

Pokročilé metody v genomice a proteomice: analýza proteinových komplexů

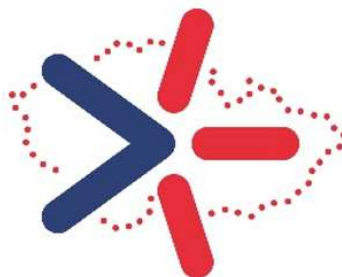
doc. Jan Paleček

jpalecek@sci.muni.cz

laboratoř Strukturních proteinů eukaryotních chromosomů
(<http://www.ncbr.muni.cz/SPEC/>)



Financováno
Evropskou unií
NextGenerationEU



**Národní
plán
obnovy**

MSMT
MINISTERSTVO ŠKOLSTVÍ,
MLÁDEŽE A TĚLOVÝCHOVY

NPO_MUNI_MSMT-16606/2022

Malý průlet světem buňky



hhmi | BioInteractive
Machinery of Life

www.BANDICAM.com

The Molecular Machinery of Life

většina ... proteinové komplexy ...

... chromosomy

dostupné: <https://www.youtube.com/watch?v=FJ4N0iSeR8U>

... a o čem uslyšíte

- Co všechno se dozvíte o genu/proteinu z databází
 - 3D (terciární) struktura proteinů
 - Proteinové interakce
 - Proteinové komplexy (kvarterní struktura)
- Jak získat nové informace o proteinových komplexech experimentálně
 - Analýza protein-proteinových interakcí
 - Analýza komplexů



NGS přináší nevídané množství dat

- rychlé sekvenování genomů poskytuje informace o proteinech v různých organismech
- proteinové databáze UNIPROT (SWISSPROT...): <https://www.uniprot.org/>
- potvrzuje představu evoluce proteinů/organismů – ukazuje na velkou konzervovanost většiny proteinů
- tyto podobnosti umožňují modelování proteinů i z málo charakterizovaných organismů (a jejich anotaci) – spolehlivé modelování pro homologie >30%

Základní alignment

- pokud pracujete s novou sekvencí (např. není v UNIPROT): BLAST – <https://blast.ncbi.nlm.nih.gov/>
- hledání příbuzných sekvencí vám napoví nakolik je protein evolučně konzervovaný, jaké má domény ... jakou mají funkci jemu podobné proteiny (např. UNIPROT databáze)

Web BLAST

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#)

Query subrange [?](#)

From

To

Or, upload file Soubor nevybrán. [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

Align two or more sequences [?](#)

Choose Search Set

Databases Standard databases (nr etc.): **New** Experimental databases

Compare Select to compare standard and experimental database [?](#)

Standard

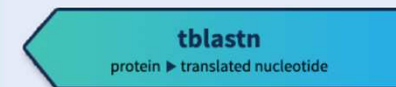
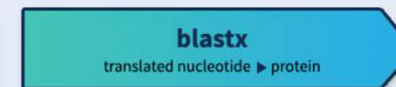
Database [?](#)

Organism Optional exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

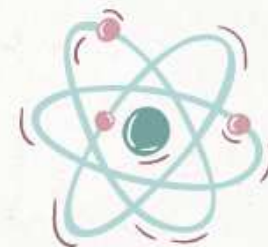
Exclude Optional Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Web BLAST



printscreen: autor

UniProt a jeho možnosti



Komplexní, vysoce kvalitní a volně přístupný zdroj sekvenčních a funkčních informací o proteinech

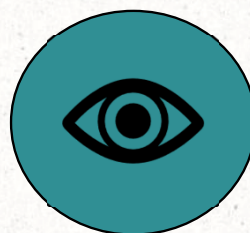
- Popis a funkce
- Zjištění přítomnosti domén daného proteinu
- Zjištění interakčních partnerů
- Struktura proteinu – PDB, Alphafold ... komplexy



**Hledání
proteinu**



Souvislosti
Funkce
Interaktom
Mutace



Vizualizace
Alphafold
Lokalizace proteinu



**Stahování
dat**

UniProt – vyhledávání

Histon H3

<https://www.uniprot.org/>

Browser address bar: <https://www.uniprot.org/uniprotkb?query=H3+cerevisiae>

UniProt navigation: BLAST Align Peptide search ID mapping SPARQL UniProtKB ▾ H3 cerevisiae Advanced | List Search

Status

Reviewed (Swiss-Prot)
(244)

Unreviewed (TrEMBL)
(308)

Popular organisms

S. cerevisiae (176)

Human (16)

Rat (7)



UniProtKB 552 results

BLAST Align Map IDs Download Add View: Cards ○ Table ● Customize columns Share ▾

Entry ▲	Entry Name ▲	Protein Names ▲	Gene Names ▲	Organism ▲	Length
<input type="checkbox"/> P61830	H3_YEAST	Histone H3	HHT1 , YBR010W, YBR0201, HHT2, SIN2, YNL031C, N2749	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	136 AA
<input type="checkbox"/> Q757N1	H3_ASHGO	Histone H3	HHT1 , ADL202C, HHT2, AER013W	Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) (Yeast) (Eremothecium gossypii)	136 AA

... i lidský

printscreen: autor

Histon H3

Informace o proteinu - UNIPROT

- Function
- Names & Taxonomy
- Subcellular Location
- Phenotypes & Variants
- PTM/Processing
- Expression
- Interaction
- Structure
- Family & Domains
- Sequence
- Similar Proteins

Functionⁱ

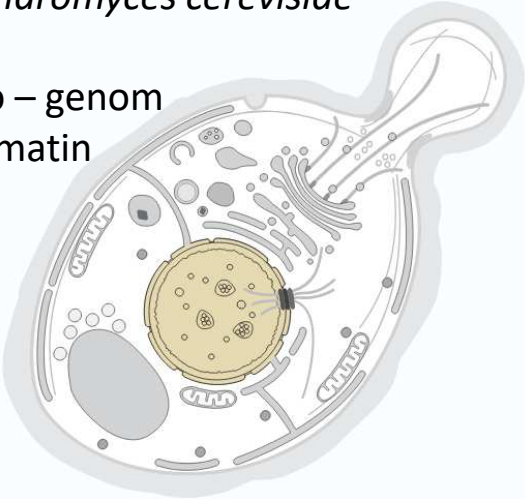
Core component of **nucleosome**. Nucleosomes wrap and compact DNA into **chromatin**, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling. Component of the UAF (upstream activation factor) complex which interacts with the upstream element of the RNA polymerase I promoter and forms a stable preinitiation complex.

Subcellular Locationⁱ

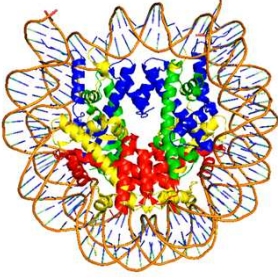
UniProt Annotation GO Annotation

Saccharomyces cerevisiae

jádro – genom
chromatin



- Nucleus Curated
- Chromosome Curated



Genová ontologie

ASPECT	TERM
Cellular Component	CENP-A containing nucleosome Source:SGD 1 Publication
Cellular Component	nucleosome Source:ComplexPortal 1 Publication
Cellular Component	nucleus Source:SGD 1 Publication
Cellular Component	replication fork protection complex Source:SGD 1 Publication
Cellular Component	RNA polymerase I upstream activating factor complex Source:ComplexPortal 1 Publication
Molecular Function	DNA binding Source:SGD 1 Publication
Molecular Function	protein heterodimerization activity Source:InterPro
Molecular Function	structural constituent of chromatin Source:InterPro
Biological Process	chromatin organization Source:SGD 1 Publication
Biological Process	global genome nucleotide-excision repair Source:SGD 1 Publication
Biological Process	nucleolar large rRNA transcription by RNA polymerase I Source:ComplexPortal 1 Publication

upozornění: informace nebývají kompletní (i chybné) – dohledat v člancích

printscreen: autor



Informace o proteinu - UNPROT



Function

Names & Taxonomy

Subcellular Location

Phenotypes & Variants



PTM/Processing

Expression

Interaction

Structure

Family & Domains

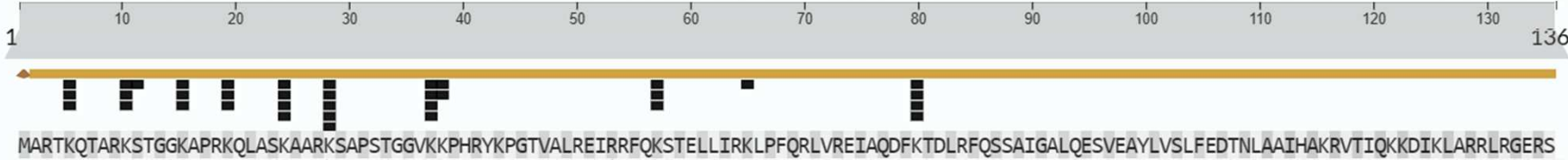
Sequence

Similar Proteins

Functionⁱ

Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called **histone code**, and nucleosome remodeling. Component of the UAF (upstream activation factor) complex which interacts with the upstream element of the RNA polymerase I promoter and forms a stable preinitiation complex.

PTM | #Acetylation
#Methylation
#Phosphoprotein



Acetylation of histone H3 leads to transcriptional activation. H3K14ac formation by GCN5, a component of the SAGA complex, is promoted by H3S10ph. Further acetylated by GCN5 to form **H3K9ac**, H3K18ac, H3K23ac, H3K27ac and H3K36ac. H3K14ac can also be formed by ESA1, a component of the NuA4 histone acetyltransferase (HAT) complex. **H3K56ac** formation occurs predominantly in newly synthesized H3 molecules during G1, S and G2/M of the cell cycle and may be involved in DNA repair. [13 Publications](#)



Informace o proteinu - UNPROT

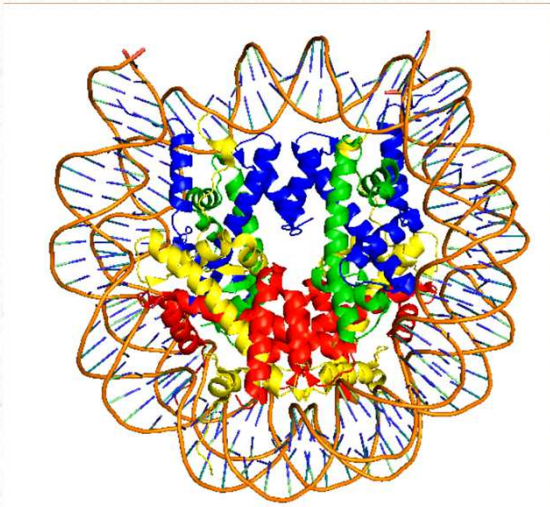
- ▶ **Function**
- Names & Taxonomy
- Subcellular Location
- Phenotypes & Variants
- PTM/Processing
- Expression
- ▶ **Interaction**
- Structure
- Family & Domains
- Sequence
- Similar Proteins

Functionⁱ

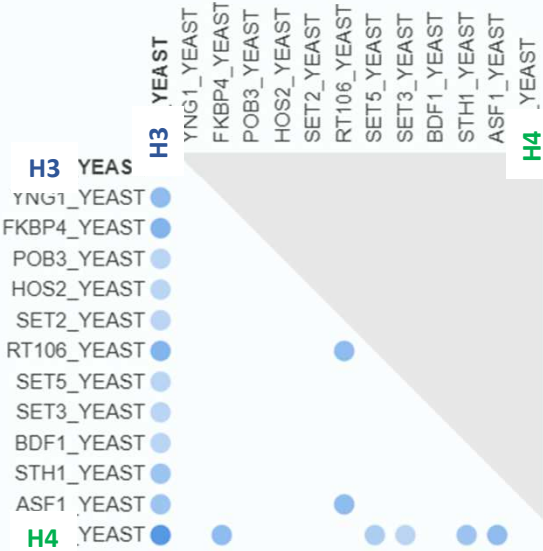
Core component of **nucleosome**. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling. Component of the UAF (upstream activation factor) complex which interacts with the upstream element of the RNA polymerase I promoter and forms a stable preinitiation complex.

Subunitⁱ

The **nucleosome** is a histone octamer containing two molecules each of H2A, H2B, H3 and H4 assembled in one H3-H4 heterotetramer and two H2A-H2B heterodimers. The octamer wraps approximately 147 bp of DNA. Histone H3 is a component of the UAF (upstream activation factor) complex, which consists of UAF30, RRN5, RRN9, RRN10, and histones H3 and H4. 1 Publication



Binary interactionsⁱ



video a printscreen: autor

Informace o proteinu - IntAct



<https://www.ebi.ac.uk/intact>

Protein-protein interaction databases

BioGRID | 32711 [↗](#) 918 interactors
35796 [↗](#) 705 interactors

ComplexPortal | **CPX-1101** [↗](#) RNA polymerase I upstream activating factor complex
CPX-1610 [↗](#) Nucleosome, variant HTA2-HTB2

DIP | **DIP-417N** [↗](#)

IntAct | **P61830** [↗](#) 153 interactors

MINT | **P61830** [↗](#)

STRING | **4932.YBR010W** [↗](#)

Select	Molecule A	Molecule B	Identifier A	Identifier B	Type A	Type B	Species A	Species B	Host Organism	Positive interaction	Detection Method	Publication IDs	Interaction Type
--------	------------	------------	--------------	--------------	--------	--------	-----------	-----------	---------------	----------------------	------------------	-----------------	------------------

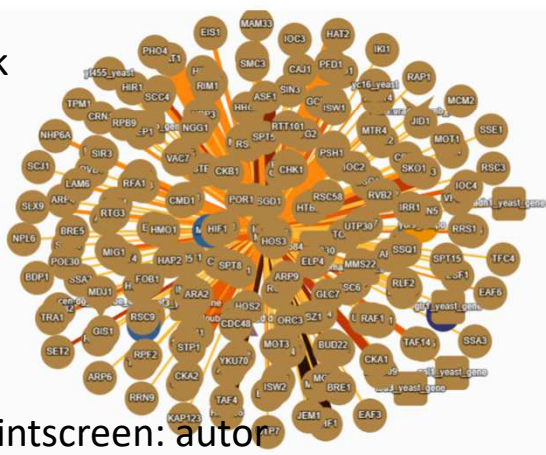
<input type="checkbox"/>		H4	H3	UniProt P02309	UniProt P61830	protein	protein						
--------------------------	--	-----------	-----------	--------------------------------	--------------------------------	---------	---------	--	--	--	--	--	--

H3 YEAS	H4 YEAS
YNG1_YEAST	<input type="checkbox"/>
FKBP4_YEAST	<input type="checkbox"/>
POB3_YEAST	<input type="checkbox"/>
HOS2_YEAST	<input type="checkbox"/>
SET2_YEAST	<input type="checkbox"/>
RT106_YEAST	<input type="checkbox"/>
SET5_YEAST	<input type="checkbox"/>
SET3_YEAST	<input type="checkbox"/>
BDF1_YEAST	<input type="checkbox"/>
STH1_YEAST	<input type="checkbox"/>
ASF1_YEAST	<input type="checkbox"/>
H4_YEAST	<input checked="" type="checkbox"/>

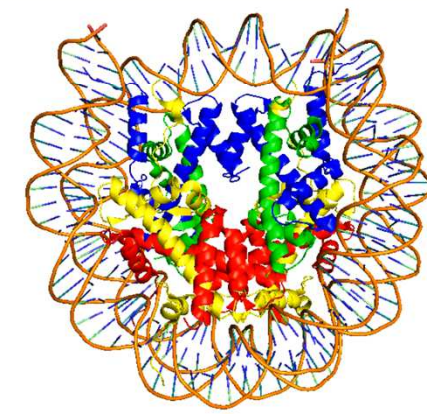
<input checked="" type="checkbox"/>	tap	16554755	physical association
		10.1038/nature04670	

... i nepřímé interakce

network sít'



- chaperon
- deacetylaza
- metyltransferasa
- chaperon
- metyltransferasa
- bromodoména
- chaperon
- histon H4



video a printscreen: auto



Protein-protein interaction databases

BioGRID | 32711 [↗](#) 918 interactors
35796 [↗](#) 705 interactors






DIP | [DIP-417N](#) [↗](#)

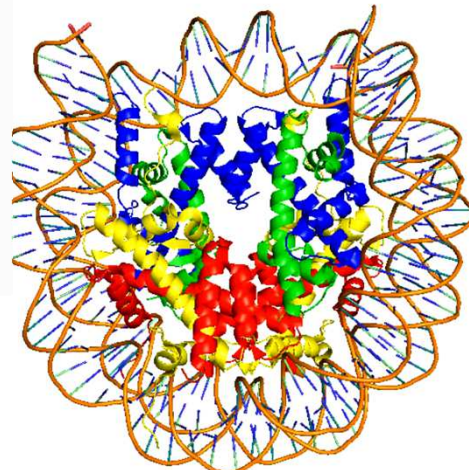
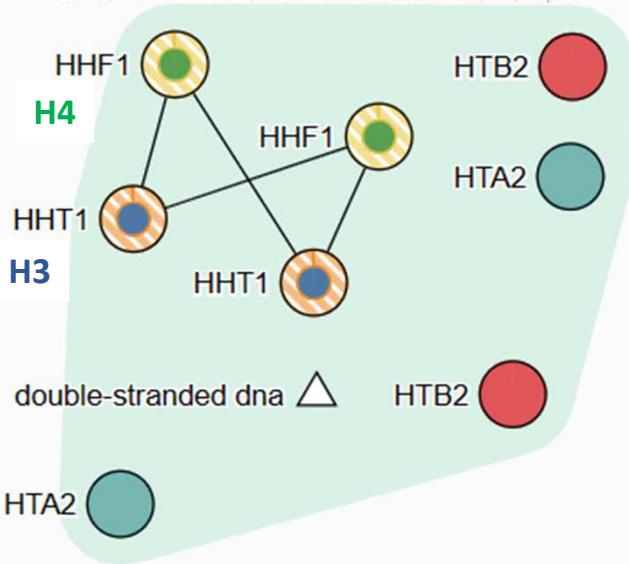
IntAct | [P61830](#) [↗](#) 153 interactors

MINT | [P61830](#) [↗](#)

ComplexPortal | [CPX-1101](#) [↗](#) RNA polymerase I upstream activating factor complex

➔ [CPX-1610](#) [↗](#) Nucleosome,
[CPX-1611](#) [↗](#) Nucleosome,
[CPX-1612](#) [↗](#) Nucleosome,
[CPX-1613](#) [↗](#) Nucleosome,
[More ComplexPortal links](#)

Legend	Description	Stoichiometry
	protein - HTA2 (unspecified role) P04912 ↗ Histone H2A.2	H2A 2
	protein - HTB2 (unspecified role) P02294 ↗ Histone H2B.2	H2B 2
	protein - HHT1 (unspecified role) P61830 ↗ Histone H3	H3 2
	protein - HHF1 (unspecified role) P02309 ↗ Histone H4	H4 2
	small molecule - double-stranded dna (unspecified role) CHEBI:4705 ↗ double-stranded DNA	1



video a printscreen: autor

Informace o proteinu - UNPROT

sekundární struktury

Histon H3

Function

Names & Taxonomy

Subcellular Location

Disease & Variants

PTM/Processing

Expression

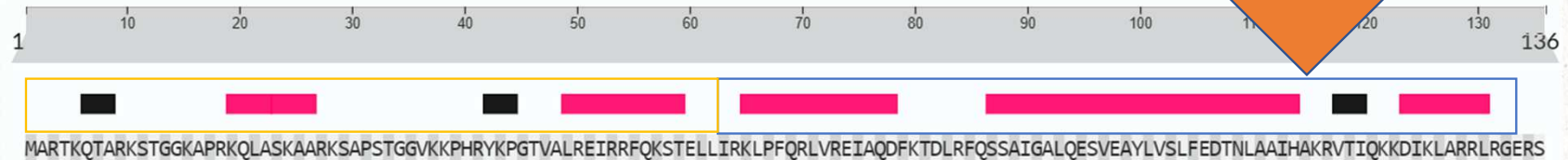
Interaction

Structure

Family & Domains

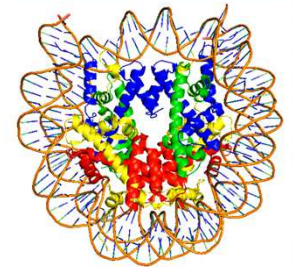
Sequence & Isoforms

Similar Proteins



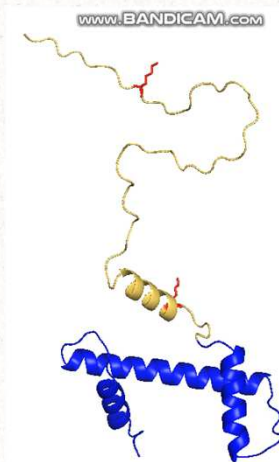
Family and domain databases

- Gene3D | 1.10.20.10 [↗](#) Histone, subunit A 1 hit
- IDEAL | IID50143 [↗](#)
- InterPro | [View protein in InterPro ↗](#)
- IPR009072 [↗](#) **Histone-fold**
- IPR007125 [↗](#) Histone_H2A/H2B/H3
- IPR000164 [↗](#) Histone_H3/CENP-A



Model Confidence:

- Very high (pLDDT > 90)
- Confident (90 > pLDDT > 70)
- Low (70 > pLDDT > 50)
- Very low (pLDDT < 50)



- PROSITE | [View protein in PROSITE ↗](#)
- PS00322 [↗](#) HISTONE_H3_1 1 hit
- PS00959 [↗](#) HISTONE_H3_2 1 hit
- Pfam | [View protein in Pfam ↗](#)
- PF00125 [↗](#) Histone 1 hit

terciární a kvarterní struktura

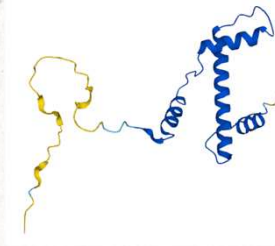
<https://alphafold.ebi.ac.uk/>

Structureⁱ

PDB	7XAY	X-ray	3.30 Å	D	2-136	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	7Z0O	EM	2.80 Å	A/C	1-136	PDBe · RCSB-PDB · PDBj · PDBsum
AlphaFold	AF-P61830-F1	Predicted			1-136	AlphaFold

video a printscreen: autor

Proteinové domény

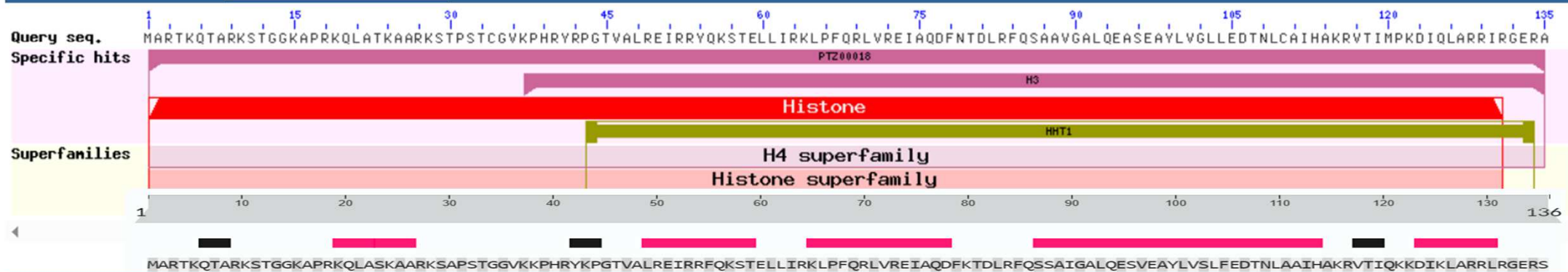


Protein Classification

histone H3 (domain architecture ID 10794185)

histone H3 is a core component of the nucleosome that wraps and compacts DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template

Graphical summary Zoom to residue level show extra options >



List of domain hits

Name	Accession	Description	Interval	E-value
[+] PTZ00018	PTZ00018	histone H3; Provisional	1-135	1.16e-85
[+] H3	smart00428	Histone H3;	37-135	5.99e-58
[+] Histone	pfam00125	Core histone H2A/H2B/H3/H4;	1-131	5.89e-49
[+] HHT1	COG2036	Archaeal histone H3/H4 [Chromatin structure and dynamics];	43-134	8.80e-30

<https://prosite.expasy.org/>, <https://www.ebi.ac.uk/interpro/entry/pfam>

printscreen: autor

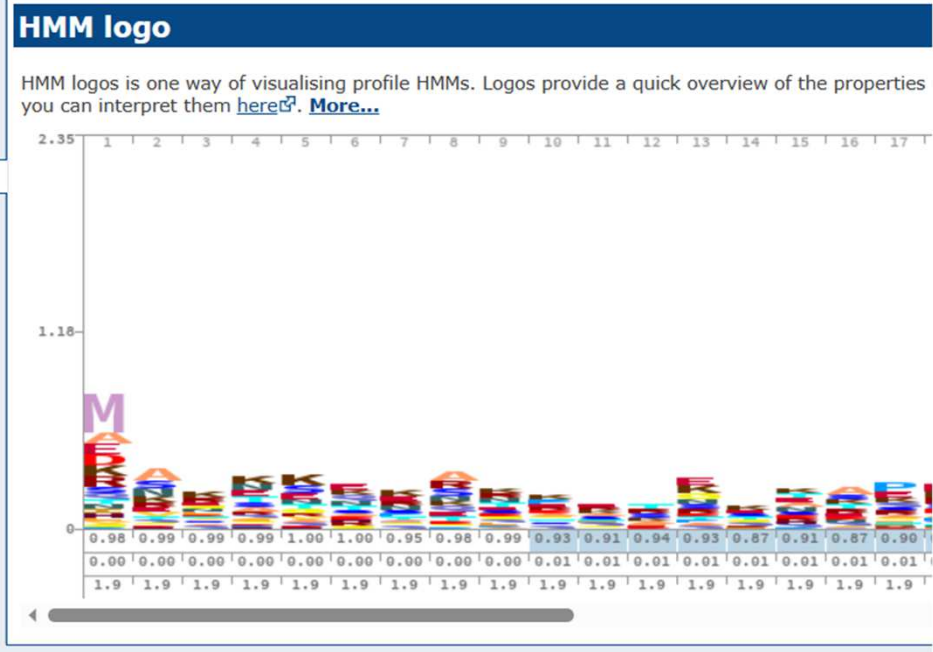
Proteinové domény

Family: *Histone* (PF00125)

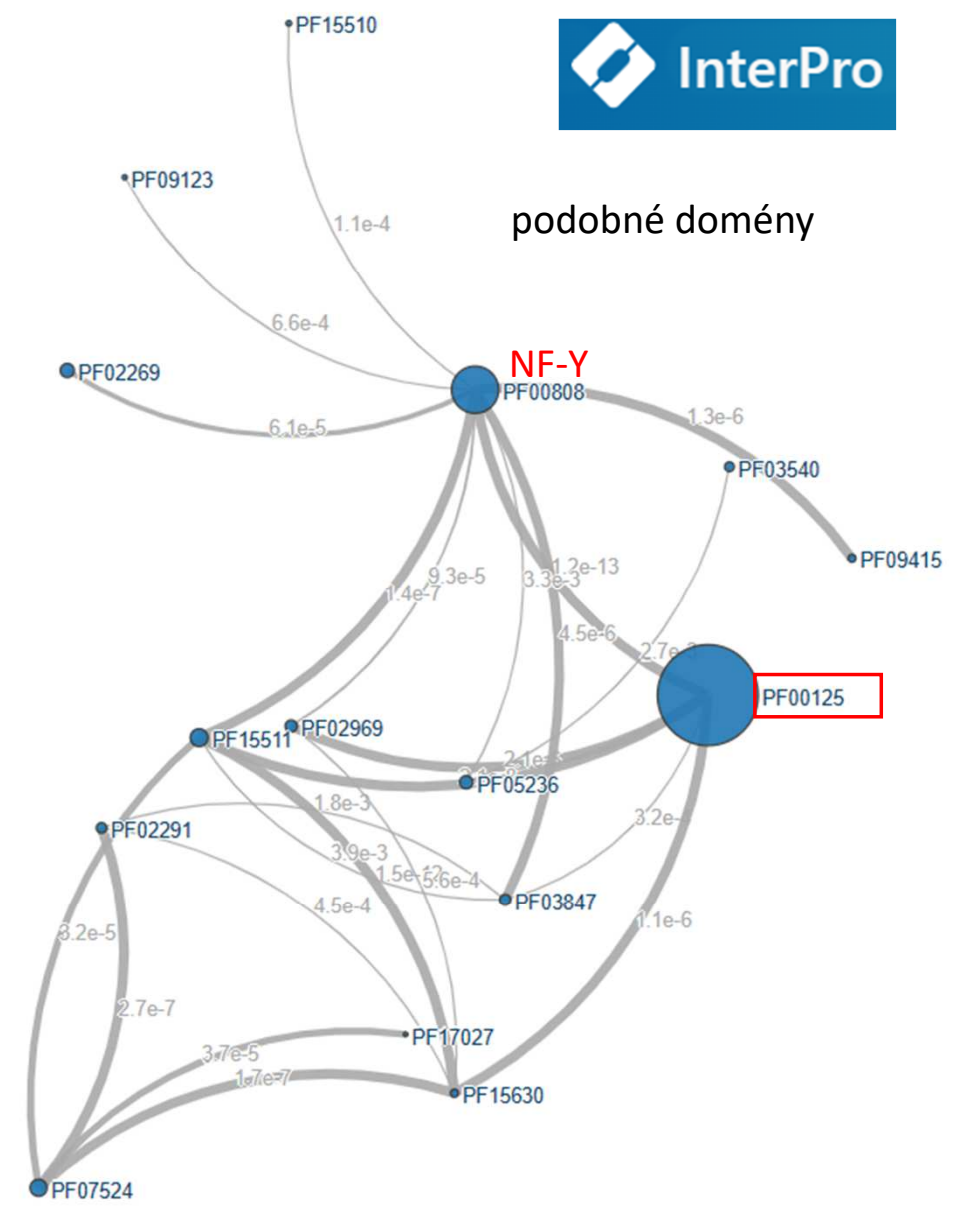
377 architecture



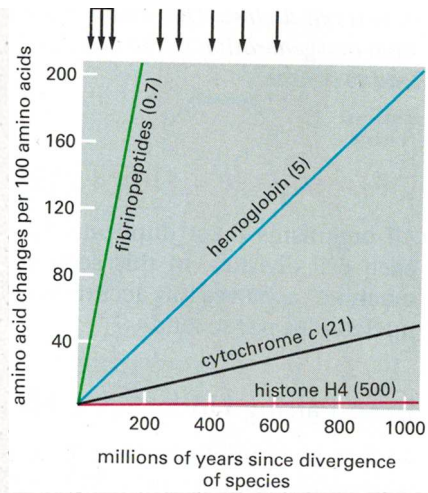
- Summary
- Domain organisation
- Clan
- Alignments
- HMM logo**
- Trees
- Curation & model
- Species
- Structures
- AlphaFold Structures
- trRosetta Structure



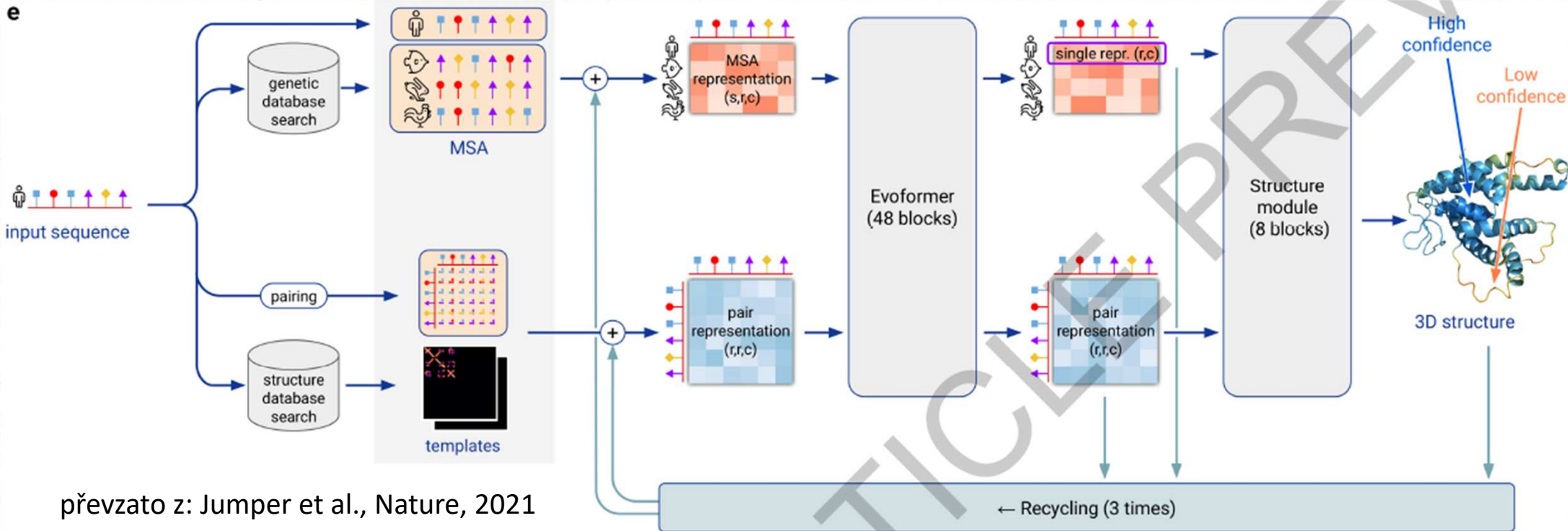
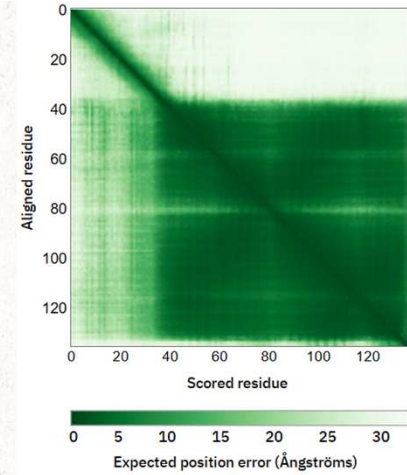
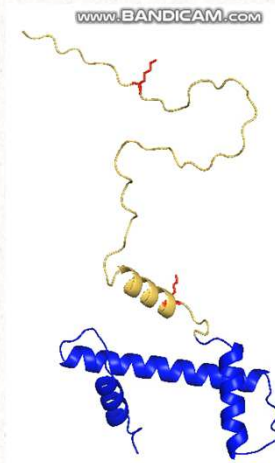
podobné domény



printscreen: autor



AlphaFold



převzato z: Jumper et al., Nature, 2021

AlphaFold – predikce 3D struktury proteinu i komplexů

- Využití online predikce Alphafold

- <https://colab.research.google.com/github/sokrypton/ColabFold/blob/main/AlphaFold2.ipynb#scrollTo=G4yBrceuFbf3>
- LatchBio: <https://console.latch.bio/workflows>

The screenshot displays the 'Workflows' page on the LatchBio platform. At the top right, there is an 'Upload Workflow' button. Below the title, there are tabs for 'Workflows' (selected) and 'All Executions'. A search bar and a dropdown menu for 'Sort: Executions Ran' are also visible. The main content area lists two workflows:

- AlphaFold2** (Verified) with 10268 executions. Description: 'AlphaFold produces highly accurate protein structure predictions'. Author: Deepmind, version v2.3.1+1.
- ColabFold** (Verified) with 5572 executions. Description: 'The ColabFold version of AlphaFold2 is optimized for extremely fast predictions on small proteins. It uses the same basic architecture as AlphaFold2, but optimizes the sequence search procedure.' Author: Sergey O., version 0.0.48-fa4cfc.

- Umožňuje i predikci 3D struktury proteinového komplexu (dimeru dvou proteinů – díky jejich **koevoluci**)

Informace o proteinu - UNIPROT

kvarterní struktura

Function

Names & Taxonomy

Subcellular Location

Disease & Variants

PTM/Processing

Expression

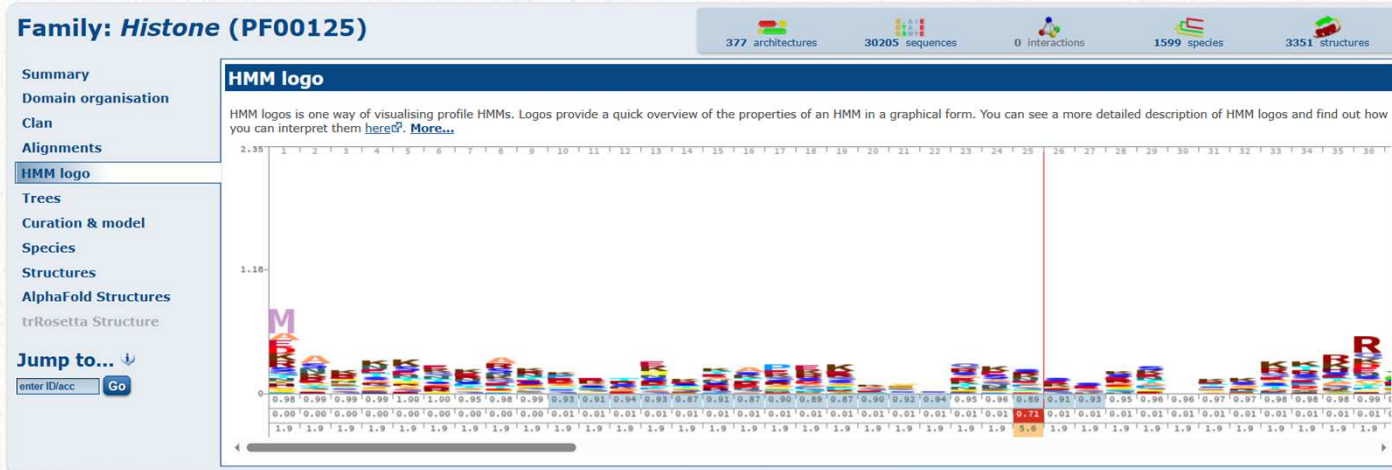
Interaction

Structure

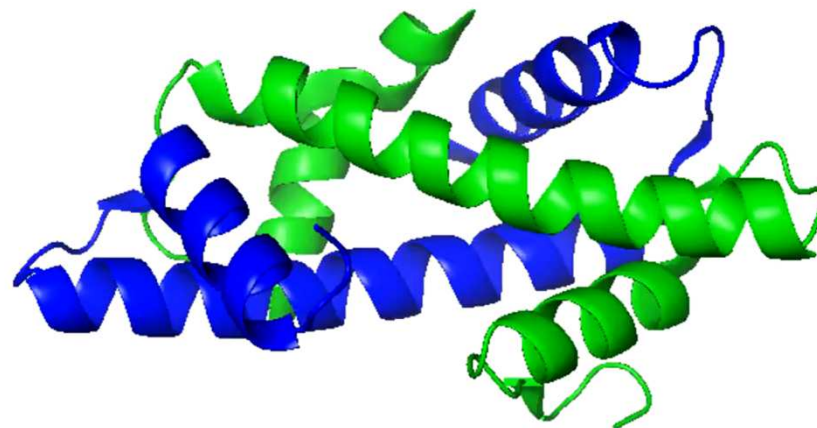
Family & Domains

Sequence & Isoforms

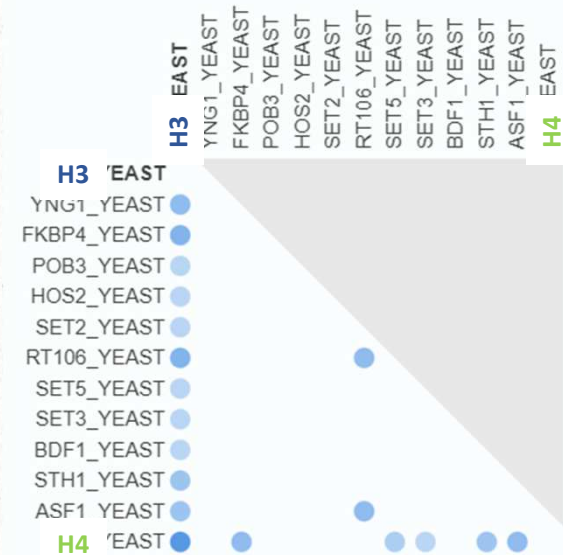
Similar Proteins



Histon fold –
typicky P-P vazba
... vazba na DNA



H3-H4 dimer



video a printscreen: autor

Histon H3

Informace o proteinu - UNPROT

Function

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Subcellular Location

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Interaction

Structure

Family & Domains

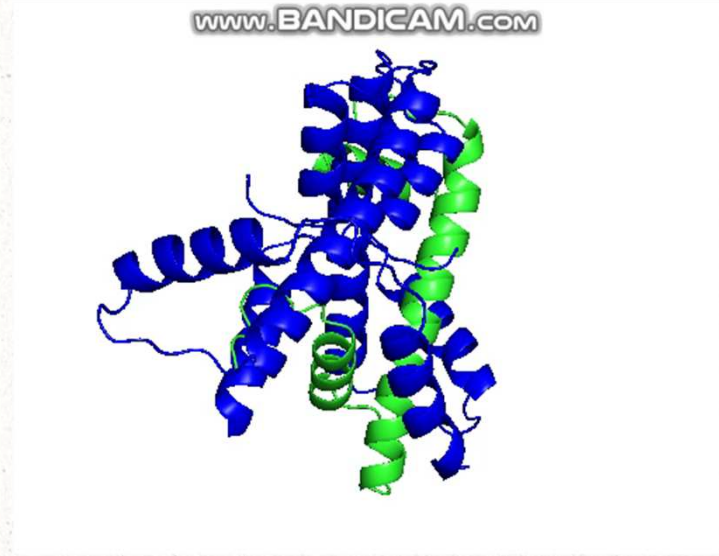
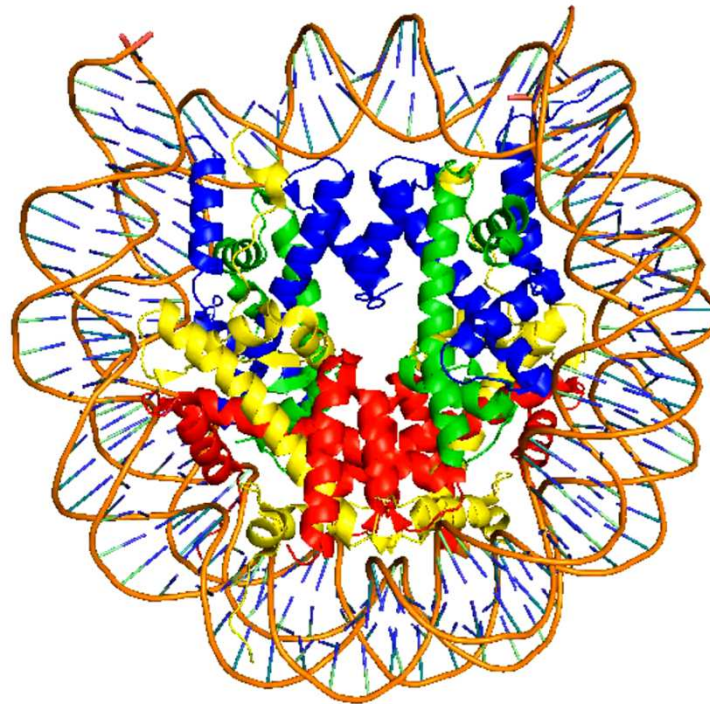
Sequence & Isoforms

Similar Proteins

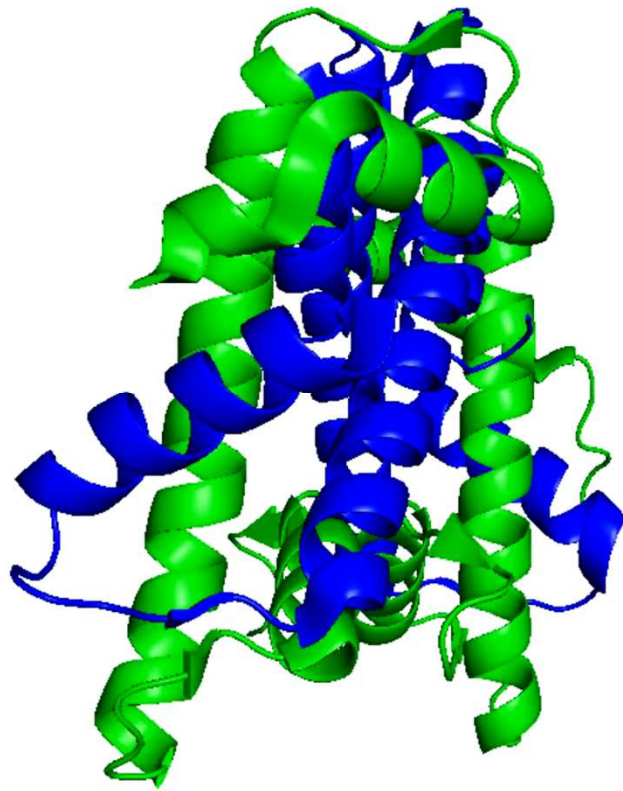
Structureⁱ

kvarterní struktura

PDB	7XAY	X-ray	3.30 Å	D	2-136	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	7Z0O	EM	2.80 Å	A/C	1-136	PDBe · RCSB-PDB · PDBj · PDBsum
AlphaFold	AF-P61830-F1	Predicted			1-136	AlphaFold



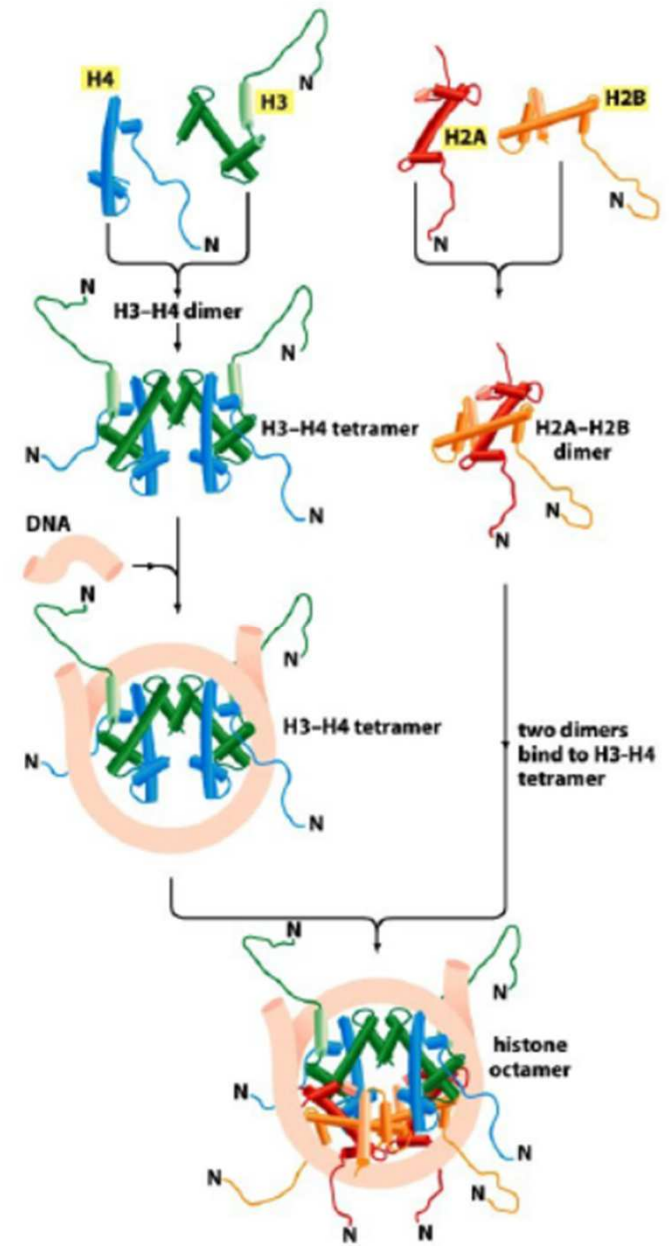
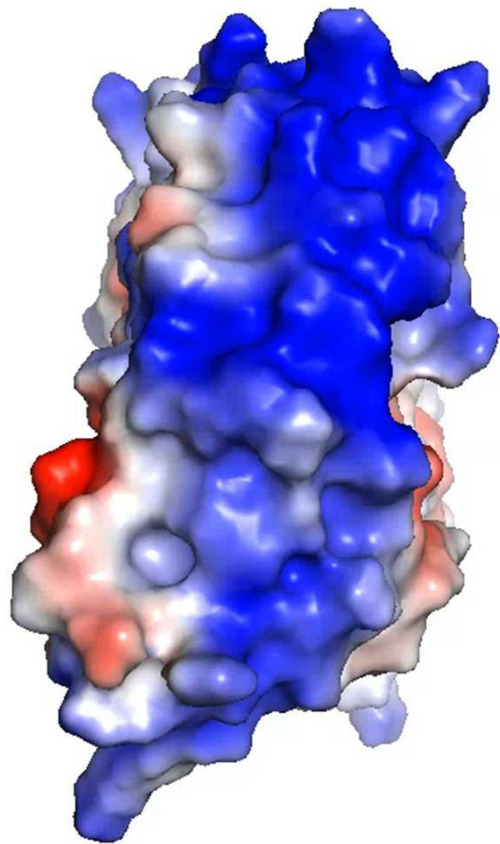
H3-H3 dimer vygeneroval alphafold jako H3-H4 dimer – až po použití H3-H4+H3 umístil H3-H3 dimer správně



nukleosom se skládá na „začátku“ (replikace DNA – vznik nové DNA ...), ale i v průběhu života buňky (oprava DNA, transkripce) – odbalení a sbalení nukleosomu regulují chaperony, remodelační komplexy ...

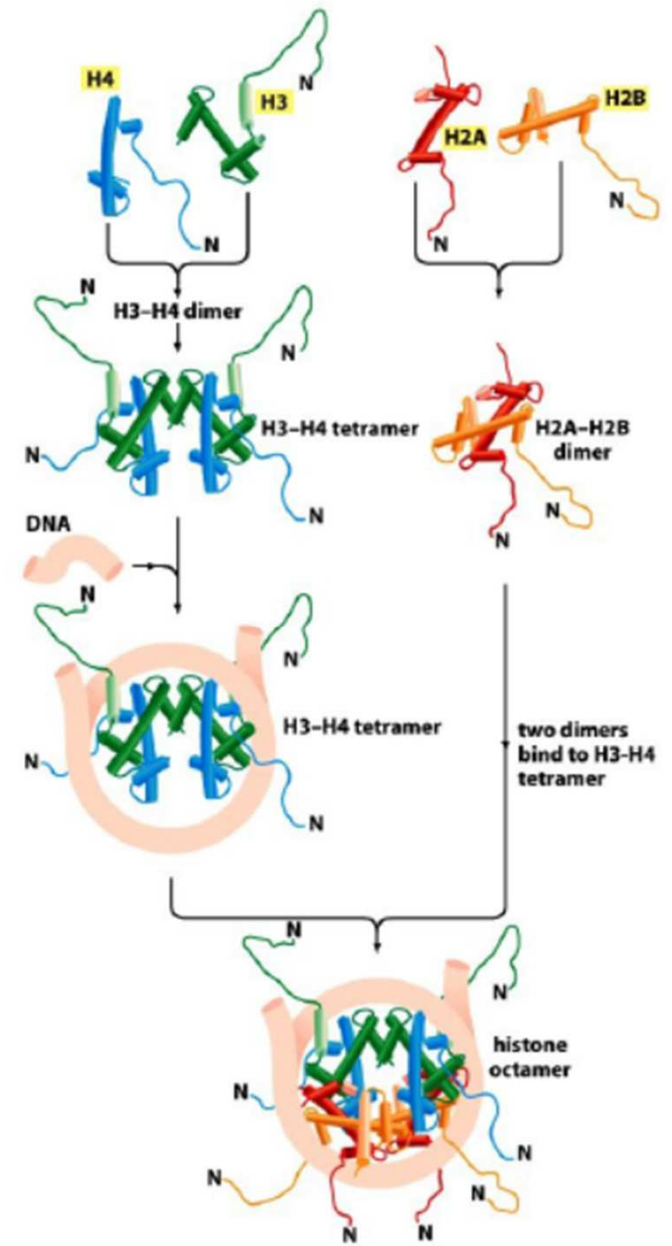
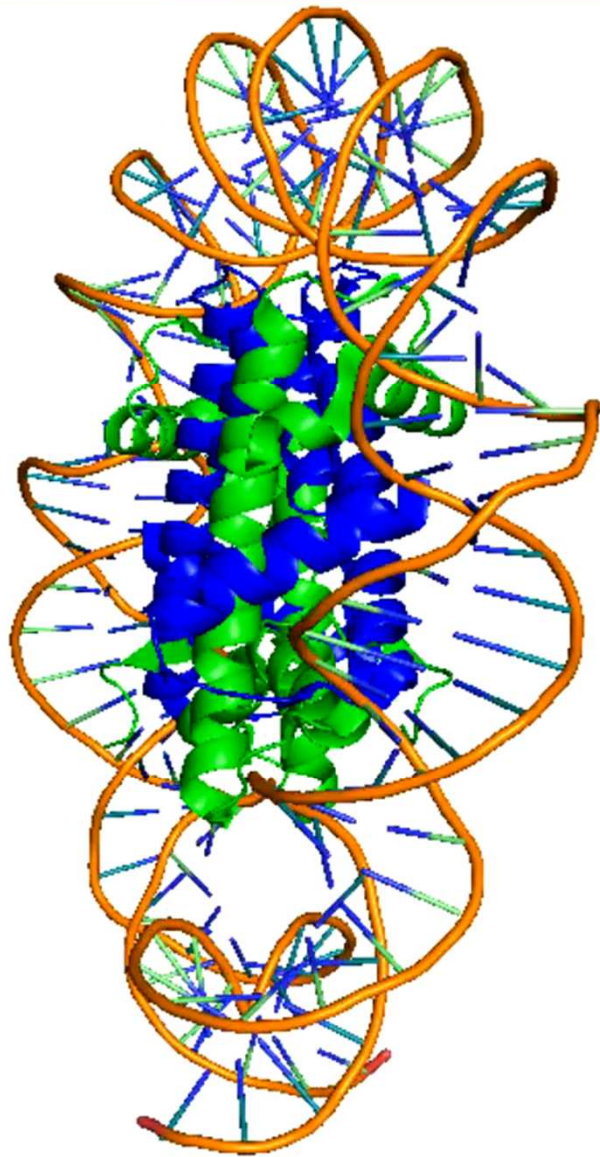
- H3-H3 interakce = $(\text{H3-H4})_2$ tetramer

video: autor



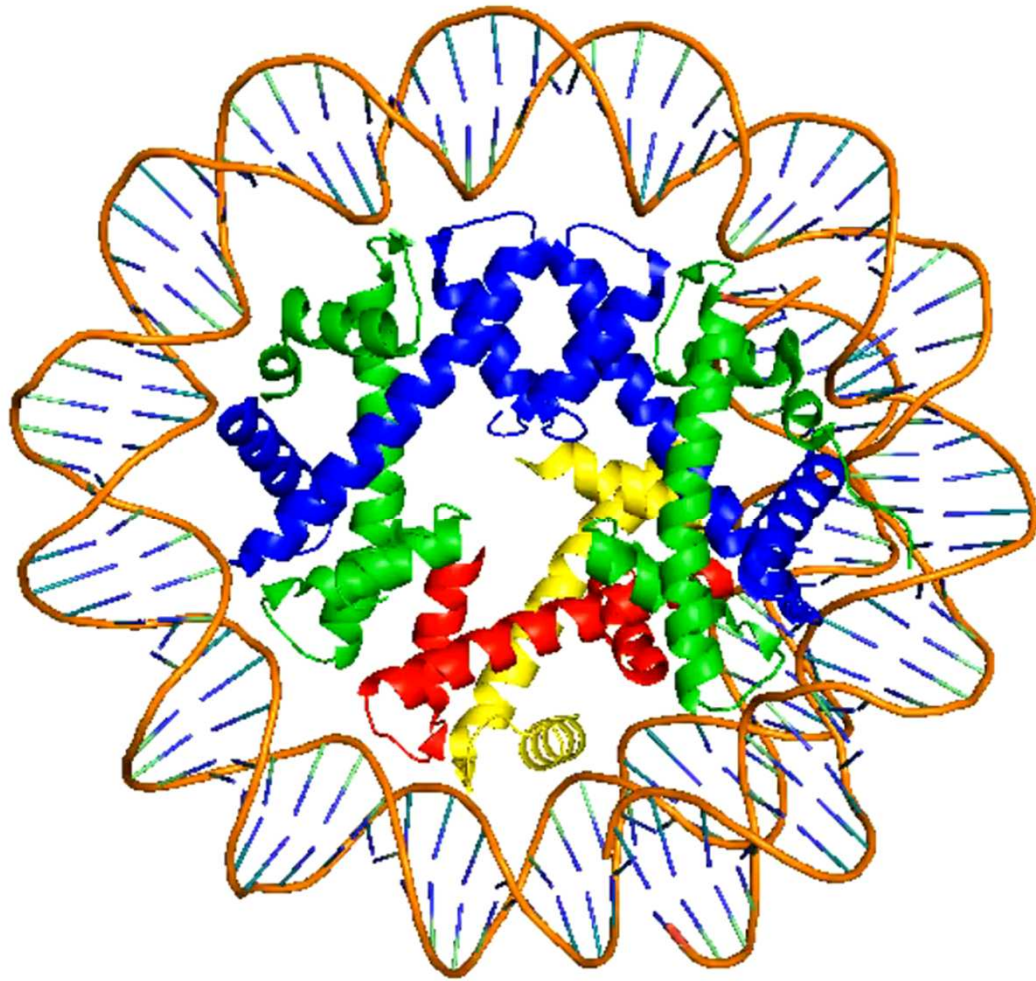
video: autor

převzato z: Alberts a kol, Mol. biol. cell, 2007



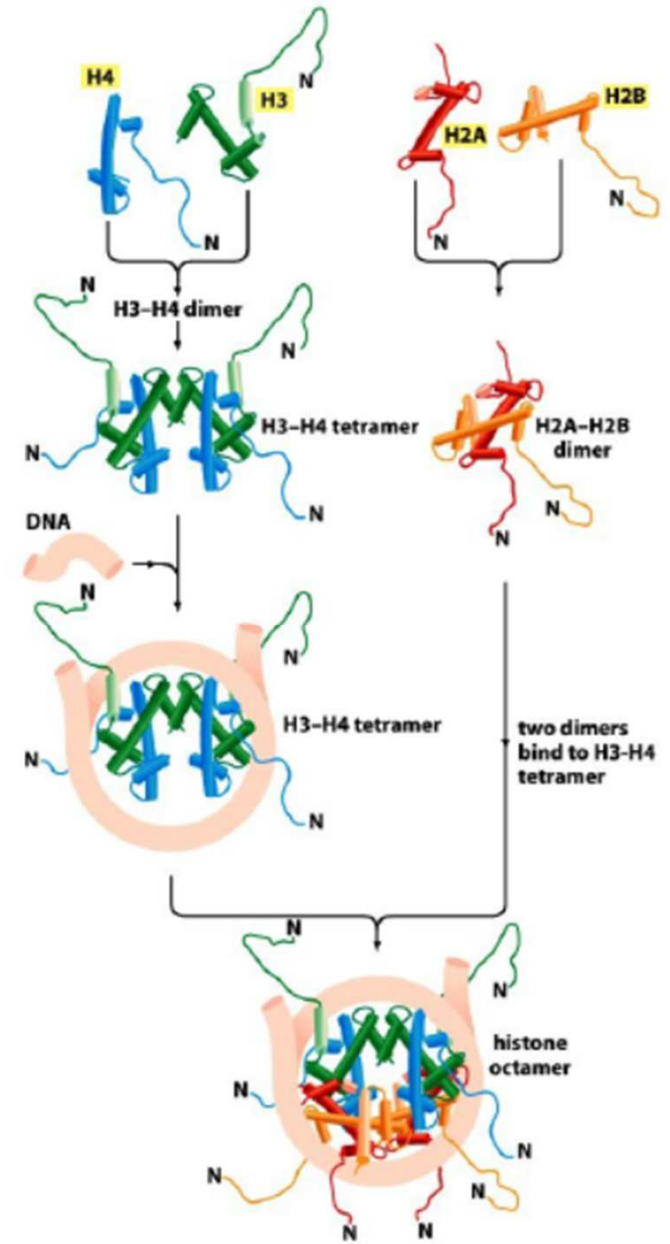
video: autor

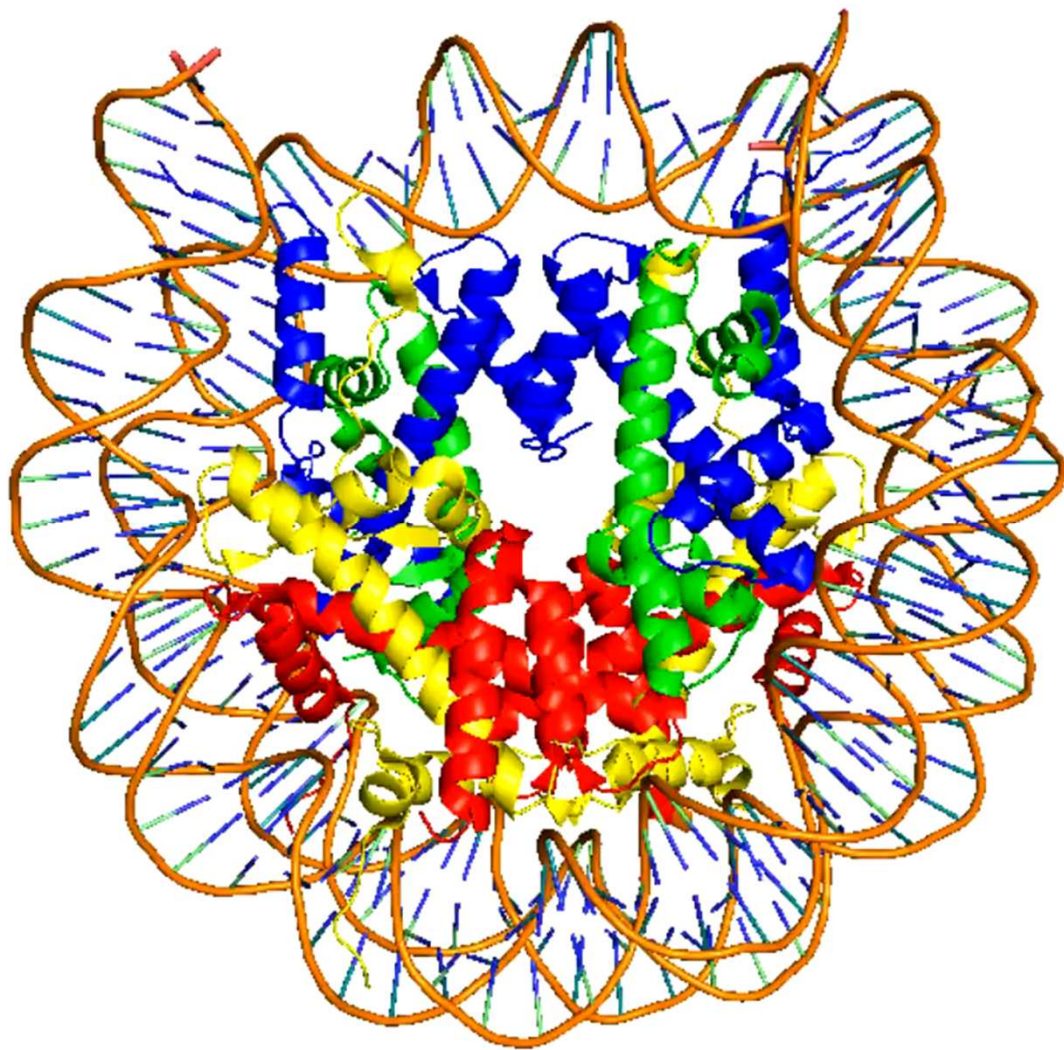
- H3-H3 interakce = $(\text{H3-H4})_2$ tetramer – vazba na DNA



- H3-H3 interakce = $(H3-H4)_2$ tetramer
- dimery H2A-H2B (H2B – váže H4)

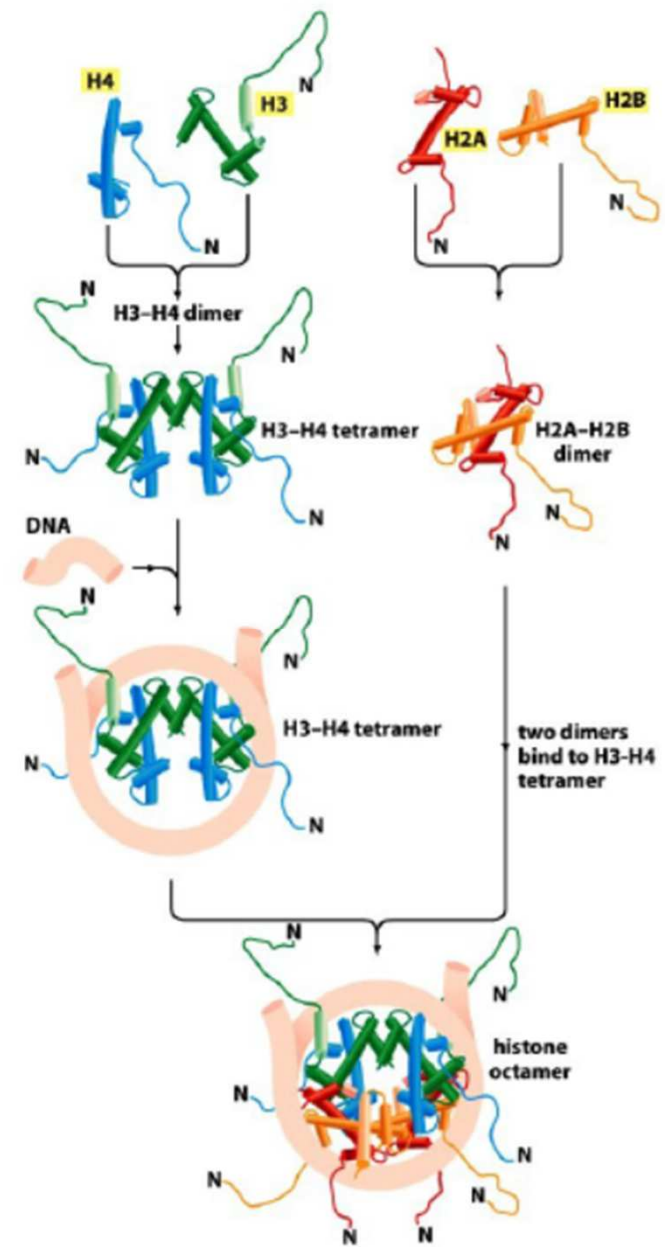
video: autor





- H3-H3 interakce = (H3-H4)₂ tetramer
- dimery H2A-H2B (H2B – váže H4)

video: autor

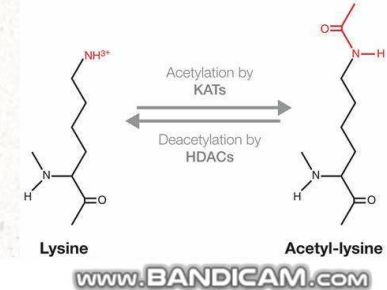
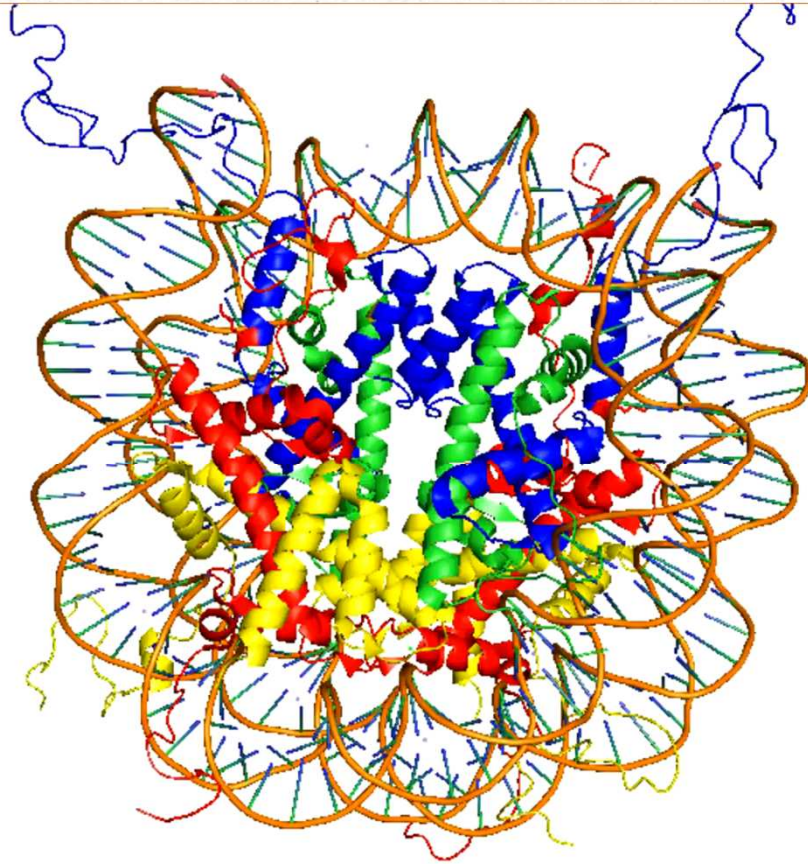


Modifikace histonů – H3K56ac

- modifikace (např. acetylace) mohou: vázat jiné proteiny (změní tvar povrchu – váže specificky bromodoména) nebo oslabit interakce (změní náboj povrchu – oslabí vazbu s DNA a rozvolní nukleosom) – pozice PTM

1KX5

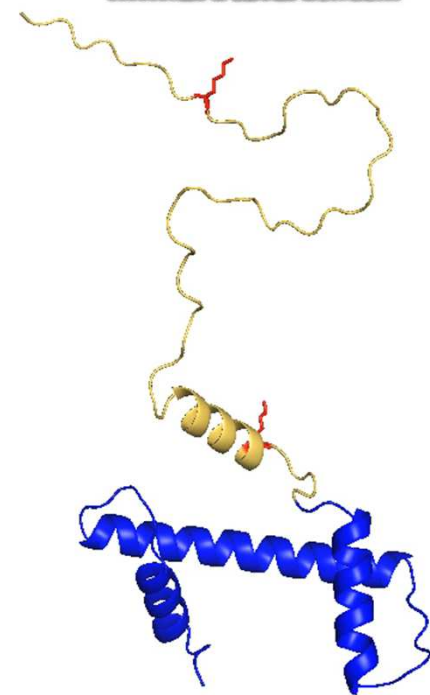
Only



H3K9ac

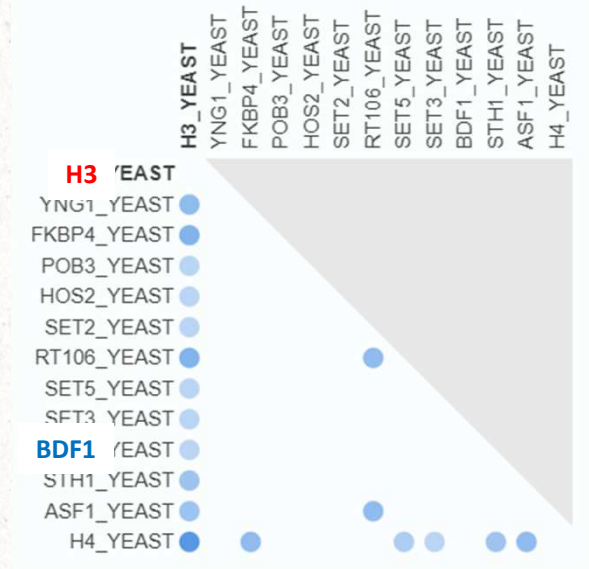
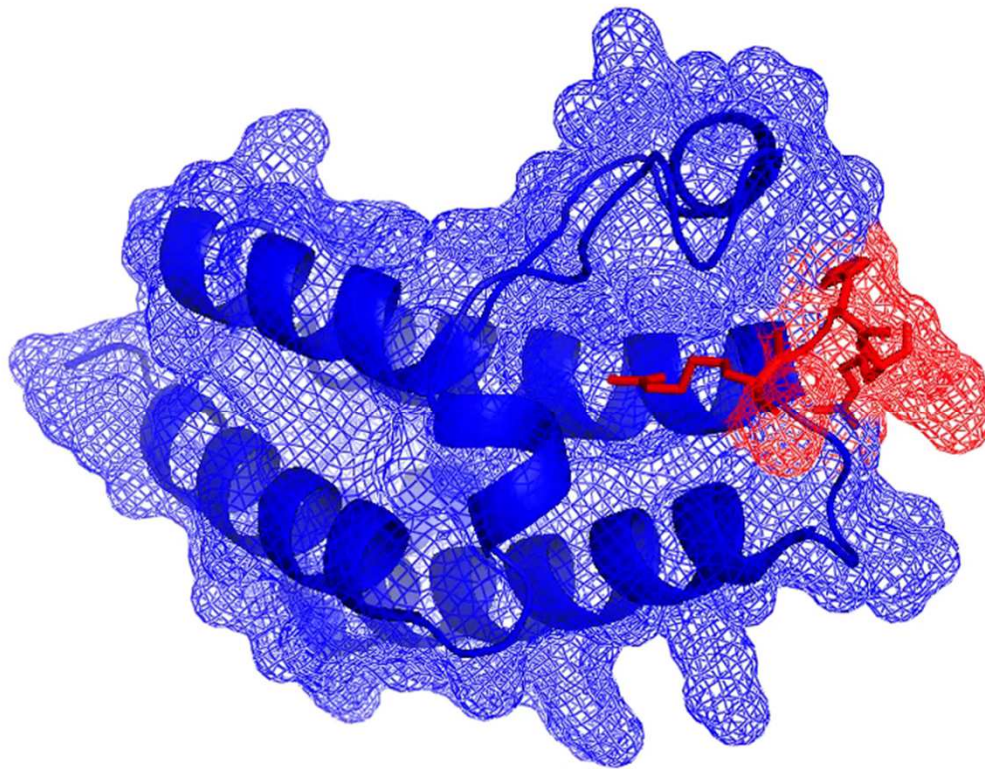
H3K56ac

video: autor



Modifikace histonů – H3K9ac

- modifikace (např. acetylace) mohou: vázat jiné proteiny (změní tvar povrchu – váže specificky bromodoména) nebo oslabit interakce (změní náboj povrchu – oslabí vazbu s DNA a rozvolní nukleosom) – pozice PTM



bromodoména váže
acetylovaný **histon**

video a printscreen: autor

Docking - hra

Bioblox 2½D Game on the Topic of Protein Docking



https://www.youtube.com/watch?v=u_-8JyCWpEQ&t=7s

Bioblox 2½D is a free mobile game on the Topic of Protein Docking. Play the Proteins Docking game. Learn about the fascinating world of bio-molecules and their interactions. Drag, Rotate, Swipe and fit the chains together like the components of a mechanism.

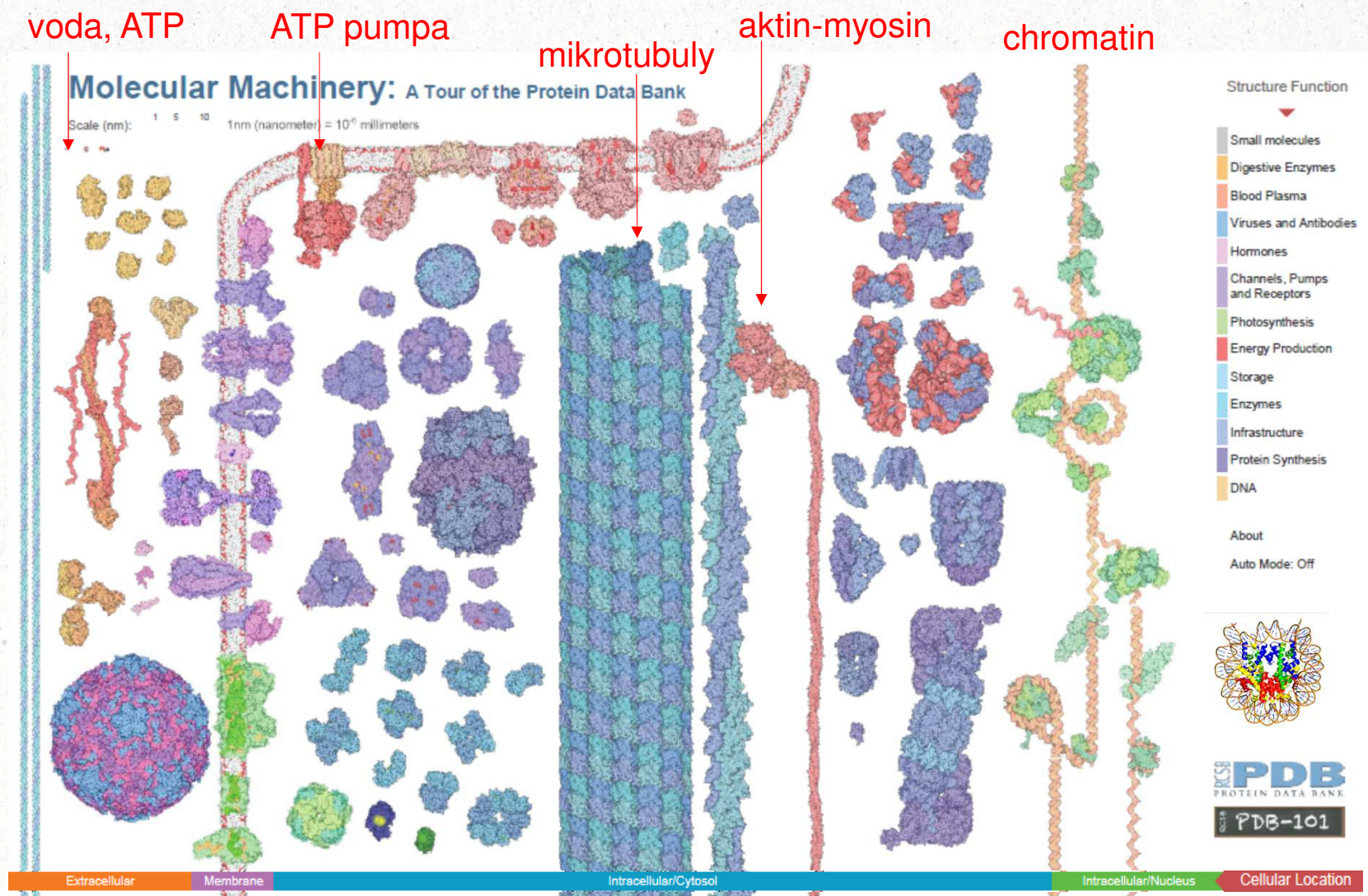


or [PLAY ONLINE](#)

printscreen: autor

<https://www.doc.gold.ac.uk/bioblox/>

Primárním zdrojem strukturálních informací = PDB



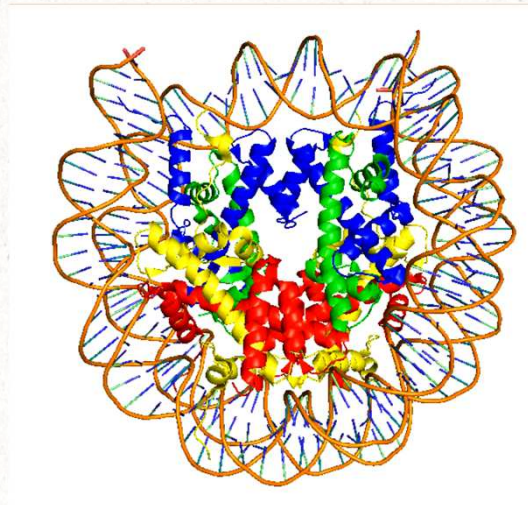
Interaktivní web PDB-101 (pro učitele): <https://pdb101.rcsb.org/>

printsreen: autor

přes 200 000 struktur

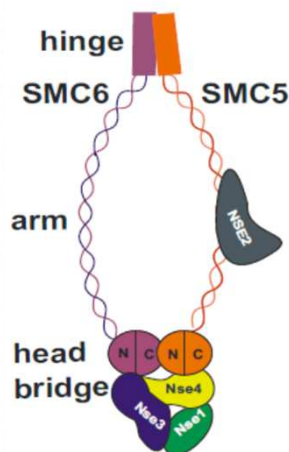
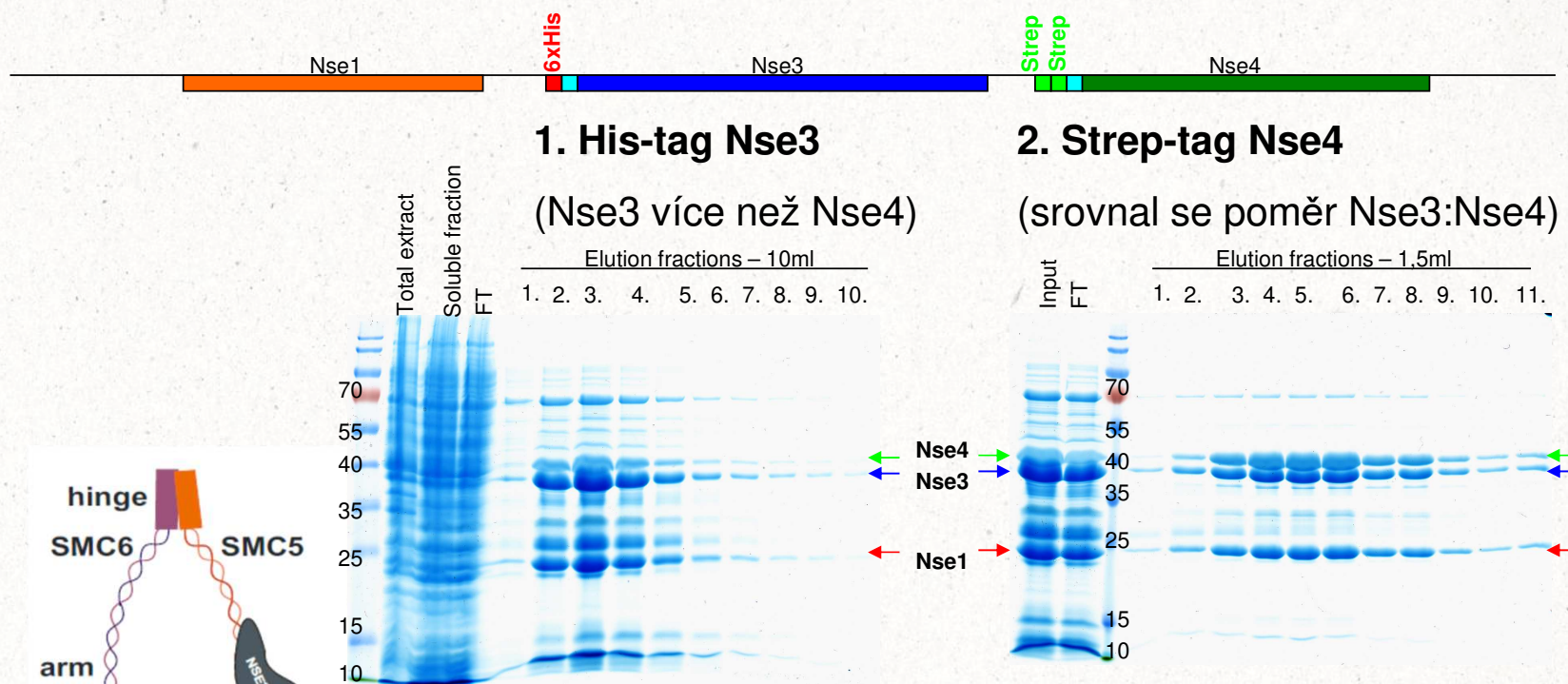
Pokročilé metody v analýze proteinových komplexů

1. - identifikace genů/proteinů ... jejich partnerů (PPI) ... izolace komplexu
 - funkce podjednotek (genetická analýza, lokalizace v buňce ...)
2. - charakterizace komplexu
 - vzájemné PPI podjednotek – architektura komplexu
3. - rekonstrukce, struktura a analýza aktivit celého komplexu *in vitro*
 - struktura: crosslink MS, X-ray, (cryo) elektronová mikroskopie, modelování, integrativní analýza



Ko-purifikace - ověření

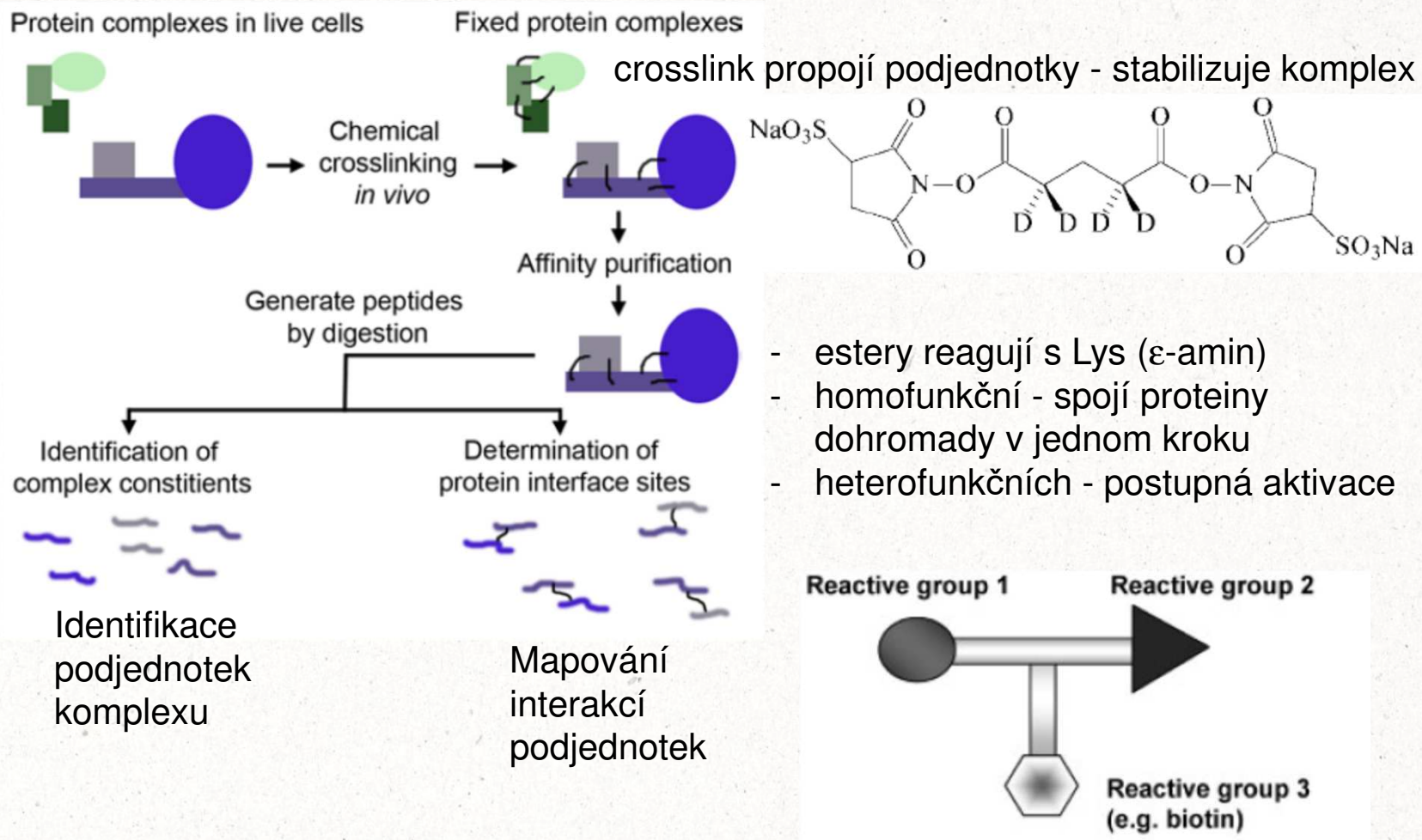
silné interakce/komplexy – proteiny lze ko-exprimovat a následně ko-purifikovat



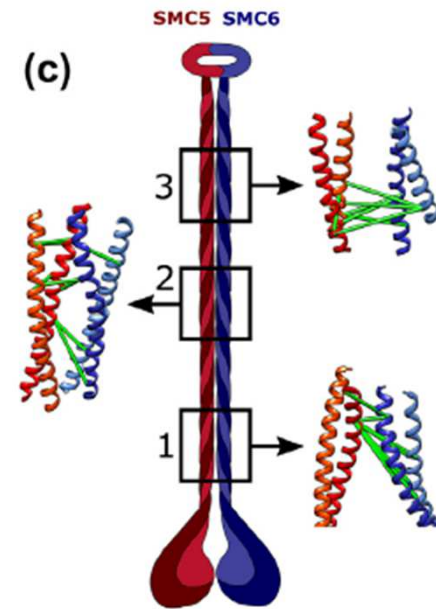
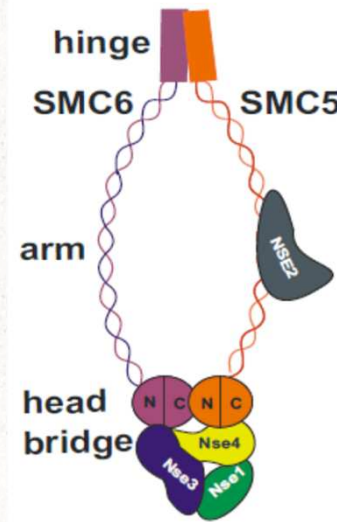
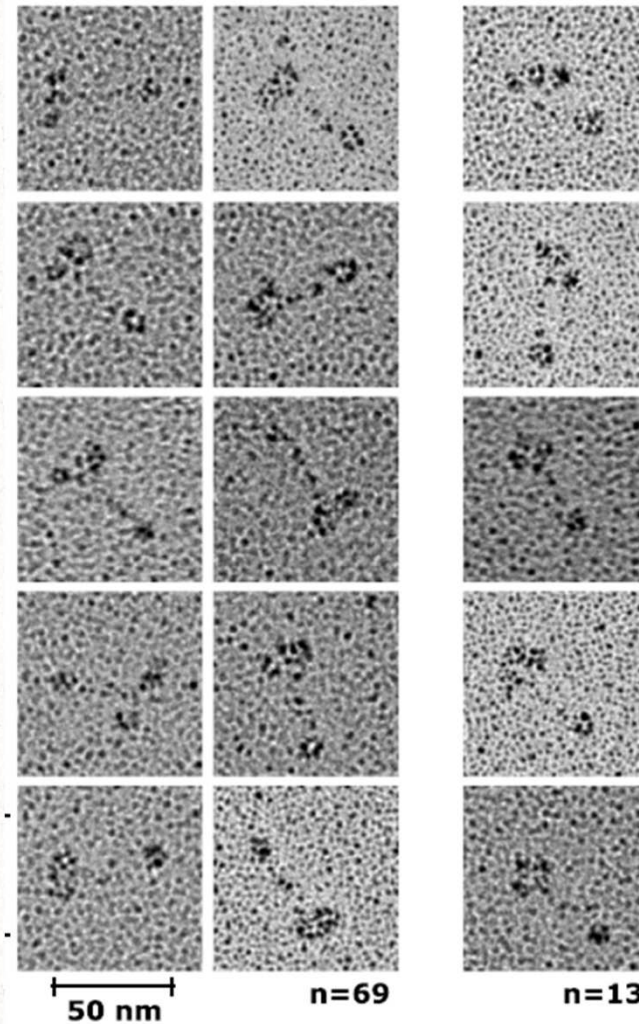
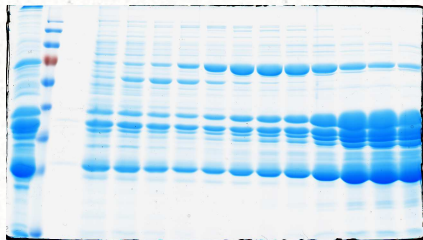
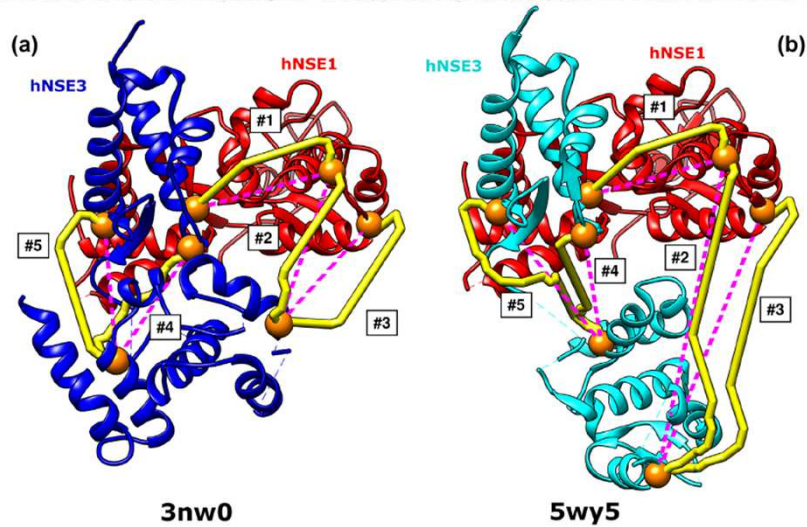
Značky na různých podjednotkách komplexu –
postupná purifikace => kompletní komplex
(přirozený poměr podjednotek v komplexu)

převzato z: Zabradý et al, NAR, 2016

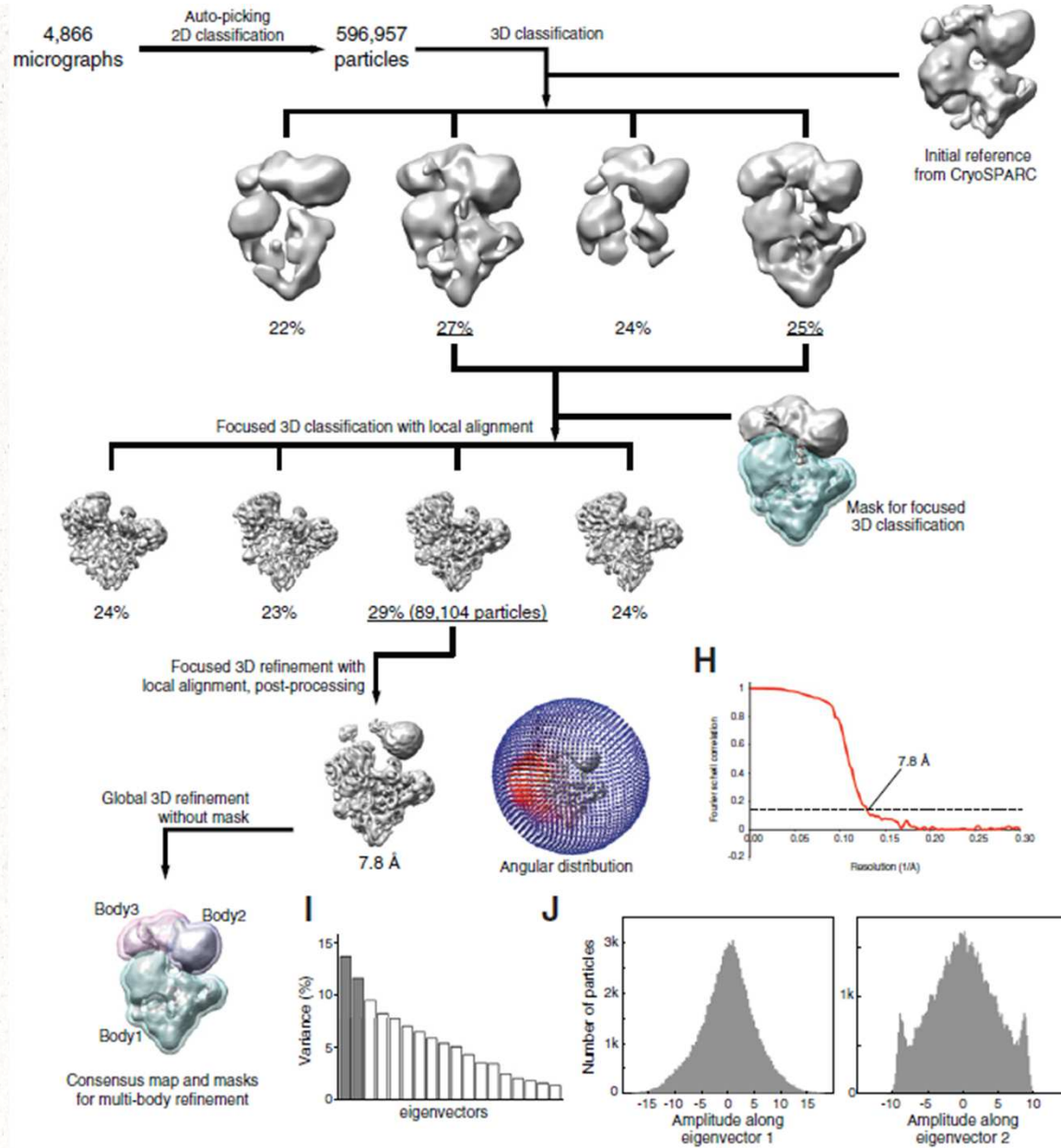
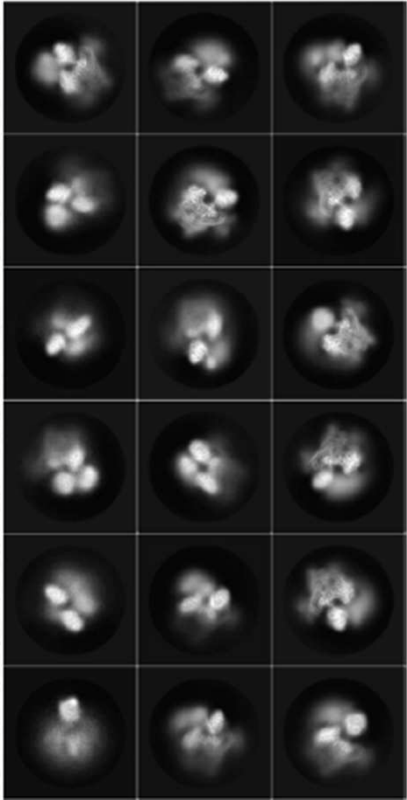
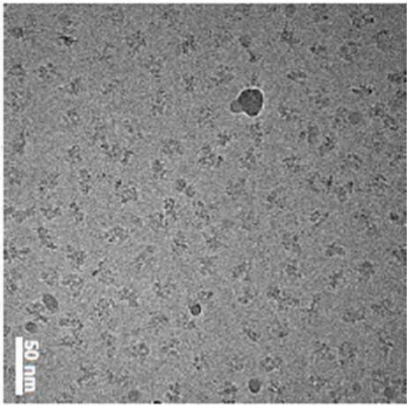
Detailní mapování komplexů - crosslinking



- krosslink pomůže upřesnit strukturální model (Nse1-Nse3)
- ukázal jak jsou ramena Smc5-Smc6 vedle sebe umístěna



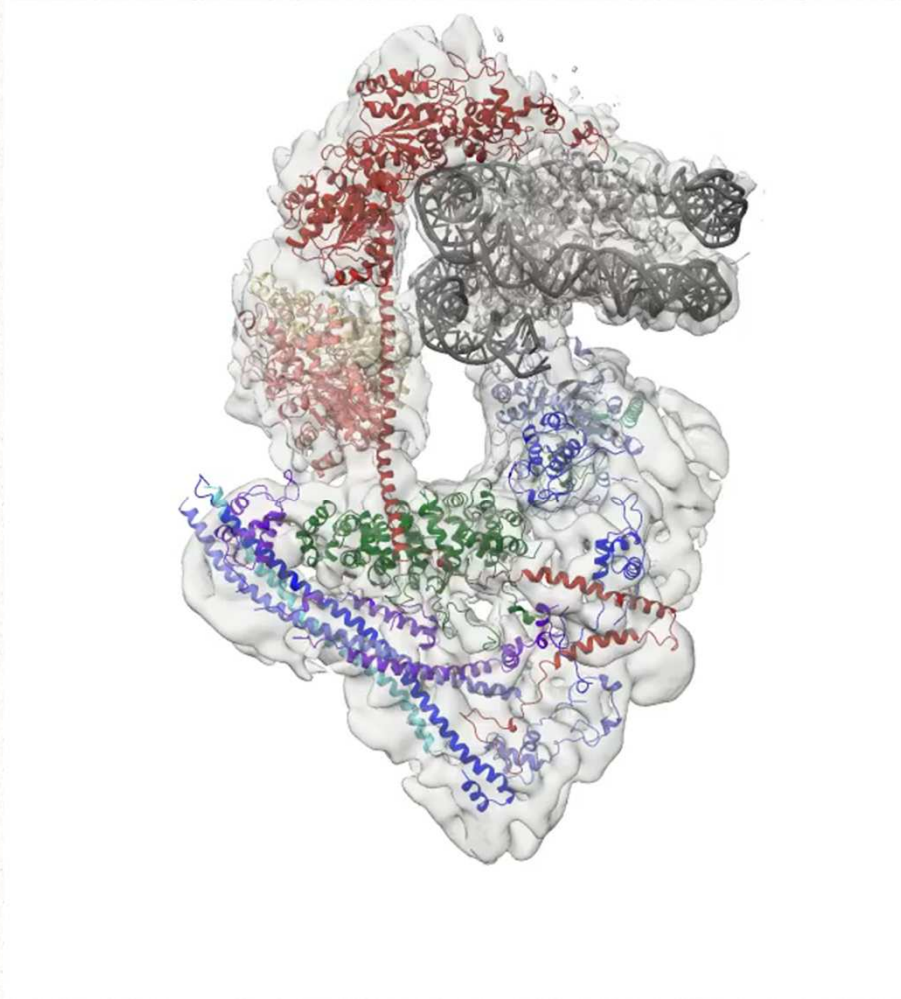
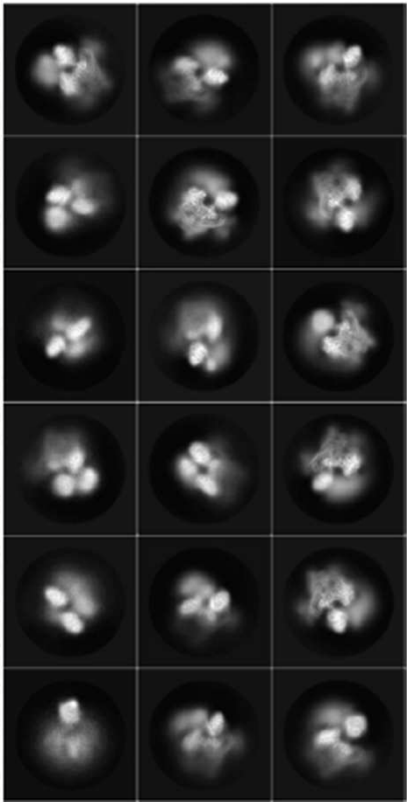
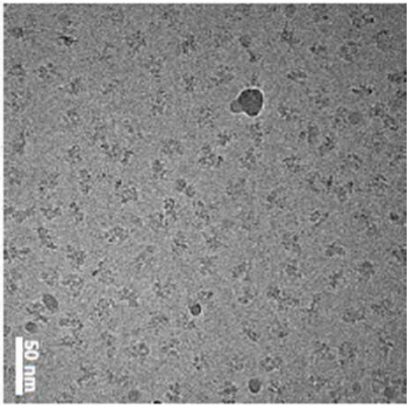
převzato z: Adamus et al, JMB, 2020



remodelační komplex

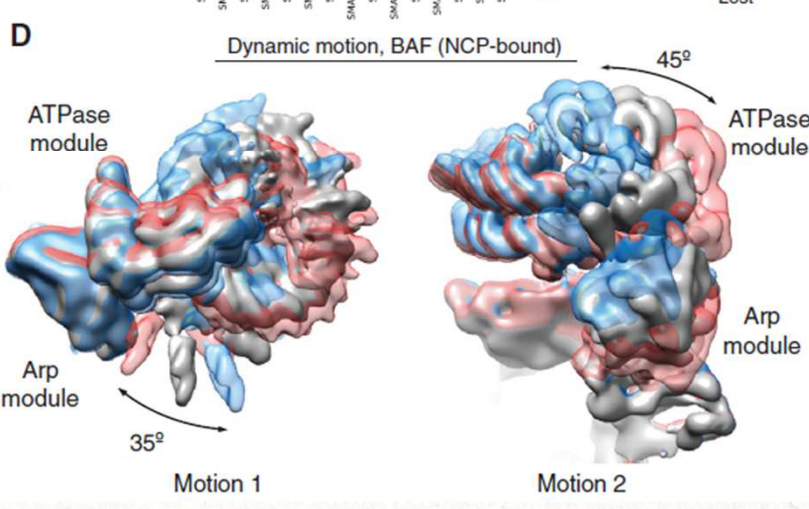
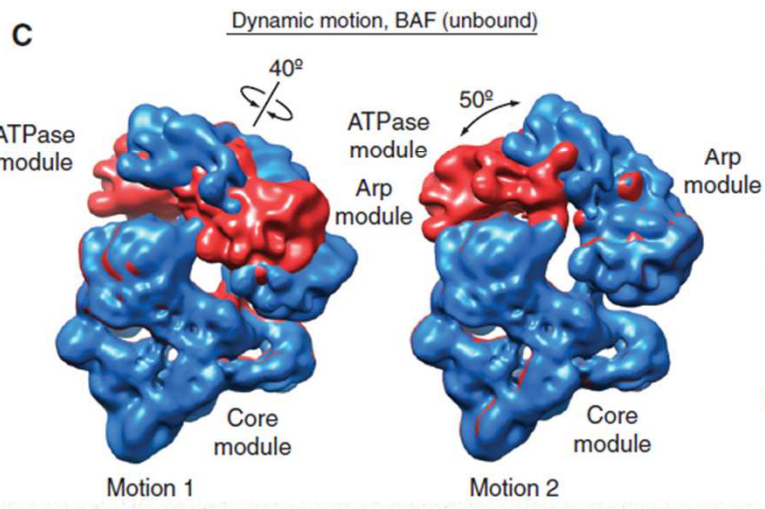
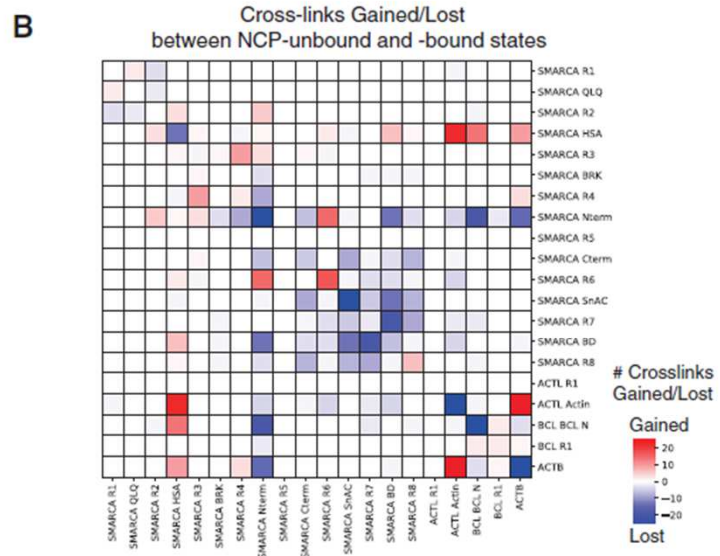
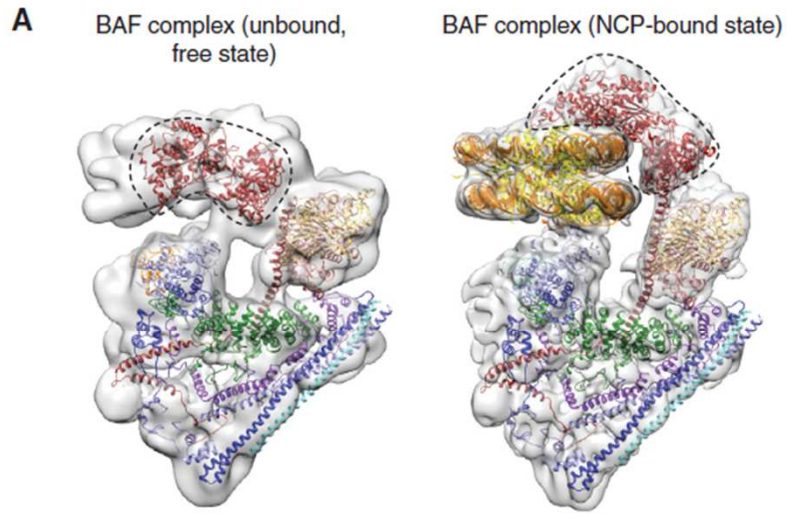
sběr velkého počtu částic, klasifikace a rekonstrukce struktury komplexu

převzato z: Mashtalir et al, Cell, 2020

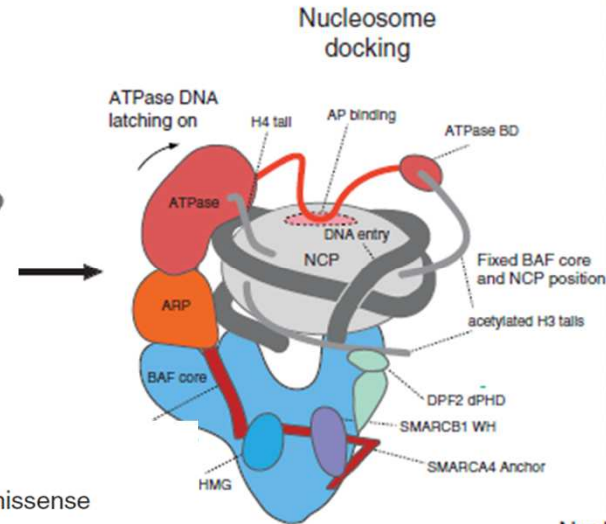
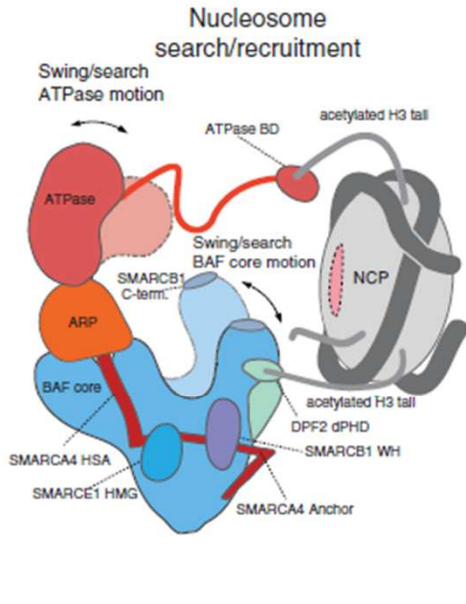
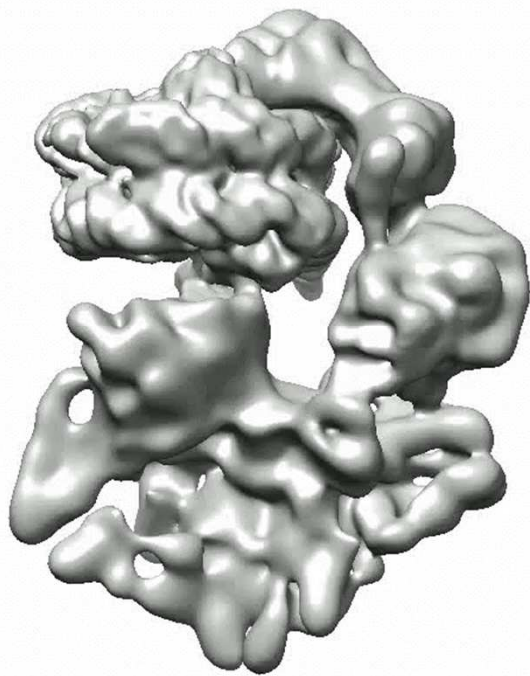


remodelační komplex

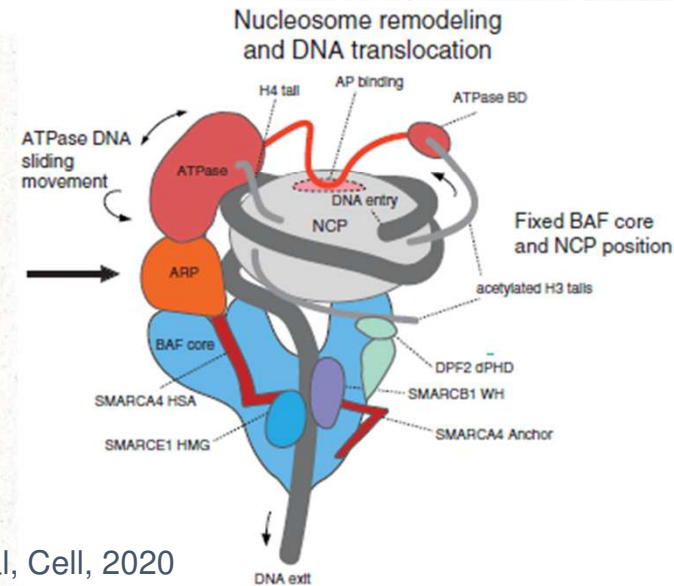
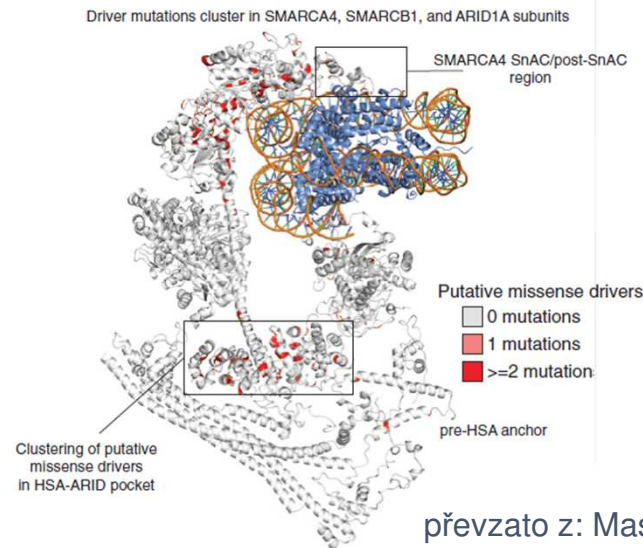
sběr velkého počtu
částic, klasifikace a
rekonstrukce struktury
komplexu



remodelační komplex
zachyceno několik konformací + rozdíly v krosslinku = dynamika



Distribution of Pan-cancer putative missense driver mutations



převzato z: Mashtalir et al, Cell, 2020

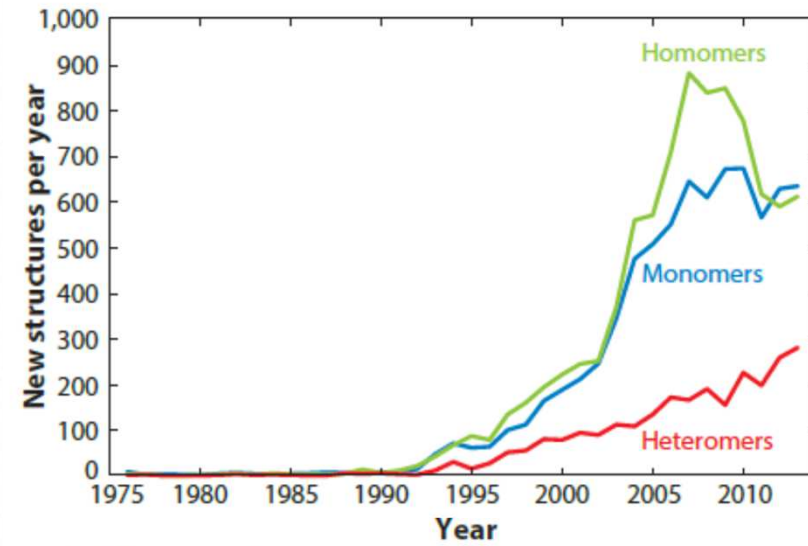
remodelační komplex

pomáhá v transaktivaci genové exprese – váže acetylované H3 (bromodomény) - uvolňuje nukleosom (volnější konce DNA)

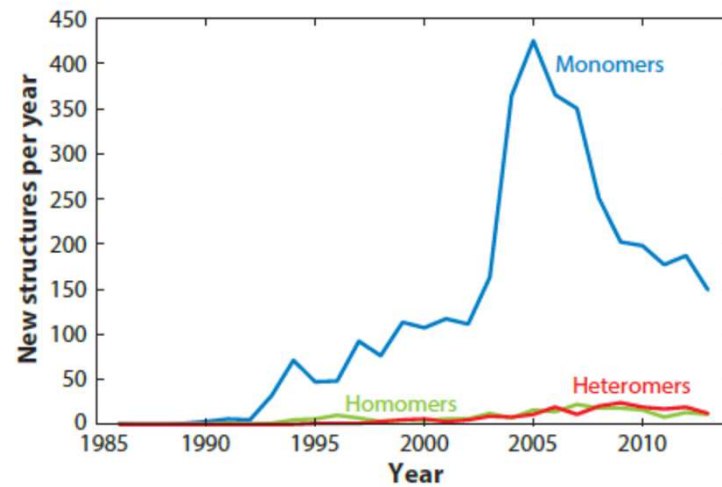
Strukturní metody

- krystalografie – nejvhodnější (boom v 1. dekádě díky sekvenačním projektům)
- NMR je limitována velikostí
- cryoEM je vhodná pro velké komplexy (boom v současnosti)

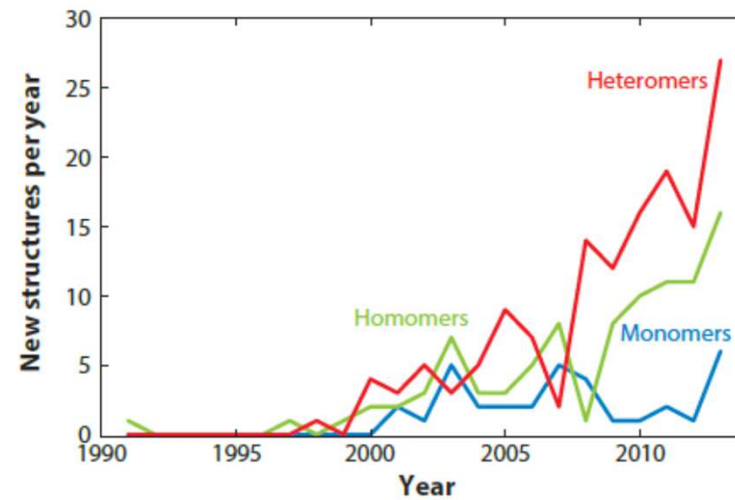
a X-ray crystallography



b NMR



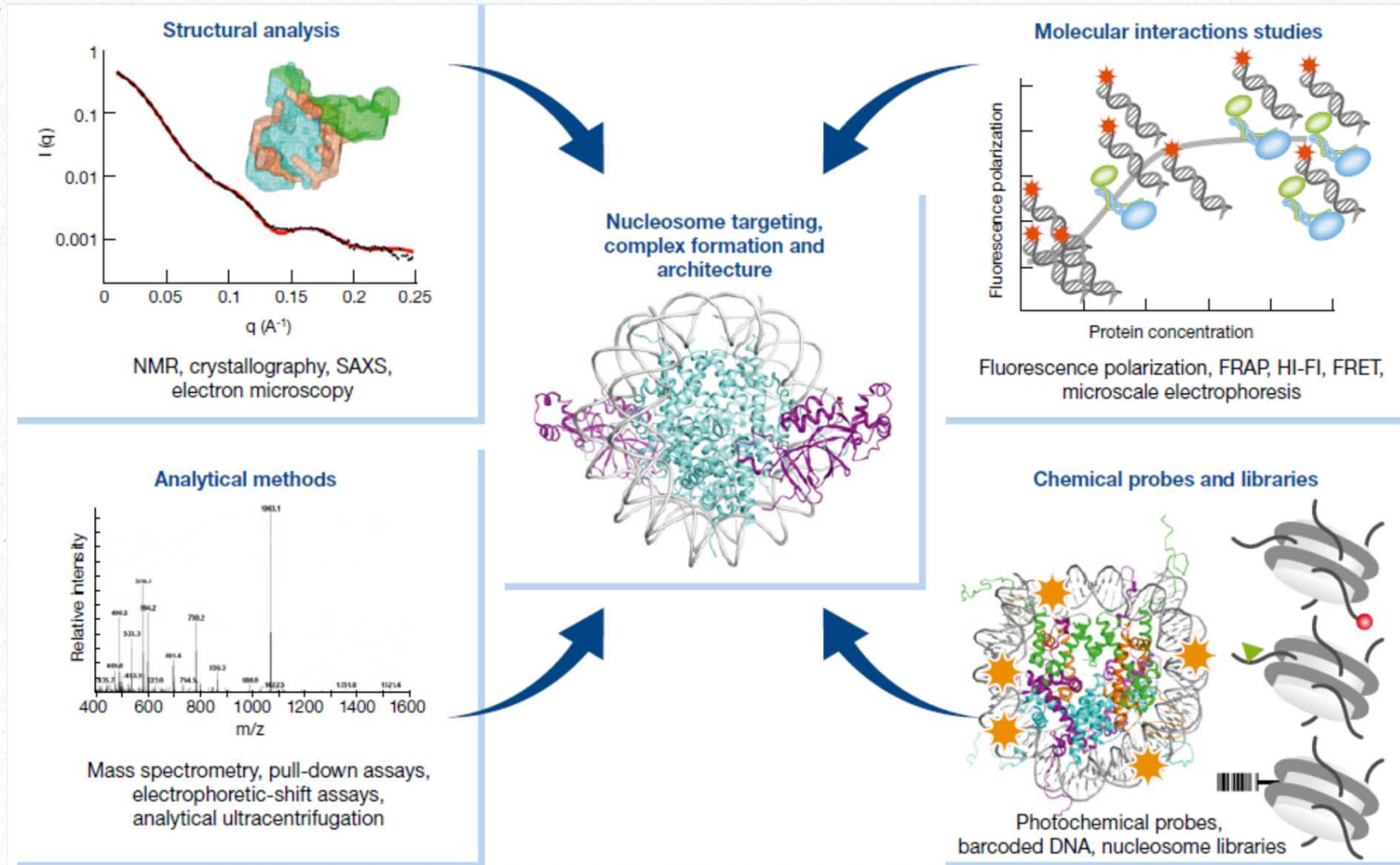
c Electron microscopy



převzato z: Marsh et al, ARB, 2015

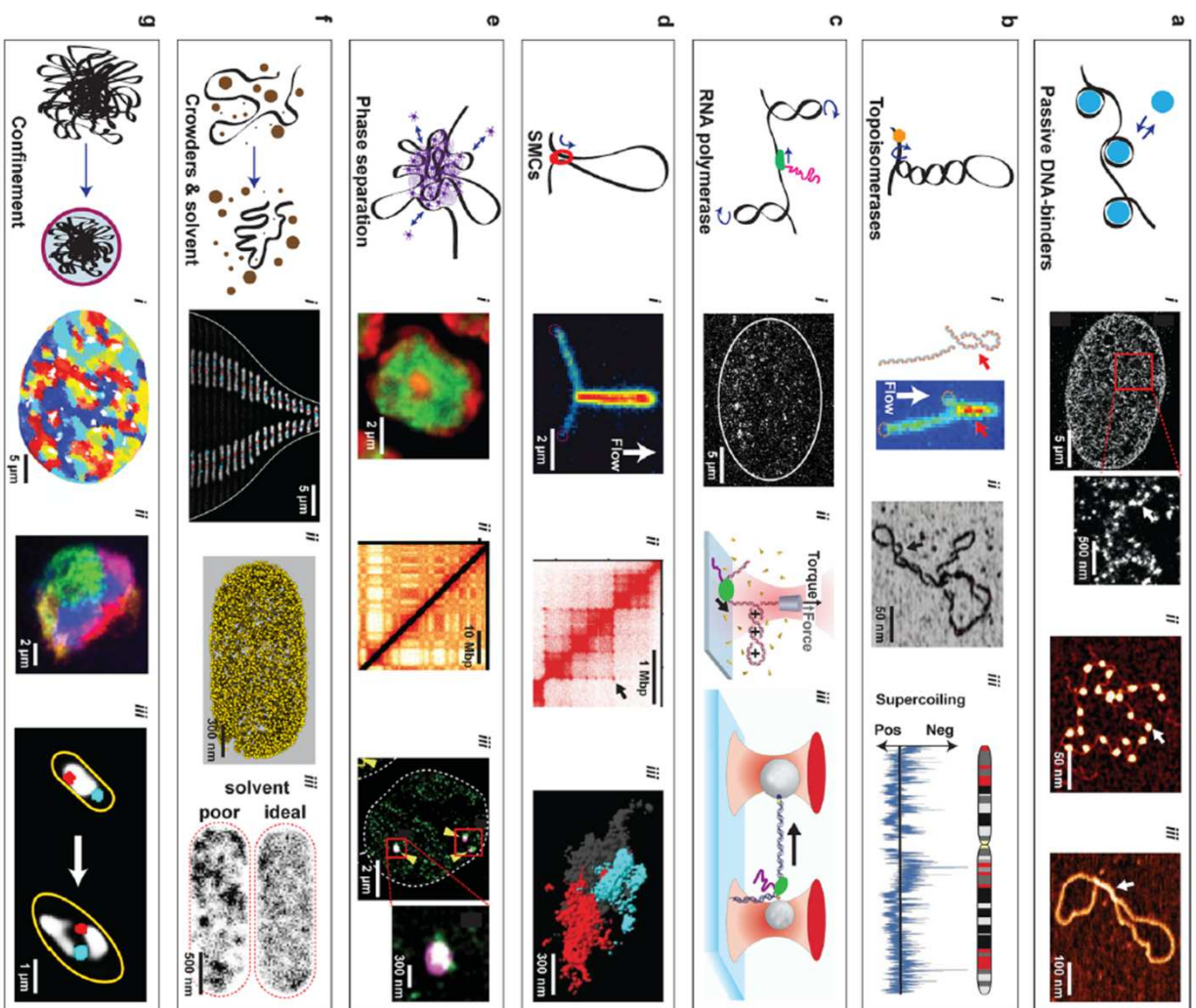
Analýza proteinových komplexů

více doc. Hofr

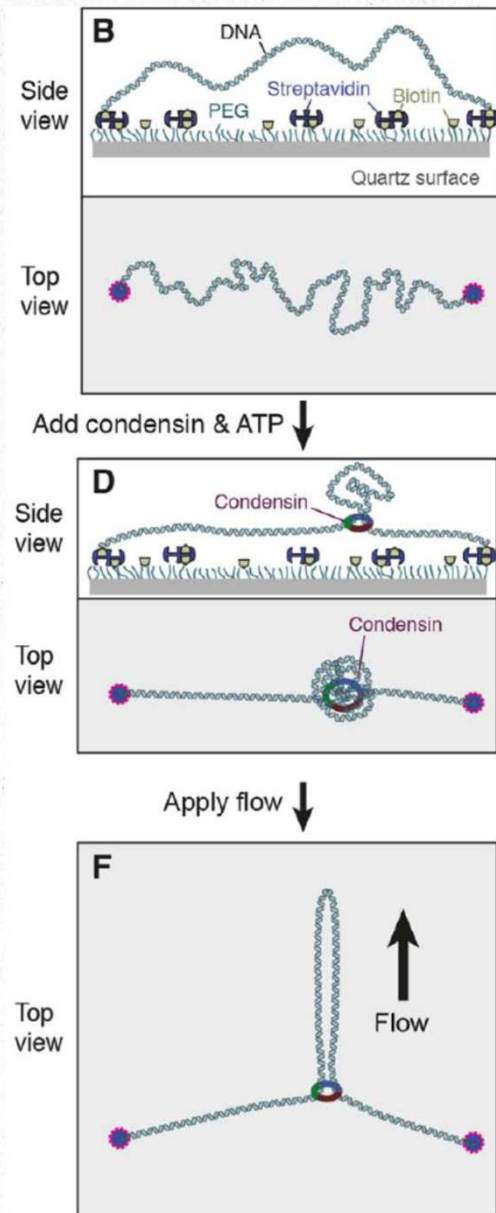


převzato z: Speranzini et al, EMBO J, 2016

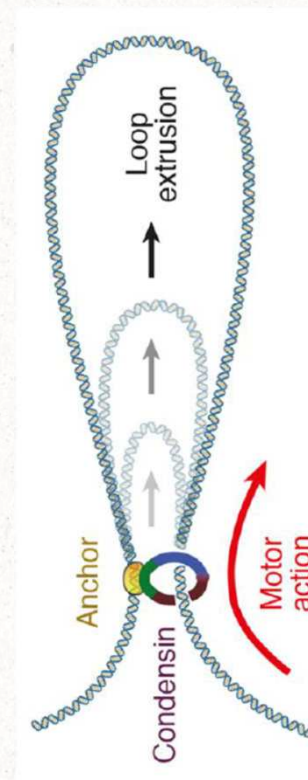
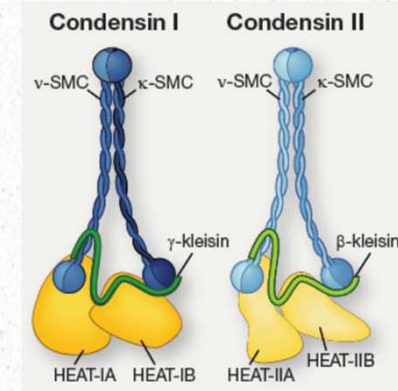
... speciální biofyzikální metody ...



převzato z: Birnie et al, ACS nano, 2020

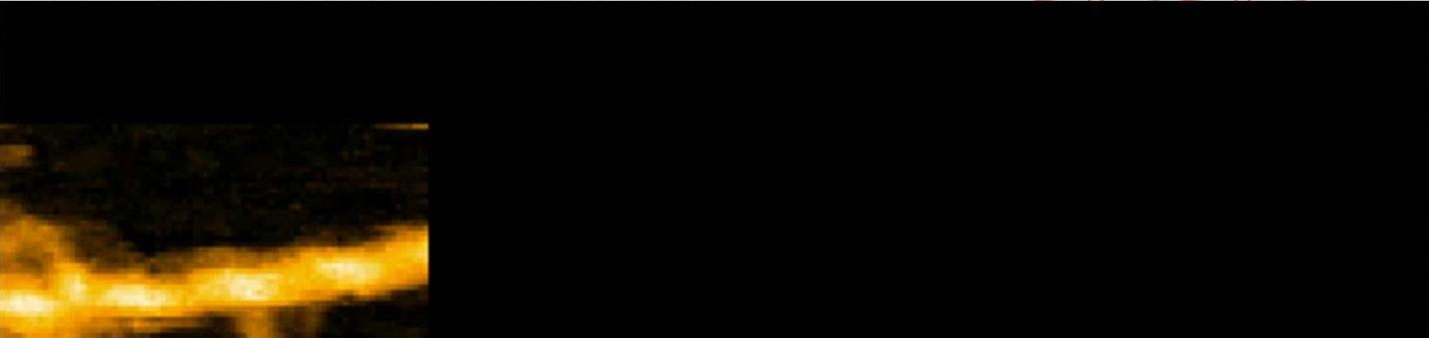
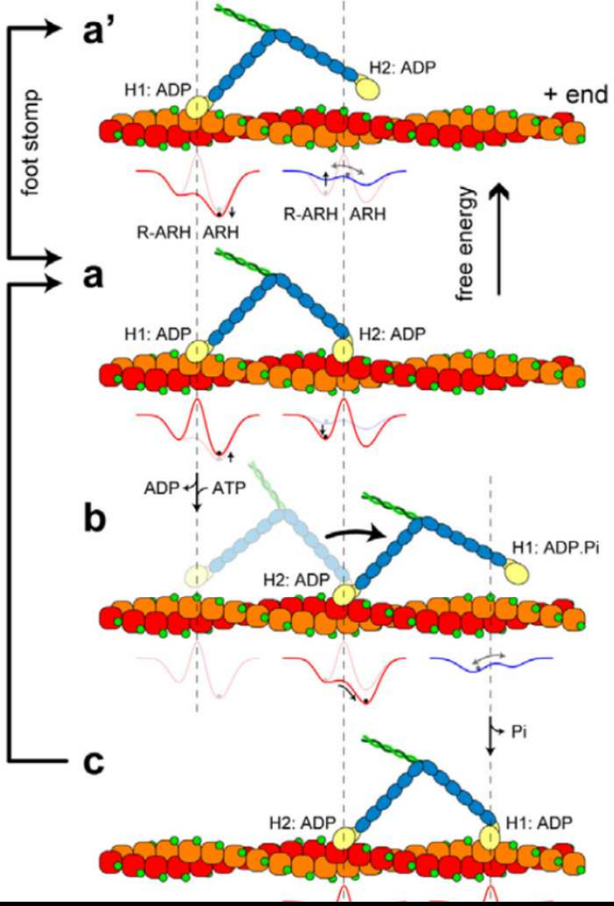
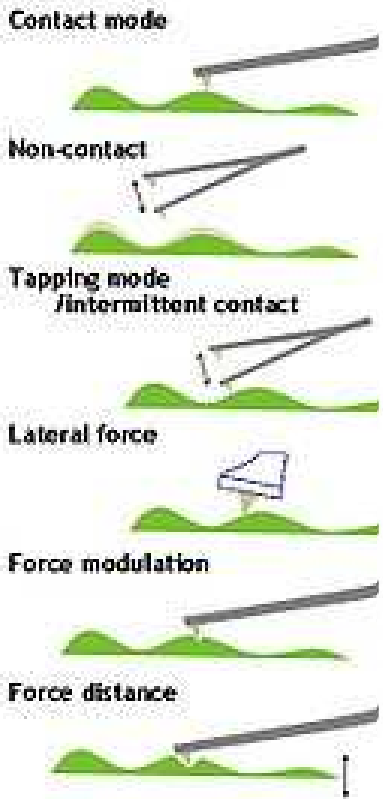
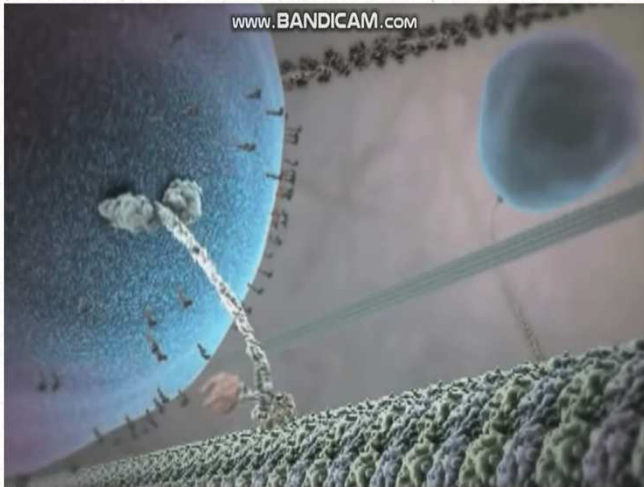


konce molekuly DNA uchyceny
 přidán SMC komplex + vazba a
 hydrolýza ATP – vytvoření
 smyčky („loop extrusion“)



převzato z: Ganji et al, Science, 2018; Takahashi, CO in CB, 2019

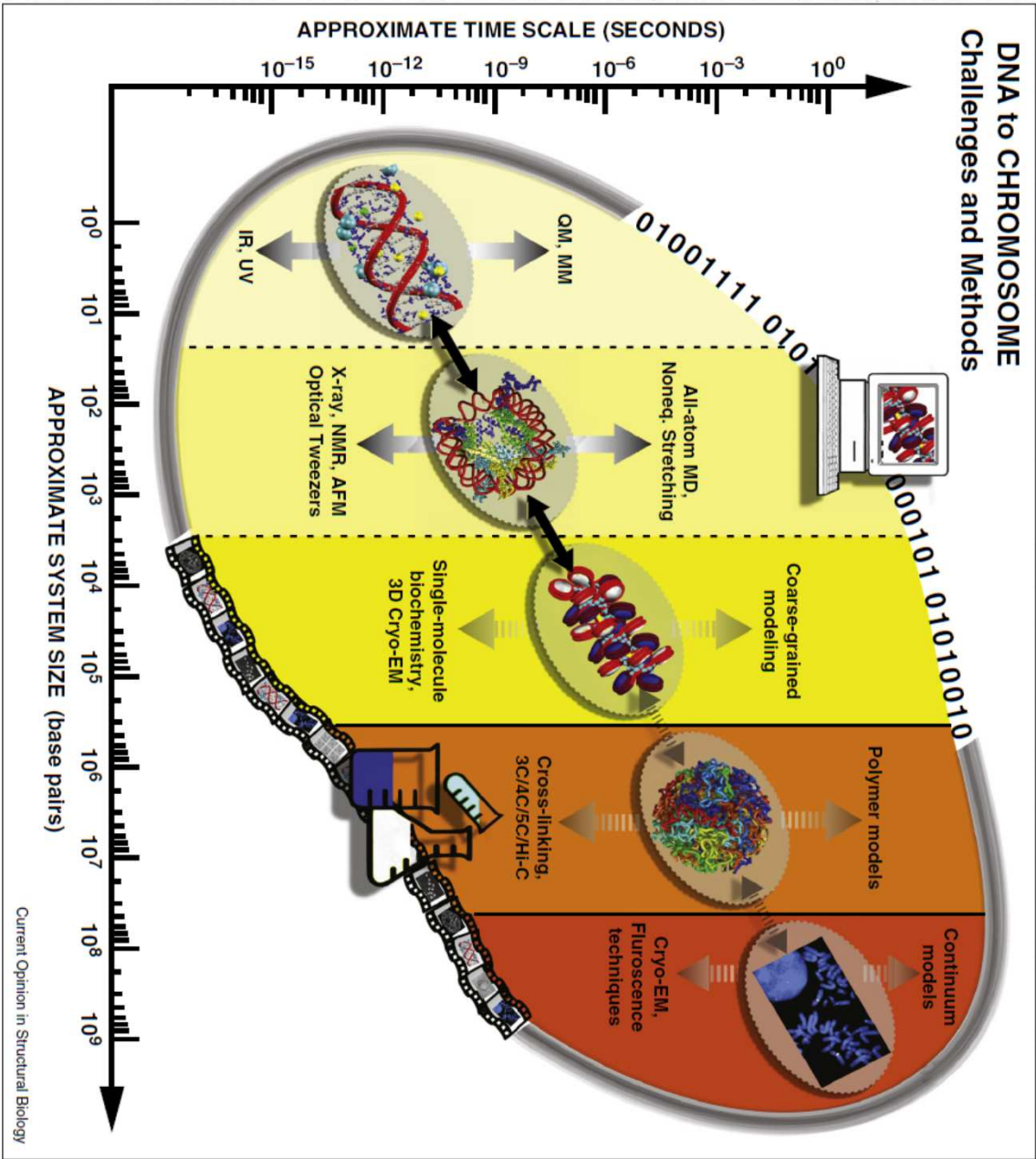
AFM (atomic force microscopy)



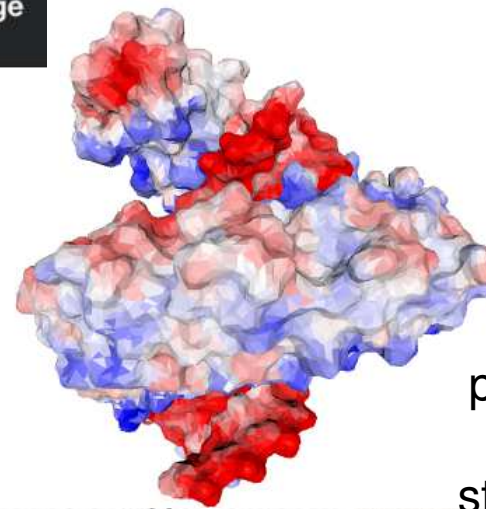
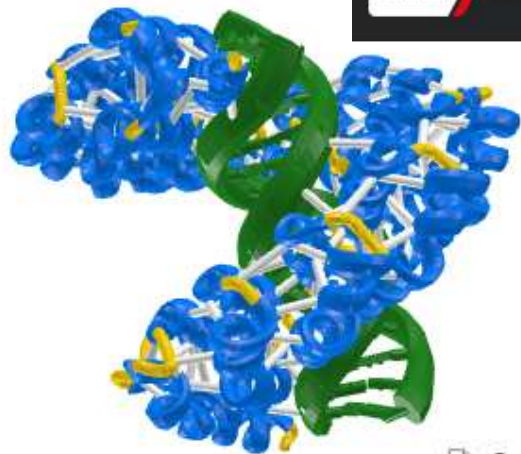
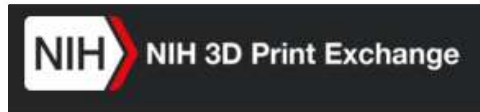
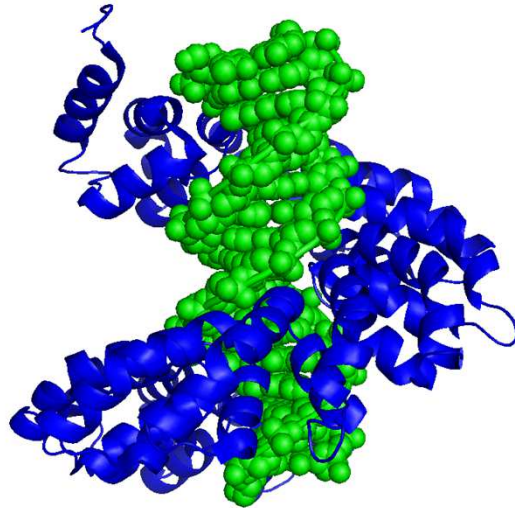
převzato z:
Ando et al, Annu Rev BioPhys, 2013

Úrovně proteinových komplexů

DNA to CHROMOSOME Challenges and Methods



Visualizace proteinových komplexů



Existuje mnoho nástrojů na vizualizaci komplexů

od **PyMOL** pro přímou vizualizaci krystalových struktur ... **3D tisk**