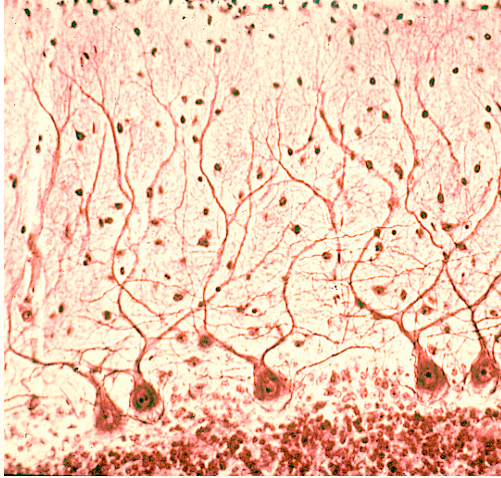


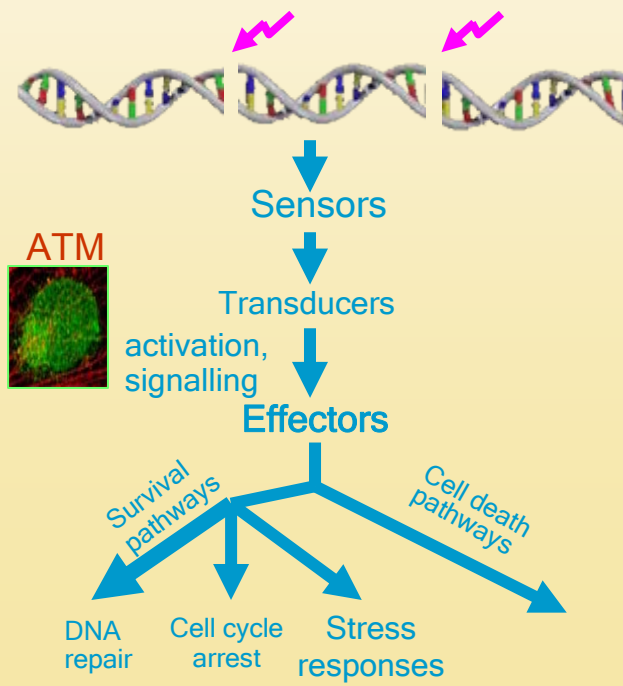


DNA repair Interest Group Cancer Center/Signal Transduction Program Seminar

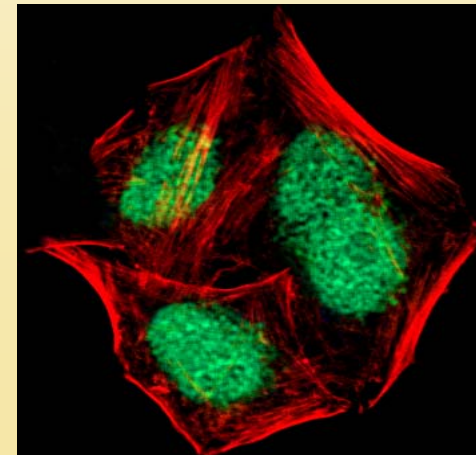
Burnham Institute for Medical
Research



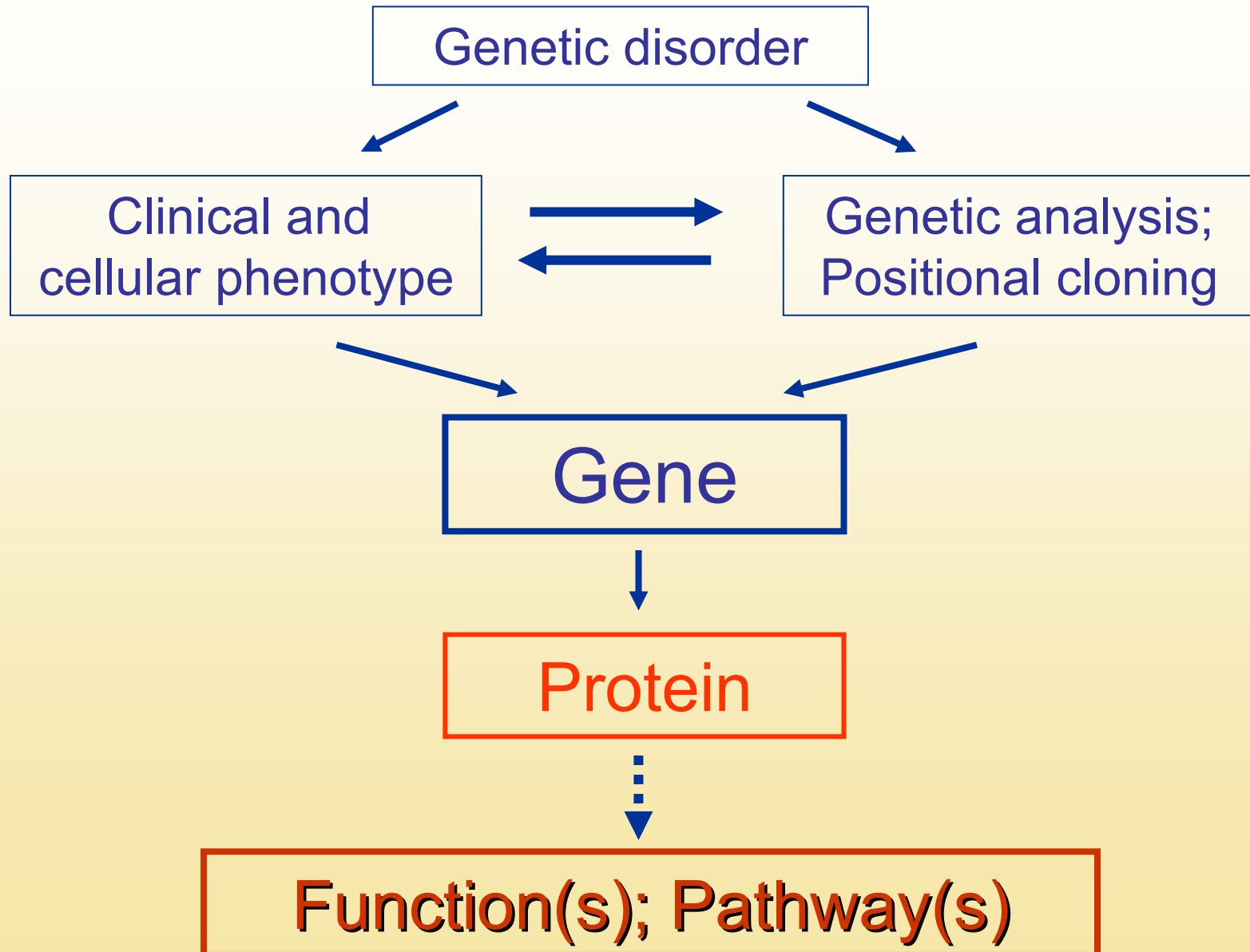
ATM: The Art of Maintaining Genome integrity



The A-T Group
Tel Aviv University

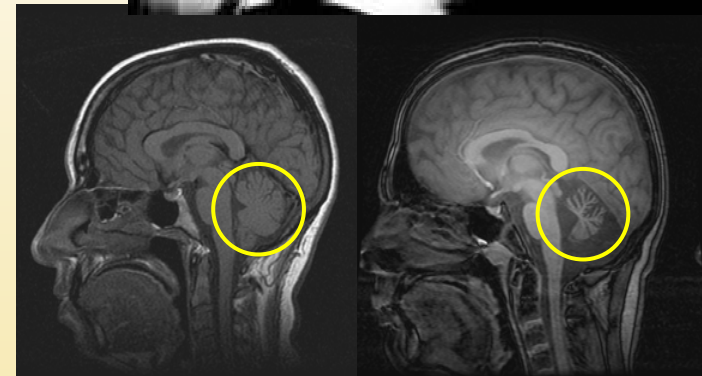


From Genetic Disorder to Function



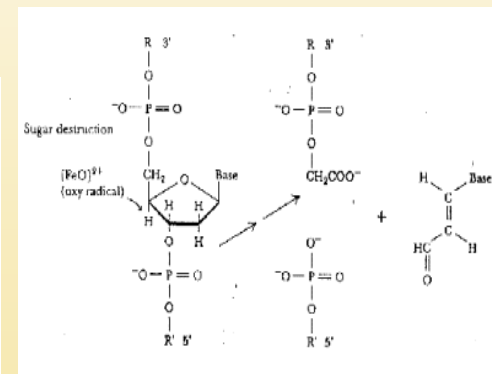
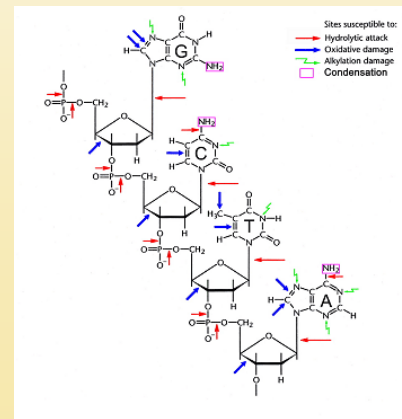
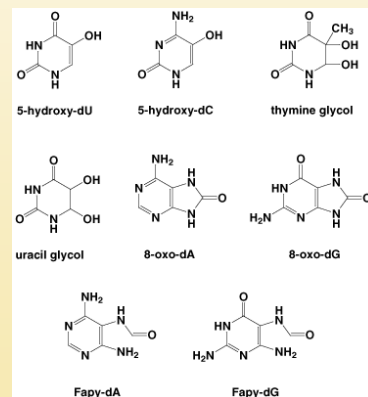
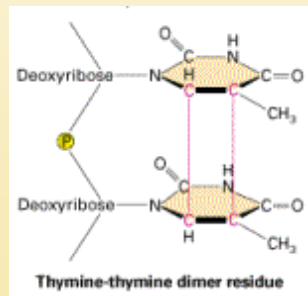
Ataxia-Telangiectasia

- Autosomal recessive
- Cerebellar ataxia (loss of Purkinje cells), severe neuromotor dysfunction
- Telangiectasia
- Immunodeficiency (B&T cells); recurrent infections
- Thymic and gonadal dysgenesis
- Retarded growth
- Premature aging
- Genomic instability
- Cancer predisposition
- Acute sensitivity to ionizing radiation
- **A profound defect in cellular responses to double strand breaks in the DNA**



DNA Damage

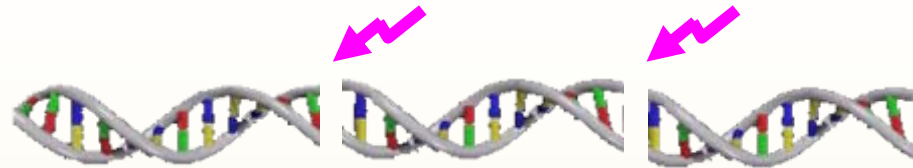
The diagram illustrates various sources of DNA damage. At the top, the title "DNA Damage" is displayed in large green letters. Below the title, six distinct sources of damage are shown, each with a pink arrow pointing down to a single DNA double helix at the bottom. The sources are: 1) A diagram of a DNA double helix with labels for "Original DNA molecule", "DNA molecule strands", "DNA molecule strands", "New strand", "New strand", and "New DNA molecule". 2) A diagram of a DNA double helix with labels for "DNA molecule strands", "DNA molecule strands", "New strand", "New strand", and "New DNA molecule". 3) A diagram of a cell showing "DNA damage" and "Cell death". 4) A diagram of a worker in a green shirt and yellow hard hat standing next to a radiation warning sign. 5) A diagram of a factory with smokestacks. 6) A diagram of a plate of food, including a large piece of meat and vegetables. 7) A diagram of a box of "Pain-Relief" capsules with a red liquid spill.



Double strand breaks



Repair DNA Double Strand Breaks



Physiologic Double-Strand DNA Break/Repair

1. RAG1,2 breaks (RAG1,2)
2. Class switch breaks (AID, UNG, APE)

Pathologic Double-Strand DNA Break/Repair

1. Ionizing radiation
2. Oxidative free radicals
3. Replication across a nick

cleavage phase

cleavage phase

joining phase

Nonhomologous DNA End Joining (NHEJ)

Ku70/86
Artemis:DNA-PKcs
XRCC4:DNA ligase IV

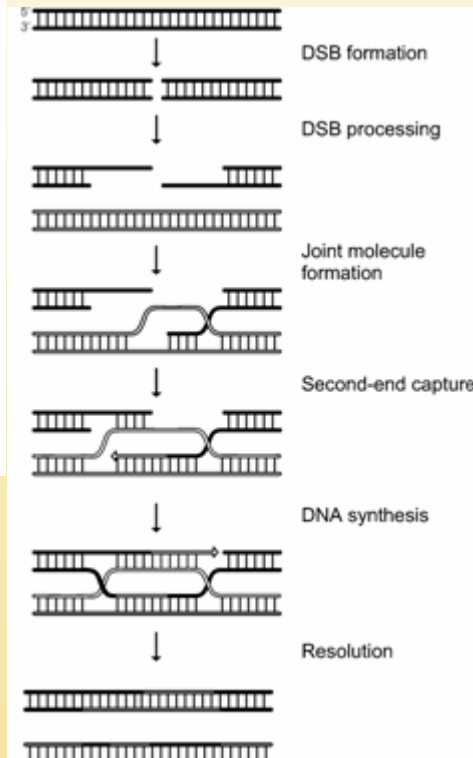
Homologous Recombination (HR)

RAD50, MRE11, XRS2,
RAD51, 52, 54, 55, 57

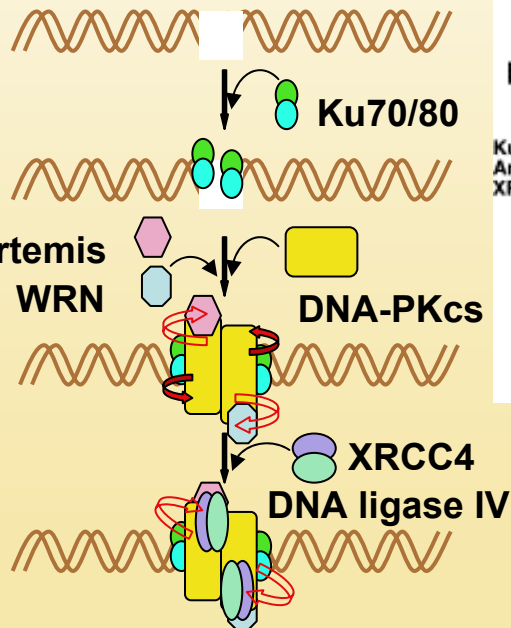
entire cell cycle

late S, G2

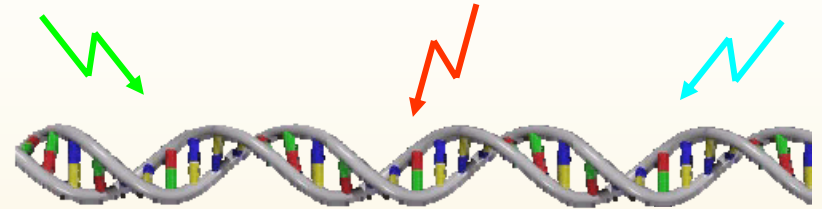
HR



NHEJ

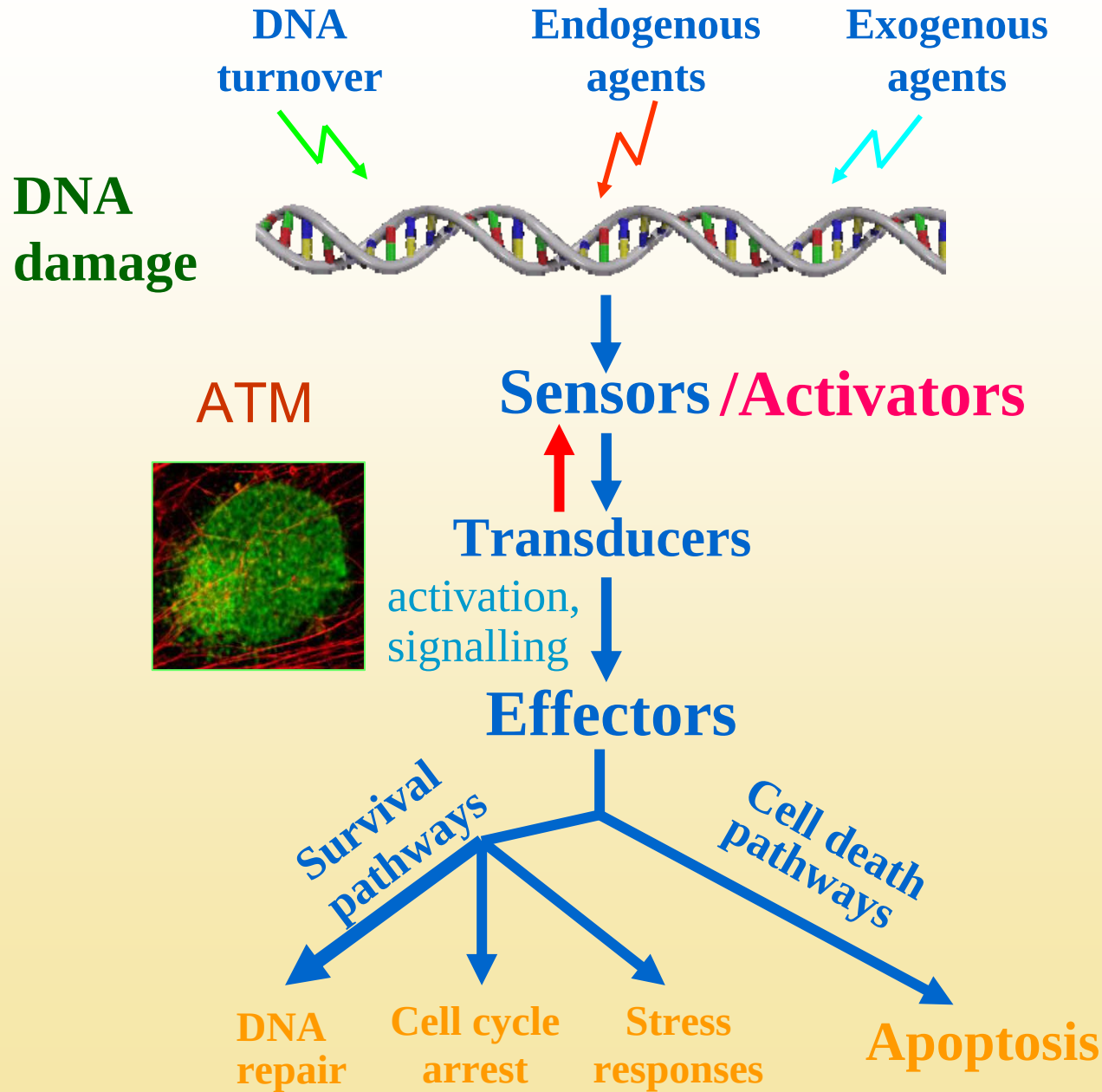


The DNA Damage Response



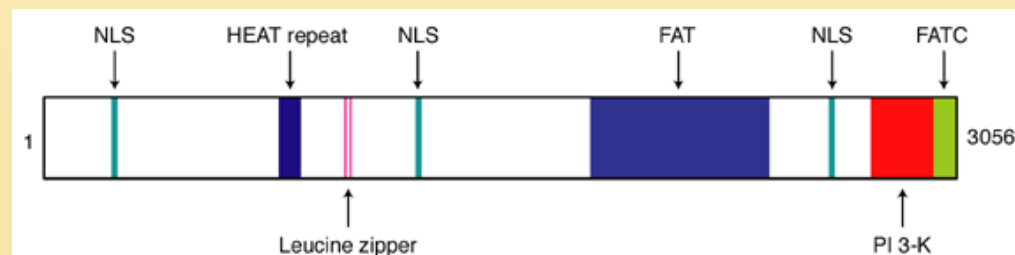
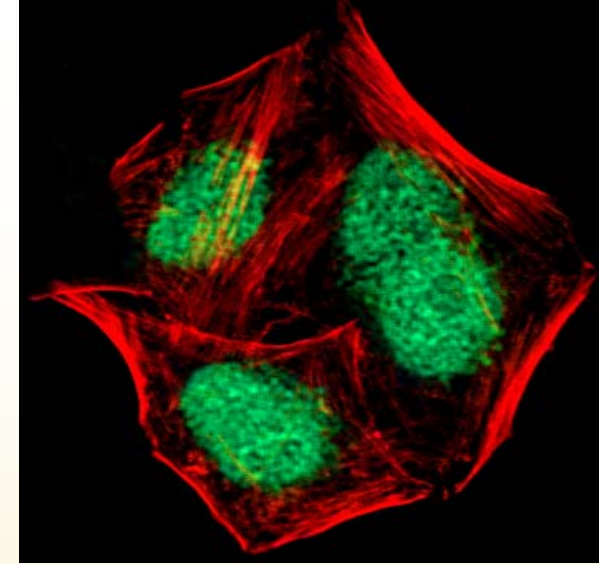
- DNA repair
- Cell cycle checkpoints
- Affects numerous cellular processes
- Modulates gene expression
- Concerted action of numerous, interlocked signaling pathways creating an intricate web
- Activated instantaneously and vigorously, particularly by DSBs

Cellular Responses to DNA Damage

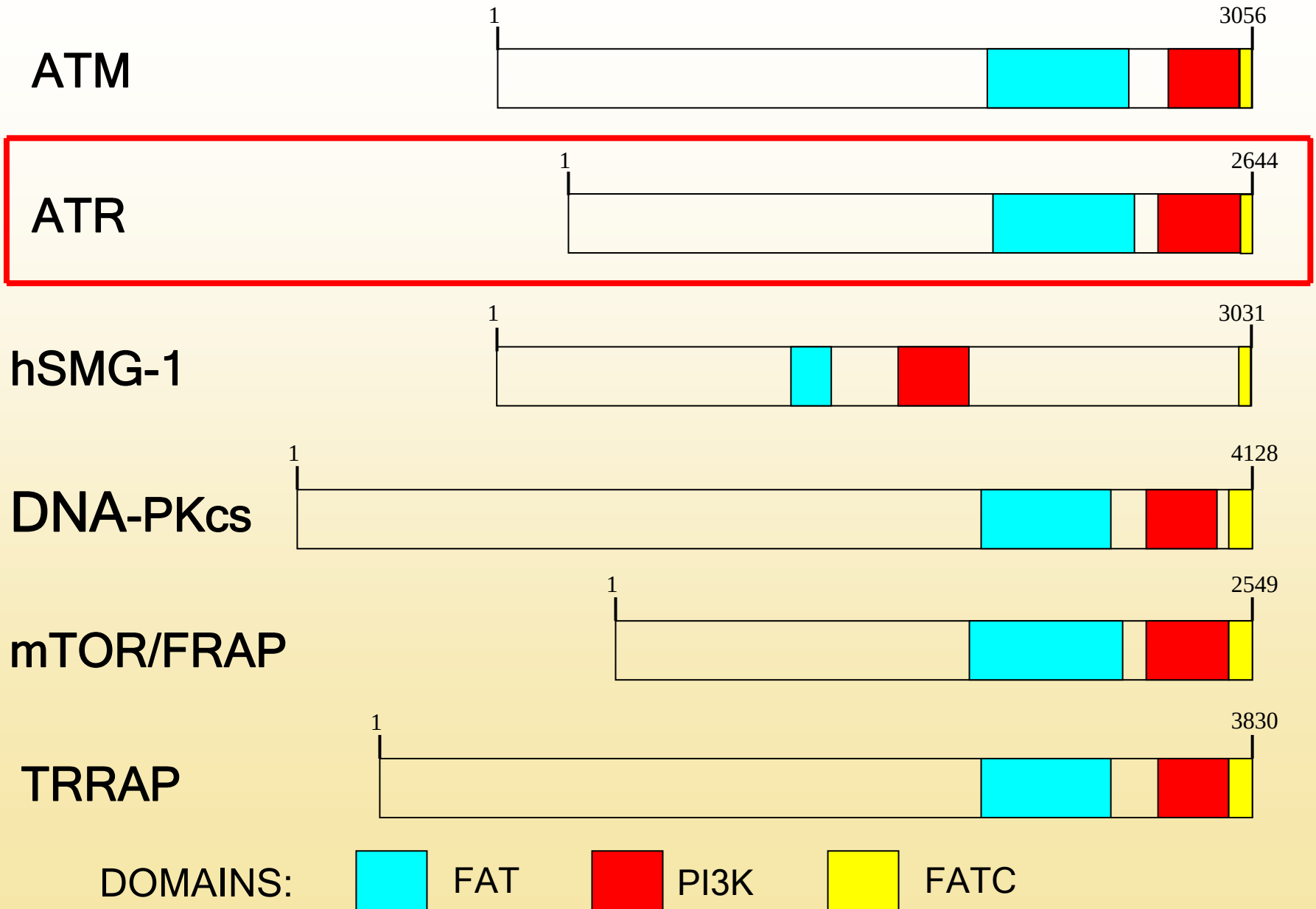


The ATM Protein

- Identified by positional cloning of the A-T gene
- Completely missing or inactivated in A-T patients
- A large (370 kDa), nuclear phosphoprotein
- A carboxy-terminal PI3-kinase-like motif
- Protein kinase activity (serine-threonine)
- ATM targets: preference for **SQ** or **TQ**
- The primary activator of the cellular response to double strand breaks (DSBs)
- Activated by DSBs



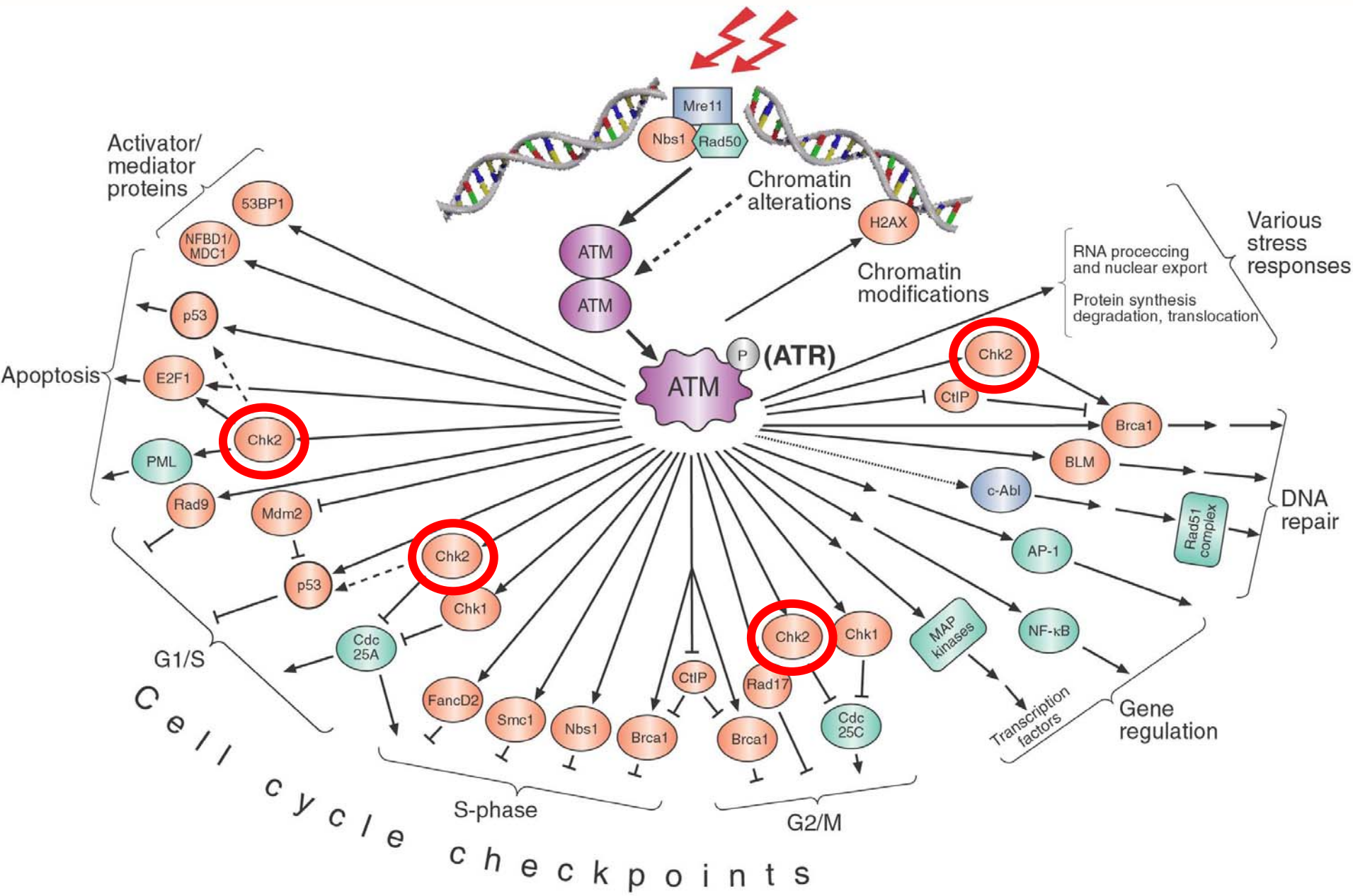
PI3-Kinase-Related Protein Kinases (PIKKs)



ATM

Control of signaling networks by
phosphorylation of key players

ATM-Mediated DNA Damage Responses



DSBs



ATM

Recruitment to
DSB sites
(Andegeko et al., 2001)

Dormant dimers turn into
active monomers
(Bakkenist & Kastan, 2003)

Activated
ATM

Phosphorylation

Effectors

Survival pathways

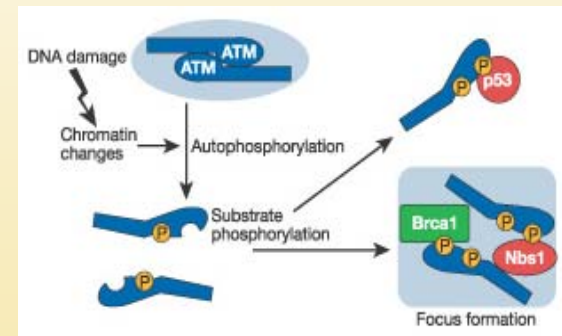
Cell death pathways

DSB
repair

Cell cycle
checkpoints

Stress
responses

Apoptosis

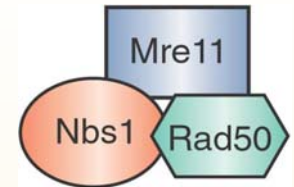


DSBs



binding to DSBs;
damage processing

MRN
complex



Processed
DNA lesions



Activation
Association with
processed DSBs



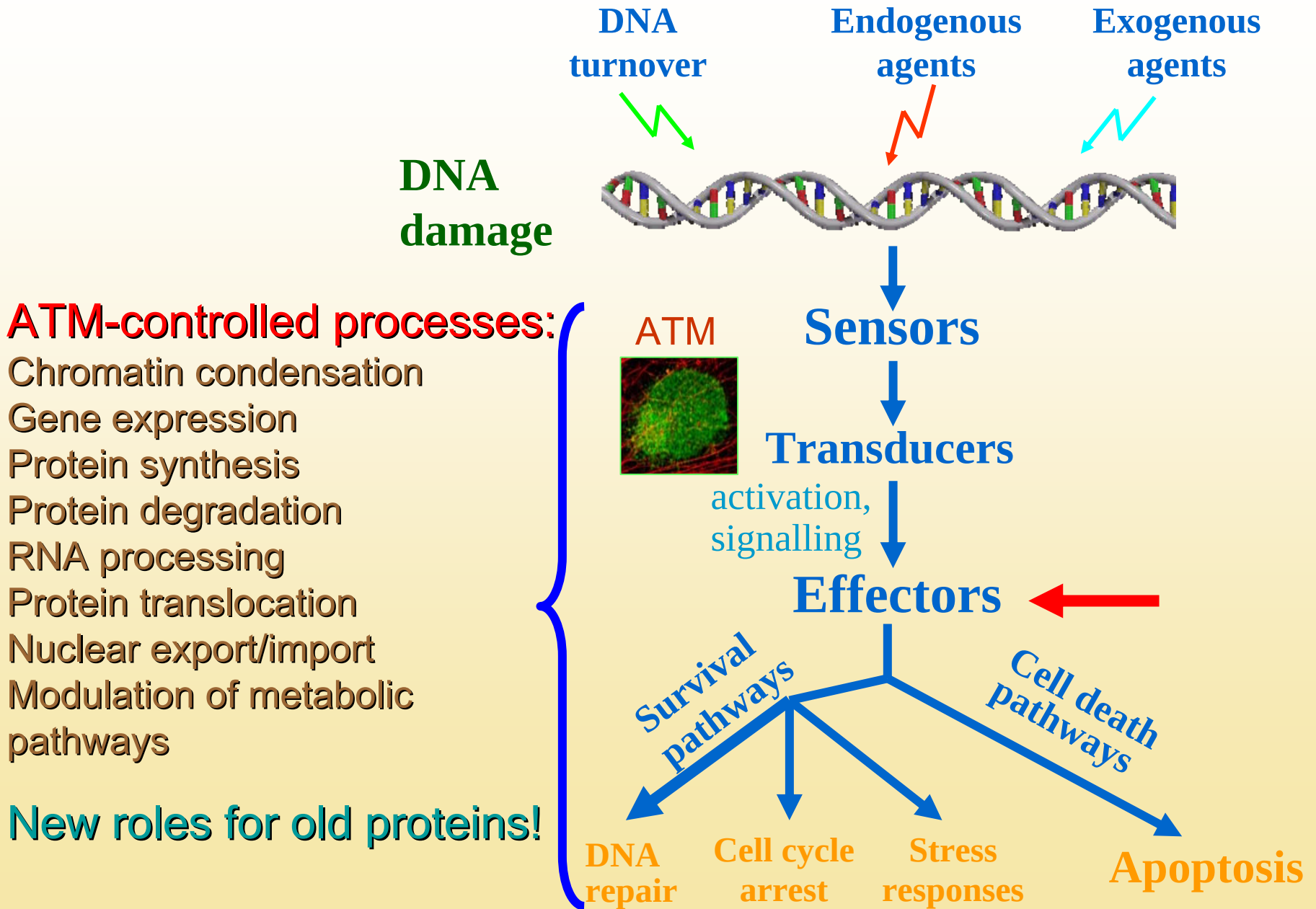
phosphorylation

Target proteins

Signaling pathways



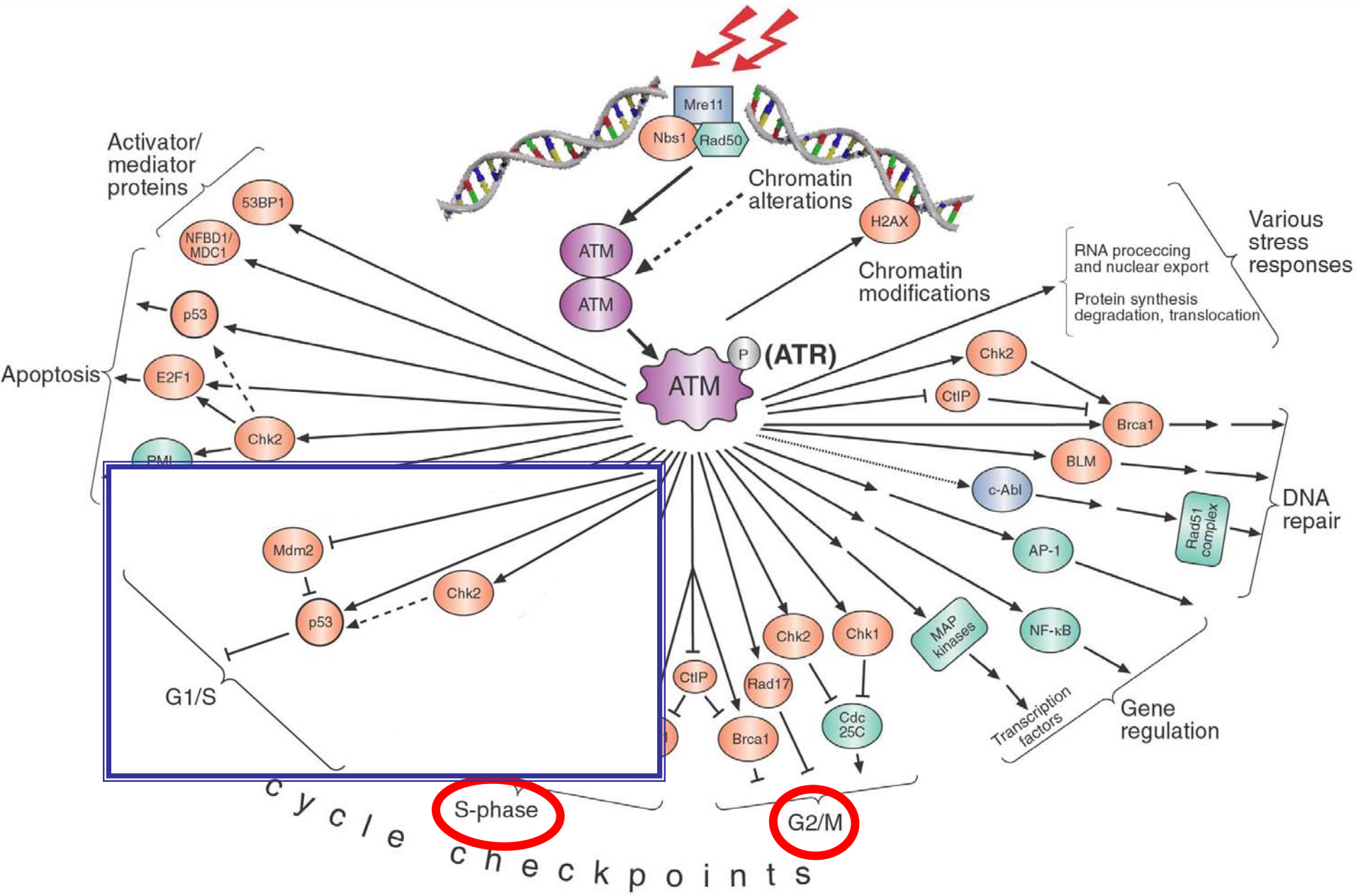
Cellular Responses to DNA Damage

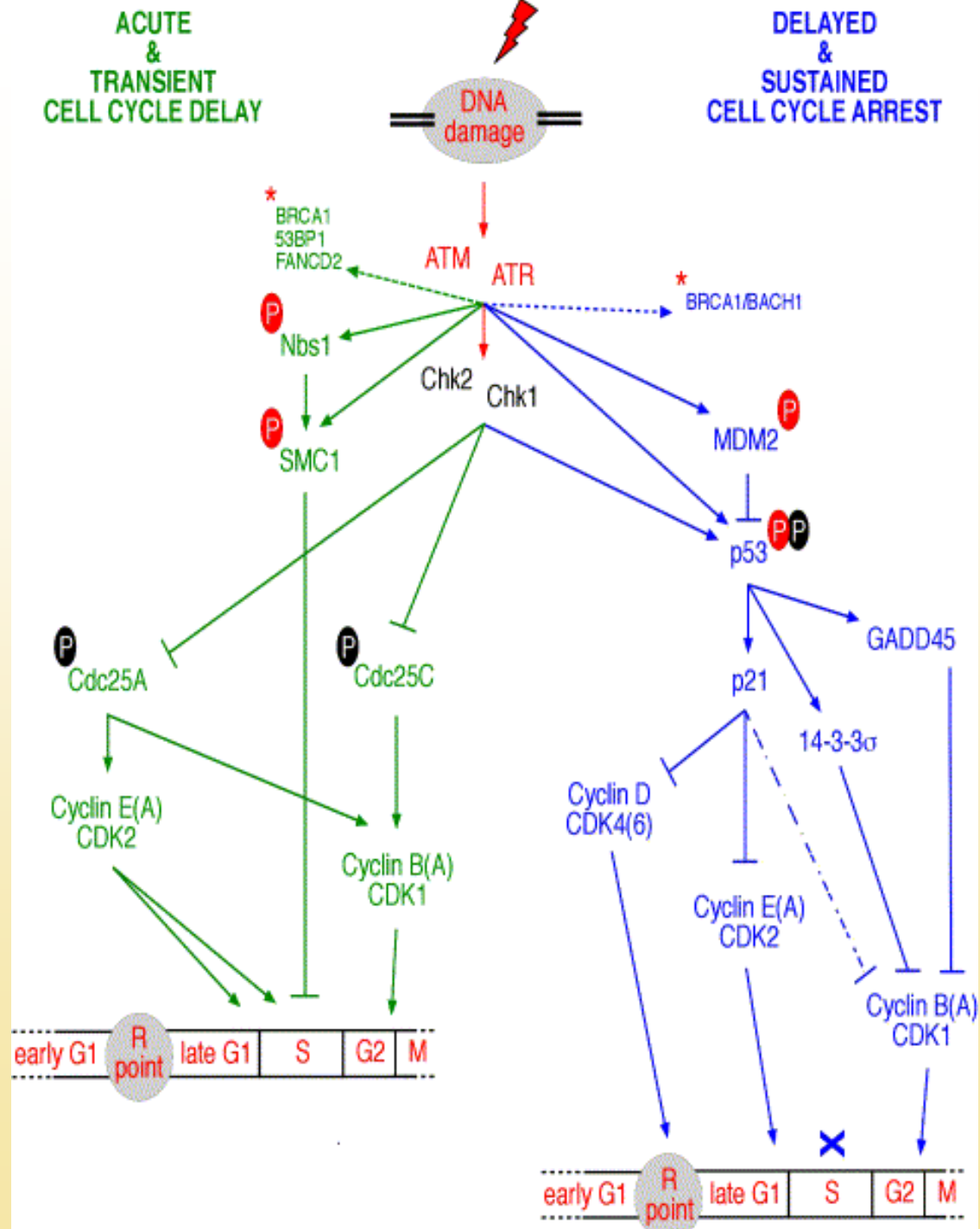


The SHARP Map, May 20, 2006

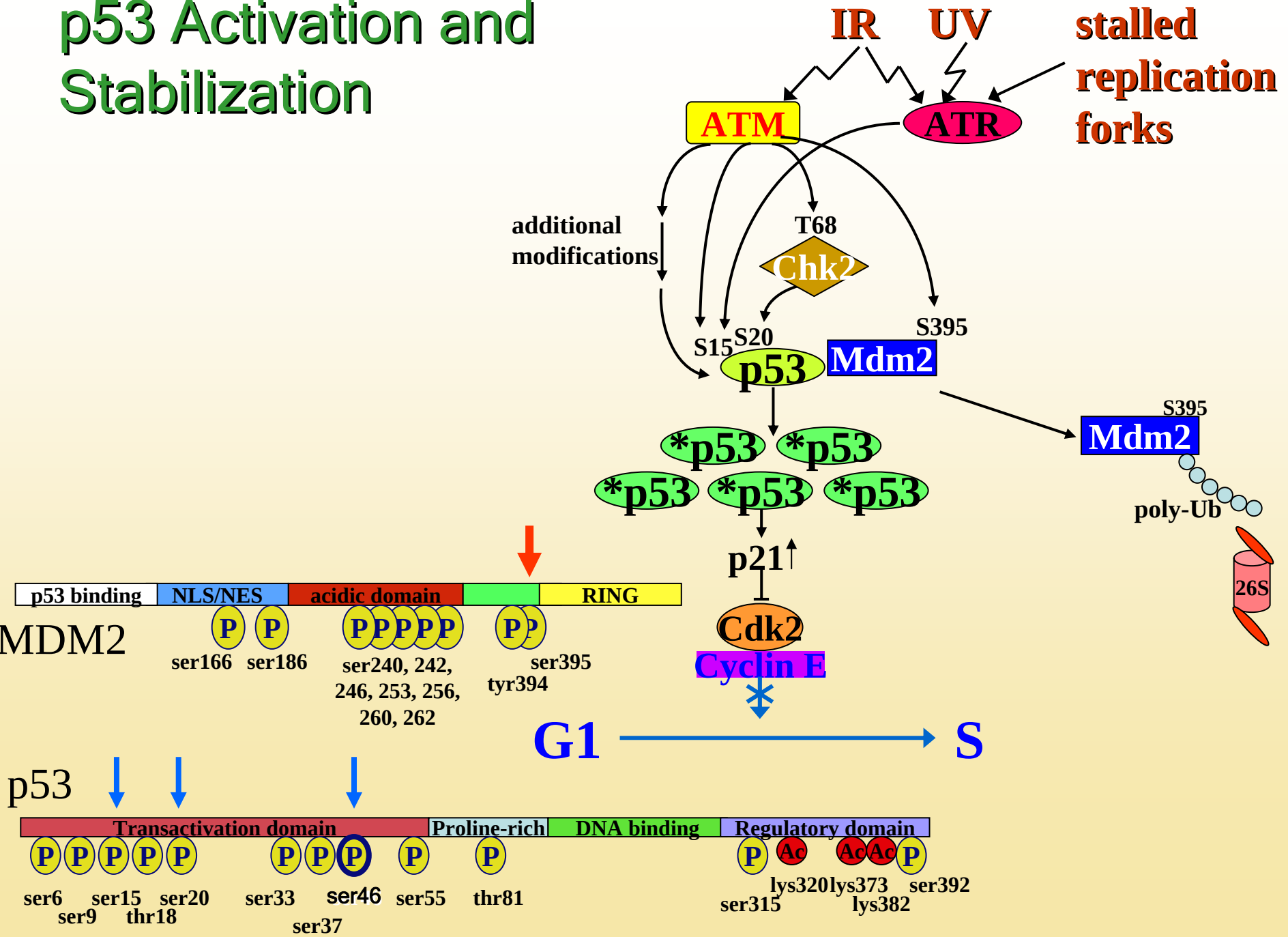


ATM-Mediated DNA Damage Responses

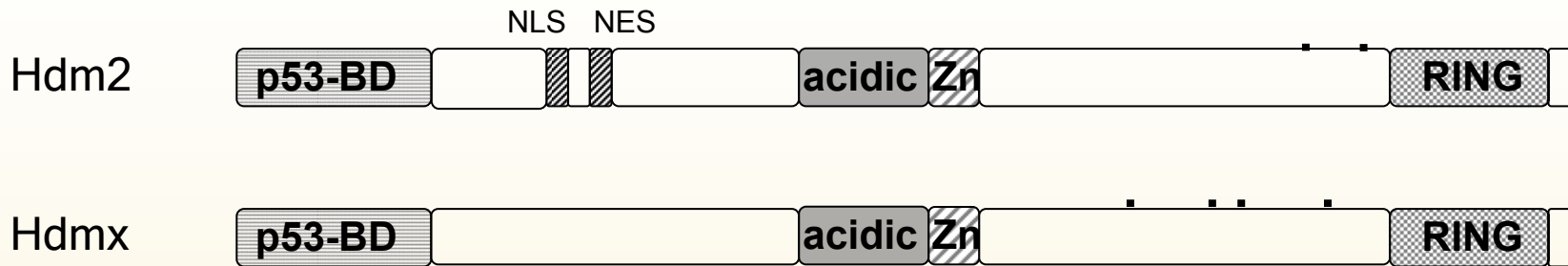




p53 Activation and Stabilization



Aother Player in the p53 Control Loop: Mdmx



Yaron Pereg

Dganit Shkedy

Rami Khosravi

Sharon Biton

Aart G. Jochemsen (Leiden)

Petra de Graaf

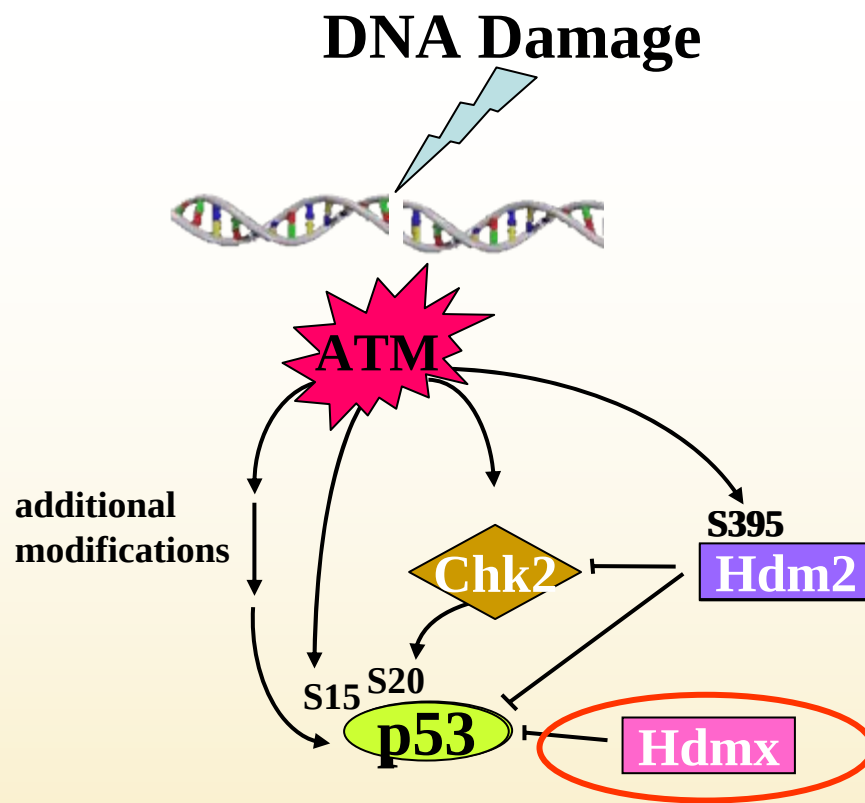
Eric Meulmeester

Wolf Lehmann (Heidelberg)

Marina Edelson-Averbukh

Koji Okamoto (Tokyo)

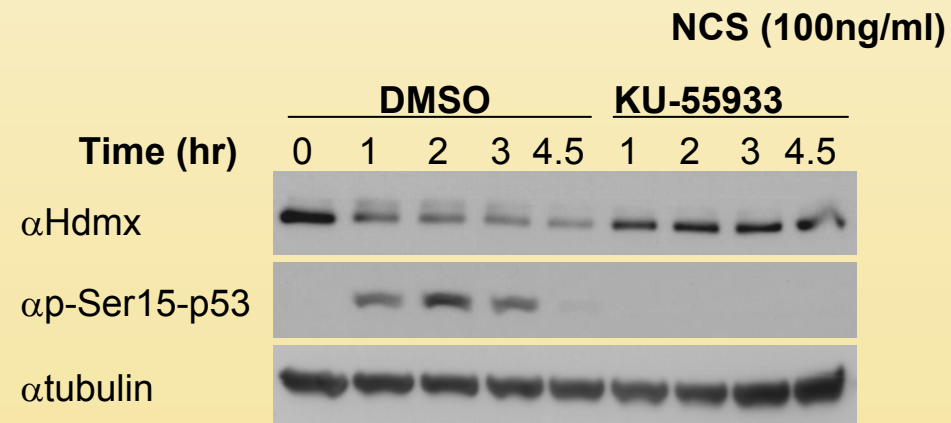
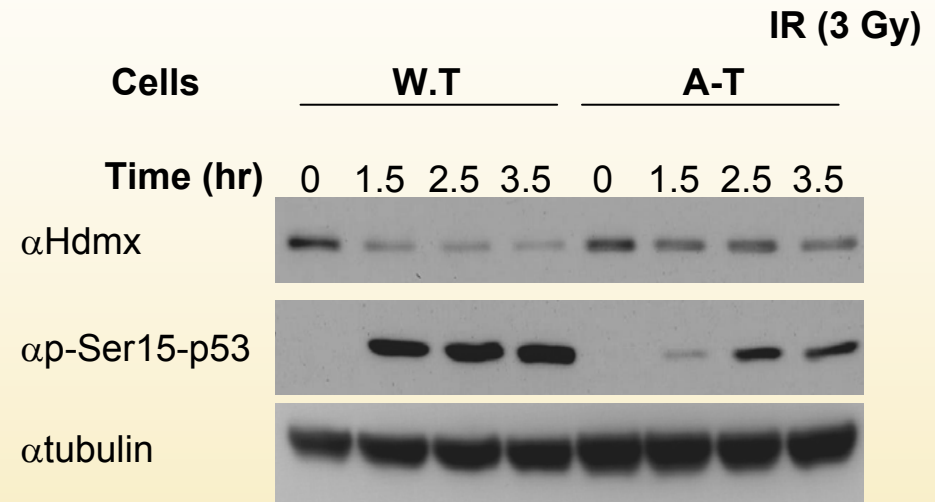
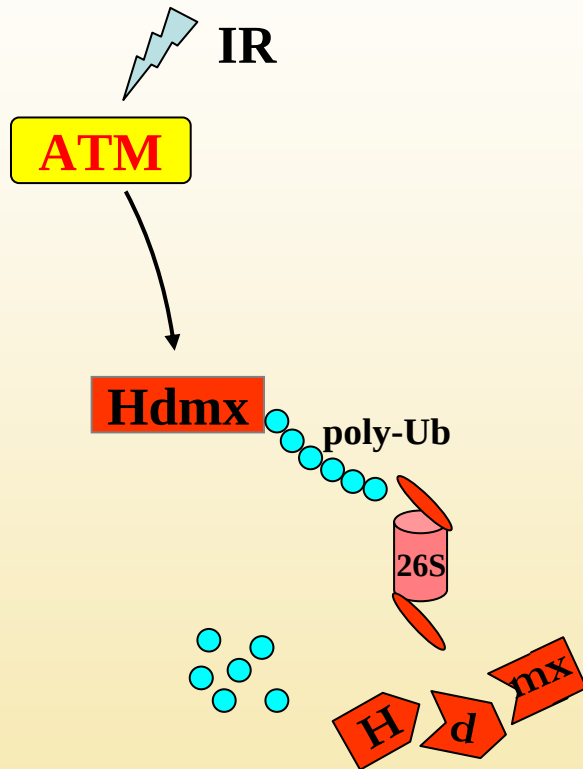
Yoichi Taya (Tokyo)



Following DNA damage Hdmx is degraded in an Hdm2-dependent manner (Pan & Chen, 2003; Kawai et al., 2003)

Is Hdmx degradation ATM-dependent?

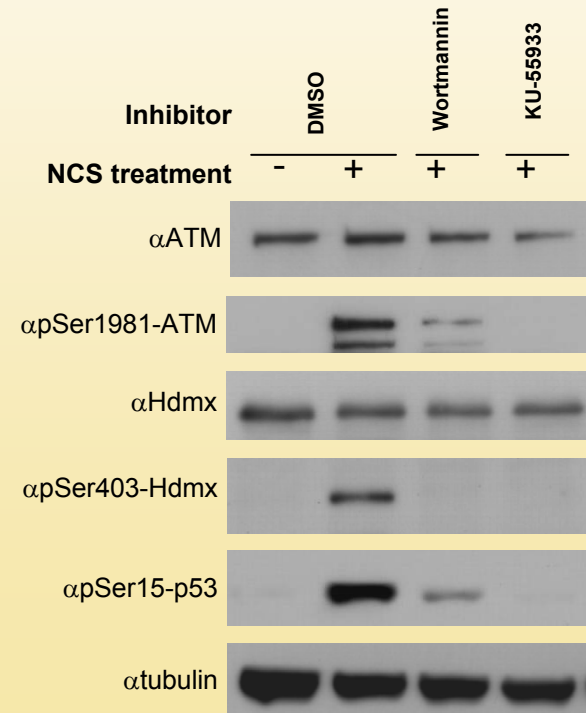
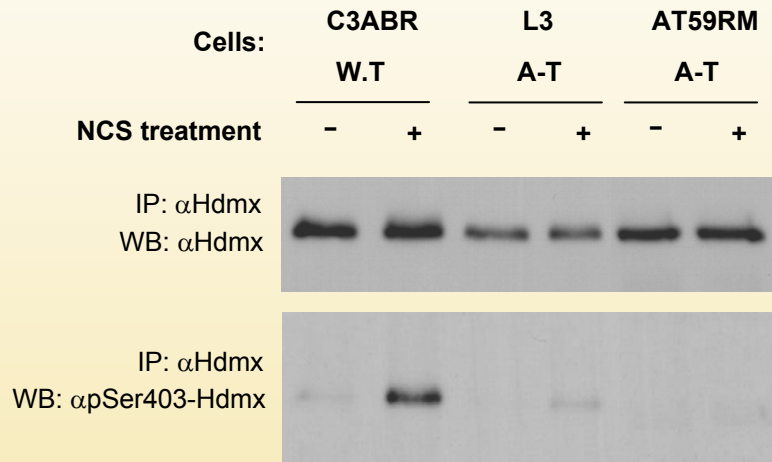
ATM Dependence of Damage-Induced Degradation of Hdmx



ATM-Mediated Phosphorylation of Ser403

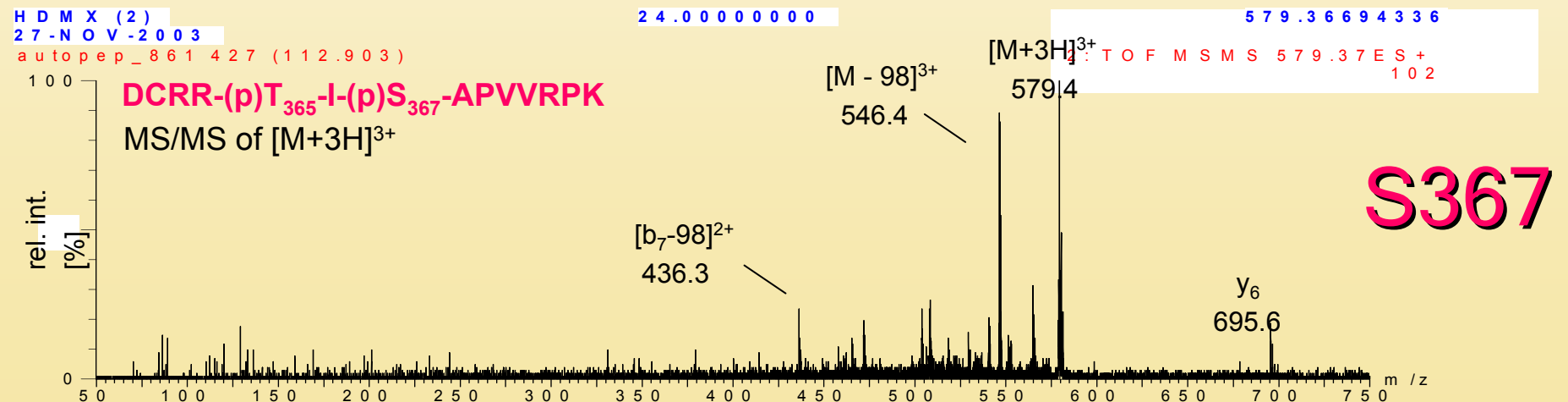
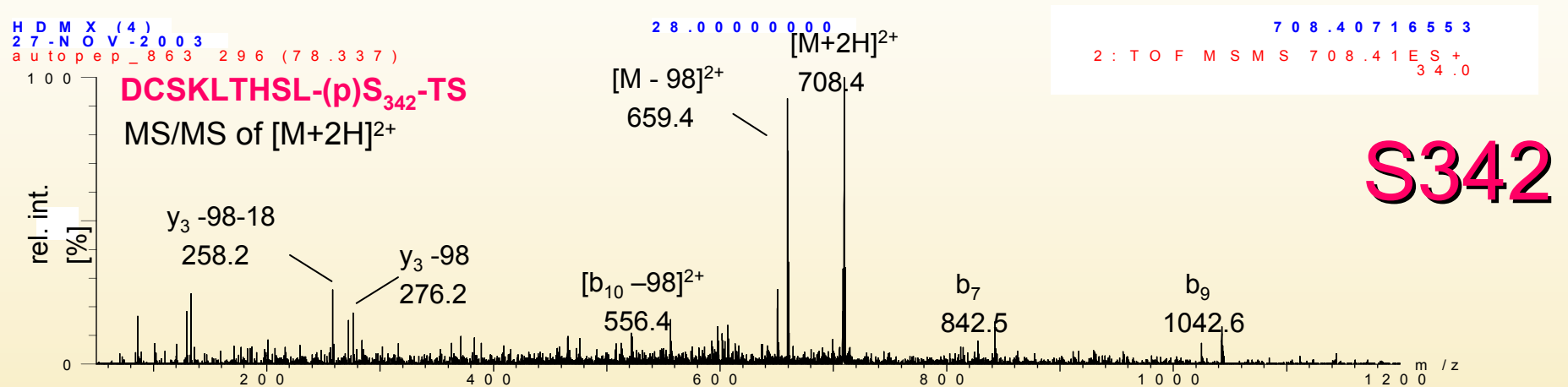
Ser 403

Hdmx

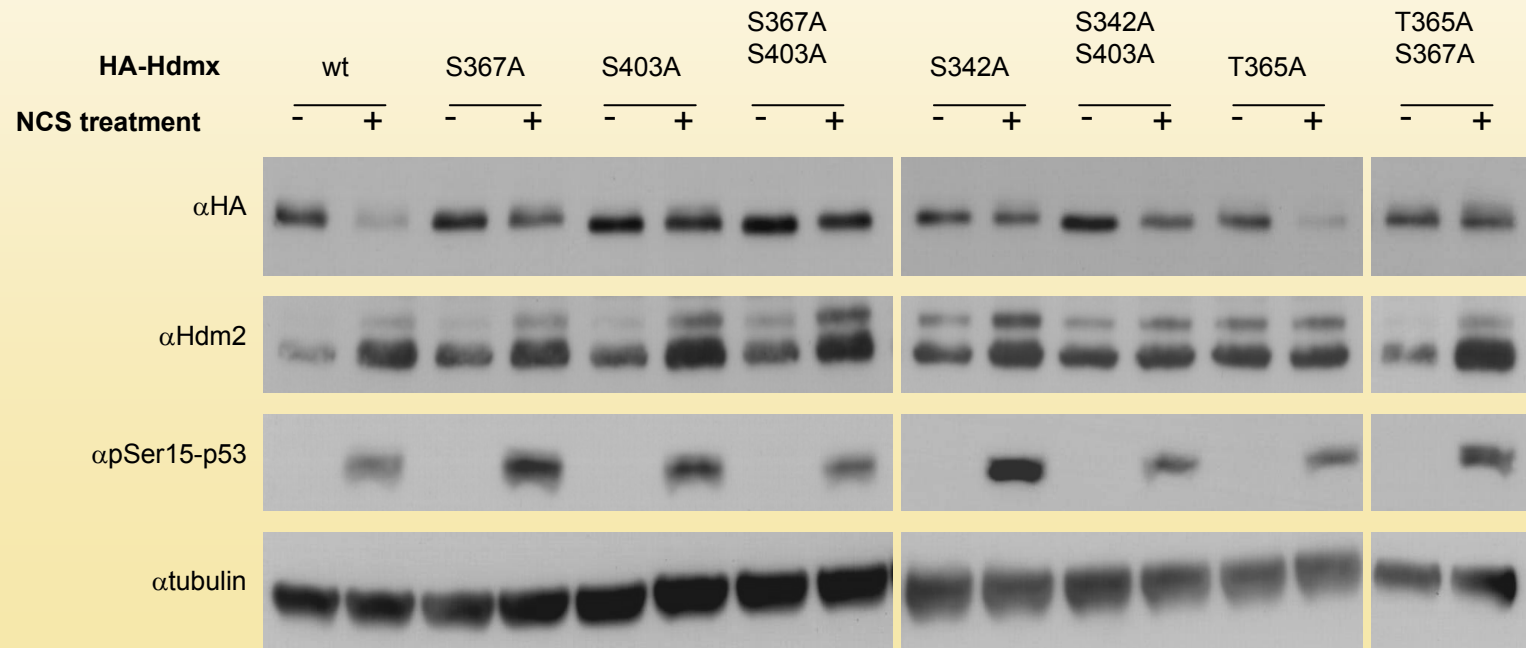
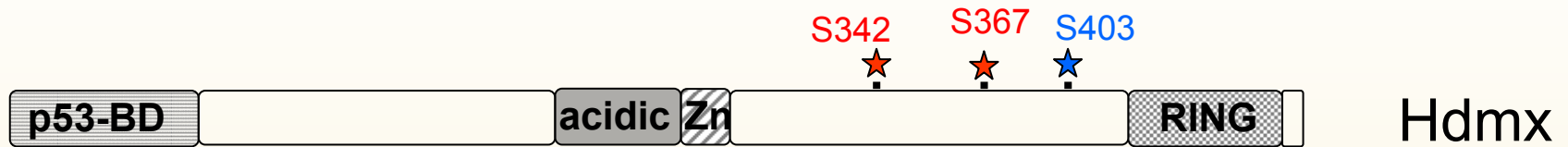


Identification of Protein Phosphorylation using Mass Spectrometry

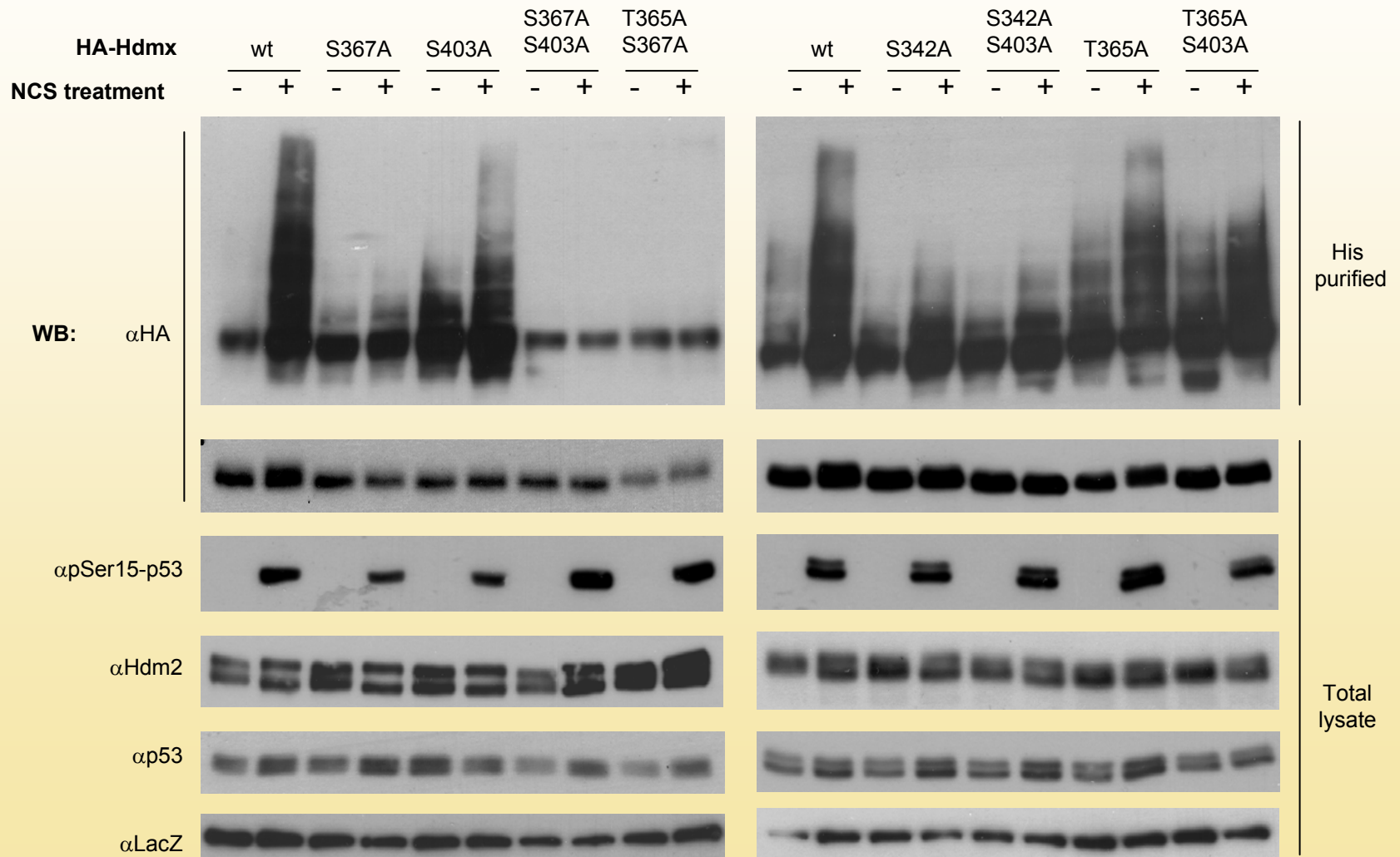
Wolf Lehmann

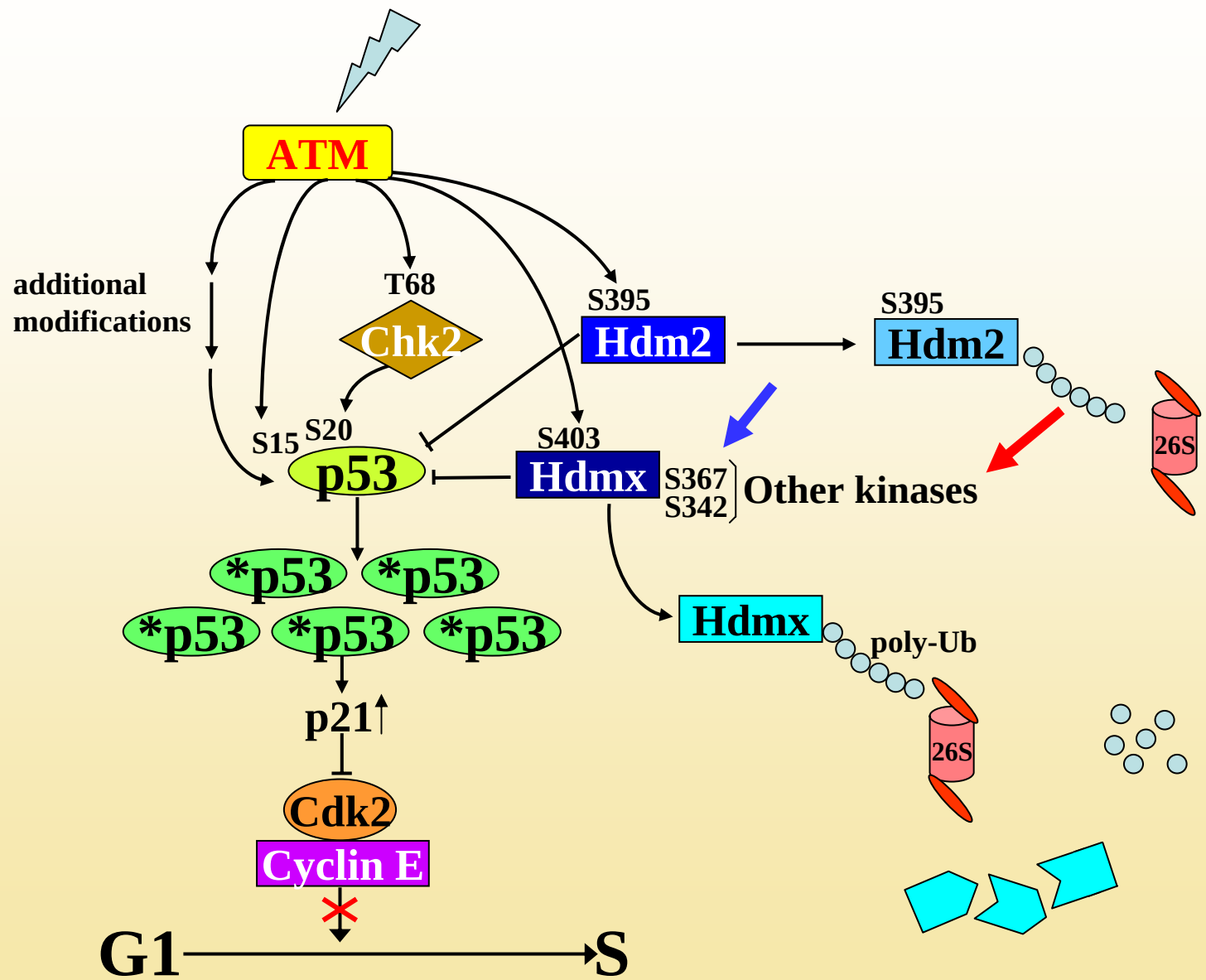


Role of Phosphorylations in Hdmx Degradation

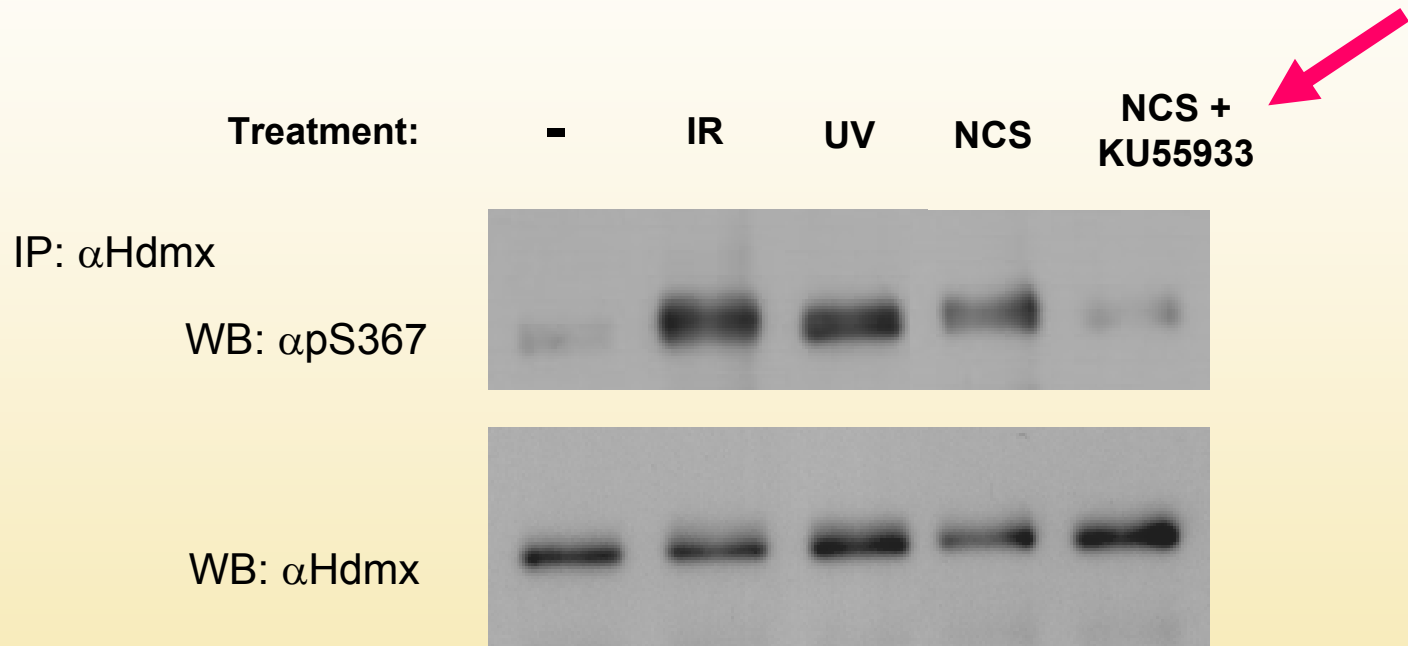


Role of Hdmx Phosphorylations in its Ubiquitination



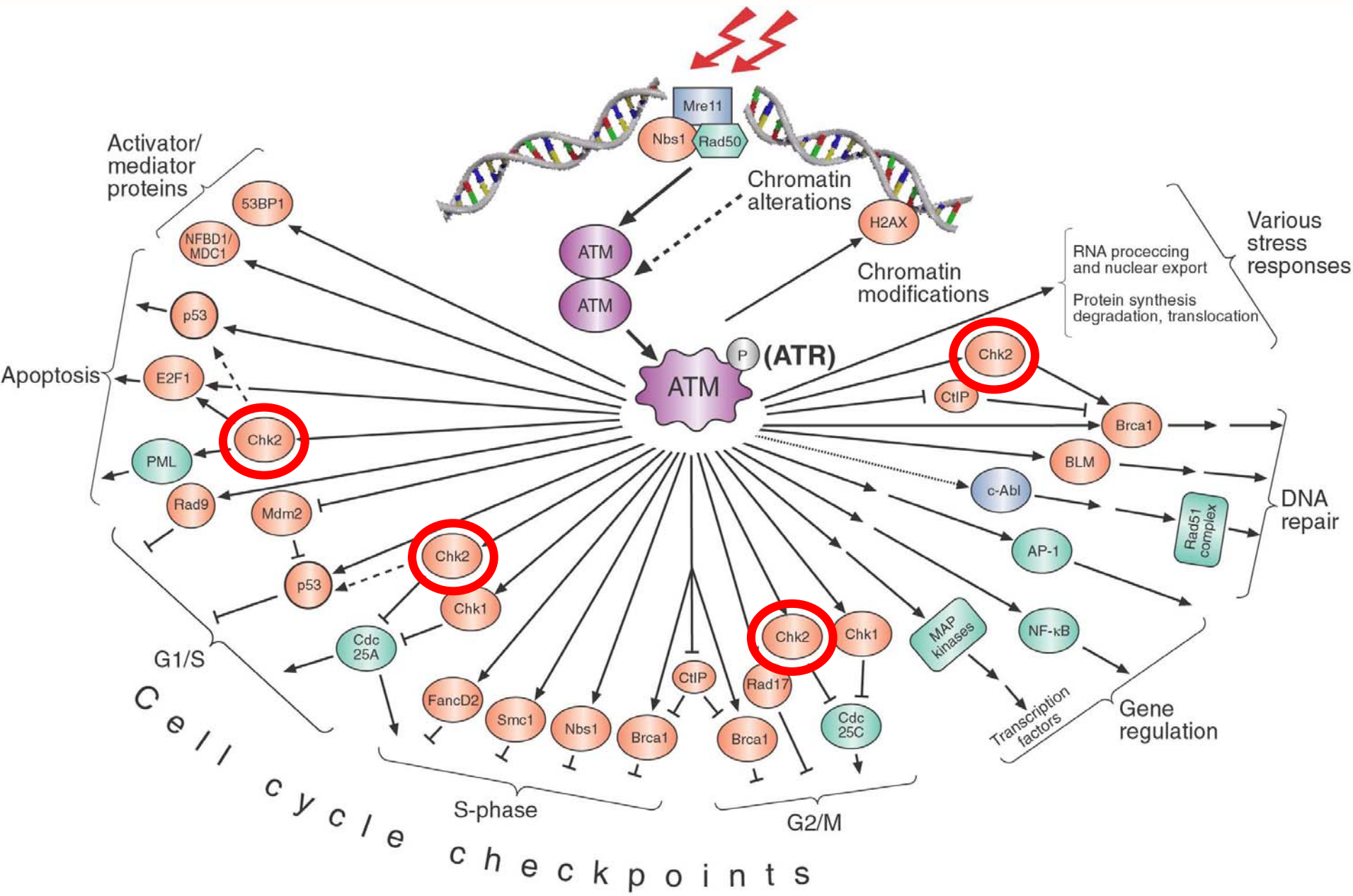


Ser367 Phosphorylation in Response to DNA Damage



Candidate kinase?

ATM-Mediated DNA Damage Responses

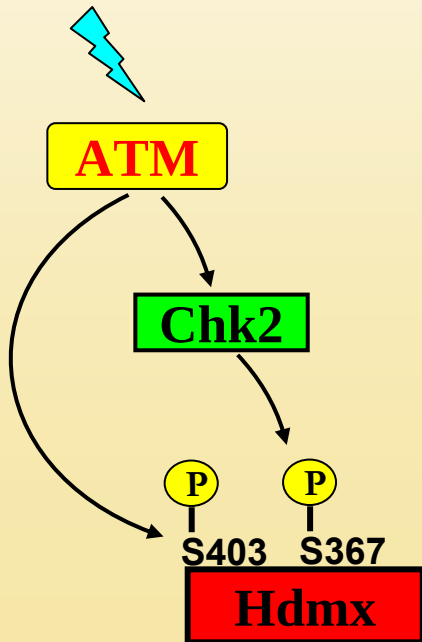


Chk2: Candidate Kinase for Ser367 Phosphorylation



Chk2 consensus phosphorylation site:

on site: **R** X X **S**
 | : : |
Hdmx: **R** T I **S**
 \
 S367

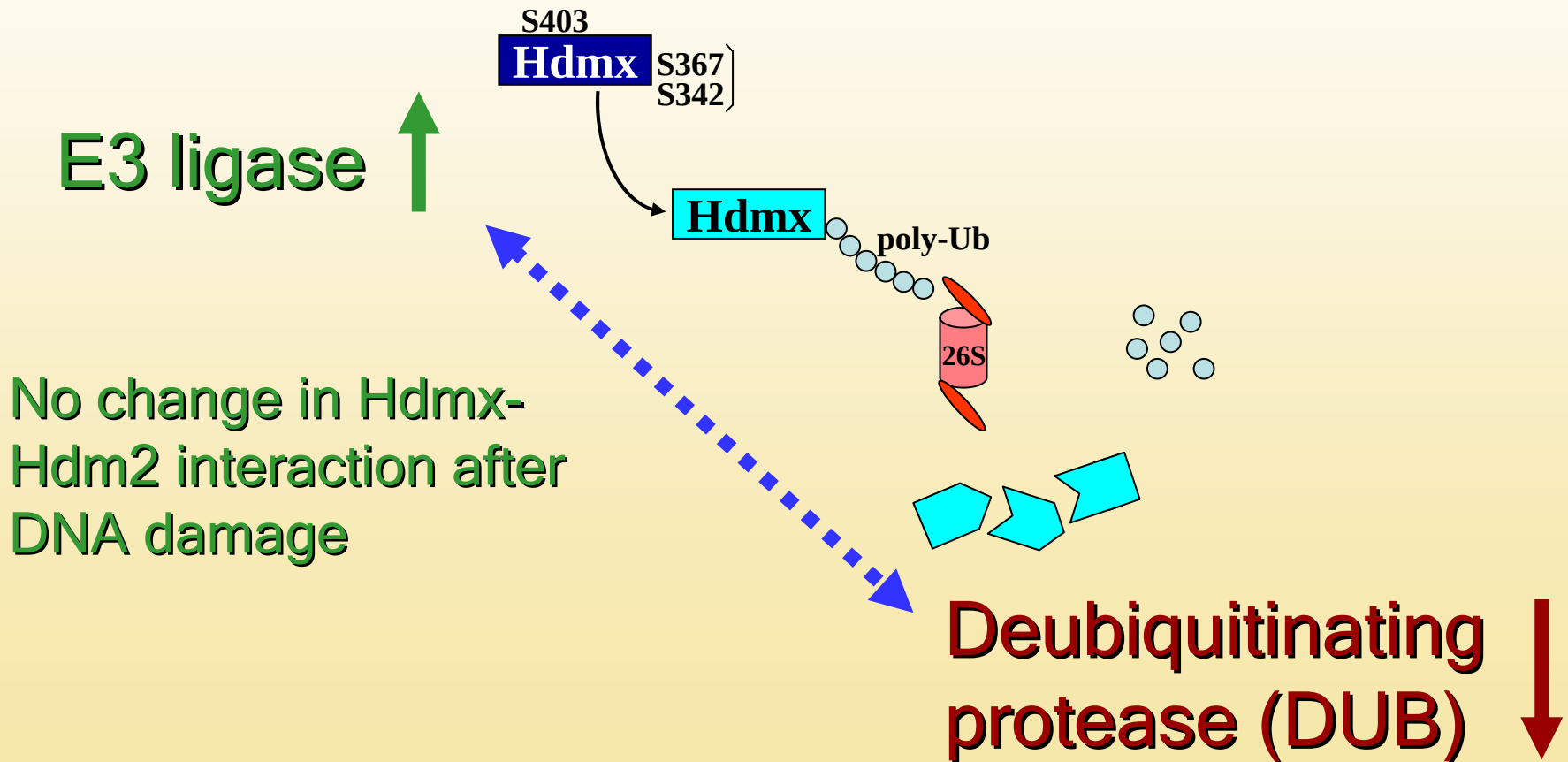


IP: αHdmx

shRNA:	GFP		Chk2		ATM	
NCS treatment:	-	+	-	+	-	+
WB: α pS367						
WB: α Hdmx						

Mechanism, Mechanism....

Protein degradation via the proteasome pathway

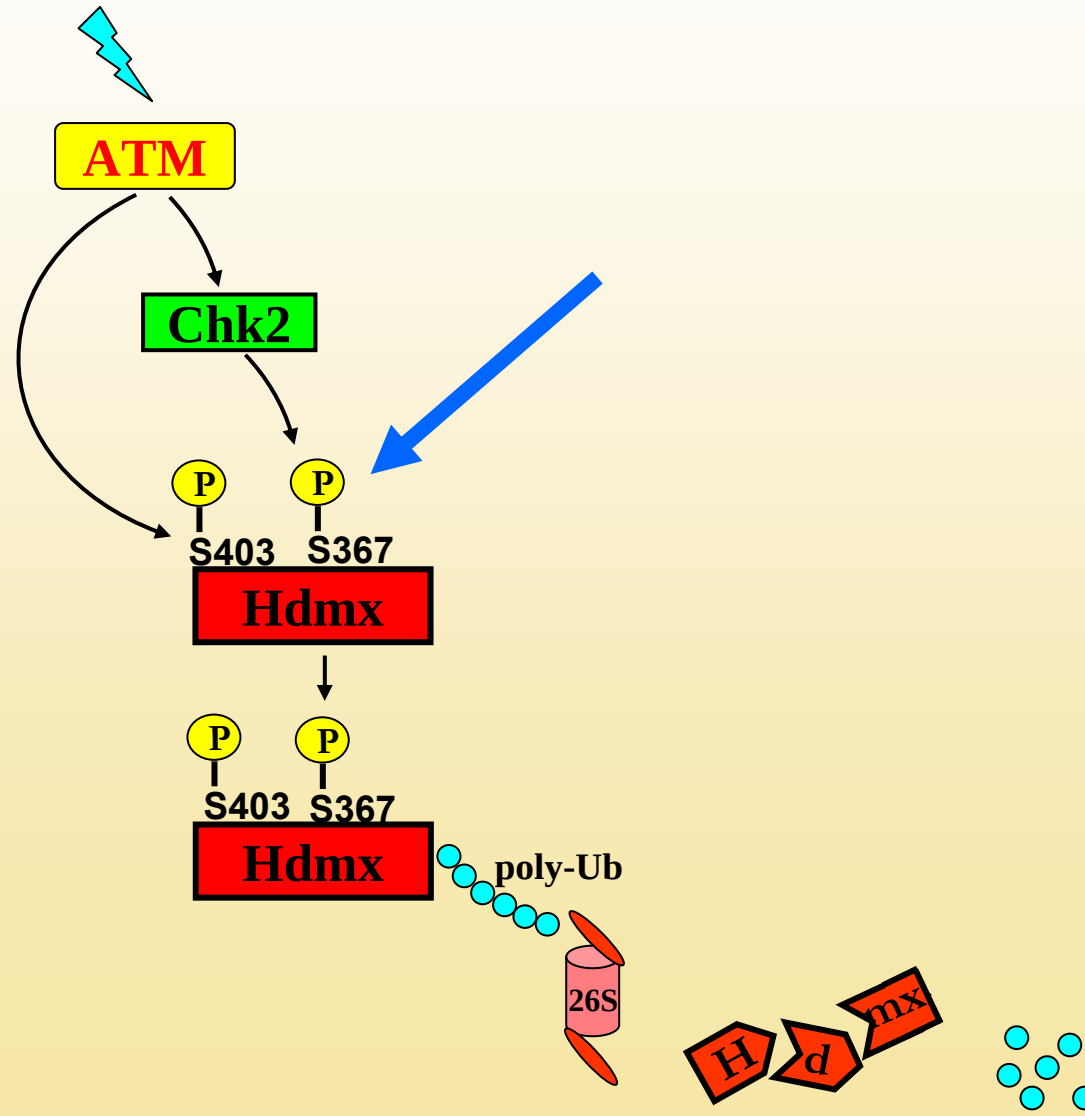


HAUSP is a DUB for Hdmx

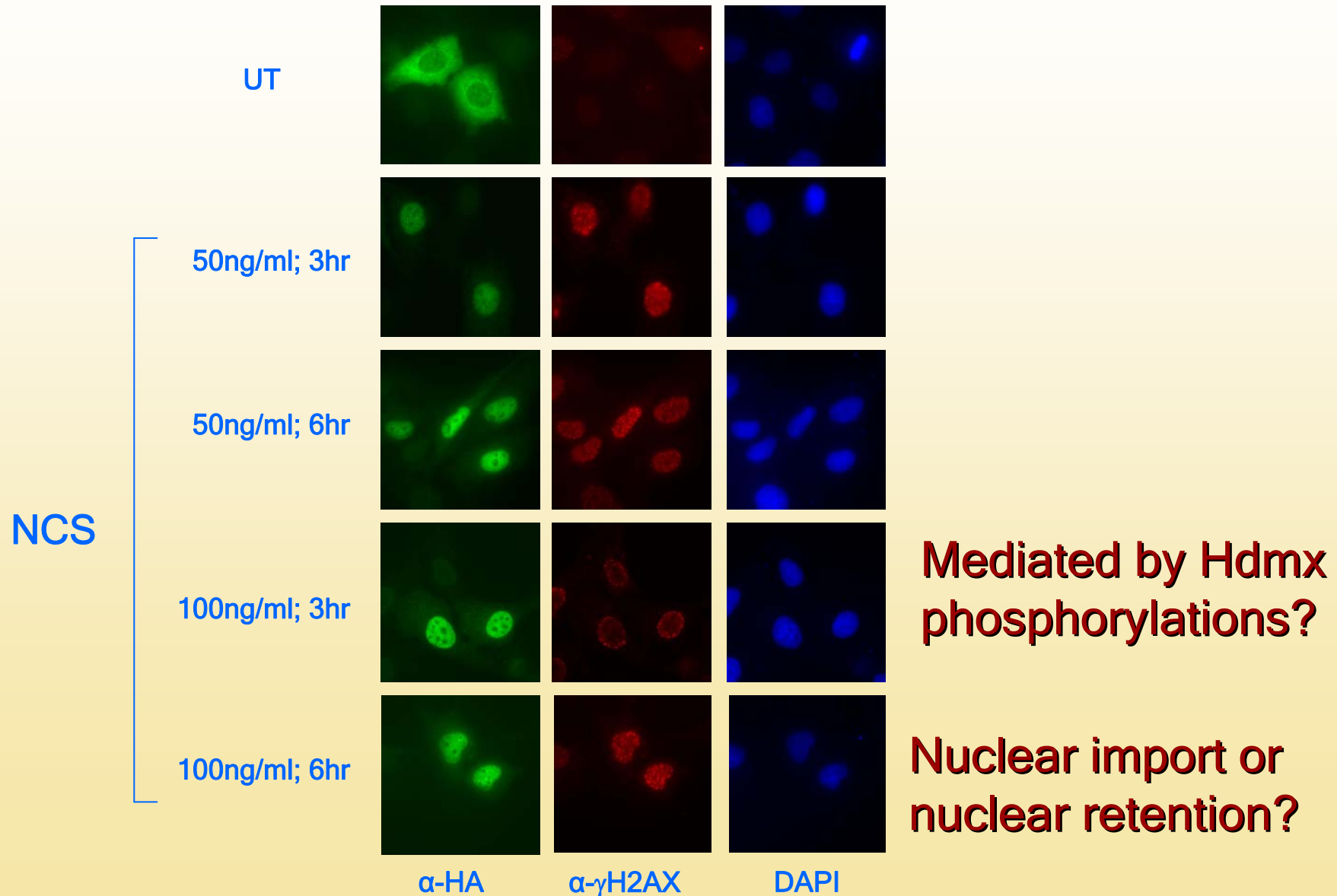
E. Meulmeester et al., 2005

- Herpes virus-associated ubiquitin specific protease (also known as USP7)
- Previously known to deubiquitinate p53 and Hdm2
- HAUSP binds, deubiquitinates and stabilizes Hdmx
- DNA damage does not alter HAUSP's enzymatic activity, stability or subcellular localization
- DNA damage reduces HAUSP's **binding** to Hdmx and Hdm2 but NOT p53
- The reduction in HAUSP-Hdmx affinity is ATM-dependent and is due to phosphorylation of Hdmx

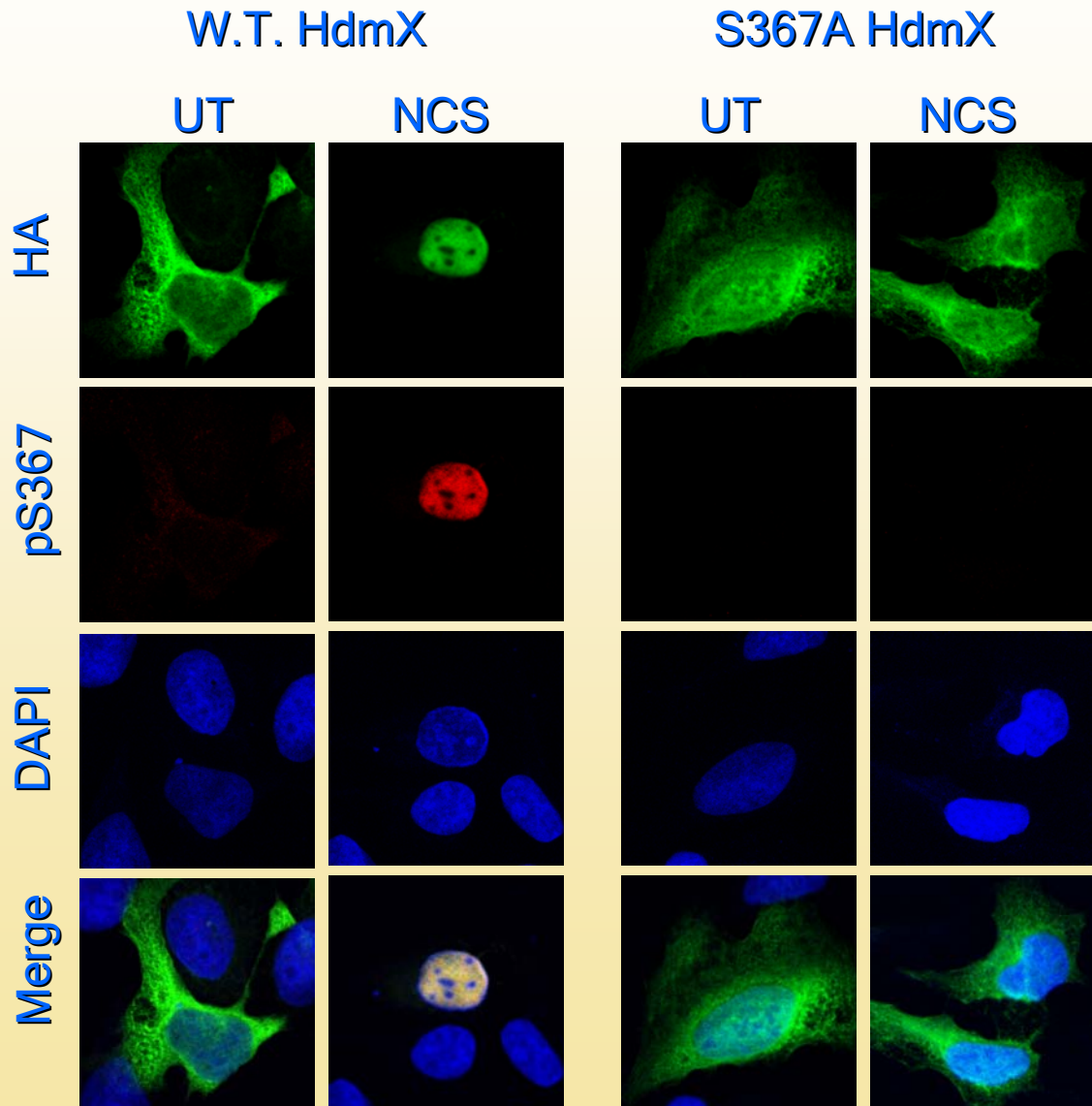
Significance of S367 Phosphorylation



Nuclear Accumulation of Hdmx in Response to DSB



Nuclear Accumulation of Hdmx in Response to DSB is Dependent on S367



Ser403 is NOT required for nuclear accumulation of Hdmx

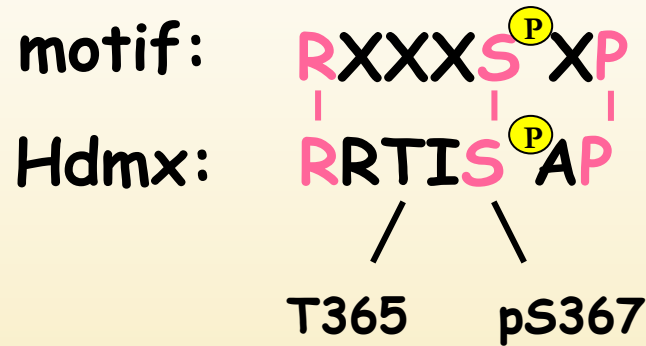
S367 phosphorylation takes place in the nucleus!

Hdmx undergoes nuclear retention

S367 Phosphorylation Creates a 14-3-3 Binding Site

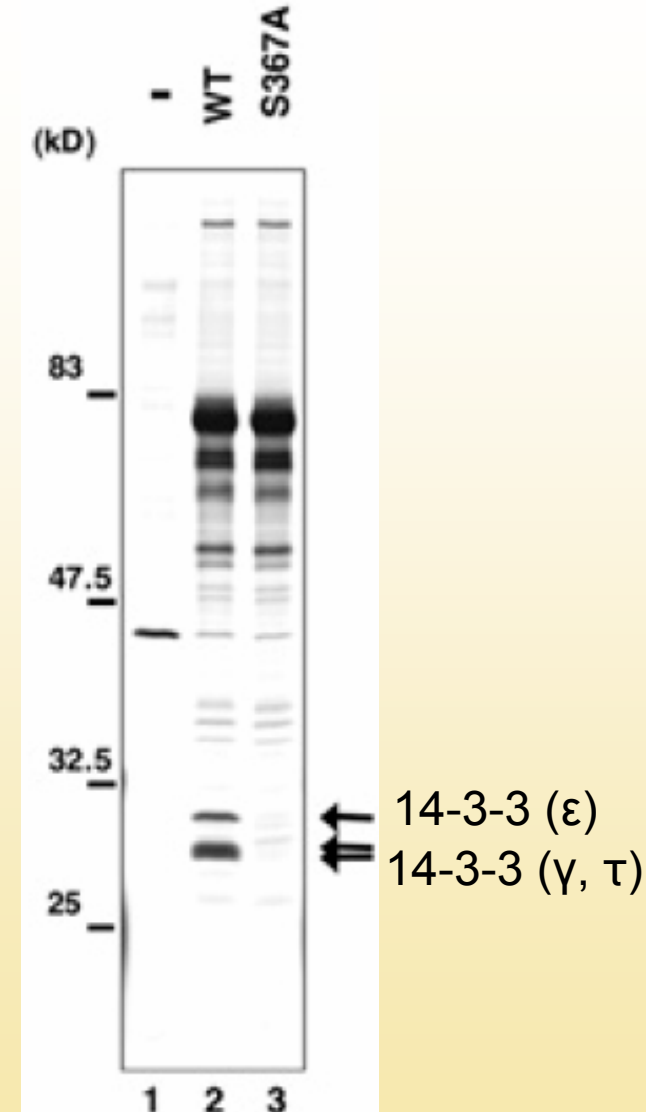
K. Okamoto et al., 2005

14-3-3 binding motif:

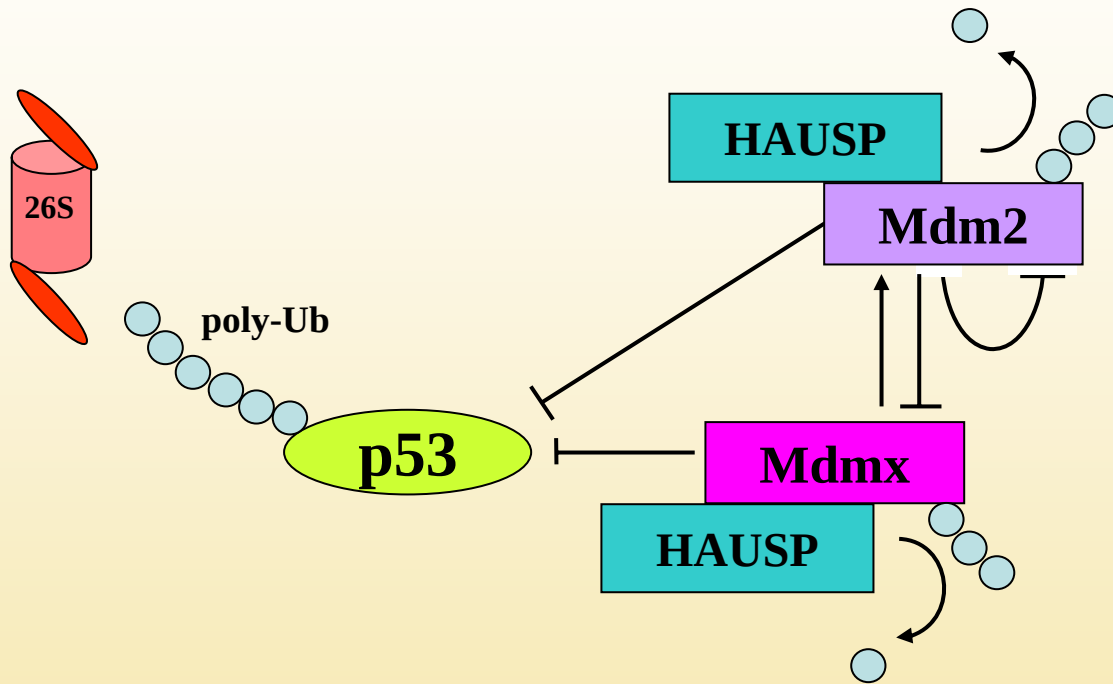


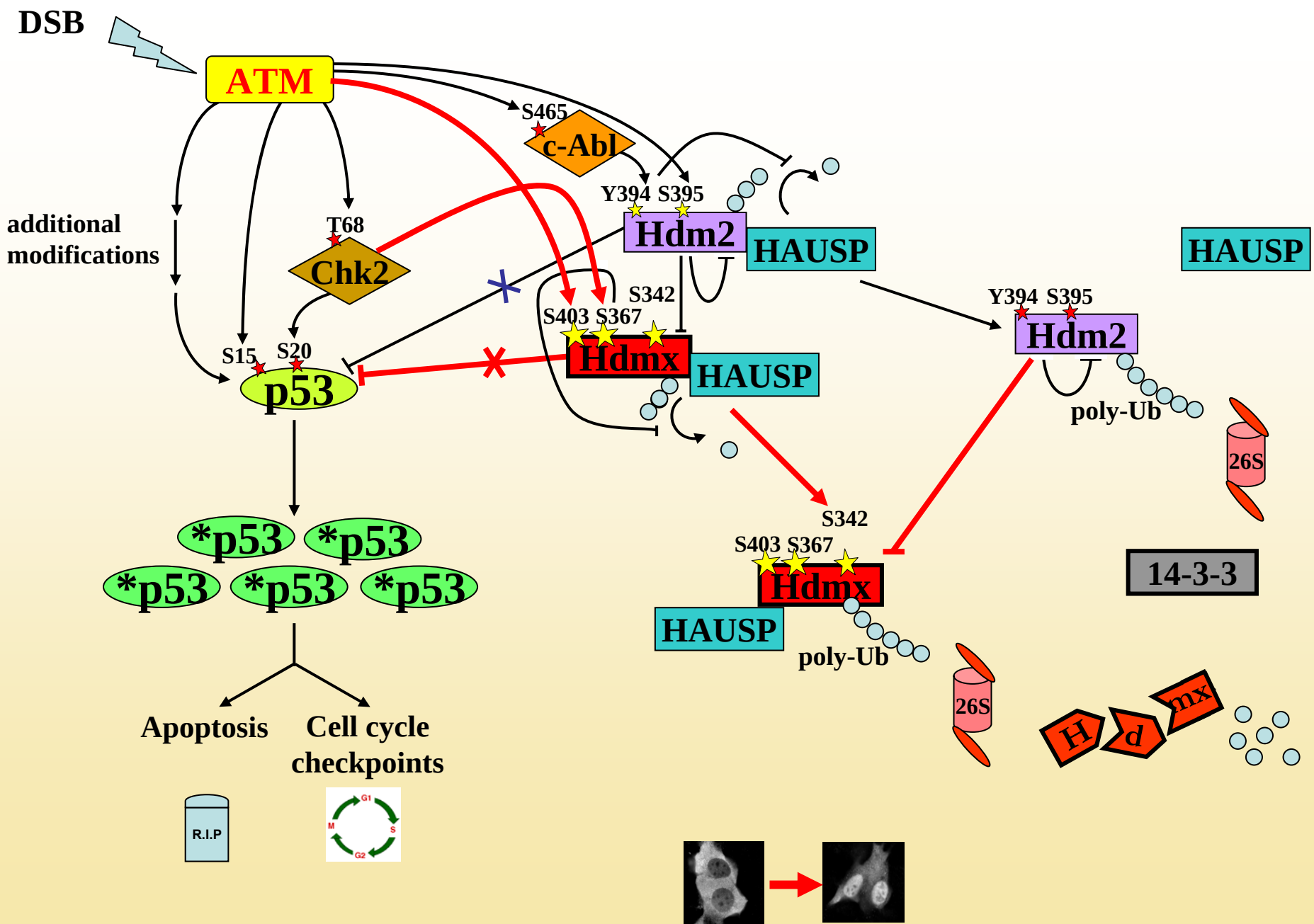
14-3-3 binding is enhanced by DNA damage and is important for Hdmx degradation

14-3-3 binding is essential for nuclear accumulation of Hdmx

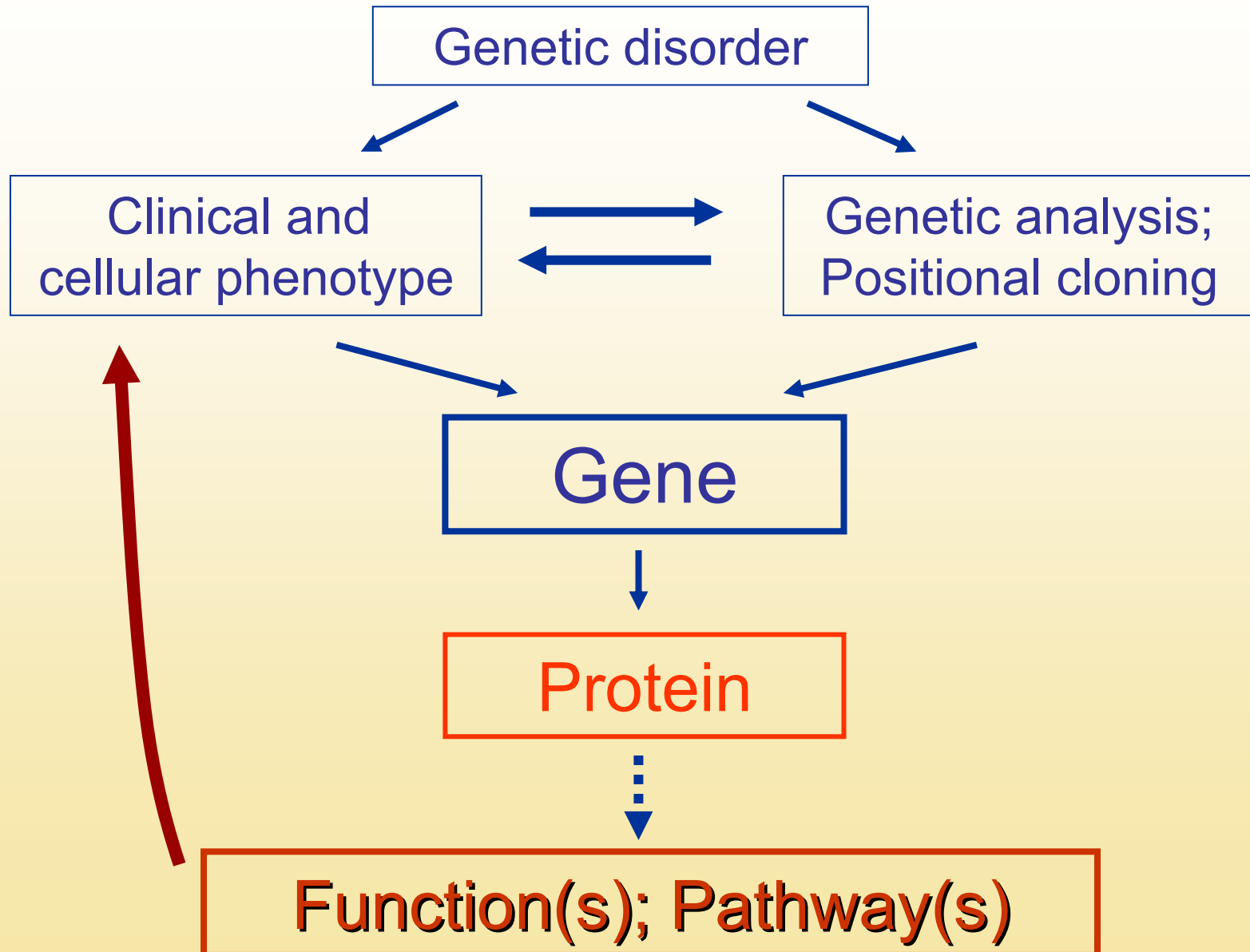


Non-Stressed Cells



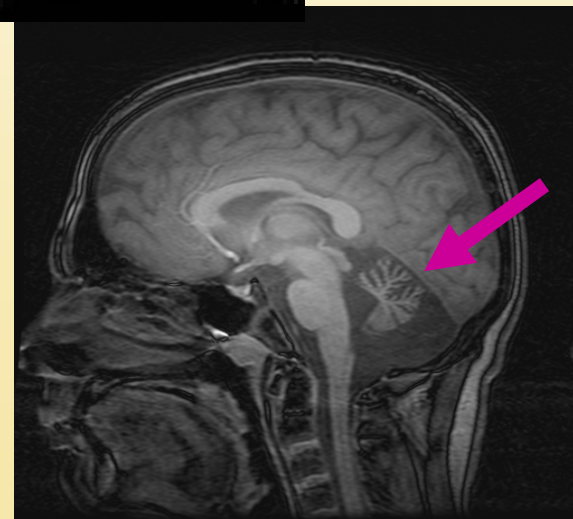


From Genetic Disorder to Function



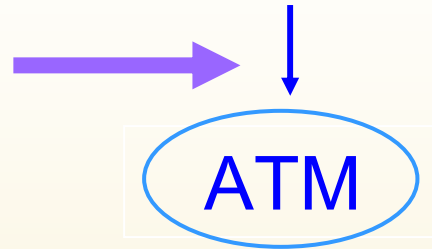
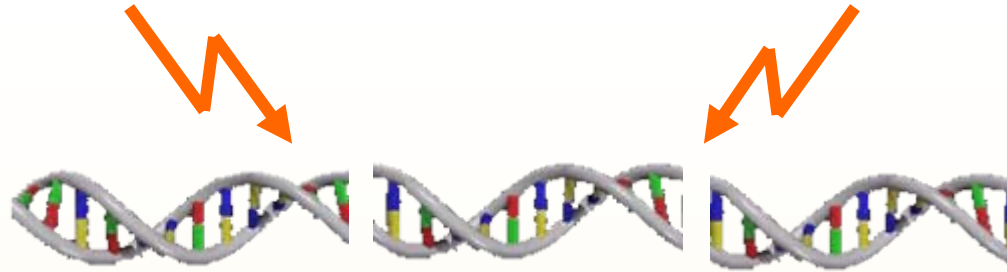


Normal brain



A-T Patient

DSBs

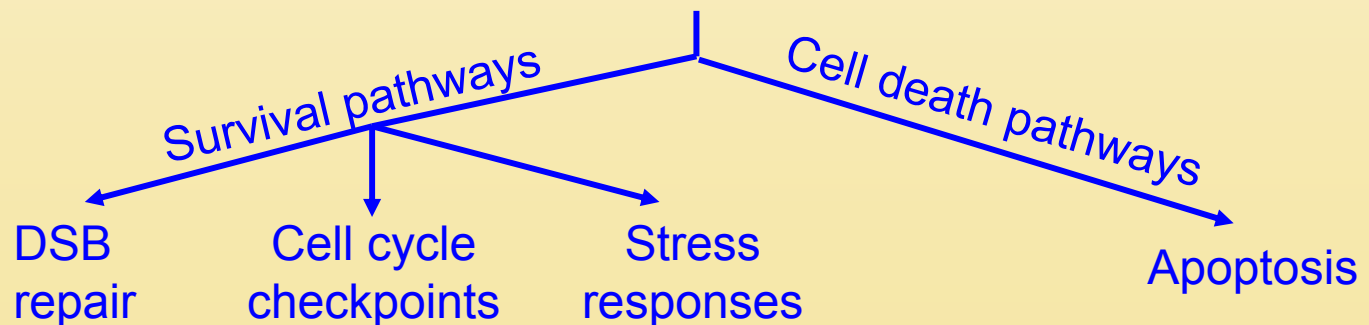


Observations in
genomic instability
syndromes...

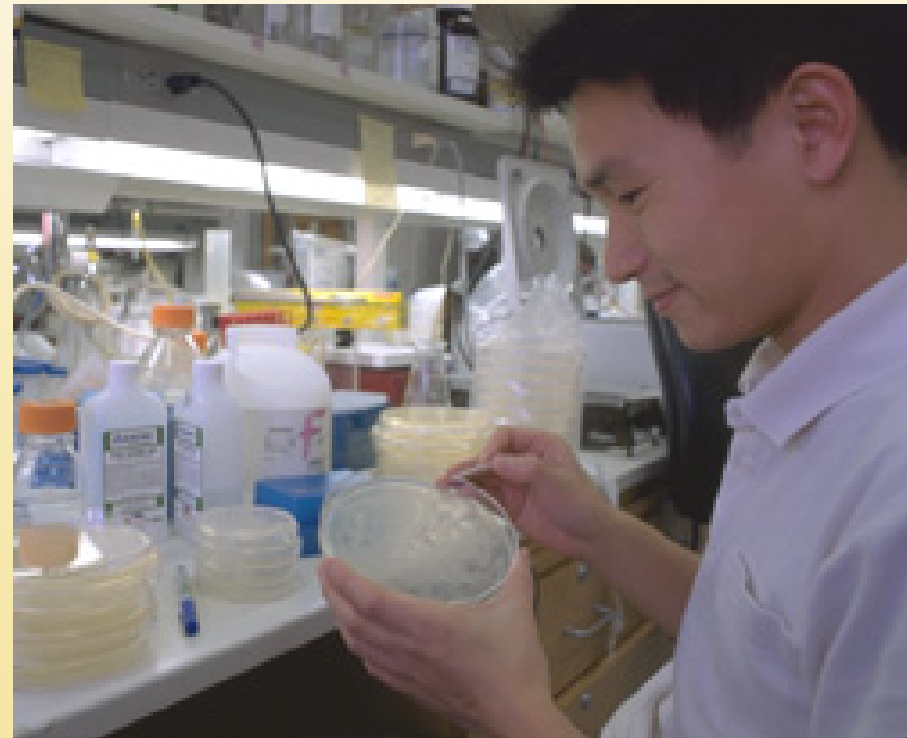


Phosphorylation

Effectors



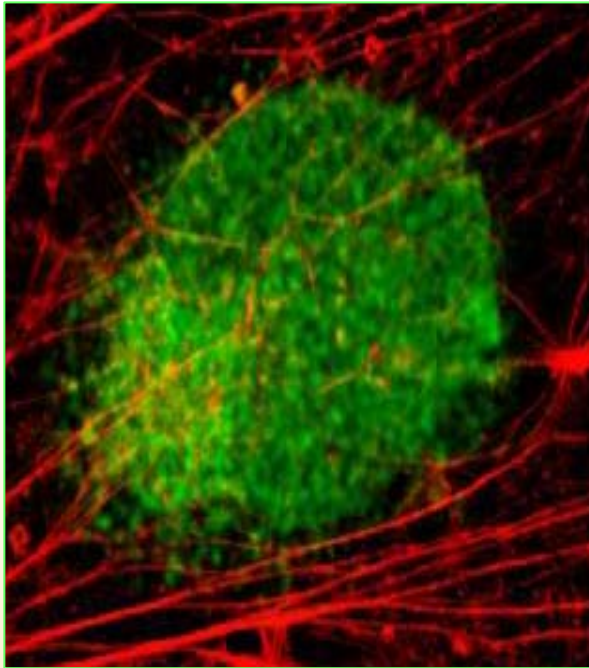
Cross-talk Between the Clinic and the Lab



A-T-Like Disease (A-TLD)

- Has most of the major characteristics of A-T with later onset and slower progression
- Hypomorphic mutations in the *MRE11* gene
- A-TLD is the only A-T-like disorder in which there is no mutation in the *ATM* gene and the ATM protein is intact and active





Tamar Uziel:

Is the **response** of ATM to DNA damage dependent on functional MRN complex?

Requirement of the Mre11-Rad50-Nbs1 Complex for ATM Activation by DNA Damage

(Uziel et al., 2003)

A-TLD cells:

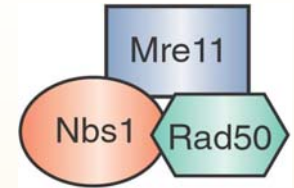
- Defects in all parameters of ATM activation and in downstream pathways
- Phenotypic reconstitution of A-TLD cells by ectopic expression of Mre11 restores normal ATM activation
- Knocking down Mre11 results in defective ATM activation

DSBs



binding to DSBs;
damage processing

MRN
complex



Processed
DNA lesions

ATM

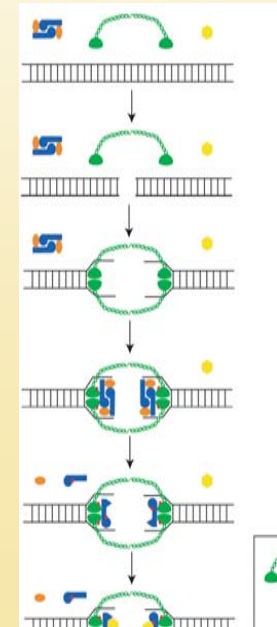
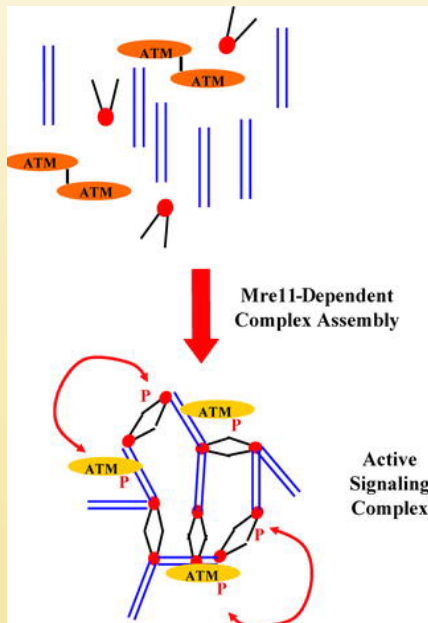
Activation
Association with
processed DSBs



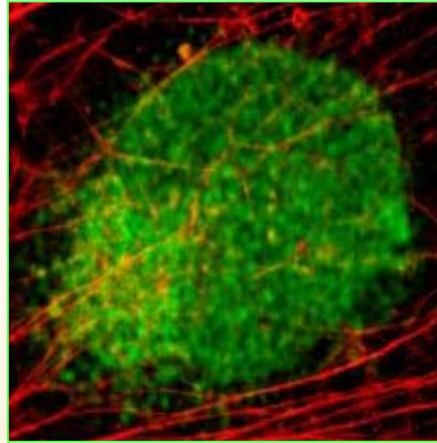
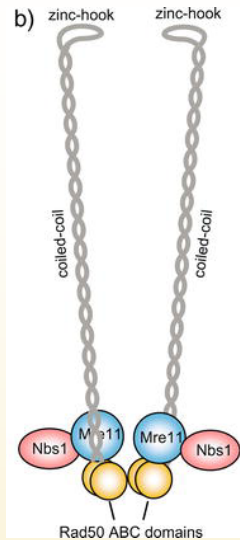
phosphorylation

Target proteins

Signaling pathways



Insights from Understanding A-TLD

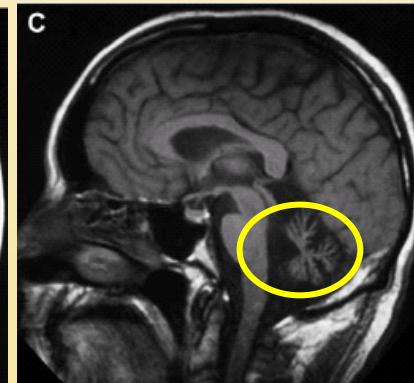


- Inability to activate ATM properly is sufficient to cause an A-T-like phenotype
- **The cerebellar degeneration in A-T patients probably results from their defective response to DNA damage**

Normal



A-T



ATM Localization and Function in Neuronal Cells

➤ Human neuron-like cells:

- ❑ In vitro differentiation of neuroblastoma cell lines
- ❑ Neuronal differentiation of human embryonic stem cells (with B. Reubinoff)
- ❑ Cerebellar neural stem cells (with NeuralStem, Inc.)

➤ Murine cerebellar cells (Ari Barzilai):

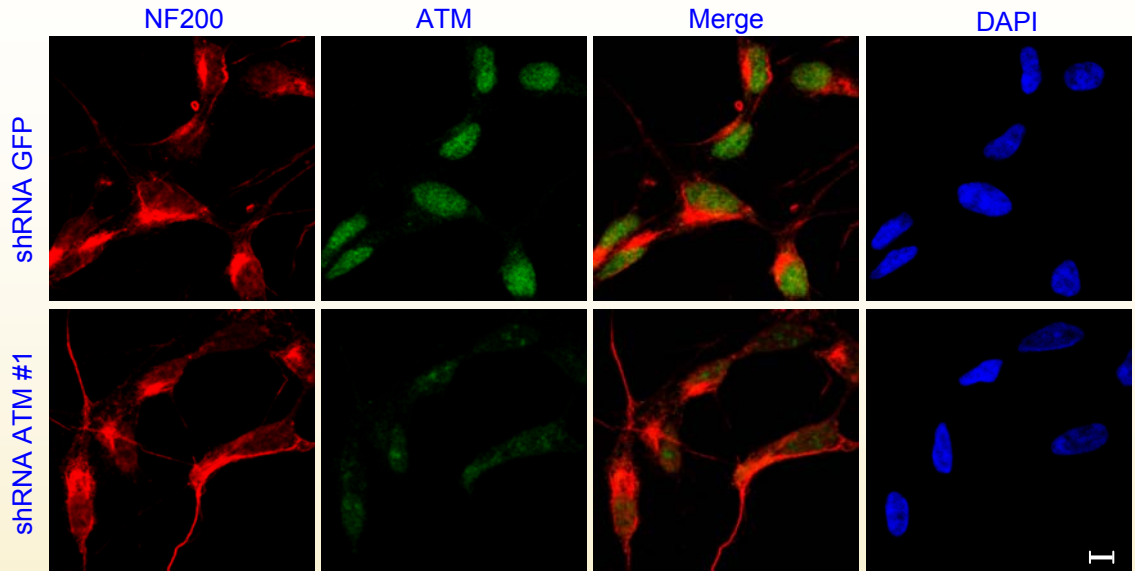
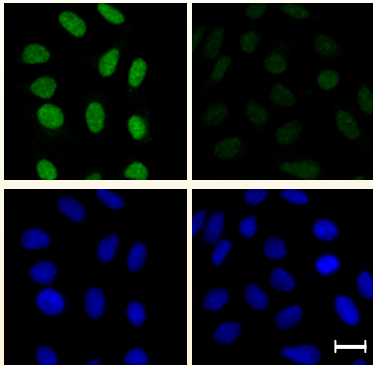
- ❑ Tissue sections
- ❑ Slice cultures

ATM is Nuclear Human Neuron-Like Cells

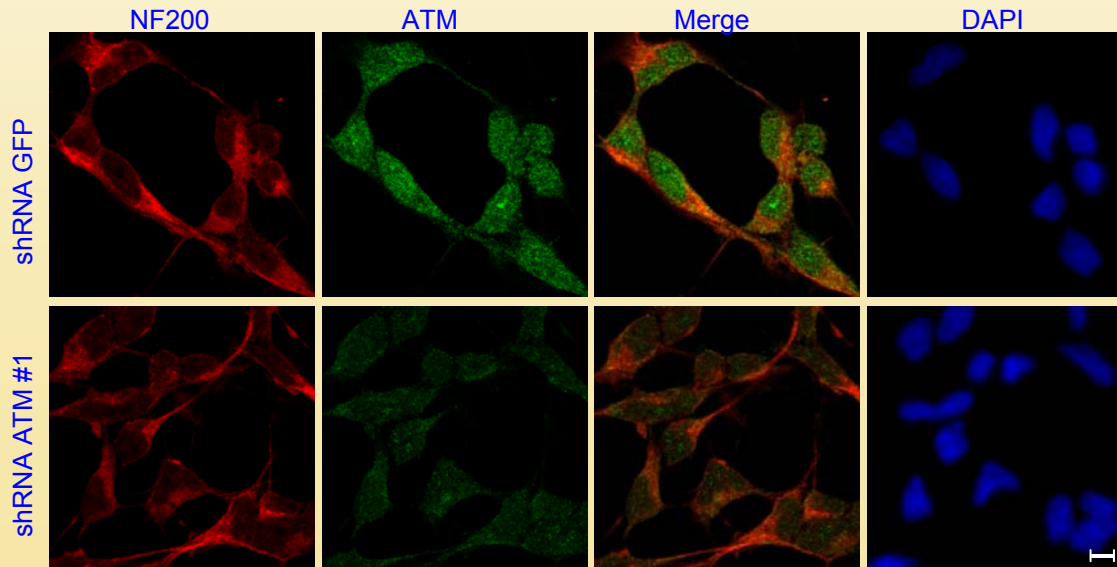
Sharon Biton

SH-SY5Y NLCs

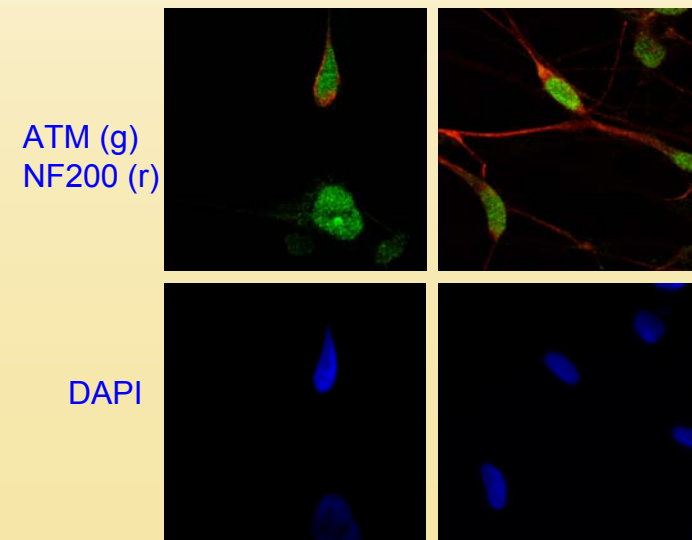
HeLa cells
shRNA: LacZ shRNA: ATM



LA-N-5 NLCs



Differentiated hESC



ATM- Dependence DNA Damage Responses

shRNA

GFP

ATM

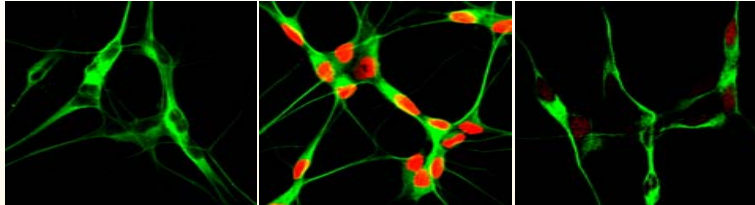
NCS

-

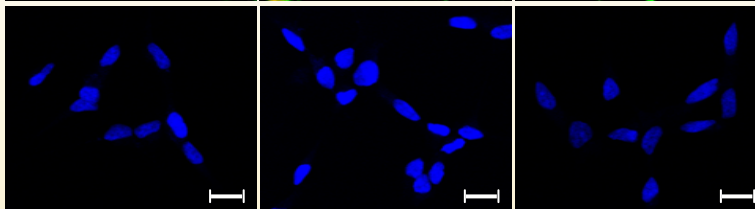
+

+

pS824-
KAP-1



DAPI



NCS

-

+

+

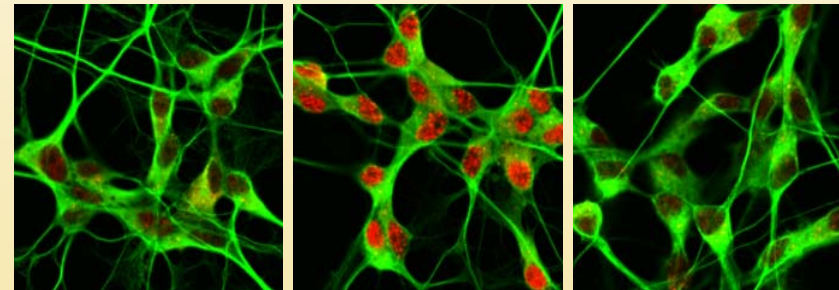
KU-55933

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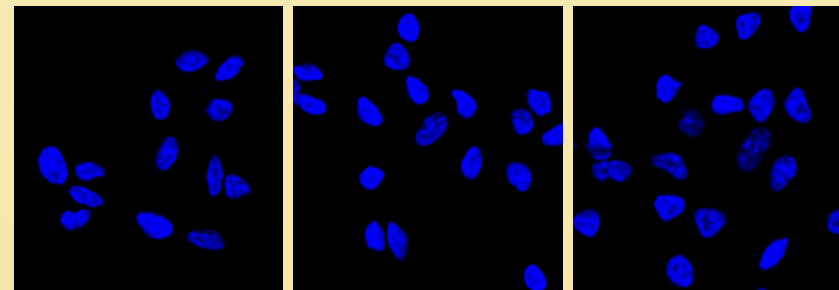
-

+

α - Tuj1 (g)
 α - SQ/TQ (r)

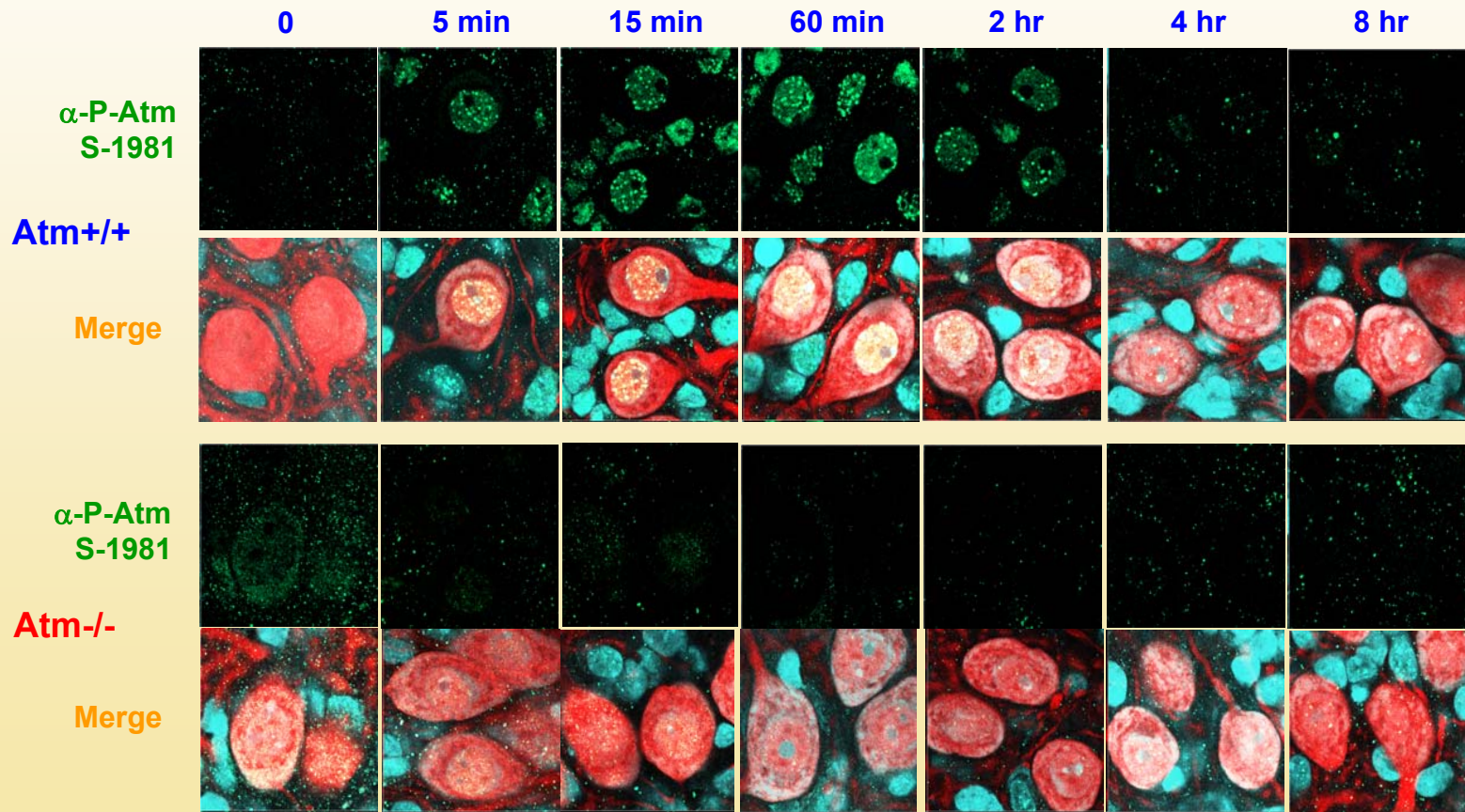


DAPI



ATM-Dependent DNA Damage Responses in Mouse Cerebellar Neurons

Inbal Dar
Ari Barzilai

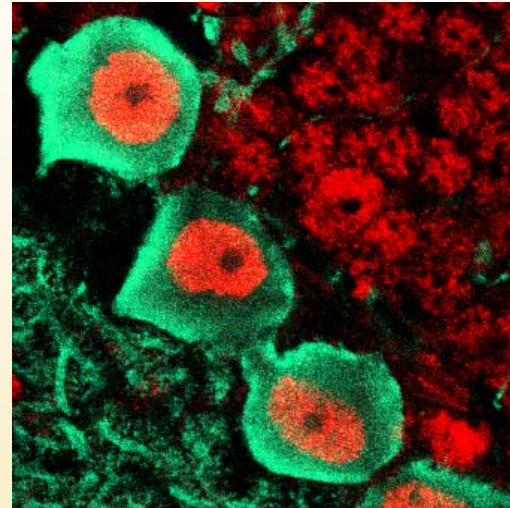
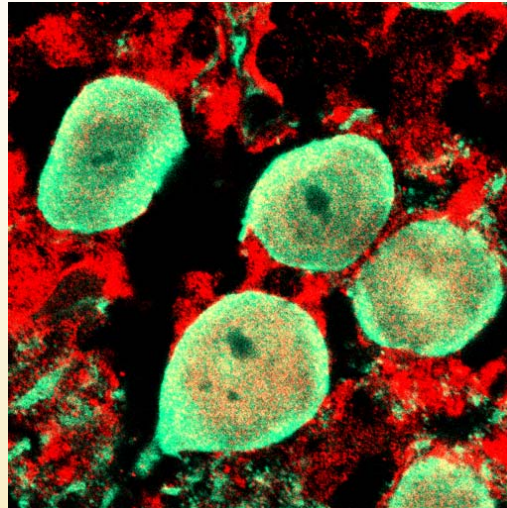


ATM Autophosphorylation in Mouse Cerebellar Neurons

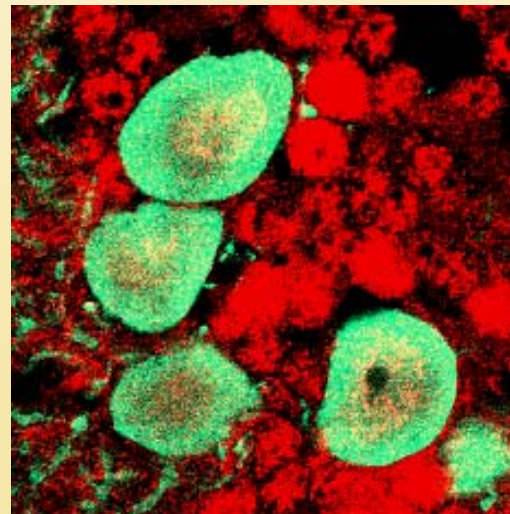
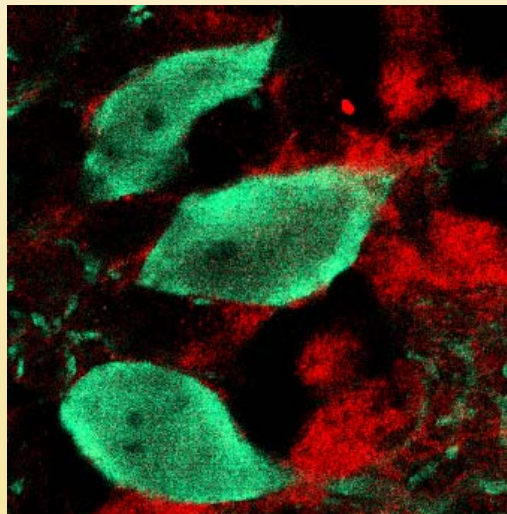
UT

20 Gy

Atm+/+

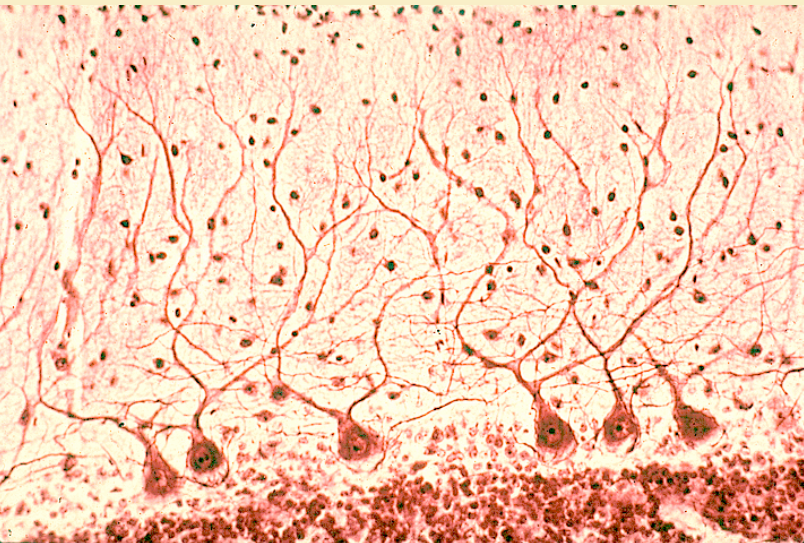
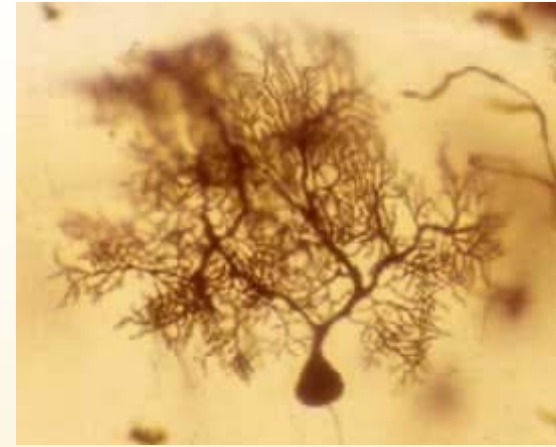


Atm-/-



Importance of the DNA Damage Response in Neurons

- Long life-span
- Extensive metabolic activity
- Oxidative stress
- High transcriptional activity

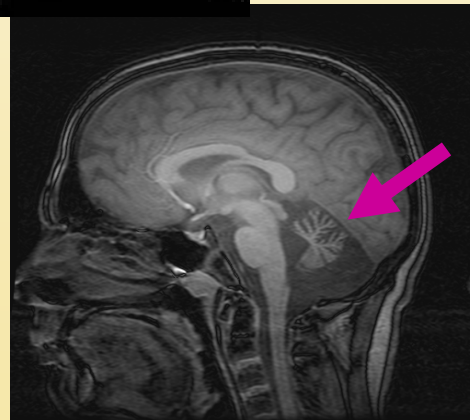


Differences between the DNA damage response in proliferating and post-mitotic cells...

New treatment Modalities?



Normal brain



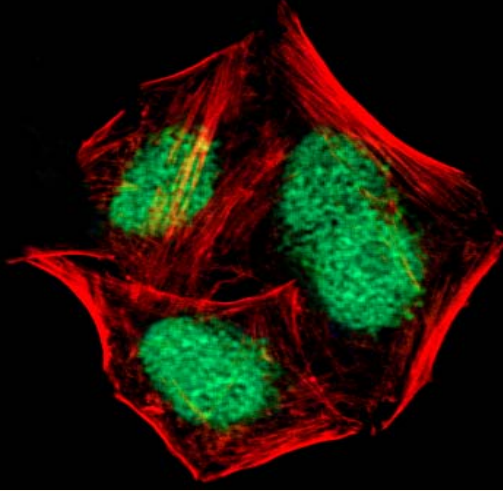
A-T Patient

High Throughput Drug Screening

- Readout representing the DNA damage response
- Search for drug that will stimulate ATM-redundant functions
- Stimulation as low as 10% of the normal response may lead to considerably milder phenotype
- Possible mechanism: stimulation of redundant kinases?

Center for Chemical Genomics,
National Human Genome
Research Institute, NIH





Thank You

