
SIMULACIÓN Y EXPERIMENTOS EN FÍSICA MACROMOLECULAR

Javier Martínez de Salazar

Grupo de Biofísica Macromolecular(BIOPHYM)

Departamento de Física Macromolecular

Instituto de Estructura de la Materia – CSIC

<http://www.biophym.iem.csic.es/>

BREVE HISTORIA DEL GRUPO BIOPHYM

ESTRUCTURA DE MEMBRANAS
CELULARES-DISTORSIONES POR
PROTEÍNAS

1976-1994

**morphology/structure vs.
Physical properties (solid)**



1996-2004

**molecular architecture
vs. physical properties
melt**



**Computational chemistry
(MM and QM, DFT)**

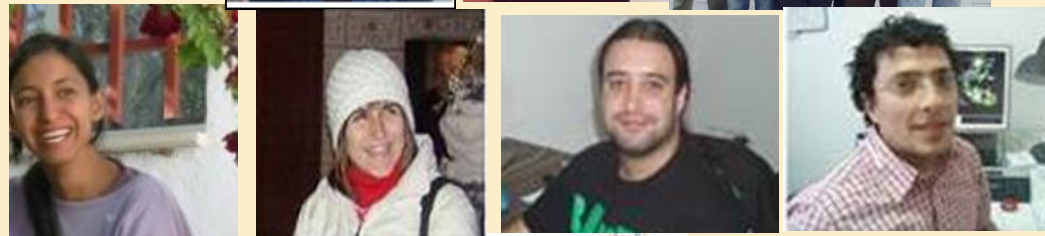
2004 - 2008

**Macromolecular simulation
(MC, MD): crystallization +
melt**

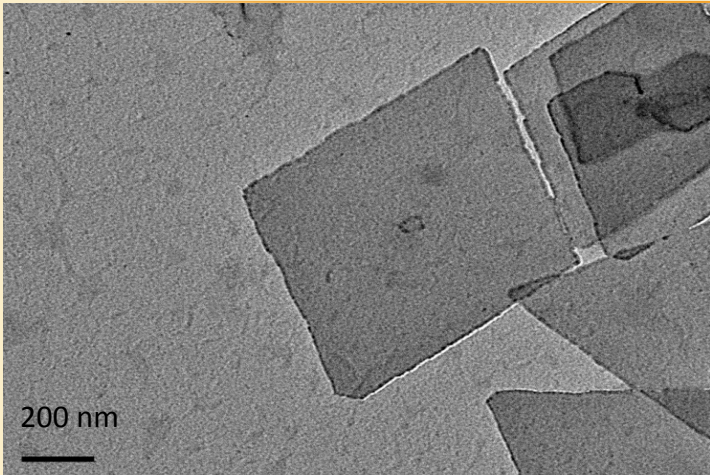


2008 - 2018

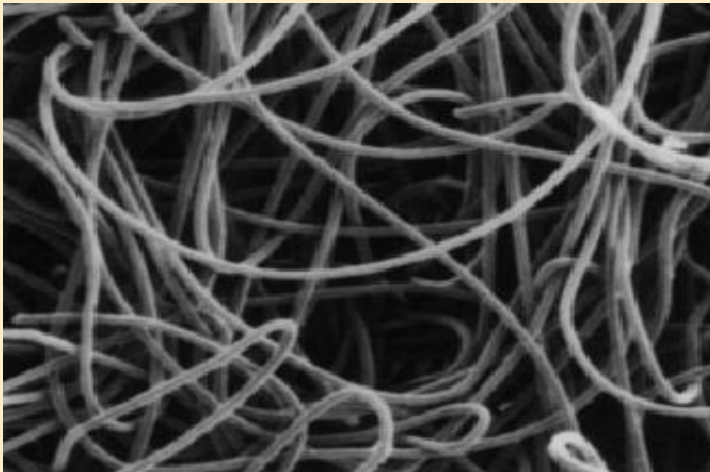
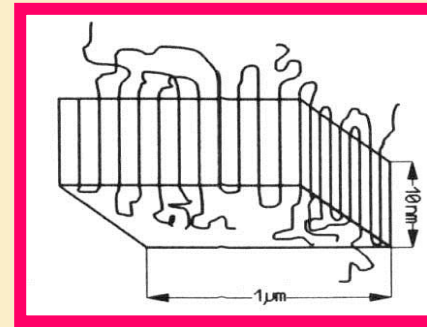
Macromolecular/ BIO



Las macromoléculas adoptan conformaciones extremas



plegada \longrightarrow laminas

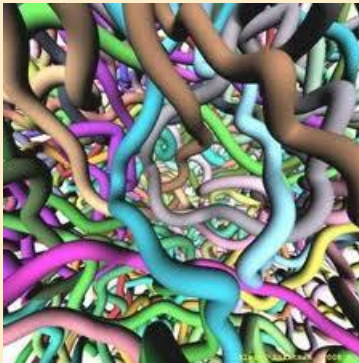
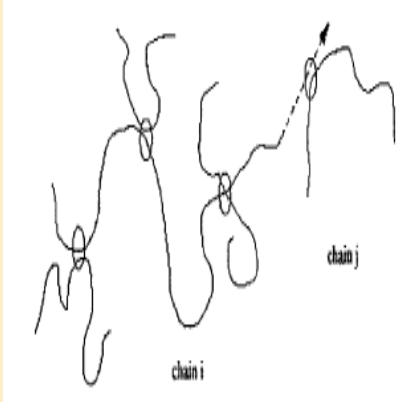


extendida \longrightarrow fibras

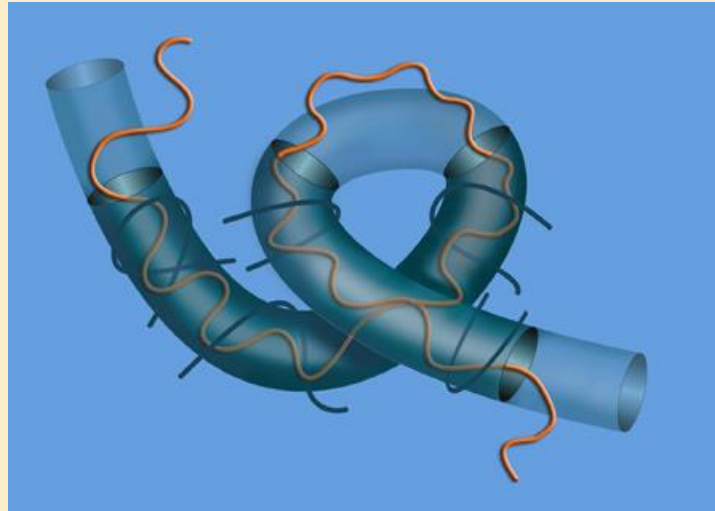


FORMAN UNA RED COOPERATIVA CON EFECTOS NO LINEALES

UNO AFECTA A TODOS

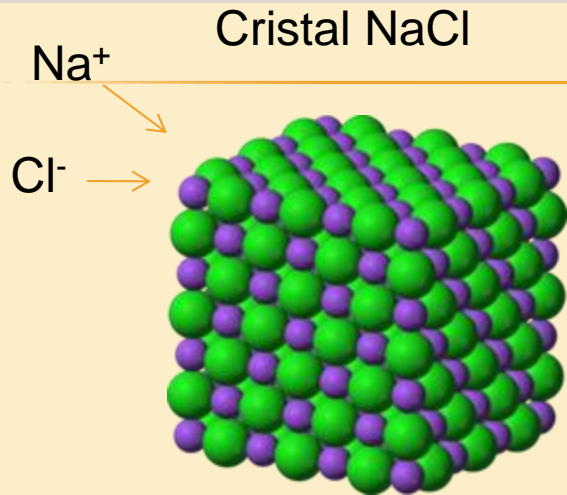


Las macromoléculas forman un sistema (**red de entrecruzamientos**) en la que cada elemento (molécula) repta en un **tubo** cuyo contorno queda fijado por el resto



Se manifiestan fenómenos cooperativos (sistemas altamente correlacionados)

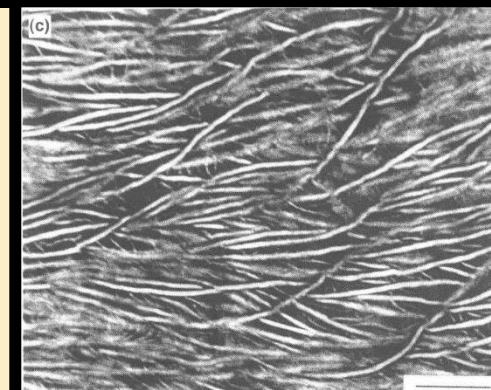
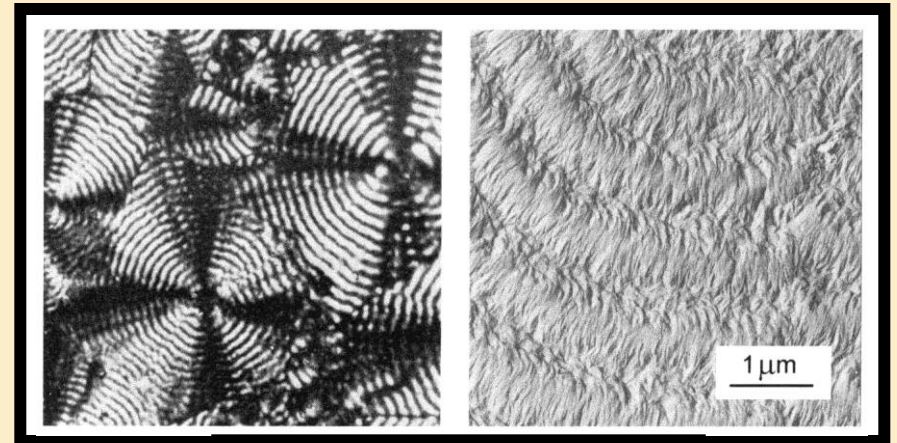
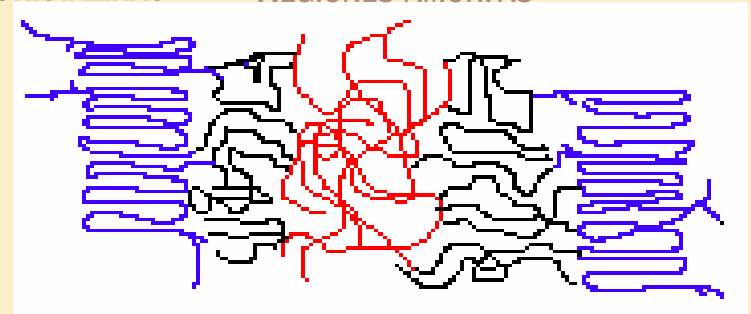
EL SISTEMA ES MÁS QUE LA SUMA DE SUS ELEMENTOS (ESTRUCTURAS COMPLEJAS)



POLIMEROS SEMICRISTALINOS

REGIONES CRISTALINAS

REGIONES AMORFAS



¿POR QUÉ HACER SIMULACIÓN COMPUTACIONAL?

- ✘ TRATAMOS CON SISTEMAS MULTICOMPONENTES EN EL QUE SUS ELEMENTOS SE ORGANIZAN ESTRUCTURALMENTE DANDO LUGAR A **FENÓMENOS NO PREDECIBLES** POR LAS TEORIAS EXISTENTES

- ✘ **LIMITACIONES** EN LA OBTENCIÓN DE SEÑALES **EXPERIMENTALES**

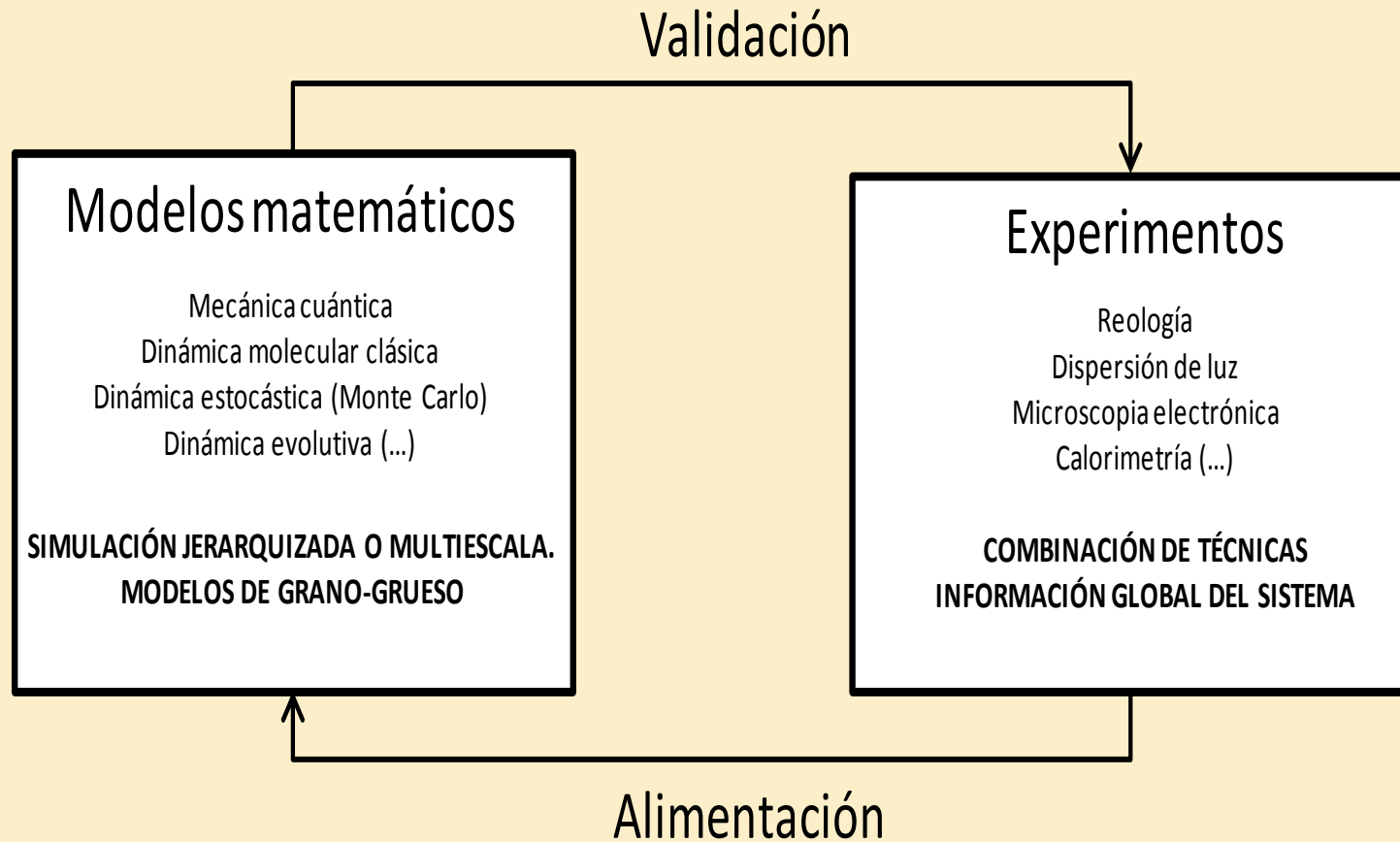
MUCHAS PREGUNTAS BÁSICAS SIN RESPUESTA

¿Cómo solidifican los polímeros?
teorías actuales no explican muchos resultados
experimentales

¿PARADIGMA INVÁLIDO?

¿Como se forman las fases en el fundido?
la termodinámica no da respuestas
concluyentes

APROXIMACIÓN SISTÉMICA A LOS PROCESOS DE ENSAMBLAJE Y SEÑALIZACIÓN EN MACROMOLÉCULAS.

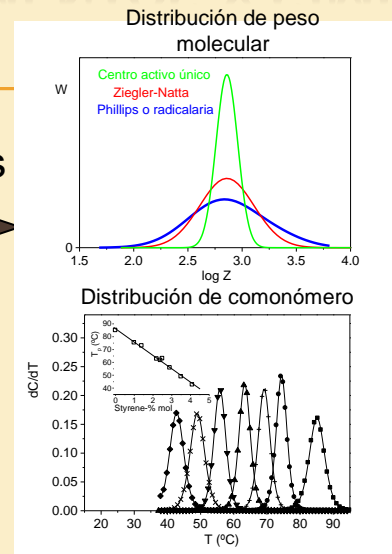


ESTABLECIENDO SINERGIAS ENTRE EXPERIMENTOS Y SIMULACIÓN



Experimentos

Resultados experimentales

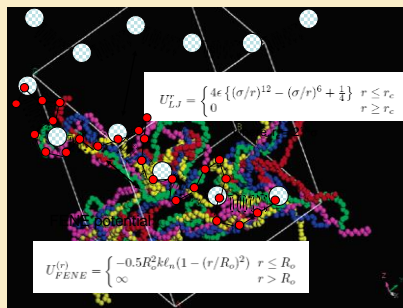


Modelo valido

Modificación del modelo

Abstracción
Simplificación

Problema en un Sistema Real



Modelos

Parametrización
Abstracción
Implementación

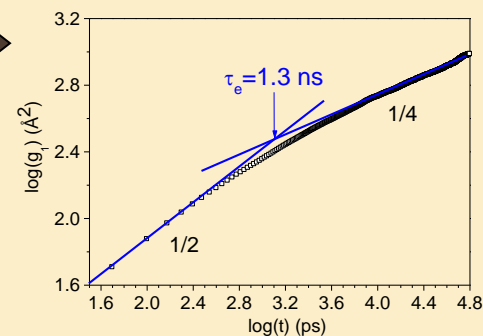


```

+
COPIES MATRIX B INTO A
DO 10 I=1,N
DO 10 J=1,N
A(I,J)=B(I,J)
10 CONTINUE
C
RETURN
END
*DECK DMD113
SUBROUTINE DMD113(A,B,C,N)
REAL*8 A(1),B(50,1),C(1)
DATA ZERO/0.0D0/
C
A=B*C
DO 10 I=1,N
DO 10 J=1,N
A(I)=A(I)+B(I,J)*C(J)
    
```

Métodos computacionales

| Force Field | $\langle R^2 \rangle (\text{Å}^2)$ | $\langle R_g^2 \rangle (\text{Å}^2)$ | $\langle R^2 \rangle / \langle R_g^2 \rangle$ | C_∞^c | $l_p (\text{Å})^d$ | $M_e (\text{kg/mol})^e$ |
|--------------------------------|------------------------------------|--------------------------------------|---|--------------|--------------------|-------------------------|
| Trappe-UA ^a | 19805 ± 50 | 3299 ± 6 | 6.00 ± 0.03 | 8.34 ± 0.01 | 9.22 ± 0.02 | 0.71 ± 0.01 |
| Karayianis et al. ^b | 19335 ± 56 | 3187 ± 6 | 6.07 ± 0.03 | 8.06 ± 0.01 | 9.54 ± 0.02 | <u>0.79 ± 0.01</u> |



El concepto de multiescala

Investigar y diseñar nuevos materiales desde la síntesis a su aplicación.

Química Cuántica (DFT)

Electrones explícitos.

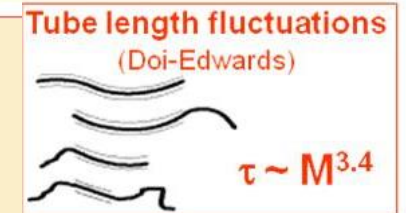
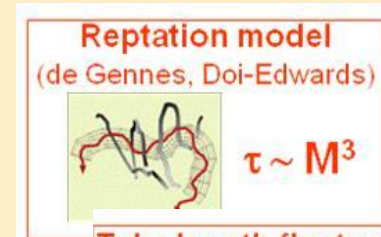
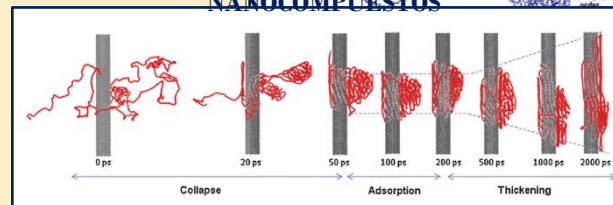
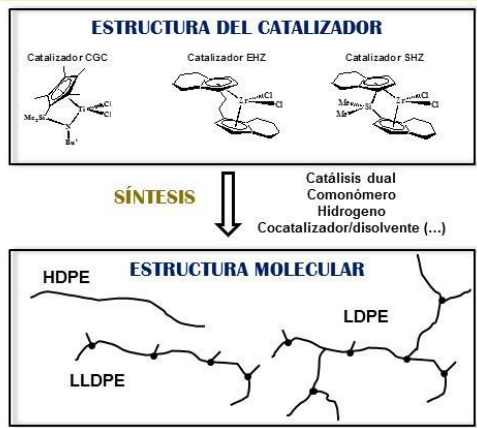
Modelos atómicos

Física clásica con "force field" atómicos (dinámica molecular y Monte Carlo).

Modelos mesoscópicos

Grano-grueso (CG) o modelos moleculares. Potenciales efectivos.

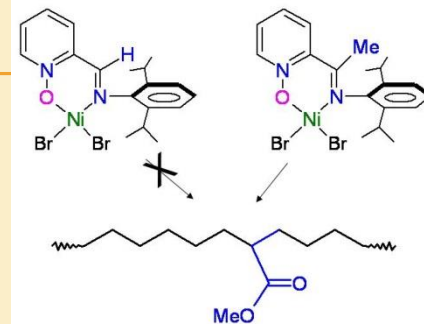
Escala espacial



Escala temporal

SIMULACIÓN Y EXPERIMENTOS EN FÍSICA MACROMOLECULAR.

Modelización de las reacciones de polimerización mediante catalizadores organometálicos.



Copolímeros de etileno y metacrilato.
Biocompatibilidad

J. Ramos, S. Martínez, V.L. Cruz and J. Martínez-Salazar, *J. Molecular Mod.* (2011)

J. Ramos, V. L. Cruz, J. Martínez-Salazar, M. Brasse, P. Palma and J. Campora *J Pol Sci: Pol Chem* (2010)

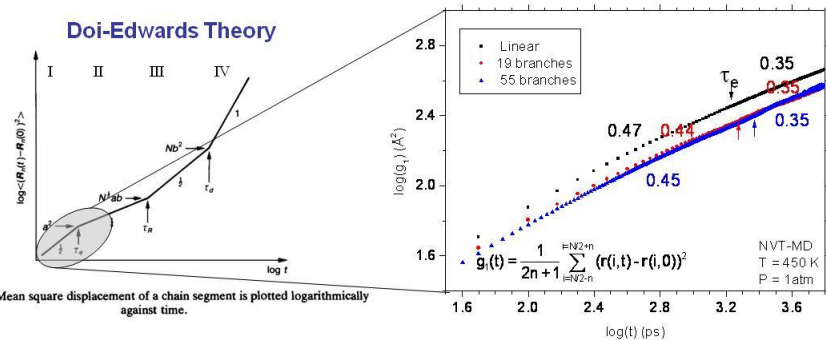
Comportamiento viscoelástico y dinámica molecular de polímeros sintéticos

Procesabilidad Viscoelasticidad

J.F. Vega, J.Ramos and J. Martínez-Salazar, *Rheologica Acta* (2011)

J. Ramos, J.F. Vega, D.N. Theodorou and J. Martínez-Salazar, *Macromolecules* (2008)

Entanglement relaxation time by MD simulations



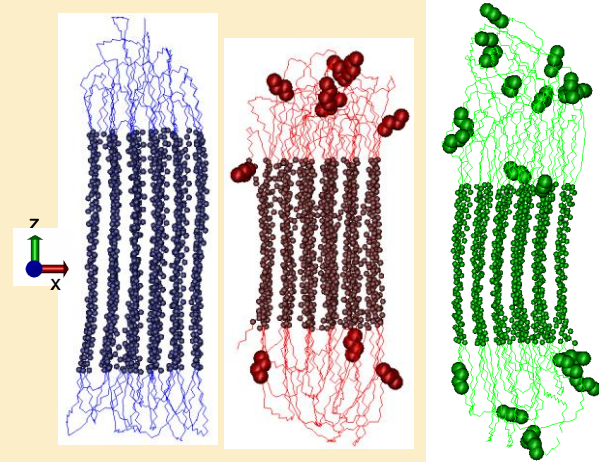
Cristalización de polímeros en disolución.
Efecto de la arquitectura molecular

Teorías de cristalización

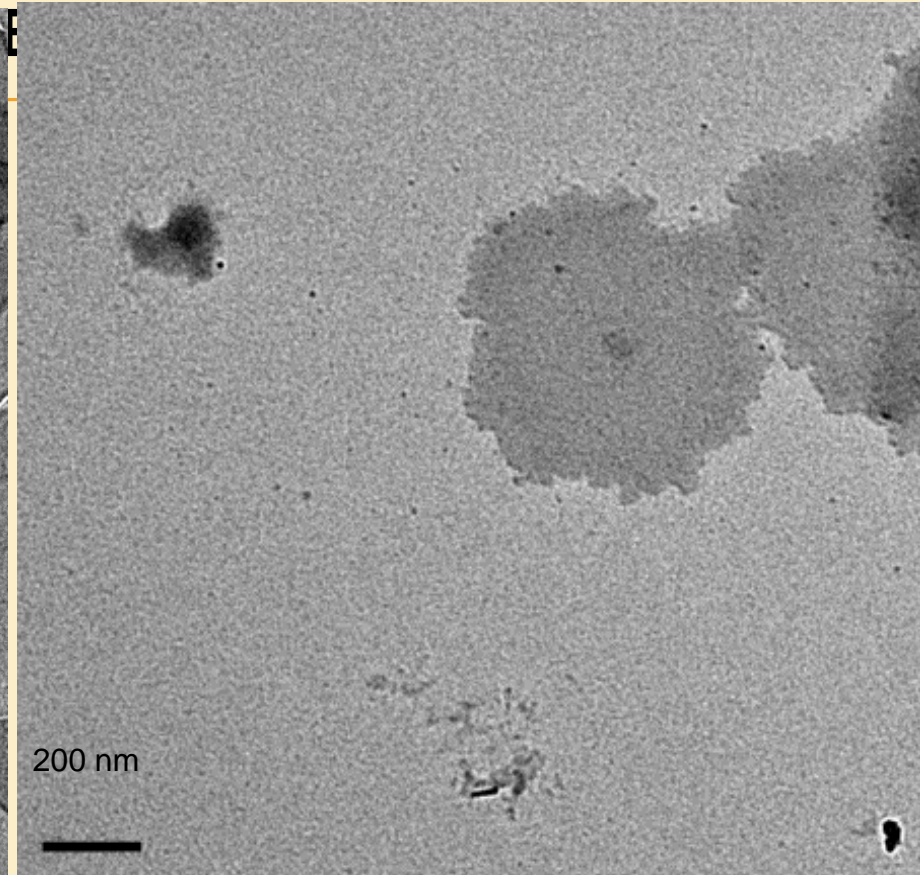
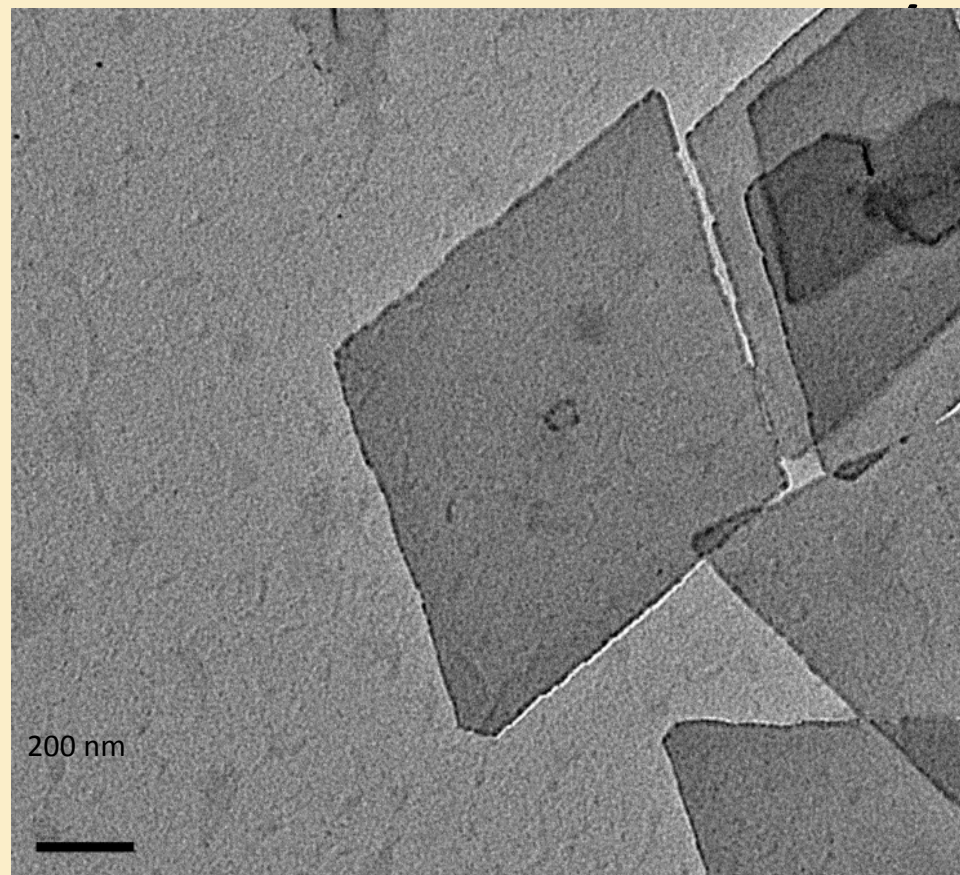
Propiedades mecánicas

S. Sanmartín, J. Ramos and J. Martínez-Salazar *Macromolecular Symposia* (2011)

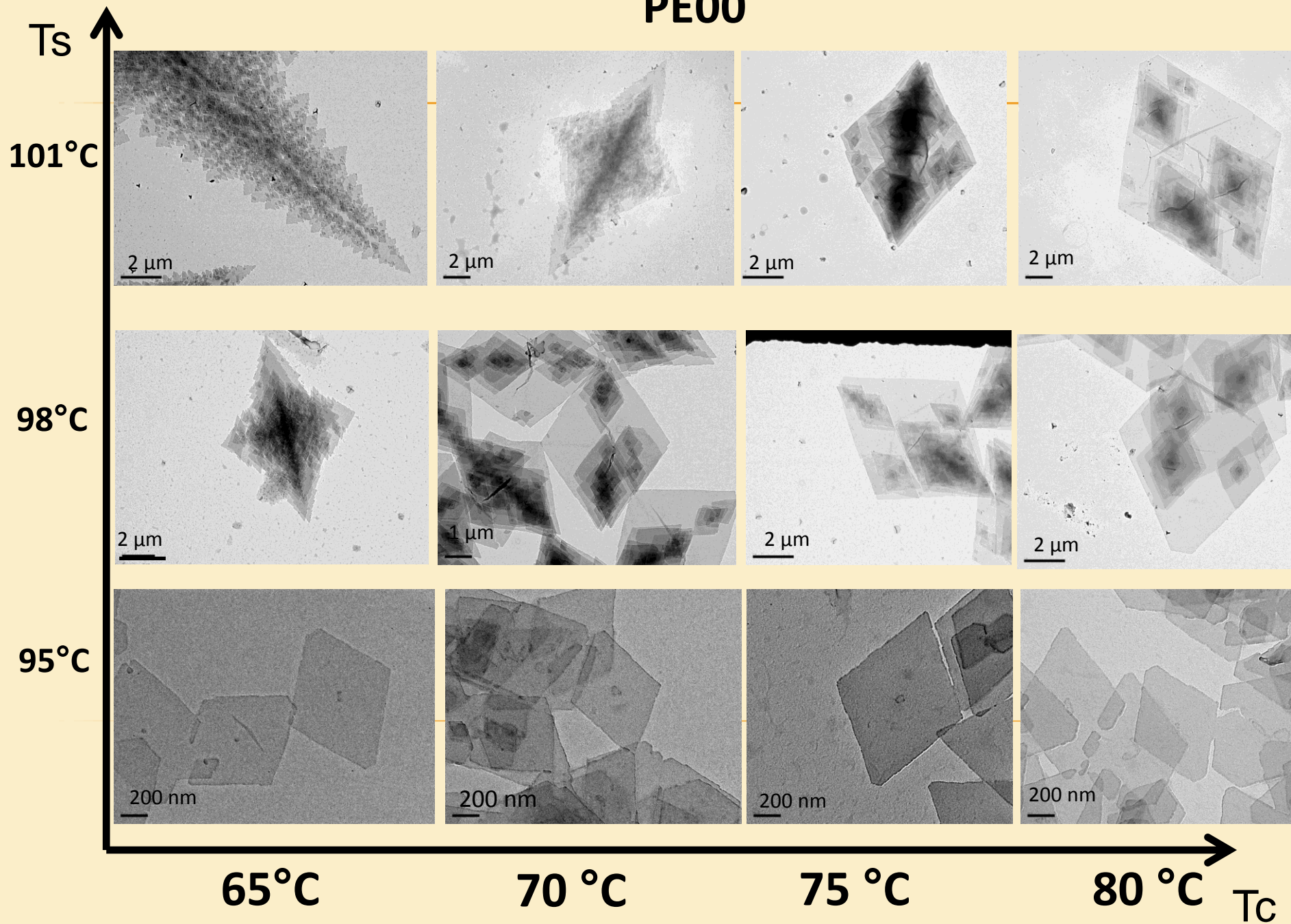
J. Ramos and J. Martínez-Salazar *J Pol Sci: Pol Phys* (2011)



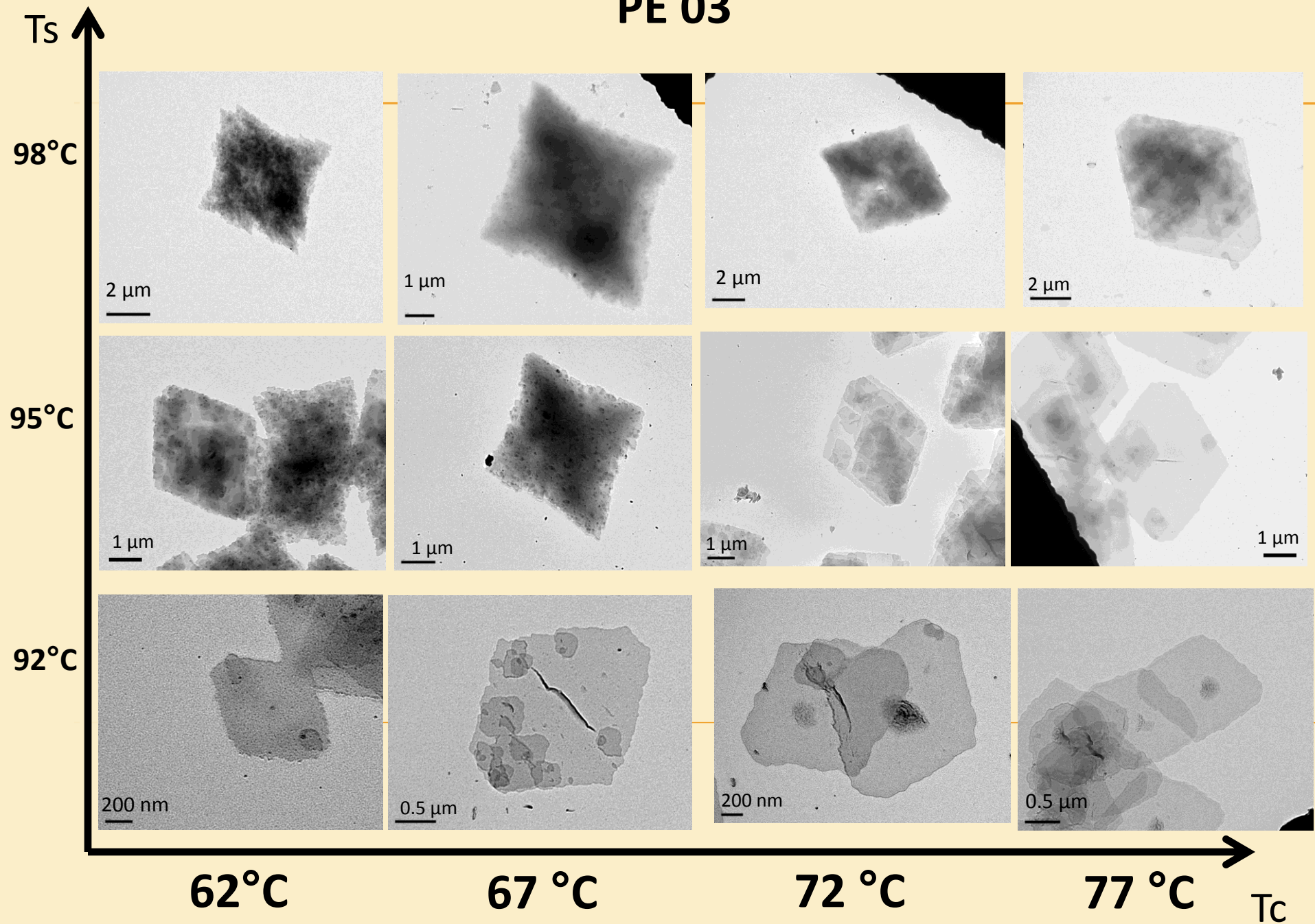
EXPERIMENTAL MORFOLOGIA MONOCRISTALES



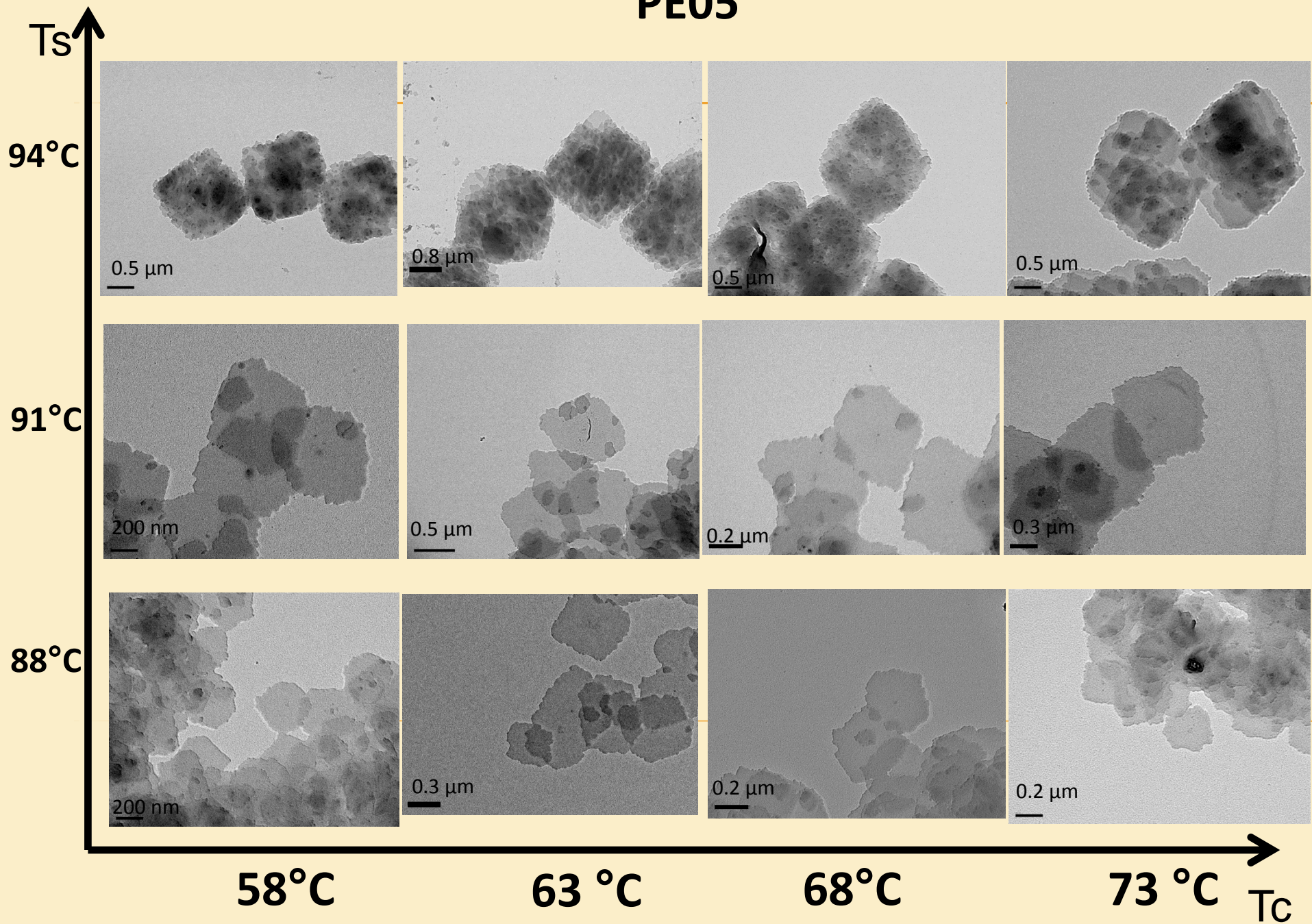
PE00



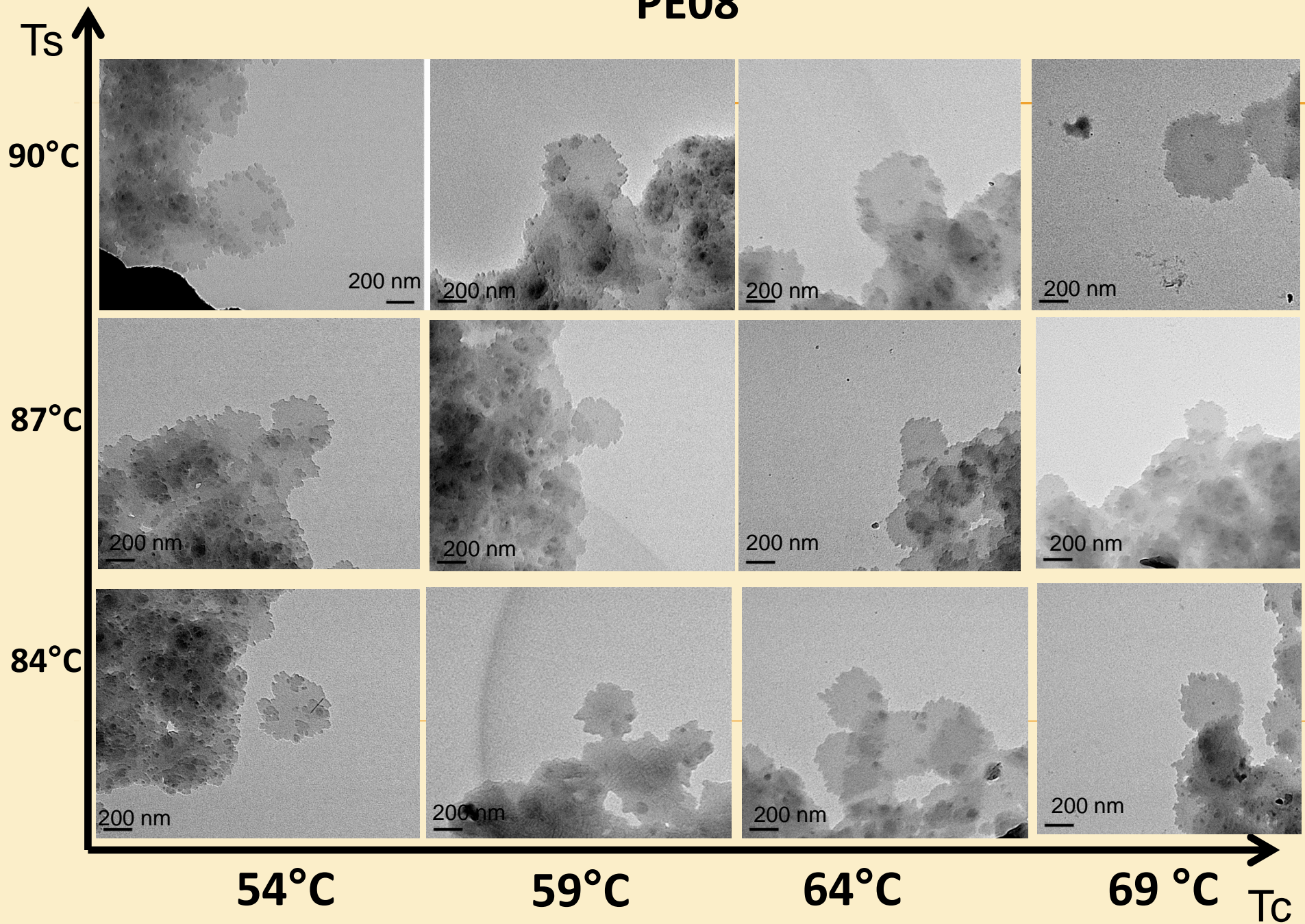
PE 03



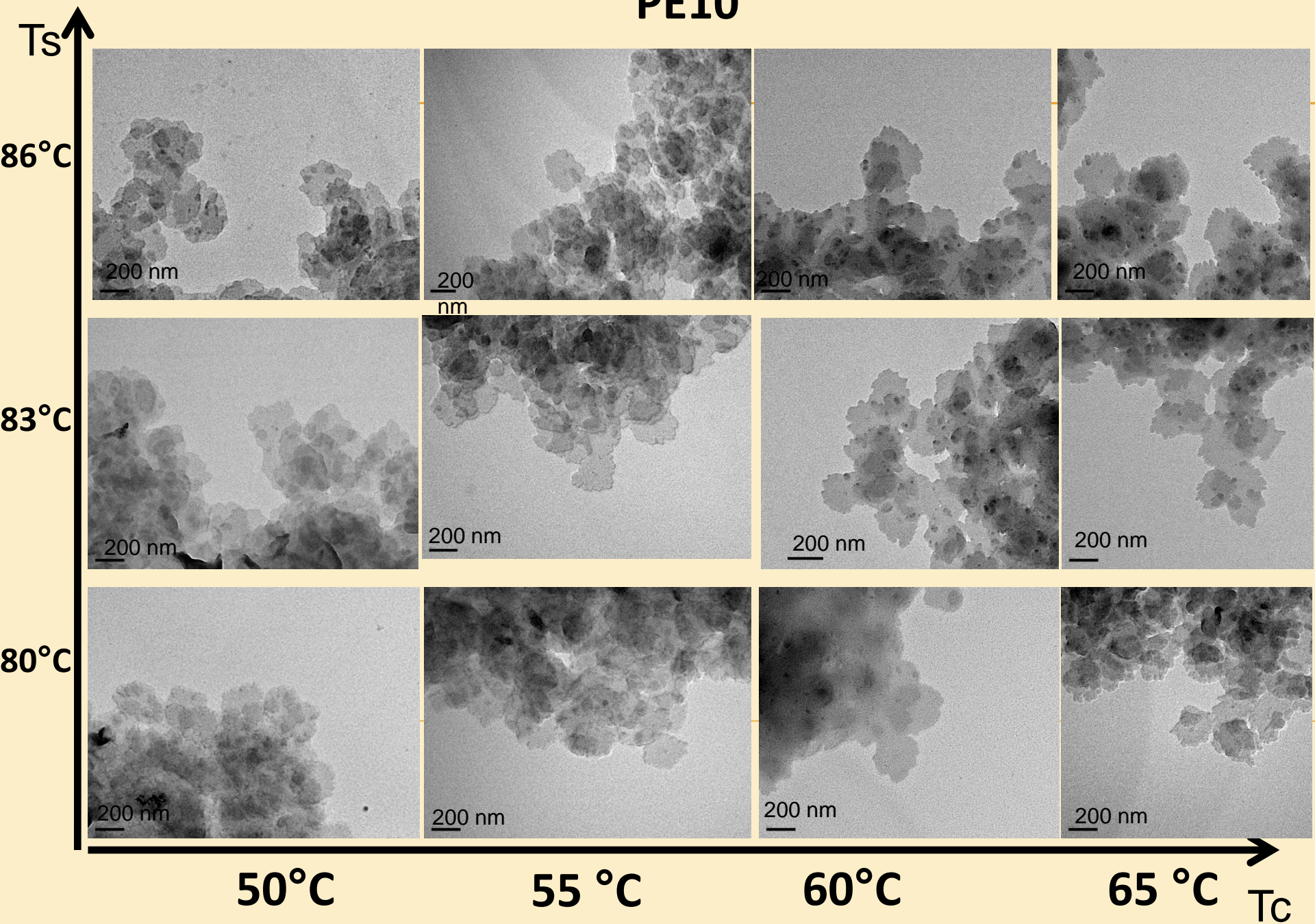
PE05



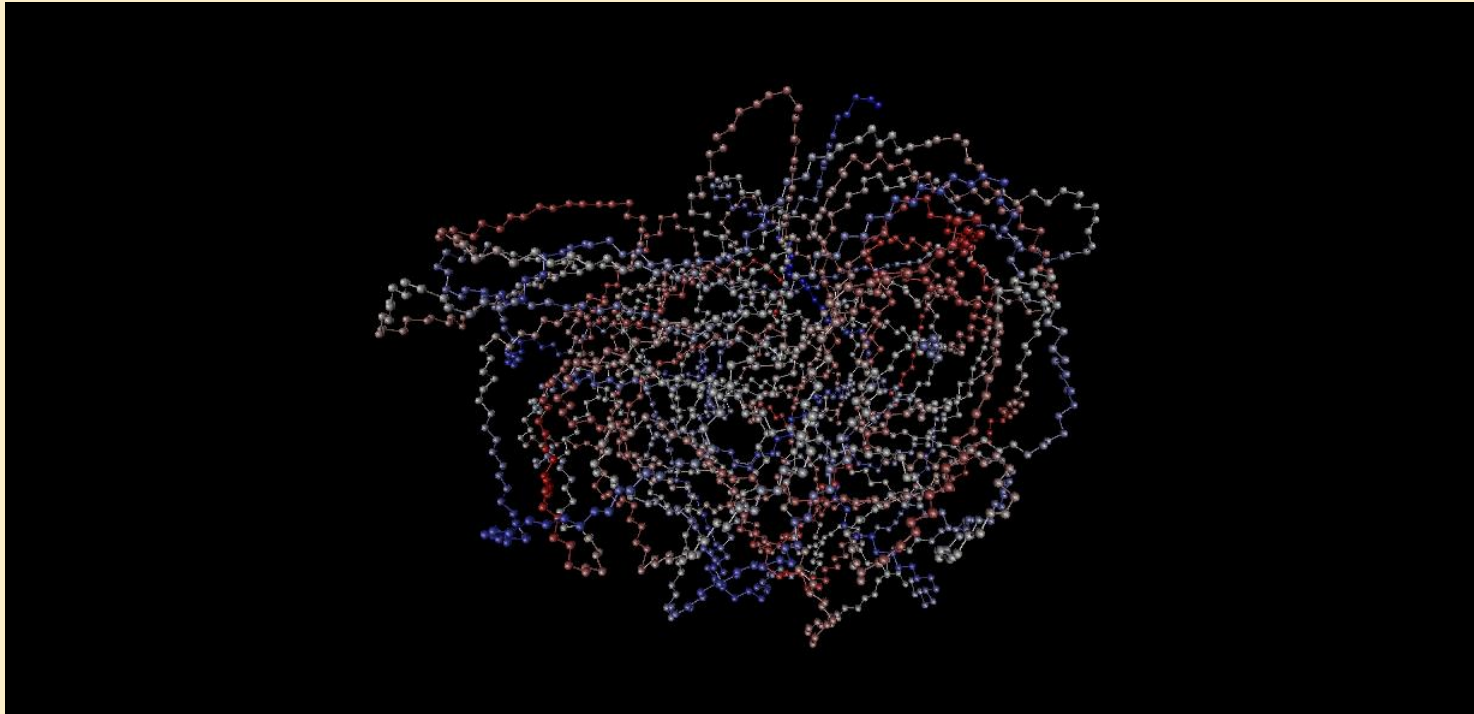
PE08



PE10



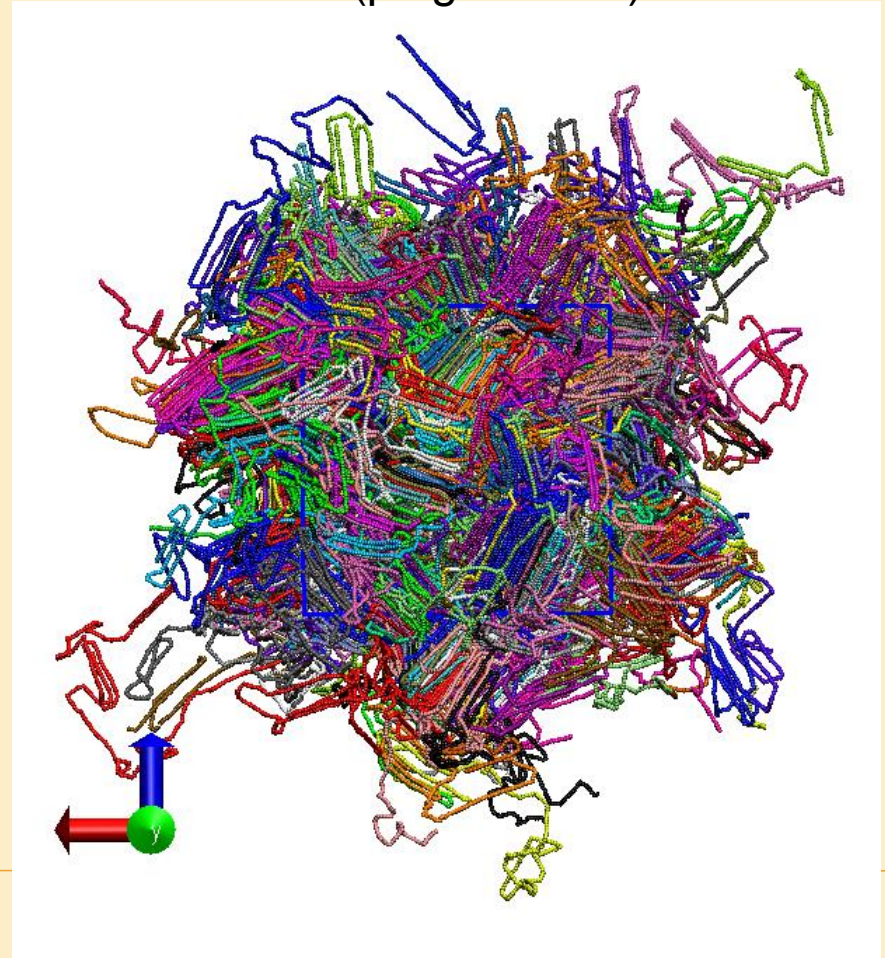
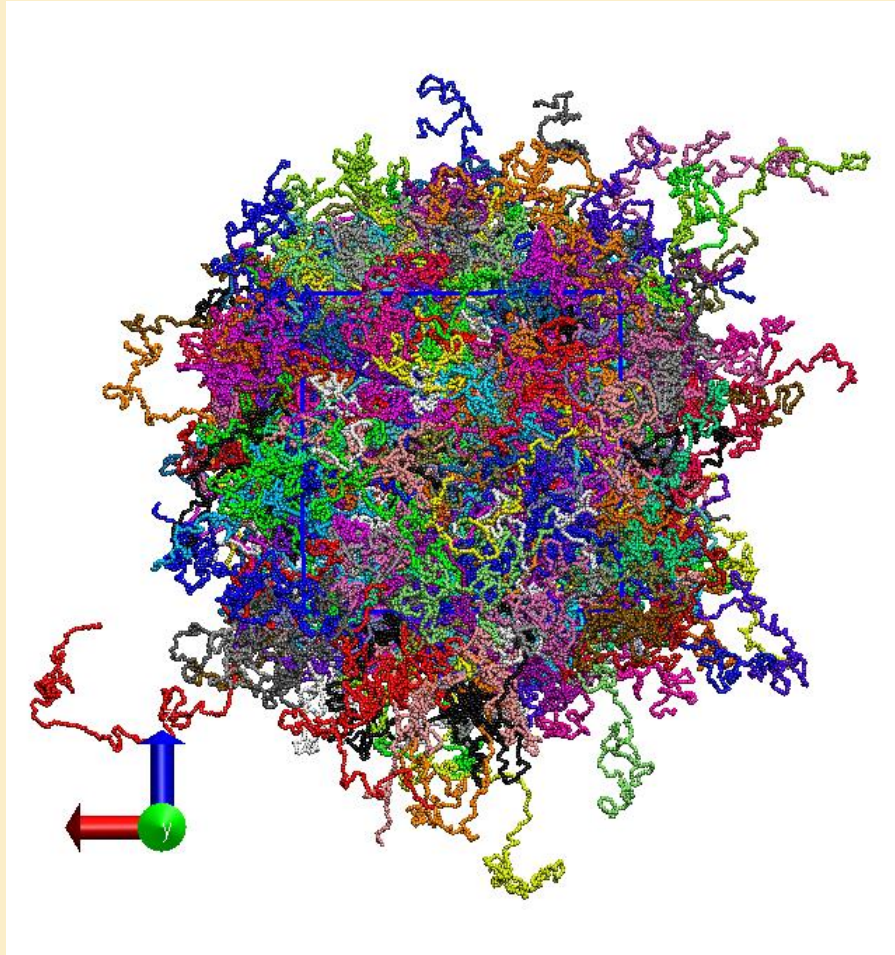
Plegamiento de una macromolécula



$T^* = 1$
(fundido)

tiempo

$T^* = 0.5$
(plegamiento)



SIMULACION Y EXPERIMENTOS EN MONOCRISTALES

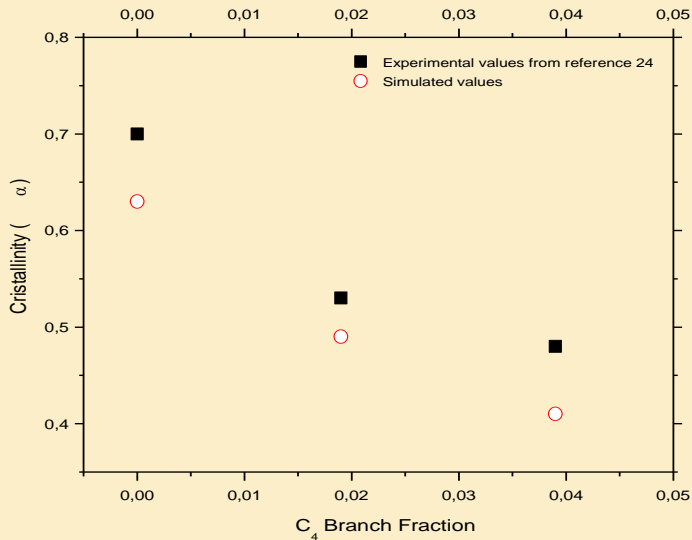
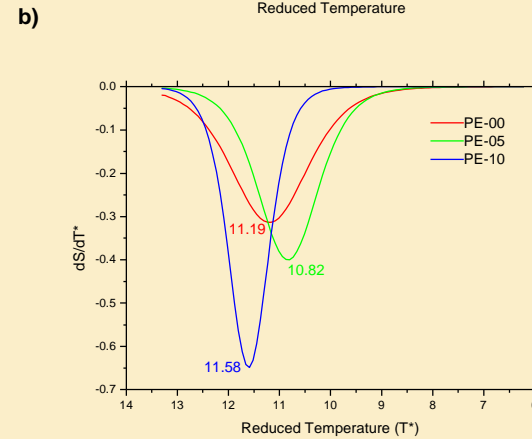
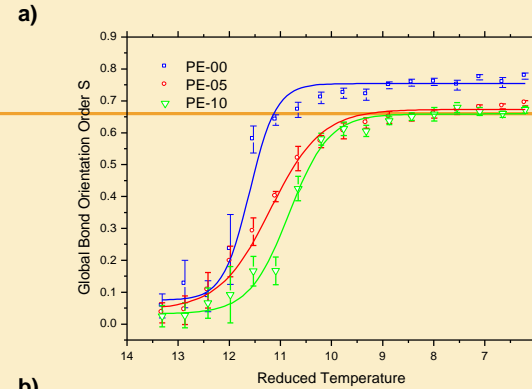
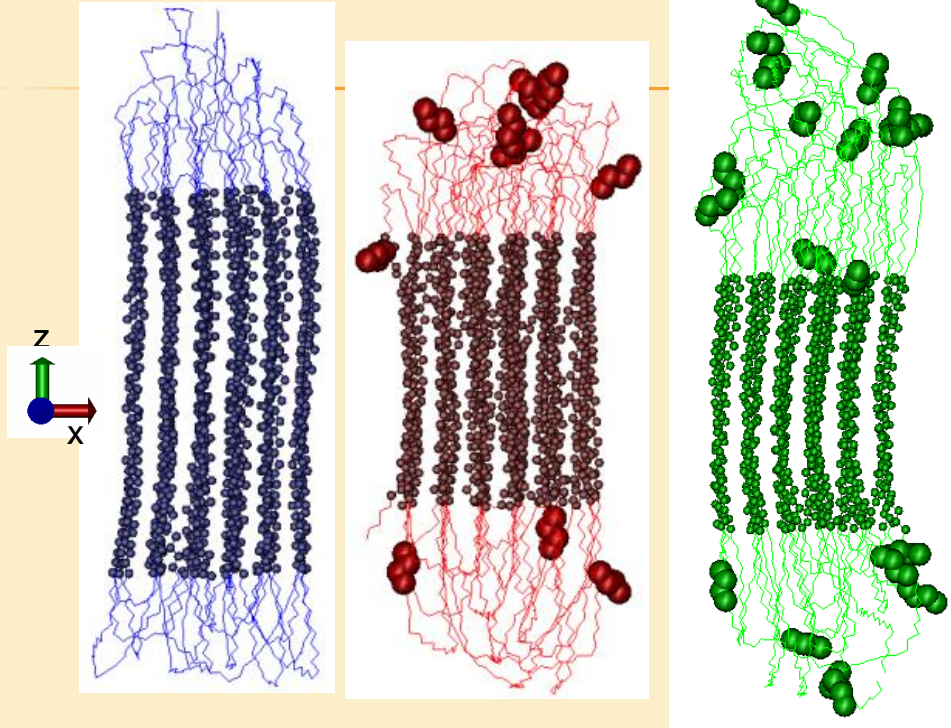


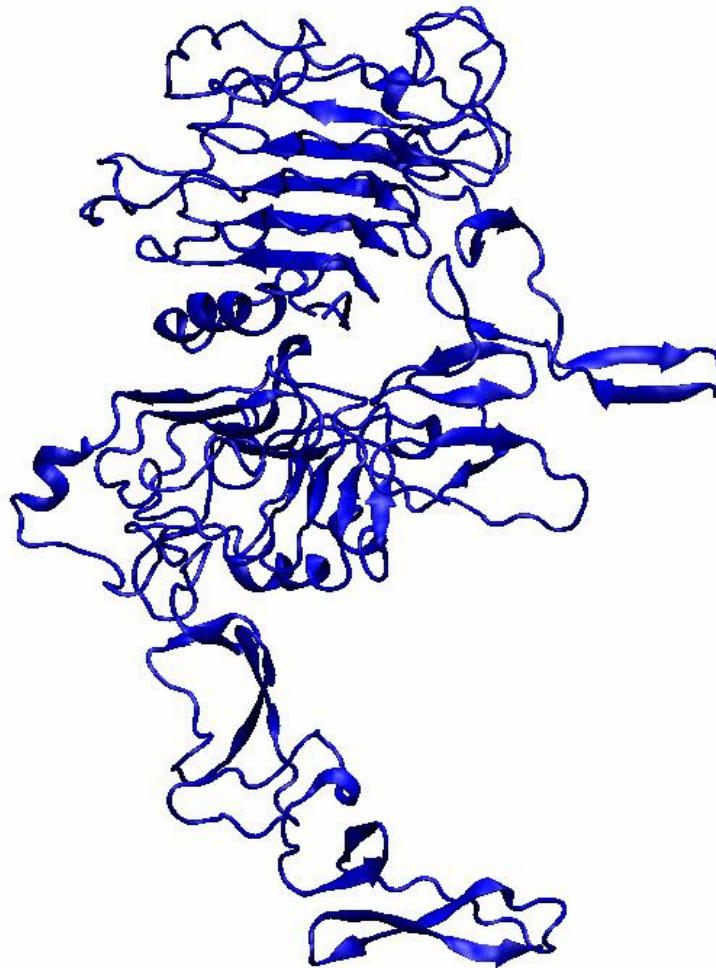
Table 2: Simulated densities as a function of the degree of branching.

| | PE-00 | PE-05 | PE-10 |
|---|--------------|--------------|--------------|
| Crystalline(ρ_c) | 0.933 | 0.917 | 0.915 |
| Amorphous(ρ_a) | 0.858 | 0.863 | 0.860 |
| <i>Amorphous experimental</i> ²⁵ | <i>0.861</i> | | |
| Total(ρ) ^a | 0.906 | 0.889 | 0.882 |
| <i>Total Experimental</i> ²⁵ | <i>0.952</i> | <i>0.931</i> | <i>0.922</i> |

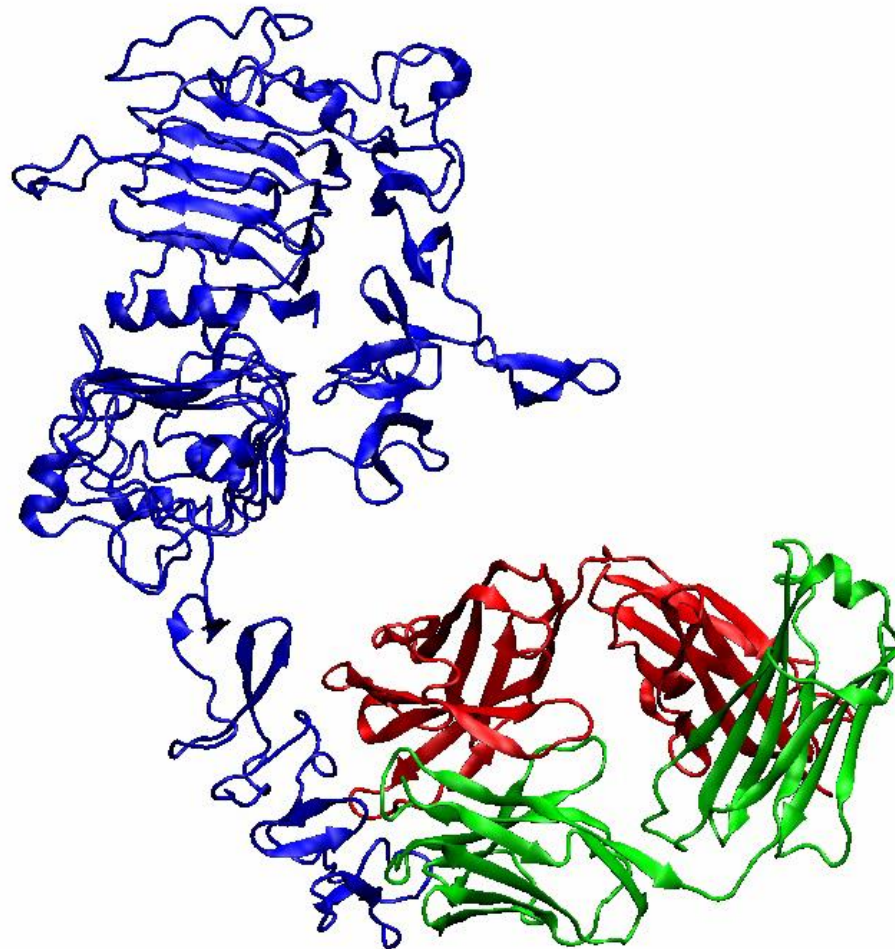
^a Calculated as: $\rho_c = \alpha \rho_c + (1-\alpha)\rho_a$ where α is the simulated crystallinity reported in Fig 8. Experimental values are in italics style. Units are given in g/cm^3 .

PROPIEDADES HIDRODINÁMICAS DEL COMPLEJO HER2/TZM

HER2



HER2 / TDM

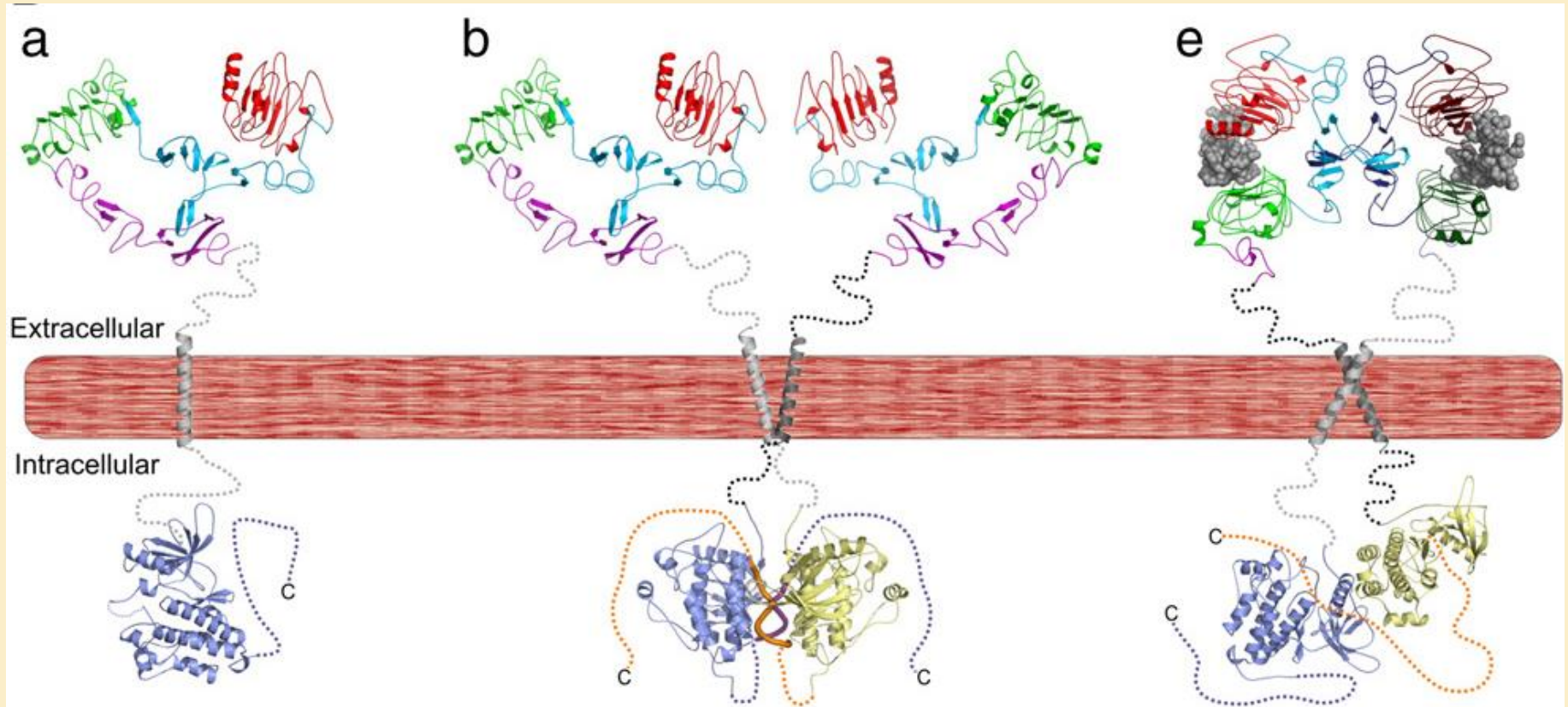


-
- ✘ HER2 pertenece a una familia de receptores que son potentes mediadores en el crecimiento y desarrollo celular

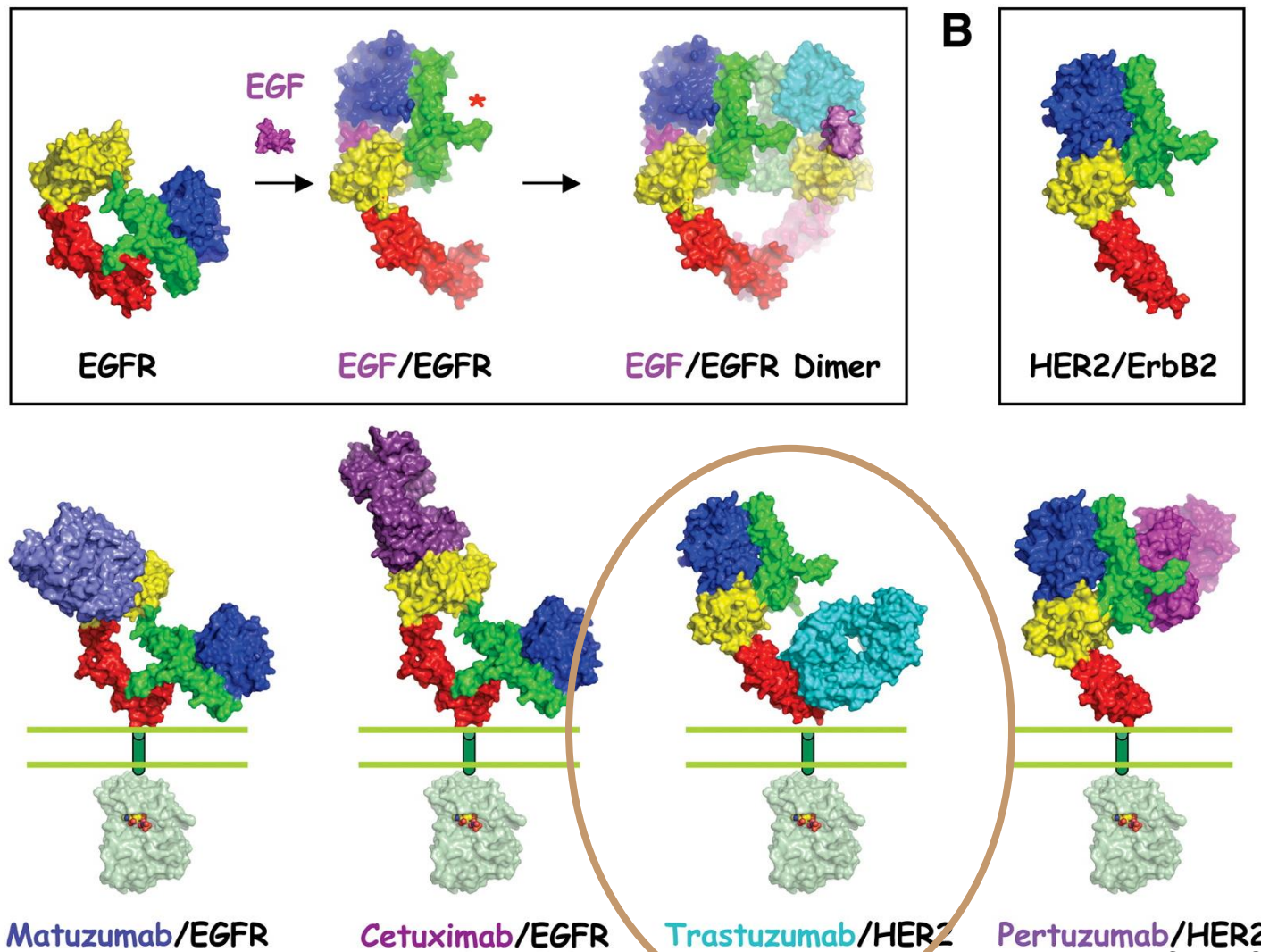
| Receptor | Enfermedad | Estrategias |
|------------------------------|--|---|
| HER2 Se sobre- expresa | Cáncer de mama Cáncer gastrico Cáncer de ovario Cáncer pulmonar | Inhibidores tirosina- kinasa, proteínas de choque térmico, inhibidores de dimerización y conjugación entre anticuerpos-quimioterapia. |
| | Tratamiento actual | Anticuerpos monoclonales especificos |

MECANISMOS DE TRANSFERENCIA:

Dimerización

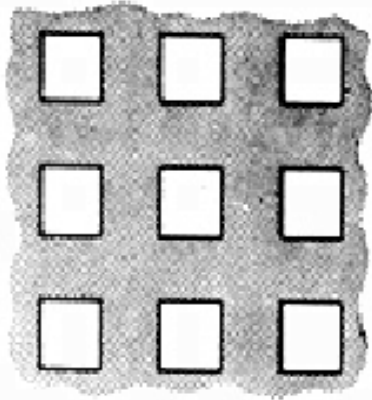


Interacción anticuerpo ErbB

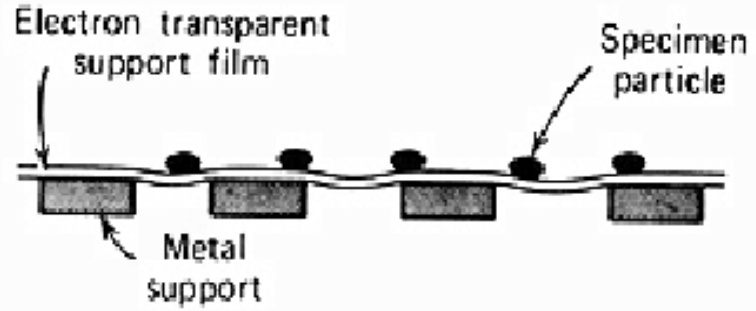


Transmission Electron Microscopy

Sample grid

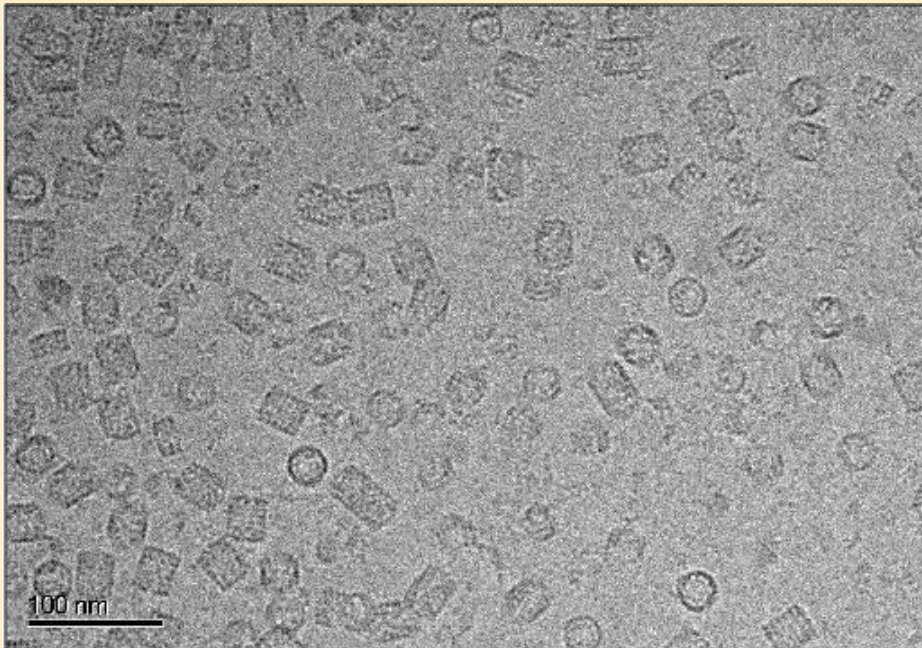


(a)

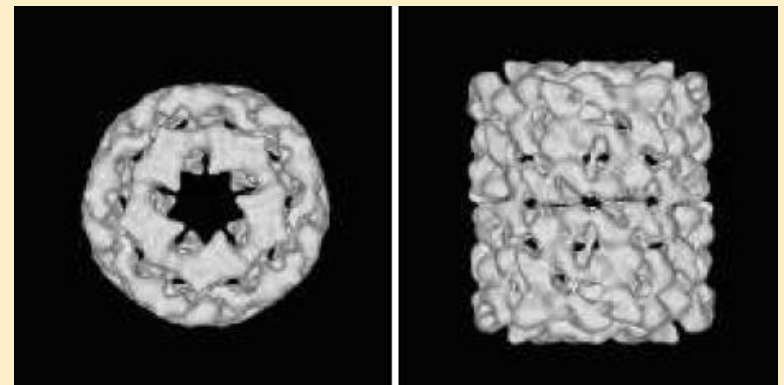


(b)

Image



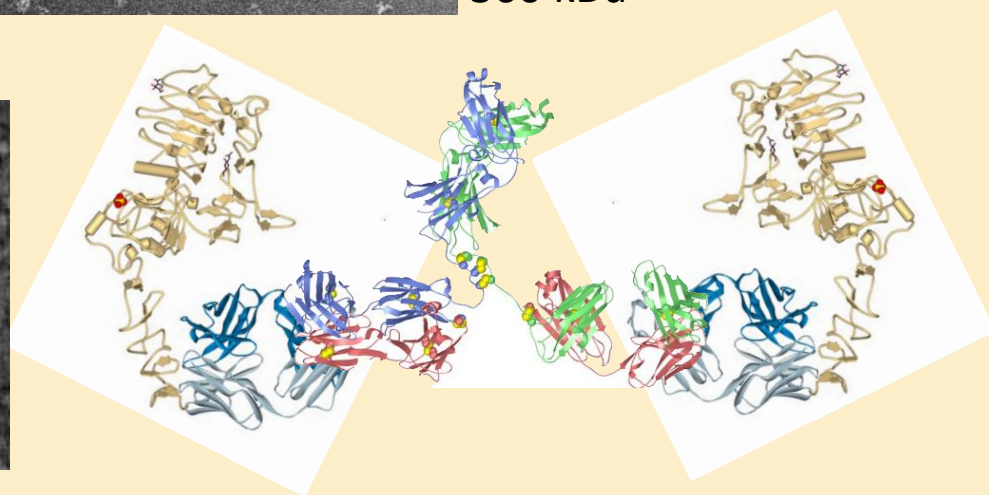
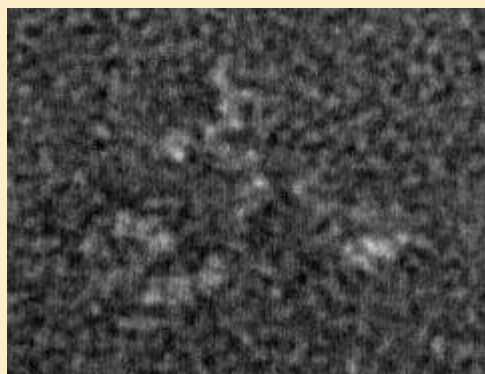
Reconstruction





360 kDa

HER2/TZM (C2)



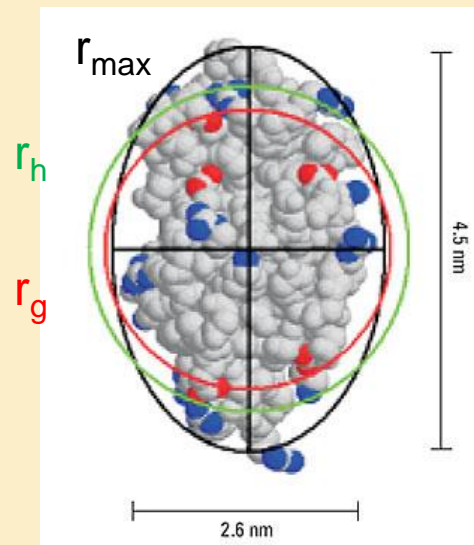
Dynamic Light Scattering

Diffusion Coefficient

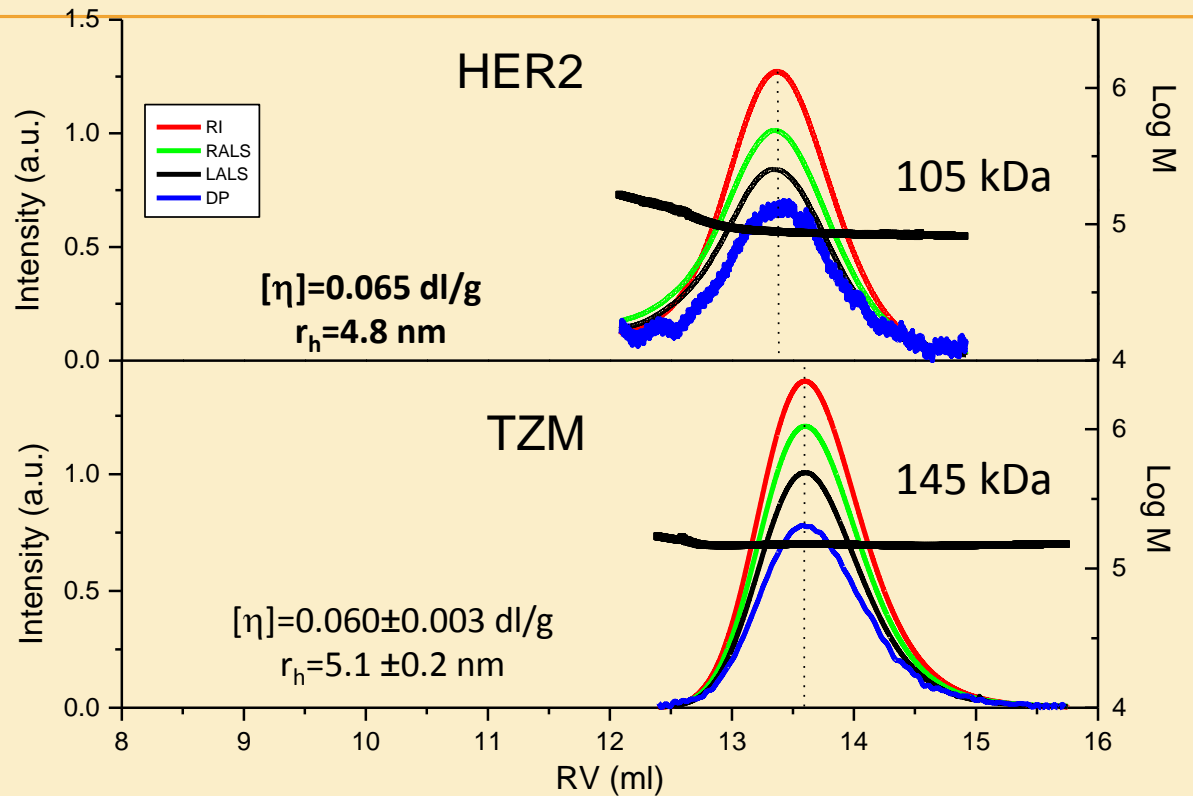
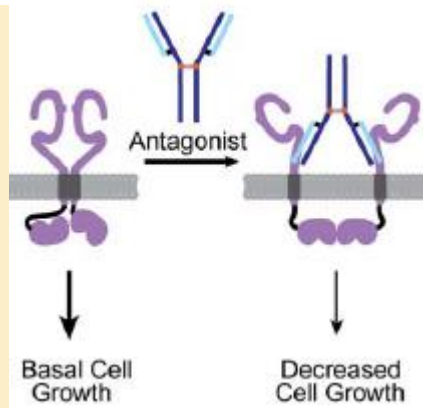
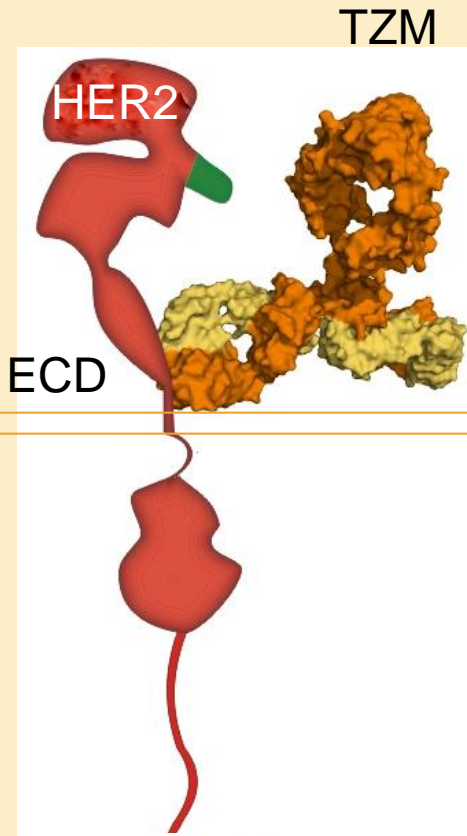
Stokes-Einstein relation

- D = Diffusion coefficient
- k = Boltzmann's coefficient
- T = Temperature
- η = Viscosity
- R = hydrodynamic radius

$$D = \frac{kT}{6\pi\eta R}$$



HER2/TZM



Calibration

BSA
 $[\eta]=0.038 \pm 0.002 \text{ dl/g}$
 $r_h=3.42 \pm 0.06 \text{ nm}$

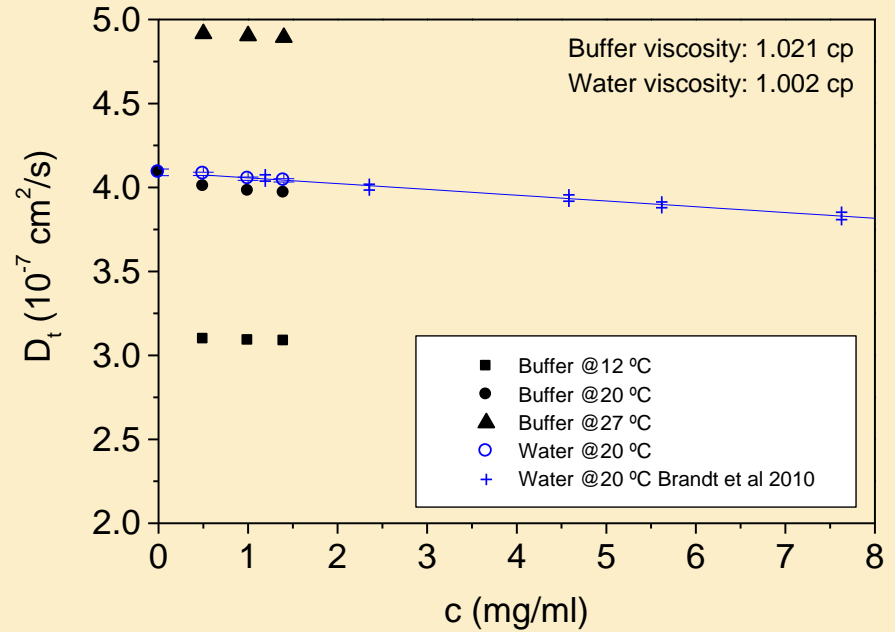
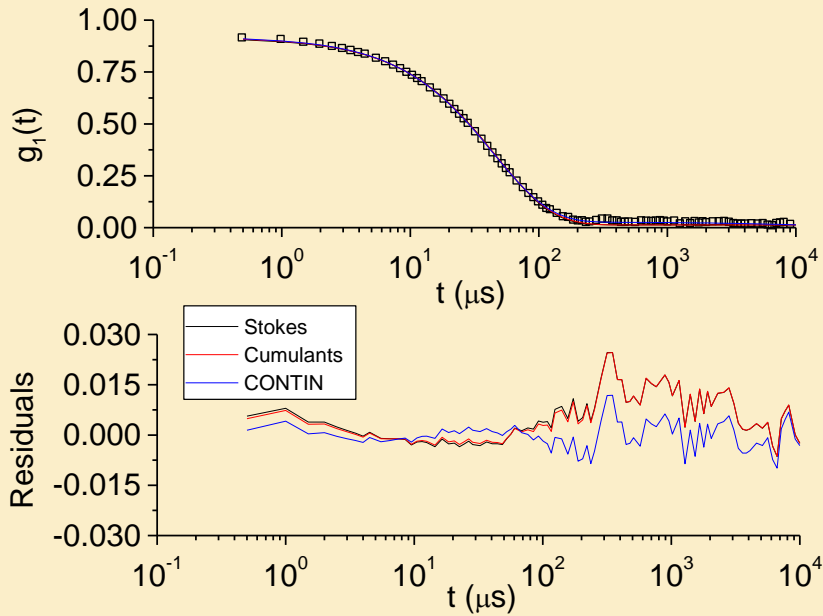
BSA Literature
 $[\eta]=0.033-0.042 \text{ dl/g}$
 $r_h=3.27-3.54 \text{ nm}$

TZM (Literature)

$[\eta]=0.064 \pm 0.002 \text{ dl/g}$
 $r_h=5.3 \pm 0.1 \text{ nm}$
 $M_w \sim 150 \text{ kDa}$

Diffusion Coefficient and Size

TZM (monodisperse)



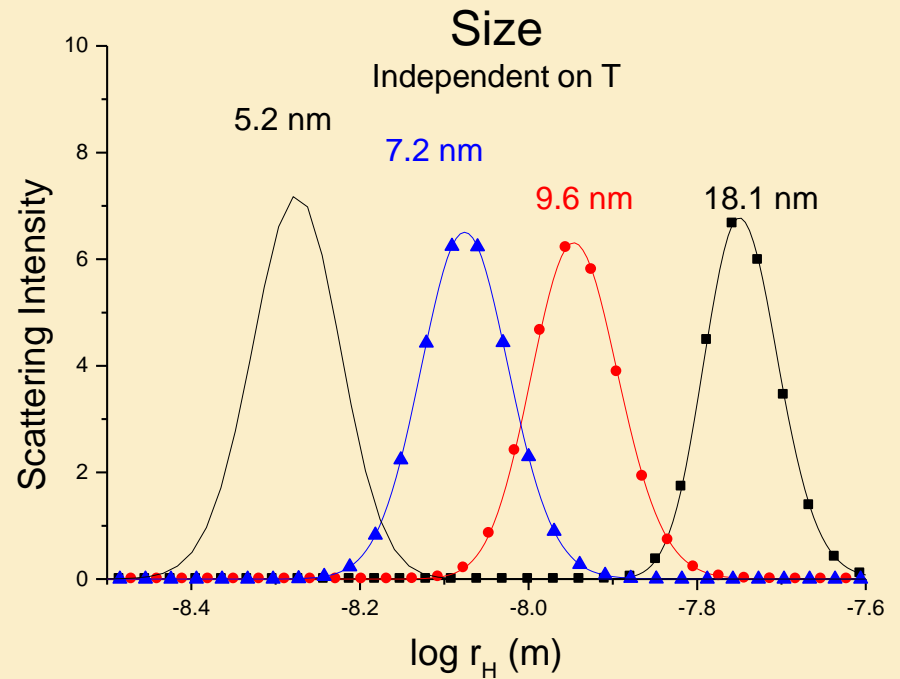
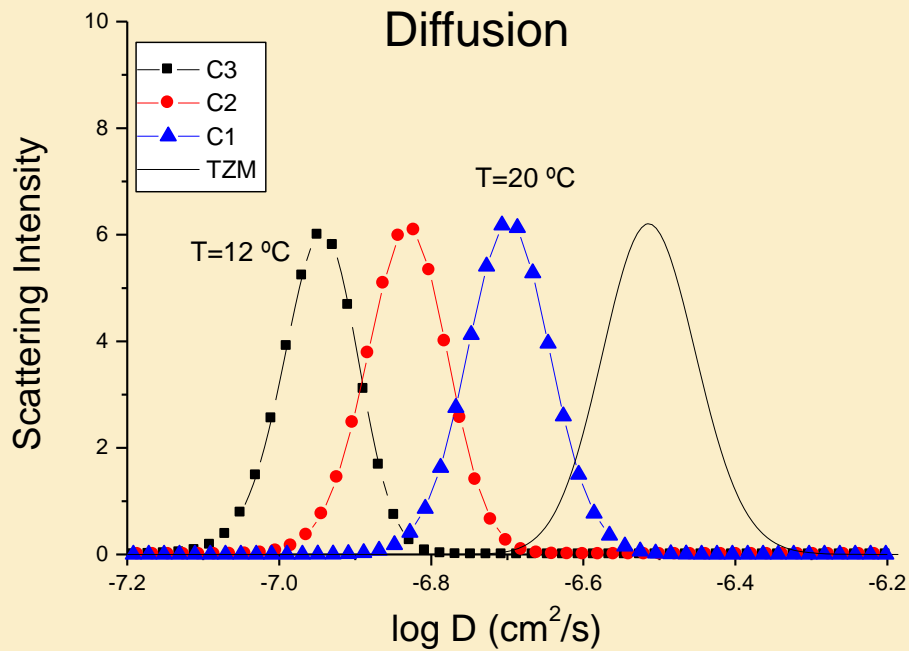
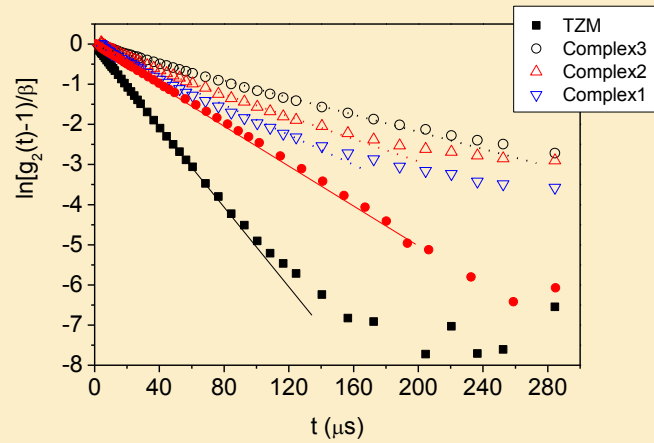
$$D_t (\text{Buffer @ } 20 \text{ }^\circ\text{C}) = 4.01 \cdot 10^{-7} \text{ cm}^2/\text{s}$$

$$D_t (\text{Water @ } 20 \text{ }^\circ\text{C}) = 4.09 \cdot 10^{-7} \text{ cm}^2/\text{s}$$

$$r_h (\text{Stokes-Einstein}) = 5.23 \text{ nm}$$

$$r_h (\text{TDA-SEC}) = 5.16 \text{ nm}$$

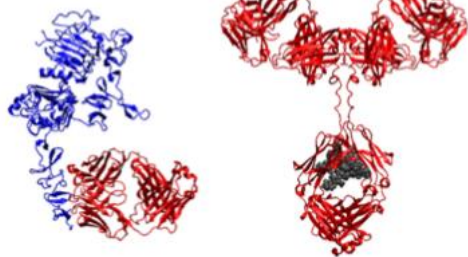
Diffusion Coefficient and Size Complexes



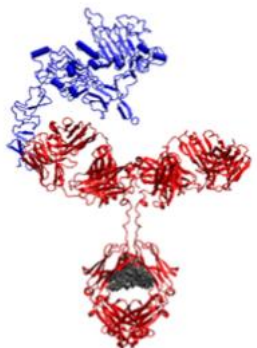
Study of the interaction in extracellular domain ErbB2-Transtuzumab complexes by hydrodynamic properties and computational models

Generating atomistic structures from MD simulations

1N8Z (Extracellular ErbB2-Fab TZM) TZM model construction from [2]

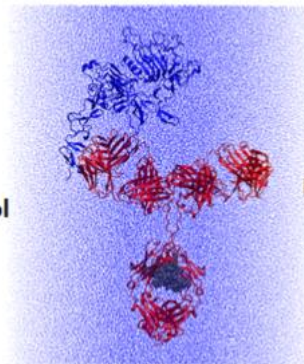


Superimpose by fitting the common Fab domain and removing the duplicated Fab domain with Pymol



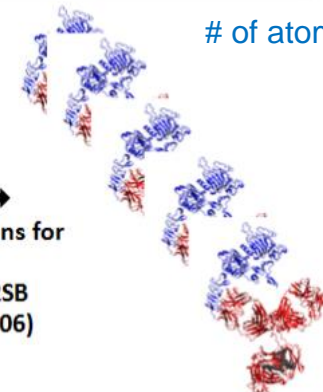
TZM-ErbB2 complex

TIP3P water and equilibration protocol (AMBER12SB FF+Glycam06)



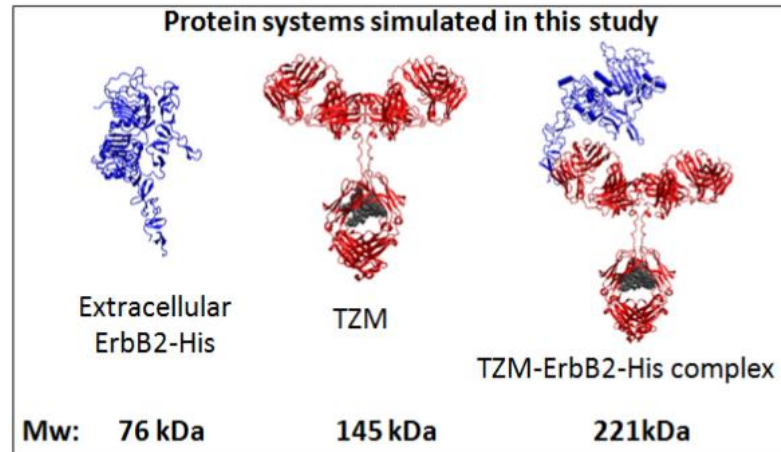
Solvated TZM-ErbB2 complex

Production runs for 50 ns (AMBER12SB FF+Glycam06)

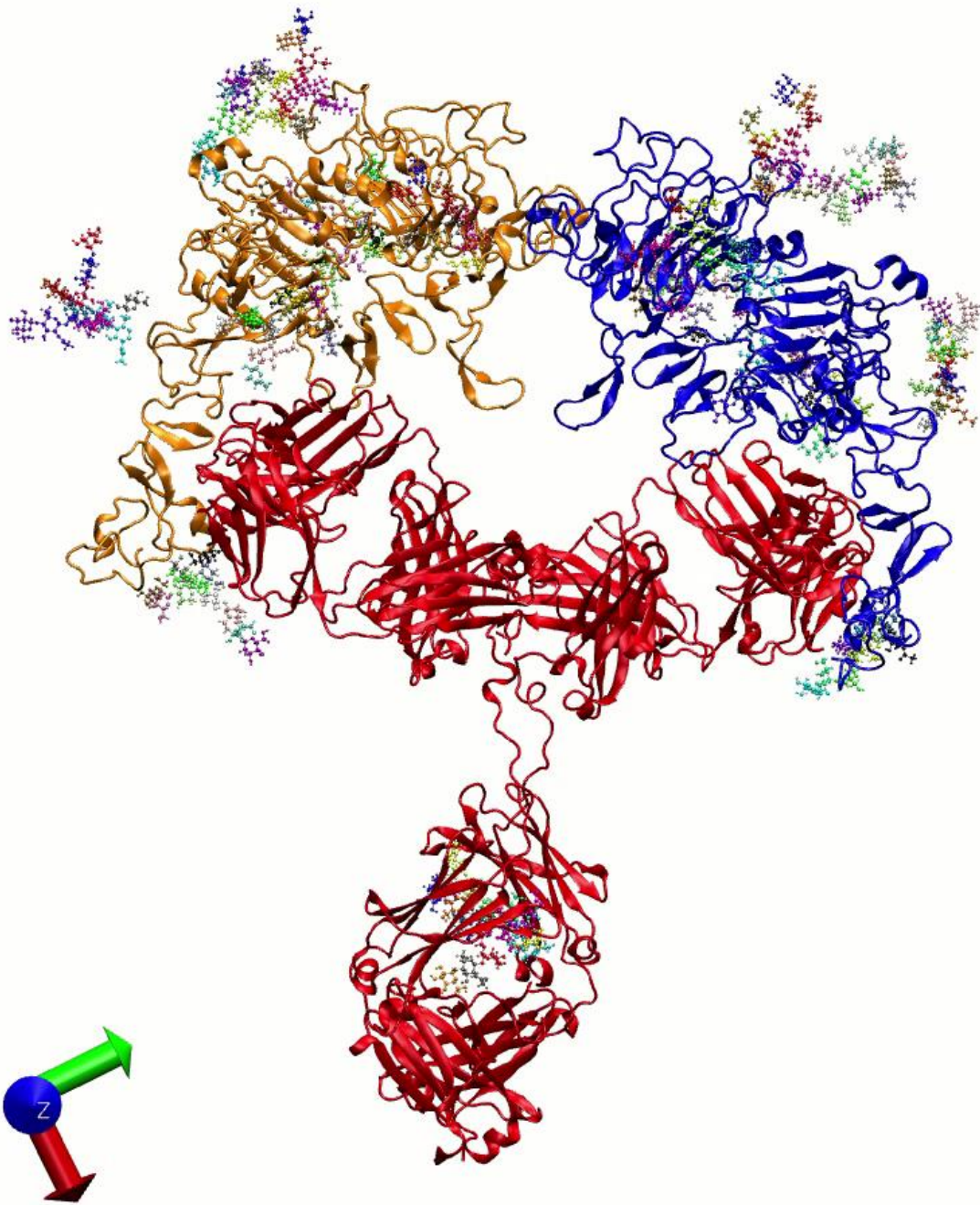


Multiple Trajectory (T1-T10)

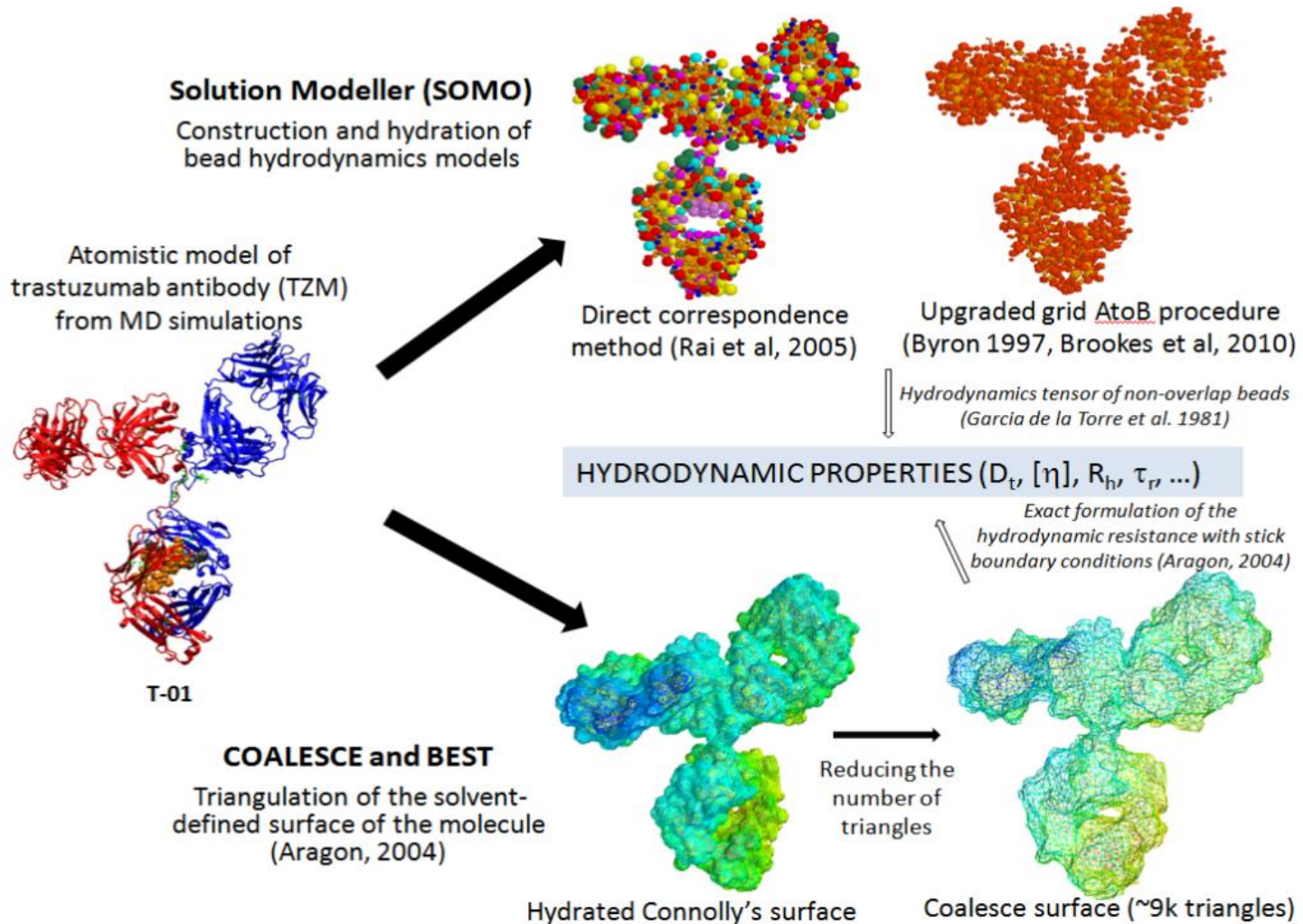
of atoms > 5×10^5



All calculations were run using AMBER14 on GPUs



Study of the interaction in extracellular domain ErbB2-Transtuzumab complexes by hydrodynamic properties and computational models

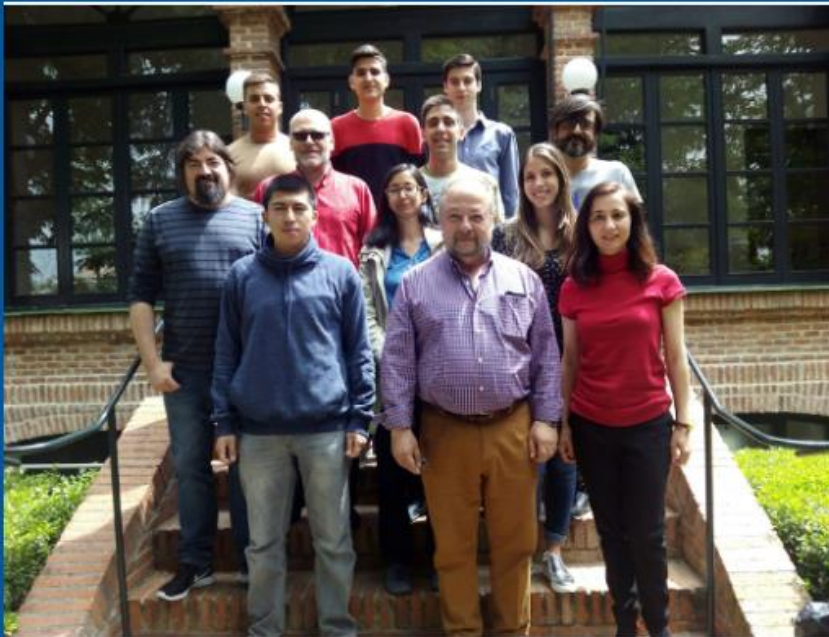


Study of the interaction in extracellular domain HER2-Transtuzumab complexes by hydrodynamic properties and computational models

Table 3. Comparison of experimental and calculated hydrodynamic results for the structures studied, including the TZM as model case, at $T = 293\text{ K}$

| <i>Sample</i> | $[\eta]$ (cm ³ -g ⁻¹) | $[\eta]$ (cm ³ -g ⁻¹) | $D \times 10^7$ (cm ² -s ⁻¹) ^a | $D \times 10^7$ (cm ² -s ⁻¹) ^a |
|--|--|--|--|--|
| | SEC | SIM | DLS | SIM |
| <i>TZM</i> | 6.5 ± 0.1 | 6.6 ± 0.2 | 4.09 ± 0.02 (5.2 nm) | 3.95 ± 0.03 (5.3 nm) |
| <i>eHER2</i> | n.d. | 5.7 ± 0.2 | n.d. | 5.32 ± 0.04 (4.0 nm) |
| <i>g-eHER2</i> | 6.4 ± 0.2 | 6.5 ± 0.2 | 4.56 ± 0.02 (4.7 nm) | 4.77 ± 0.04 (4.5 nm) |
| <i>g-eHER2 dimer</i> | 6.9 ± 0.5 ^a | 6.9 ± 0.2 | 3.57 ± 0.02 (6.0 nm) | 3.71 ± 0.02 (5.8 nm) |
| <i>Complex 1:1 (TZB-erbb2)</i> | 7.4 ± 0.2 | 7.9 ± 0.2 | 3.16 ± 0.02 (6.8 nm) | 3.20 ± 0.02 (6.7 nm) |
| <i>Complex 1:2 (TZB-erbb2)₂</i> | 8.6 ± 0.2 | 8.4 ± 0.2 | 2.38 ± 0.02 (9.0 nm) | 2.80 ± 0.02 (7.6 nm) |

^a In parentheses the corresponding value of r_h obtained from Eq. 6 in water at $T = 293\text{ K}$.



Group members (left to right): *Top:* Mr. Rubén Casas, Mr. Alejandro Clemente, Mr. Guillermo Juárez. *Middle:* Dr. Javier Ramos, Dr. Victor Cruz, Dra. Virginia Souza-Egipsy, Mr. Eduardo Sanchez, Mrs. Anna Espasa, Dr. Juan Francisco Vega. *Bottom:* Mr. Alexis Julián Amagua, Prof. Javier Martínez-Salazar, Dra. Sonia Martínez.

BIOPHYM is a group devoted to experimental and computational research activities related to the fundamental physical properties of macromolecular systems: molecular dynamics, assembling and functionality of synthetic polymers and biomacromolecular systems.

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THE END

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