

Evolution of snRNA

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snRNA

- snRNA := small nuclear RNA; $\text{snRNA} \subset \text{ncRNA}$
- snRNP := ribonucleoprotein particles
- spliceosome = snRNP + proteins

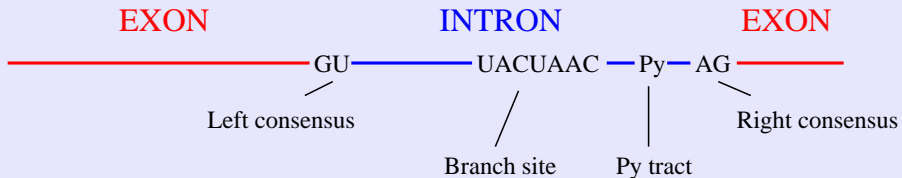
- snRNA \neq snoRNA (small nucleolar RNA)

snRNP for Splicing

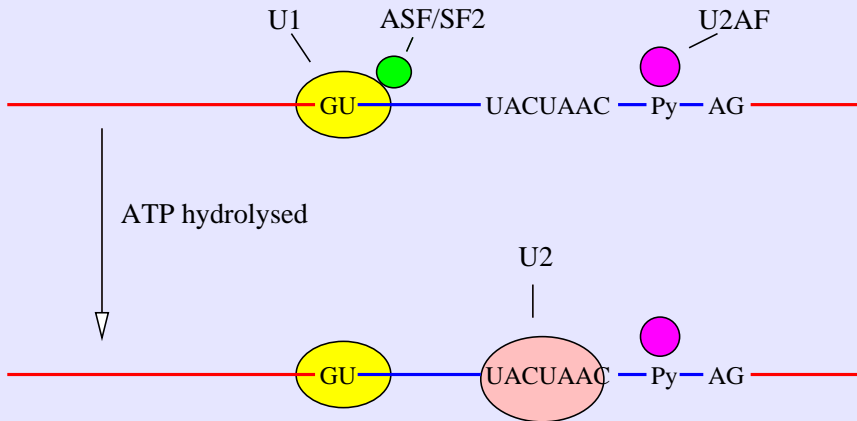
- U1, U2, U3, U5, U4/U6
- name from corresponding snRNA
- each contains snRNA + > 20 Proteine

- alternativly to main spliceosome: minor spliceosome
U11, U12, U5var, U4atac/U6atac
- conserved Sm-binding site: $PuAU^nG Pu$, $n \in \{3, 4, 5, 6\}$
(not U6)

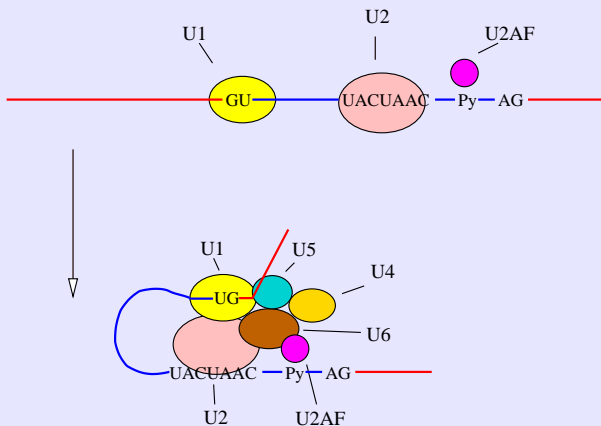
Example: Yeast



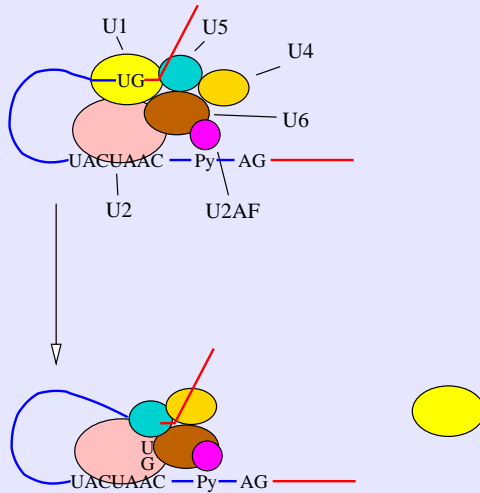
E complex, A complex



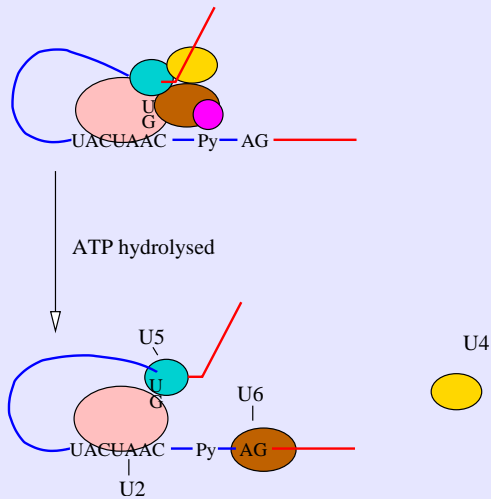
B1 complex



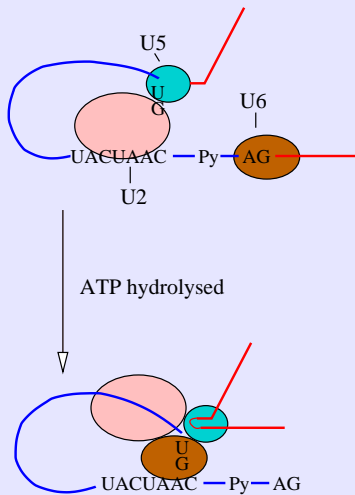
B2 complex



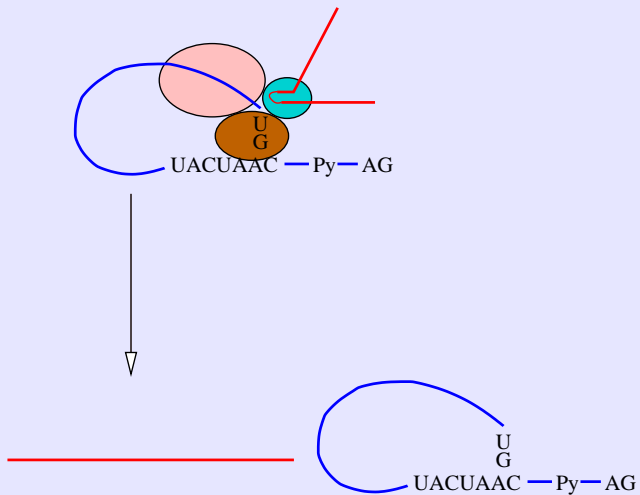
C1 complex



C2 complex



Spliced RNA



What has be done so far?

- description of diffent subunits in different taxons
- which parts essential
- which parts conserved
- very incomplete and confusing

Lost in RNA-World

- Lost in RNA-World - Non coding RNA and the Spliceosome in Eukaryotic Ancestor (Lesley J. Collins; 2004)
- Searching for ncRNA in eukaryotic genomes: Maximizing biological input with RNAmotif (Collins, Macke, Penny; 2004)

Aims

- find all subunits in all complete genomes which are known!
- find all copies!
- which are pseudogenes? how many of them?
- build phylogenetic tree
- publish new found U5, phylogenetic tree

Programs

- Blast
- RNAmotif
- Hypa

Blast

Taxon	Copies	Chromosomes
Homo	6	1(3),15(3)
Mus	6	1(1), 4(3), 9(2)
Rattus	9	2(1), 5(3), 7(1), 8(2), 13(1), 19(1)
Gallus	7	7(8)
Drosophila	7	2L(5), 3L(1), X(1)
Pan	7	1(3), 2(1), 8(1), 16(2)
Dog	7	2(1), 7(2), 10(1), 15(2), 17(1)

Hypa

```
ire = stem1 loop cstem1
where stem1:=.{3,20}
      loop:= CYR .{3,5}
      cstem1:=^[1,0,2]stem1
      << freeE(stem1(loop)cstring) <= -4;
```


Hypa

```
hairpin(%loop) = (stem:=.{3,10}) %loop ^stem  
tata = TATA[CG][AU]  
stopcodon=TGA|TA[GC]
```

```
hairpinTata=hairpin(tata);  
hairpinStopcodon=hairpin(stopcodon);
```

```
hairpinTata2=(stem:=.{3,10}) (TATA[CG][AU]) ^stem;  
hairpinStopcodon=(stem:=.{3,10}) (TGA|TA[GC]) ^stem;
```