

# Cell Adhesion and Integrin Mechanosensing *in silico*

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Mechanical Engineering



Molecular Cell  
Biomechanics Lab



BERKELEY  
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# Biomechanics vs Mechanobiology

**Biomechanics:** The study of mechanical behavior and properties of living systems and biological structures.

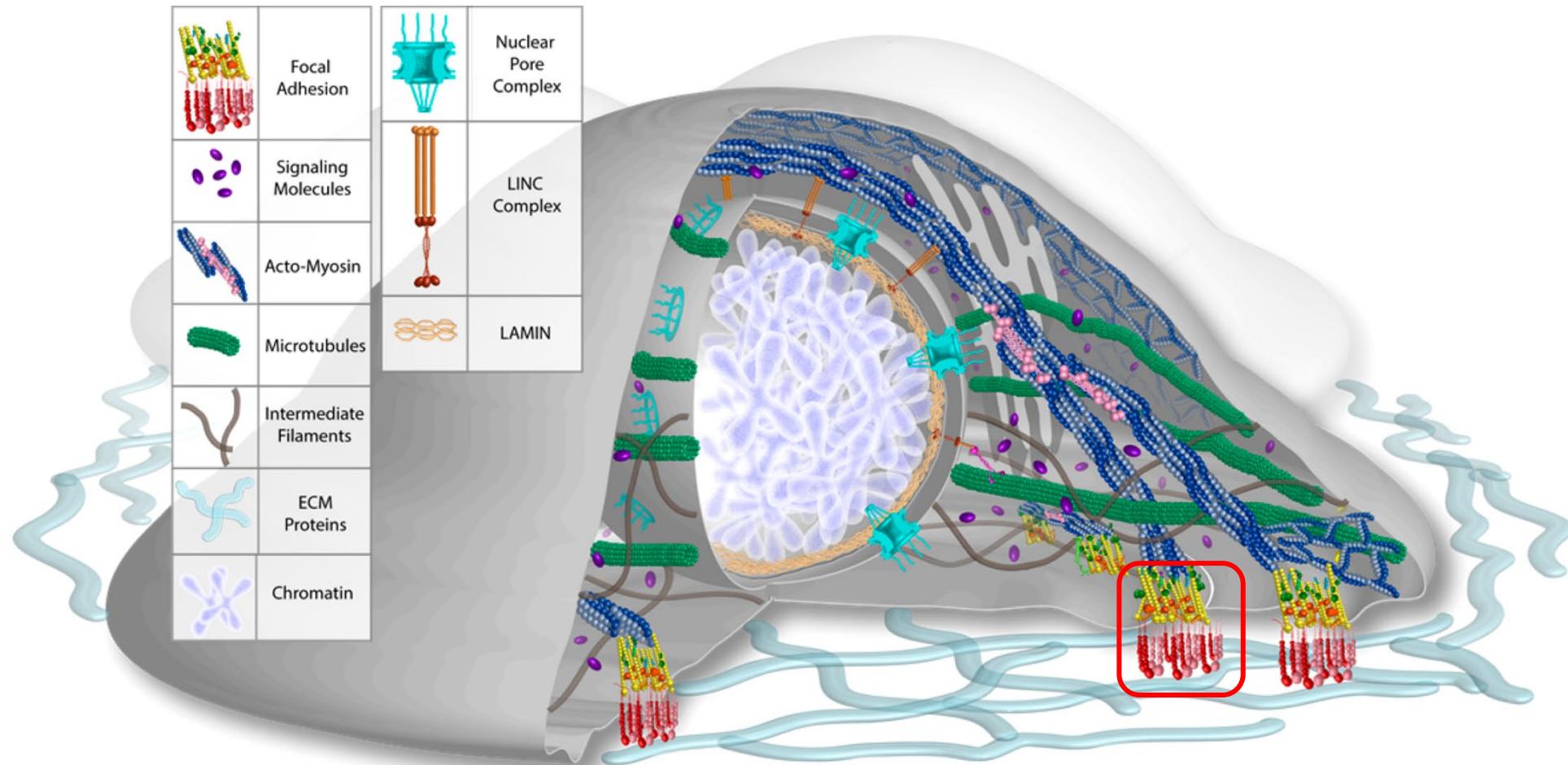
**Mechanobiology:** The study of how mechanics interacts with and governs the biological behavior of living systems and biological structures.

# Biomechanics vs Mechanobiology

**Biomechanics:** Studying **biology** through the lens of **mechanics**.

**Mechanobiology:** Studying how **mechanics** influences **biology**.

# The mechanical system of the cell

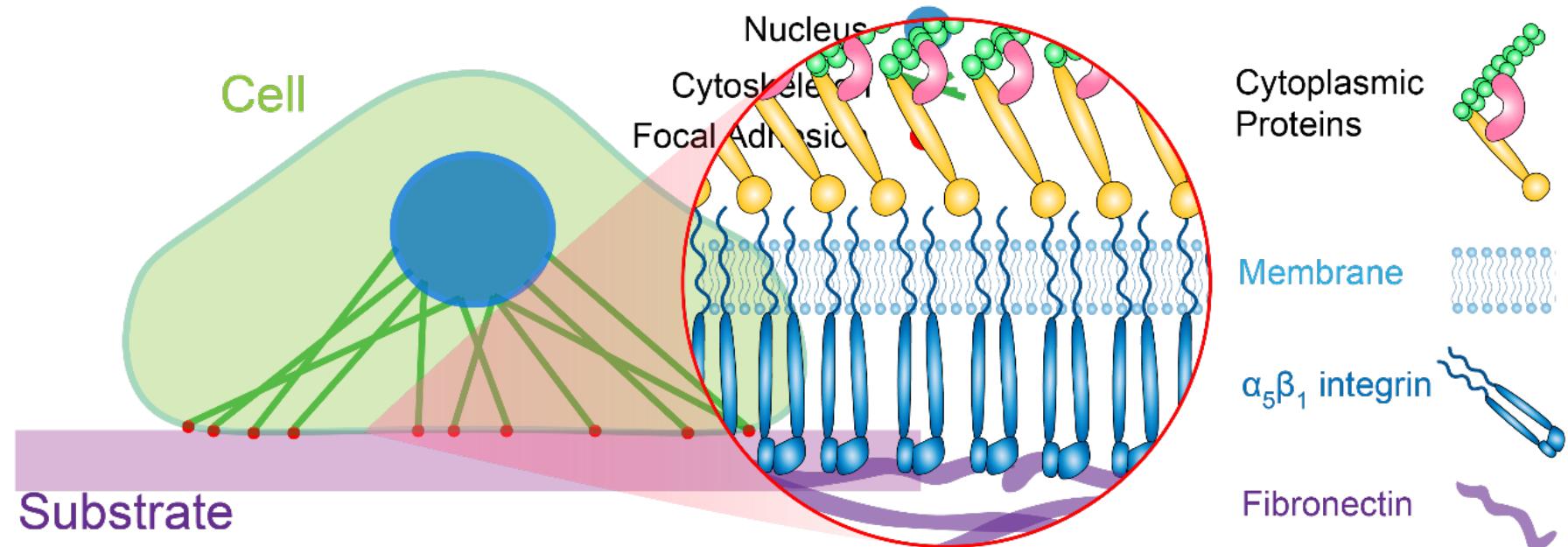


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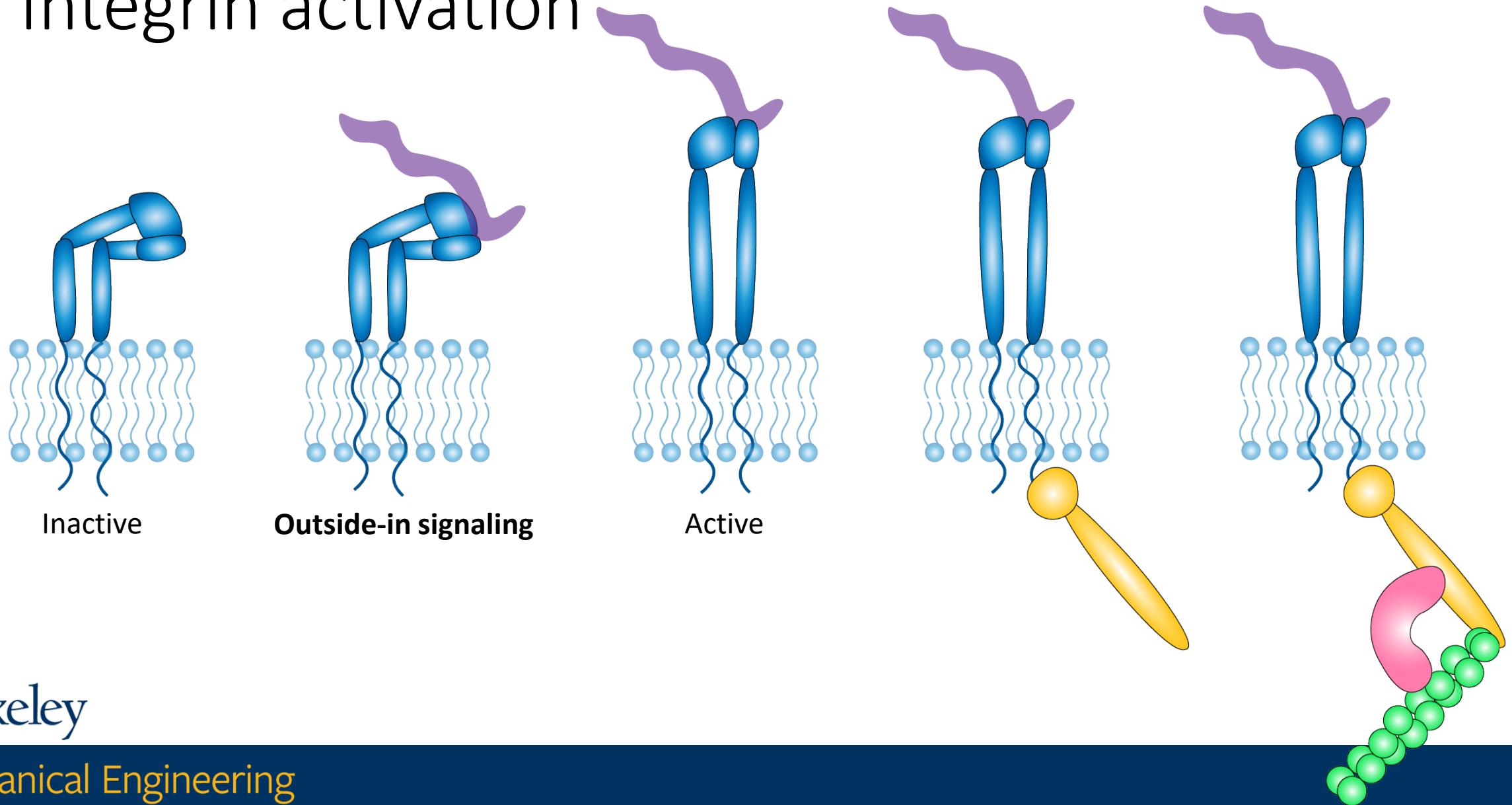
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Shams et al. ACS Biomaterials Sci & Eng. 2017.

Integrin is a cell adhesion molecule with an instrumental role in disease and cell biology



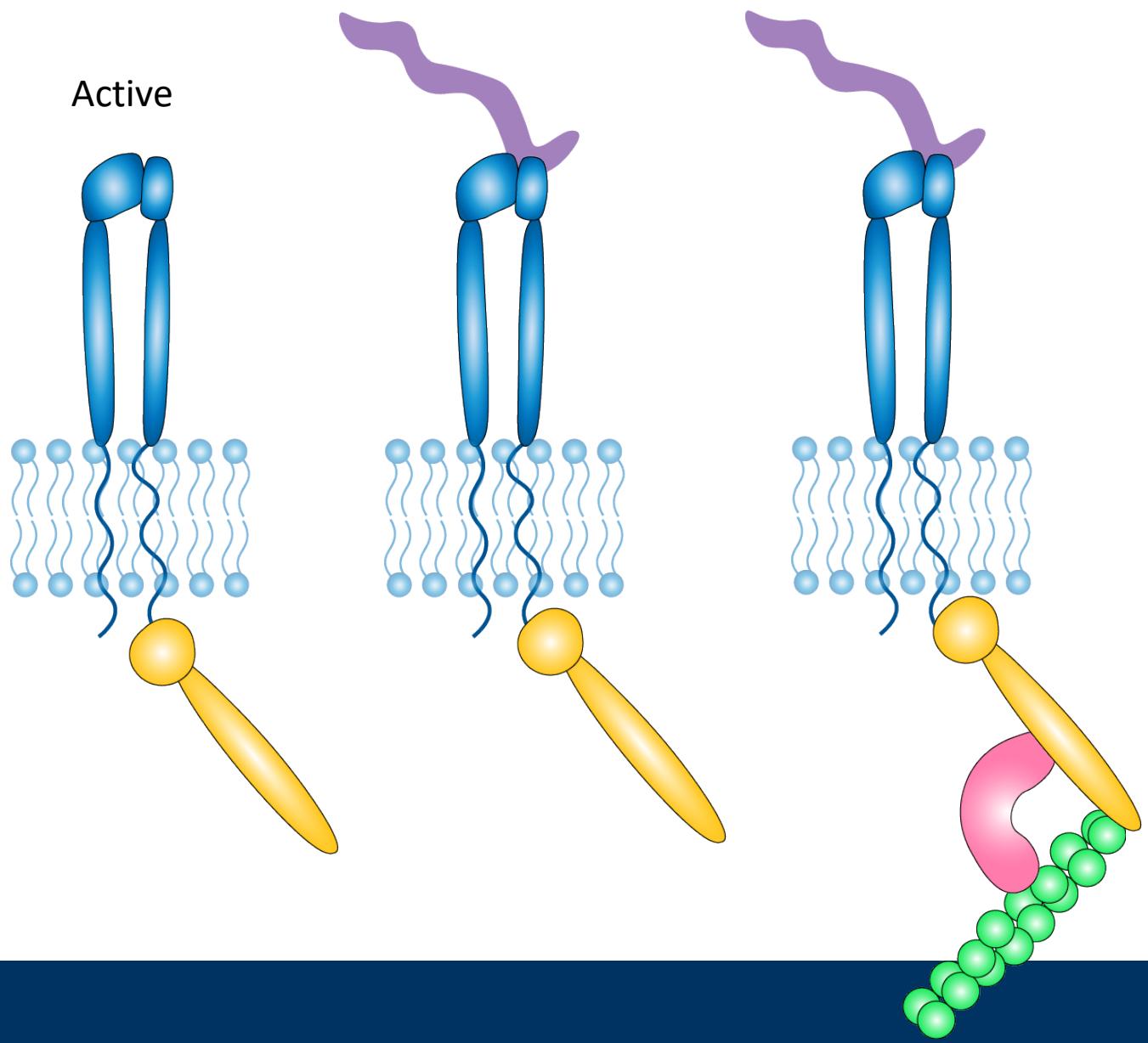
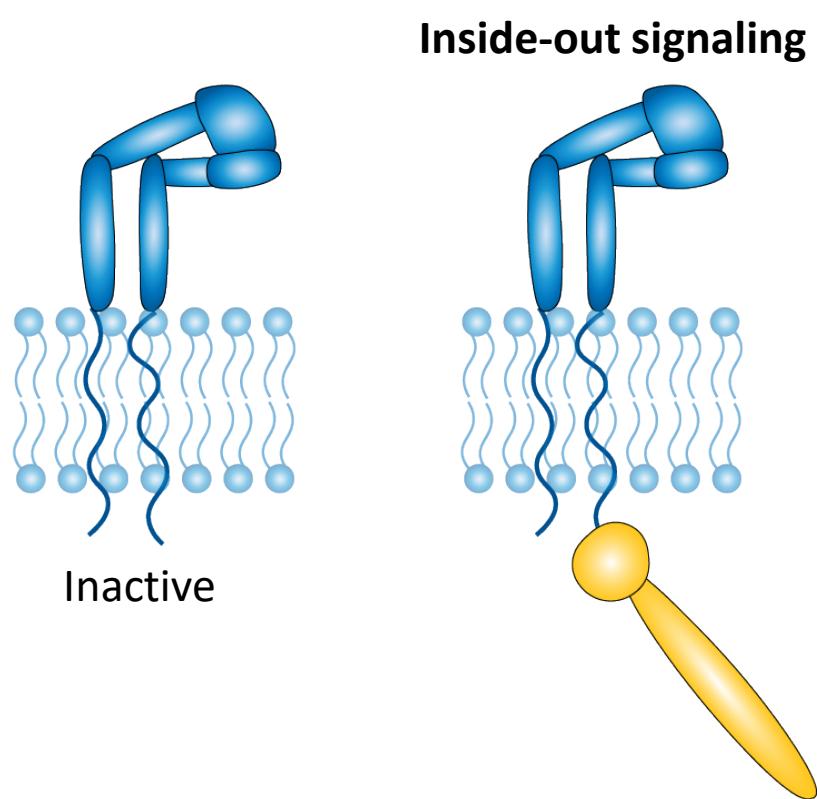
# Integrin activation



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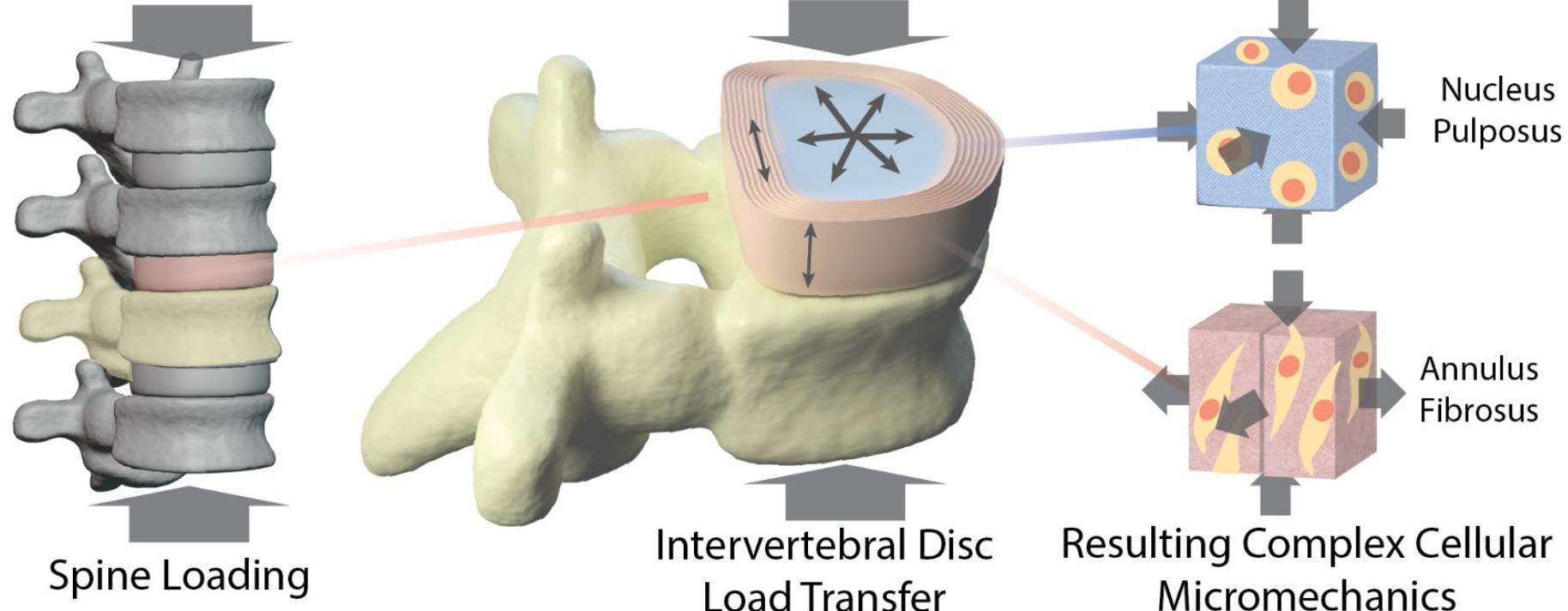
# Integrin activation



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# Integrin is a cell adhesion molecule with an instrumental role in disease and cell biology

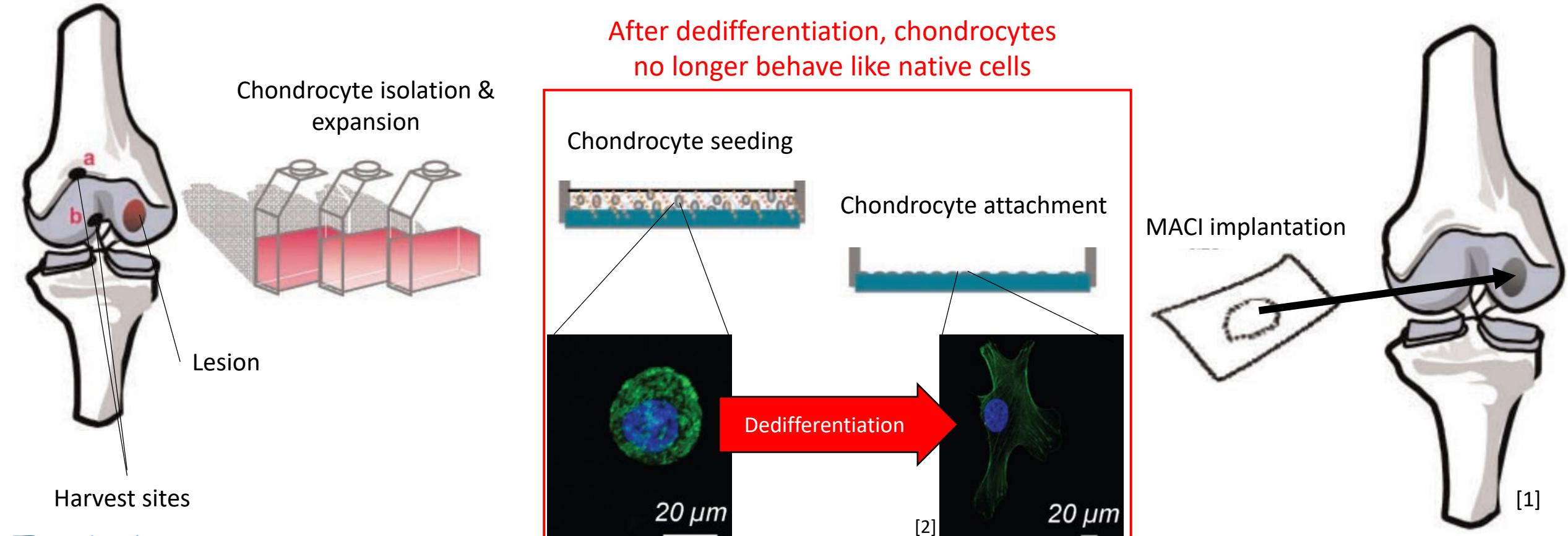


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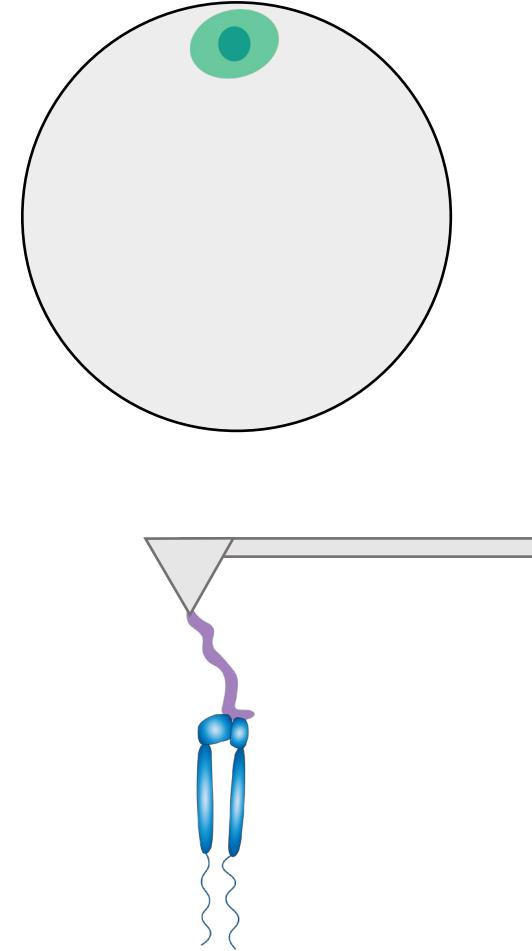
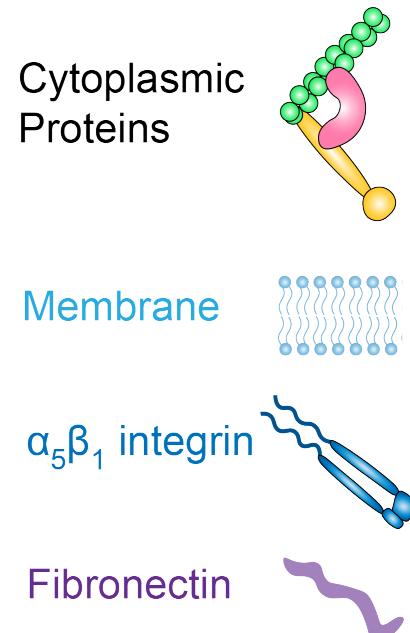
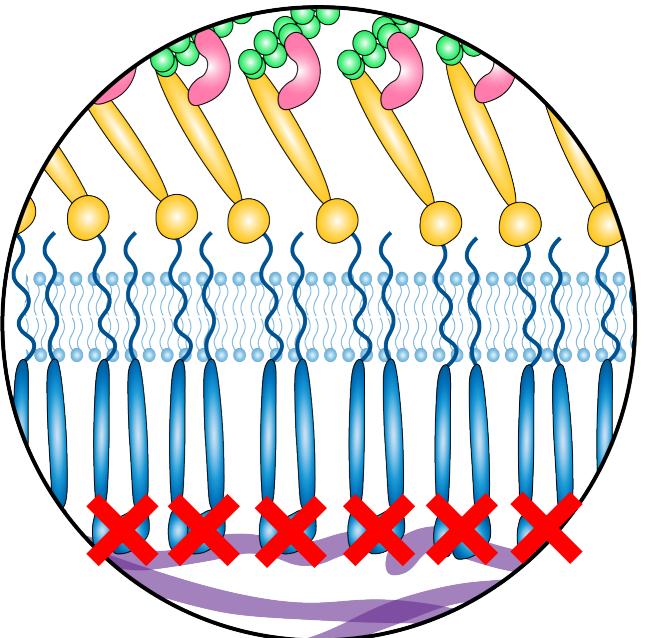
Jonathan McKinley. Figure used with permission.

# Integrin is a cell adhesion molecule with an instrumental role in disease and cell biology



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# Integrin is a cell adhesion molecule with an instrumental role in disease and cell biology



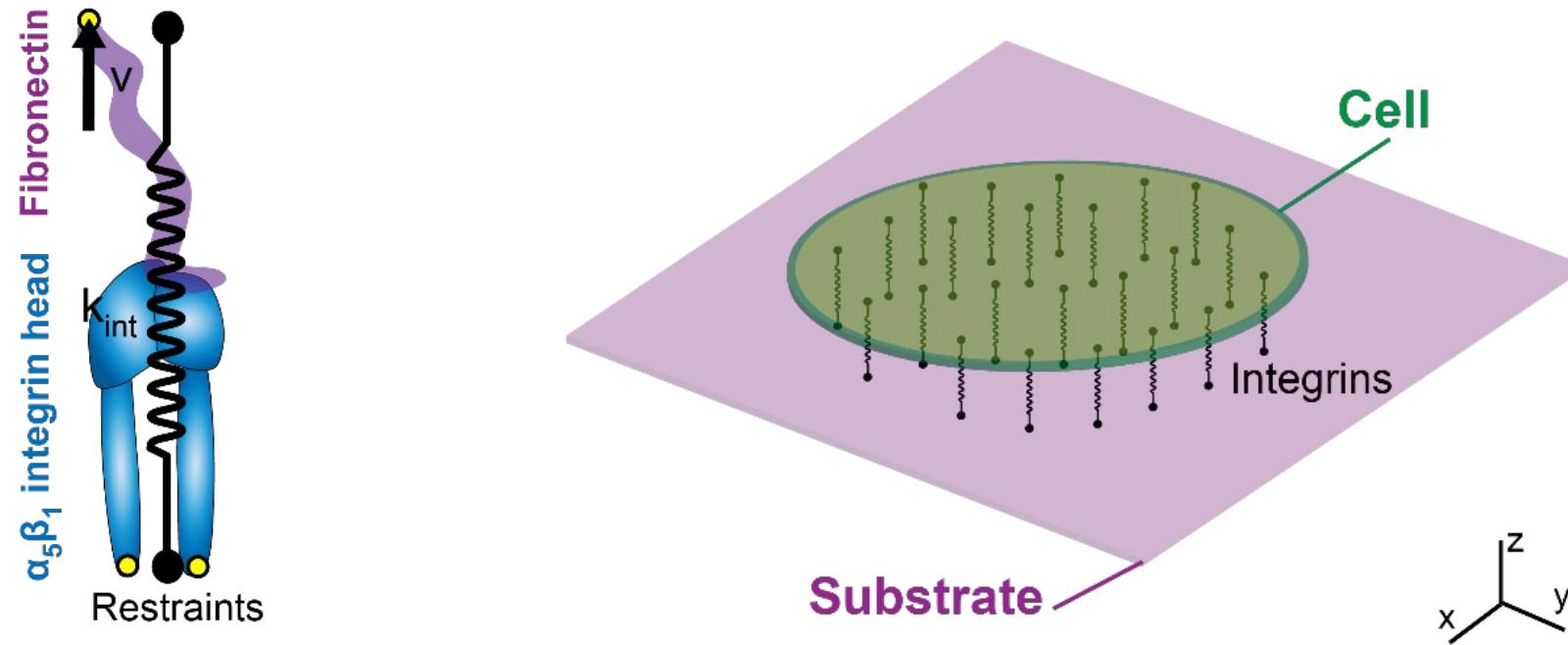
**Cell Adhesion**  
Friedland et al. *Science*. 2009.

**Rupture Force**  
Li et al. *Biophysical*. 2002.

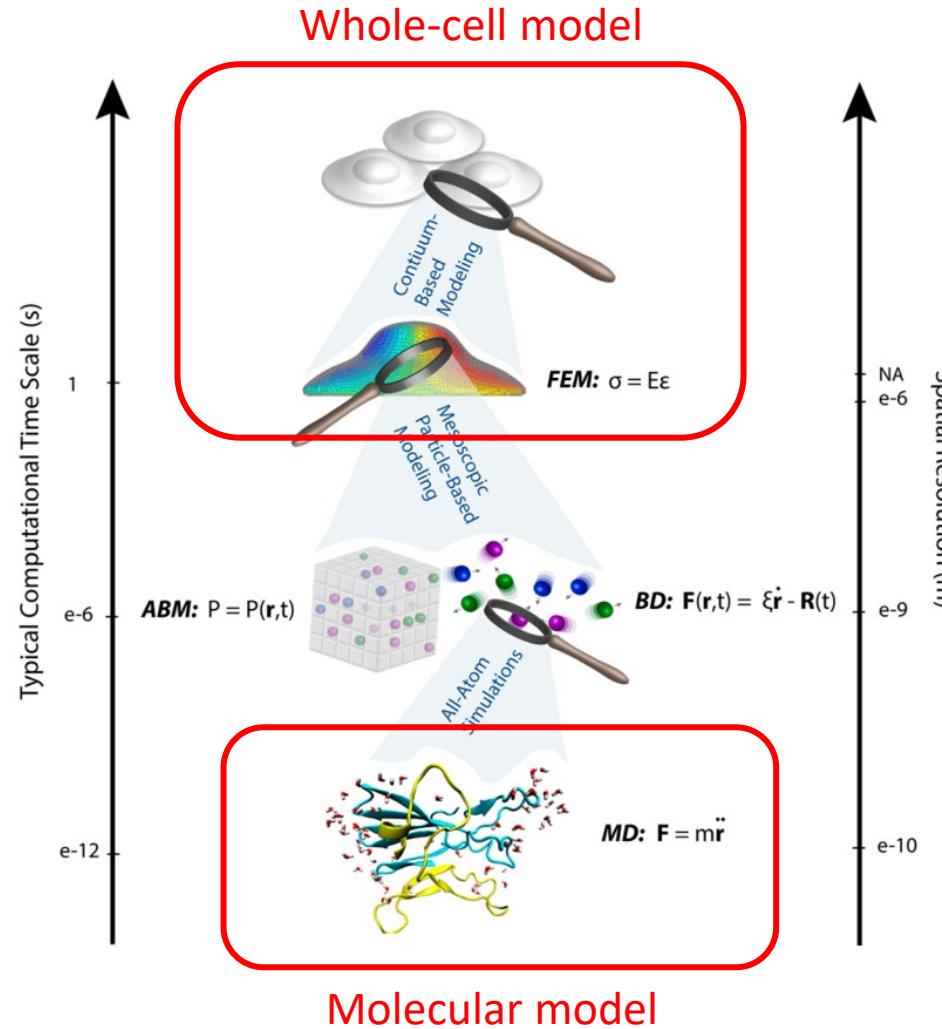
But how does disrupting  $\alpha_5\beta_1$  integrin reduce cell adhesion?

What are the multiscale mechanics?

# Multiscale model to link the nanomechanics of integrin to the whole-cell micromechanics



# Tools we can use to investigate multiscale mechanics



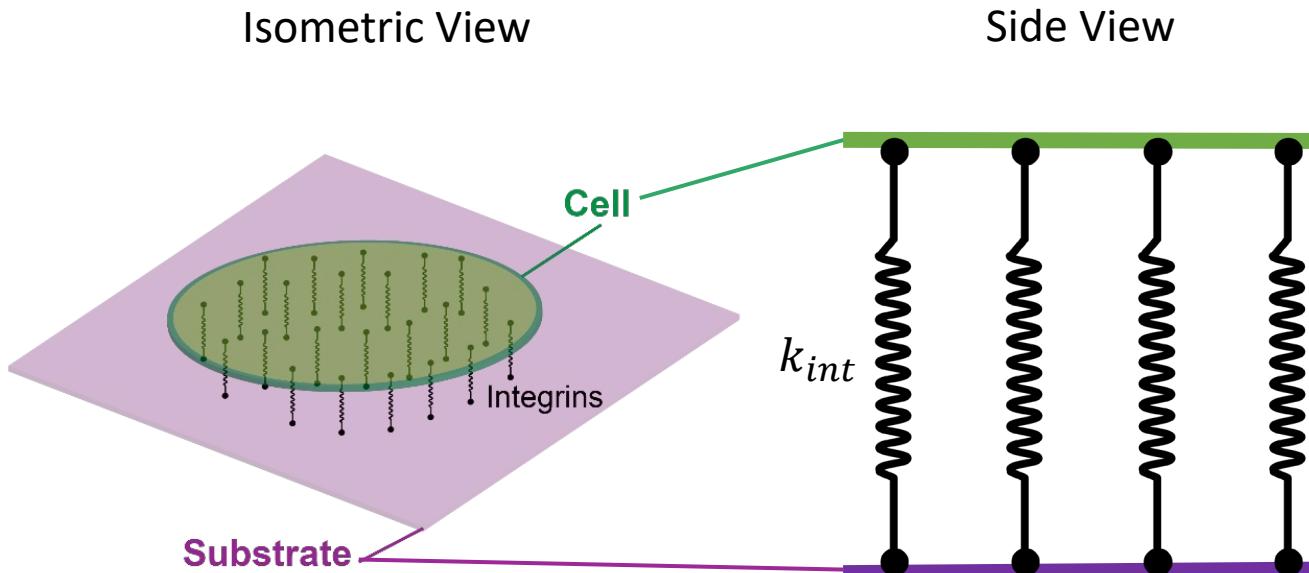
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Shams et al. ACS Biomaterials Sci & Eng. 2017.

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# Whole-cell Finite Element Model



$$\Sigma \mathbf{F} = \mathbf{f}_{ext} + \nabla \boldsymbol{\sigma} = \rho \mathbf{a}$$

Cell:  $\mathbf{f}_{int} - \nabla(\boldsymbol{\sigma}_c^{pas} + \boldsymbol{\sigma}_c^{act}) = \rho_c \mathbf{a}_c$

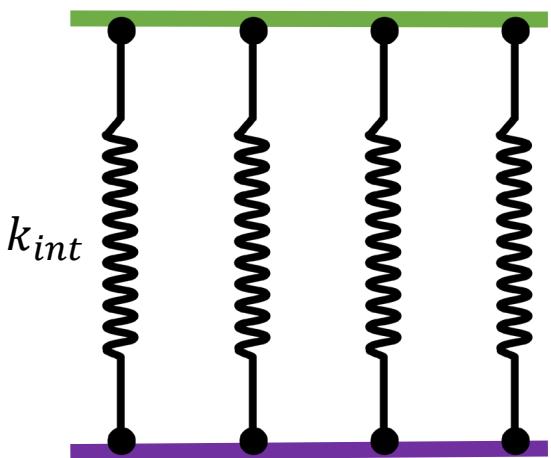
Substrate:  $\mathbf{f}_{int} - \nabla \boldsymbol{\sigma}_s^{pas} = \rho_s \mathbf{a}_s$

Hooke's Law:  $\mathbf{f}_{int} = N_{int} k_{int} \mathbf{u}_{int}$

$$\mathbf{f}_{int} = C N_{max} k_{int} \mathbf{u}_{int}$$

# Whole-cell Finite Element Model

Side View



$$f_{int} = CN_{max}k_{int}u_{int}$$

$$C_{t+\Delta t} = C(1 - K_{off}\Delta t) + K_{on}\Delta t(1 - C)$$

$$K_{off} = K_a e^{\frac{|f_{int}|}{F_a}} + K_b e^{\frac{-|f_{int}|}{F_b}}$$

$$K_a : 0.004 \text{ s}^{-1} [2]$$

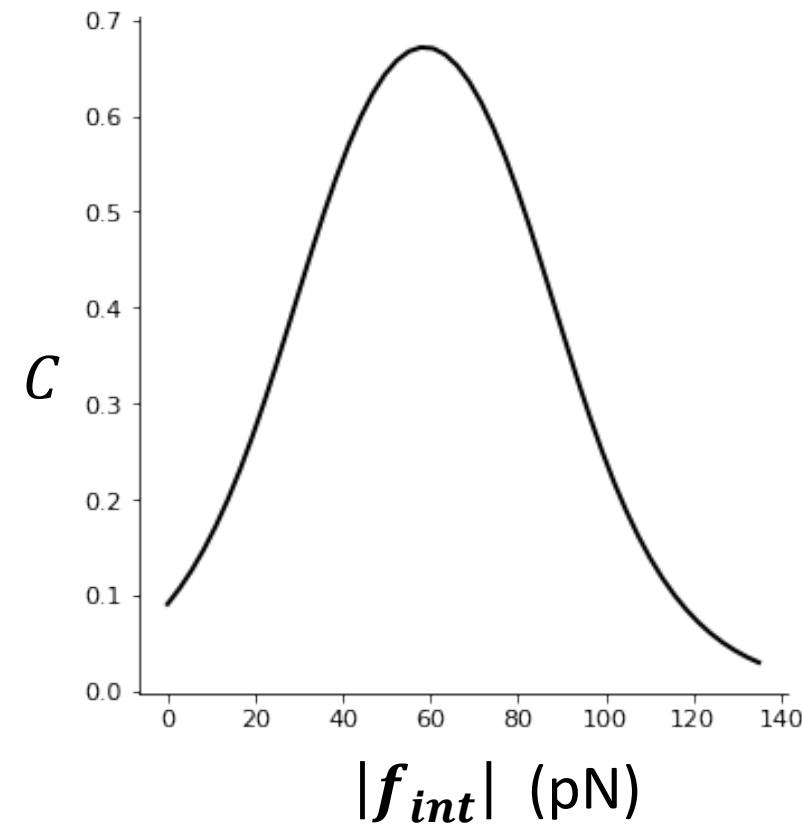
$$K_b : 10 \text{ s}^{-1} [2]$$

$$F_a : 15 \text{ pN} [2]$$

$$F_b : 15 \text{ pN} [2]$$

$$K_{on} : 0.002 \text{ s}^{-1} [1]$$

$$\Delta t : 0.01\text{s}$$



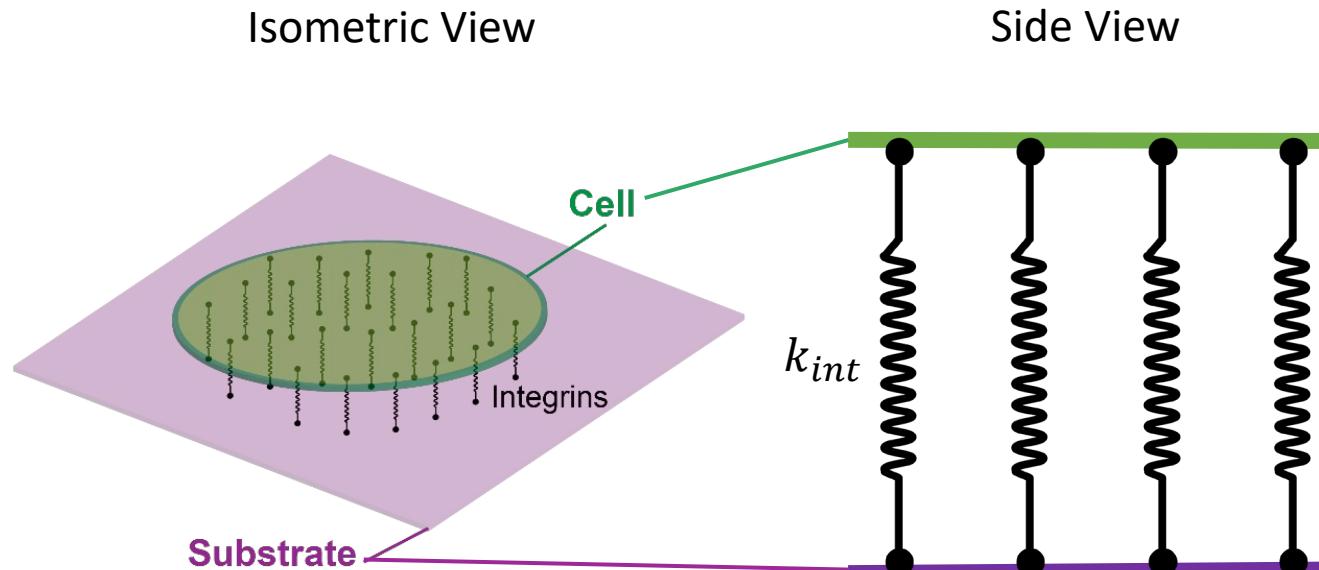
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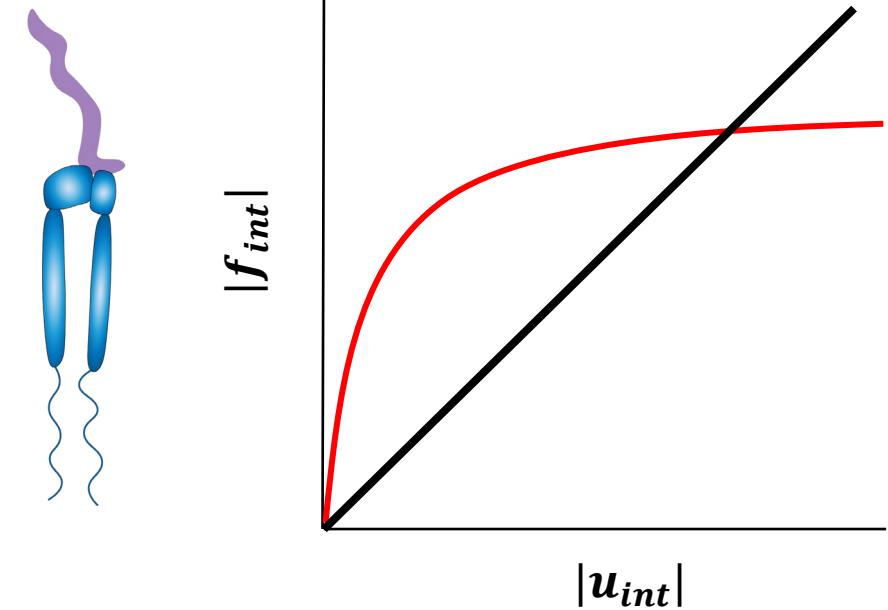
Bell GI. Science. 1978.

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# Multiscale Coupling



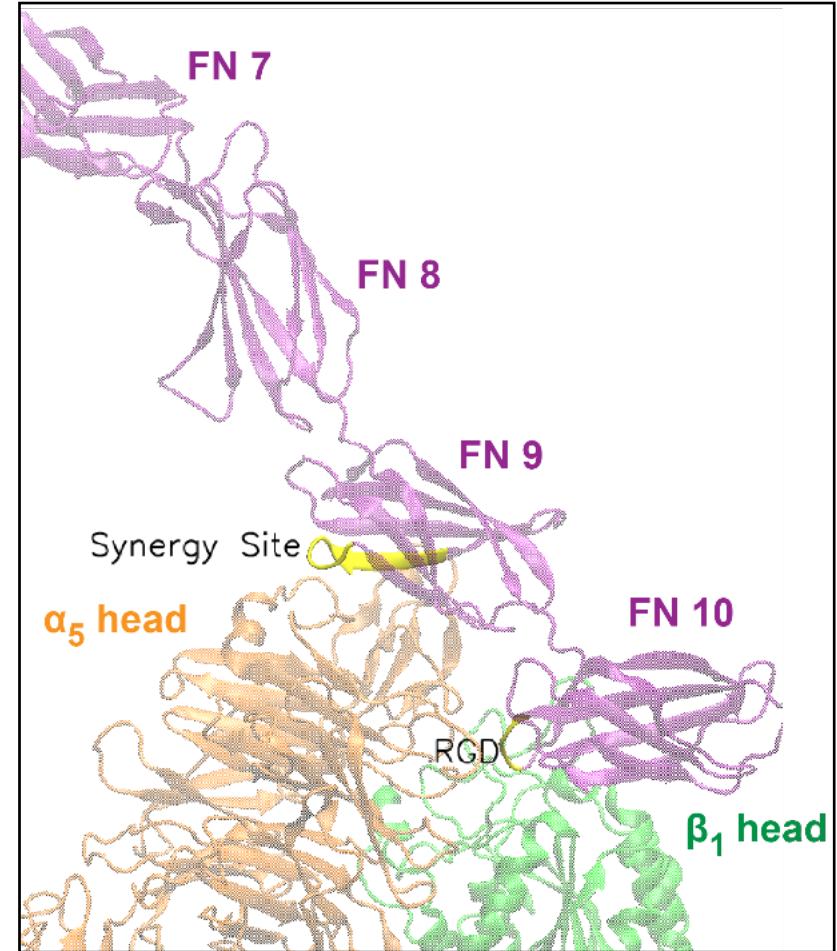
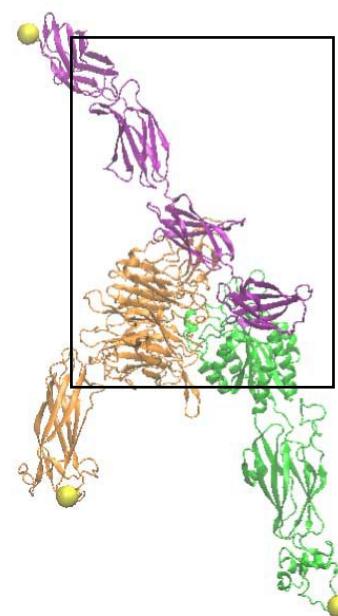
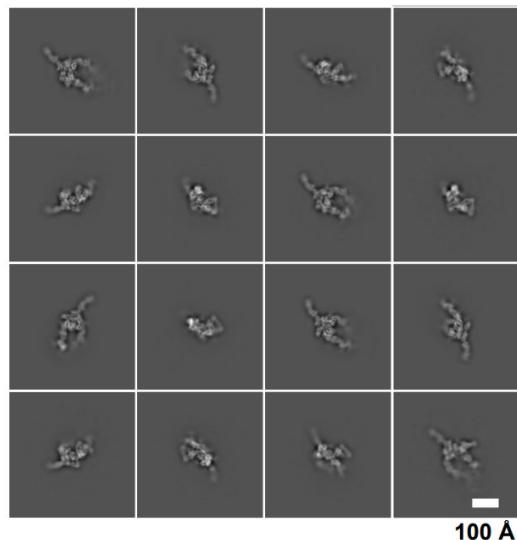
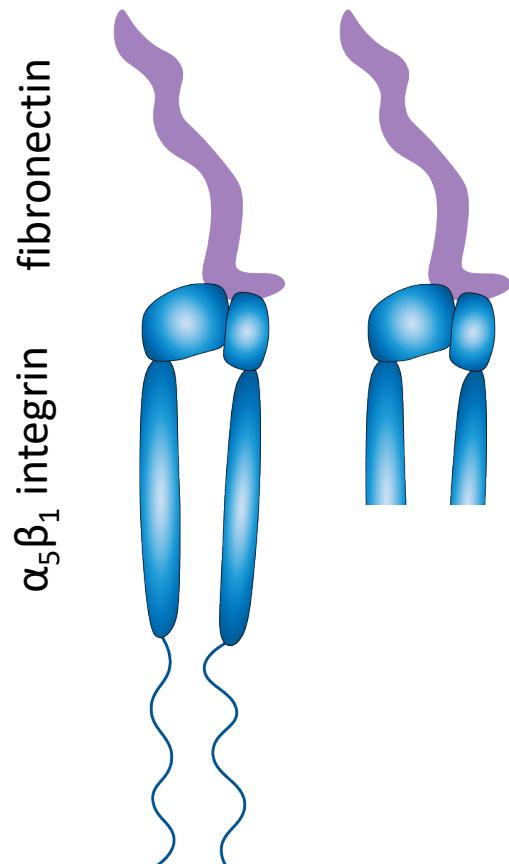
$$f_{int} = C N_{max} k_{int} u_{int}$$



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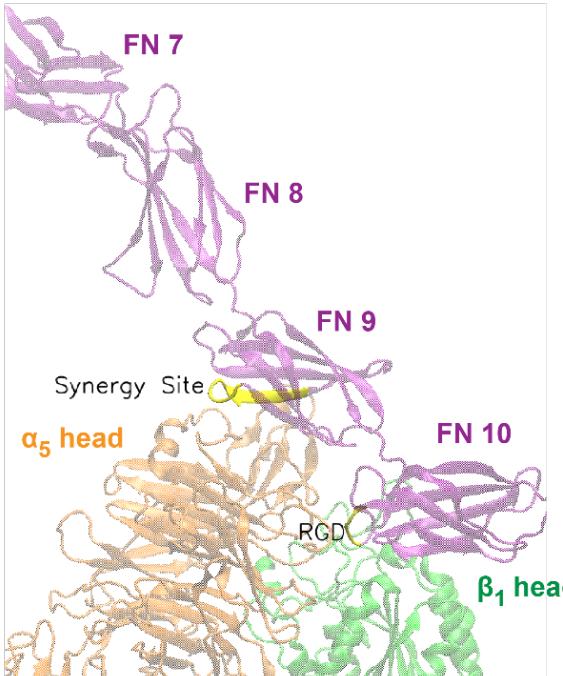
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# $\alpha_5\beta_1$ integrin-fibronectin structure



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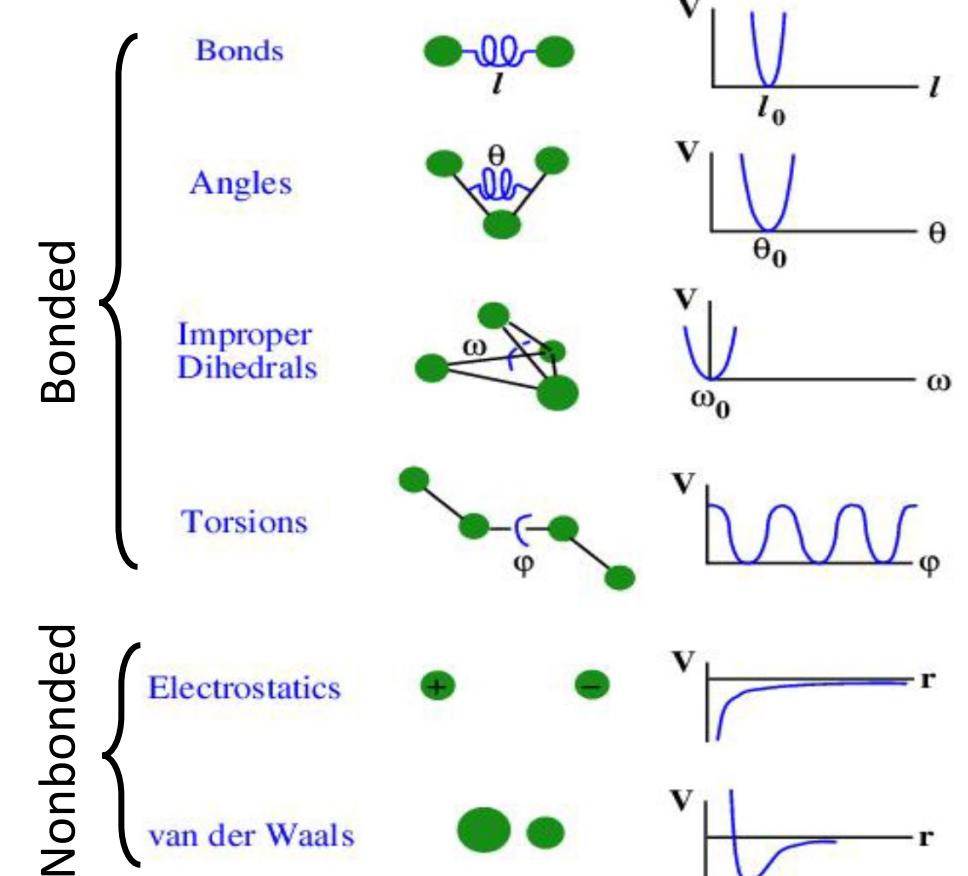
# Molecular Dynamics



## 1. Initialize

Positions:  $\mathbf{r}^N = (\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N)$

Potentials:  $V(\mathbf{r}^N) = V_{bonded} + V_{nonbonded}$



[bioinformatics.niaid.nih.gov/cmm/intro\\_simulation/intro\\_simulation.pdf](http://bioinformatics.niaid.nih.gov/cmm/intro_simulation/intro_simulation.pdf)

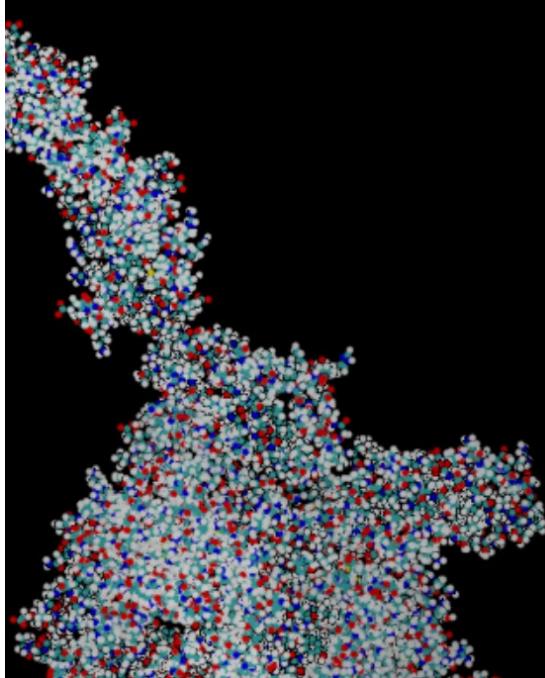
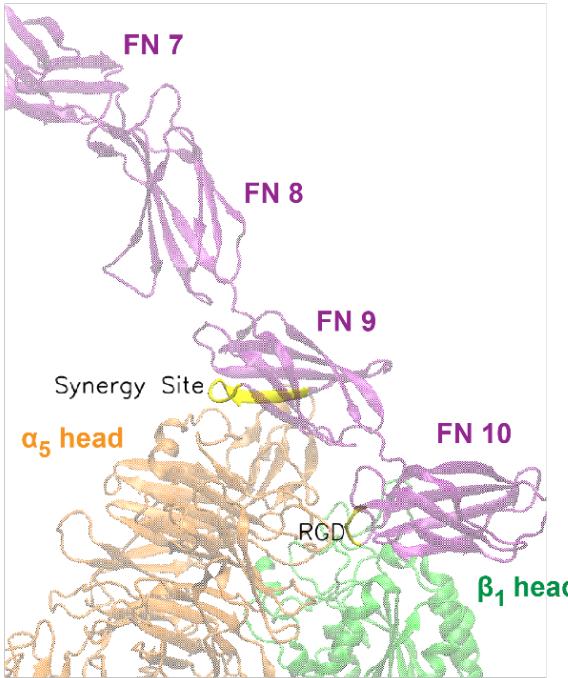
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Gromacs MD manual.gromacs.org

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# Molecular Dynamics



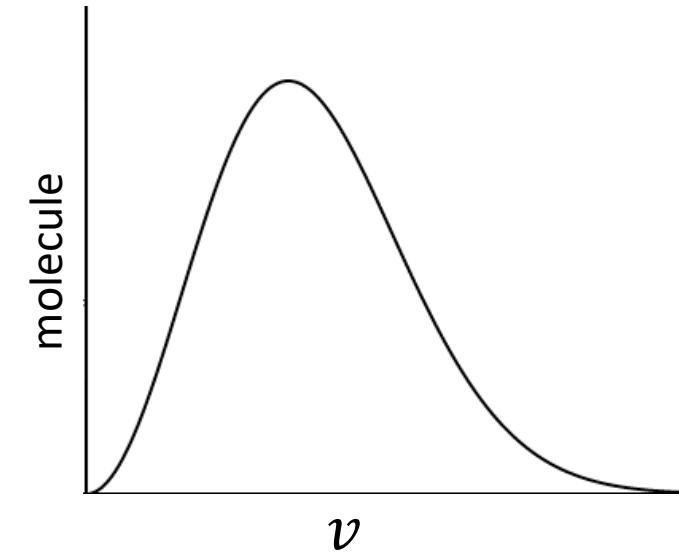
## 1. Initialize

Positions:  $\mathbf{r}^N = (\mathbf{r}_1, \mathbf{r}_2, \dots, \mathbf{r}_N)$

Potentials:  $V(\mathbf{r}^N) = V_{bonded} + V_{nonbonded}$

Velocities:  $\mathbf{v}^N = (\mathbf{v}_1, \mathbf{v}_2, \dots, \mathbf{v}_N)$

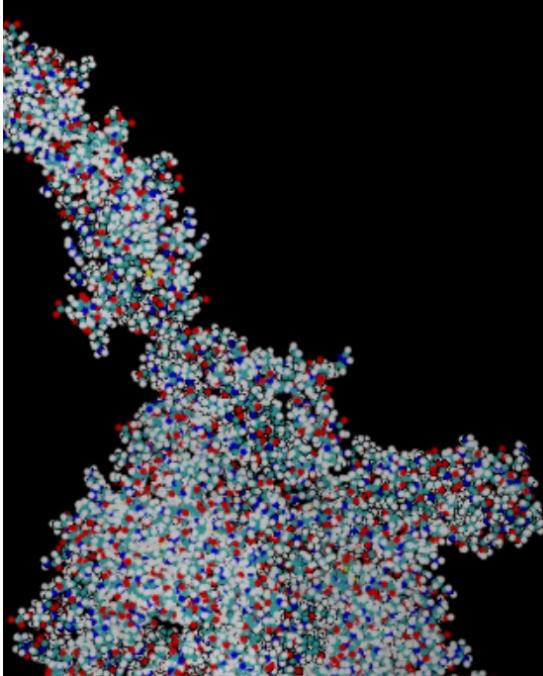
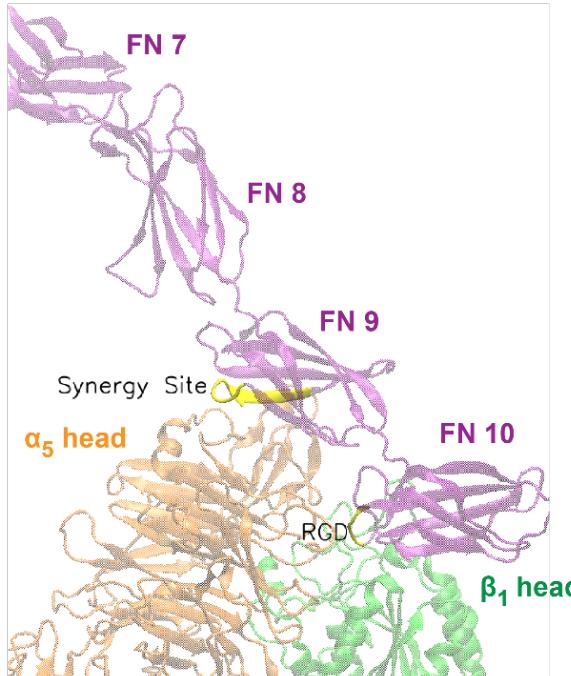
$$p(v_i) = \sqrt{\frac{m_i}{2\pi kT}} \exp\left(-\frac{m_i v_i^2}{2kT}\right)$$



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# Molecular Dynamics



2. Compute forces & energies

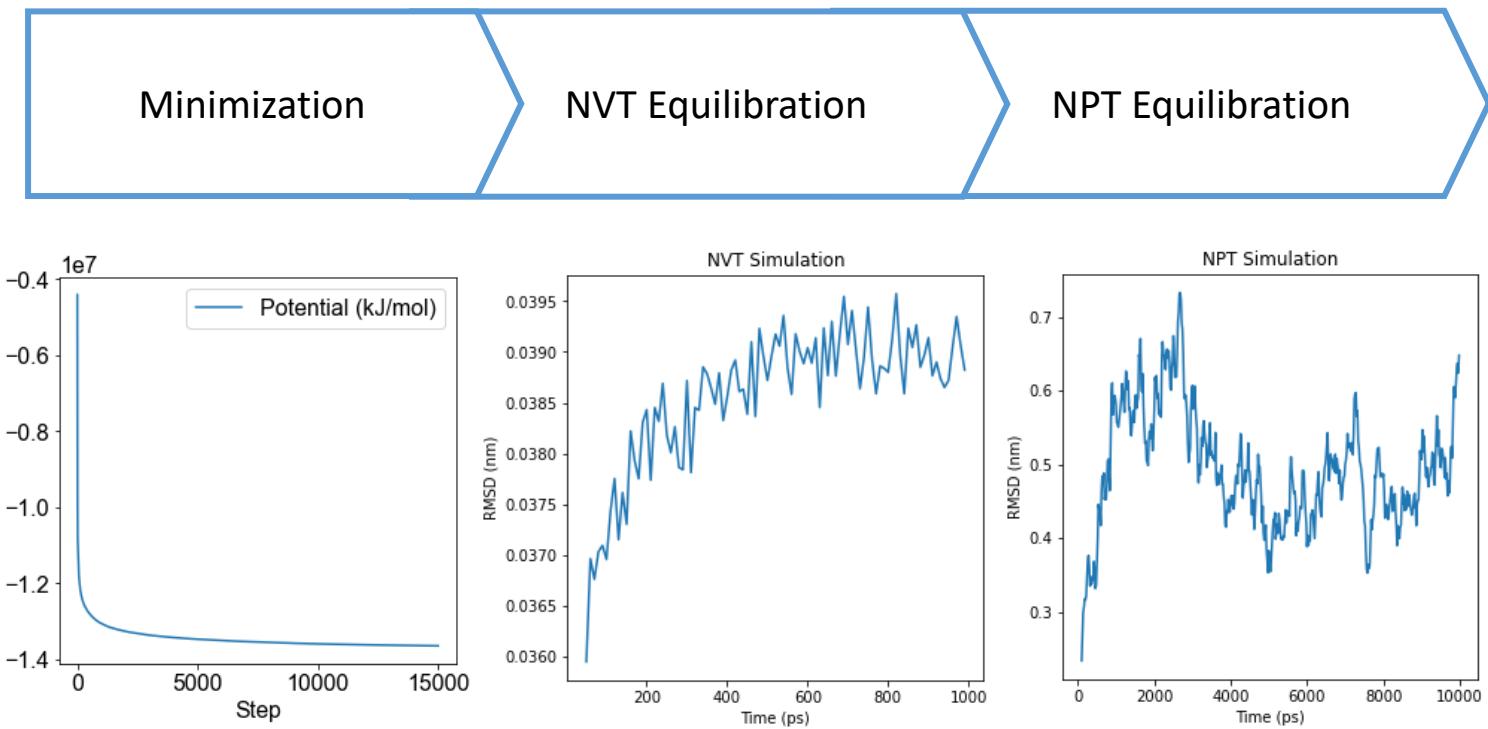
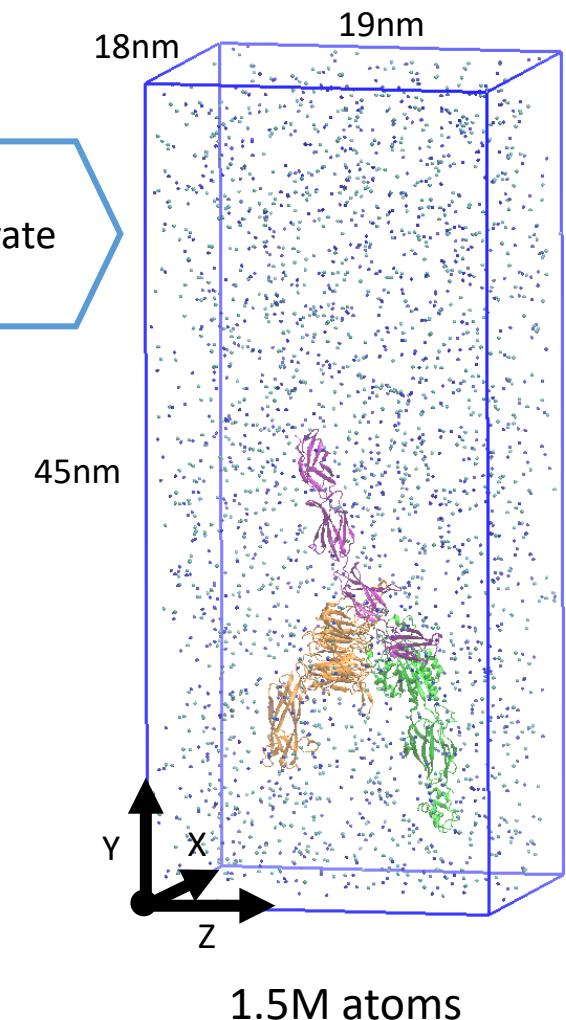
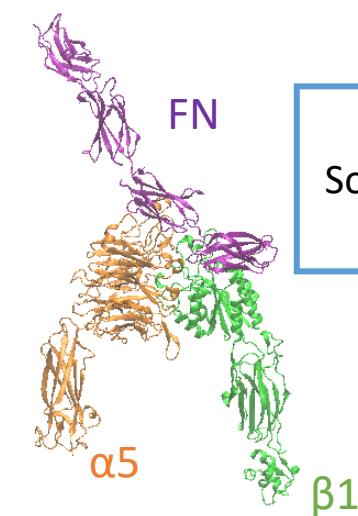
$$\mathbf{F}_i = -\frac{\partial V}{\partial \mathbf{r}_i}$$

3. Update positions & velocities

$$\frac{d^2 \mathbf{r}_i}{dt^2} = \frac{\mathbf{F}_i}{m_i} \quad \frac{d\mathbf{r}_i}{dt} = \mathbf{v}_i \quad \frac{d\mathbf{v}_i}{dt} = \frac{\mathbf{F}_i}{m_i}$$

4. Output trajectory

# Molecular Dynamics Workflow

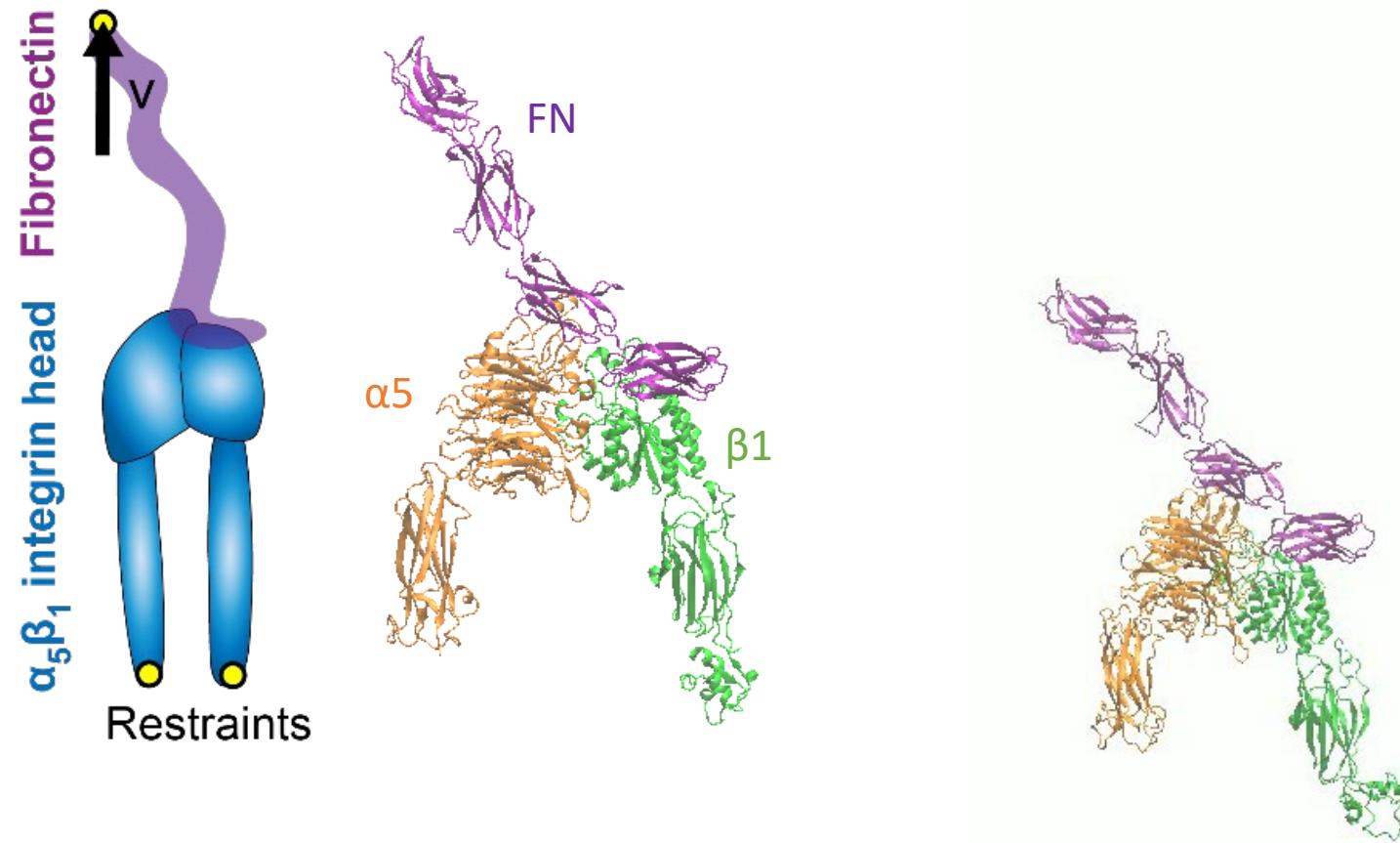


$$RMSD = \sqrt{\frac{1}{M} \sum_{i=1}^N m_i \|r_i(t_1) - r_i(t_2)\|^2}$$

N: Atoms P: Pressure  
V: Volume T: Temperature

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# Molecular Dynamics

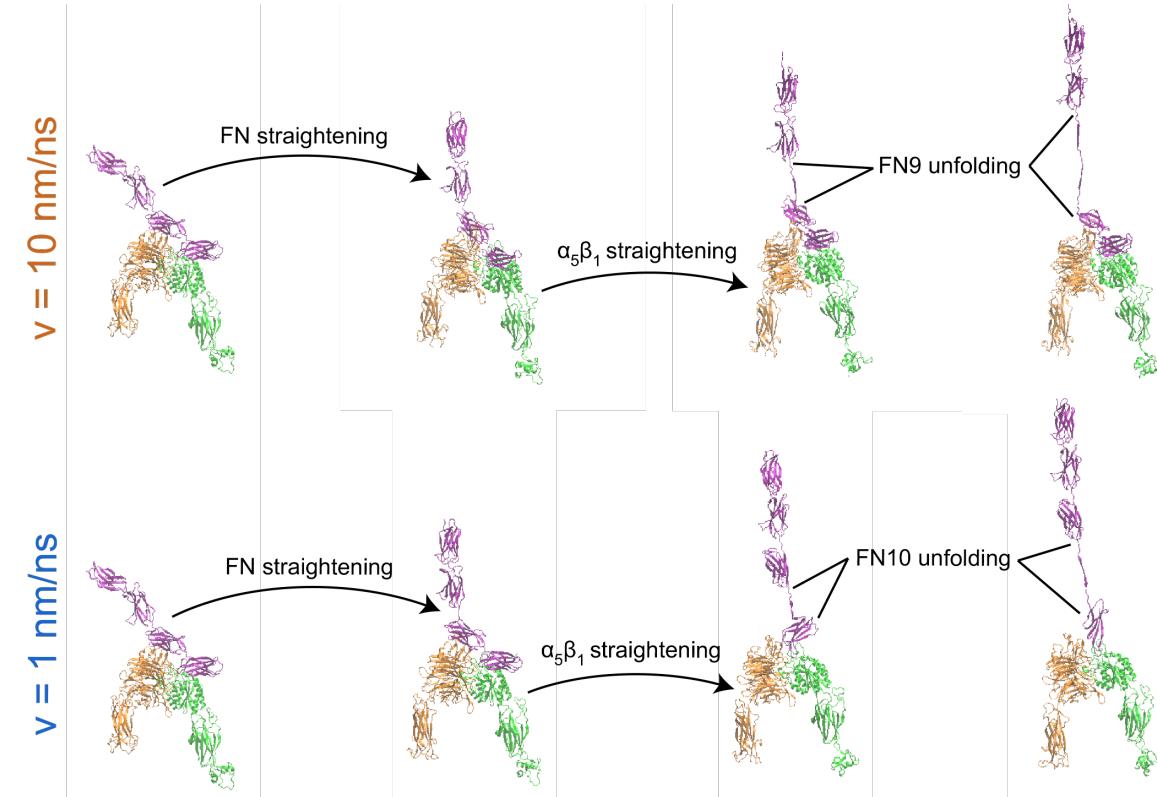
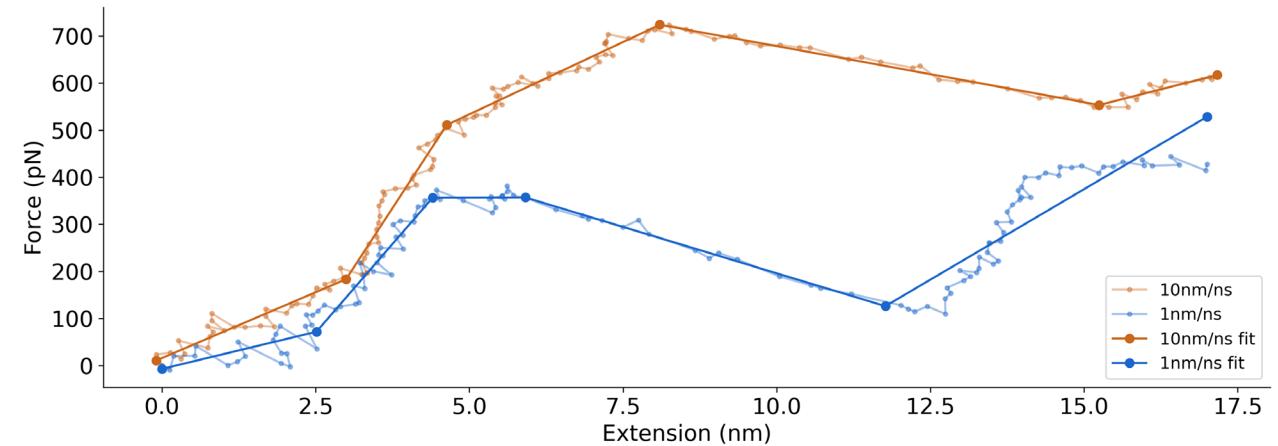
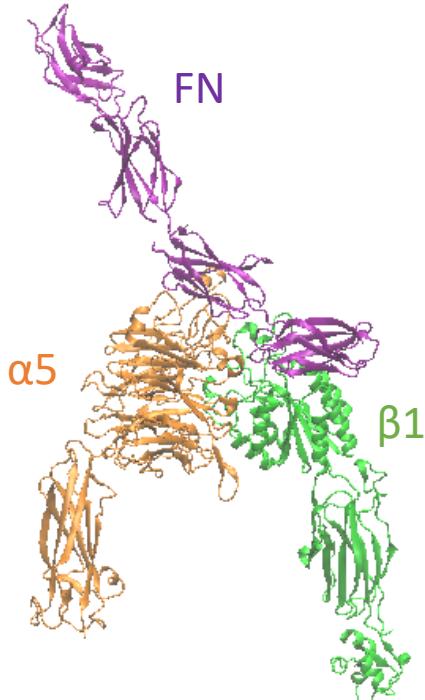
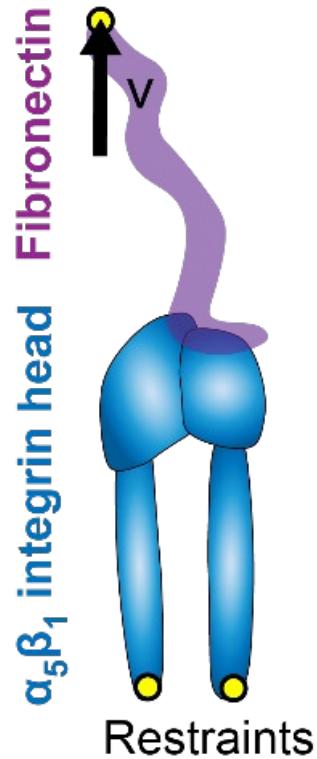


10 nm/ns

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# Molecular Dynamics

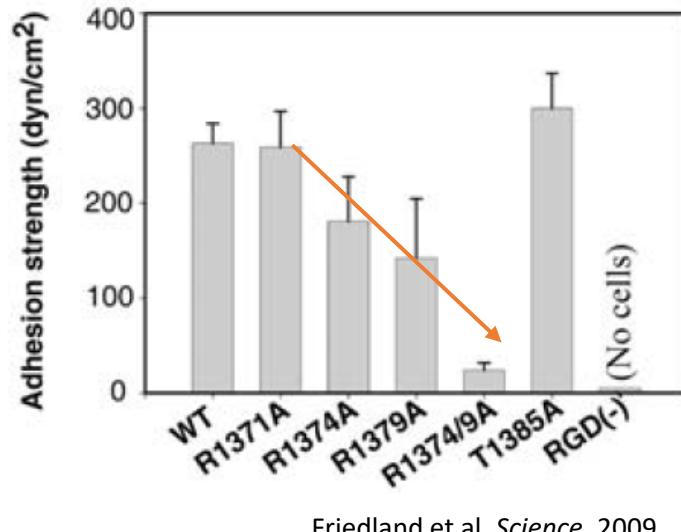


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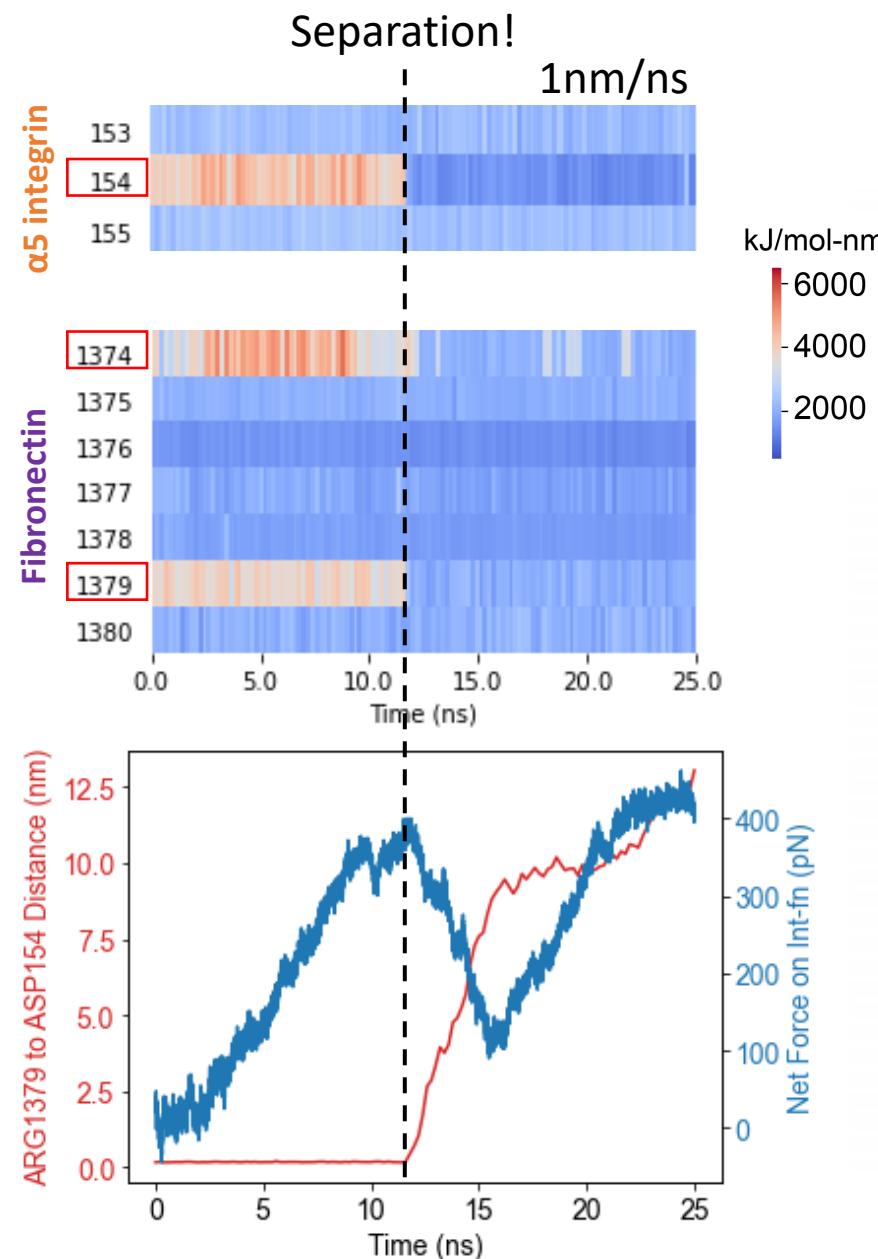
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# Individual amino acid interactions confirms key adhesion mediators

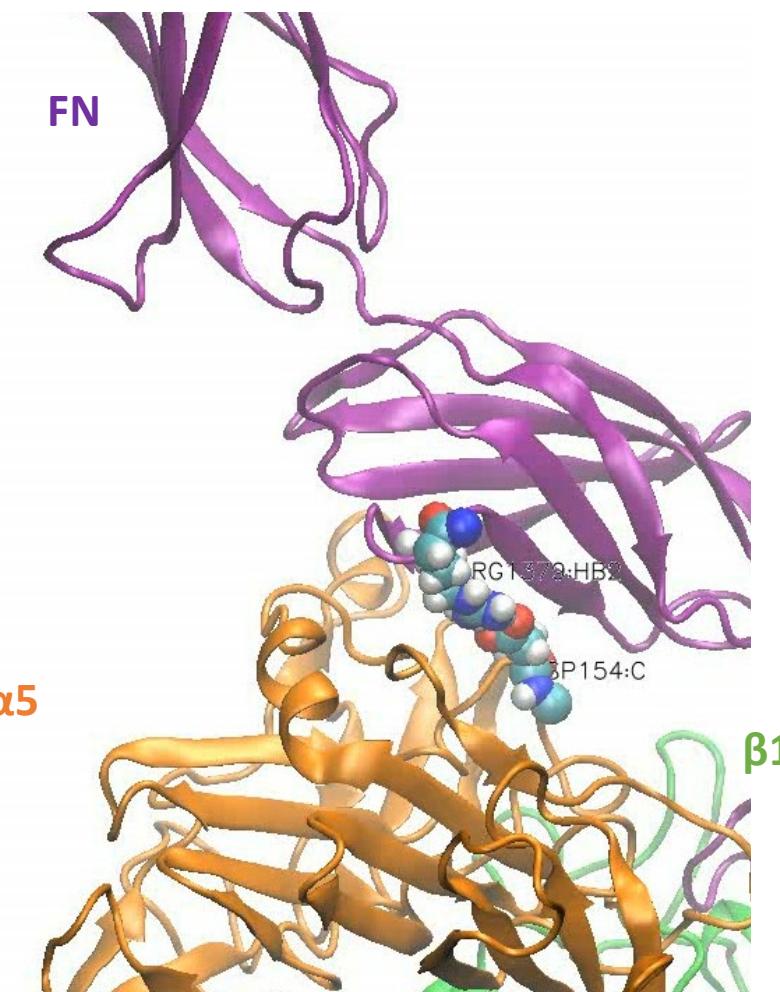
Mutation of 1379 reduces cell adhesion strength per spinning disk assay



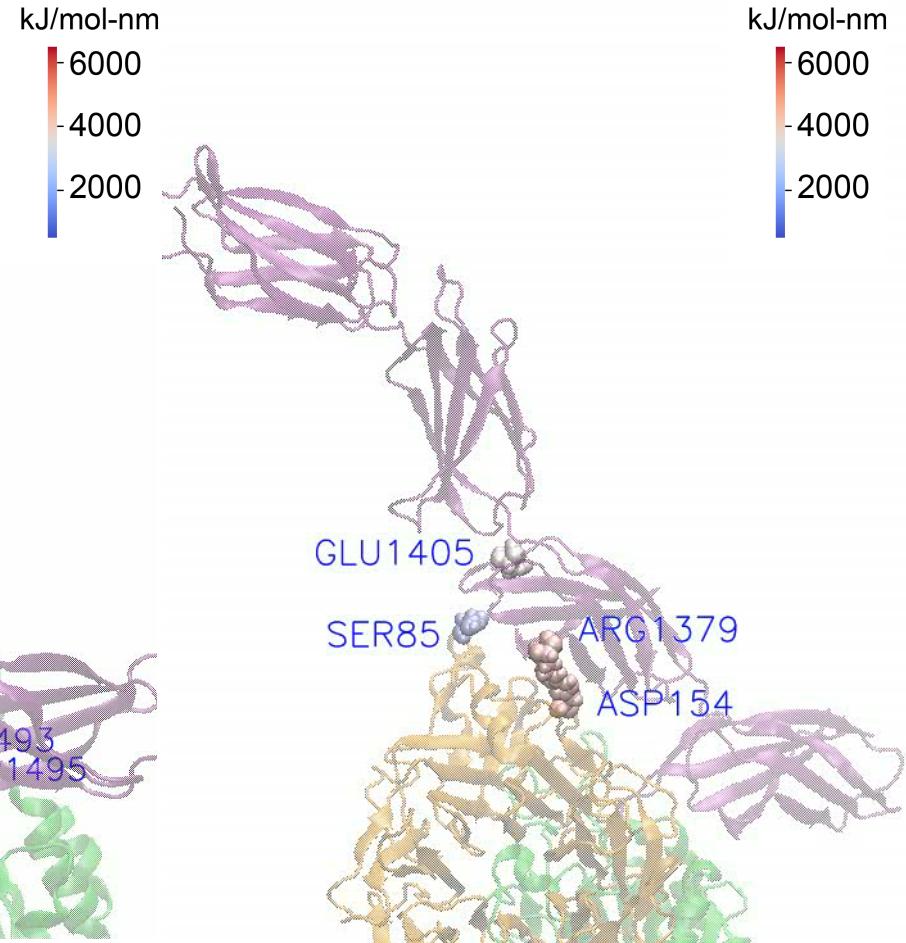
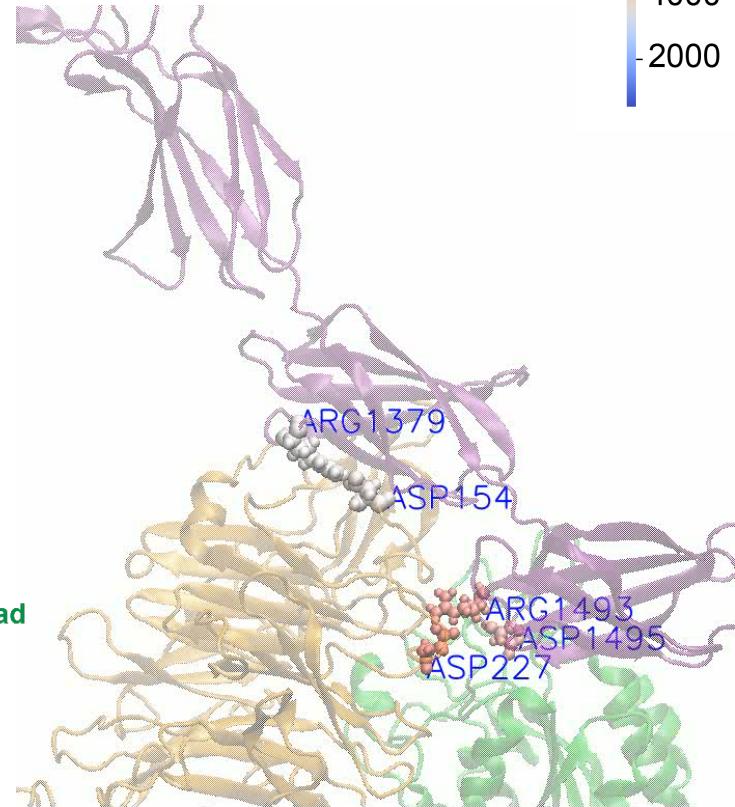
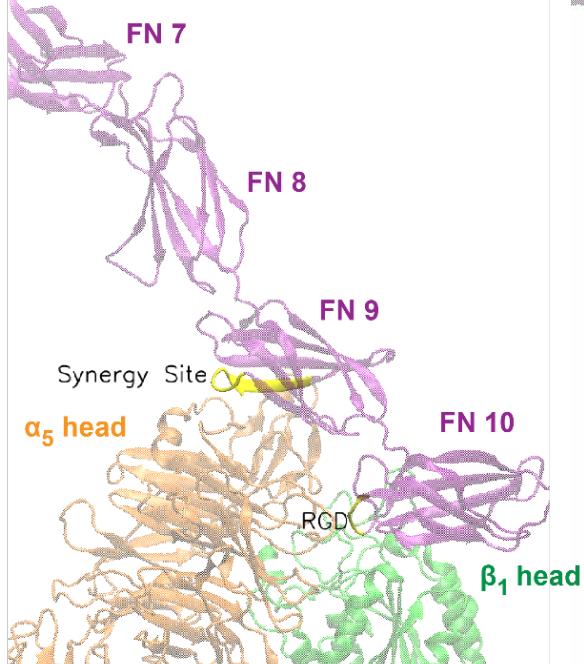
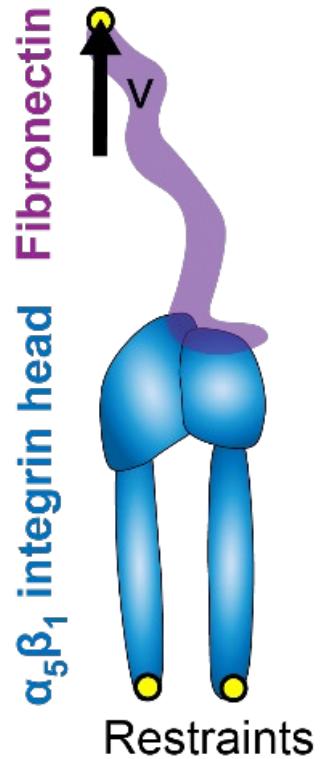
Friedland et al. *Science*. 2009.



Movie shows moment of separation



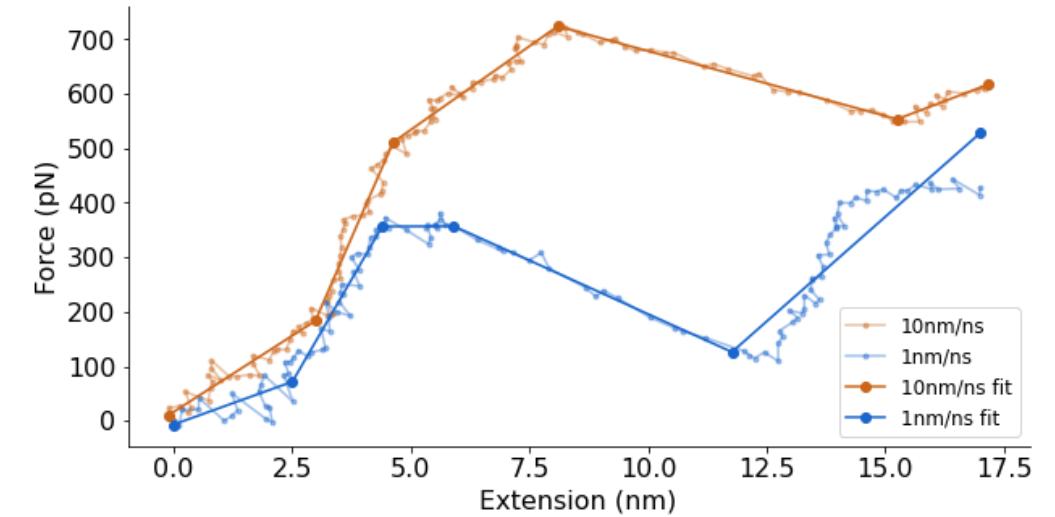
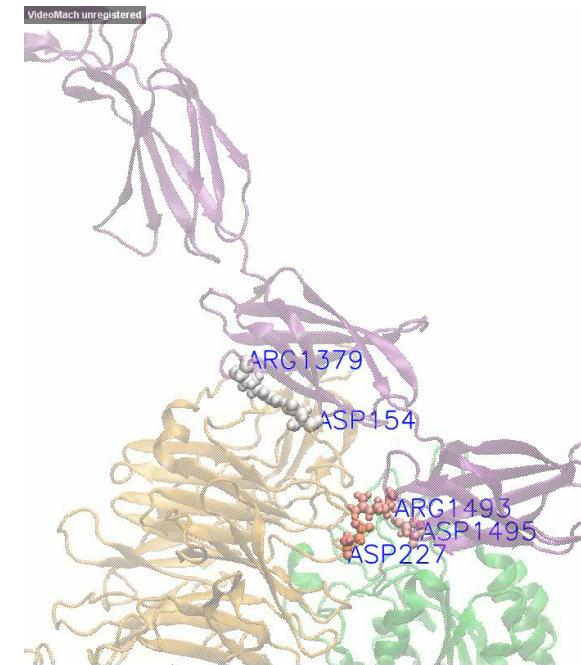
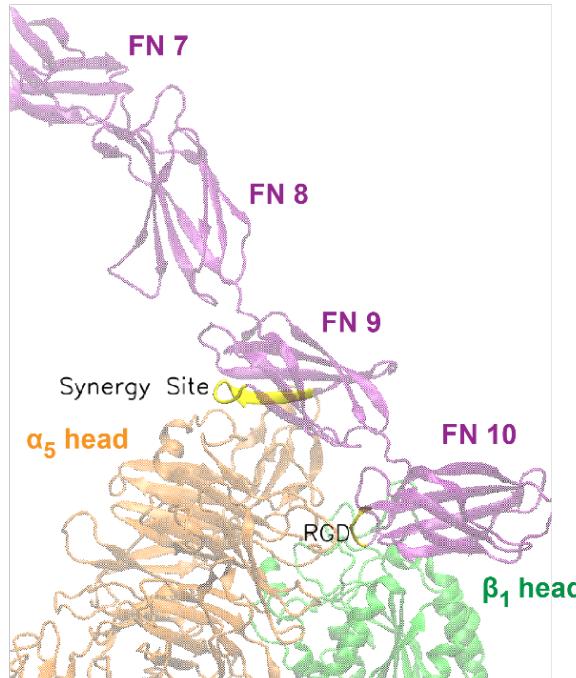
# Individual amino acid interactions confirms key adhesion mediators



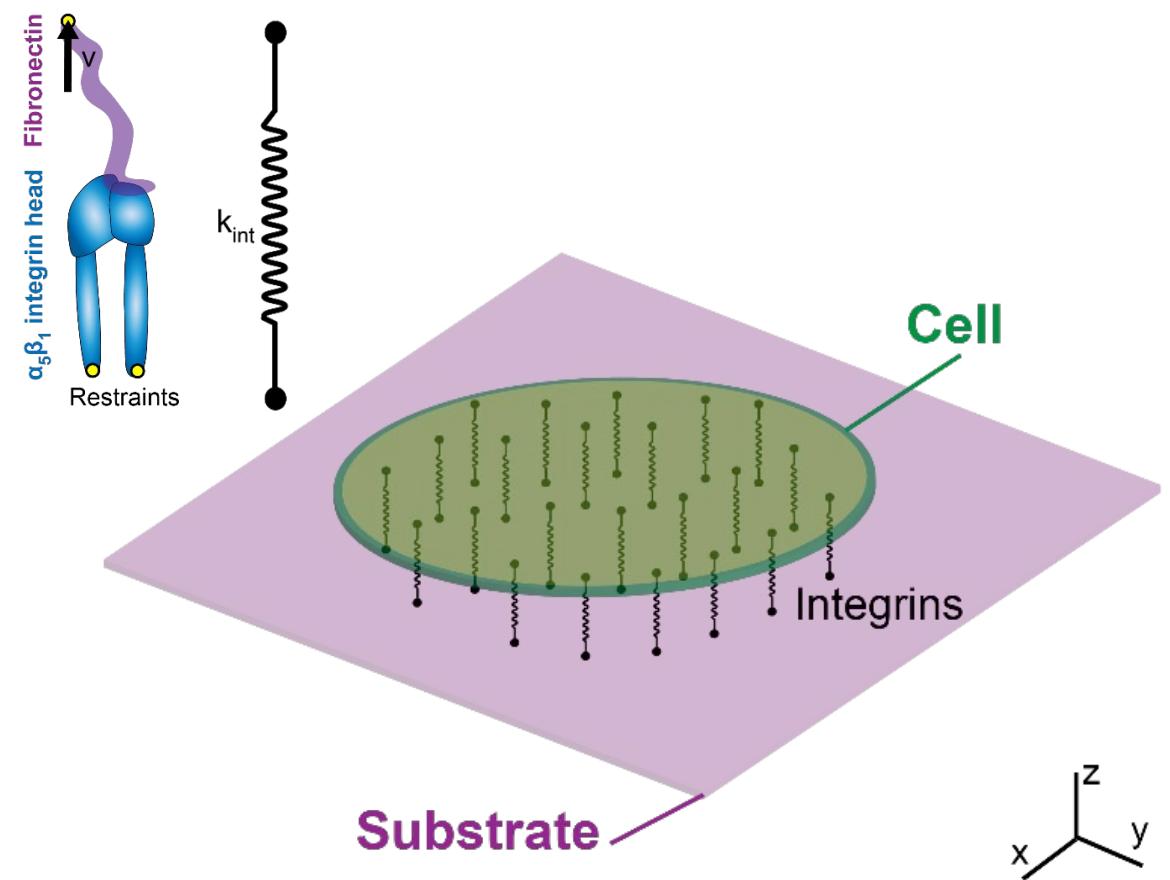
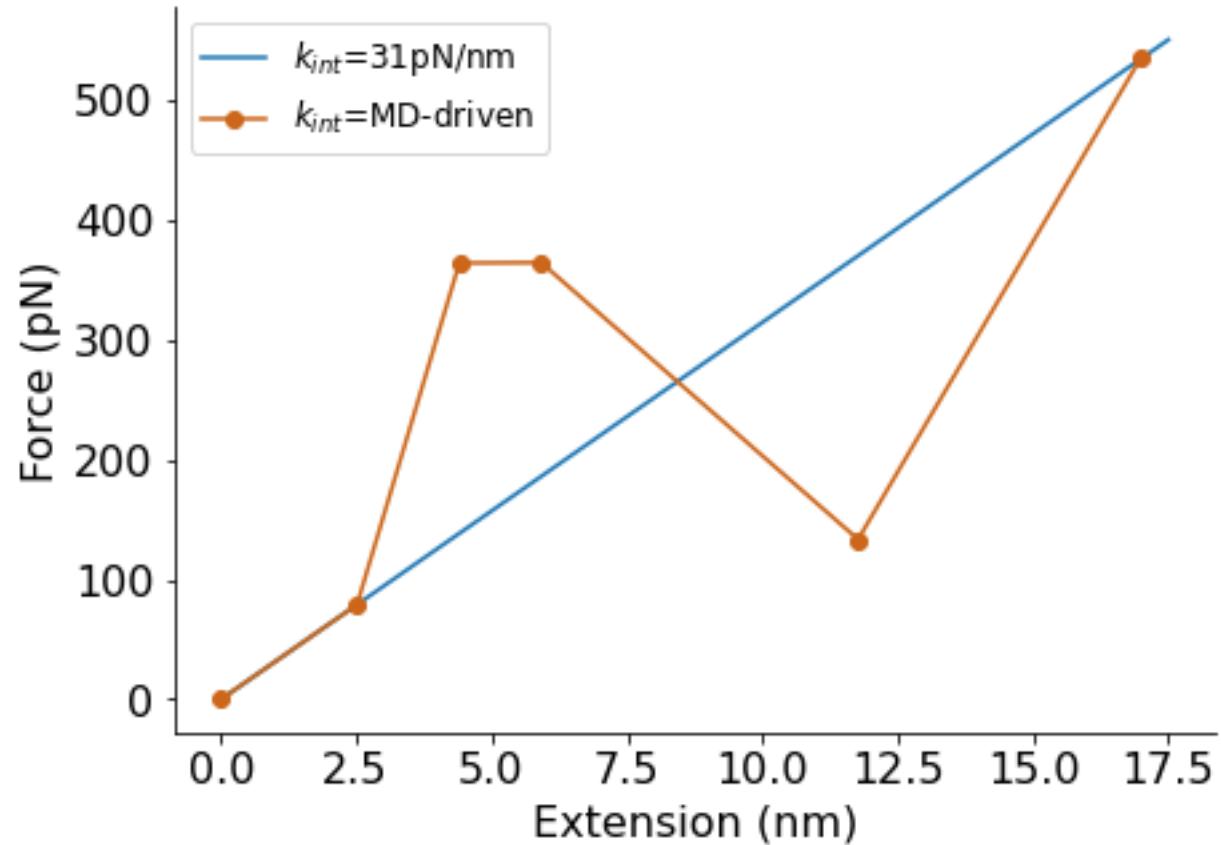
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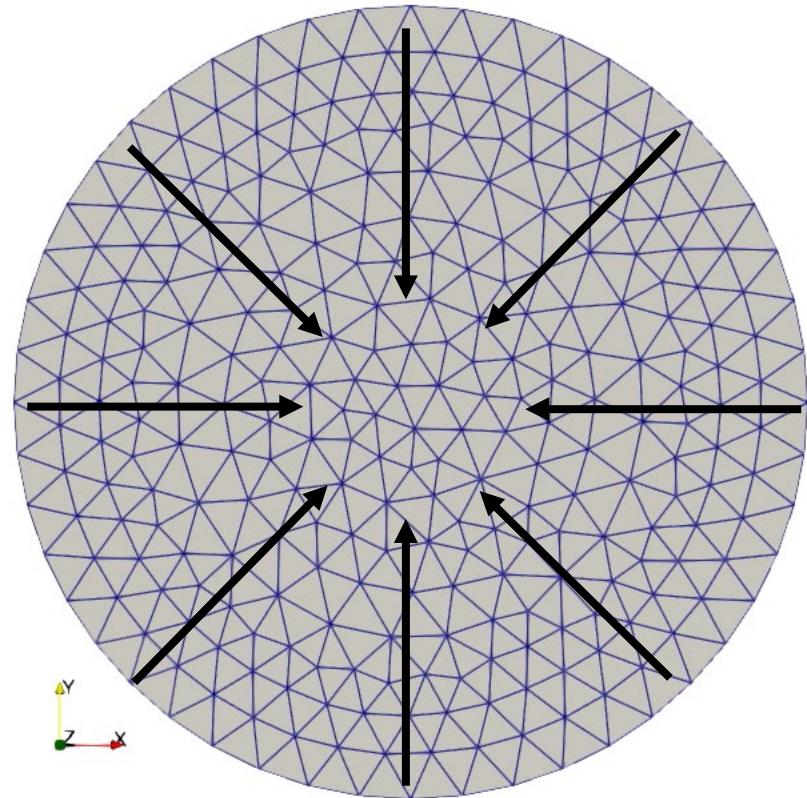
# Amino acid interactions at synergy site contribute to the nonlinear force-extension behavior of $\alpha_5\beta_1$ -FN



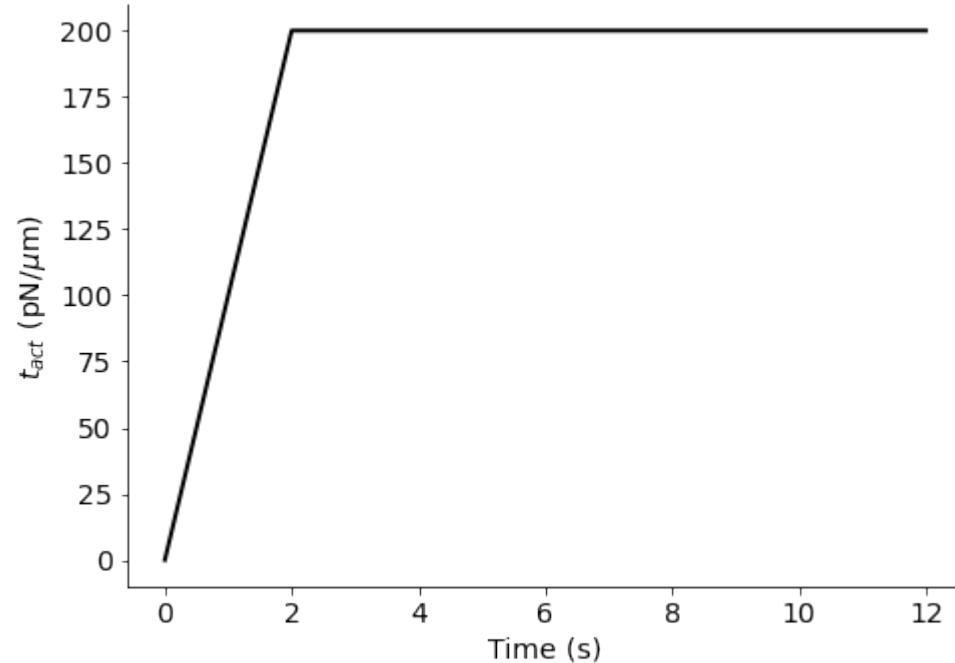
# Multiscale coupling



# Isotropic cell contractility



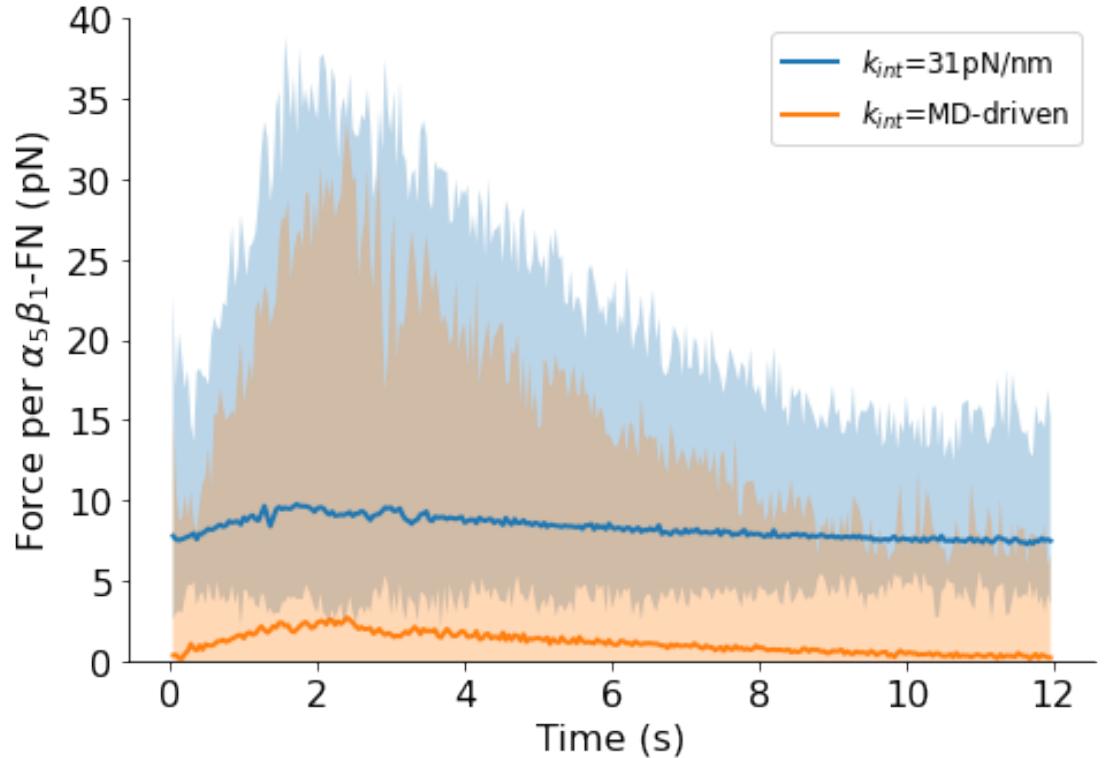
$$f_{int} - \nabla(\sigma_c^{pas} + \sigma_c^{act}) = \rho_c \mathbf{a}_c$$
$$\sigma_c^{act} = t_{act} \mathbf{I}$$



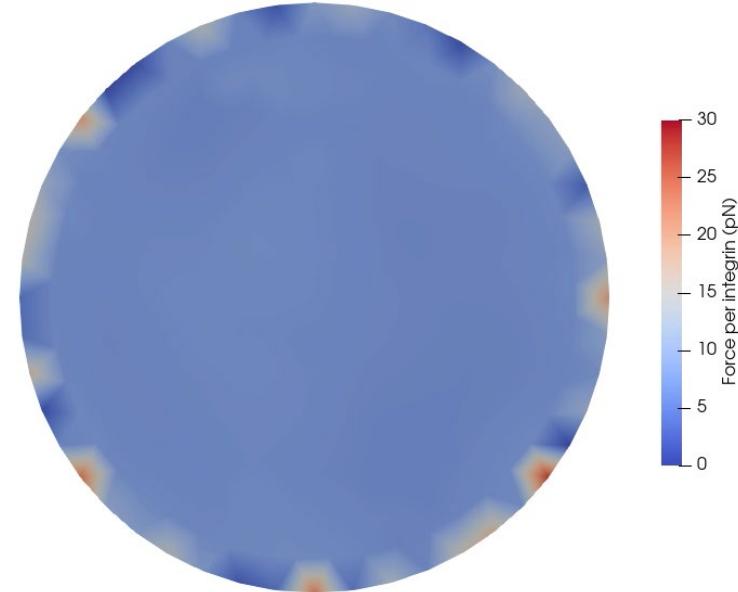
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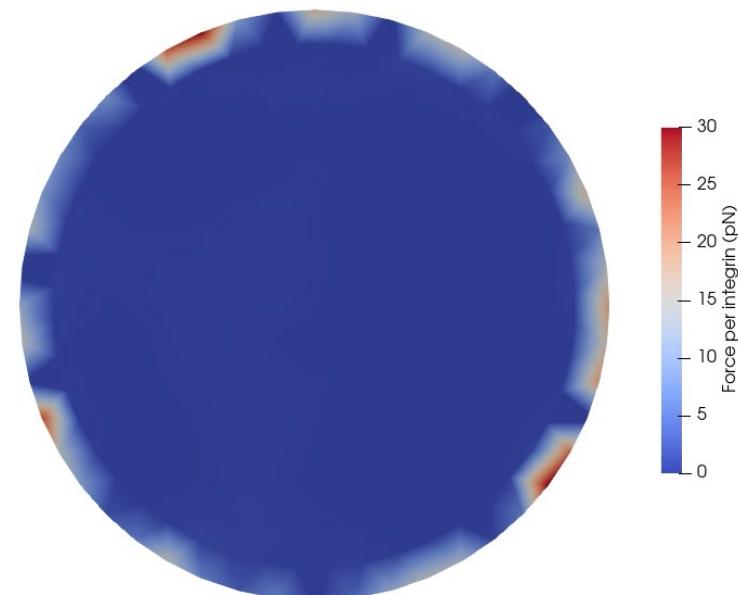
# Force per integrin is damped



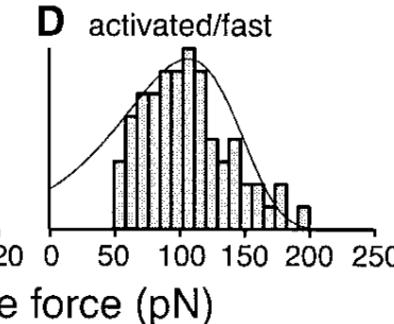
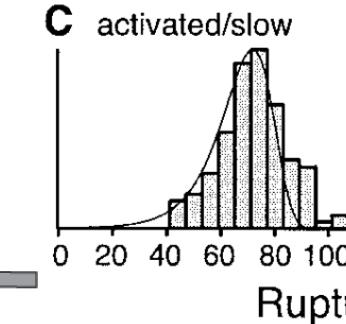
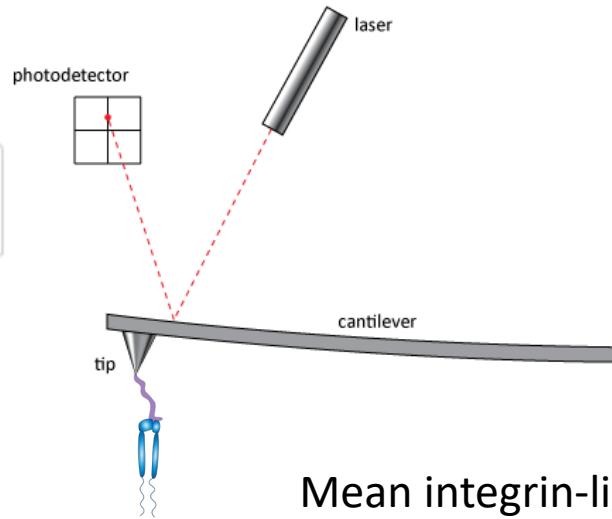
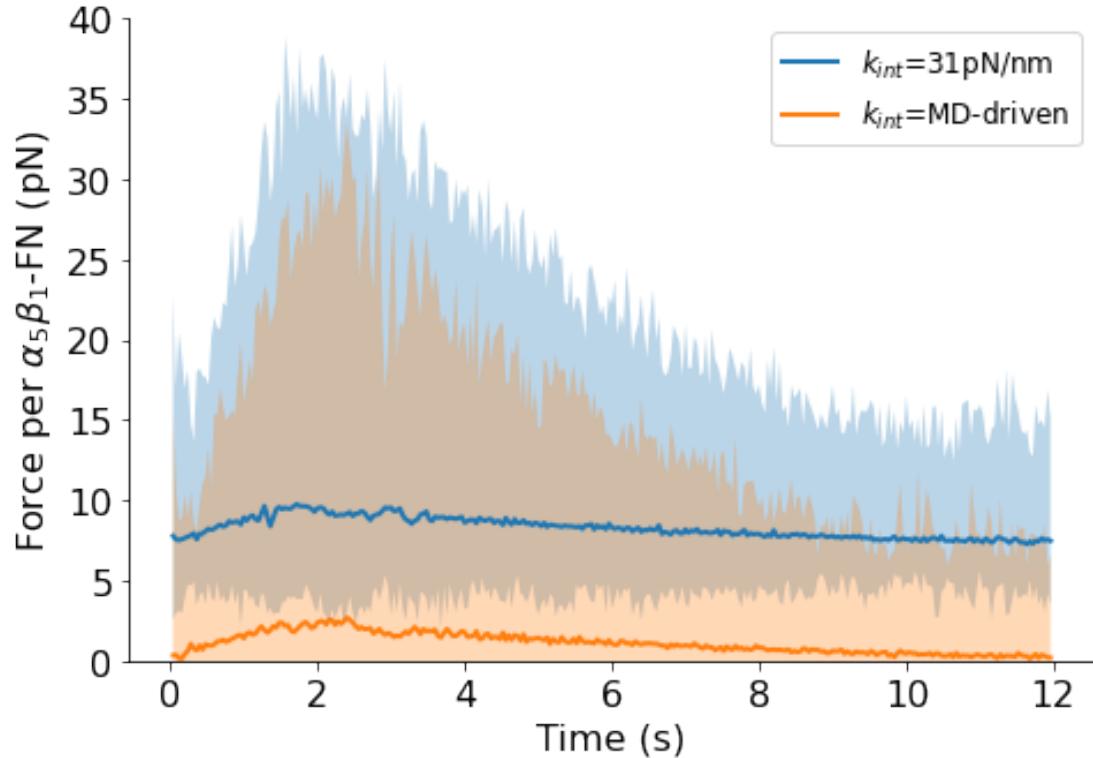
Constant 31 pN/nm



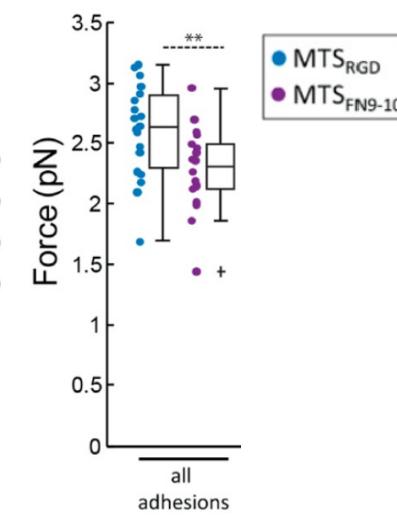
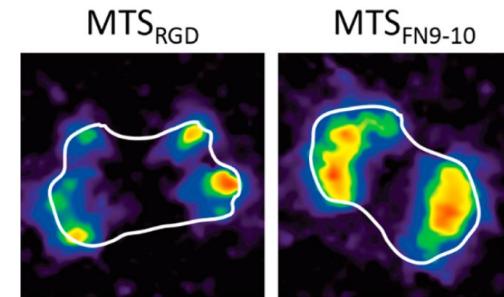
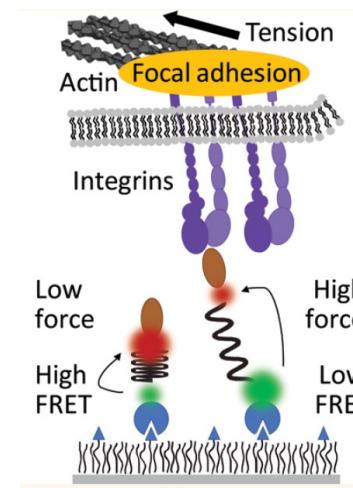
MD-driven



# Comparing to FRET-based sensors and AFM



Mean integrin-ligand rupture forces: 70 – 100 pN [1]



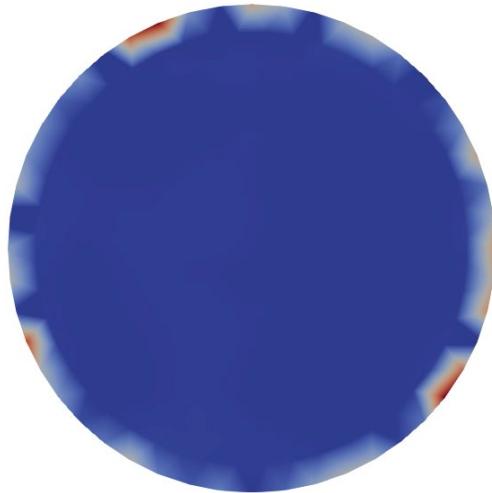
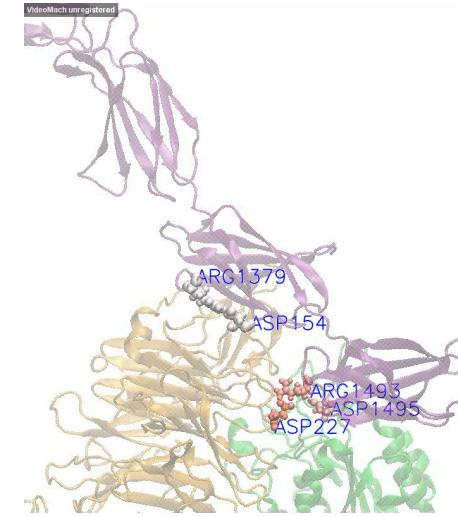
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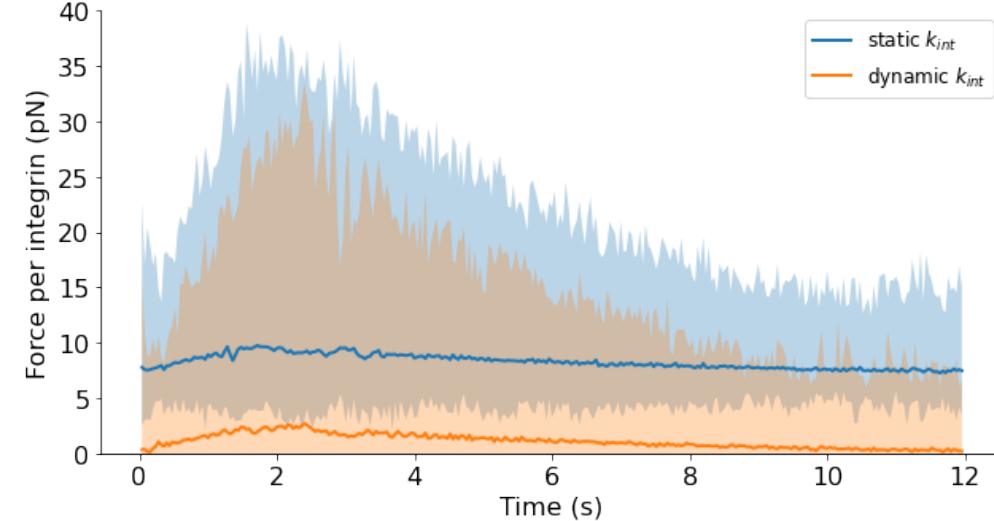
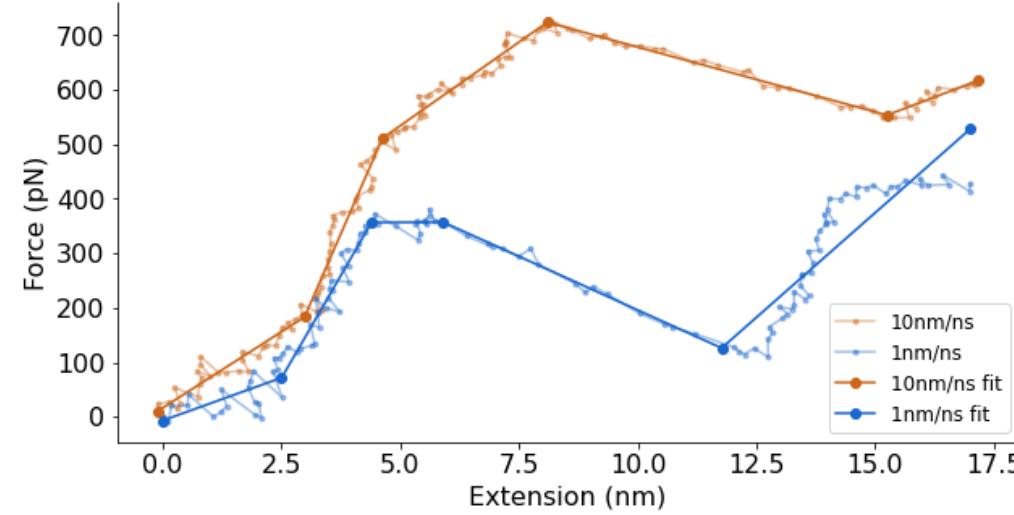
[1] Li et al. *Biophysical Journal*. 2003. [2] Chang et al. *ACS Nano*. 2016.

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Amino acid interactions at synergy site contribute to the nonlinear force-extension behavior of  $\alpha_5\beta_1$ -FN, which can lead to damped whole-cell adhesion force landscapes



30  
25  
20  
15  
10  
5  
0  
Force per integrin (pN)

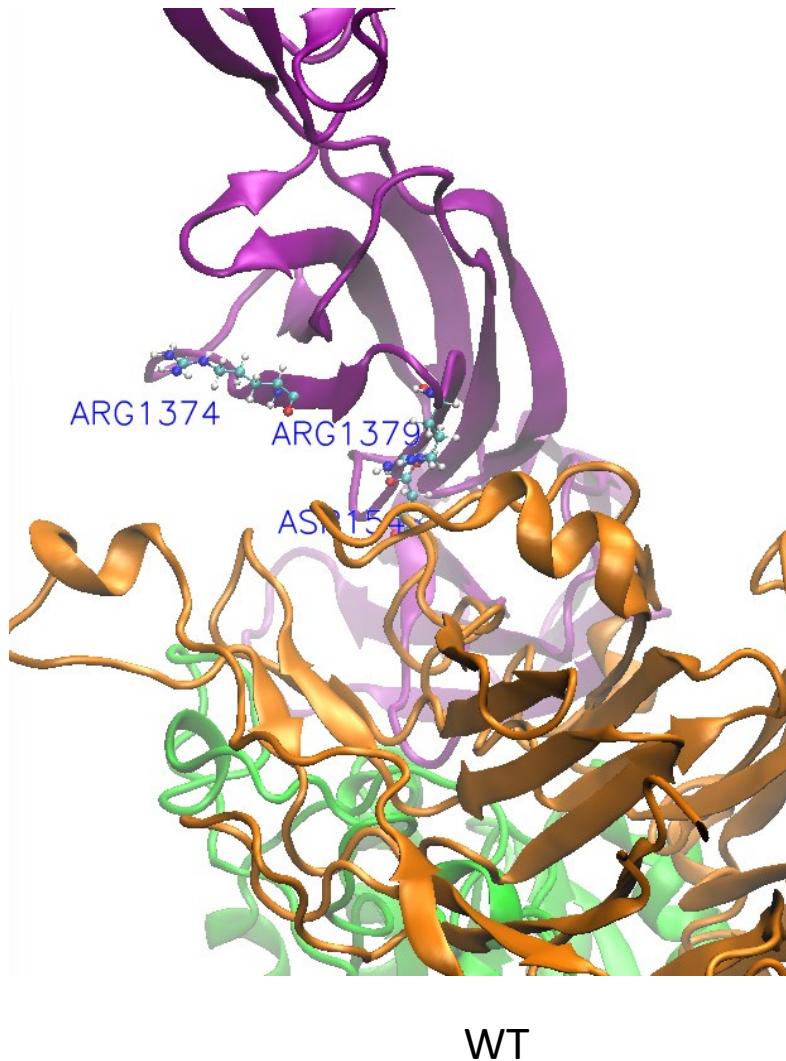
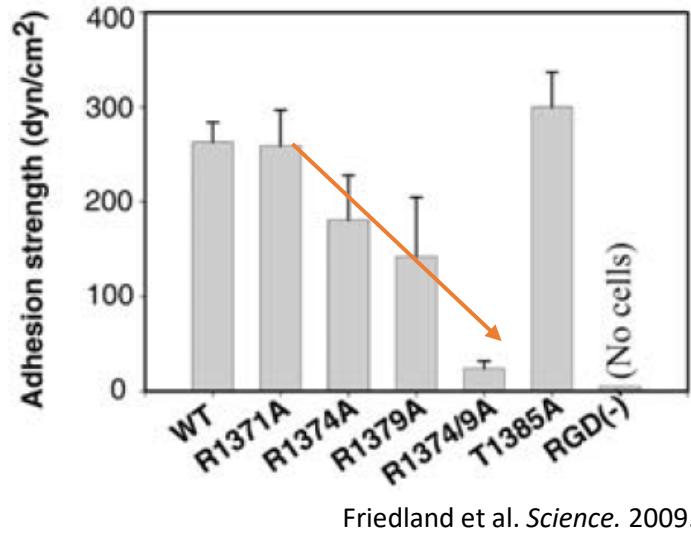


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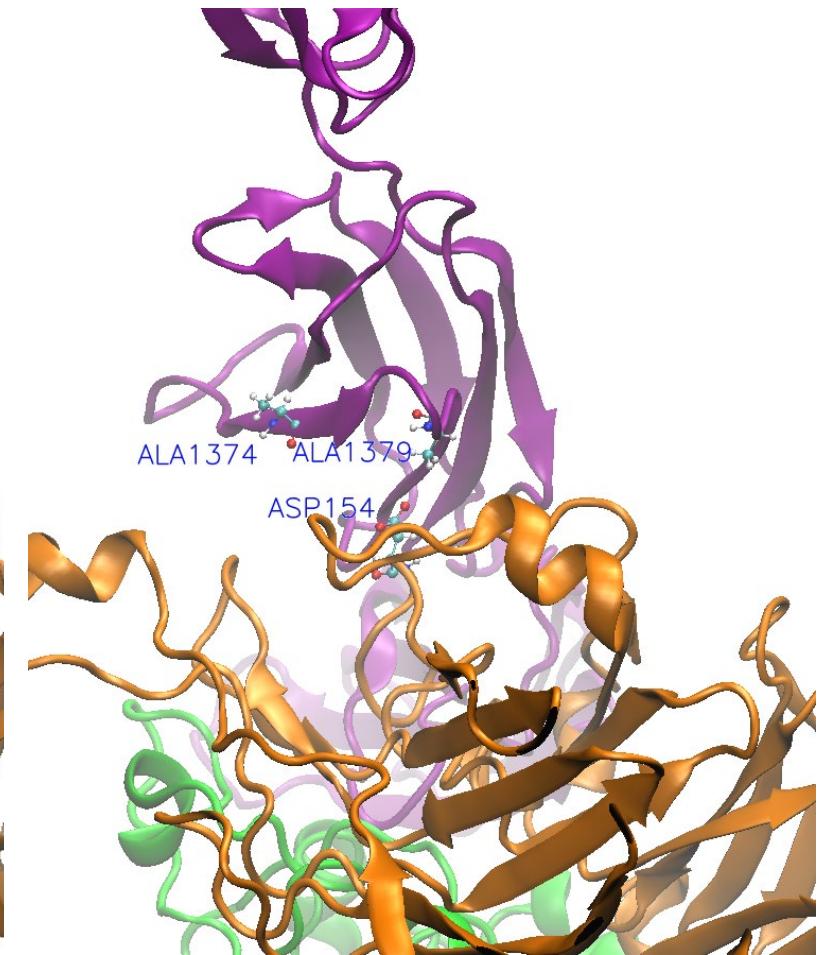
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# Ongoing Work

Virtual mutation of R1374/9A



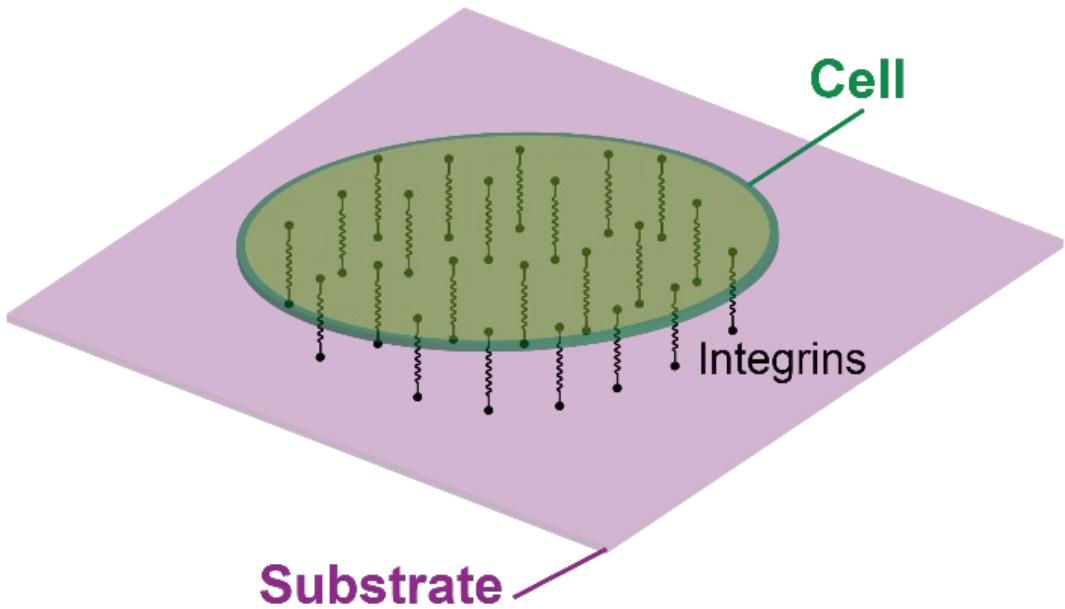
WT



R1374/9A

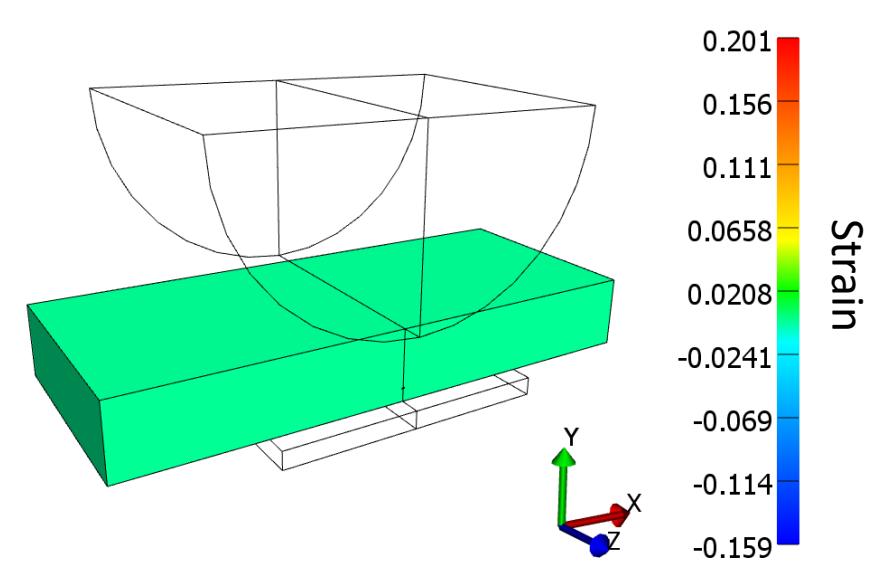
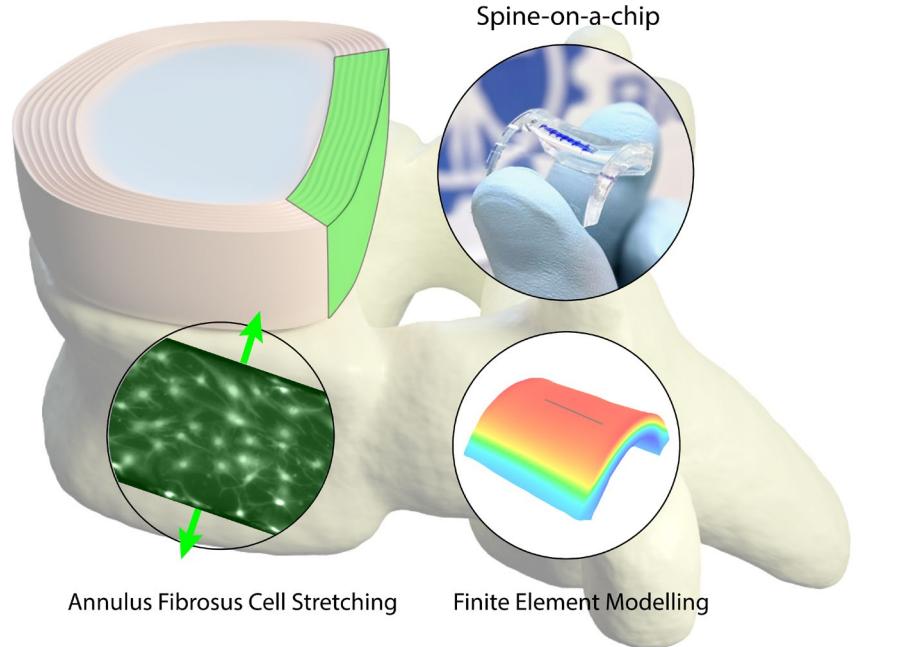
# Ongoing Work

Stretching the substrate

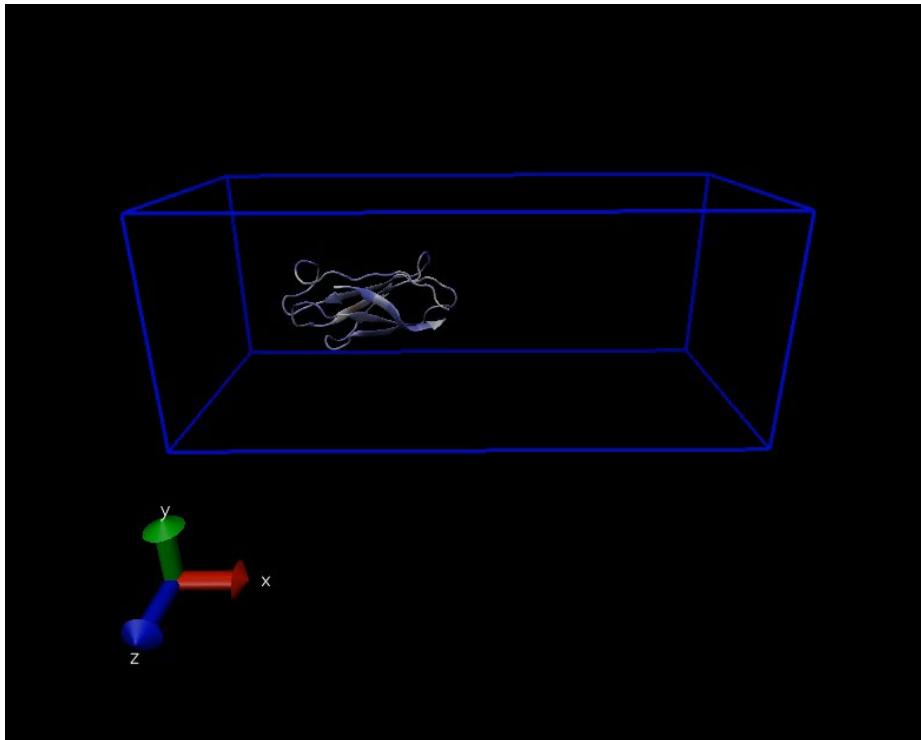


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# Fibronectin Steered Molecular Dynamics and Force Distribution Analysis Demo



Available: [github.com/dredremontes/fn\\_MD\\_FDA](https://github.com/dredremontes/fn_MD_FDA)

More info: [dredremontes.github.io](https://dredremontes.github.io)

Your feedback is appreciated



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