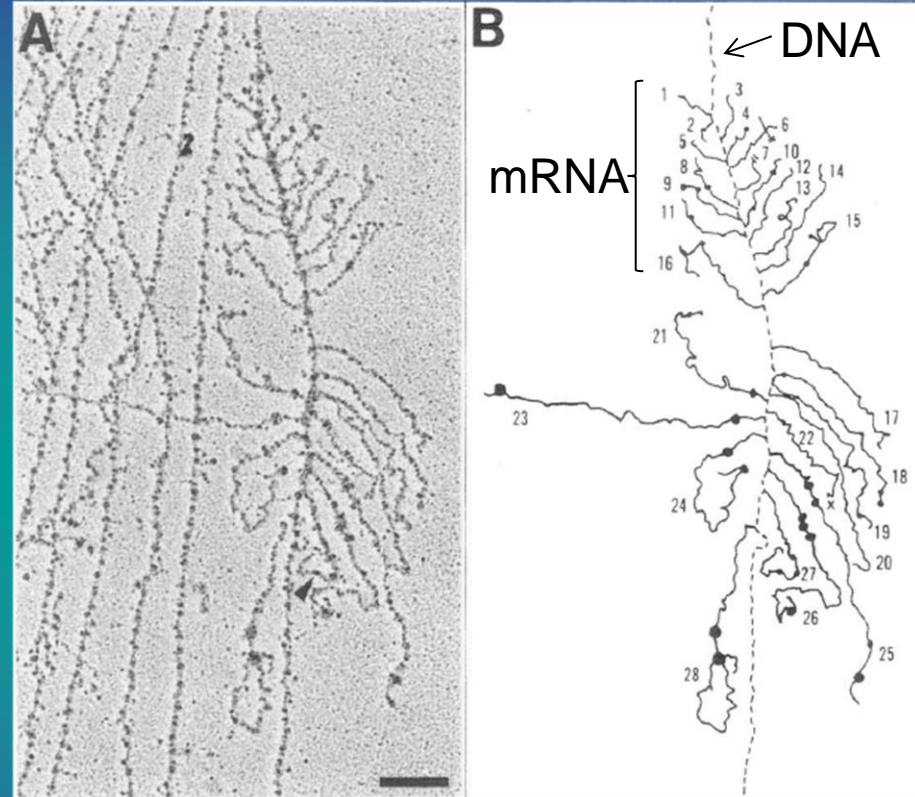


Single molecule dynamics of gene expression measured on single genes in living cells

Yaron Shav-Tal
Bar-Ilan University
Ramat Gan, Israel

mRNA transcription in 'real-time'



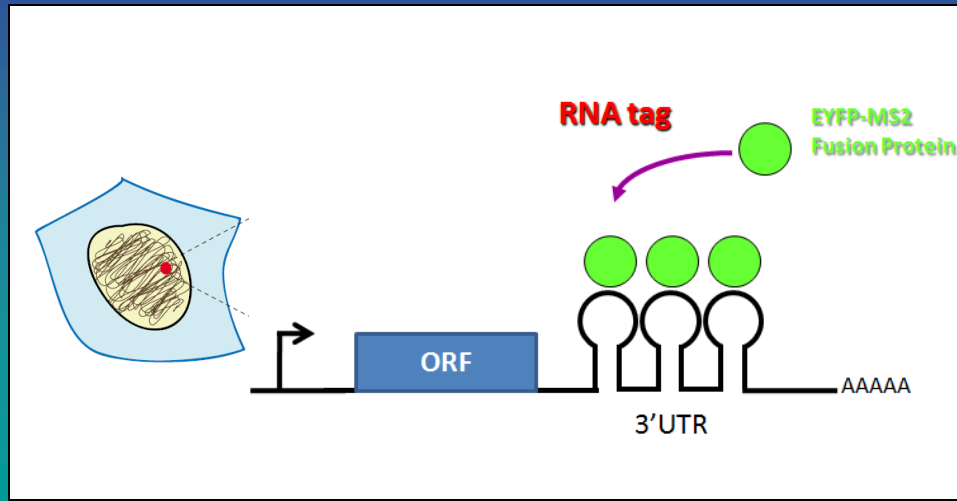
Beyer & Osheim. *Genes Dev.* 1988

How to study gene expression in living cells?

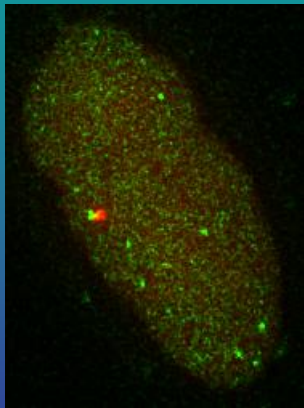
Polymerase

mRNA

Following mRNA dynamics in living cells

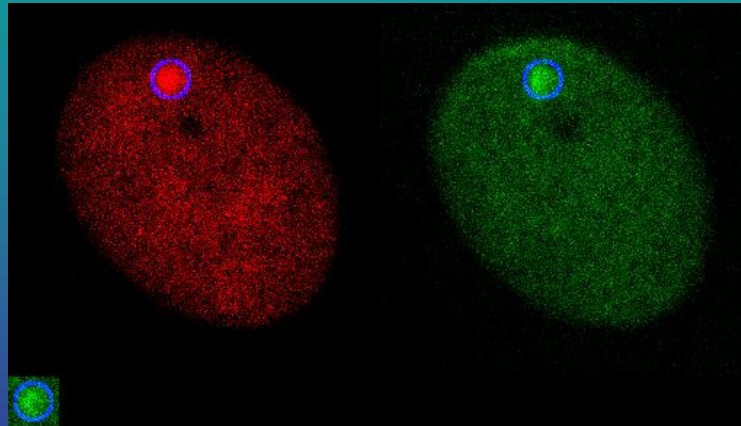


mRNP diffusion



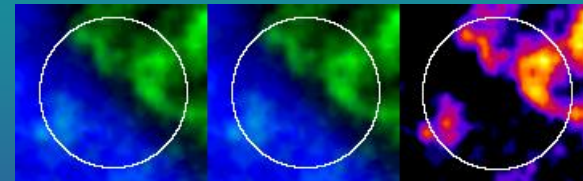
Shav-Tal et al. *Science* 2004

Transcription kinetics



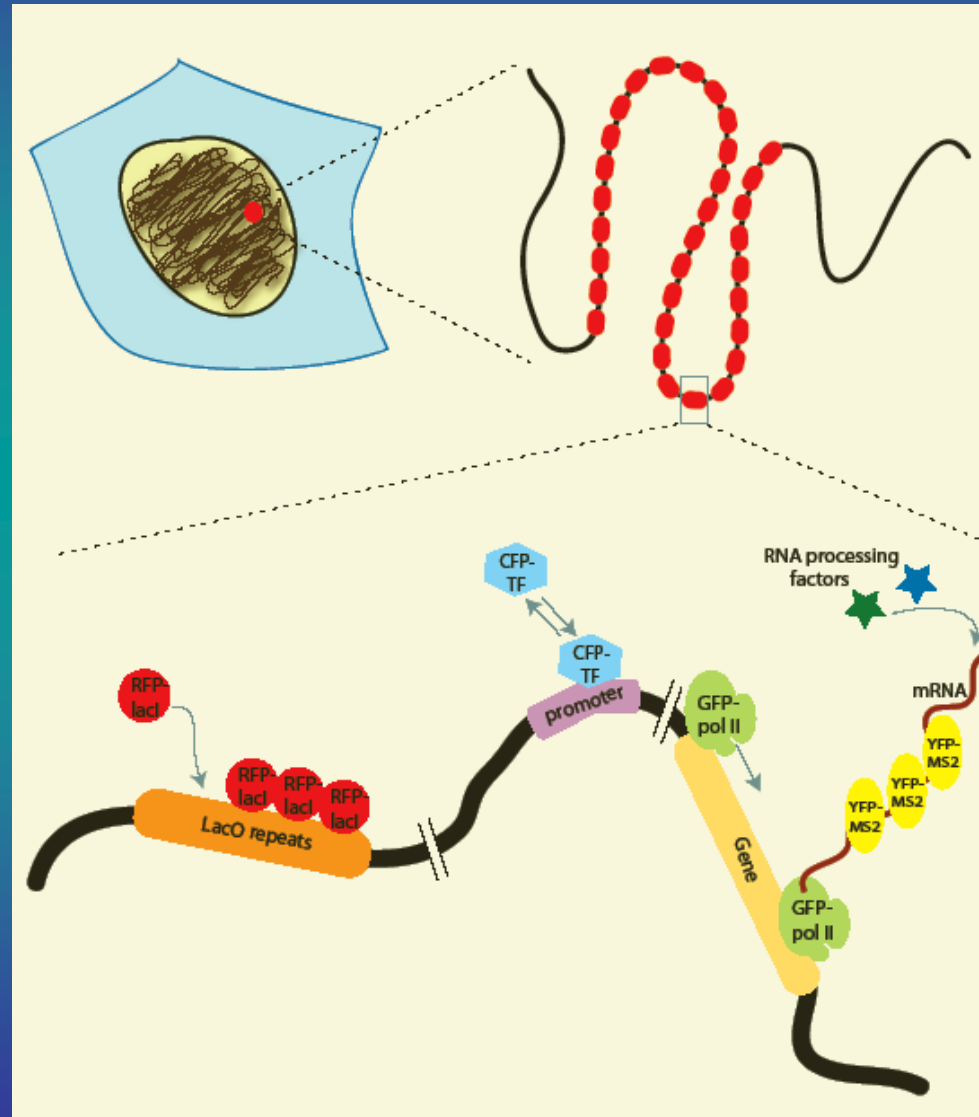
Darzacq et al. *Nat. Struct. Mol. Biol.* 2007

mRNP export

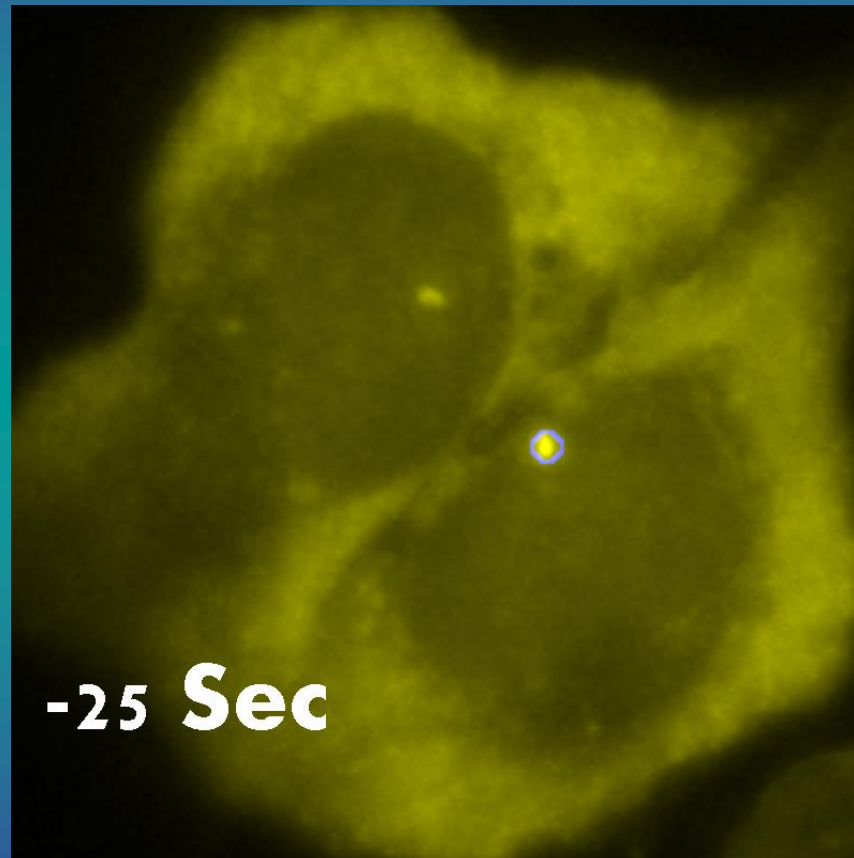


Mor et al. *Nat. Cell. Biol.* 2010

Tandem array gene systems for following gene expression in living cells



Tandem array gene systems for following gene expression in living cells



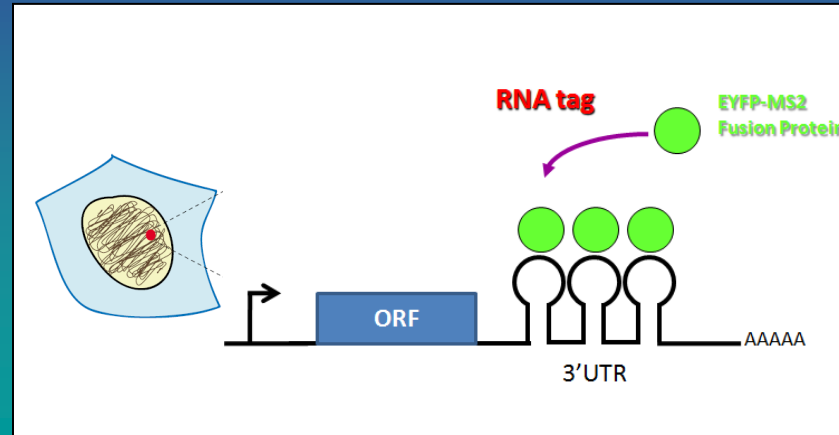
mRNA transcription (FRAP)
(mRNA = yellow)

Measuring transcriptional kinetics of single genes

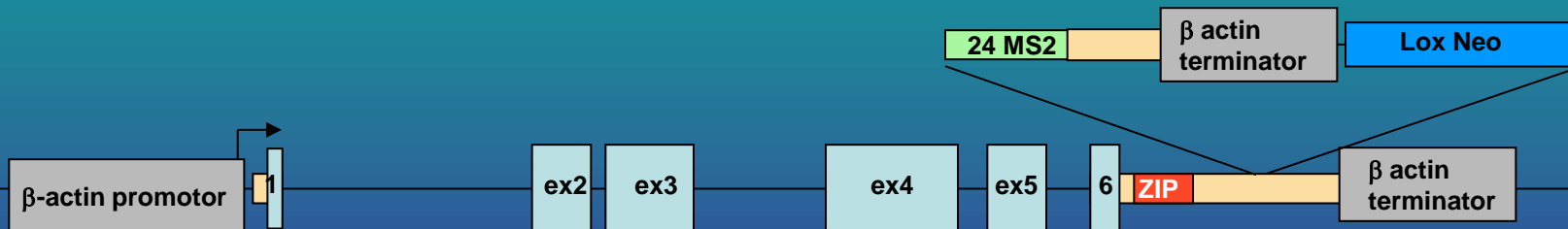
Approach A

Tagging of an endogenous gene

β -actin transcription observed in primary cells from a MS2-knock-in mouse



Mouse Chr 5

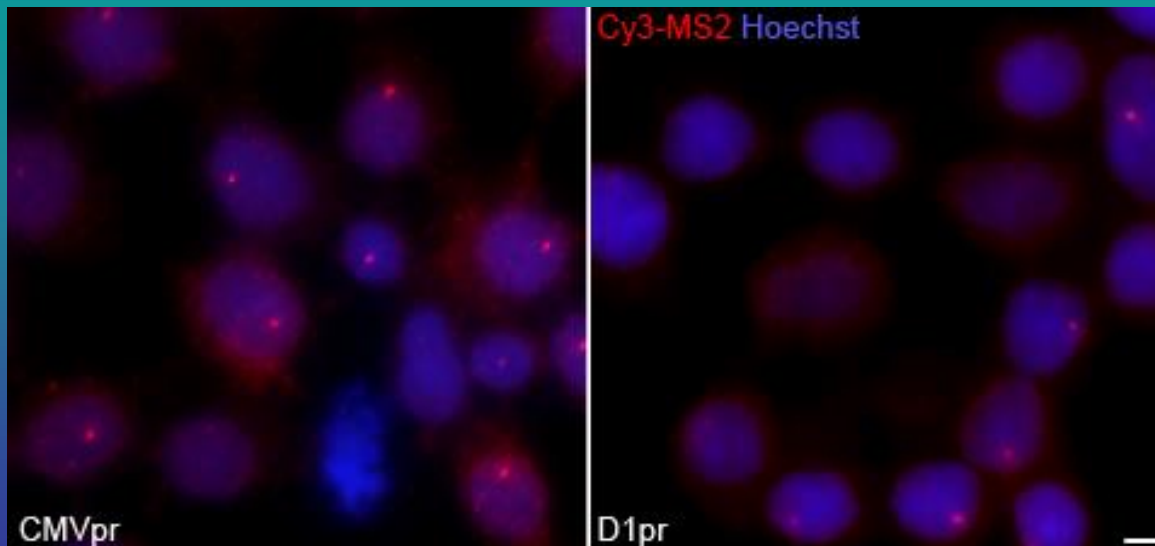
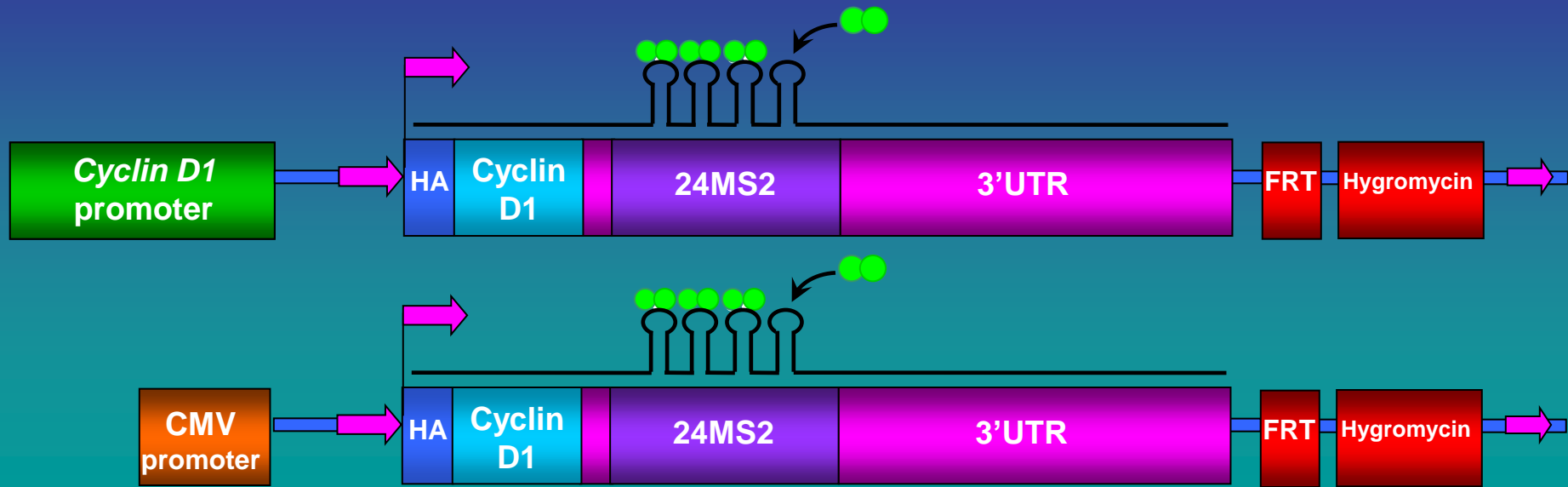


Measuring transcriptional kinetics of single genes

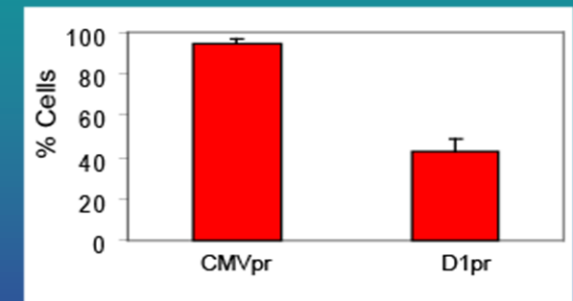
Approach B

Site-specific single-allele recombination

Detection of transcription activity on single alleles D1 alleles

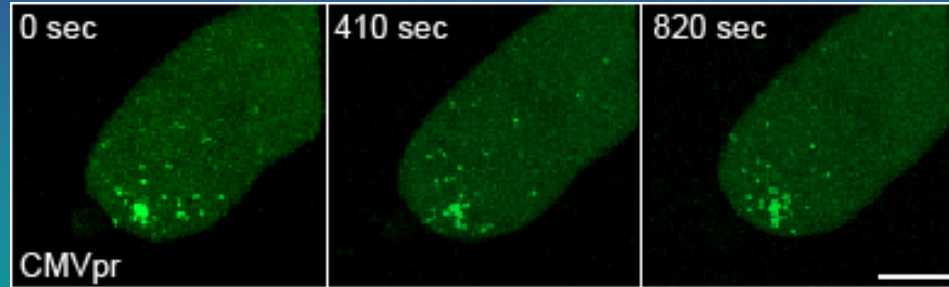
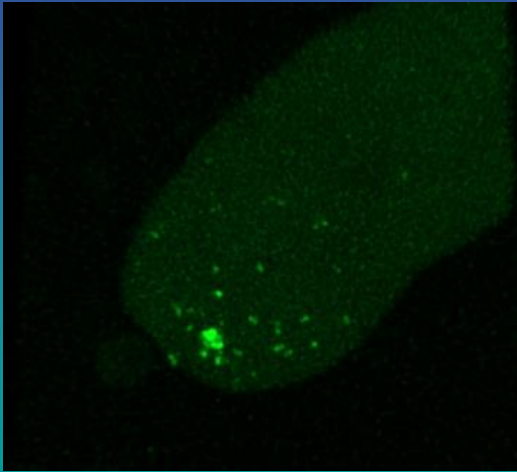


HEK293 cells

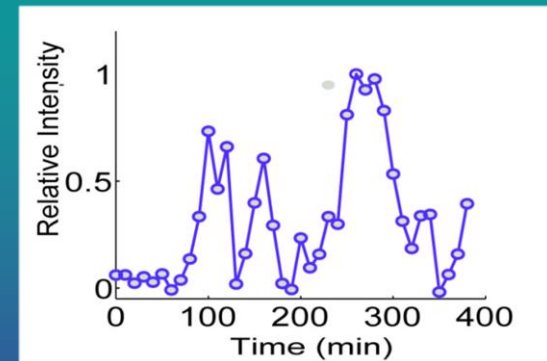
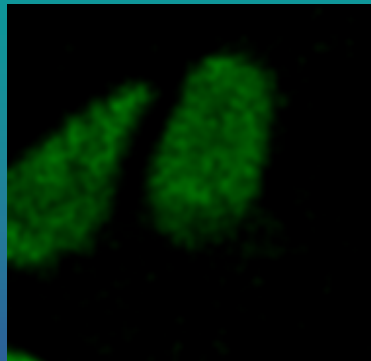
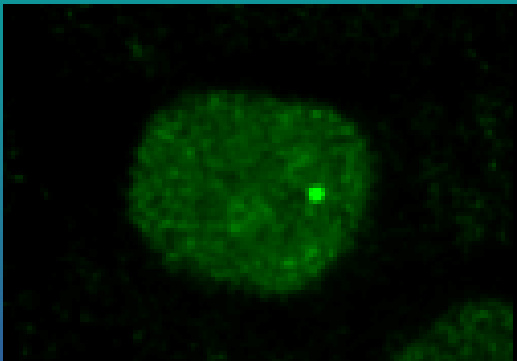


Detection of active *cyclin D1* alleles

CMV promoter

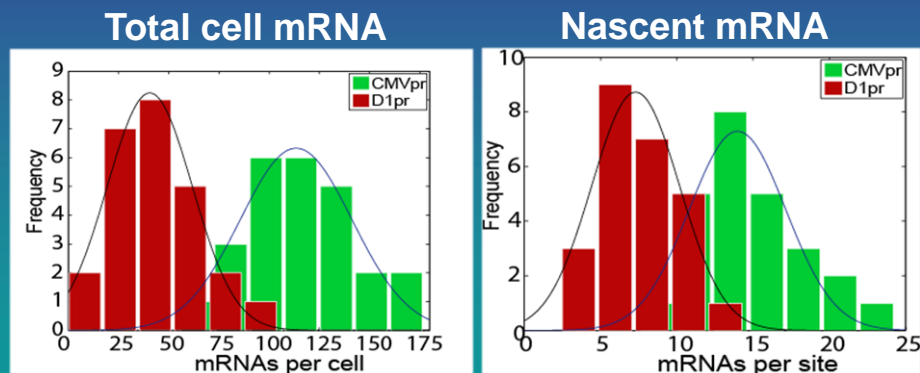
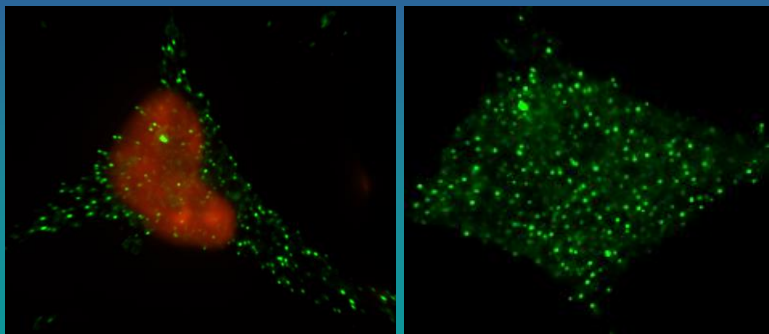


Endogenous *CCND1* promoter

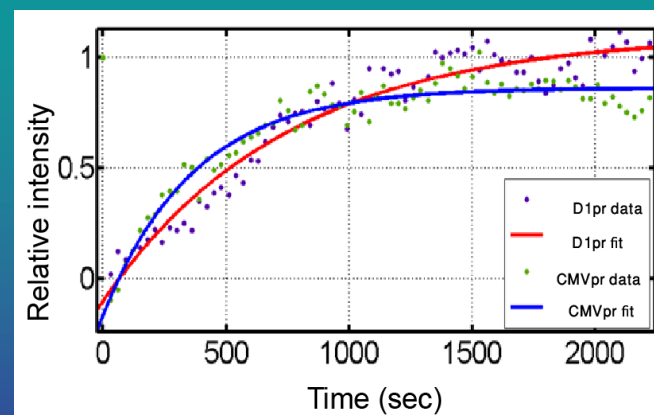
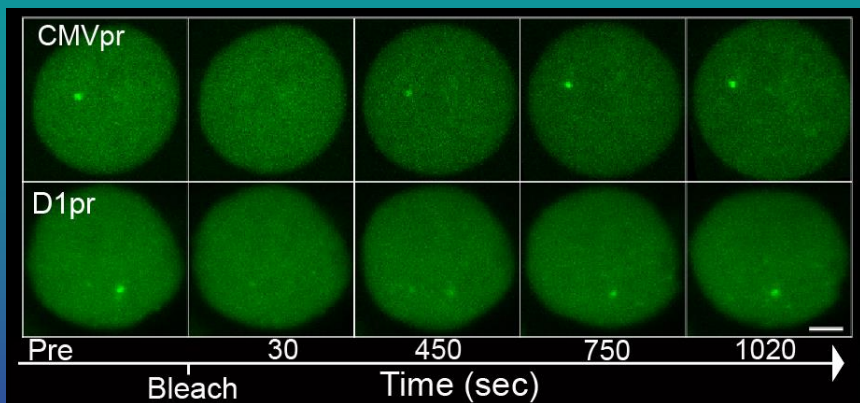


The kinetic difference between the CMV and *CCND1* promoters

Single mRNA quantification

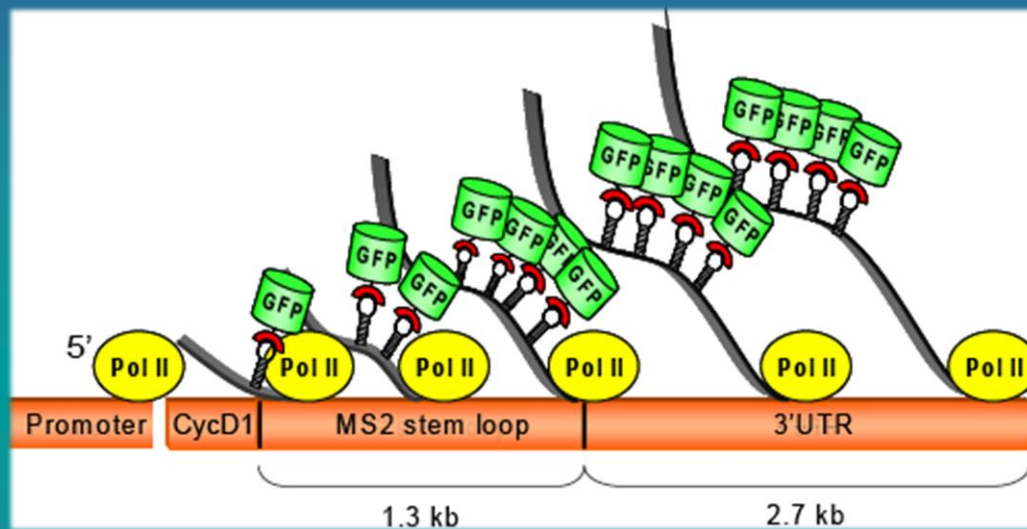


FRAP – transcription kinetics



The kinetic difference between the CMV and *CCND1* promoters

Model: FRAP analysis + RNA quantification

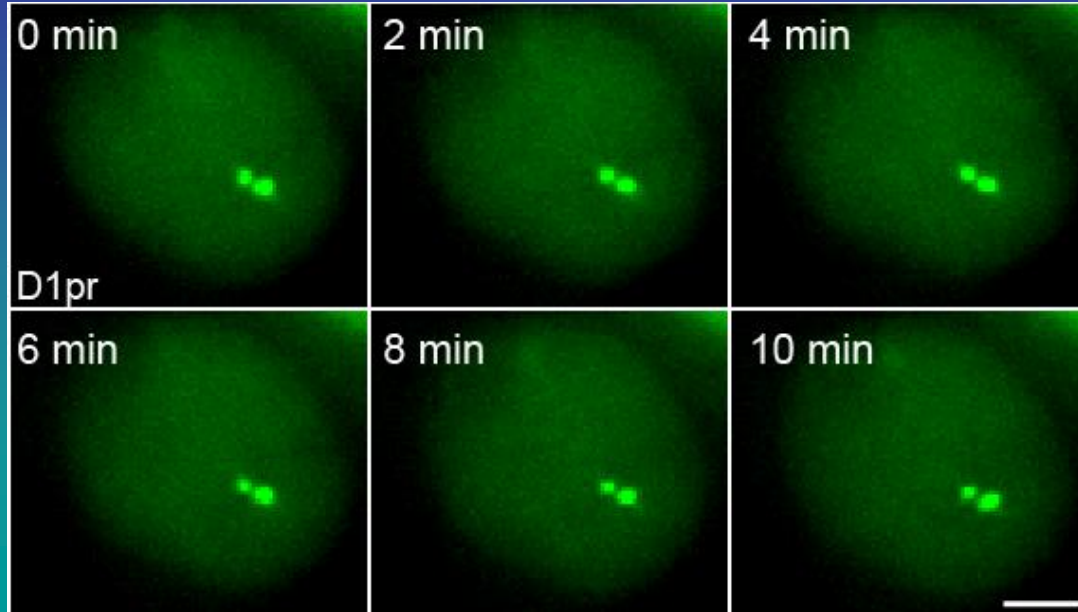


	CMVpr	D1pr
RNAs per cell	114±40	41±30
RNA per allele	14±4	7±4
Polymerase spacing (nt)	237	335
Promoter firing (sec)	22	52
Transcription rate	~0.3-0.8kb/min	

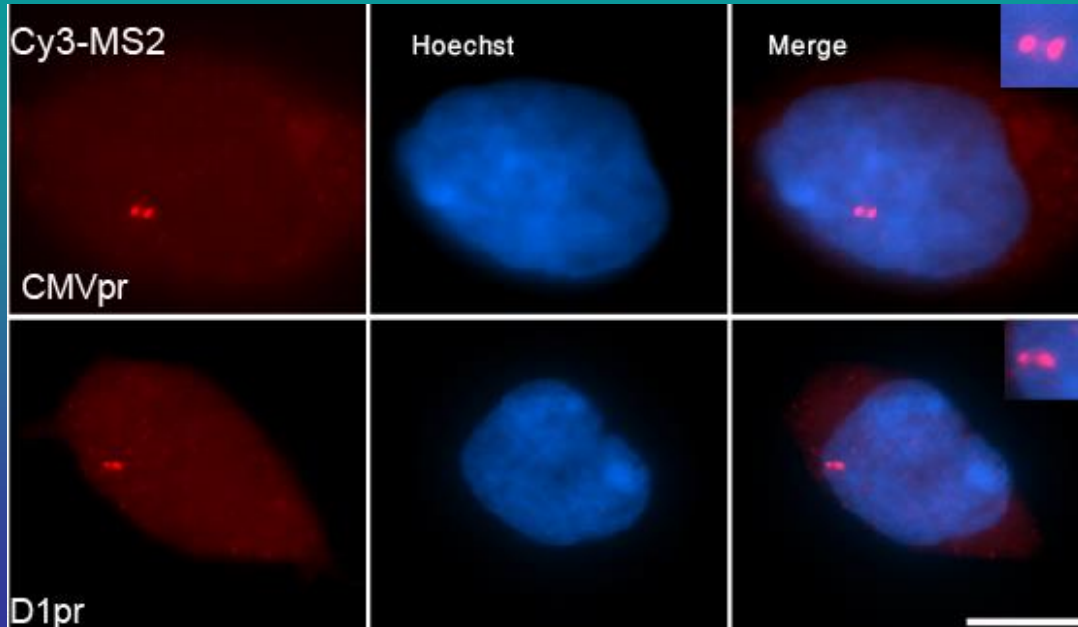
Transcription kinetics throughout the cell cycle

Transcription site doublets

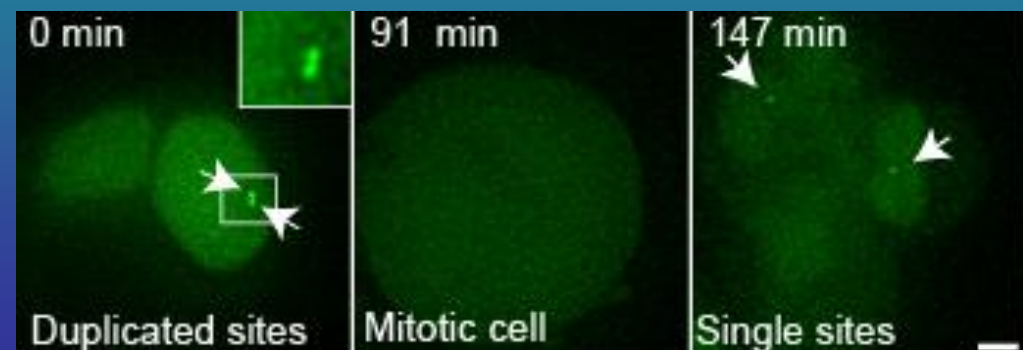
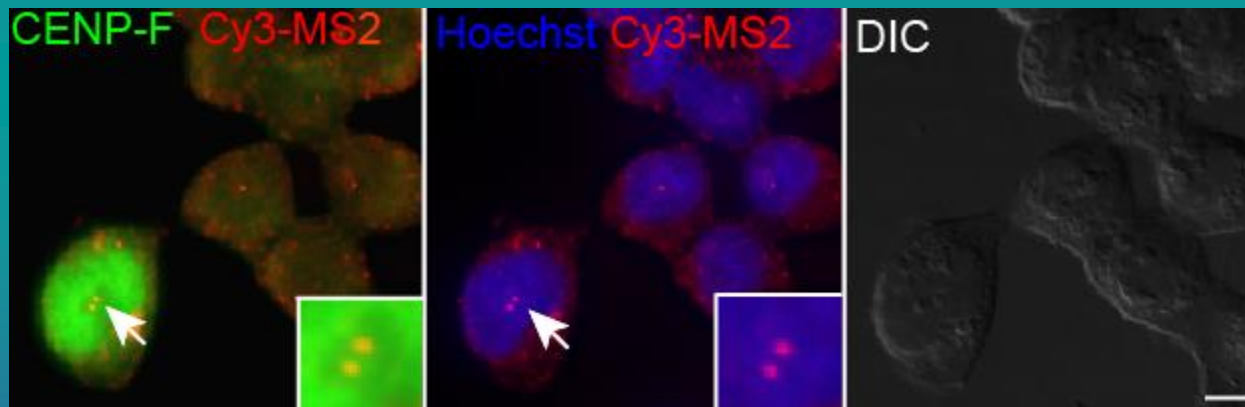
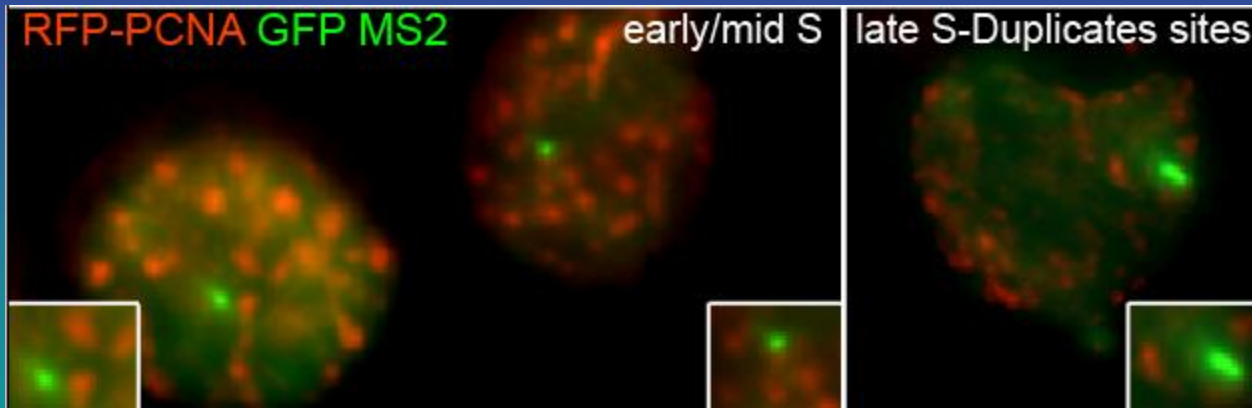
Living cells



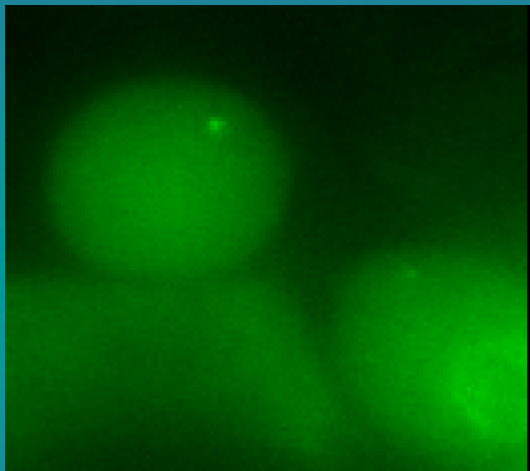
RNA FISH



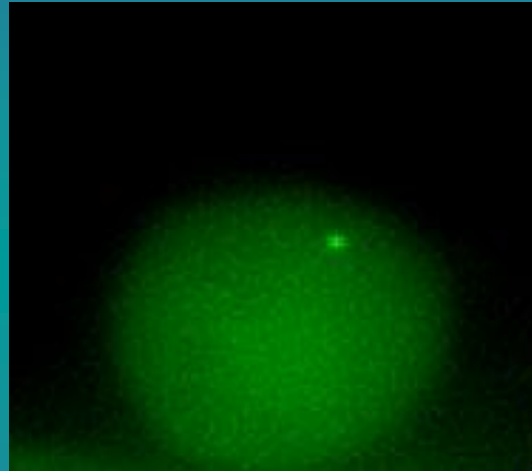
Two transcription sites are prominent from late S phase and onwards



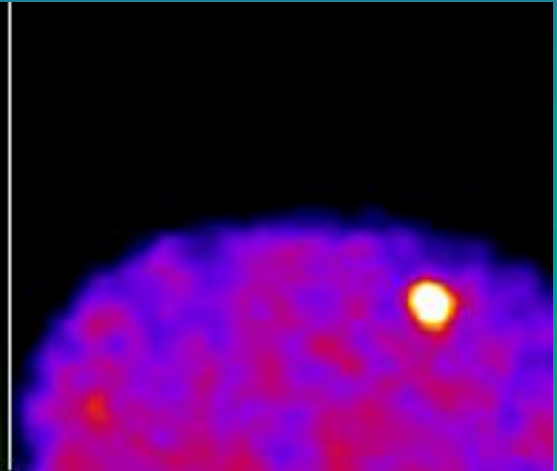
The formation of a second transcription site



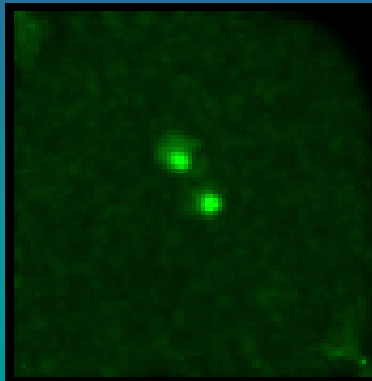
65 min



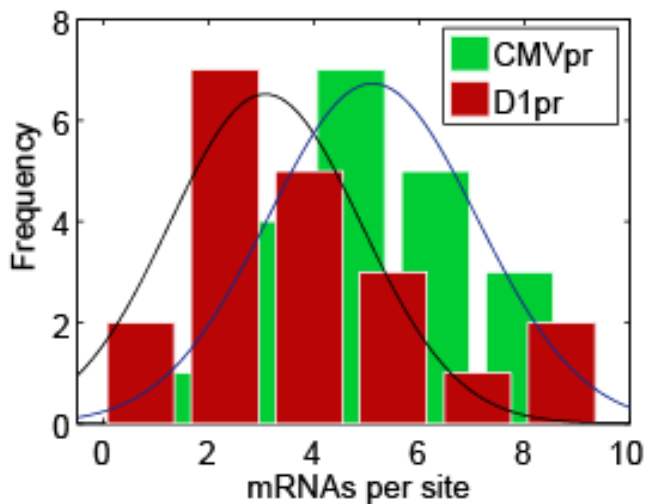
44 min



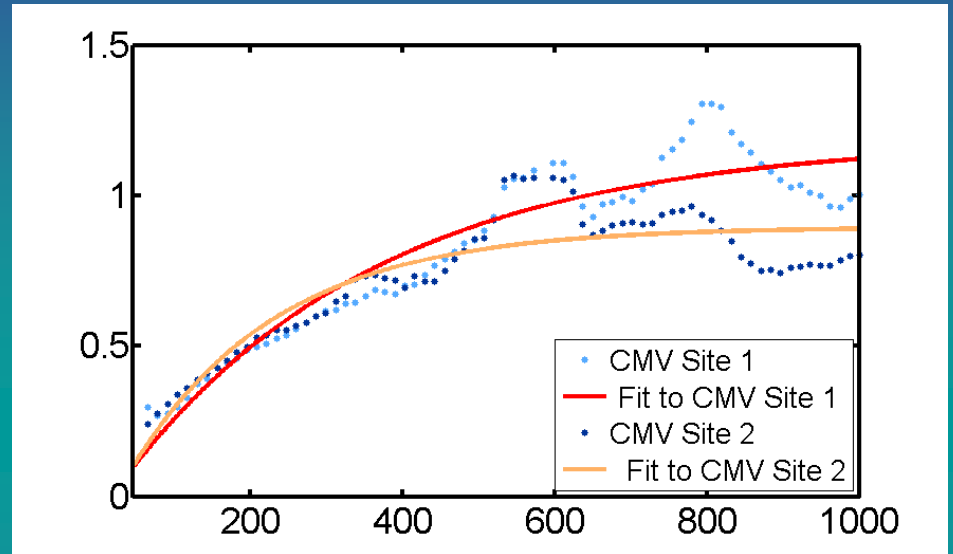
Duplicated transcription sites are less potent



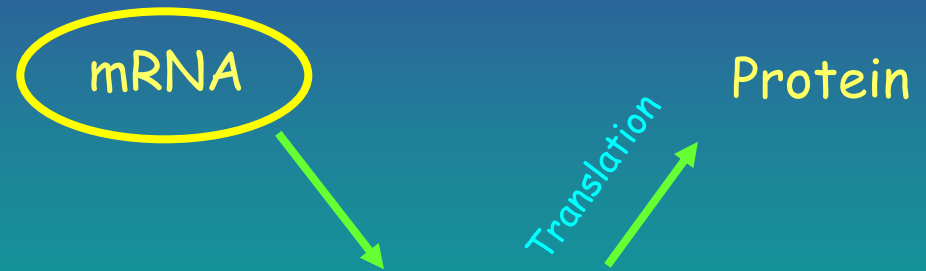
Nascent mRNA quantification



FRAP on 2 sites



Transcription kinetics



mRNA processing:

*5'-end capping

*Editing

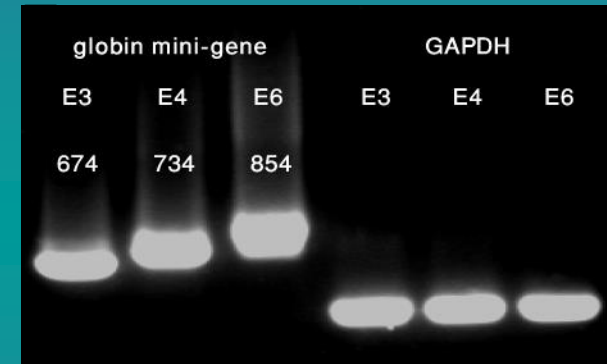
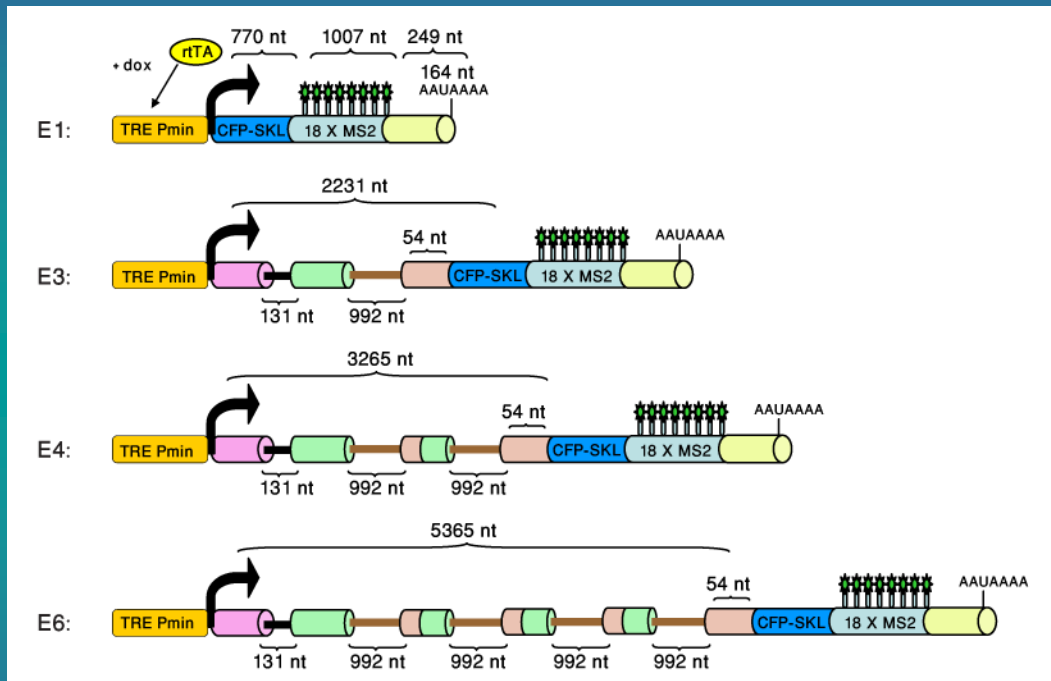
*Splicing

*3'-end processing

mRNA export



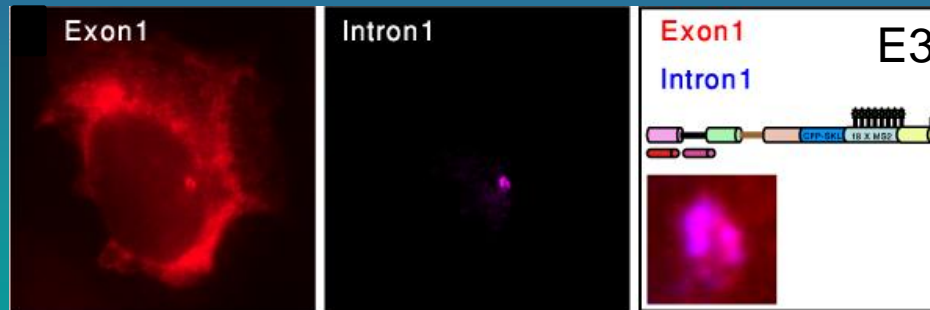
Studying the effect of splicing on transcription kinetics



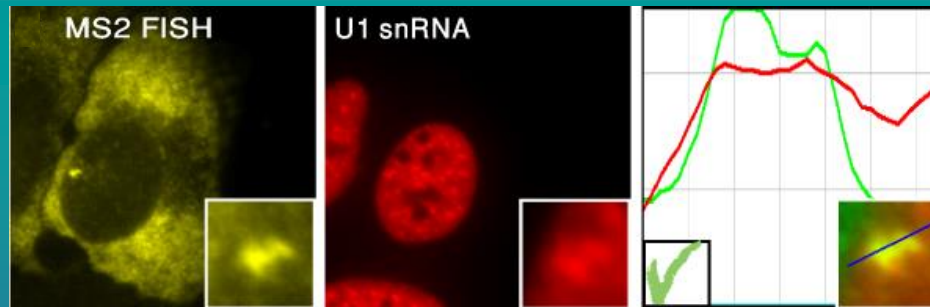
Splicing is co-transcriptional

Detected at
transcription sites

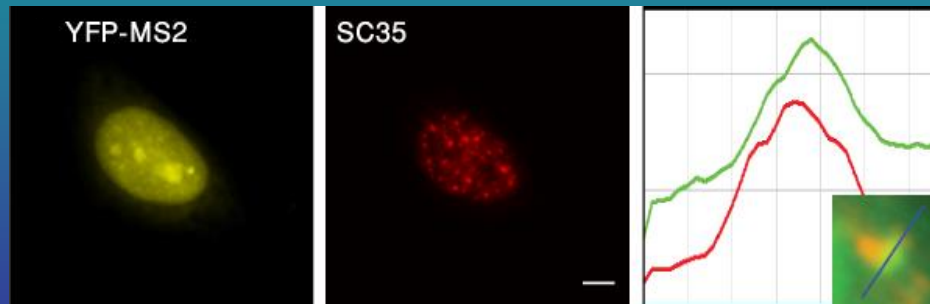
Exons
and
introns



Core
splicing
machinery
(U snRNAs)



Splicing
factors



Are splicing factors recruited to an intronless gene?

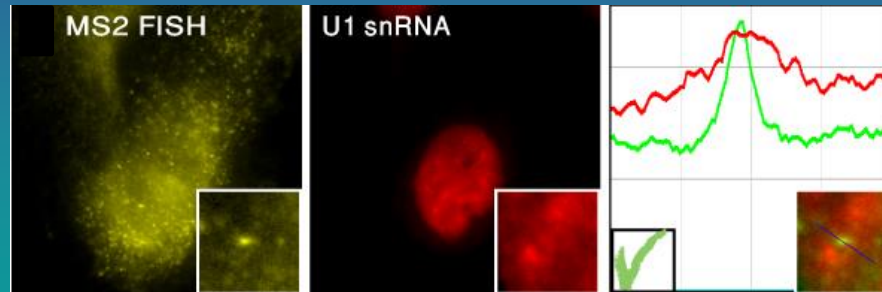


(de Almeida and Carmo-Fonseca 2008)

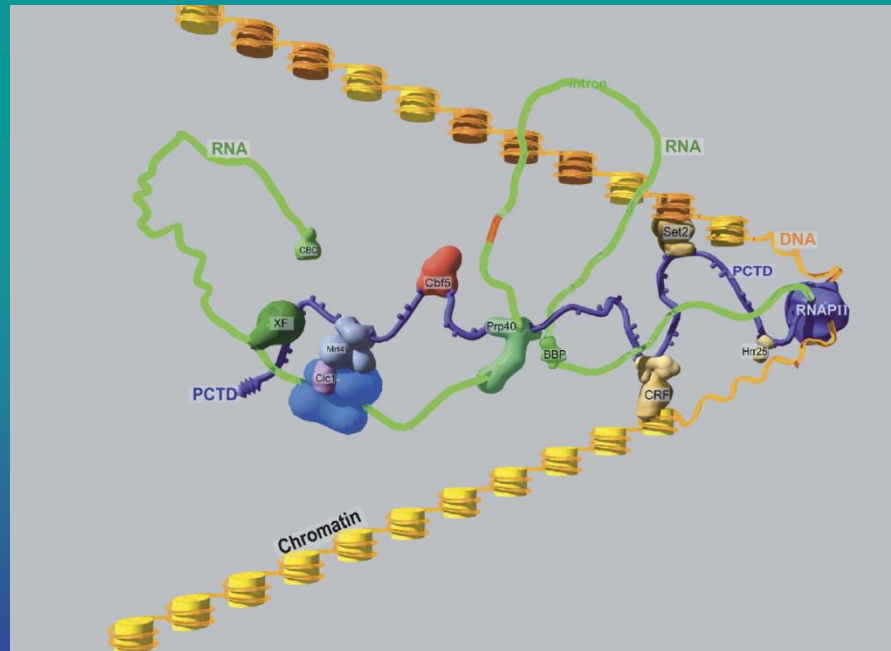
U1 snRNP is recruited to an intronless gene



U1 snRNA



U2 snRNA

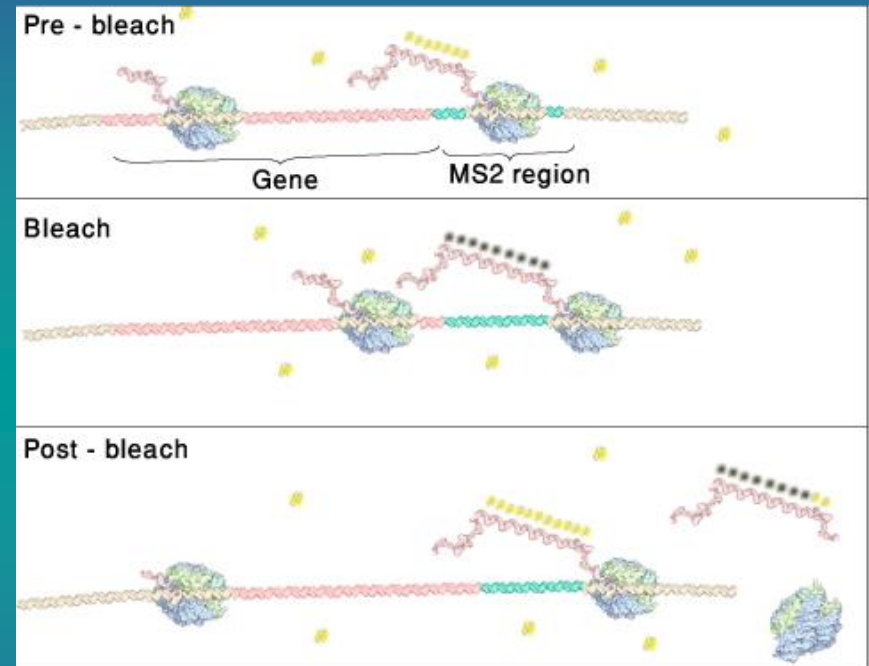
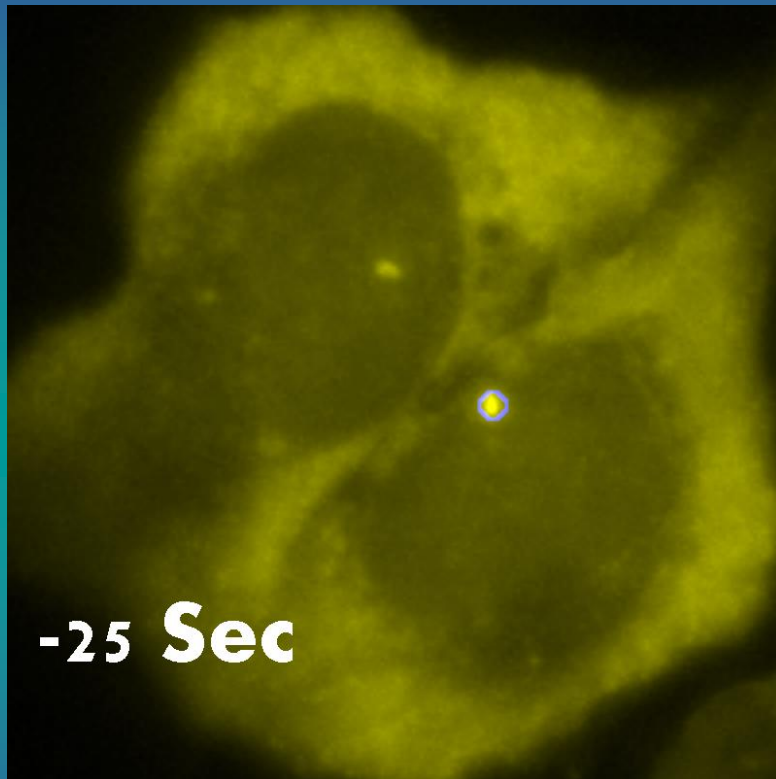


U4 snRNA

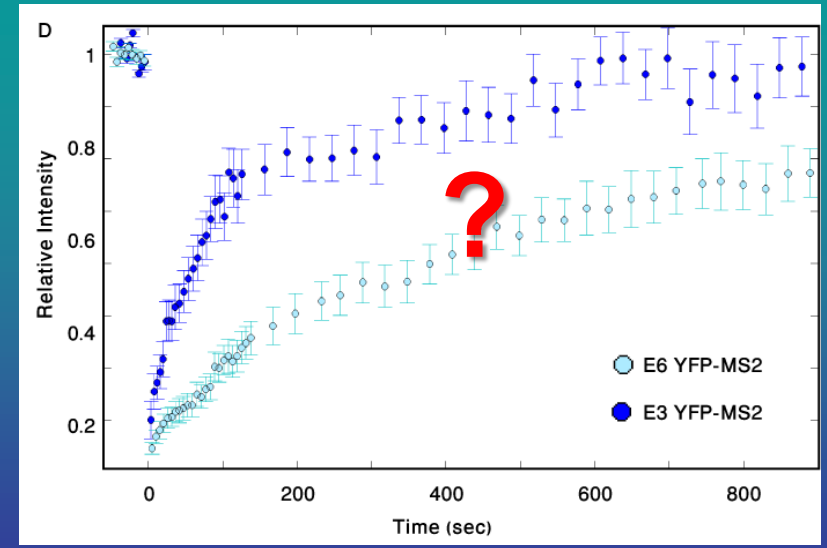
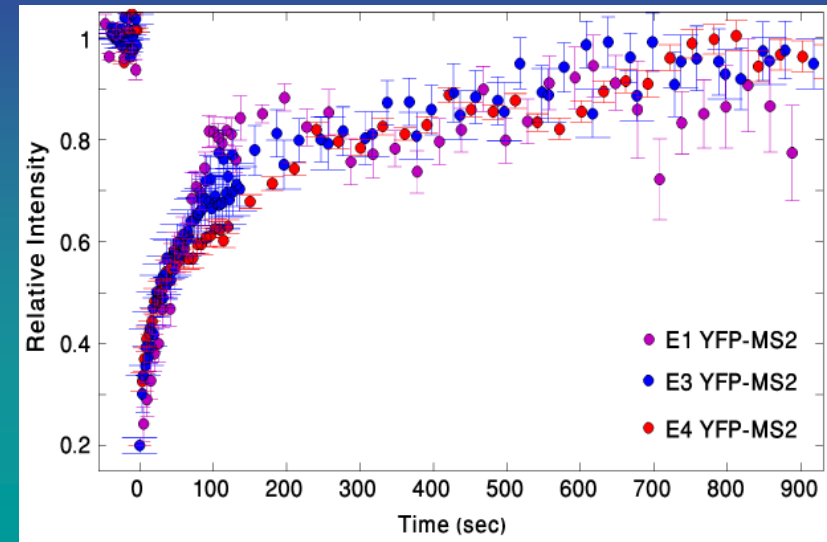
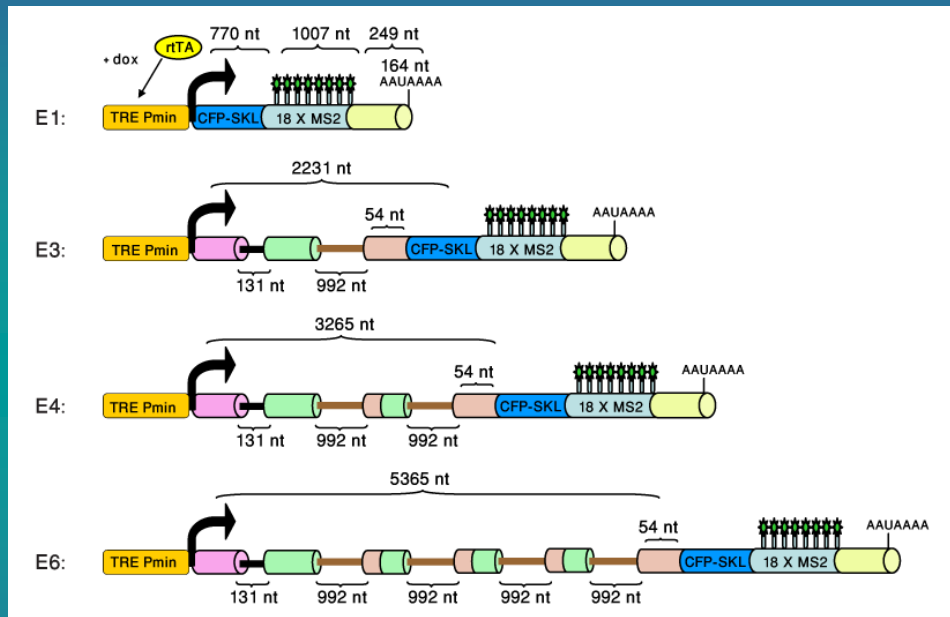
(Phatnani and Greenleaf, *Genes Dev* 2006)

Measuring elongation kinetics using FRAP

FRAP (mRNA)

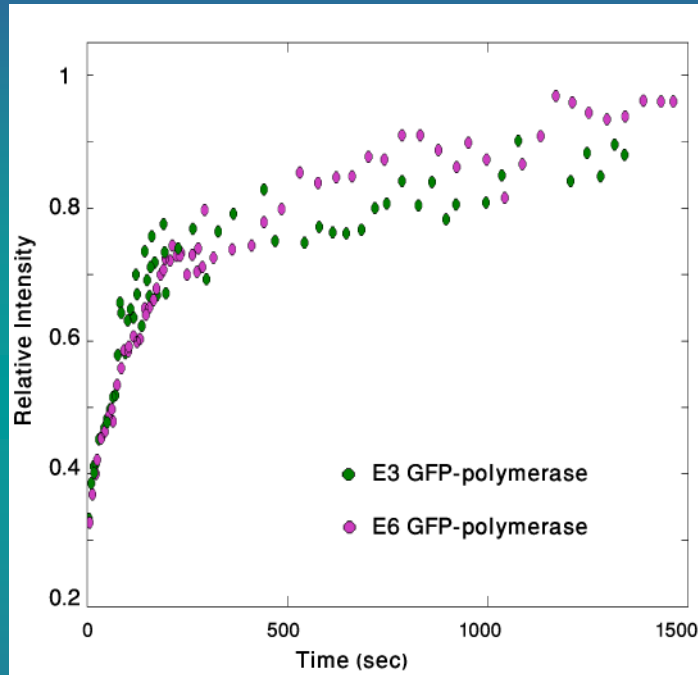


Measuring elongation kinetics using FRAP

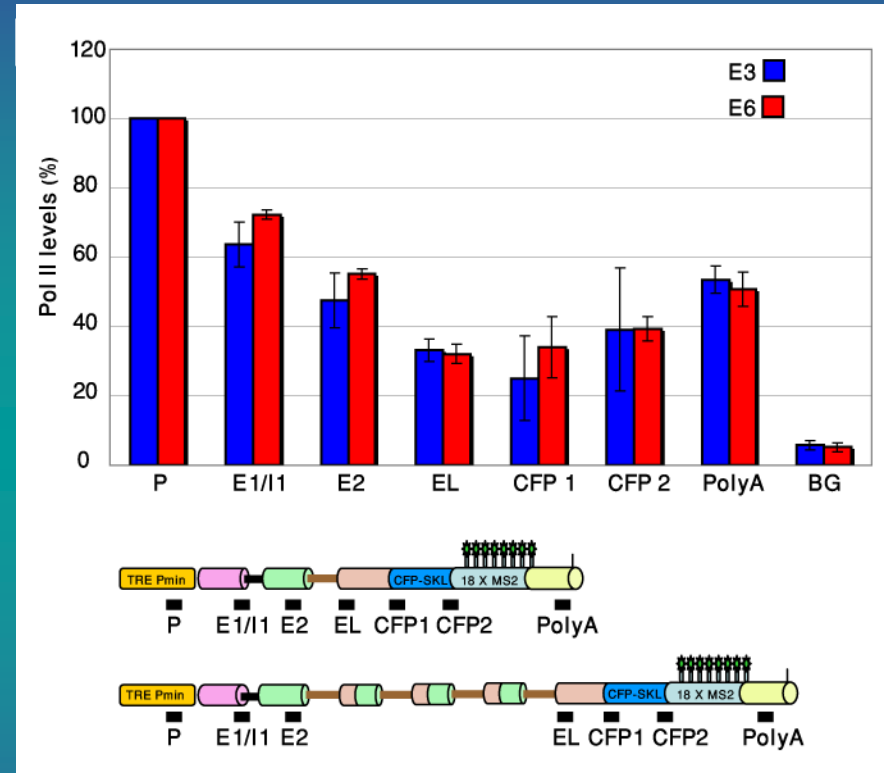


Total polymerase kinetics remain unchanged

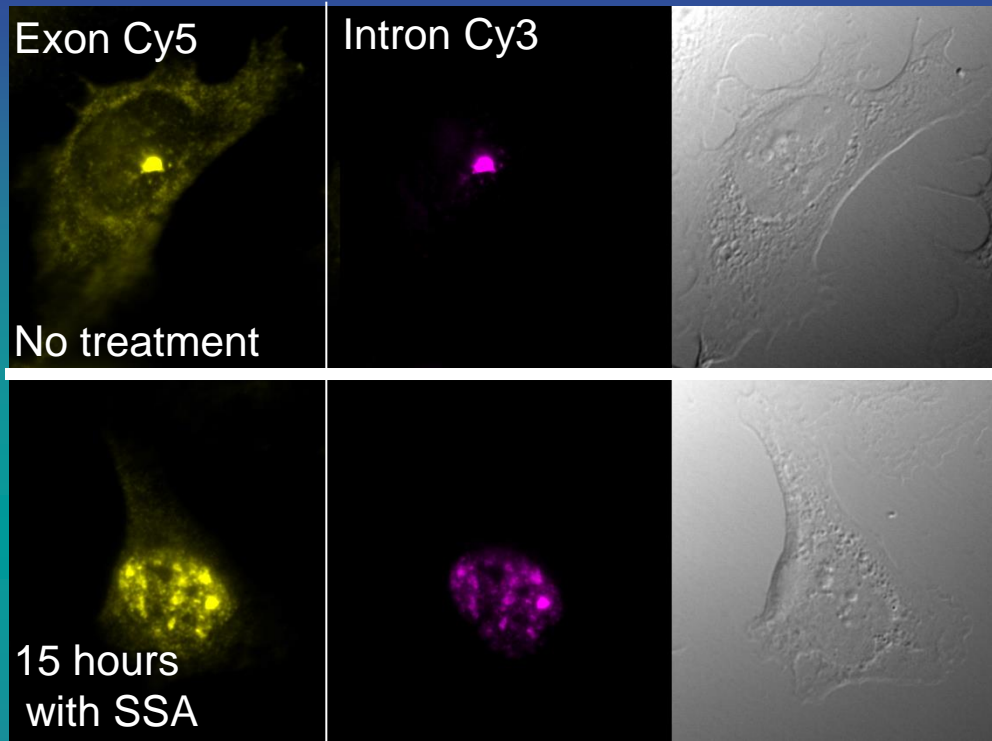
FRAP (GFP- Pol II)



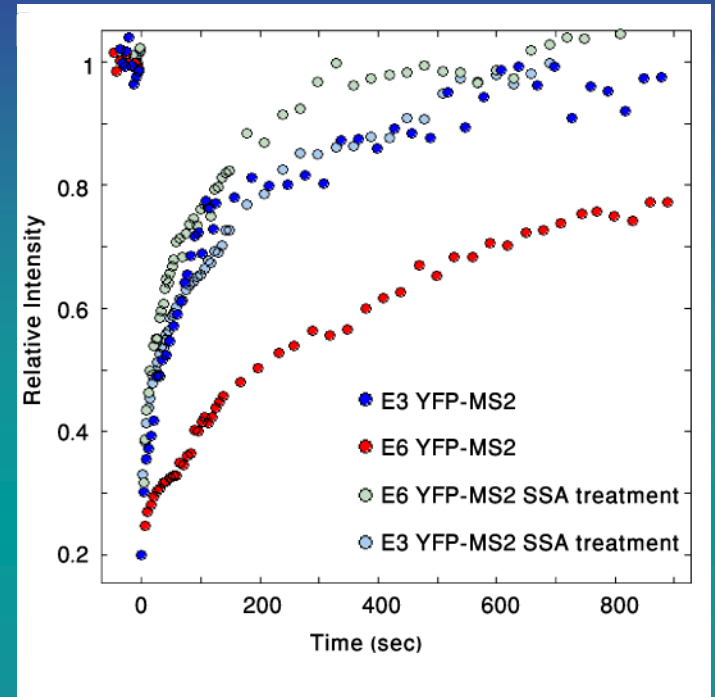
DNA ChIP (Pol II)



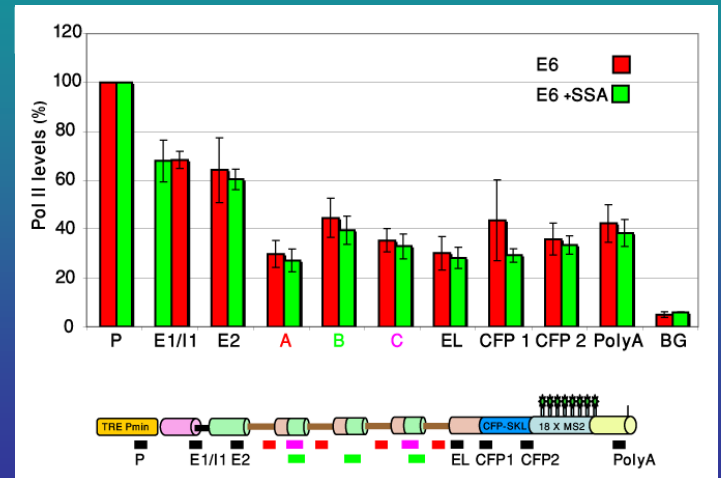
Splicing inhibition affects E6 kinetics



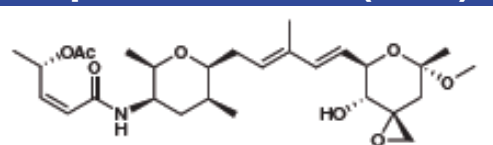
FRAP (mRNA)



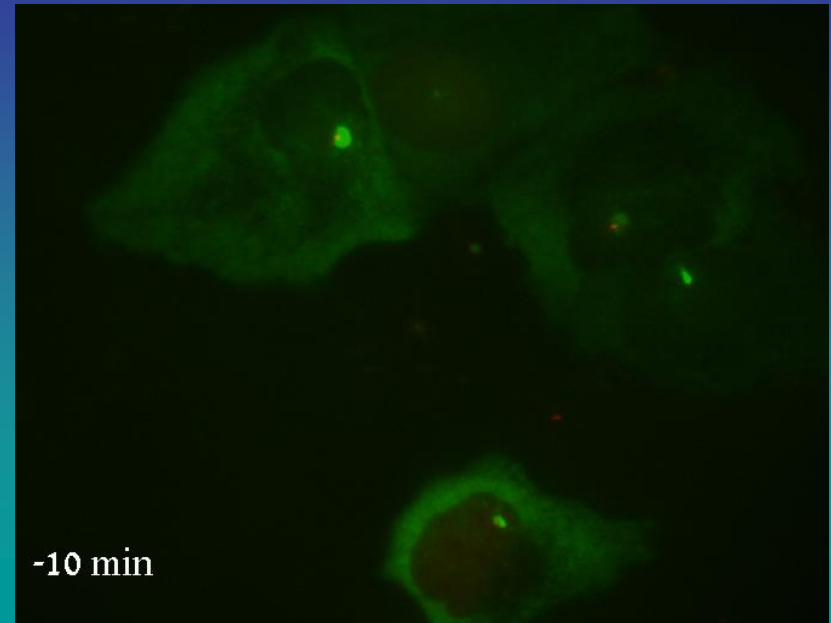
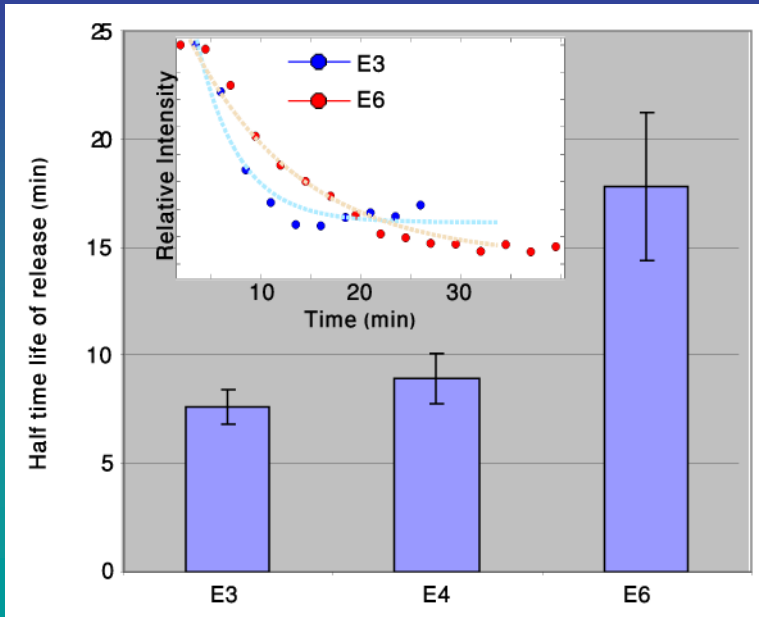
DNA ChIP (Pol II)



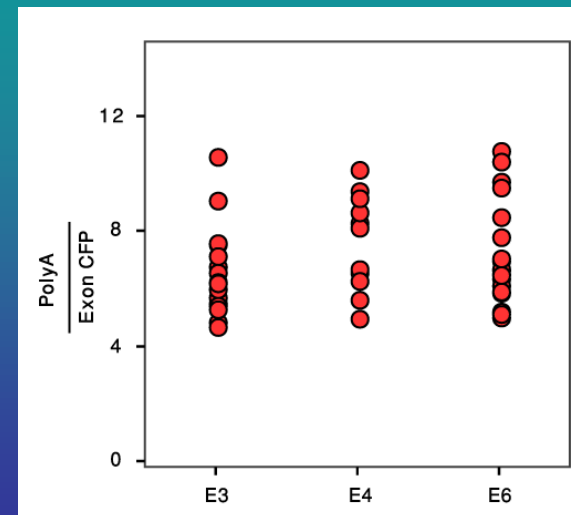
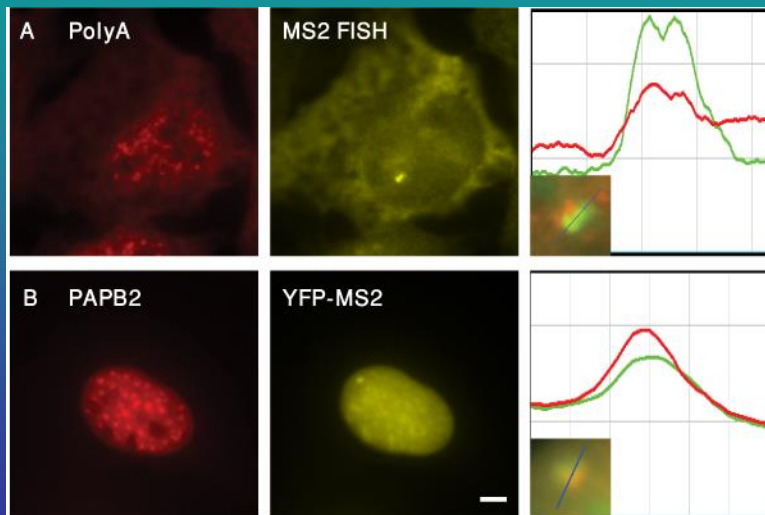
Spliceostatin A (SSA)



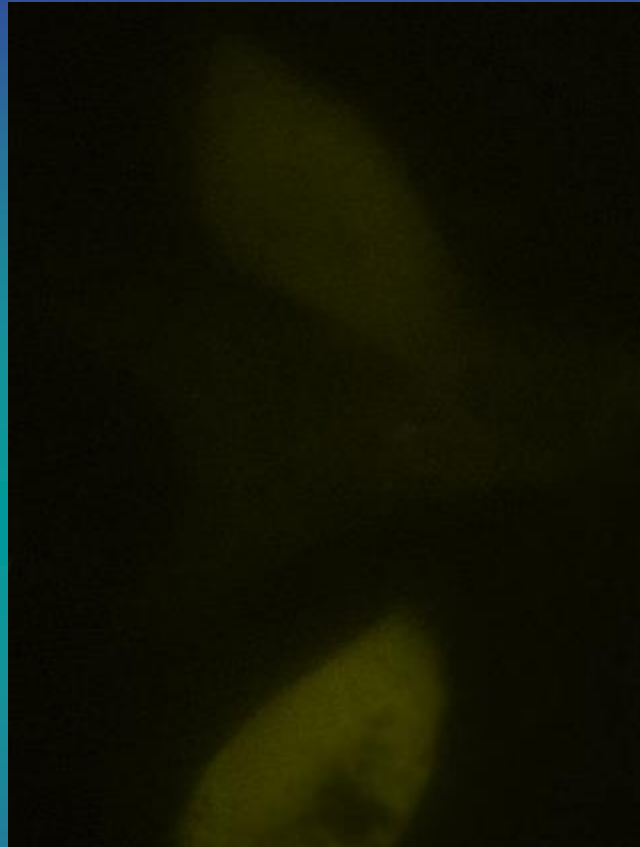
mRNAs are stalled on the E6 gene



This is not accumulation of aberrant transcripts



Kinetics of mRNP nucleoplasmic transport

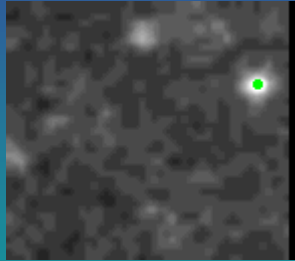


Every 6 min for 6:45 hrs

mRNPs appeared in the nucleoplasm 5-10 min after transcription induction. After another ~10 min the mRNPs could be detected in the cytoplasm.

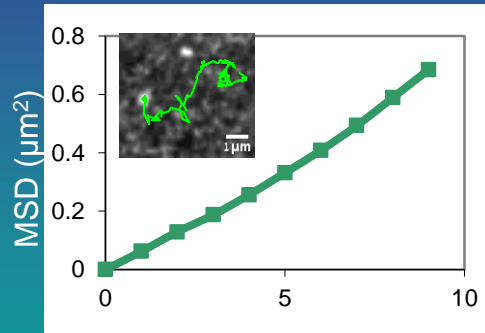
mRNP transport kinetics

2D and 3D tracking

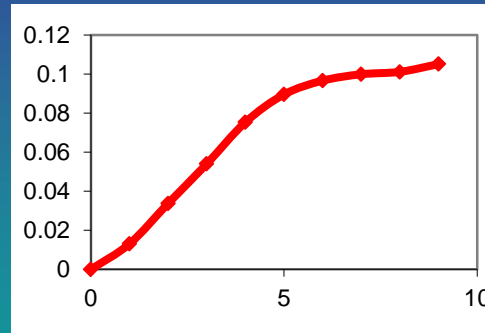


X10 original speed

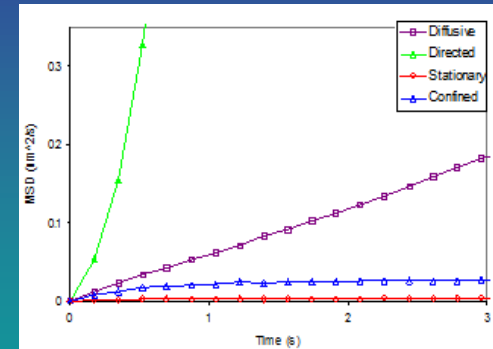
Diffusive



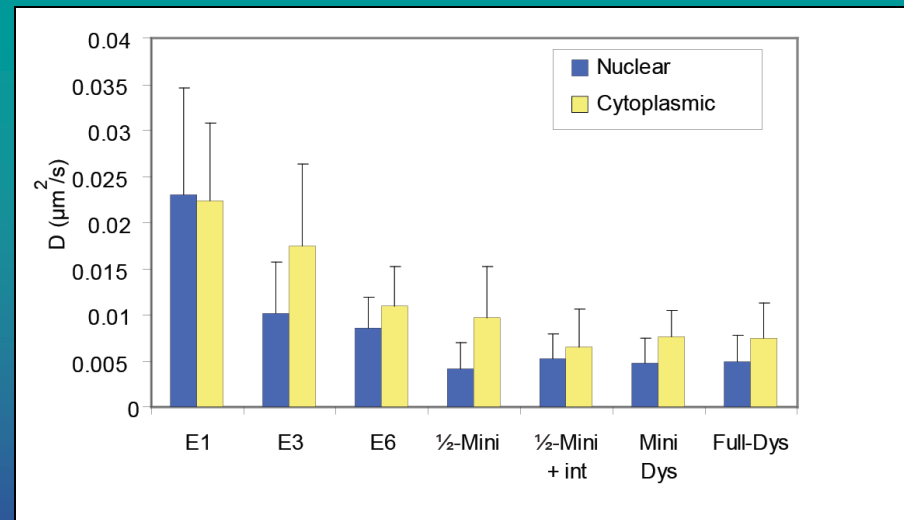
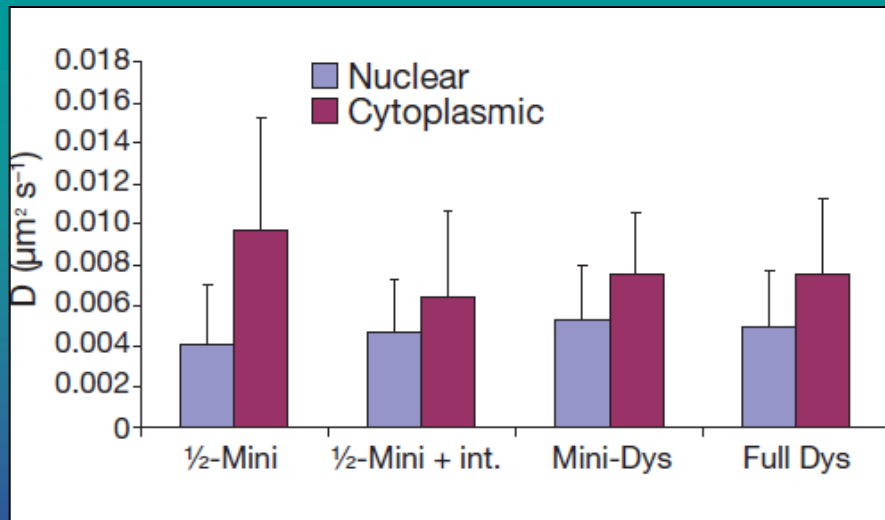
Corralled



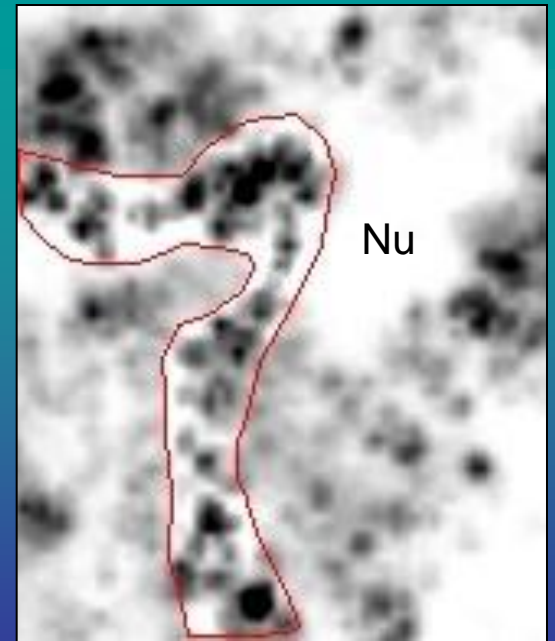
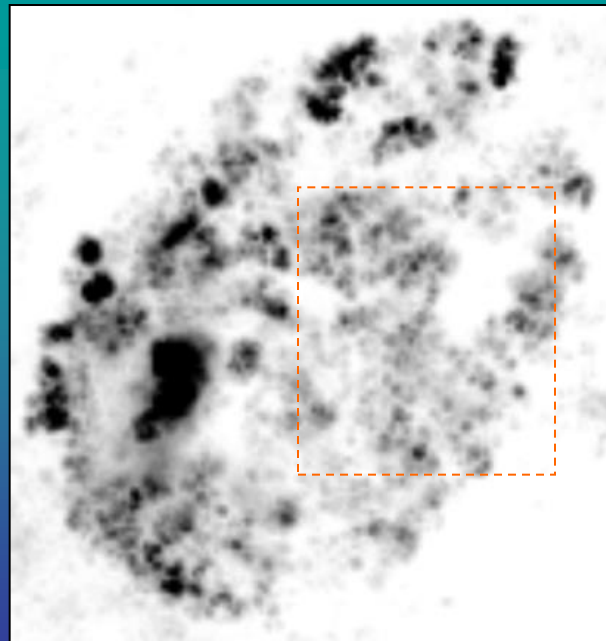
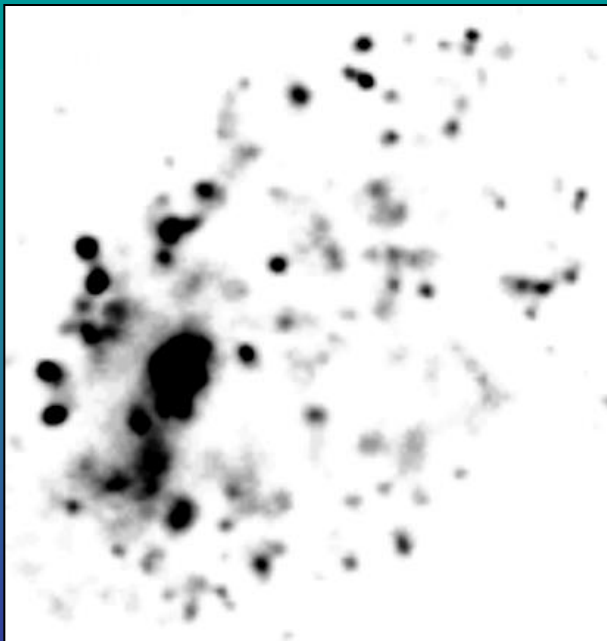
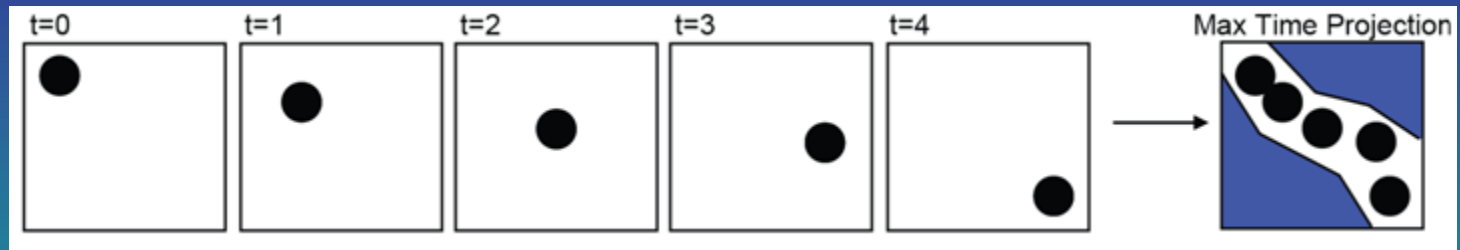
Mean square displacement analysis



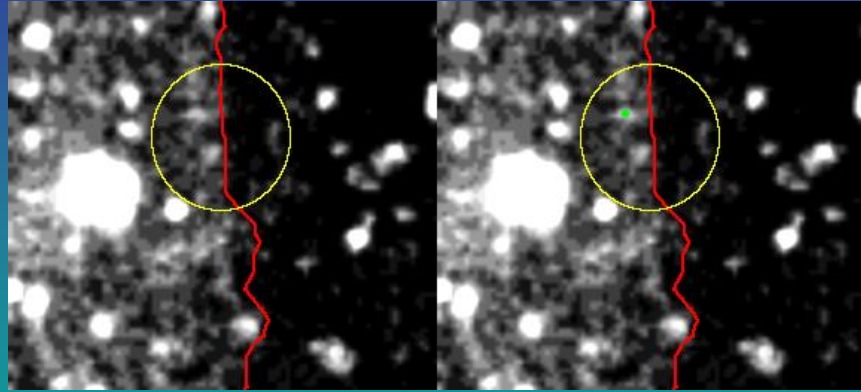
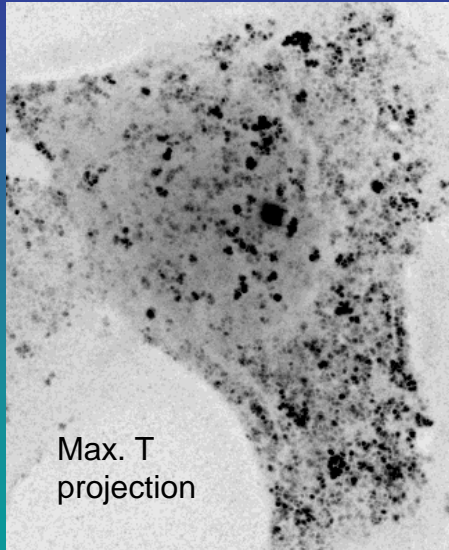
time (sec)



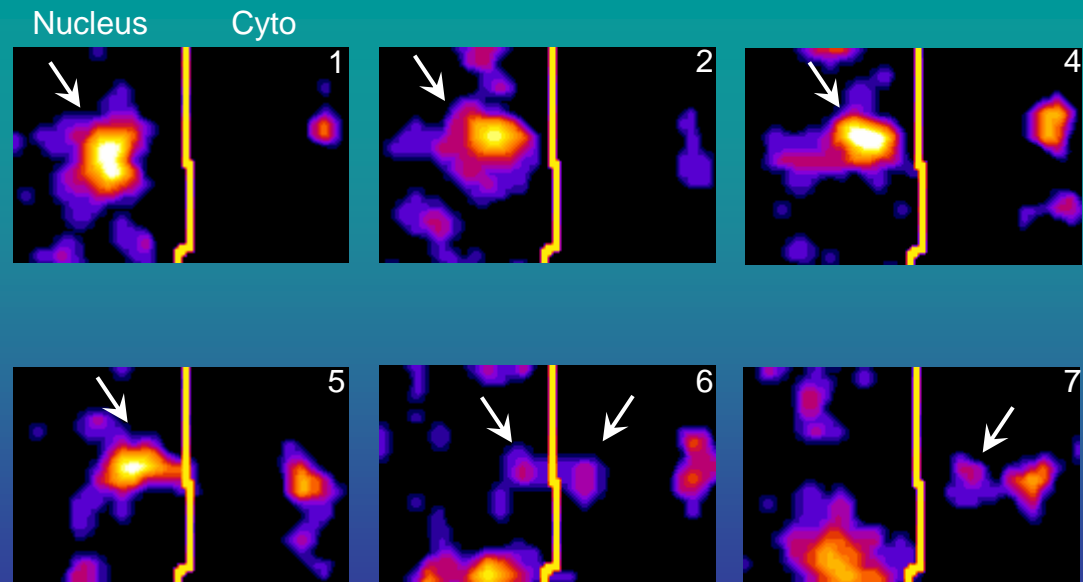
mRNP tracks



mRNP export



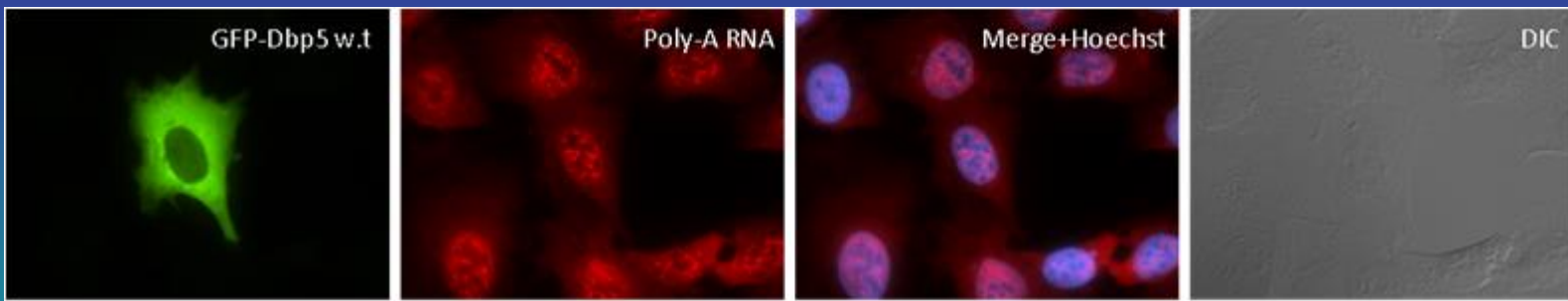
7 sec



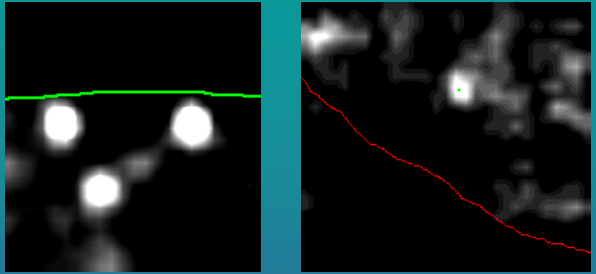
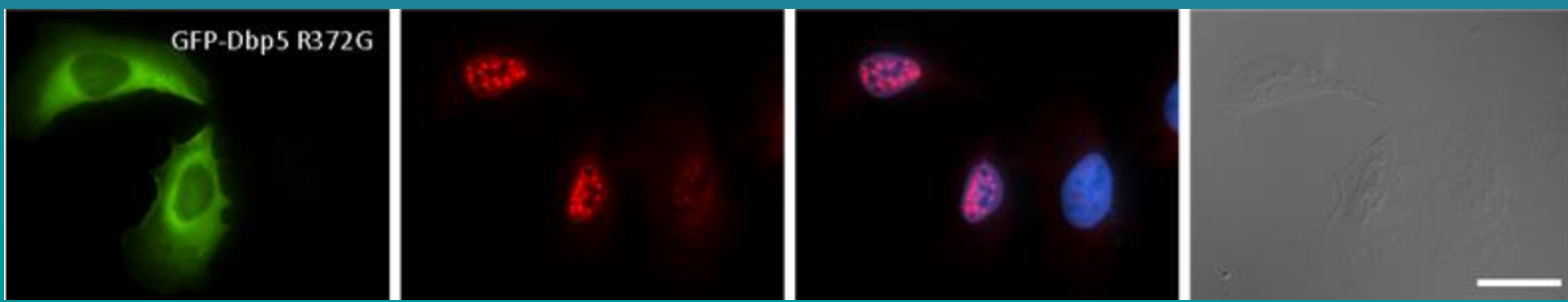
Dbp5 is required for mRNA export in human cells

RNA FISH

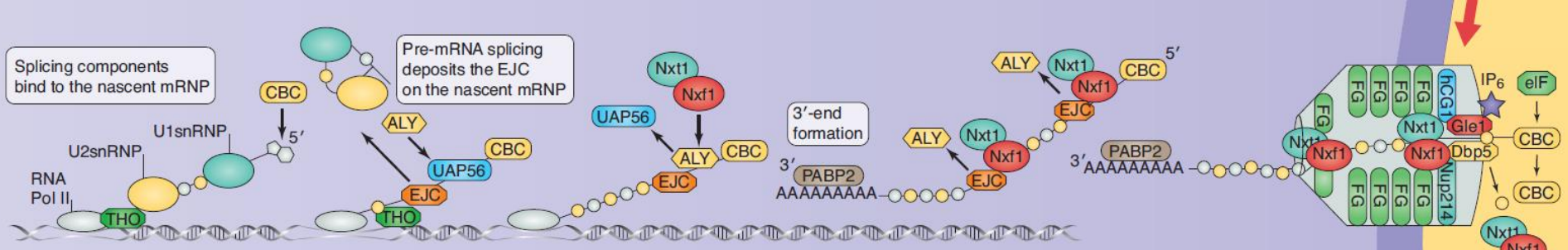
W.T



Dominant Negative R372G



(Hodge et al. *Genes Dev* 2011) (Noble et al. *Genes Dev* 2011)





משרד המדע, הטכנולוגיה והחלל
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Oliver Vugrek

Ruđer Bošković Institute



INNOmOL
Innovation Pipeline