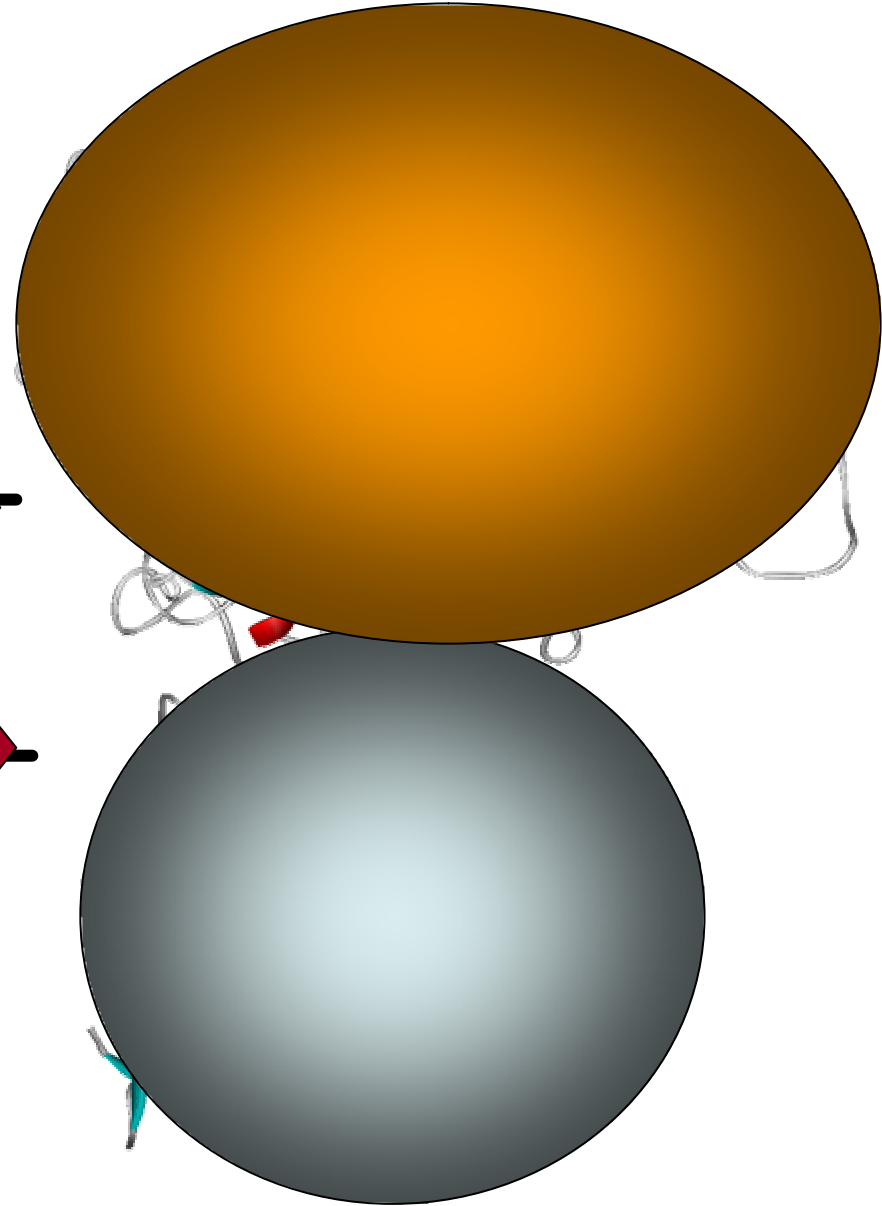
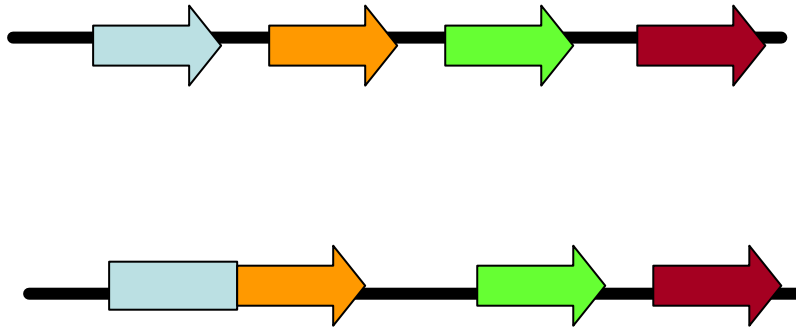
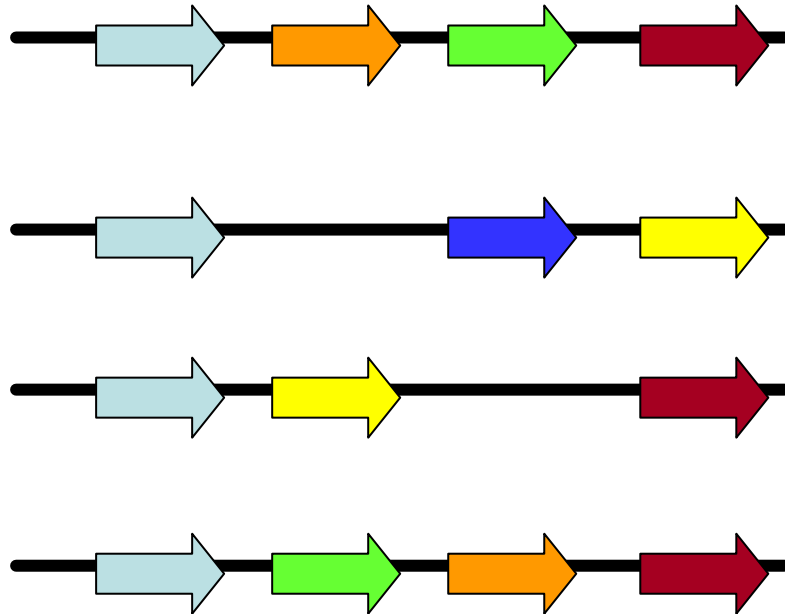


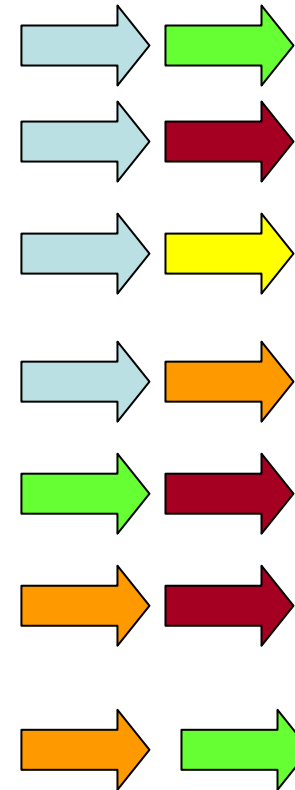
Prediction of interactions

Gene fusion

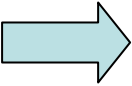
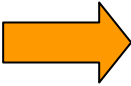
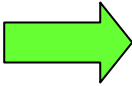
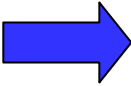
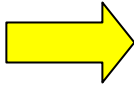


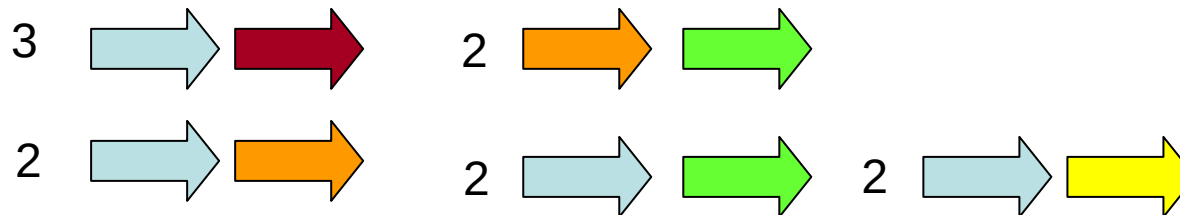


Gene neighbours

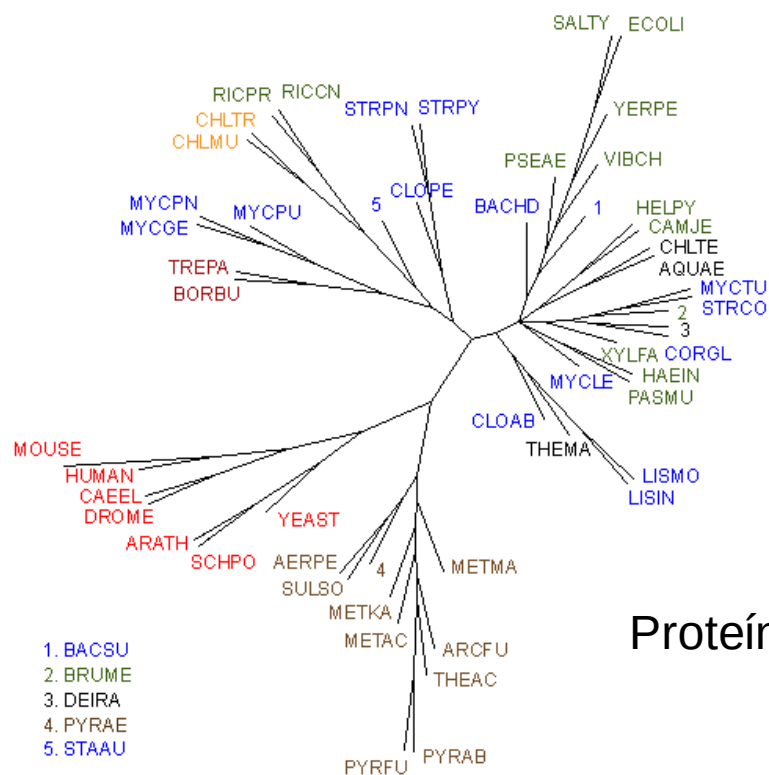


Gene co-occurrence

							
	X	X	X	X			human
	X				X	X	drosophila
	X			X		X	elegans
	X	X	X	X			mouse



phylogenies

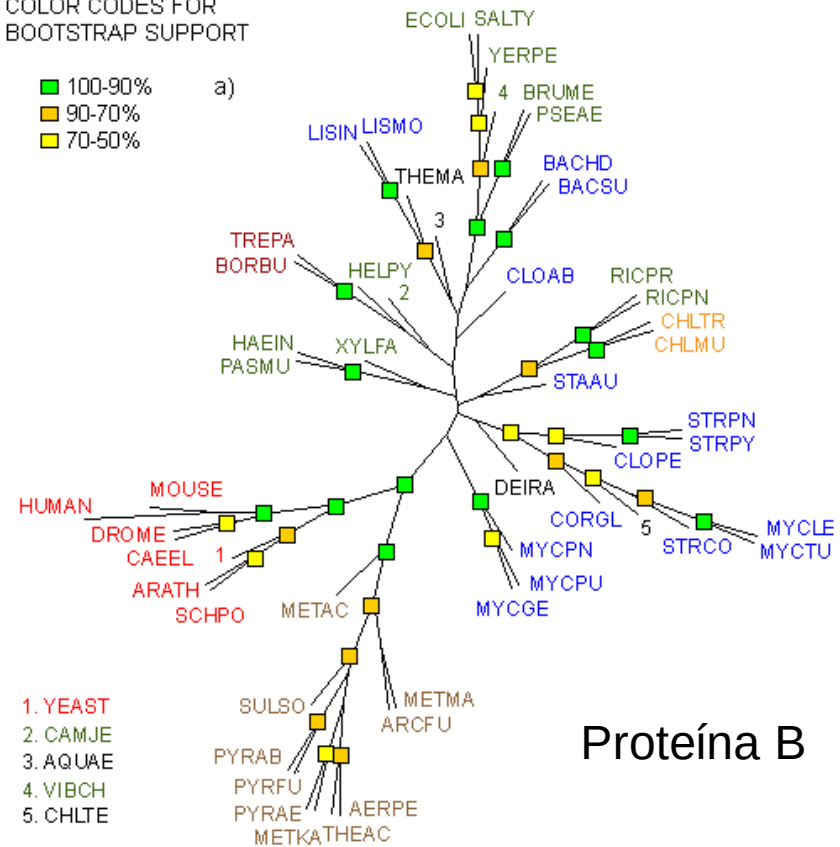


Proteína A

COLOR CODES FOR
BOOTSTRAP SUPPORT

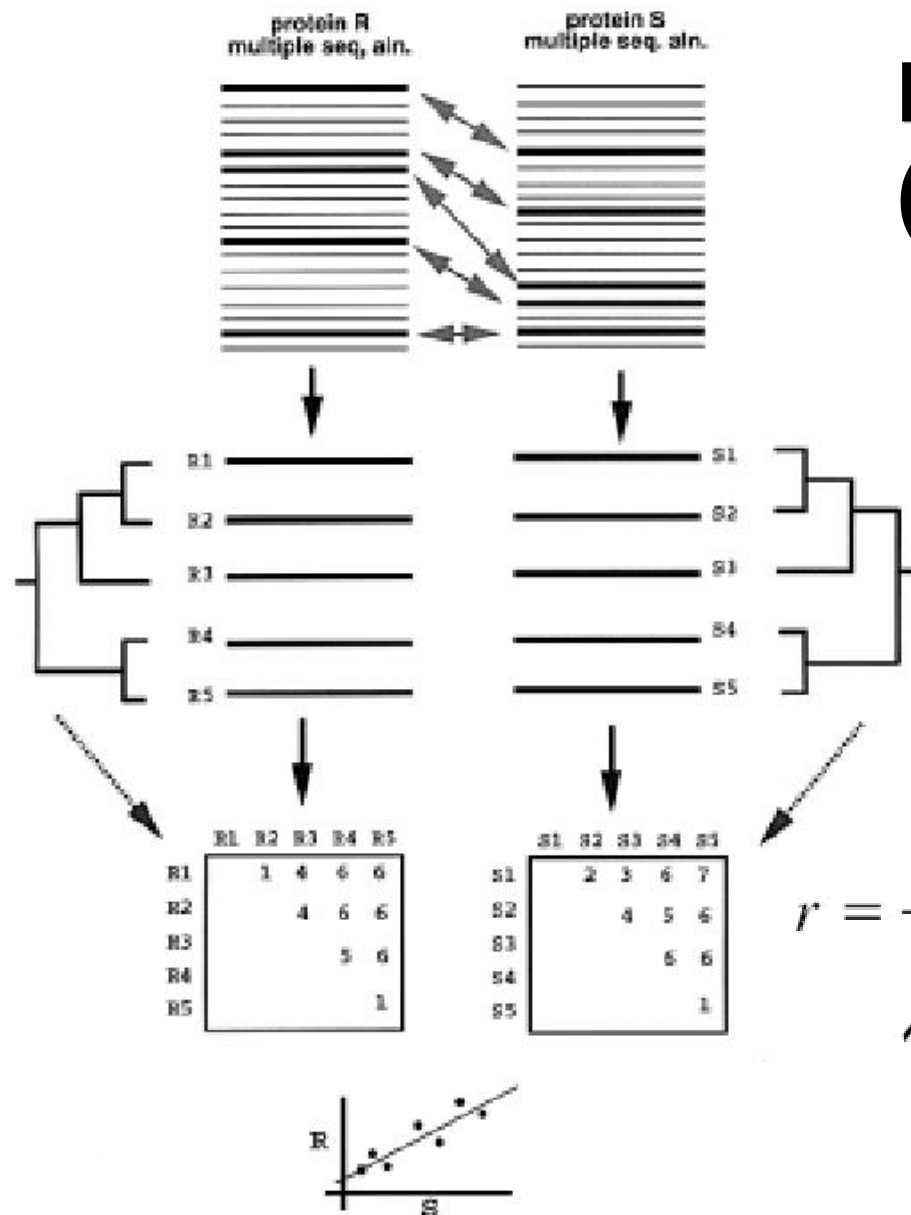
- 100-90%
- 90-70%
- 70-50%

a)



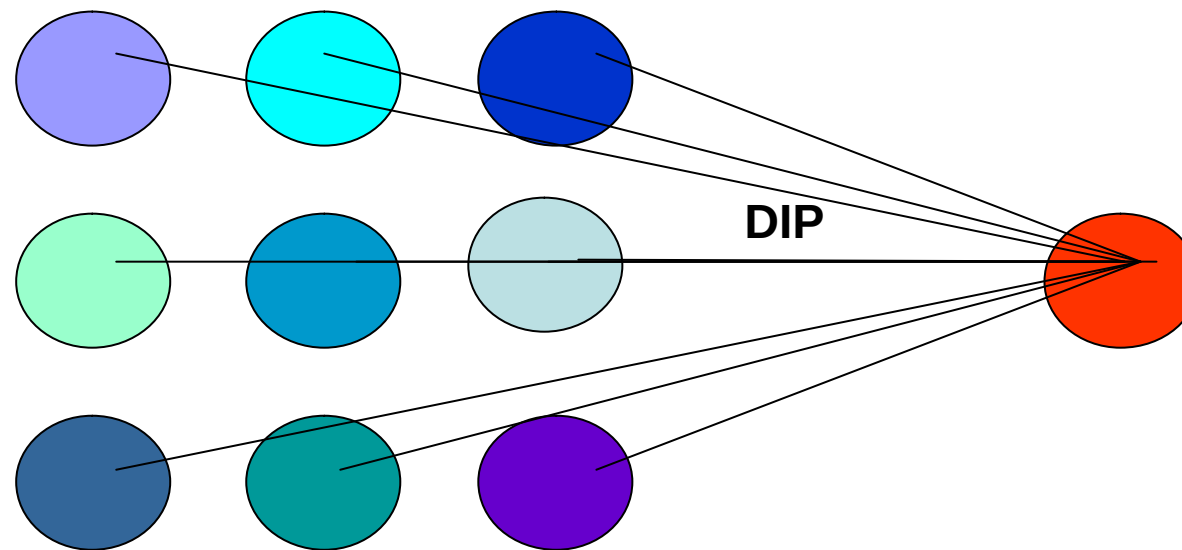
Proteína B

Profiles (phylogeny)



$$r = \frac{\sum_{i=1}^N (R_i - \bar{R}) (S_i - \bar{S})}{\sqrt{\sum_{i=1}^N (R_i - \bar{R})^2} \sqrt{\sum_{i=1}^N (S_i - \bar{S})^2}}$$

Expand interactions:
Using “interologs”



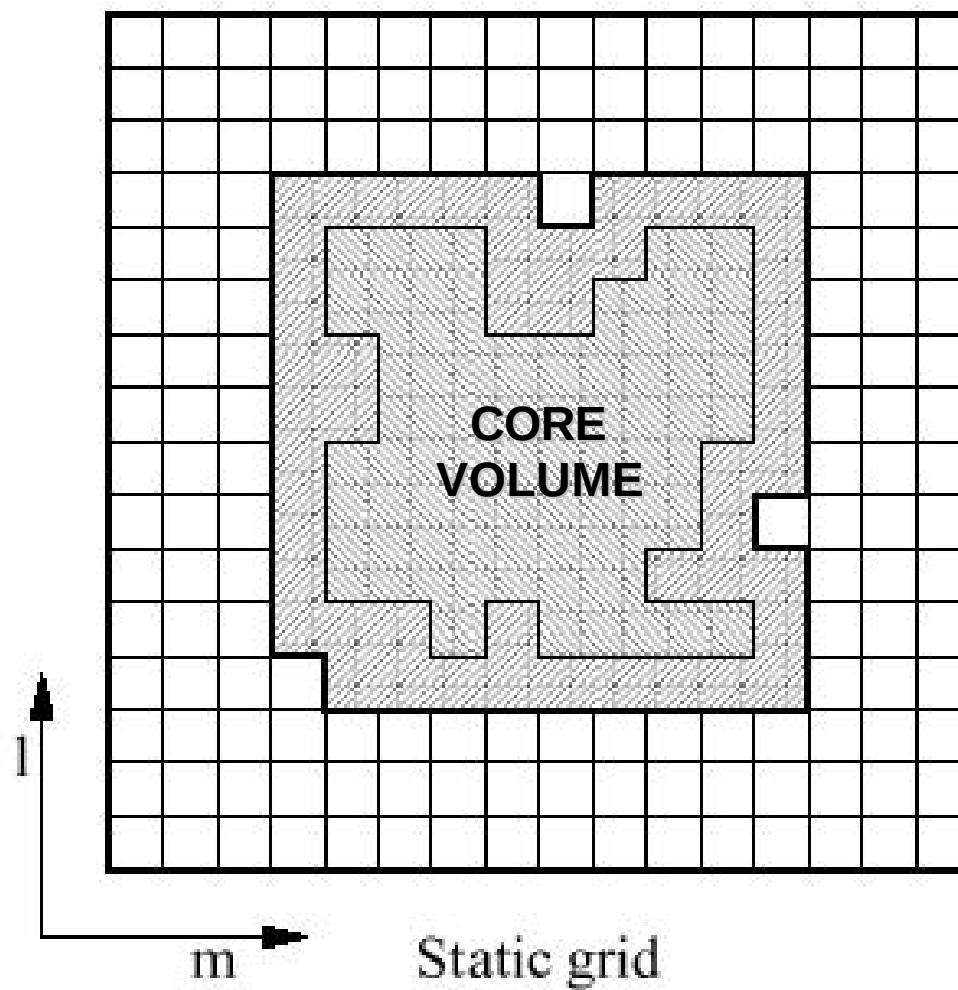
COG members

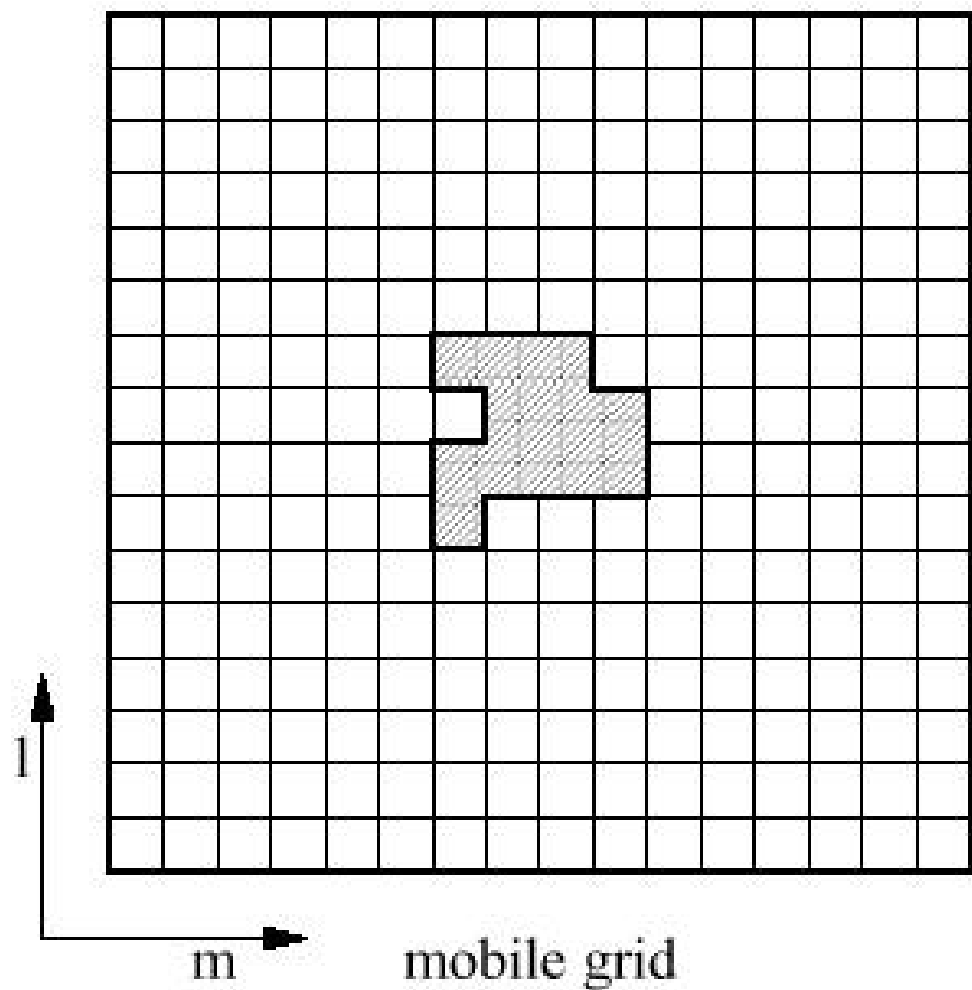


Predicción basada en estructura



Surface and core regions





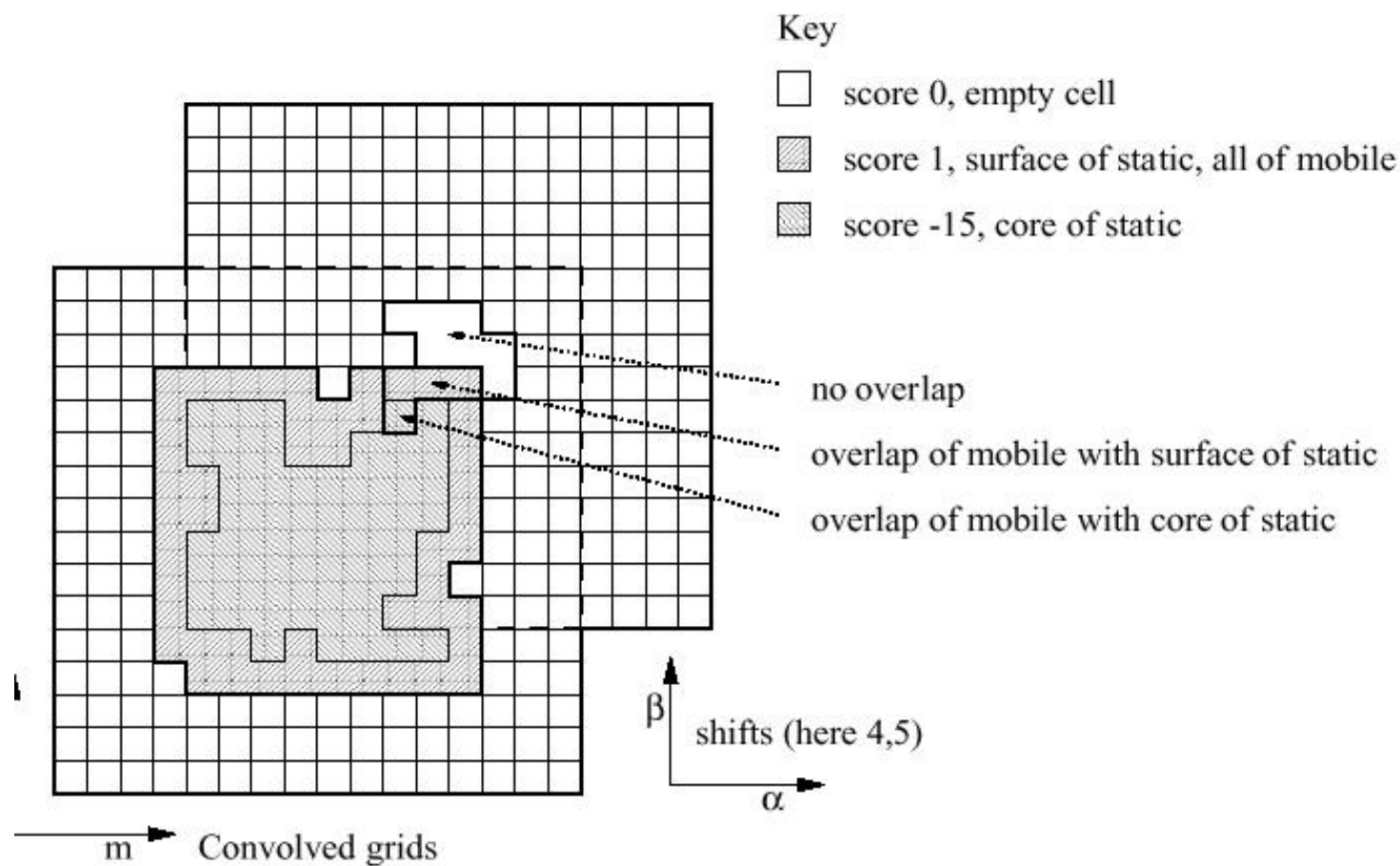
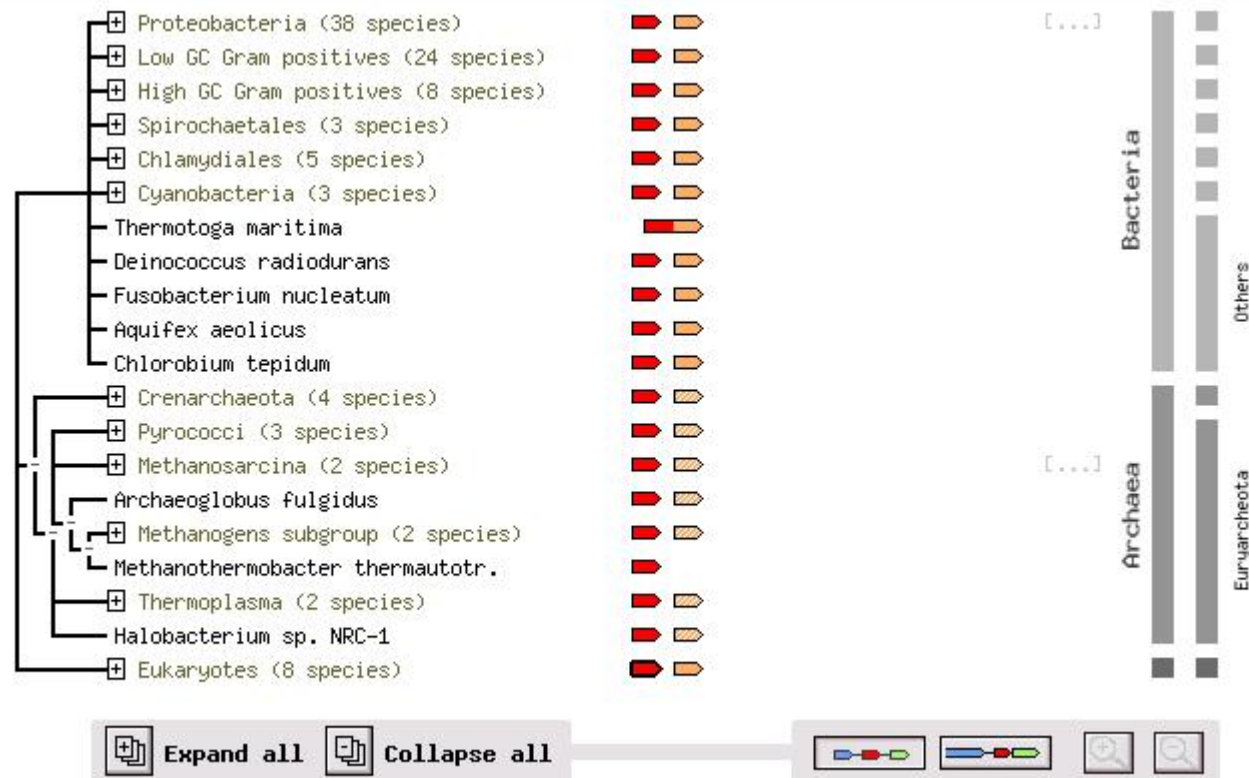


Figure 2: Grid discretisation of molecules and calculation of surface complementarity

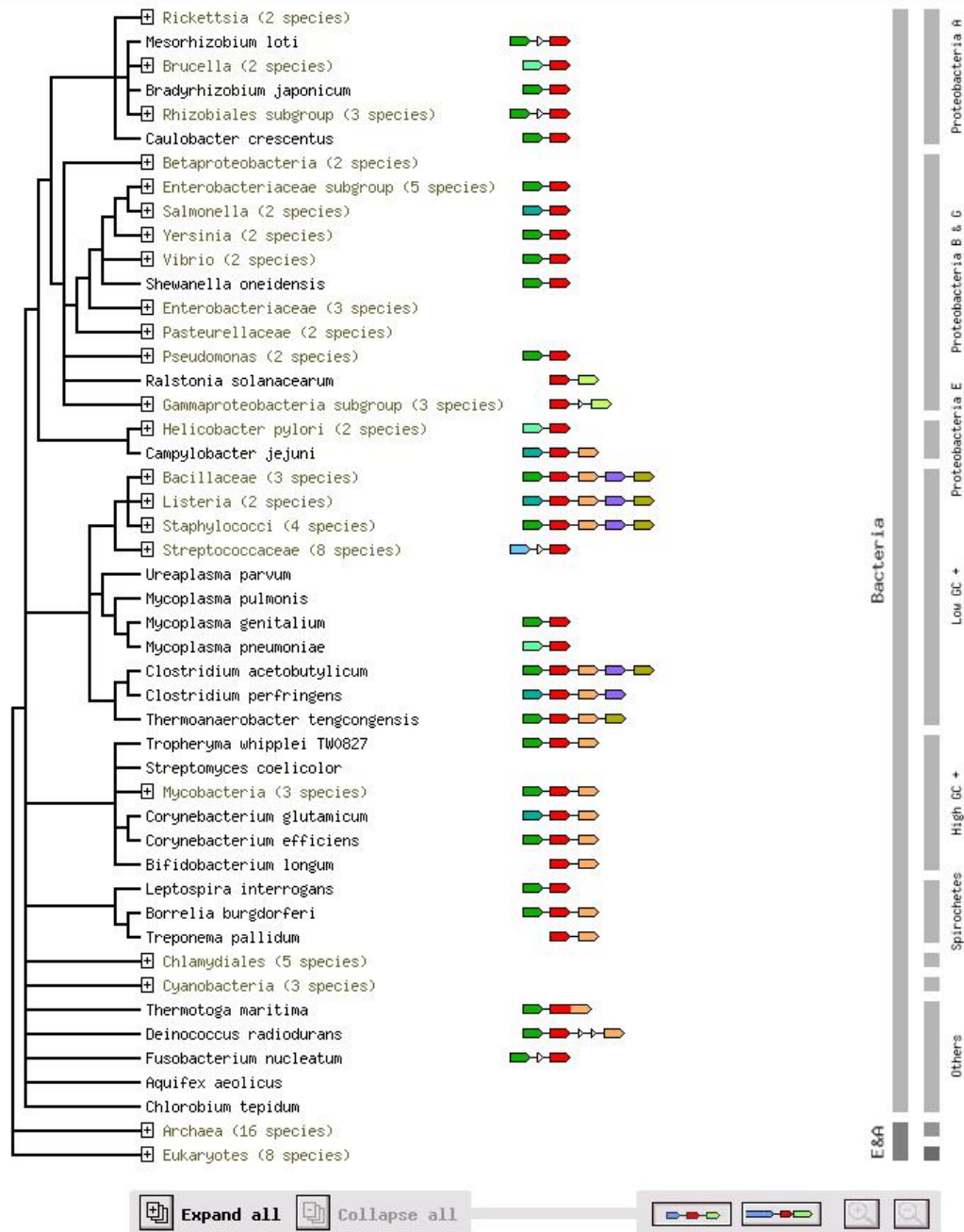
STRING use of database

<http://string.embl.de>

Gene fusion



Gene neighborhood

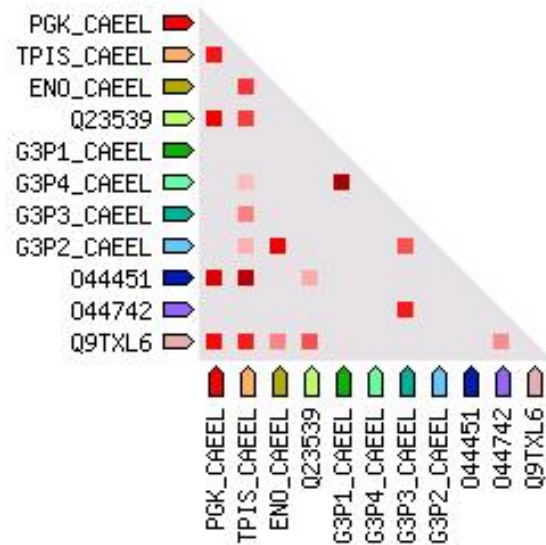


Gene co-expression

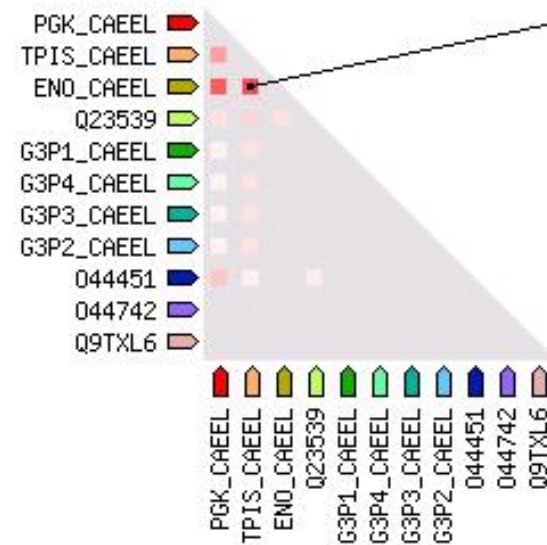
- Coexpression -

association score  0.0 1.0

... from Coexpression in
Caenorhabditis elegans:



... from Coexpression in
other species (transferred):



from *H. pylori*

Show

Text Mining

Biosynthesis of the side chain of yeast glycosylphosphatidylinositol anchors is operated by novel mannosyltransferases located in the endoplasmic reticulum and the Golgi apparatus.

PubMed

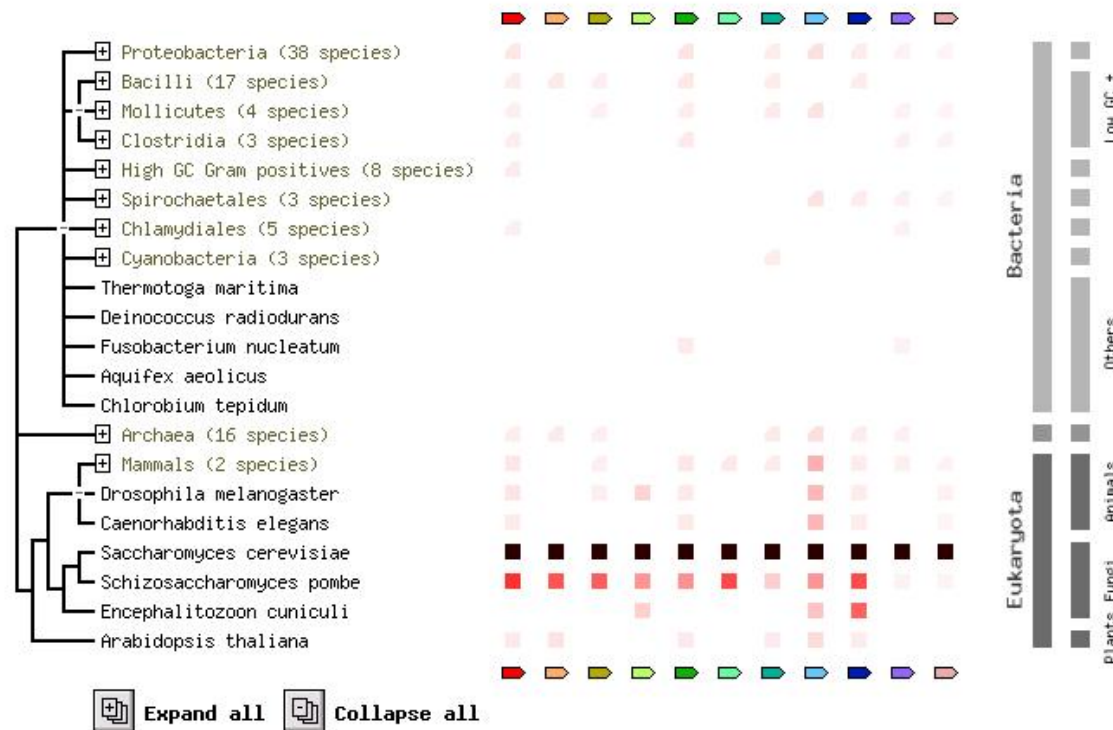
Glycosylphosphatidylinositol (GPI) anchors of the yeast *Saccharomyces cerevisiae* have been reported to contain three different types of side chains attached to contain three different types of side chains attached to the alpha 1,2-linked mannose of the conserved protein-ethanolamine-PO4-Man alpha 1,2Man alpha 1,6Man alpha 1,4GlcNH2-inositol glycan core. The possible side chains are Man alpha 1,2- or Man alpha 1,2Man alpha 1,2- or Man alpha 1,3Man alpha 1,2- (Fankhauser, C., Homan, S. W., Thomas Oates, J. E., McConville, M. J., Desponds, C., Conzelmann, A., and Ferguson, M. A. (1993) *J. Biol. Chem.* 268, 26365-26374). To determine in what subcellular compartment these side chains are made, we metabolically labeled GPI-anchored membrane proteins with myo-[2-3H]inositol in secretion mutants blocked at various stages of the secretory pathway and analyzed the anchor structure of the labeled glycoproteins. When the exit of vesicles from the endoplasmic reticulum or entry into the cis-Golgi were blocked in *sec12* or *sec18* cells, all anchors contained a side chain consisting of a single alpha 1,2-linked mannose. GPI proteins trapped in the cis-Golgi of *sec7* contained Man alpha 1,3Man alpha 1,2- but no Man alpha 1,2Man alpha 1,2-side chains. Mutants blocked at later stages of the secretory pathway made increased amounts of side chains containing two mannoses. Man alpha 1,2Man alpha 1,2- and Man alpha 1,3Man alpha 1,2- side chains were preferentially associated with ceramide- and diacylglycerol-containing GPI anchors, respectively. *Mnn1* (■), *mnn2* (■), *mnn3*, *mnn5*, and *mnt1*(=*kre2*), i.e. mutants which lack or down-regulate 1,2- and 1,3- mannosyltransferases used in the elongation of N- and O-glycans in the Golgi, add the fifth mannose to GPI anchors normally. The same conclusion was reached through the analysis of deletion mutants in *KTR1*, *KTR2*, *KTR3*, *KTR4*, and *YUR1* which all are open reading frames with high homology to *MNT1* (■). Mutants deficient in the Golgi elongation of N-glycans such as *anp1* (■), *van1* (■), *mnn9* (■) are deficient in the maturation of the N-glycans of GPI-anchored glycoproteins, but process the GPI anchor side chain normally. Data are consistent with the idea that the fourth mannose is added to proteins as part of the anchor precursor glycolipid in the endoplasmic reticulum, whereas the fifth mannose is added by not yet identified alpha 1,3- and alpha 1,2-mannosyltransferases located in the Golgi apparatus.

Active recycling of yeast Golgi mannosyltransferase complexes through the endoplasmic reticulum.

PubMed

Mnn9p (■) is a component of two distinct multiprotein complexes in the *Saccharomyces cerevisiae* cis-Golgi that have both been shown to have alpha-1,6-mannosyltransferase activity in vitro. In one of these complexes, *Mnn9p* (■) associates with four other membrane proteins, *Anp1p* (■), *Mnn10p* (■), *Mnn11p* (■), and *Hoc1p* (■), whereas the other complex consists of *Mnn9p* (■) and *Van1p* (■). Members of the *Mnn9p* (■)-containing complexes were incorporated into COPII vesicles made in vitro from endoplasmic reticulum (ER) membranes isolated from cycloheximide-treated cells. This behavior is consistent with an active Golgi to ER recycling process. To examine this path in vivo, we monitored retrograde transport of subunits of the complex in cells blocked in anterograde transport from the ER. In this situation, specific relocation of the proteins from the Golgi to the ER was observed in the absence of new protein synthesis. Conversely, when retrograde transport was blocked in vivo, subunits of the mannosyltransferase complex accumulated in the vacuole. Packaging of *Mnn9p* (■) in COPI-coated vesicles from purified Golgi membranes was also investigated using a coatamer-dependent vesicle budding assay. Gradient fractionation experiments showed that *Mnn9p* (■) and the retrograde v-SNARE, *Sec22p*, were incorporated into COPI-coated vesicles. These observations indicate that the *Mnn9p* (■)-containing mannosyltransferase complexes cycle back and forth between the ER and Golgi.

Gene co-occurrence



Your Input:

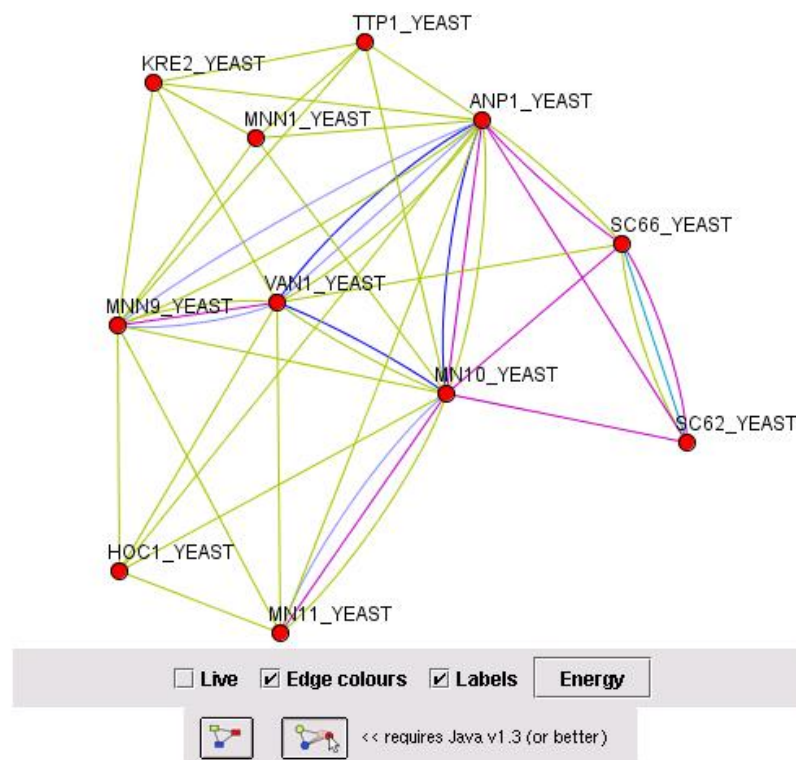
ANP1_YEAST Mannan polymerase II complex ANP1 subunit (M-Pol II subunit ANP1) (Ami [...])

Predicted Functional Associations:

MN10_YEAST	Probable alpha-1,6-mannosyltransferase MN10 (EC 2.4.1.-) (Mannan poly [...])
VAN1_YEAST	Mannan polymerase I complex VAN1 subunit (M-pol I subunit VAN1) (Vanad [...])
SC66_YEAST	Translocation protein SEC66 (HSS1 protein) (206 aa)
HOC1_YEAST	Putative glycosyltransferase HOC1 (EC 2.4.-.-) (Mannan polymerase II c [...])
MNN9_YEAST	Mannan polymerase complexes MNN9 subunit (M-pol I subunit MNN9) (M-Pol [...])
MN11_YEAST	Probable alpha-1,6-mannosyltransferase MN11 (EC 2.4.1.-) (Mannan poly [...])
SC62_YEAST	Translocation protein SEC62 (283 aa)
KRE2_YEAST	Glycolipid 2-alpha-mannosyltransferase (EC 2.4.1.131) (Alpha-1,2-manno [...])
TTP1_YEAST	TTP1 protein (Mannan synthesis protein MNN2) (597 aa)
MNN1_YEAST	Alpha-1,3-mannosyltransferase MNN1 (EC 2.4.1.-) (762 aa)

Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining [Homology]	Score
		•		•		•	0.969
		•		•		•	0.822
			•			•	0.814
				•		•	0.802
						•	0.802
						•	0.801
			•			•	0.784
						•	0.769
						•	0.762
						•	0.745

GRAPH


Your Input:

■ ANP1_YEAST Mannan polymerase II complex ANP1 subunit (M-Pol II subunit ANP1) (Ami [...])

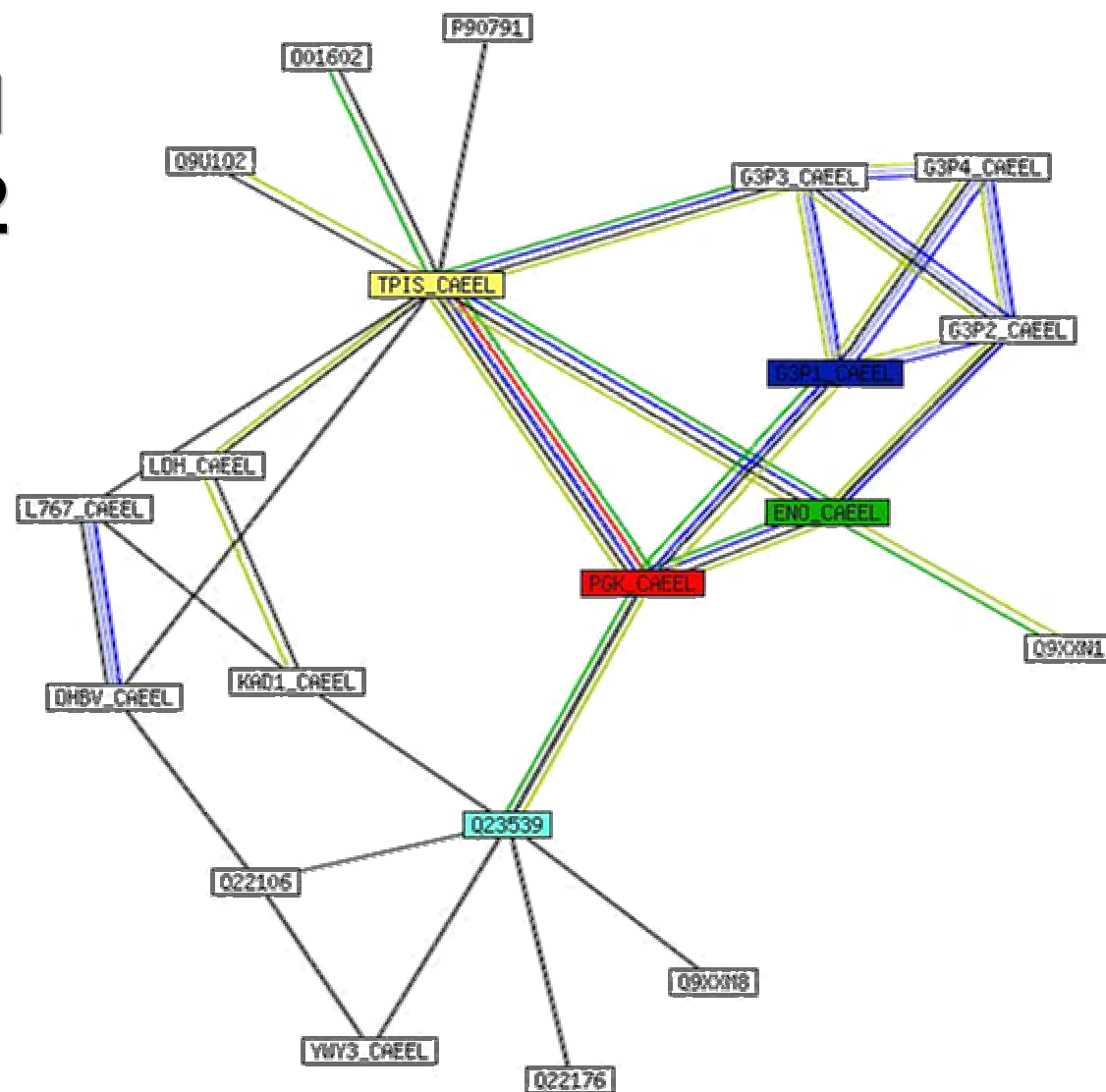
Predicted Functional Associations:

■ MN10_YEAST	Probable alpha-1,6-mannosyltransferase MNN10 (EC 2.4.1.-) (Mannan poly [...])
■ VAN1_YEAST	Mannan polymerase I complex VAN1 subunit (M-pol I subunit VAN1) (Vanad [...])
■ SC66_YEAST	Translocation protein SEC66 (HSS1 protein) (206 aa)
■ HOC1_YEAST	Putative glycosyltransferase HOC1 (EC 2.4.-.-) (Mannan polymerase II c [...])
■ MNN9_YEAST	Mannan polymerase complexes MNN9 subunit (M-pol I subunit MNN9) (M-Pol [...])
■ MN11_YEAST	Probable alpha-1,6-mannosyltransferase MNN11 (EC 2.4.1.-) (Mannan poly [...])
■ SC62_YEAST	Translocation protein SEC62 (283 aa)
■ KRE2_YEAST	Glycolipid 2-alpha-mannosyltransferase (EC 2.4.1.131) (Alpha-1,2-manno [...])
■ TTP1_YEAST	TTP1 protein (Mannan synthesis protein MNN2) (597 aa)
■ MNN1_YEAST	Alpha-1,3-mannosyltransferase MNN1 (EC 2.4.1.-) (762 aa)

Neighborhood	Gene Fusion	Cooccurrence	Experiments	Databases	Textmining	[Homology]	Score
		•	•	•	•	•	0.969
		•	•	•	•	•	0.822
			•	•	•	•	0.814
			•	•	•	•	0.802
				•	•	•	0.802
				•	•	•	0.801
			•				0.784
				•	•	•	0.769
				•	•	•	0.762
				•	•	•	0.745

GRAPH

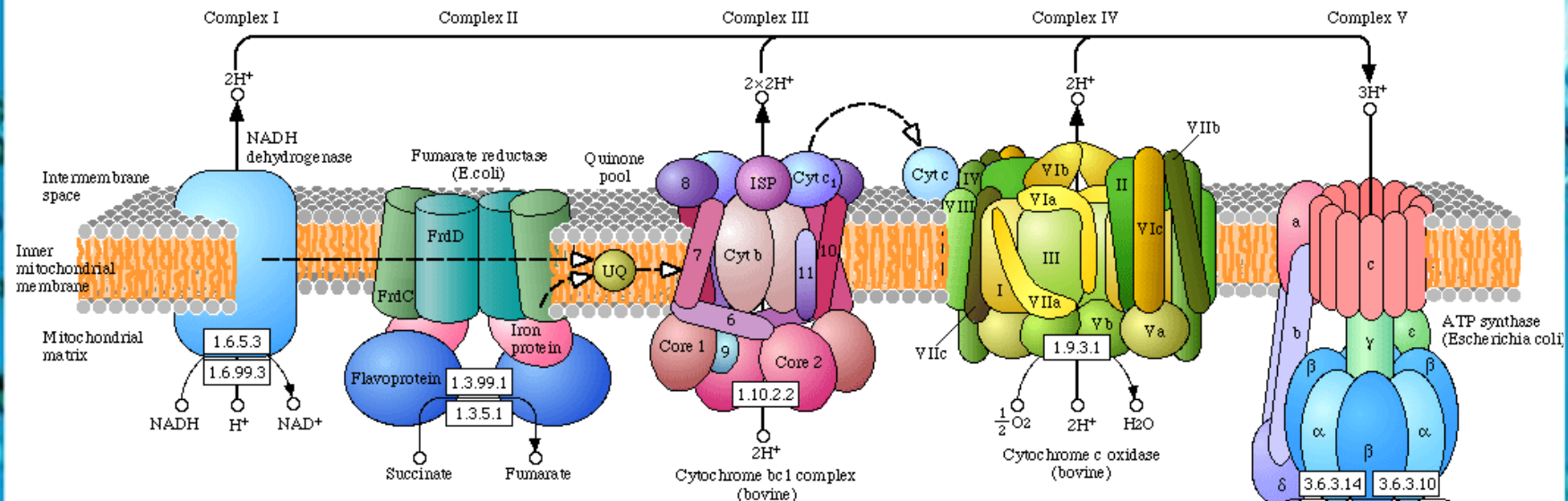
Depth 2



<< requires Java v1.3 (or better)

Prediction of metabolic pathways

OXIDATIVE PHOSPHORYLATION



NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6
---	-----	-----	-----	-----	------	-----	-----

B/A/E	NuoA	NuoB	NuoC	NuoD	NuoE	NuoF	NuoG	NuoH	NuoI	NuoJ	NuoK	NuoL	NuoM	NuoN
-------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Succinate dehydrogenase / Fumarate reductase

E	SDHC	SDHD	SDHA	SDHB
---	------	------	------	------

B/A	SdhC	SdhD	SdhA	SdhB
	FrdA	FrdB	FrdC	FrdD

Cytochrome c reductase

E/B/A	ISP	Cyt b	Cyt c1							
E				COR1	QCR2	QCR6	QCR7	QCR8	QCR9	QCR10

Cytochrome c oxidase

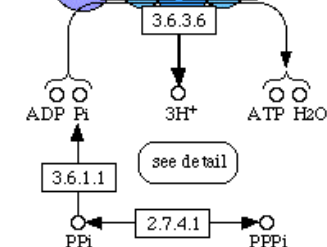
E	COX10	COX3	COX1	COX2	COX4	COX5A	COX5B	COX6A	COX6B	COX6C	COX7A	COX7B	COX7C	COX8	COX10	E/B/A	COX11	COX15	COX17
B/A	CyoE	CyoD	CyoC	CyoB	CyoA	CoxD	CoxC	CoxA	CoxB	QoxD	QoxC	QoxB	QoxA						

Cytochrome c oxidase, cbb3-type

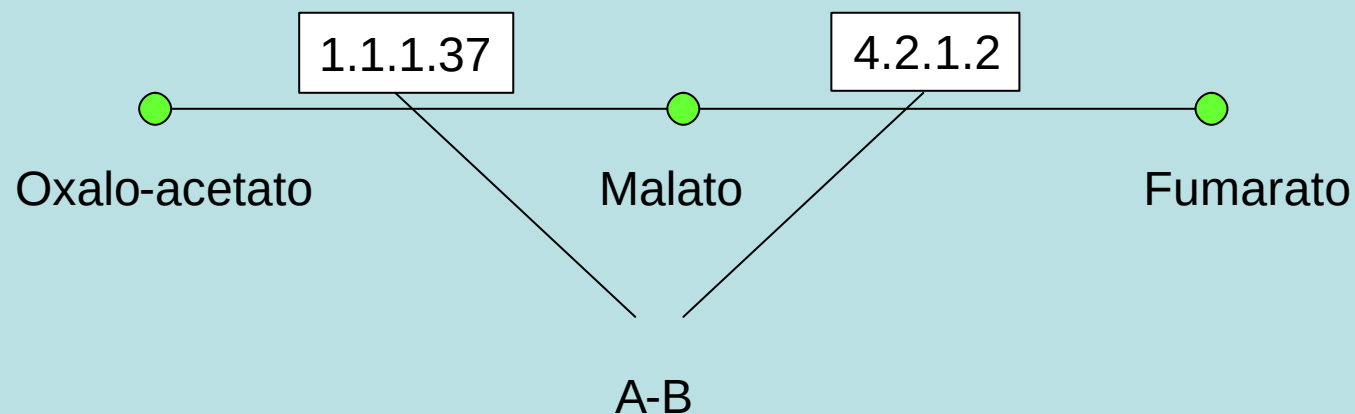
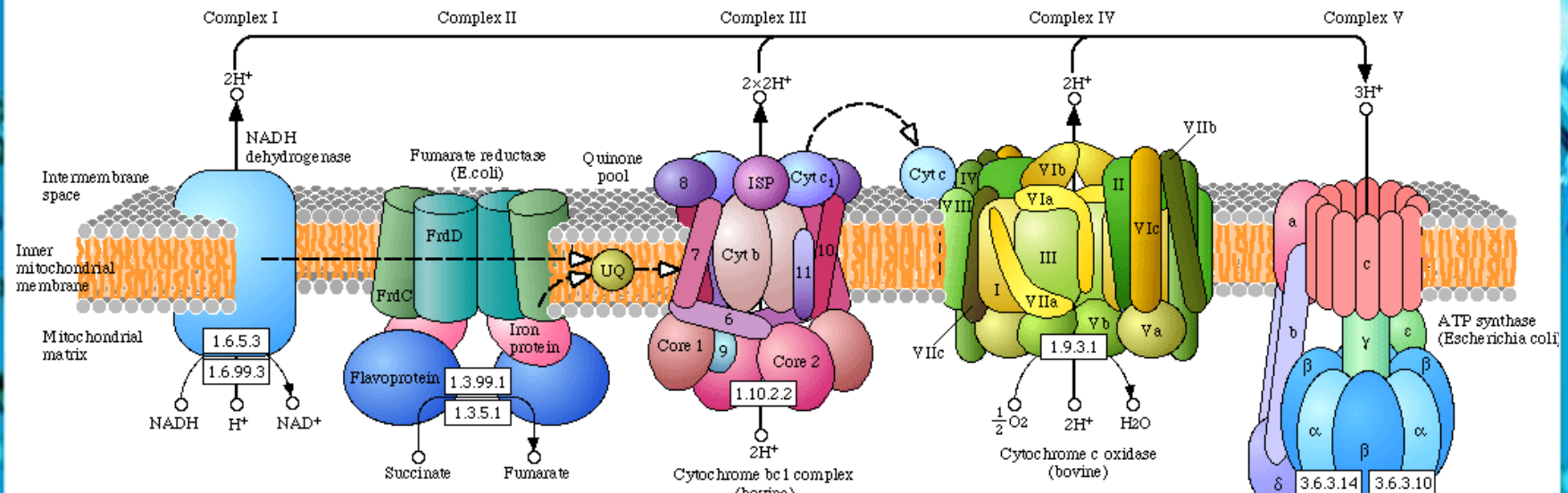
B	I	II	IV	III
---	---	----	----	-----

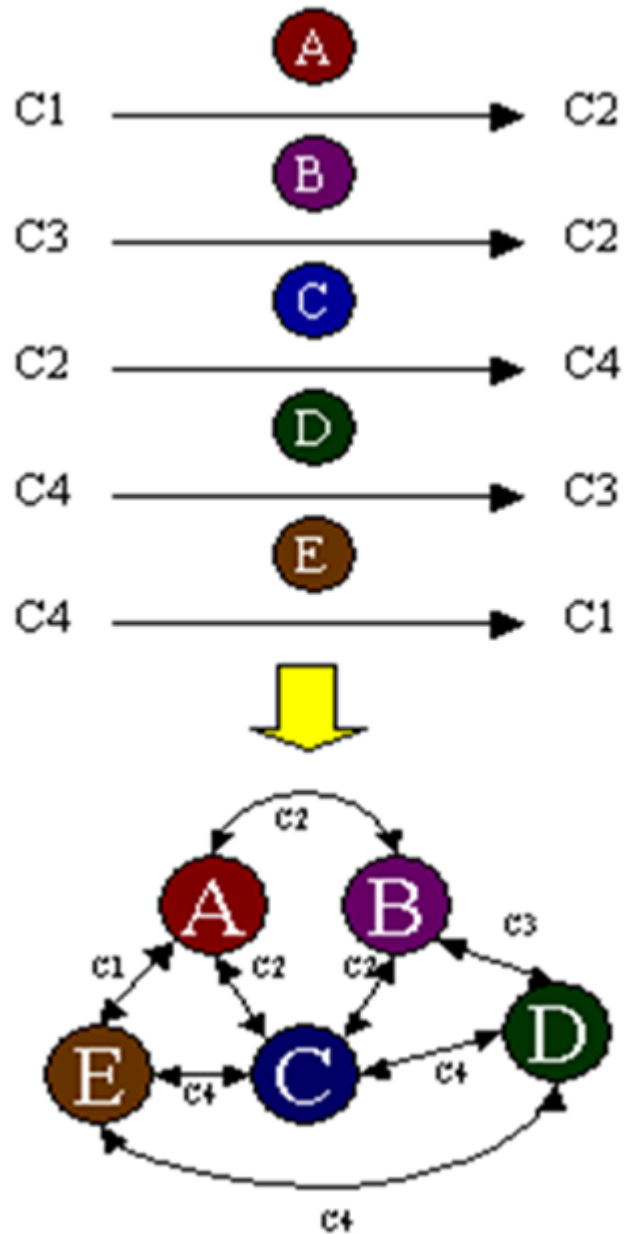
Cytochrome bd complex

B/A	CydA	CydB
-----	------	------



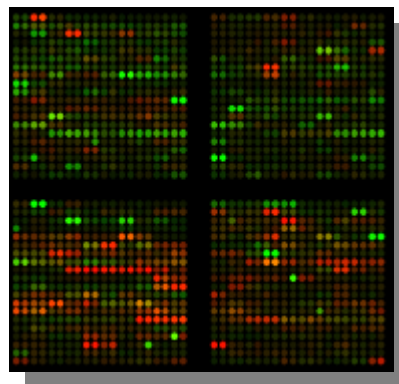
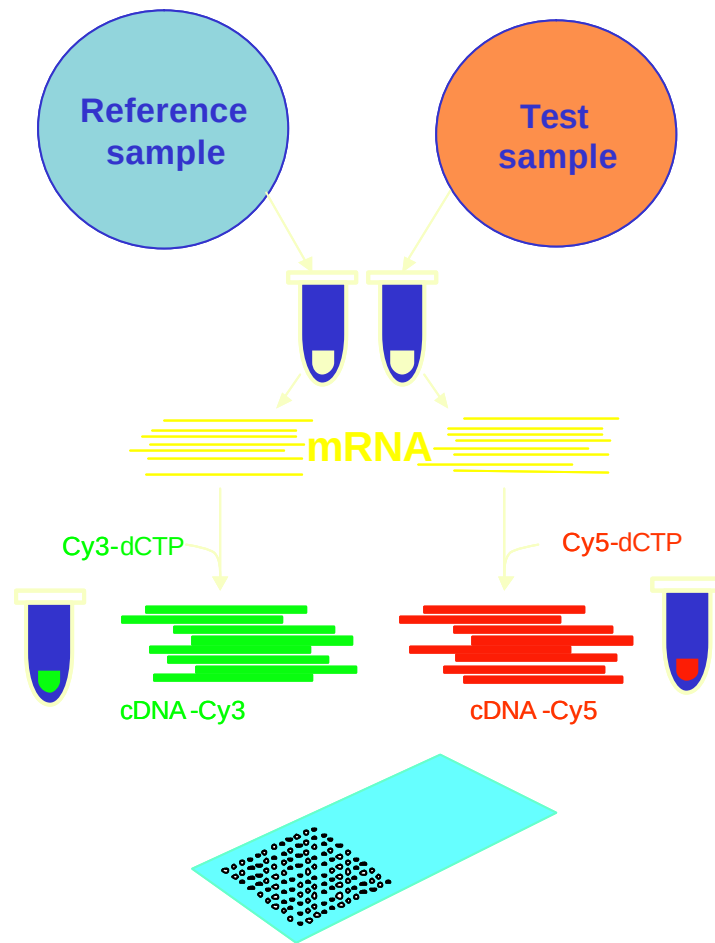
OXIDATIVE PHOSPHORYLATION



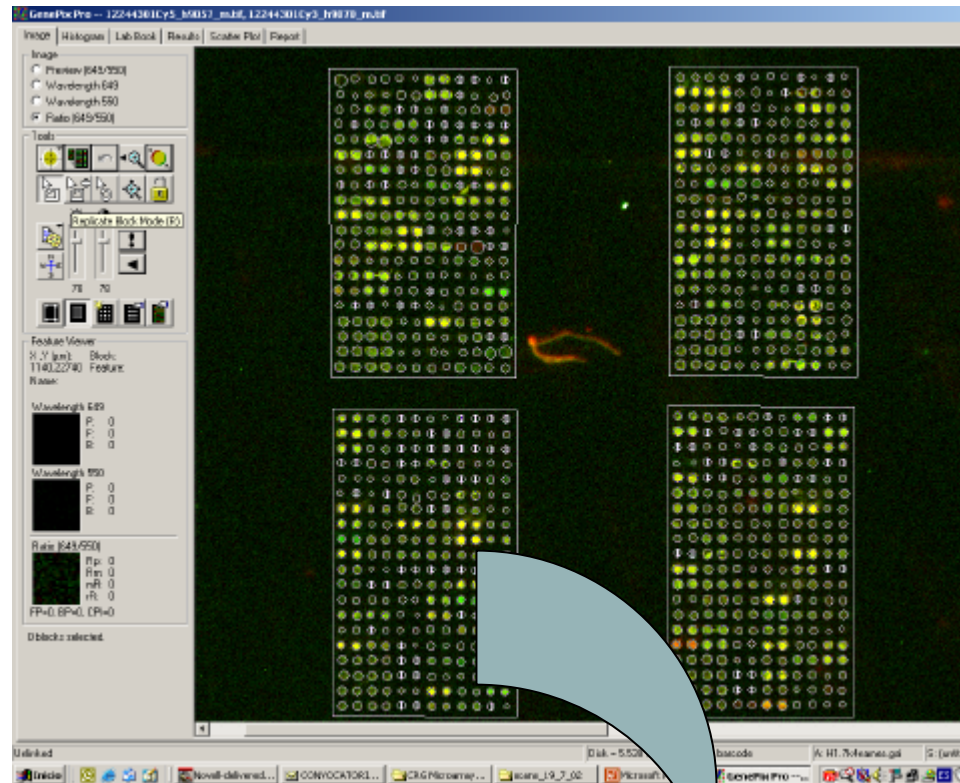


**Pathway based
in common
substrates and
products
(except water)**

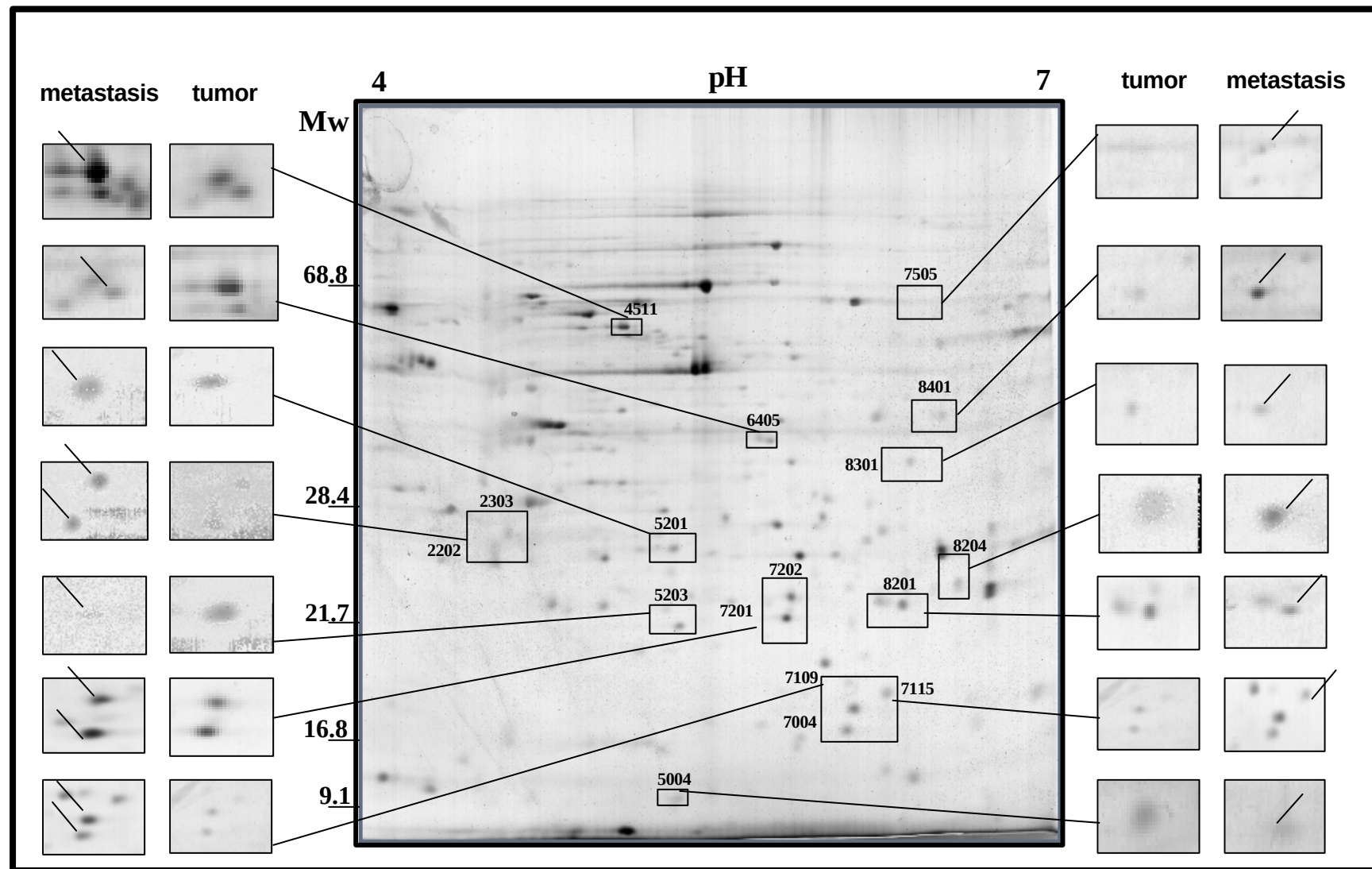
Applications in proteomics



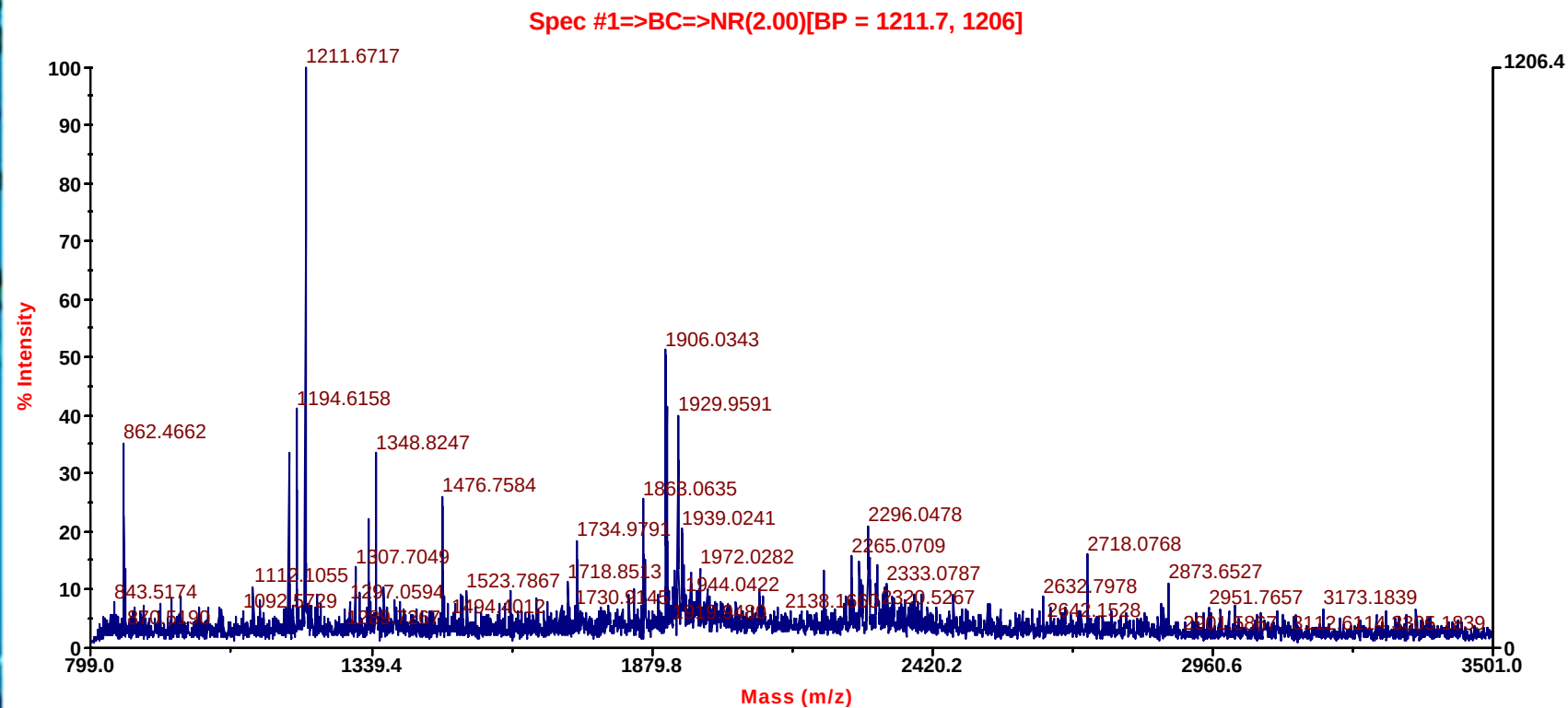
Dr. L. Sumoy
(CRG)



Block	Column	Row	ID	F649 Median	B649 Mean	F550 Median	B550 Mean	...
1	1	1	gen 1	5356	240	115	256	...
1	2	1	gen 1	5472	298	115	221	...
1	3	1	gen 2	8986	270	115	295	...
1	4	1	gen 2	6729	270	115	364	...
1	5	1	gen 3	8981	270	115	276	...
1	6	1	gen 3	9287	270	115	308	...
1	7	1	gen 4	5138	270	11082	434	...
1	8	1	gen 4	5438	270	9594	257	...
1	9	1	gen 5	7634	270	13316	363	...
1	10	1	gen 5	9056	270	14402	291	...
1	11	1	gen 6	12181	702	16383	433	...
1	12	1	gen 6	15159	552	18793	263	...
1	13	1	gen 7	6805	243	14445	298	...
1	14	1	gen 7	6715	261	13874	199	...
1	15	1	gen 8	6073	319	12385	439	...
1	16	1	gen 8	5041	355	9371	335	...
...	...	...	...	...	...	...	...	...



Dra. A. Sierra (IRO)



Dr. D. Andreu (UPF)

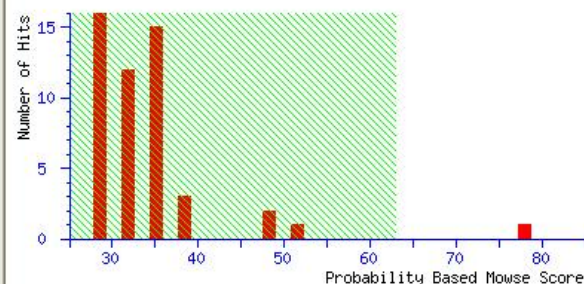
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{MATRIX} Mascot Search Results

User : Cristina Chiva
Email : cchiva@imim.es
Search title : 7004
Database : NCBIInr 20020615 (1010557 sequences; 318889261 residues)
Taxonomy : Homo sapiens (human) (114351 sequences)
Timestamp : 18 Jun 2002 at 14:14:19 GMT
Top Score : 78 for [gi|5031851](#), (NM_005563) stathmin 1; stathmin; oncoprotein 18; phosphoprotein 19; metablastin; prosolin;

Probability Based Mowse Score

Score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 63 are significant ($p < 0.05$).



Protein Summary Report

[Switch to Concise Protein Summary Report](#)

To create a bookmark for this report, right click this link: [Protein Summary Report \(7004\)](#)

Re-Search All

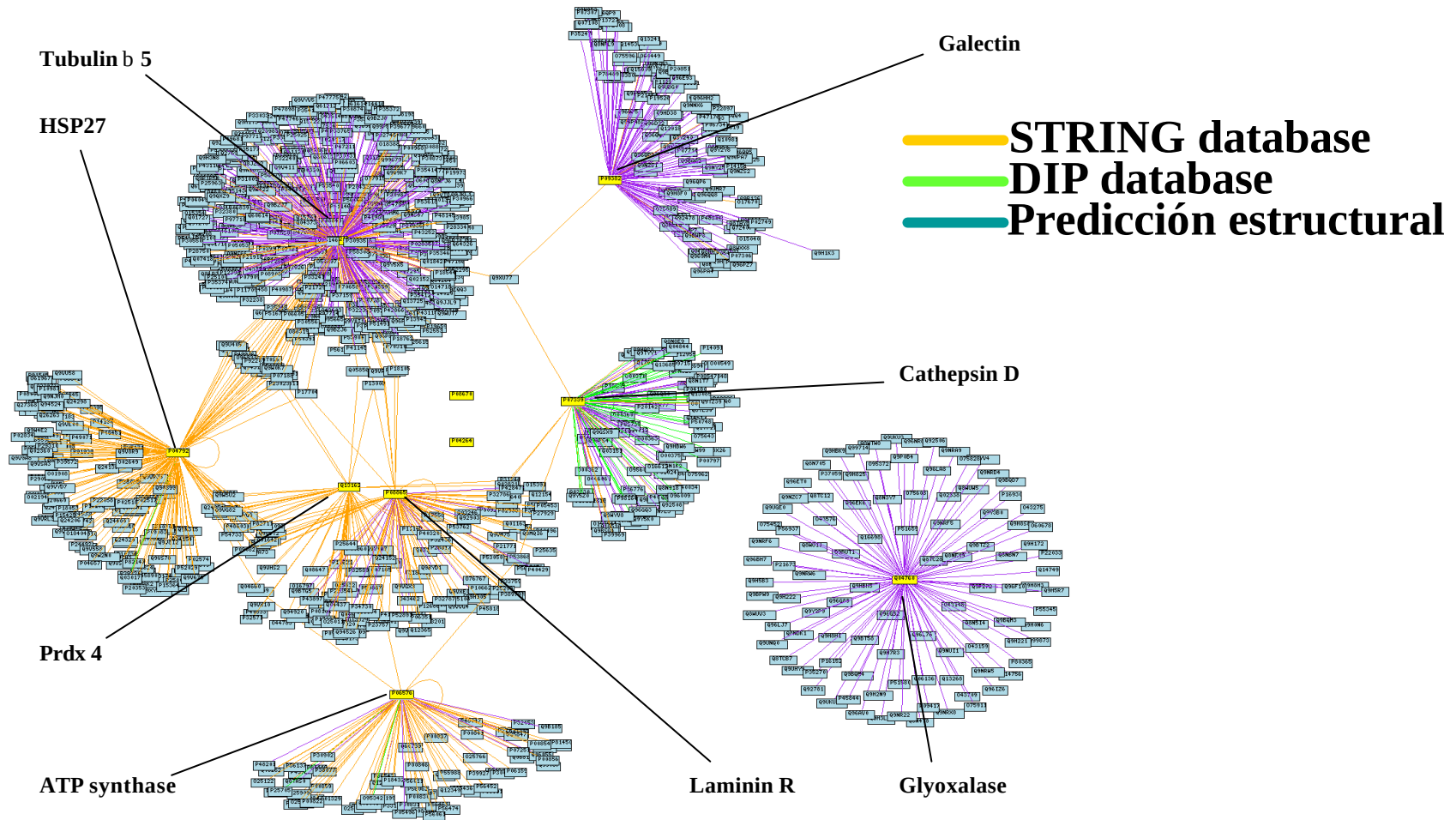
Search Unmatched

Index

Accession	Mass	Score	Description
1. gi 5031851	17292	78	(NM_005563) stathmin 1; stathmin; oncoprotein 18; phosphoprotein 19; metablastin; prosolin;
2. gi 15680064	17326	51	(BC014353) Similar to stathmin 1/oncoprotein 18 [Homo sapiens]
3. gi 65682	38387	49	cytochrome P450 2A3, hepatic - human (fragment)
4. gi 5669088	3008	47	(AF119714) phosphodiesterase I/nucleotide pyrophosphatase 3 [Homo sapiens]
5. gi 7981325	5636	39	(AL121575) dJ914N13.3 (phosphodiesterase I/nucleotide pyrophosphatase 3) [Homo sapiens]
6. gi 20468564	17863	38	(XM_120047) hypothetical protein XP_120047 [Homo sapiens]
7. gi 337930	27614	38	(M22146) scar protein [Homo sapiens]
8. gi 35903	29221	37	(X57959) ribosomal protein L7 [Homo sapiens]
9. gi 17456938	17874	37	(XM_062716) hypothetical protein XP_062716 [Homo sapiens]
10. gi 8922663	17002	37	(NM_018215) hypothetical protein FLJ10781 [Homo sapiens]

SPOTS

^a Spot No.	Protein Identity	Acc. No.	pI	M _r (kDa)	Function	Differential expression in breast cancer
2202	Multicatalytic endopeptidase complex zeta chain	P28066	4.7	26.58	Proteolysis	Su et al., 2001 ; Perou et al., 1999 ; Ross et al, 2000
2303	Tyrosine3/tryptophan5	NP_006752	4.6	29.33	Transduction	
4511	ATP synthase beta chain	P06576	5.3	56.53	Synthesis of ATP	Chen et al, 2001
5004	Beta-tubulin cofactor A	O75347	5.3	12.90	Complex Assembly	Perou et al., 1999
5201	Ran-BP1 (Ran binding protein 1)	P34022	5.2	23.74	GTPase activating	_____
5203	My 032 protein	AF061735	6.6	15.82	_____	_____
6405	F-actin capping protein alpha-1 subunit	P52907	5.5	33.07	Complex Assembly	Su et al., 2001 ; Ross et al., 2000
7004	Stathmin 1	P16949	5.8	17.29	Transcription	Perou et al, 1999 ; Curmi et al, 2000 ; Brattsand G., 2000 ; Bieche et al, 1998
7109	Familial Als mutant G37r	IAZV_A	5.9	16.12	Redox	Chandel, 2000
7115	Non-metastatic cells 1 protein nm-23	P15531	5.8	17.31	Transcription	Su et al., 2001 ; Nakopoulou et al 1999 ; Kapranos , 1996
7201	Thioredoxin peroxidase B	1QMV_A	5.4	21.91	Redox	Su et al., 2001 ; Perou et al., 1999; Ross et al, 2000 ; Husbeck et al ,2001 ; Berggren 2001 et al. ; Harvey et al , 2001
7202	Glutathione transferase	P09211	5.4	23.57	Glut. transferase	Perou et al., 1999 ; Ross et al, 2000 Dialyna et al, 2001; Ghalia et al, 2000; Huang et al, 2000
7505	Aminoacylase 1	Q03154	5.8	46.08	Hydrolysis	Su et al., 2001 ; Perou et al., 1999 ; Ross et al, 2000
8201	Hypothetical protein MGC15429	NP_116139	5.9	22.45	_____	_____
8204	Peroxiredoxin3	P30048	7.1	28.05	Redox	Su et al., 2001 ; Perou et al., 1999 ; Ross et al, 2000
8301	Carbonyl reductase 3	O75828	5.8	31.23	Redox	_____
8401	Enolase 1	P06733	7.1	47.78	Transcription	Su et al., 2001 ; Perou et al., 1999 ; Ross et al , 2000

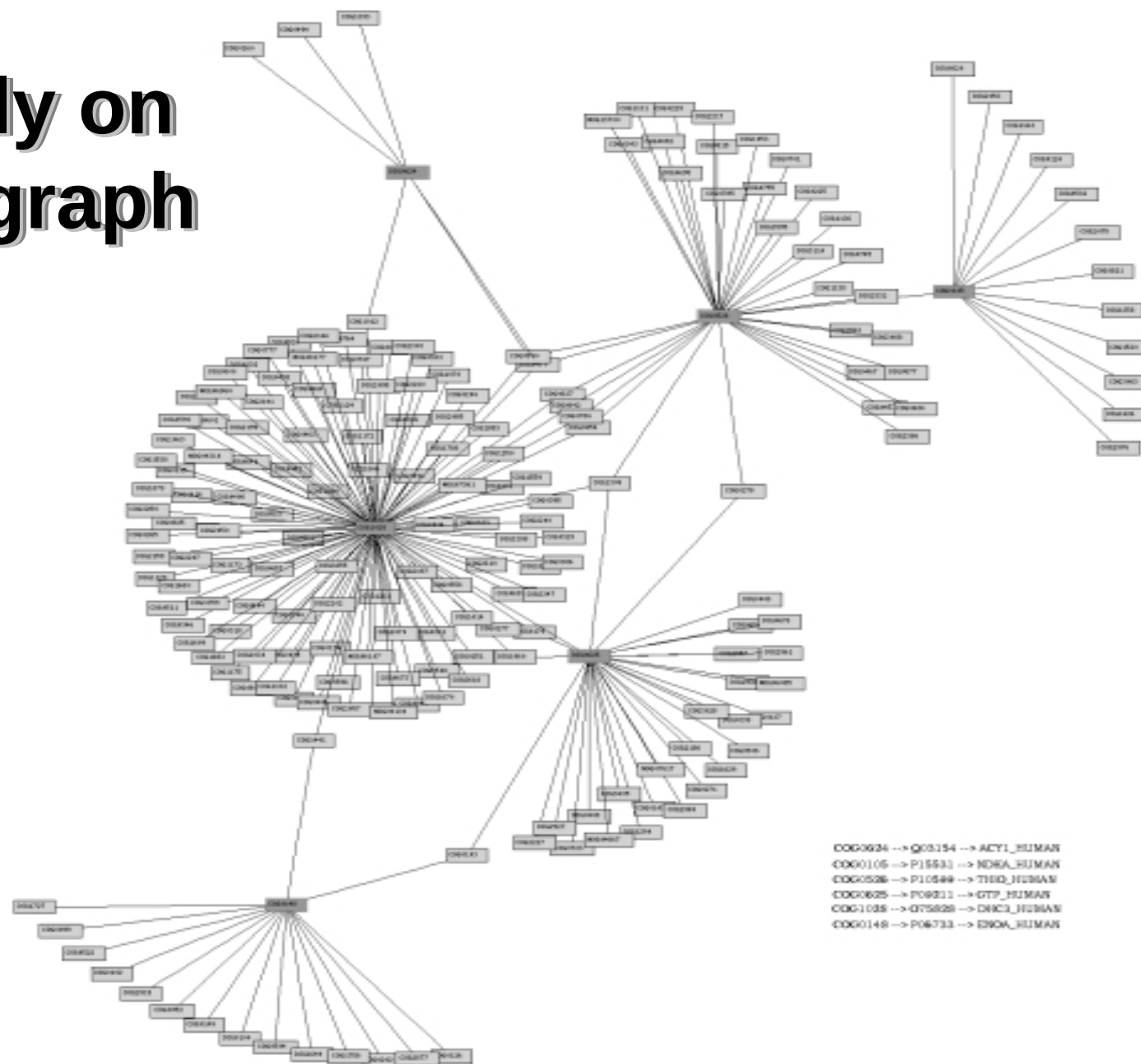


Proteínas identificadas

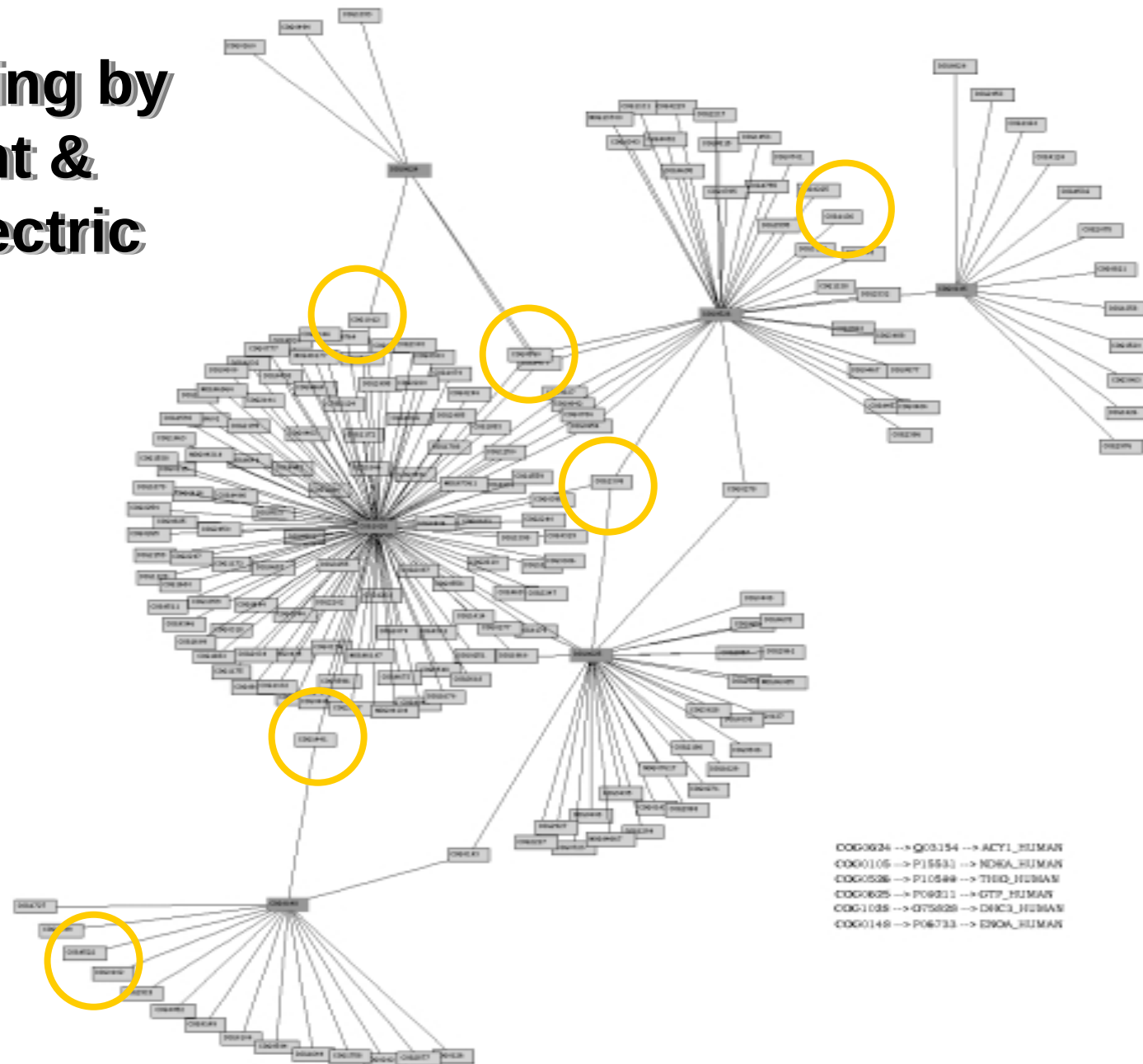
Proteínas propuestas

Help to solve 2D page gels

Apply on the graph



Filtering by weight & isoelectric point



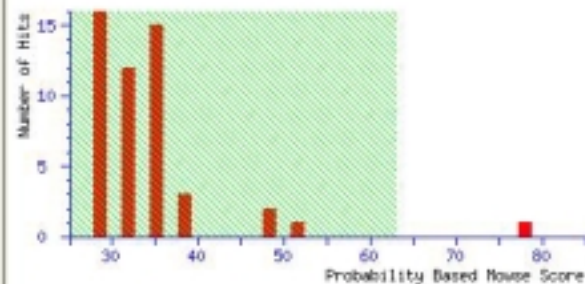
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{MATRIX} Mascot Search Results

User : Cristina Chiva
Email : cchiva@imim.es
Search title : 7004
Database : NCBI nr 20020615 (1010557 sequences; 318889261 residues)
Taxonomy : Homo sapiens (human) (114351 sequences)
Timestamp : 18 Jun 2002 at 14:14:19 GMT
Top 10 hits : 78 for [gi118031851](#), (NM_005563) stathmin 1; stathmin; oncoprotein 18; phosphoprotein 19; metablastin; prosolin;

Probability Based Mowse Score

Score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 65 are significant ($p < 0.05$).



Protein Summary Report

[Switch to Concise Protein Summary Report](#)

To create a bookmark for this report, right click this link: [Protein Summary Report \(7004\)](#)

Re-Search All

Search Unmatched

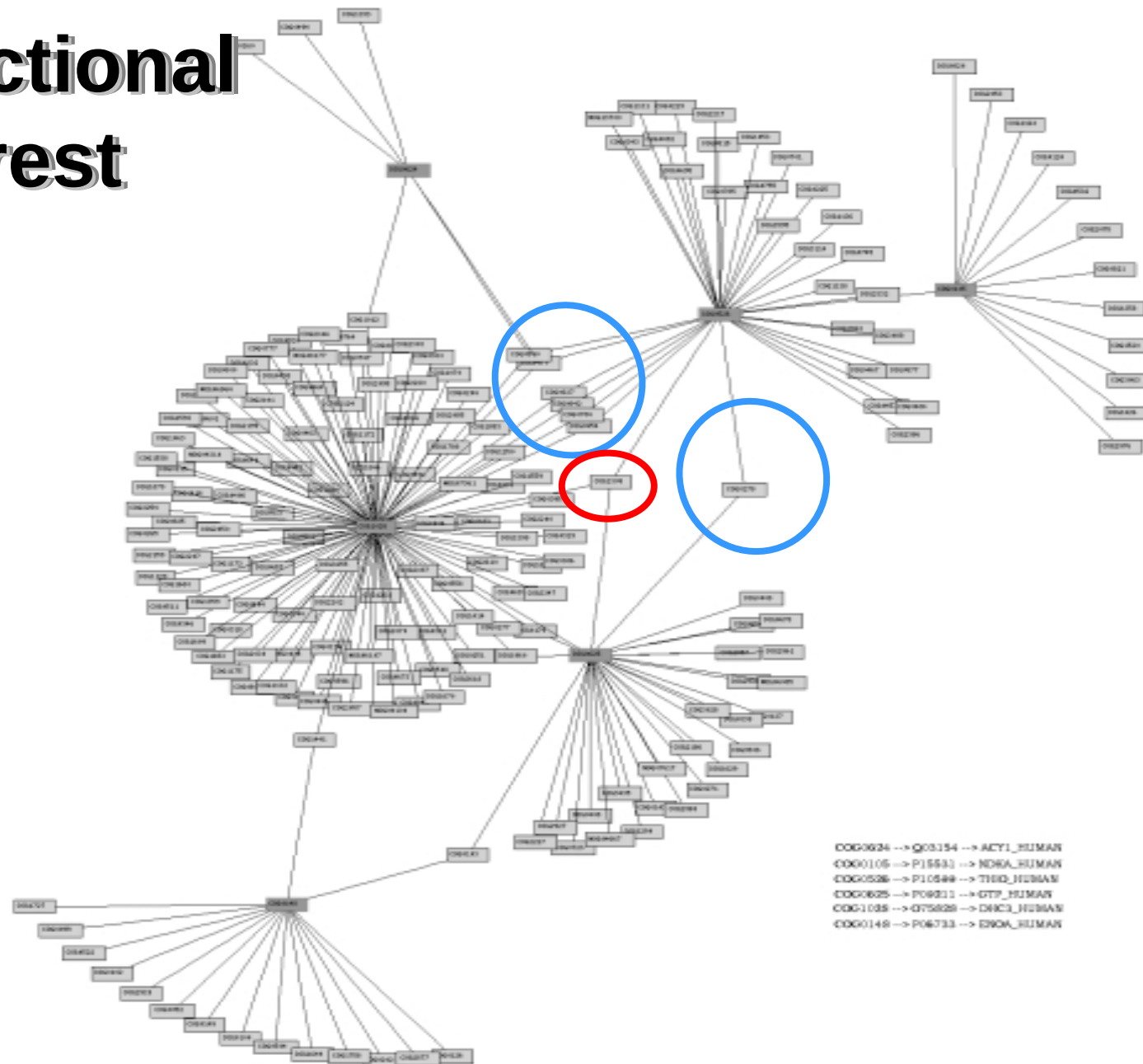
Index

Accession	Mass	Score	Description
1. gi118031851	17292	78	(NM_005563) stathmin 1; stathmin; oncoprotein 18; phosphoprotein 19; metablastin; prosolin;
2. gi115680064	17326	51	(AF119714) similar to stathmin 1/oncoprotein 18 [Homo sapiens]
3. gi1165682	38357	39	(U00006) Cytochrome P450 2A3, hepatic - human (fragment)
4. gi11669088	17300	39	(AF119714) phosphodiesterase I/nucleotide pyrophosphatase 3 [Homo sapiens]
5. gi11798182	17300	39	(AL121575) dJ914N13.3 (phosphodiesterase I/nucleotide pyrophosphatase 3) [Homo sapiens]
6. gi11111366	17563	38	(XM_120047) hypothetical protein XP_120047 [Homo sapiens]
7. gi11111366	27614	38	(M22146) scar protein [Homo sapiens]
8. gi1135903	29221	37	(X57959) ribosomal protein L7 [Homo sapiens]
9. gi117456938	17874	37	(XM_062716) hypothetical protein XP_062716 [Homo sapiens]
10. gi118922663	17002	37	(NM_018215) hypothetical protein FLJ10781 [Homo sapiens]

LISTA DE CANDIDATOS

Explaining biological processes

Functional interest

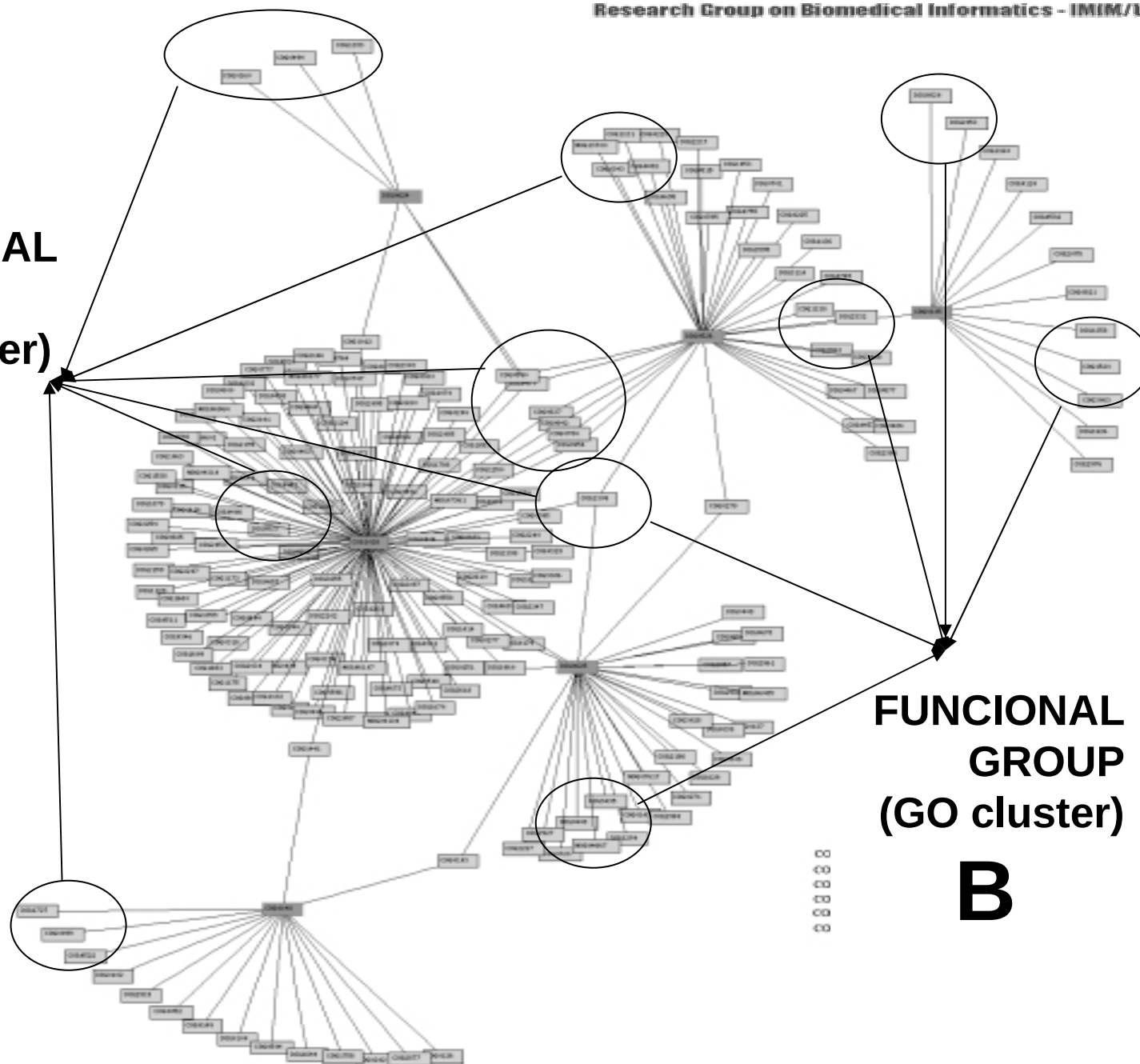


**FUNCIONAL
GROUP
(GO cluster)**

A

**FUNCIONAL
GROUP
(GO cluster)**

B



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