

DNA

Sequenzen

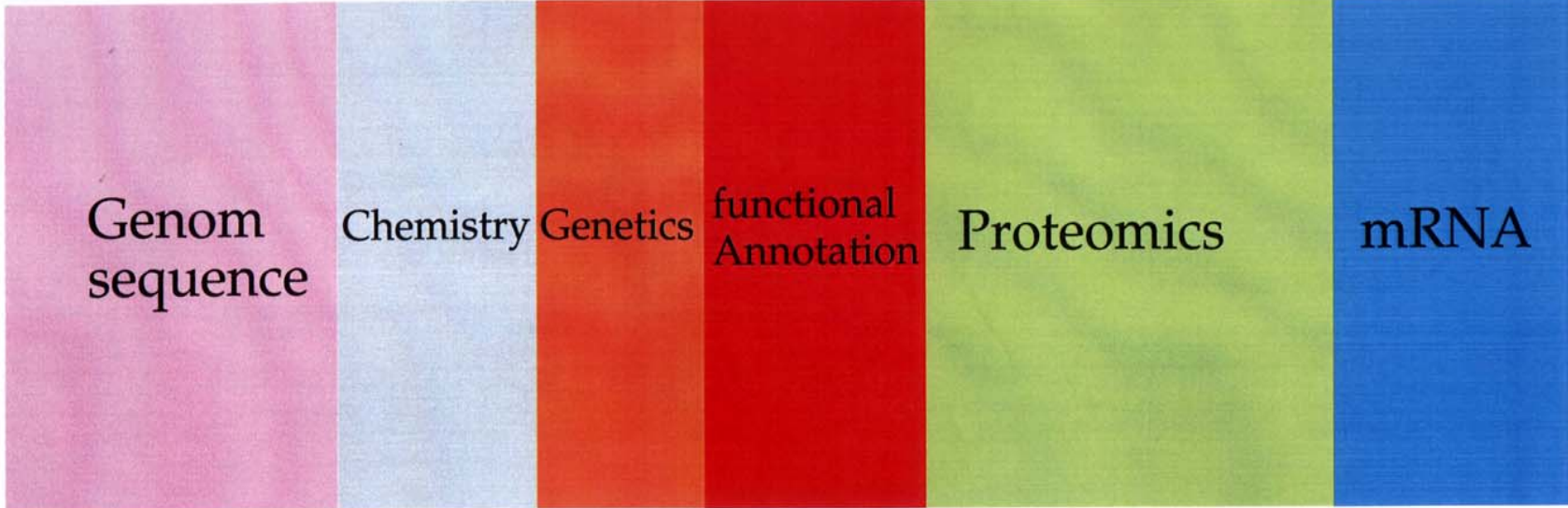
Proteine, RNA

Strukturen

Vorhersage, Interaktionen

Netzwerke

regulatorische, metabolische



Gene ID	Gene Name	Accession	Start	End	Protein	Function	Category	Count 1	Count 2	Count 3
545 0	G791_e02748	130261	132515	2182517	6 60	ruap	ruap, BACSU	799	598	0
547 0	G791_e02715	130268	130261	7425485	7 54	mb	mb, BACS F	147	970	0
						ruapF	ruapF	400	400	1 803
						ipO	ipO	579	997	0 1 0
						ipB	ipB	744	570	994
								1 908	1095	945
								1 992	099	0

- Listerien
- Blochmannien
- Arabidopsis
- Mensch
- Maus

Example:  
*Mycoplasma pneumoniae*



# Genematcher II

18.000 ASICS

32 CPU cluster

(post-processing)

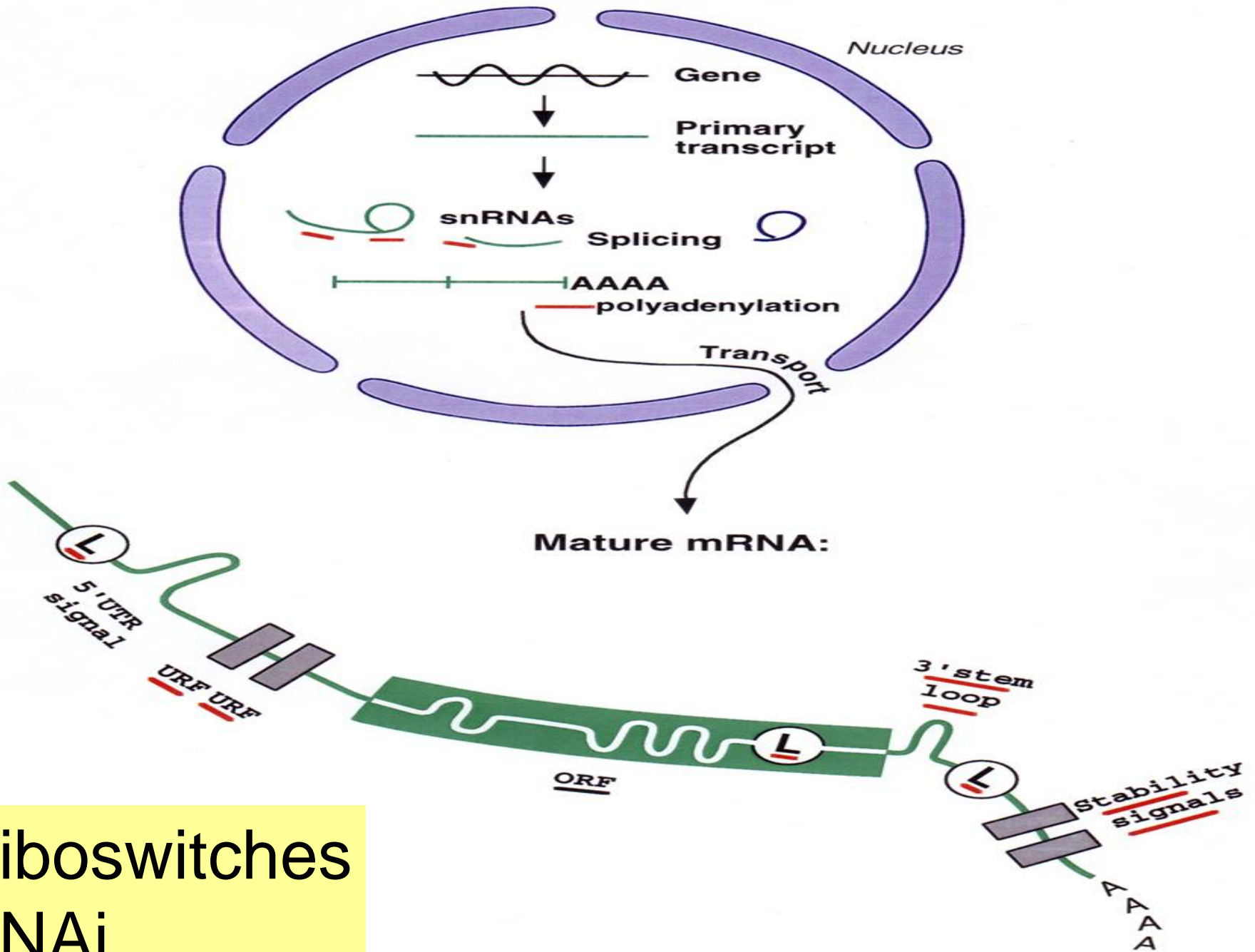
sehr schnelle

Genomvergleiche

Pathogenomik

EST-Daten

SMART



Riboswitches  
RNAi

# Komparative Genomik: Annotierung von Proteindomänen



## AnDom Annotation of domains

Schmidt *et al.*, 2002

[Usage](#)  
[Example](#)  
[New Search](#)

### Color Code

SCOP-Class

- 1 all alpha
- 2 all beta
- 3 alpha + beta
- 4 alpha / beta
- 5 multidomain
- 6 membrane / cell surface
- 7 small proteins



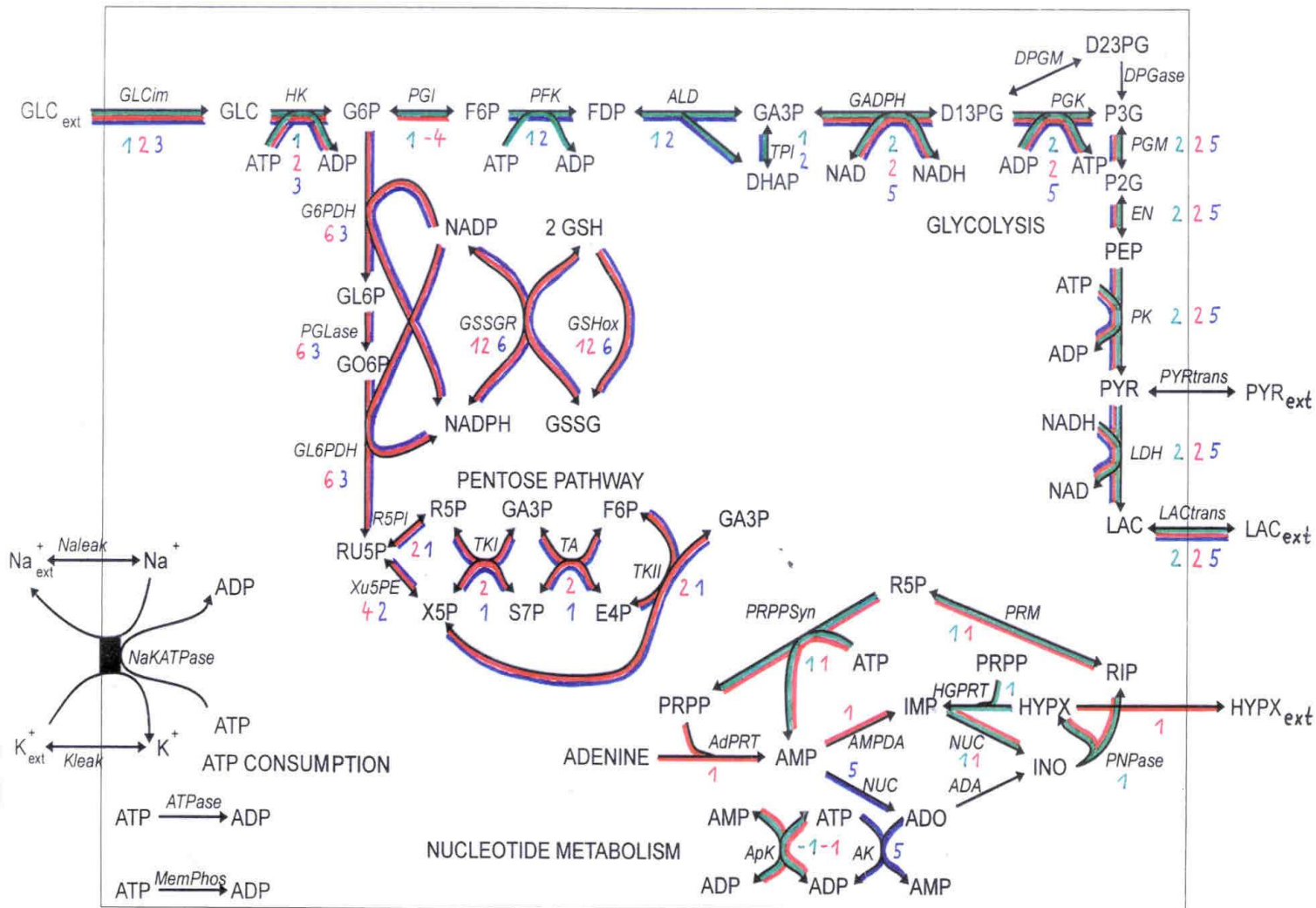
Sequences producing significant alignments:

PDB	SCOP		Score (bits)	E Value
<a href="#">d1e0ta2</a>	<a href="#">c.1.12.1</a>	(A:1-69,A:168-344) Pyruvate kinase, N-terminal ...		<a href="#">257</a>
<a href="#">d1dxea</a>	<a href="#">c.1.12.5</a>	(A:) 2-dehydro-3-deoxy-galactarate aldolase (Es...		<a href="#">109</a>
<a href="#">d1e0ta1</a>	<a href="#">b.58.1.1</a>	(A:70-167) Pyruvate kinase (PK) (Escherichia coli)		<a href="#">94</a>
<a href="#">d1a49a1</a>	<a href="#">b.58.1.1</a>	(A:116-217) Pyruvate kinase (PK) (Rabbit (Oryct...		<a href="#">94</a>
<a href="#">d1pk1a1</a>	<a href="#">b.58.1.1</a>	(A:88-186) Pyruvate kinase (PK) (Leishmania mex...		<a href="#">92</a>
<a href="#">d1e0ta3</a>	<a href="#">c.49.1.1</a>	(A:354-470) Pyruvate kinase, C-terminal domain ...		<a href="#">92</a>

[Comments &  
suggestions](#)

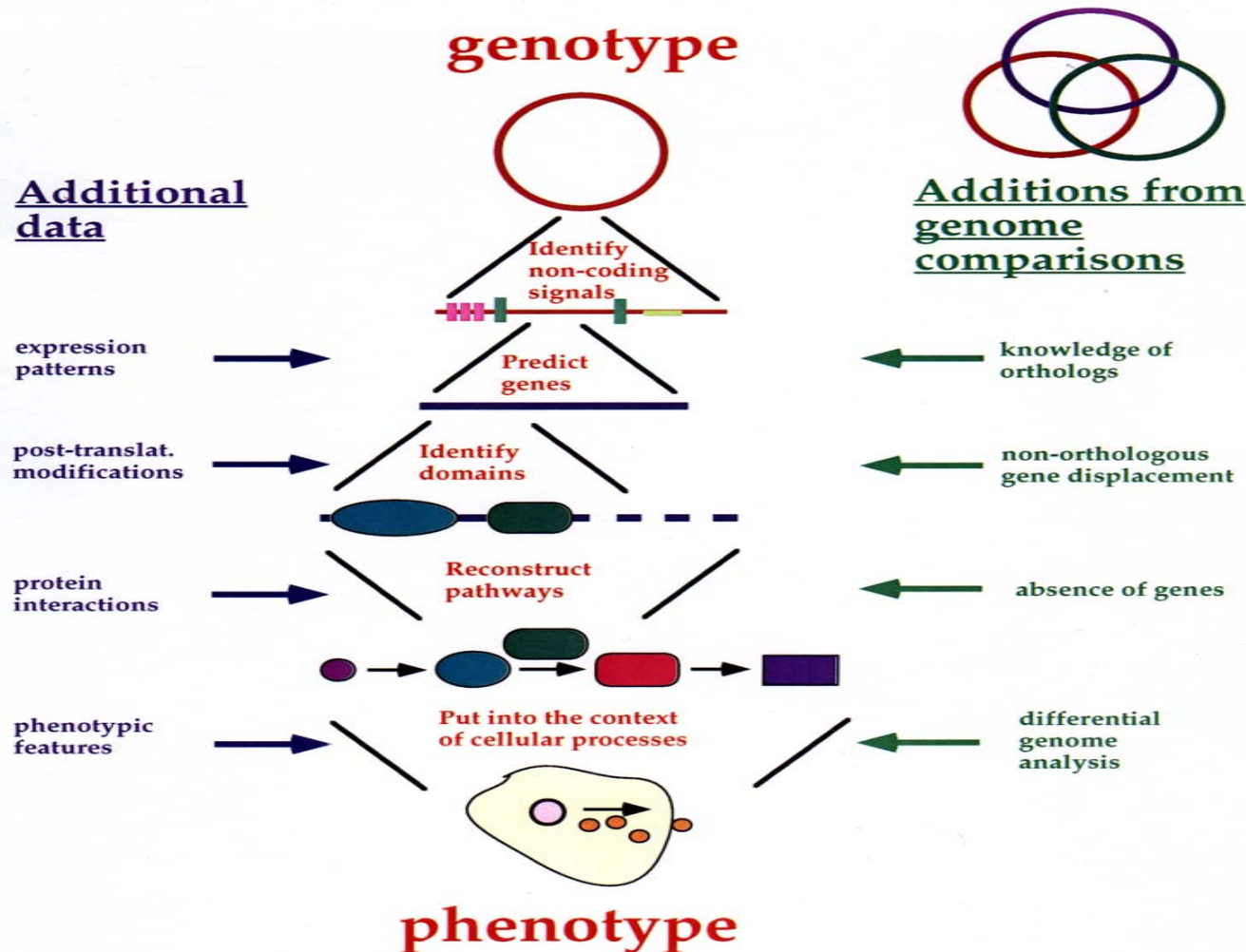
# AG Dandekar: Netzwerkmodellierung

Elementar  
Moden  
analyse



- Phagosom
- Listerien
- Blochmannien
- Erythrozyt
- Thrombozyt
- Mykoplasmen
- Mensch

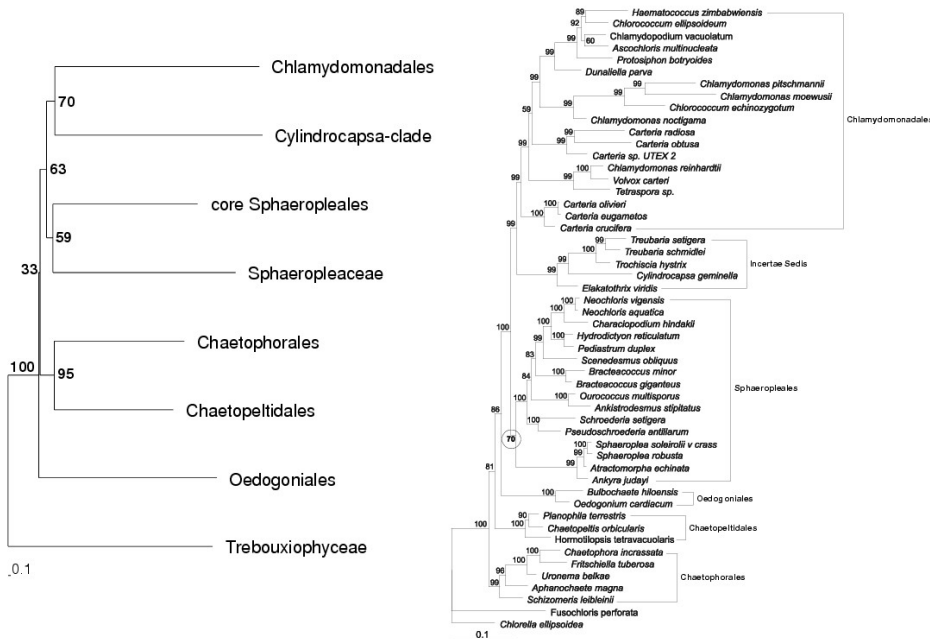
# AG Dandekar: Netzwerkmodellierung



Analyse  
verschie-  
dener  
Ebenen  
zellulärer  
Prozesse

Plättchen  
Phagosom  
Lymphome  
Arabidopsis  
Rezeptoren

# AG Wolf: Phylogenetik



## Profile distances

(accurate and robust phylogeny estimation)

## RNA secondary structures

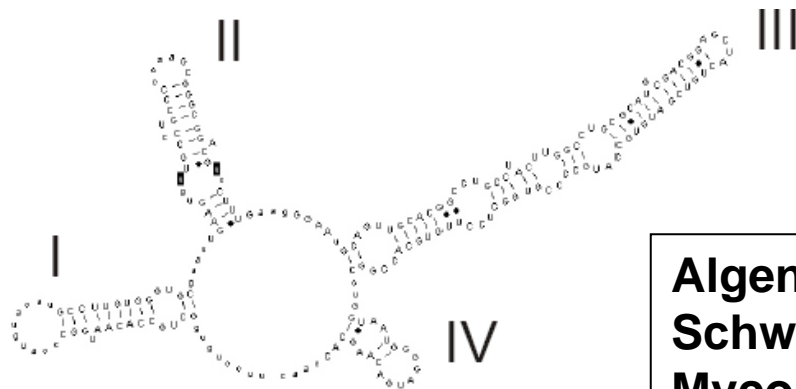
(internal transcribed spacer 2 (ITS2))

## PGK

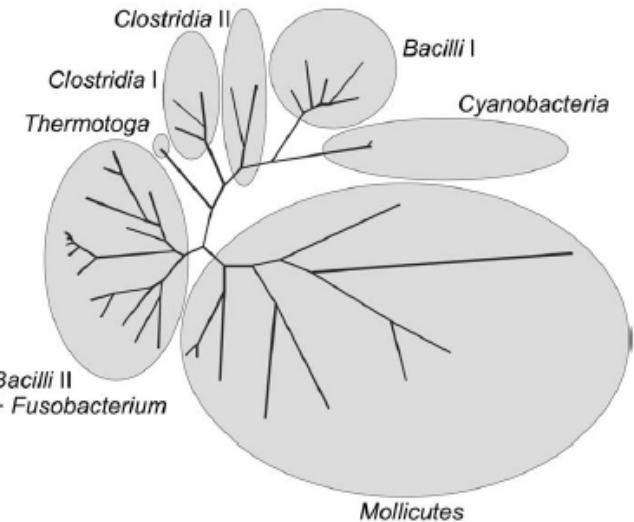
(Protein evolution)

**A**

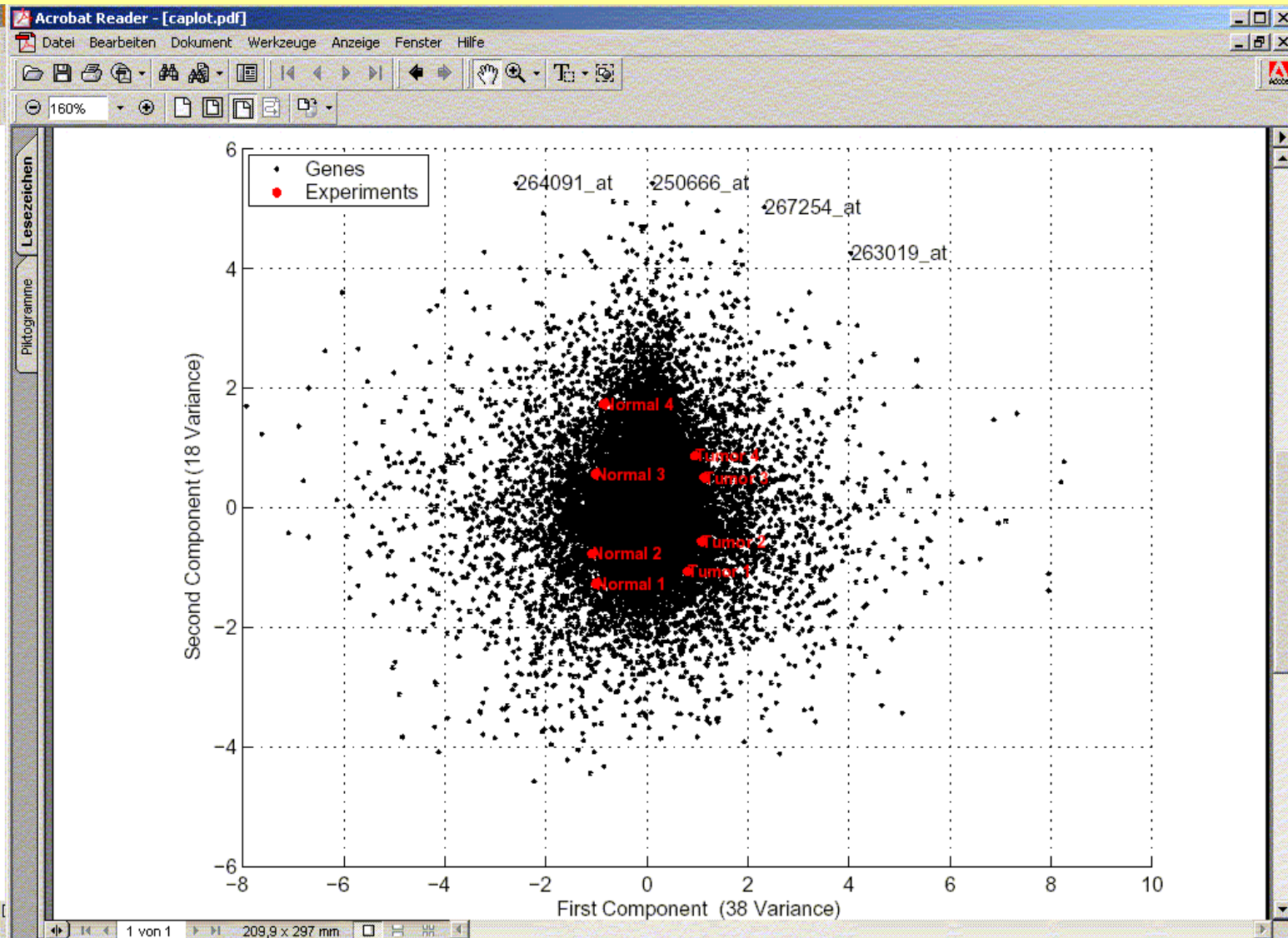
**B**



**Algen  
Schwämme  
Mycoplasmen**



# AG Müller: Statistische Modellierung

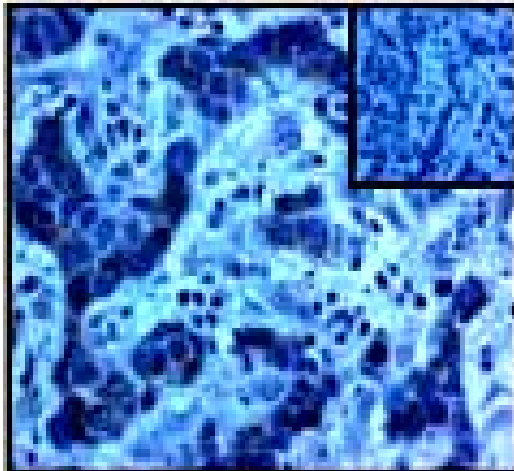


Maus  
Arabidopsis  
Mensch

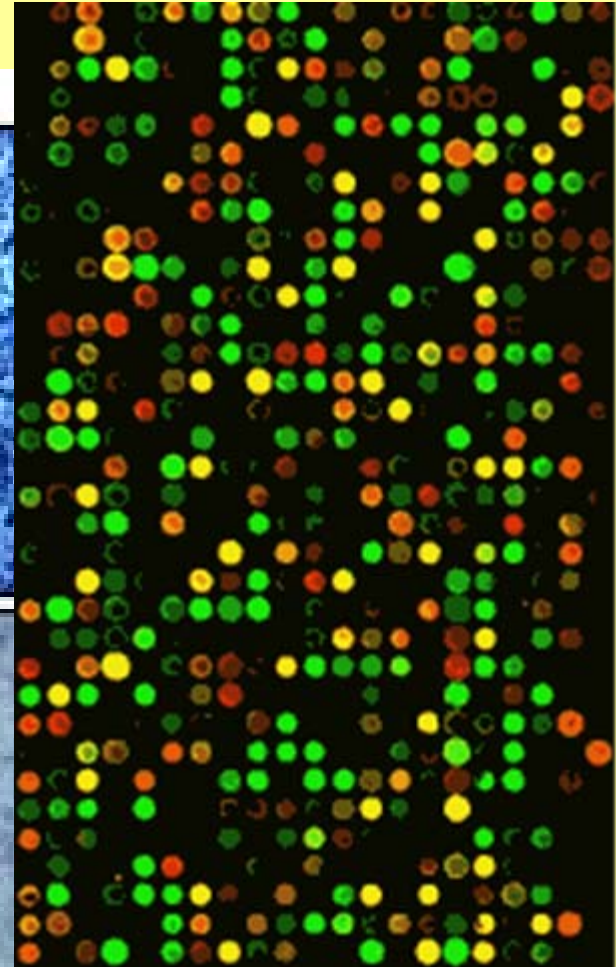
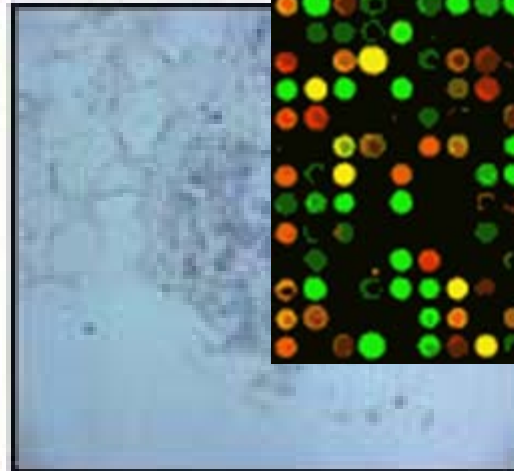
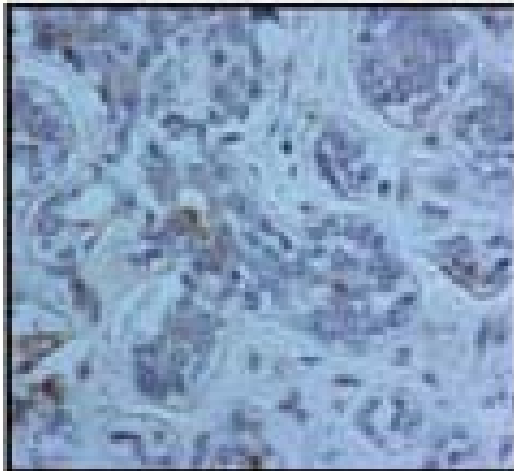
Domänen  
Tumoren  
Stammbäume

# *Überexpression des RAS Onkogen*

**Tumor 1**



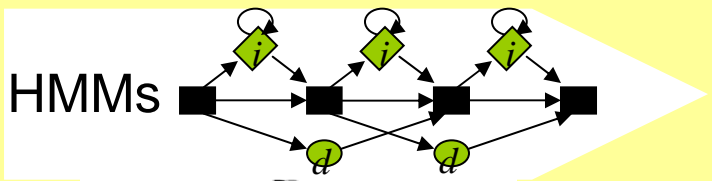
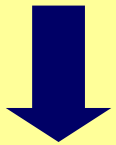
**Normal**



# AG Schultz: Large scale domain analysis



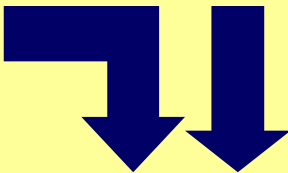
665 SMART domains



~90 Enzymatic SMART domains



Primary literature



52 Known catalytic mechanism

*e!* Ensembl peptide sets (version 18)

```
11a1vvgfSRvylgvHypsD
+a+++++SR+++++H++ D
CWAVFCSLSRITDNRHHWWD
```



Annotated HMMs

inactive PTP  
D2B (diverged cleft)



„catalytic“ positions  
slow evolving positions

# AG Schultz: Large scale domain analysis multi-functional

## Protein Tyrosine Phosphatases Family

