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Core Facility Day 2024

Life Sciences

16 OCTOBER, 2024
CEITEC, E35/211 + ATRIUM

Curious about what expert services are available to researchers on campus? What instruments can you use in shared mode and under what conditions? Do you want to see everything for yourself?

Register at: muni.cz/go/fba265





CEITEC MUNI Core Facility Proteomics CF

Zbyněk Zdráhal, CF Day Life Sciences, 16 October 2024

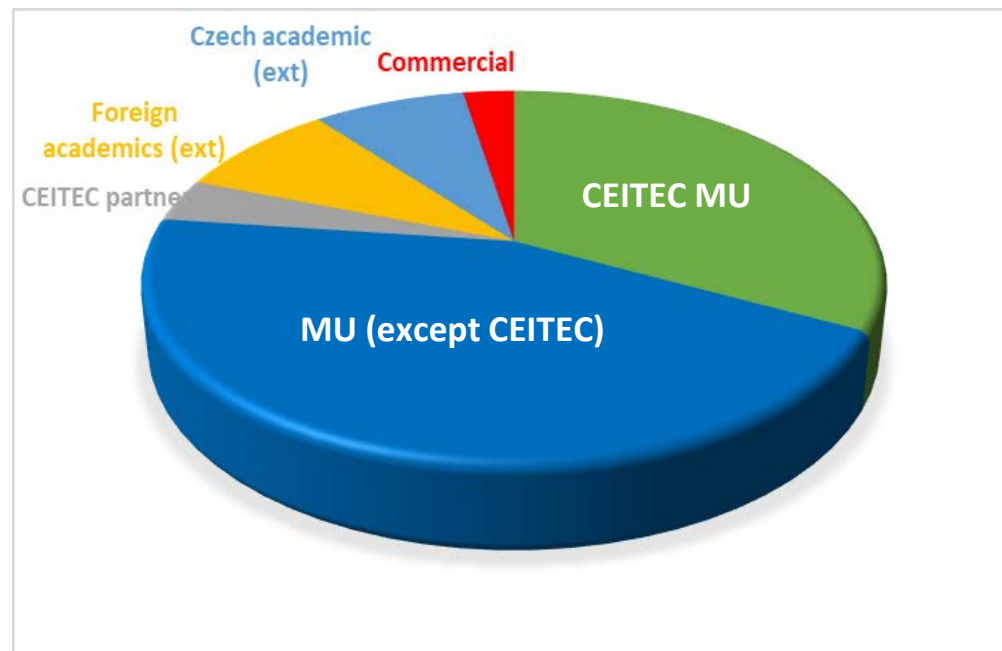
Content

- CF overview
- Services
- Access rules
- News
- New instrumentation
- Acknowledgment
- Result example

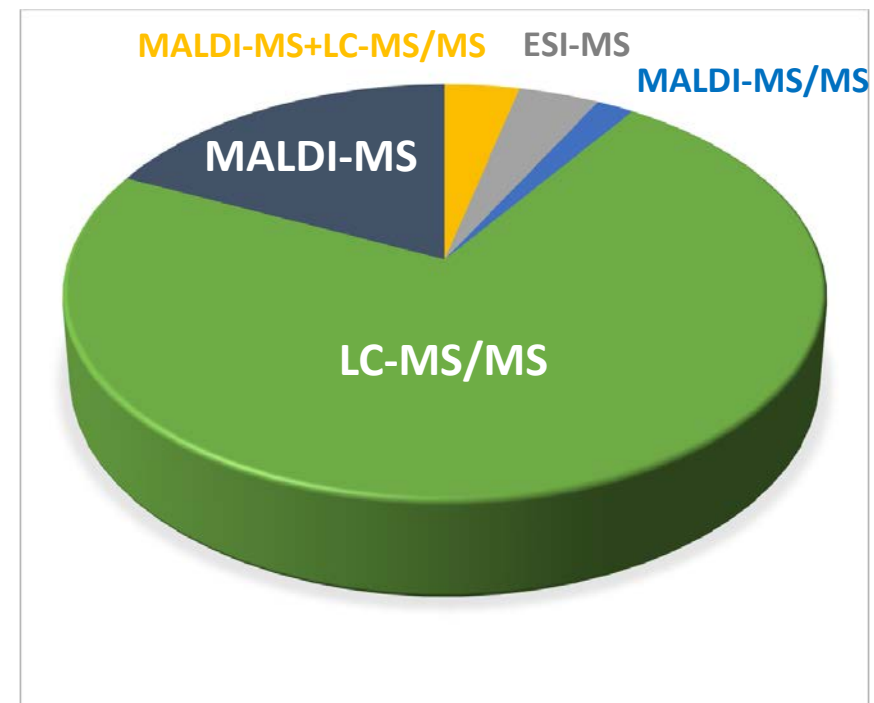
CF overview 2023

187 users (78 students) ● 472 orders ● 5040 samples ● ~ 25 000 hrs

User community distribution

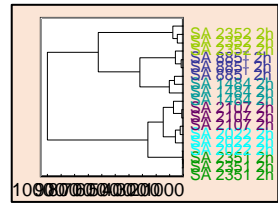


Distribution of samples according to analysis type



● **33 clear acknowledgements to our CF (~ 30 % of CIISB)**

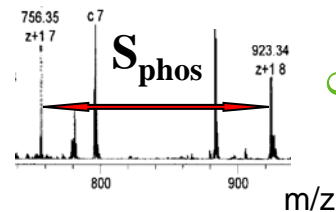
Services



- **Intact mass measurement**
(MW, MALDI-MS profiling)

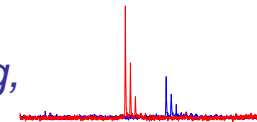
- **protein identification**
(de novo sequencing)

- **protein complexes analysis**
(-protein, -RNA, -DNA)



- **characterization of protein modifications**
(phosphorylation, acetylation, methylation etc.)

- **quantification of complex protein mixtures**
(relative and absolute quantitation, isotopic labeling, label-free)



Overview of our services is available at
<https://www.ceitec.eu/proteomics-core-facility/cf95>

Access rules

Full service mode



Register • Order • Bring sample • Pick-up report

<https://www.ceitec.cz/centralni-laborator-proteomika/cf95>

please talk to us:

prior you start a proteomic experiment in your lab

Personal discussion is highly recommended.

Selection of optimal design of the whole experiment (**also on your side**) enables to maximize obtained information, **saves a lot of your (and our) time and work.**

Prices - 2025

- As usual, **the pricelist will be updated** for 2025 in the beginning of the year, **slight changes are expected**
- Payment at quarterly basis
- Prepayments should be spent ideally during the following year
- The CIISB discount **will stay on 85 % of full costs**

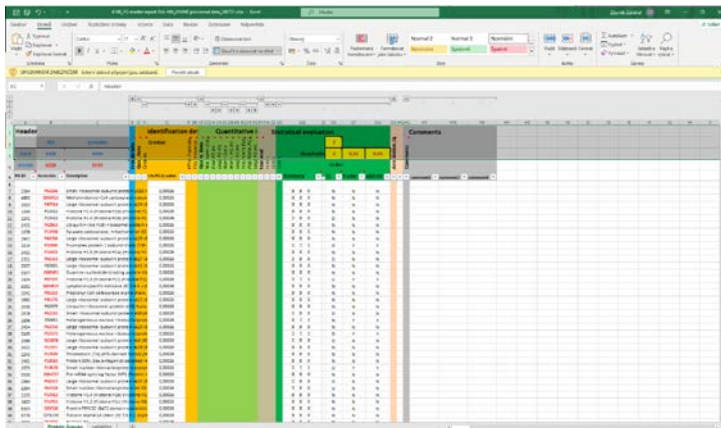
15 % to pay



News

- **New format of our reports**
stand-alone, portable, offline

Excel



Proteo-Visualizer



- basic training in January/February 2025
- user manual is under progress

New Instrumentation

timsTOF Pro 2



spring 2025



timsTOF HT



- **Deeper proteome coverage**

Max. injection amount:

250 ng



2 000 ng

Scan rate:

100 Hz



300 Hz

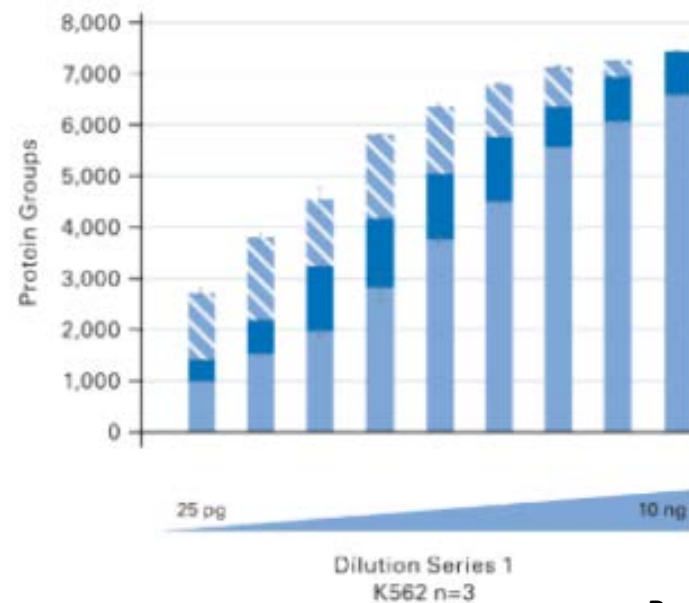
New Instrumentation

timsTOF Ultra 2

spring 2025



- Ultimate sensitivity
- Scan rate - 300 Hz



Bruker.com

- Spatial proteomics
- Single cell proteomics

Sample preparation protocols should be established

Acknowledgment

- **Preferred version:** *„CIISB, Instruct-CZ Centre of Instruct-ERIC EU consortium, funded by MEYS CR infrastructure project LM2023042, is gratefully acknowledged for the financial support of the measurements at the CEITEC Proteomics Core Facility.“*

Computational resources were provided by the e-INFRA CZ project (ID:90254), supported by the Ministry of Education, Youth and Sports of the Czech Republic

- **Short version:** *„We acknowledge CEITEC Proteomics Core Facility of CIISB, Instruct-CZ Centre, supported by MEYS CR (LM2023042).“*

Result example

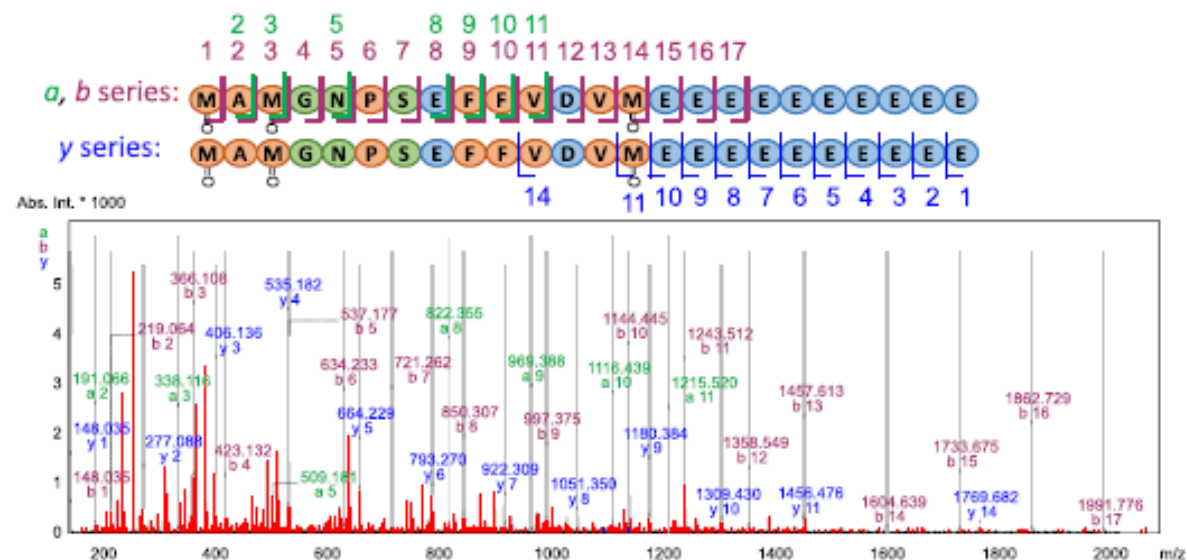
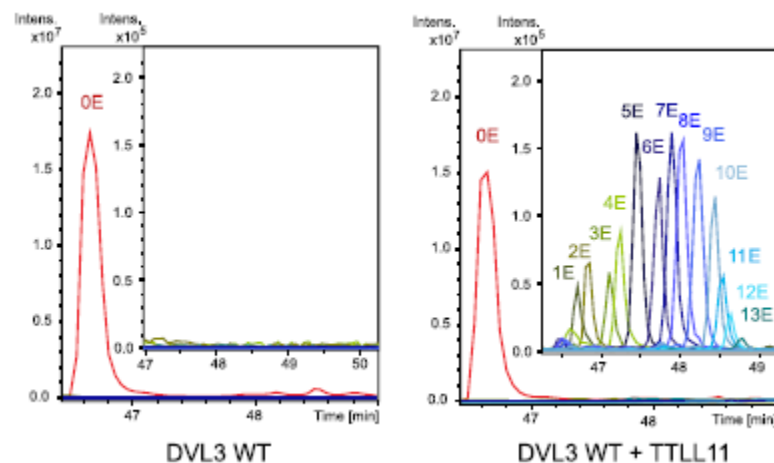


Vita Bryja's lab

Kravec M. *et al.*

Carboxy-terminal polyglutamylation regulates signaling and phase separation of the Dishevelled protein

- new type of PTM



<https://doi.org/10.1038/s44318-024-00254-7>



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Thank you for your attention! Questions?

core.facility@ceitec.muni.cz

ceitec.eu/core-facilities/

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CEITEC MUNI Core Facility Biomolecular Interactions and Crystallography (CF BIC)

Josef Houser, CF Day Life Sciences, 16 October 2024

Expertise

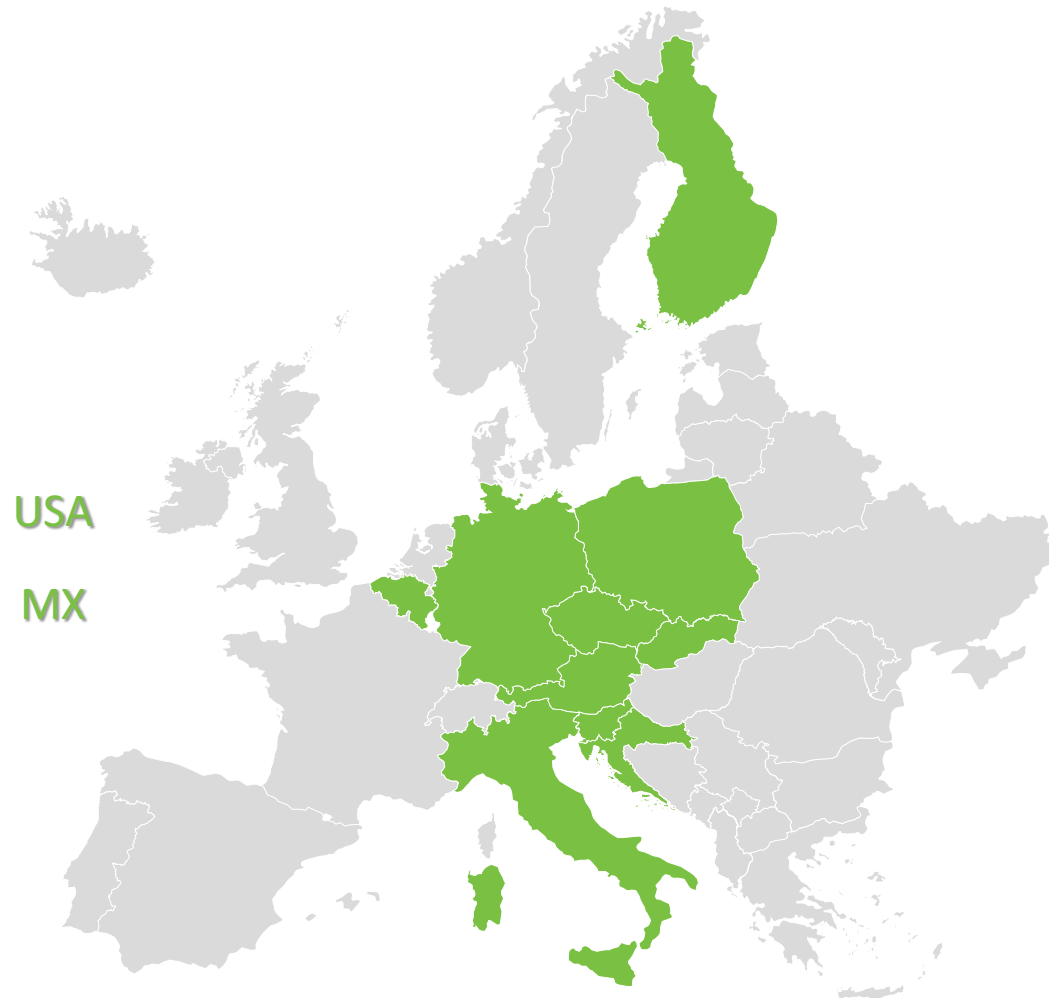


20 techniques with 30 instruments

- Studies of **physical properties** of the molecules, e.g. size distribution, homogeneity, stability, structural content
- Characterization of (bio)molecular **interactions** including thermodynamics and/or kinetics parameters
- High-throughput **crystallization** screening and optimization of conditions for a crystal growth
- **X-ray diffraction** and 3D structure solving

International network

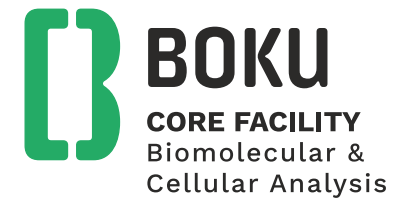
Users



Projects



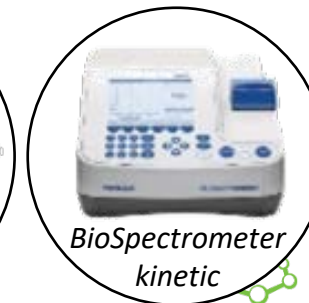
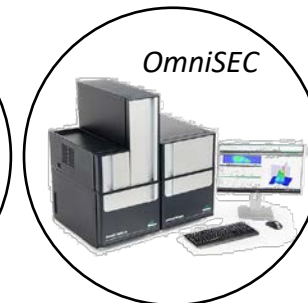
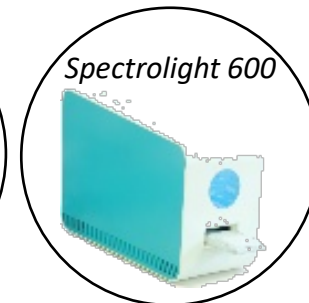
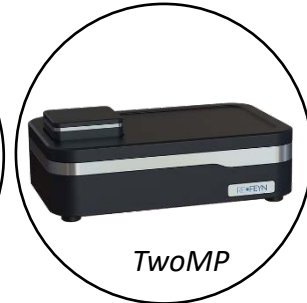
Collaboration



Biophysical characterization

- Homogeneity
 - Molecular mass
 - Oligomeric state
 - Aggregation
- Stability
 - Temperature
 - Buffer composition
- Folding
 - Secondary structure
 - Shape

- Analytical ultracentrifugation (AUC)
- Size exclusion chromatography (SEC-LS)
- Dynamic light scattering (DLS)
- Differential scanning fluorimetry (DSF)
- Differential scanning calorimetry (DSC)
- Circular dichroism spectroscopy (CD)
- Small-angle X-ray scattering (SAXS)
- Mass photometry (MP)
- UV/VIS spectroscopy



Biomolecular interactions

- Various principles

- In solution
- On surface
- Cell-based

- Parameters

- Affinity
- Thermodynamics
- Kinetics

- Types of molecules

- Proteins, nucleic acids, small molecules

- Isothermal titration calorimetry (ITC)

- Micro-scale thermophoresis (MST)

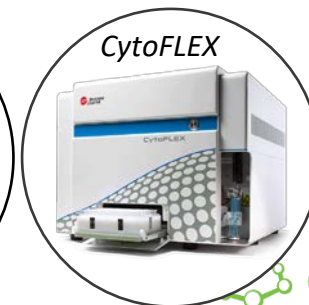
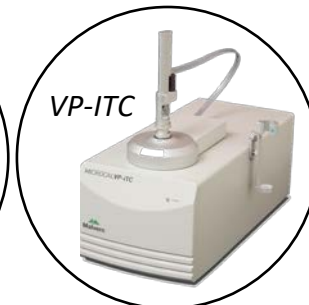
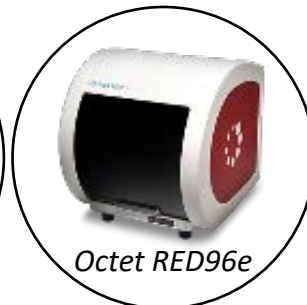
- Bio-layer interferometry (BLI)

- Surface plasmon resonance (SPR)

- Analytical ultracentrifugation (AUC)

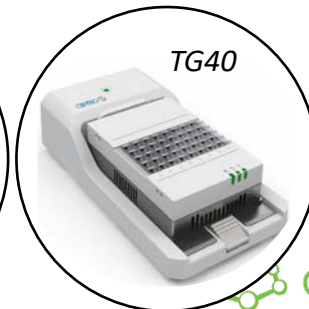
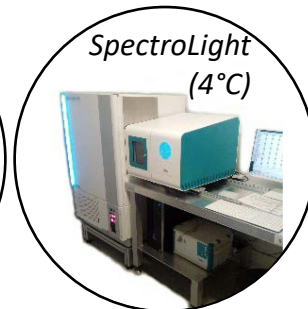
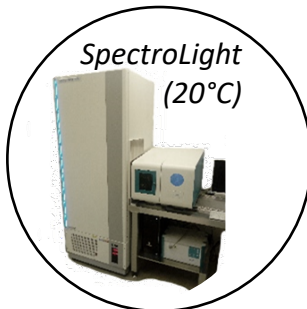
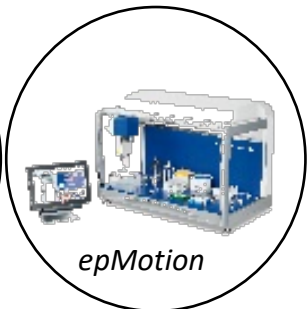
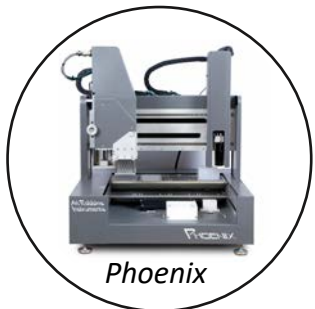
- Fluorescence anisotropy (FA)

- Cell sorting (FACS)



Crystallography

- Complete instrumentation for crystallization screening
 - Optimization of crystallization
 - Diffraction data collection
 - 3D structure determination
- Crystallization plates set-up robotics
 - Plates storage and imaging
 - Crystallization temperature optimization
 - Optical microscopes
 - X-ray diffraction
 - Accessories for cryo-crystallography



High throughput

- Robotization and automation for HTS
- Pipetting from 500 pl to 1 ml
- Microarrays
- 96 and 384-well plates handling
 - Aliquoting
 - Gradient preparation

- **Parallelization**

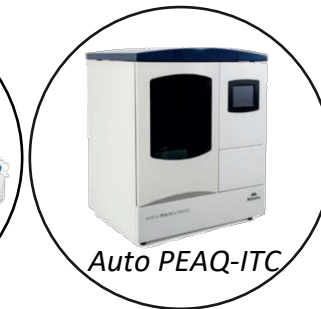
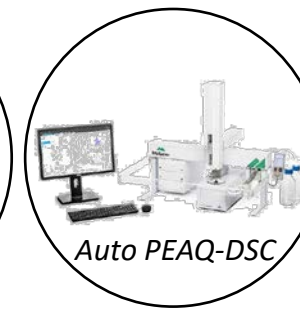
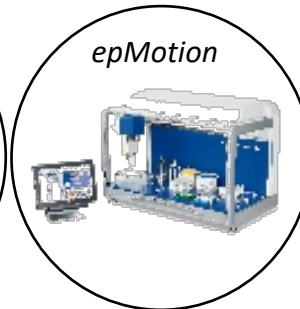
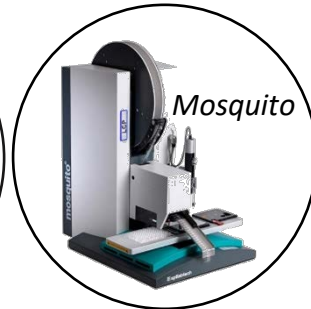
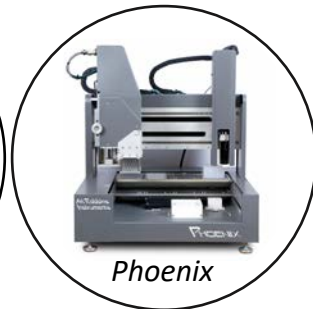
- In plates – DLS, BLI, crystallization
- In capillaries – DSF

- **Autosamplers**

- Walk-away operation, 24/7
- SPR, ITC, DSC, SEC-LS

- **Pipetting robotics**

- SBS plate preparation
- Microarrays



Equipment news

- **Fluorimeter** – Fluorolog QM
 - **Fluorescence anisotropy**
 - Time resolved single-photon count
 - Temperature controlled

- **CD spectrometer** – Chirascan V100
 - **Secondary structure analysis**
 - High stability, sensitivity and precision
 - Temperature control (4-100 °C)



Equipment news

- **Mass photometer** – Refeyn MP2

- Sample **homogeneity** and **mass analysis**
- Broad concentration range
- Proteins and their complexes



- **Analytical size-exclusion chromatography** – fraction collector

- Collection of separated fractions
- Pre-step for **MS** or **EM** analysis



Case study – 14-3-3 ζ protein

- Important **human regulatory protein**
- Various roles in organism
- **Monomer-dimer transition** depending on phosphorylation

Phosphomimicking mutants

ζ _S58E

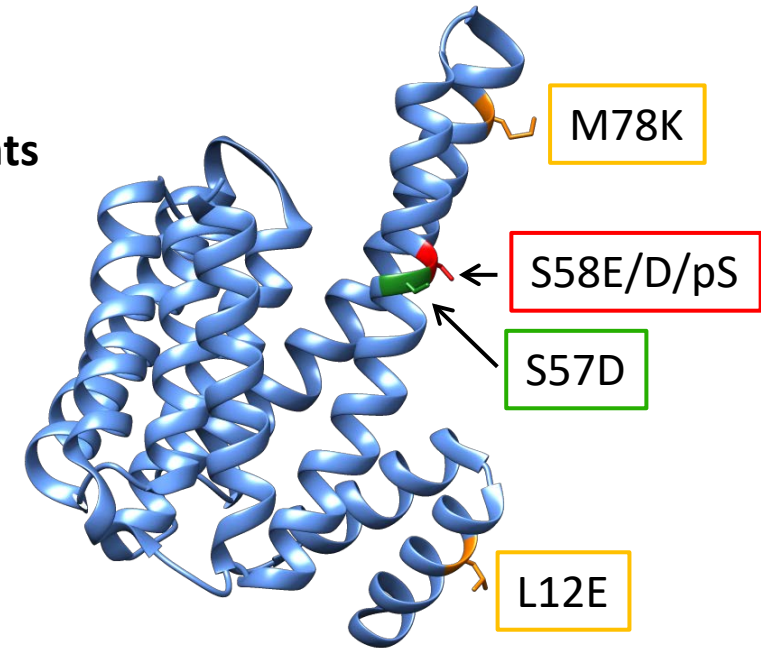
ζ _S58D

ζ _S57D_S58D

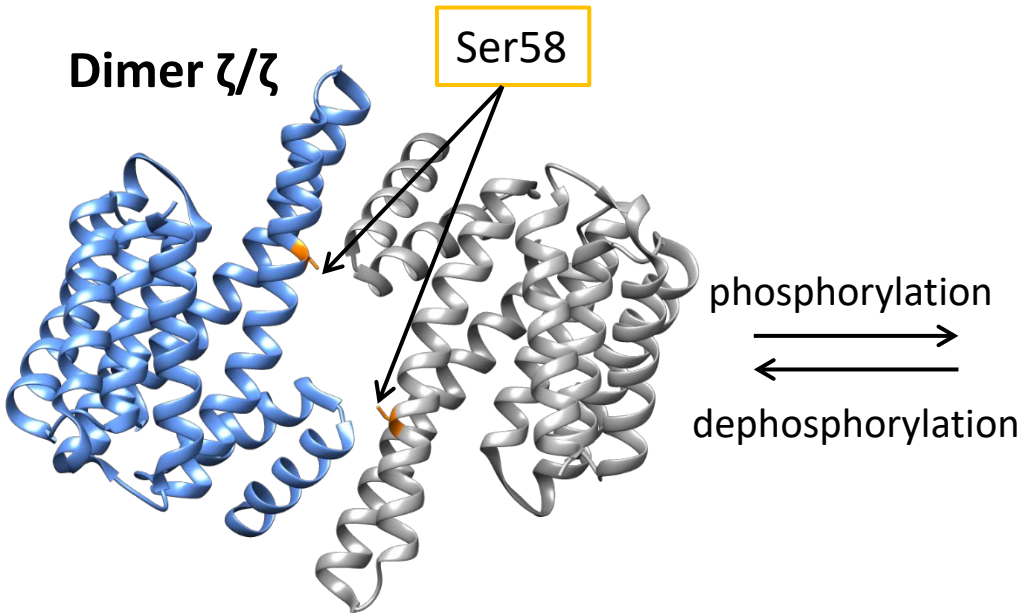
Monomeric mutants

ζ _L12E_M78K = ζ _m

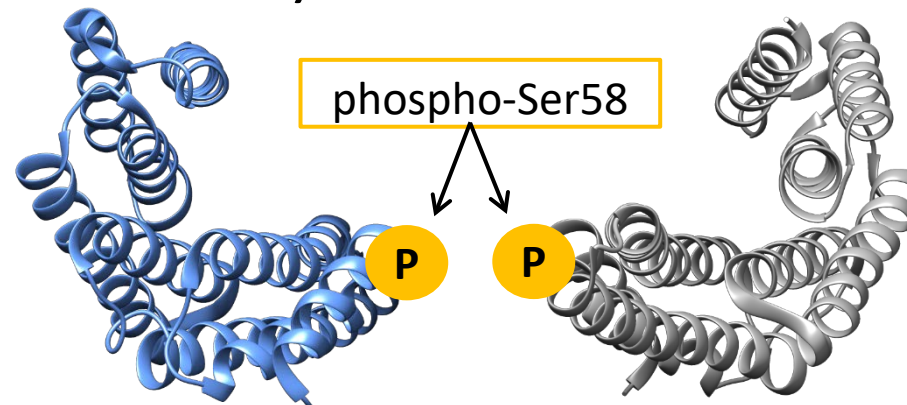
Phosphorylated ζ _pS58



Dimer ζ/ζ



P ζ Monomers

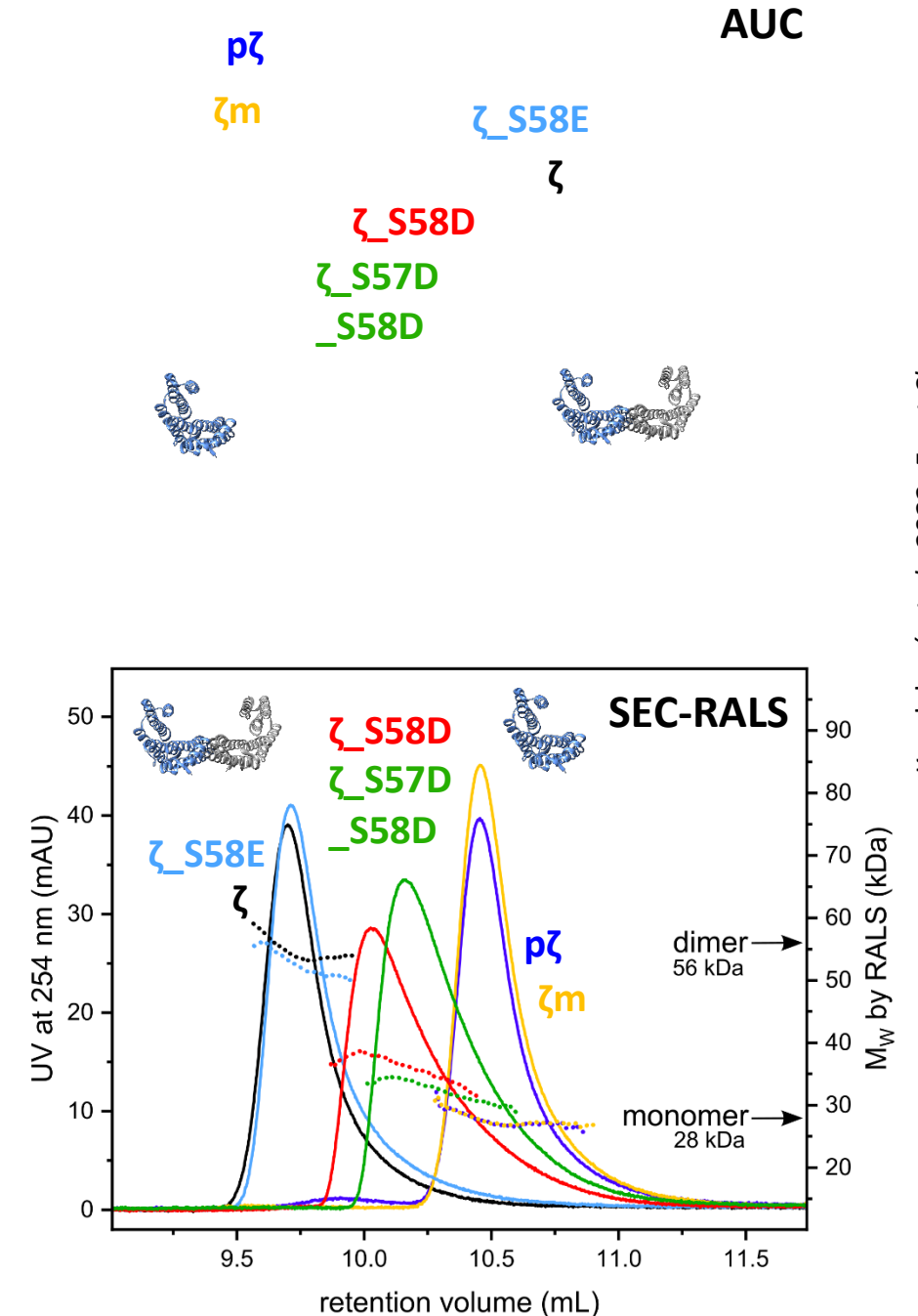


Jozef Hritz

Case study – 14-3-3 ζ protein

- Combination of multiple methods
- FRET, MST, AUC, SEC-LS, nanoDSF, DSC
- **High-variability** among “phosphor-mimicking” mutations (K_D varies by 4 orders)

14-3-3 construct	K_D (AUC/SEC)	T_m (nanoDSF) [°C]	T_m (DSC) [°C]
ζ_{WT}	5.5 ± 0.8 nM	60.35 ± 0.15	60.28 ± 0.01
ζ_{S58E}	0.35 ± 0.25 μ M	58.19 ± 0.09	57.64 ± 0.01
ζ_{S58D}	132 ± 7 μ M	54.21 ± 0.03	53.89 ± 0.01
ζ_{S57D_S58D}	348 ± 19 μ M	53.58 ± 0.10	53.70 ± 0.01
ζ_m	4.6 ± 0.1 mM	53.04 ± 0.12	53.34 ± 0.02
ζ_{pS58}	7.6 ± 0.8 mM	50.70 ± 0.11	50.88 ± 0.02



How to use CF BIC?

- CF BIC is **opened to everyone**
- Majority of users from CEITEC and Masaryk University

Modes of access

- Service mode
- User mode

Pricing

- Full prices – based on cost matrix
- **Reduced fee** – national/international projects
- Collaboration – specific cases

- Compliance with **CF BIC rules** required
- **Acknowledgement** obligatory



Workshops in 2025

- Methods for Characterization of **Biomolecular Interactions**

- Lectures on various biophysical techniques
- Available to students as subject S2004/S2005

27 – 31 Jan 2025

- **Bio-SAXS** practical course

- Annual event co-organized with CMS at Biocev
- Lectures and practicals on SAXS applications

Sep 2025

- Potential workshops

- inQuiQ (Delta LS) – instrument demo
- Mass photometry
- ...

To be announced...

Check bic.ceitec.cz and **CEITEC newsletters**
for more information



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Institute of Technology

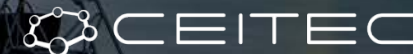
Thank you for your attention!

core.facility@ceitec.muni.cz

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CEITEC MUNI Core Facility Josef Dadok National NMR Centre

Pavel Kadeřávek, CF Day Life Sciences, 16 October 2024

Content

- **CF overview**
 - Who is Josef Dadok
 - What is NMR good for
 - What you need to use our services
- **Equipment**
- **Users and applications**
- **Access, Training, Data policy**
- **People**
- **Financial support and acknowledgments**
- **Selected publications**

Josef Dadok

- * 28. 2. 1926
- Pioneer of nuclear magnetic resonance spectroscopy in Czechoslovakia
- Important figure in the NMR instrumentation and methodology worldwide.
- Developed instruments for high resolution NMR spectroscopy later produced by Tesla Brno (3rd country in the world, after USA and Japan)
- Since late 1960s lived and worked in USA – Carnegie Mellon Univ., Pittsburgh
- First 600 MHz (14.1 T) magnet suitable for high resolution NMR spectroscopy in 1970s.
- Doctor honoris causa of Masaryk University (2013).



NMR Spectroscopy

Strengths:

- Atomic resolution – detailed information
- Applicable both in solution and solid state
- Good for compound identification, quality control, structure determination
- Can study dynamics & interactions
- Gentle to the sample



Weaknesses:

- Low sensitivity
- Needs lot of sample, measurements long, often needs isotope enrichment
- Data interpretation laborious
- Expensive equipment



What you need to use our CF

Sample:

- Liquid or solid
 - **Quantity**
 - 0.1 to 30 mg for liquids, depending on nucleus and MW
 - dissolved in 600 μ l to 180 μ l, \sim 10 mg for solids
 - **Solubility**
 - water, chloroform, benzene, DMSO, DMF (deuterated)
 - **Stability**
 - at least minutes
 - **Temperature (liquid)**
 - 0 $^{\circ}$ C to 80 $^{\circ}$ C normal, -80 $^{\circ}$ C to 150 $^{\circ}$ C extended
- **Know what are you trying to find out**
 - *Send the publication that inspired you!*
 - Nuclei ^1H , ^{13}C , ^{15}N , ^{31}P , ^{19}F routinely, many others possible
 - Type of spectra
 - 1D, 2D homonuclear, heteronuclear, etc.



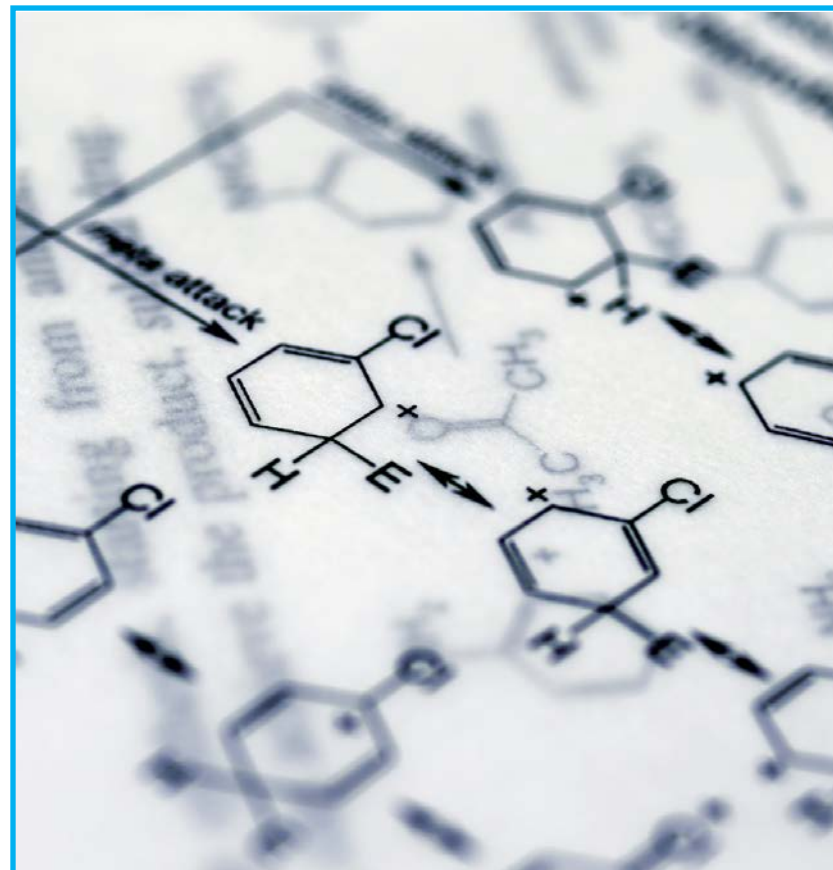
Equipment

- **6 NMR spectrometers**
 - 500 MHz, 600 MHz, two 700 MHz, 850 MHz, 950 MHz
 - 5 cryoprobes, solid-state possible at 500 and 700 MHz
 - Simple X-band EPR spectrometer
- **Extensive upgrades in 2020 - 2022**
 - New electronics (Neo generation)
 - LN2 recycling
 - 4 new cryoprobes, ^{19}F possible everywhere
 - extended temperature range $<-40^{\circ}\text{C}, +150^{\circ}\text{C}>$
 - Diffusion probe 700 MHz
- **No new equipment in 2024**
 - (planned new probe for industry applications and helium liquefier)
- **Future plans**
 - Combined EPR/NMR system for hyperpolarized NMR experiments (with Neugebauer RG, CEITEC BUT)
 - Sample changer for 600MHz
 - Solid-state MAS probe with fast rotation (better resolution)
 - 700MHz TCI probe



Users and applications

- **CEITEC research groups**
 - Biomolecular applications - Structure, dynamics and interactions of proteins and nucleic acids
- **Other MUNI**
 - Faculty of Science, Medicine, Pharmacy
 - Organic and inorganic compounds, perspective pharmaceuticals
- **Outside academic users**
 - Charles University, UTB Zlín, Institute of Physics of Materials CAS, Cancer Research Institute SAS, Institute of Neuroimmunology SAS, Vienna University, JKU Linz, Universidad Politécnica de Santa Rosa Jáuregui (Mexico)
 - Proteins, DNA, metabolites
- **Industry**
 - PIB, Synthon, Ratiochem, Al | ffinity
 - Quality control



Access, Training, Data policy

- **Access: User or service mode**
- User mode – trained users only
- **Training** - Practical NMR Spectroscopy of Biomolecules (C7995)
Non-students/outside users welcome
- Experienced NMR spectroscopist can get certified based on their previous experience/publications.
- **Booking** - CEITEC reservation system
 - <https://booking.ceitec.cz/en/planning-board/>
- **Monitoring system**
 - <https://nmrinfo.ncbr.muni.cz/nmr/monitoring/>
- **Data policy**
 - Users shall work under their own logins
 - Users are owners of their data, no permanent storage in the CF (quotas)
 - Data backed up every night

Financial support

CIISB (Czech, world)

<https://www.ciisb.org/open-access/proposal-submission>

INSTRUCT (EU)

<https://instruct-eric.org/submit-proposal>



People

- **Pavel Kadeřávek**
 - CF head, **teaching and user training**, management of CIISB and Instruct projects, methods development (pulse sequence etc.), **spectra measurement for outside users – biomolecules**.
- **Radovan Fiala**
 - Deputy head, **spectra measurement for outside users – biomolecules**, **teaching and user training**.
- **Jaromír Toušek**
 - **booking system**, NMR monitoring and information system software, **spectra measurement for outside users – liquide + solid state**, NMR calibration and testing, cryogen refills.
- **Otakar Humpa**
 - **spectra measurement for outside users – organic chemistry**, gasses and cryogenic liquids logistics, cryogen refills, communication with Campus Facilities.
- **Kateřina Bouzková**
 - **spectra measurement for outside users – solid-state and organic chemistry**, cryogenic liquids logistics, cryogen refills.
- **Petr Padrta**
 - Maintenance of computers and network, installations and maintenance of NMR software, troubleshooting, **accounts for new users**.



Acknowledgement text – CIISB

- **Preferred version:** *„CIISB, Instruct-CZ Centre of Instruct-ERIC EU consortium, funded by MEYS CR infrastructure project LM2023042, is gratefully acknowledged for the financial support of the measurements at the CF Josef Dadok National NMR Centre.“*
- **Short version:** *„We acknowledge CF Josef Dadok National NMR Centre of CIISB, Instruct-CZ Centre, supported by MEYS CR (LM2023042).“*
- *Co-authorship (creative input, substantial contribution)*

Selected publications

Notable publications acknowledging CF

Protein-nucleic acid interactions

PAPAGEORGIU, Anna C.; POSPÍŠILOVÁ, Michaela; CIBULKA, Jakub; ASHRAF, Raghif; WAUDBY, Christopher A. et al. Recognition and coacervation of G-quadruplexes by a multifunctional disordered region in RECQ4 helicase. Online. Nature Communications. 2023, vol. 14 (1) <https://doi.org/10.1038/s41467-023-42503-z>.

Nucleic acids

LUO, Yu; ŽIVKOVIĆ, Martina Lenarčič; WANG, Jiawei; RYNEŠ, Jan; FOLDYNOVÁ-TRANTÍRKOVÁ, Silvie et al. A sodium/potassium switch for G4-prone G/C-rich sequences. Online. Nucleic Acids Research. 2024, vol 52 (1) 448-461, <https://doi.org/10.1093/nar/gkad1073>.

Plants

JANKOVSKÁ, Dagmar, JURČOVÁ, Nikol, KUBÍNOVÁ, Renata, VÁCLAVÍK, Jiří, ŠVAJDLENKA, Emil, MASCELLANI, Anna, MARŠÍK, Petr, BOUZKOVÁ Kateřina, MALANÍK MilaN, Anticholinesterase Activity of Methanolic Extract of *Amorpha fruticosa* Flowers and Isolation of Rotenoids and Putrescine and Spermidine Derivatives, Plants, 2024 vol. 13 (9), <https://doi.org/10.3390/plants13091181>

Material Science

SKODA, David; ZHU, Ran; HANULIKOVA, Barbora; STYSKALIK, Ales; VYKOUKAL, Vit et al. Propylene Metathesis over Molybdenum Silicate Microspheres with Dispersed Active Sites. Online. ACS Catalysis. 2023, vol 13 (19), 12970-12982, <https://doi.org/10.1021/acscatal.3c02045>.

Small molecules

NOVOTNÝ, Jan, Jan CHYBA, Anna HRUZÍKOVÁ, et al. Flipping hosts in hyperfine fields of paramagnetic guests. Cell Reports Physical Science [online]. 2023, 4(7), doi:10.1016/j.xcrp.2023.101461



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Thank you for your attention! Questions?

Building C04

nmr@ceitec.muni.cz

<https://nmr.ceitec.cz>

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Core Facility Day 2024

Life Sciences

16 OCTOBER, 2024
CEITEC, E35 / 211 + ATRIUM

Curious about what expert services are available to researchers on campus? What instruments can you use in shared mode and under what conditions? Do you want to see everything for yourself?

Register at: muni.cz/go/fba265



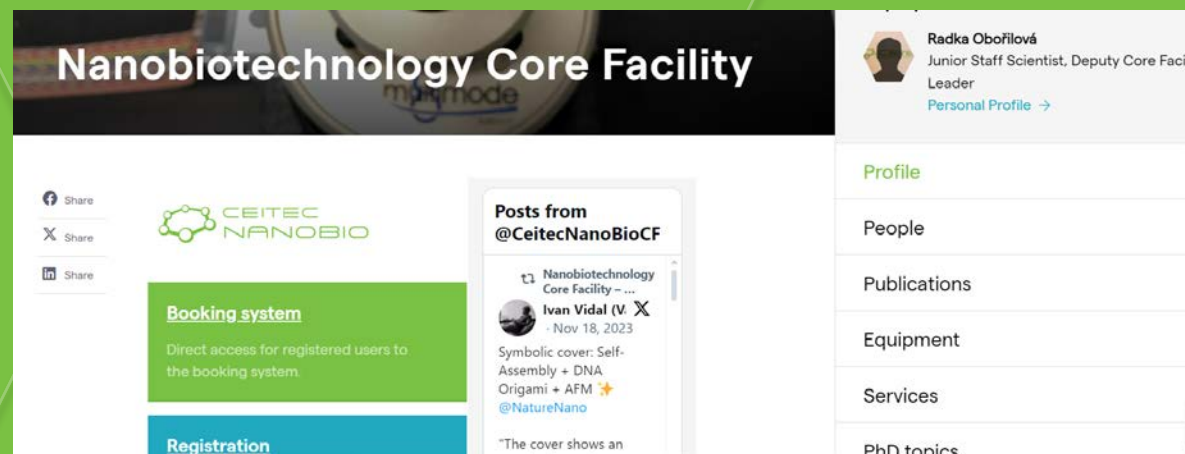


CEITEC MUNI Core Facility NanoBiotechnology

Jan Příbyl CF Day Life Sciences, 16 October 2024

Web page: ceitec.eu/nanobio

- People
- Equipment
- Services
- Access
- Acknowledgement info



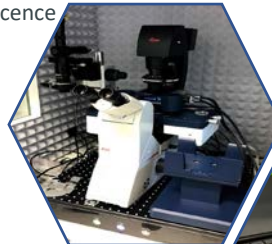
Follow us on X: [@CeitecNanoBioCF](https://twitter.com/CeitecNanoBioCF)



Core Facility Nanobiotechnology

Imaging, mechanical mapping, Raman microscopy

Atomic Force Microscopy of biosamples
Combined with fluorescence microscopy



Atomic Force Microscopy of biosamples
High-resolution imaging

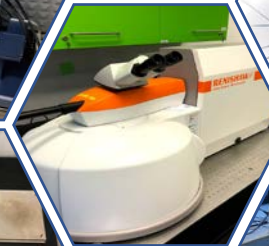


Multielectrode Array (MEA)
Cellular electrophysiology

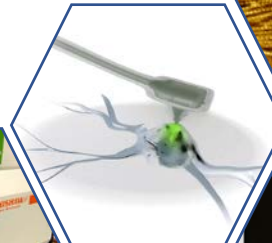
NanoIndenter
Indentation of soft samples



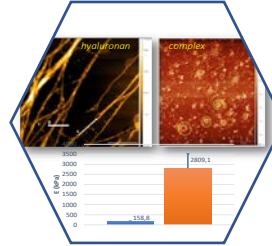
Raman microscopy
Chemical mapping of surface



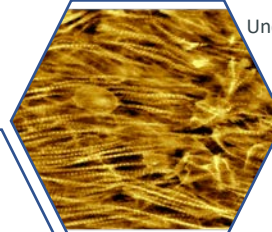
FluidFM
AFM based microfluidics



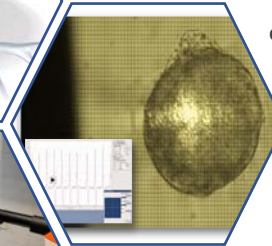
Structure and biomechanics of biomolecules
(AFM imaging and nano-indentation)



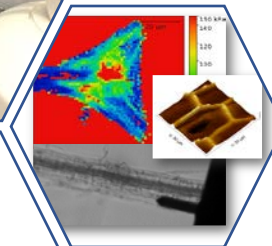
Structure of biomolecules
Under native conditions



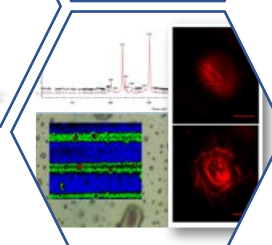
Biomechanics of contractile cells
Toxicology and cell development



Stiffness mapping of cells and tissues
Nanoindentation under semi-physiology

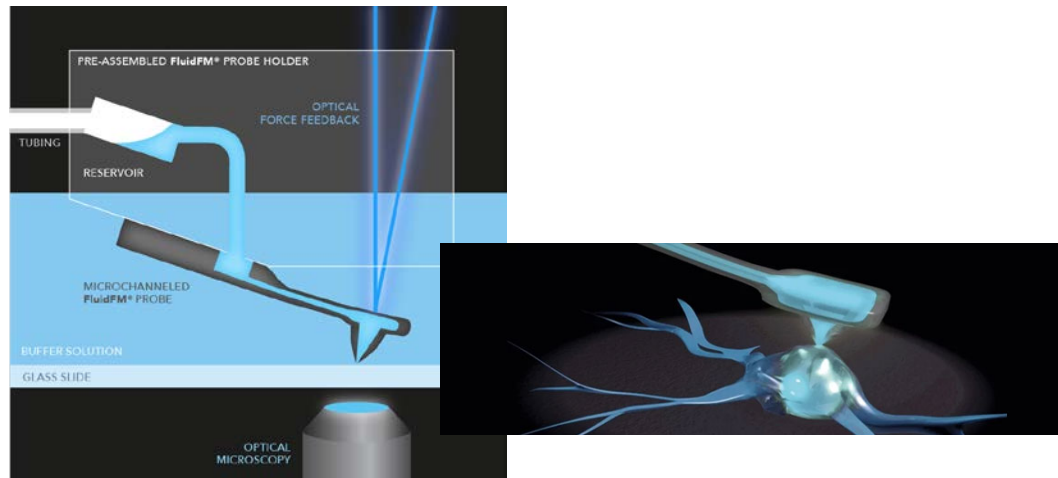
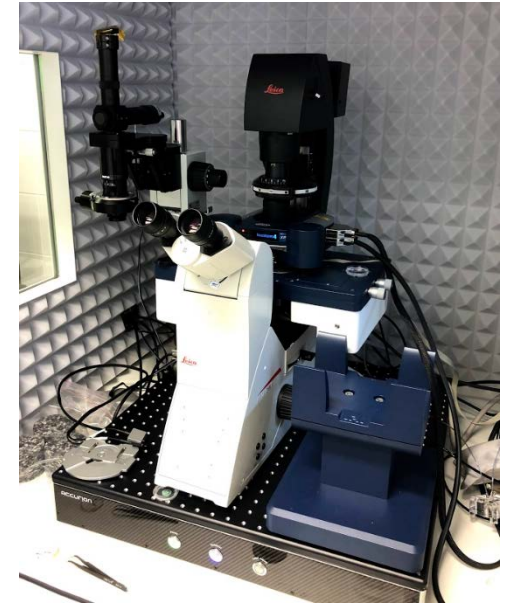
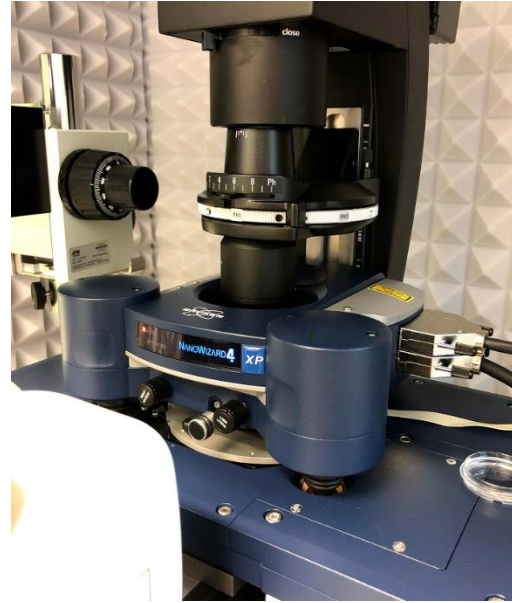
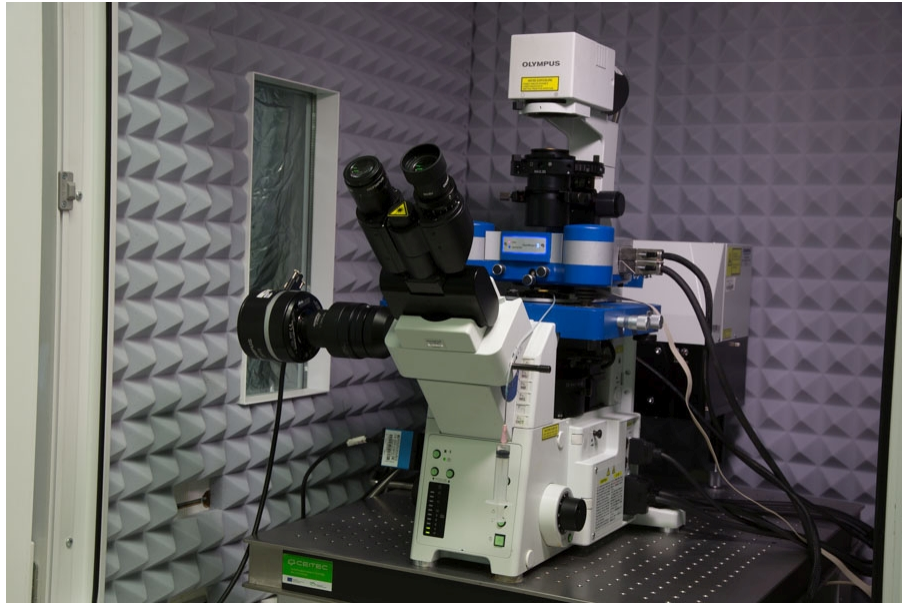


Fluorescence and Raman microscopy
Structural and chemical characterization

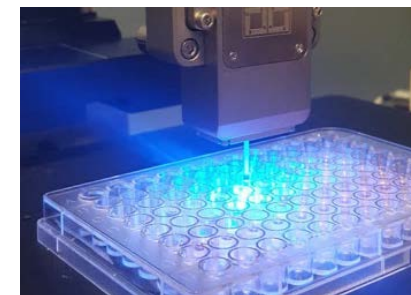


JPK NanoWizard 3 and 4 with extended scanning range

BioAFM – living cells and tissues

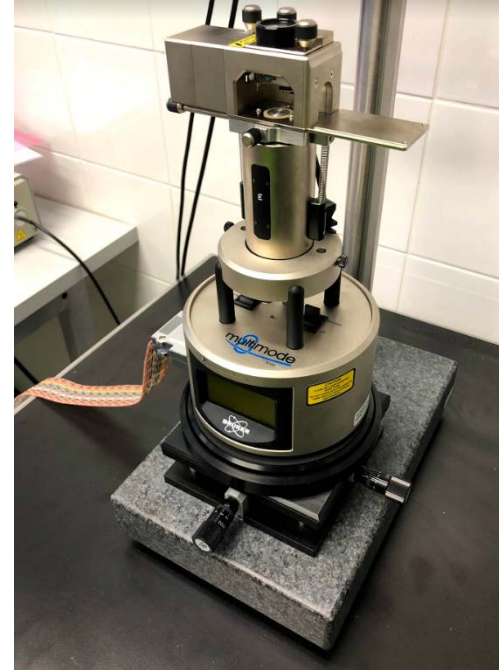
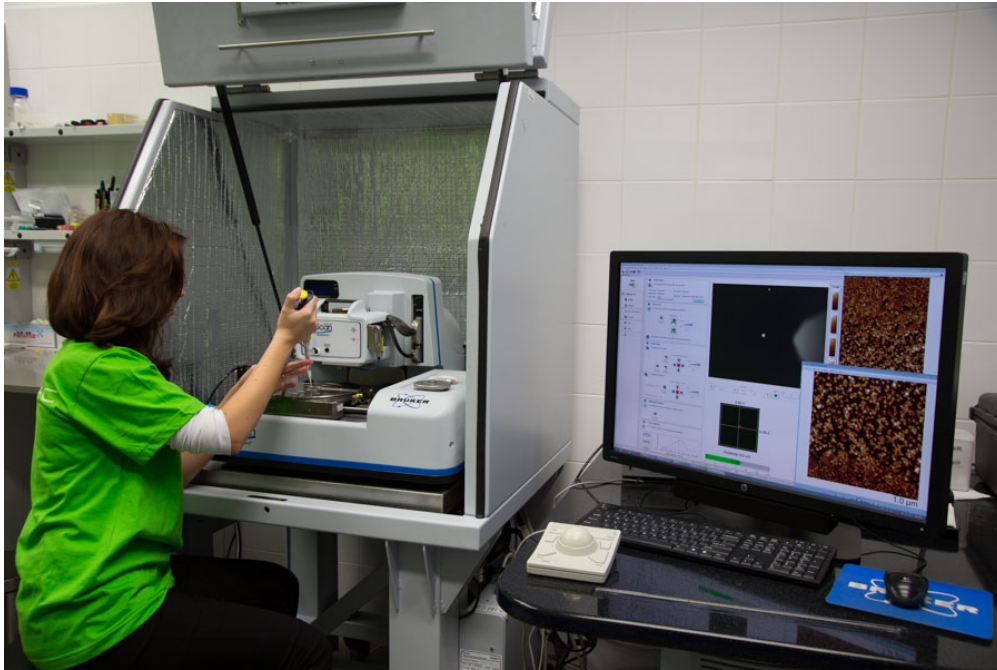


+ CytoSurge FluidFM module



+ BioSoft NanoIndenter 

BioAFM – molecules, nanoobjects, molecular complexes



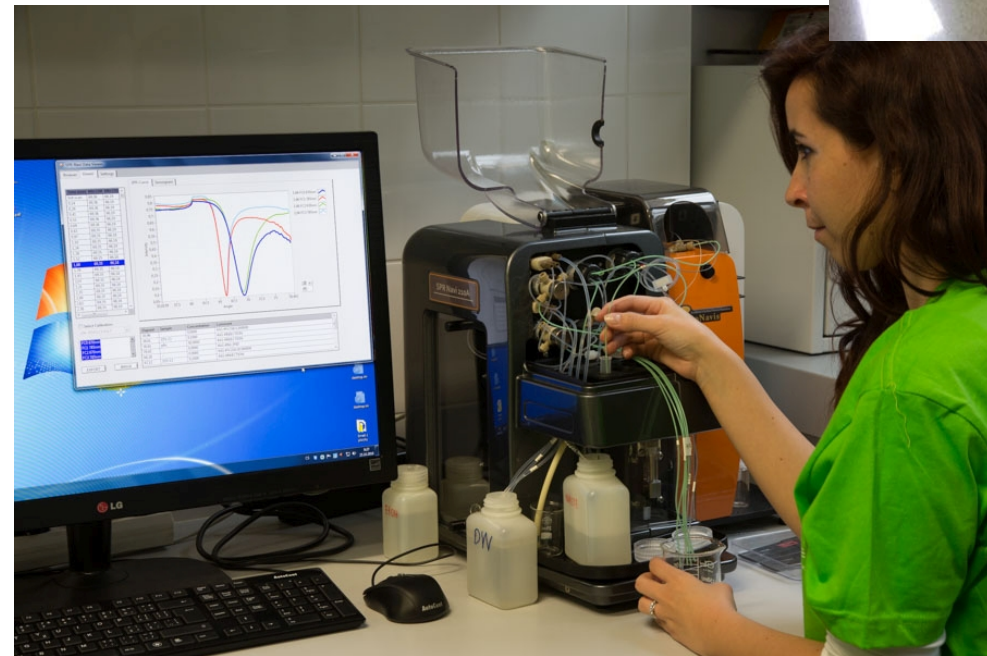
**Bruker Dimension Icon FastScan and MultiMode 8HR
NTMDT Ntgra Vita**

Raman microscopy, SPR affinity biosensor, Upconverting particles UCNP reader

Renishaw InVia Raman microscope

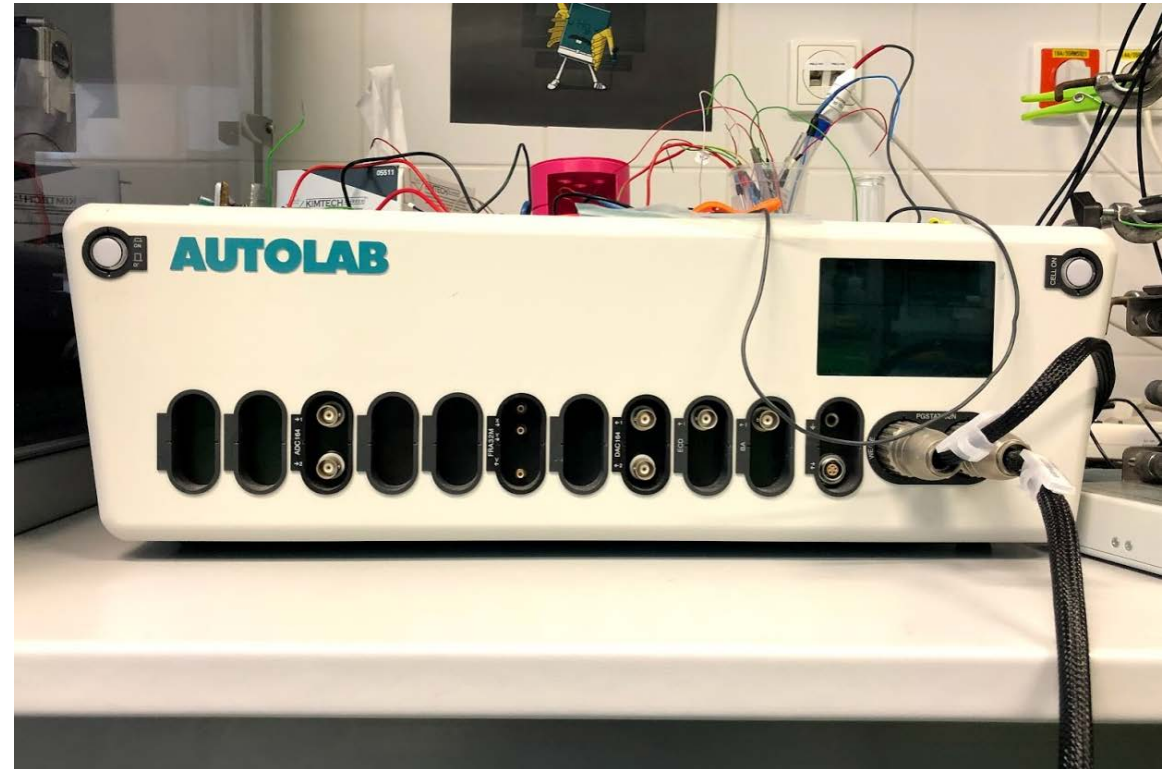
Bionavis SPR biosensor device

Labrox UPCON reader



Bioelectrochemistry, Cellular electrophysiology

**Autolab Modular potentiostat
MultiChannel MEA2100Lite**



- 1. Cells – mechanical properties**
- 2. Cells - imaging**
- 3. Biomolecules - imaging**
- 4. Nano-objects imaging**
- 5. Raman-AFM combined microscopy**
- 6. Raman microscopy**
- 7. Electrochemical measurements**
- 8. Nanodeposition system**
- 9. SPR biosensor**
- 10. Scanning of upconversion luminescence**
- 11. Multielectrode array recording of cellular potential**

What's new and what's planned?

Upgrades and upgrade plans

OP JAK – infrastructure investments 2023-26

Název infrastruktury	Plánované investiční výdaje 2023–2026 (tis. Kč) ¹	Maximální výše způsobilých výdajů výzvy Výzkumné infrastruktury I OP JAK (tis. Kč) ²
Czech-Biolmaging	1 233 722	493 489
COMPASS	1 050 000	420 000
CzechNanoLab	904 000	361 600
CIISB	720 153	288 061
CZ-OPENSREEN	577 400	188 700
BBMRI-CZ	369 043	184 522
CCP	357 000	178 500
EATRIS-CZ	281 162	140 581
RECETOX RI	248 600	124 300
METROFOOD-CZ	230 600	115 300
MGML	219 400	109 700
NanoEnviCz	212 720	106 360
CZECRIN	209 682	104 841
ELIXIR-CZ	188 500	94 250
CICRR	159 000	79 500
NCMG	135 300	67 650

40% of the initial plan

CF Nanobio: 16 000 tKč

-15% overhead costs

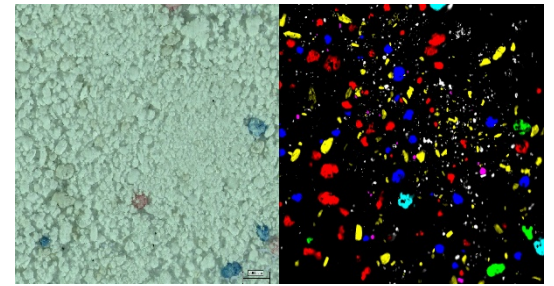
-29% possible reduction

= 9 000 tKč ~ 380 tEUR

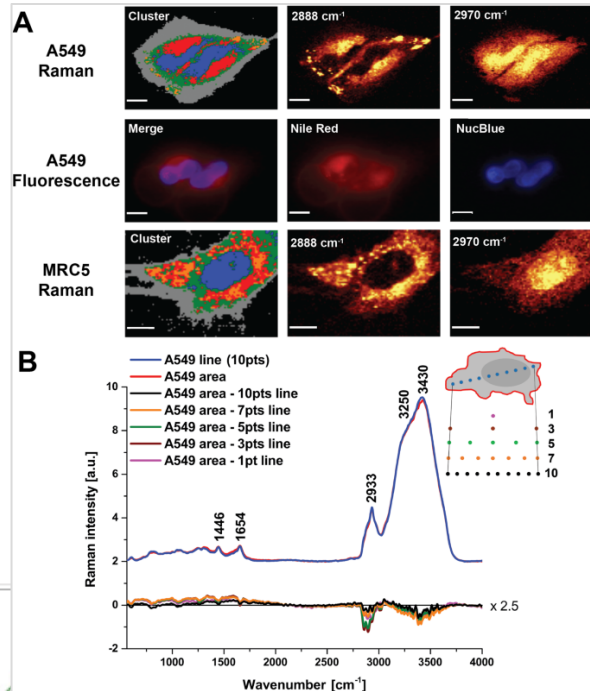
29% over total budget

1. Raman microscope upgrade

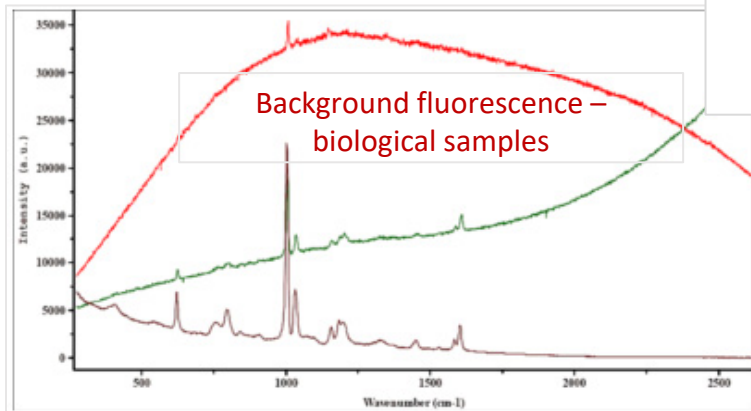
Renishaw InVia confocal Raman microscope



White light and Raman images of powder



Surmacki, J.M., et al. *Sci Rep* 8, 12604 (2018).



<https://www.azom.com/article.aspx?ArticleID=2950>

Raman part - upgrade

+ laser 785 nm, 100 mW (fluorescence decrease)

+ 1 x 785 nm polarization

+ 1 x 633 nm polarization

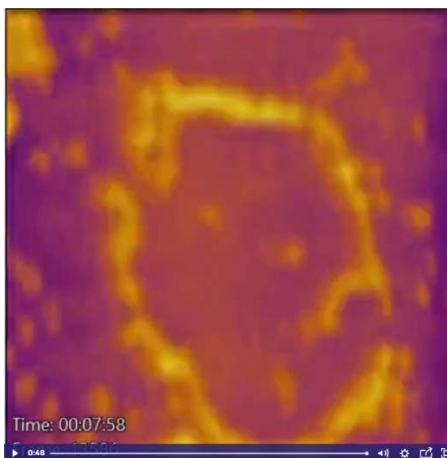
+ Software upgrade to version **WiRE 5.6**

(incl. **particle analysis** and spectral database modules – **microplastics**)

Full integration with AFM

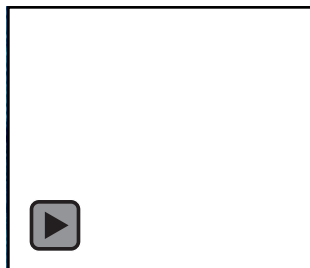
- AFM correlative software
- AFM microscope antivibration solution

2. High-Speed (Video-Rate) AFM

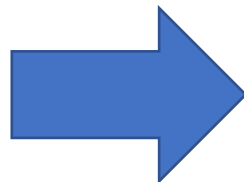


Size: **425 nm**, line scan rate of **1250 lines/second**
160×32 pixels, (**28 fps**). The playback rate 10×
Source: <https://afm.oxinst.com/Video-Rate-AFM-Movies?wvideo=abneb64e3y>

Asylum Cypher VRS1250
Video-Rate High-Speed AFM



Prices from 500 tEUR



Bruker MultiMode 8HR upgrade

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Optics and photonics Personalized health Robotics and autonomous systems Soft matter and flexible structures Laboratories LBNI Open Hardware

Research

Open Hardware

AFM head for small cantilevers, with photothermal drive

Equipment

Publications

Teaching

Join LBNI

Funding

People

Contact

Open Hardware

We believe that the concept of open science should go beyond publishing papers in open access journals and sharing source code.

AFM head for small cantilevers, with photothermal drive

SPM Controller/Software

Find out about our custom SPM controller and its software

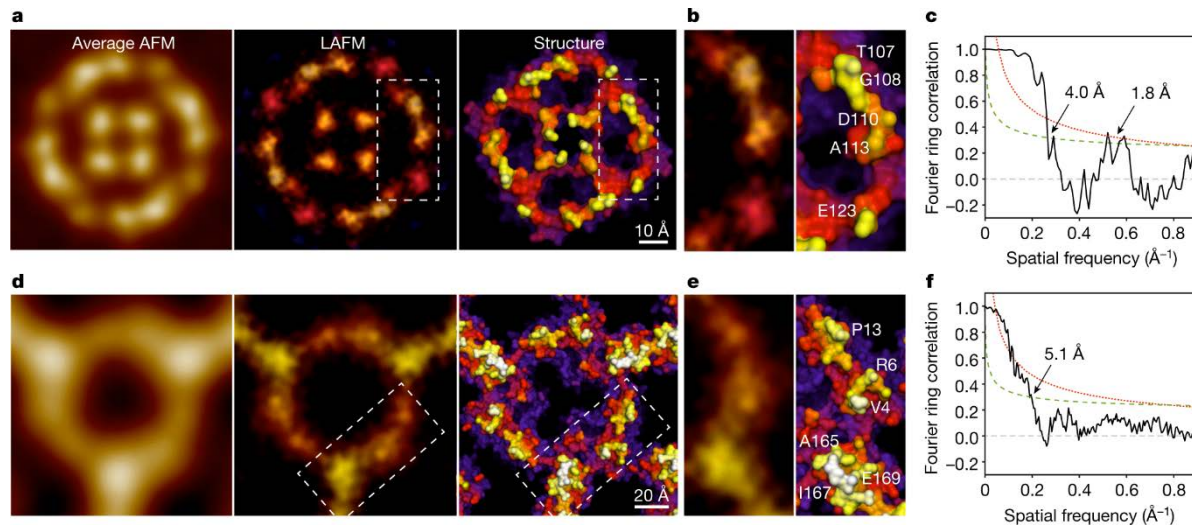
<https://www.epfl.ch/labs/lbni/openhardware/>

Price 65 tEUR

Advanced data processing

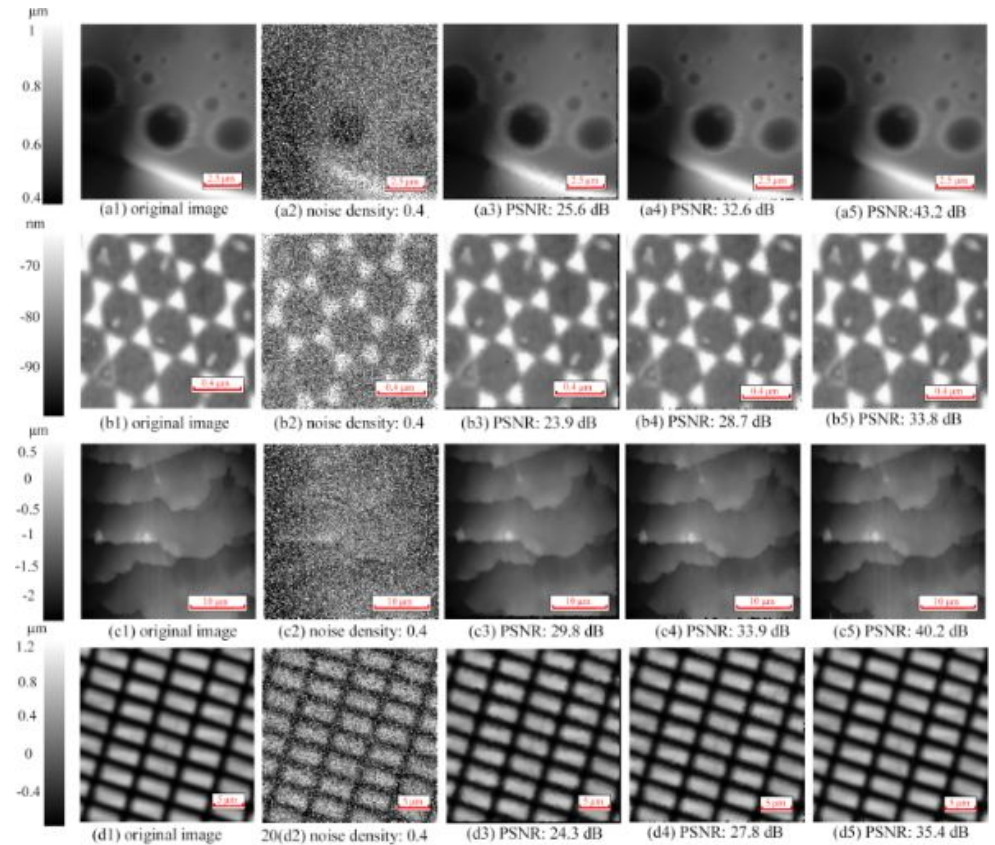
Deconvolution image processing

Deconvolution filters – 50-100 images
input (HS-AFM):



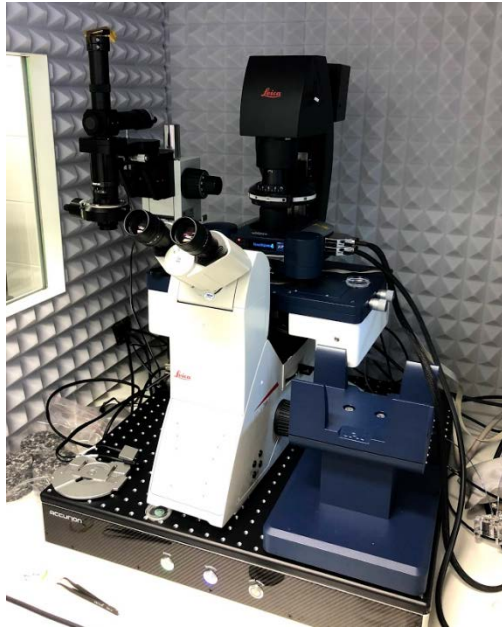
Heath, G.R., Kots, E., Robertson, J.L. *et al. Nature* **594**, 385–390 (2021).

Denoising with AI:

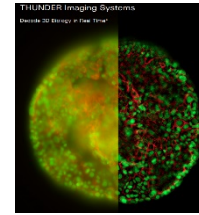


Beilstein J. Nanotechnol. **2019**, *10*, 2346–2356.

3. Leica Microscope Upgrade



Leica DMi8
(combined with JPK NW4XP)



Leica THUNDER Imaging Systems

Easily tackle biologically relevant 3D models with THUNDER Imagers.

They bring you high-speed, multicolor imaging of thin and thick samples with increased temporal resolution in the first attempt itself.

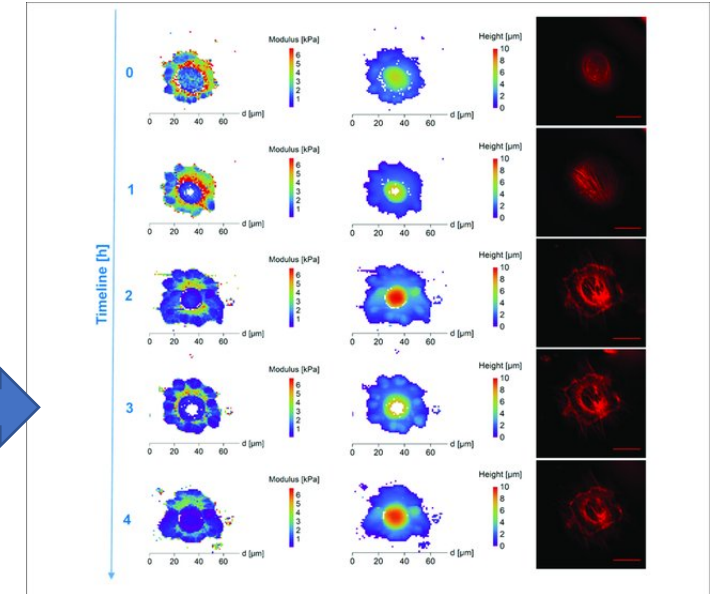
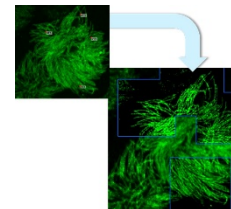
+



Telight LiveCodim

From conventional to super-resolution microscopy

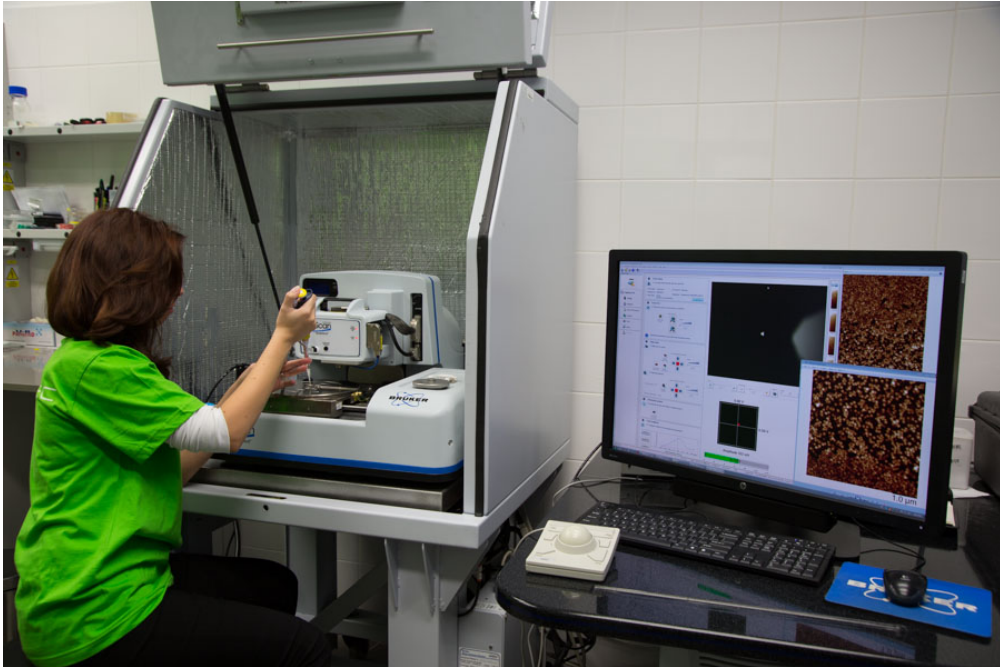
LiveCodim is a universal, super-resolution imaging platform, designed to interface with any standard fluorescence microscope. It is the solution for live imaging with high resolution and low phototoxicity.



AFM – confocal correlation microscopy

Price 120 tEUR

4. Bruker Dimension FastScan Upgrade



In everyday operation from 2014



AFM controller upgrade:



Price 80 tEUR



OP VVV CZ.02.1.01/0.0/0.0/18_046/0015974

Thank you for your attention!



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CEITEC MUNI Core Facility

CEMCOF - Cryo-electron microscopy and tomography core facility

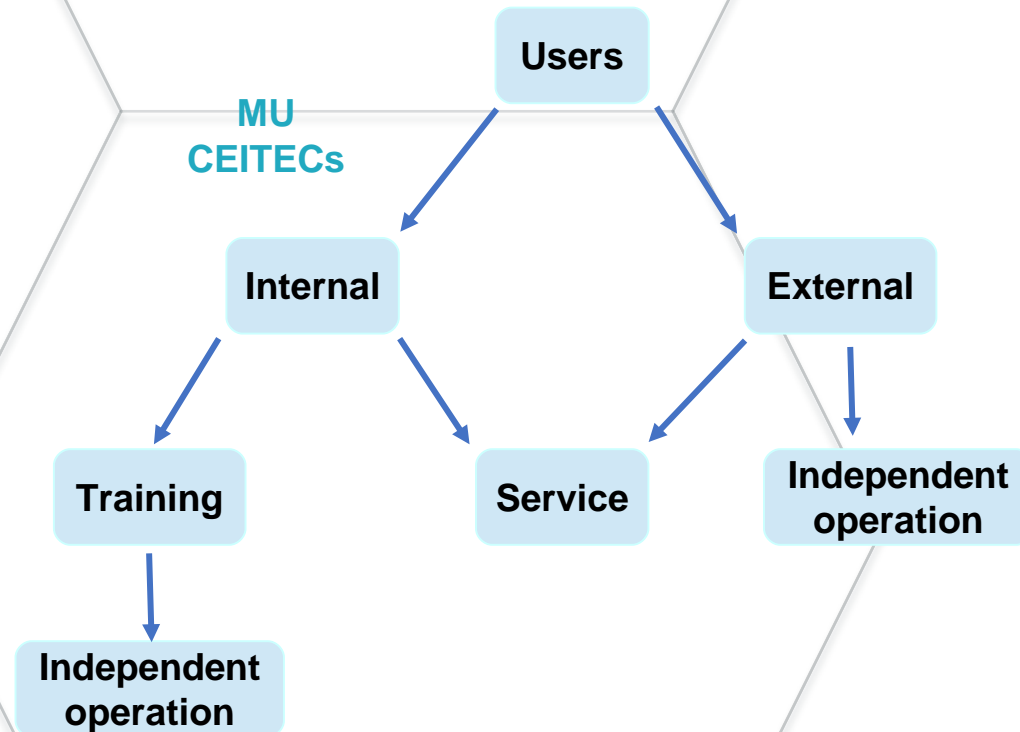
Jiri Novacek, CF Day Life Sciences, 16 October 2024

Users & services

- **Services:**

- TEM/SEM imaging
- Sample vitrification
- Resin embedding
- FIB-SEM tomography
- Initial structural screening
- Initial cryo-EM screening
- Analytical techniques (EDS)
- Cryo-FIB lamella preparation
- SPA data collection
- Cryo-ET data collection
- Electron diffraction tomography
- (cryo-)volume EM
- Data analysis

User mode or service mode available on all instruments



Users & services

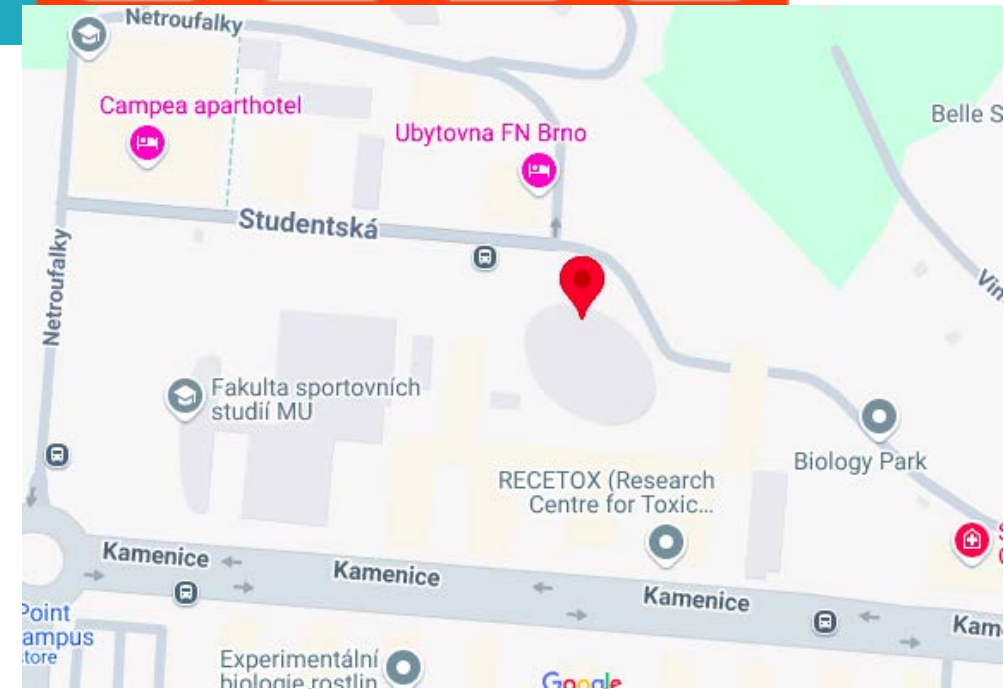
- **New users:**

- select access route
- Fill in project/application form
- Arrange service via email
- Get trained for corresponding instrument

- **Active users:**

- remember to renew your project application – email - single mouse click
- Instruct – one Visit (access) limited to 2 days of microscope time
- ask CF staff for help anytime needed
- report issues

<https://cryo.ceitec.cz>



New instrumentation & services

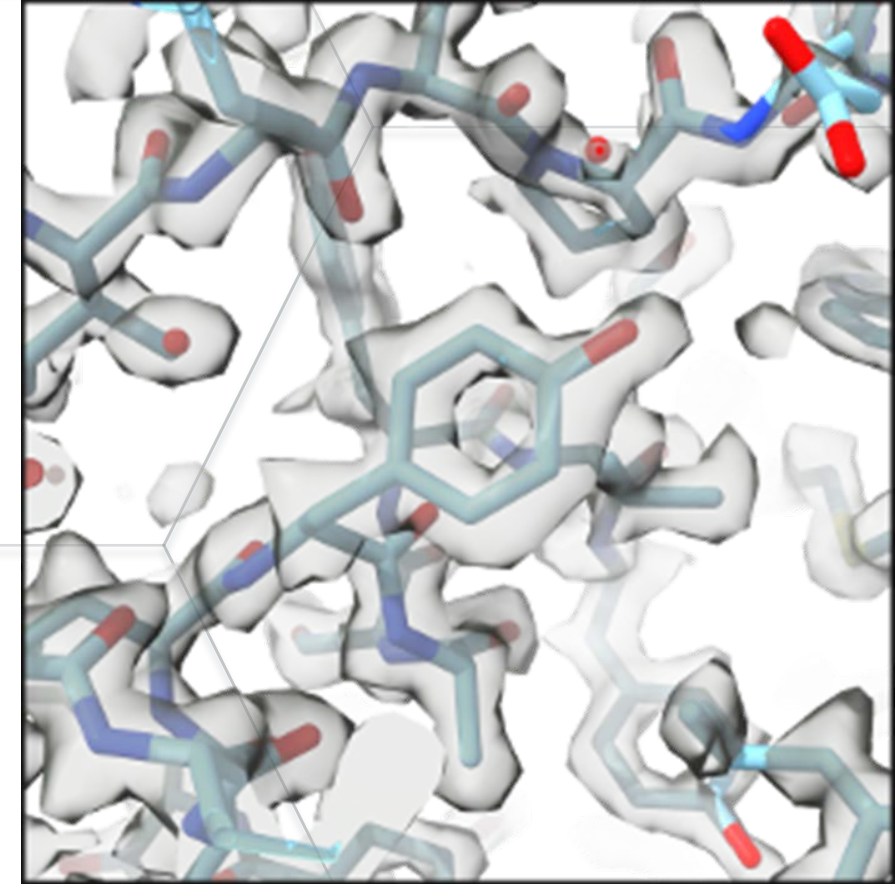
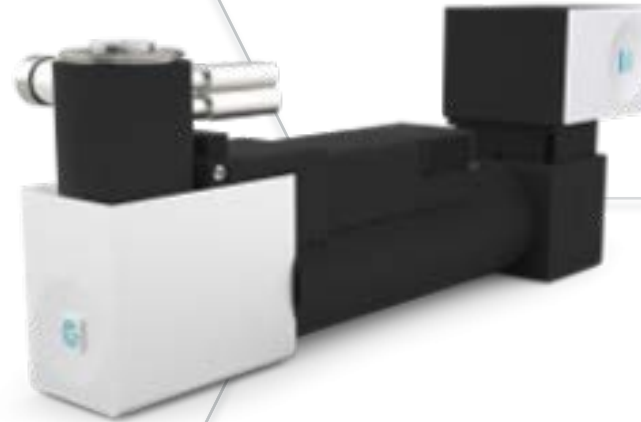
- **Talos Arctica upgrade – Selectris & Falcon4i**

- Community:

- Structural Biology

- Features:

- high stability
- simple and robust operation
- second high-end cryo-TEM (together with Titan Krios)
- SPA
 - throughput – 600-900 movies/hour
 - quality – benchmark data on apoferritin $< 1.8\text{\AA}$
- cryo-ET
 - tomography on cellular lamellae



New instrumentation & services

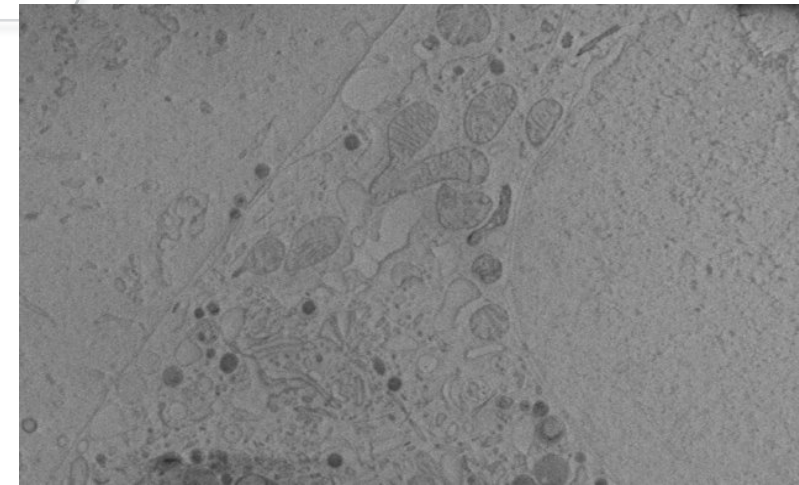
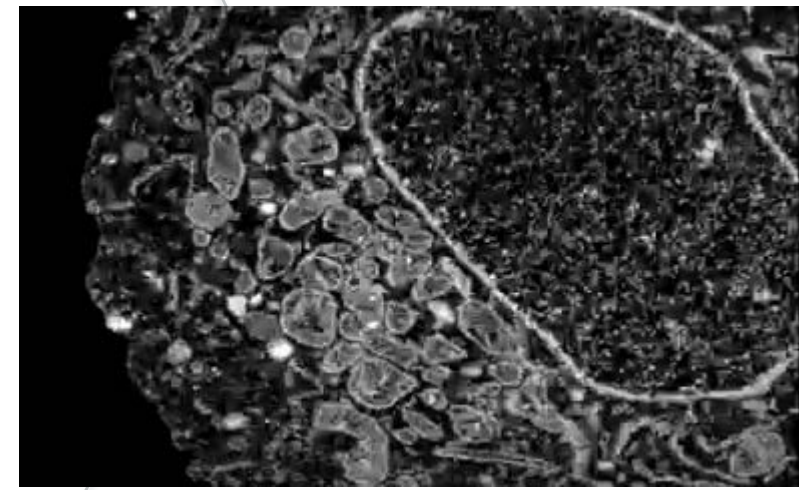
- **pFIB/SEM – Helios Hydra V**

- Community:

- Cellular & Structural Biology

- Features:

- high-resolution SEM imaging (immersion)
- cryo-EM & RT applications
 - volume EM of resin samples
 - cryo-volume EM – HPF specimen
- lamella preparation for cryo-ET
- correlative volume EM – internal development of on-chamber confocal microscope – Pavel Krepelka
- development of new techniques on Versa – AFM&SEM



New instrumentation & services

- **Blot free vitrification device – Chameleon**

- Community:

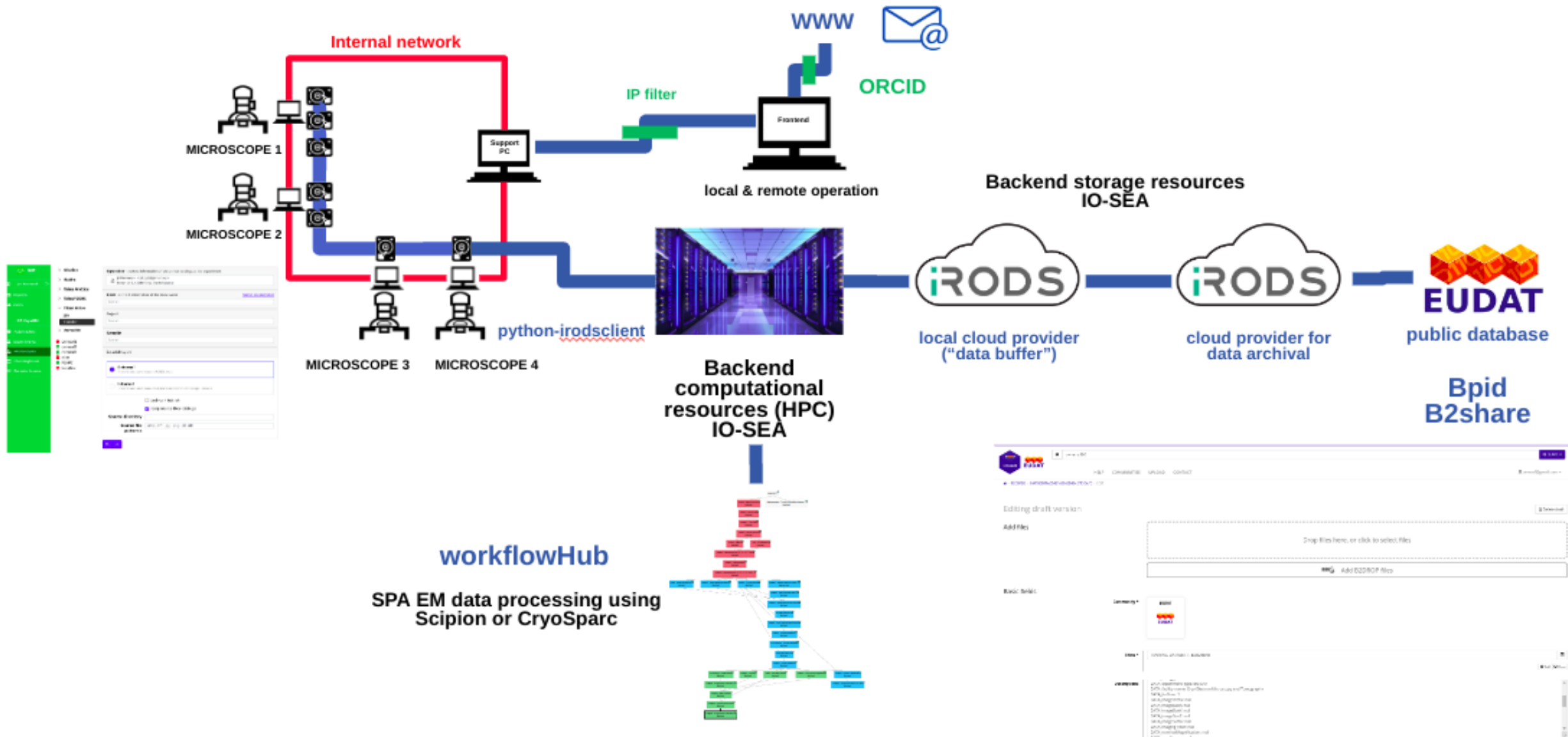
- Structural Biology

- Features:

- available from December 2024
- low sample volume (x higher sample concentration)
- high-level of automation – minimal user interaction (grid handling)
- Increased reproducibility and repeatability of sample preparation by freezing sample preparation
- primarily for SPA



Data management



WorkflowHub interface showing a workflow diagram and a code editor with a terminal output window.

Data management

- web-browser based operation
- accessible directly from the instrument/microscope
- secure access from outside the microscope network:
 - Google
 - eduID
 - ORCID
- instrument specific setup
- implementation of different data analysis workflows
 - simple data transfer (e.g. cryo-EM screening)
 - single particle analysis
 - cryo-ET
- data-model with four different components:
 - the laboratory (center)
 - the user (data owner)
 - the sample
 - the data
- based on ISPyB data model
- real-time job status
- automated user notification (email)
- local database of the projects

The sidebar menu for CEMCOF SIP includes the following items: CEMCOF SIP (with a gear icon), Jiri Nováček (with a user icon and email), Users, CF CryoEM, Autoloaders, Dewars, Experiments, Microscopes (highlighted in dark green), Planningboard, and Remote Access.

<https://aperture.ceitec.muni.cz>

The instrument selection sidebar lists the following instruments: Glacios (yellow), Hydra (light green), Talos Arctica (blue), TalosF200C (purple), Titan Krios (green), Transfer SPA (black), and Versa3D (orange). Below these are several microscopes: ARC8-SPC, cemcof, emcf21, emcf22, emcf23, and karolina.

The experiment configuration form includes the following sections: Operator (contact information of the person setting up the experiment, with a dropdown menu showing 'Jiří Nováček <jiri.novacek@ceitec.muni.cz>'), User (contact information of the data owner, with a dropdown menu showing 'Same as operator'), Project (text input field), Sample (text input field), Data Lifecycle (radio buttons for External, Internal, and Company), Source directory (text input field), and a 'Run job' button with a checked checkbox for 'Send user link to this experiment'.

To prevent cluttering microscope drives, the selected source directory will be automatically purged after 1 week

Data management

- every experiment has a unique experiment card
 - shared with data owner via email
 - information about experiment (including notes)
 - data acquisition report (quality control)
 - single site for the interaction with data status
 - notification by email before data expiration or publication
- for users: read carefully the data management policy a requested status for particular dataset
- for PIs: each dataset will be assigned with DOI upon publication (after embargo period or upon request) - can be used for raw data publication (currently through EUDAT)
- Future development – implementation of deposition initiation to method-specific database (EMPIAR)

experiment card

241013_IR - Sample test 1

Center	CF CryoEM
Operator	
User	
Experiment started	10/14/2024 7:37:15 AM
Instrument	TitanKrios
Experiment technique	EM-SPA
Sample	Sample test 1
Sample keywords	testovaci; test

Data status: Draft creation requested

[Do not archive and publish this dataset](#)

Embargo ends: 14.10.2027 (in 2 years, 11 months)

Since this dataset has been marked to be archived, it is expected to be assigned public identifier (DOI) and made publicly available either automatically after embargo period or earlier on your decision.

[Request publication now](#)

Data access

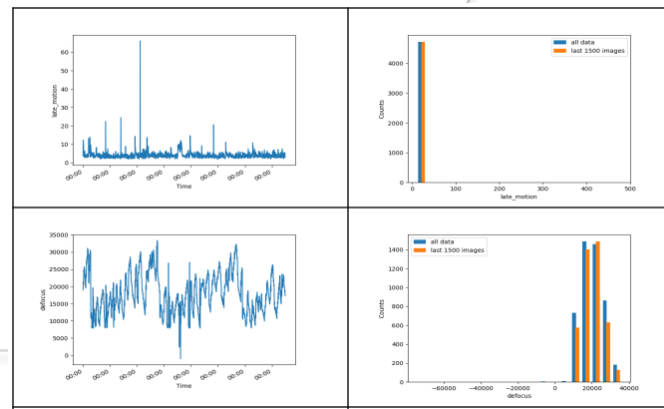
The dataset has been stored at the following location, and you can access it provided that you were given credentials (username/password/ssh key) by the facility:
storage-brno14-ceitec.metacentrum.cz:/gpfs/vol1/export/nfs4/shared/cemcof/internal/DATA_24/241013_IR

On Windows , you can use for example [WinSCP](#) program to access and copy the data.

On Linux  / **macOS** , you can use for example the rsync utility:
`rsync -av --progress [username]@storage-brno14-ceitec.metacentrum.cz .`

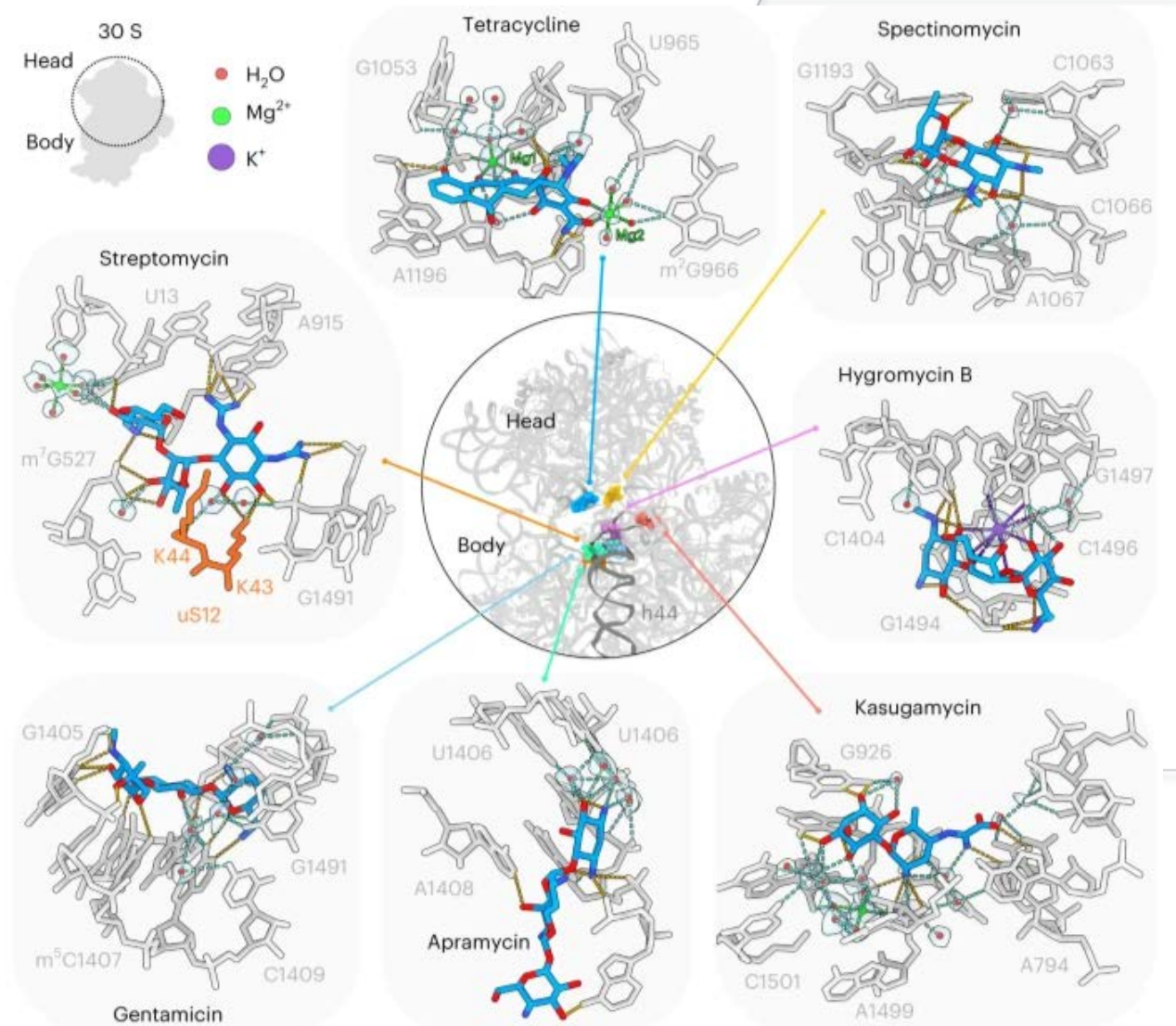
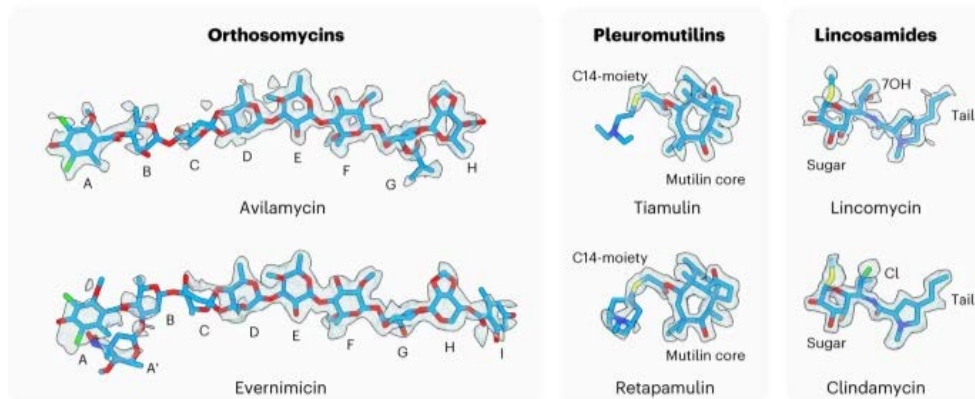
Single particle analysis workflow using cryoSPARC processing engine

Diameter: 100 Å
Defocus max: 35000 Å
Defocus min: 10000 Å
Voltage: 300 kV
Spherical aberration: 2.7 mm
Frame Rate: 1.5 e/s
Pixel Size: 0.3113 Å/pix



User projects/results

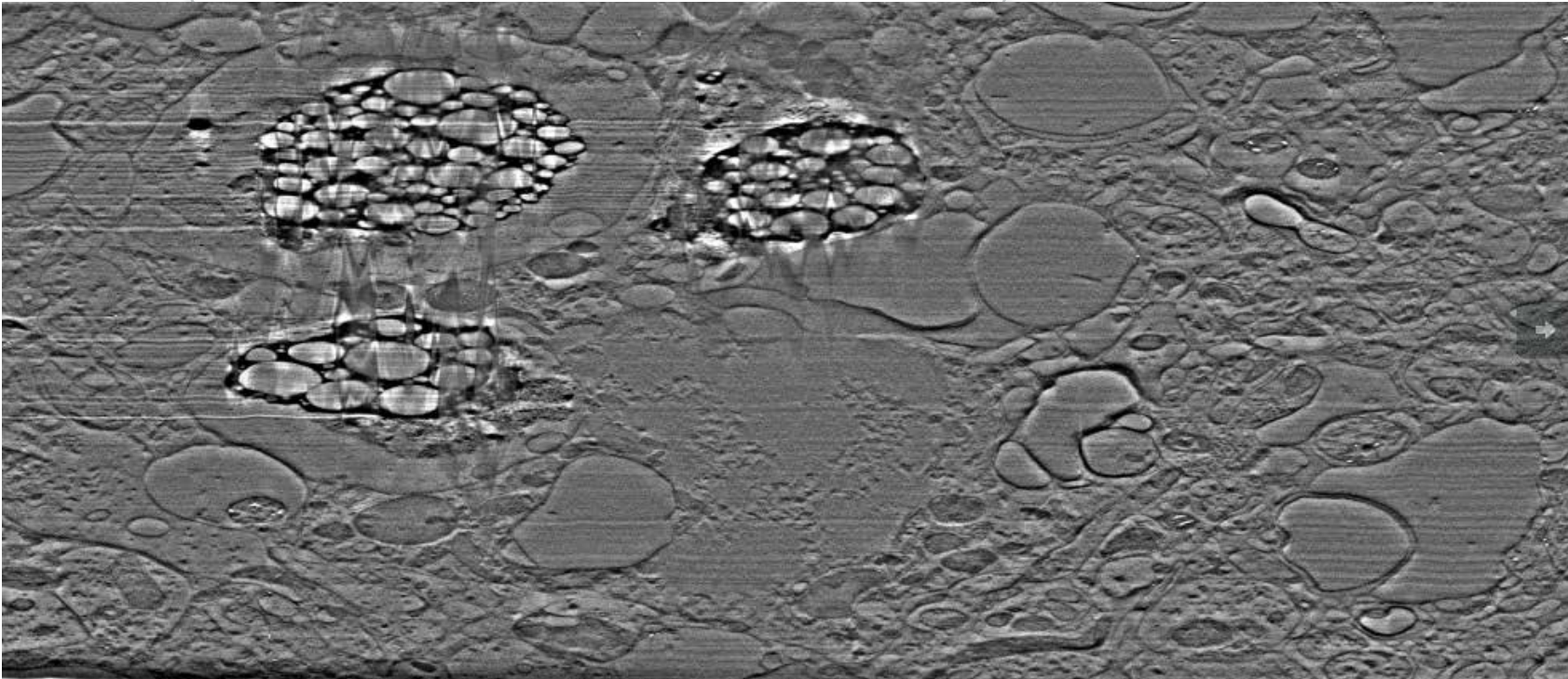
- Daniel Wilson group (University of Hamburg)
- sub-2Å resolution structures of 17 different antibiotics bound to bacterial ribosome
- antibiotic-RNA interaction network
- conservation of binding mode for antibiotics with the same scaffold
- visualisation of water molecules in the binding site



Patternoga et. al (2023), NSMB, doi.org/10.1038/s41594-023-01047-y

User projects/results

- Hana Nedožralova (Lukas Zidek RG, CEITEC)
- cryo-volume EM of Alzheimer patient's brain
- no heavy metal contrasting -> near-native state (high-pressure frozen)
- volumetric analysis of selected brain tissue regions



Akcnowledgements





ceitec_brno



CEITEC_Brno



CEITEC



CEITEC -
Central European
Institute of Technology

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core.facility@ceitec.muni.cz

ceitec.eu/core-facilities/

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CEITEC MUNI Core Facility Cellular Imaging Core Facility CELLIM

Milan Esner, CF Day Life Sciences, 16 October 2024



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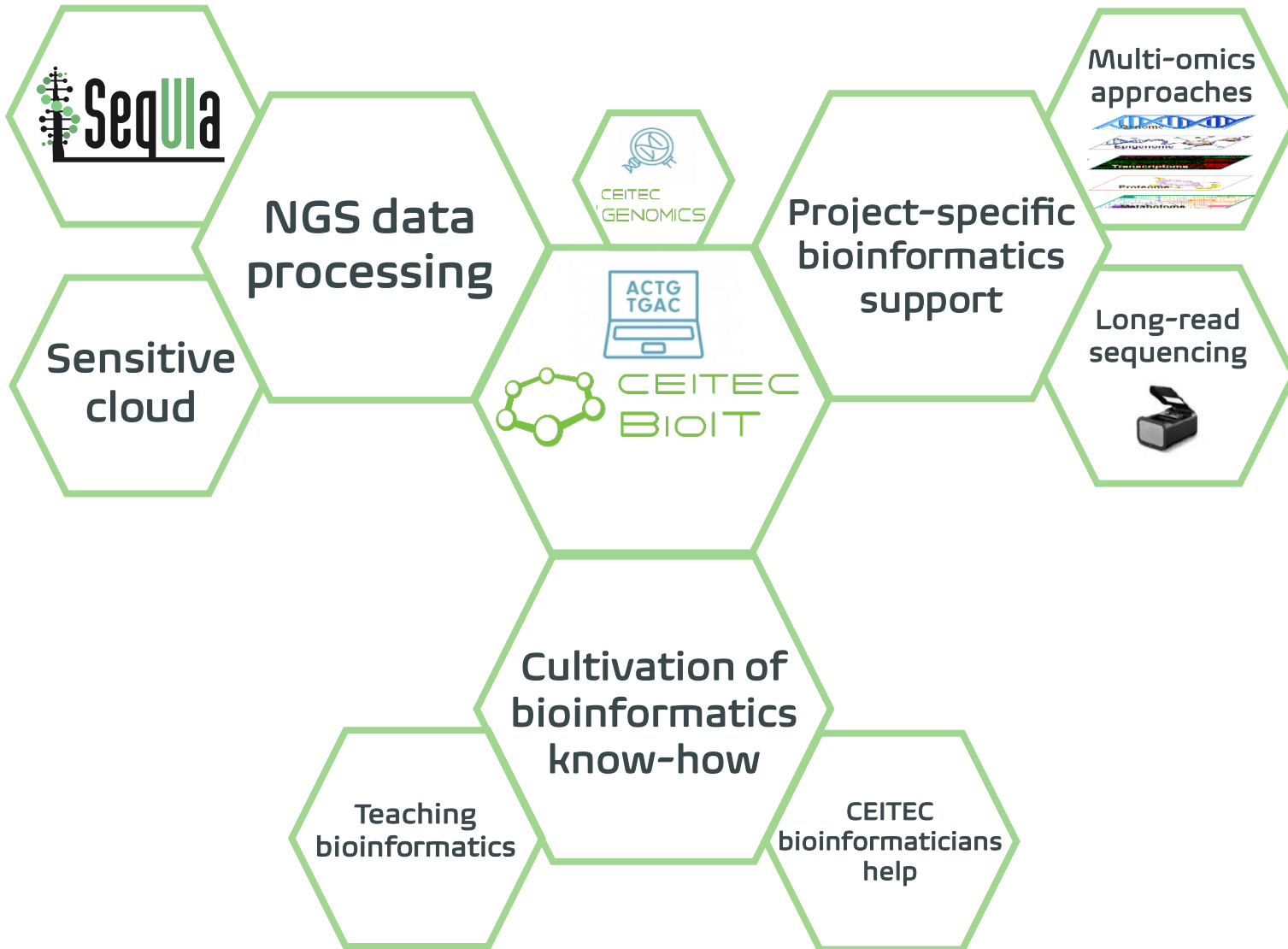
Register at: muni.cz/go/fba265

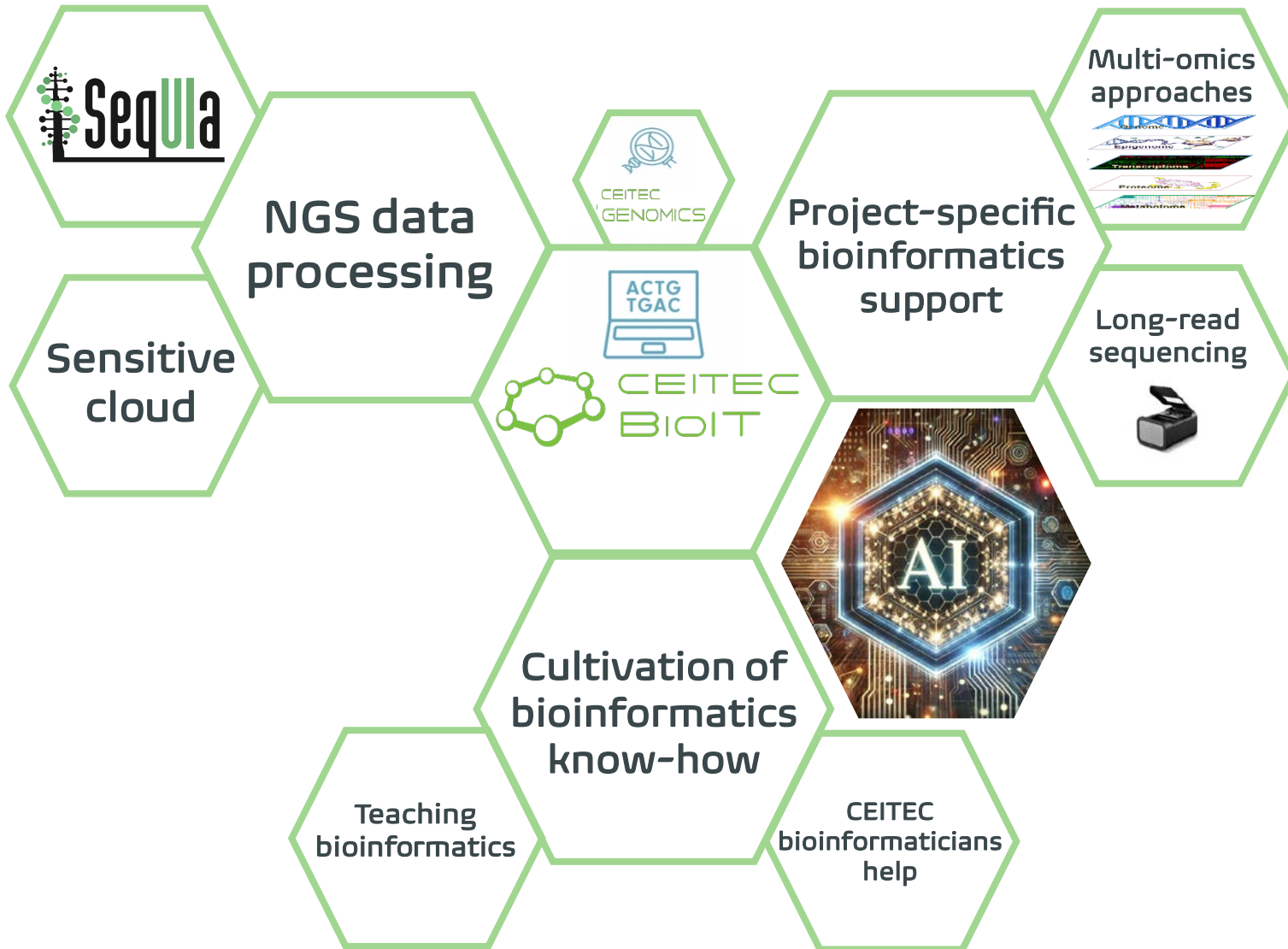


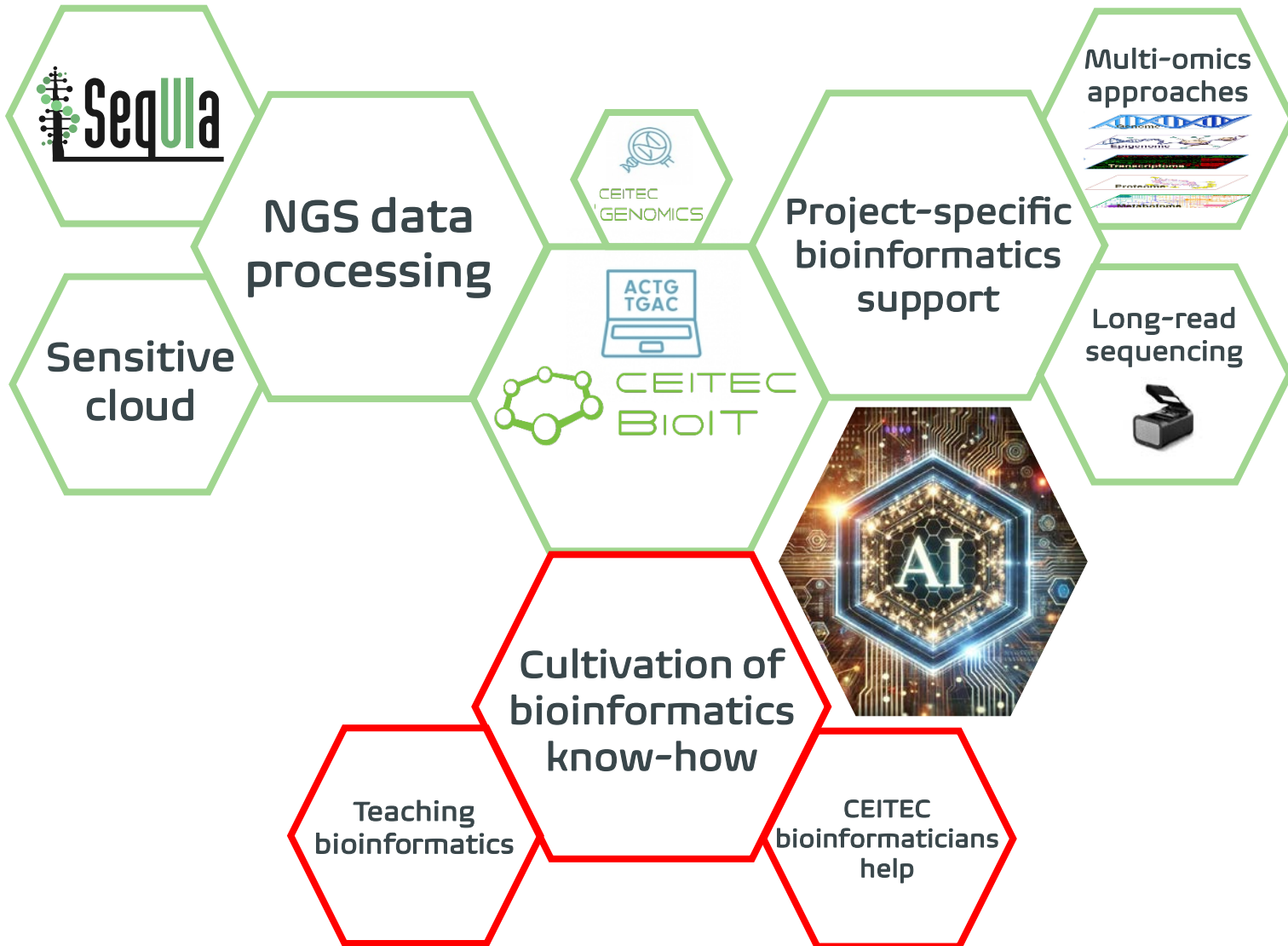


CEITEC MUNI Core Facility Bioinformatics - BioIT

Vojtěch Bystrý, CF Day Life Sciences, 16 October 2024

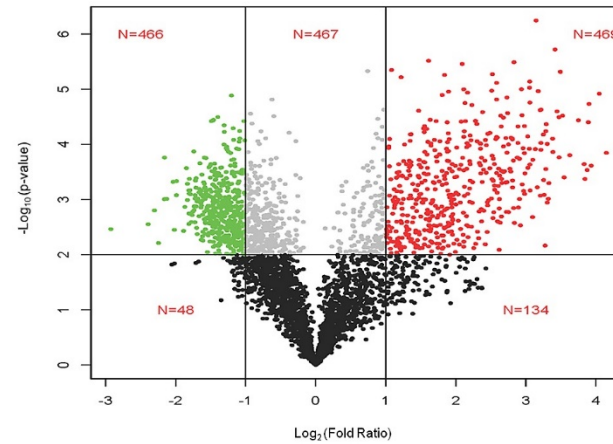








Genes	LogFC	FDR	Genes	LogFC	FDR
RNASE2	-4.2668	1.25E-24	LMO2	-2.02467	1.26E-04
CLC	-4.94929	1.05E-13	CD24	-2.24512	1.65E-04
PRG3	-3.90837	2.93E-12	MRC1	-2.06384	2.36E-04
RNASE3	-4.31871	5.08E-12	CRISP3	-2.73151	2.55E-04
PRG2	-5.93443	1.01E-09	MS4A3	-2.17214	2.61E-04
MPO	-2.52454	8.15E-09	ZNF358	2.042213	2.66E-04
DEFA4	-2.22389	1.70E-08	MS4A6A	-2.21587	3.54E-04
ELANE	-4.39842	1.94E-08	IL4R	-2.1392	3.74E-04
EPX	-3.18113	9.02E-08	PXDC1	-2.08509	4.67E-04
ARMC7	2.314169	2.21E-07	CD320	2.241042	4.83E-04
CAMP	-3.0549	9.82E-07	CD163	-2.52643	5.17E-04
IGHG1	-3.7307	2.23E-06	LUM	-3.58203	5.20E-04
CTSH	-2.87845	3.55E-06	CXCL8	-2.40243	5.26E-04
AIF1	-2.16656	4.43E-06	NOD2	-2.95453	5.26E-04
LST1	-2.19262	8.38E-06	SI00A8	-2.70373	5.61E-04
IGLJ3	-4.49176	1.13E-05	CXCL2	-2.71229	5.61E-04
CLPP	2.32109	1.65E-05	IGHD	-4.07084	5.84E-04
LTF	-3.89554	1.65E-05	HMOX1	-2.36868	5.99E-04
FABP4	-2.79511	3.18E-05	MS4A4A	-3.38126	6.11E-04
LYVE1	-2.9819	3.18E-05	HIF1A	-2.13129	6.18E-04
NRP1	-2.08155	3.34E-05	VNN2	-2.4071	6.18E-04
SI00A12	-2.16333	3.34E-05	MAFB	-3.4547	6.41E-04
CEACAM8	-3.52708	4.20E-05	ALDH1A3	-2.01185	6.80E-04
IGLV1-44	-4.8402	6.64E-05	LHFP	-2.18934	6.98E-04
KCTD12	-2.56891	6.99E-05	SI00A9	-2.3273	8.20E-04
CD14	-3.15551	7.82E-05	MNDA	-3.14832	9.14E-04
RPS11	2.079562	8.44E-05	HLA-DPA1	-2.64283	9.63E-04
IGK	-3.99784	9.70E-05	TGFB1	-2.93660	9.89E-04
P2RY13	-2.46684	1.05E-04	MAGEA4	2.361871	9.92E-04
DTX2	2.071491	1.05E-04	MROH7	-2.03615	9.95E-04



FC, fold change; FDR, false discovery rate.

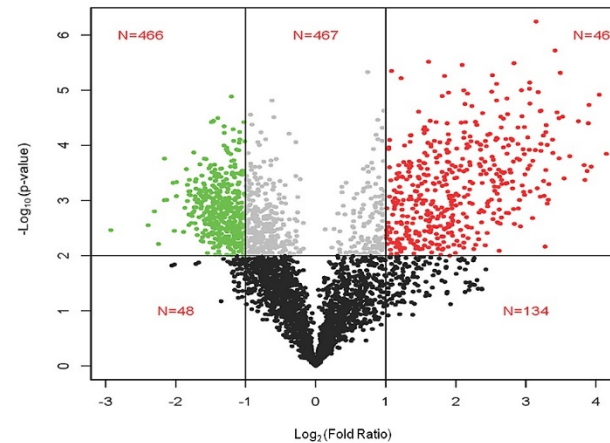


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<https://github.com/education>

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All without coding—let AI write the code for you!

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Second edition: 21 – 22 JANUARY 2025

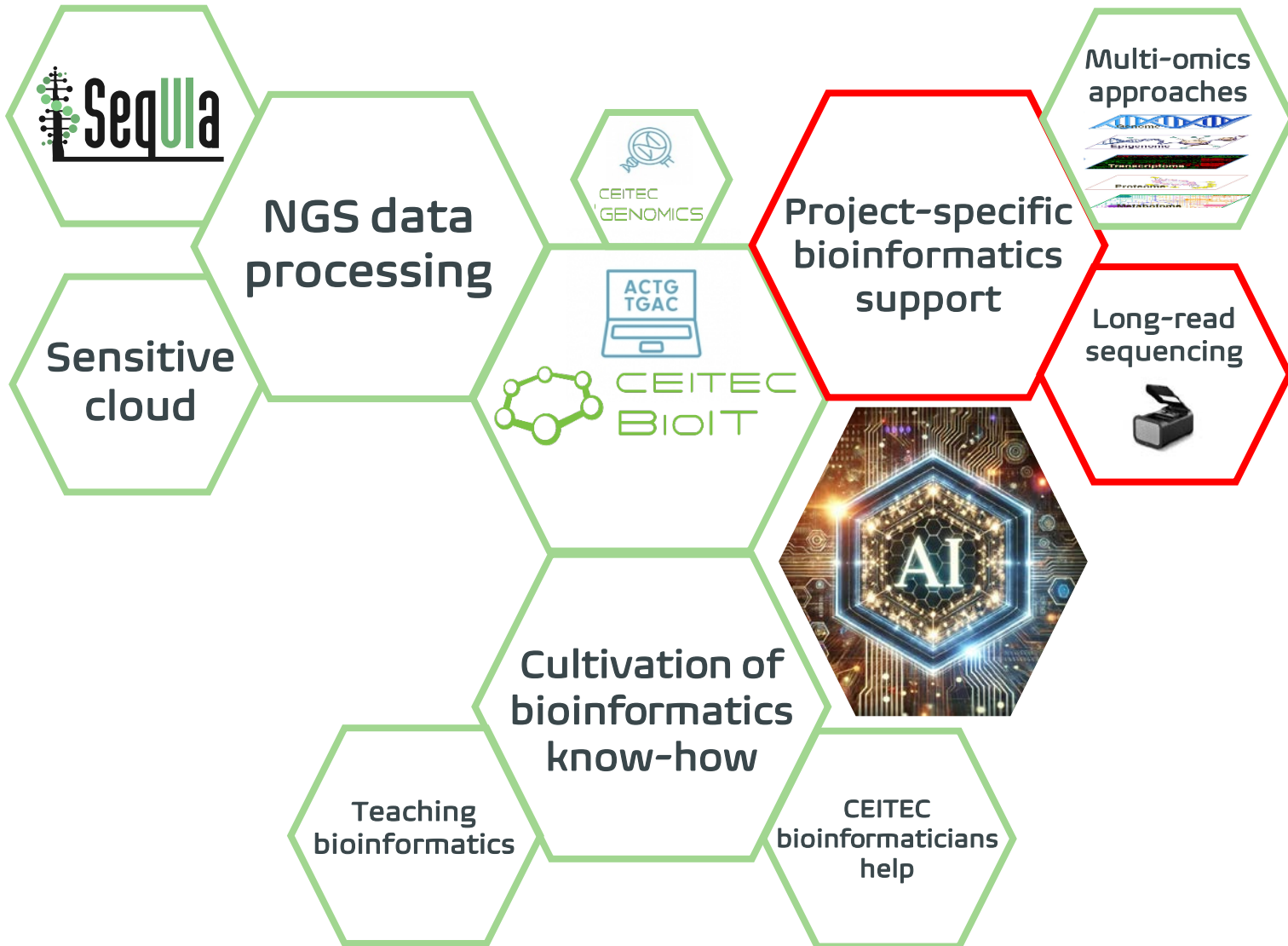
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Deep learning and direct sequencing of labeled RNA captures transcriptome dynamics








 Vlastimil Martinek,  Jessica Martin,  Cedric Belair,  Matthew J Payea,  Sulochan Malla,  Panagiotis Alexiou,  Manolis Maragkakis

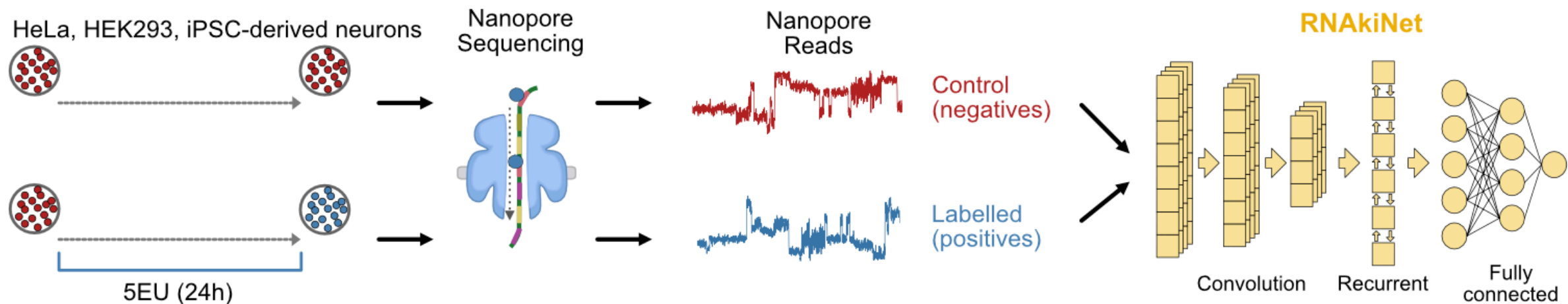


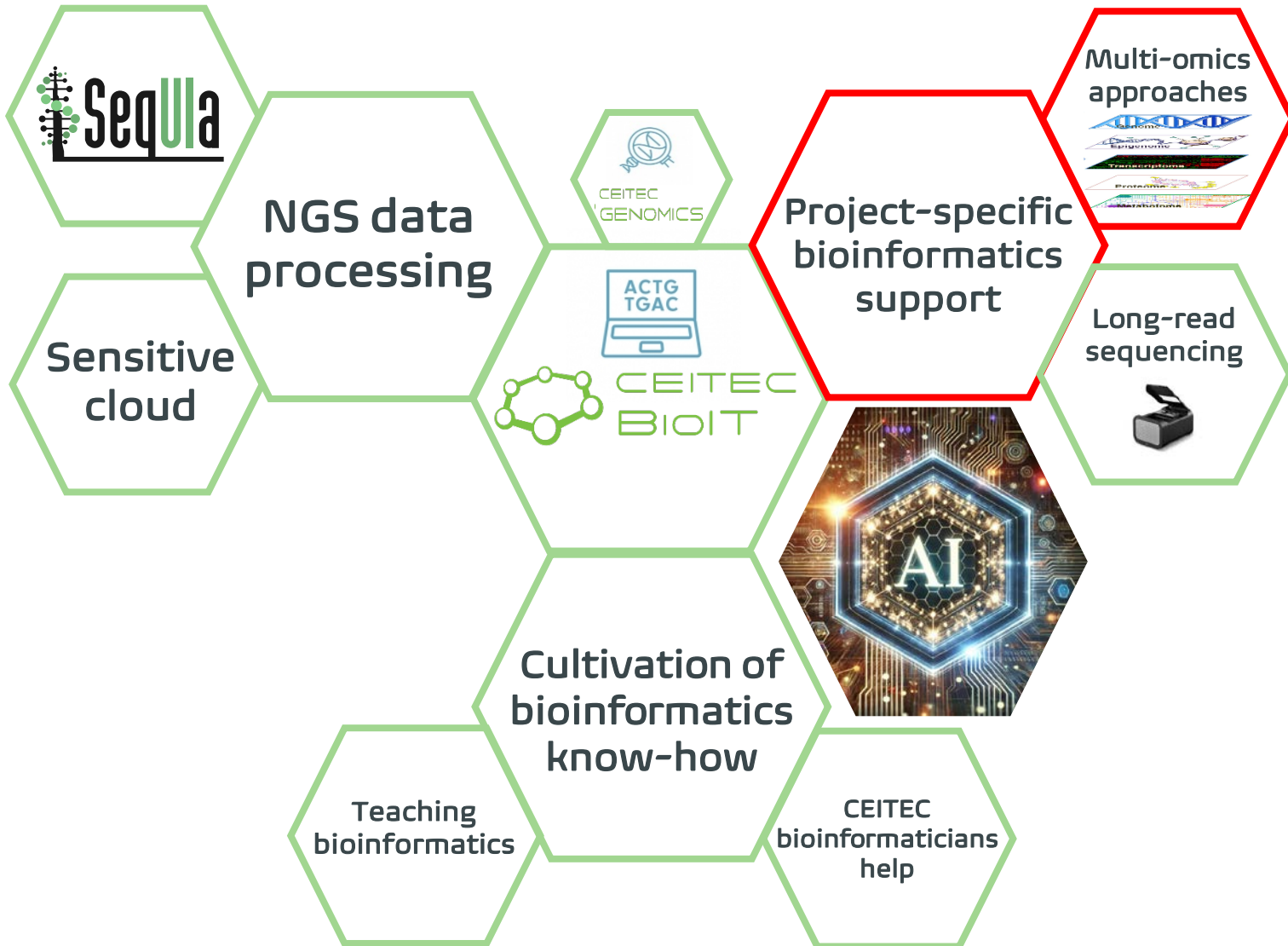
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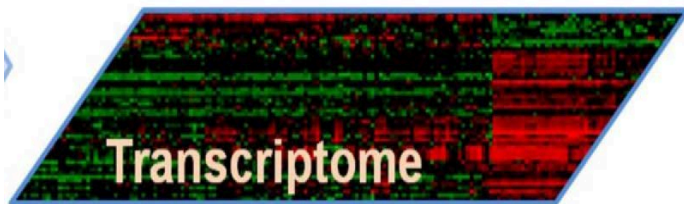
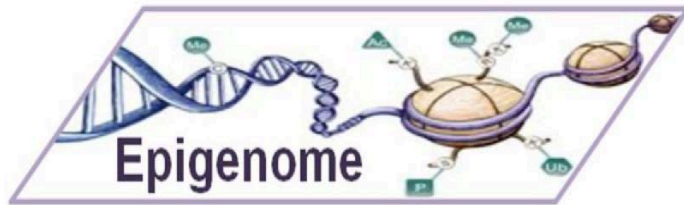
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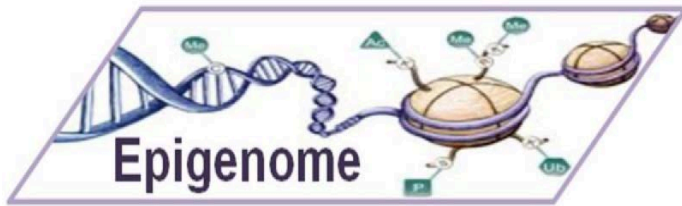




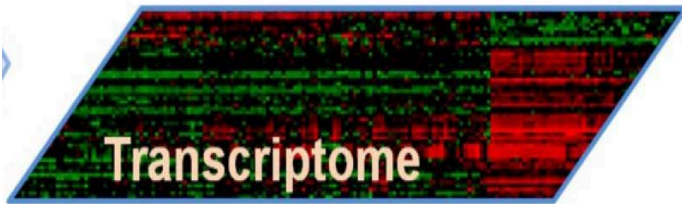
Protein sequence



Genome



Epigenome



Transcriptome

MAGICS-LAB/ DNABERT_2

[ICLR 2024] DNABERT-2: Efficient Foundation Model and Benchmark for Multi-Species Genome



EpiGePT: a Pretrained Transformer model for epigenomics

[Zijing Gao](#),^{1,#} [Qiao Liu](#),^{2,#*} [Wanwen Zeng](#),² [Rui Jiang](#),^{1,*} and [Wing Hung Wong](#)^{2,3,*}

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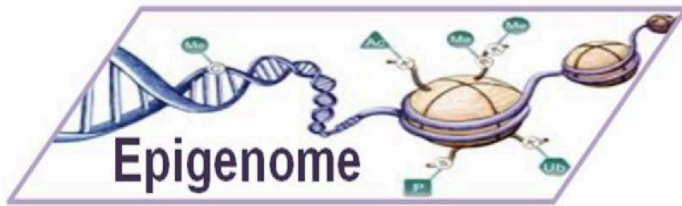
Protein sequence



Genome

MAGICS-LAB/ DNABERT_2

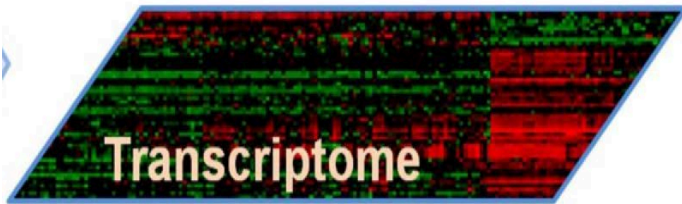
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Transcriptome

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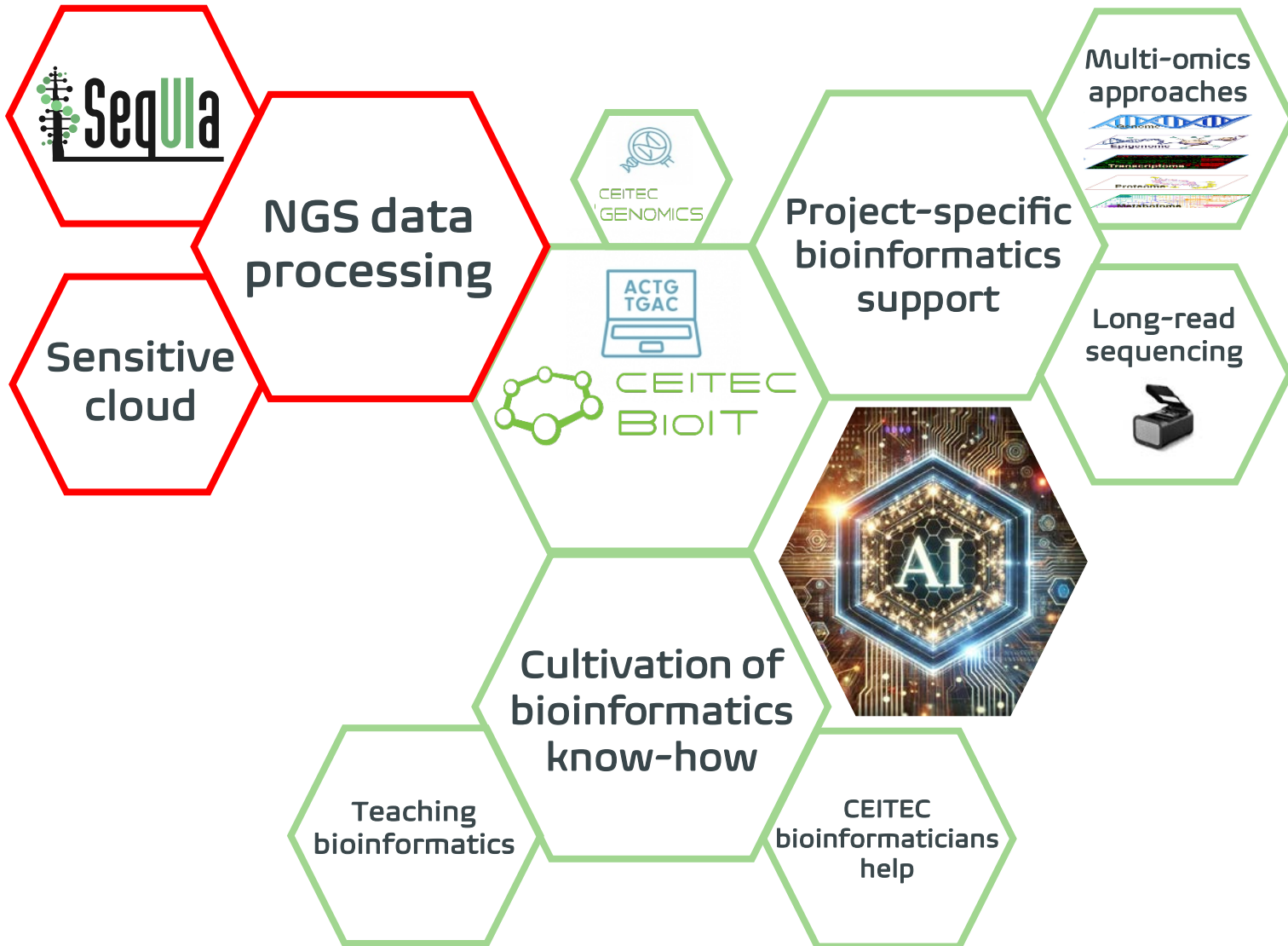
Differential Expression

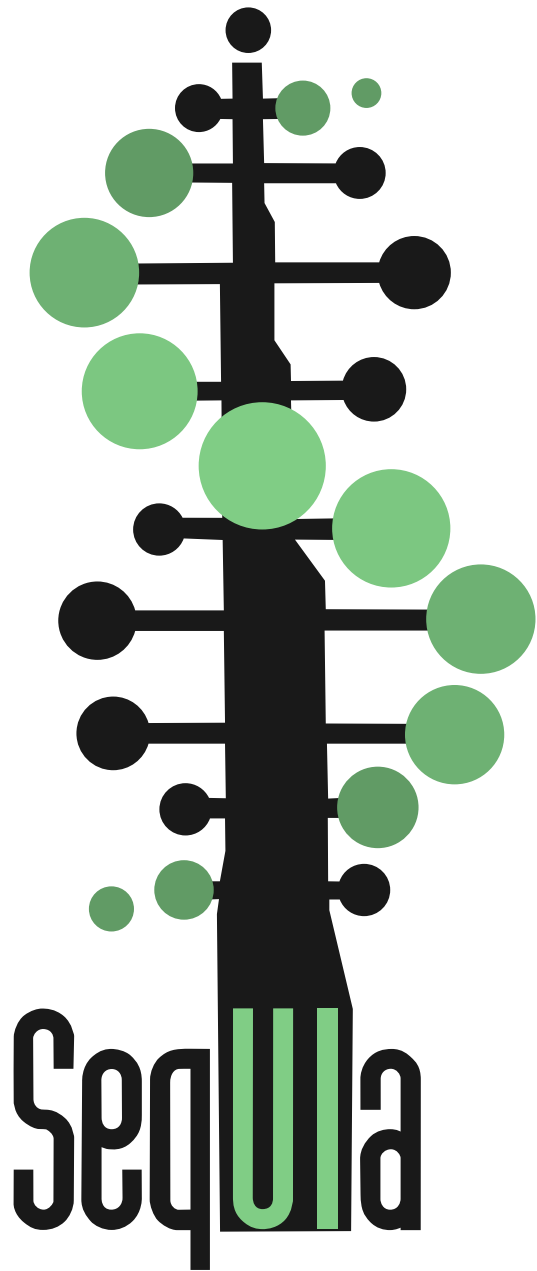
Differential
Expression

Differential
Expression

Differential
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Expression

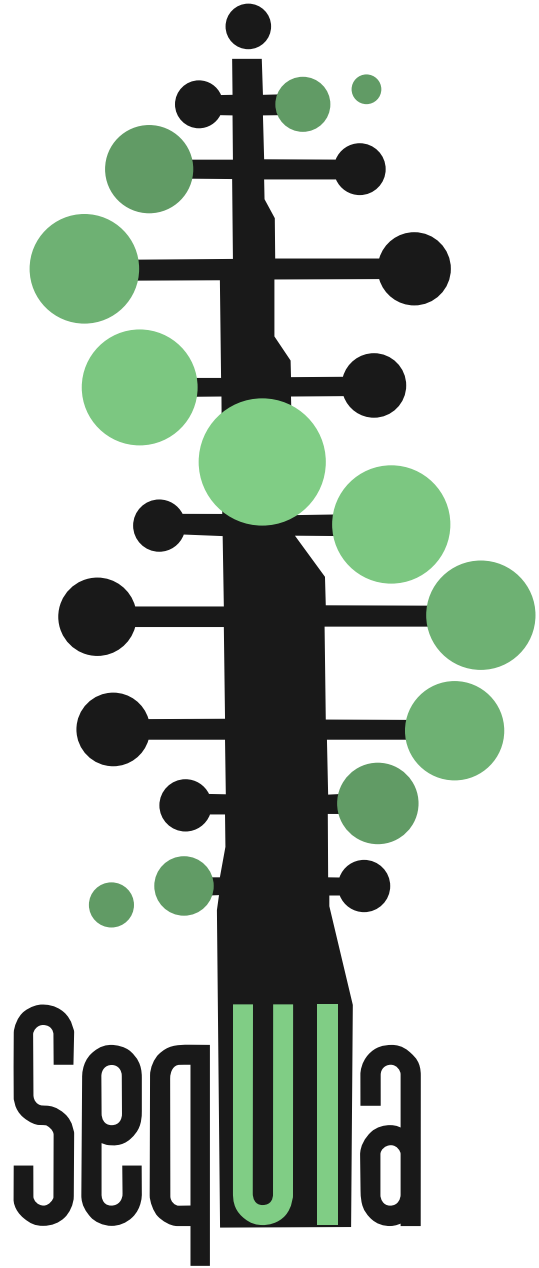




Runs [Add run](#) [Download runs outputs](#) [Run outputs](#)

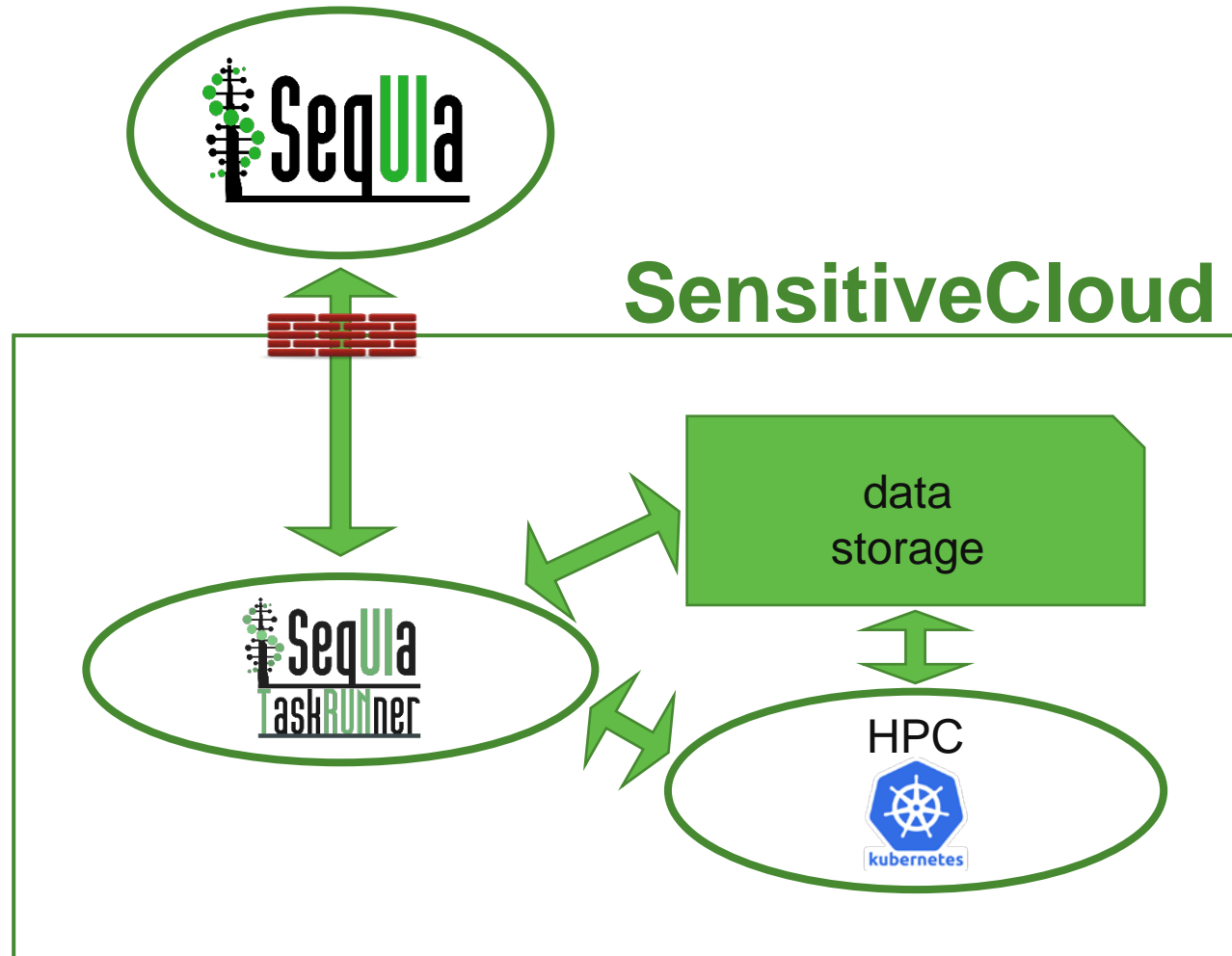
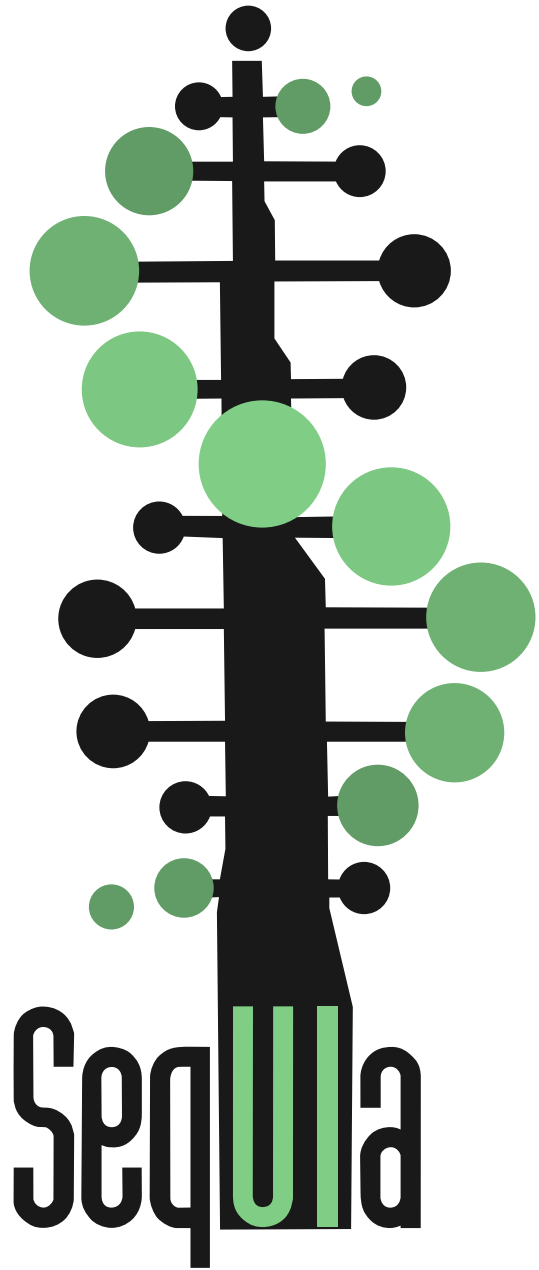
Runs

Run name	Libraries	Last edit	Paired output - name	Paired output - flowcell	Status	Action
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CMBG_MGI_300_20241018	<ul style="list-style-type: none"> Next_tM_NHA Run assigned Next_tN_NHA Run assigned Next_tO Run assigned Next_tP Run assigned 	2024-10-15	--- click to pair ---		Libraries assigned	
CMBG_MGI_300_20241011	<ul style="list-style-type: none"> Next_tK Analysis success Next_tL Analysis success A153 Analysis success AMP111 Analysis success Navrk95 Analysis success 	2024-10-13	CMBG_MGI_30020241011	F350038847	Analysis success	
BabyFox_003	BabyFox_003 Run data paired	2024-10-10	BabyFox_003	HKCLMDRX5	Data paired	
BabyFox_002	BabyFox_002 Run data paired	2024-10-09	BabyFox_002	HKFYDRX5	Data paired	
	Navrk93 Analysis success					



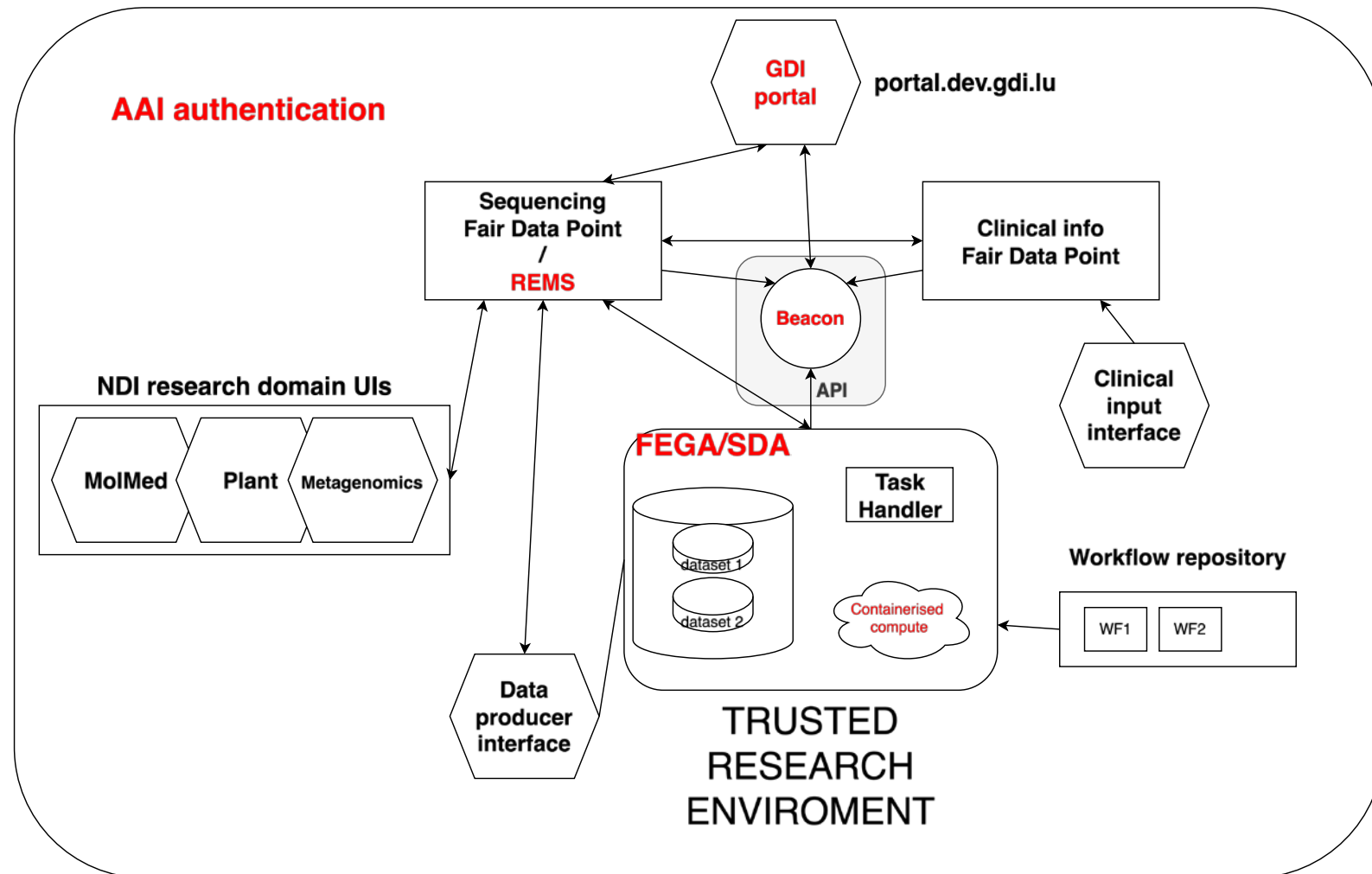
new sequencers data processing

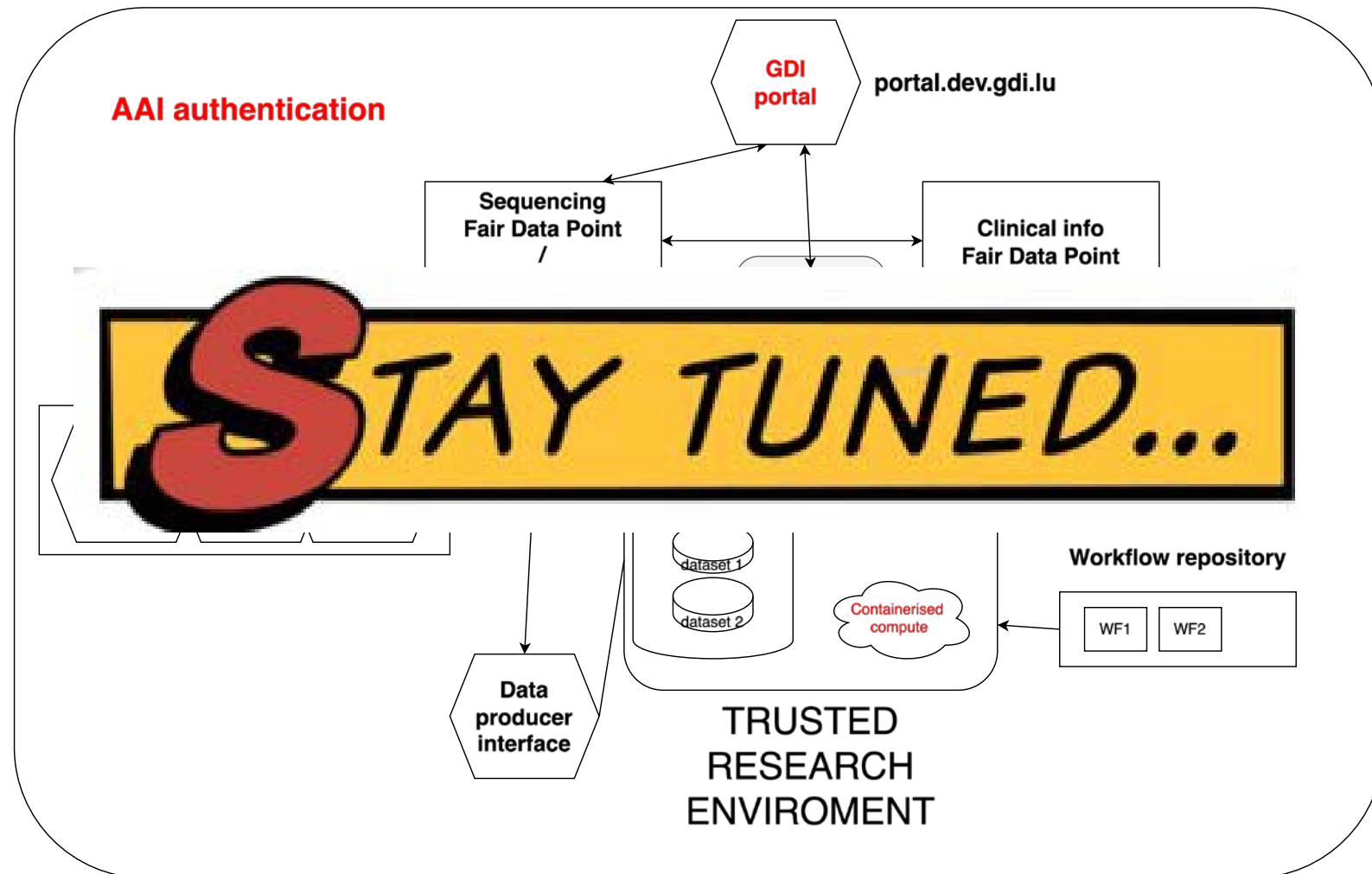






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Acknowledgement text – NCMG

- *„We acknowledge the CF Bioinformatics supported by the NCMG research infrastructure (LM2023067 funded by MEYS CR) for their support with the bioinformatics analysis of scientific data presented in this paper.“*



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SensitiveCloud as an Environment within e-INFRA CZ

CEITEC Core Facility Day Life Sciences 2024
2024-10-16

Michal Růžička <ruzicka@ics.muni.cz>, Petr Holub <hopet@ics.muni.cz> et al.
Prepared in cooperation with the EOOSC CZ Secretariat



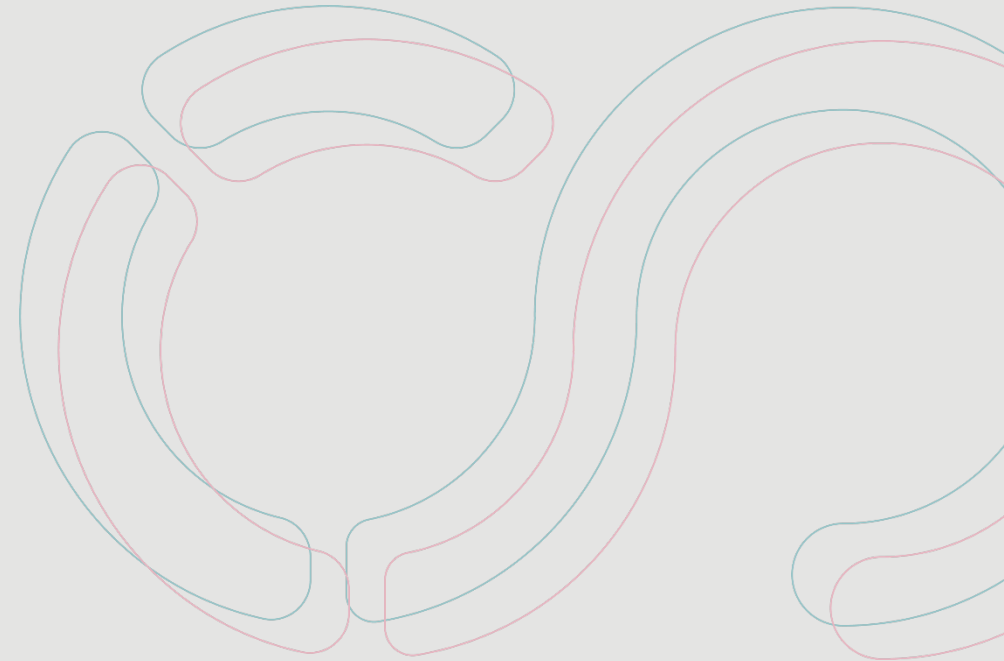
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SensitiveCloud

Infrastructure for Sensitive Data within e-INFRA CZ



Motivation

- Security is an increasingly emphasized area.
 - Users are gradually placing more and more emphasis on the security of their data.
 - Various parts of the university (Med, CEITEC, RECETOX, CERIT-SC, ...) work with medical and other sensitive data.
- Two “hot topics” in data management and processing.
 - **Open and FAIR data** – The principles of Open and FAIR data (Findable, Accessible, Interoperable, Reusable, ...) are needed as the simple availability of data does not guarantee its usability.
 - **Sensitive Data** – Primarily in Health and Life Science, which creates a clear demand for processing sensitive data.
- A strategic goal of CERIT-SC / e-INFRA CZ – Supporting life-science and high-value users.

Our Team

- Selected specialists from CERIT-SC team.
 - **Technical** implementation (storage and computation software and hardware, data networks, datacenters personnel, ...).
 - **Compliance**, risk management, ...
 - Service **design**.
 - **Legal** consultation.
 - Security **research** (forensic readiness).

Environment Design and UX

- Higher security == worse **UX**.
- Higher security == requirement for **higher service maturity** (ITIL, ISO, ...).
- Environment design based on:
 - “General security best-practice”.
 - User interviews and testing.
- Developed semi-formal framework:
 - **On-boarding process** for users: first contact, interview(s), contract signing, access and training, deployment.
 - Description of the environment.
 - User rights and responsibilities.
 - Contract template.
 - General conditions of use of the service.

Implementation

- Two components:
 - SensitiveCloud **Compute** (including GPUs).
 - SensitiveCloud **Storage**.
- SensitiveCloud Compute is provided as a PaaS built on Kubernetes with Rancher:
 - The user only manages the application, not the entire VM.
 - Ideal SaaS – R-Studio, Jupyter Notebook, ...
- SensitiveCloud Storage.
 - Integration within computing via NFS-CSI.
- Separate network, WireGuard VPN access, Perun AAI with multi-factor, iron behind the lock with camera surveillance, ...

General Security Best Practice

- Rational search for possible vulnerabilities, attacks and countermeasures.
 - From formal risk analysis to wise men over coffee meetings...
- ISO 27k:
 - Not a prerequisite, not a sufficient condition.
 - By itself, **addressing process** maturity and higher security de facto is a by-product.
 - SensitiveCloud **certified in summer** **2023**.
- BUT:
 - The correct solution implicitly must necessarily be ISO 27k compliant.
- Forensic readiness.
 - The security methods research applied to SensitiveCloud infrastructure.

Continuous Process

- ISO 27k is about **continuous** planning, monitoring and **improvements**.
- In the **process** of applying for projects planning to use SensitiveCloud.
 - Possible extension of hardware resources.
 - Possible new integrations with infrastructures.
 - Possible new use-cases.
- Continuous improvements of processes, technical security measures, onboarding process, and SensitiveCloud public presentation, ...
- Thinking of SensitiveCloud 2.0, 3.0, ...
 - Full virtual machines, virtual desktops in the secure environment.
 - Dedicated Kubernetes/OpenStack platform deployed on-demand.

SensitiveCloud Infrastructure

- SensitiveCloud **up and running**.
 - ISO 27k certified.
 - Onboarding process, processes, technical measures, service agreement template, ...
- Continuous **process of improvements**.
 - Projects in progress, FEGA.
 - Thinking of SensitiveCloud 2.0, 3.0, ...



1.

We find out whether SensitiveCloud fulfils your requirements.



2.

We explore all the specifics of your use case and, if necessary, make appropriate changes.



3.

We sign an agreement confirming our duties and expectations.



4.

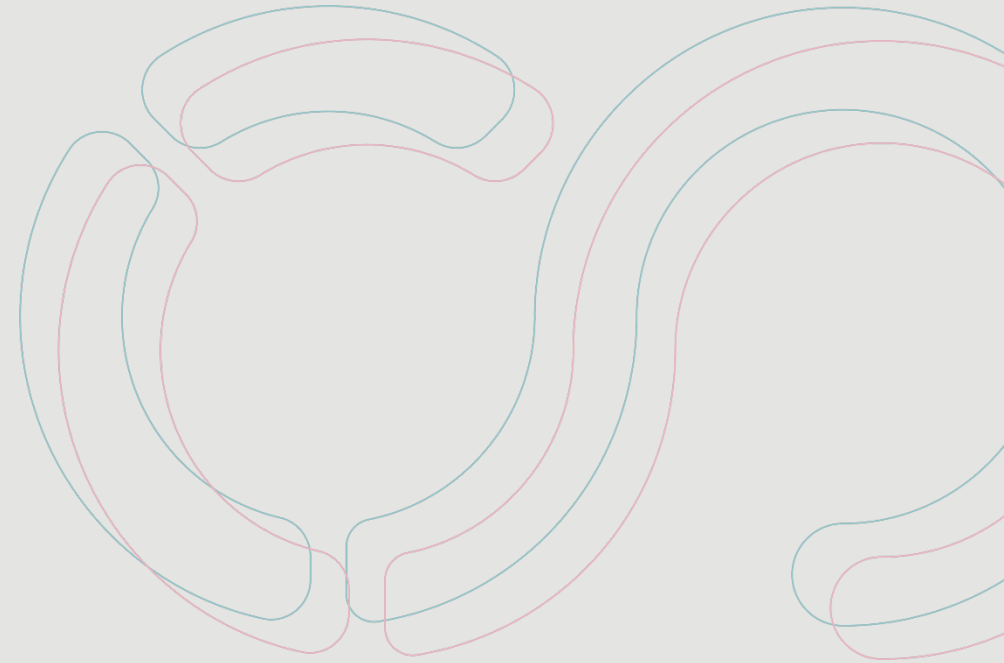
We train you to harness the most of the environment.



5.

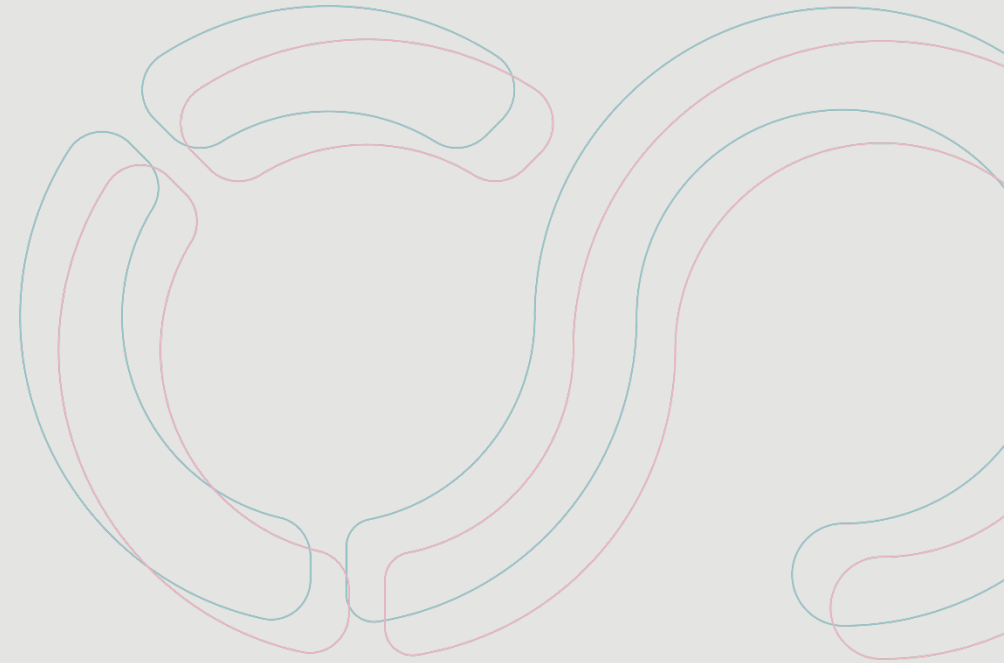
You work on your research, and we continuously monitor your needs and satisfaction.

<https://www.cerit-sc.cz/infrastructure-services/sensitivecloud>



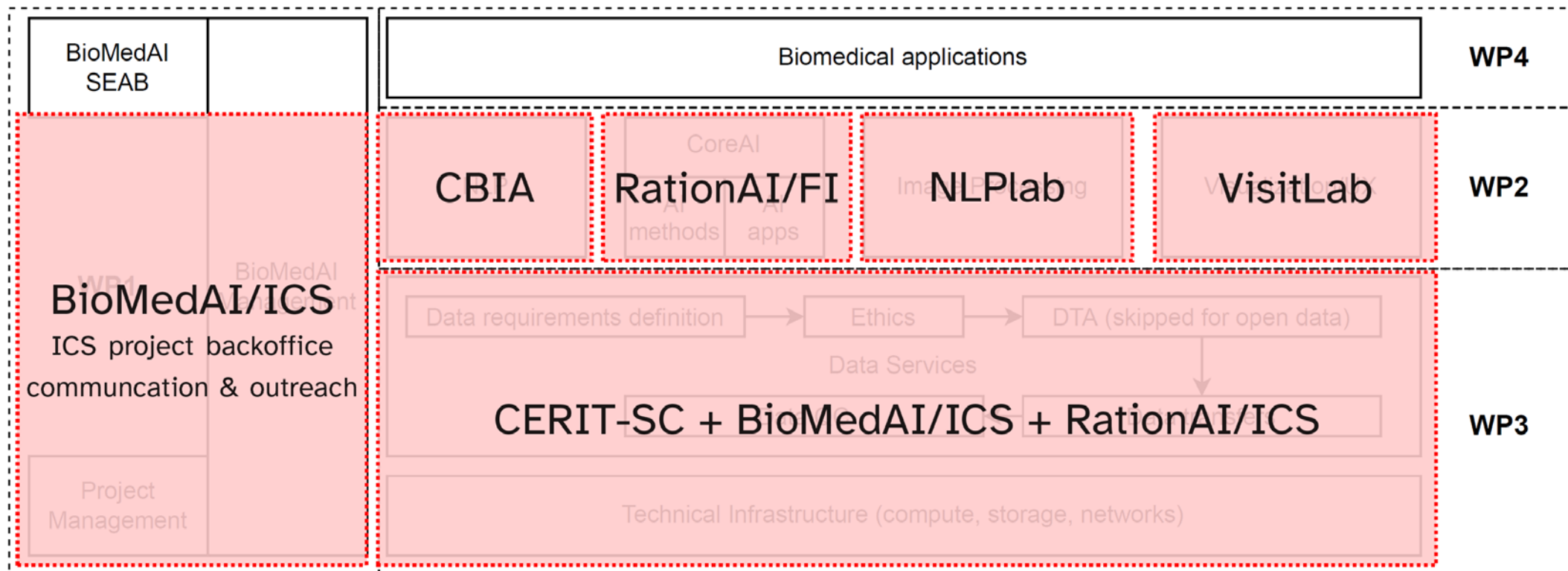
RationAI

SensitiveCloud Use-Case



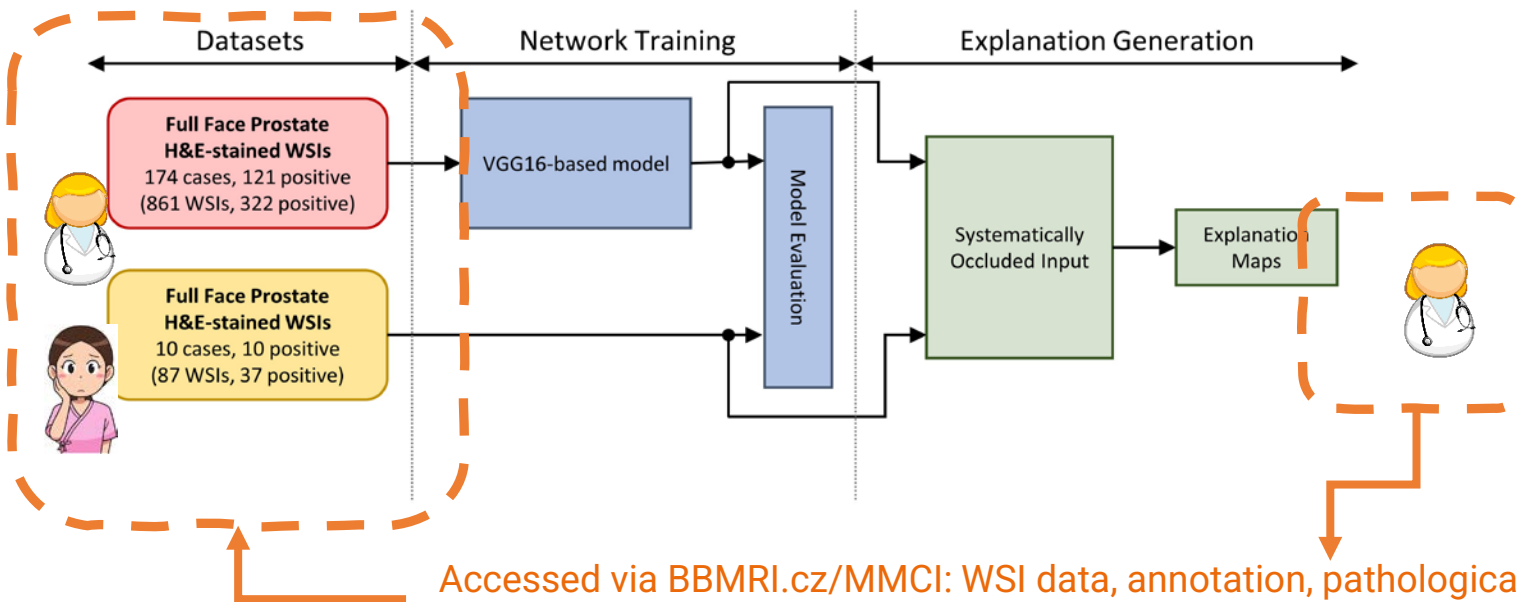
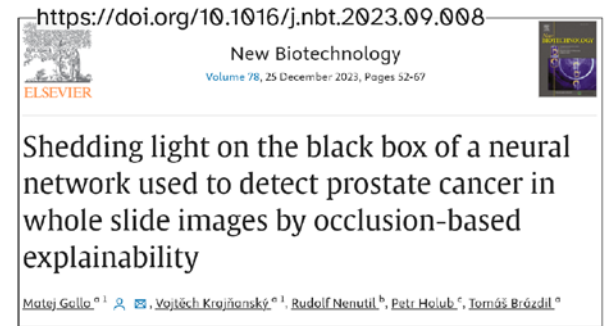
RationAI Use of SensitiveCloud

- **RationAI**: Research group at FI/ICS MUNI.
 - Main focus: Rational application of **AI in biomedical domain** – primarily those with **clinical impact**.
- **BioMedAI Center**: Infrastructure, data, and research groups (MU, MMCI, FN Brno, BBMRI.cz, ...).



RationAI Use of SensitiveCloud: Selected Results

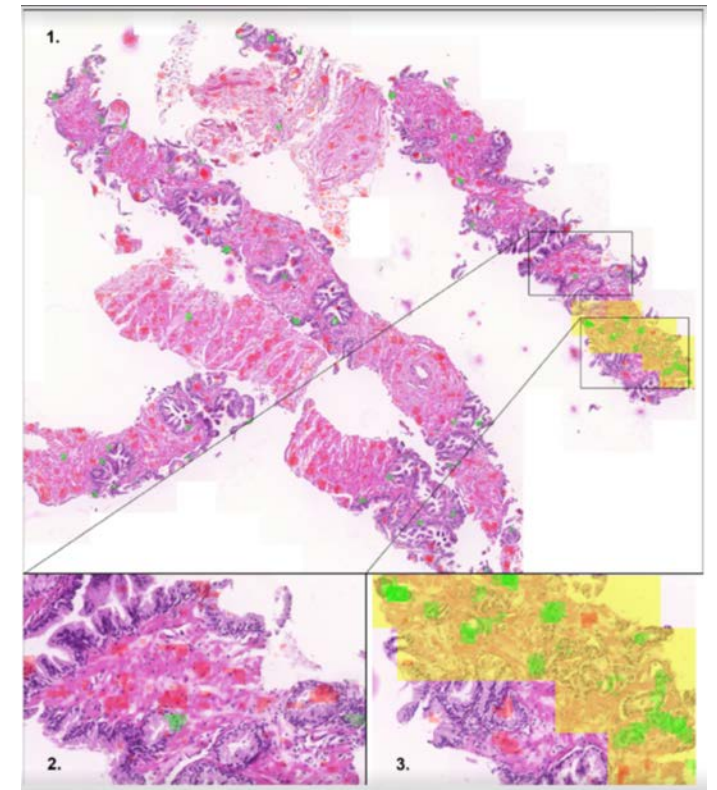
- Prostate cancer diagnosis support using explainable AI.
 - Developed using supervised training of AI models with robust application of explainability.
 - Internal clinical validation and use at MMCI.



Accessed via [BBMRI.cz/MMCI](https://bbmri.cz/MMCI): WSI data, annotation, pathologica expertise. Data hosted and processed in SensitiveCloud.

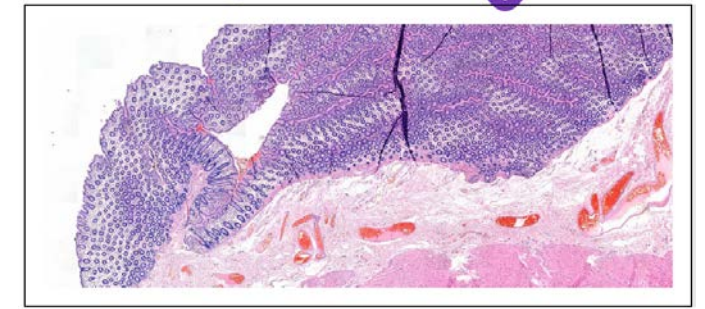
15 October 2024

SensitiveCloud | Ružička, Holub

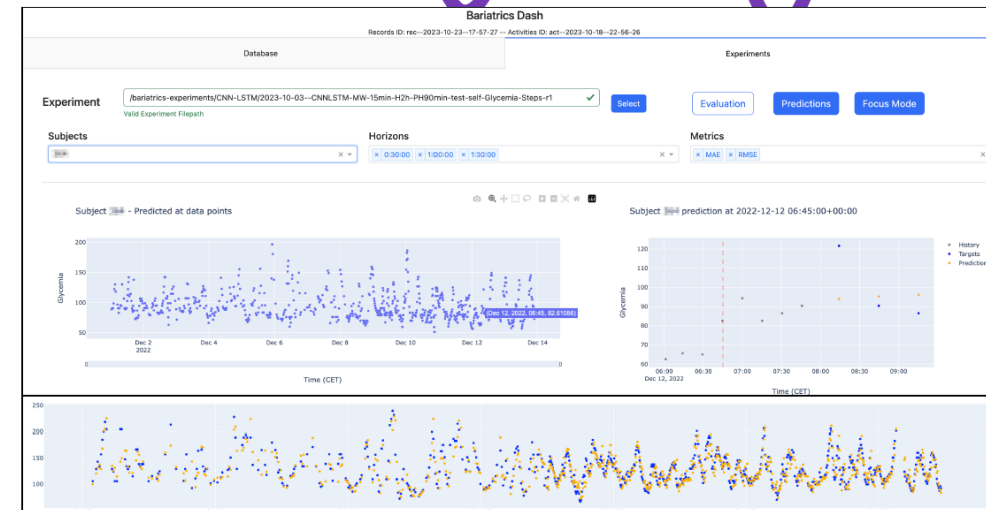
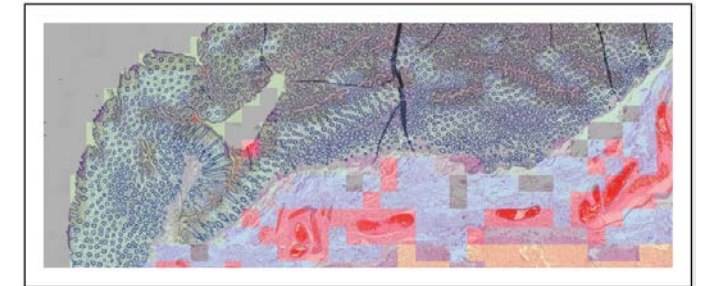


RationAI Use of SensitiveCloud: Selected Results

- Ki67 model trained entirely on real-world clinical data without any additional manual annotations.
- Model for deduplication and cleanup of National.
- Oncology Register in collaboration with UZIS.
- Extracting “knowledge” from existing models.
E.g., Testing with Concept Activation Vectors (TCAV).
- Explainable models for blood glucosis
level predictions – collaboration with 1st Faculty
of Medicine, Charles University.

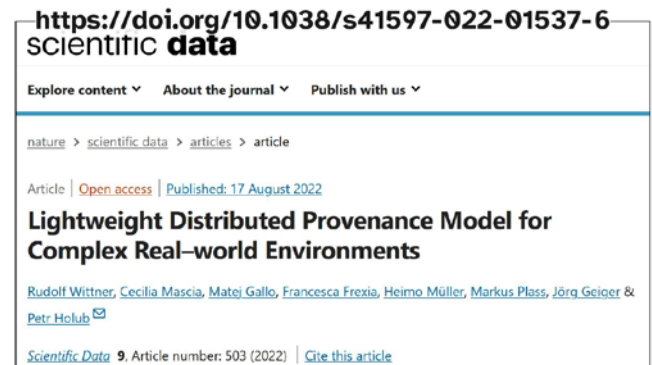


↓ TCAV

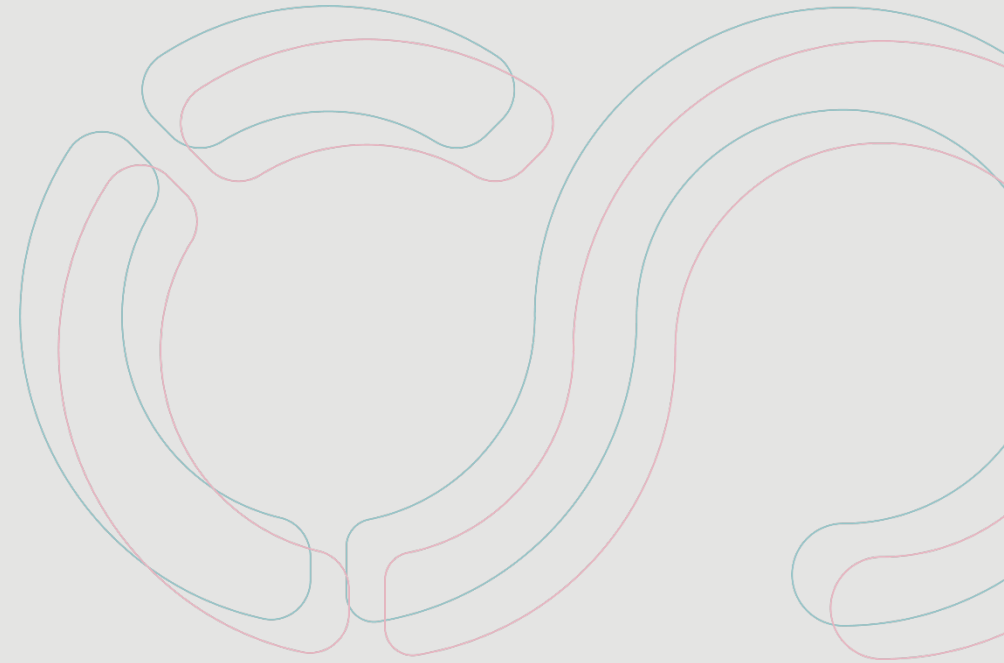


RationAI Contributing to the Infrastructure

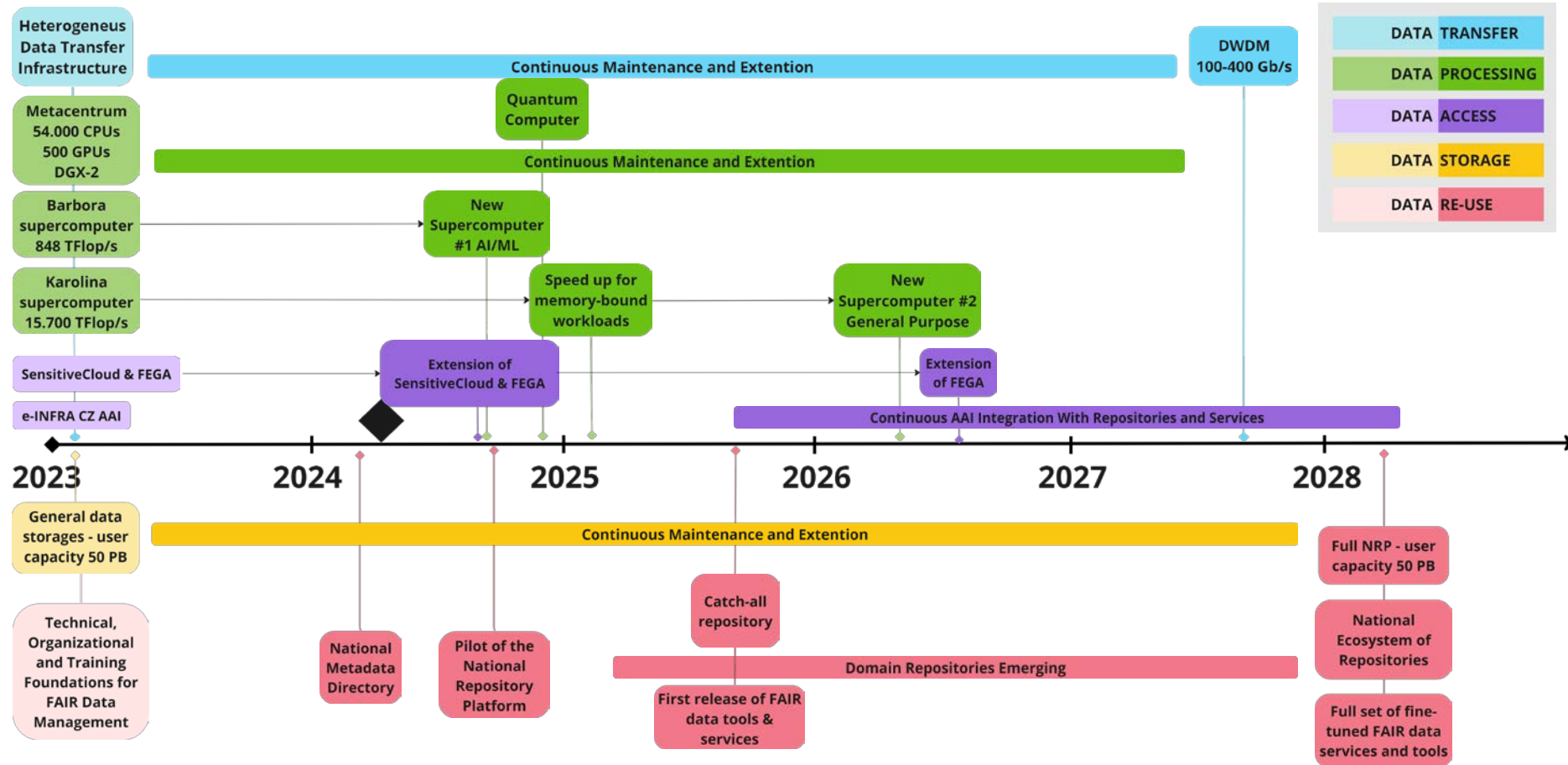
- Reusable Mlflow-based pipeline system for development of AI models in SensitiveCloud.
 - **RatioPath** – training and inference pipelines for digital pathology and management of experiments.
 - **RatioViz** – visualization system for digital pathology, including WSIs, annotation, results and exploration of AI models.
 - **RatioCast** – training, inference and visualization system for time series data.
- Methods for **sharing digital pathology data as anonymous data** published in Nature Comms.
- **QC algorithms** for working with digital pathology data.
- **Provenance information infrastructure** for documenting history of data and AI models.



EOSC Implementation in the Czech Republic



EOSC Services in Wider Context





From Storage to Repositories

26 November 2024

Prague

Registration for on-line stream still open!

<https://www.eosc.cz/>



National EOSC CZ Conference

Questions?



Zdroj: Communicate_communication_conference_2028004 od OpenClipart-Vectors z Pixabay



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Curious about what expert services are available to researchers on campus? What instruments can you use in shared mode and under what conditions? Do you want to see everything for yourself?

Register at: muni.cz/go/fba265





CEITEC MUNI Core Facility BioData: Biological data management and analysis

Radka Svobodová, CF Day Life Sciences, 16 October 2024

BioData overview

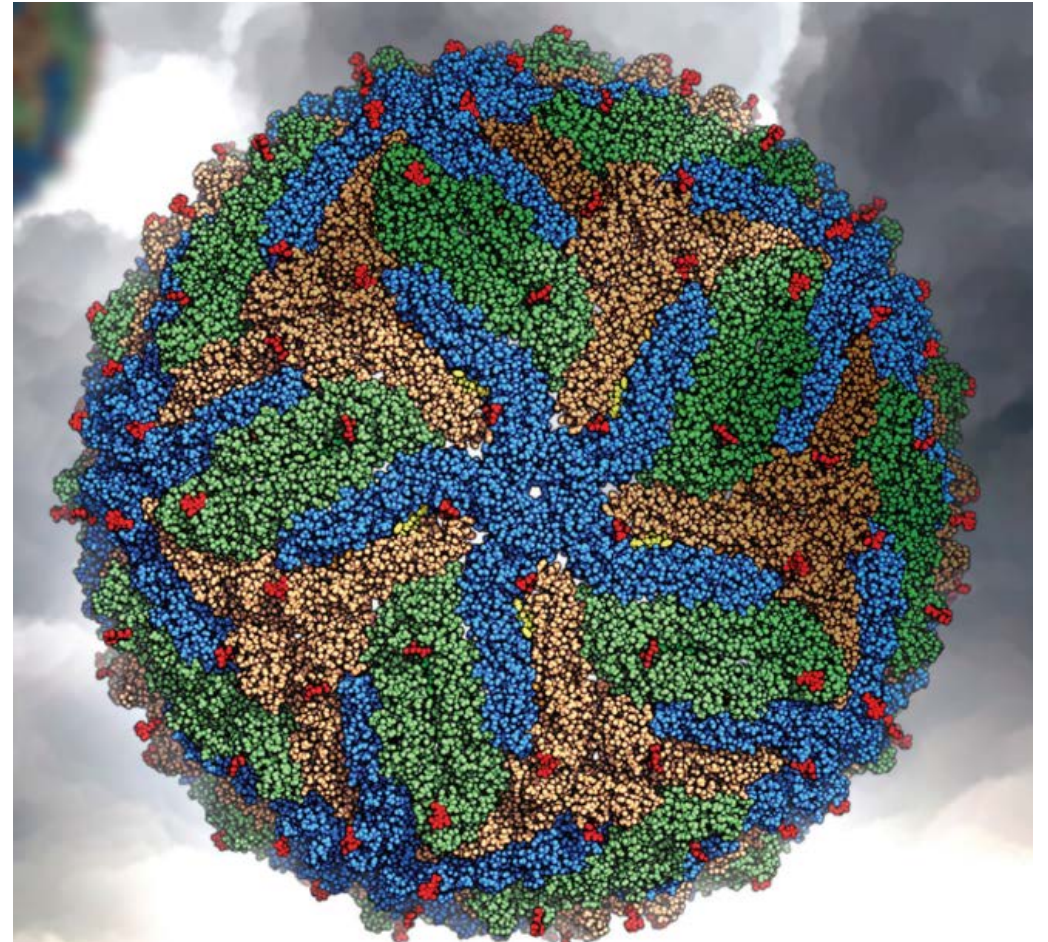
Why data management?

Biological data are:

- Interesting
- Expensive
- Larger and larger
- We have them more and more...

The data deserve to be:

- Findable
- Accessible
- Interoperable
- Reusable



About BioData CF



- **Mission:** Analysis and management of biological data

- **Expertise:**

- Computer science
- Data management
- Structural bioinformatics



- **Members of ELIXIR and EOSC research infrastructures**

BioData services

Data

Data management

- Data repositories
- Access to ICT data resources
- Booking support
- **EOSC networking**

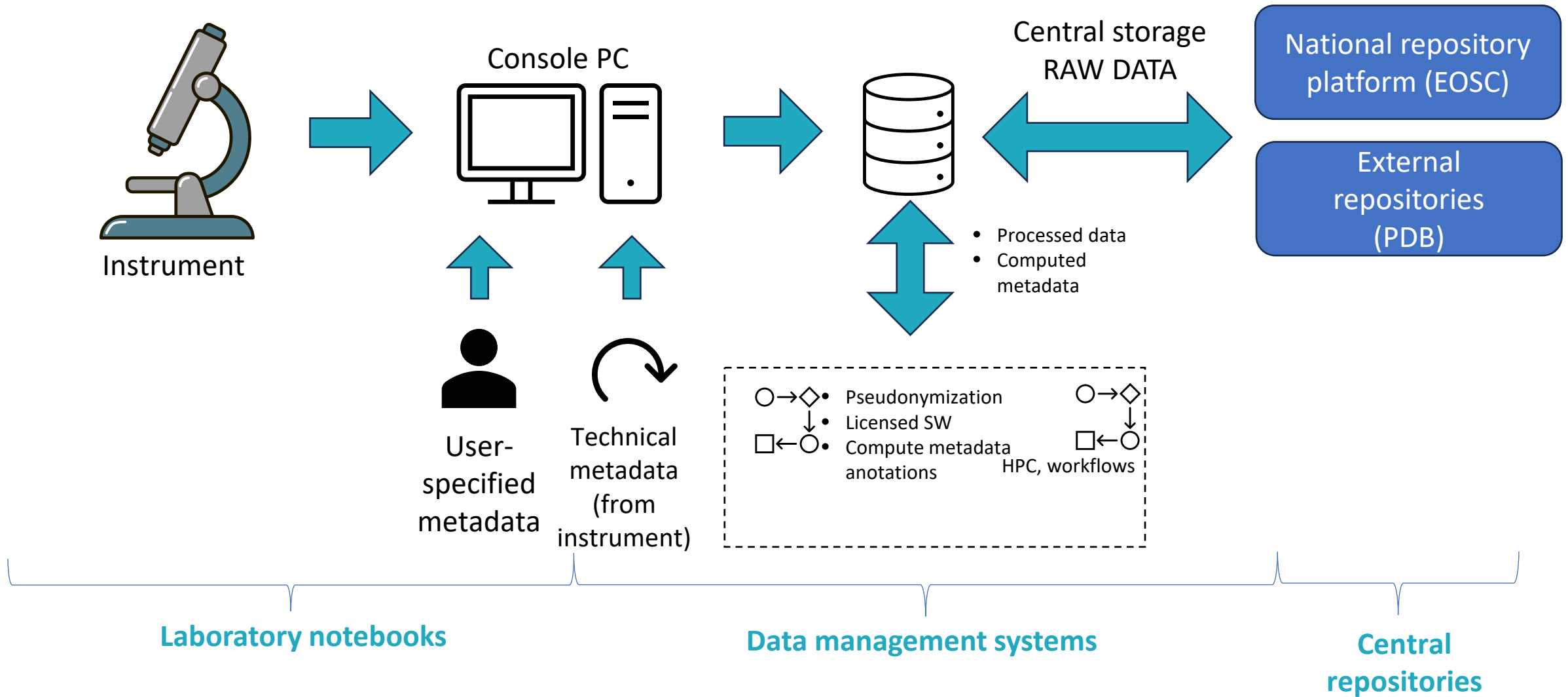
Bio

Structural bioinformatics

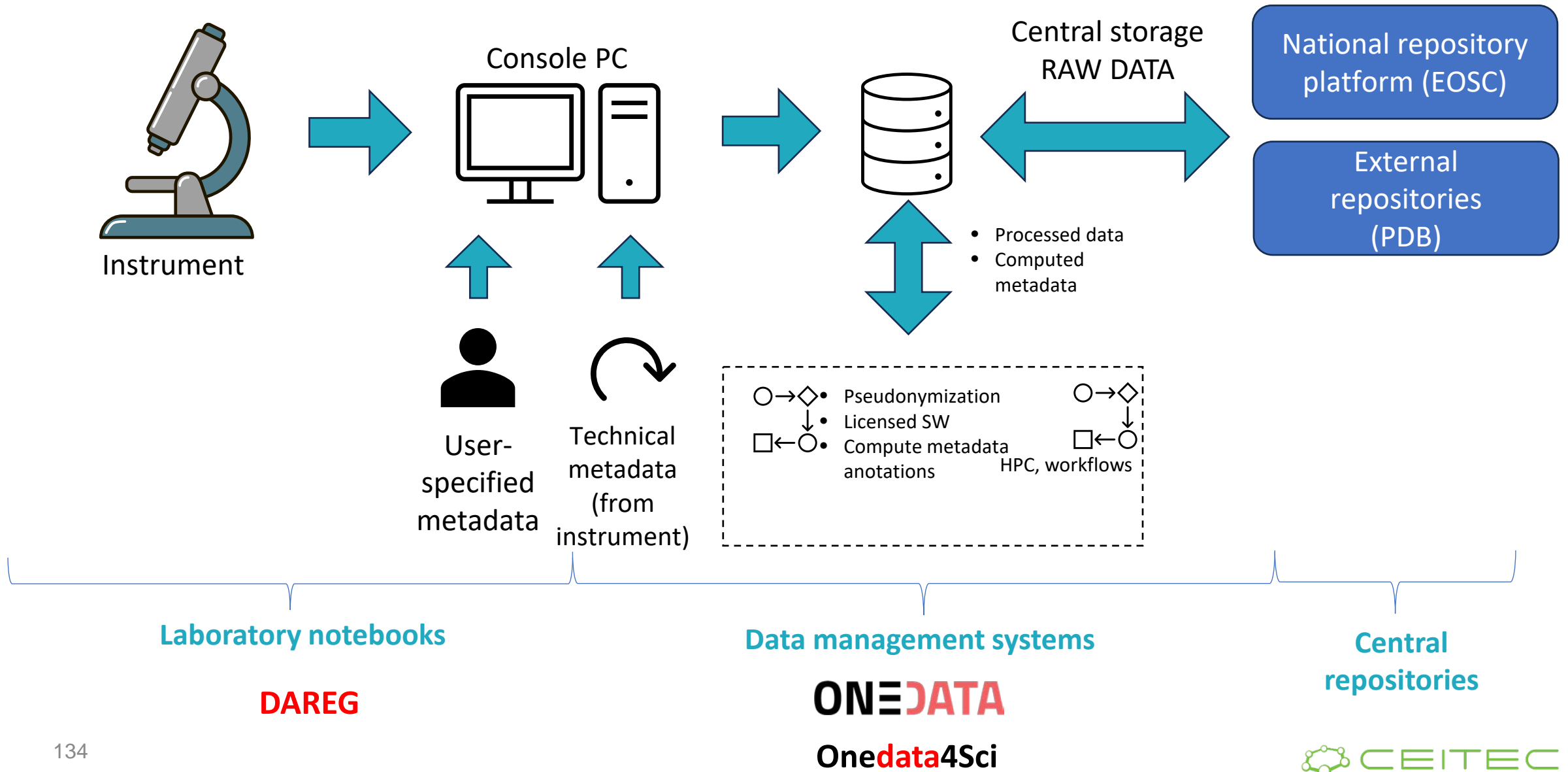
- Analyses of protein structures
- Validation and deposition
- AlphaFoldology
- Tools and databases
- **ELIXIR networking**

Our **Data** services + examples

Data: Data repositories



Data: Data repositories



Data: Data repositories – our tools

Onedata4Sci: Life science data management solution based on Onedata

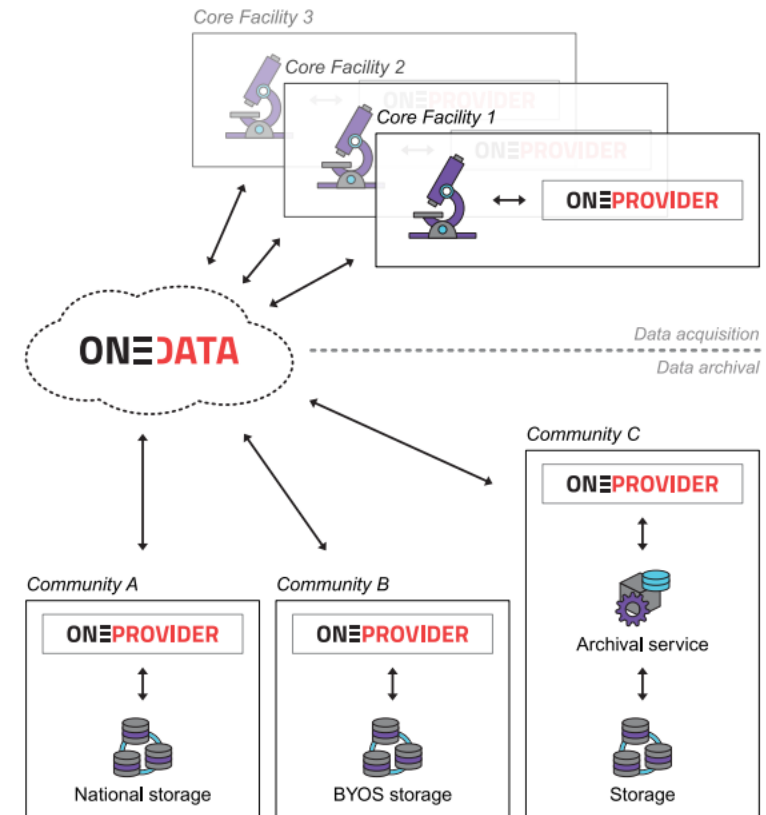
Svoboda T., Raček T., Handl J., Sabo J., Rošinec A., Opiola L., Jesionek W., Ešner M., Nováček J., Pernisová M., Valasevich N. M., Křenek A., Svobodová R.: *Onedata4Sci: Life science data management solution based on Onedata*,

<https://doi.org/10.48550/arXiv.2311.16712>

DAREG: Dataset Registry

A web portal that allows users to manage their datasets, stored using Onedata, and enrich them with metadata.

<https://dareg.biodata.ceitec.cz/>



Data: Data repositories – examples

- RG of prof. Rektor
- CF Plant sciences
- CF Cellular imaging
- CF Multimodal and Functional Imaging (MAFIL DB)
- CF Biomolecular Interactions and Crystallization

Data: Access to IT resources of MU

MUNI
ICS

- Web servers
- Virtual machines
- Compute
- Storage

✓ Species
Marchantia polymorpha, 16402 genes, 3 stages

✓ Genomic interval
Analyzing interval <-1000; 1000> bp relative to ATG, bucket size 30 bp

Motif mapping ATG	Genomic interval Min [bp] -1000
Motifs are mapped relative to TSS or ATG	
Genomic interval Max [bp] 1000	Bucket size [bp] 30
Relative to ATG	Interval used to group the results

Data: Access to IT resources of MU

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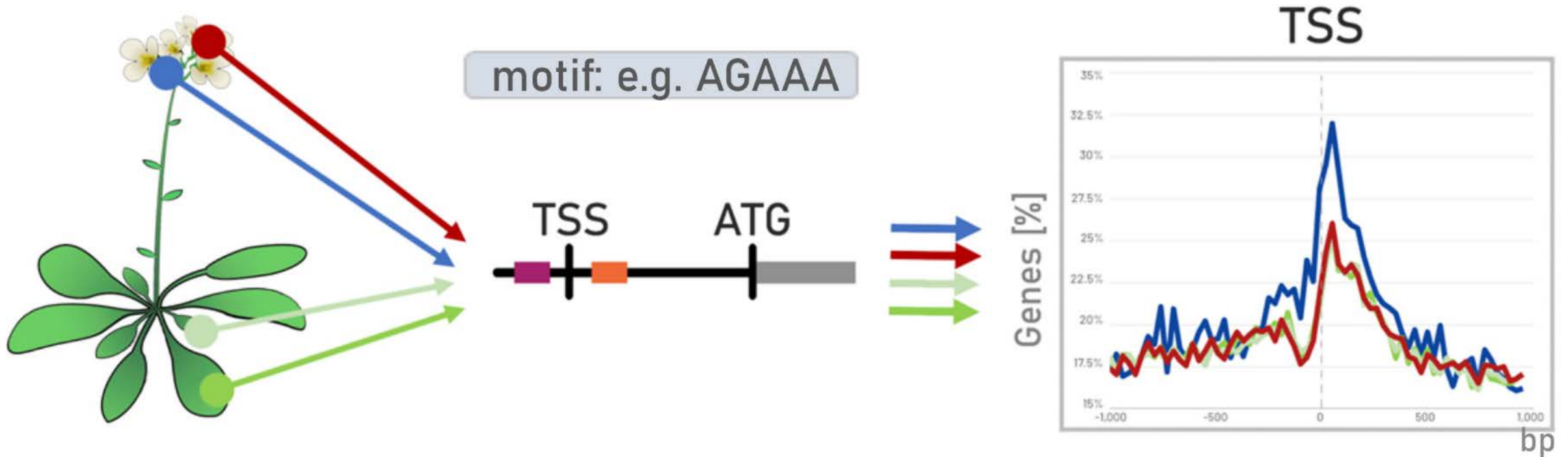
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Data: Access to IT resources of MU – examples GOLEM

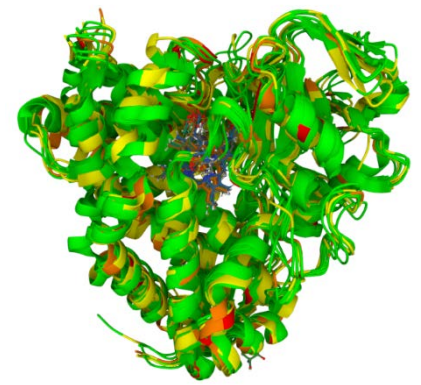


Nevosád L., Klodová B., Honys D., Svobodová R., Raček T., **Procházková Schrumpfová P.**: *A tool for visualizing the distribution of Gene regulatOry eLEMents within the plant promoters with a focus on male gametophyte*, in review (The Plant Journal)

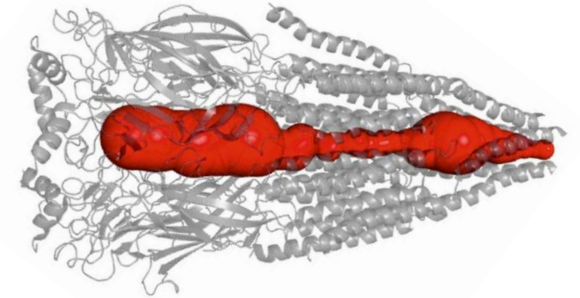
Our **Bio** services + examples

Bio: Structural bioinformatics support

- Analyses of protein structures
- Validation and deposition
- AlphaFoldology
- Structural bioinformatics training



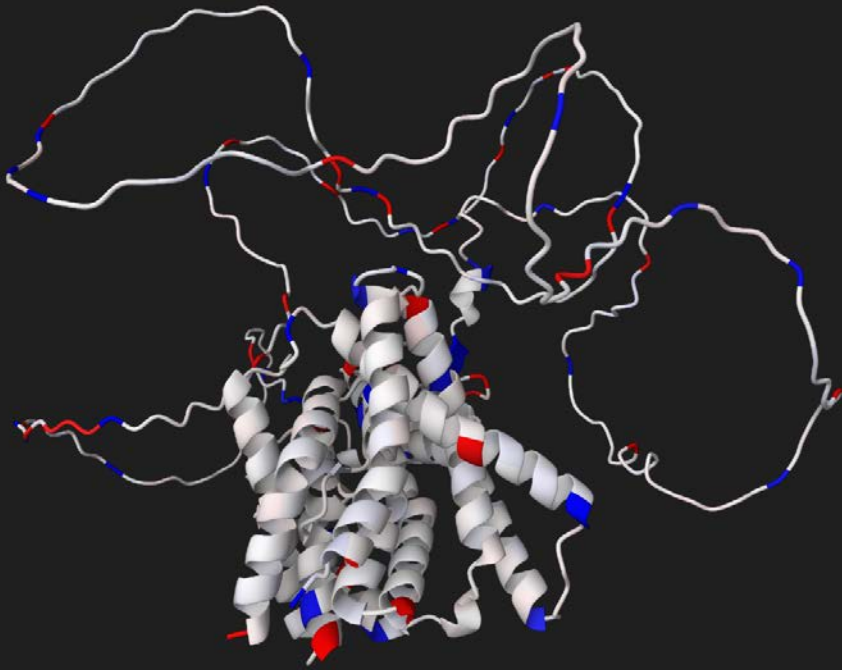
Mol*



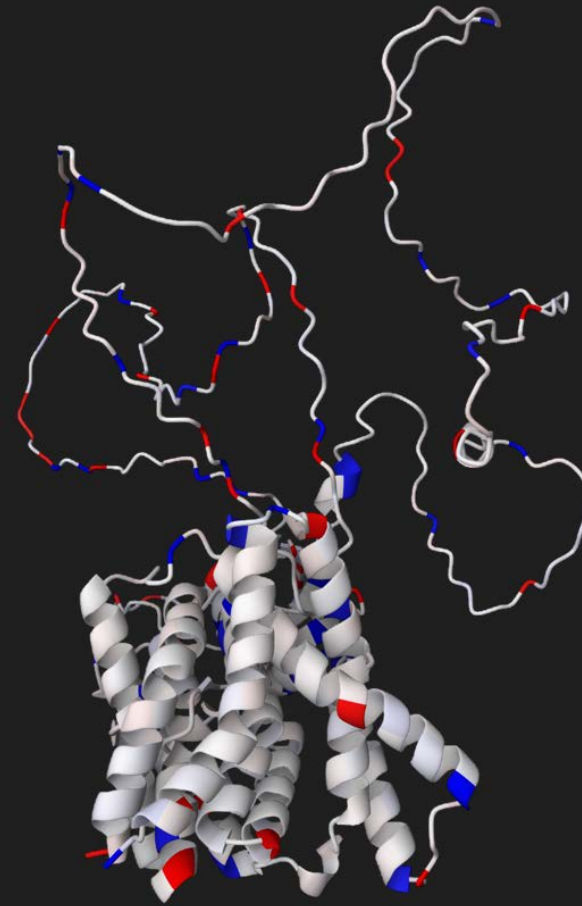
 **PDBe**
Protein Data Bank in Europe

EMBL-EBI 

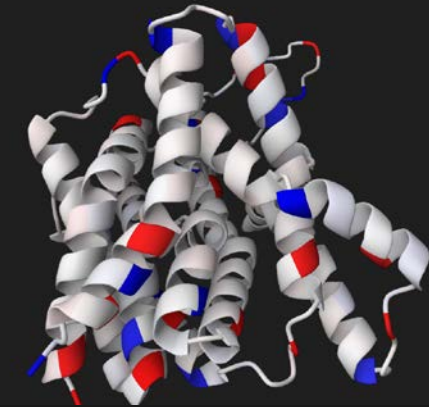
Bio: Structural bioinformatics support - example PIN anatomy



PIN3



PIN7

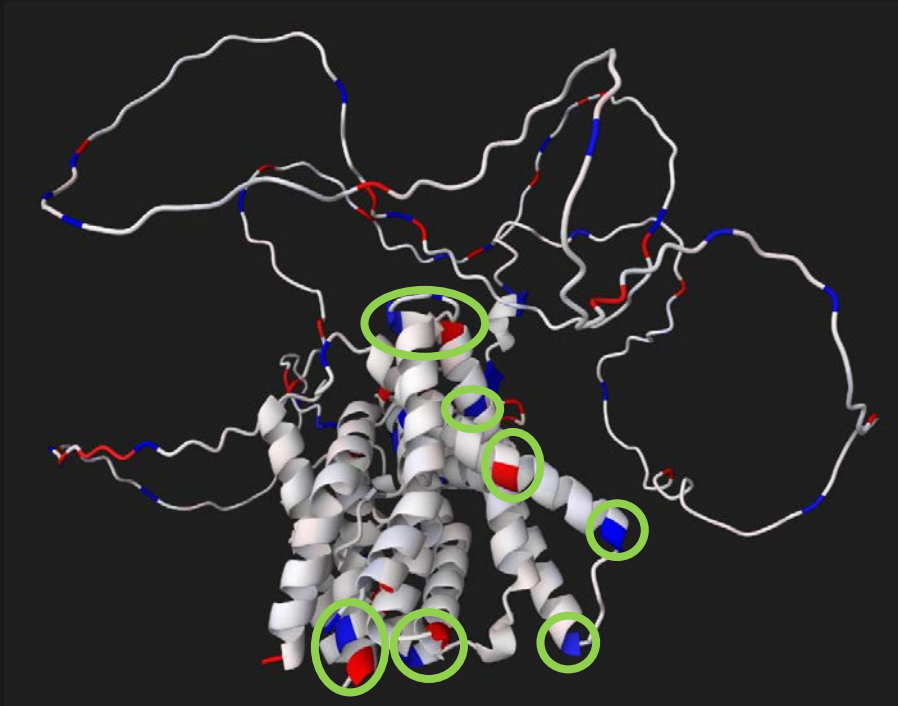


PIN5

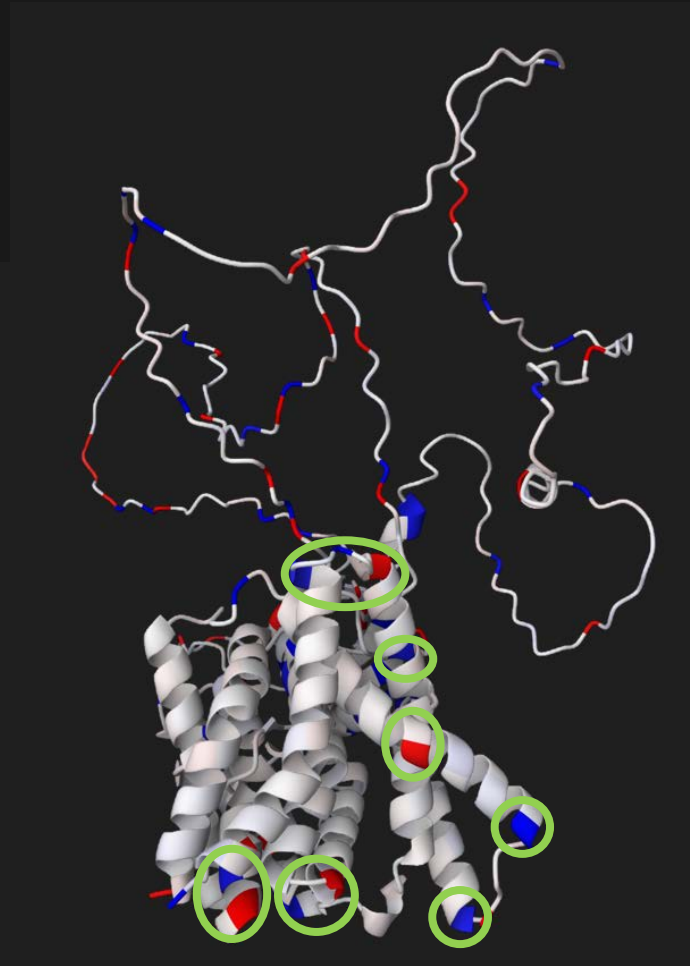
Bio: Structural bioinformatics support - example

PIN anatomy

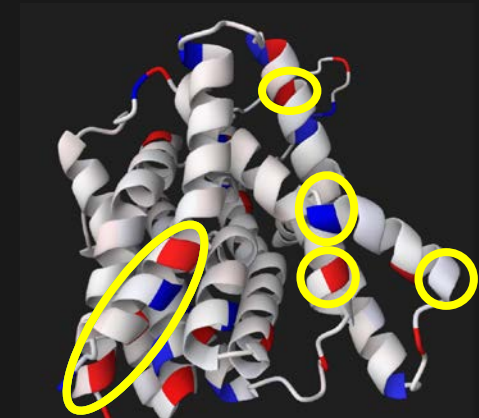
Legend:
Similar charges
Different charges



PIN3



PIN7



PIN5

Bio: Structural bioinformatics tools – new

AlphaFind (<https://alphafind.fi.muni.cz>):

Searching of similar proteins in AlphaFold DB

aCharges (<https://alphacharges.ncbr.muni.cz>)

Web application for calculation of partial atomic charges on AlphaFold2 structures

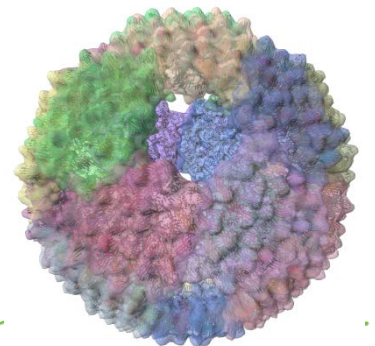
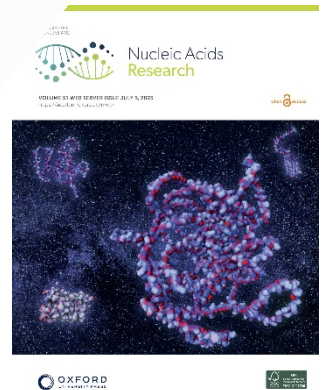
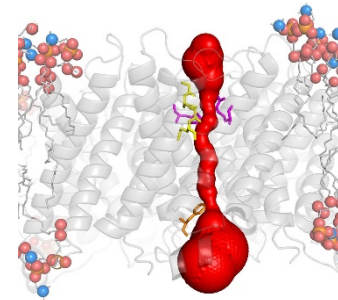
ChannelsDB (<https://channelsdb.biodata.ceitec.cz>)

Database of channels and pores in proteins

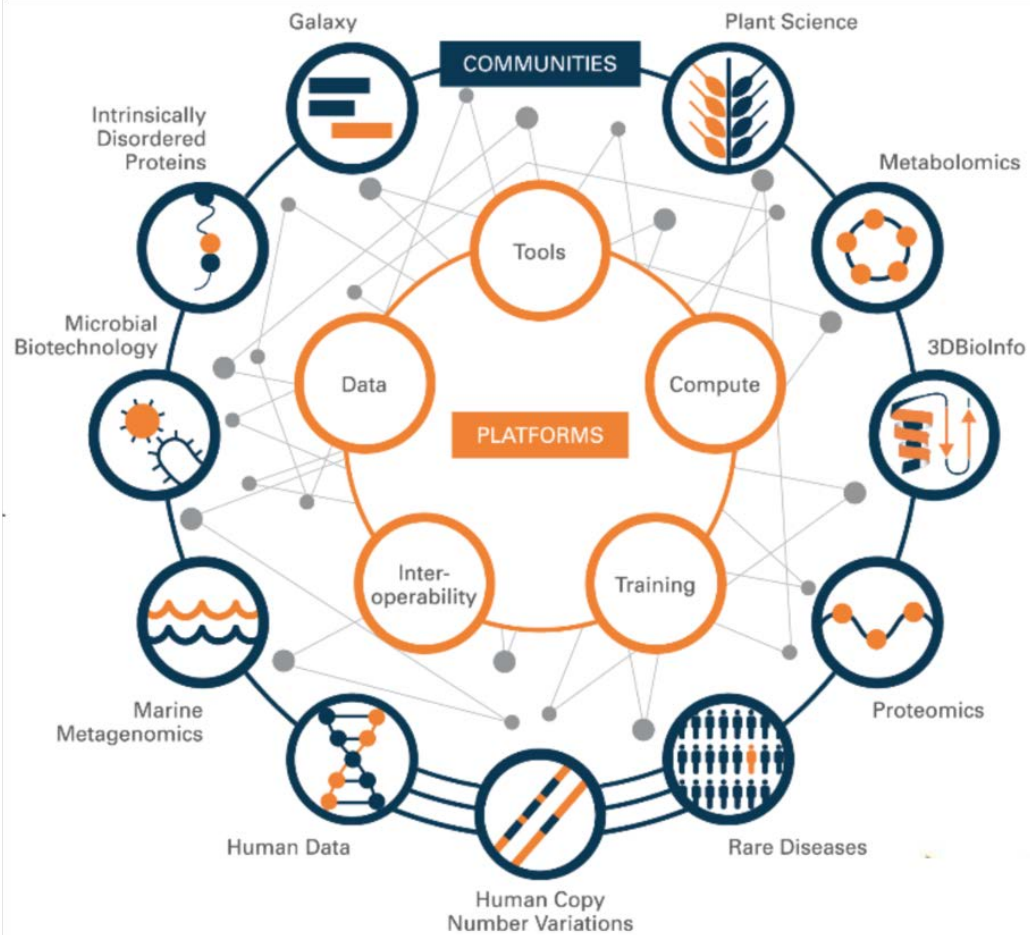
Mol *VS (<https://molstarvalseg.ncbr.muni.cz>)

Web application for visualization and interpretation of cell imaging data

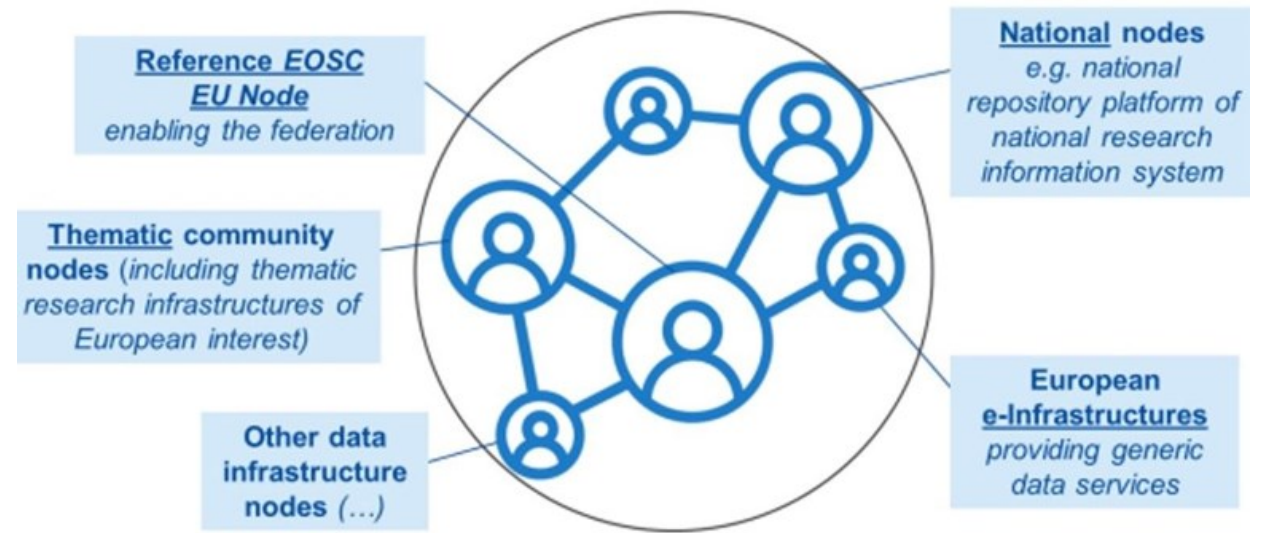
All published in **Nucleic Acids Research 2023-2024**



Bio: ELIXIR networking



Data: EOSC networking



Other information

Cooperation & Funding

- **ELIXIR & ELIXIR CZ**
 - Node at Masaryk university
 - funding 2023 - 2026
- **EOSC**
 - National repository platform (KA5)
 - Bio/Health/Food cluster
 - funding from 03/2024
- **EMBL-EBI**
 - Cooperation with Protein Data Bank, CATH, etc.



People

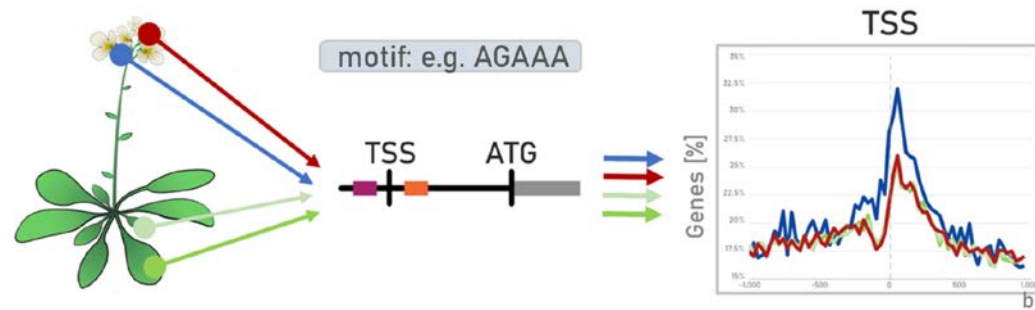


Acknowledgement text

- *„Biological Data Management and Analysis Core Facility of CEITEC Masaryk University, funded by ELIXIR CZ research infrastructure (MEYS Grant No: LM2023055), is gratefully acknowledged for supporting the research presented in this paper.“*

Summary

- For researchers:
 - We can help you to **store / make accessible / publish** your data



- For students:
 - Join us and **do research / build infrastructure** with us





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CEITEC -
Central European
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Thank you for your attention! Questions?

Radka Svobodová
radka.svobodova@ceitec.muni.cz

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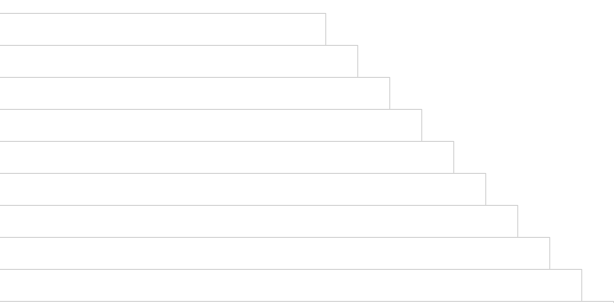
MUNI
CERIT-SC

CERIT-SC (part of e-INFRA CZ)

Luděk Matyska

CERIT-SC director

Institute of Computer Science MU



Who we are? A little bit of history

- Till 2019, CERIT-SC has been a separate Large Research Infrastructure, together with CESNET and IT4Innovations
- Since 2020, these three LRIs created an **e-INFRA CZ consortium** and work together as a complex (and unique) large national research e-infrastructure
- CERIT-SC is also founding member of ELIXIR CZ, Czech node of ELIXIR
- Collaboration with other LRIs

So, who we are? e-Infrastructure!

- Part of the [MetaCentrum](#)
- Resources
 - Compute capacity
 - Including GPUs
 - Storage capacity
- Service and tools layer
 - Batch processing (more at other parts of e-INFRA CZ)
 - OpenStack Cloud
 - Containers and Kubernetes
 - Jupyter notebooks
 - AAI

So, who we are? e-Infrastructure with expertise

- Efficient use of the resources and tools
 - Lukáš Hejtmánek, Viktoria Spišaková, Radek Polášek and the whole cloud team
- Optimization of algorithms and analyses
 - Aleš Křenek group
- GPU acceleration and
 - Jiří Filipovič research group
- General data analytics
 - Tomáš Rebok research group

What we have?

- 9000 CPUs
 - 3500 within Kubernetes environment
- 80 GPUs
 - 39 within Kubernetes environment
- Almost 15 PB storage capacity
 - 2,6 PB within the Kubernetes environment
 - Additional 4 PB on the way
 - Not repository features (e.g. guaranteed data retention)

Cloud, Containers, Kubernetes

- OpenStack cloud environment
 - Whole virtual machines/clusters
- Kubernetes and Containers support
 - Containers support reproducibility of computations/analyses
 - Kubernetes the management environment for containers
 - Very flexible environment (see next slide)
 - Extensible application catalogue
 - Rancher applications: Ansys, Matlab, Rstudio, VMD, UI for LLM, ...

Containers and Kubernetes applications

- Static always running applications, e.g. webs and portals
- HPC workflows (batch processing), including long-term running applications
- Interactive workloads
 - Jupyter Hubs, virtual desktops, GUIs, ...
- But also semi-interactive HPC workflows (e.g. CryoEM sw)
- Bursty workloads

- Ability to restart applications, increased reliability of the environment

JupyterHub

- <https://hub.cloud.e-infra.cz>
- Integrated with e-INFRA CZ storage
 - Integration with Onedata datasets in progress
- No explicit runtime limit
- Set of prepared applications already available
- Allows to spawn additional jobs from the notebook (cascading)
- Notebook environment for advanced users
 - <https://binderhub.cloud.e-infra.cz>
 - Build notebook image from source
 - Possible to request special resources (RAM, CPU, GPU, ...)

Aplhafold

- Web UI for Apphafold tools
- Supports several different tools
 - Alphafold, Colabfold, Omegafold, Emsfold
- Colabfold
 - Running our mmseqs server (no rate limits)
 - Added possibility to limit number of models
- Integrated Mol* viewer and e-INFRA CZ storage

- Also collaboration on the development and support for AlphaFind

Aleš Křenek group

- Building application specific computational environments for scientific data processing, analysis, and interaction with data repositories
 - CryoEM, MD, protein similarities
- Joint development of advanced computational techniques in scientific data processing using ML and quantum computing
 - Mass spectroscopy, MD
- Operation and development of Galaxy service, generic environment for FAIR data processing
 - <https://usegalaxy.cz>

Jiří Filipovič Group

- Methods for Automatic Code Optimization
 - OpenCL and CUDA Autotuning with kernel Tuning Toolkit
 - Optimization of Computation Kernels Granularity
- Application in Computation Chemistry and Biology
 - Caverdock 2.0
 - Optimization and acceleration of EM software (Xmipp sw package)
- Related areas of research interest
 - Runtime systems
 - Performance Engineering
 - Performance Prediction Methods
 - Real-time simulations

Tomáš Rebok Group

- Data analytics environment for heterogeneous and multisource unstructured data
 - Central processing, personal datasets and „assistents“, ...
- Originally developed for Police
 - Need of high privacy, personal data processing
 - Highly unstructured data combined with structured ones
- Work with Institute for Global Change (CzechGlobe)
- Currently offered as the Core Data Center facility and services for the eLTER-ERIC under preparation

CERIT-SC interaction with EOSC

- Coordinating the EOSC-CZ project
 - Partners are CESNET and VSB-TUO (IT4Innovations)
 - The strategic project of OP JAK
 - To oversee, monitor and support the EOSC implementation in CR
 - Hosting EOSC CZ secretariat
- Collaborating with CARDS project (NTK)
 - Mirek Bartošek one of the major architects for PNG
- Member of NRP for research data project
 - Coordinated by CESNET
 - CERIT-SC leading service oriented workpackages there

CERIT-SC interaction with EOSC

- Collaborating with UK on preparation of the Open Science II project
 - Helping to coordinate MU involvement
- Providing also wider Open Science support at MU
 - MU Open Science strategy
 - Support for Open Access
 - Coordinating the OpenAccess/Open Science managers at MU
 - Cultivating support and environment for the Data Curators

Summary for CERIT-SC

- CERIT-SC provides resources together with the advanced expertise for their use
 - From batch processing to highly interactive tasks
 - Indirect support for AI (LLM) processing on GPUs
- Part of large research infrastructures
 - Formally e-INFRA CZ and ELIXIR CZ
 - eLTER(-ERIC) in progress
- Collaboration with other LRIs
 - BBMRI CZ, RECETOX, CzeCOS, ...
-

Thank you for your attention