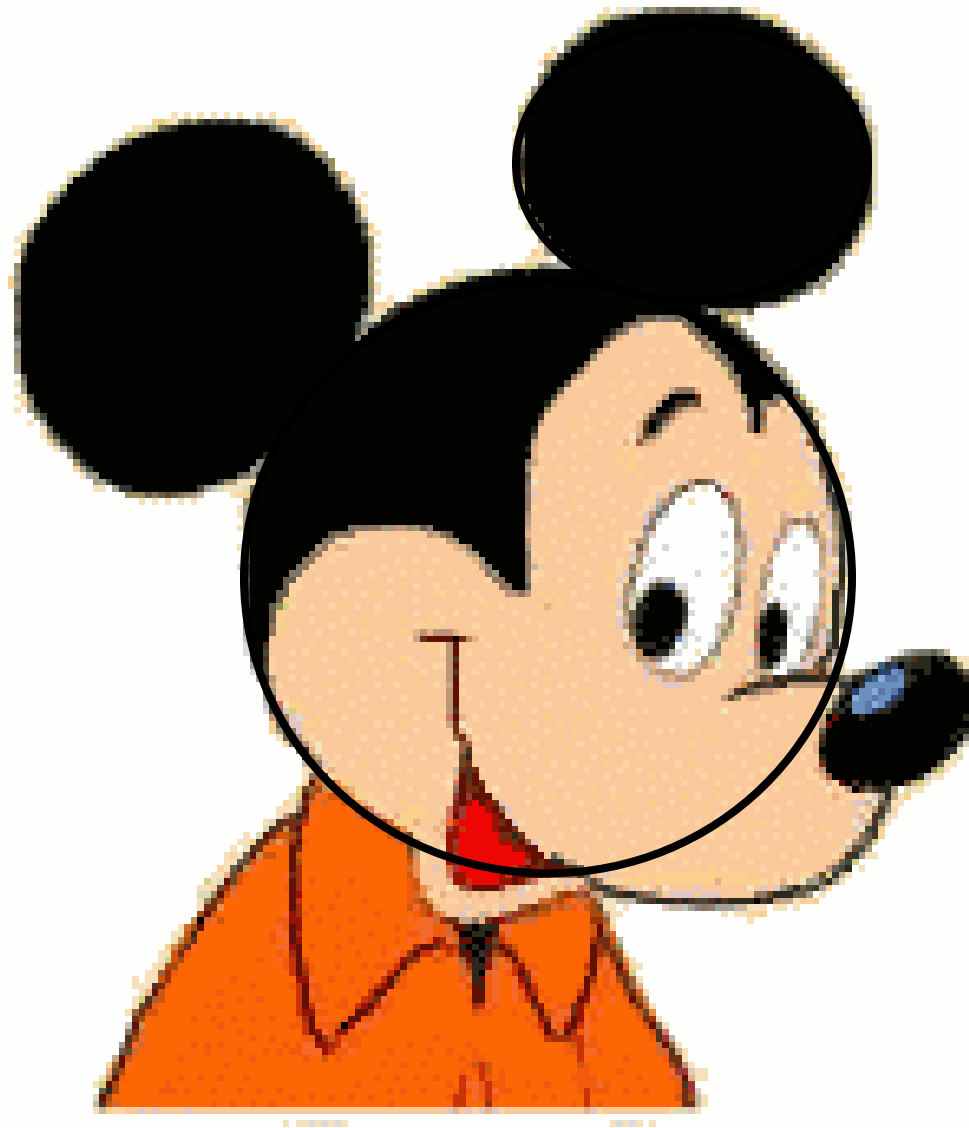


Modelni organizmi

Ne stori drugemu, kar nočeš, da on stori tebi (pa kaj še!).



Wikipedia: A **model organism** is a non-human [species](#) that is extensively studied to understand particular [biological phenomena](#), with the expectation that discoveries made in the organism model will provide insight into the workings of other organisms.

Modelni organizmi

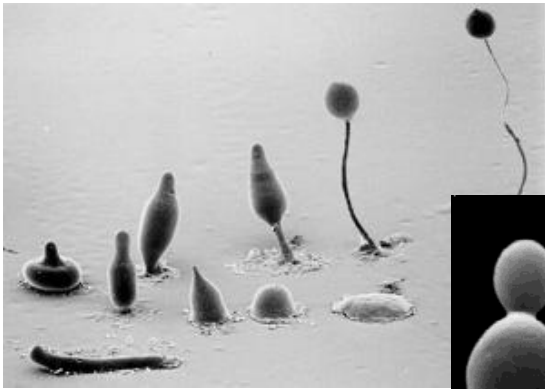


flybase.org

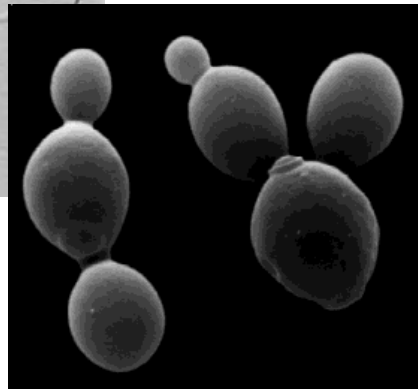
wormbase.org



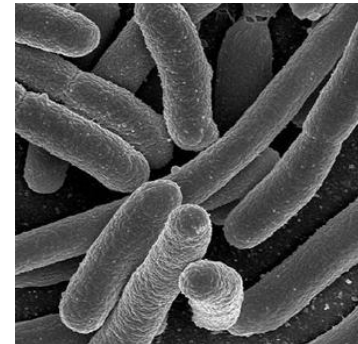
arabidopsis.org



dictybase.org



yeastgenome.org



ecogene.org

Model Organisms

Organism	Genome Size (Mb)	Genes	Homologous Recombination	Meiotic Recombination	Biochemistry
<i>E. coli</i>	4.6	4,288	Yes	No	Excellent
<i>S. cerevisiae</i>	12.1	6,144	Yes	Yes	Good
<i>S. pombe</i>	14	4,900	Yes	Yes	Good
<i>C. elegans</i>	97	18,266	Difficult	Yes	Poor
<i>Drosophila</i>	180	13,338	Difficult	Yes	Fair
<i>Arabidopsis</i>	100	25,706	No	Yes	Poor
Mouse	2500	22,011	Yes	Yes	Good
Human*	2900	22,808	Yes*	Yes	Good

*cultured cells

Table 1 | Interaction networks in selected model organisms and in humans

Species	Network type*	Details	Refs
<i>Saccharomyces cerevisiae</i>	Y2H	~3,000 interactions; ~2,000 proteins	14
	AP-MS	~7,000 interactions; ~2,700 proteins	16
	AP-MS	~500 complexes; ~2,700 proteins	17
	Drug-gene	~6,000 genes; ~400 drugs or conditions	152
	Genetic	~5.4 million measured interactions; ~4,500 genes	40
<i>Schizosaccharomyces pombe</i>	Genetic	~1.6 million measured interactions; ~2,400 genes	38
	Drug-gene	~440 genes; 21 drugs or conditions	64
	Drug-gene	~2,500 genes; 6 drugs or conditions	153
<i>Caenorhabditis elegans</i>	Genetic	~65,000 measured interactions; ~162 genes	50
	Y2H	~3,800 interactions; ~2,600 proteins	154
<i>Drosophila melanogaster</i>	AP-MS	~550 complexes; ~5,000 proteins	155
	Y2H	~4,800 filtered interactions; ~4,700 proteins	156
	Genetic	~30,000 measured interactions; 93 genes	46
	Genetic	~17,000 measured interactions; ~500 genes	157
<i>Escherichia coli</i>	AP-MS	~6,000 interactions; ~1,800 proteins	158
	Genetic	~235,000 measured interactions; ~820 genes	39
	Drug-gene	~4,000 genes; 324 drugs or conditions	36
<i>Homo sapiens</i>	Fractionation-mass spectrometry	~14,000 interactions; ~3,000 proteins	159
	Y2H	~3,200 interactions; ~1,700 proteins	160
	Y2H	~2,800 interactions; ~1,500 proteins	161
	Drug-gene	70 genes; 87 drugs	145
	Genetic	878 validated interactions; 12 genes, each tested for interactions using genome-wide RNA interference	47
	Genetic	Pairwise genetic interactions among a set of 60 genes through double knockdown using RNA interference	45

AP-MS, affinity purification-mass spectrometry; Y2H, yeast two-hybrid. *In cases in which multiple networks of the same type were available for a single species, details of the largest network are provided. For cases in which no network was clearly larger, both networks are included.

quick search **GO**

advanced search

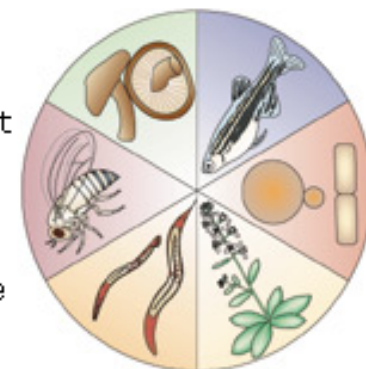


The Art and Design of Genetic Screens

A collection of reviews from *Nature Reviews Genetics*, continually updated. Select the links below for full-text access.

In this age of genomics, one could be forgiven for thinking that classical genetic screens are a thing of the past. But whereas genome projects provide us with an inventory of genes, genetic screens can provide important clues about what those genes do. When genetic screens are reported, the details of the screen itself are often overshadowed by the excitement surrounding the genes that are identified. But the way a screen is designed can profoundly influence which genes are uncovered, and the exquisite design of some genetic screens can inspire related experiments in other systems.

This Web Focus contains a series of articles that celebrates the art and design of genetic screens, which we will update with new articles over the next few months. These reviews are intended to provide an up-to-date account of genetic screening in the main genetic experimental systems. By highlighting recent genetic screens, these articles will illustrate the elegance and power of genetic screens, and the thinking that underlies them.



Genetic screens can provide the first hint about the molecular events that underpin a particular biological process. The results are sometimes exhilarating and sometimes mundane - but if the screen is any good, they are usually biologically meaningful. Either way, genetic screens have a certain mystique, and for the foreseeable future, they are here to stay.



Home

Analyze

Sequence

Function

Literature

Community

A budding *S. cerevisiae* cell imaged by X-ray tomography

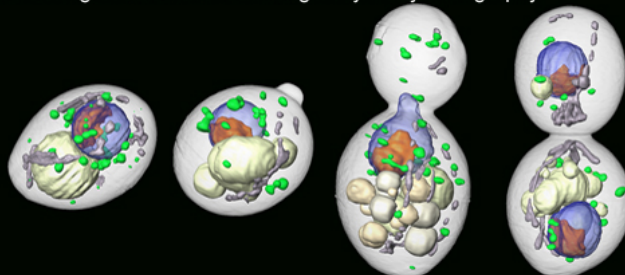


Image courtesy of Carolyn Larabell, Ph.D., University of California, San Francisco

About SGD

The *Saccharomyces* Genome Database (SGD) provides comprehensive integrated biological information for the budding yeast *Saccharomyces cerevisiae* along with search and analysis tools to explore these data, enabling the discovery of functional relationships between sequence and gene products in fungi and higher organisms.

Upcoming Meetings

Biocuration 2012 - The Conference of the International Society for Biocuration

April 2, 2012 - Washington, DC

Abstract submission now closed

10th Francophone Yeasts Meeting, Levures, Modèle et Outils-10

April 2, 2012 - University of Toulouse, France

Abstract deadline: February 8, 2012

General Meeting of the American Society for Microbiology

June 16, 2012 - San Francisco, CA

Abstract deadline: January 17, 2012

EMBO Conference 2012 on Gene Transcription in Yeast "From Mechanisms to Gene Regulatory Networks"

June 16, 2012 - St. Feliu de Guixols, Girona, Spain

Abstract deadline: March 16, 2012

Model Organisms to Human Biology: Cancer Genetics

June 17, 2012 - Omni Shoreham, Washington, DC

New & Noteworthy

Engineering Magnetic Yeast

03/02/2012

With a bit of genetic manipulation and a hearty diet of iron, Nishida and Silver report in the latest issue of PLOS Biology that they have caused yeast cells to become magnetic. And this isn't just a parlor trick. Their research could one day help other scientists create new therapies for the sick and new applications for research and industry. The first step in the process was to load the yeast up with magnetic...[read more >](#)

The latest in Yeast(Genome) technology!

02/23/2012

Sitting in seminar and need some ORF info fast? There's an app for that! SGD has developed the YeastGenome app for the iPhone, iPad, and iPod touch, and we want your input. A limited number of spots are available on a first-come, first-served basis. Sign up today to become a beta tester and be the envy of your lab! ...[read more >](#)

Symposium in remembrance of Jon Widom, 1955 - 2011

02/22/2012

As many of you know, Jonathan Widom died suddenly last summer. He was a Professor in the Department of Molecular Biosciences at Northwestern University. The beauty of Jon's scientific research was more than matched by his surpassing intellectual brilliance and personal warmth, and he is deeply missed by those who knew and loved him. Jon's family and colleagues have organized a symposium celebrating his life and work, which will be held at Northwestern's Evanston campus on March 16,...[read more >](#)

Finally Great Tasting, Low Alcohol Beer

02/17/2012

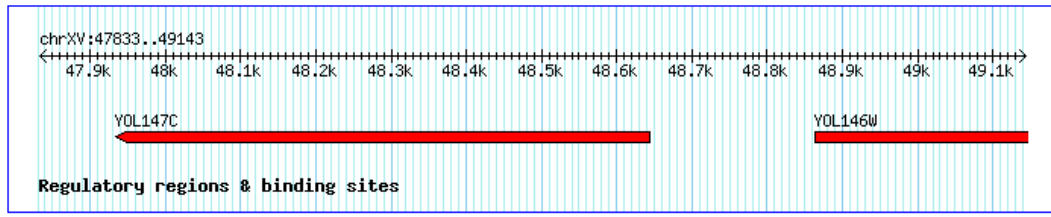
Let's face it: low alcohol beer just doesn't taste that great. This is because the alcohol is either diluted or removed chemically after fermentation. Both methods wreak havoc with a beer's flavor. Dr. John Morrissey of University College Cork is trying to change this. His lab is working to generate a strain of yeast that turns some but not all of its sugar into alcohol. That way the beer process is the same, just with less...[read more >](#)

PEX11/YOL147C Summary ?

- Summary
- Locus History
- Literature
- Gene Ontology
- Phenotype
- Interactions
- Expression
- Regulation
- Protein
- Wiki

Standard Name	<i>PEX11</i> ¹
Systematic Name	YOL147C
Alias	<i>PMP24</i> ² , <i>PMP27</i> ^{3, 4}
Feature Type	ORF, Verified
Description	Peroxisomal protein required for medium-chain fatty acid oxidation; also required for peroxisome proliferation, possibly by inducing membrane curvature; localization regulated by phosphorylation; transcription regulated by Adr1p and Pip2p-Oaf1p (3, 5, 6, 7, 8 and see Summary Paragraph)
Name Description	PEroXin 1

Chromosomal Location [ChrXV:48643 to 47933](#) | [ORF Map](#) | [GBrowse](#)
Note: this feature is encoded on the Crick strand.

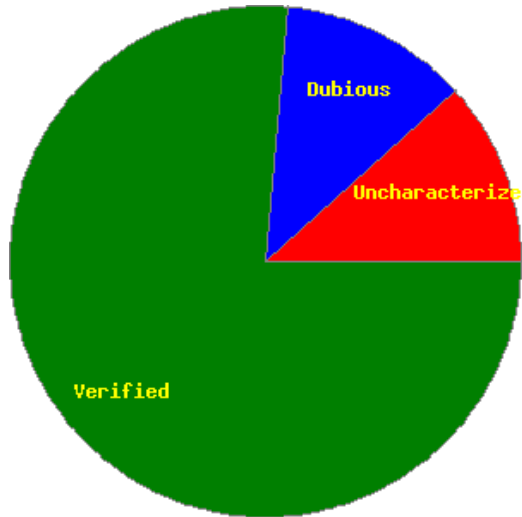


GENE ONTOLOGY ANNOTATIONS [All PEX11 GO evidence and references](#)

View Computational GO annotations for PEX11	
Molecular Function Manually curated	<ul style="list-style-type: none"> molecular_function unknown (ND [Ⓔ])
Biological Process Manually curated	<ul style="list-style-type: none"> fatty acid oxidation (IMP [Ⓔ]) peroxisome fission (IMP [Ⓔ])
Cellular Component Manually curated	<ul style="list-style-type: none"> endoplasmic reticulum (IDA [Ⓔ]) peroxisomal membrane (IDA [Ⓔ])

Genom kvasovke *Saccharomyces cerevisiae*

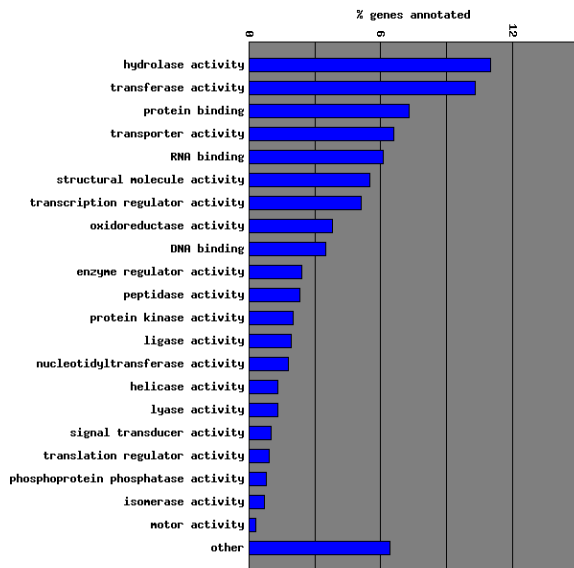
Science (1996) 274:546



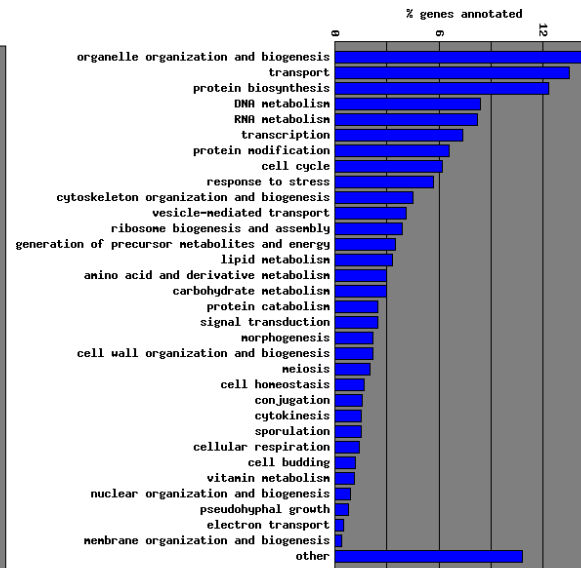
16 kromosomov, 12.2 Mbp, ~70% genoma = ORFs

5091 ORFs, 77,05% 786 ORFs, 11,90% 730 ORFs, 11,05%

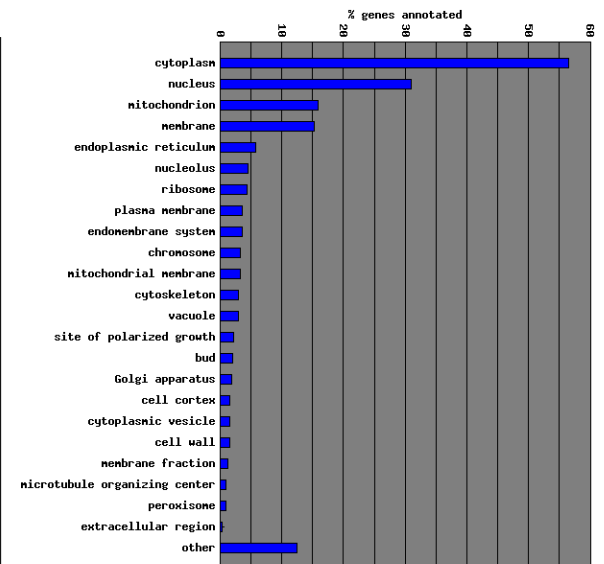
SGD Genome Snapshot, 12. marec 2014



GO Molecular Function

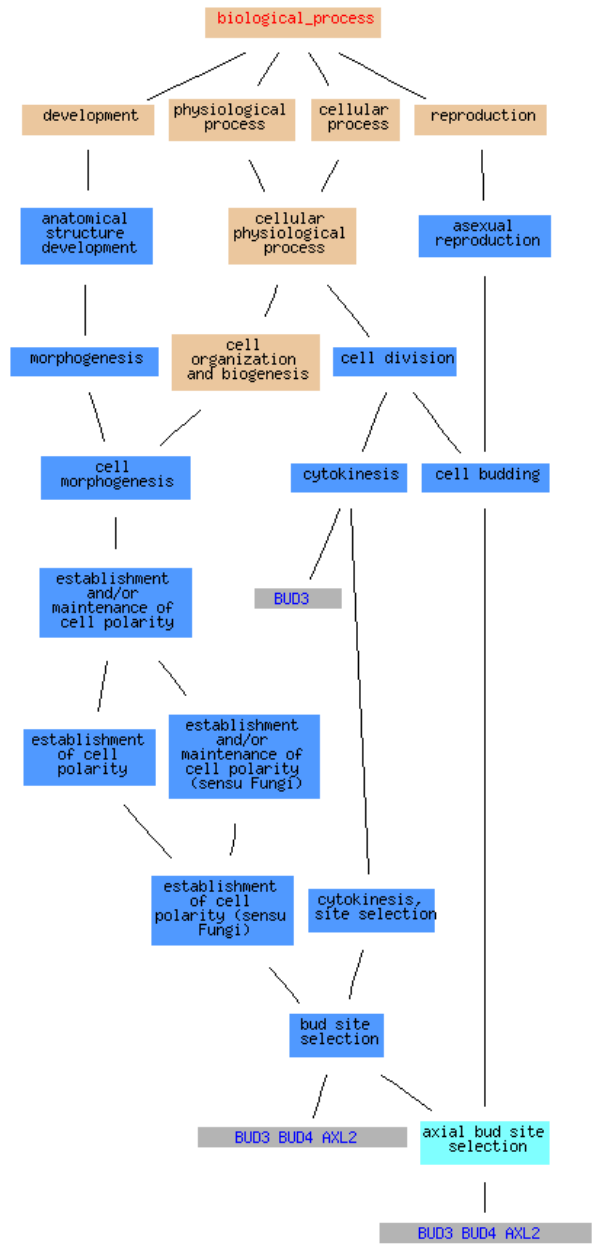


GO Biological Process

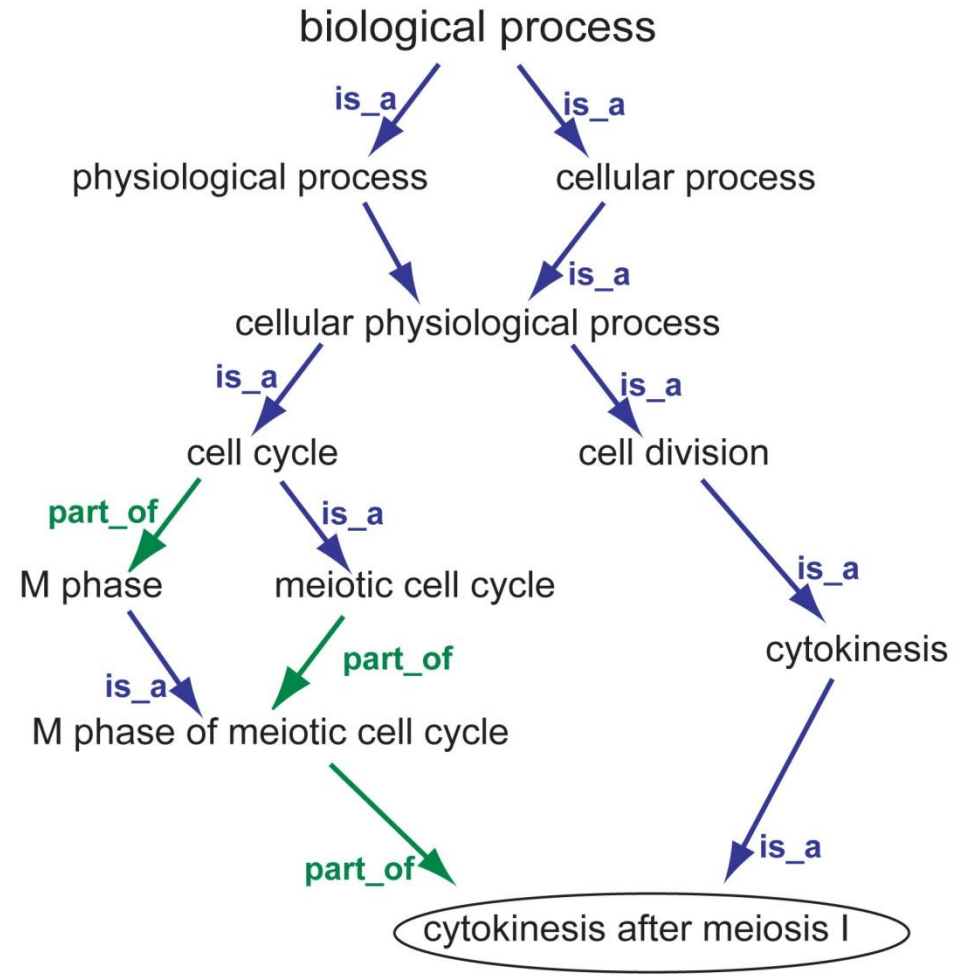


GO Cellular Localization

pvalue: <=1e-10 1e-10 to 1e-8 1e-8 to 1e-6 1e-6 to 1e-4 1e-4 to 1e-2 >0.01

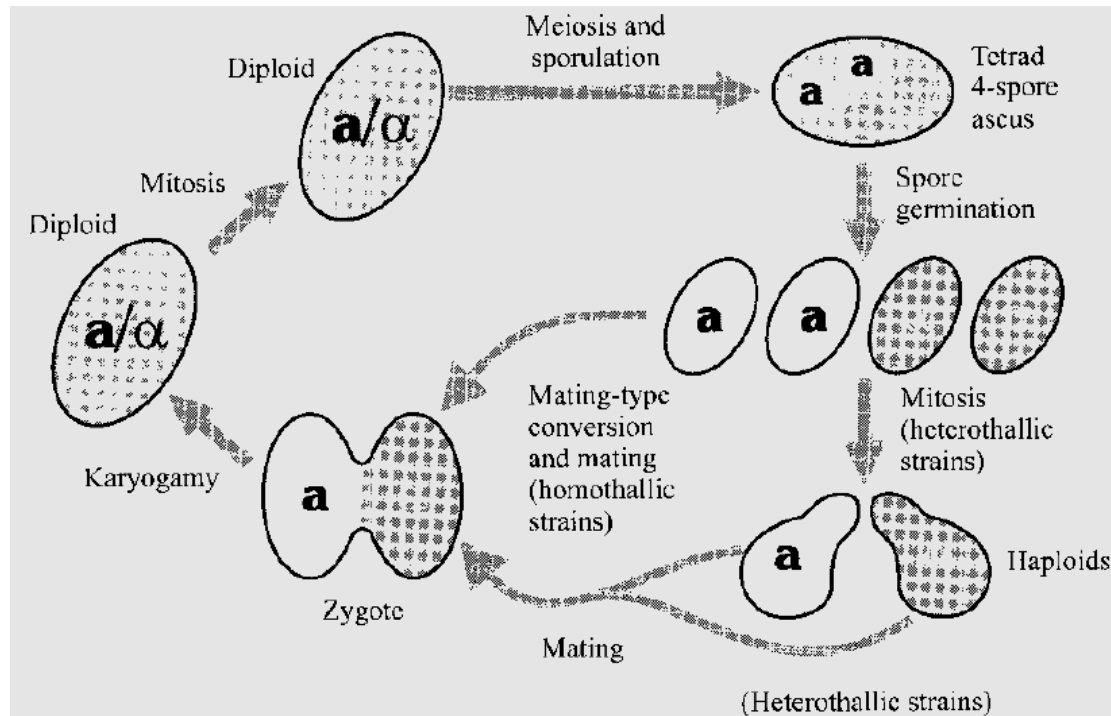


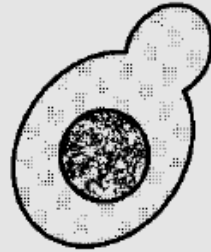
pvalue: <=1e-10 1e-10 to 1e-8 1e-8 to 1e-6 1e-6 to 1e-4 1e-4 to 1e-2 >0.01



Saccharomyces cerevisiae (budding yeast, baker's yeast, ...)

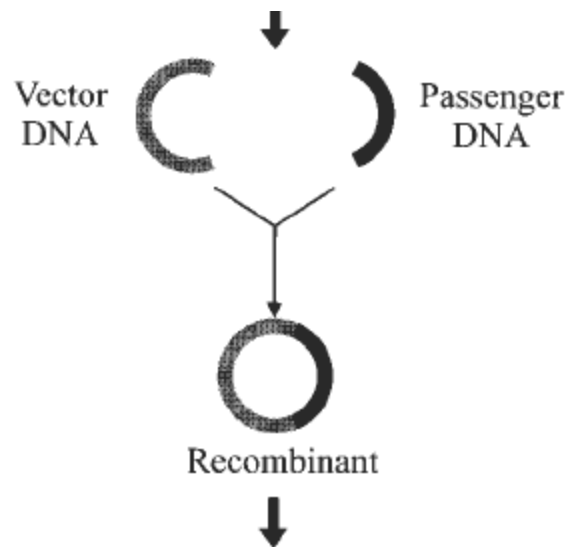
- enocelični evkariont (*Eukaryota*; *Fungi/Metazoa group*; *Fungi*; *Dikarya*; *Ascomycota*; *Saccharomycotina*; *Saccharomycetes*; *Saccharomycetales*; *Saccharomycetaceae*; *Saccharomyces*)
- uveljavljen modelni organizem (NL – celični cikel (Nurse, Hartwell, 2001), telomere (Blackburne, Szostak, 2009))
- GRAS
- posebnosti metabolizma (Crabtreejev efekt)





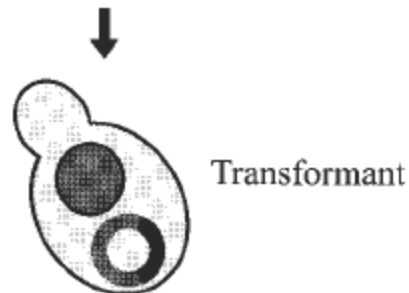
Vector DNA	Passenger DNA
Integrating plasmids YIp Yeast Integrative Plasmid Autonomously replicating plasmids YRp Yeast Replicating Plasmid YEpl Yeast Episomal Plasmid YCp Yeast Centromeric Plasmid	DNA-fragments containing target gene Genomic fragment cDNA fragment PCR fragment Chemically synthesized fragment
Specialized plasmids YLp Yeast Linear Plasmid YAC Yeast Artificial Chromosome YXp Yeast Expression Plasmid YDp Yeast Disintegration Plasmid	Selectable genetic markers Recessive markers <i>HIS3, LEU2, LYS2, TRP1, URA3, ADE2</i> Dominant markers <i>CUP1, SFA1, SMR1</i> Resistance to geneticin G418, hygromycin, methotrexate, chloramfenicol, diuron, canavanine, zeocin





Transformation Strategies

- Spheroplasts*** Cell walls are digested with lytic enzymes, PEG added, brief heat shock and regeneration
- Chemical*** Cells are permeabilized with lithium salts (e.g. acetate), DNA and PEG added and cells briefly heat shocked
- Electrical*** Cells and DNA are electrically pulsed in an electroporation device
- Biolistic*** DNA-coated tungsten microprojectile particles are propelled in a 'gene gun' at high speed into the cell



Druge vrste kvasovk

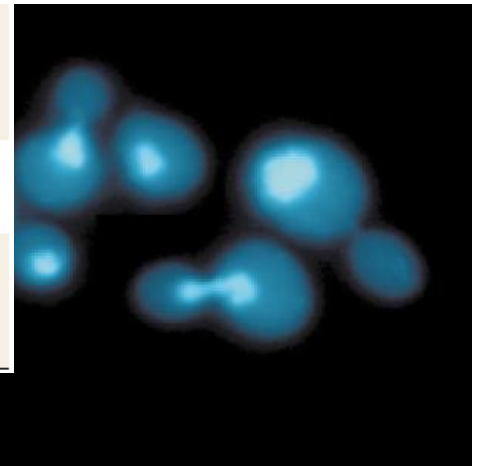
Table 1 | **Nomenclature in the two yeast species**

	<i>S. cerevisiae</i>	<i>S. pombe</i>
Wild-type gene	<i>YFG1</i>	<i>yfg1⁺</i>
Deletion (null) mutant	$\Delta yfg1$ <i>yfg1</i> Δ	$\Delta yfg1$ <i>yfg1</i> Δ
Recessive mutant	<i>yfg1-1</i>	<i>yfg1-1</i>
Dominant mutant	<i>YFG1-2</i>	<i>yfg1-2</i>
Protein	Yfg1 YFG1p	Yfg1 yfg1p

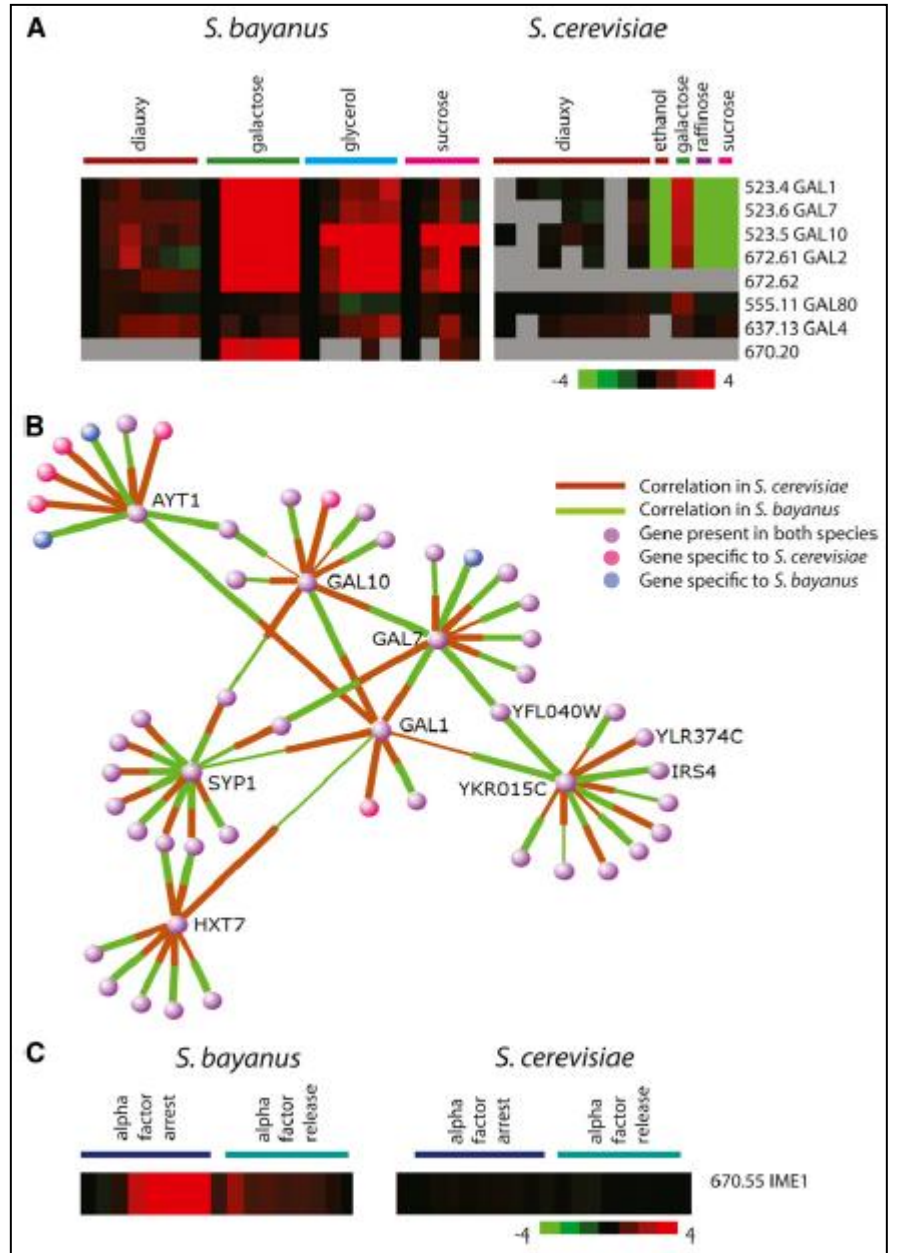
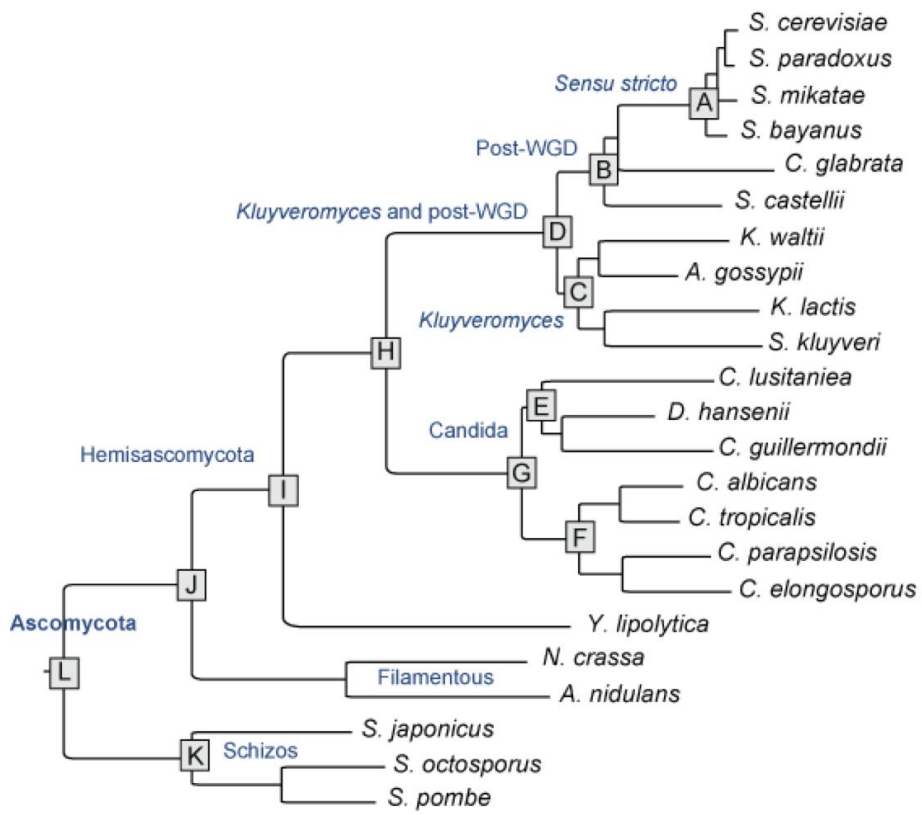
Table 2 | **Corresponding tools in the two yeast species**

	<i>S. cerevisiae</i>	<i>S. pombe</i>
Regulated promoter	<i>GAL</i> (galactose regulated)	<i>nmt</i> (thiamine regulated)
Plasmid replication origins	<i>ARS1</i> or 2 μ	<i>ars1</i>
Auxotrophic markers		
Uracil, orotidine 5'-phosphate decarboxylase Select against with 5-FOA	<i>URA3</i>	<i>ura4⁺</i>
Leucine, β -isopropylmalate dehydrogenase	<i>LEU2</i>	<i>leu1⁺</i>
Adenine, phosphoribosyl-aminoimidazole carboxylase Accumulates red colour	<i>ADE2</i>	<i>ade6⁺</i>

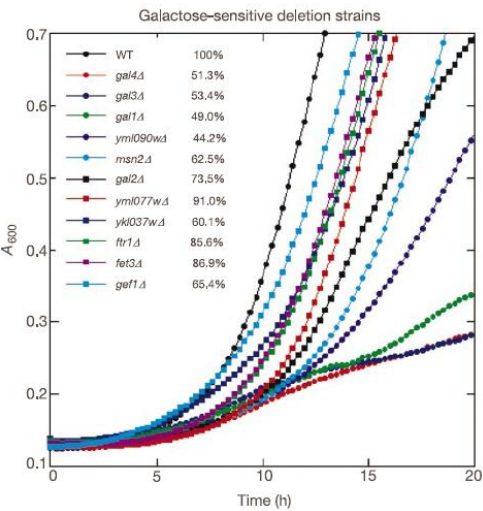
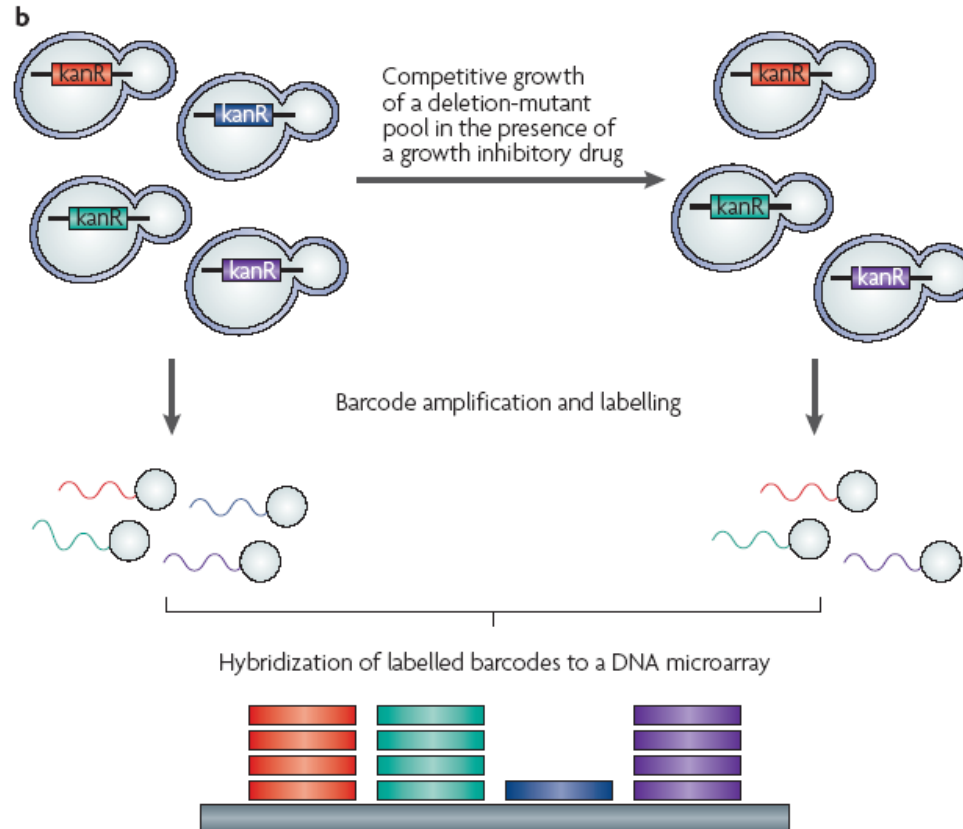
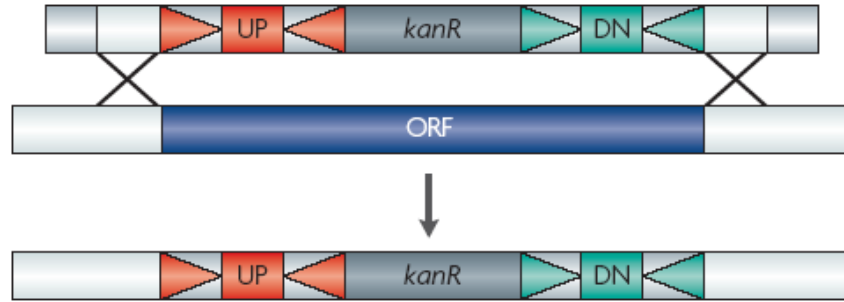
Saccharomyces cerevisiae

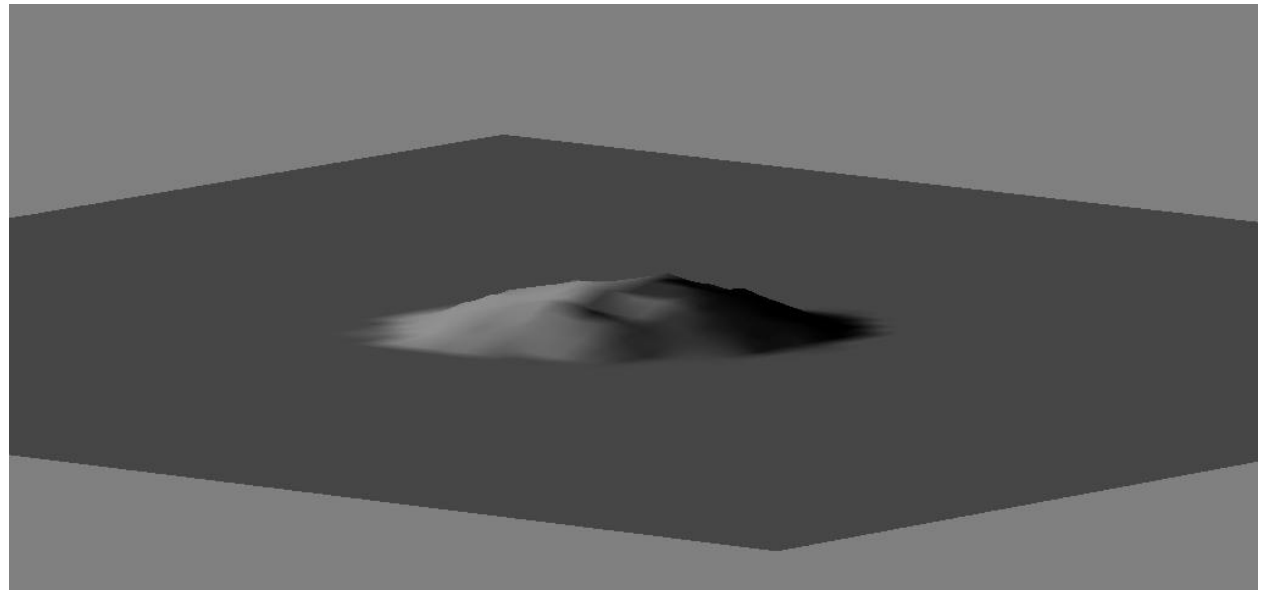
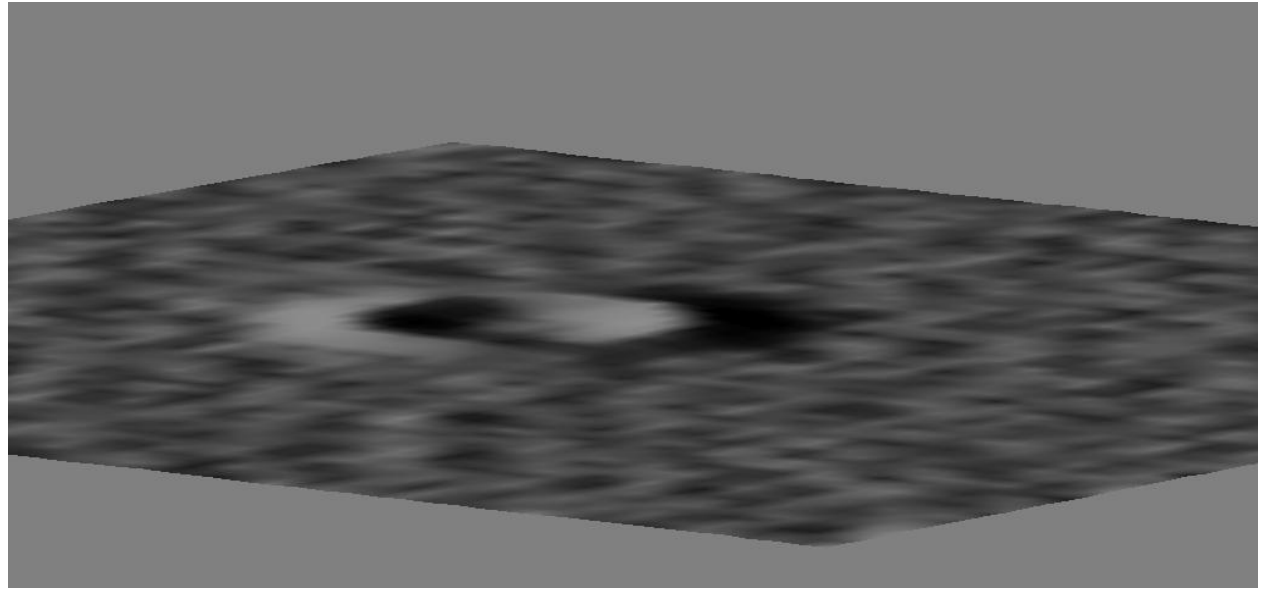
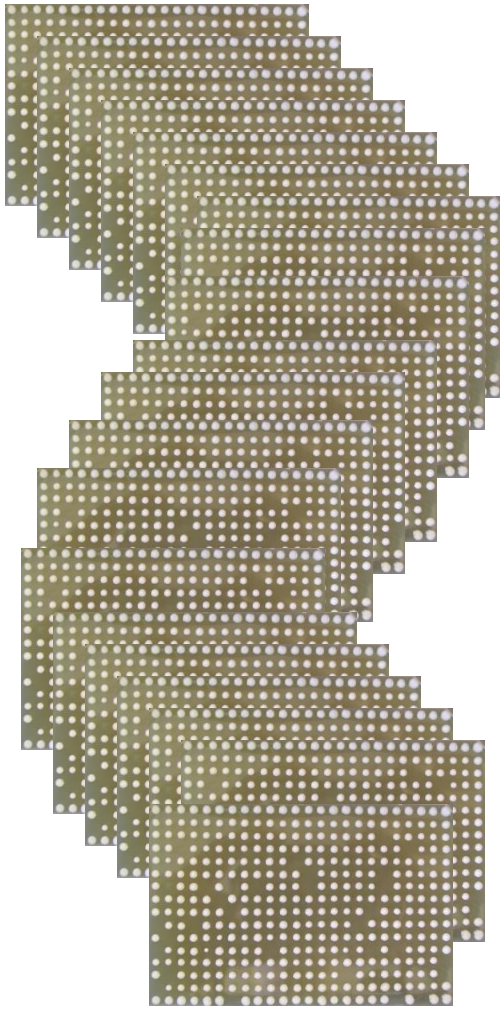


Schizosaccharomyces pombe (fission yeast)

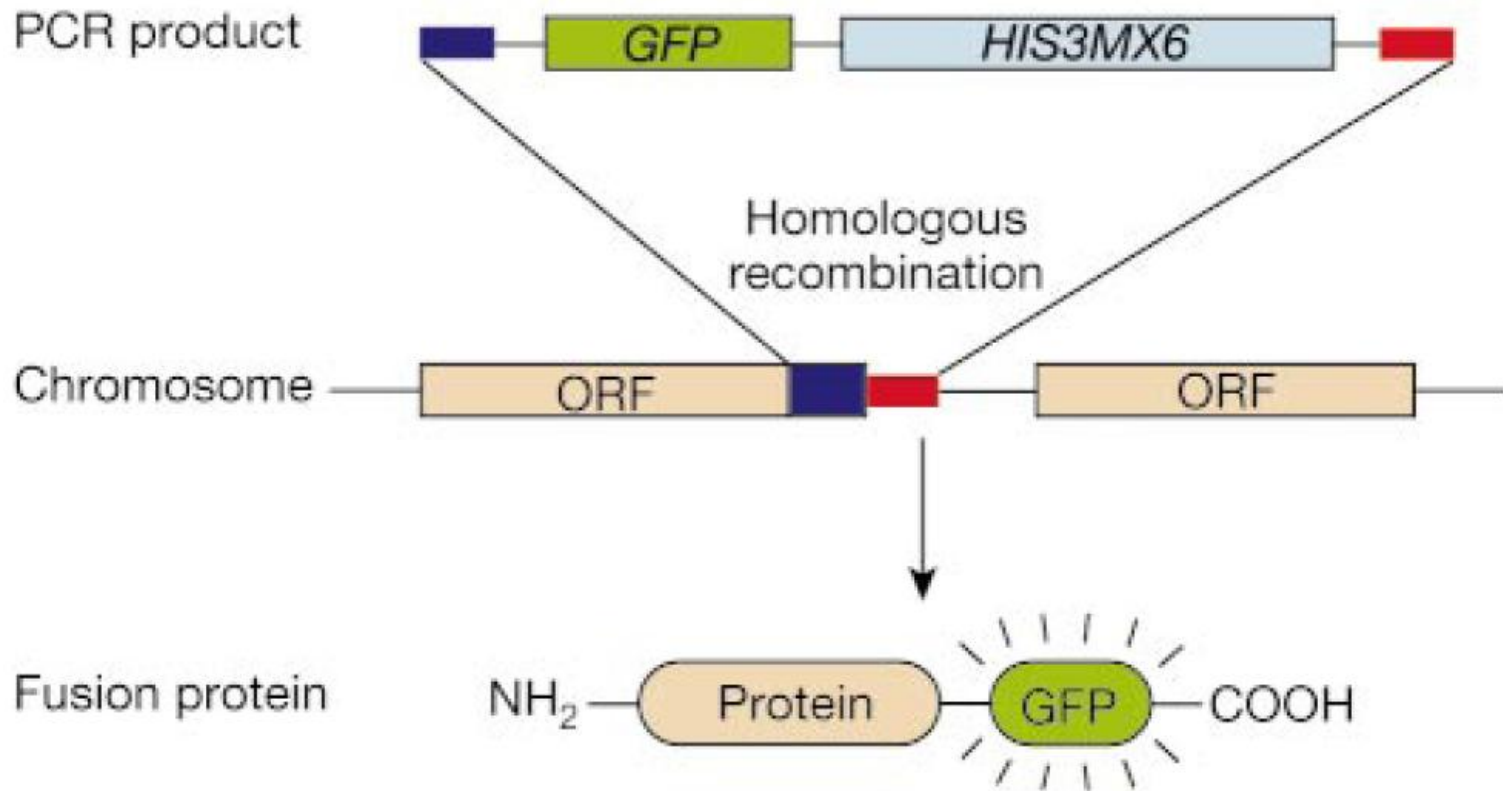


Delecijski projekt na genomski ravni (‘forward’ : ‘reverse’ genetika)

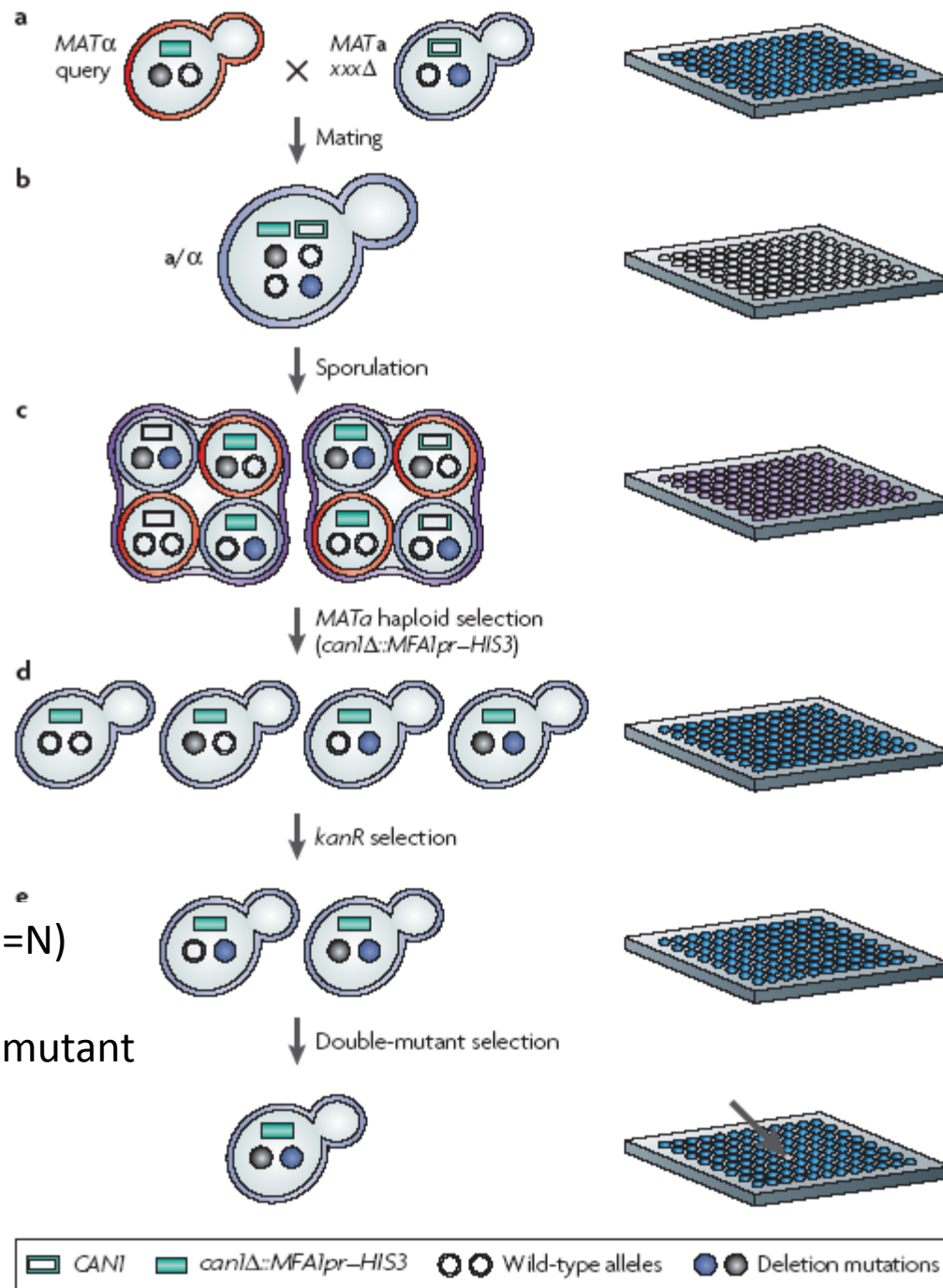




Sistematično označevanje proteoma



**SGA –
synthetic
genetic array
analysis**



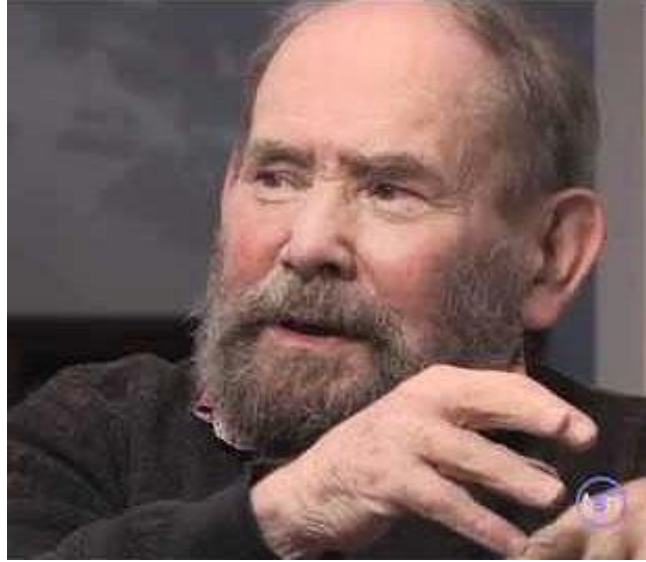
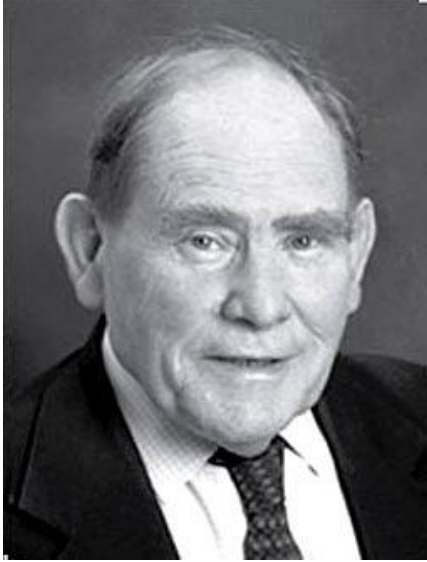
S. cerevisiae: 5800 genov (=N)

Število dvojnih delecijских mutant
($N \times (N-1) / 2$): $1,68 \times 10^7$

Caenorhabditis elegans



Sydney Brenner

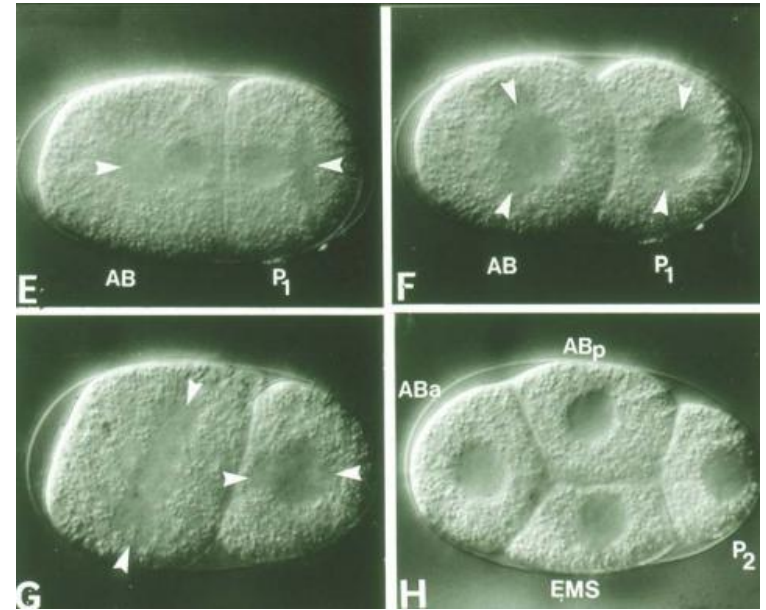
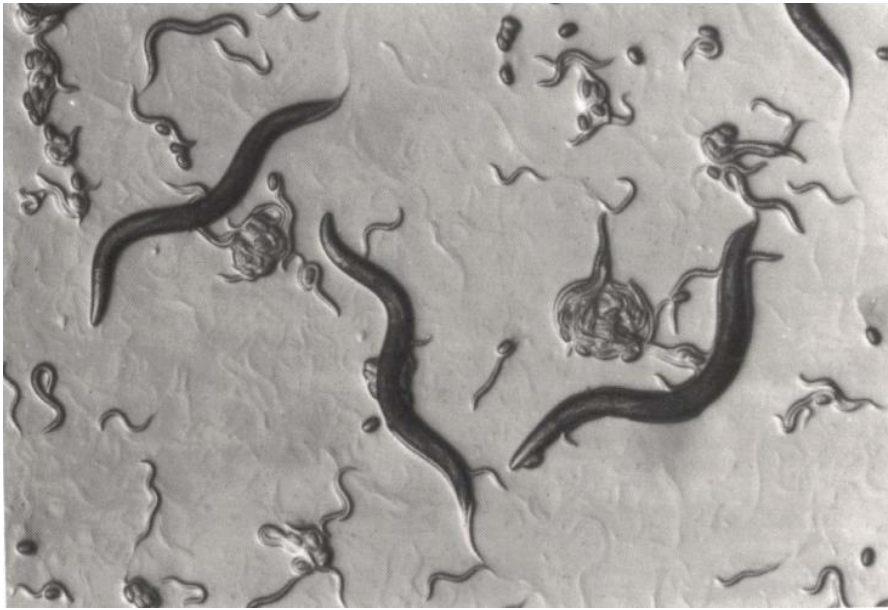


NL – razvoj organov in programirana celična smrt (Brenner, Horvitz, Sulston, 2002),
RNA interferenca (Fire, Mello, 2006), GFP (Chalfie, 2008)



- večcelični organizem: *Eukaryota*; *Fungi/Metazoa group*; *Metazoa*; *Eumetazoa*; *Bilateria*; *Pseudocoelomata*; *Nematoda*; *Chromadorea*; *Rhabditida*; *Rhabditoidea*; *Rhabditidae*; *Peloderinae*; *Caenorhabditis*
- 959 somatskih jeder (1031 pri samcih), od tega 302 nevrona
- ~20.000 genov, 36% ima človeške homologe
- znan 'fate map'
- možnost zamrznitve kultur
- nekateri kompleksnejši fenotipi, npr. odvisnos

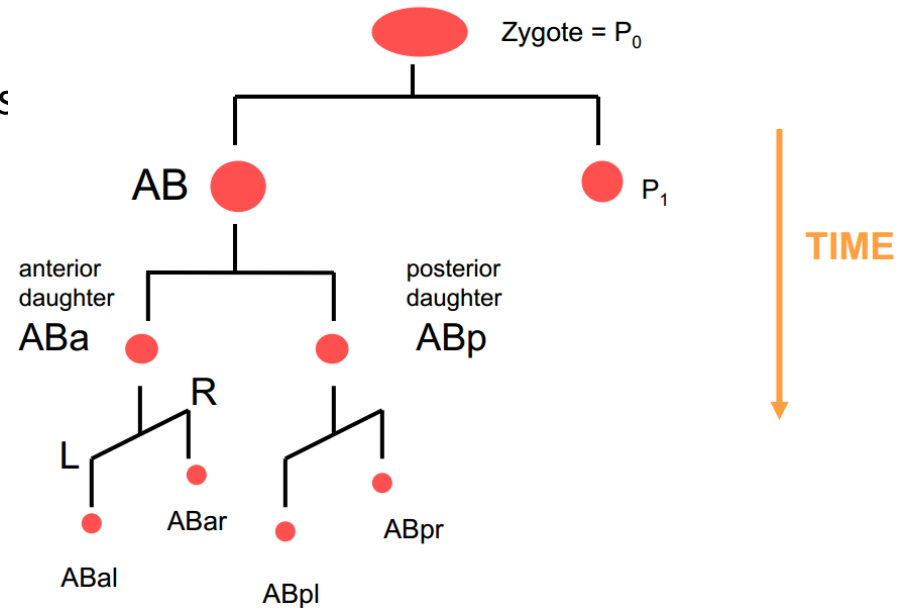




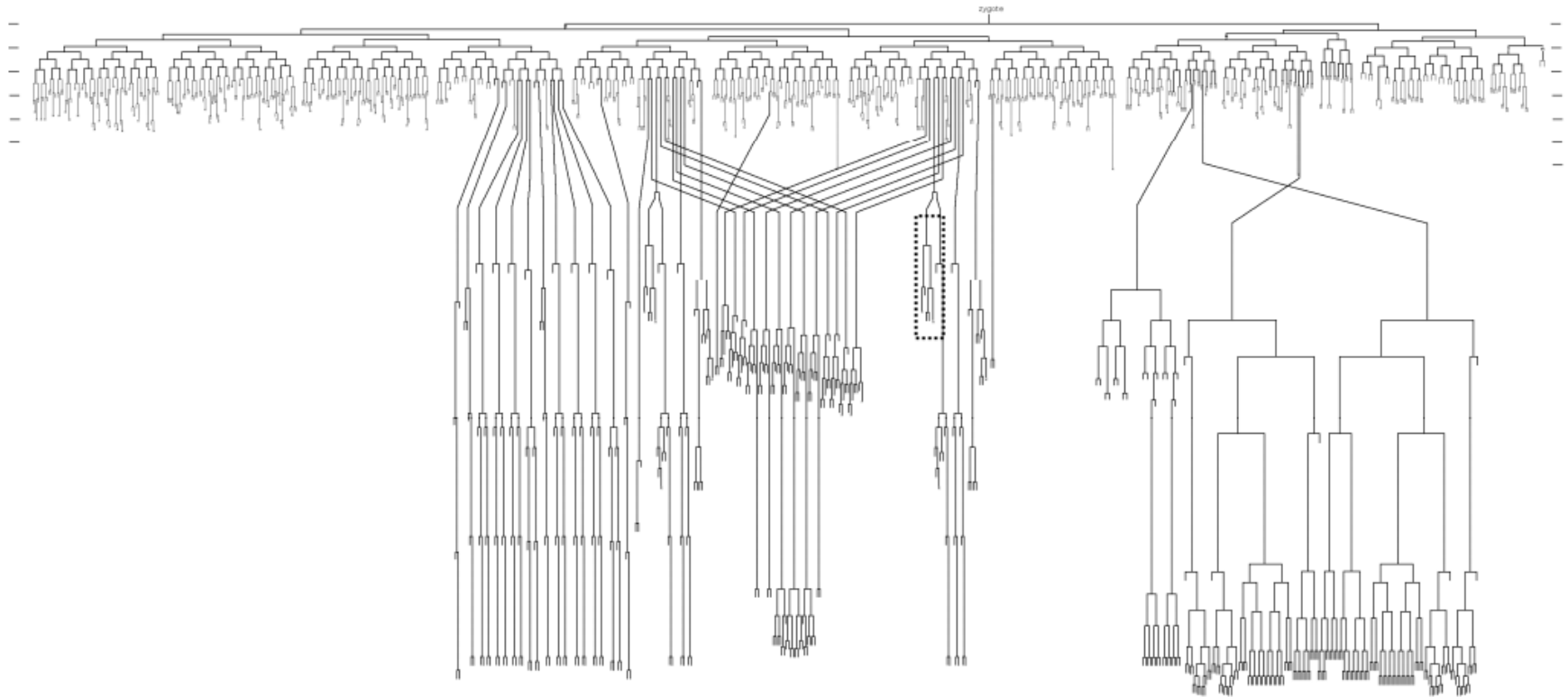
Ocena 1: nematodi predstavljajo 80% vseh živals
(‘drugih’ 80% predstvaljajo žuželke...)

Ocena 2: nematodi predstavljajo 80% vseh živals

Cell lineage diagrams

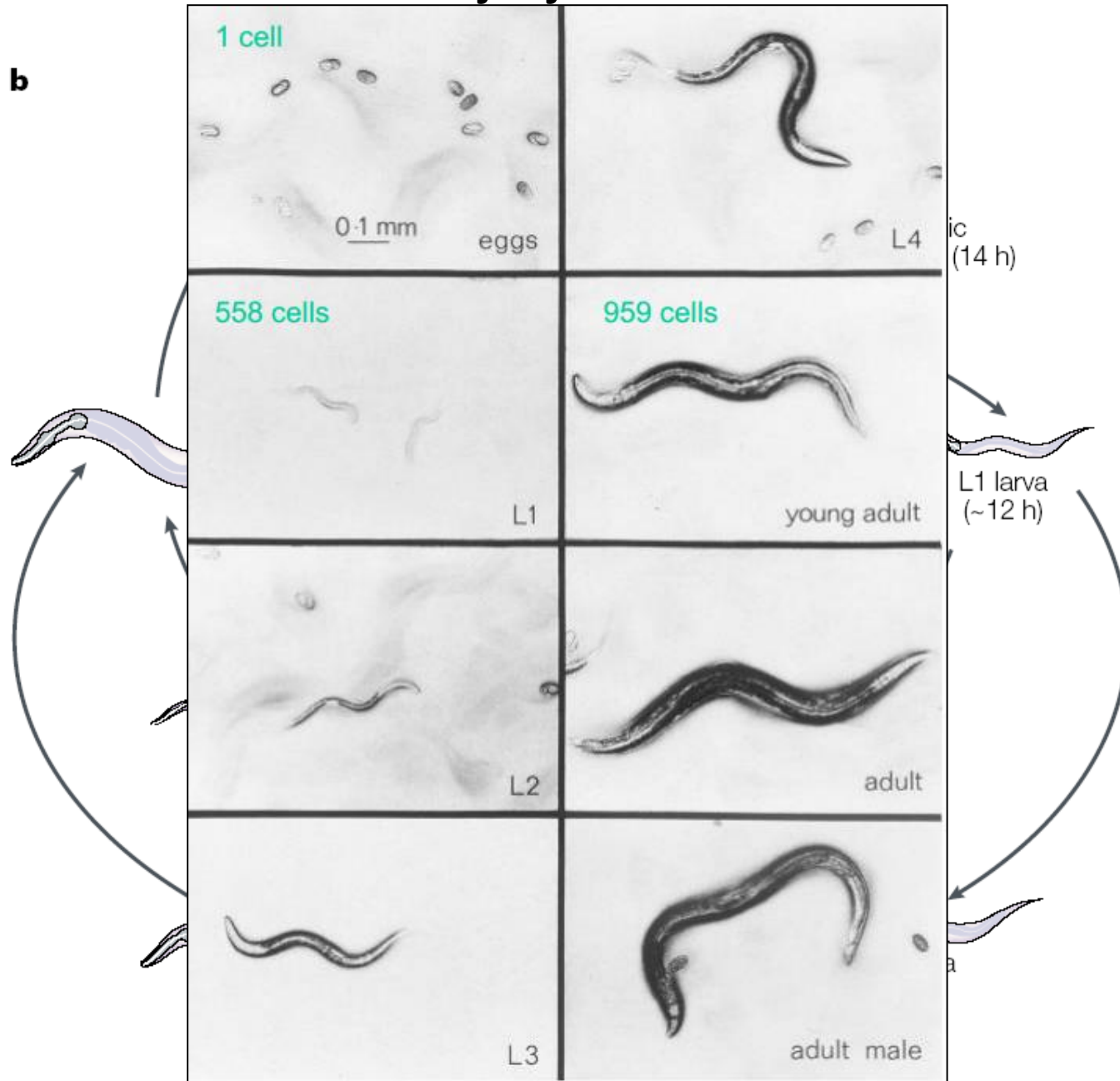


Izvor ('pokolenje') vseh celic v telesu *C. elegans*

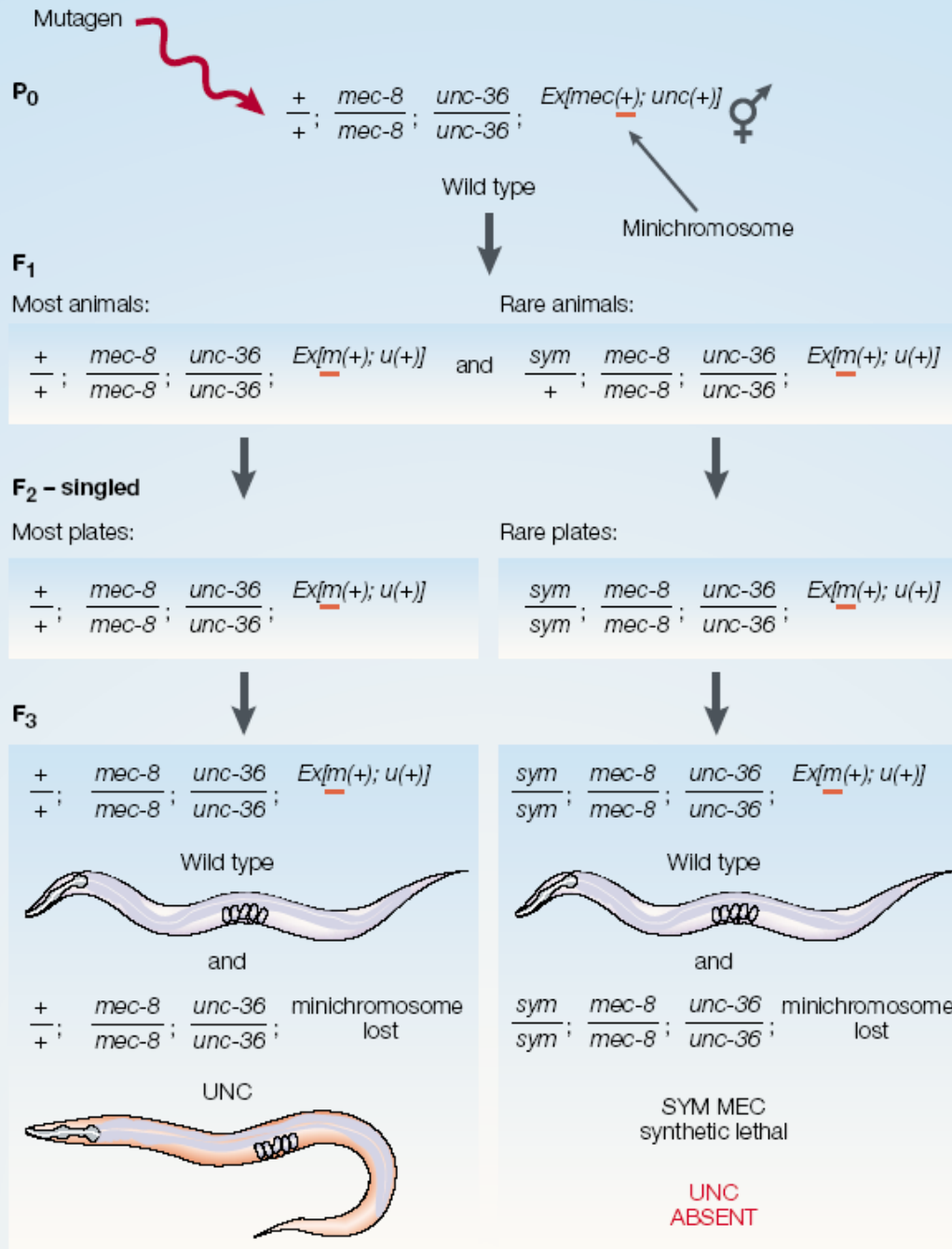


Življenjski cikel

b



Test sintetske letalnosti



Utišanje genov pri metazojih

C. elegans



Long
>150 bp
dsRNA

Drosophila

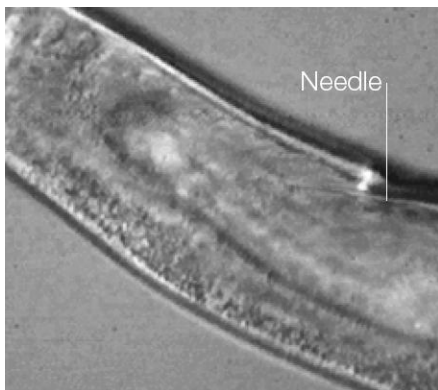
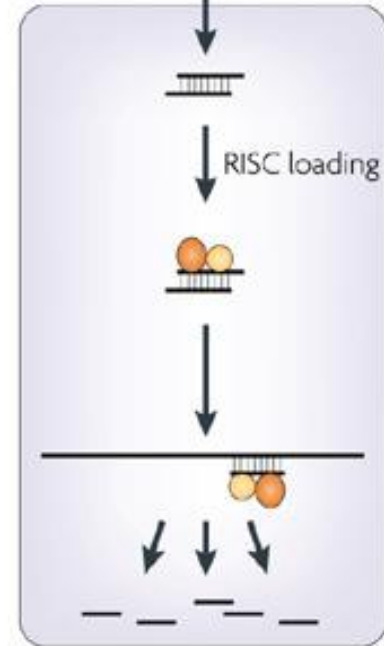
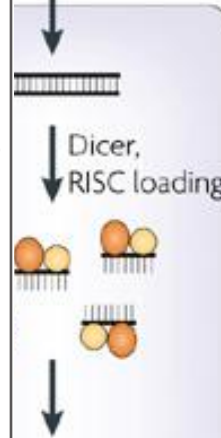
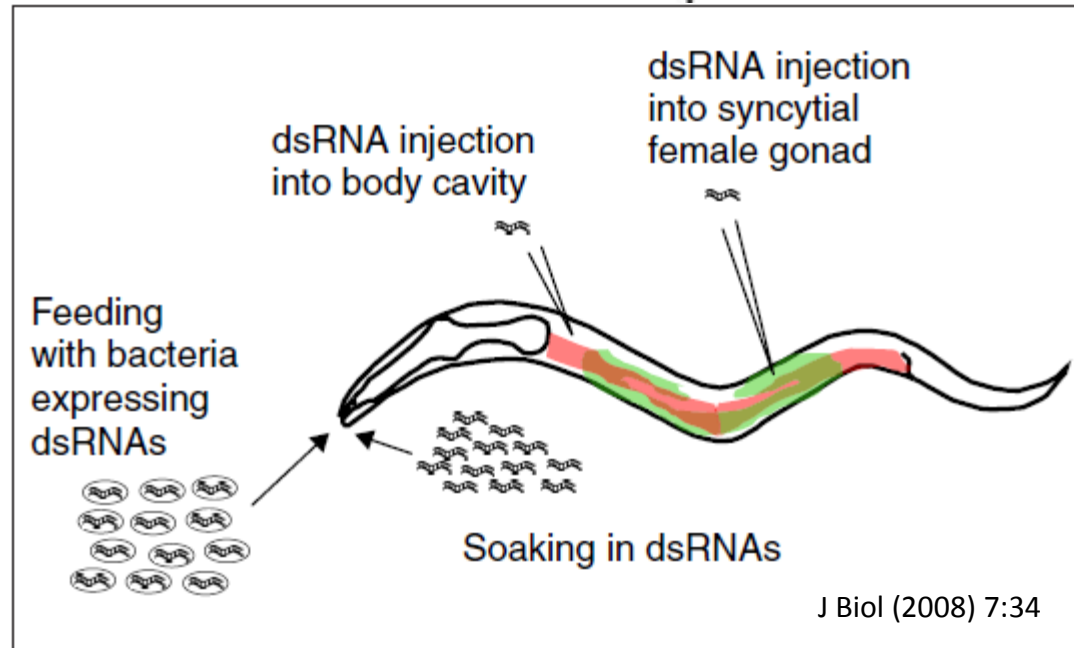
Long dsRNA
>100 bp

Bathing

Humans

siRNA
21 bp

Transfection

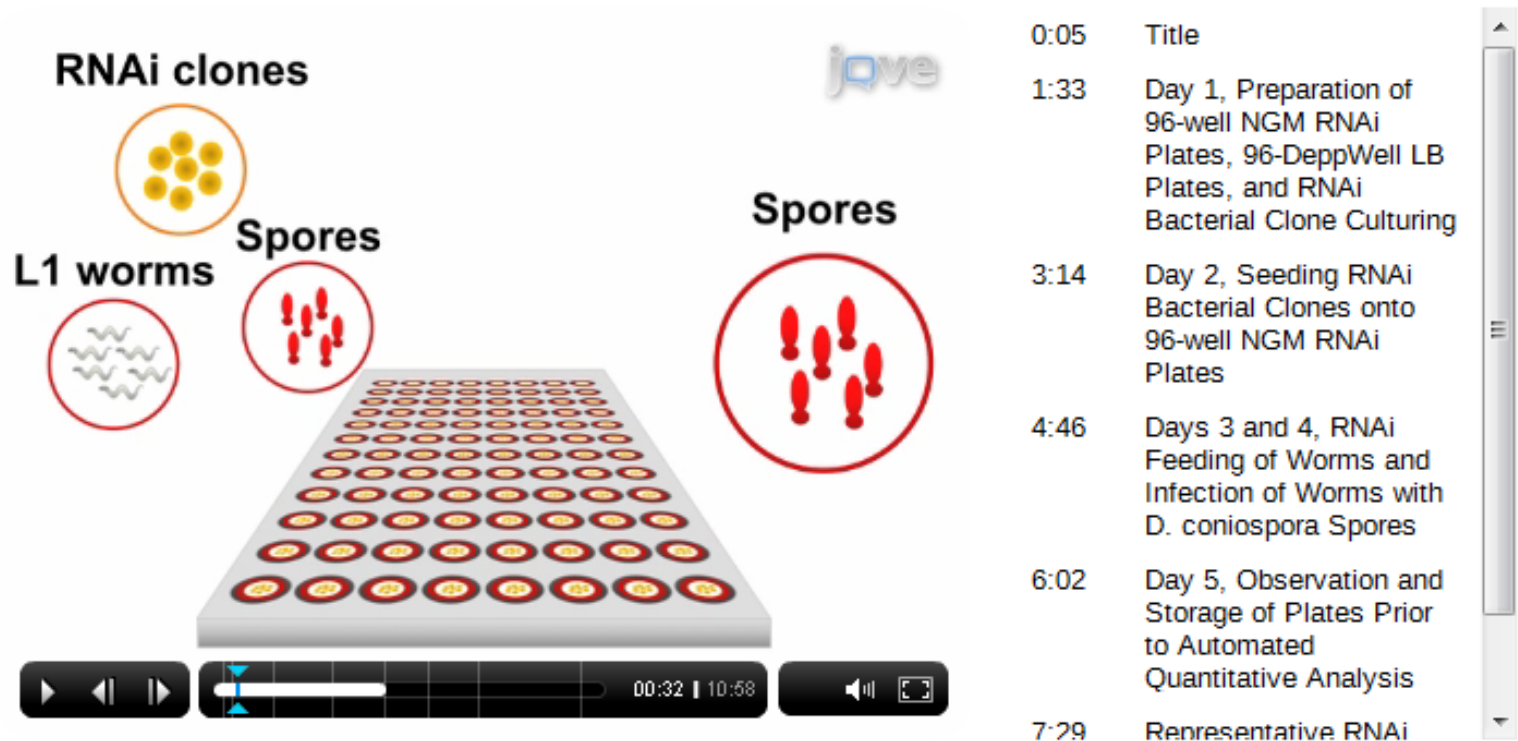


Domaća naloga

Quantitative and Automated High-throughput Genome-wide RNAi Screens in *C. elegans*

Barbara Squiban, Jérôme Belougne, Jonathan Ewbank, Olivier Zugasti

Centre d'Immunologie de Marseille-Luminy, Université de la Méditerranée



0:05 Title

1:33 Day 1, Preparation of 96-well NGM RNAi Plates, 96-DeppWell LB Plates, and RNAi Bacterial Clone Culturing

3:14 Day 2, Seeding RNAi Bacterial Clones onto 96-well NGM RNAi Plates

4:46 Days 3 and 4, RNAi Feeding of Worms and Infection of Worms with *D. coniospora* Spores

6:02 Day 5, Observation and Storage of Plates Prior to Automated Quantitative Analysis

7:29 Representative RNAi



HTML



Preprints


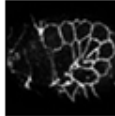
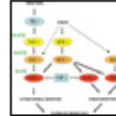
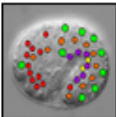
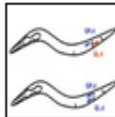

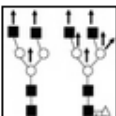
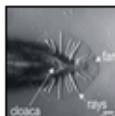

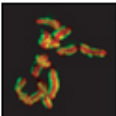

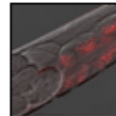


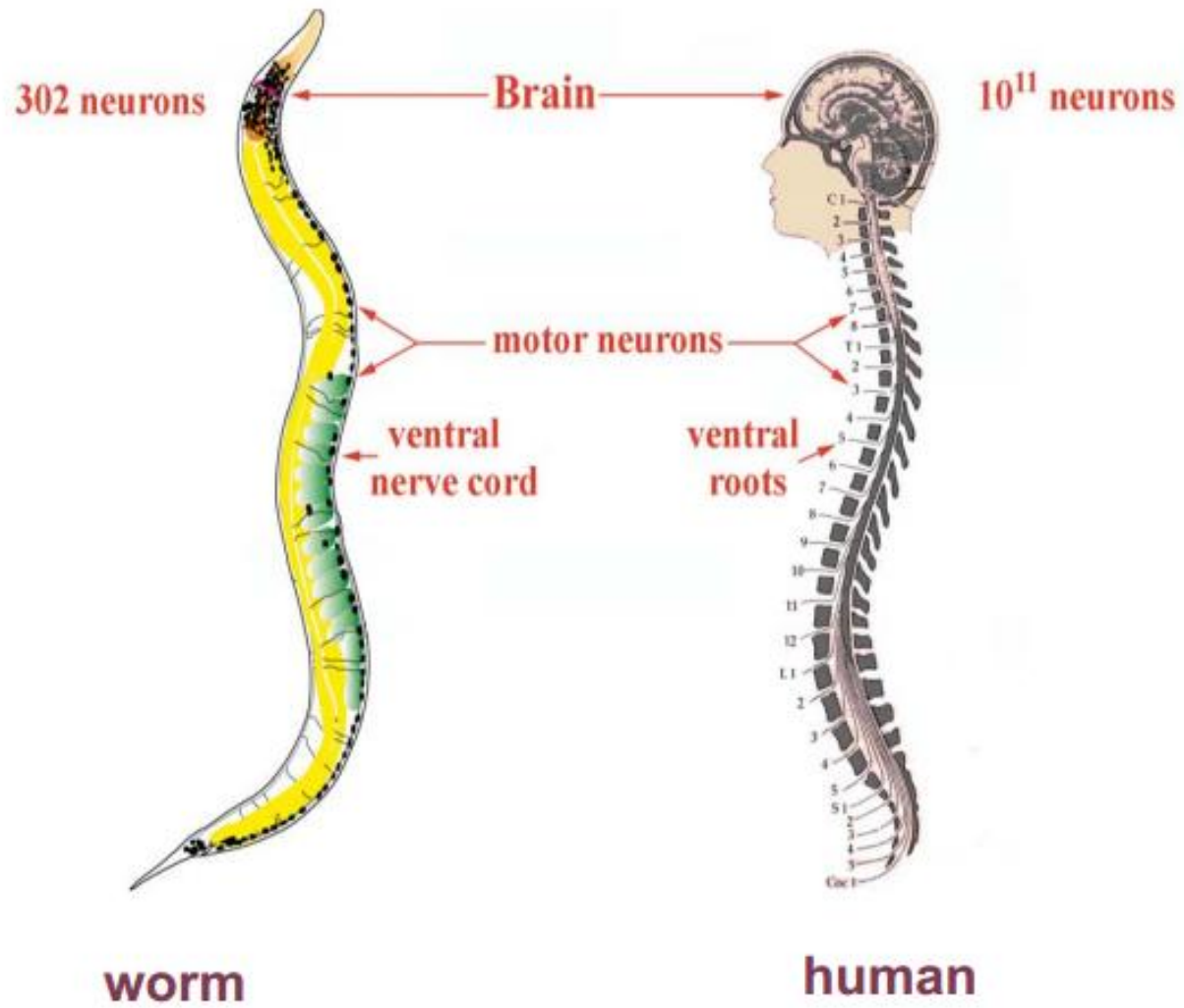
PDF

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C. elegans

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 Cell biology	 The germ line	 Disease models and drug discovery



Drosophila melanogaster: študij po primeru

Sexual Deprivation Increases Ethanol Intake in *Drosophila*

G. Shohat-Ophir,^{1,2*} K. R. Kaun,^{1,2} R. Azanchi,^{1,2} U. Heberlein^{1,2*}

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