# Reconstruct ancestral DNA for your proto-gene

1. Describe what you see in the DNA sequence at the start of your proto-gene in the other species/ancestors. Do you see the start of an ORF in the other species (i.e an ATG codon)? If there is one present, is it the same or different frame as the ORF in *S. cerevisiae*?

2. In what species or ancestor did the ORF first appear? (i.e. what species or ancestor furthest from *S. cerevisiae* can you find the first ATG in the same frame as the proto-gene in *S. cerevisiae*). Use the tree below for reference.
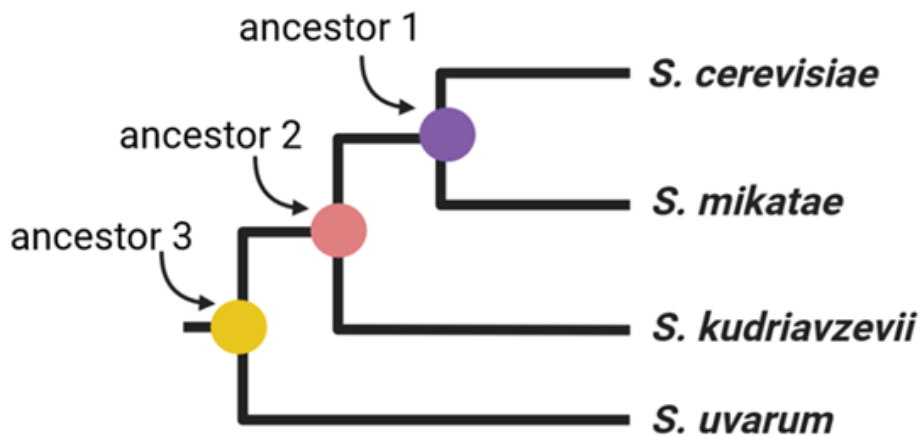
3. Using the region homologous to your proto-gene, how similar are the DNA sequences between your proto-gene sequence in *S. cerevisiae* compared to the ancestors and other species? Fill in the percentage ID in the table:

	% DNA sequence identity with Scer sequence
Scer	100
Anc_node 1	
Smik	
Anc_node 2	
Skud	
Anc_node 3	
Suva	

4. Does the DNA sequence similarity between *S. cerevisiae* and the other species/ancestors decrease with evolutionary distance (ie does DNA sequence similarity decrease as you get further from *S. cerevisiae)*?

5. Using the region homologous to your proto-gene, how similar are the amino acid sequences between your proto-gene sequence in *S. cerevisiae* compared to the ancestors and other species? Fill in the percentage ID in the table:

	% amino acid sequence identity with Scer sequence
Scer	100
Anc_node 1	
Smik	
Anc_node 2	

Skud	
Anc_node 3	
Suva	

6. Does the amino acid sequence similarity between *S. cerevisiae* and the other species/ancestors decrease with evolutionary distance? (i.e. does amino acid sequence similarity decrease as you get further from *S. cerevisiae)*