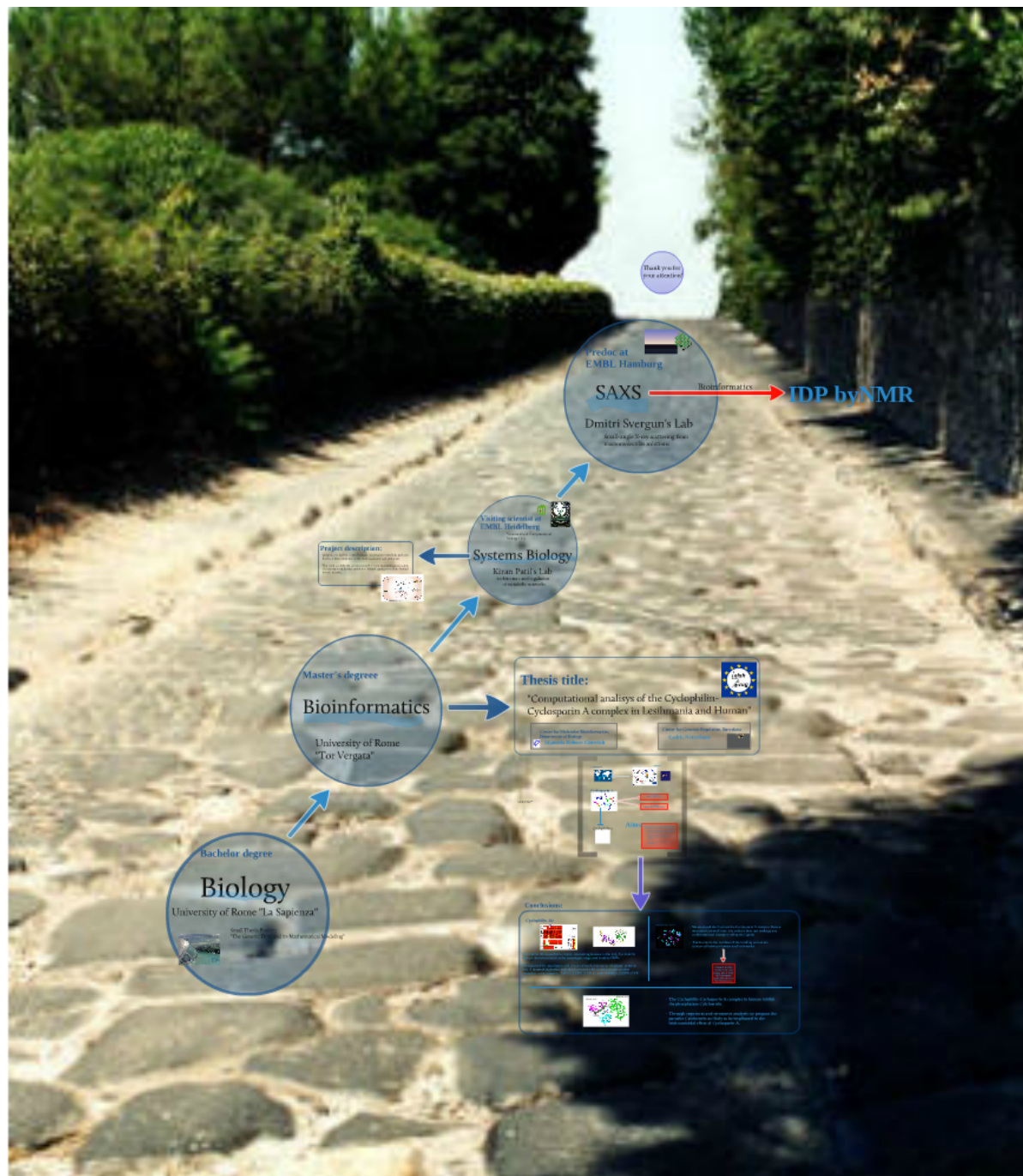






BIOINFORMATICS

University of Rome
"Tor Vergata"

Bachelor degree

Biology

University of Rome "La Sapienza"



Small Thesis Project:
"The Genetic Drift and its Mathematical Modeling"

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Valencia

- Microbiology
- Biochemistry
- Molecular Biology
- Physiology

- Microbiology
- Biochemistry
- Molecular Biology
- Physiology

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of Rome "La Sapienza"

Small Thesis Project:

"The Genetic Drift and its Mathematical Modeling"

Bachelor degree

Biology

University of Rome "La Sapienza"

Small Thesis Project:
"The Genome Era" and its Mathematical Modeling"



Master's degree

Bioinformatics

University of Rome "Tor Vergata"

Project description:

Creation of a bioinformatics pipeline for the analysis of the pathways that have been changed in the metabolic network of the yeast *S. cerevisiae*. The pipeline is based on the use of the software *CytoScape* and *Pathway Tools*. The results of the analysis are presented in a report.



Visiting scientist at EMBL Heidelberg

Systems Biology

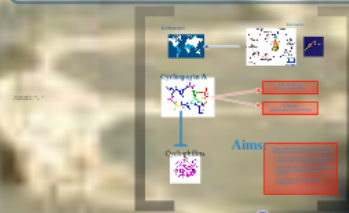
Kiran Patil's Lab
Architecture and regulation of metabolic networks

Thesis title:

"Computational analysis of the Cyclophilin-Cyclosporin A complex in *Leishmania* and Human"

Centre for Molecular Biomedicine, Department of Biology, Mammalia Veltner University

Centre for Genetic Regulation, Barcelona, Cedric Notredame



Conclusions:

Cyclophilin A:

Cyclophilin A is a highly conserved protein in the eukaryotic kingdom. It is involved in the regulation of the cell cycle and the cell growth. It is a member of the cyclophilin family of proteins. It is a member of the cyclophilin family of proteins. It is a member of the cyclophilin family of proteins.

Cyclosporin A:

Cyclosporin A is a cyclic peptide. It is a member of the cyclosporin family of peptides. It is a member of the cyclosporin family of peptides. It is a member of the cyclosporin family of peptides.

The Cyclophilin-Cyclosporin A complex:

The Cyclophilin-Cyclosporin A complex is a complex of Cyclophilin A and Cyclosporin A. It is a member of the cyclophilin-cyclosporin family of complexes. It is a member of the cyclophilin-cyclosporin family of complexes. It is a member of the cyclophilin-cyclosporin family of complexes.

Through sequence and structure analysis we propose the possible Cyclophilin as likely to be implicated in the biochemical effect of Cyclosporin A.

Small-angle X-ray scattering from macromolecular solutions

Master's degree

Bioinformatics

University of Rome
"Tor Vergata"

Thesis title:

"Computational analysis of the Cyclophilin-Cyclosporin A complex in Leishmania and Human"



Center for Molecular Bioinformatics,
Department of Biology



Manuela Helmer Citterich

Center for Genomic Regulation, Barcelona

Cedric Notredame



Leishmaniasis



Leishmania



Cyclosporin A



In Leishmania:
Anti-parasitic effects

Cyclosporin A comp

**Center for Molecular Bioinformatics,
Department of Biology**



Manuela Helmer Citterich

Psychomania and Human"

Center for Genomic Regulation, Barcelona

Cedric Notredame



Center for Molecular Bioinformatics,
Department of Biology



Manuela Helmer Citterich

Center for Genomic Regulation, Barcelona

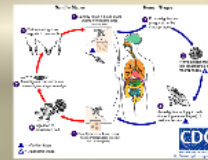
Cedric Notredame



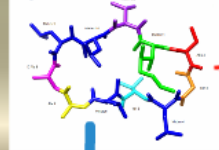
Leishmaniasis



Leishmania



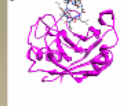
Cyclosporin A



In Leishmania:
Anti-parasitic effects

In Human:
Immunosuppressant effects

Cyclophilins



Aims:

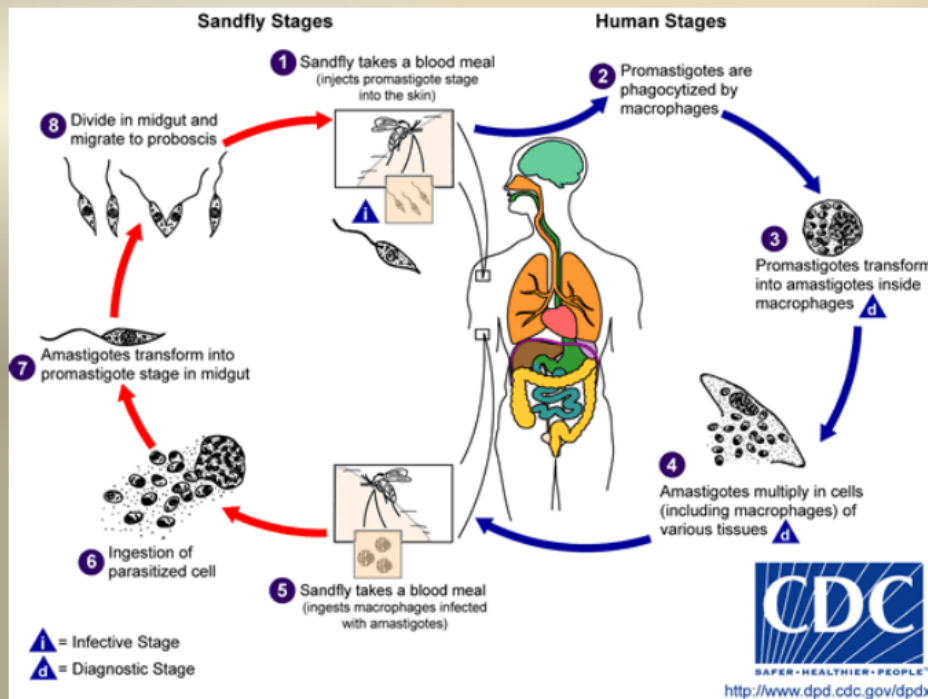
- Because of the immunosuppressant activity the Cyclosporin A cannot be used as anti-leishmaniasis
- Find the way to the creation of a Cyclosporin A analog specific for leishmanin Cyclophilins
- Detect all the differences between human and leishmanin Cyclophilins/Cyclosporin A complexes
- Study the anti-parasitic mechanism of Cyclosporin A.

Leishmaniasis

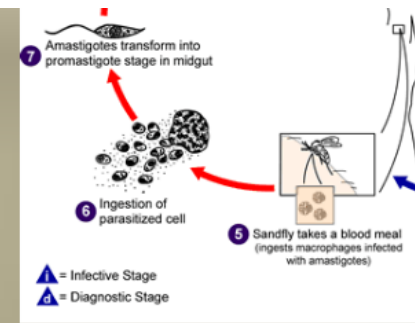


Cyclosporin A

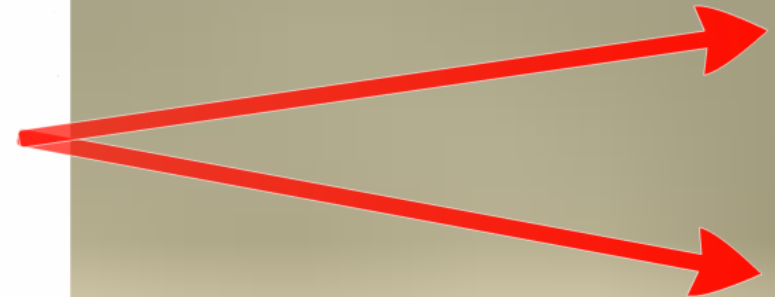
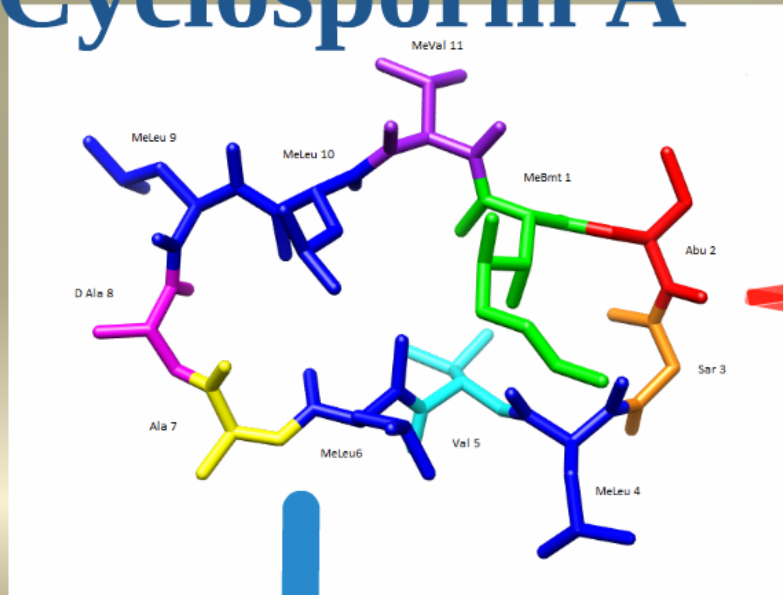
Leishmania



In Leishmania:



Cyclosporin A



Aims:

6 Ingestion or parasitized cell

5 Sandfly takes a blood meal (ingests macrophages infected with amastigotes)

▲ = Infective Stage

▲ = Diagnostic Stage



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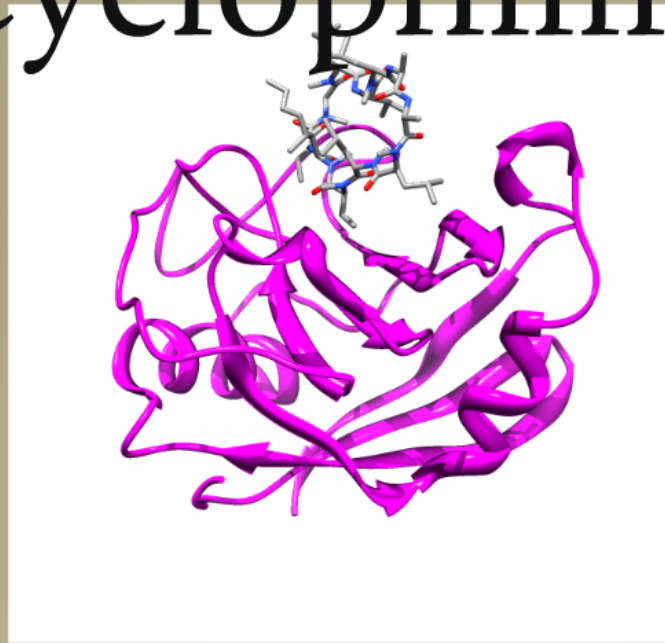
**In Leishmania:
Anti-parasitic effects**

**In Human:
Immunosuppressant effects**

Aims:

Because of the immunosuppressant activity the

Cyclophilins



Aims:

Because of the immunosuppressant activity the Cyclosporin A cannot be used to treat leishmaniasis

- Pave the way to the creation of a Cyclosporin A analog specific for leishmania Cyclophilins
- Detect all the differences between human and leishmania Cyclophilin-Cyclosporin A complexes.
- Study the anti-parasitic mechanism of Cyclosporin A.

Cyclophilins

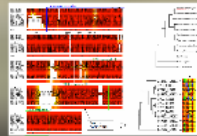


Aims:

Because of its immunosuppressive activity, Cyclosporin A (CsA) is used in the treatment of various diseases. However, its use is limited by side effects and toxicity. The aim of this study was to analyze the structure of Cyclophilin A (CYP4) and to propose a lethal phenotype in the parasite: A4I935_LEIIN (CYP 4) and A4HSQ3_LEIIN (CYP 2).

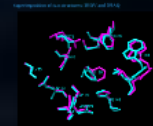
Conclusions:

Cyclophilin 40:



Cyclophilin 40 seemed to be highly interesting because is the only Cyclophilin that get phosphorylated at the amastigote stage and binds to HSPs.

We searched for paralogues and proposed two *Leishmania infantum* proteins that, if mutated together with the Cyclophilin 40, could generate a lethal phenotype in the parasite: A4I935_LEIIN (CYP 4) and A4HSQ3_LEIIN (CYP 2).



- We analyzed the Cyclophilin-Cyclosporin A complex from a structural point of view: the protein does not undergo any conformational change binding the ligand.
- Furthermore the residues of the binding pocket are conserved between human and *Leishmania*.

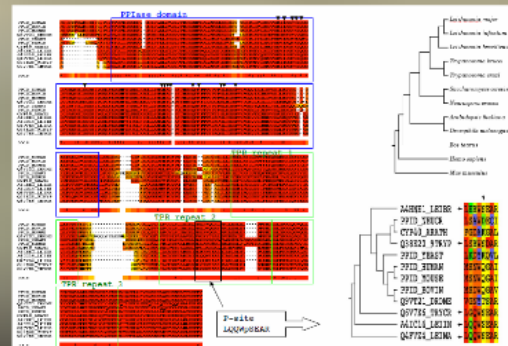
Obstacle for the creation of a CsA analog able to bind the *Leishmania* cyclophilins but not the human ones.



- The Cyclophilin-Cyclosporin A complex in human inhibit the phosphatase Calcineurin.
- Through sequences and structures analysis we propose the parasite Calcineurin as likely to be implicated in the leishmanicidal effect of Cyclosporin A.

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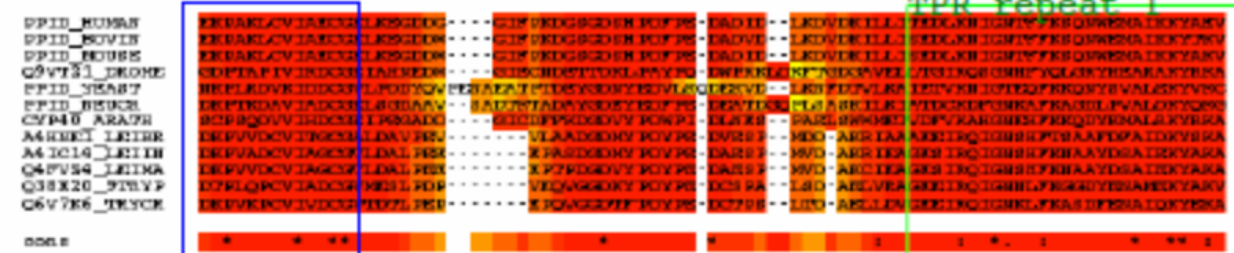
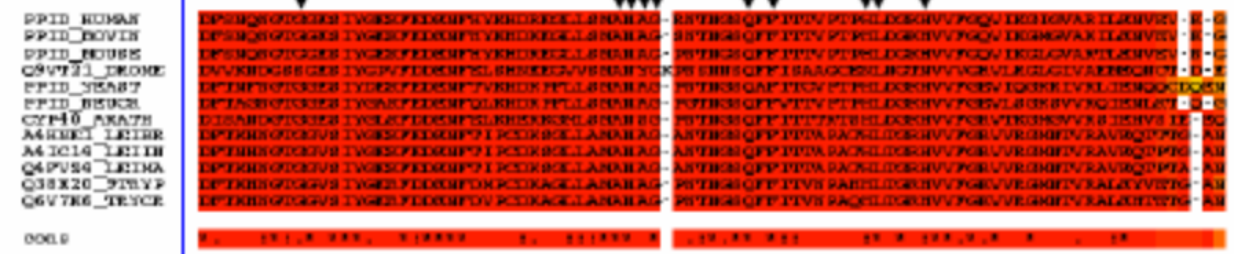
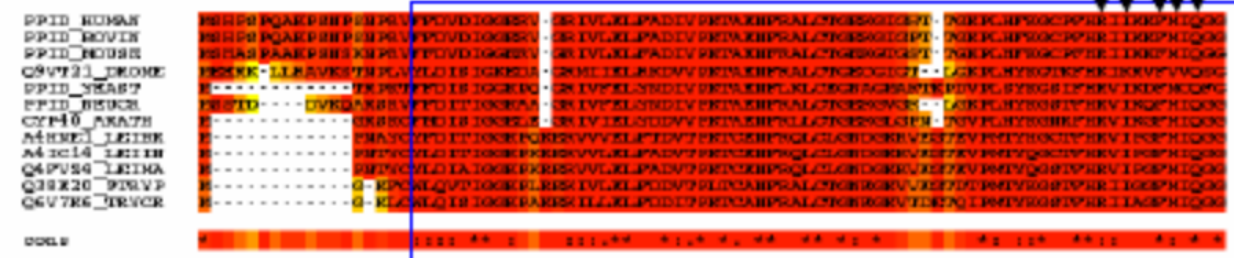


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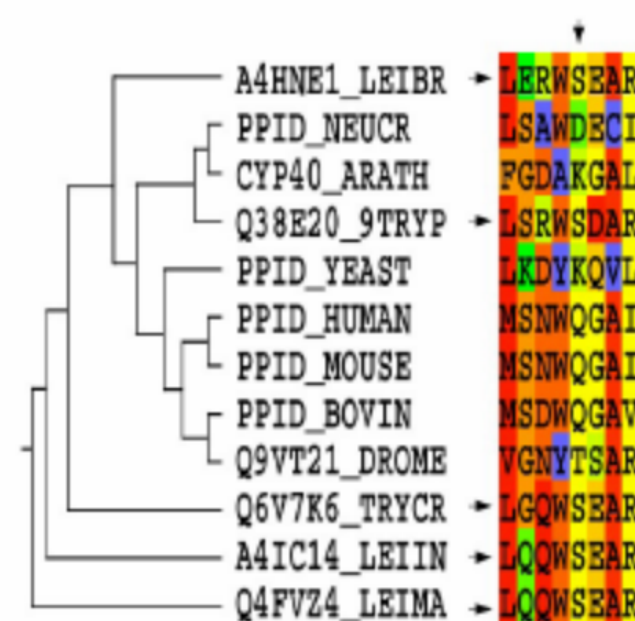
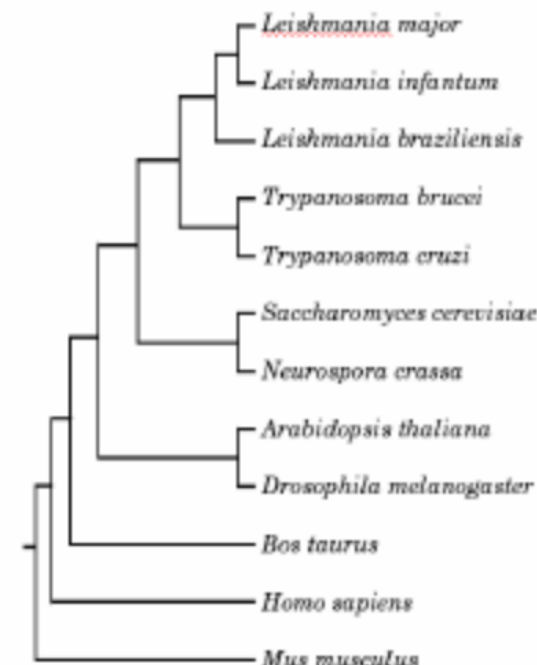
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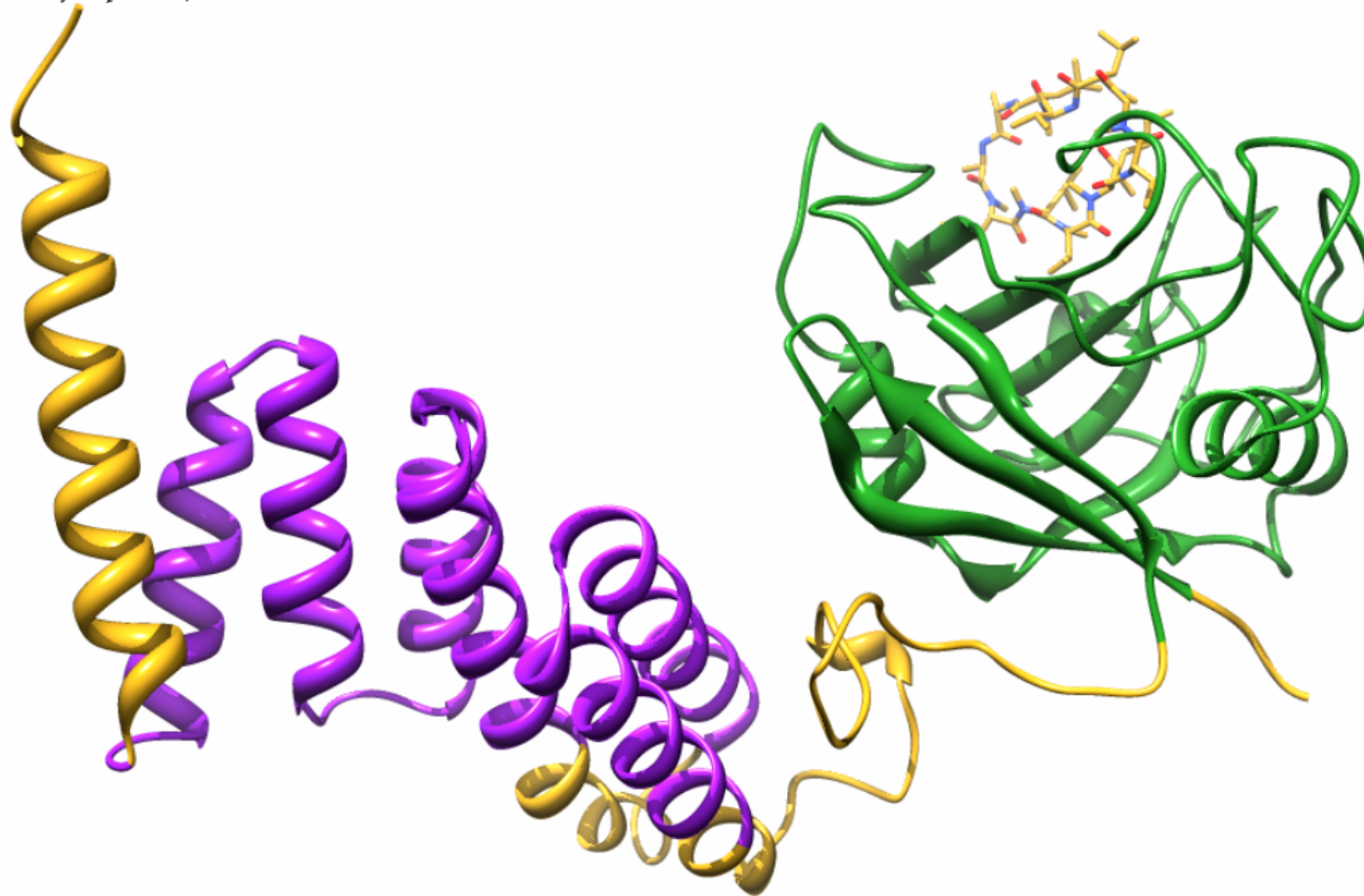
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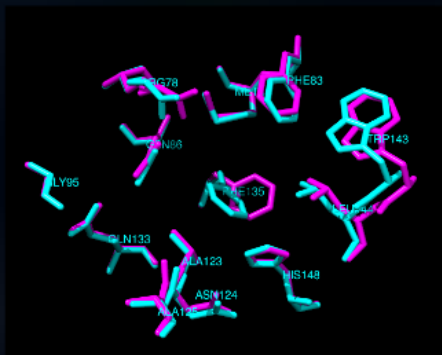
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Leishmania infantum model of Cyclophilin 40



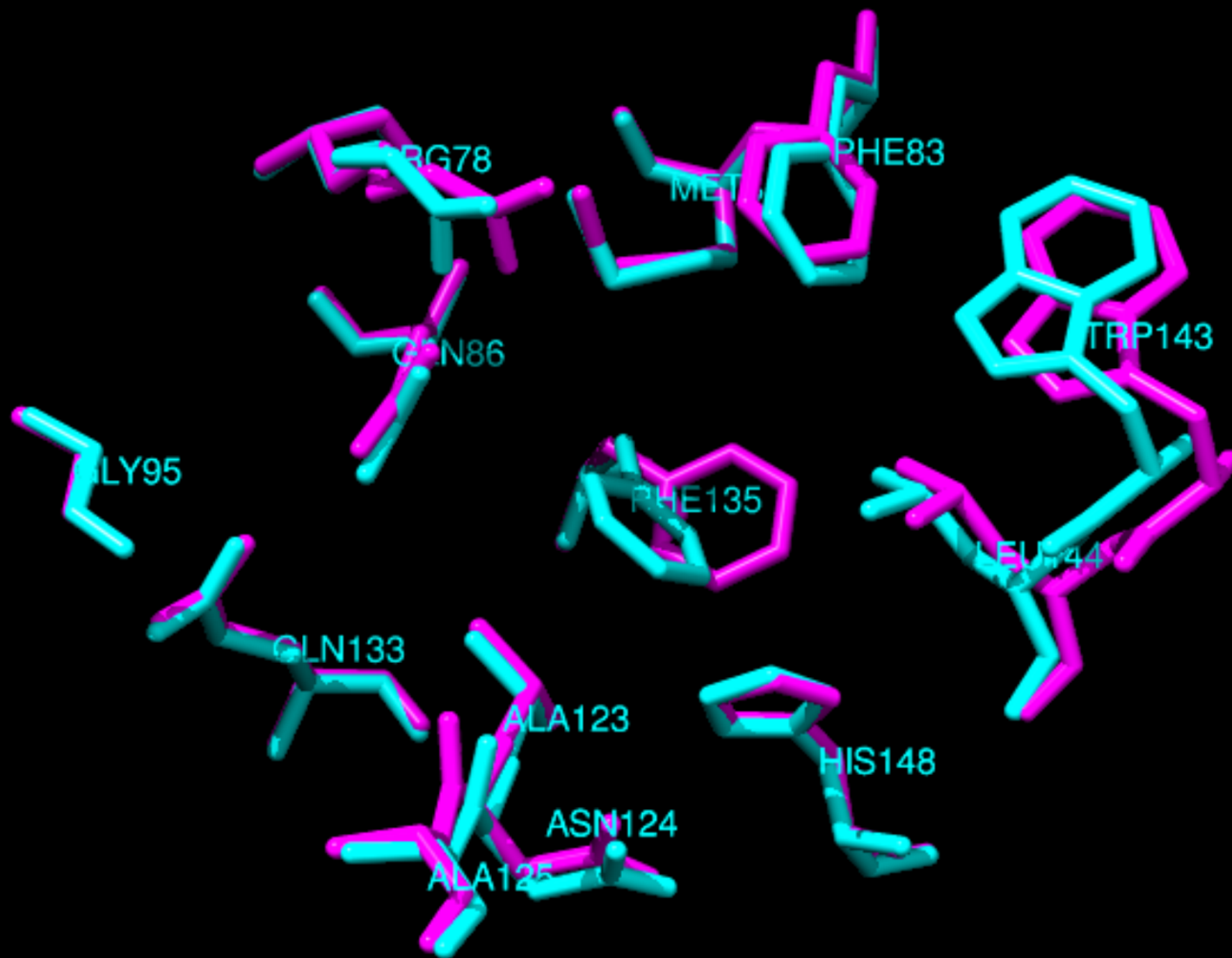
Superimposition of two structures: 3EOV and 3HAQ



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- Furthermore the residues of the binding pocket are conserved between human and leishmania.



Obstacle for the creation of a CsA analog able to bind the leishmania cyclophilins but not the human ones.



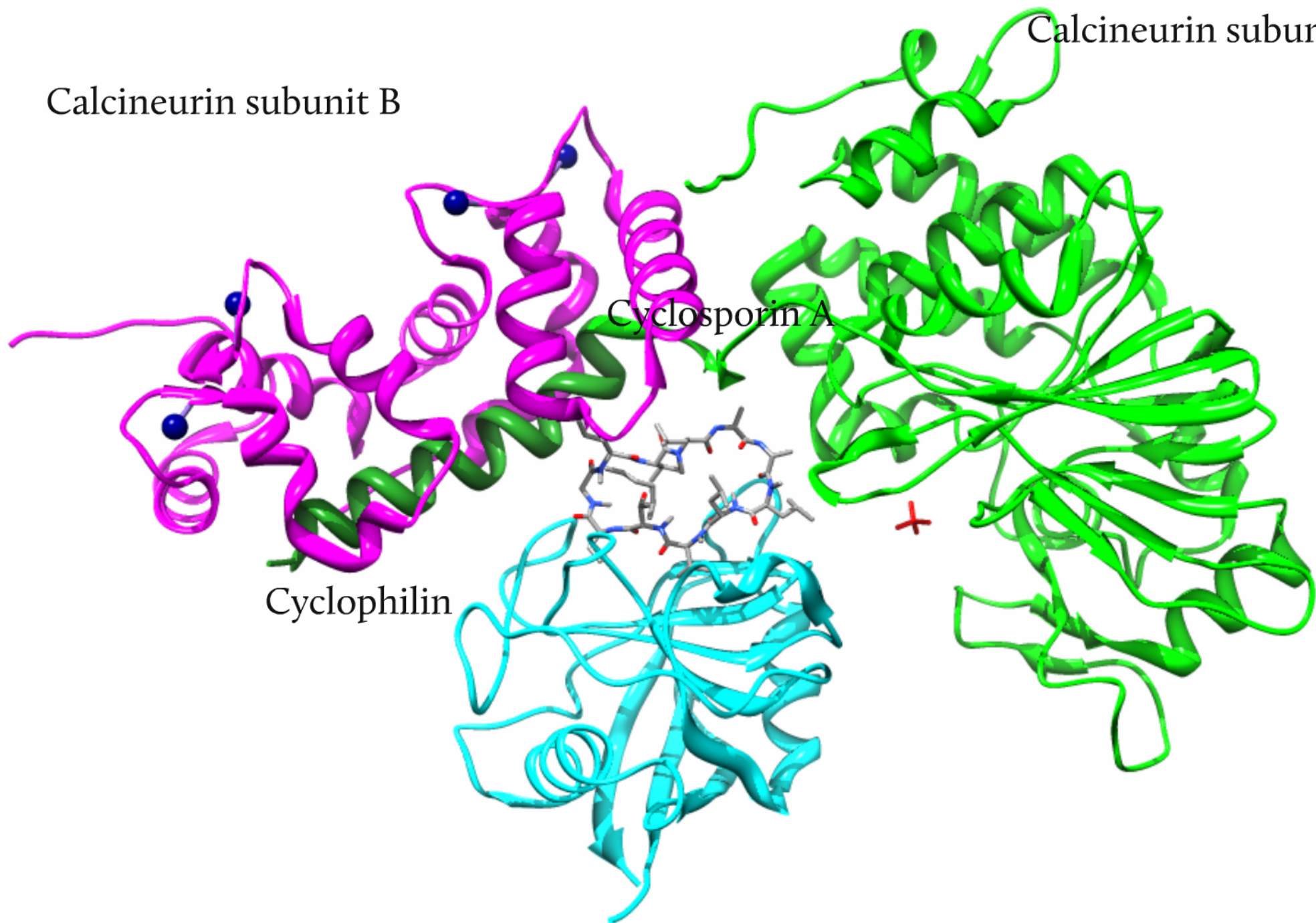
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Calcineurin subunit B

Calcineurin subunit A

Cyclosporin A

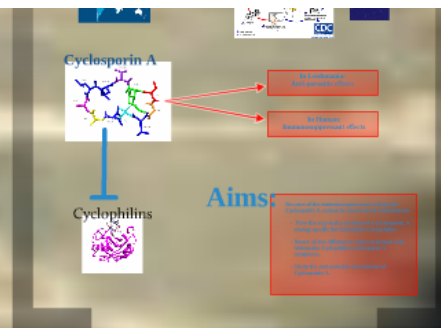
Cyclophilin





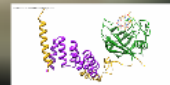
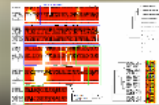
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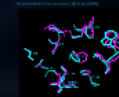
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Visiting scientist at EMBL Heidelberg

Structural and Computational
Biology Unit

Systems Biology

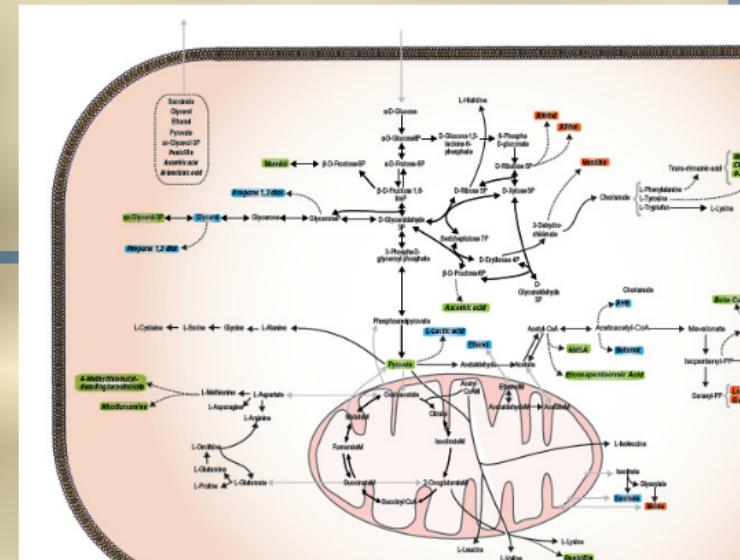
Kiran Patil's Lab

Architecture and regulation
of metabolic networks

Project description:

Creation of a tool for system biologist showing new metabolic pathways that have been integrated in the yeast *Saccharomyces cerevisiae*.

This work can help the computationally-driven engineering production of important metabolites useful for different applications, from biofuel to food industry.





Thank you for
your attention!

Predoc at
EMBL Hamburg



SAXS

Bioinformatics

IDP by

Dmitri Svergun's Lab

Small-angle X-ray scattering from
macromolecular solutions

Visiting scientist at
EMBL Heidelberg
Structural and Computational
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Systems Biology

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Master's degreee

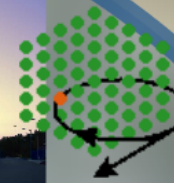
Bioinformatics

Thesis title:

"Computational analisys of the Cyclophilin-
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**Predoc at
EMBL Hamburg**



SAXS

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Dmitri Svergun's Lab

Small-angle X-ray scattering from
macromolecular solutions

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your attention!



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