



# PREDICCIÓN DE ESTRUCTURA TRIDIMENSIONAL DE PROTEÍNAS

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# Temario



- Estructura de proteínas.
  - ▣ Reglas estructurales y excepciones.
  - ▣ Predicción de estructuras secundarias.
  - ▣ Cálculo de estructuras secundarias.
- Búsqueda de homólogos.
  - ▣ Reconocimiento de Plegamientos.
- Modelamiento Comparativo
  - ▣ Suite Modeller.
  - ▣ Suite Rossetta.
  - ▣ Análisis de Modelos.
  - ▣ Validación otras técnicas experimentales.

# Temario

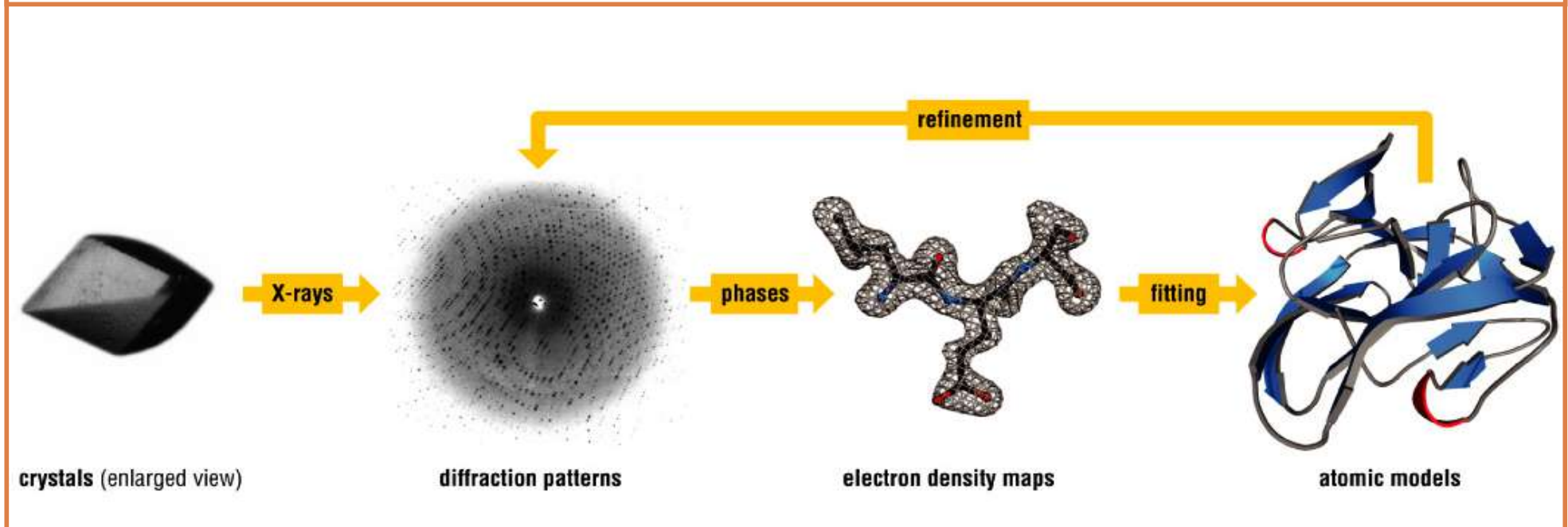
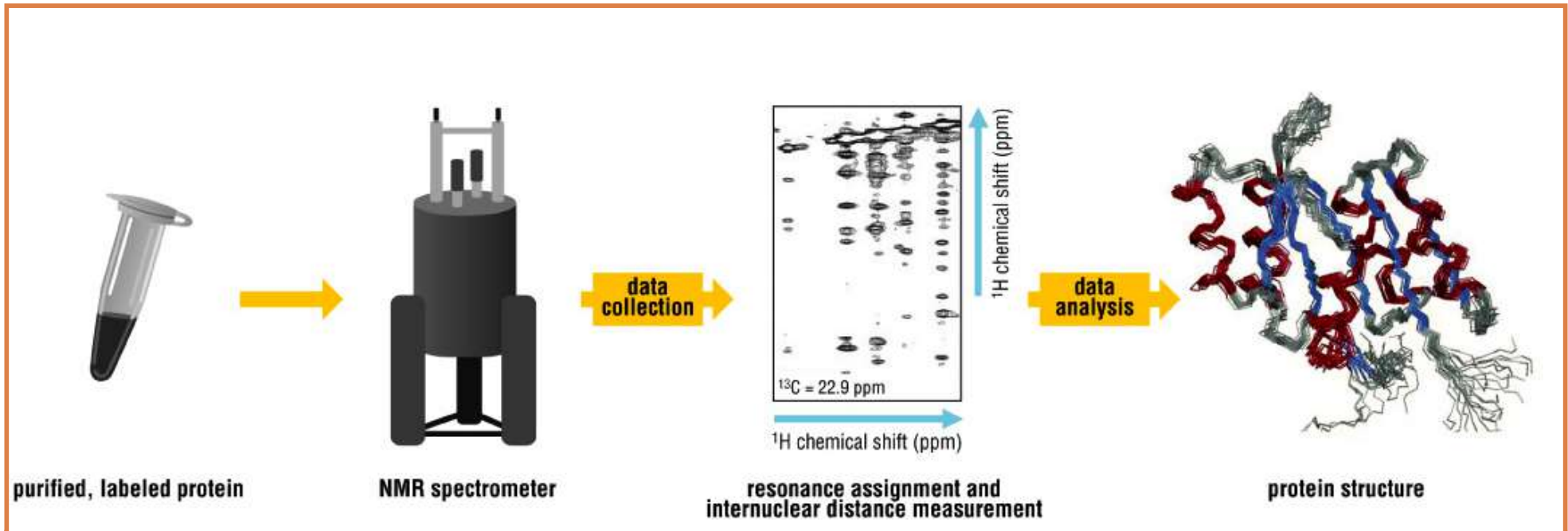


- Modelamiento ab initio.
- Modelamiento proteínas de membrana.
- Modelamiento CDR anticuerpos.
- Modelamiento de Lazos.
- Modelamiento de Mutaciones.



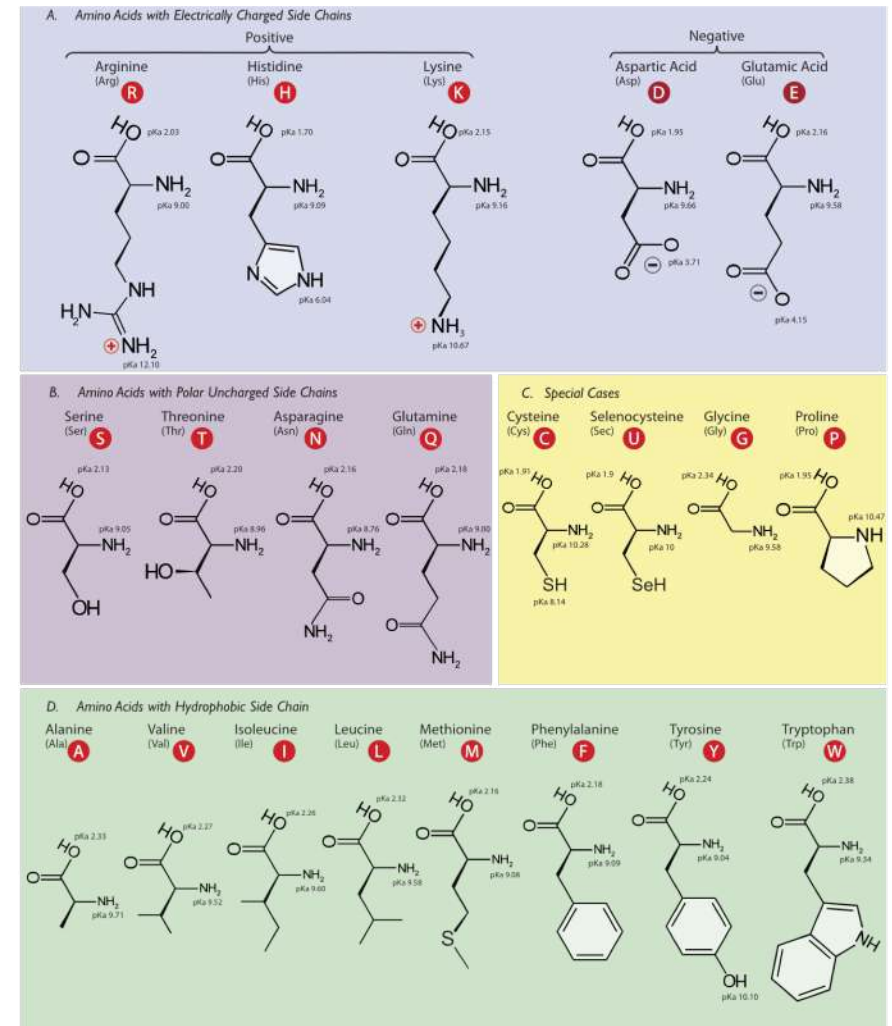
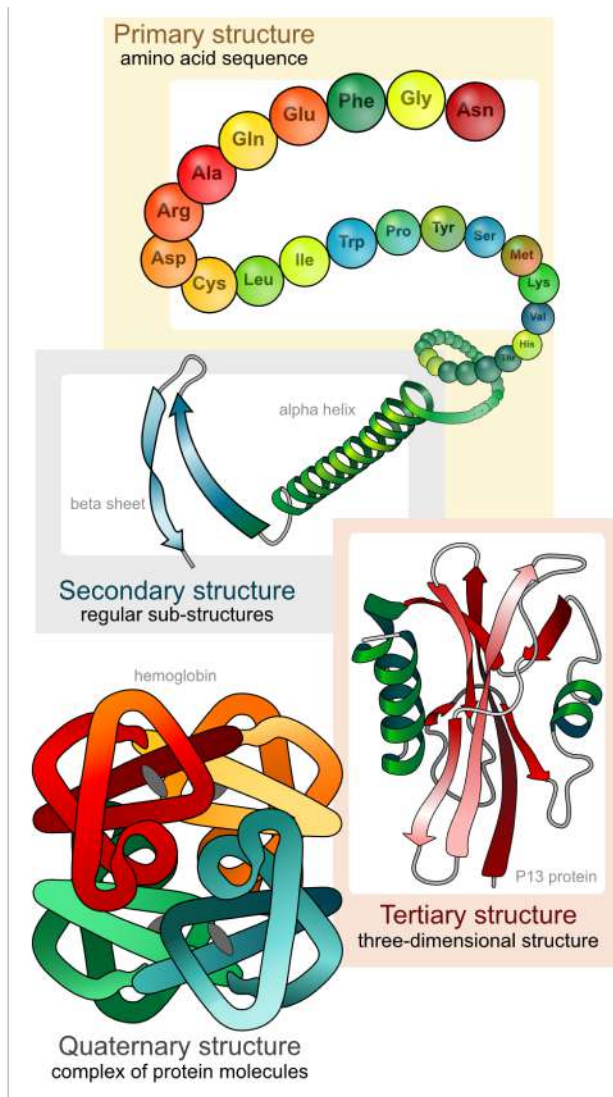
# Estructura de Proteínas

# METODOS EXPERIMENTALES DE DETERMINACION DE ESTRUCTURA DE PROTEINAS



# Estructura de Proteínas:

## Niveles

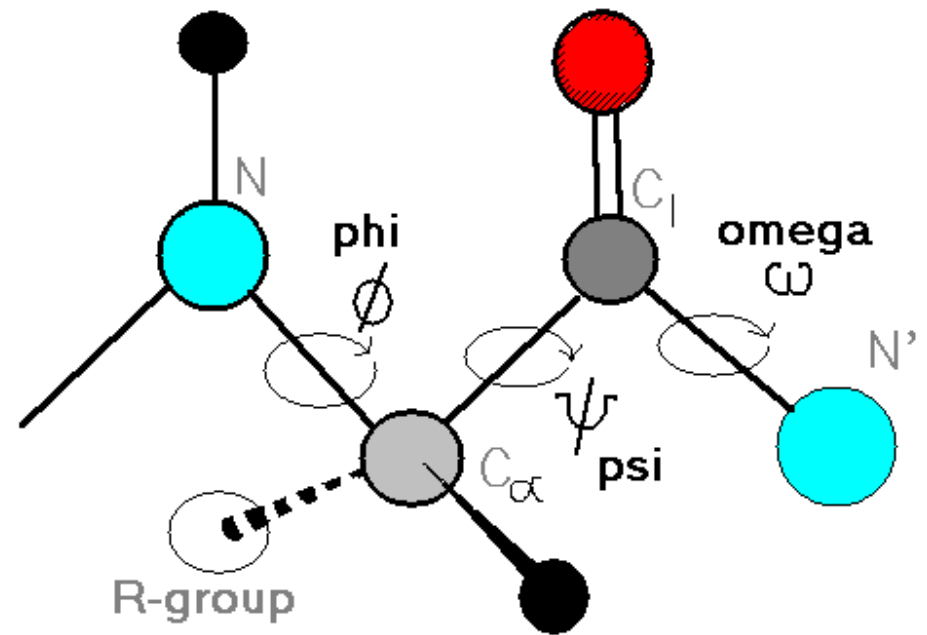
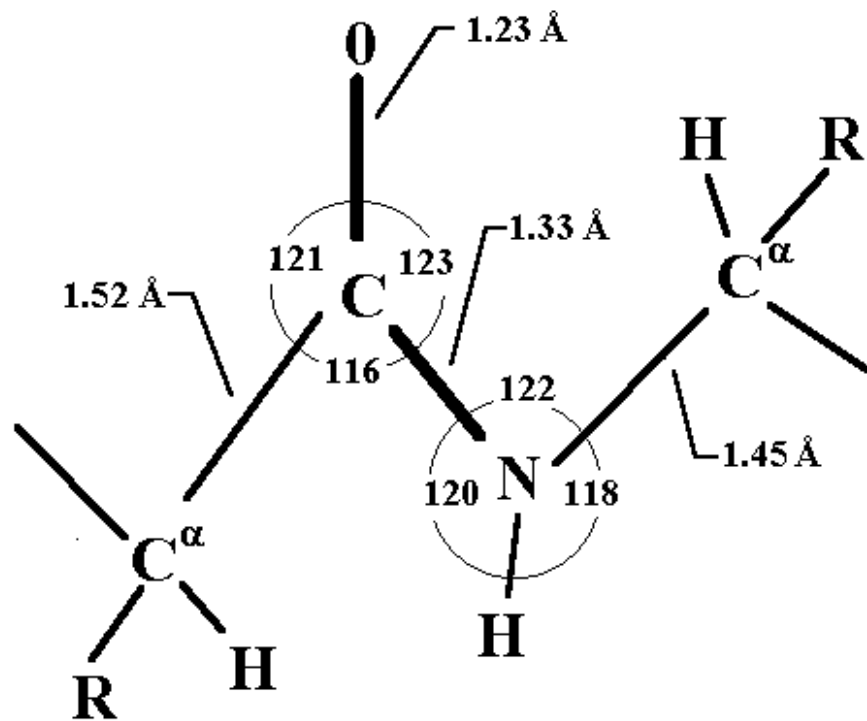


# Estructura de Proteínas:

## Estructura Secundaria

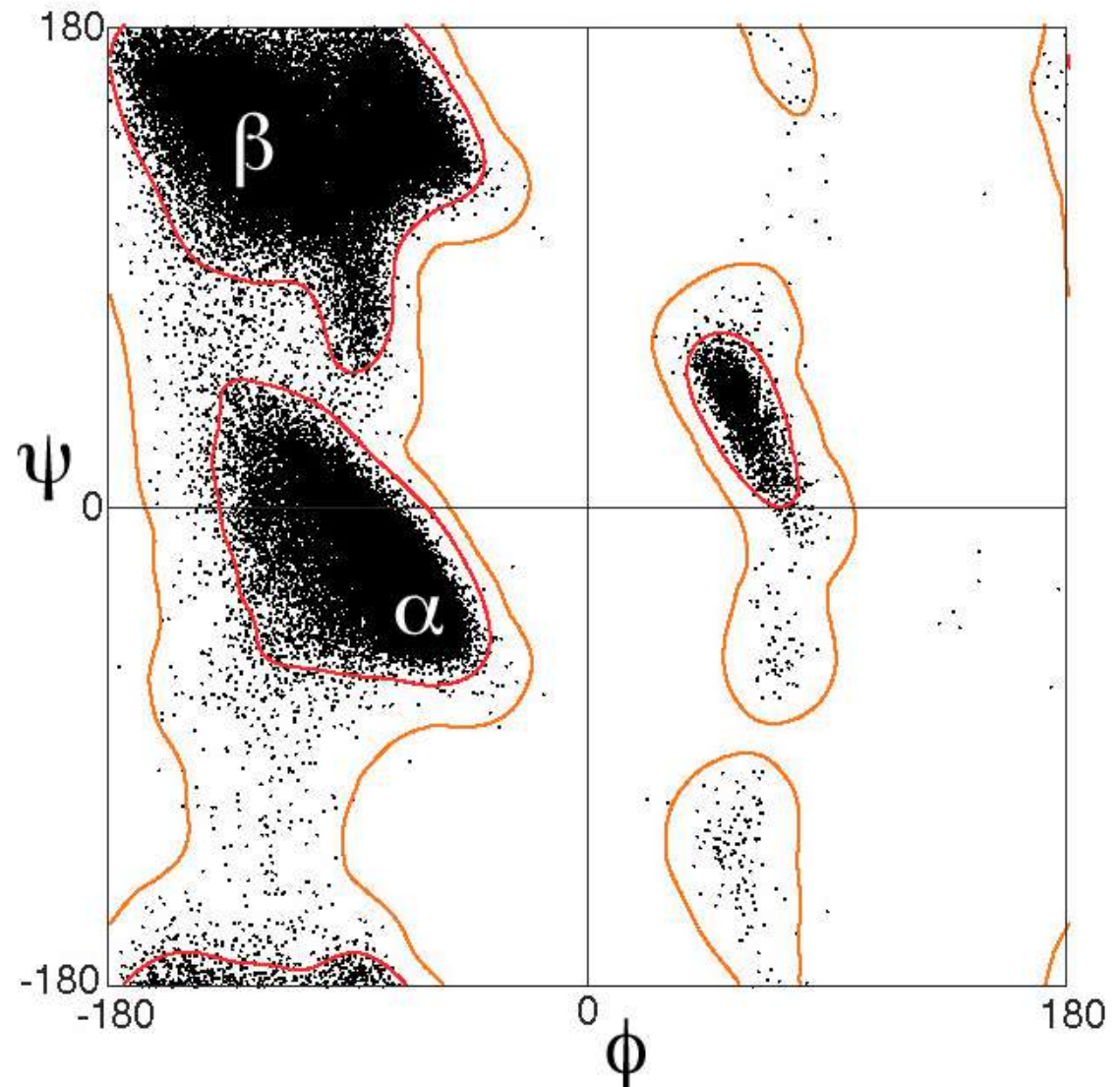
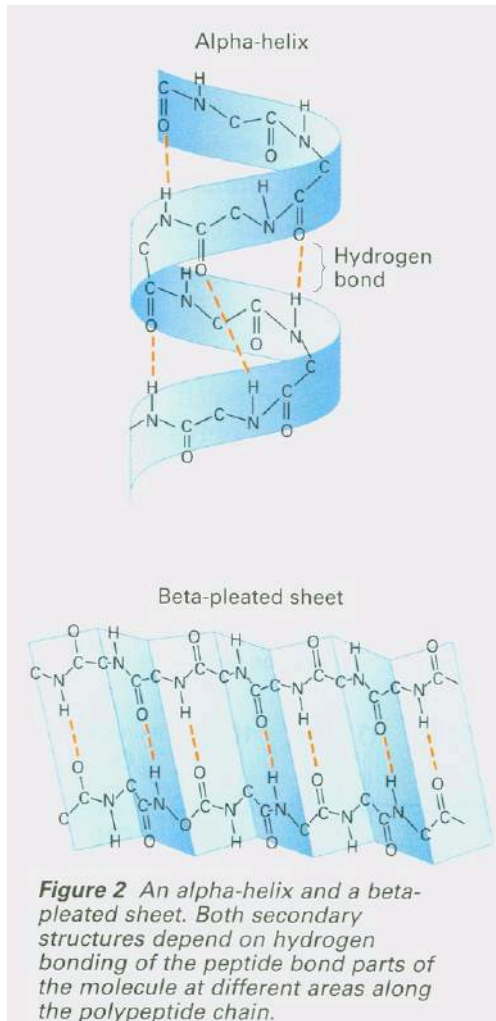
- Alfa Hélices.
  - ▣ Posee 3.6 aminoácidos por vuelta con puentes H cada 4 residuos.
  - ▣ El largo promedio es de 10 aminoácidos o 10 Å y van desde 5 a 40 (1.5 a 11 vueltas).
  - ▣ Rica en LEMA / pobres en PSGY.
- Hojas Beta.
  - ▣ 5 a 10 aminoácidos consecutivos que interaccionan con otros 5 a 10 en forma paralela o antiparalela.
- Lazos.
  - ▣ Son regiones de una cadena proteica que están entre  $\alpha$  hélices y hojas  $\beta$ , de longitudes variadas y configuraciones 3D y en la superficie de la estructura. Pueden ser tan cortos como 2 aminoácidos (horquillas).
- Vueltas.
  - ▣ Son tipos de lazos con configuraciones determinadas.

# Ángulos y Largos del Esqueleto Proteico





# Gráficos de Ramachandran



# Estructura de Proteínas:

## Definiciones

### □ Dominio.

- **Estructural.** Una región compacta y globular que es semi-independiente del resto de la cadena polipeptídica; esta región puede ser uno o más segmentos de una cadena de AA, la cadena entera o varias cadenas.
- **Evolutivo.** Una región de la proteína que se encuentra en la naturaleza aislada o en más de un contexto de múltiples dominios.
- **Funcional.** Una región de la estructura de una proteína que está asociada con una determinada función.

### □ Motivo. Región contigua dentro de una proteína que se distingue por propiedades bien definidas:

- **Secuencial.** Patrón de AA conservados que es común a un grupo de proteínas.
- **Estructural.** Es una combinación de elementos estructurales secundarios con un arreglo geométrico específico. Por ejemplo:  $\beta$ -sandwiches, helix-turn-helix (HTH), helix-hairpin-helix, etc.

### □ Repeticiones. Simetría y duplicación estructural son muy comunes en proteínas. Eventos de duplicación y re-arreglos genómicos.

### □ Complejos. 50-70% de las proteínas se encuentran en complejos homoméricos.

- Superficies isologas (homologas).
- Superficies heterologas.

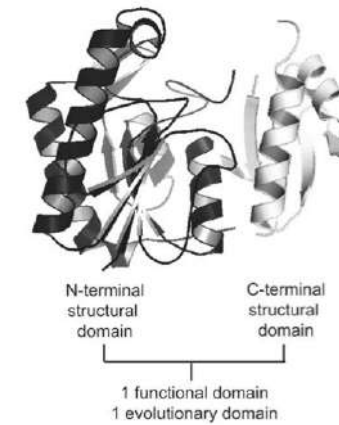


Fig.1. Domains in the structure of  $\alpha$ -aminopeptidase DppA (pdb 1hi9).

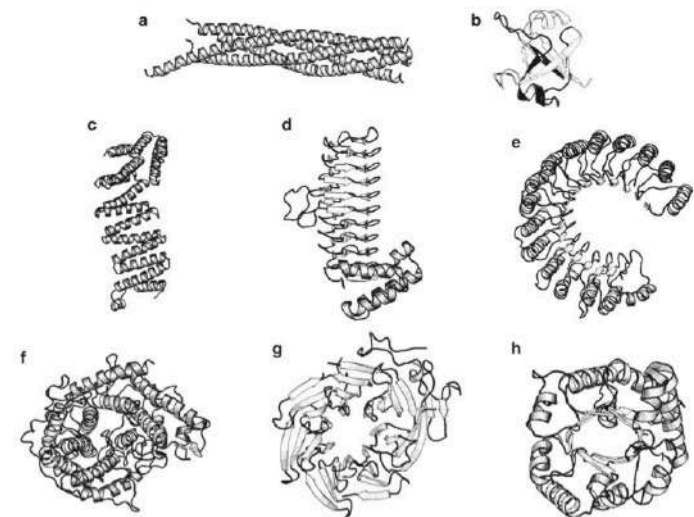


Fig. 4. Representative repetitive structures. (a) Coiled coil (pdb 1n7s), (b) structural repeats in globular domain (pdb 1cz4), (c)  $\alpha$ -solenoid (pdb 1qge), (d)  $\beta$ -solenoid (pdb 2lf2), (e)  $\beta\alpha$ -solenoid (pdb 2bnh), (f)  $\alpha$ -toroid (pdb 1ga1), (g)  $\beta$ -toroid (pdb 1erj), and (h)  $\beta\alpha$ -toroid (pdb 2jk2).

# Reglas estructurales y excepciones.

- **Una secuencia muchos plegamientos.** Equilibrio entre al menos dos estados conformacionales.
- **Secuencias camaleónicas.** Cadenas de aminoácidos idénticos adoptan estructuras secundarias alternativas ( $\alpha$ -hélice, hoja- $\beta$ , vuelta).
- **Decaimiento del plegamiento.** Es un evento de deleción que afecta el plegamiento común de la proteína.
- **Transiciones de plegamiento.** Una parte de una proteína puede tener u a lata similaridad pero se pliega en una estructura secundaria diferente.
- **Transiciones de arquitectura.** Inserción de estructura secundaria adicional a plegamiento común puede desencadenar una nueva arquitectura.
- **Permutaciones circulares.** Cambios en el orden secuencial de los extremos de una proteína.
- **Intercambio y vuelta de hojas beta.** Cambios en la orientación de una hoja beta con respecto al core.

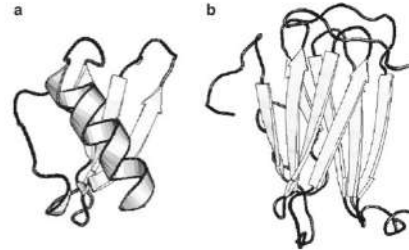


Fig. 5. The structures of two alternative folds of lyphotactin (Ltn10). (a) Monomeric Ltn10 (pdb 1j8l) and (b) dimeric Ltn10 (pdb 2jp1).

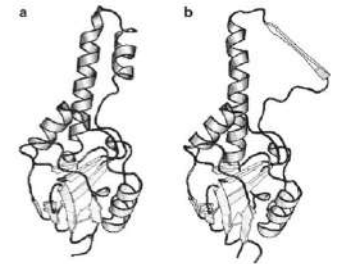


Fig. 7.  $\alpha$ -Apical domain of thermosome. (a) Structure of isolated domain, (b) structure of a subunit in the closed thermosome.

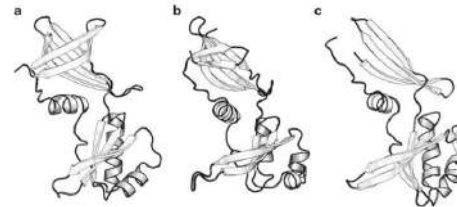


Fig. 9. Fold decay. Structures of exonuclease domains of (a) *Escherichia coli* DNA polymerase (pdb 1q8l), (b) *Sulfolobus solfataricus* DNA polymerase (pdb 1s5j), (c) *Thermococcus gorgonarius* DNA polymerase (pdb 1tgc).

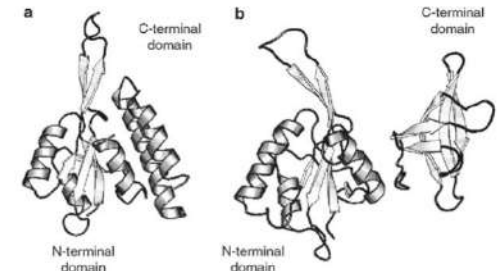


Fig. 10. Fold transition. Structures of (a) RfaH and (b) NusG.

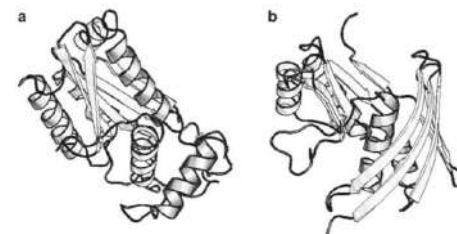


Fig. 11. Architecture transition. Structures of (a) restriction endonuclease BamHI (pdb 1bam) and (b) YaeQ (pdb 2g3w).

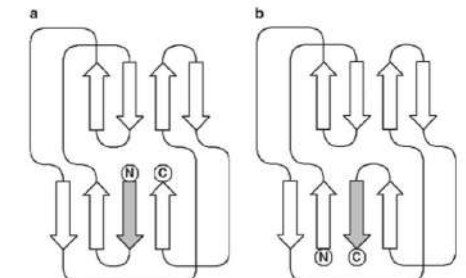
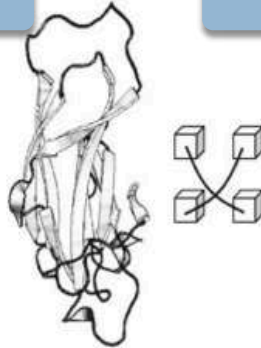


Fig. 12. Circular permutation. Topology diagram of (a) synaptotagmin C2-domain, (b) phospholipase C $\alpha$  C2-domain. Circularly permuted strand is shown in grey.

# Reglas estructurales y excepciones.

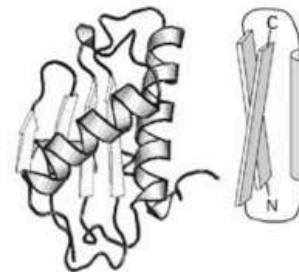
Ecotina 1IFG



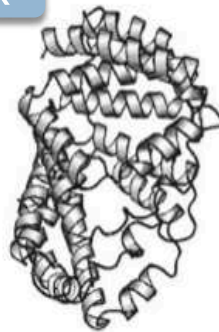
YibK 1MXI



Ribonucleasa P 1A6F



Peridinina 1PPR



DinB 2F22



- ❑ Conexiones entre estructuras secundarias nunca se cruzan y hacen nudos.
- ❑ Conexiones de beta-X-beta son hacia la derecha.
- ❑ La relación de hojas beta o hélices es compacta en un core hidrofóbico.
- ❑ Las piezas de estructura secundaria adyacentes están en estrecho contacto.

# Predicciones Estructurales de Proteínas.



- The Critical Assessment of protein Structure Prediction (CASP) experiments.

<http://predictioncenter.org>



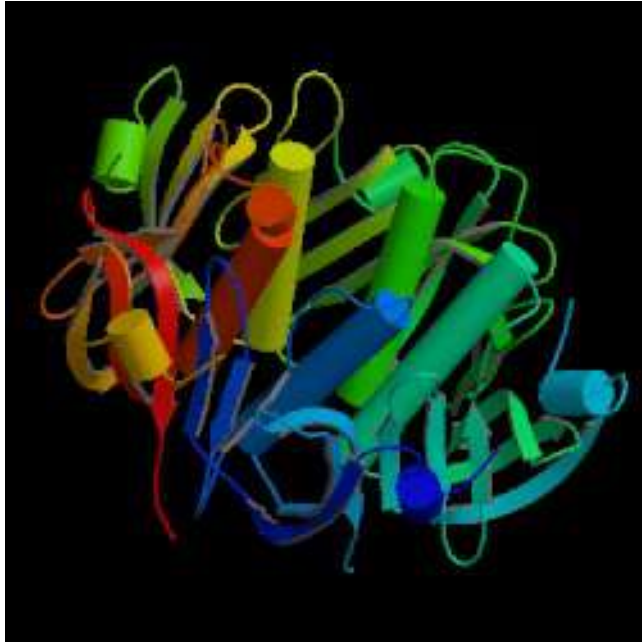
# Similaridad de Secuencias

Similaridad de secuencias implica rasgos comunes estructurales, funcionales y evolutivos. Es cuantificable y es uno de los parámetros para determinar homología entre proteínas.

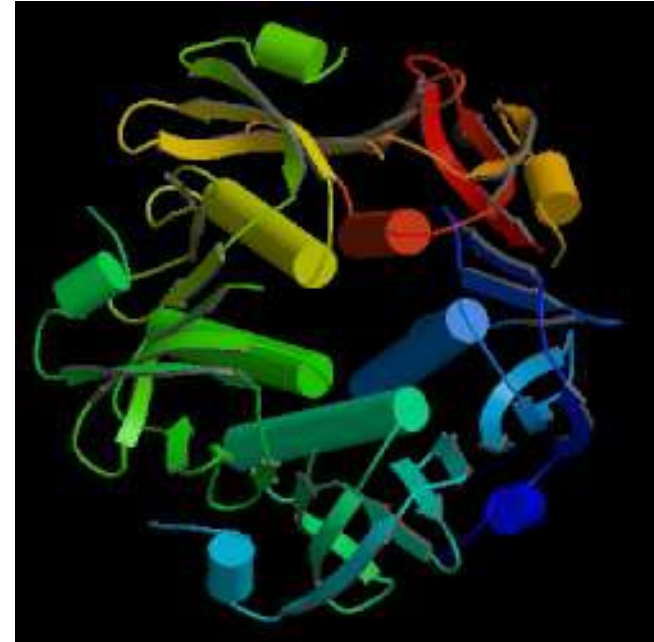


# Proteínas Similares:

## Enterotoxina y Toxina del Cólera



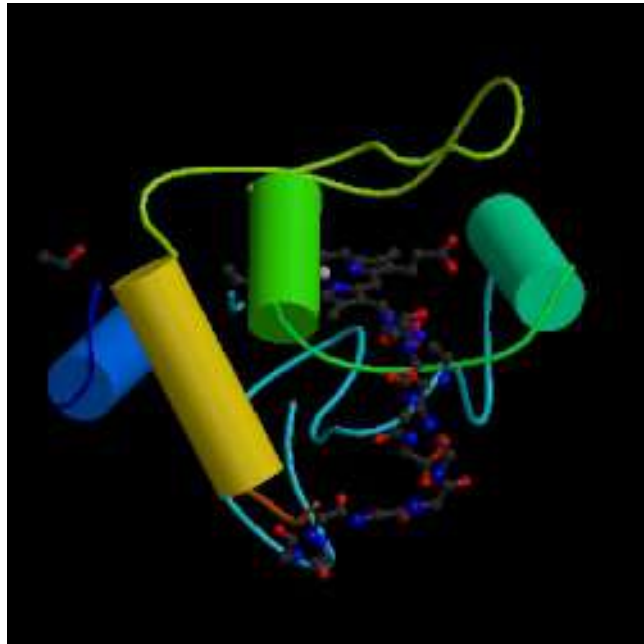
Enterotoxina



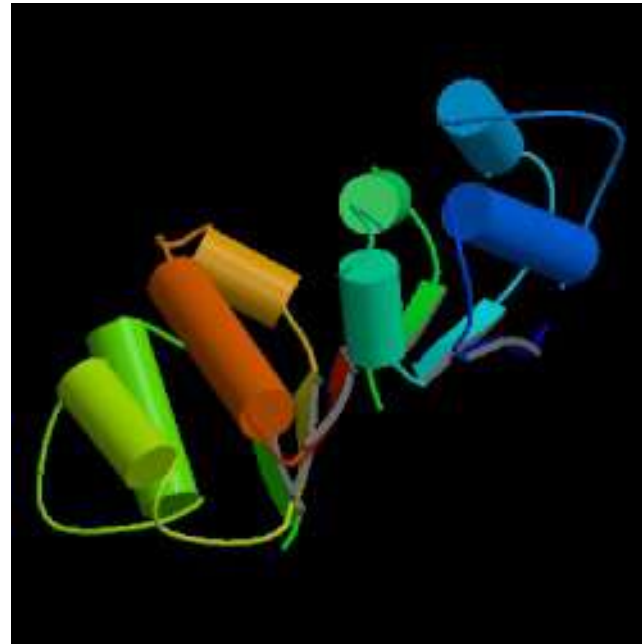
Tóxina del cólera

80% de identidad

# Proteínas No Similares: Citocromo y Barstar



Citocromo

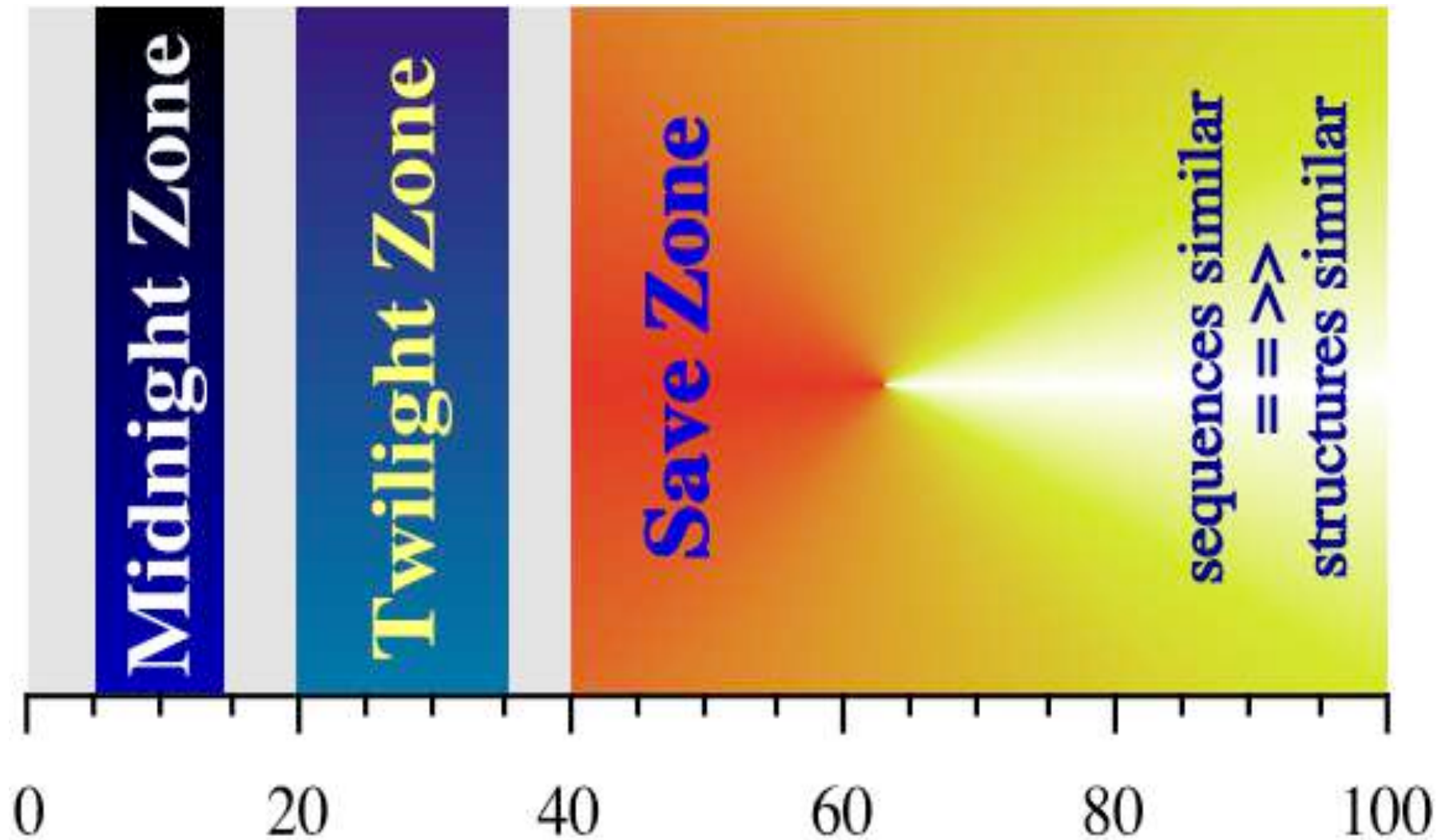


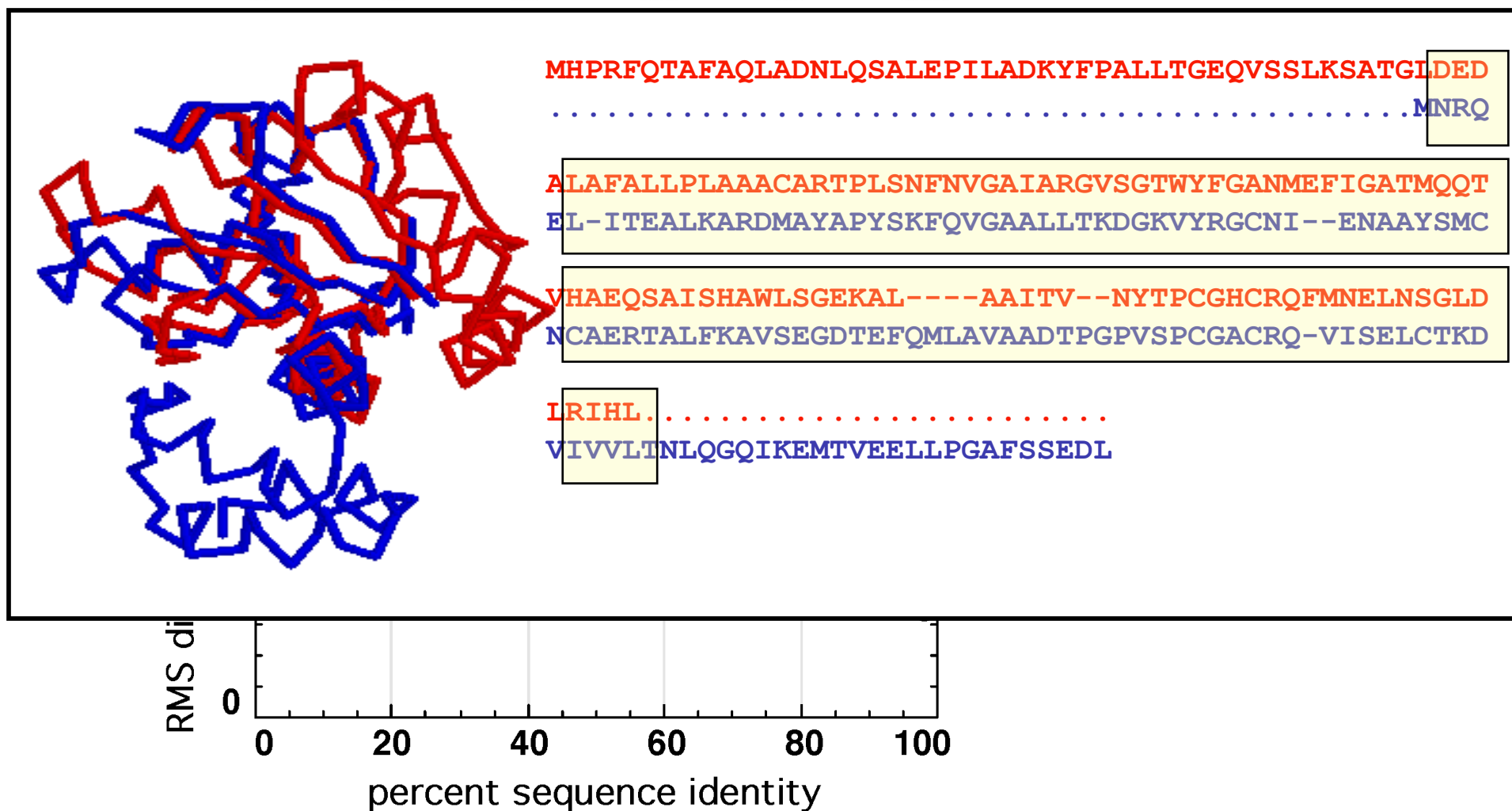
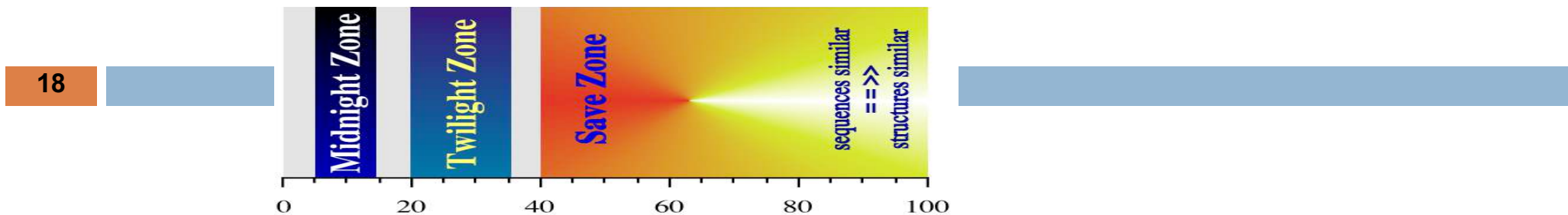
Barstar

Menos de un 20% de identidad



# Zonas de Similaridad





# Búsqueda de homólogos:

## Métodos para detección de homología.

BLAST	Sequence–Sequence	<a href="http://blast.ncbi.nlm.nih.gov/">http://blast.ncbi.nlm.nih.gov/</a>
FASTA/Ssearch	Sequence–Sequence	<a href="http://fasta.bioch.virginia.edu/">http://fasta.bioch.virginia.edu/</a> <a href="http://www.ebi.ac.uk/Tools/sss/fasta/">http://www.ebi.ac.uk/Tools/sss/fasta/</a>
CS-BLAST	Sequence (profile)–Sequence	<a href="http://toolkit.lmb.uni-muenchen.de/cs_blast/">http://toolkit.lmb.uni-muenchen.de/cs_blast/</a>
PSI-BLAST	Profile–Sequence	<a href="http://blast.ncbi.nlm.nih.gov/">http://blast.ncbi.nlm.nih.gov/</a>
CSI-BLAST	Profile–Sequence	<a href="http://toolkit.lmb.uni-muenchen.de/cs_blast/">http://toolkit.lmb.uni-muenchen.de/cs_blast/</a>
HMMER	HMM–Sequence	<a href="http://hmmer.org/">http://hmmer.org/</a>
SAM	HMM–Sequence	<a href="http://compbio.soe.ucsc.edu/HMM-apps/">http://compbio.soe.ucsc.edu/HMM-apps/</a>
COMPASS	Profile–Profile	<a href="http://prodata.swmed.edu/compass/">http://prodata.swmed.edu/compass/</a>
PROCAIN	Profile–Profile + additional sequence features + SS <sup>a</sup>	<a href="http://prodata.swmed.edu/procain/">http://prodata.swmed.edu/procain/</a>
COMA	Profile–Profile	<a href="http://www.ibt.lt/bioinformatics/coma/">http://www.ibt.lt/bioinformatics/coma/</a>
HHsearch	HMM–HMM + SS <sup>a</sup>	<a href="http://toolkit.lmb.uni-muenchen.de/hhpred/">http://toolkit.lmb.uni-muenchen.de/hhpred/</a>
PRC	HMM–HMM	<a href="http://supfam.org/PRC">http://supfam.org/PRC</a> <a href="http://www.ibi.vu.nl/programs/prcwww/">http://www.ibi.vu.nl/programs/prcwww/</a>



# Búsqueda de homologos:

## Métodos MSA.

1	ClustalW	Método de alineamiento progresivo Incluye procesamiento multicore	<a href="http://www.ebi.ac.uk/clustalw">http://www.ebi.ac.uk/clustalw</a>	(Thompson y col. 1994)
2	Muscle	Refinamiento sucesivos con árbol calculado	<a href="http://www.drive5.com/muscle">http://www.drive5.com/muscle</a>	(Edgar 2004)
3	T_Coffee	Preprocesamiento de Pares de alineamiento Incluye procesamiento multicore	<a href="http://www.tcoffee.org">http://www.tcoffee.org</a>	(Notredame y col. 2000)
4	Mafft	Transformada rápida de <u>Fourie</u> para identificar regiones homologas (FFT).	<a href="http://align.genome.jp/mafft">http://align.genome.jp/mafft</a>	(Katoh y col. 2002)
5	Mafft ginsi	MAFFT Alineamiento global	<a href="http://align.genome.jp/mafft">http://align.genome.jp/mafft</a>	(Katoh y col. 2002)
6	Mafft linsi	MAFFT Alineamiento local	<a href="http://align.genome.jp/mafft">http://align.genome.jp/mafft</a>	(Katoh y col. 2002)
7	Mafft einsl	MAFFT Para secuencias con zonas extensas no alineadas	<a href="http://align.genome.jp/mafft">http://align.genome.jp/mafft</a>	(Katoh y col. 2002)
8	Kalign	Implementación de algoritmo de Wu-Manber	<a href="http://msa.cgb.ki.se">http://msa.cgb.ki.se</a>	(Lassmann y col. 2009)
9	ProbCons	Incluye consistencia probabilística	<a href="http://probcons.stanford.edu">http://probcons.stanford.edu</a>	(Do y col. 2005)
10	Dialign-TX	Zonas altamente similares son utilizadas como semillas de alineamiento.	<a href="http://dialign-tx.gobics.de">http://dialign-tx.gobics.de</a>	(Subramanian y col. 2008)
11	Probalign	Partición de las probabilidades de función. Pares HMM	<a href="http://probalign.njit.edu">http://probalign.njit.edu</a>	(Chikkagoudar y col. 2007)
12	MsaProbs	Incluye consistencia probabilística y calculo multicore	<a href="http://sourceforge.net/projects/msaprobs">http://sourceforge.net/projects/msaprobs</a>	(Liu y col. 2010)
13	Prank	Usa filogenia y reconoce inserciones y delecciones	<a href="http://www.ebi.ac.uk/goldman-srv/webPRANK">http://www.ebi.ac.uk/goldman-srv/webPRANK</a>	(Löytynoja y Goldman 2005; Löytynoja y Goldman 2008b)
14	Picxaa PF	Probabilístico y No progresivo, metodo de evaluación de paridad factor	<a href="http://www.ece.tamu.edu/~bjyoon/picxaa">http://www.ece.tamu.edu/~bjyoon/picxaa</a>	(Sahraeian y Yoon 2010)

# Filogenia

<http://itol.embl.de>

HOME TREE OF LIFE OTHER TREES SHARED PROJECTS DATA UPLOAD SAVED VIEWS HELP ABOUT & CONTACT

## ITOL INTERACTIVE TREE OF LIFE

Welcome to ITOL!

Interactive Tree Of Life is an online tool for the display and manipulation of phylogenetic trees. It provides most of the features available in other tree viewers, and offers a novel circular tree layout, which makes it easy to visualize mid-sized trees (up to several thousand leaves). Trees can be exported to several graphical formats, both bitmap and vector based. [more...](#)

News

- Version 2.1 introduces a new dataset type, [circles](#). Recent additions also include the ability to assign dataset values with internal nodes. These will be displayed only when associated clades are collapsed. Check the [Help pages](#) for details.
- Second ITOL article was published in 2011 NAR Web server issue ([abstract](#), [full text PDF](#)).

The Tree Of Life

Various ITOL generated tree images

Examples

Protein domain architectures

ITOL can easily display protein domain architectures directly on the tree.

ITOL account login

Login: Password:

☐ Remain logged-in?

Firefox toolbar

If you are using Mozilla Firefox to access ITOL, try our [Firefox toolbar](#).

Recent changes

Version 2.2

- multiple binary datasets will be automatically spread to prevent overlap
- if labels are present in a color strip dataset, a legend containing the labels will be added to exported trees

Version 2.1.1

- branches can be marked with [custom labels](#)
- Dataset legends are optional in exported trees

Version 2.1

- New dataset type: [circles](#)
- Several datasets (binary, bar chart, multi-value bar chart, protein domains) support display of values assigned with internal nodes of the tree. These values will only be displayed when associated clades are collapsed.

Version 2.0.1

- Pie chart position on each branch can be defined: [example](#)

Version 2.0

- New dataset type: [connections](#)

Version 1.9

- [custom information](#) can be displayed in node popups; basic HTML and CSS are supported, with links and images

Version 1.8.3

- trees can be rerooted when exported through [batch access](#)

Version 1.8.2

- name based node filtering in the automatic NCBI tree generator

Version 1.8.1

- protein IDs/ACCEs (uniprot and NCBI) supported in the automatic NCBI tree generator

Version 1.8

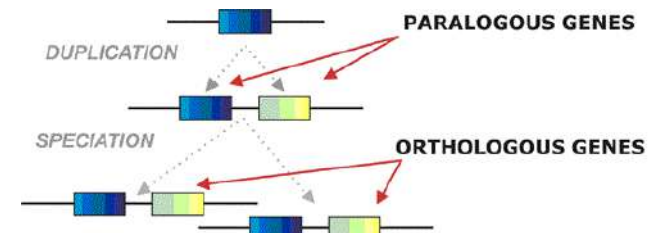
- new tree display mode: [unrooted](#)
- branches can be automatically colored based on bootstrap values

[Full version history](#)

Ortólogos.  
Parólogos.

INPARANOID7

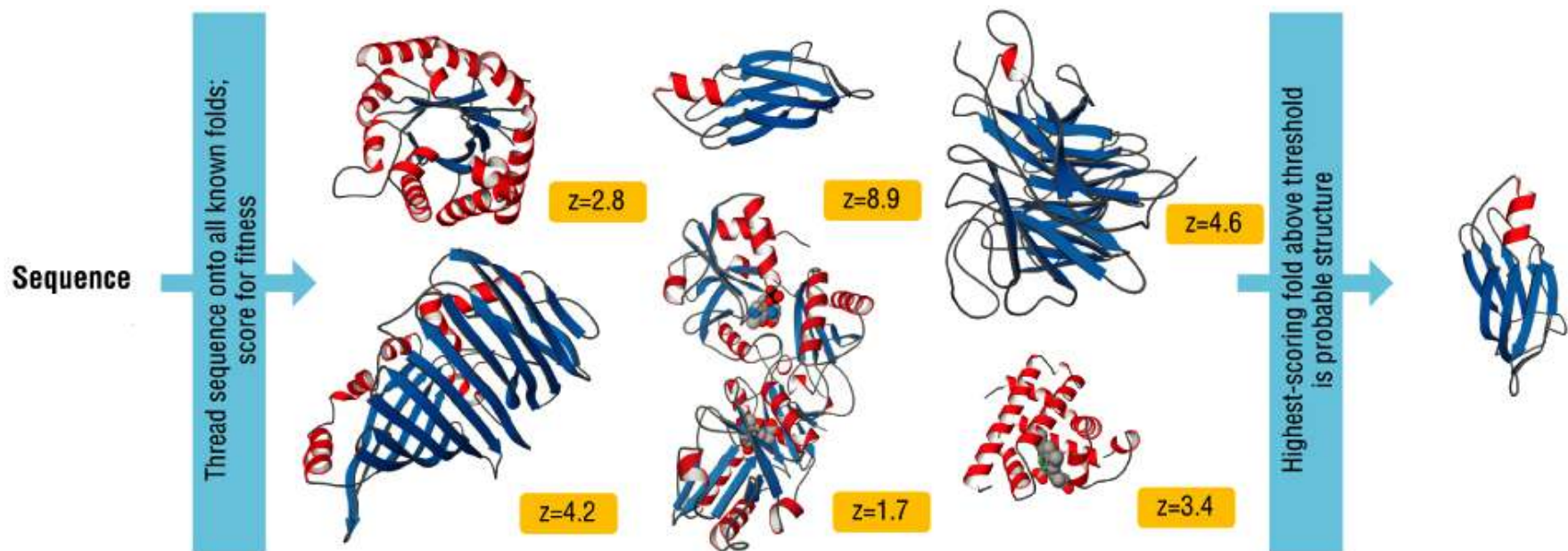
<http://inparanoid.sbc.su.se>



Letunic, I. & Bork, P. (2011)  
'Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy.'  
*Nucleic Acids Res* **39**(Web Server issue), W475-W478.

Ostlund, G.; Schmitt, T.; Forslund, K.; Köstler, T.; Messina, D. N.; Roopra, S.; Frings, O. & Sonnhammer, E. L. L. (2010)  
'InParanoid 7: new algorithms and tools for eukaryotic orthology analysis.'  
*Nucleic Acids Res* **38**(Database issue), D196-D203.

# Threading





# Búsqueda de moldes.

## Phyre2

<http://www.sbg.bio.ic.ac.uk/phyre2>

The screenshot shows the Phyre2 web interface. At the top left is the 'Phyre2' logo. To its right is a subscription box for Google Groups with an email input field and a 'Subscribe' button. Below the logo, it says 'Protein Homology/analogy Recognition Engine V 2.0'. In the center, there are five icons: a calendar, a magnifying glass, a question mark, an envelope, and a book. Below these is a link 'What's New in Phyre2'. The main form area has a dark sidebar on the left with labels: 'E-mail Address', 'Optional Job description', 'Amino Acid Sequence' (with a file upload icon), and 'Modelling Mode' (with a file upload icon). To the right of the sidebar are input fields for the first three labels. The 'Modelling Mode' section has two radio buttons: 'Normal' (selected) and 'Intensive'. At the bottom of the form are 'Phyre Search' and 'Reset' buttons. At the very bottom of the page, it says '192033 submissions since Feb 14 2011'.

Kelley LA and Sternberg MJE. (2009).  
Protein structure prediction on the web: a  
case study using the Phyre server.  
*Nature Protocols* 4, 363-371

3DPSSM <http://www.sbg.bio.ic.ac.uk/~3dpssm/index2.html>

Busca homólogos remotos, para ello combina perfiles de secuencia con información estructural (potenciales de solvatación e información de estructura secundaria) para realizar el reconocimiento de plegamiento

The screenshot shows the 3D-PSSM Protein Fold Recognition (Threading) Server website. The browser window title is "3D-PSSM Protein Fold Recognition (Threading) Server - Microsoft Internet Explorer". The address bar shows "http://www.sbg.bio.ic.ac.uk/~3dpssm/index2.html". The website has a dark blue background with yellow and green text and buttons. The main header includes the "3D-pssm" logo and "Imperial College of Science, Technology & Medicine Fold Recognition Server". A navigation menu on the left lists: Home, Recognise a Fold, Fold Library, Authors, Links, and Help. A status bar at the top right indicates "Fold Library Last Updated: Tue Jun 15 06:00:00 2004: [9864] Structures". A central banner displays "Welcome to the 3D-PSSM Web Server V 2.6.0" and describes it as "A Fast, Web-based Method for Protein Fold Recognition using 1D and 3D Sequence Profiles coupled with Secondary Structure and Solvation Potential Information." Below this, a message states: "The successor to 3dpssm is ready for use (beta-testing). The new system is known as **Phyre** and has an up-to-date fold library, 10-15% better coverage than 3d-pssm, and a new interface." A note specifies: "Please Note: 3D-PSSM is now for **academic use only**." Two news items are listed: "3D-PSSM frozen - new system shortly" dated Jun 18 2004, and "Completely new protein structure prediction system" dated Apr 5 2004. The bottom of the page features a "Submit a Protein Sequence" button and a taskbar with various open applications including "Universidad de Concepci...", "BRENDA: Entry of mande...", "3D-PSSM Protein Fol...", "Microsoft PowerPoint - [fol...", "Paint Shop Pro - race", and "Métodos automáticos de ...". The system clock shows 12:01.

3D-PSSM Protein Fold Recognition (Threading) Server - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Address <http://www.sbg.bio.ic.ac.uk/~3dpssm/index2.html> Go Links »

**3D-pssm** Imperial College of Science, Technology & Medicine  
Fold Recognition Server

Home  
Recognise a Fold  
Fold Library  
Authors  
Links  
Help

Contact  
[Lawrence Kelley](#)

BMM  
GlaxoWellcome

Fold Library Last Updated: Tue Jun 15 06:00:00 2004: [9864] Structures

[Disclaimer and Terms of Use](#)

Last updated: 06/22/2005 11:09:04 Visitors To Date: **276,193**

**Welcome to the 3D-PSSM Web Server V 2.6.0**

A Fast, Web-based Method for Protein Fold Recognition using 1D and 3D Sequence Profiles coupled with Secondary Structure and Solvation Potential Information.

The successor to 3dpssm is ready for use (beta-testing)  
The new system is known as **Phyre** and has an up-to-date fold library, 10-15% better coverage than 3d-pssm, and a new interface.

Please Note: 3D-PSSM is now for **academic use only**.

**3D-PSSM frozen - new system shortly** Jun 18 2004  
I have today frozen the updates for 3D-PSSM. New pdb structures will no longer be added to the fold database. I intend to release our new server to the public in September. Benchmarking has shown the new system to be a substantial improvement over 3D-PSSM.  
Lawrence Kelley

**Completely new protein structure prediction system** Apr 5 2004  
A brand new fold recognition system is on its way. The new system is nearing completion. Benchmarking suggests it is far superior to 3D-

Submit a Protein Sequence

Start | Universidad de Concepci... | BRENDA: Entry of mande... | 3D-PSSM Protein Fol... | Microsoft PowerPoint - [fol... | Paint Shop Pro - race | Métodos automáticos de ... | Internet | 12:01



**FUGUE** <http://www-cryst.bioc.cam.ac.uk/fugue/prfsearch.html>

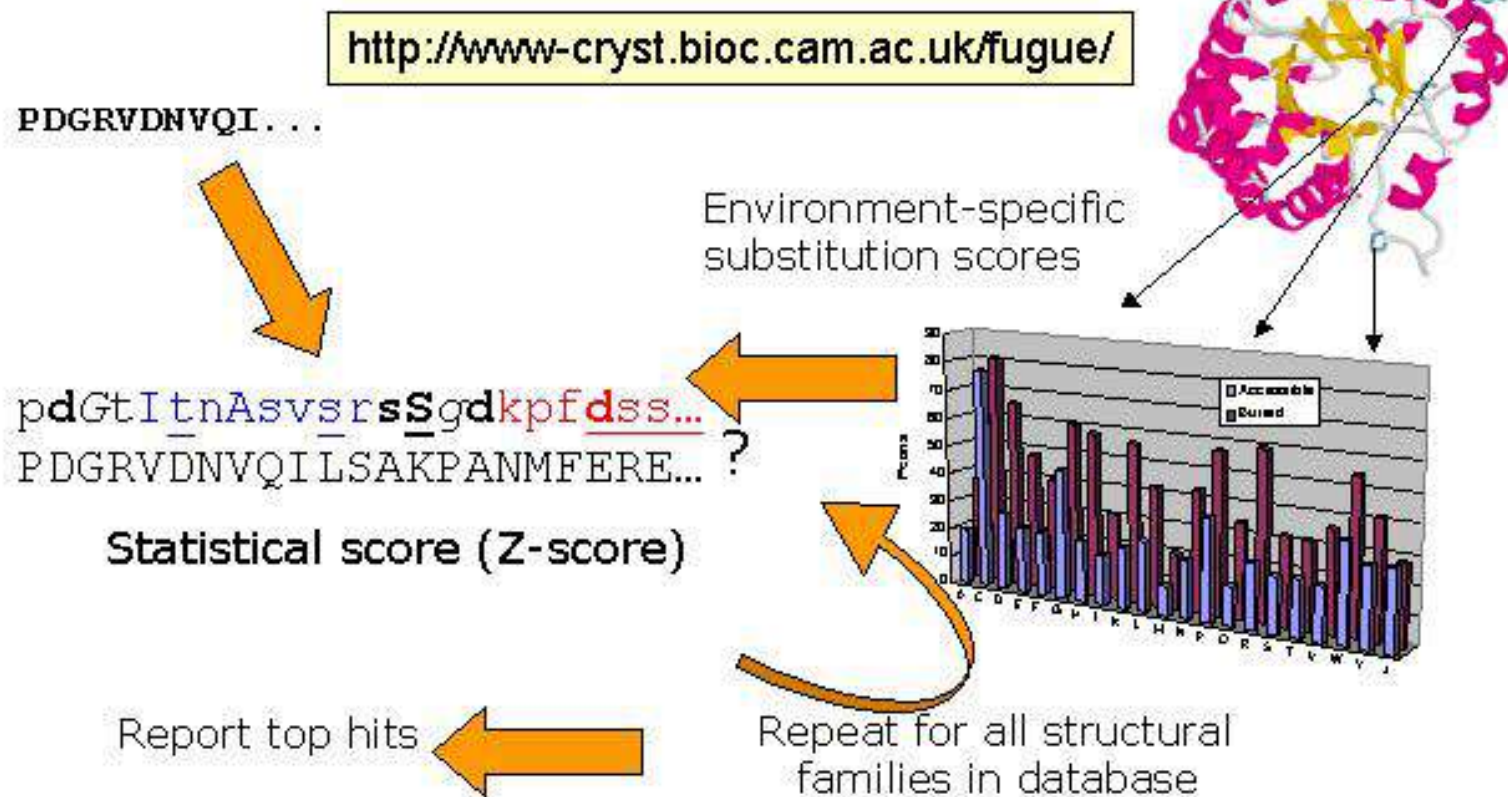
Emplea tablas de sustitución específicas para ambientes y penalizaciones para los gaps que son dependientes de estructura, donde los score para el emparejamiento de aminoácidos y las inserciones y deleciones son evaluadas dependiendo del ambiente local de cada aminoácido dentro de una estructura conocida

The screenshot shows a web browser window titled "FUGUE Profile Lib Search - Microsoft Internet Explorer". The address bar displays the URL <http://www-cryst.bioc.cam.ac.uk/fugue/prfsearch.html>. The page content is on a blue background and includes the following elements:

- Header:** The Crystallography and Biocomputing Group logo (a crest) and text: "Crystallography and Biocomputing Group", "Department of Biochemistry", "University of Cambridge", "CB2 1GA, UK".
- Section Title:** "FUGUE (Ver 2.0) Profile Library Search Against HOMSTRAD".
- Citation:** "Citation: Shi, J., Blundell, T. L. & Mizuguchi, K. (2001), *J Mol Biol*, 310(1), 243-57."
- Warning:** "NB: Please note that Fugue has been updated (since 2nd of May 2002) and consequently the recommended z-score cut-offs used are different from previous versions. Please do refer to the new set of cut-offs when verifying your result (New cut-offs will be shown on the resulting page or resulting email sent to you.)"
- Form Fields:**
  - "E-mail:  (where the results will be sent to)"
  - "Note: if you are a group member, just enter your user name to save your typing. (i.e. user => user@crystbioc.cam.ac.uk)"
  - "Password (registered user only - for future use): "
  - "Name of your sequence (optional): "
  - "Please upload your sequence file here:  Browse..."
  - "OR"
  - "Enter your amine acid sequence below." followed by a large text input area.

The Windows taskbar at the bottom shows several open applications: Start, Universidad de..., BFENDA: Entr..., PHYRE Protei..., 3D-PSSM Prot..., Phyre Job Stat..., FUGUE Pro..., Microsoft Pow..., Paint Shop Pro..., Métodos auto..., and secuencias - ... The system clock shows 12:11.

# FUGUE: Sequence-structure homology recognition using environment-specific substitution tables and structure-dependent gap penalties



Shi, J., Blundell, T.L., Mizuguchi, K. *J. Mol. Biol.* **310**, 243-257 (2001)

# Búsqueda de homologos:

COPS: <http://topsearch.services.came.sbg.ac.at>

(a) Enter a PDB code like 3bey and press enter/return or the Search button.

qCOPS 3bey Search

(b) Search results are listed in the Selection Widget. The rows in the Selection Widget correspond to the domains of the given PDB file. The first domain is automatically selected (see below) and the respective Equivalent layer is opened (see (c)).

20 Domains found for Query: 1z6t

Query	Size	S30	S90	Equivalent	Species	Compound	PDB-Header
c1z6tA1	94	3121	2937	76971	Homo sapiens	Apoptotic protease activating factor 1	APOPTOSIS
c1z6tA2	180	8614	13719	76970	Homo sapiens	Apoptotic protease activating factor 1	APOPTOSIS
c1z6tB2	188	8614	13719	12693	Homo sapiens	Apoptotic protease activating factor 1	APOPTOSIS

Color By: Structure Find Download: TXT Total: 20

(c) After the search (a) has been finished the first domain is automatically selected (b) and its parent on the lowest COPS layer (*Equivalent*) is retrieved from the system. The *Tree Result Table* displays all descendants of the parent of a selected layer. Below, the *Related* layer is selected as indicated by the last opened (red) folder icon.

COPS - Parent: c1n3ka\_ with 47 descendants

Node	1	Size	S30	S90	Struct-Id	Species	Compound
c1pn5A_	93	15582	32590	7137	Homo sapiens	NACHT-, LRR- and PYD-containing protein 2	
c1ucpA_	91	7286	17724	20614	Homo sapiens	Apoptosis-associated speck-like protein containing a CARD	
c1z6tA1	94	3121	2937	14747	Homo sapiens	Apoptotic protease activating factor 1	
c1z6tB1	96	3121	2937	14747	Homo sapiens	Apoptotic protease activating factor 1	
c2a5yB1	109	10013	17291	7613	Caenorhabditis	ced-4	

Customize Table Color By: Species Find Download: TXT Parent Node

COPS provee 5 niveles de clasificación:

- Distant (30%)
- Remote (40%)
- Related (60%)
- Similar (80%)
- Equivalent (99%)

