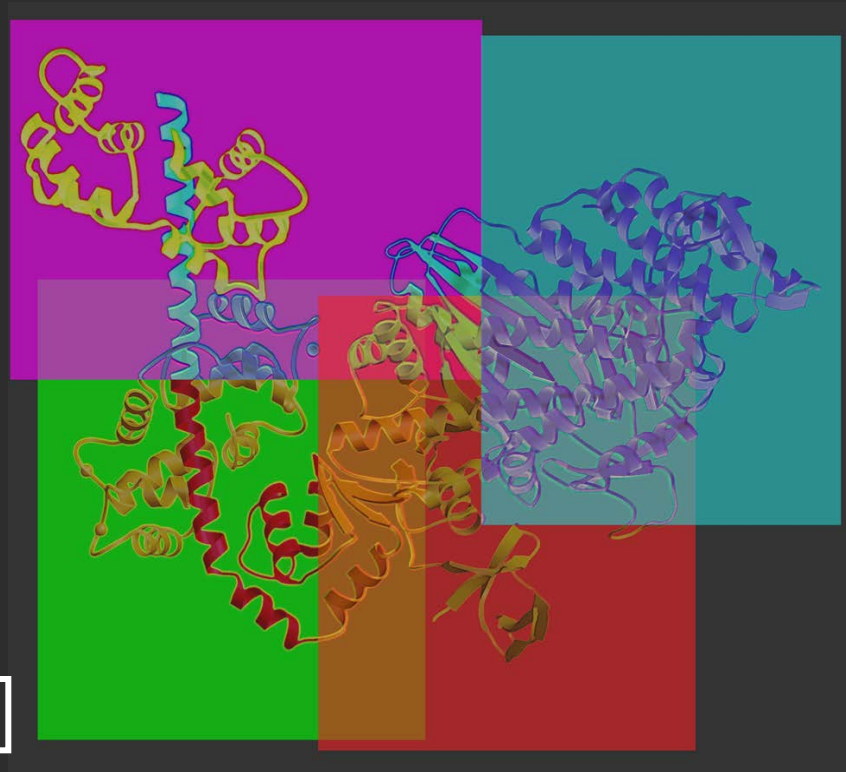


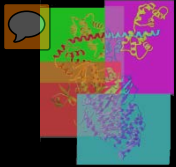
Défis et succès dans l'étude de la production de force et du rôle cellulaire des nanomoteurs myosines.



The Structural Motility Group



*Colloque annuel - ITMO Bases moléculaires et structurales du vivant, Paris, France.
Anne Houdusse – 24th of May 2013*

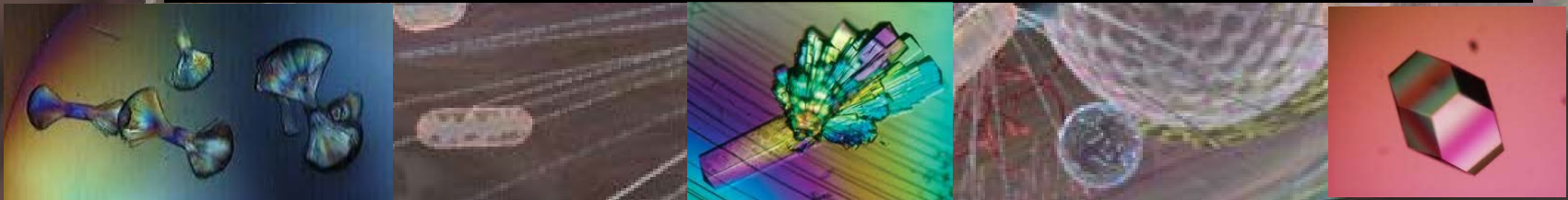


The cytoskeleton, a dynamic city plan for the cell

Molecular motors are essential for cell polarity and division

Cellular traffic – cell division – cell migration

« Seeing is necessary for understanding »
Our goal : Visualize the motor conformational changes
necessary for function and regulation



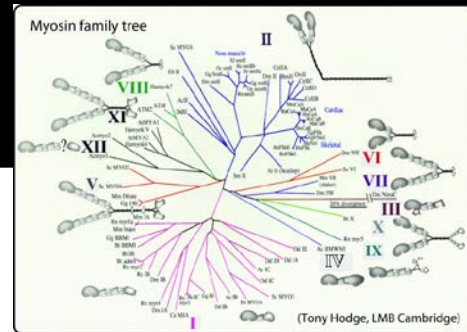
**Molecular Understanding of
Transport and Tension Generation
by Molecular Motors**

The myosin superfamily

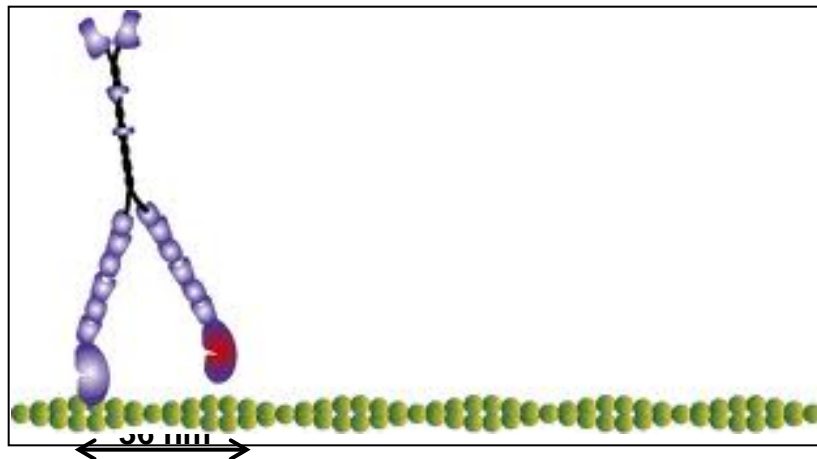
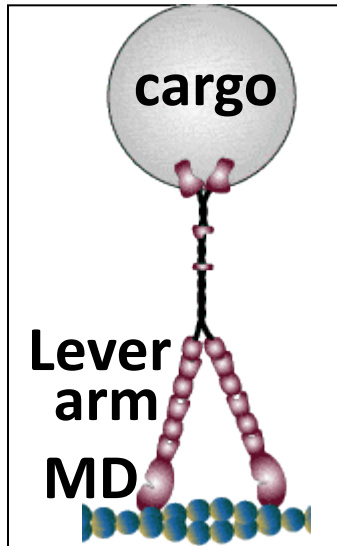
Myosin motors

Actin-based molecular motors

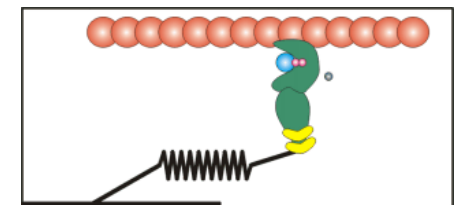
How do they convert chemical energy into force production



Myosin V steps on actin



Powerstroke



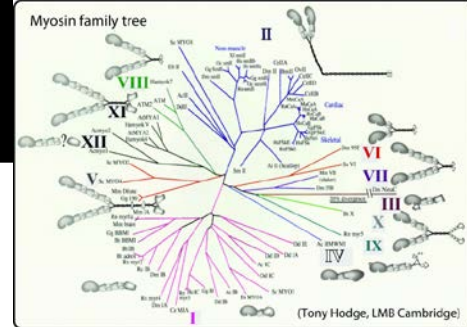
The myosin superfamily

Myosin motors

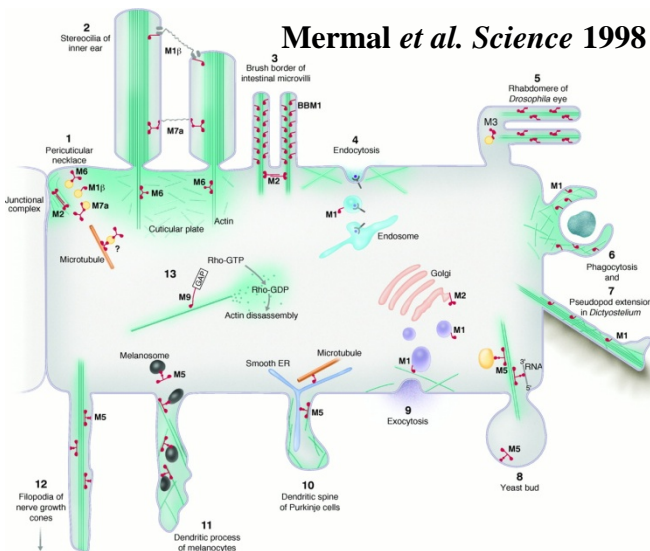
Actin-based molecular motors

How do they convert chemical energy into force production

How do they tune their activity for different cellular functions



Mermel et al. Science 1998



Various myosins can either contract rapidly or hold force

Actin filament contraction

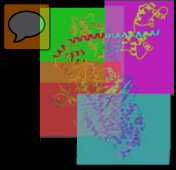
Molecular transporters of cargoes in the cell

Tension sensors

Anchoring function - Dynamic tethers

Role in membrane deformation and fission

Sequence differences can tune motor activity – or impair the motor



OUTLINE

**Myosin motors - force production, regulation,
cellular roles :**

**What is currently known
for force production by the myosin superfamily.**

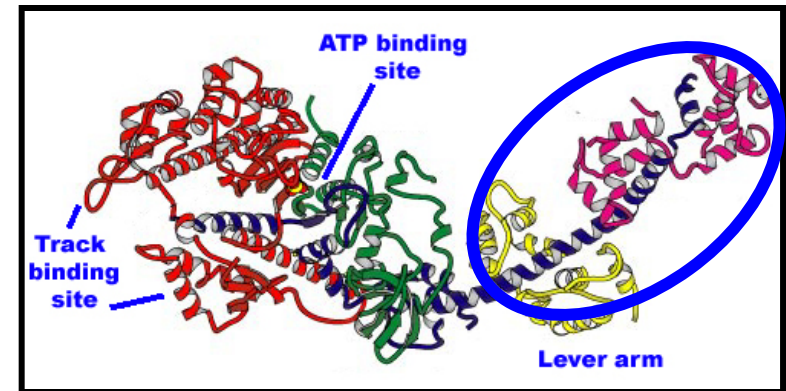
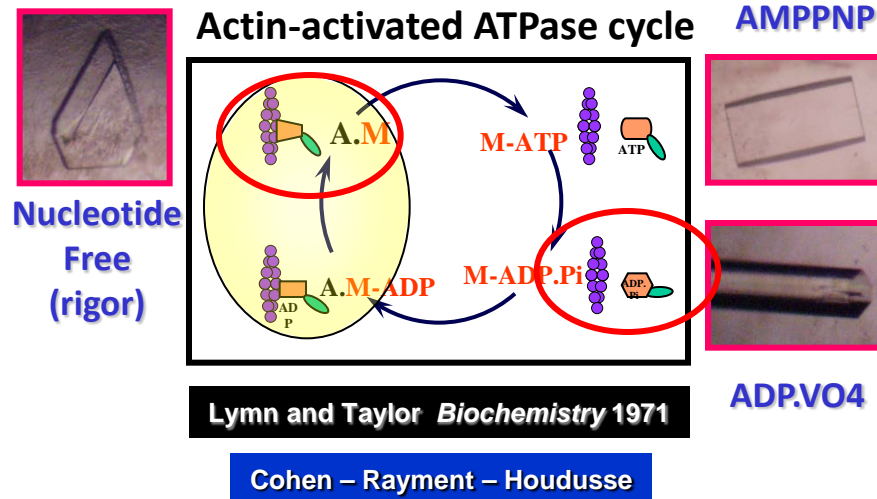
Testing the theory with a reverse motor

Current challenges

Allostery, basis to convert chemical energy into force production

Myosin motors

Myosin II MD + lever arm = 125 kDa



Rayment et al. Science 1993

– Allostery –

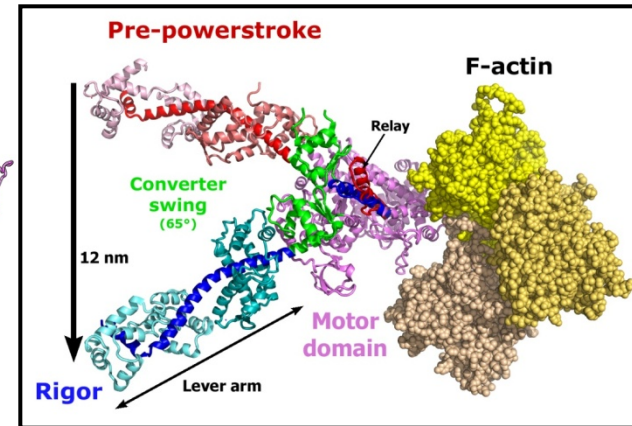
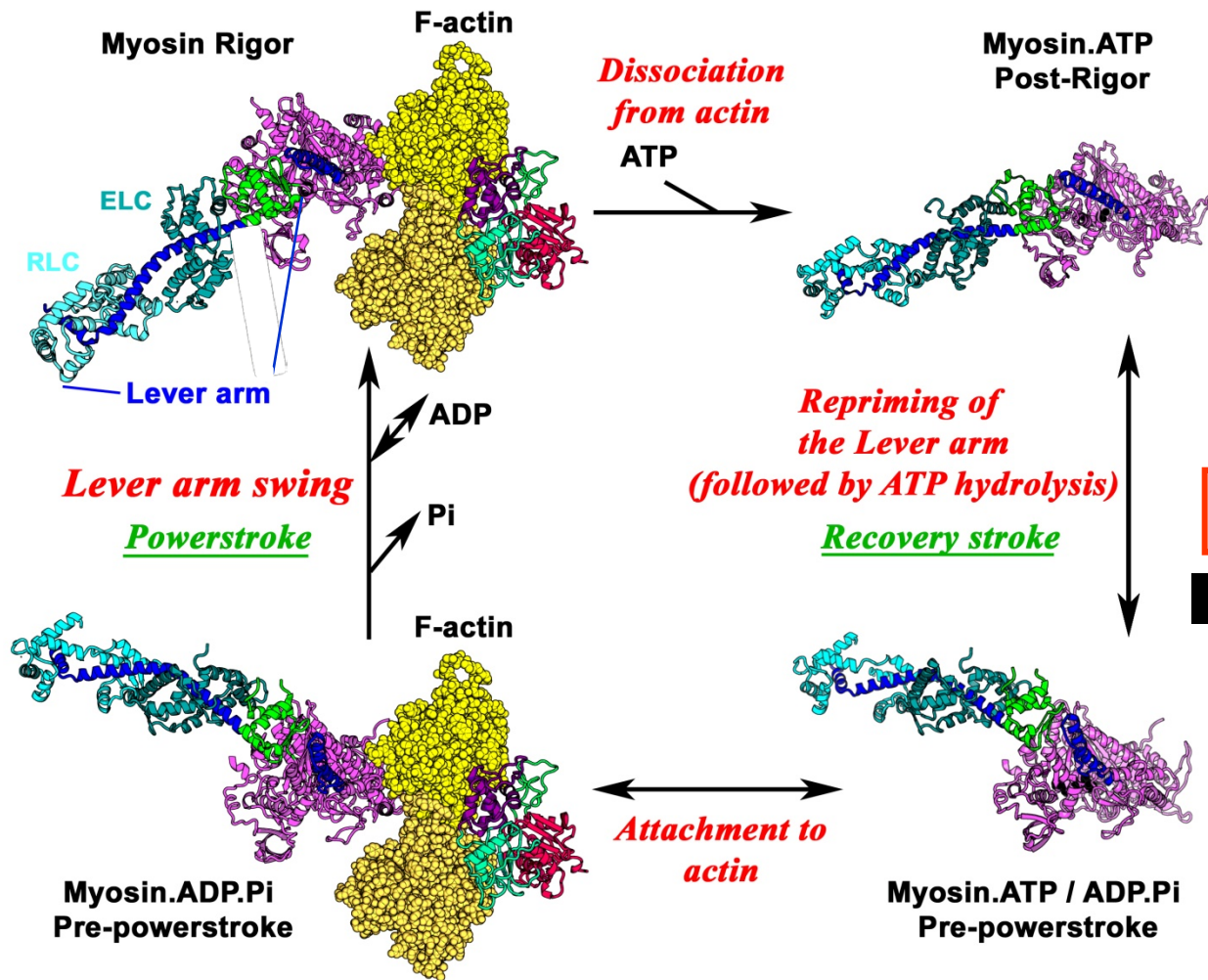
Communication across the enzyme at several nm distances

6 nm actin binding site / lever arm – 3.5 nm active site / lever arm

Changes in the three allosteric sites must be precisely synchronized

The simplified actomyosin cycle

How ATP hydrolysis is converted in mechanical energy



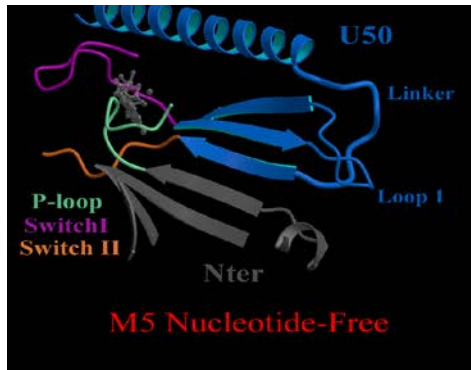
Swinging lever arm theory

Holmes & Geeves 1999 *Ann Rev Biochem* 68:687

Principle of force production:
an extended lever arm amplifies
the conformational changes
of the MD

Rotation of the
converter/lever arm

Long range pathways of
communication
Within the motor



**Twisting of the central
beta sheet
controls cleft closure
and actin affinity**

Transducer

Transducer



Coupling between nucleotide- and actin- binding sites

Detachment from the actin track upon ATP binding

Coureux et al. 2003 *Nature* 425:419-423.

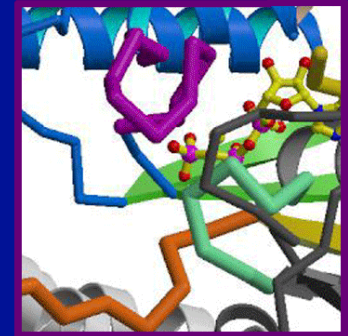
Coureux et al. 2004 *Embo J.* 23:4527-37.

Cecchini, Houdusse, Karplus. *Plos Comput Biol* 2008.

N.F → ATP

2-10 ms

Active Site



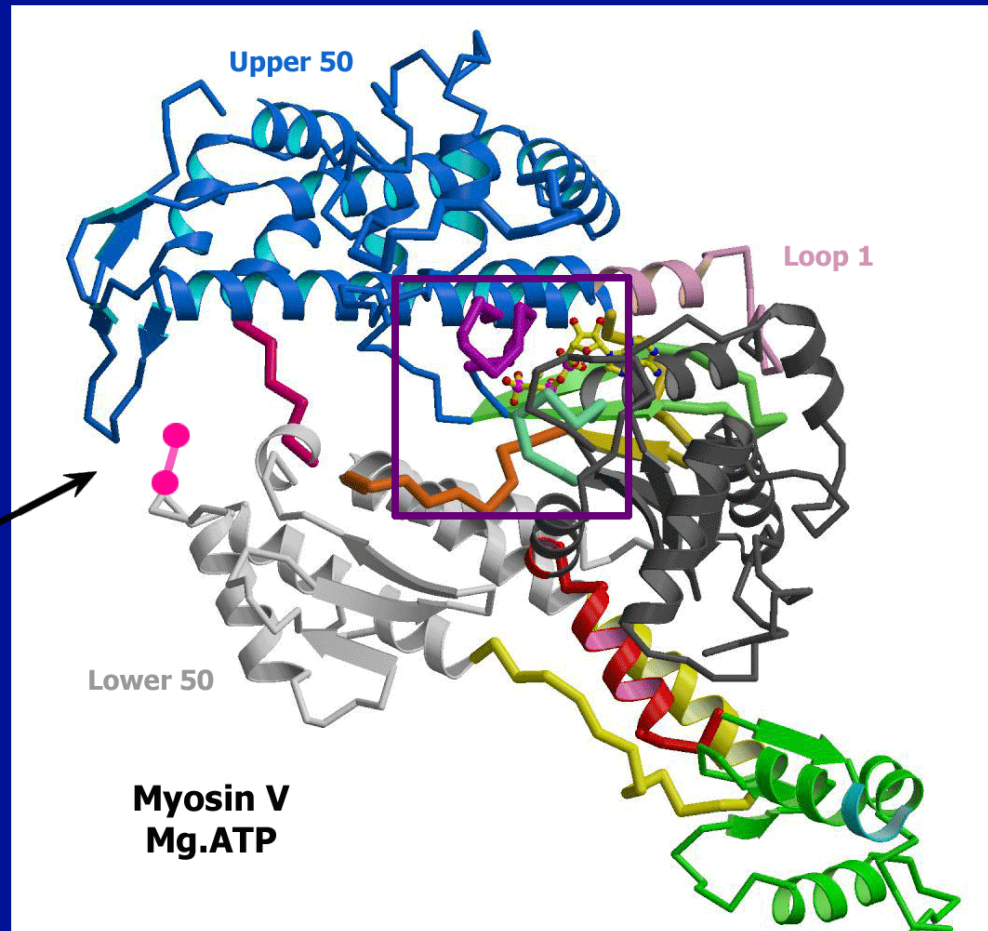
**Switch I
near**

**Switch II
P-loop**

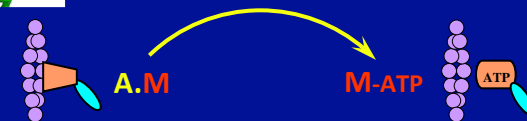
**Weak
Actin binding
Interface**

**50 kDa Cleft
Open**

**Total cleft closure
in the rigor state**



These large scale rearrangements are largely encoded in the low-frequency normal modes of the motor. The transition requires local rearrangements combined with these vibration modes.



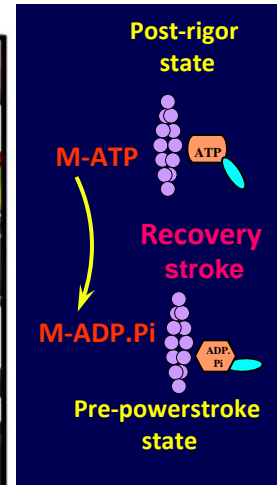
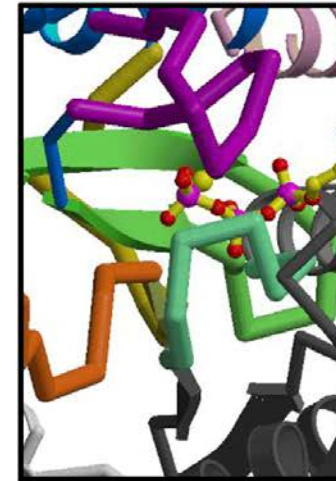
The recovery stroke promoting ATP hydrolysis

ATP ↔ ATP ↔ ADP.Pi

1-60 ms

Repriming linked to hydrolysis

MgATP

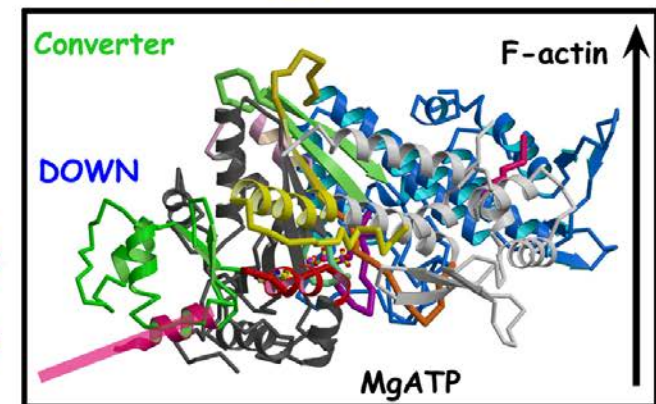


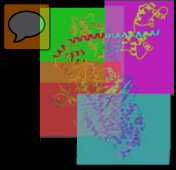
Backdoor
OPEN

Switch II
out

Switch II
Relay
SH1 Helix

Converter
DOWN





OUTLINE

**Myosin motors - force production, regulation,
cellular roles :**

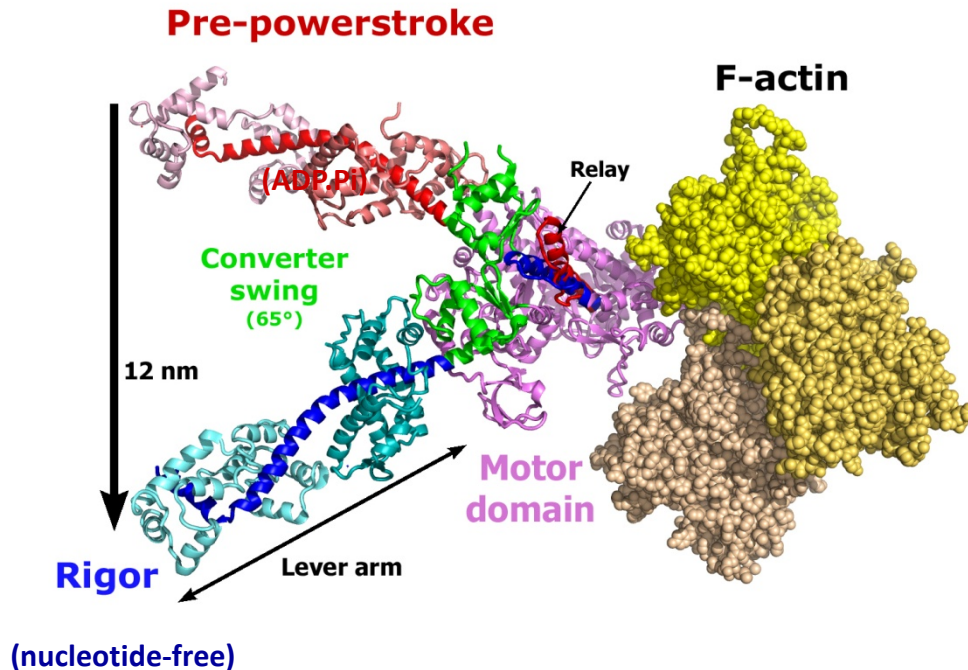
What is currently known
for force production by the myosin superfamily.

Testing the theory with a reverse motor

Current challenges

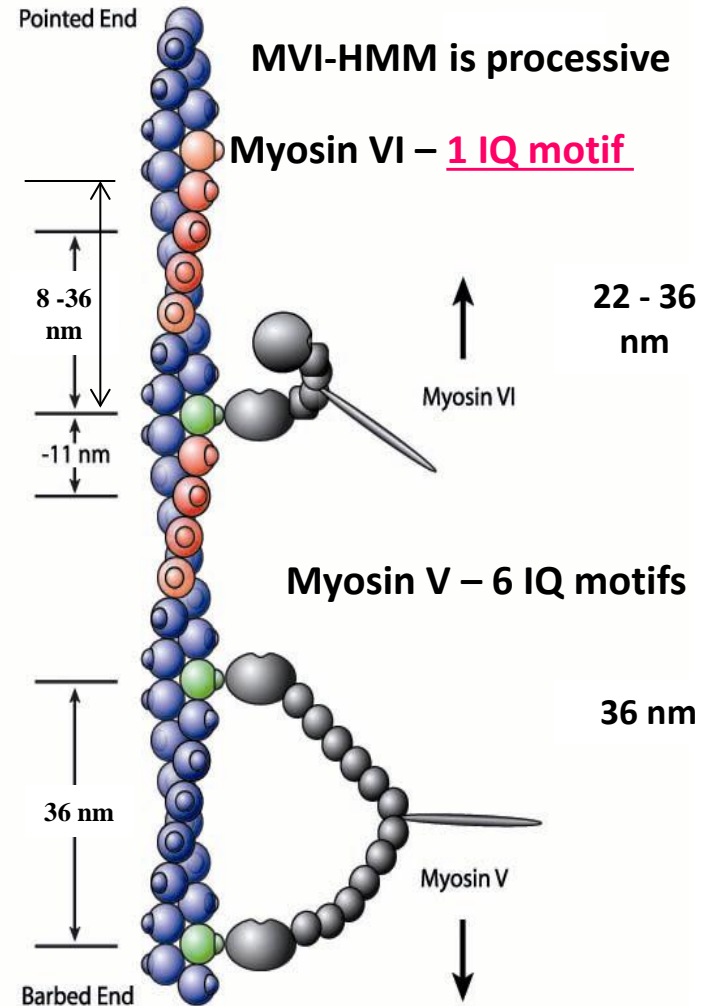
Directionality and step size

Holmes and Geeves Annu. Rev. Biochem. 1999



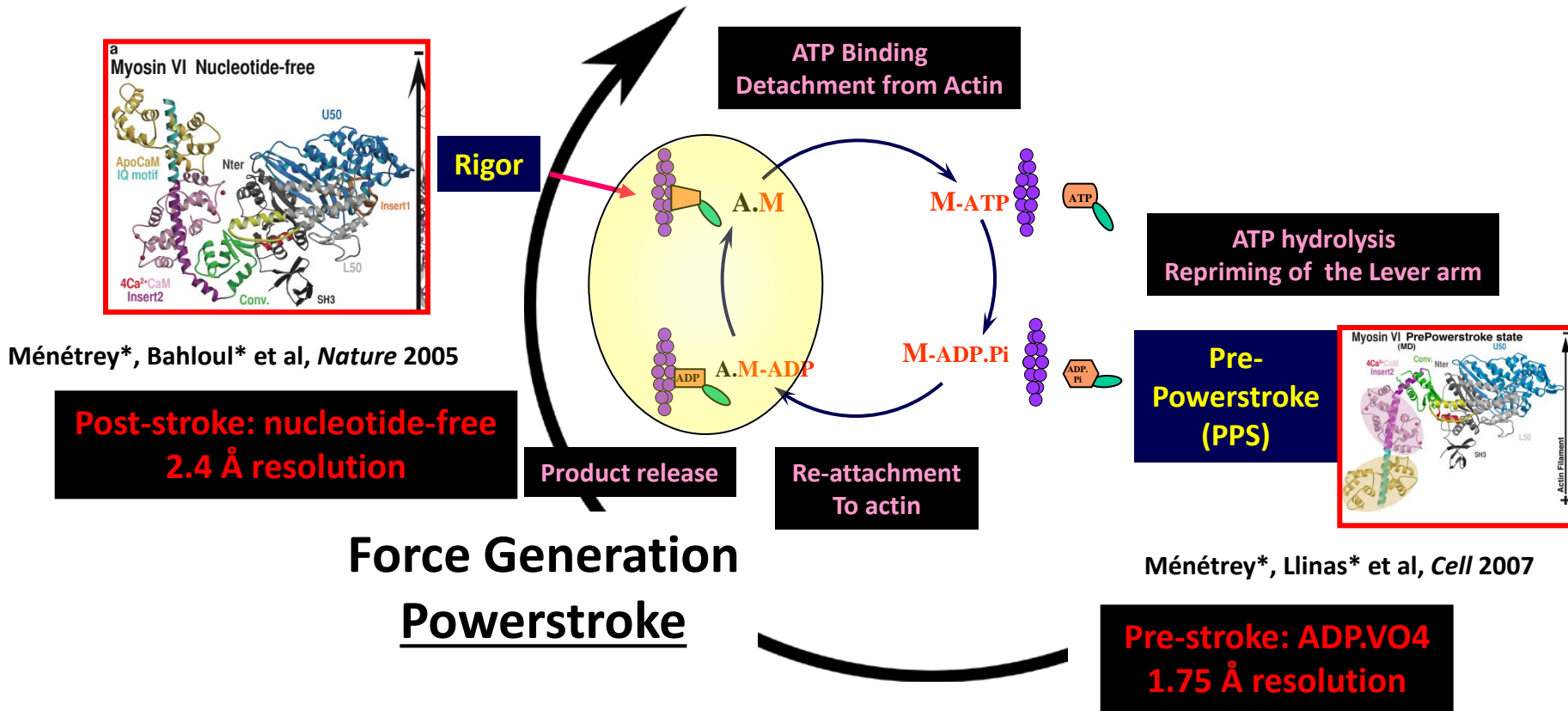
The swinging lever arm theory does not seem compatible with the step size of myosin VI

Rock et al. (2001) *PNAS USA* 98, 13655-9.



What are the structural elements that define the directionality of the force produced ?
What are the adaptations of the motor that allow to generate so big steps ?

Direct visualization of the M6 powerstroke



Identify the structural features that control directionality in this reverse motor.

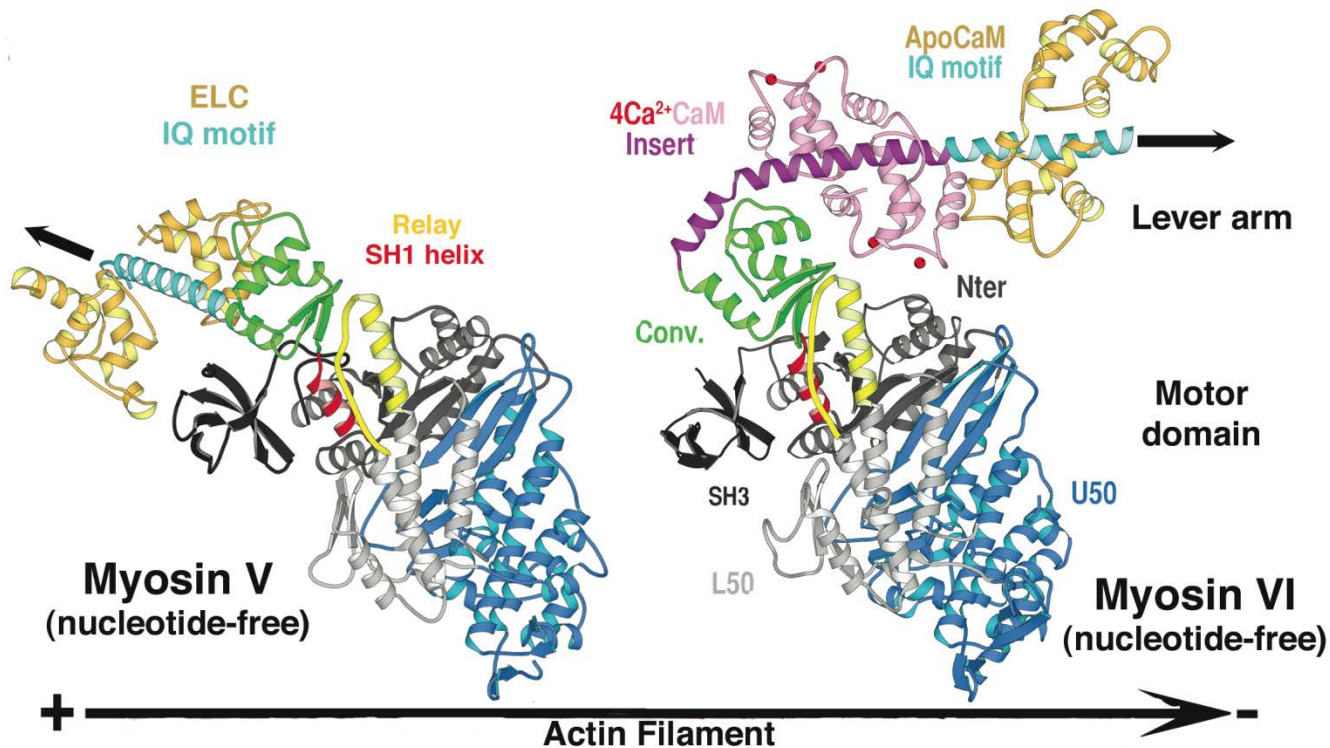
Understanding how this motor can produce a big stroke.

Directionality in myosin motors

Visualization of the conformation at the end of the stroke

The structure of the nucleotide-free state of the myosin VI motor reveals the mechanism of **directionality reversal**, Ménétrey J.*, Bahloul A.*, Wells A., Yengo C., Morris C., Sweeney H.L. and Houdusse A.

(Nature, 2005, 435 :779-85) * co-authors



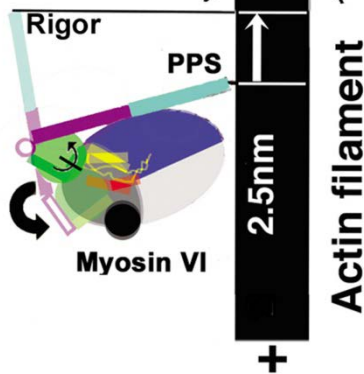
Myosin V and Myosin VI at the end of Force Production

How myosin VI generates a big stroke

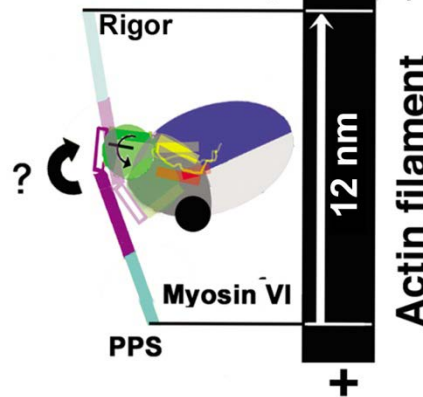
Myosin VI at the beginning of Force Production

Model of Myosin VI

PPS with
(+) end Myosin
converter rotation



Measured Movement of Myosin VI Lever Arm



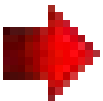
Measured working stroke
of **12 nm**

from single molecule studies

Rock et al. (2005) *Mol Cell* 17:603-9.

**Only 2.5 nm predicted
from modeling**

**Model based on the pre-powerstroke state observed for plus-end motors –
just adding the insert/CaM after the converter**



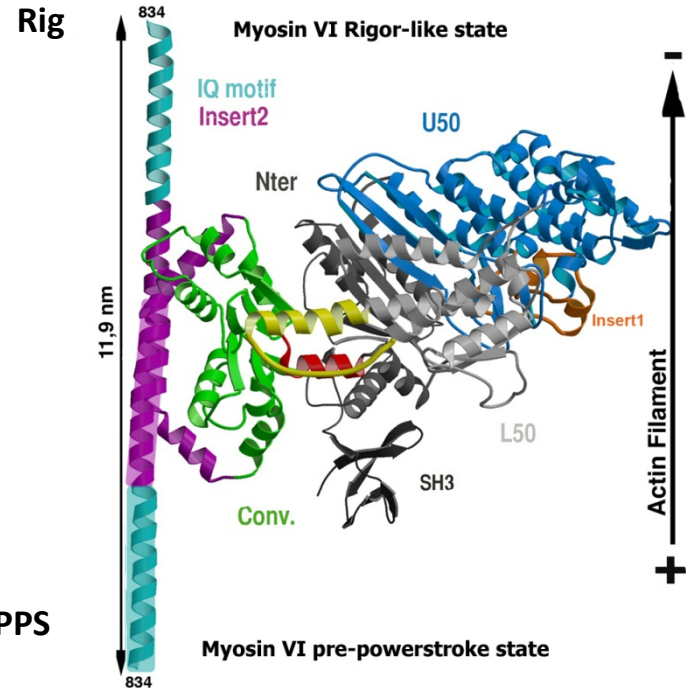
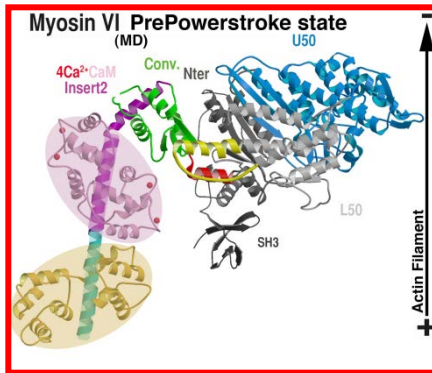
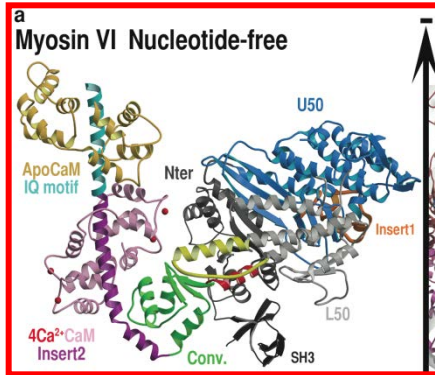
The Myosin VI Pre-power stroke must be different from that of other myosins !

How myosin VI generates a big stroke

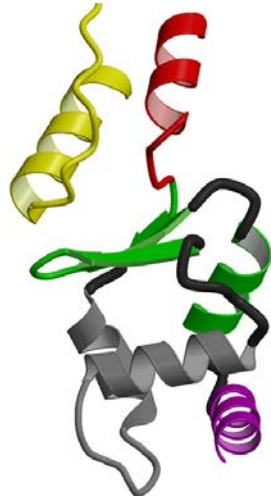
The structural basis for the large powerstroke of myosin VI.

Ménétrey J.*, Llinas P.*, Mukherjea M., Sweeney H. L. and Houdusse A.

(Cell, 2007, 131:300-308) * co-authors

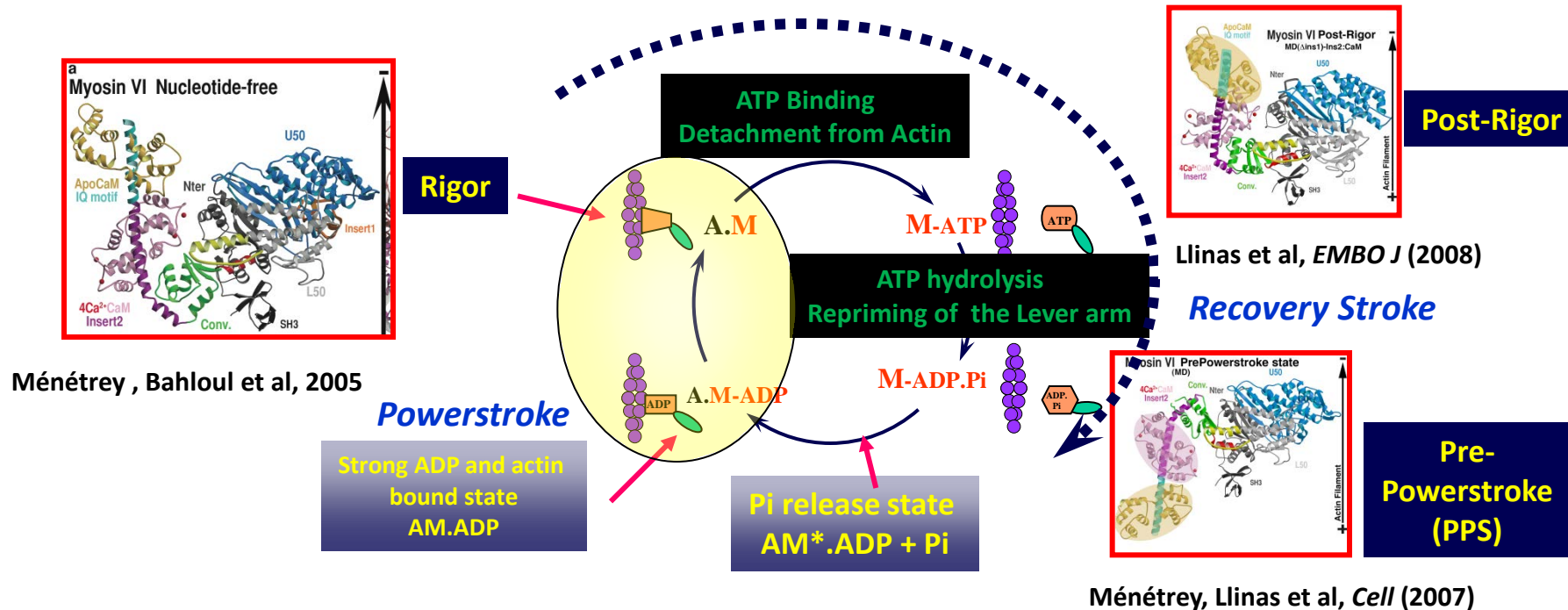


Pre-powerstroke state



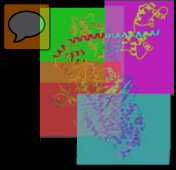
These two M6 structures predict a 180° reorientation of the lever arm parallel to the actin filament and a 12 nm stroke for the S1 fragment

Three structural states of the M6 motor



These M6 structures show that the swinging lever arm theory applies to correctly predict the beginning and the end of the stroke for M6!

The communication pathway between the active site and the converter is conserved in minus-end motors.



OUTLINE

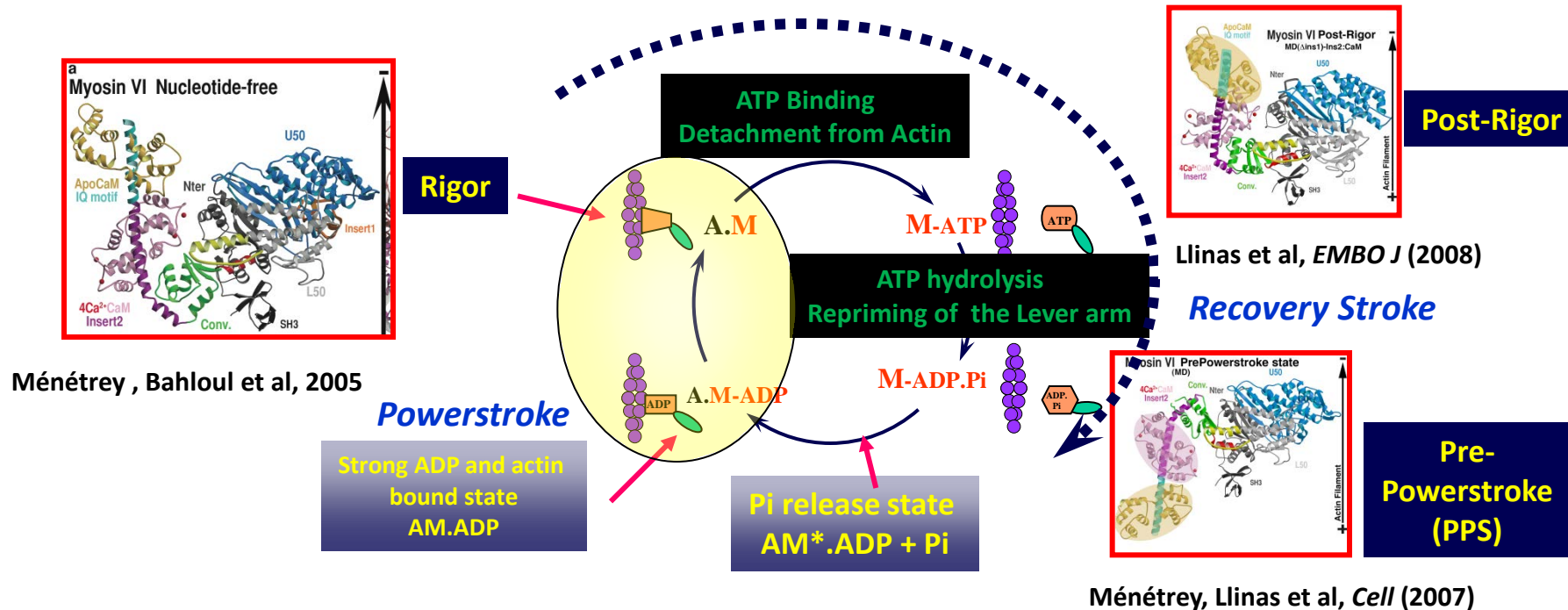
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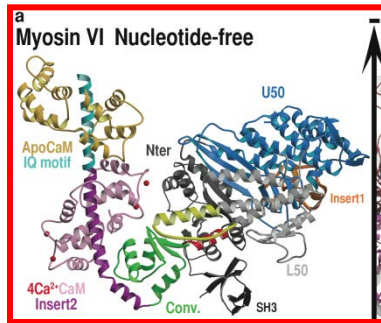


To be a motor, myosin must trap its hydrolysis products. Interestingly, the recovery stroke is reversible with ATP bound, but not with ADP.Pi bound. The dynamics in the myosin head is highly sensitive to the content of the active site.

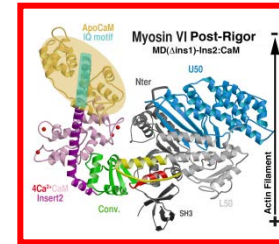
Actin promotes a different type of rearrangement to release Pi.

The powerstroke is NOT a reversal of the recovery stroke !

How does myosin produce force



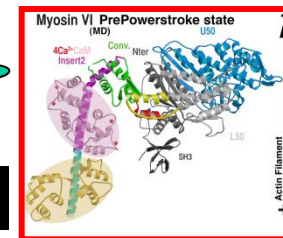
Ménétreay, Bahloul et al, 2005



Post-Rigor

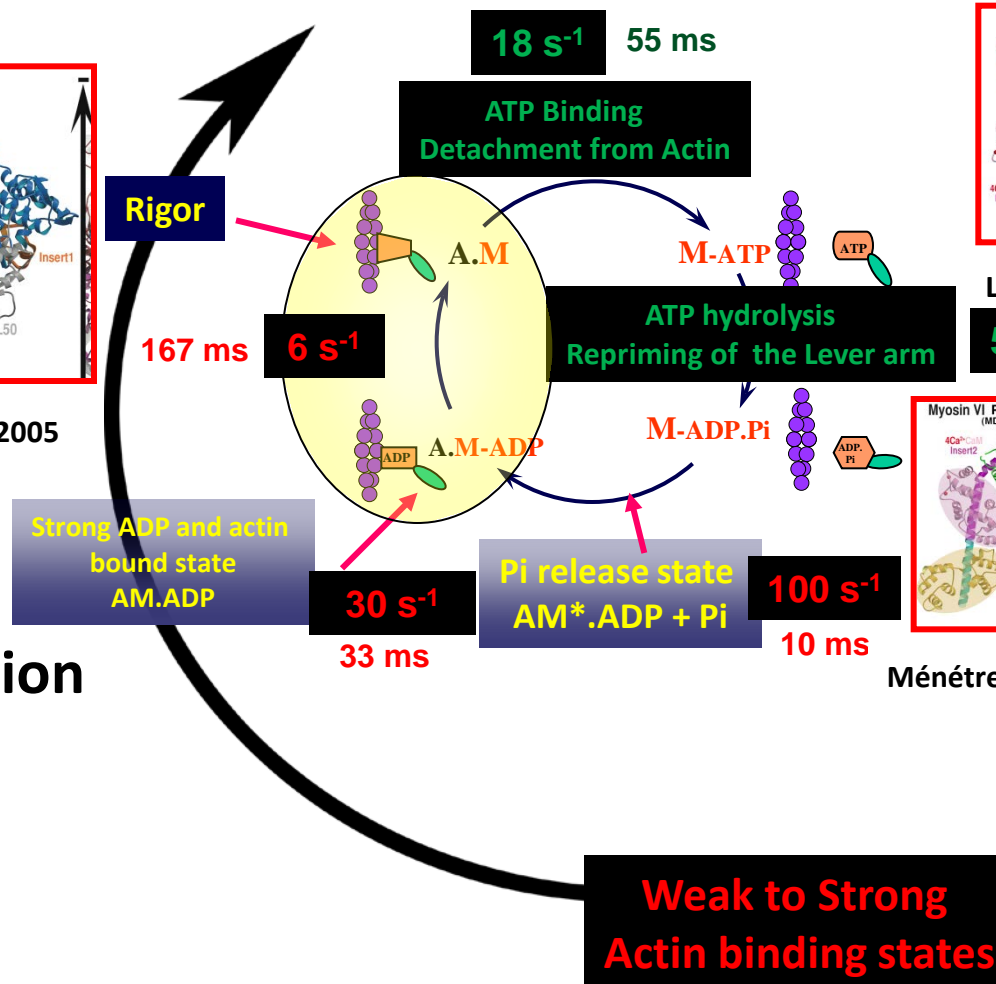
Llinas et al, *EMBO J* (2008)

53 s⁻¹ 18 ms

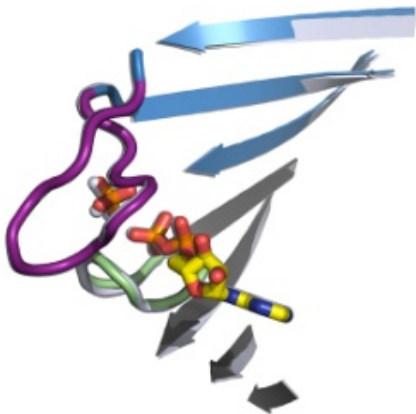


Pre-Powerstroke (PPS)

Ménétreay, Llinas et al, *Cell* (2007)

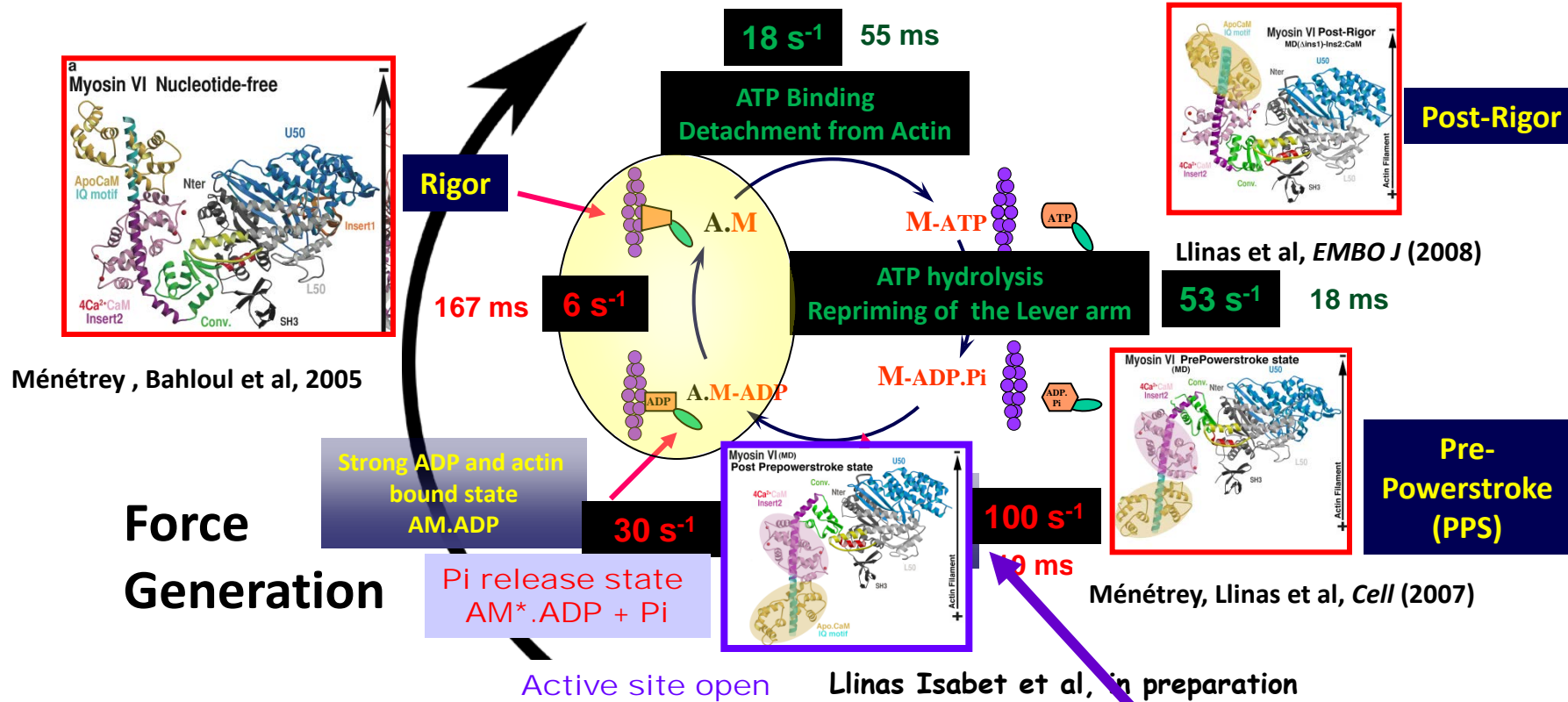


When does the cleft close and the transducer rearrange ?
When does the lever arm swing ?
Which transitions promote product release ?



How does myosin produce force

Pi release on actin



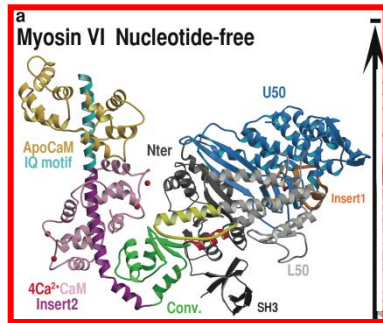
How myosin releases its Pi at the beginning of force production

The Pi release state should have the active site open and the lever arm primed

This state should have a higher affinity for actin than PPS but not as high as AM.ADP or AM

This state should promote commitment of the motor on actin

The mechanism of Force Generation by myosin motors



Ménétrey, Bahloul et al, 2005

Lever arm swing between ADP states

Force
Generation

Rigor

ADP release

6 s⁻¹

30 s⁻¹

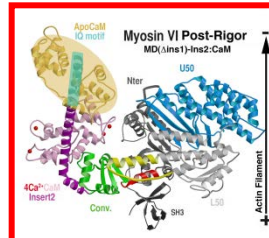
ATP Binding
Detachment from Actin

M-ATP

ATP hydrolysis
Repriming of the Lever arm

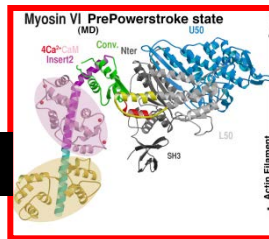
M-ADP.Pi

100 s⁻¹



Post-Rigor

Llinas et al, *EMBO J* (2008)



Pre-
Powerstroke
(PPS)

Ménétrey, Llinas et al, *Cell* (2007)

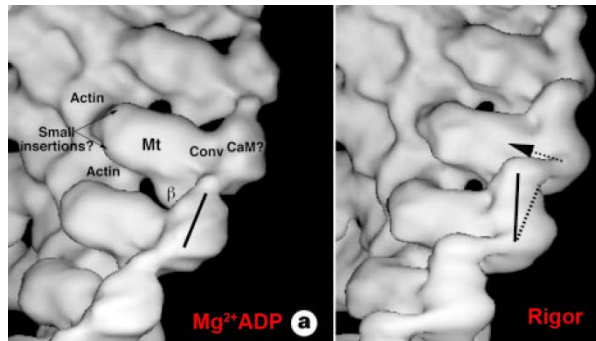
Backdoor closed

Llinas Isabet et al, in preparation

Backdoor open

Cleft closure to populate
Strong ADP state
Lever arm swing
upon pyrene quenching

Pi release state
AM*.ADP + Pi





Structural Studies

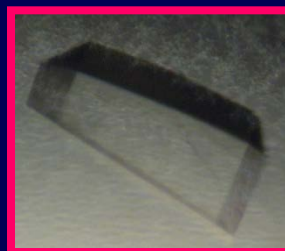
Tatiana Isabet
Serena Sirigu
Paola Llinas
Olena Pylypenko
Julie Ménétrey
Hannah Benisty
Anne Houdusse



Structural Motility Group



Special Thanks



Protein Expression Functional Assays

Allan B. Zhong
Xiaoyan Liu
Li-Qiong Chen
Dan Safer
Lee Sweeney



Computational Studies

Marco Cecchini
Martin Karplus