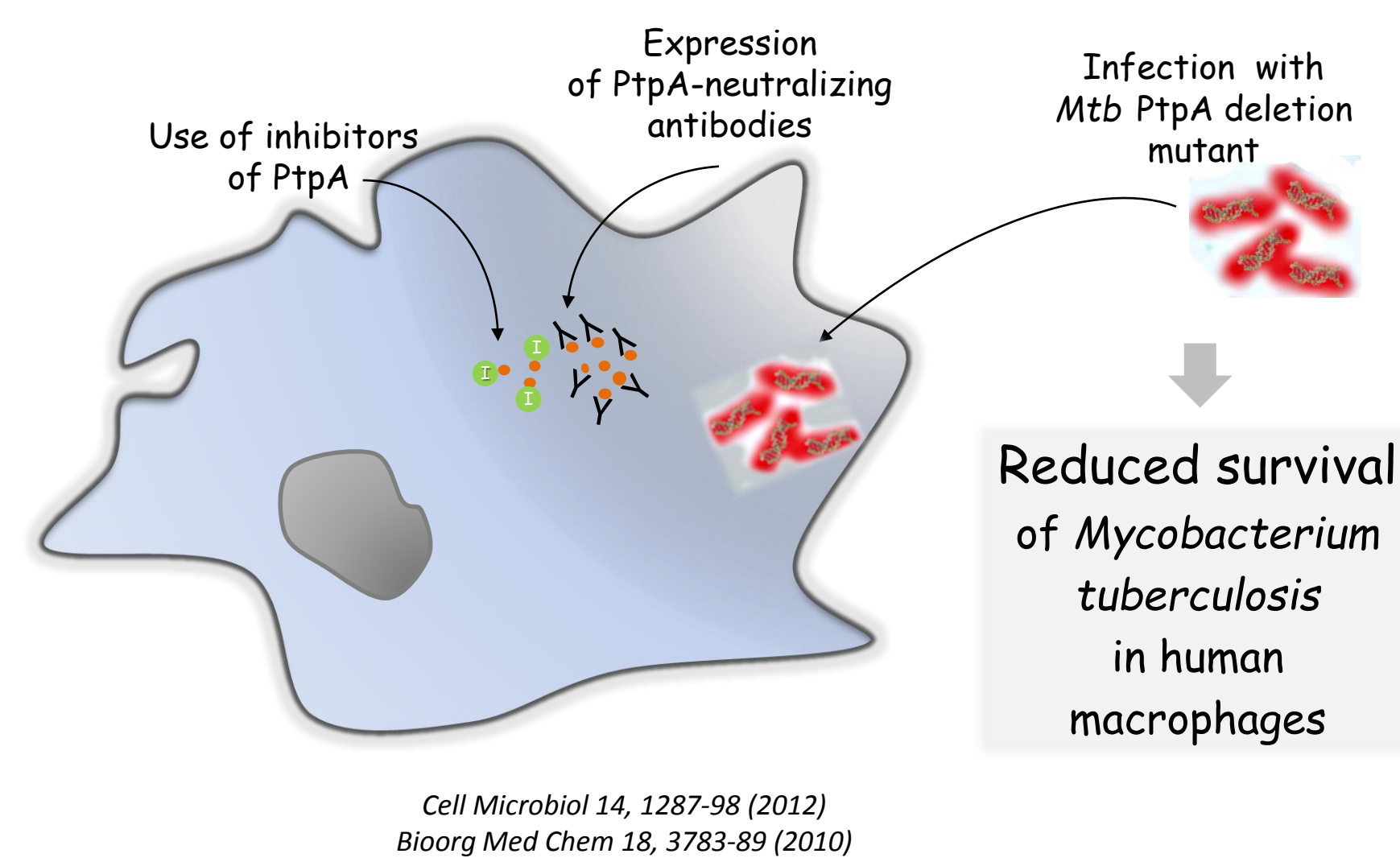
Decoding the eukaryotic signaling pathways



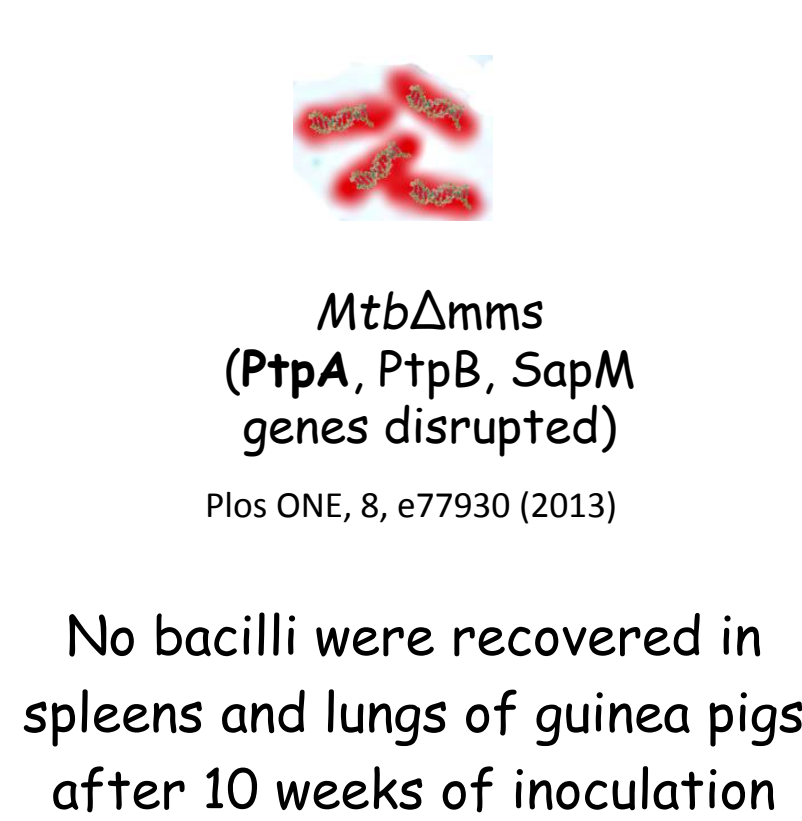
✓ The tyrosine phosphatase PtpA from *Mycobacterium tuberculosis* has been detected in the cytosol of infected macrophages



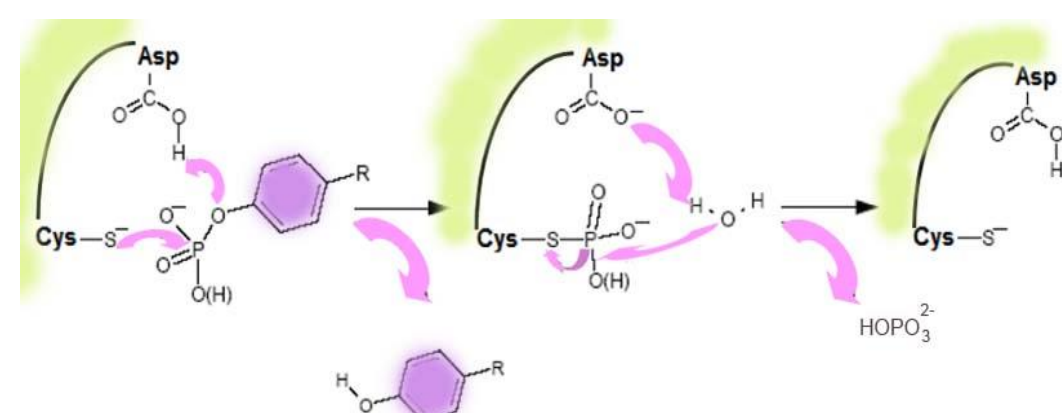
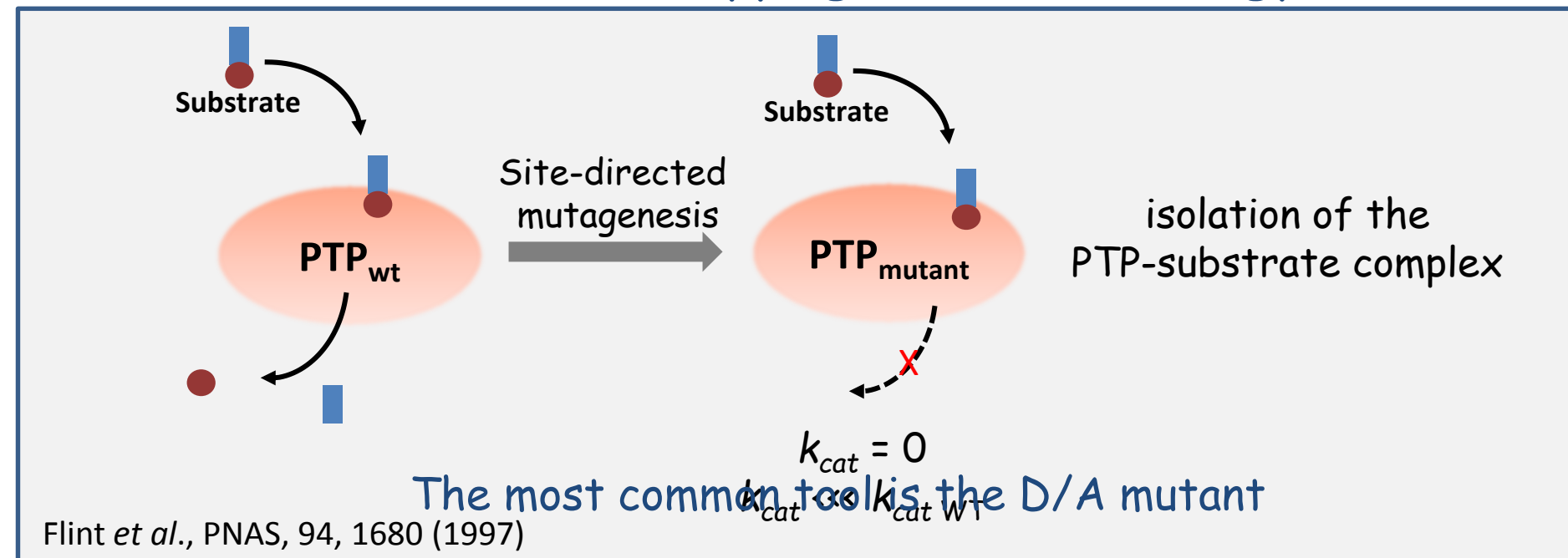
✓ PtpA is a key virulent factor



✓ Important role of mycobacterial phosphatases in the colonization of spleen and lung



"PTP substrate trapping mutants strategy"



We obtained the PtpA D/A mutant

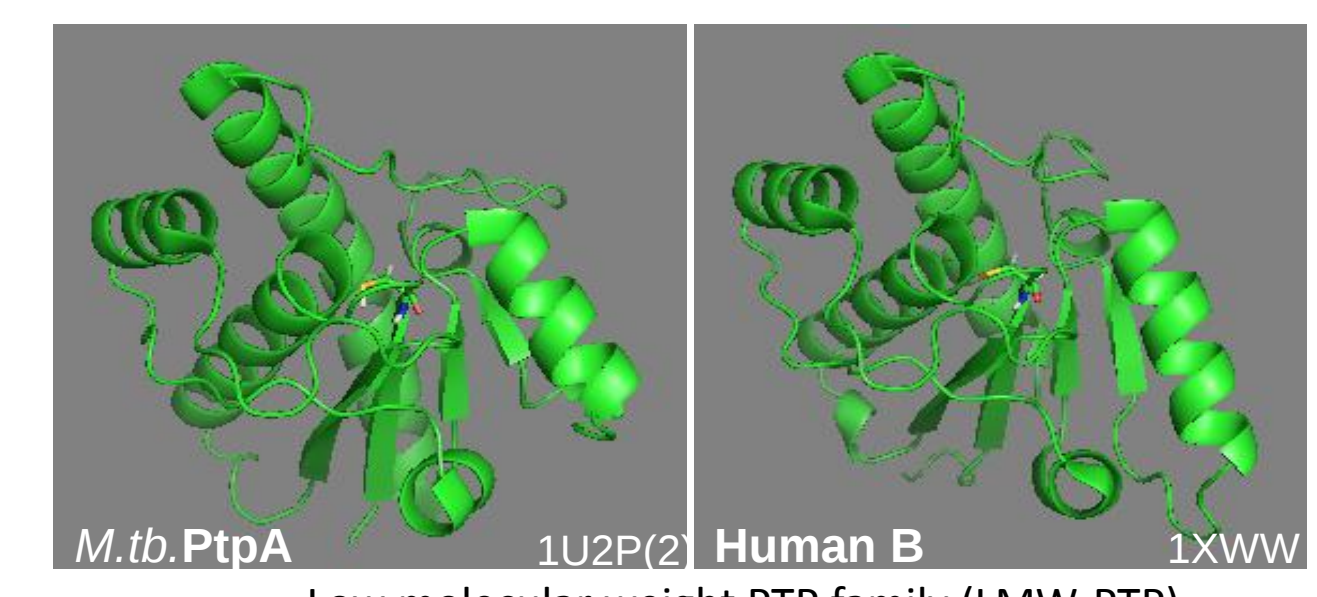
The Asp 126 is a catalytic residue and is not considered crucial in defining substrate specificity

1-Which are the eukaryote substrates of these phosphatases?

"Improved PTP substrate trapping strategy"

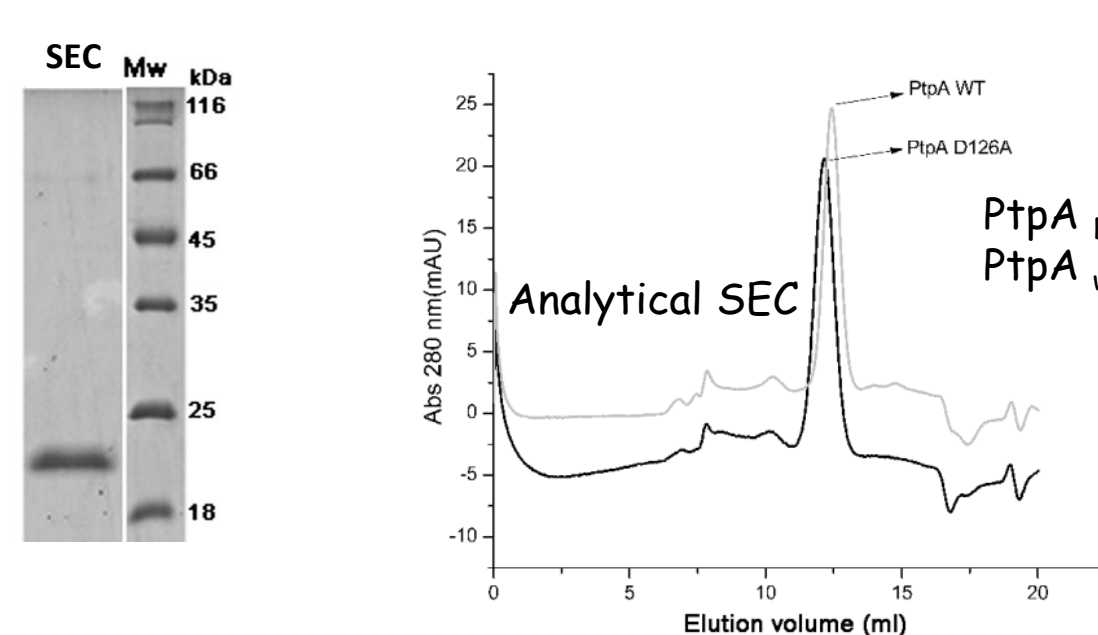
- Verification of the structural and biochemical properties of the PtpA D126A mutant to ensure its adequacy for substrate trapping
- Preparation of extracts of human-macrophage-like THP-1 cells preserving phospho-tyrosine (P-Y) modifications
- Analysis by SPR of the interaction between the phosphatase and the macrophage protein extracts, selection of conditions for washing and elution steps.
- Substrate trapping assay using stringent experimental conditions defined by SPR to reduce non-specific interactions
- Validation of protein candidates as substrates of PtpA

PtpA shows 37% of sequence identity and high structural similarity to its human orthologue HCPTPB.



Verification of the structural and biochemical properties of the PtpA D126A mutant to ensure its adequacy for substrate trapping

PtpA_{D126A} behaved similarly to the PtpA_{wt} through the whole expression and purification procedure

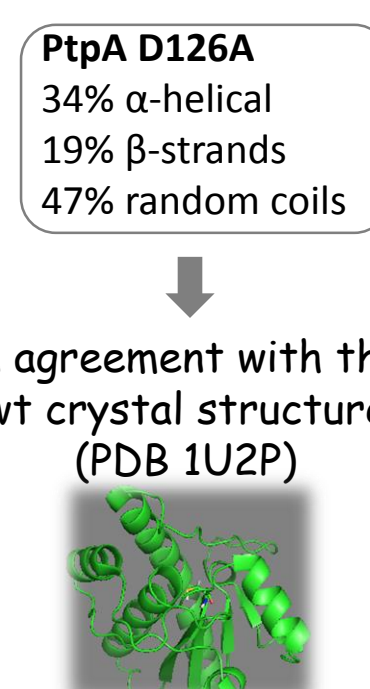


PtpA_{D126A} in aqueous solution is a monomer as PtpA_{wt}

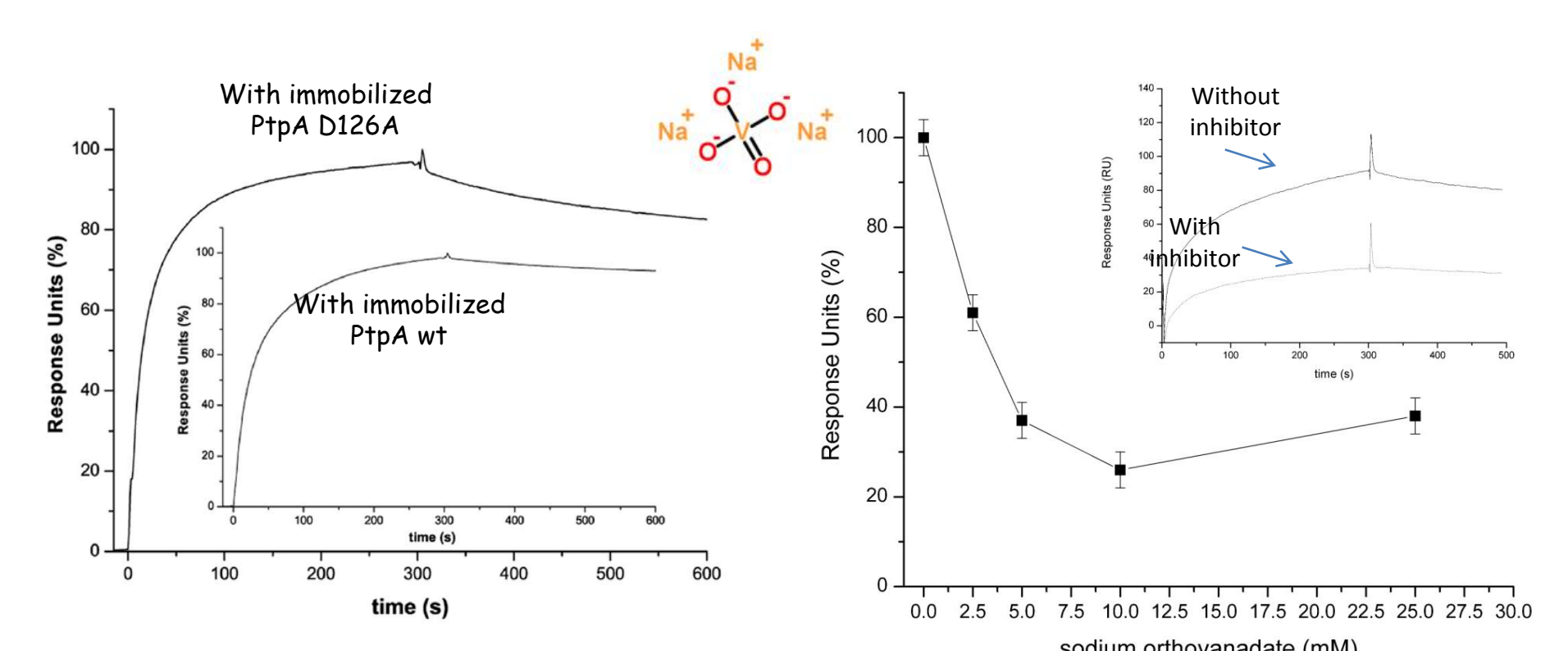
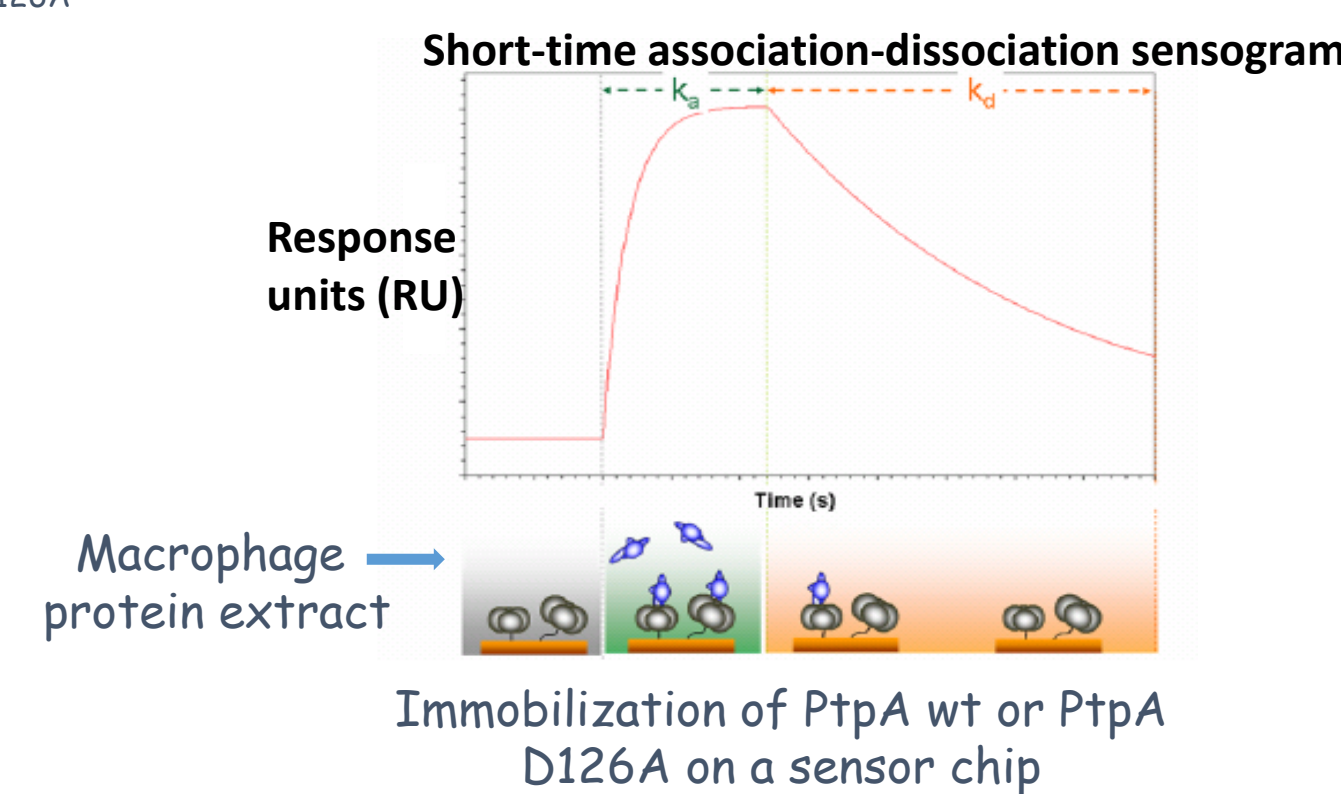
The D/A mutation did not significantly alter the enzyme structure

The secondary structure of PtpA_{D126A} and PtpA_{wt} are basically equal

Circular dichroism studies (CD)

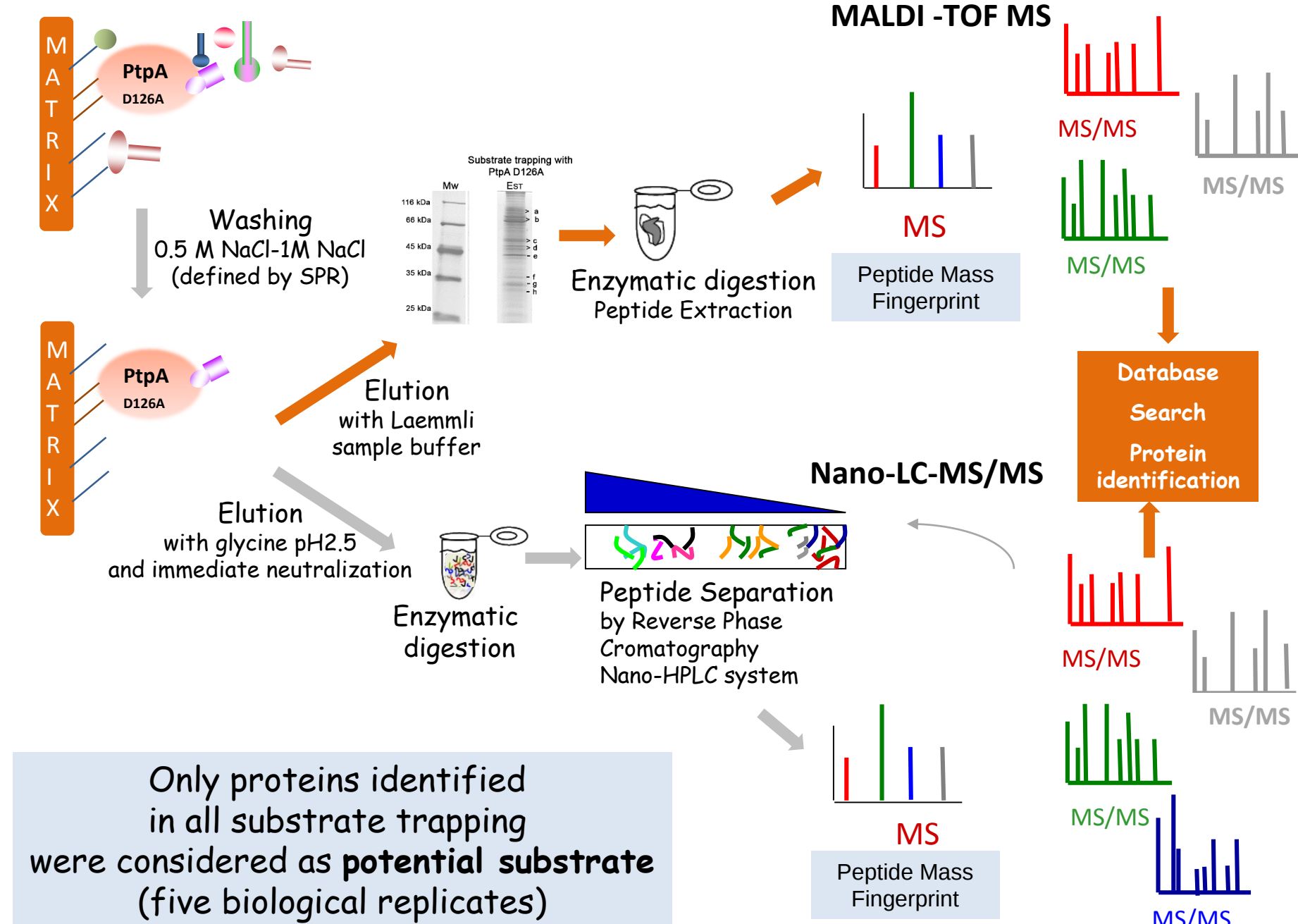


Study by Surface Plasmon Resonance (SPR) how PtpA interacts with macrophage protein components



The macrophage extract contained components which were capable of binding to PtpA mutant through the active site

Substrate trapping assay



Four novel putative PtpA substrates

Biological process ^a	Protein accession	Protein name	Mascot score ^b	Mass (Da)	No. of matched ions ^a	No. of peptide sequences ^a
Lipid metabolism; fatty acid beta-oxidation	ECHA_HUMAN	Tri-functional enzyme subunit alpha, mitochondrial	2422	82947	63	23
Sulfide oxidation, using sulfide: quinone oxidoreductase	SQRD_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial	705	49929	28	10
Respiratory electron transport chain	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial	531	59714	16	7
Glycolysis	K6PP_HUMAN	6-phosphofructokinase, platelet type	922	85542	47	15

^a Only the main biological processes with traceable author statement are shown. From UniProt (<http://www.uniprot.org/>) database (released on January 2014)[®].

^b The value of score, number of matched ions and peptide sequences is the best value obtained.

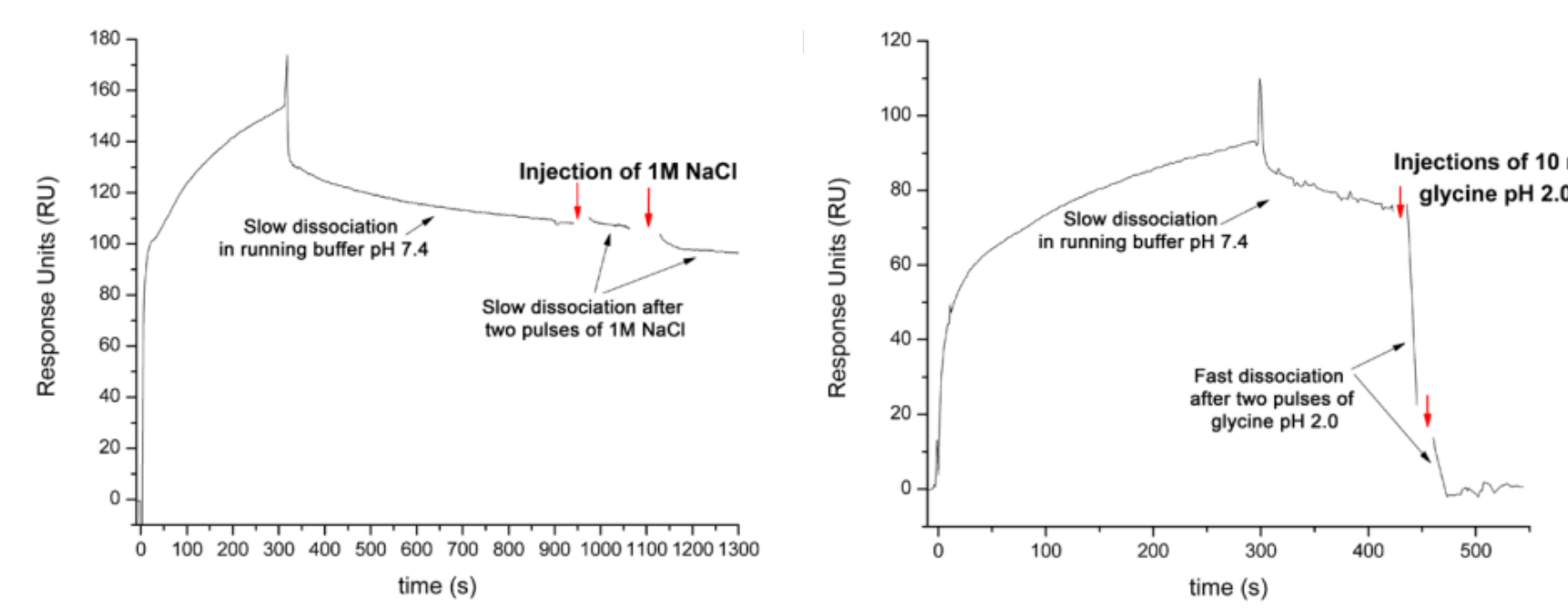
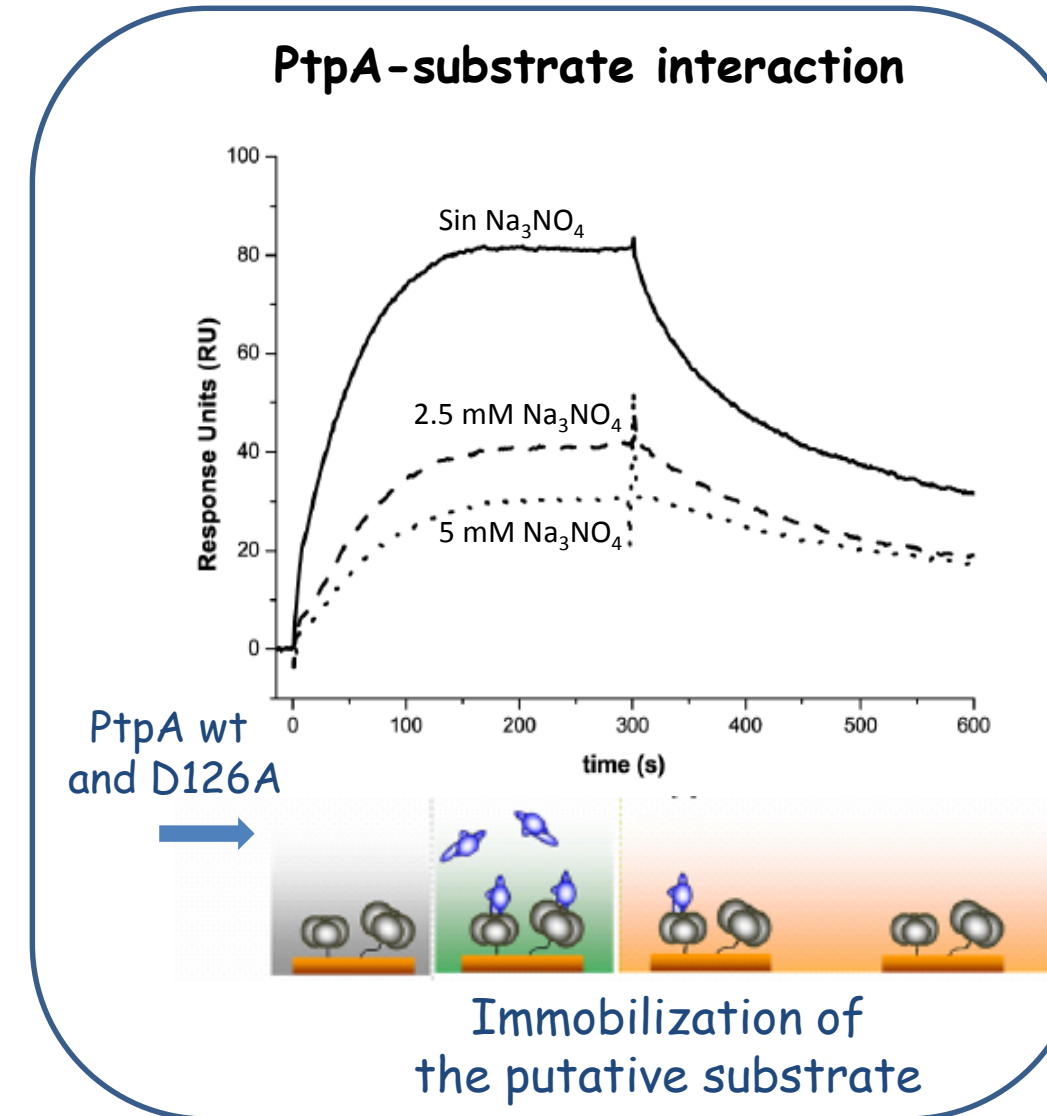
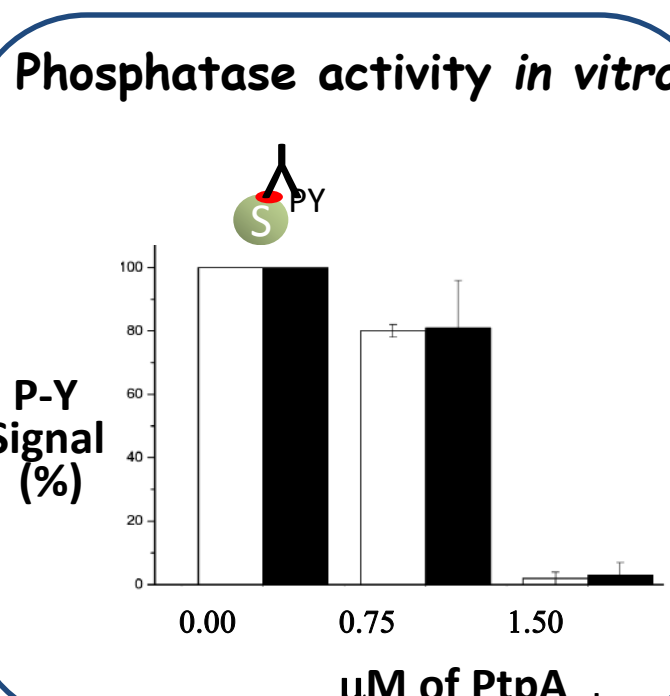
High salt concentration seems to be a good choice for washing steps to reduce non-specific binding

and low pH would be useful for eluting the proteins bound to PtpAD126A.

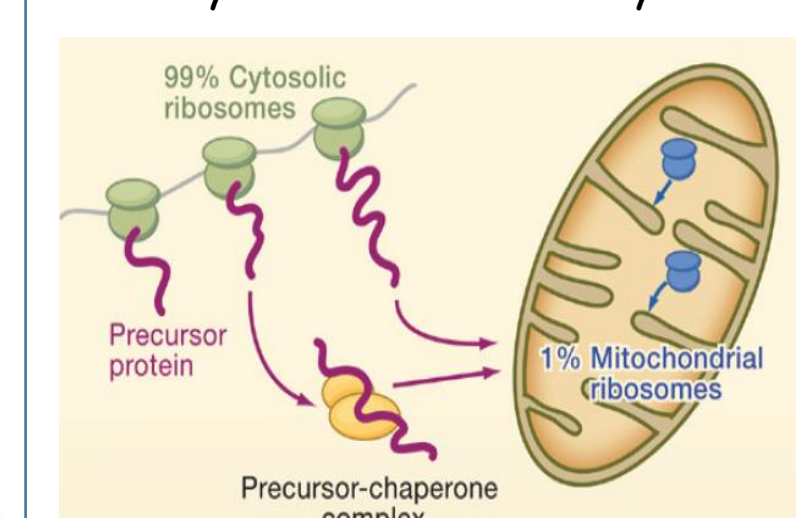
By different approaches we are addressing the validation of these proteins candidates as PtpA substrates.

Immunoprecipitation of each potential substrate

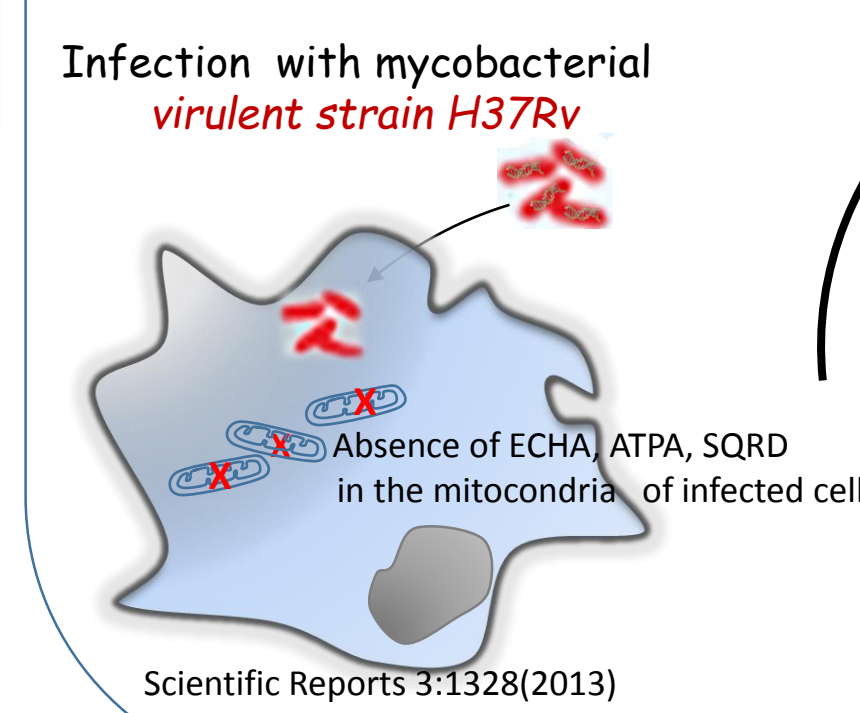
Dynabeads



ECHA, ATPA, SQRD are synthesized in the cytosol



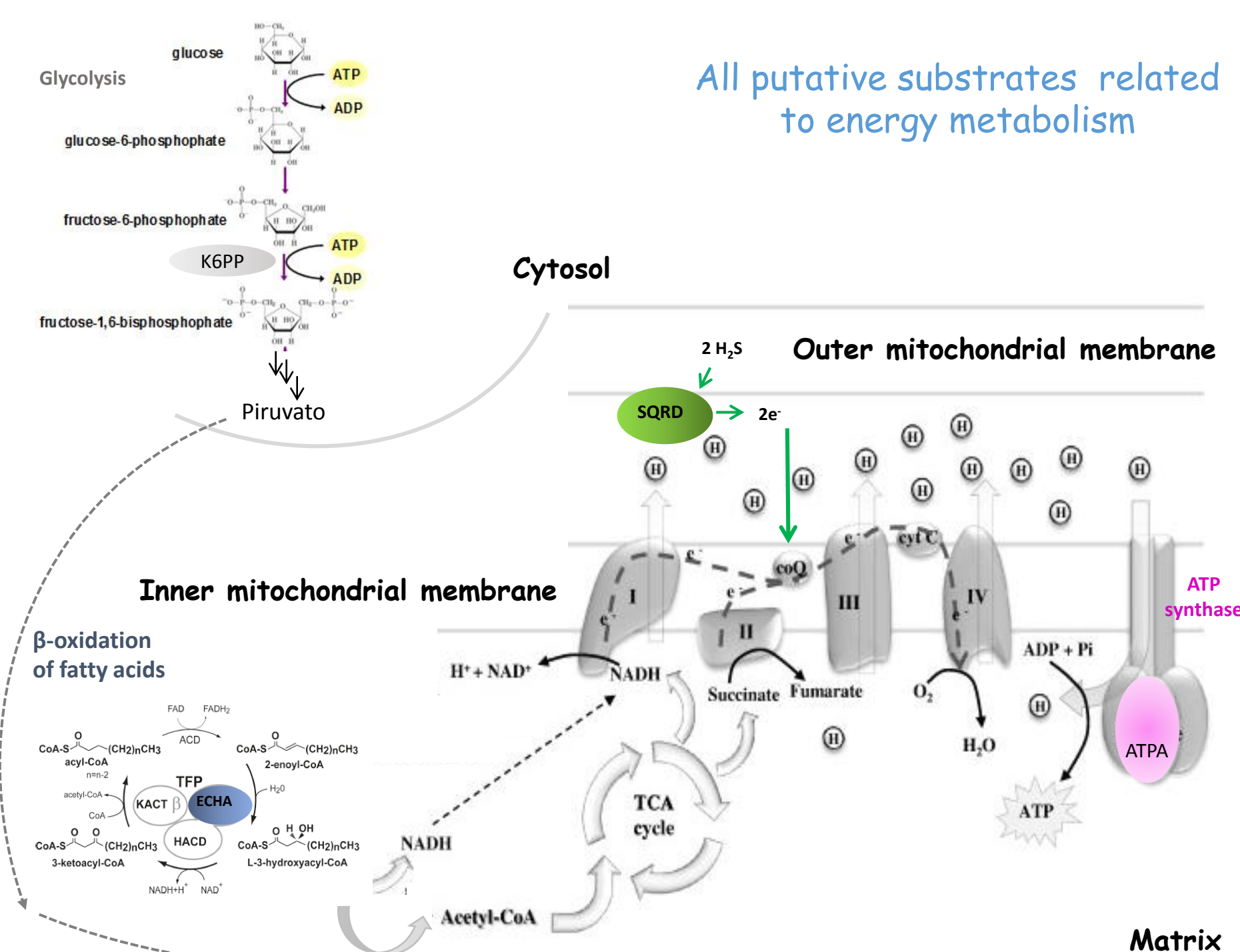
PtpA has been localized in the cytosol of infected macrophages



PtpA mediated dephosphorylation of these proteins in the cytosol?

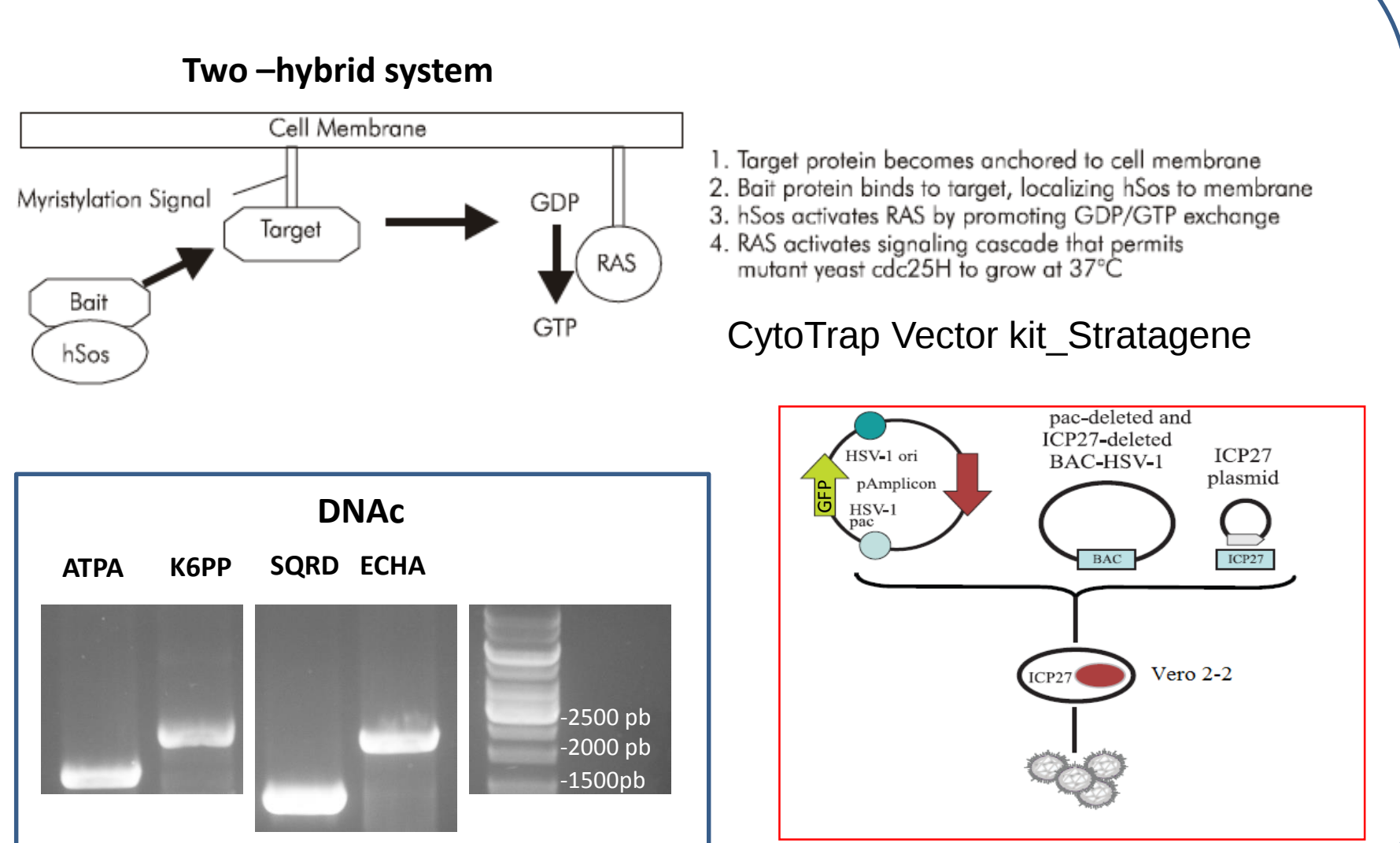
Altering their activity and/or translocation to the mitochondria?

Affecting pathways involved in cell energy metabolism?



All putative substrates related to energy metabolism

Interaction at a cellular level



Decoding the eukaryotic signaling pathways

