

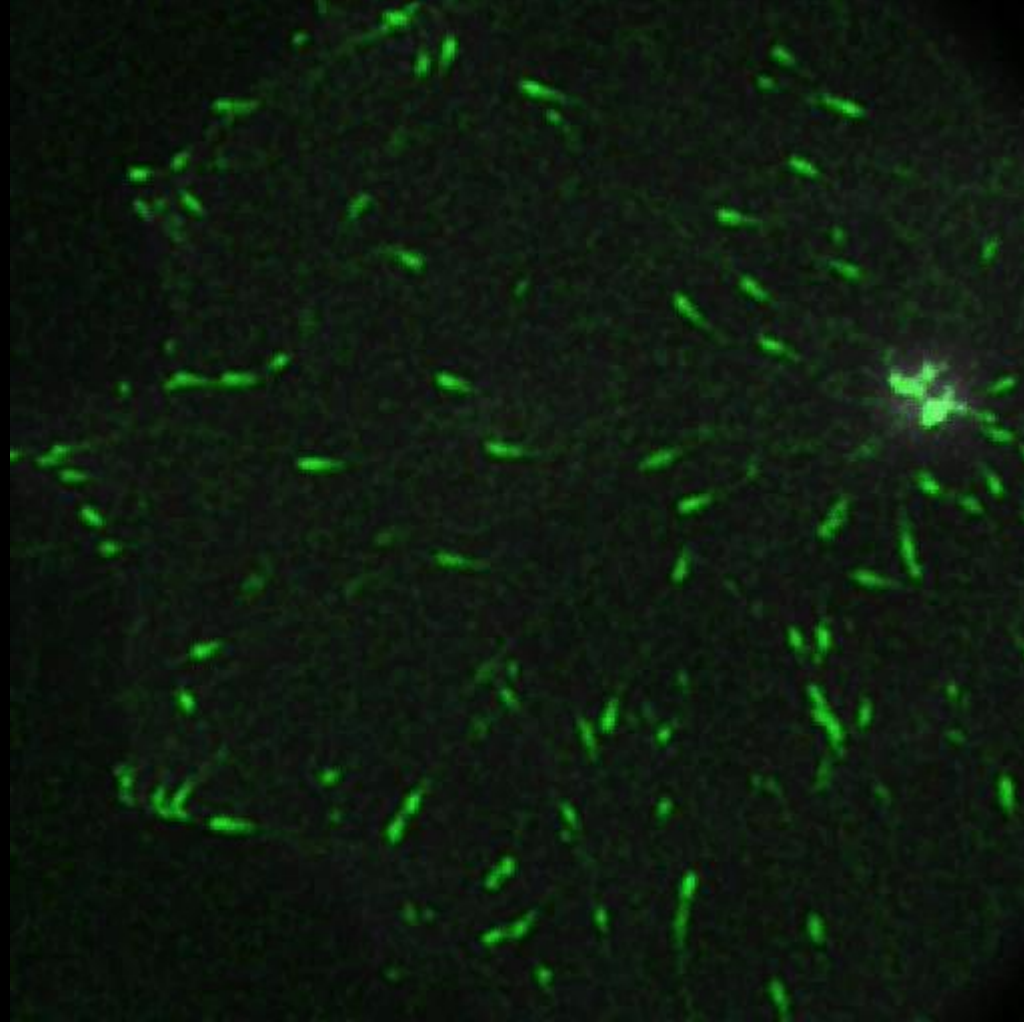


Anna Akhmanova

Cell Biology

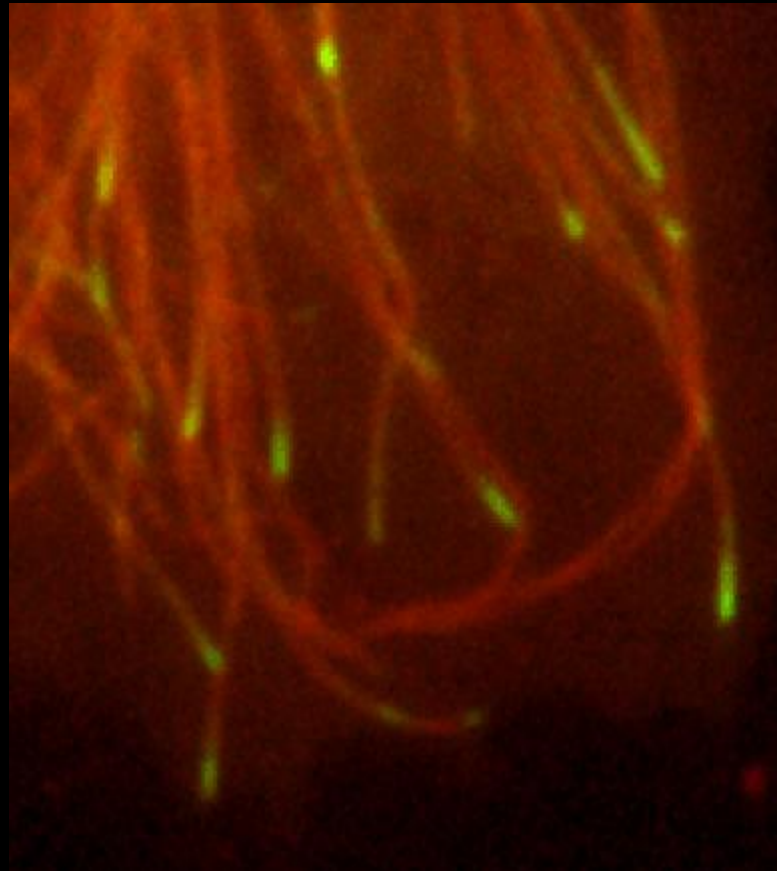
Utrecht University

The Netherlands



A zoo at the tip: a dynamic protein network  
controls the fate of microtubule ends

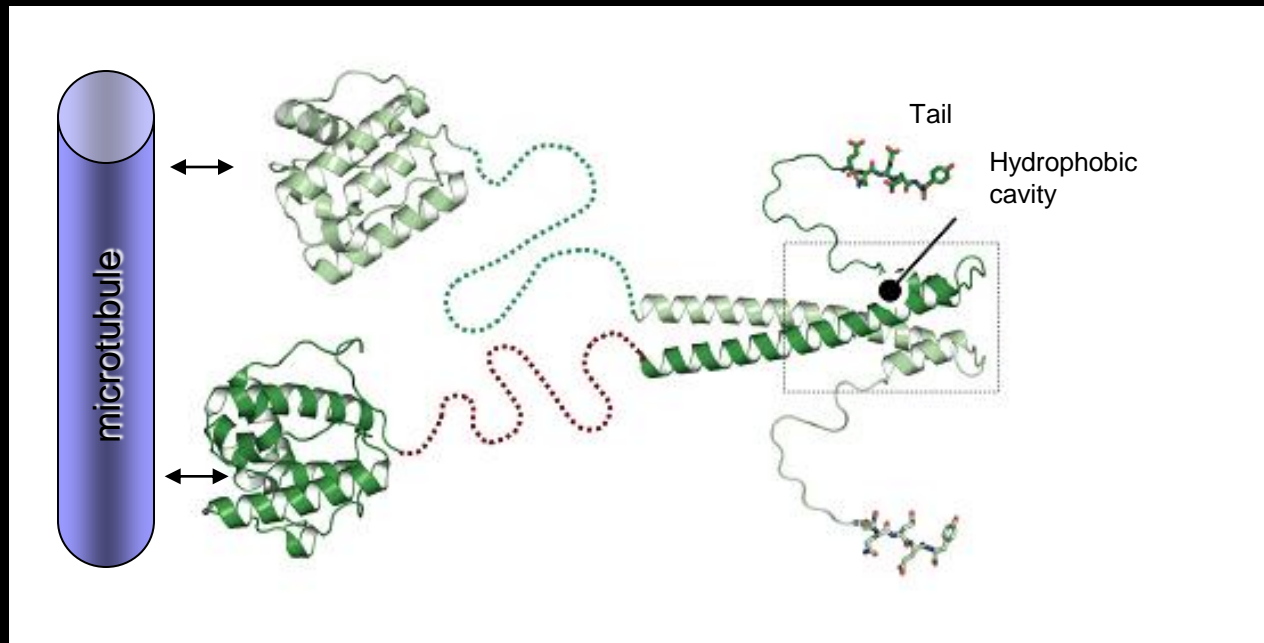
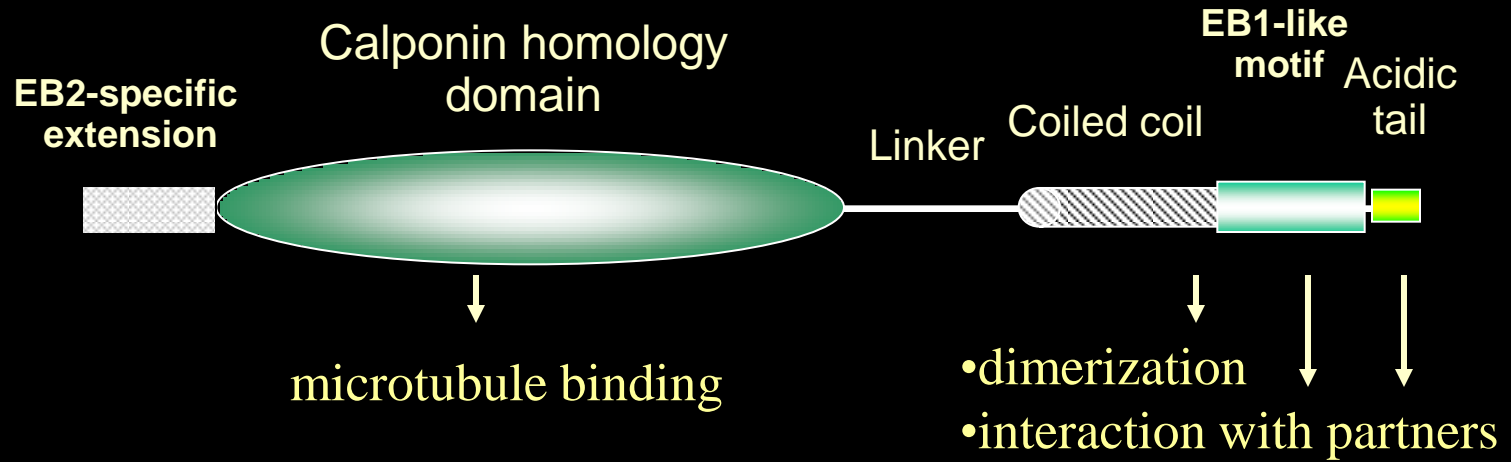
# Plus end-tracking proteins accumulate at the growing microtubule ends



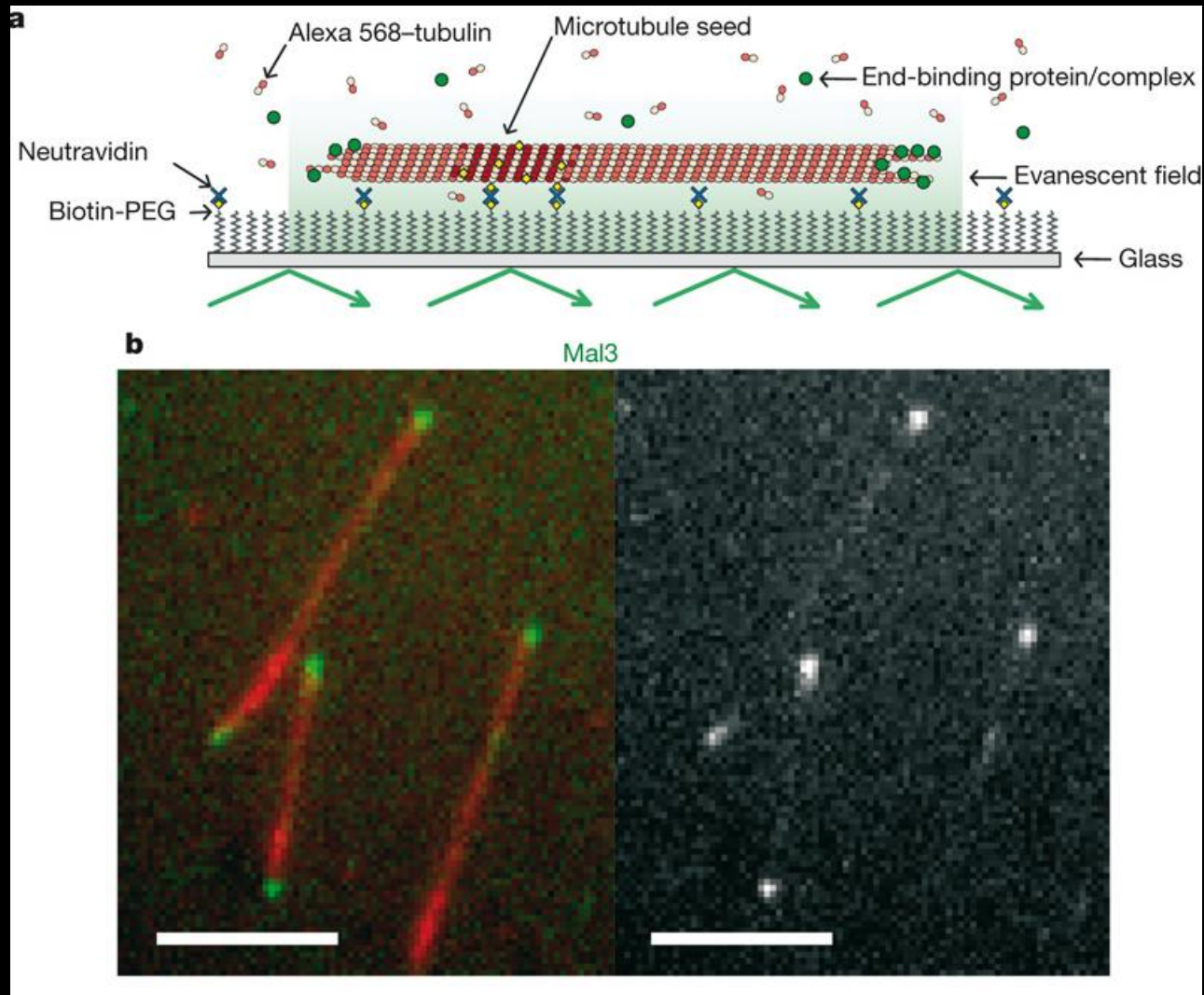
GFP-EB3 and mCherry- $\alpha$ -tubulin  
in a MRC5 human lung fibroblast

0.5s/frame

# EB1 family members: EB1, EB2 (RP1) and EB3 (EBF3)

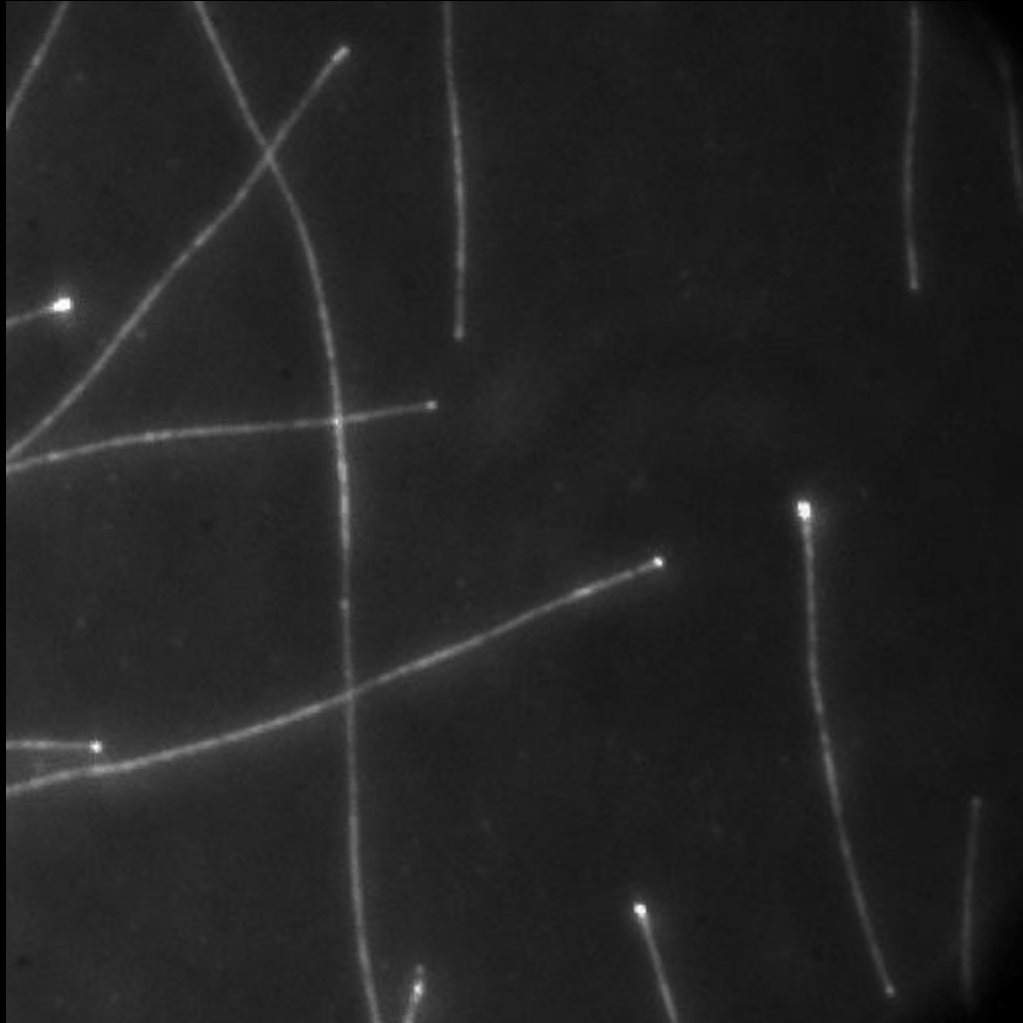


# Plus end tracking in vitro

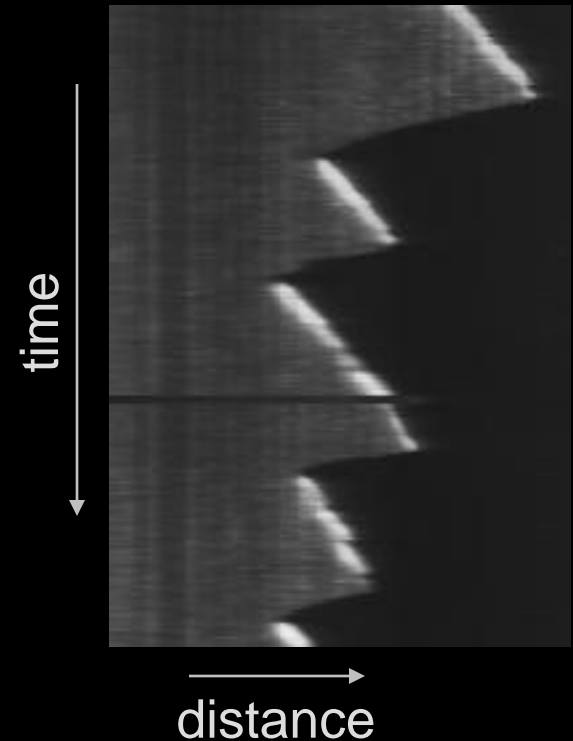


# EB family members autonomously track growing microtubule ends

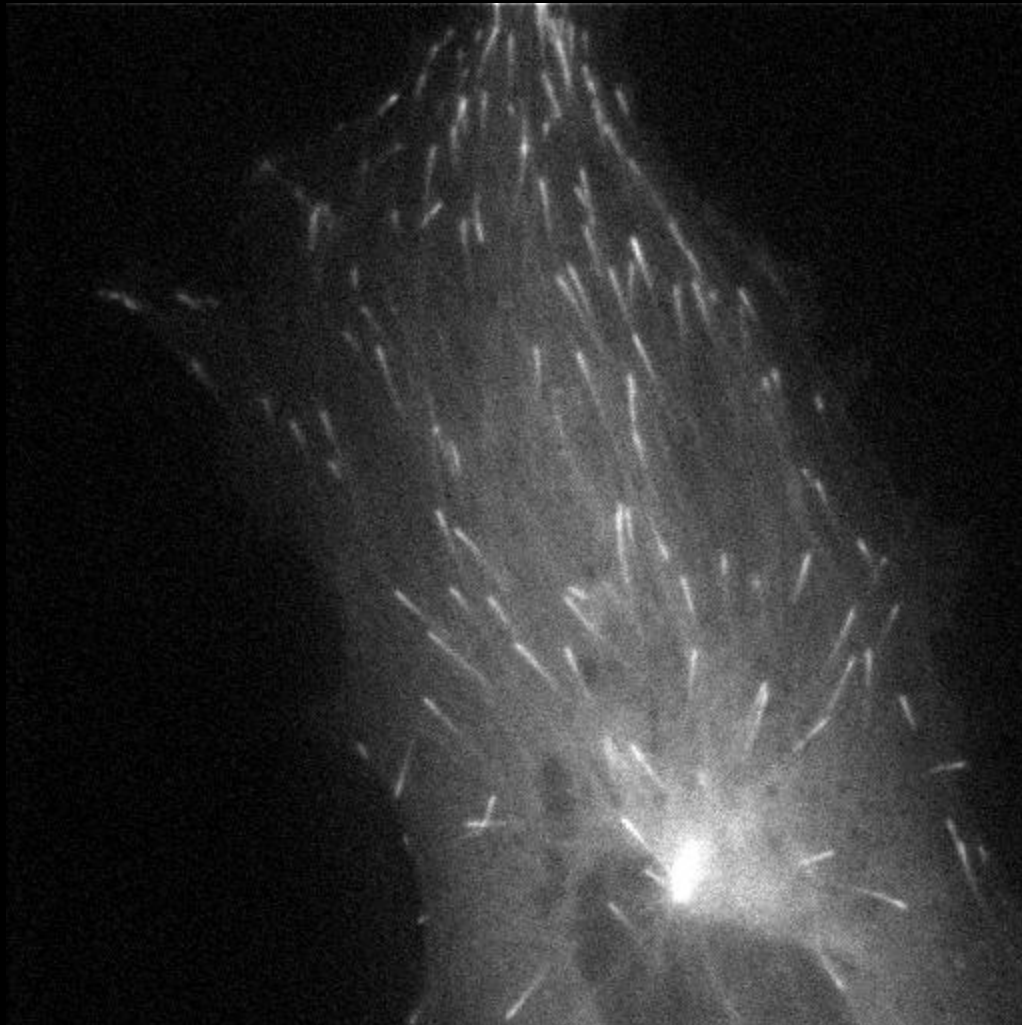
**GFP-EB3**



**kymograph**



# Persistent growth of microtubules the role of EB proteins



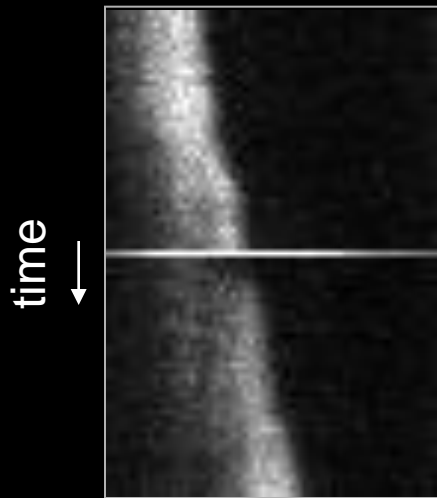
EB3-GFP in a CAR  
goldfish fibroblast

*movie: Ilya Grigoriev*

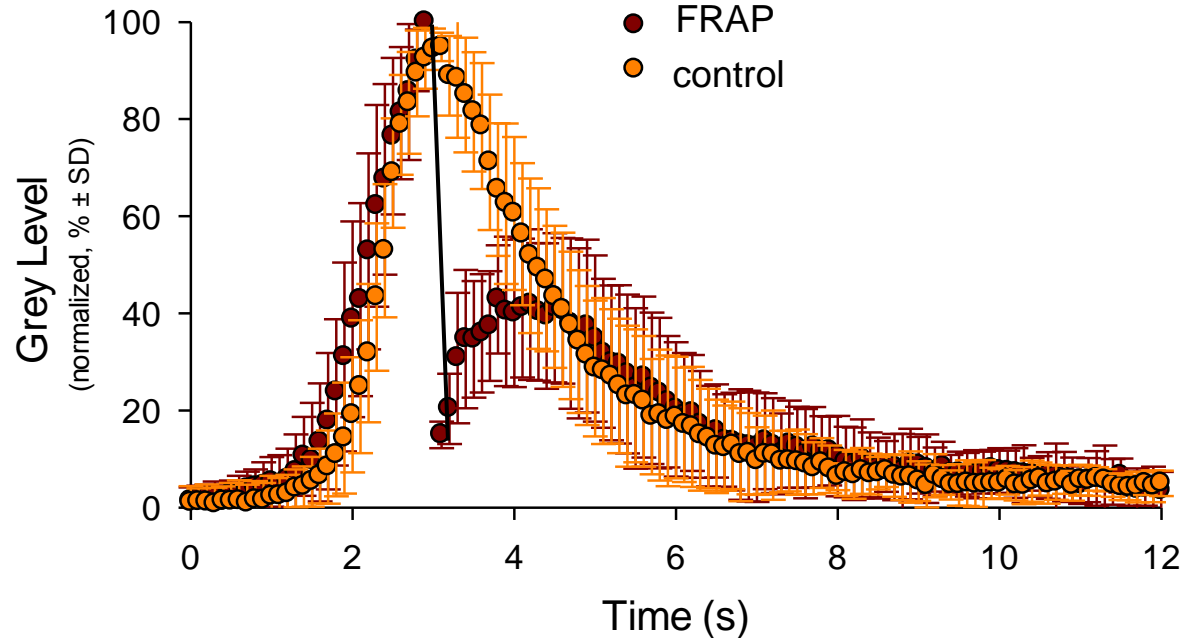
# FRAP-based analysis of protein exchange on microtubule ends



30 fps



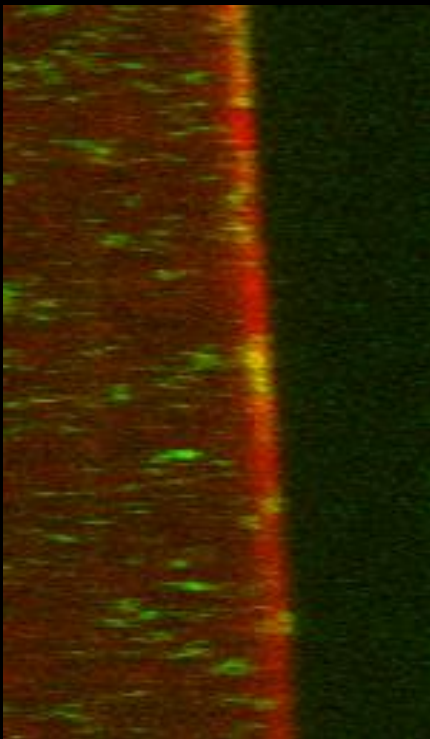
EB3-GFP residence time 0.3-0.4 s



# Single molecule analysis of EB3 interaction with microtubules

GFP-EB3

mCherry-EB3



Association Rate (n per 1 $\mu\text{m}$ per 1 nM per 1 s)		Dwell Time (s)	
Lattice	Tip	Lattice	Tip
$2.3 \pm 0.9$	<u><math>6.5 \pm 0.5</math></u>	$0.16 \pm 0.03$	<u><math>0.34 \pm 0.04</math></u>

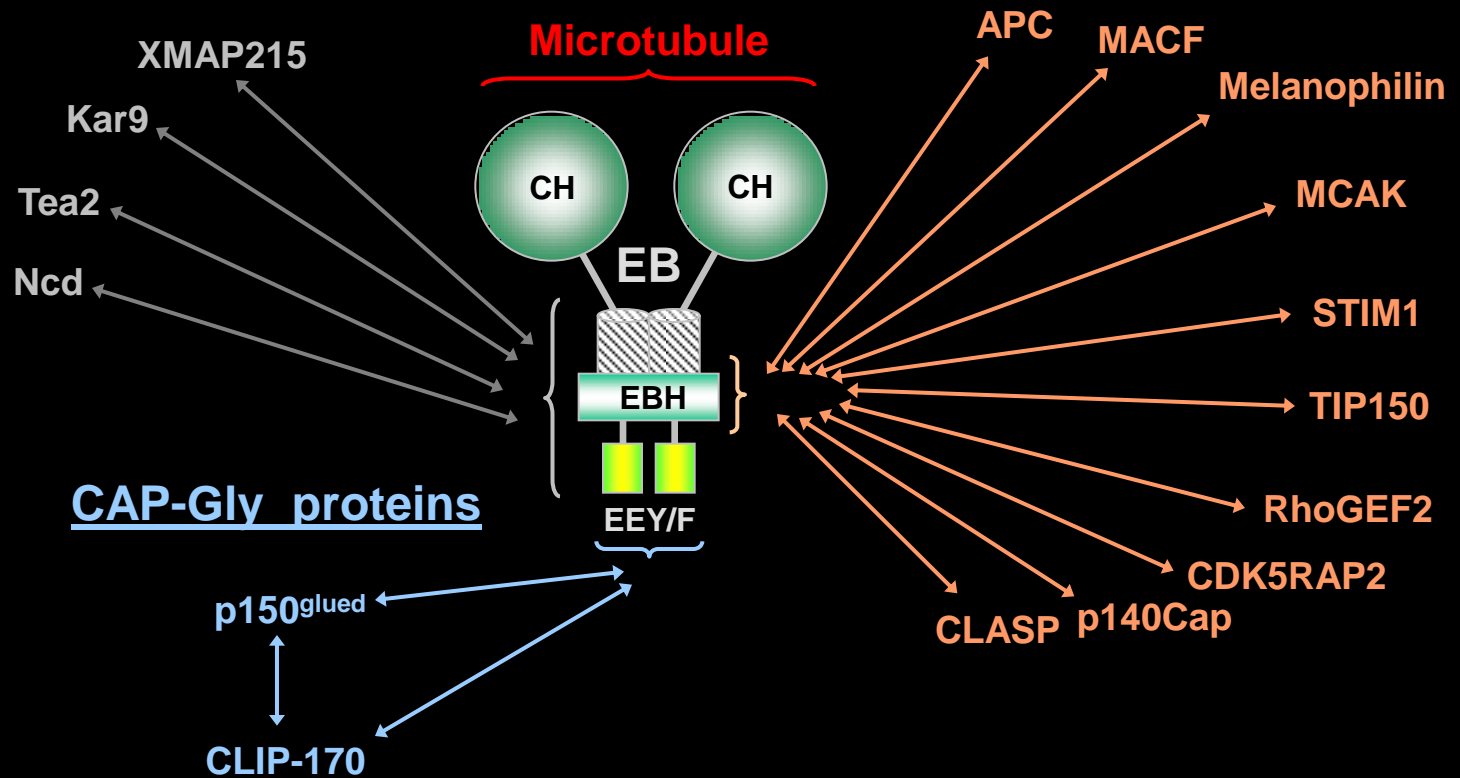
*Kris Leslie, Lukas Kapitein*



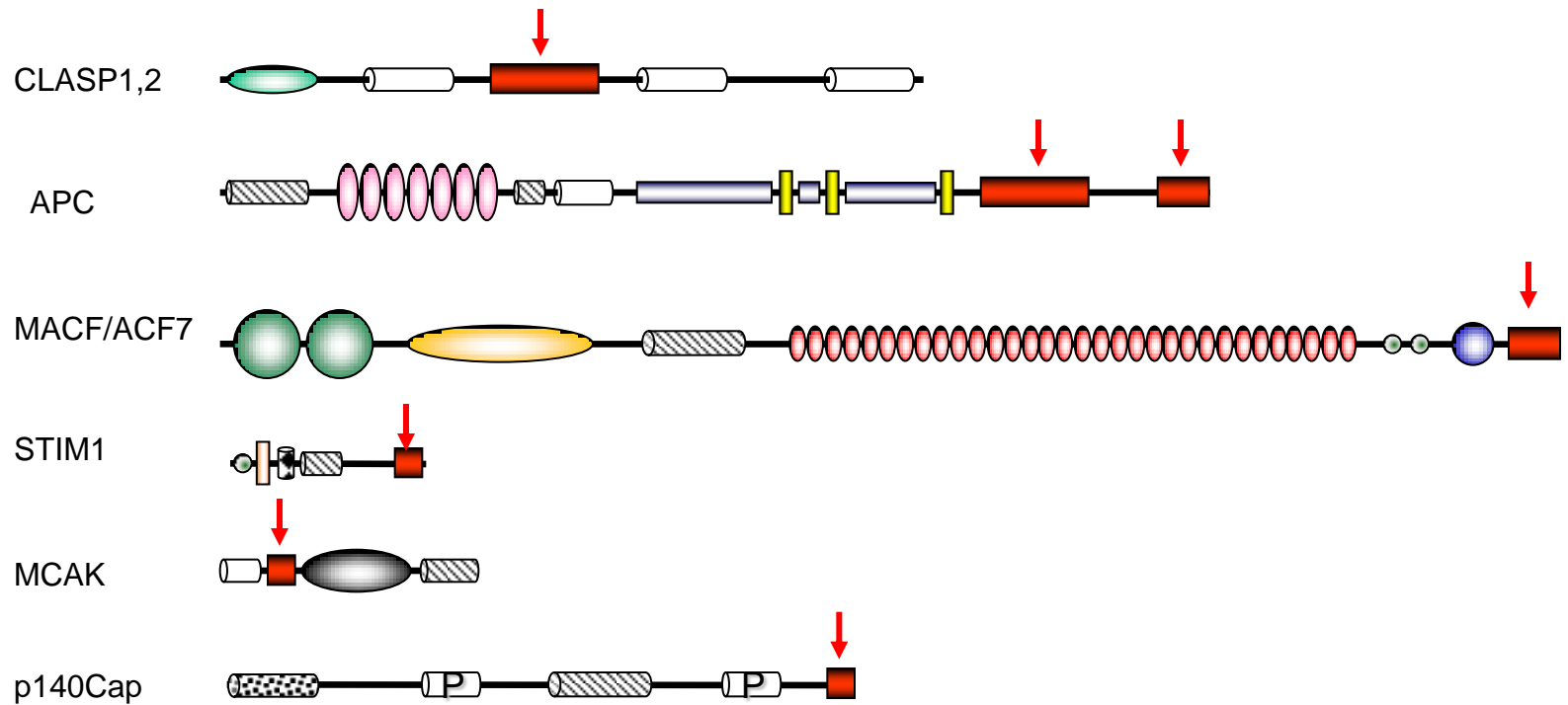
# EBs – the “core “ of +TIP network

## Proteins with yet unknown EB-binding mechanisms

## SxIP proteins



# +TIPs with basic/serine-rich regions



# SxIP motif is a common feature of +TIPs with basic/serine rich regions

hMACF2	PQTH <b>HRPTPRAGSRPSTAKPSKIP</b> TPQ <b>RKSPASKL</b> DKSSKR*
hAPC	FNYN <b>PSPRKSSAD</b> STSA <b>RPSQ</b> IP <b>TPVNNNT</b> KKR <b>DSKTD</b> ST <b>ES</b>
hCLASP1	GLTGGSS <b>RGPPVTPSS</b> EK <b>RSKIP</b> RSQGC <b>SRETS</b> PN <b>RIGLAR</b> RSQGC <b>SRETS</b> PN <b>RIGLAR</b> S <b>SRI</b> PR <b>PSMSQGC</b> RD <b>TSRE</b> SS <b>R</b>
CLASP2	TVSSGVQ <b>RVLVNSASAQ</b> K <b>RSKIP</b> RSQGC <b>SREAS</b> PS <b>RLSVAR</b> RSQGC <b>SREAS</b> PS <b>RLSVAR</b> S <b>SRI</b> PR <b>PSVSQGC</b> RE <b>ASRE</b> SS <b>R</b>
hMCAK	NLPLQ <b>ENV</b> TIQ <b>KQKRR</b> SVN <b>SKIP</b> AP <b>KE</b> SL <b>RSR</b> ST <b>RM</b> STV <b>SE</b>
hDDA3	<b>RLPRP</b> QGAA <b>AKSSSQLP</b> IP <b>SA</b> IP <b>RPAS</b> RM <b>PLTS</b> RS <b>VPPGR</b>
mSTIM1	<b>DPDTPSP</b> VGD <b>NRALQGS</b> RN <b>TRIP</b> HLAG <b>KKAMA</b> E <b>ED</b> NGS <b>IGE</b>
mMelan	AAL <b>RAAGLTVKPSGKPRKSG</b> IP <b>IFLPRVTEK</b> LD <b>RIPKTPP</b>

# Dimerization stimulates EB1-binding and plus end tracking of IP motif peptides

hMACF2-18

GS**R**PSTAK**P**SKIP**T**P**Q****R**KSPASK

monomer



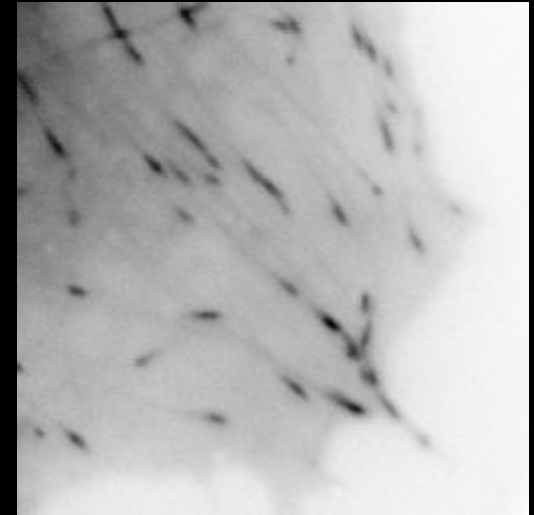
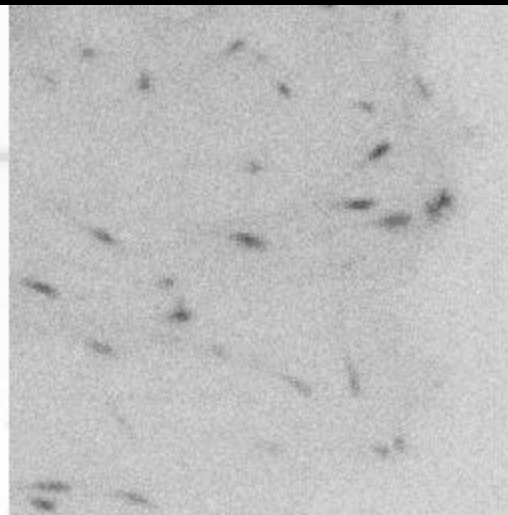
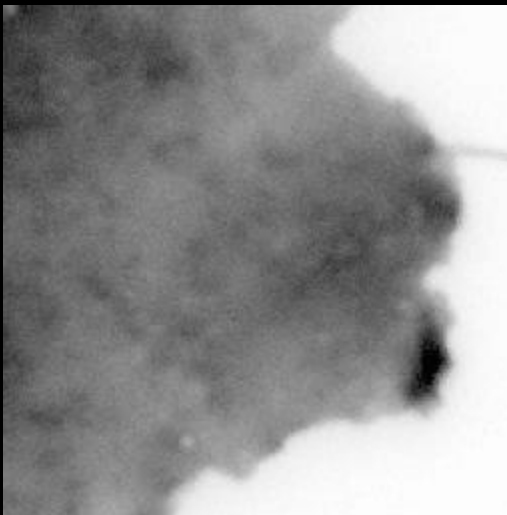
dimer



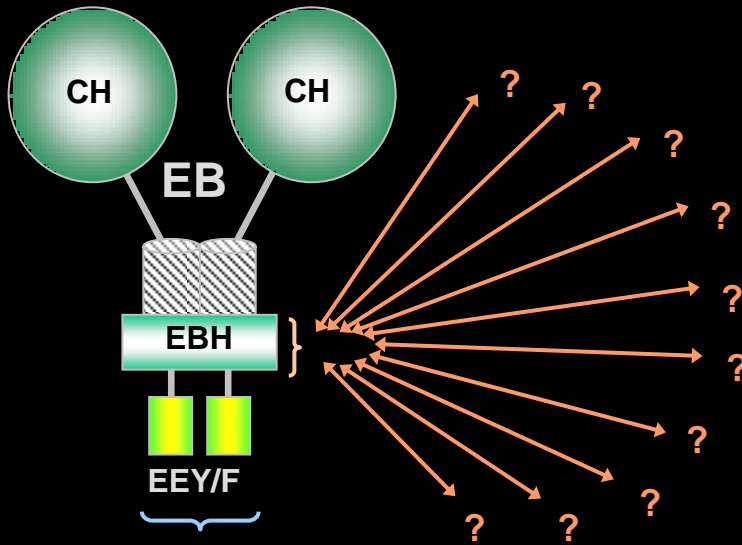
hMACF2-12

A**K**P**S**KIP**T**P**Q****R**K

dimer

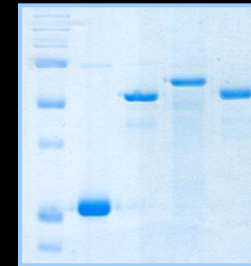


# Searching for new SxIP +TIPs



Bioinformatics  
approaches

GST-EB pull downs  
+ Mass Spec



# Bioinformatics prediction of SxIP motifs

		-5	SxIP-9AA	+5	
APC	2796	D	STSA R P S Q I P T P V N N N T K		2814
APC2	2075	R	T T S E S P S R L P V R A P A A R P		2093
CLASP1	711	T	P S S E K R S K I P R S Q G C S R E		729
CLASP1	734	R	I G L A R S S R I P R P S M S Q G C		752
CLASP2	487	S	A S A Q K R S K I P R S Q G C S R E		505
CLASP2	510	R	L S V A R S S R I P R P S V S Q G C		528
TIP150	916	S	V T A P R R S L L P A P K S T S T P		934
Dystonin	7543	R	P S T A K P S K I P T P Q R K S P A		7561
MACF1	5402	R	R G L N K P S K I P T M S K K T T T		5420
MCAK	91	Q	R R S V N S K I P A P K E S L R S		109
STIM1	635	A	L Q A S R N T R I P H L A G K K A V		653
p140Cap	1031	E	K P S A S R T S I P V L T S F G A R		1049
FGFR10P	165	T	S A Q T T P S K I P R Y K G Q G K K		183
Melanophilin	503	S	G K P R R K S N L P I F L P R V A G		521
DDA3	274	S	S Q L P I P S A I P R P A S R M P L		292
CDK5RAP2	929	T	N R E A K K S R L P I L I K P S R S		947

$x_1x_2$   $x_3$   $x_4x_5x_6$

$x_1-x_2$ -S/T- $x_3$ -I/L-P- $x_4-x_5-x_6$  9AA

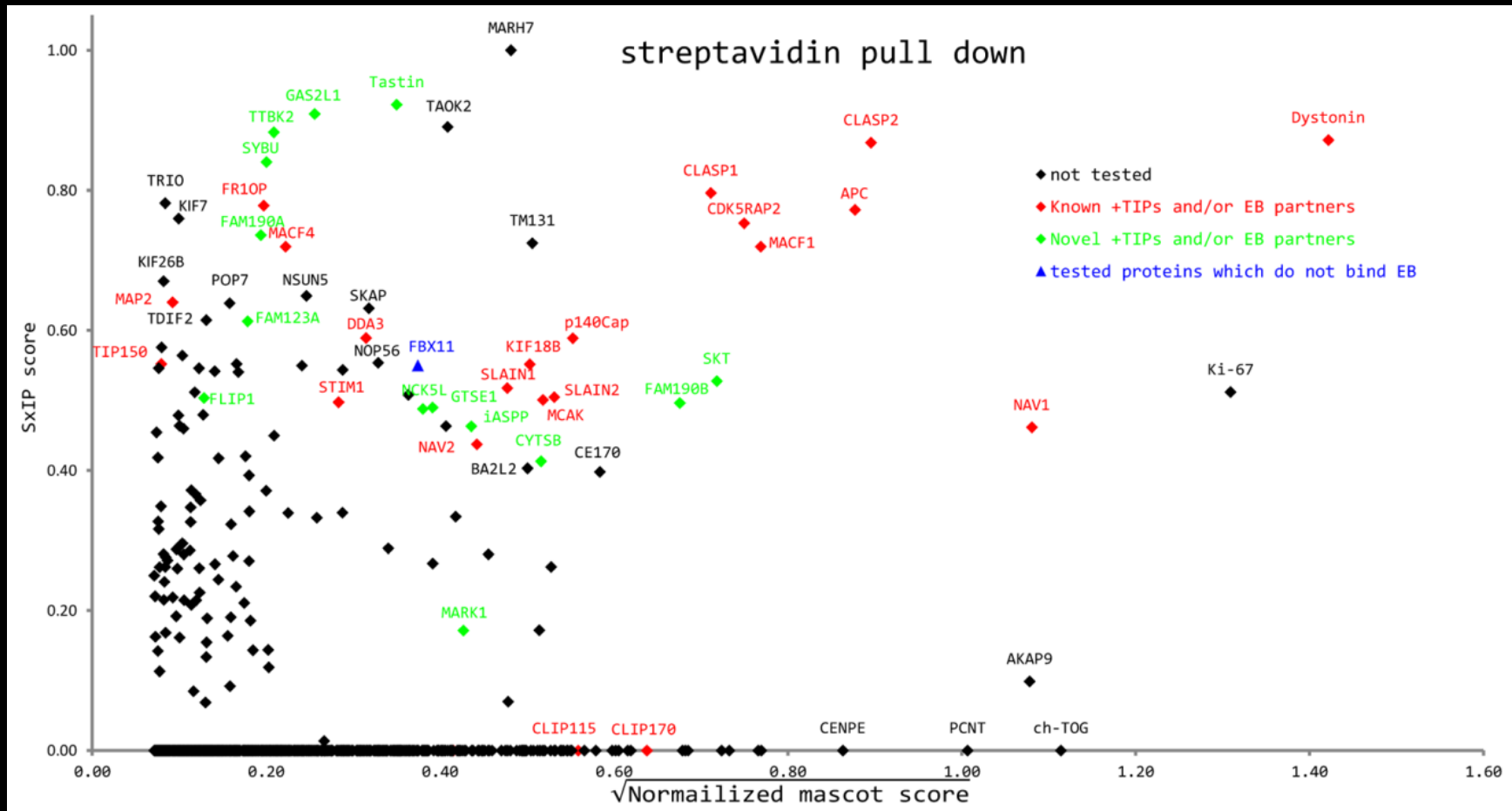
$x_1-x_4$ : at least one of them is R or K

$x_1-x_6$ : none of them are D or E

Folding and Conservation

833 proteins  
(~4%)

# Comparison between EB pull down and bioinformatics prediction



# Back-tracking +TIPs:

## DDA3 (proline/serine-rich coiled-coil 1)



CC SxIP



Regulated by p53/p73

*(Lo et al., Oncogene 1999; (Hsieh et al., Oncogene 2002)*

Binds to EB3

*(Hsieh et al., Oncogene 2007)*

Targets kinesin-13 KIF2A (MT depolymerase)  
to the spindle

*(Jang et al., JCB 2008)*

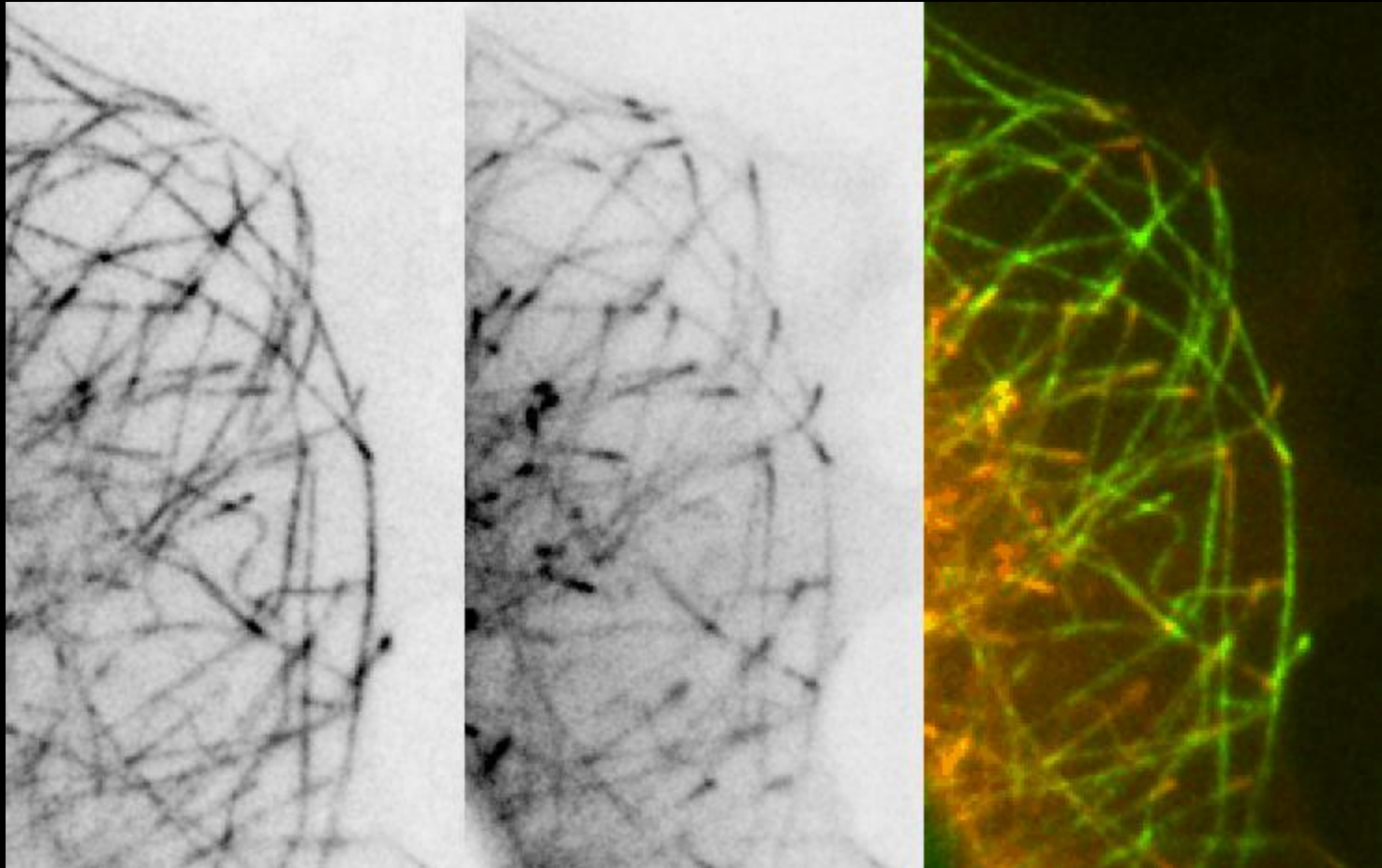


# Back-tracking +TIPs: DDA3

GFP-DDA3

EB3-RFP

GFP-DDA3/ EB3-RFP

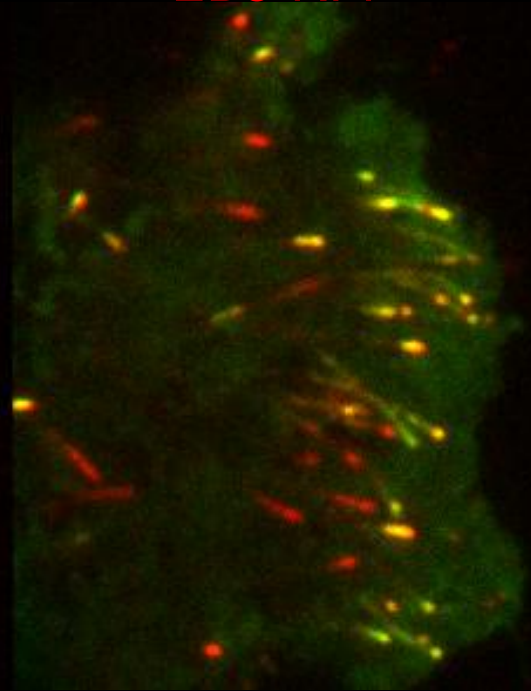
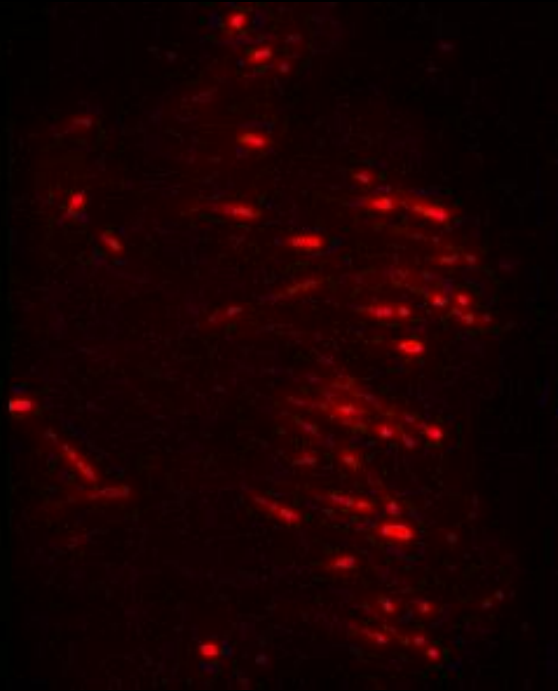
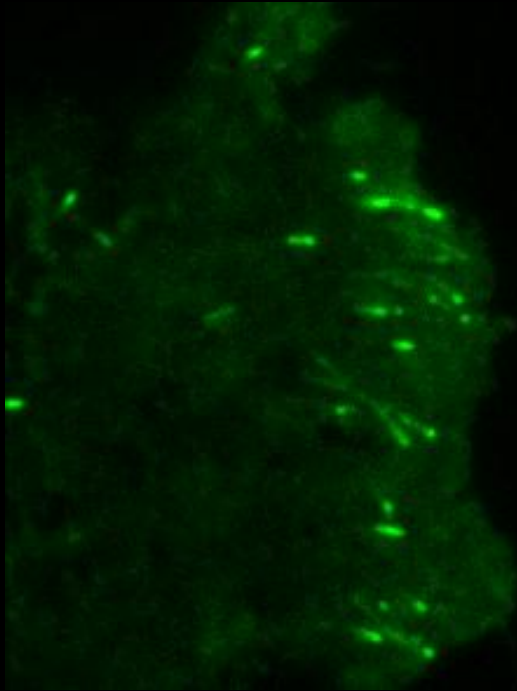


# Plasma membrane binding: FAM123A/AMER2 (homologue of WTX)

GFP-FAM123A

EB3-RFP

GFP-FAM123A /  
EB3-RFP



Membrane binding

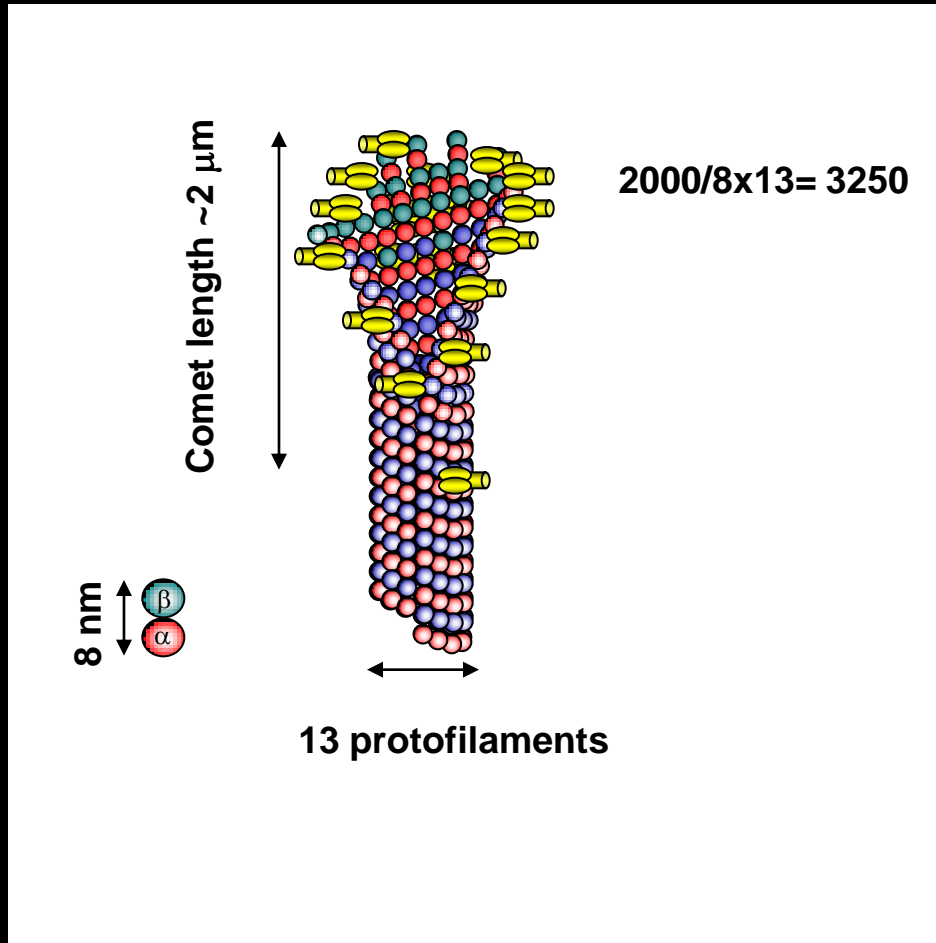
SxIPSxIP



WTX=AMER1 (Wilms Tumor gene on the X chromosome)  
Regulates Wnt signaling, binds to APC,  
Binds to PIP2 on the plasma membrane

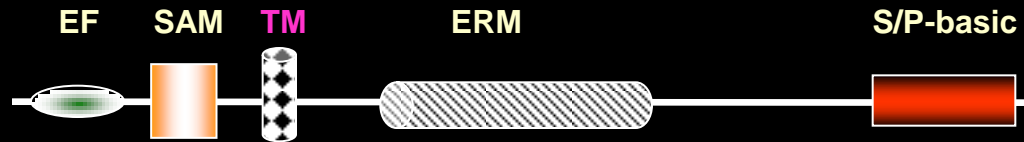
How many different proteins can bind to one microtubule tip at the same time?

# Growing Microtubule Tip



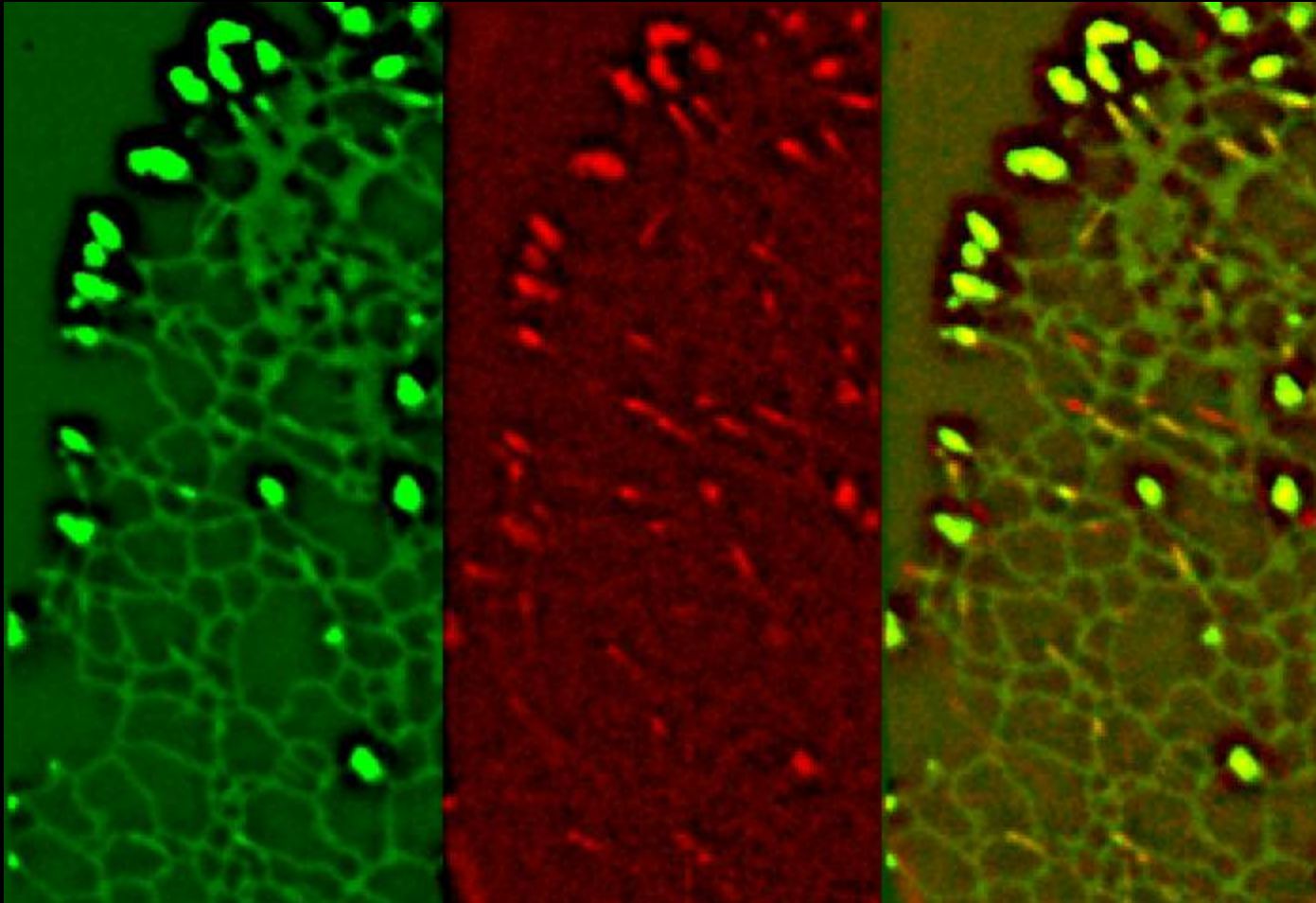
Are all growing microtubule tips  
in the same cell the same?

# Stromal Interaction Molecule: STIM



- STIM1 is a transmembrane protein, which localizes predominantly to the ER
- STIM 1 is as a sensor of ER luminal  $\text{Ca}^{2+}$  and is essential for store-operated  $\text{Ca}^{2+}$  entry
- Upon  $\text{Ca}^{2+}$  release from the ER, STIM1 locally activates  $\text{Ca}^{2+}$  channels in the plasma membrane

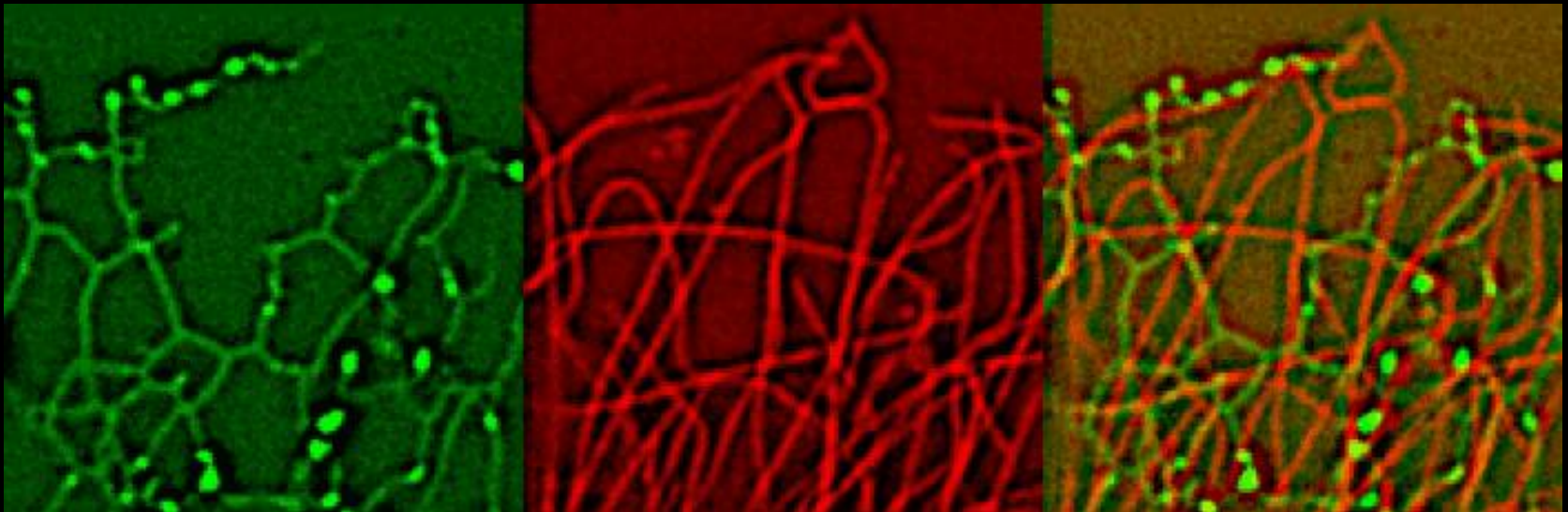
# GFP-STIM1 colocalizes with plus end marker EB3



GFP-STIM1 and EB3-mRFP  
in a MRC5 human lung fibroblast

1 s/ frame

# Tip Attachment Complex-mediated ER protrusion



GFP-STIM1 and mCherry-tubulin  
in a MRC5 human lung fibroblast

1 s/frame



What do +TIPs do?

# Regulation of microtubule dynamics

# SLAINs

- SLAIN1 and SLAIN2 are present in all vertebrates
- SLAIN1 was identified as a novel embryonic stem cell gene  
Hirst, CE et al., Dev Biol. 2006 May 1;293(1):90-103
- SLAINs were named after amino acid stretch in SLAIN1:

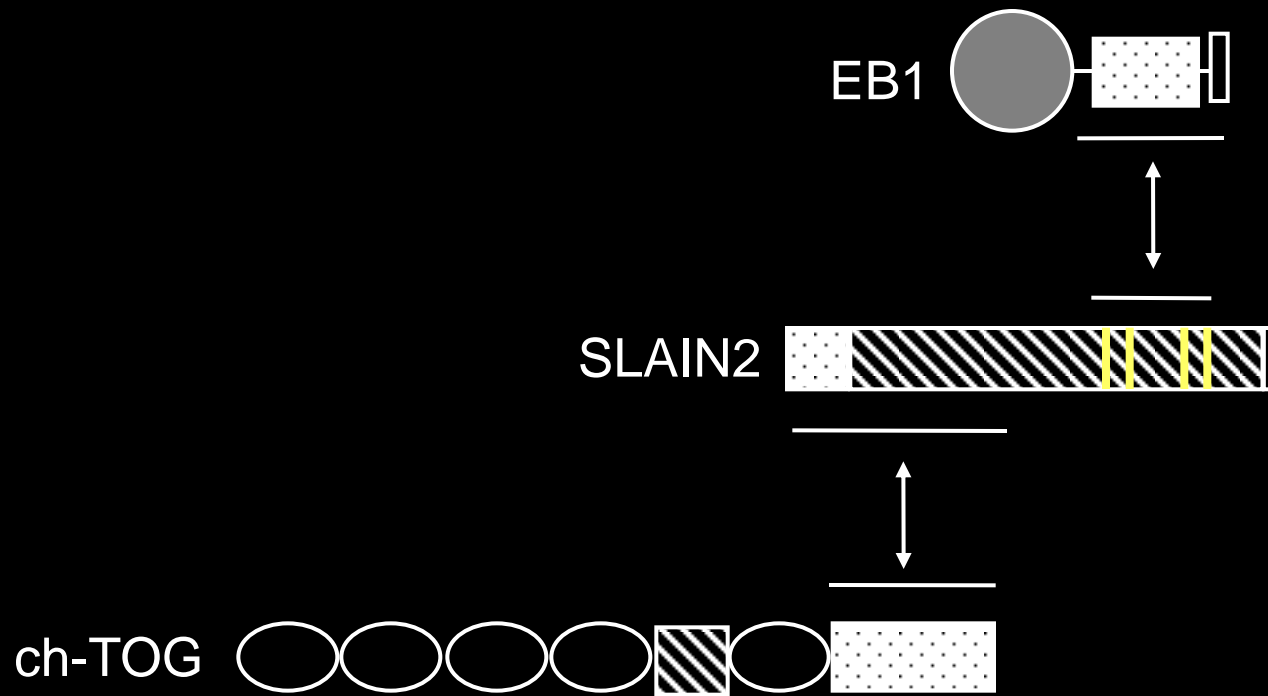
HsSL1 528-ALPRPSLAINGSN

HsSL2 466-GLPRPSAPSAGGI

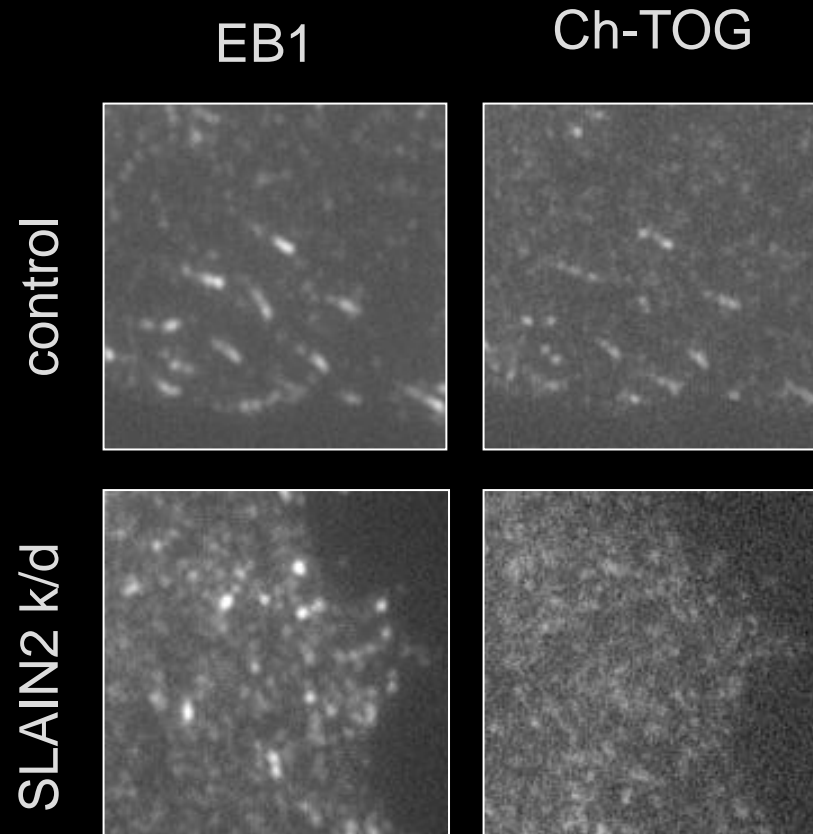
- Protein structure:



# SLAINs link EB1 to the microtubule polymerase ch-TOG

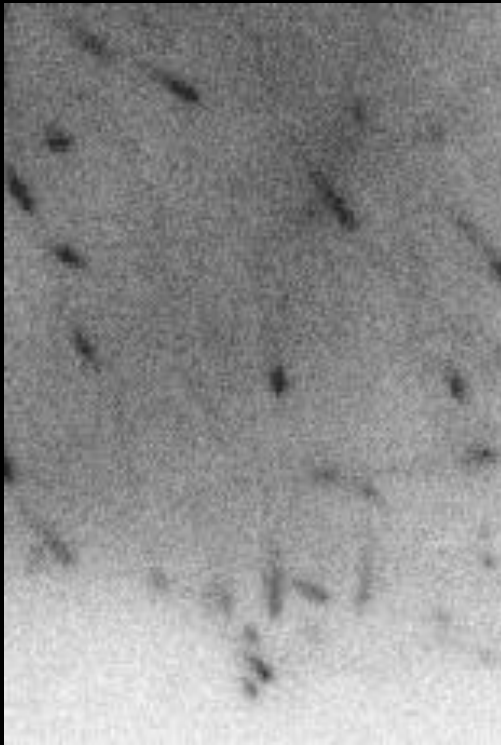


# SLAIN2 depletion causes loss of ch-TOG from microtubule tips

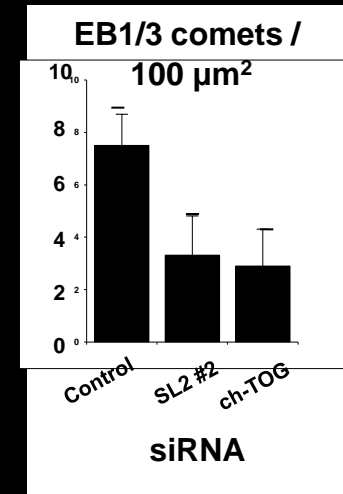


# SLAIN2 knockdown in HeLa cells

Control siRNA



SLAIN2 siRNA



Stable EB3-GFP HeLa cell line

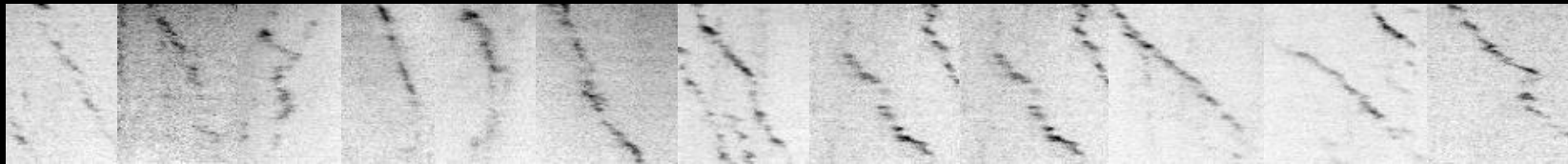
# Knockdown of SLAIN2 and ch-TOG gives a similar MT dynamics phenotype

time  
↓  
kymographs  
→  
distance

Control  
siRNA



SLAIN2  
siRNA

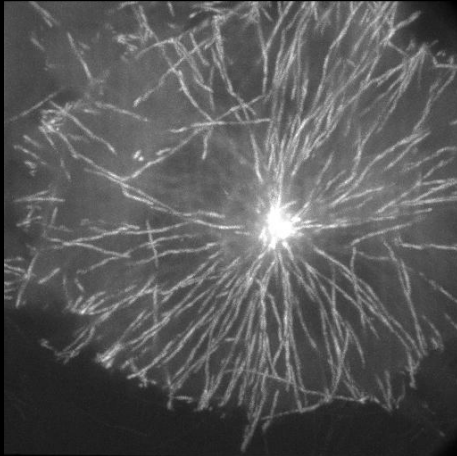


ch-TOG  
siRNA

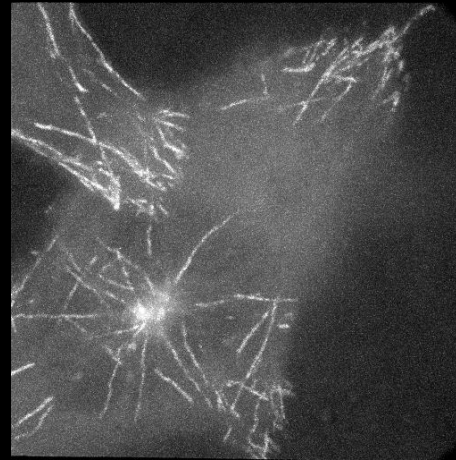


# SLAIN2 and ch-TOG depletion increases catastrophe frequency in CHO cells

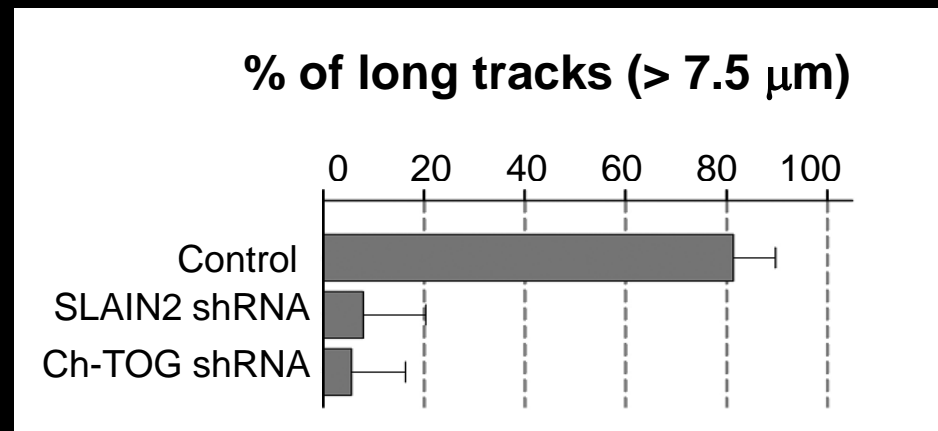
**Control shRNA**



**SLAIN2 shRNA**



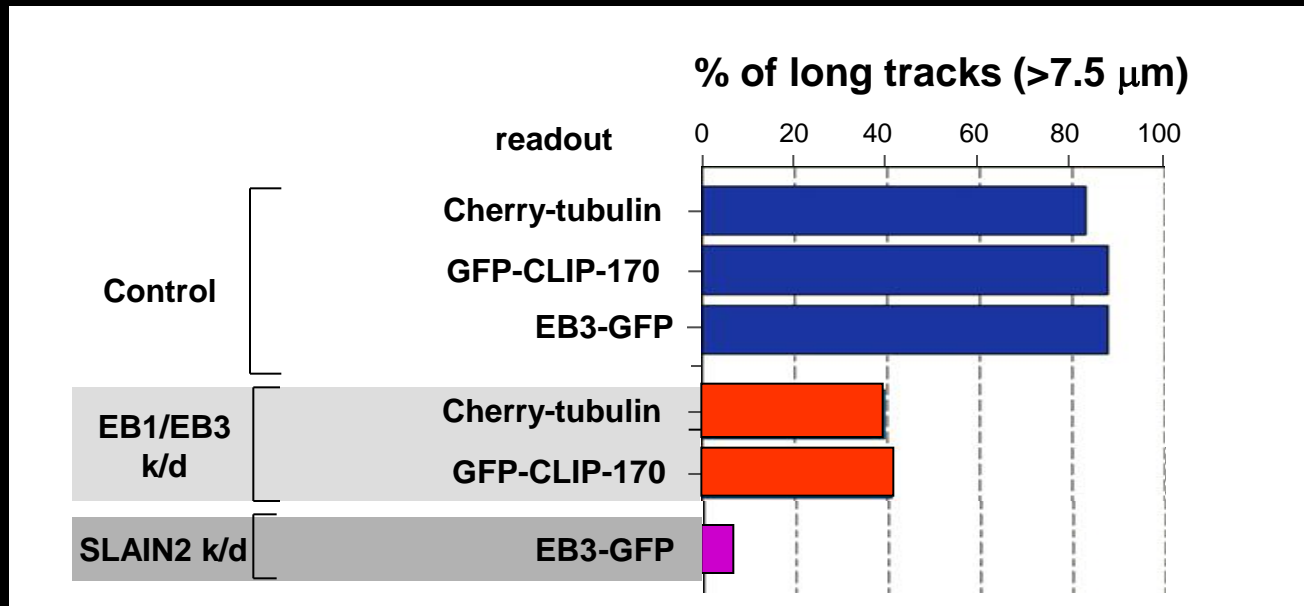
EB3-GFP,  
Projection analysis





SLAINs are part of a complex protein network that promotes microtubule growth

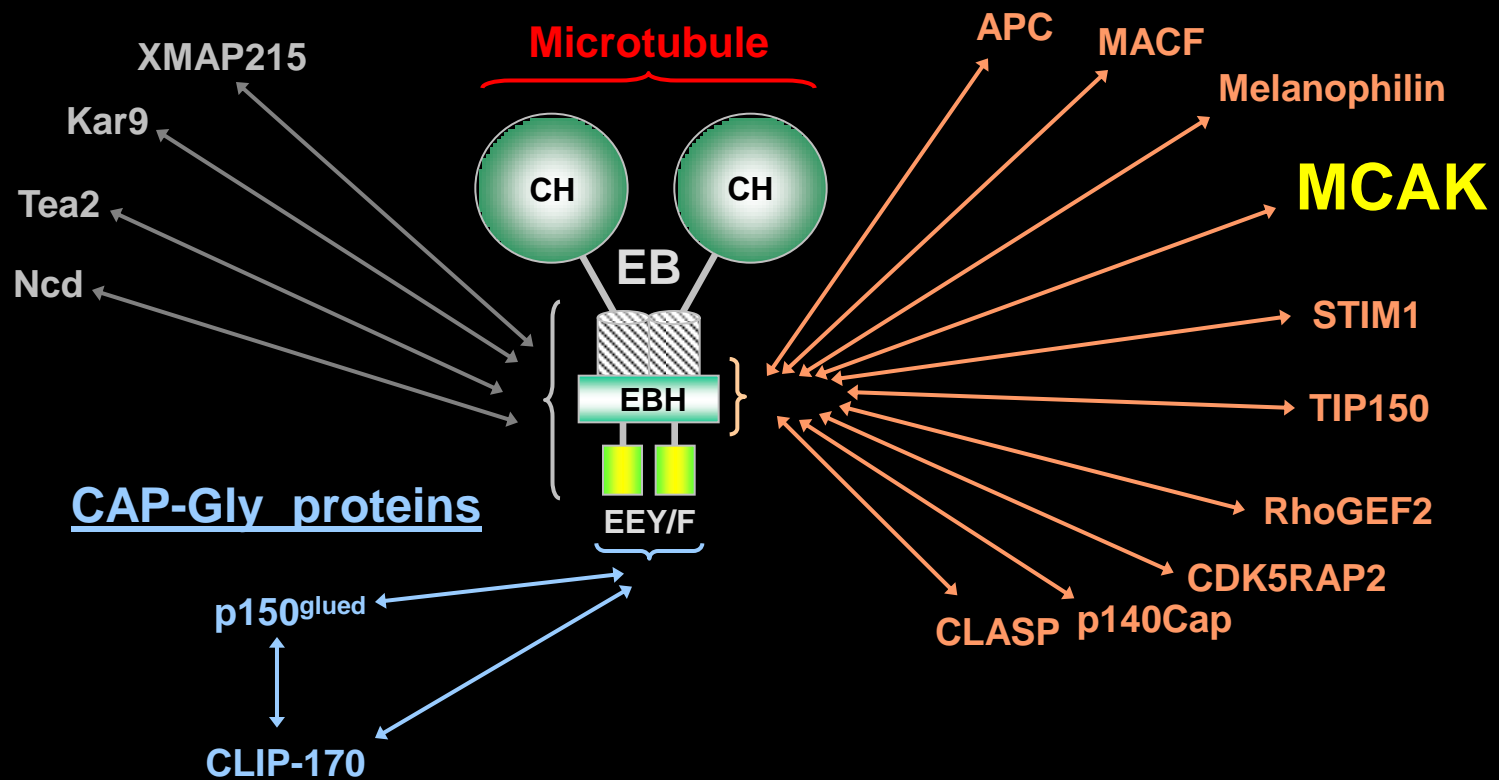
# EB1+EB3 depletion increases catastrophe frequency, but not as dramatically as SLAIN depletion



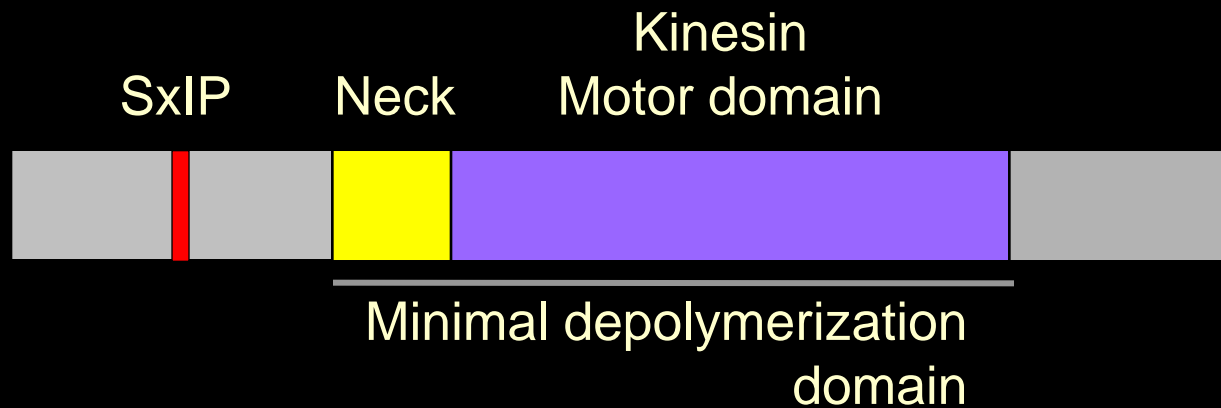
# EBs bind not only to MT stabilizers but also to destabilizers

## Proteins with yet unknown EB-binding mechanisms

## SxIP proteins



# MCAK is a microtubule depolymerase

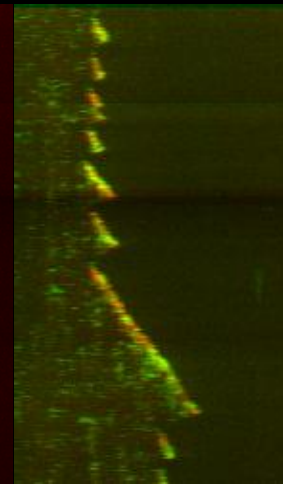
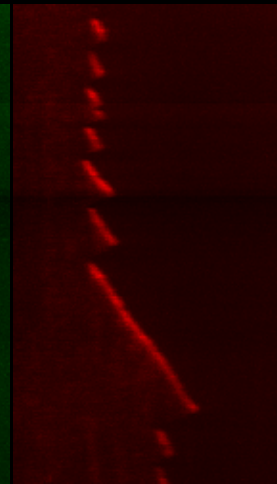
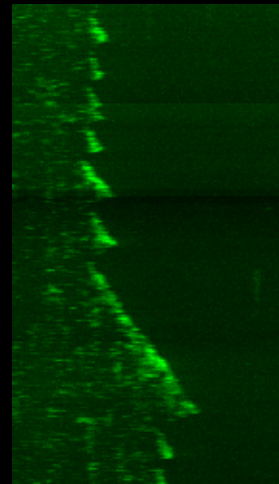


# GFP-MCAK + mCherry-EB3 (+ATP)

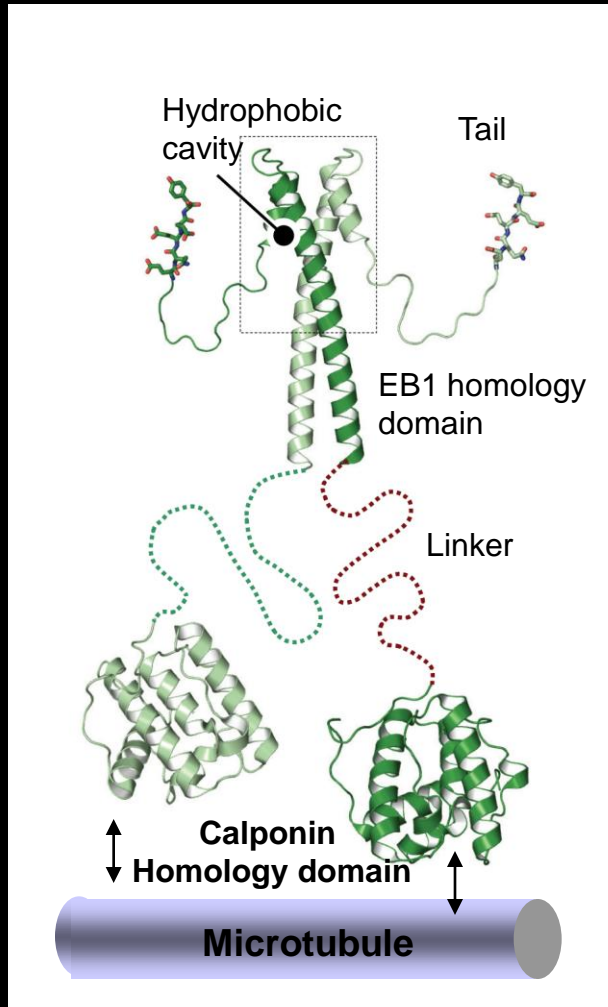


GFP-MCAK  
6 nM

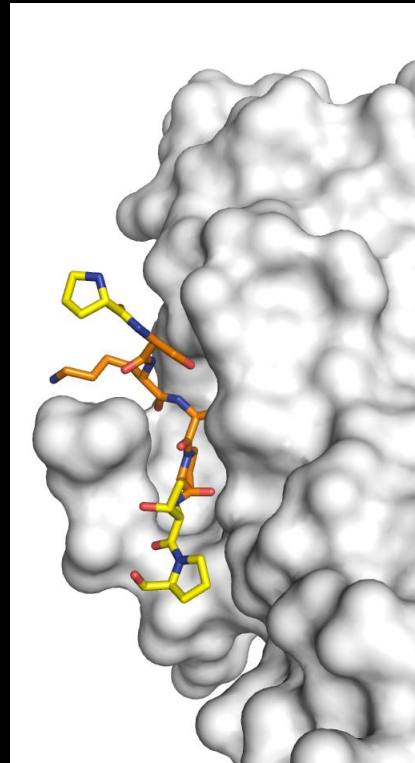
mCherry-  
EB3 300 nM



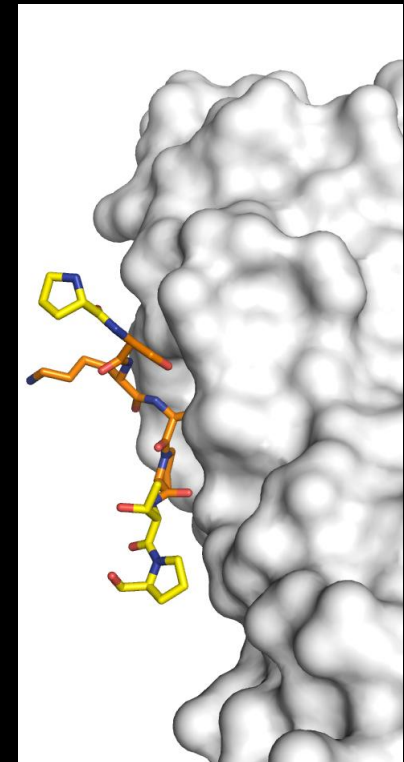
# The proximal part of EB1 tail participates in binding to SxIP peptides



EB1c  
-SxIP peptide

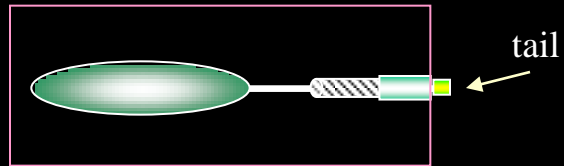


EB1c- $\Delta$  tail  
-SxIP peptide

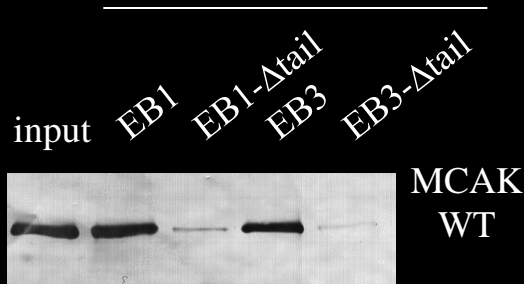


# EB3 lacking the tail does not bind to MCAK and does not target it to the tips

EB- $\Delta$ tail

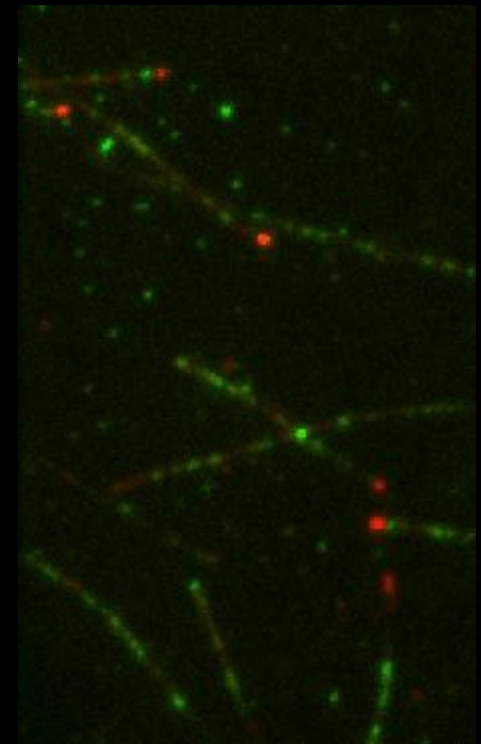


GST pull down



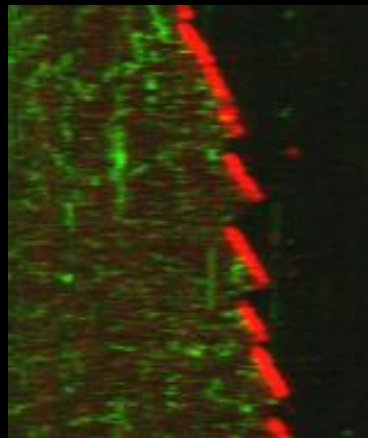
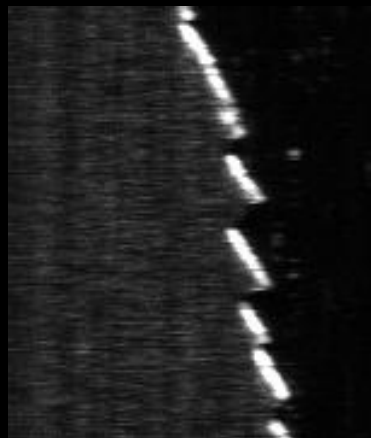
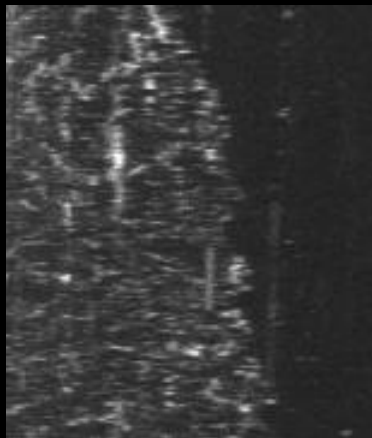
GFP-MCAK  
mCherry-EB3  $\Delta$ tail

ATP



GFP-MCAK  
12 nM

mCherry-EB3  
 $\Delta$ tail (75 nM)



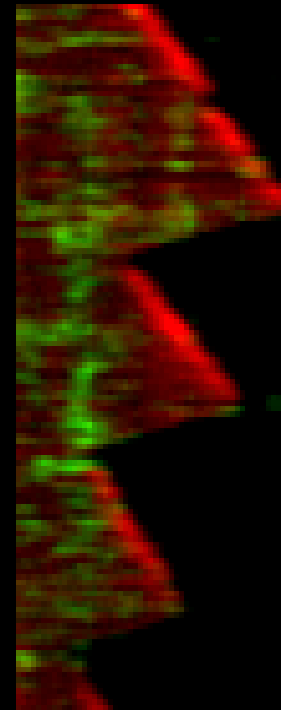
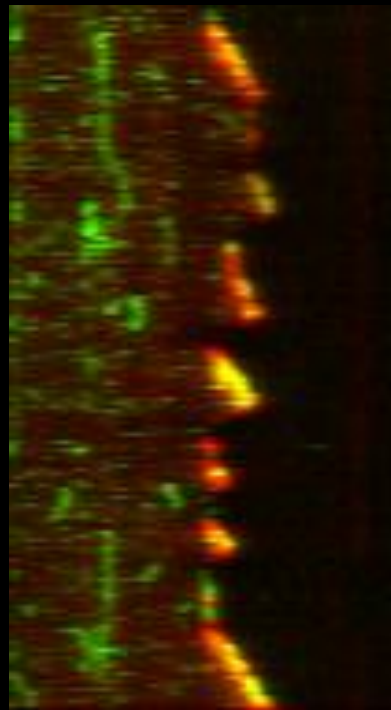
# Targeting to microtubule tips by EB3 promotes MCAK-mediated catastrophe induction

**GFP-MCAK**  
**6 nM**

**GFP-MCAK**  
**24 nM**

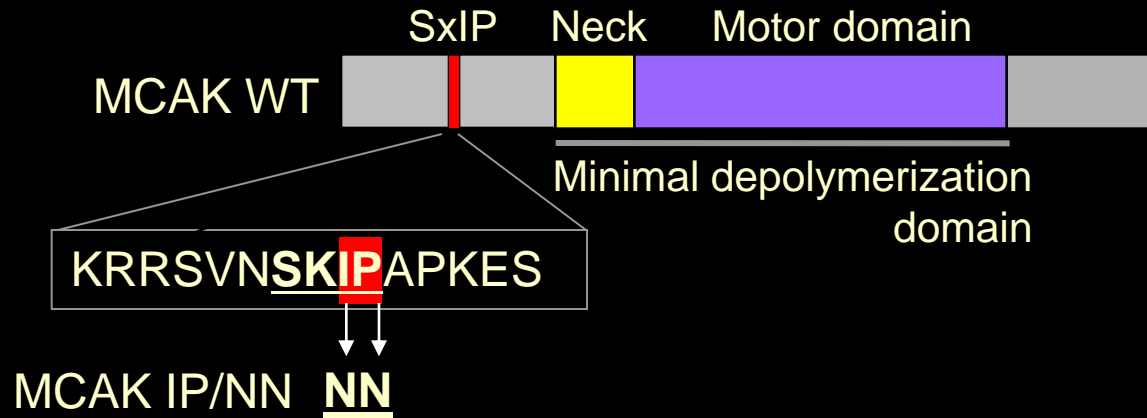
**mCherry-EB3**  
**75nM**

**mCherry-EB3 $\Delta$ T**  
**75 nM**



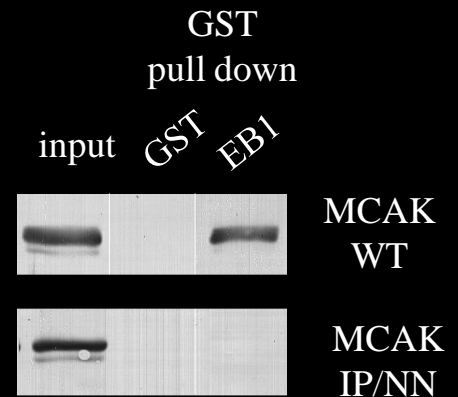
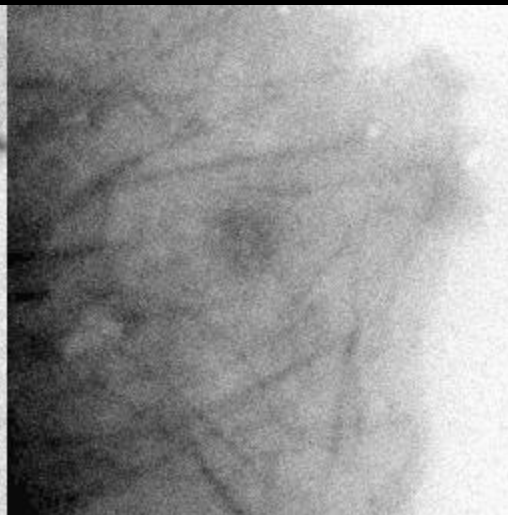
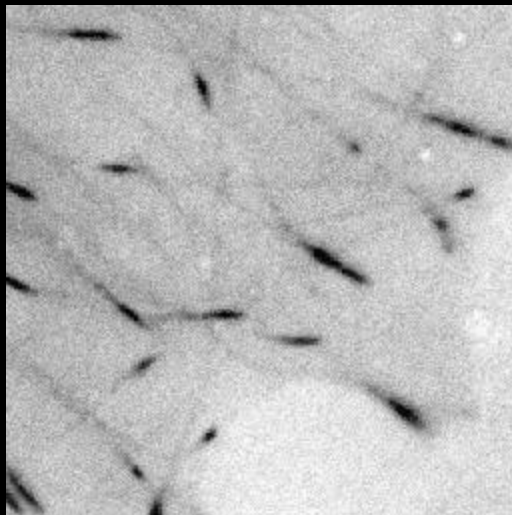


# IP->NN mutation in MCAK abolishes plus end tracking in cells

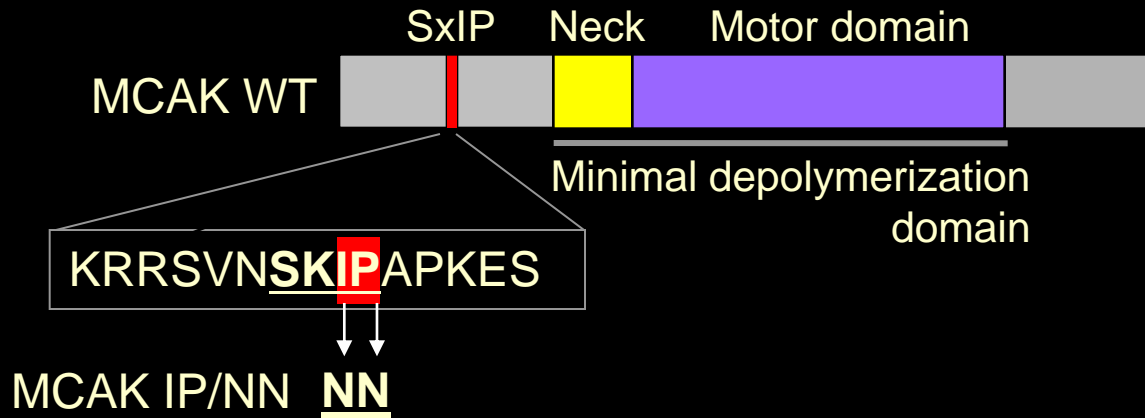


MCAK WT

MCAK IP/NN

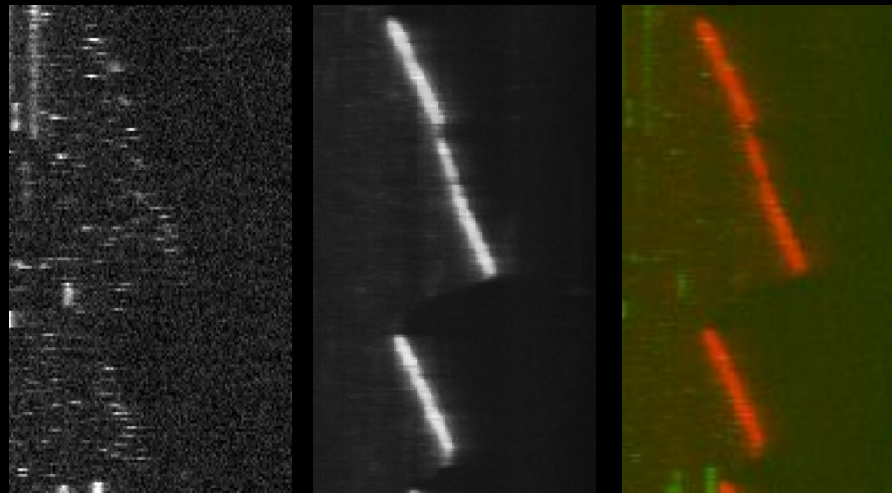


# IP->NN mutation in MCAK abolishes plus end tracking in vitro



GFP-MCAK  
IP/NN

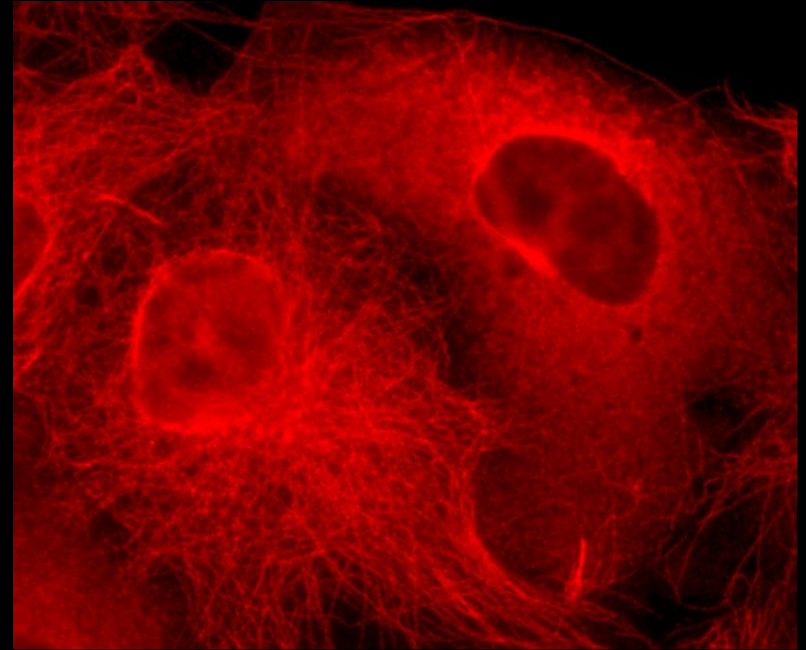
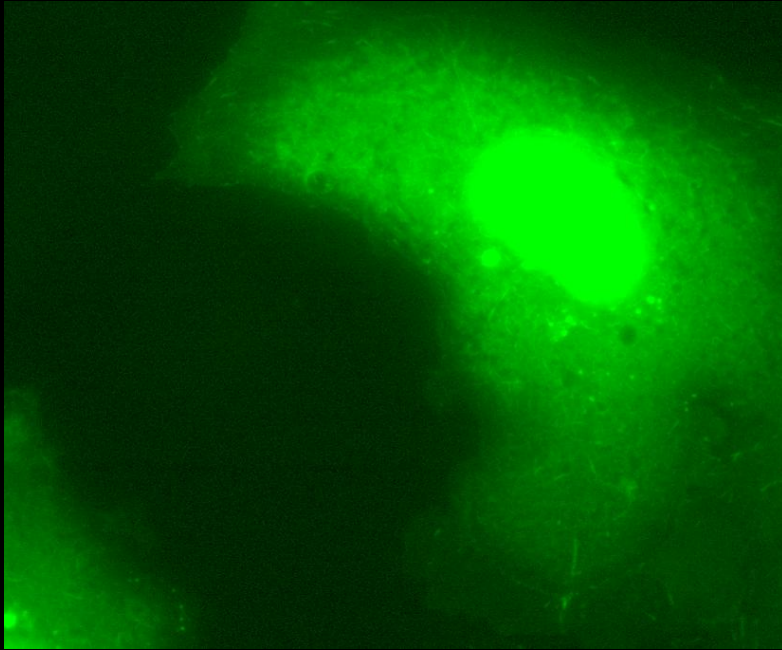
mCherry-EB3



# MCAK is a microtubule depolymerase

**GFP-MCAK**

**$\beta$ -tubulin**



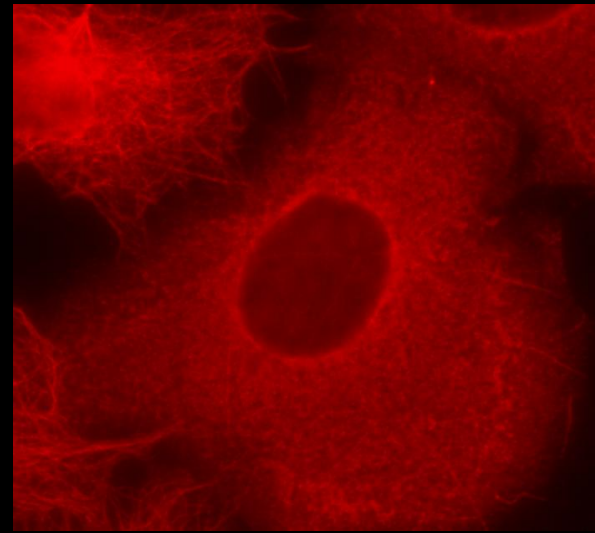
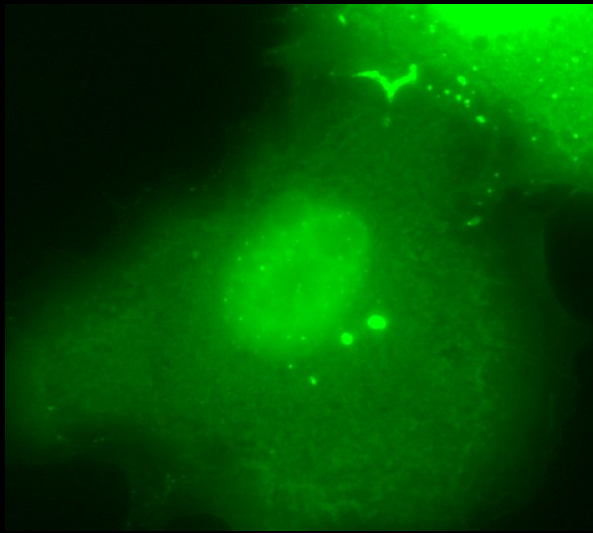
Does plus end targeting enhance or inhibit depolymerization activity?

# MCAK IP->NN mutant depolymerizes microtubules less efficiently

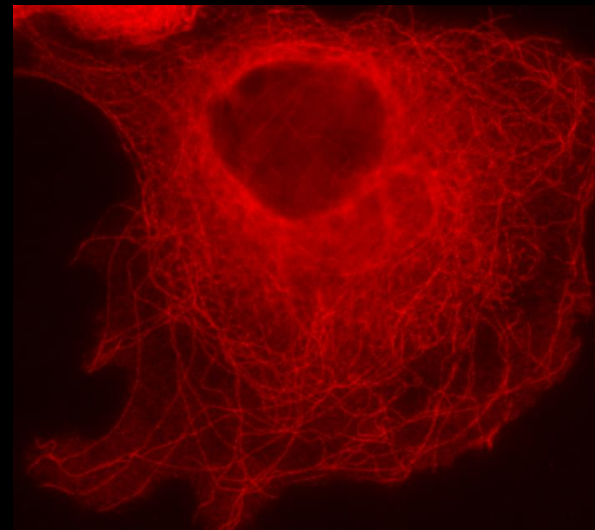
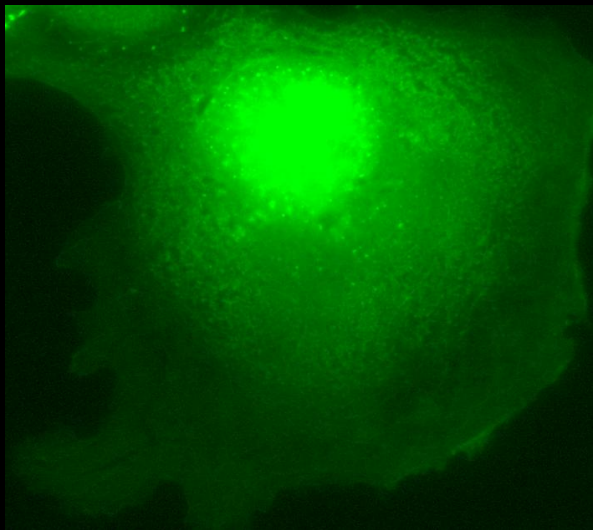
**GFP-MCAK**

**$\beta$ -tubulin**

**MCAK WT**



**MCAK IP/NN**



EB-dependent targeting of MCAK to  
microtubule tips makes it a more potent  
catastrophe inducer

A complex and flexible network of  
microtubule tip-interacting proteins and their  
partners controls the dynamics of individual  
microtubule ends

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