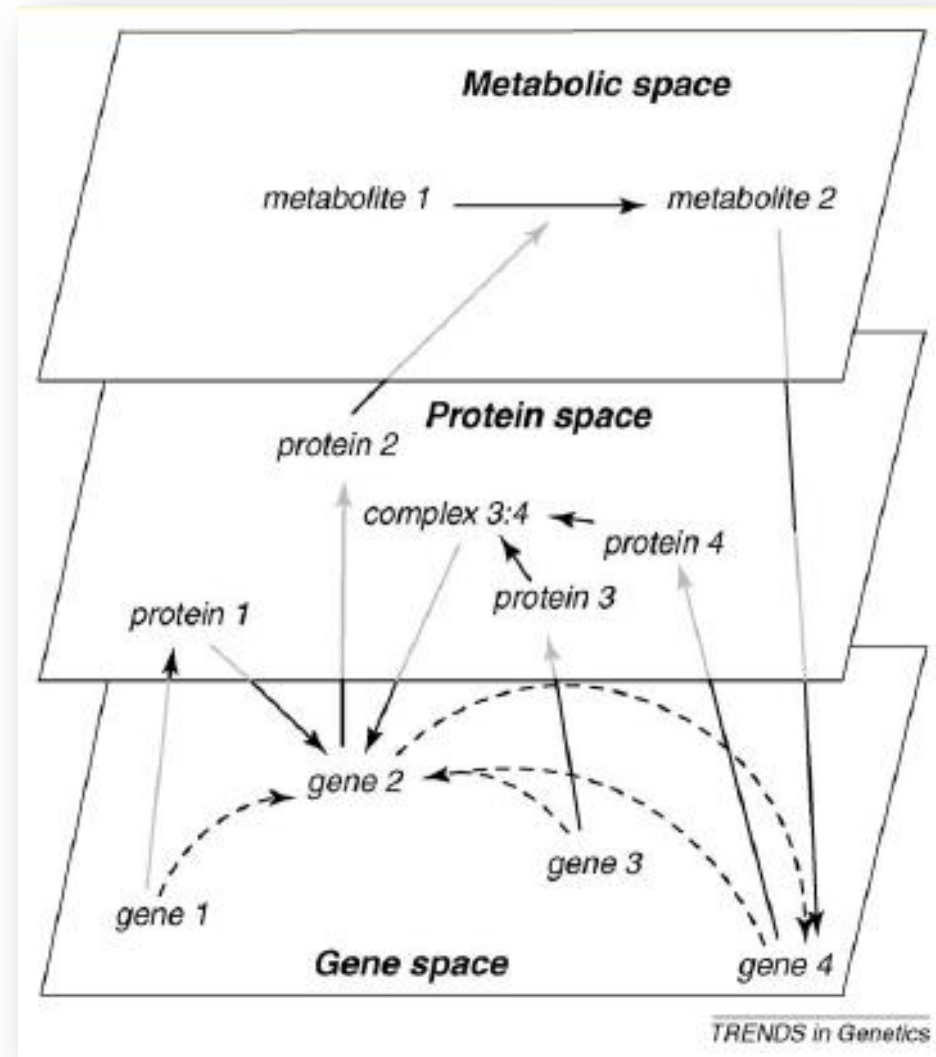
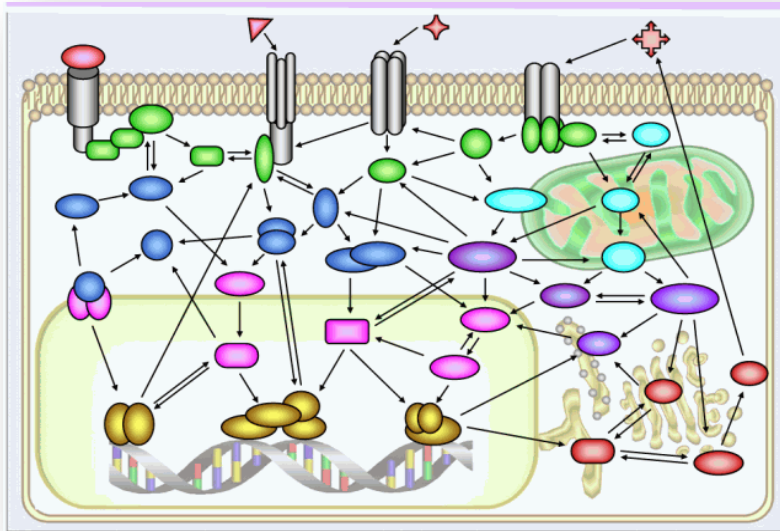
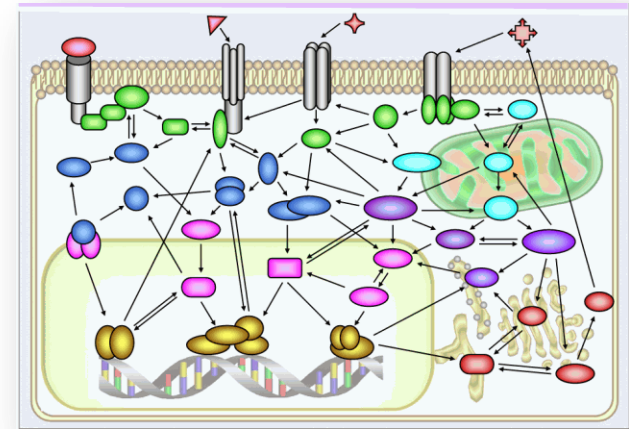


# Redes Biológicas

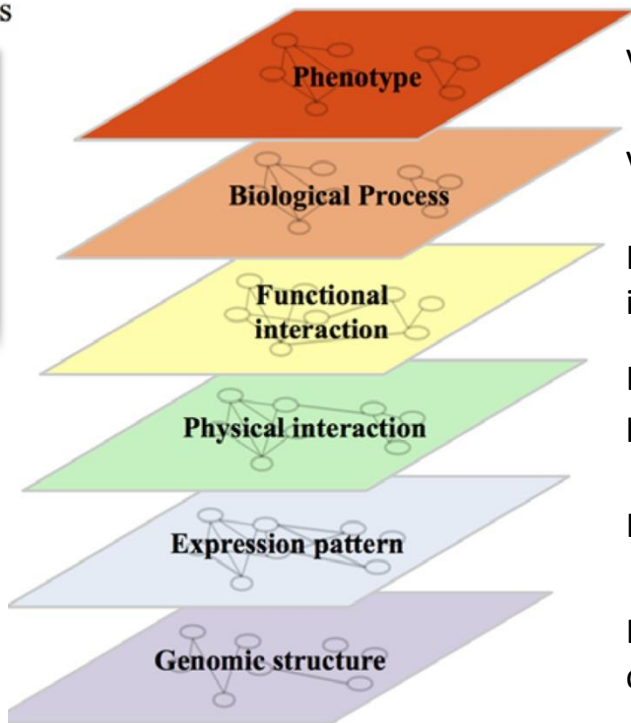
# La metáfora de redes



# Niveles interactuando



Abstraction levels



VI – Relaciones entre biomoléculas y fenotipos o enfermedades

V – Relaciones funcionales de más alto nivel entre biomoléculas

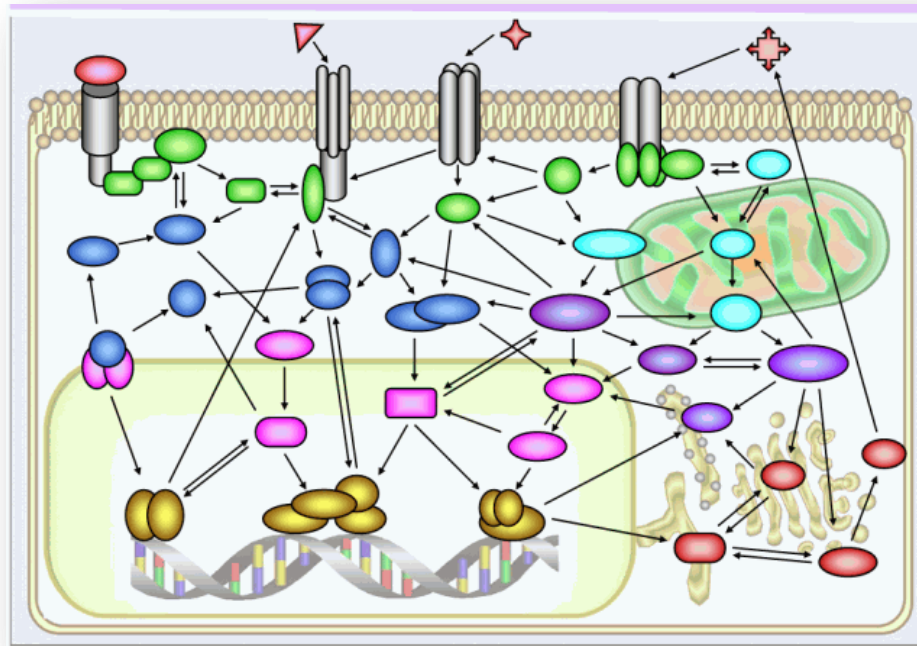
IV – Relaciones funcionales entre biomoléculas (e.g. redes de interacción genética, redes de señalización, vías metabólicas)

III – Patrón de interacciones físicas: proteína-proteína, proteína-DNA, proteína-RNA

II – Patrones de expresión génica

I - Estructura y organización del genoma (e.g. relaciones de cercanía u homología entre genes)

# En la era de grandes datos



**Visión global** obtenida gracias al acceso experimental a **omas**:

Genoma

Transcriptoma

Proteoma

Metaboloma

Interactoma

Fenoma

Biblioma

....

# En la era de grandes datos

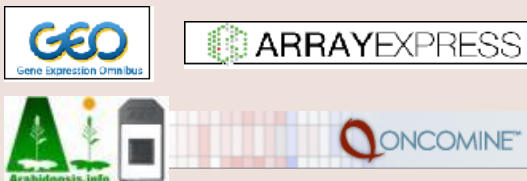
## Protein Interactions



## Prot/DNA

Chip-Chip db  
Chip-Seq db

## Gene Expression



## Ontologies/Standardizations

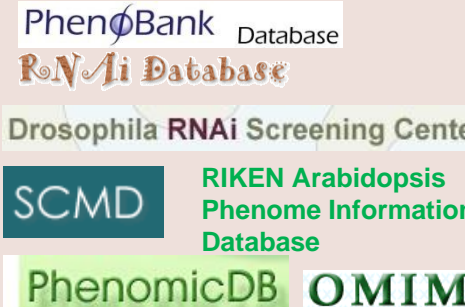
PATO -Human Phenotype Ontology  
SNOMED – UMLS - MeSH  
Exp Factor Ontology  
Disease Ontology



## Metabolic/Signalling Pathways

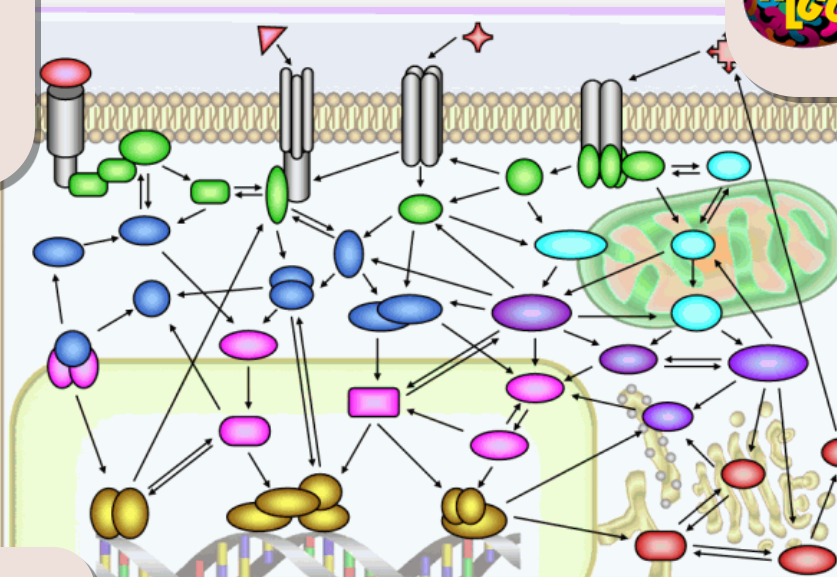


## Phenomics



## Others DB

PharmaGKB

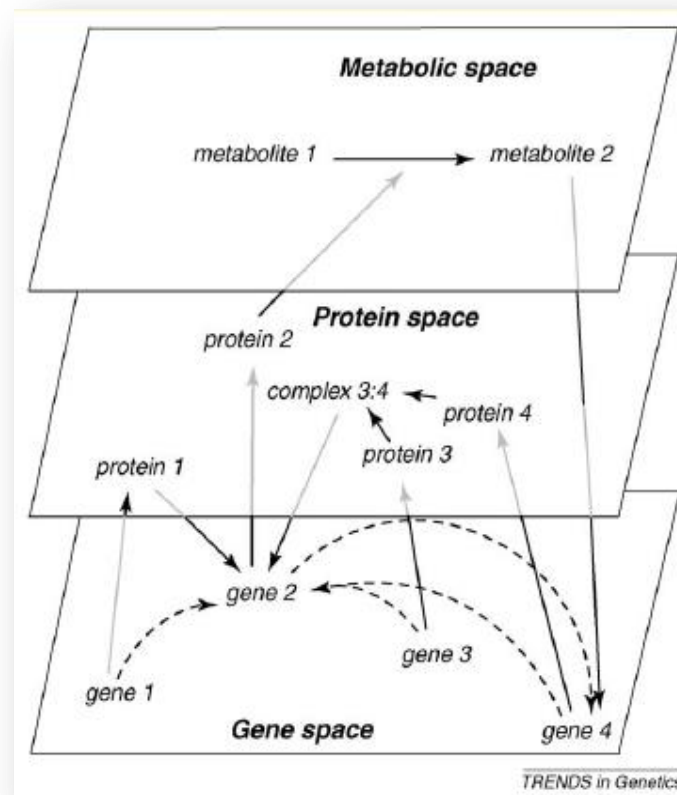


# Redes de Interés Biológico

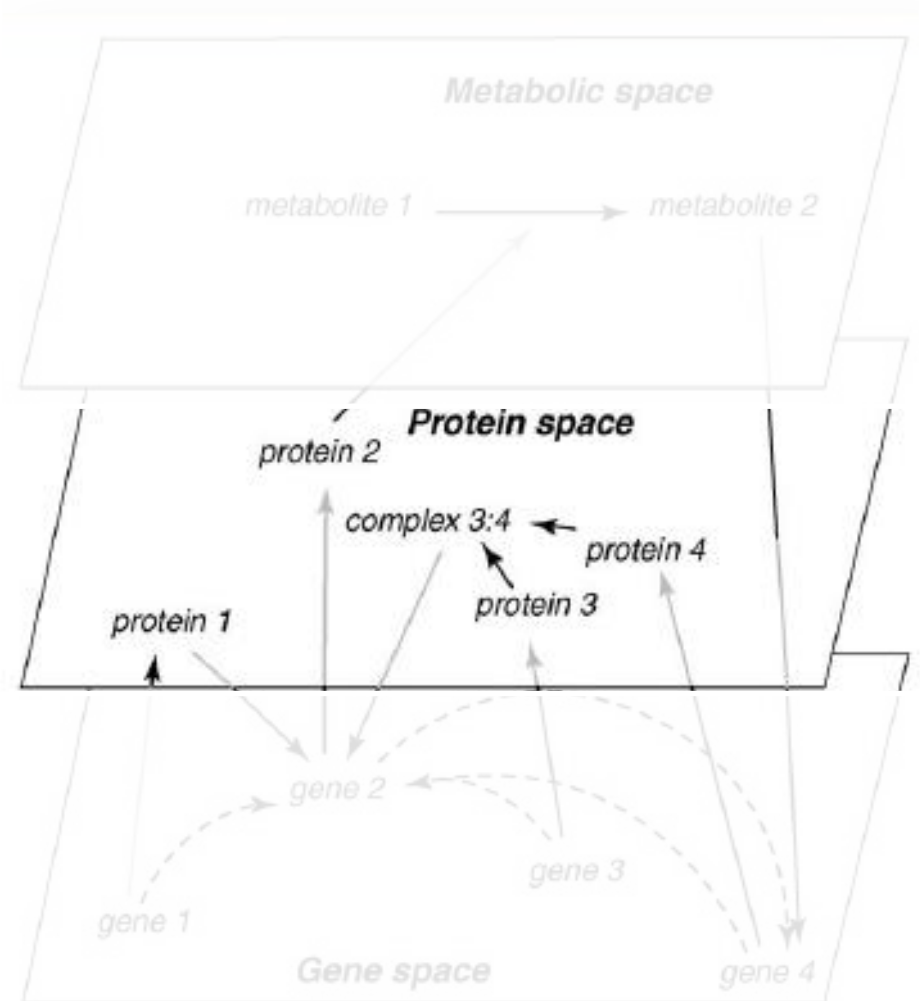
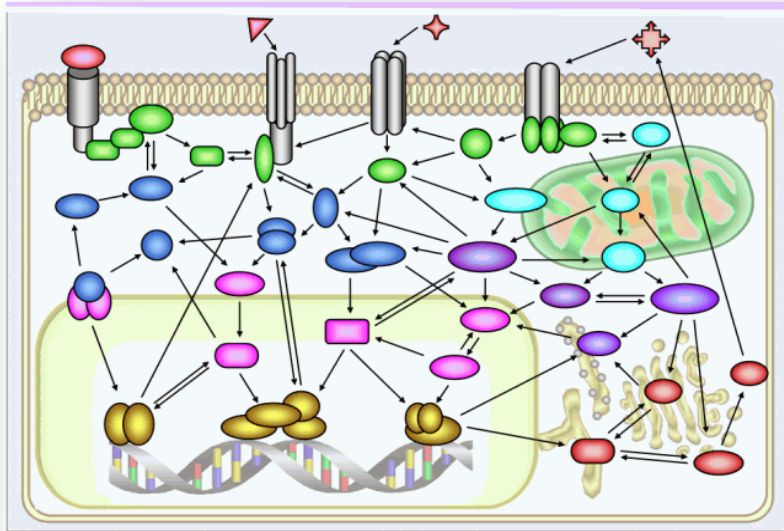
Datos, datos...y mas datos —> Redes, redes...y mas redes

Redes moleculares que “soportan” a la funcionalidad biológica celular

Tipo de Red	Interacción
Protein Protein	Interacción física
Metabolic	Metabolic and transport reactions
Red Regulacion Genica	Protein / DNA interactions
Modificaciones Postraduccionales	Fosforilacion kinasa/sustrato

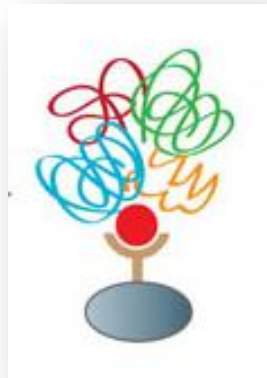
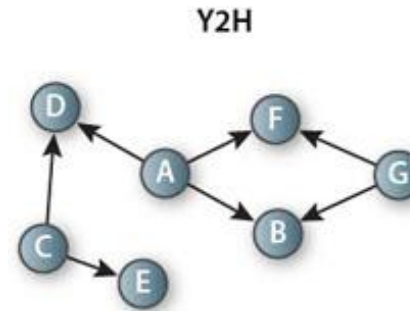
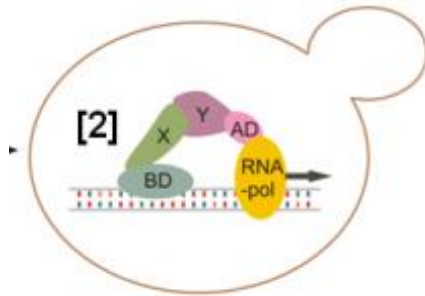


# Redes de interacción proteína-proteína

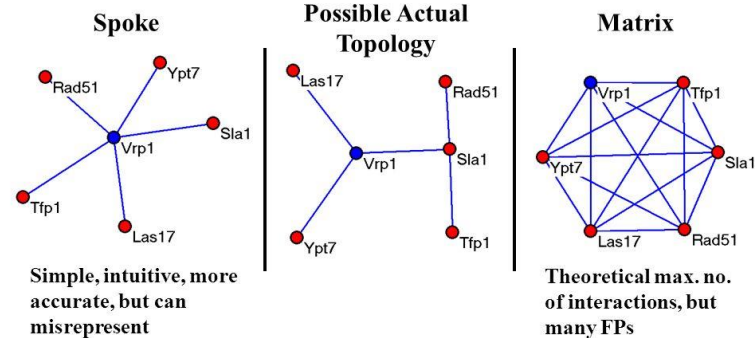




# Del experimento a la red



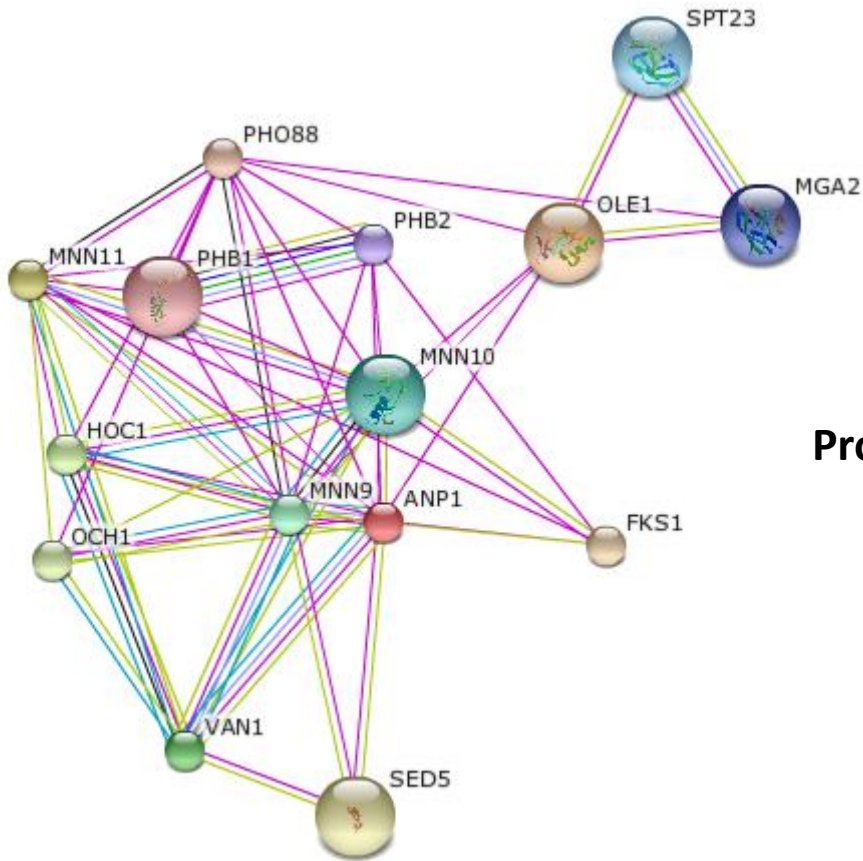
## Spoke and matrix models of PPI



Bader GD, et al. Nat Biotechnol. 2002 20(10):991-7.



# Redes Interaccion Proteina-Proteina



## Desafios:

Datos de diferentes tecnicas experimentales.

Diferentes contextos

Interacciones reportadas en diferentes organismos.

## Propuestas

Integracion en BD y metaBDs

Asignacion de score de confianza basado en

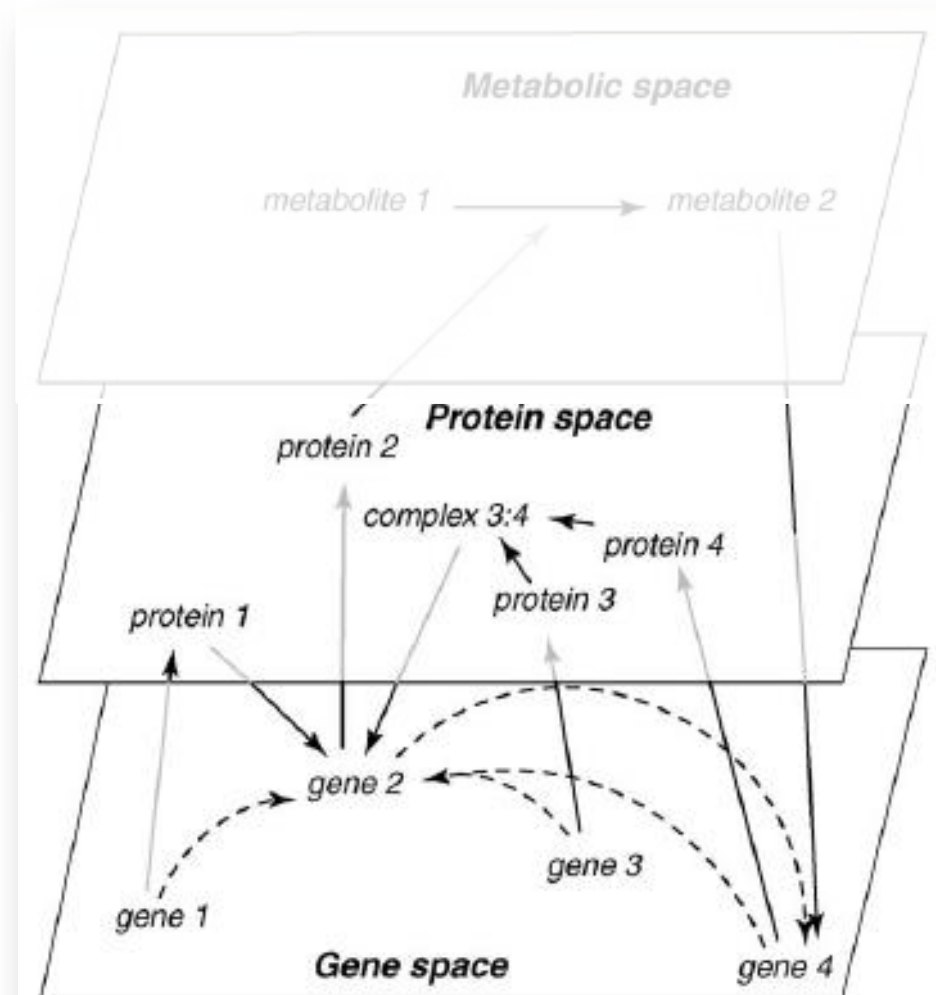
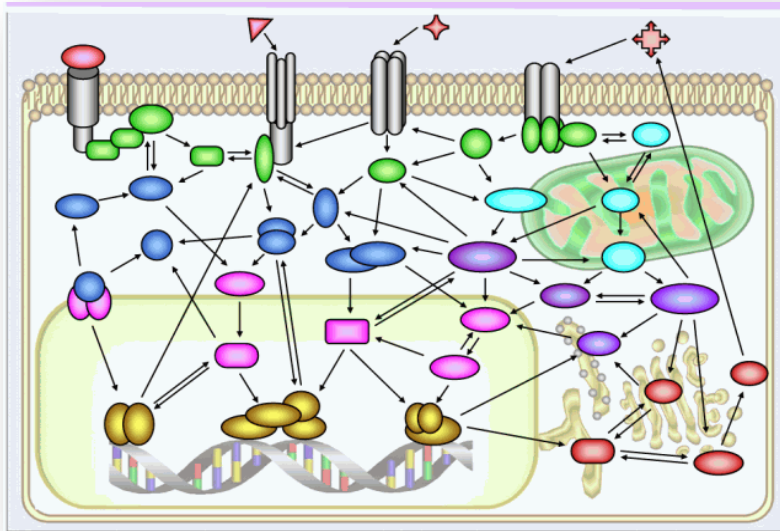
- [quality score tecnica exp](#)
- # de estudios donde se reporta la interaccion

Filtrado

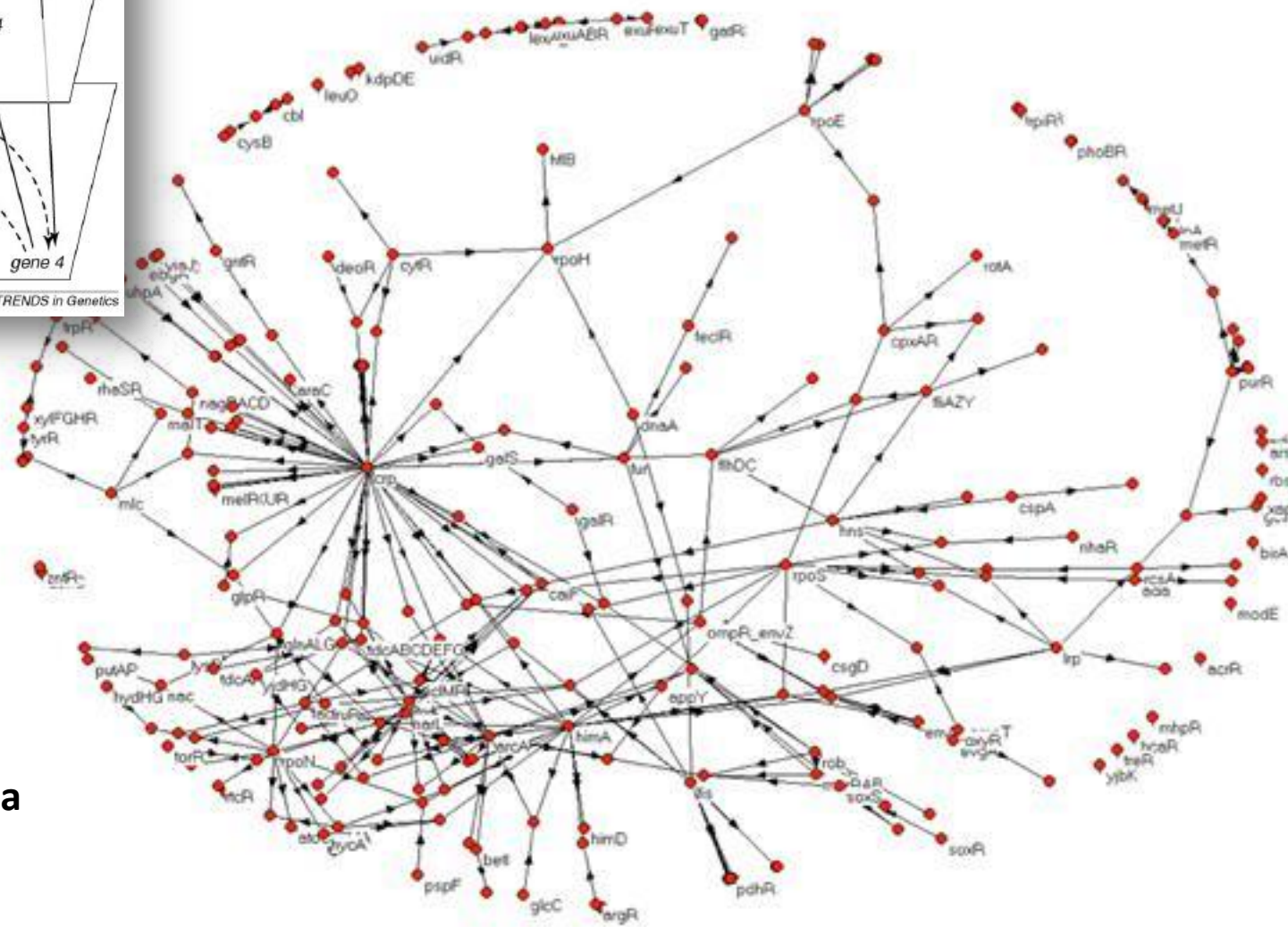
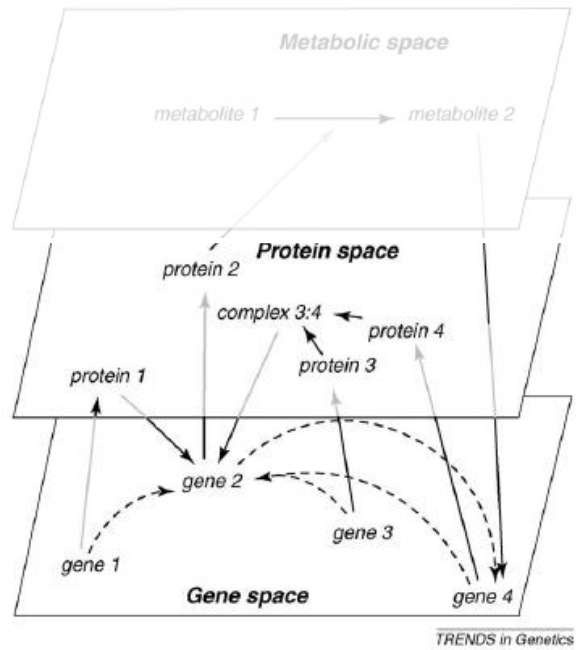
Tejido

Funcional

# Redes de regulación génica (RRG)



# RRG *E.coli*



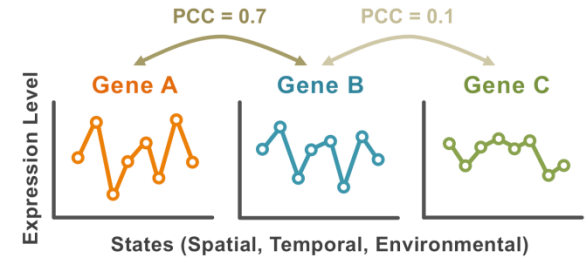
Red phenomenologica  
Grafo dirigid0  
FT -> gen target

# Redes de Interés Biológico

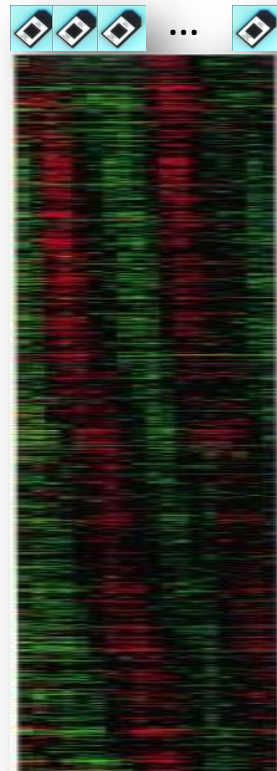
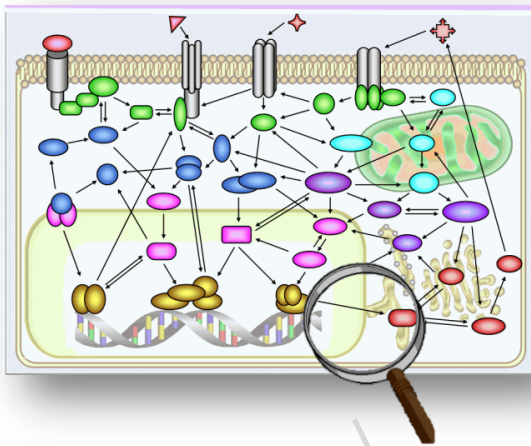
Datos, datos...y mas datos  $\longrightarrow$  Redes, redes...y mas redes

## Redes fenomenológicas:

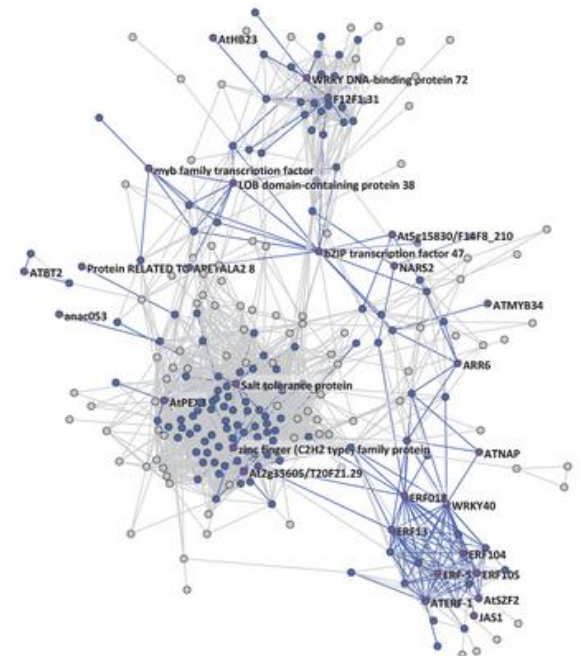
Tipo de Red	Criterio de vinculación
Coexpresión Genica	Correlacion en patrones de expresion



Estímulo



Genes funcionalmente relacionados generalmente presentan perfiles de expresión correlacionados



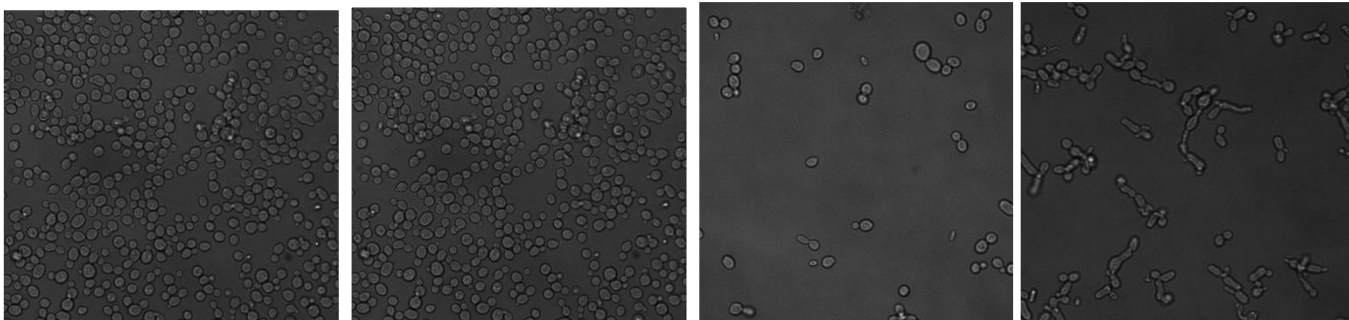
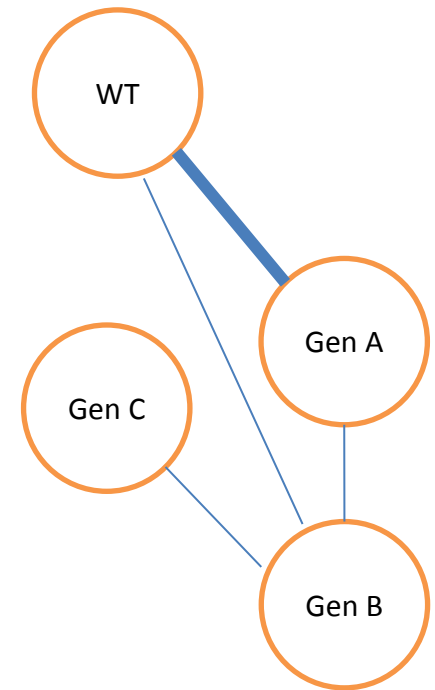
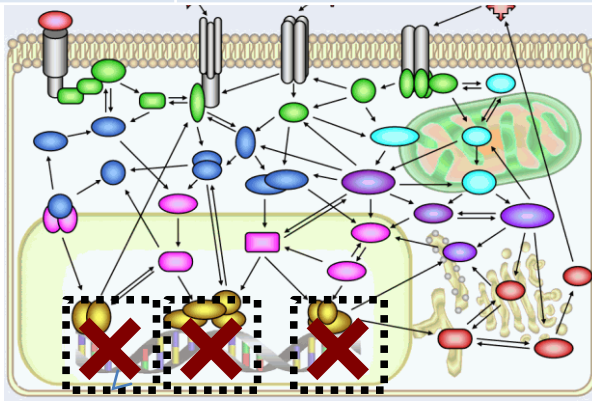


# Redes de Interés Biológico

Datos, datos...y mas datos  $\longrightarrow$  Redes, redes...y mas redes

## Redes fenomenológicas:

Tipo de Red	Criterio de vinculación
Coexpresión Genica	Correlacion en patrones de expresion
Genéticas (delección única )	Fenotipo

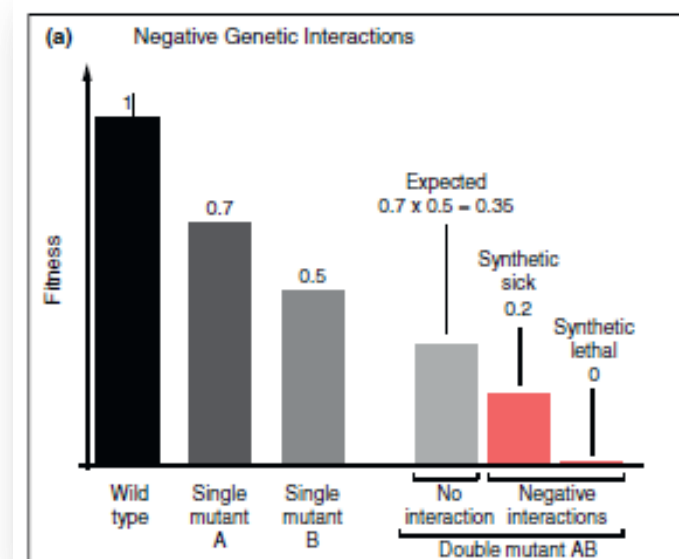
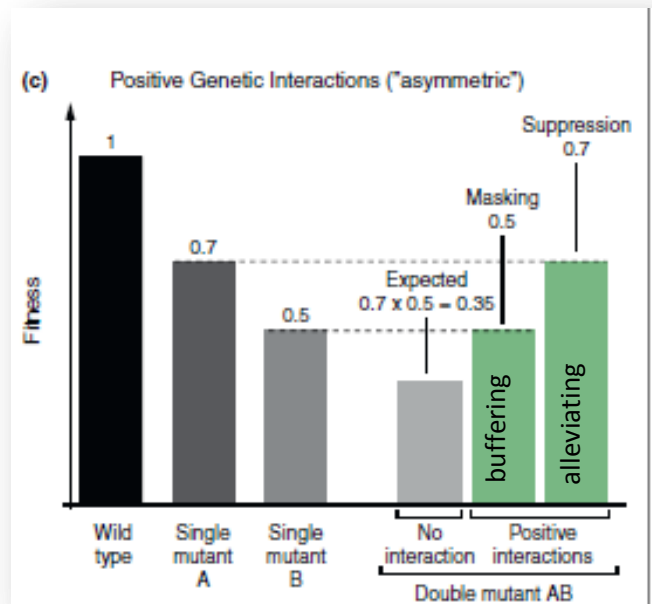


# Redes de Interés Biológico

Datos, datos...y mas datos —> Redes, redes...y mas redes

## Redes fenomenológicas:

Tipo de Red	Criterio de vinculación
Coexpresión Genica	Correlacion en patrones de expresion
Genéticas (delección única )	Fenotipo
<b>Interacción Genética (delecciones dobles)</b>	<b>Fenotipo</b>

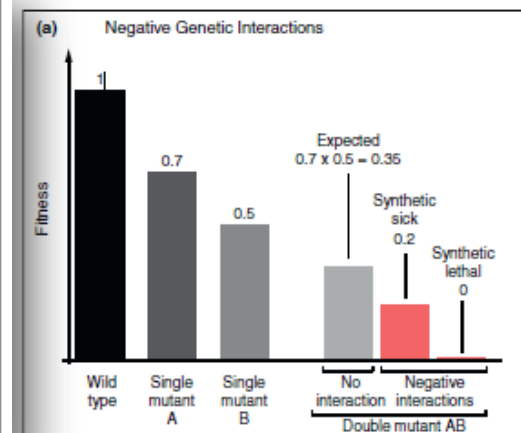
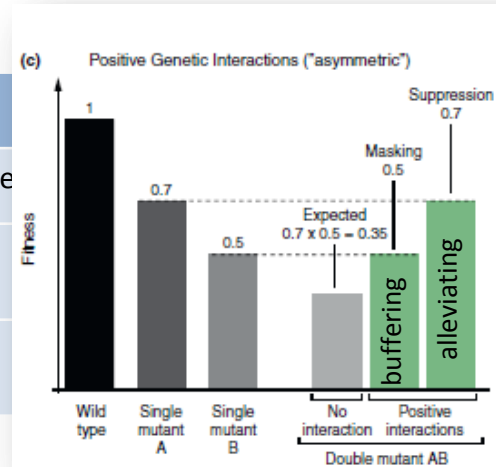


# Redes de Interés Biológico

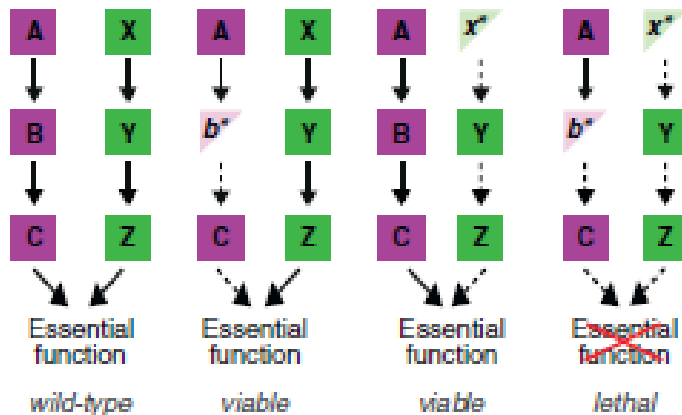
Datos, datos...y mas datos → Redes, redes...y mas redes

## Redes fenomenológicas:

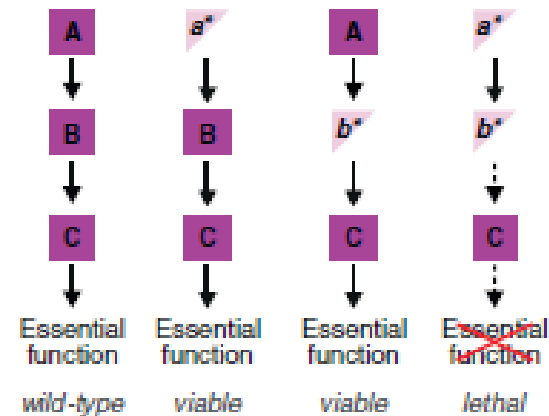
Tipo de Red	Criterio de vinculación
Coexpresión Genica	Correlacion en patrones de expresi
Genéticas (delección única)	Fenotipo
Interacción Genética (delecciones dobles)	Fenotipo



(a) Between Pathway Genetic Interactions (non-essential pathways)



(c) Within Pathway Genetic Interactions (essential pathway)





# Redes de Interés Biológico

Datos, datos...y mas datos → Redes, redes...y mas redes

Redes "soporte"

Tipo de Red	Interacción
Protein Protein	Interacción física
Metabolic	Metabolic and transport re
Red Regulacion Genica	Protein / DNA interactions
Modificaciones Postraduccionales	Fosforilacion kinasa/sustrato
Text Mining	Coaparicion

The screenshot shows a PubMed search result for a paper from *J Biol Chem*. The abstract text is as follows:

**The presenilin proteins are components of multiple membrane-bound complexes that have different biological activities.**  
[Gu Y](#), [Sanjo N](#), [Chen F](#), [Hasegawa H](#), [Petit A](#), [Ruan X](#), [Li W](#), [Shier C](#), [Kawarai T](#), [Schmitt-Ulms G](#), [Westaway D](#), [St George-Hyslop P](#), [Fraser PE](#).

Several lines of evidence have indicated that the presenilin proteins function within macromolecular complexes and are necessary for the regulated intramembranous proteolysis of certain type 1 transmembrane proteins, including the amyloid precursor protein, Notch, and p75. Data from multiple complementary experiments now suggest that there may be several distinct presenilin complexes. We show here that presenilin mutations and certain detergents affect the abundance and componentry of the presenilin complexes, and these structural effects correlate with their effects on gamma-secretase activity. Our data suggest that there are at least three complexes, including a approximately 150-kDa nicastrin-aph-1 complex (which is likely to be a precursor complex). There is a stable and abundant intermediate complex of approximately 440 kDa, which contains aph-1, pen-2, nicastrin, and PS1. However, it is the very low abundance, high mass (>=670 kDa) heteromeric complexes that are associated with the highest gamma-secretase-specific activity.