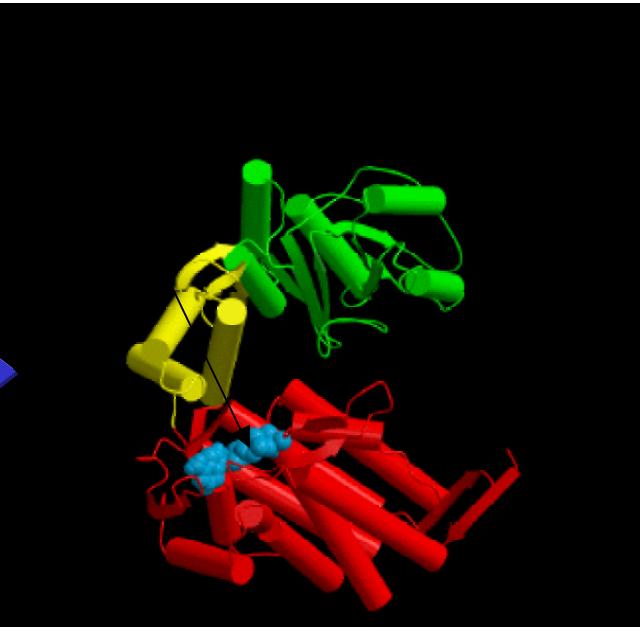
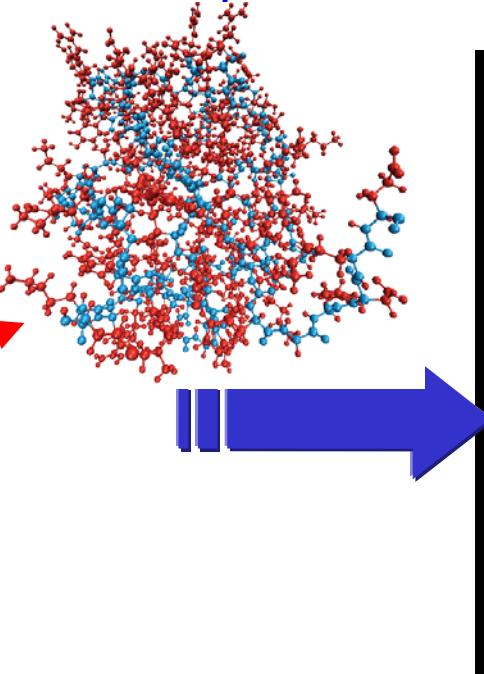
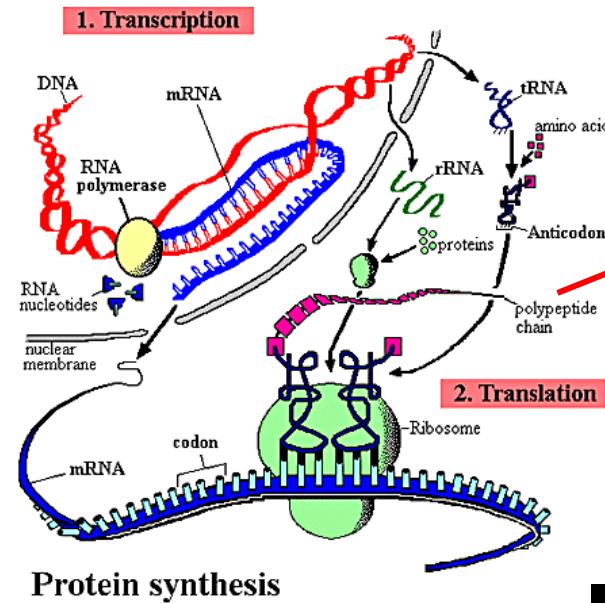

Estructura de Proteínas

Introducción

Características del Espacio de Estructuras

Florencio Pazos (CNB-CSIC)

Estructura de proteínas



Molecular chaperonin
GroEL

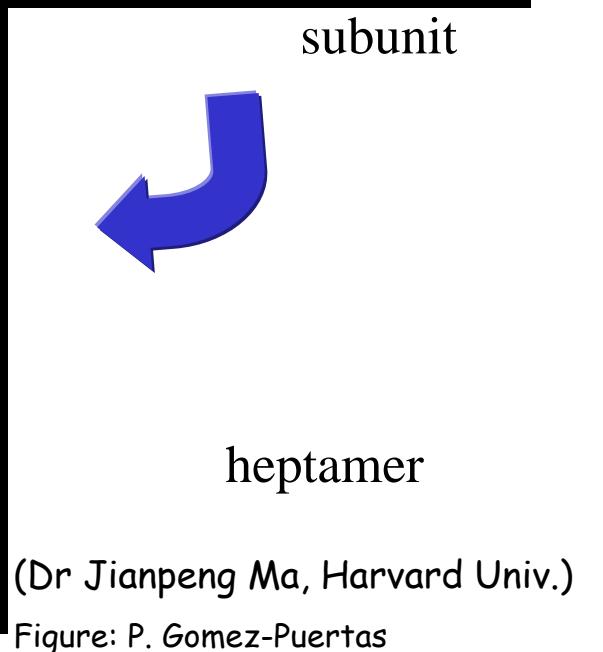
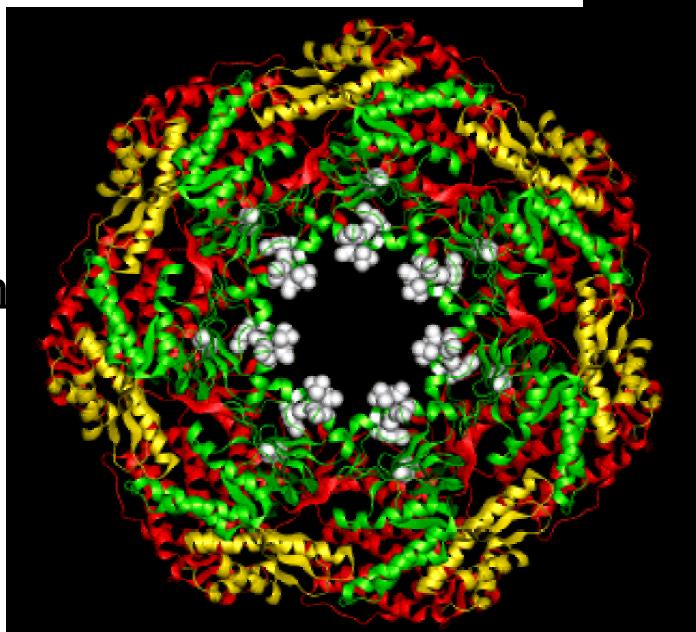
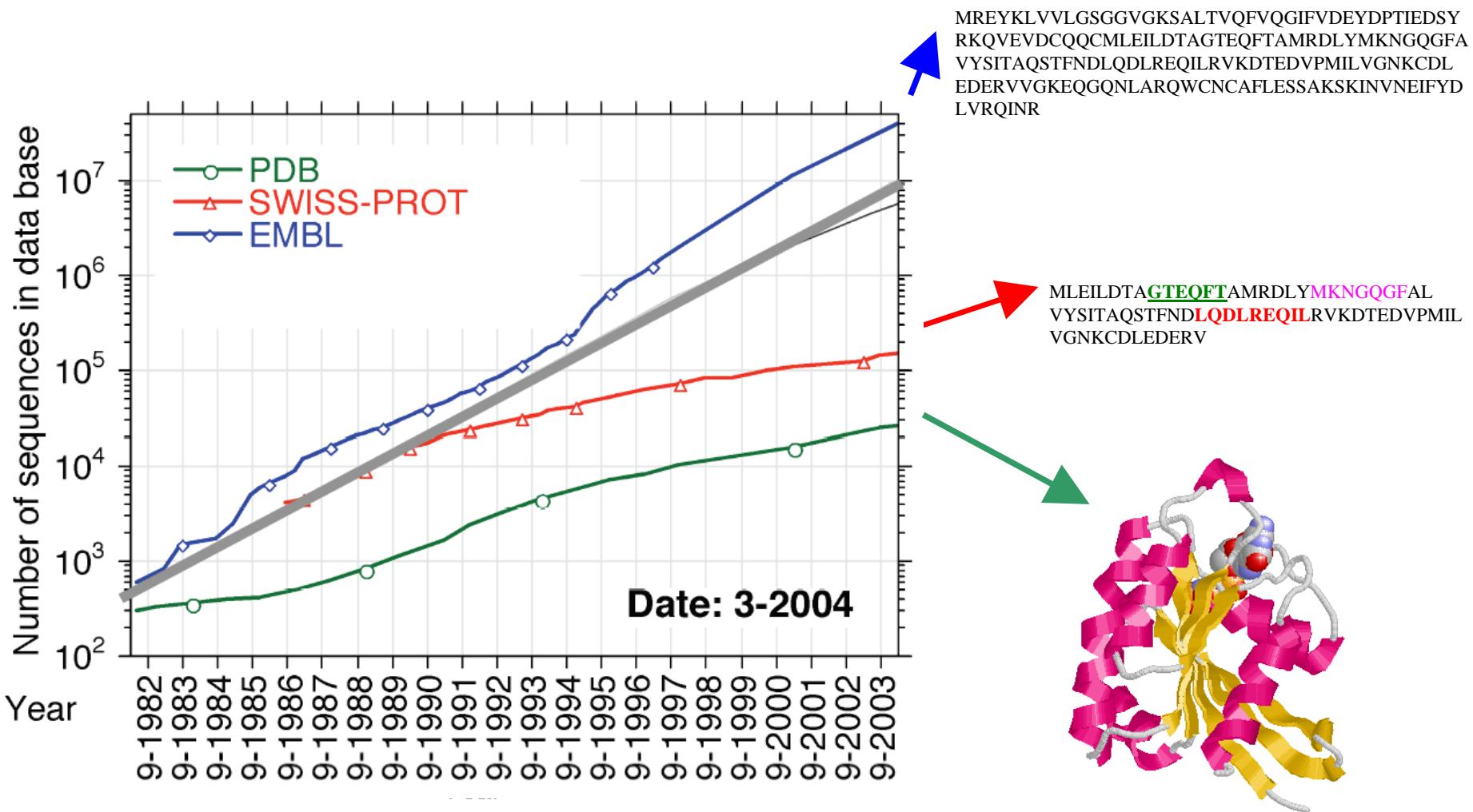
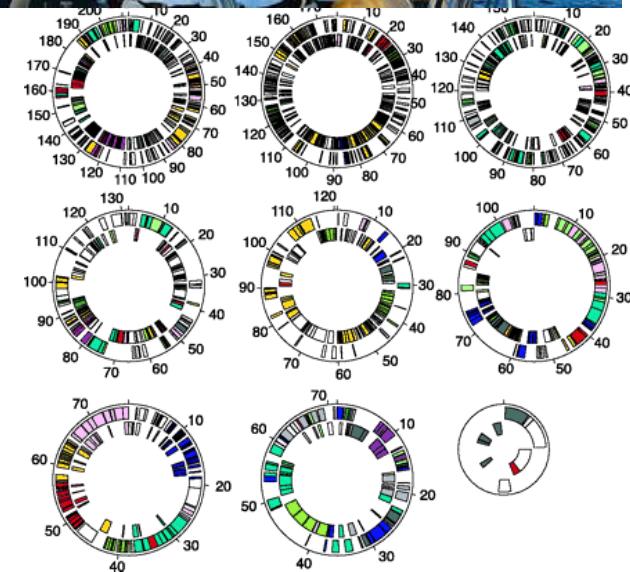
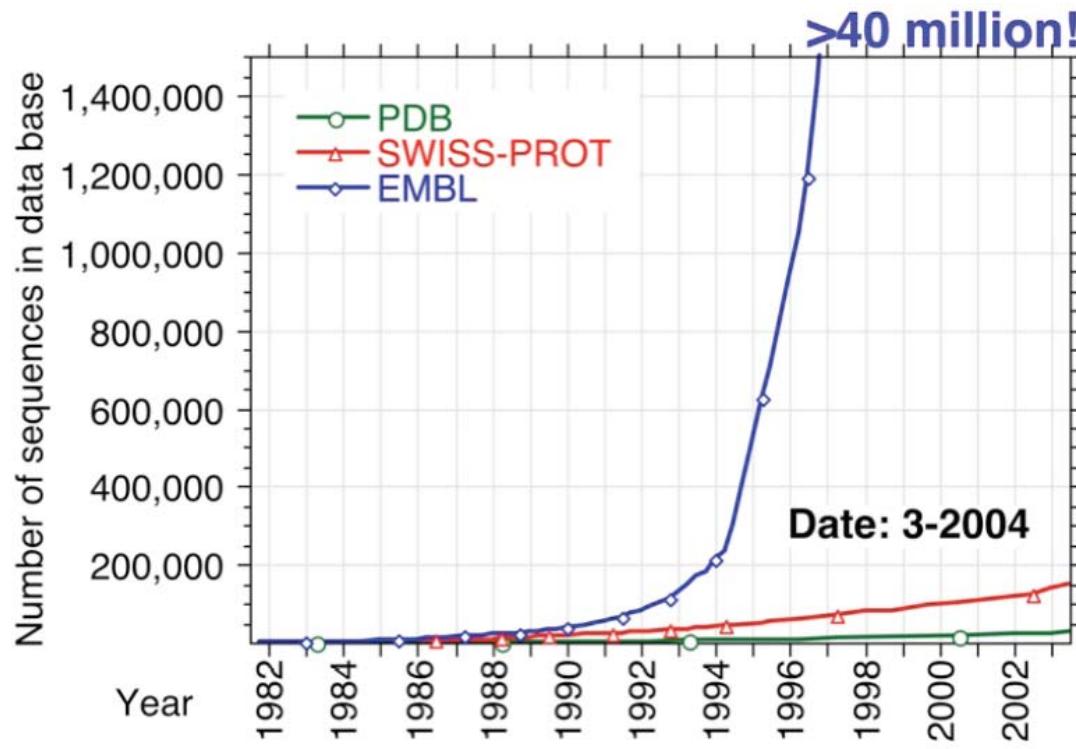
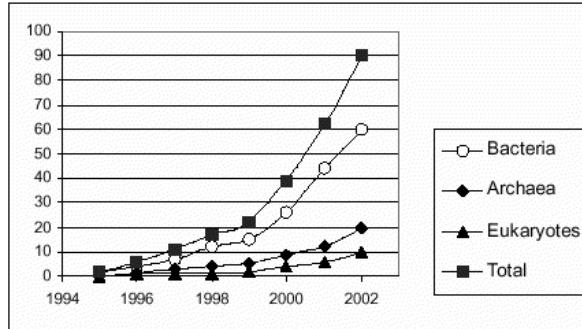


Figure: P. Gomez-Puertas

Conocimiento experimental de secuencias, funciones y estructuras de proteínas

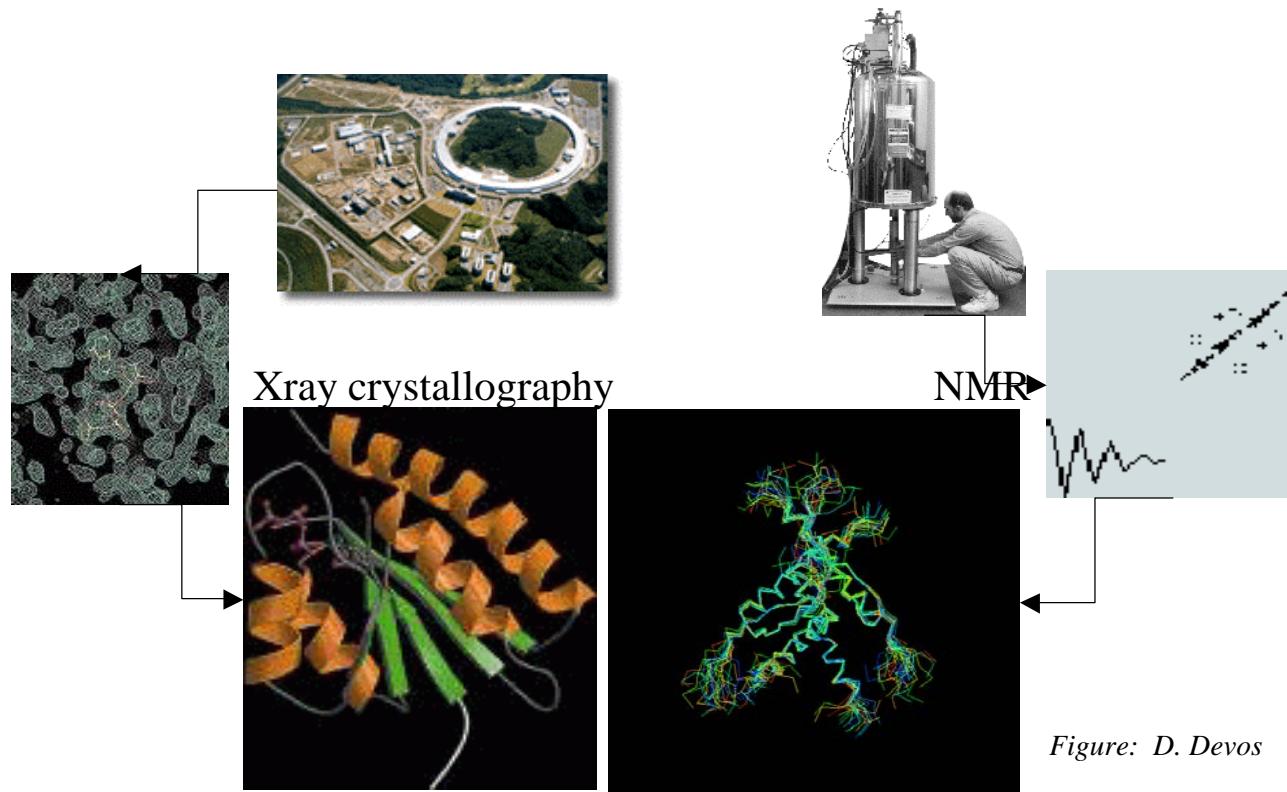


Secuenciación de Genomas Completos y “Metagenomas”

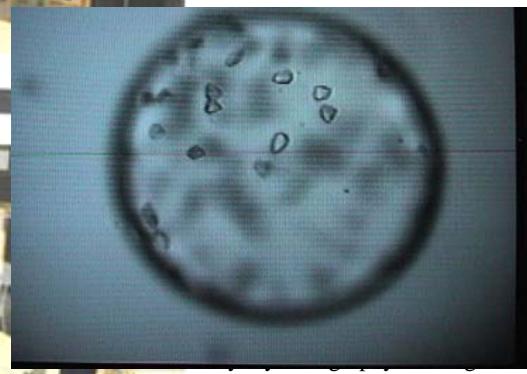
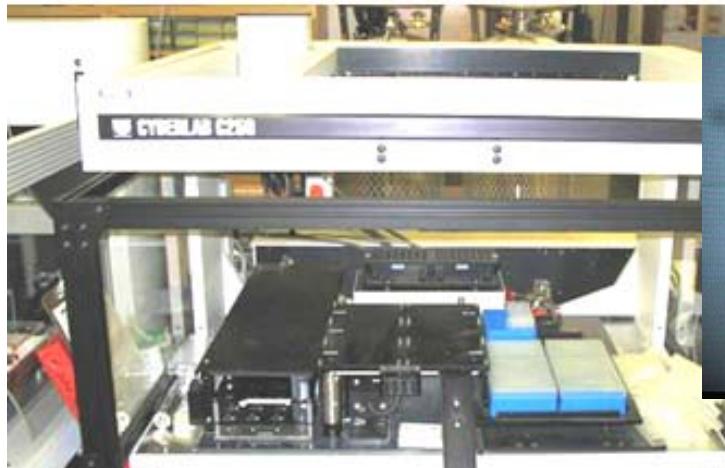


- Collins, F.S., Green, E.D., Guttmacher, A.E. & Guyer, M.S. (2003) A vision for the future of genomic research. *Nature*, **422**, 835-847.
- Venter, J. C. *et al.* Environmental genome shotgun sequencing of the Sargasso Sea. (2004). *Science* **304**, 66-74.

Determinación experimental de estructura de proteínas



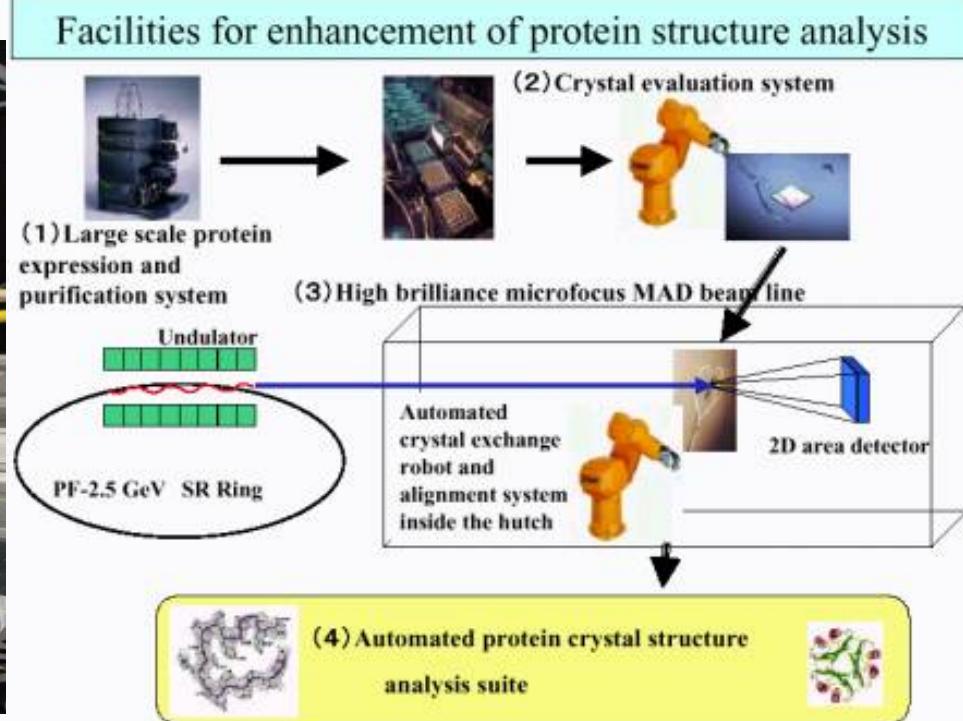
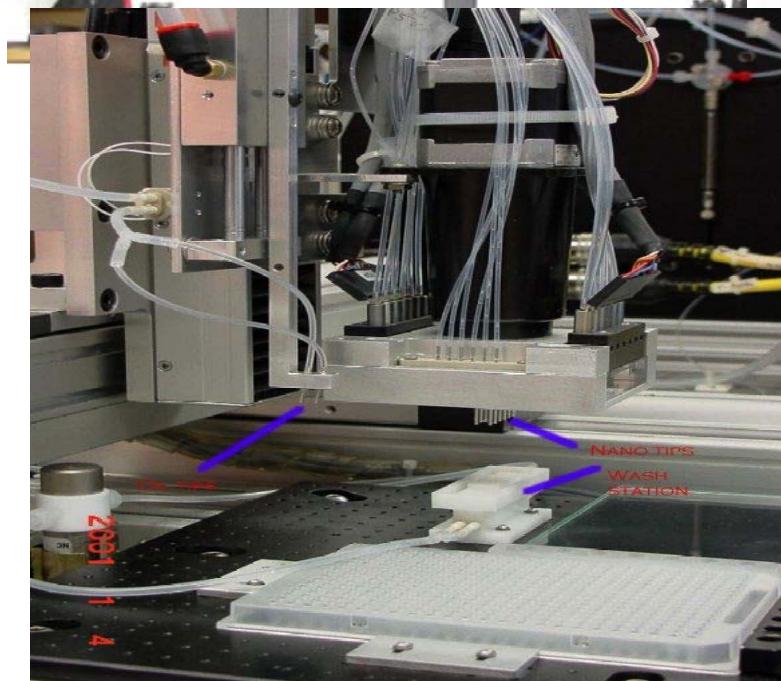
Genómica estructural



part of two minimal genomes, Mycoplasma genitalium and Thermotoga maritima, crystallography are being used for structural

structure determination of biologically important proteins in Arabidopsis. The

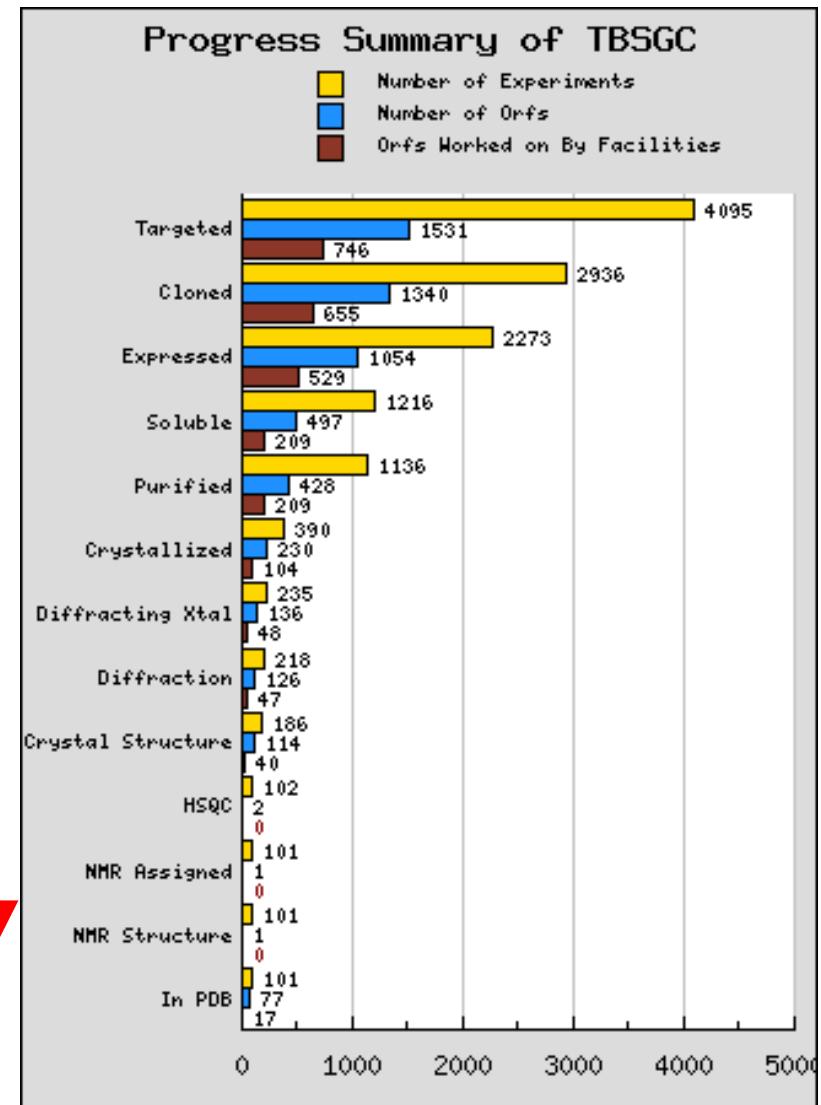
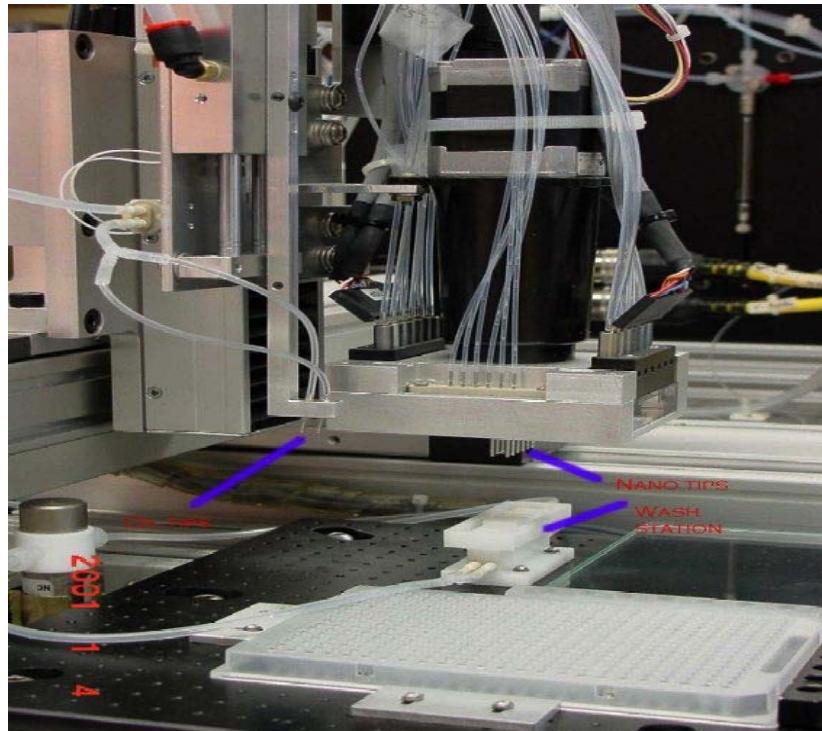
and the main proteins of interest are signaling proteins involved in the response to light in *Thermotoga maritima*, and creating a high-throughput system for structural determination.



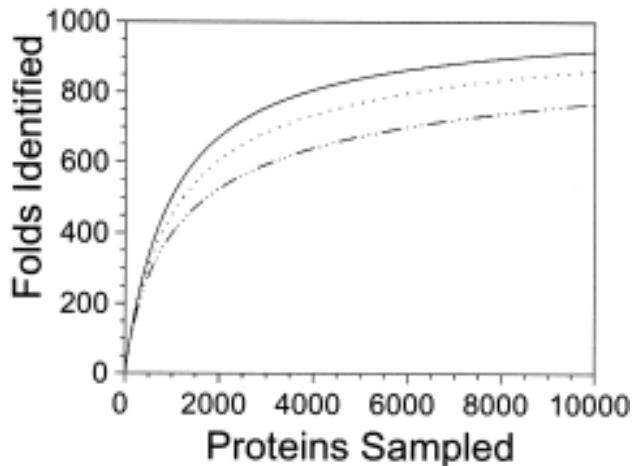
Goldsmith-Fischman, S. and Honig, B. (2003) Structural genomics: Computational methods for structure analysis. *Protein Sci*, **12**, 1813-1821.

Vitkup, D., Melamud, E., Moult, J. and Sander, C. (2001) Completeness in structural genomics. *Nat Struct Biol*, **8**, 559-566.

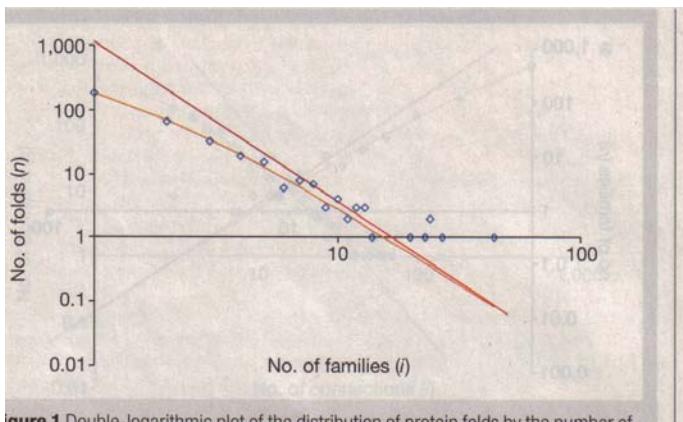
Genómica Estructural



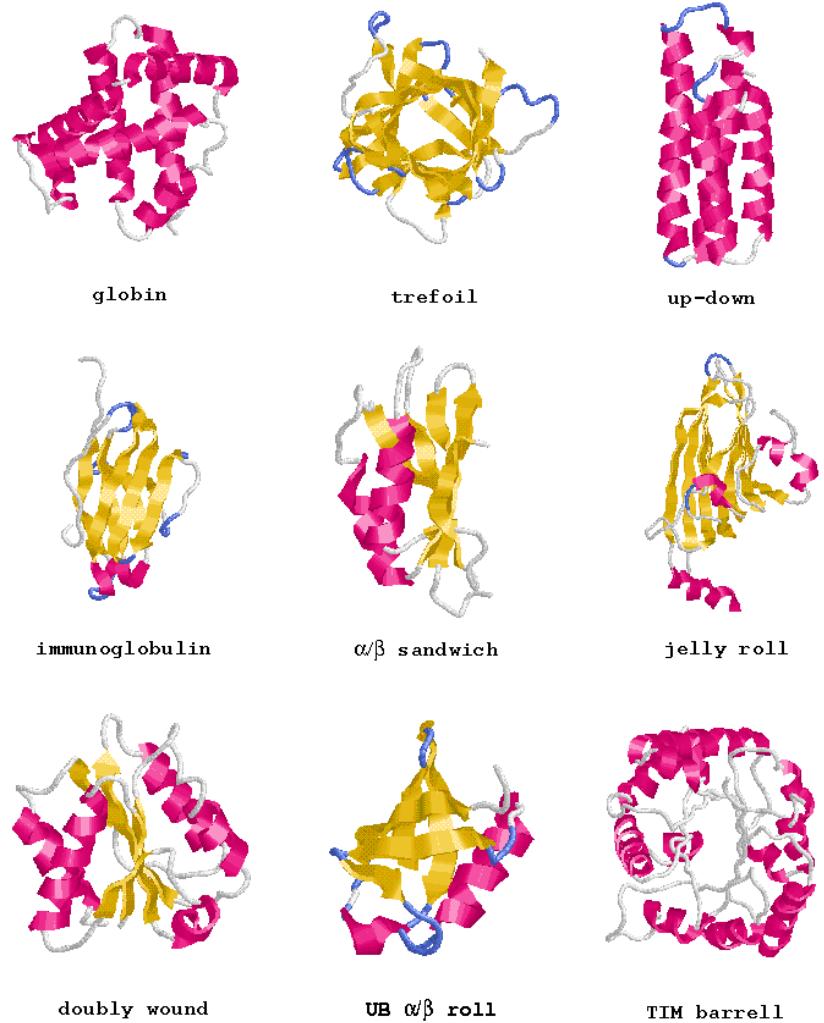
Características del Espacio de Estructuras



Leonov, H., Mitchell, J.S. & Arkin, I.T. (2003) Monte Carlo estimation of the number of possible protein folds: effects of sampling bias and folds distributions. *Proteins*, **51**, 352-359.



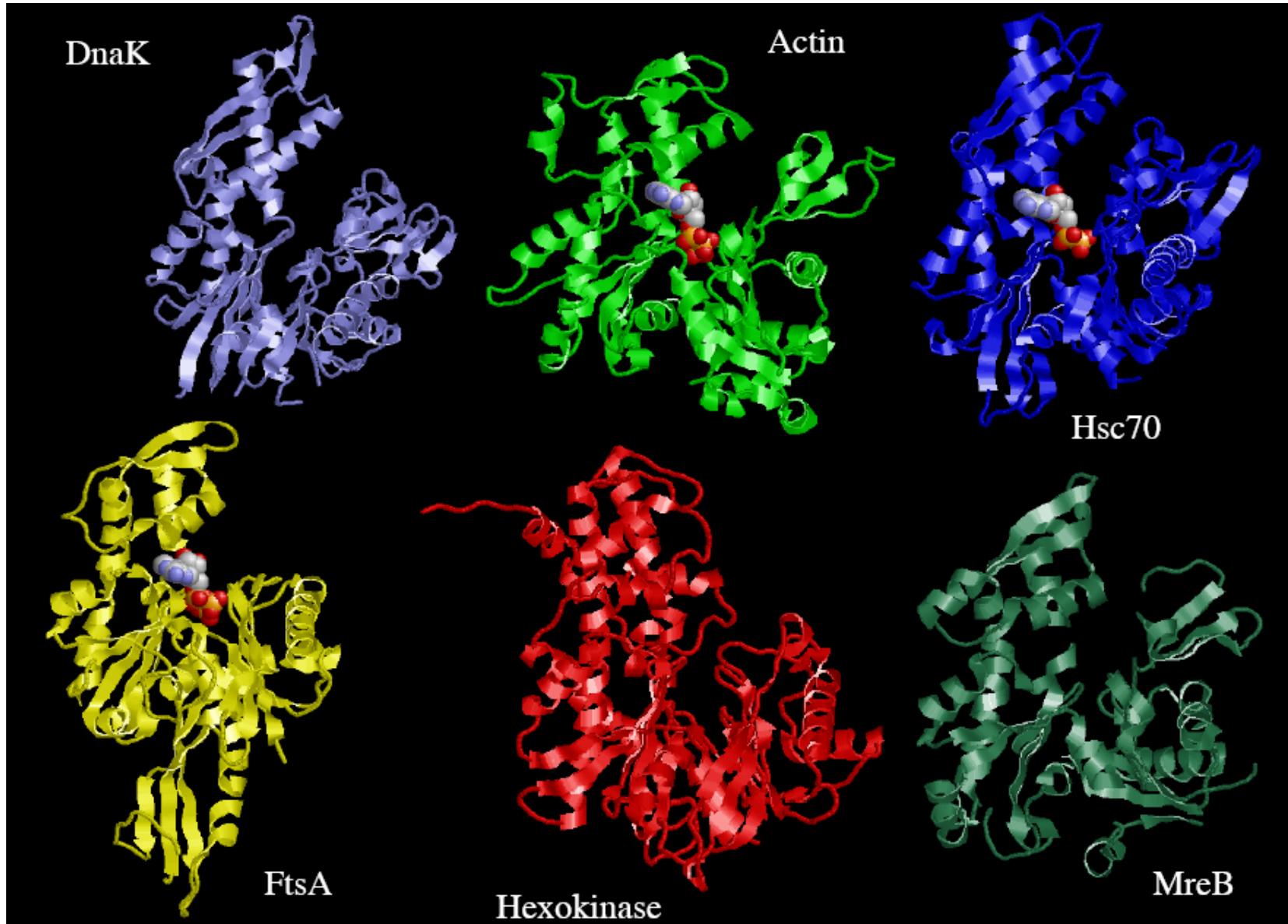
Koonin, E.V., Wolf, Y.I. & Karev, G.P. (2002) The structure of the protein universe and genome evolution. *Nature*, **420**, 218-223.



Orengo, C.A., Jones, D.T. & Thornton, J.M. (1994) Protein superfamilies and domain superfolds. *Nature*, **372**, 631-634.

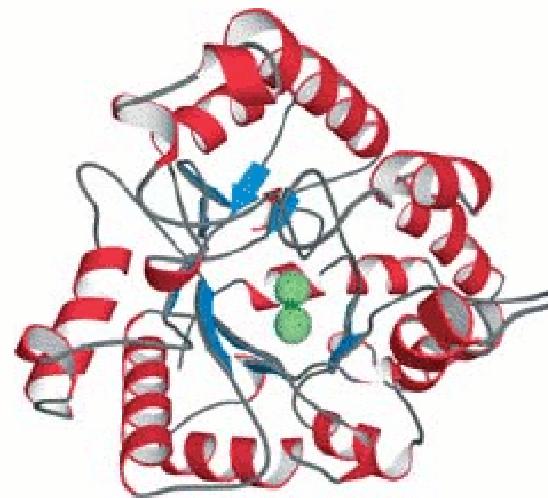
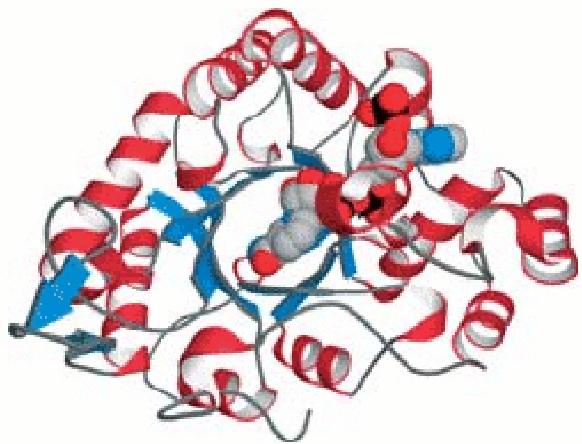
Características del Espacio de Estructuras

Relación con el espacio de secuencias



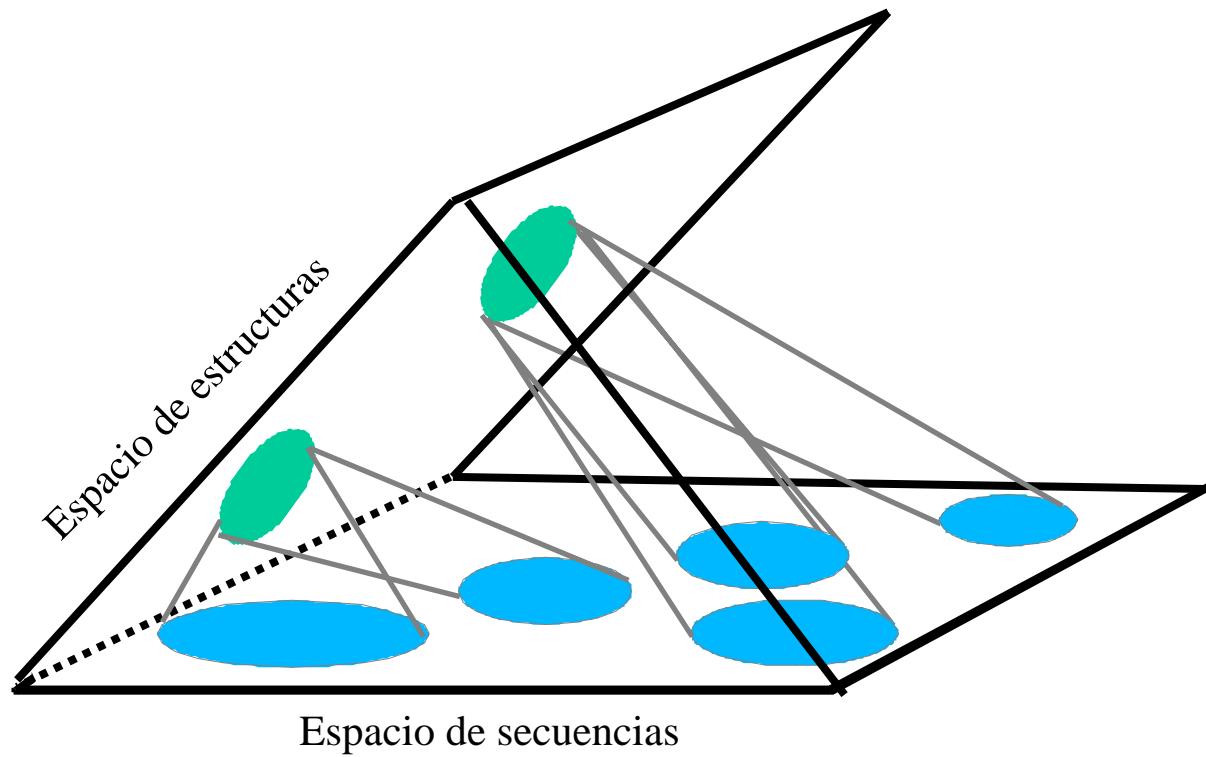
Características del Espacio de Estructuras

Relación con el espacio de secuencias

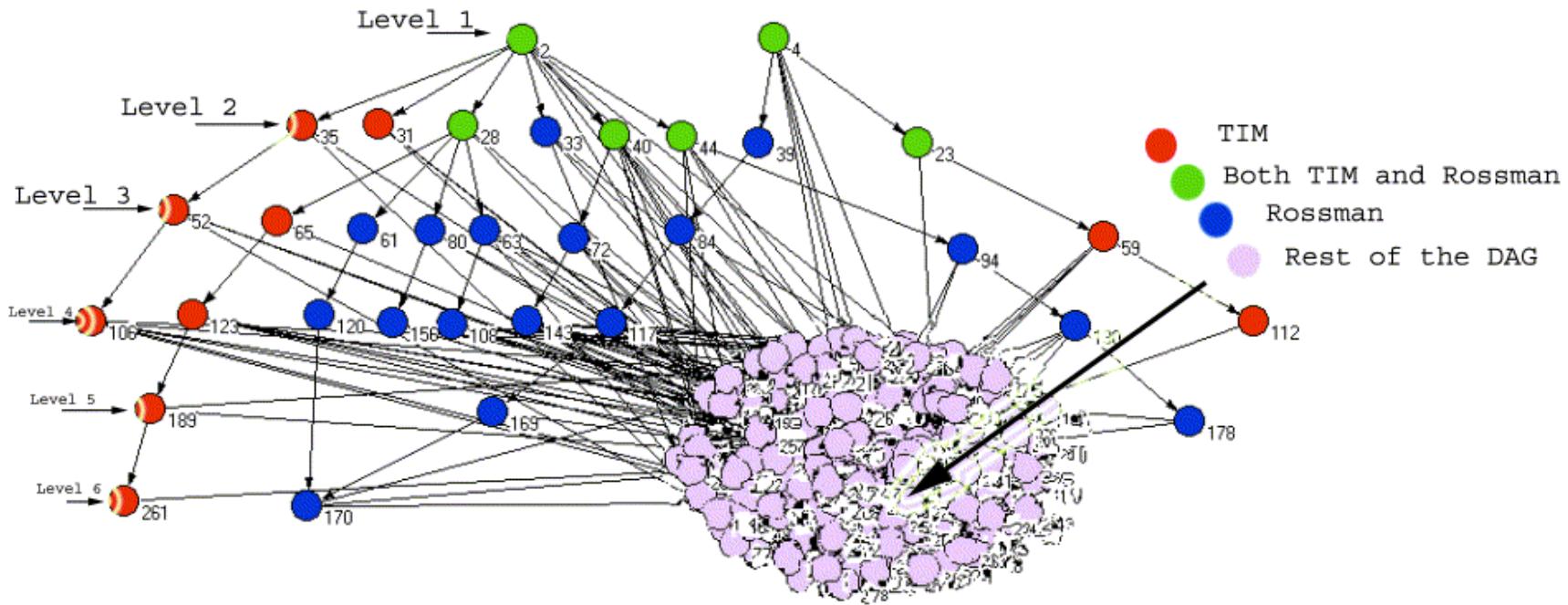


Características del Espacio de Estructuras

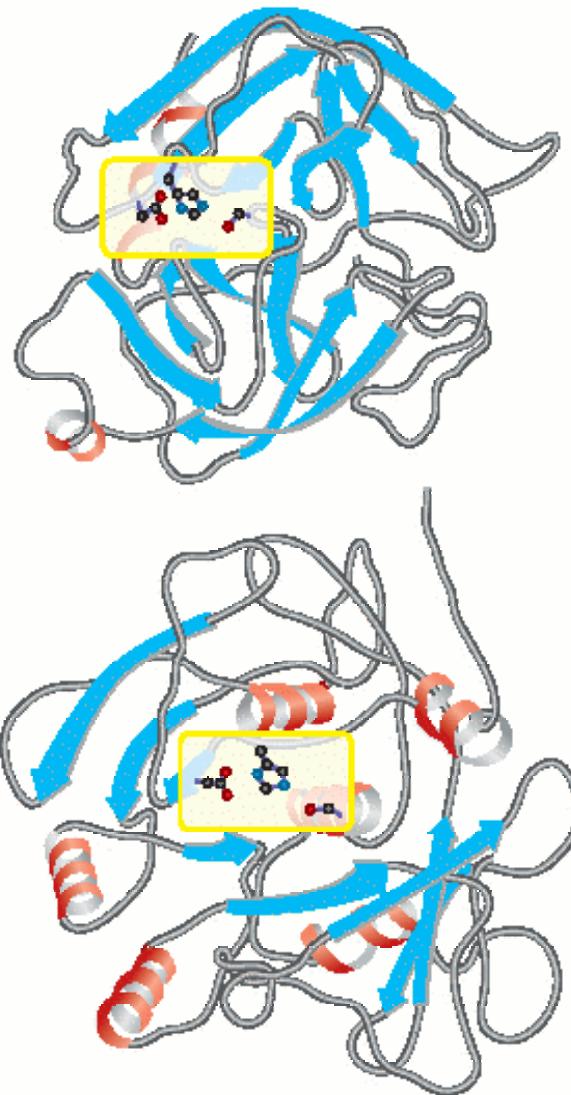
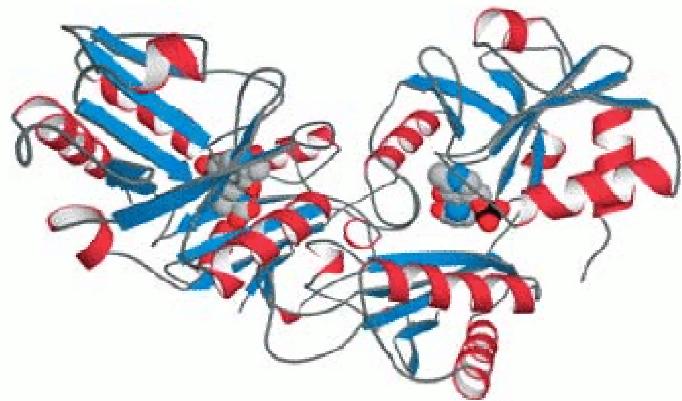
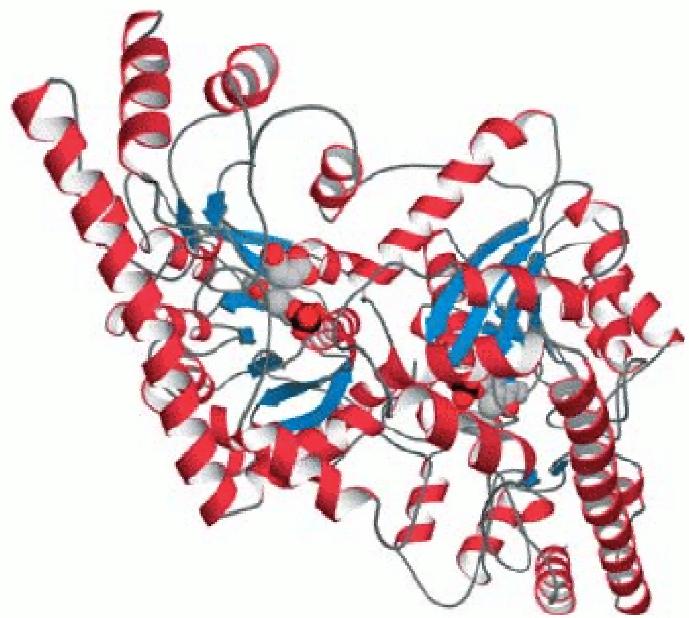
Relación con el espacio de secuencias



Características del Espacio de Estructuras Relación con el “espacio de funciones”

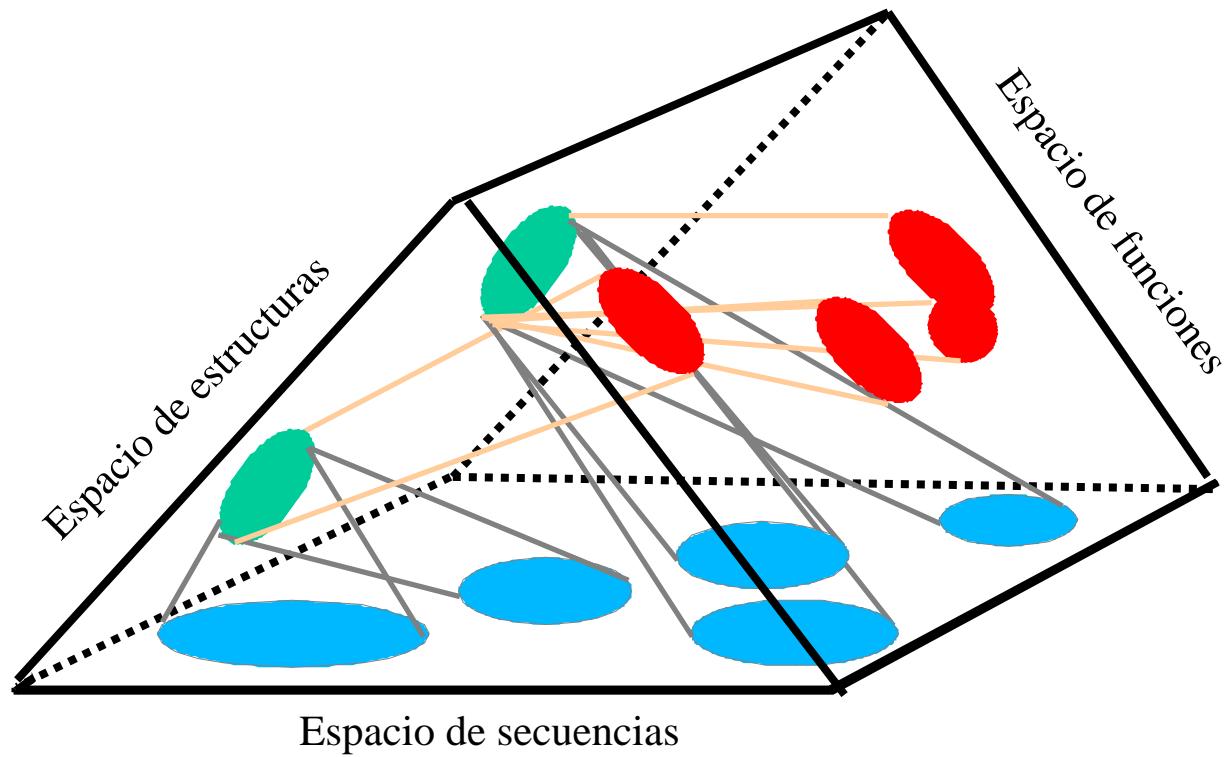


Características del Espacio de Estructuras Relación con el “espacio de funciones”

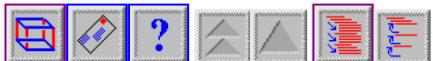


Características del Espacio de Estructuras

Relación con el espacio de secuencias y funciones



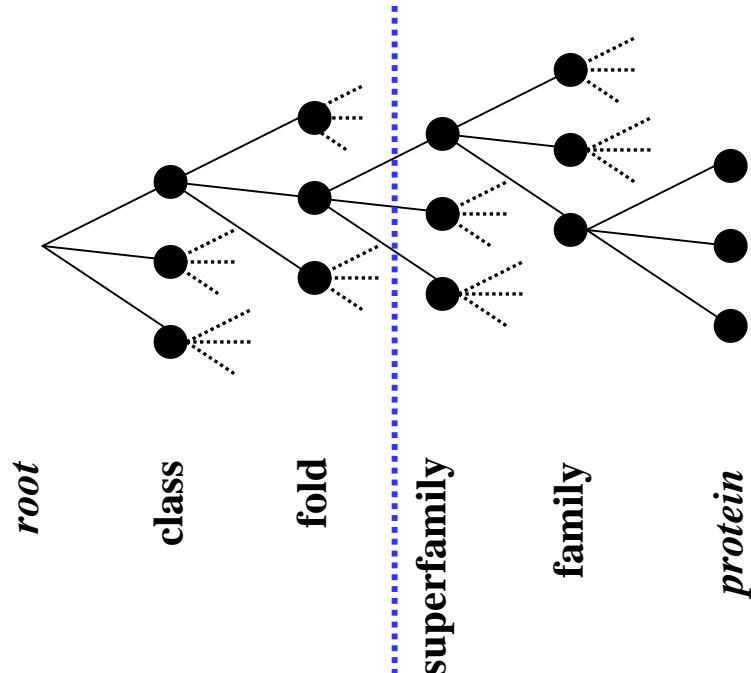
Clasificación jerárquica de estructuras de proteínas (SCOP)



Root: scop

Classes:

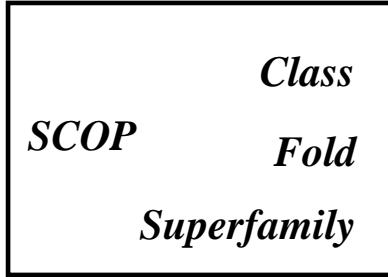
1. [All alpha proteins](#) [46456] (218)
2. [All beta proteins](#) [48724] (144)
3. [Alpha and beta proteins \(a/b\)](#) [51349] (136)
Mainly parallel beta sheets (beta-alpha-beta units)
4. [Alpha and beta proteins \(a+b\)](#) [53931] (279)
Mainly antiparallel beta sheets (segregated alpha and beta regions)
5. [Multi-domain proteins \(alpha and beta\)](#) [56572] (46)
Folds consisting of two or more domains belonging to different classes
6. [Membrane and cell surface proteins and peptides](#) [56835] (47)
Does not include proteins in the immune system
7. [Small proteins](#) [56992] (75)
Usually dominated by metal ligand, heme, and/or disulfide bridges
8. [Coiled coil proteins](#) [57942] (6)
Not a true class
9. [Low resolution protein structures](#) [58117] (24)
Not a true class
10. [Peptides](#) [58231] (116)
Peptides and fragments. Not a true class
11. [Designed proteins](#) [58788] (42)
Experimental structures of proteins with essentially non-natural sequences. Not a true class



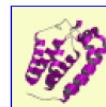
Andreeva, A., Howorth, D., Brenner, S.E., Hubbard, T.J., Chothia, C. and Murzin, A.G. (2004) SCOP database in 2004: refinements integrate structure and sequence family data. *Nucleic Acids Res.*, **32**, D226-229.

Structural Classifications

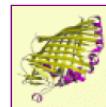
CATH



Main classification levels



Class 1: Mainly Alpha



Class 2: Mainly Beta

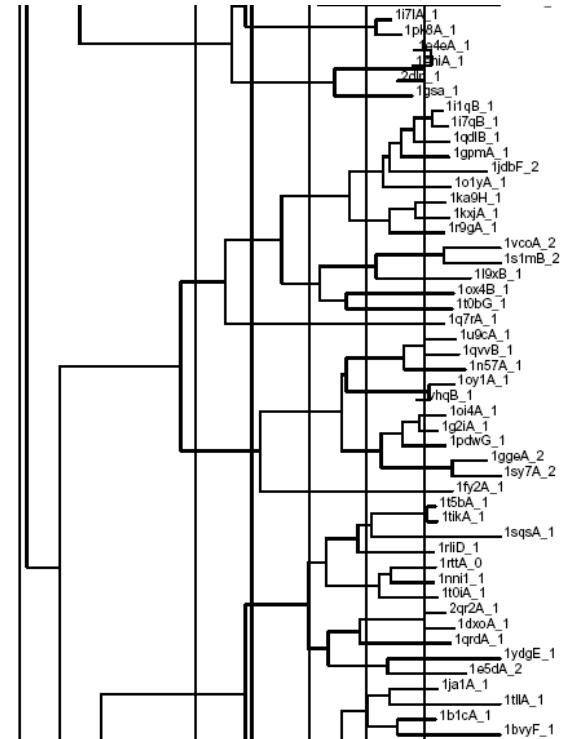


Class 3: Mixed Alpha-Beta



Class 4: Few Secondary Structures

Dali/FSSP



Pearl, F., Todd, A., Sillitoe, I., Dibley, M., Redfern, O., Lewis, T., Bennett, C., Marsden, R., Grant, A., Lee, D., *et al.* (2005) The CATH Domain Structure Database and related resources Gene3D and DHS provide comprehensive domain family information for genome analysis. *Nucleic Acids Res.*, **33**, D247-251.

Dietmann, S., Park, J., Notredame, C., Heger, A., Lappe, M. and Holm, L. (2001) A fully automatic evolutionary classification of protein folds: Dali Domain Dictionary version 3. *Nucleic Acids Res.*, **29**, 55-57.

The Protein “Universe”

10^{400} Possible sequences

10^{10} Sequences in the biosphere

10^5 Families

$10^3\text{-}10^4$ Folds

10^4 Functions (GO)

Estructura de Proteínas

Programa

Día 1

Introducción

Bases de datos con información estructural

Visualización y manipulación de estructuras

Día 2

Comparación y alineamiento de estructuras

Introducción a la predicción de estructura

Predicción de estructura secundaria y otras características 1D

Día 3

Predicción de estructura tridimensional

http://pdg.cnb.uam.es/pazos/cursos/protstr_cnb/