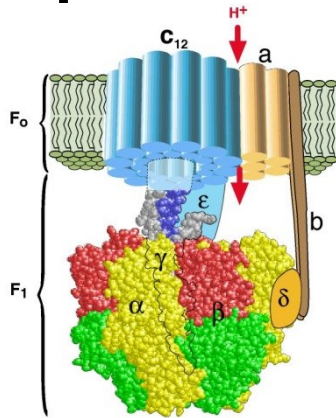


Önrendeződő fehérjék és peptidek elméleti és kísérleti tanulmányozása

Peptidkémiai Alapítvány,
MTA,
14. 11.2016

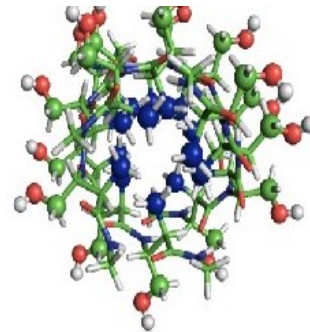
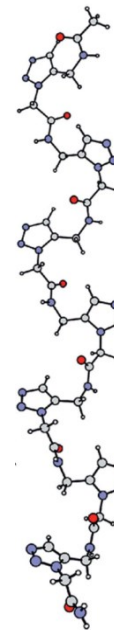
Komplex Biomolekuláris Motorok



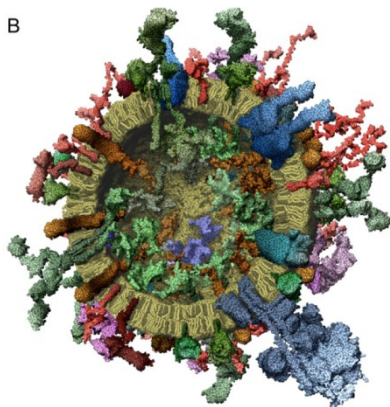
H. Wang and G. Oster (1998). Nature 396:279-282.



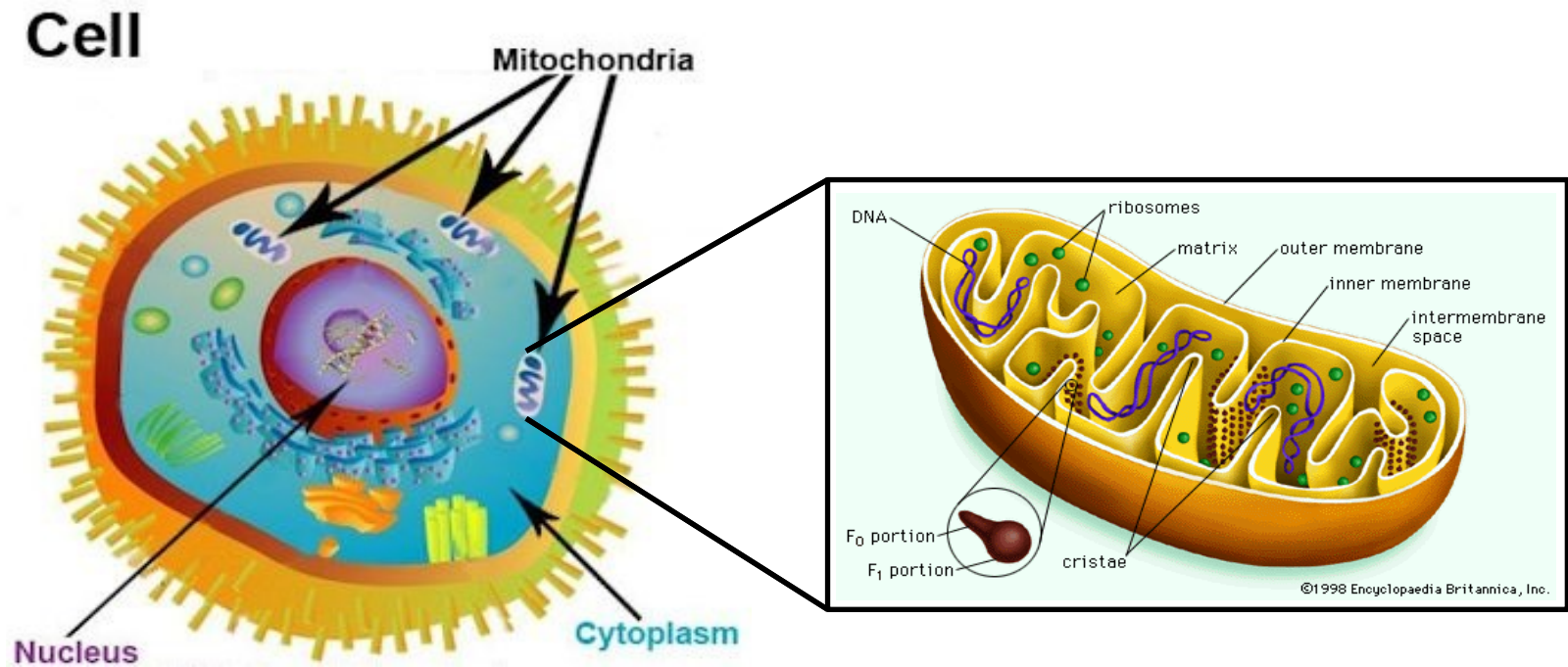
Foldamerek



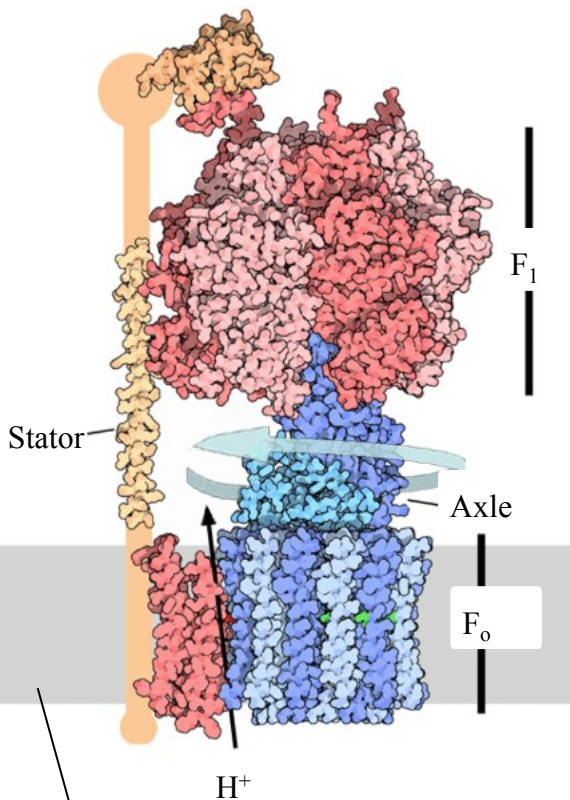
Flow - LD – Filament, Fibrillum Membrán aktív



F_0F_1 - ATP szintáz



F₀F₁ - ATP szintáz

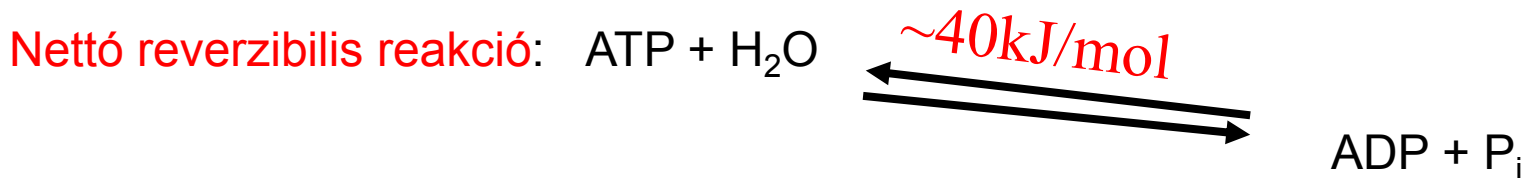


Belső membrán

The rotary catalytic mechanism of mitochondrial ATP synthase.

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MRC | Dunn Human Nutrition Unit



http://en.wikipedia.org/wiki/ATP_synthase

<http://www.youtube.com/playlist?list=UUZ7c6Hzi7XUpVmk4IBltHqQ>

Tömegtermelés: **50-75 kg/nap!!**

F₀F₁ - ATP szintáz

View from above and then below the F₁ domain along the rotating γ -subunit.

© Medical Research Council

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Nutrition Unit

F₁ • ATP

F₁ • ADP P_i

Senior *et al* BBA, 2002

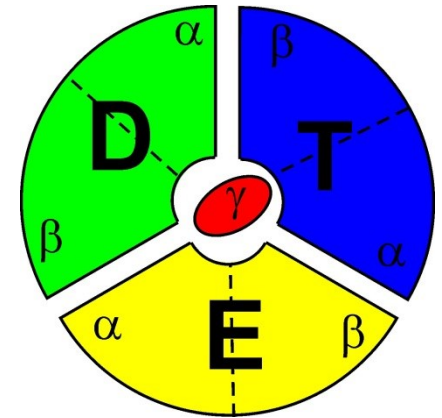
Penefsky *Methods Enzymol*, 1986

F₁ egyedül: ATP-t hidrolizál

Abrahams *et al*. Nature 1994 Adachi *et al*. Cell 2007
Kinosita *et al*. Nature 2001

Pionírok:

Dittrich *et al* Biophys. J. 2004 Strajbl *et al* PNAS, 2003
Yang *et al*. PNAS 2003



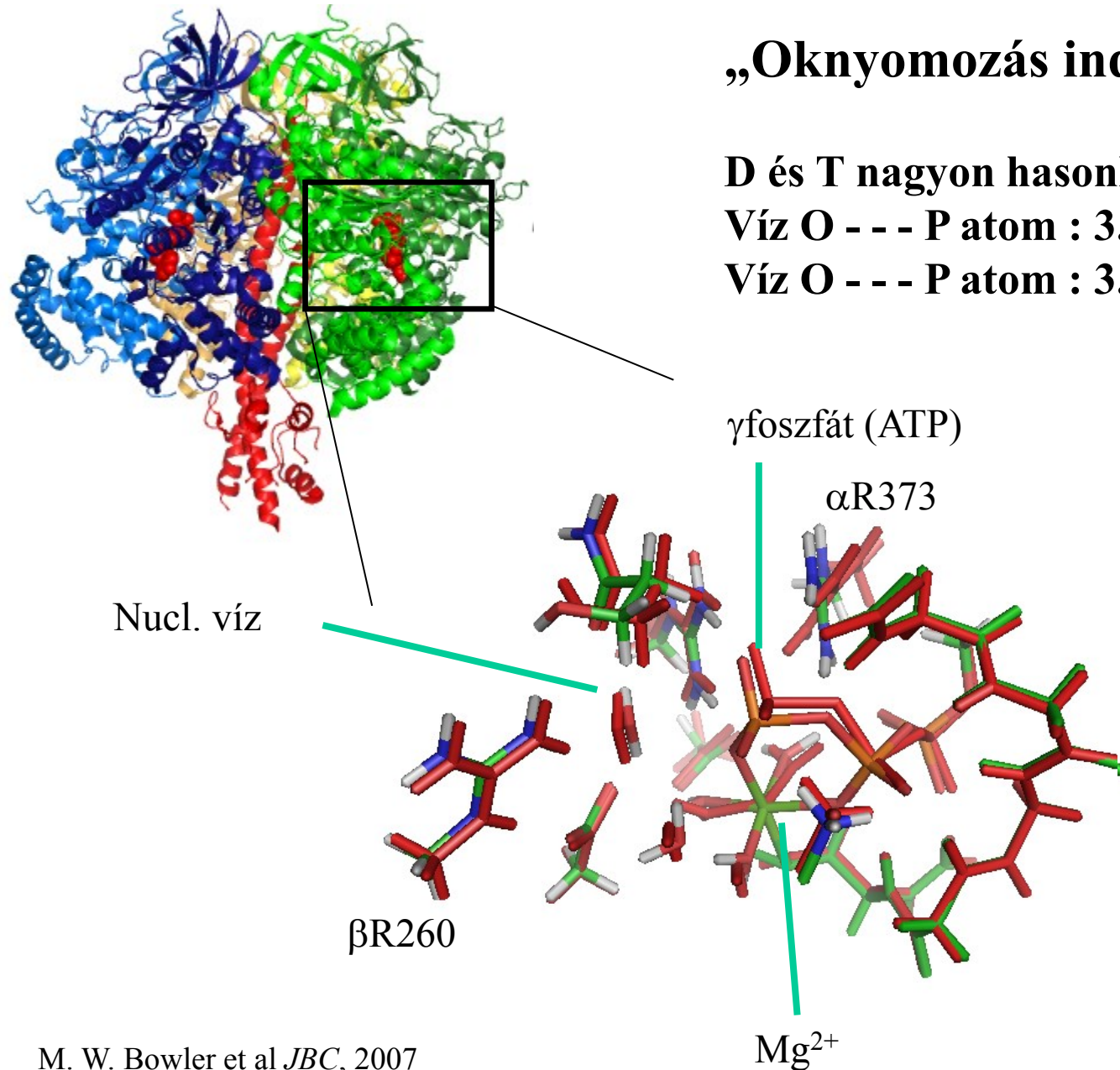
F₁ - ATPáz

„Oknyomozás indul”

D és T nagyon hasonló???

Víz O - - - P atom : 3.8Å (T)

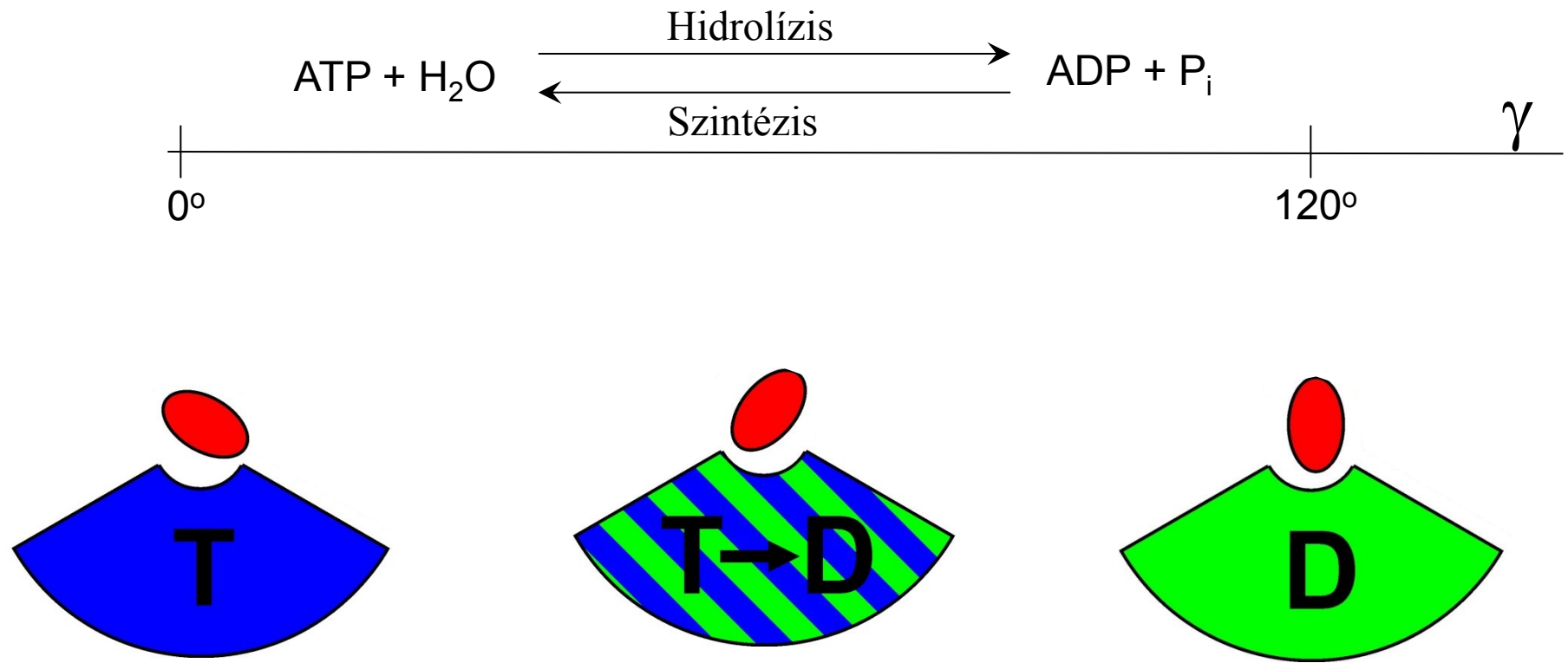
Víz O - - - P atom : 3.1Å (D)



**Hogyan kontrollál a F_1
sub-Ångström változásokat?**

Hogy változtatja ez a reakciót?

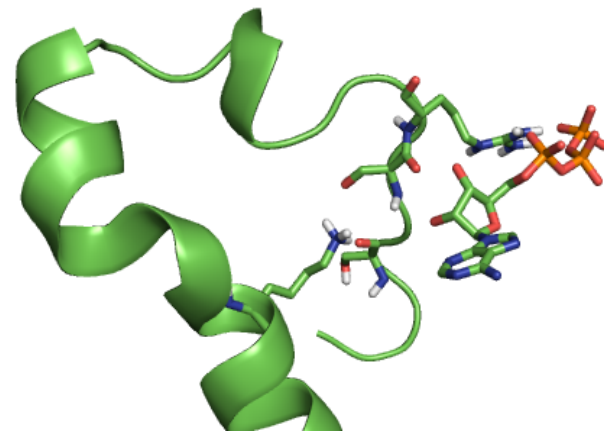
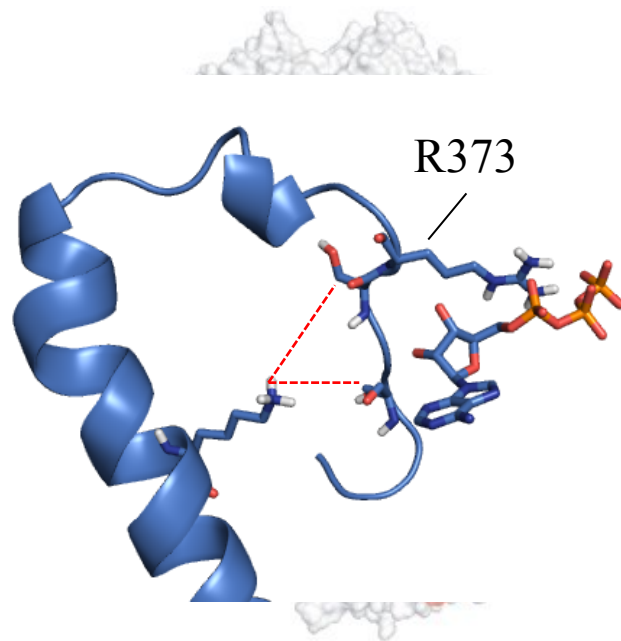
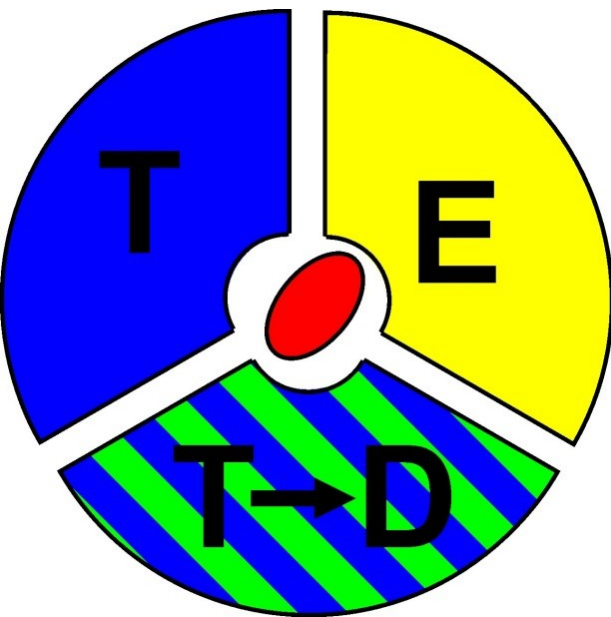
Macroskála



T: ATP, or Tight site

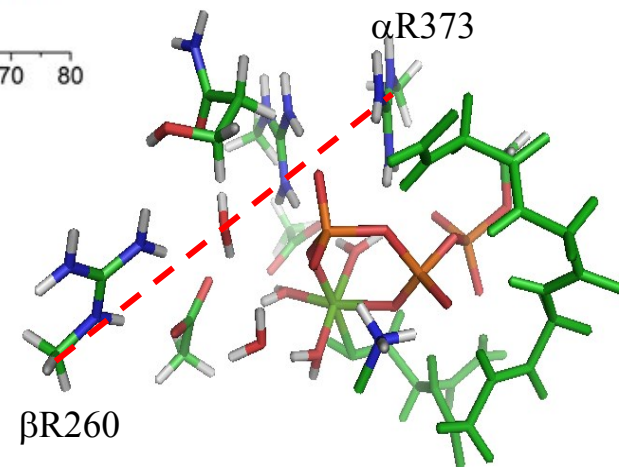
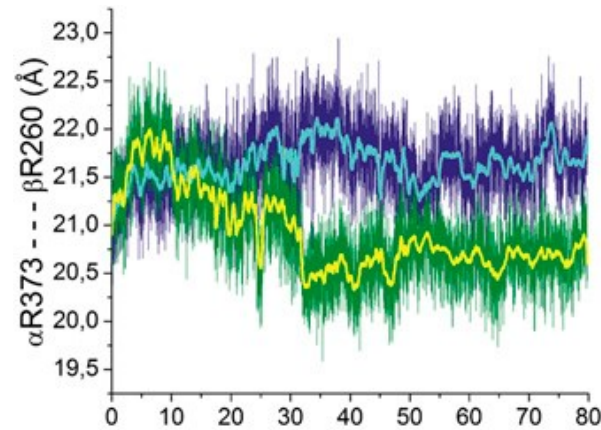
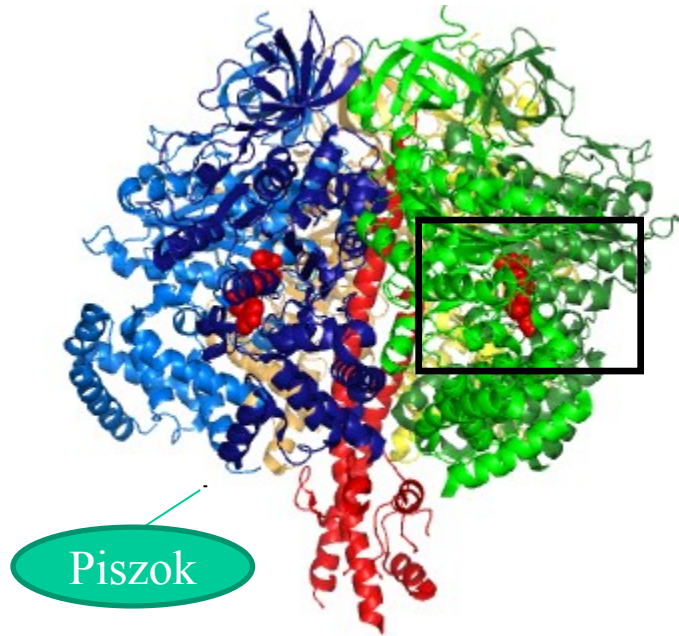
D: ADP, or Loose site

Makroskála



T: ATP, or Tight site
D: ADP, or Loose site

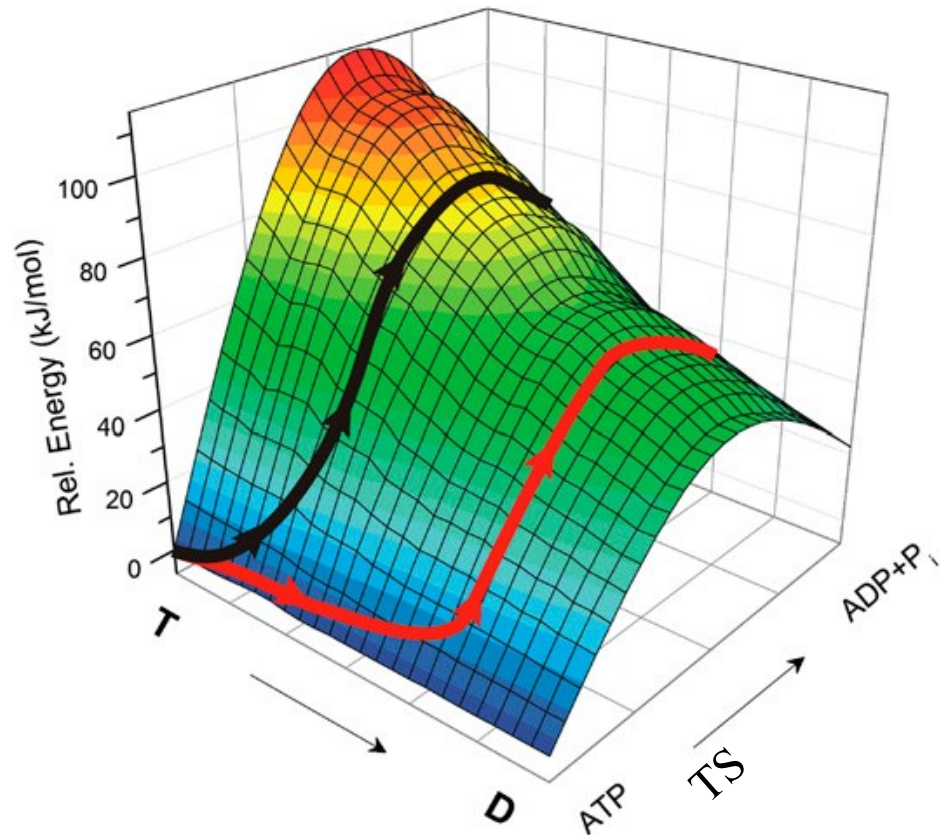
Makroskála



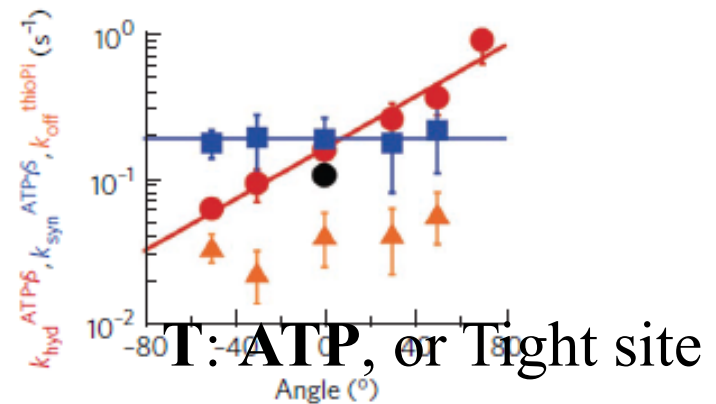
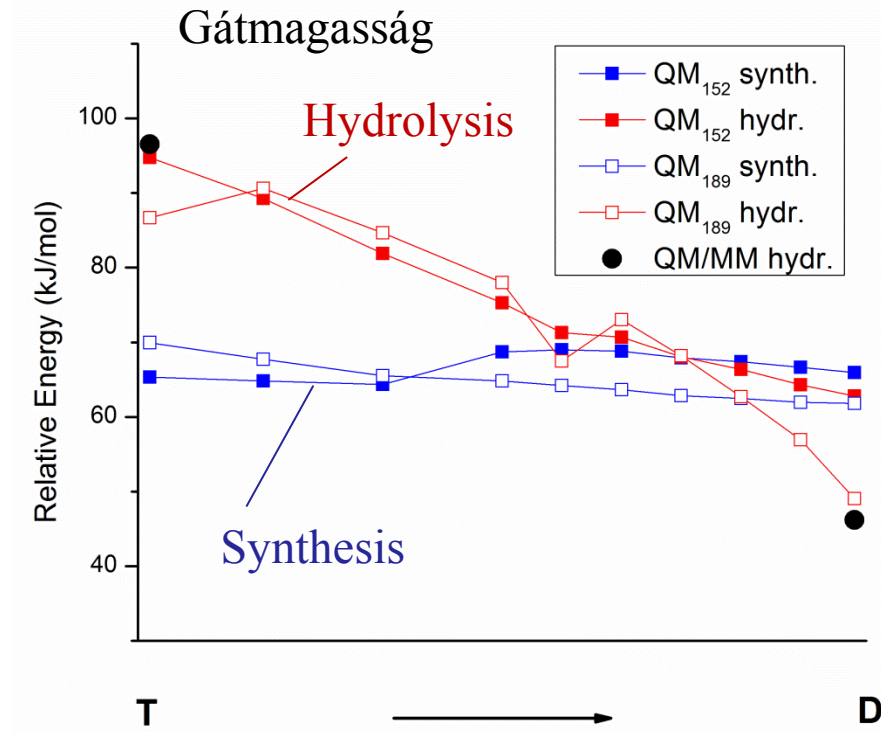
**Hogyan kontrollál a F_1
sub-Ångström változásokat?**

Hogy változtatja ez a reakciót?

Mikroskála



QM (152, 189 atom, 12 modellben)
QM/MM (152/7000, 3 modellben)



T: ATP, or Tight site

D: ADP, or Loose site

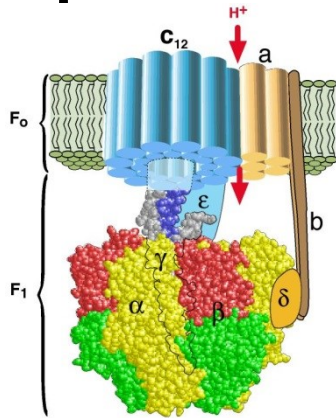
Összegzés

F_1 – Finomhangolja az aktív centrum konformációját

Asszimetrikusan változtatja a reakciósebességet a két ellentétes irányba

Létrehoz egy racsni-mechanizmust, amely biztosítja a hatékony ATP szintézist

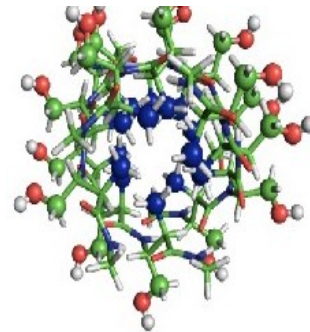
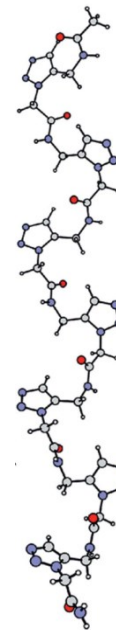
Komplex Biomolekuláris Motorok



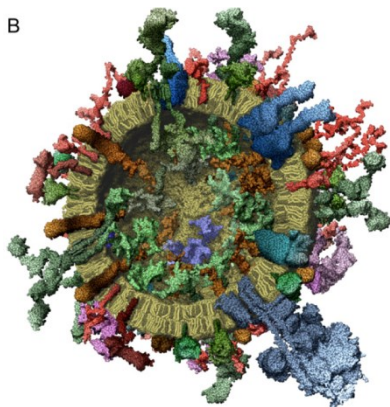
H. Wang and G. Oster (1998). Nature 396:279-282.



Foldamerek



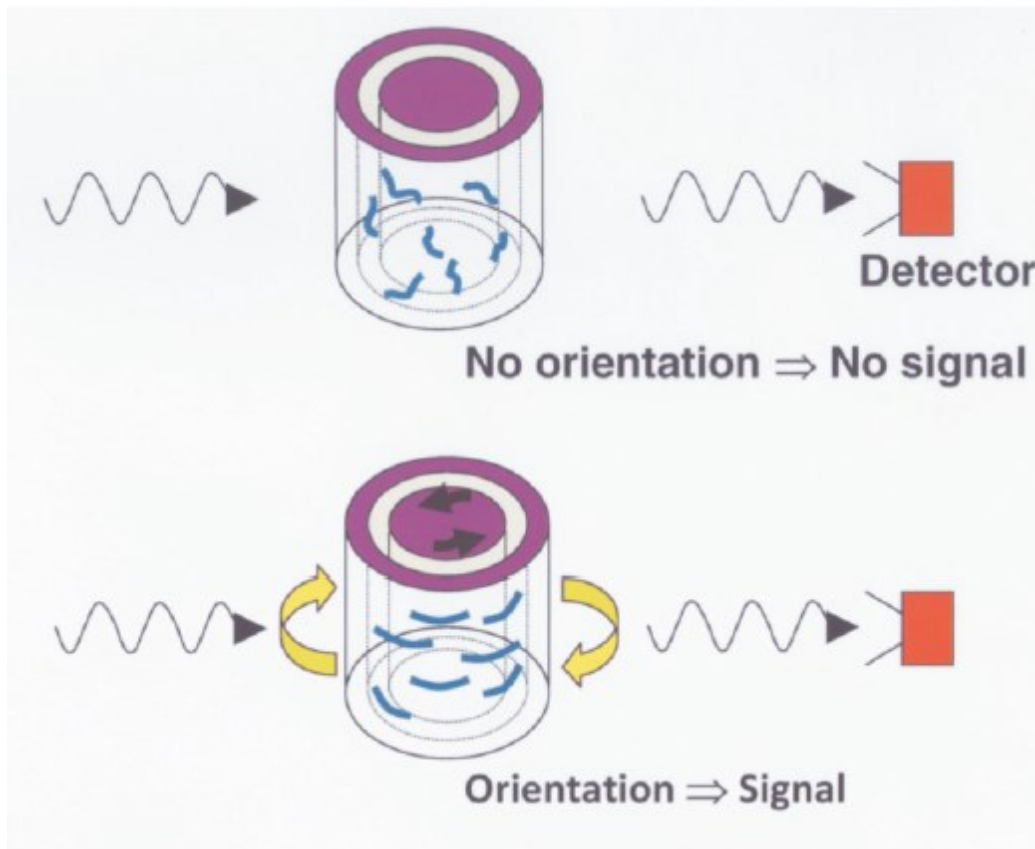
Flow - LD – Filament, Fibrillum Membrán aktív



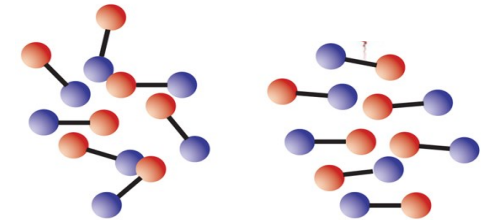
Lineáris Dikroizmus (oldatfázis) – Flow LD

$$LD = A_{\parallel} - A_{\perp}$$

Couette folyadék cella



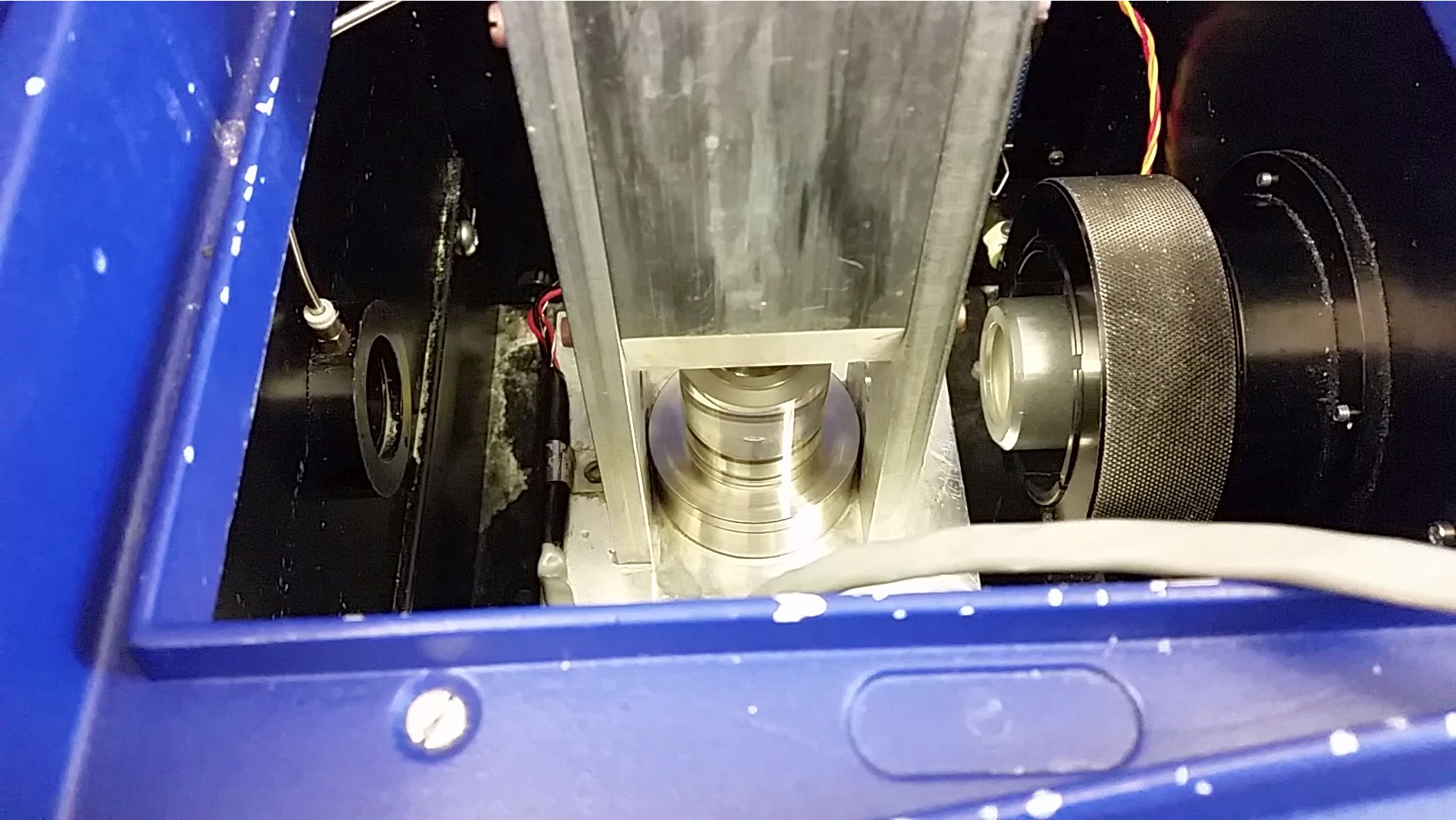
Orientációs faktor



$S = 0$

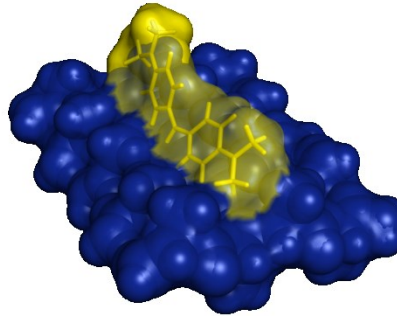
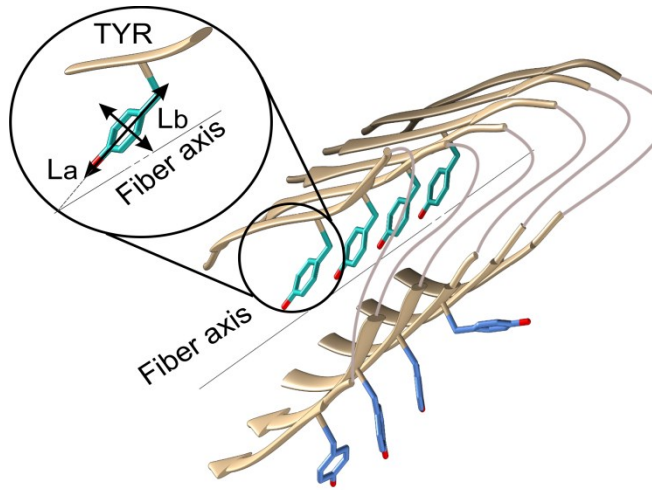
$S \approx 1$

Lineáris Dikroizmus (LD) Spektroszkópia



Flow LD – Fibrillumok és filamentumok

Amyloid fibrillumok



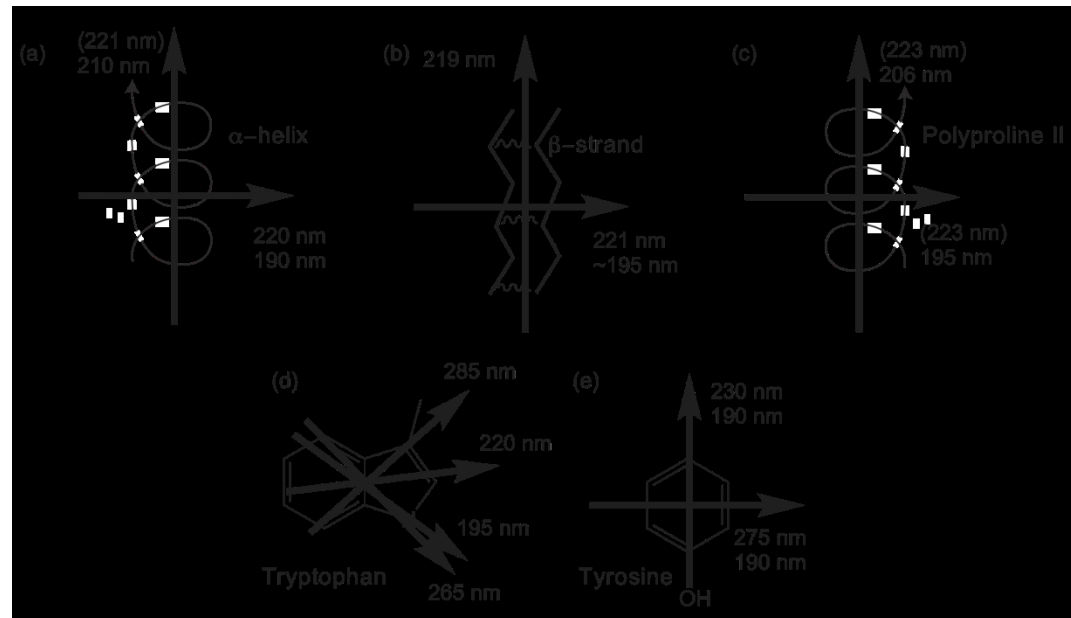
Reymer, Frederick, Rocha, Beke-Somfai, Kitts, Lindquist, Nordén *PNAS*, 2014

Kitts, Beke-Somfai, B. Nordén *Biochemistry*, 2011

DNS, DNS-fehérje rendszerek



Reymer, Takahashi, Nordén, 2009 *PNAS*

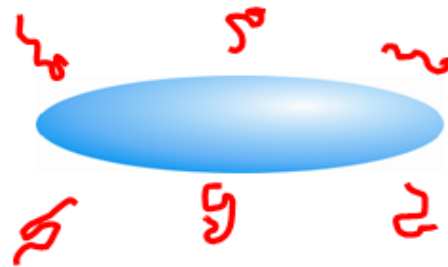


Rodger, Dafforn, Nordén, 2010 *RSC Publishing*

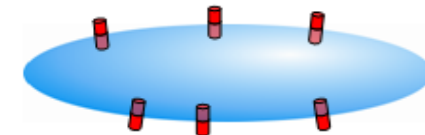
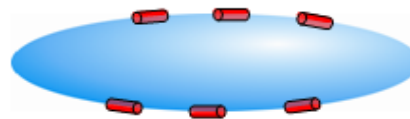
Membrán rendszerek

$$LD = A_{II} - A_{\perp}$$

Áramlás által
generált
nyíróerő



$$S \approx 0.06 - 0.1$$



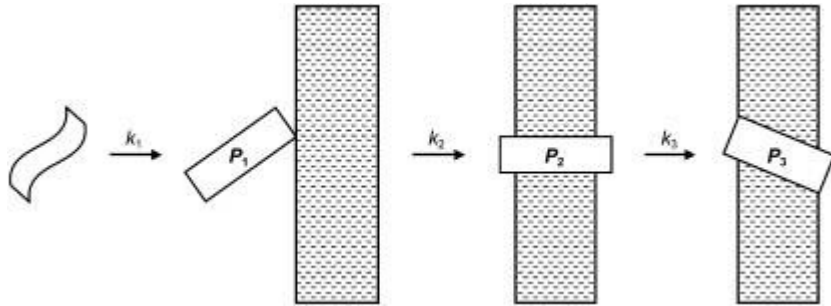
<https://www2.warwick.ac.uk/fac/sci/chemistry/research/arodger/arodgergroup/>

Kogan, Nordén, Beke-Somfai *Chem Phys Lip*, 2013, 175, 105

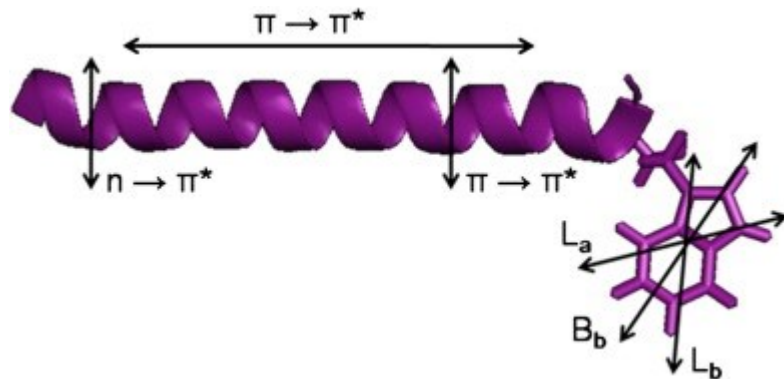
Rocha, Kogan, Beke-Somfai, Nordén, *Langmuir*, 2016, 32, 2841

Membrán rendszerek

Peptid adszorpció és beépülési kinetika

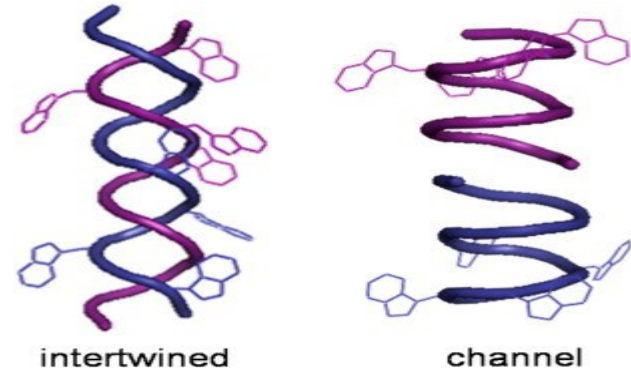


Rodger et al. Biophys J. 2009 96 1399

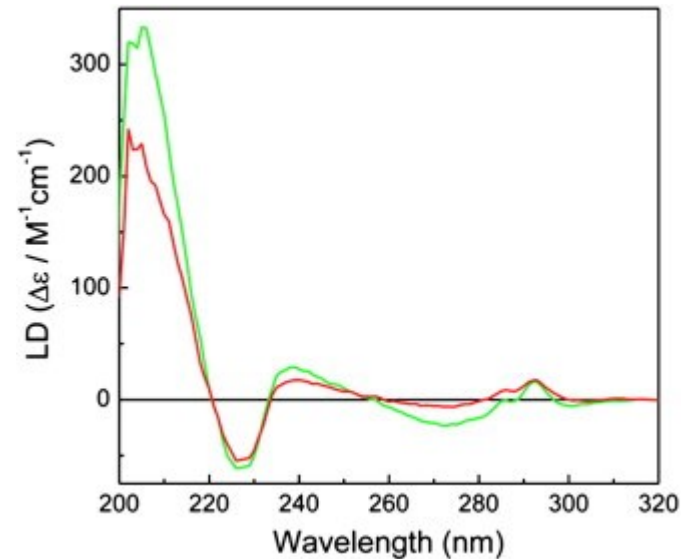


Svensson et al. BBA-Biomemb. 2011 1808 211

Konformáció, kötődési geometria, Konformáció változások



Svensson et al. BBA-Biomemb. 2011 1808 211



Köszönöm a figyelmet, (és a támogatást - 2005) !

Anna Reymer

Bengt Nordén

Johan Johansson

Nina Kann

Sandra Rocha

Takahashi Masayuki

Bobo Feng

Maxim Kogan

Per Lincoln

Biological Nanochemistry group
Biomolecular Self-assembly group
Szigyártó Imola Csilla
Keszthelyi Tamás
Ferenc Zsila



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