ISMB/ECCB
2025
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# CLOSING CEREMONIES

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# THANK YOU CONFERENCE CHAIRS

**Carole Goble**

**João Carlos Setubal**

**Janet M Thornton**

# THANK YOU VOLUNTEERS!

# THANK YOU ISCB Staff!

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# AWARDS

The RCSB PDB Poster Prize will be awarded for the best poster related to structure and function prediction. The award will consist of a complimentary ISCB membership.

# Jude Wells

## College London, UK

***Design in voxel space, decode in smiles space: Plixer generates drug-like molecules for protein pockets***

# BioVis:
# Biological Data Visualizations

biovis

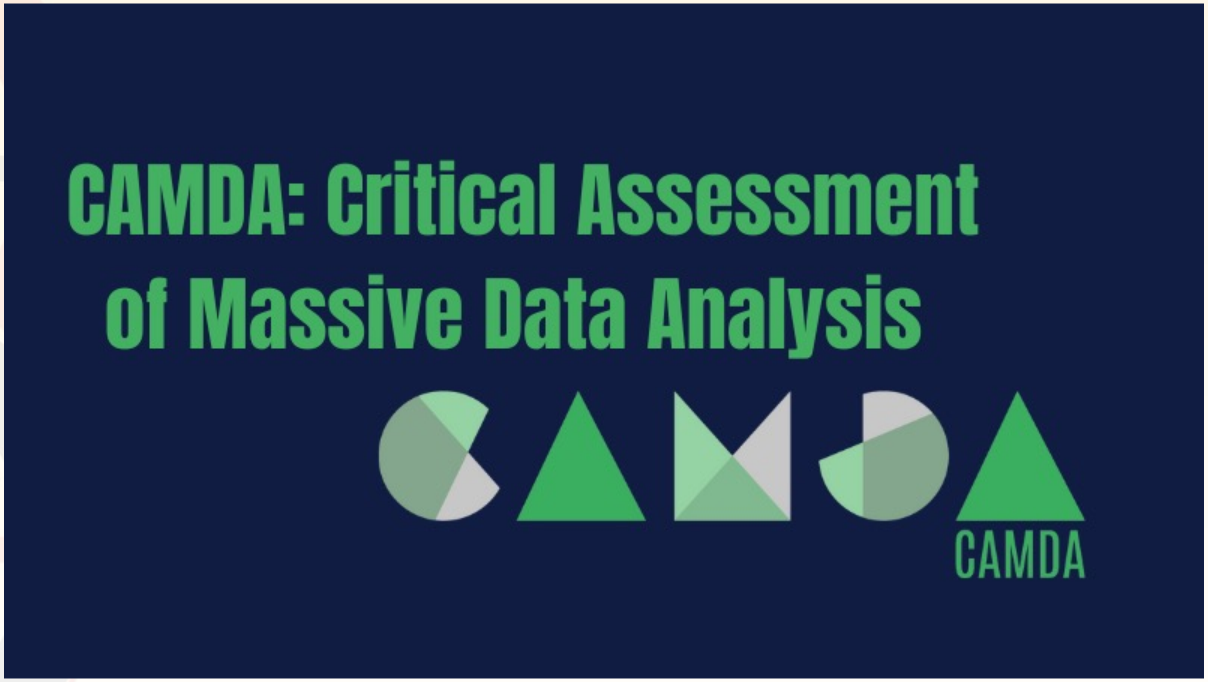
BioVis:
Biological Data
Visualizations

# Honorary Mention
# Best Abstract

# Thomas C. Smits

## Harvard Medical School

### *Automatic Generation of Natural Language Descriptions of Genomics Data Visualizations for Accessibility and Machine Learning*

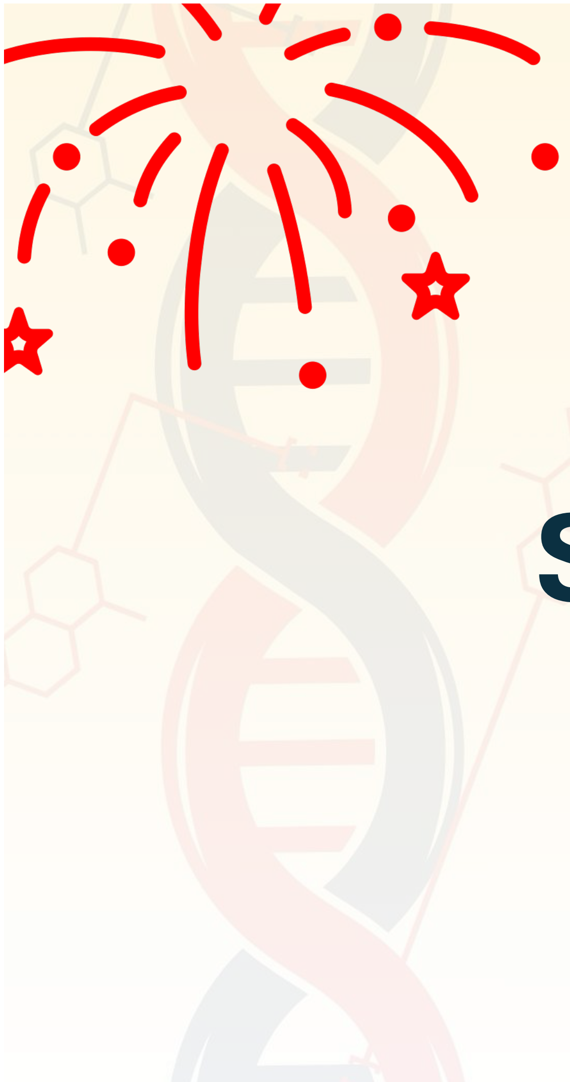


CAMDA: Critical Assessment of Massive Data Analysis

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA

# Honorary Mention



# Serghei Mangul

### University of Suceava

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA

# 3rd place

# Owen Visser

## University of Florida

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA

# 2nd place

# Rafael Pérez-Estrada

UNAM, Mexico

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA

# WINNER

# Anton Pashkov

UNAM, Mexico

BioVis:
Biological Data
Visualizations

# Best Abstract

# Bum Chul Kwon

IBM Research

## *GENET: AI-Powered Interactive Visualization Workflows to Explore Biomedical Entity Networks*

# EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

## EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

# Best Poster

# Vikram Shivakumar

## Johns Hopkins University

***Mumemto: efficient maximal matching across pangenomes***

EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

# Best Short Talk

# Maureen Stolzer

### Carnegie Mellon University

## *Evolution of the Metazoan Protein Domain Toolkit Revealed by a Birth-Death-Gain Model*

EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

# Best Long Talk

# Emilia Hurtado

## The University of British Columbia

## *A Probabilistic Method for Inferring Cell Phylogenies from Mitochondrial Variants*

# Function: Gene and Protein Function Annotation

Function: Gene and Protein Function Annotation

Function

# Runner-up Best Poster

# Hannelore Longin

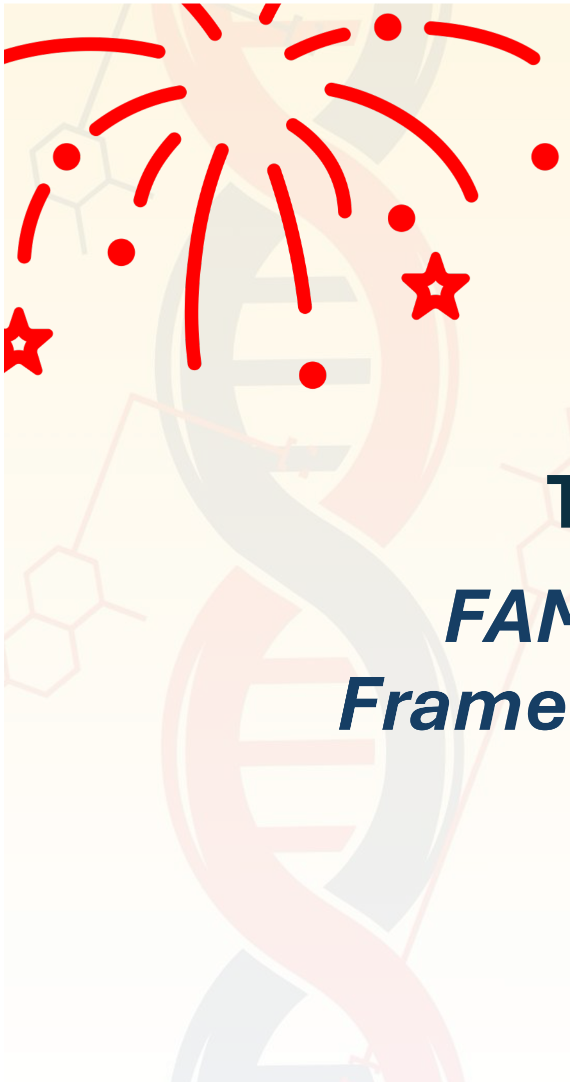
KU Leuven, Belgium

## *Fold first, ask later: structure-informed function prediction in Pseudomonas phages*

Function: Gene and Protein Function Annotation

Function

# Best Poster



# Guy Shur

## Tel Aviv University, Israel

## *FAMUS: A Few-Shot Learning Framework for Large-Scale Protein Annotation*

Function: Gene and Protein Function Annotation

Function

# Runner-up Best Talk

**Jun Kim**

**Stanford University**

# *Semi-Supervised Data-Integrated Feature Importance Enhances Performance and Interpretability of Biological Classification Tasks*

Function: Gene and Protein Function Annotation

Function

# Best Talk

## Harsh Srivastava

### New York University

*Fine-tuning protein language models with a disorder-aware vocabulary improves intrinsic disorder classification and function prediction*

## Rund Tawfiq

### KAUST, Saudi Arabia

*On the completeness, coherence, and consistency of protein function prediction: lifting function prediction from isolated proteins to biological systems*

# HiTSeq: High Throughput Sequencing Algorithms & Applications

HiTSeq

HiTSeq: High Throughput Sequencing
Algorithms & Applications

HiTSeq

# Early Career Poster Award

# Qiuyu Lian

## University of Cambridge

### *Harmonization, integration, and annotation of single-cell protein and transcriptomic atlases via unified cell ontology learning*

HiTSeq: High Throughput Sequencing
Algorithms & Applications

HiTSeq

# Early Career Talk Award

# Netanya Keil

**University of Florida**

## *Quality assessment of long read data in multisample lrRNA-seq experiments using SQANTI-reads*

# iRNA: Integrative RNA Biology

IRB
Integrative RNA Biology
group

iRNA:
Integrative
RNA Biology

# Best Poster

## Rahaf Issa

**University of Regensburg**

*In-Vivo Analysis of pre-mRNA Splicing Kinetics and Regulation in Mouse Models*

## Louis-Philippe Chaumont

**Université de Sherbrooke**

*Deciphering the coordinated regulation between snoRNAs and their host genes during neurogenesis*

## Yu-Jen Lin

**University of California Berkeley**

*RISE: Relative Impact of Splicing and Expression in transcriptome studies*

# NetBio:
# Network Biology

**NetBio:**
**Network Biology**

NetBio

# Best Poster

## Method

**Arne Wehling**

**CSL Behring**

*The power of regulation: Solving target discovery with expression profiles and directed graphs*

## Case-study/Application

**Sebastian Urquiza-Zurich**

**University of Chile**

*Integrative Transcriptomic Profiling Reveals Novel lncRNA–circRNA–miRNA–mRNA Regulatory Networks in a Neurohormonal Model of Cardiac Hypertrophy*

## Tool

**Estefania Torrejon**

**NOVA Medical School**

*EV-Net: Extracellular vesicles-mediated intercellular communication networks involved in metabolic disease pathophysiology*

**NetBio:**
**Network Biology**

NetBio

# Best Talk

# Beatriz Urda-Garcia

## Barcelona Supercomputing Center, Spain

*Disentangling the genetic and non-genetic origin of disease co-occurrences*

NetBio:
Network Biology

NetBio

# NetBio Cytoscape Network Visualization Contest Winners

# Alejandra Paulina Perez Gonzalez, Michael Costanzo, Jong Chan Lim

# RegSys: Regulatory & Systems Genomics

RegSys:
Regulatory &
Systems
Genomics

RegSys

# Best Poster

# Erick Isaac Navarro Delgado

## The University of British Columbia

### *RAMEN: A reproducible framework for dissecting individual, additive and interactive gene-environment contributions in genomic regions with variable DNA methylation*

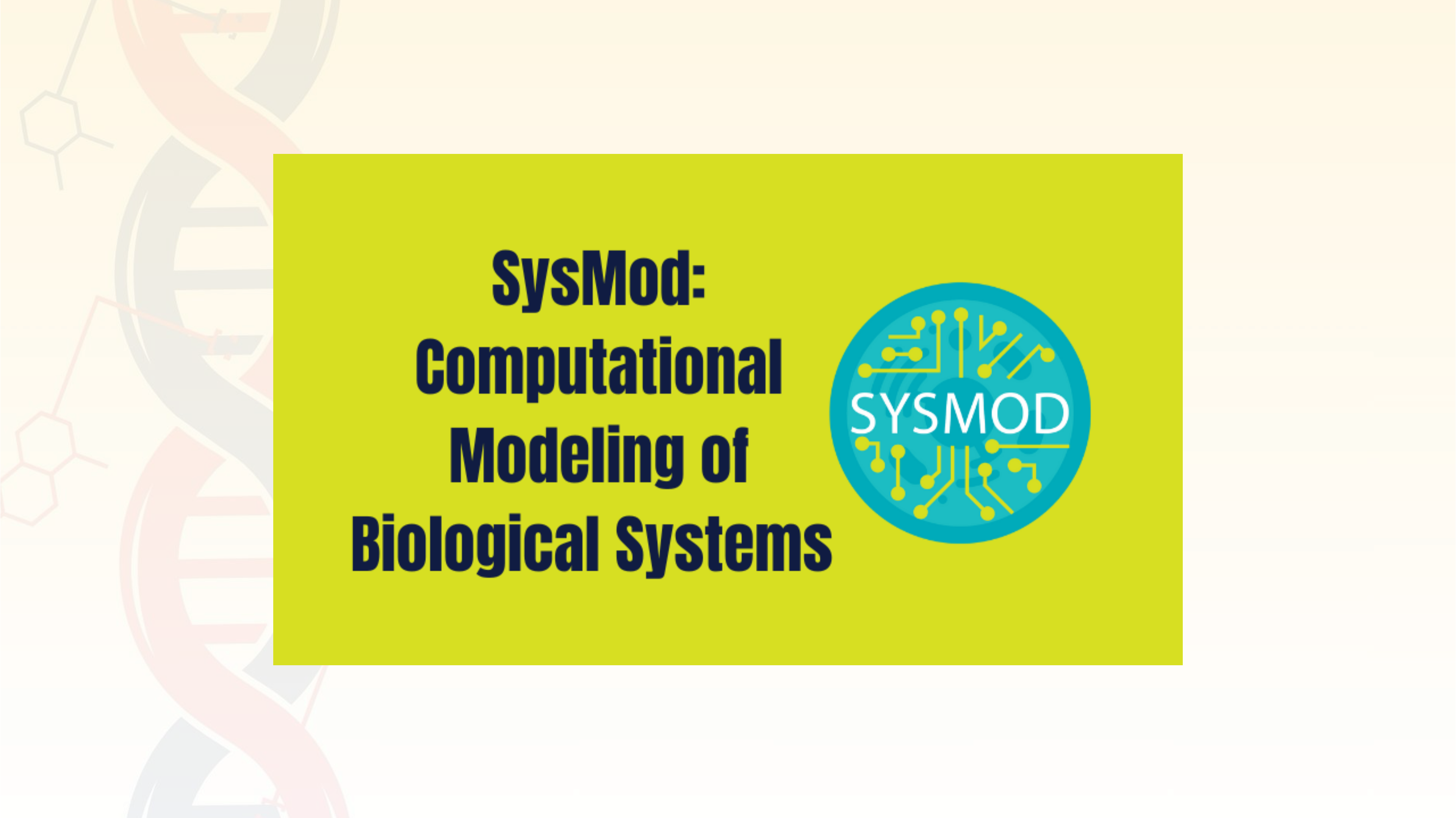
RegSys:
Regulatory &
Systems
Genomics

# Best Talk

# Surag Nair

## Genentech Inc

## *Nona: A unifying multimodal masked modeling framework for functional genomics*



# SysMod: Computational Modeling of Biological Systems

**SysMod: Computational Modeling of Biological Systems**

SYSMOD

# 3rd Place Poster

# Sebastian Huß

## University of Potsdam

*NeuralFlux: Estimation of reaction fluxes at a genome-scale level from time-resolved isotope labeling patterns using deep learning*

SysMod:
Computational
Modeling of
Biological Systems

SYSMOD

# 2nd Place Poster

# Rupinder Kaur

UKSH Campus Kiel

## Computational Prediction of Targeted Nutritional Interventions for Host–Microbiome Modulation in *C. elegans*

SysMod:
Computational
Modeling of
Biological Systems

SYSMOD

# 1st Place Poster

# Yanjun Liu

University of Galway

## Systems-Level Analysis of Metabolic Dysregulation in Gaucher Disease: Mitochondrial Dysfunction and Disrupted Cholesterol Homeostasis

# TransMed: Translational Medicine Informatics & Applications

TransMed:
Translational
Medicine
Informatics &
Applications

# Best Poster

## Yang Yang

### University of Chicago

*Transcription and DNA replication collisions lead to large tandem duplications and expose targetable therapeutic vulnerabilities in cancer*

## Gamze Yazgeldi Gunaydin

### University of Helsinki

*Signs of immune dysregulation in second trimester maternal blood RNA profiles in late–onset preeclampsia*

TransMed:
Translational
Medicine
Informatics &
Applications

# Best Oral Presentation

## Sophia Krix

**Fraunhofer Institute for Algorithms and Scientific Computing (SCAI)**

*Unraveling Early Changes in Alzheimer's Disease: Causal Relationships Among Sleep Behavior, Immune Dynamics, and Cognitive Performance Through Multimodal Data Fusion*

## Barry Ryan

**University of Edinburgh**

*Combining Clinical Embeddings with Multi-Omic Features for Improved Interpretability in Parkinson’s Disease Patient Classification*

# VarI: Variant Interpretation

VarI: Variant Interpretation

# Best Poster

## Anastasiia Kolchina

**Helmholtz Institute for Pharmaceutical Research Saarland (HIPS)**

*Beyond Additivity: The Challenge of Predicting Epistatic Effects in Proteins*

## Megha Hegde

**Kingston University London**

*DNA-DistilBERT: A small language model for non-coding variant effect prediction from human DNA sequences*

VarI: Variant Interpretation

VarI COSI

# Best Talk

## Alexander Gress

**Helmholtz Institute for Pharmaceutical Research Saarland (HIPS)**

*StructGuy: Data leakage free prediction of functional effects of genetic variants*

## Kilian Salomon

**Berlin Institute of Health at Charité (BIH)**

*Functional characterization of standing variation around disease-associated genes using Massively Parallel Reporter Assays*

# Ian Lawson Van Toch Memorial Award

# Outstanding Student Paper

with support from

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The Princess Margaret UHN

DATE: July 11, 2025

PAY TO: Princess Margaret Cancer Foundation $ 82,818$^{29}$

THE SUM OF: Eighty-Two Thousand Eight Hundred & Eighteen/100 DOLLARS

Team Ian Ride

AUTHORIZED SIGNATURE

# Ian Lawson Van Toch Memorial Award

with support from
The Princess Margaret Cancer Foundation UHN

## Xiang Ge Luo

ETH Zurich, Switzerland

***Bayesian inference of fitness landscapes via tree-structured branching processes***

## Minh Hoang

Princeton University

***Locality-aware pooling enhances protein language model performance across varied applications***

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# CONGRATS AWARDEES