CG920 Genomics

Lesson 6

Protein Interactions in Gene Regulations

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Literature

- Literature sources for Chapter 06:
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 - Ainger, K., Avossa, D., Morgan, F., Hill, S.J., Barry, C., Barbarese, E., and Carson, J.H. (1993). Transport and localization of exogenous myelin basic protein mRNA microinjected into oligodendrocytes. J Cell Biol 123, 431-441.
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 - Grefen, C., Stadele, K., Ruzicka, K., Obrdlik, P., Harter, K., and Horak, J. (2008).
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Outline

- Functional importance of the specificic interactions of proteins in the regulation of gene expression
 - Chromatin structure
 - Regulation of transcription
 - mRNA localization
 - Protein stability
 - Signal transduction
- Methods of analysis of protein interactions in vivo
 - Co-immunoprecipitation
 - The tandem affinity purification (TAP-tag)
 - Yeast two-hybrid assay (Y2H)
 - Bimolecular fluorescence complementation (BiFC)
 - Membrane Recruitment Assay (MeRA)
- Practical use of methods for in vivo studies of protein interactions

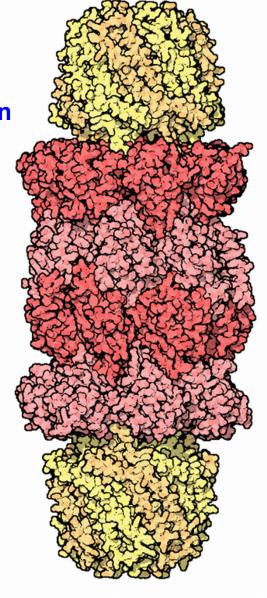
Importance of Protein Interactions

Functional importance of specific protein interactions

 Most of the proteins in the cell exist in the form of complexes which may further interact with each other

Proteasome

 protein complex responsible for the degradation of obsolete proteins in the cell









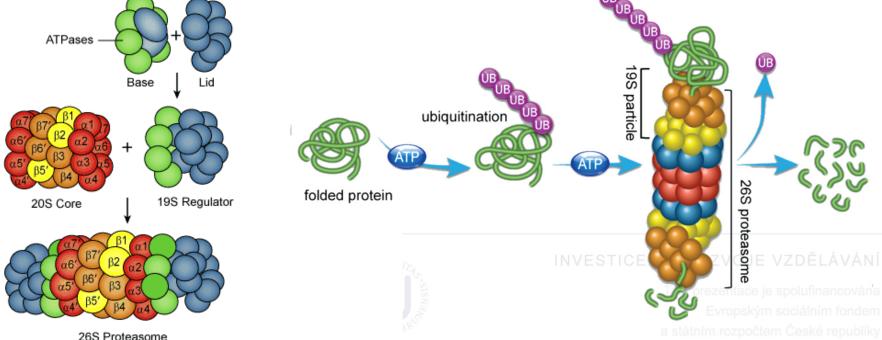


The importance of protein interactions

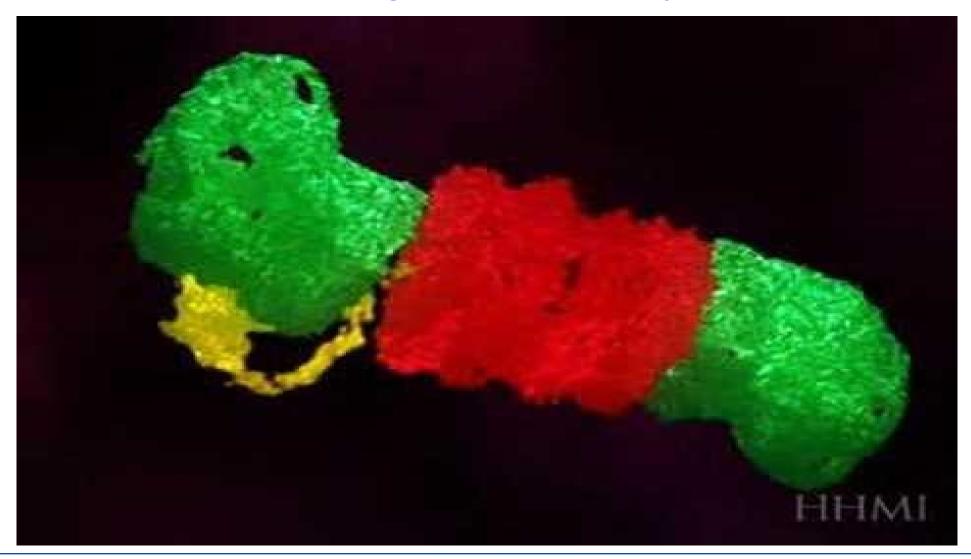
Proteasome

- Consisting of a core, also being designated as 20S and regulatory portions (19 or 11S)
- Allows targeted degradation of proteins labelled by a specific marker - small polyppetide (76 aa) called ubiquitin

20S & 26S PROTEASOME



Proteasome –targeted proteolysis









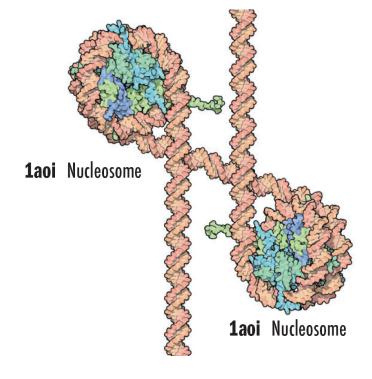




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Importance of Protein Interactions

- Functional importance of specific protein interactions
 - Chromatin structure

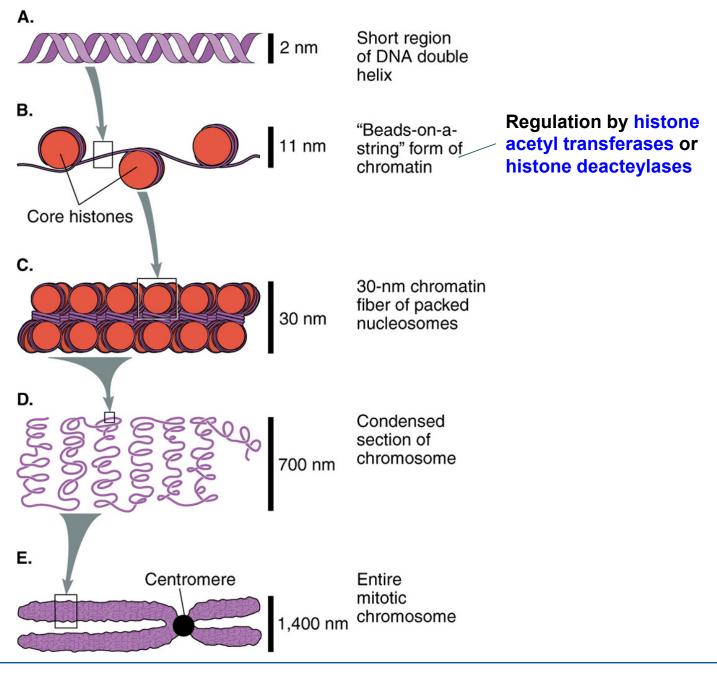






















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DNA methylation in animals vs. in plants









methylation status

methylation status

CpG

CpG or CpNpG

Cell-specific methylation allows maintain of tissue-specific gene expression profiles

CpNpNp

Imprinting and "cell memory"



Mechanism of transcriptional regulation by DNA methylation mostly unknown











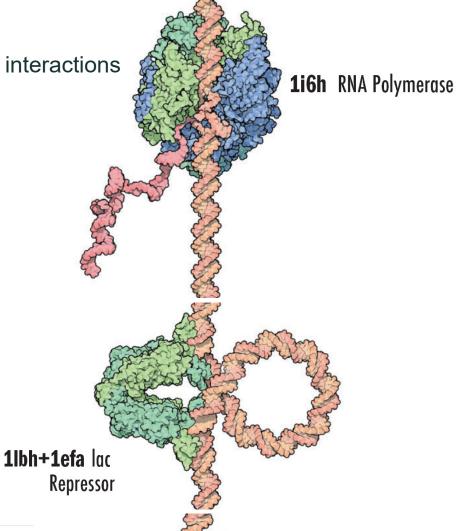
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Importance of Protein Interactions

Functional importance of specific protein interactions

Chromatin structure

Regulation of transcription





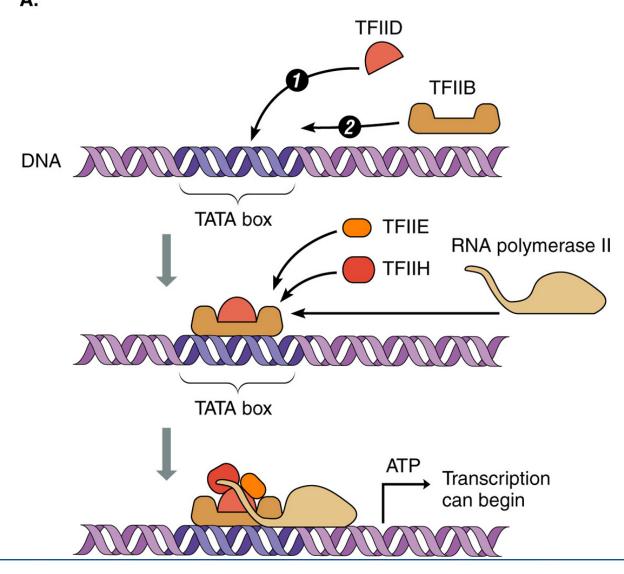






1ais TATA-binding Protein/ Transcription Factor IIB

Initiation of Transcription





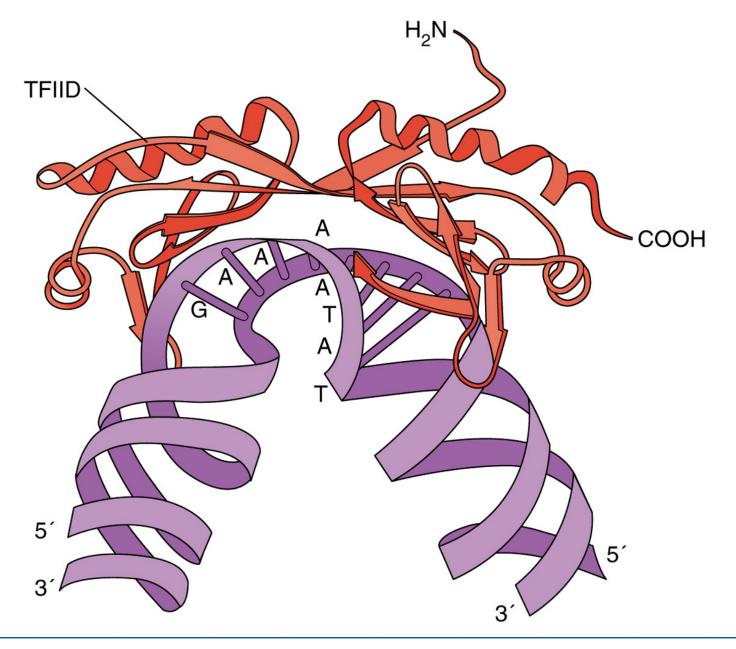








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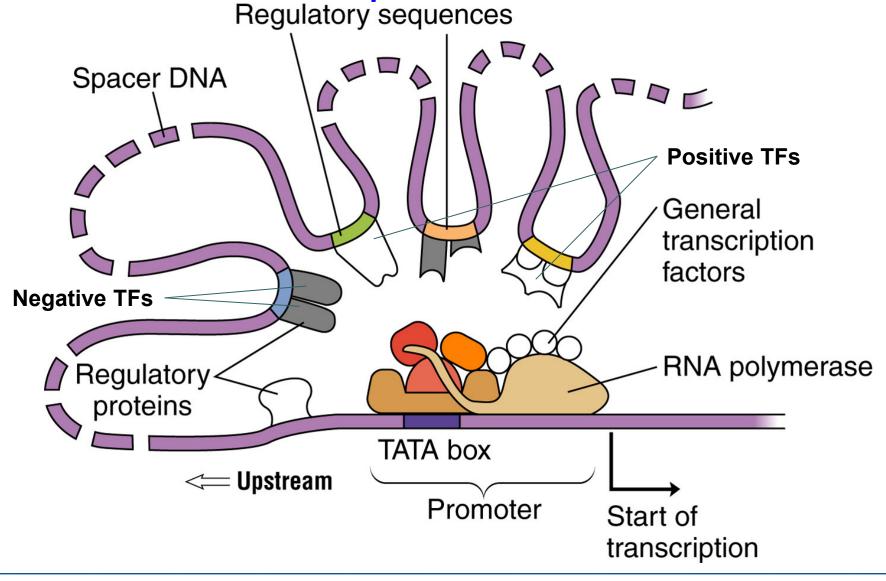






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Initiation of Transcription





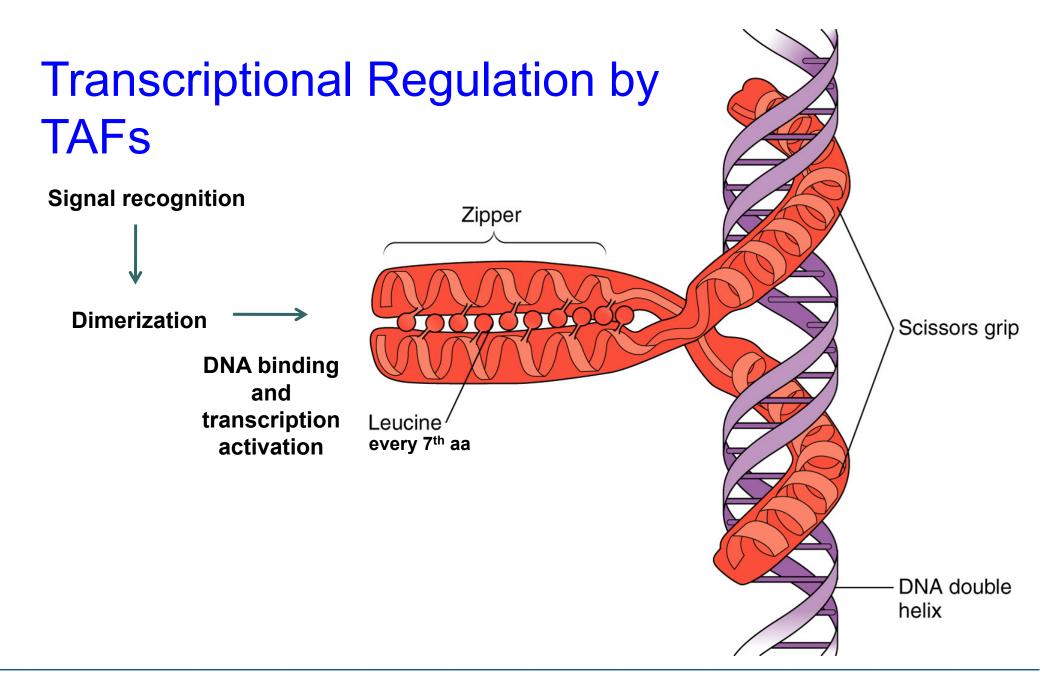








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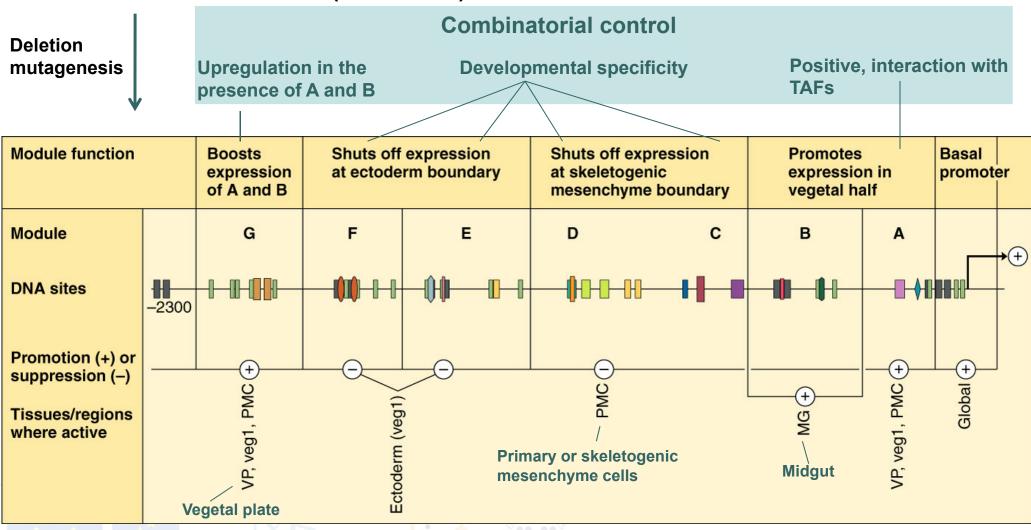




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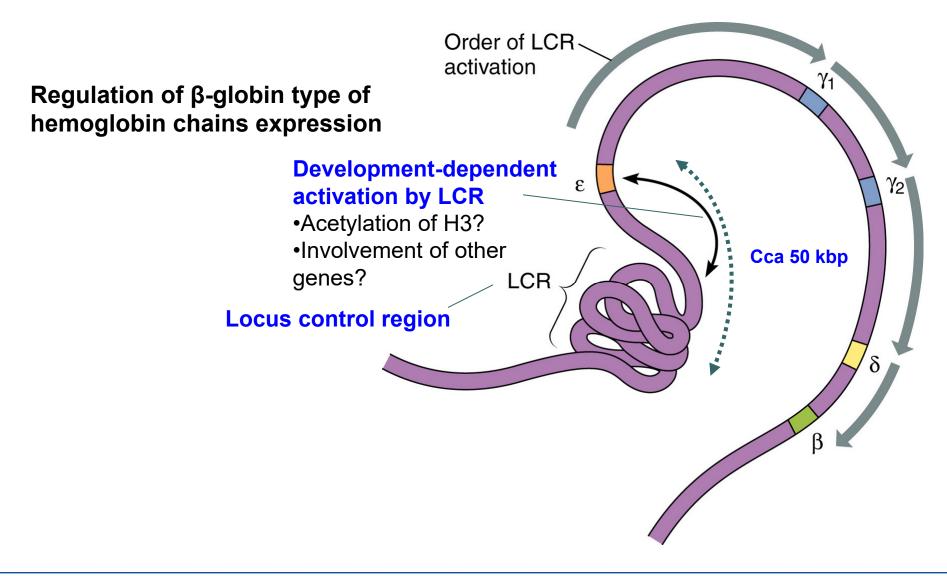
Multifactorial Promoters Control

ProENDO16:REPORTER (sea urchin)





Multifactorial Promoters Control













Importance of Protein Interactions

- Functional importance of specific protein interactions
 - Chromatin structure
 - Regulation of transcription
 - mRNA localization



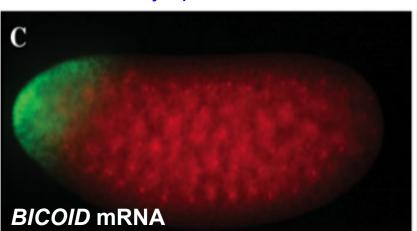


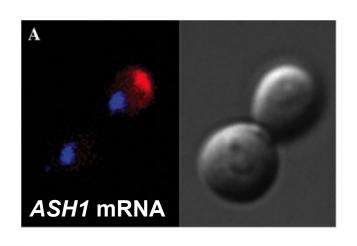


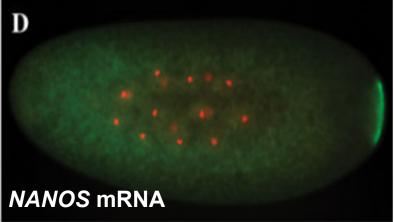




- Importance of mRNA localization
 - Control over spatiotemporal localization of gene product (protein)
 - Asymmetric cell division during development
 - Embryo polarization







Shahbabian and Chartrand, 2012



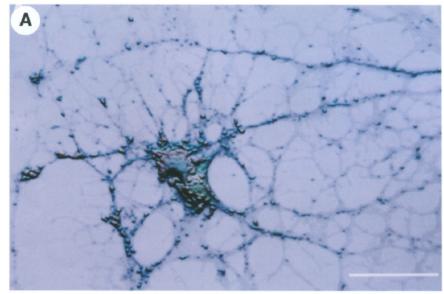


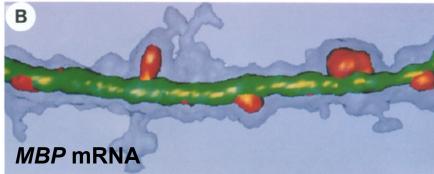






- Role of mRNA localization
 - Attenuating the expression of potentially toxic proteins
 - Localization of expression of MYELIN BASIC PROTEIN (MBP) into myelination regions of nerve cells





Ainger et al., 1993





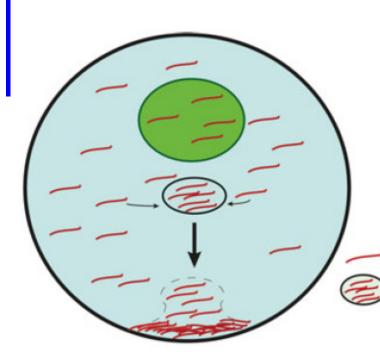






Mechanisms

Diffusion and entrapment of mRNA



- During the early stages of Xenopus oogenesis, Xcat-2 mRNA is restricted to a specific structure in the cytoplasm called the mitochondrial cloud (MC, Balbiani body)
- MC movement is partly dependent on the depolymerization of microtubuls (socalled "molecular motor")
- Entrapment on the vegetal pole via interaction of MC and ER

Xcat2 mRNA

mitochondrial cloud

Shahbabian and Chartrand, 2012







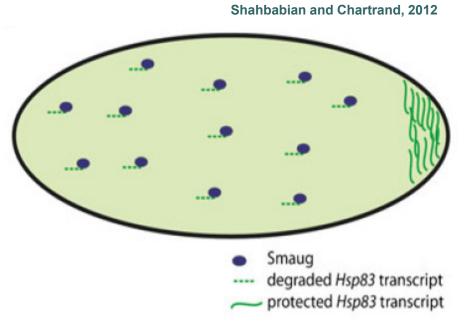




Mechanisms

Localized mRNA degradation

- During embryogenesis in Drosophila m. Hsp83 mRNA is localized at the posterior pole of embryo, similarly to NANOS mRNA
- Hsp83 mRNA is localized in the whole embryo, however, it is destabilized by cis elements both in 3'UTR (HDE) and in coding region (HIE).



- HIE elements are recognized by SMAUG protein, which mediates binding of degradation complex CCR4/POP2/NOT
- In the posterior pole the Hsp83 mRNA is protected from the effects of SMAUG by the so-called HPE element in 3'UTR; mechanism of this protection is still unknown





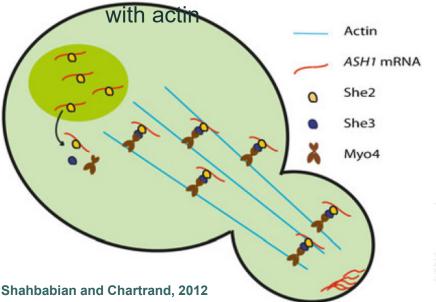


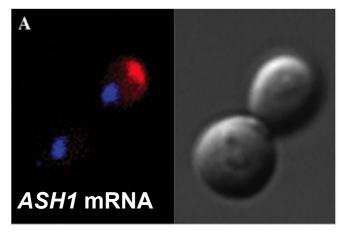


Mechanisms

Active transport of mRNA

- Asymmetric Synthesis of HO1 (ASH1) is represor of the HO endonuclease in S. cereviseae; inhibition of HO results in inhibition of mating-type switching in daughter cells
- ASH1 mRNA is actively transported by "molecular motors" associated





Shahbabian and Chartrand, 2012

- ASH1 mRNA contains 4 cis elements (3 in the coding sequence and 1 in the 3'UTR), which are recognized by RNA-binding protein SHE2
- SHE2 interacts with SHE3, an adaptor protein, which links SHE2 to the molecular motor MYO4, which then binds to actin and allows transport of ASH1 mRNA into the daughter cell

Importance of Protein Interactions

- Functional importance of specific protein interactions
 - Chromatin structure
 - Regulation of transcription
 - mRNA localization
 - hnRNA splicing











Importance of Protein Interactions

- Functional importance of specific protein interactions
 - Chromatin structure
 - Regulation of transcription
 - mRNA localization
 - hnRNA splicing
 - Protein stability



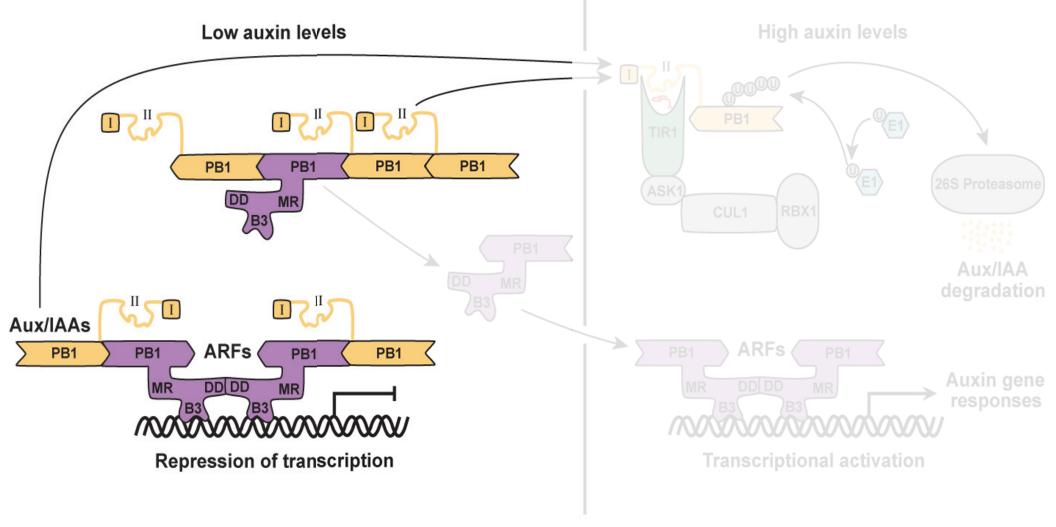


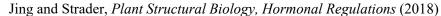






Auxin Signalling















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Importance of Protein Interactions

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 - hnRNA splicing
 - Protein stability
 - Signal transduction



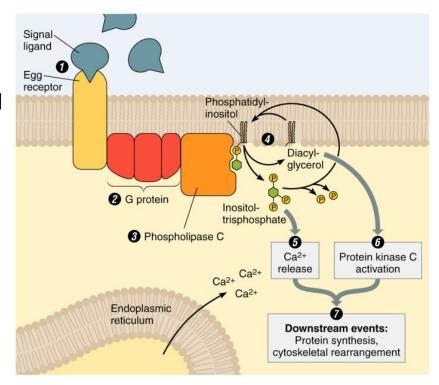


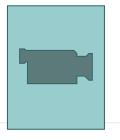




Signal transduction

- PI and signal transduction
 - through G protein and phospholipase C
 - Signalling cascades using cAMP

















Outline

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- Methods of analysis of protein interactions in vivo
 - Co-immunoprecipitation





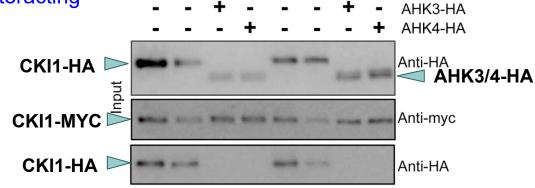




PI in vivo

Co-immunoprecipitation -ck CKI1-myc

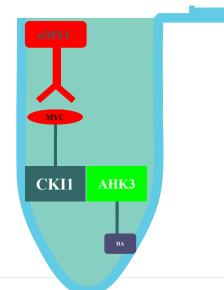
 Isolation of protein complexes using antibodies recognizing one of the interacting proteins



+CK CKI1-myc

CKI1-HA

CKI1H405Q-HA













αΗΑ



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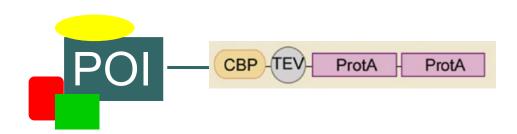




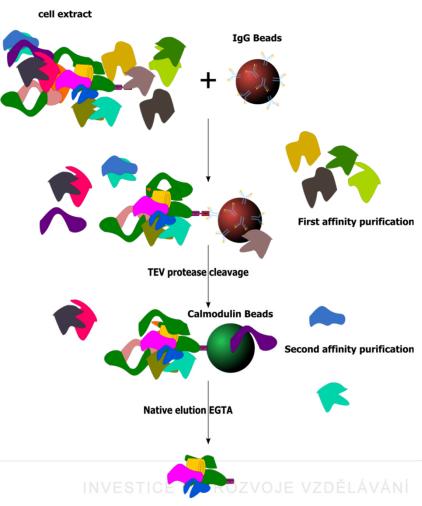
PI in vivo

Tandem affinity purification (TAP-tag)

 Isolation of protein complexes using recombinant proteins fused with two different binding domains tags



- calmodulin-binding protein (CBP)
- IgG binding domains of protein A (ProtA)
- TEV (tobacco etch virus) protease recognition site
- Isolated protein complexes are separated using 1D ELFO and then identified by MS
- Advantage: using two independent protein domains for affinity purification -> therefore high specifity



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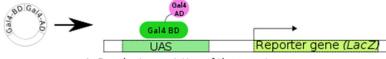




PI in vivo

Yeast two-hybrid assay (Y2H)

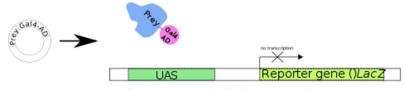
- Isolation of protein complexes using recombinant proteins, each fused to a part of Gal4 transcription factor
 - One of the proteins (bait) fused to DNAbinding domain of Gal4 (Gal4-BD)
 - The other protein (prey) fused to activation domain of Gal4 (Gal4-AD)
- Protein interactions enable reconstitution of binding domains with activation domain and triggers the expression of a reporter gene
 - Visual detection (blue color, LacZ)
 - Auxotrophic selection (growth on medium lacking histidine, His)
- Method used for searching for interaction partners in expression libraries of individual organisms



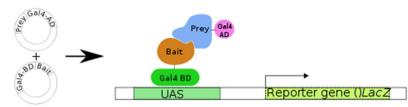
A. Regular transcription of the reporter gene



B. One fusion protein only (Gal4-BD + Bait) - no transcription



C. One fusion protein only (Gal4-AD + Prey) - no transcription



D. Two fusion proteins with interacting Bait and Prey

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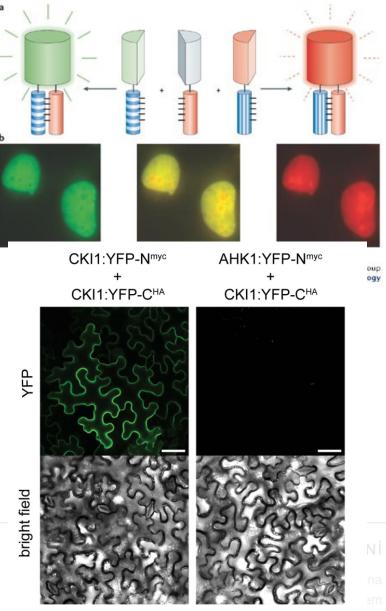




PI in vivo

Bimolecular fluorescence complementation (BiFC)

- Protein interaction is detected by reassociation of the fluorescent protein
 - Each of the potential interaction partners is fused to one of the subunits of the fluorescent protein, e.g. YFP
 - In case of interaction, the fluorescence appears
- Apart from identification of the interaction, this method allows you to localize the interaction within the cell











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PI in vivo

Membrane Recruitment Assay (MeRA)

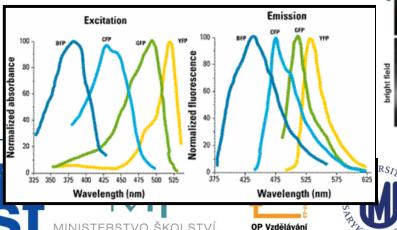
 Method for identification of interactions of cytoplasmic proteins with the membrane proteins



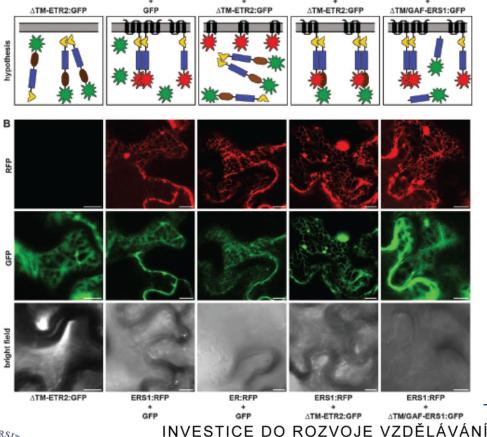
Membrane protein is fused with a fluorescecnt protein

Potential interaction partner is fused with another fluorescent protein with different emission spectra

In case of interaction the localization of the cytoplasmic protein is changed – it is colocalized on the membrane with the membrane protein



pro konkurenceschopnost

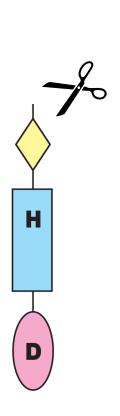


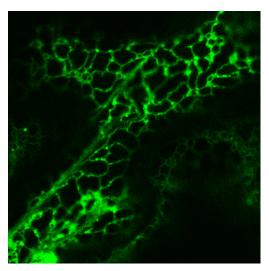


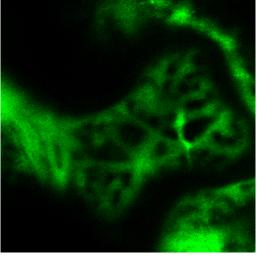
Tato prezentace je spolufinancována Evropským sociálním fondem a státním rozpočtem České republiky

PI in vivo

Membrane Recruitment Assay (MeRA)











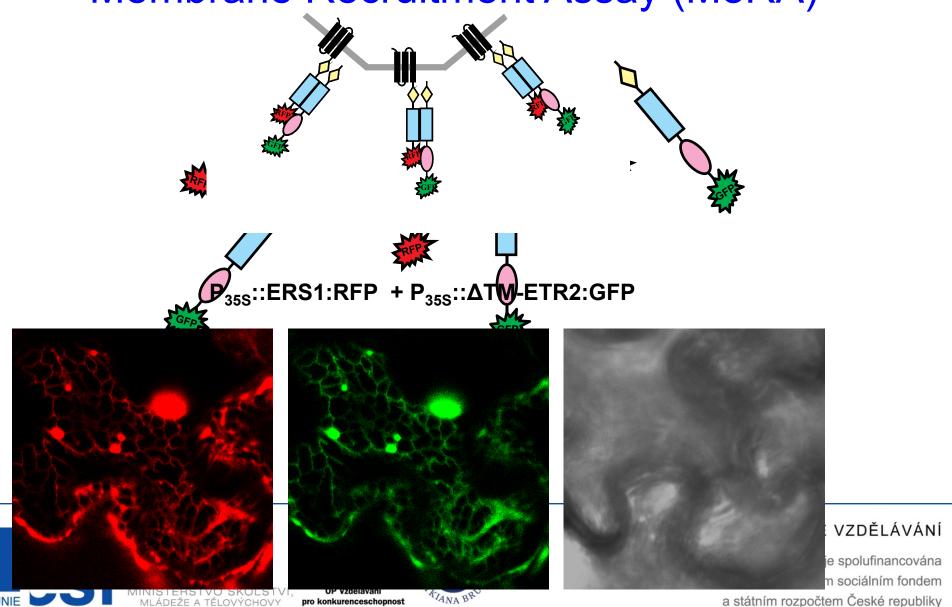






PI in vivo

Membrane Recruitment Assay (MeRA)



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 - Practical use of methods for *in vivo* studies of protein interactions

Signal Transduction via MSP

Recent Model of the CK Signaling via Multistep Phosphorelay (MSP) **Pathway** Releative Transcript Level (% maximum) **CYTOKININ** - ARR16 - ARRIS РМ -O- ARRS AHK sensor histidine kinases • AHK2 - ARR7 AHK3 ... ARR6 CRE1/AHK4/WOL 100 Time following cytokinin application HPt Proteins D'Agostino et al., Plant Phys, 2000 • AHP1-6 **CK** primary response genes Response Regulators - Type-A ARRs expression **NUCLEUS REGULATION OF TRANSCRIPTION** INTERACTION WITH EFFECTOR PROTEINS









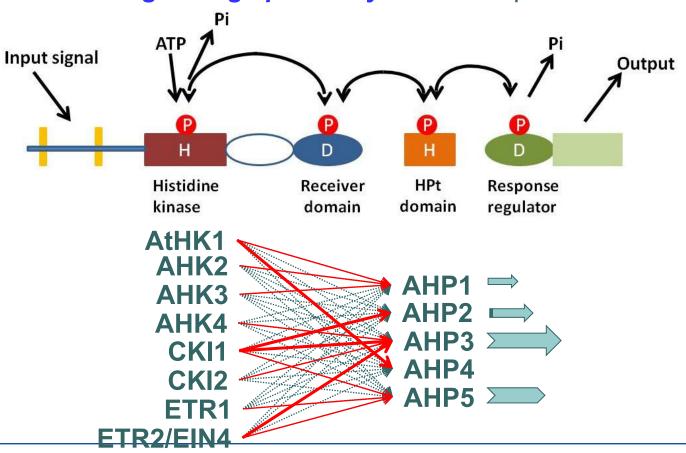


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Tato prezentace je spolufinancována Evropským sociálním fondem a státním rozpočtem České republiky

Is there any specificity in plant MSP?

Is there a signalling specificity of MSP in plants?





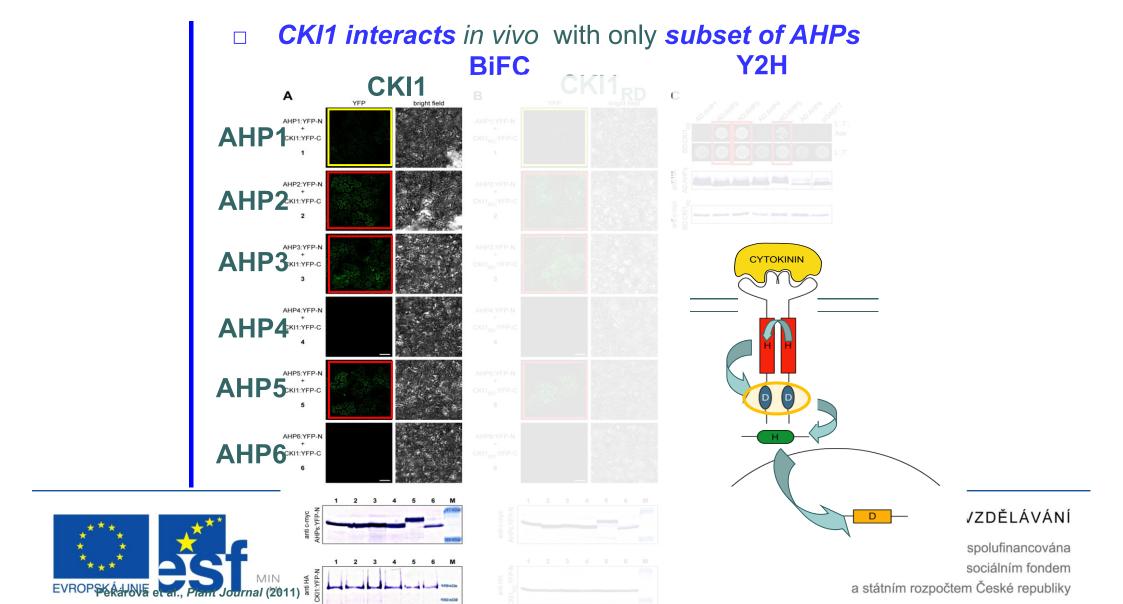






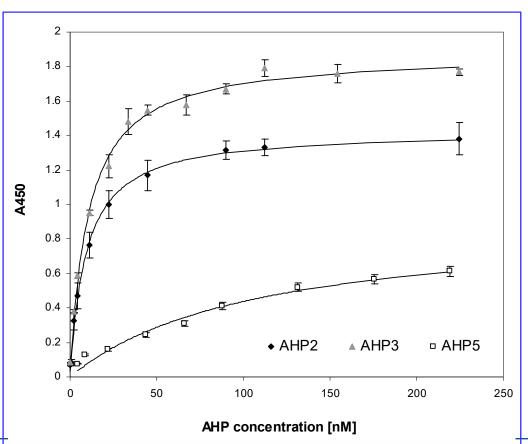


Specificity of CKI1 signalling



Specificity of CKI1 Signalling

Specificity of CKI1 interaction was confirmed in vitro



AHP3: $K_{d} \sim 10,5 \text{ nM}$

AHP2: $K_{d} \sim 9,17 \text{ nM}$

AHP5: $K_{d} \sim 108 \text{ nM}$







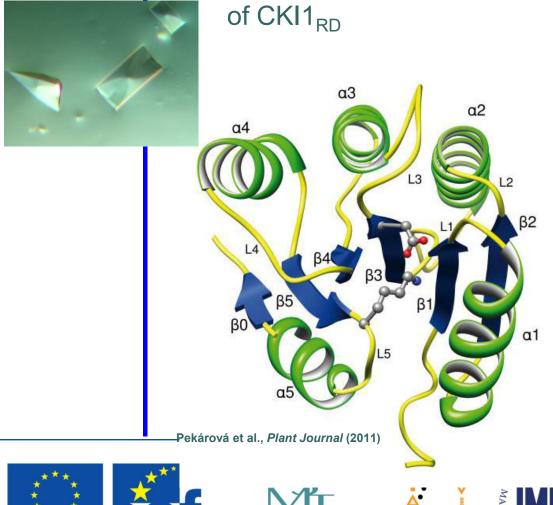


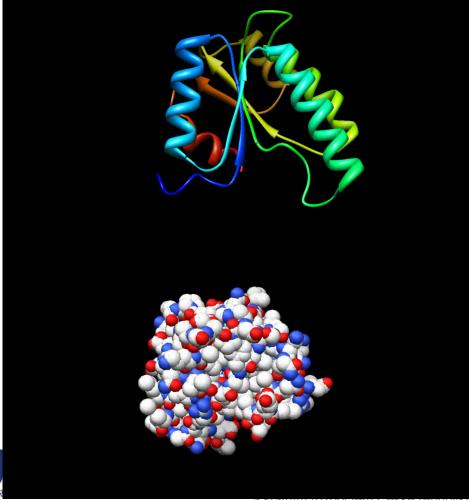




Structure of CKI1_{RD}

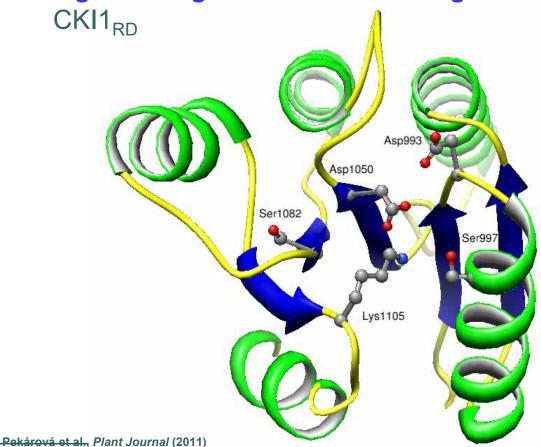
X-ray crystallography revealed conserved $(\alpha/\beta)_5$ structural fold





Dynamics of CKI1_{RD}

Mg²⁺binding leads to remodelling of active centre of









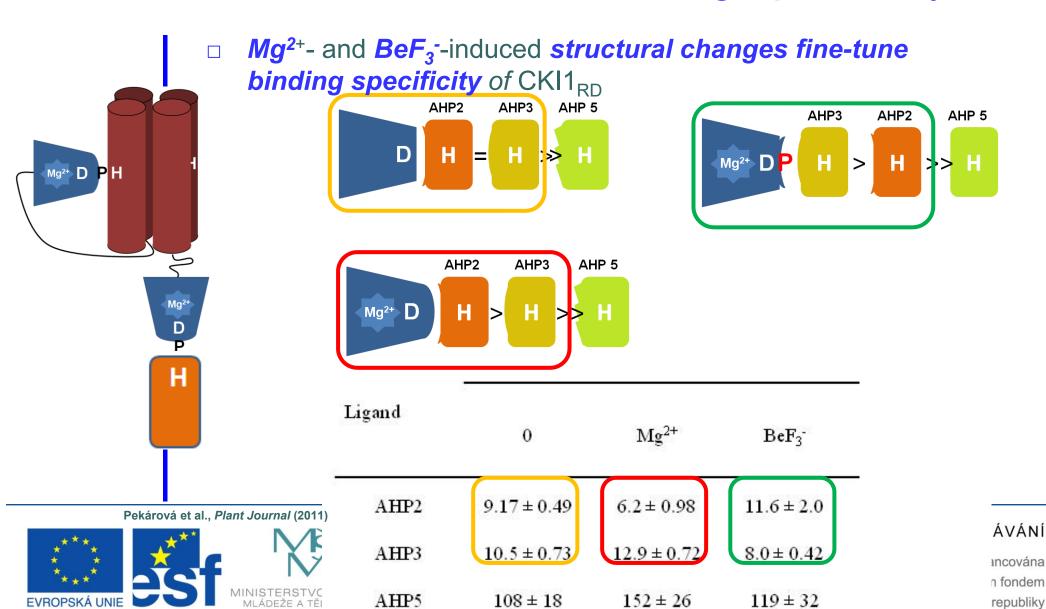




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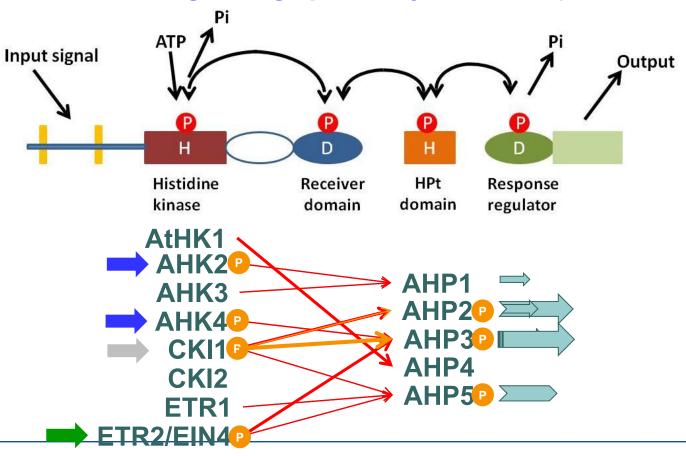
Tato prezentace je spolufinancována Evropským sociálním fondem a státním rozpočtem České republiky

CKI1_{RD} structural changes are associated with its binding specificity



Model Suggestion

YES, there is signalling specificity of MSP in plants.













Summary

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Discussion









