Computational Systems Biology Group

Center for Computational Biology and Bioinformatics

Chemical and Biological Engineering, & Computer Engineering

Koç University, Istanbul, Turkey

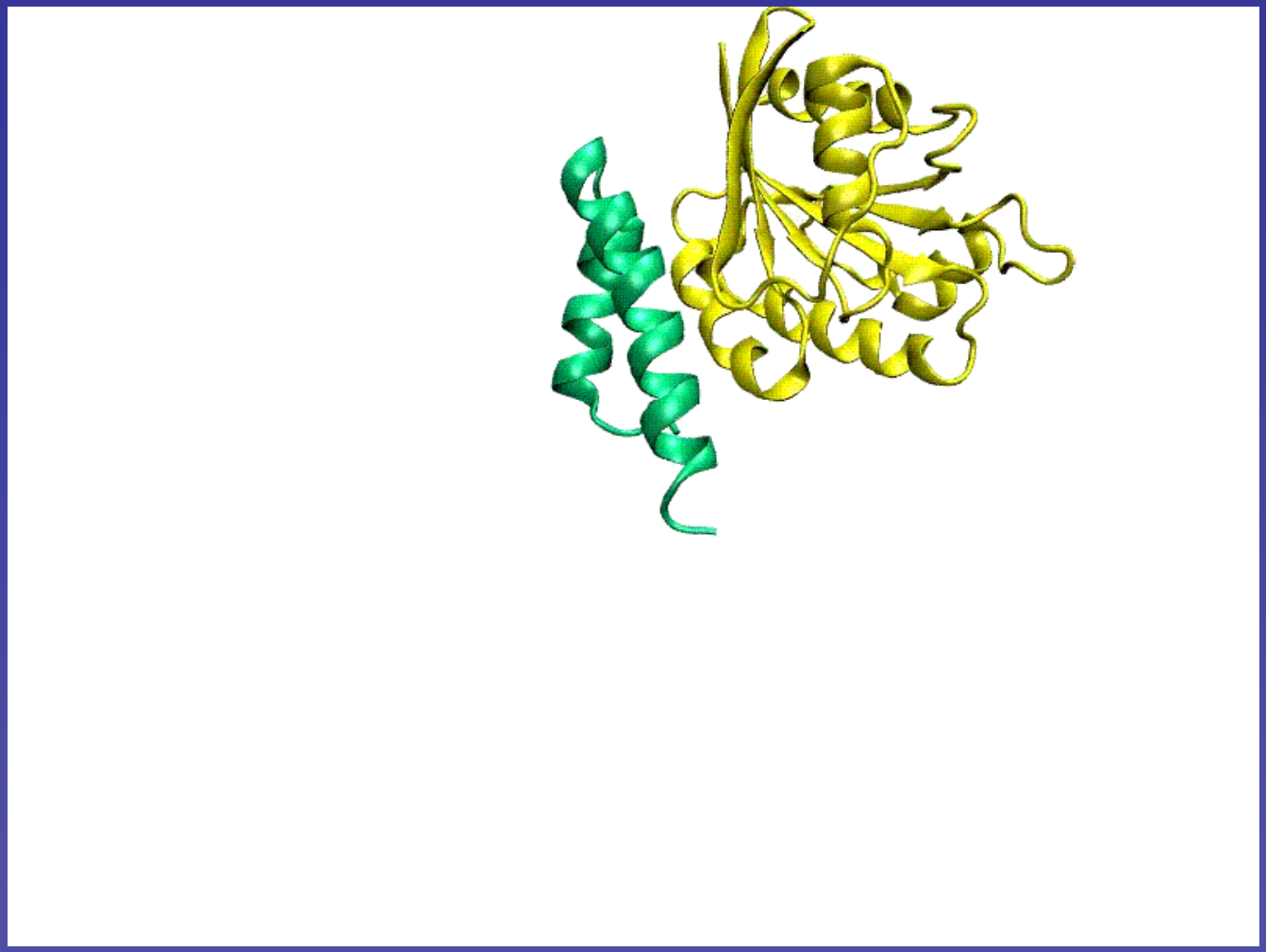
Özlem Keskin – Attila Gürsoy

COSBI

- Our research focuses on systems biology in the broad field of computational biology.

- We do:
- Develop computational methods and approaches for large scale structural modeling of protein-protein interactions
- Develop methods to find critical residues (energy hotspots) at the protein-protein interfaces
- Integrate 3D structural data of protein-protein complexes in signaling pathways that play important roles in cancer and other diseases
- Apply Molecular dynamics to study the Ras signaling pathway
- Predict interactions in the microbiome
- Provide maintain databases and computational services of the methods developed in the group to the community.

Develop tools: Protein-protein interactions



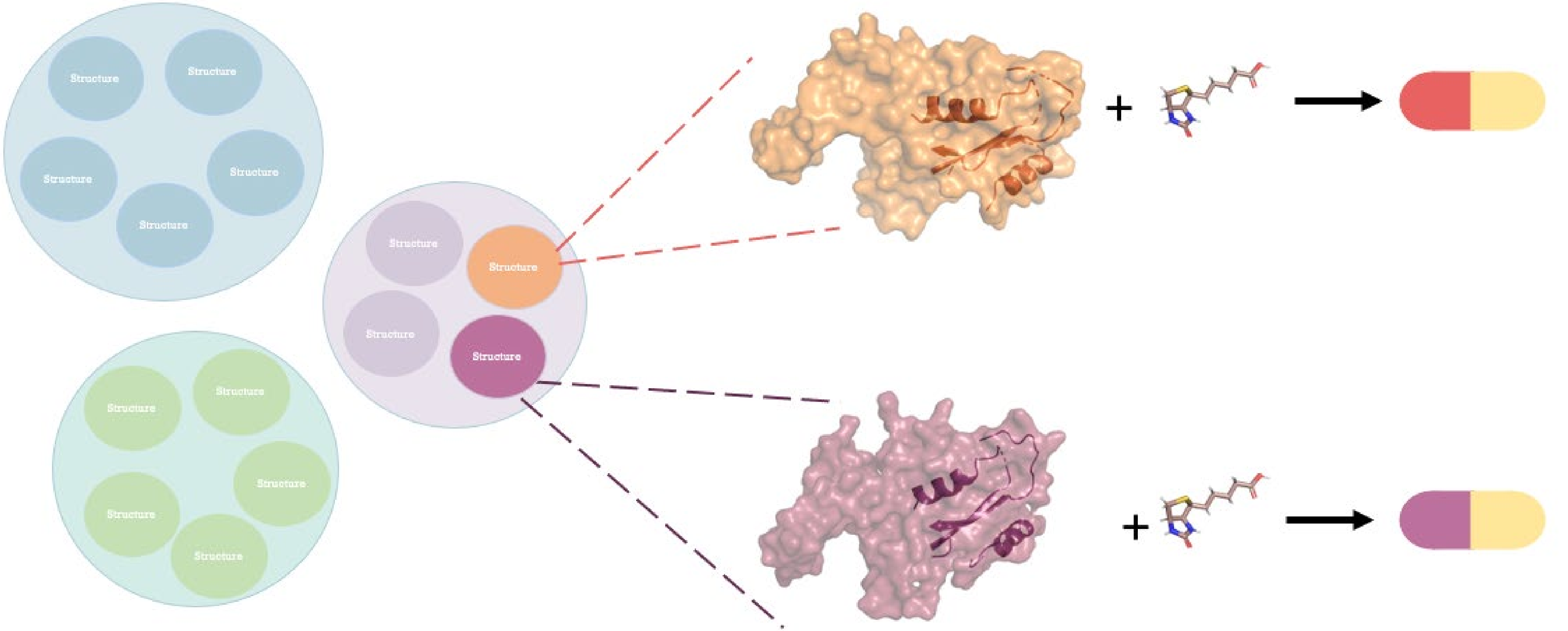
PRISM PROTOCOL
PROTEIN INTERACTIONS BY STRUCTURAL MATCHING

http://cosbi.ku.edu.tr/prism/

Tuncbag Nat Prot 2011, Curr Opğn
Tuncbag Proteins 2012

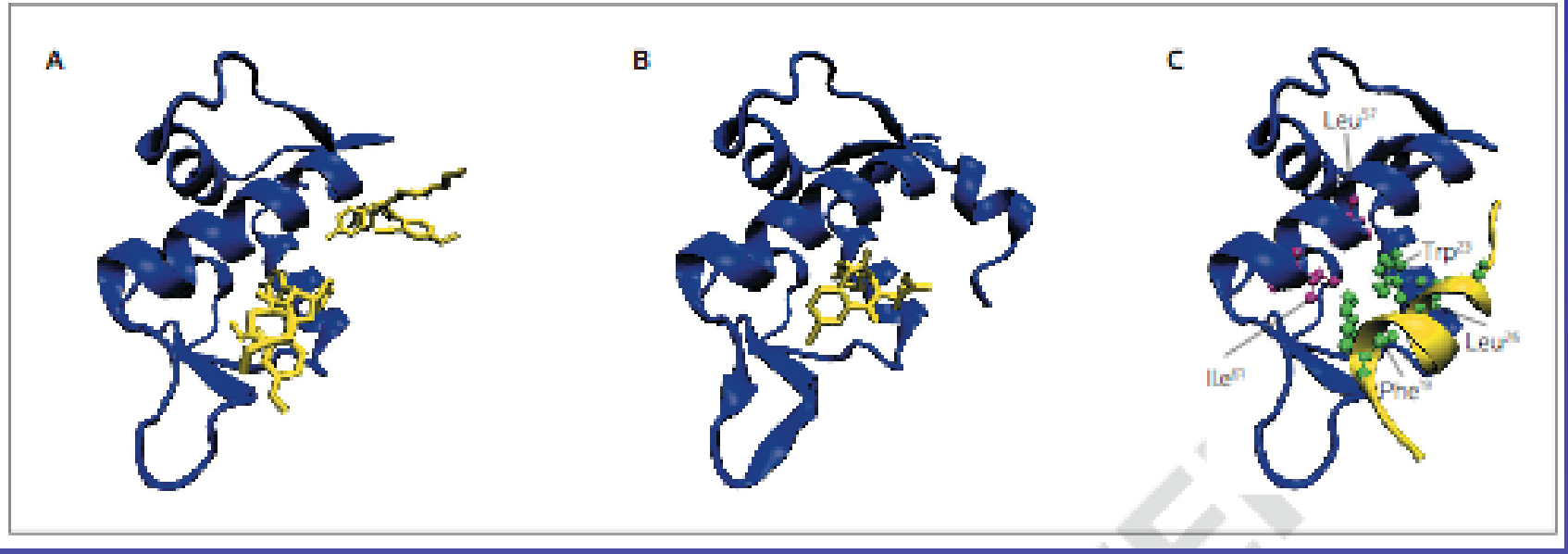
Baspinar et al NAR

Drug Repurposing



Protein-drug interaction sites

Figure 4. Structures of Mdm2 complexed with p53 and its inhibitors.



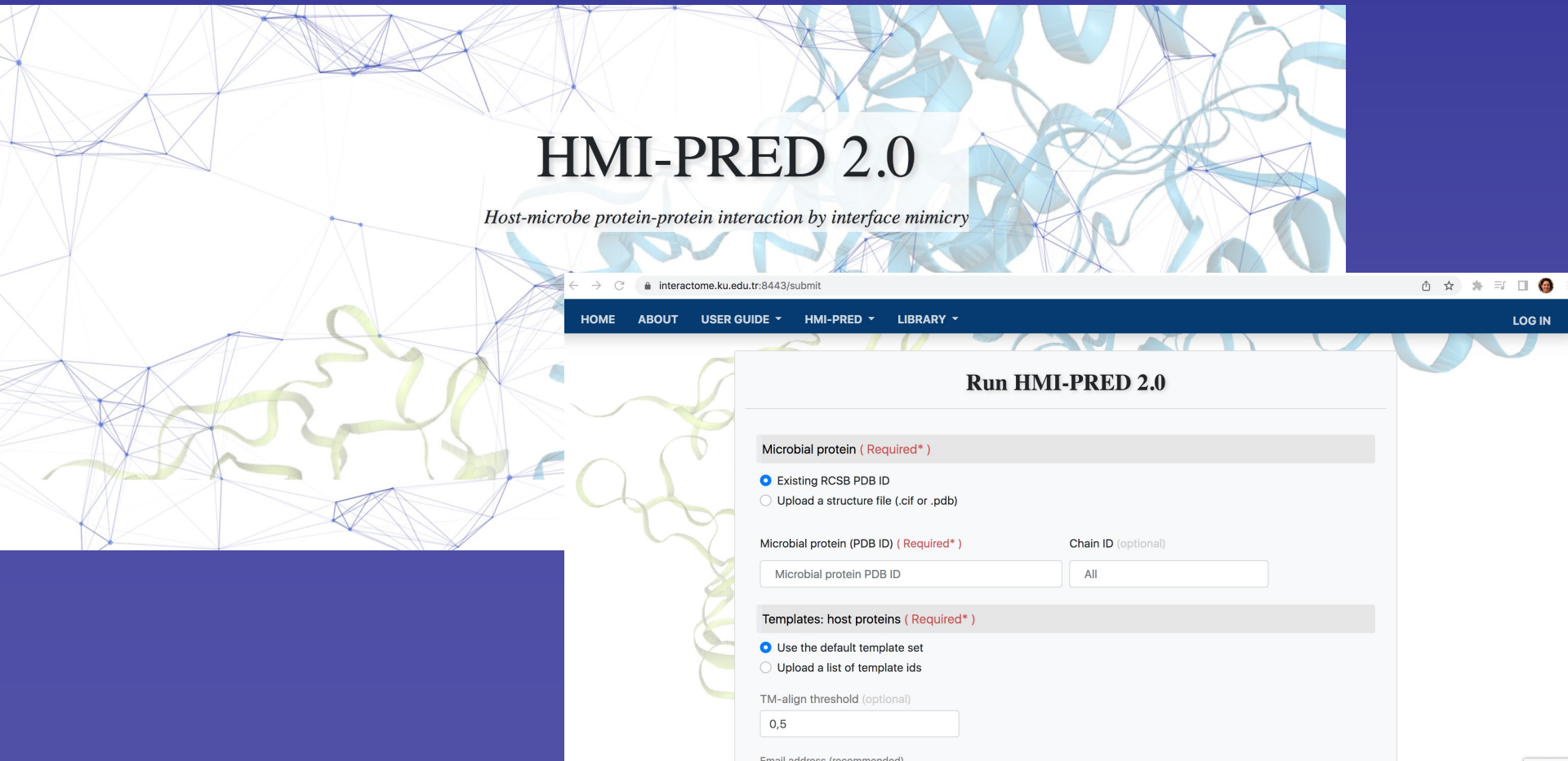
HOTREGION
A DATABASE OF COOPERATIVE HOTSPOTS

KOÇ UNIVERSITY

Acuner et al, Current Opinion in Drug Discovery & Development 2011

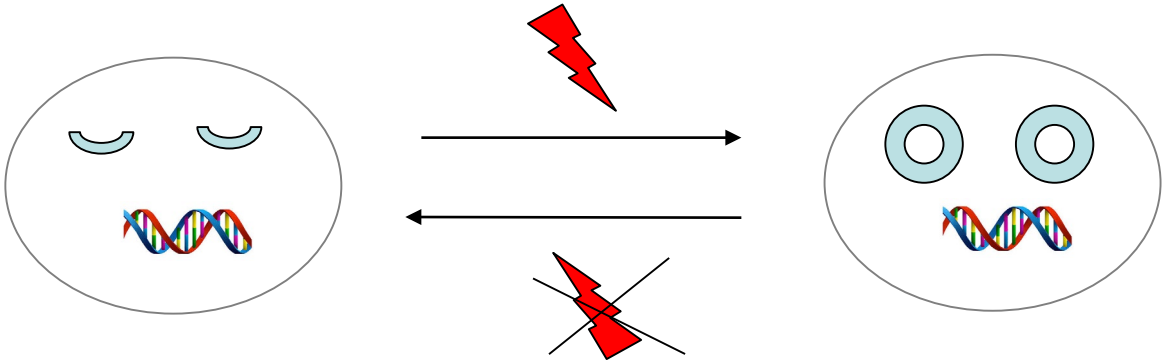
Human-microbe interactions: microbiome https://interactome.ku.edu.tr:8443/

- HMI-PRED 2.0 predicts microbial target proteins based on interface mimicry.



KRas mutations- Cancer Molecular dynamics studies

Stimulating signal



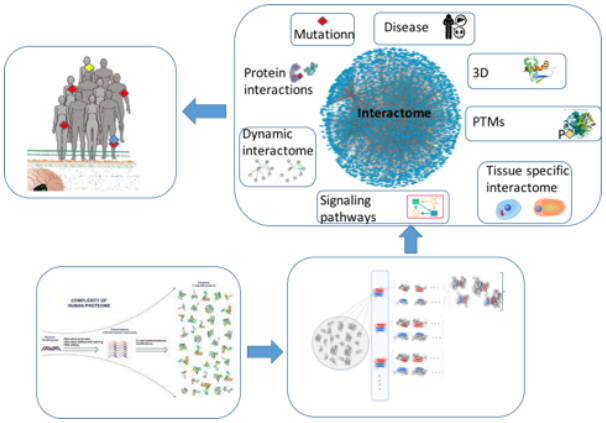
Inactive cell

Active cell

Kras on-off switch
In cancer, always on state
Cells continiously grow/divide

We are looking for PhD students/post-doctoral researches at Computational & Systems Biology Lab at Koc University, Istanbul COSBI (cosbilab.ku.edu.tr)

Human Intractome Project: Structural protein-protein interaction resource at genomic scale



The main aim of this project is to extract the comprehensive human interactome, integrate it with the knowledge of 3-dimensional structure (experimental or homology model), make the interactions more physical and meaningful, and present the most comprehensive and reliable structural interactome resource in the literature to the scientific community.

Post-doc /PhD student applicants should have:

- Ph.D. (MS) in computational sciences, computer sciences/engineering, bioinformatics, computational biology, or a closely related field
- Proficiency in programming languages such as C++, Java, JavaScript, Python, Databases (SQL)
- Good oral and written communication skills
- Preferably experience in Structure modeling and prediction, Structural bioinformatics, network biology

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TUBİTAK (The Scientific and Technological Research Council of Turkey) 2247-A National Research Leaders program research grant

Cardiovascular stress & neuronal function