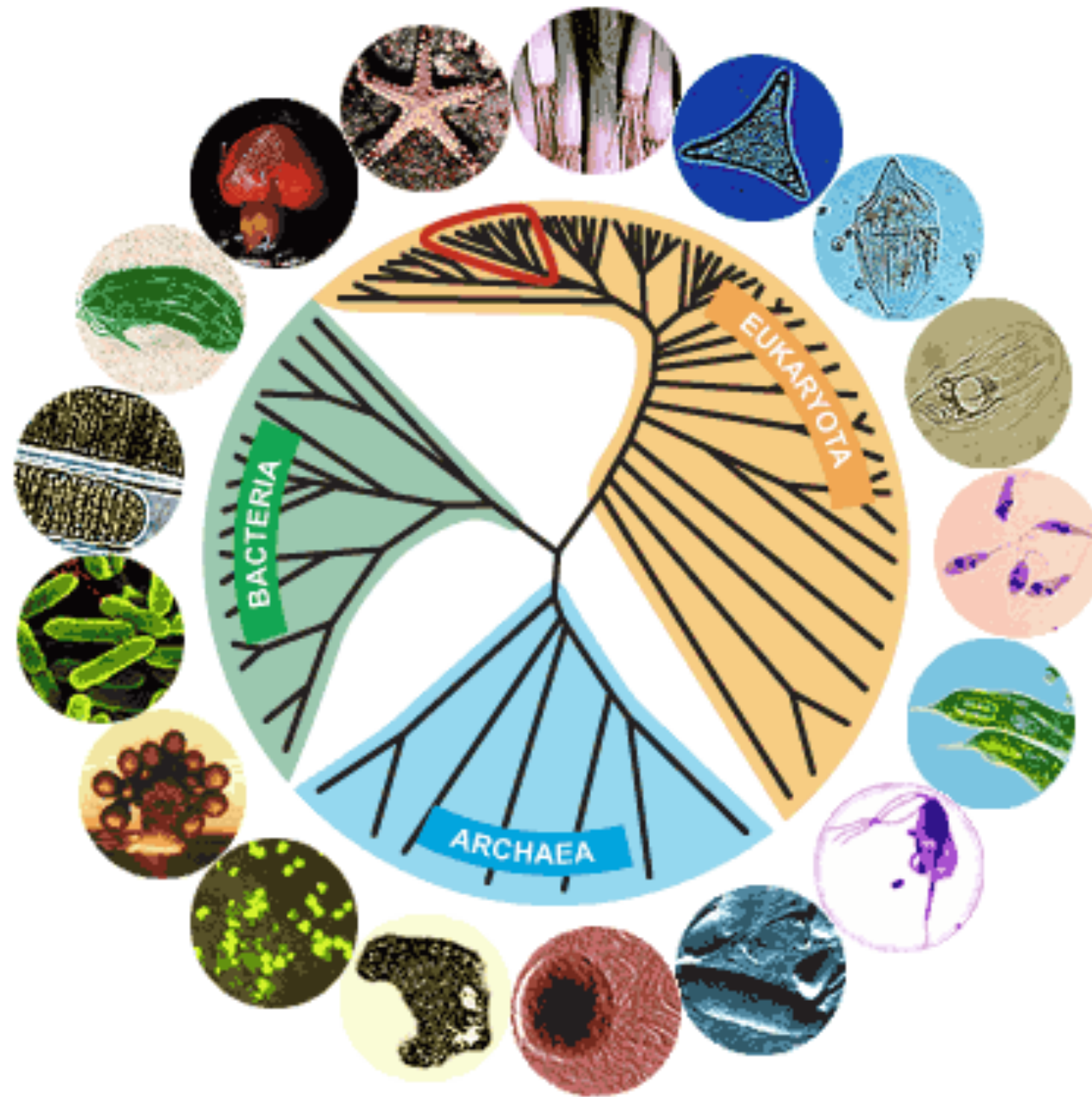


# Phylogeny of SNCA

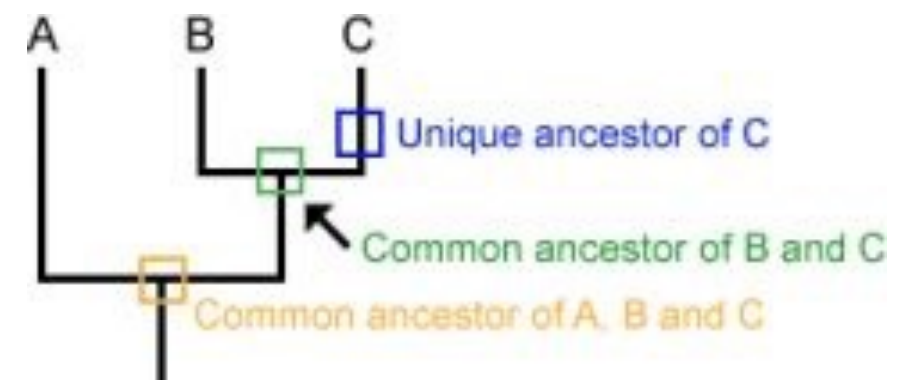
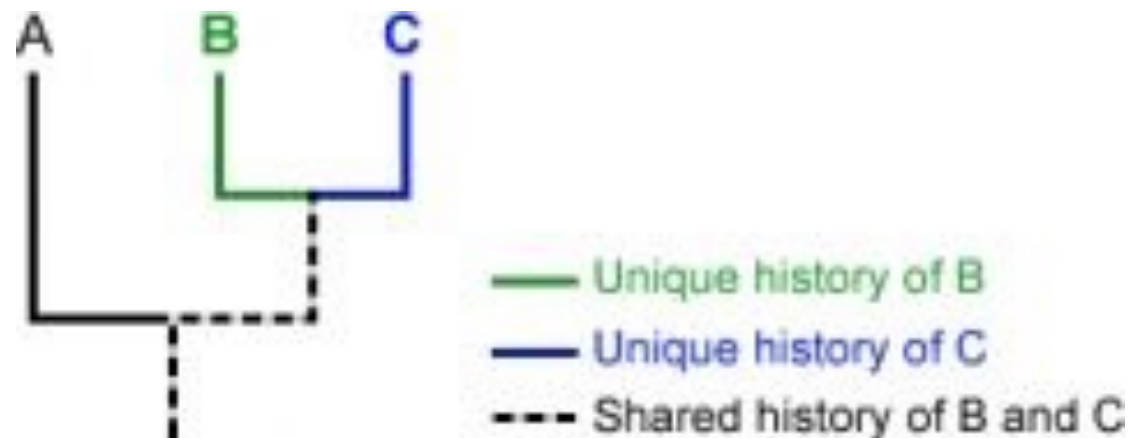
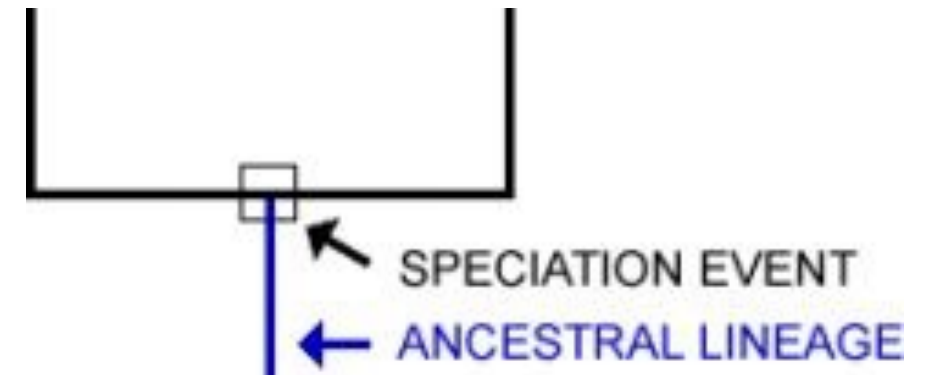
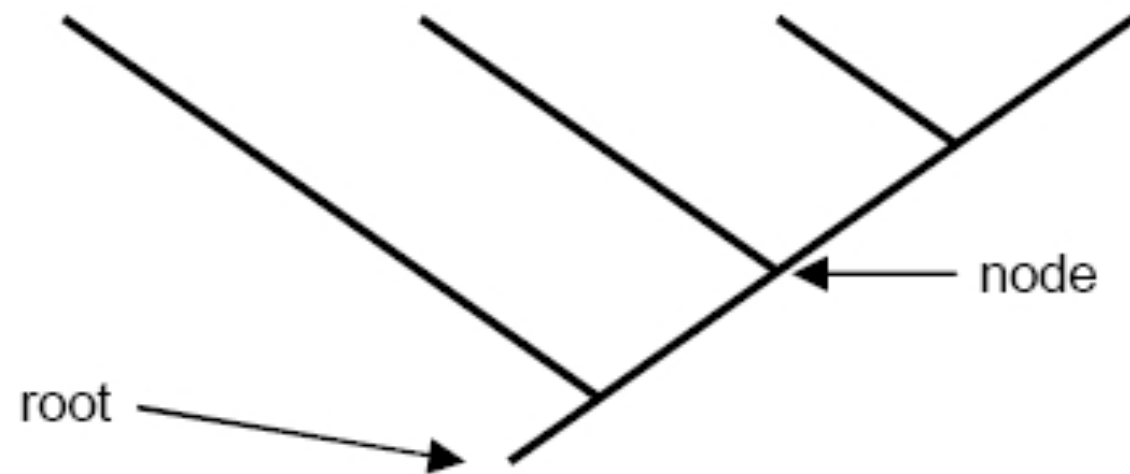
Tessa Bachinski and Rose Rogers

# What is Phylogeny?

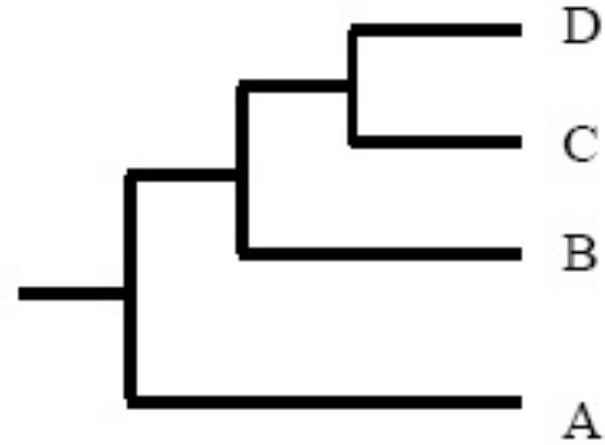
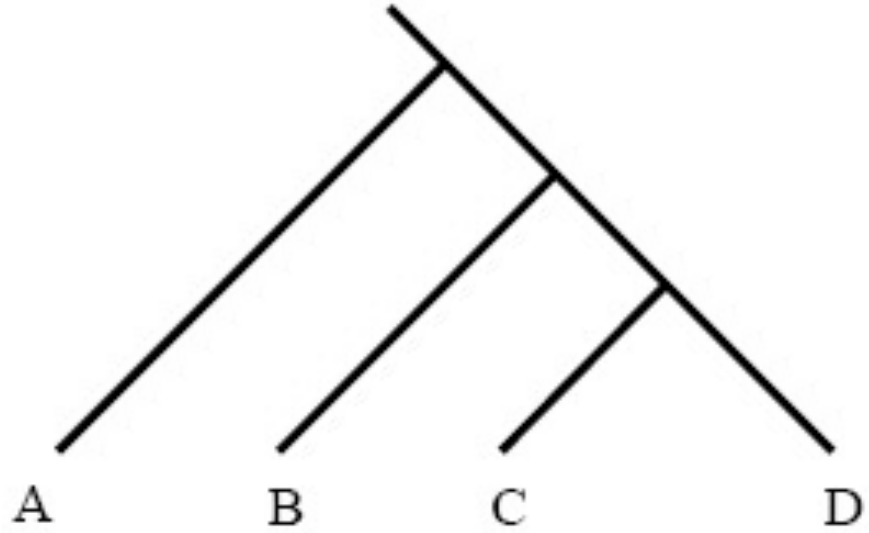


**Analysis of relationships in varying aspects of biology**

# Phylogeny Basics



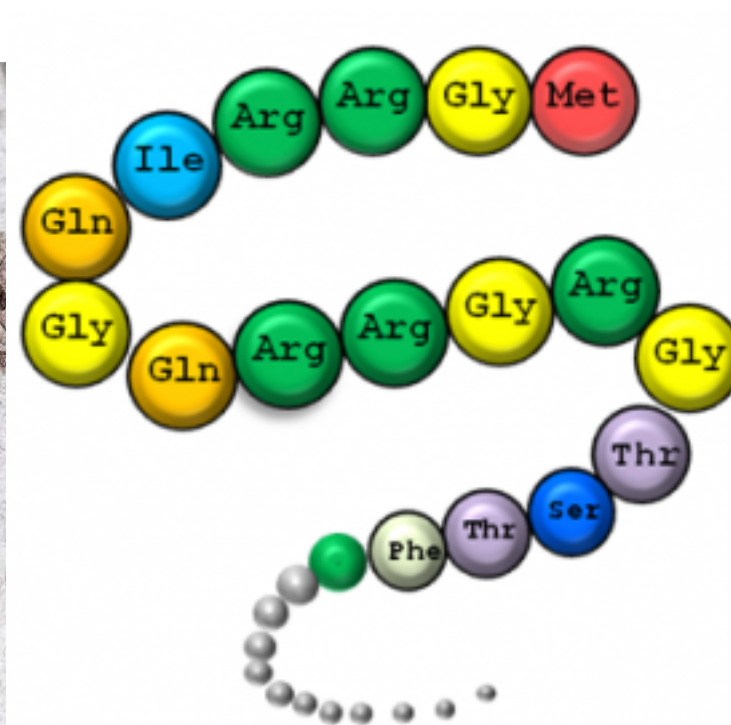
# Are these trees different?



# What kind of data can be used to make phylogeny trees?



**Features**



**Proteins/  
Biochemical  
Markers**



**DNA**

Image 1: <https://thumbs.dreamstime.com/z/backbone-fossil-fish-macro-photo-54090281.jpg>

Image 2: <http://userscontent2.emaze.com/images/2dfa0fd0-0b4f-4f43-a435-8a78be1cf2eb/974647e9-312f-458b-9559-3513779effda.PNG>

Image 3: [https://www.sciencemag.org/sites/default/files/styles/inline\\_450w\\_no\\_aspect/public/DNA\\_16x9\\_0.jpg?itok=gs07u06o](https://www.sciencemag.org/sites/default/files/styles/inline_450w_no_aspect/public/DNA_16x9_0.jpg?itok=gs07u06o)



# How do you decide what goes where?



**Character Based**



**Distance Based**

Image 1: <https://i1.wp.com/mvslim.com/wp-content/uploads/2016/02/384b1c8c-09c2-4db6-8f89-8aa85e7ca0f0.jpg?fit=758%2C474&ssl=1>  
Image 2: <https://images.unsplash.com/photo-1432753759888-b30b2bdac995?ixlib=rb-1.2.1&ixid=eyJhcHBfaWQiOjEyMDd9&w=1000&q=80>

# How do you build a tree with character based methods?

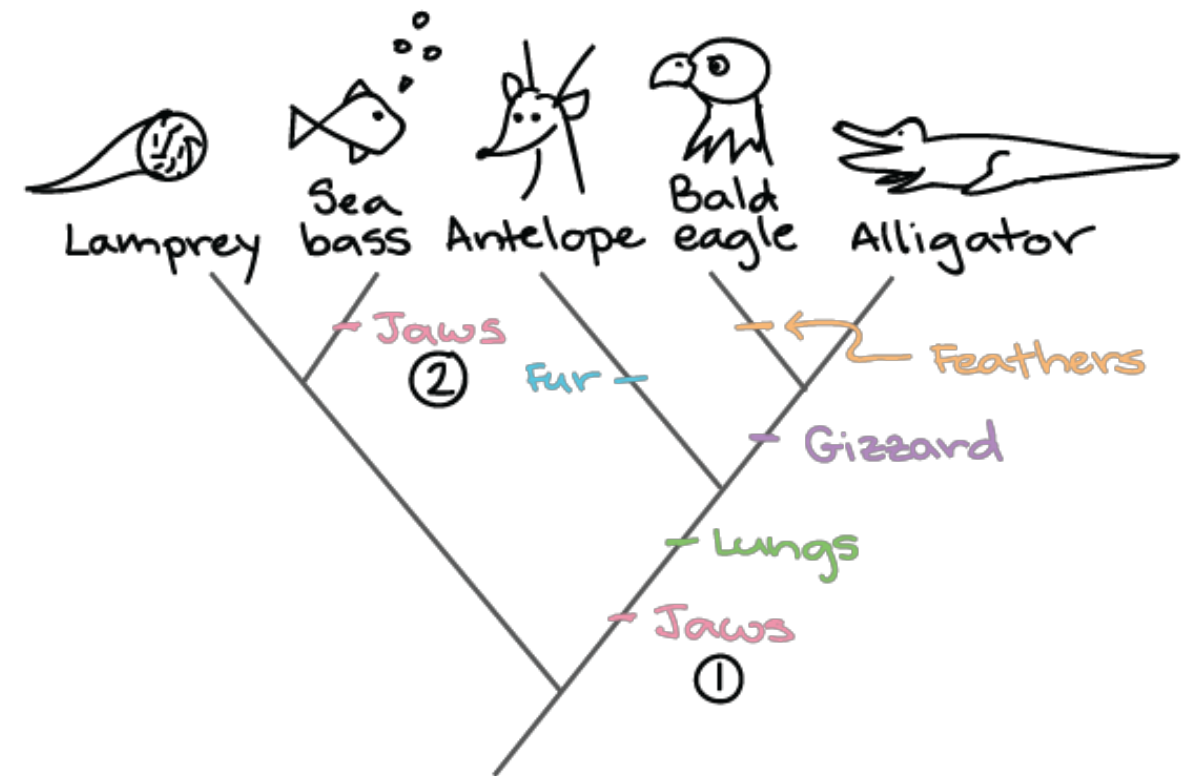
Feature	Lamprey	Antelope	Bald eagle	Alligator	Sea bass
Lungs	0	+	+	+	0
Jaws	0	+	+	+	+
Feathers	0	0	+	0	0
Gizzard	0	0	+	+	0
Fur	0	+	0	0	0



# Maximum Likelihood



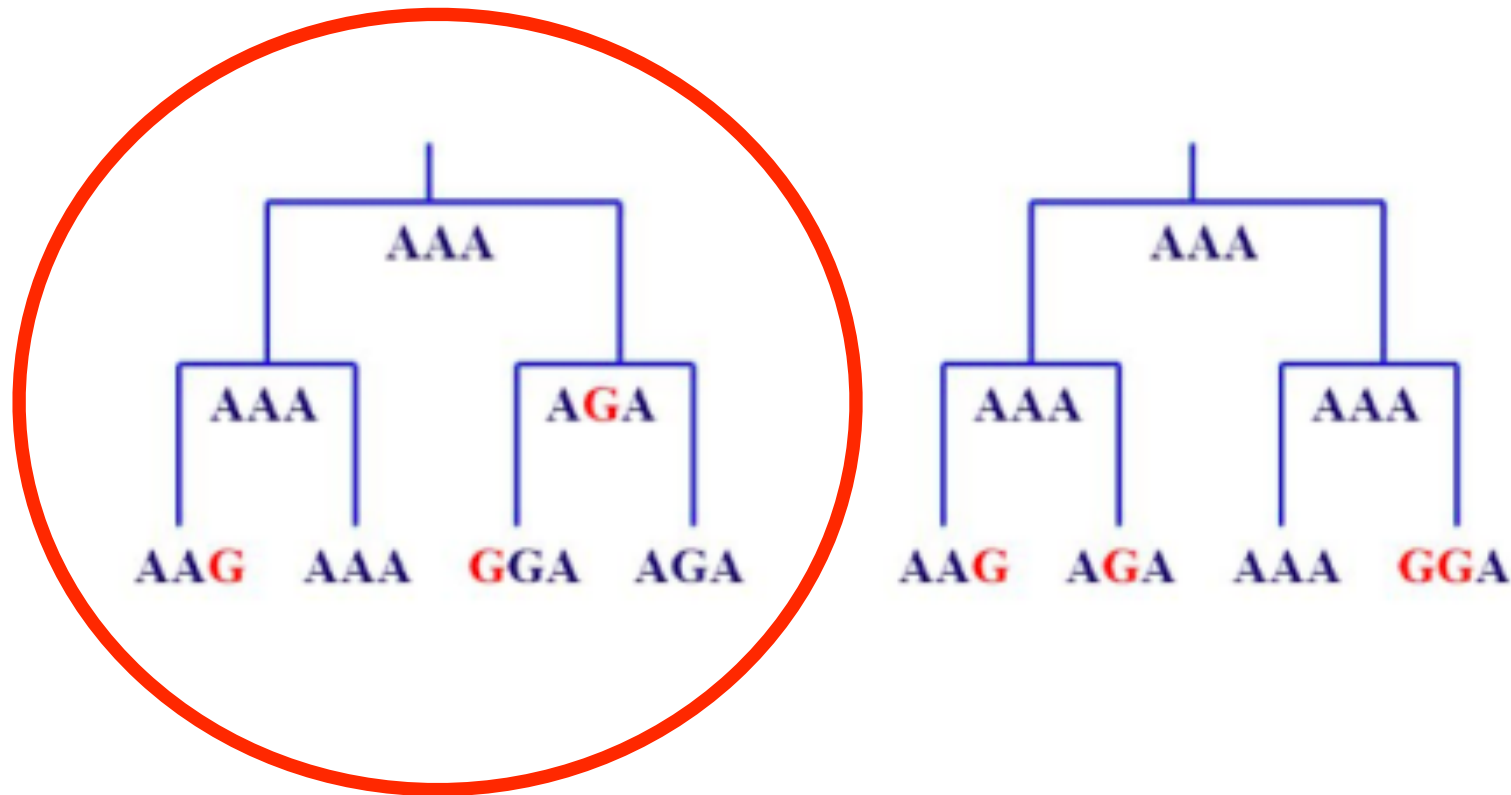
VS



**What was more likely to happen?**



# Maximum Parsimony



**Parsimony requires the fewest changes to get from a common ancestral sequence to the current sequences**

# How do we use DNA?



## Step 1: Align

```
T ATGGCGCTGGGCATACTGAGC
T A  GCGCAGGGCATACTGAGC
T A  GCGCAGGGGATACTGAGC
TTATGGCGCTGGGCATTCTGAGC
```

## Step 2: Find the SNPs

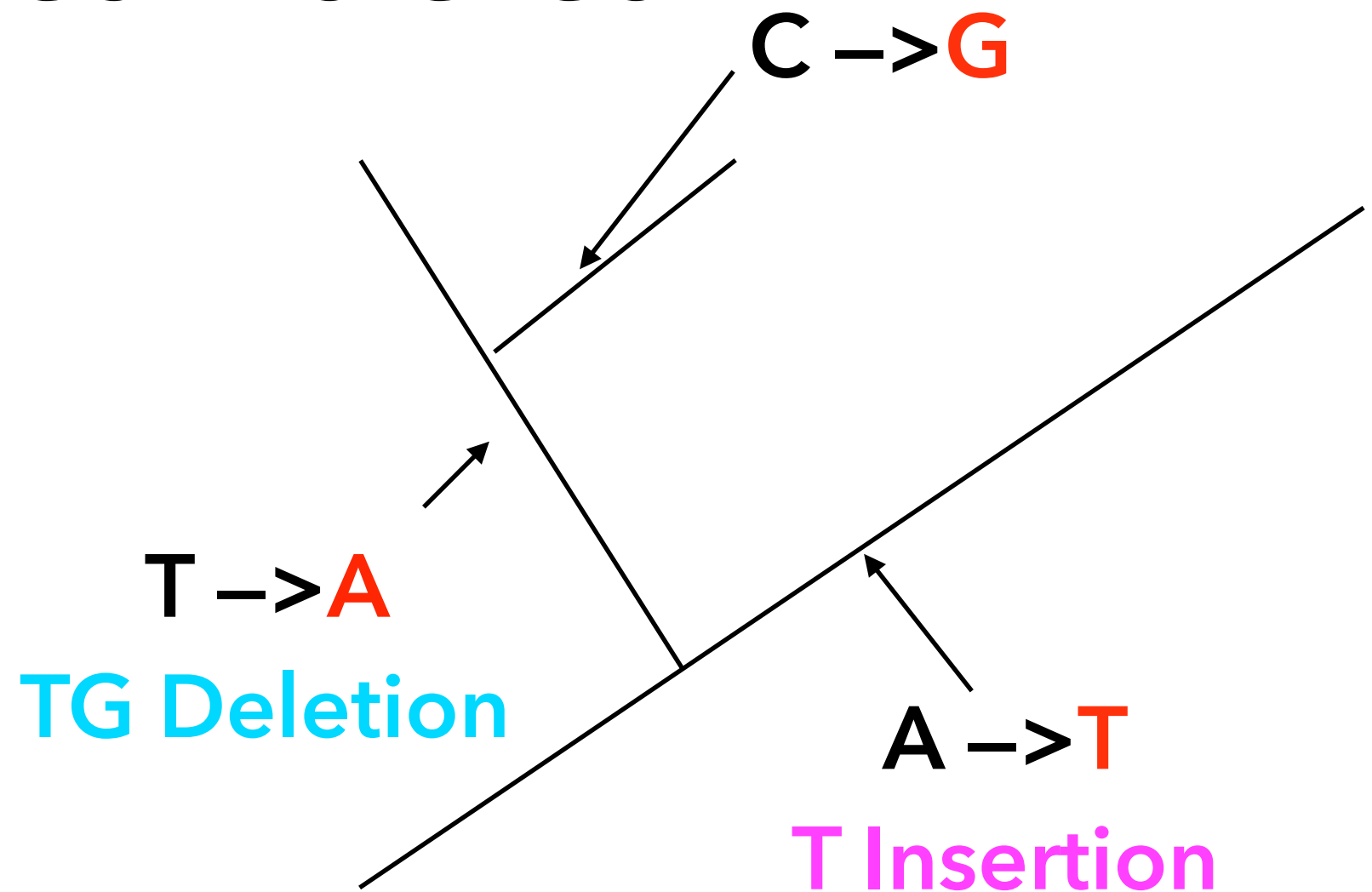
```
GCTGGGCATACTGAGC
GCAGGGCATACTGAGC
GCAGGGGATACTGAGC
GCTGGGCATTCTGAGC
```

## Step 3: Find the Indels

```
T ATG GCGC
T A  GCGC
T A  GCGC
TTATG GCGC
```

## How do we use that information to build a tree?

TATGCGCTGGGCATACTGAGC  
TAAGCGCAGGCATACTGAGC  
TAAGCGCAGGGATACTGAGC  
TTATGCGCTGGGCATTCTGAGC





## How do we use distance methods to determine trees?

Species A

ATGGCTATTCTTATAGTACG

Species B

ATCGCTAGTCTTATATTACA

Species C

TTCACTAGAACCTGTGGTCCA

Species D

TTGACCAGAACCTGTGGTCCG

Species E

TTGACCAGTTCTCTAGTTTCG

NUMBER OF CHANGES

=

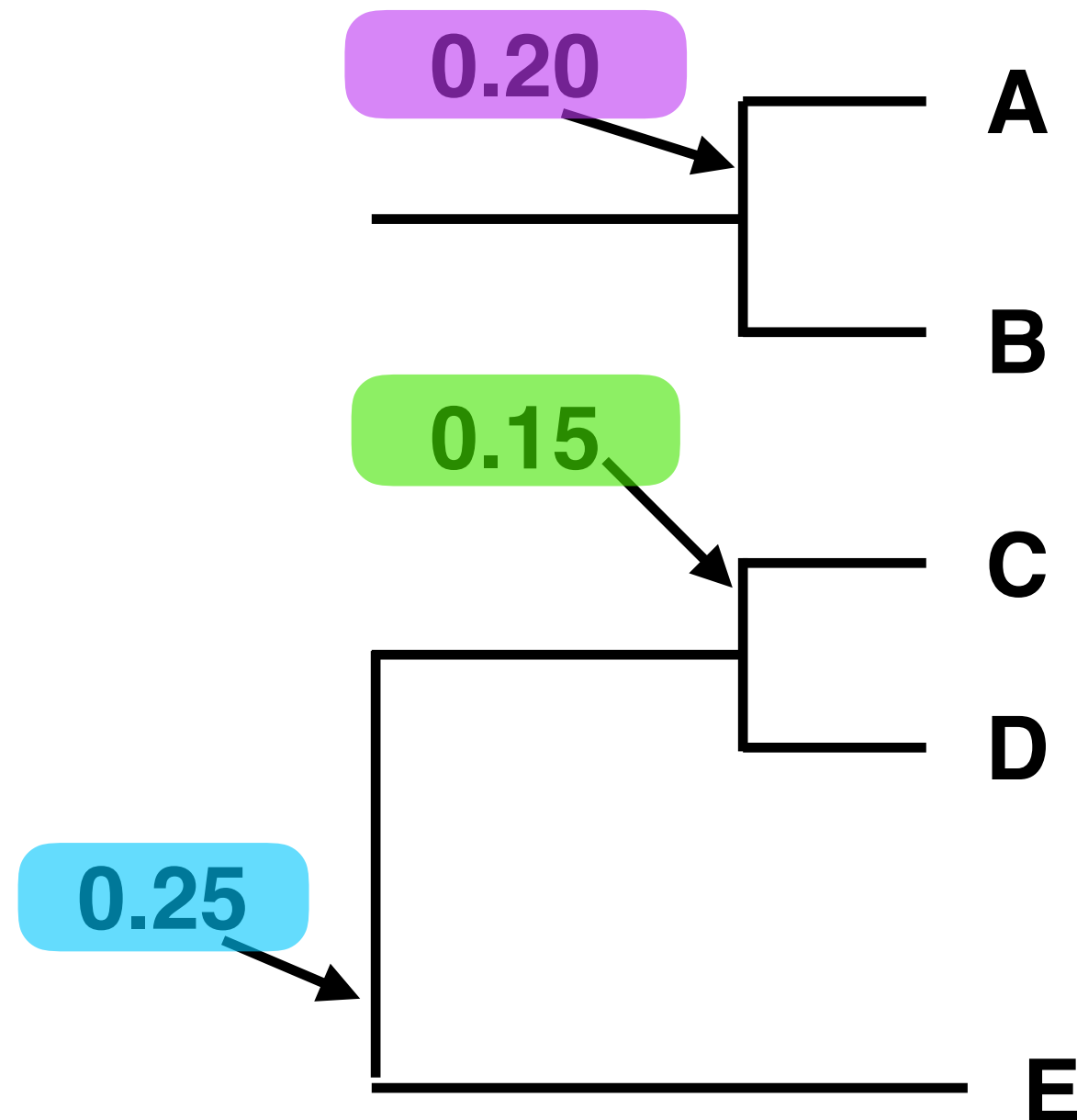
\_\_\_\_\_

TOTAL LENGTH

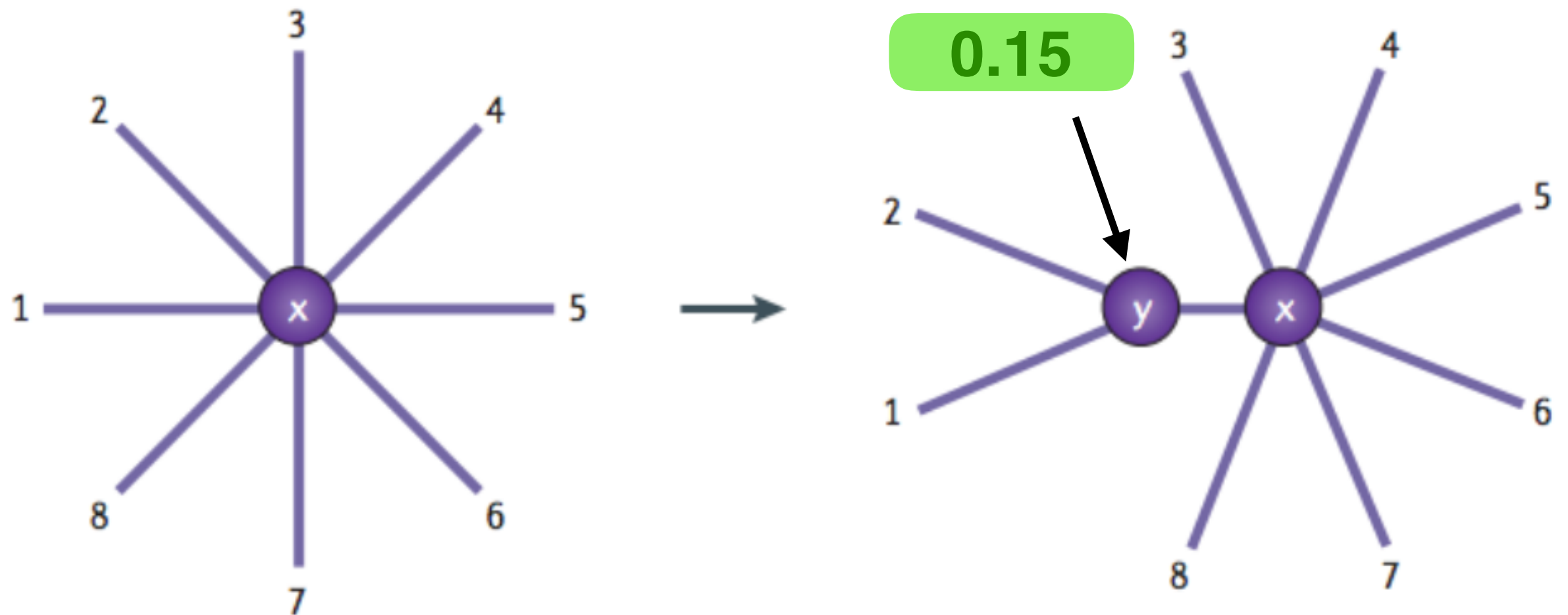
# Distance Matrix Method - Neighbor Joining

		A	B	C	D	E
Species	A	-----	0.20	0.50	0.45	0.40
Species	B		-----	0.40	0.55	0.50
Species	C			-----	0.15	0.40
Species	D				-----	0.25
Species	E					-----

# How do you use the numbers to build a tree?



# How do you use the numbers to build a tree?





# **What are advantages and disadvantages of each method?**

## **Character Based**

**Easy to see and calculate  
(computer/hand)**

**May require assumptions**

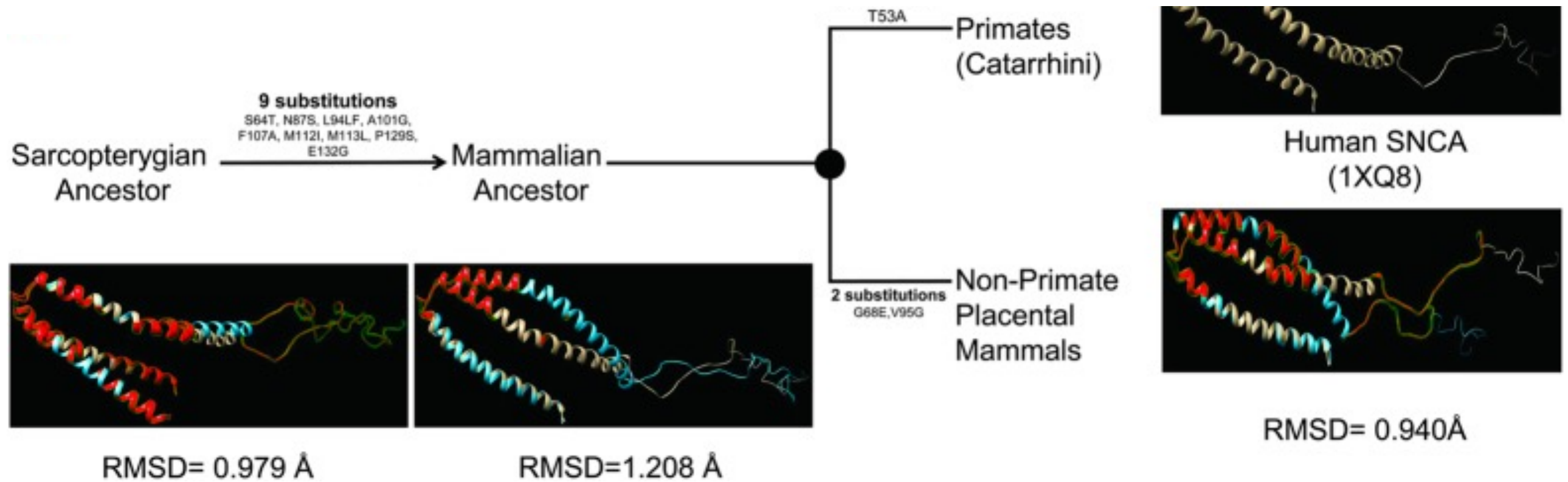
## **Distance Based**

**Very quick and easy to  
compute**

**Not good if there is poor  
alignment**

**Very distant things are  
hard to calculate**

# Why do I need this?

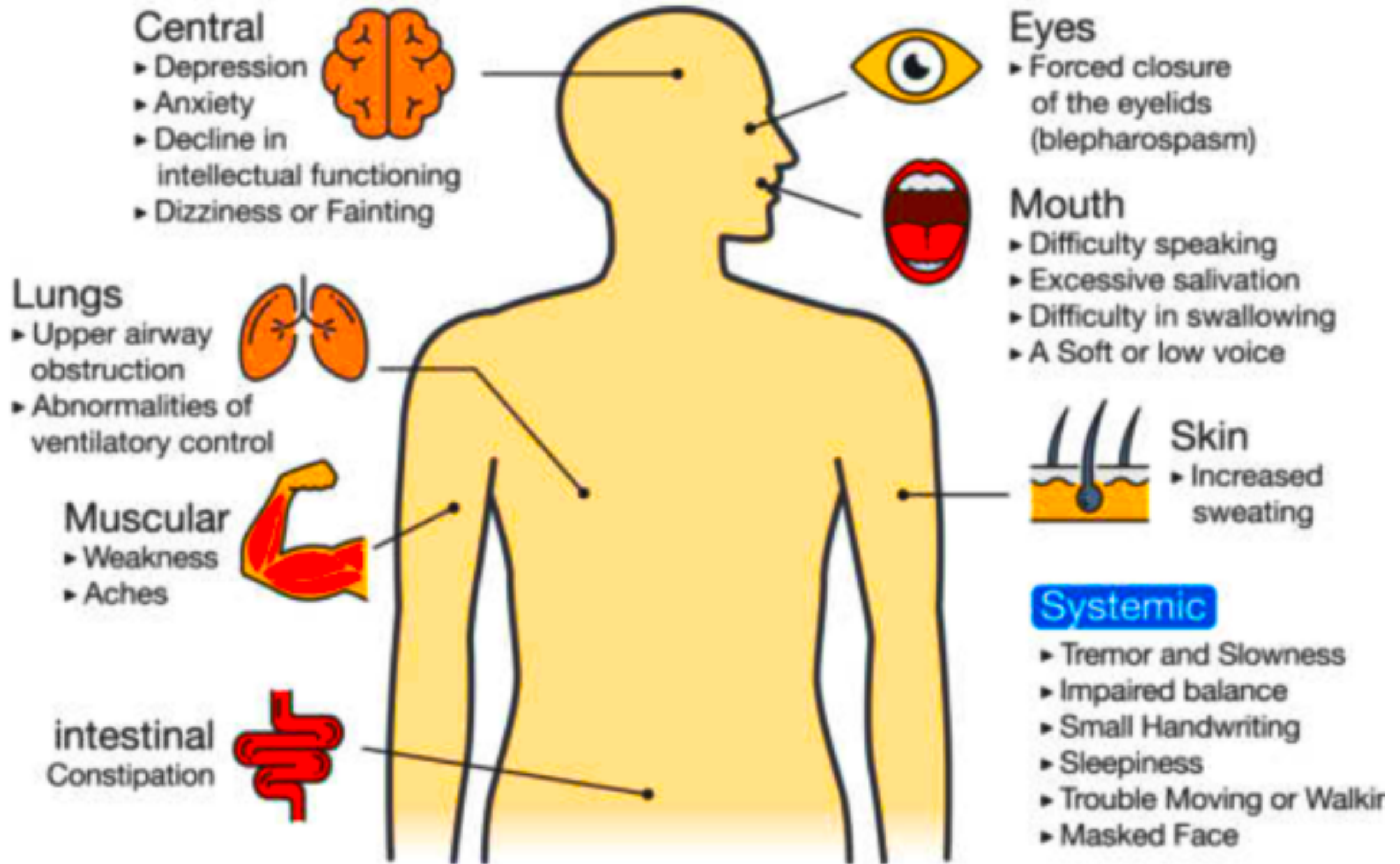


## Population Genetics Evolution Gene Tracking



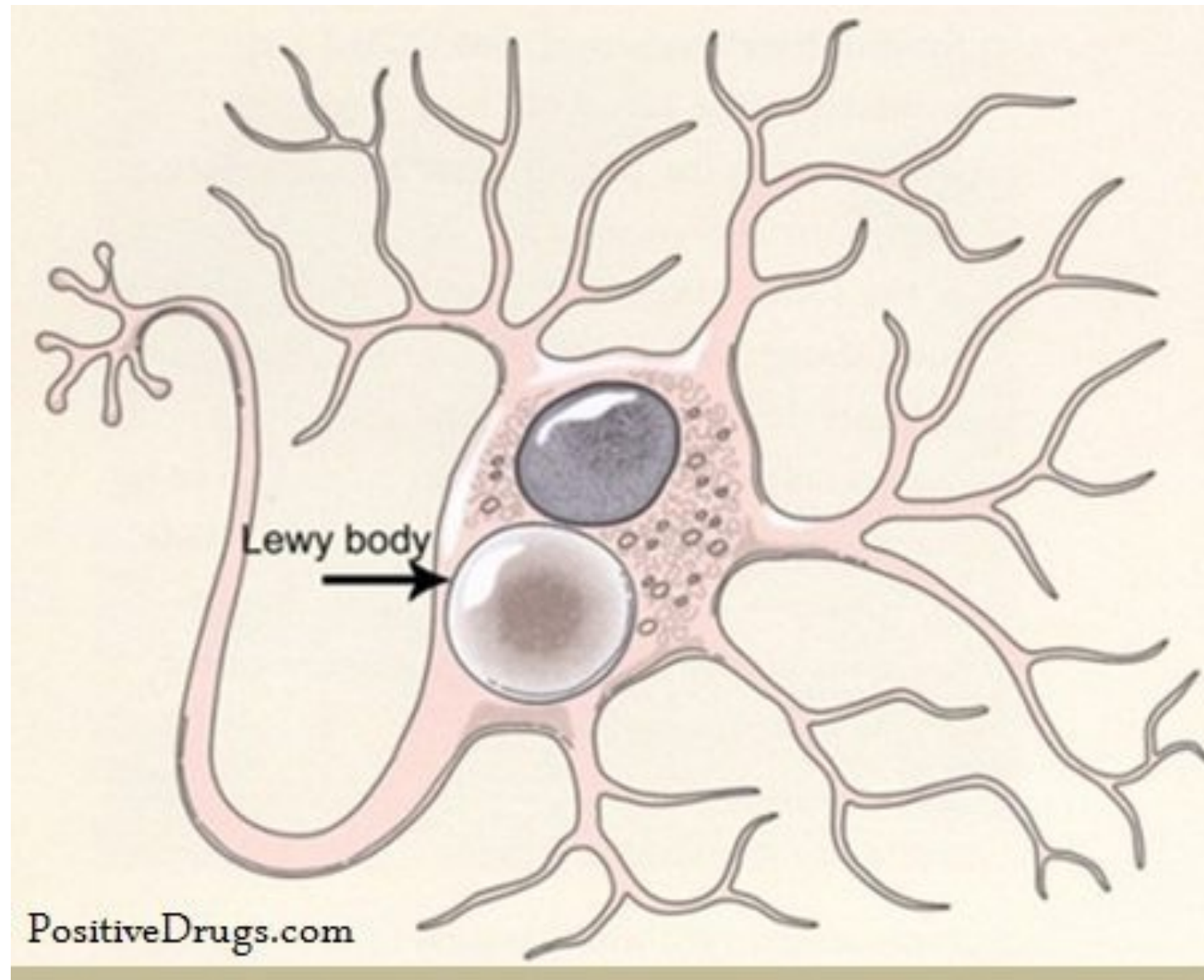


# Symptoms



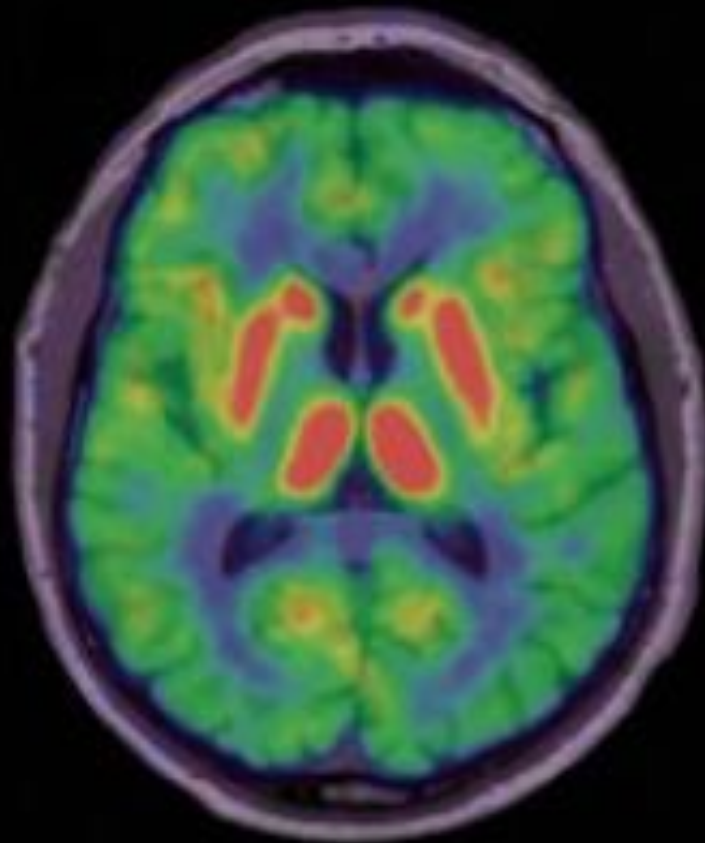


# On a molecular level, what leads to Parkinson's Disease?

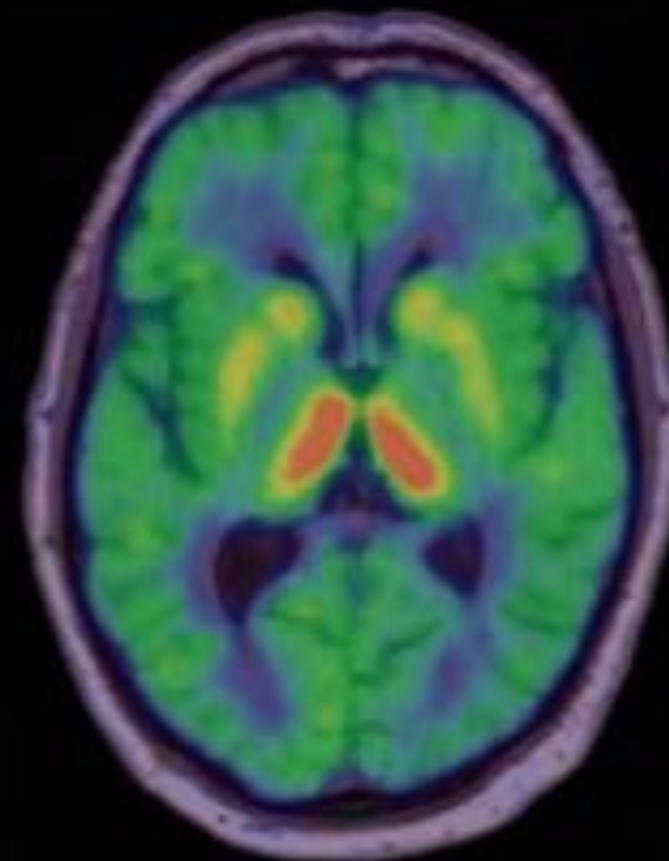


# On a molecular level, what leads to Parkinson's Disease?

Healthy Brain

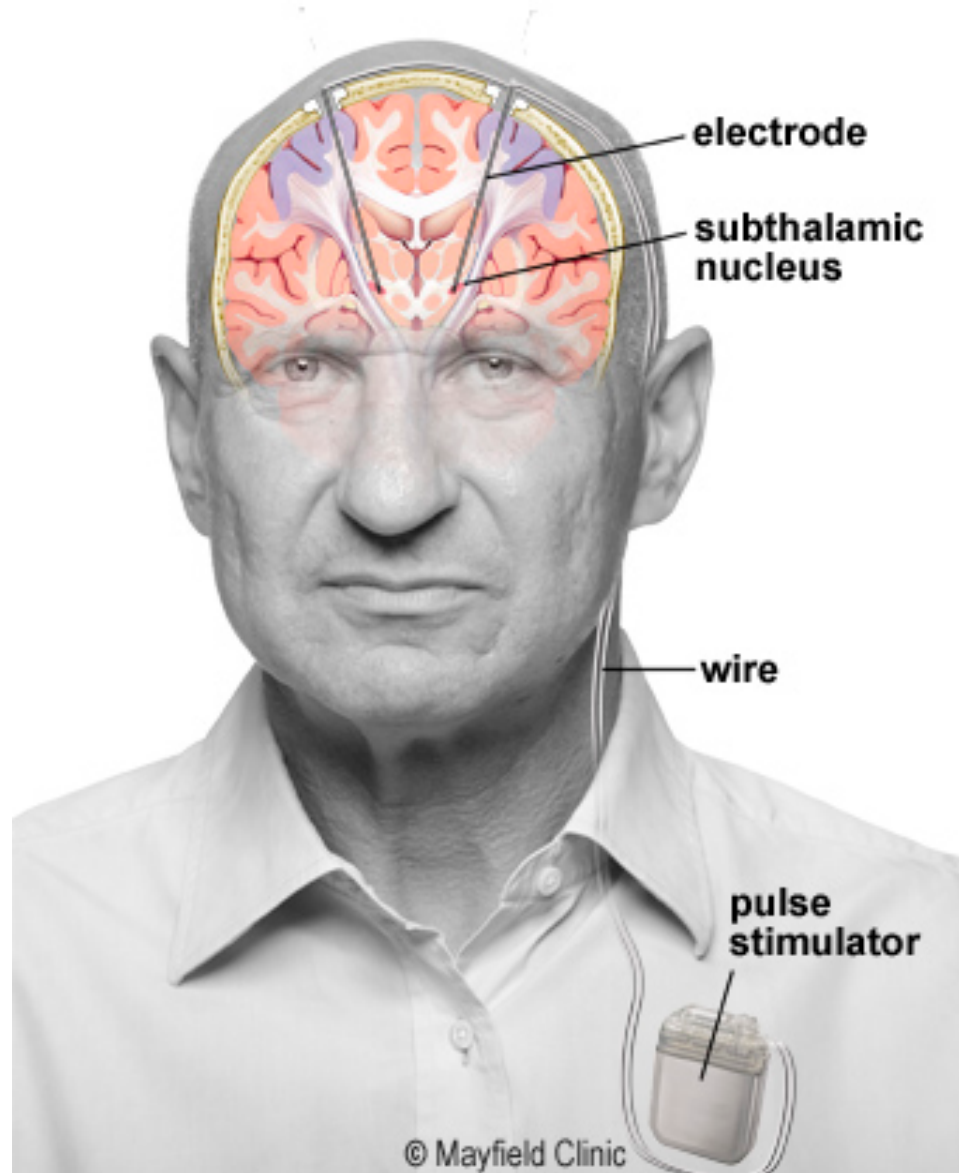


Parkinson's Brain



LOW  HIGH

# Treatments





# SCIENTIFIC REPORTS



**OPEN**

## **The Parkinson Disease gene SNCA: Evolutionary and structural insights with pathological implication**

Received: 11 October 2015

Accepted: 30 March 2016

Published: 15 April 2016

Irum Javaid Siddiqui, Nashaiman Pervaiz & Amir Ali Abbasi

After Alzheimer, Parkinson's disease (PD) is the second most common neurodegenerative disorder. Alpha synuclein (SNCA) is deemed as a major component of Lewy bodies, a neuropathological feature



# What is SNCA?

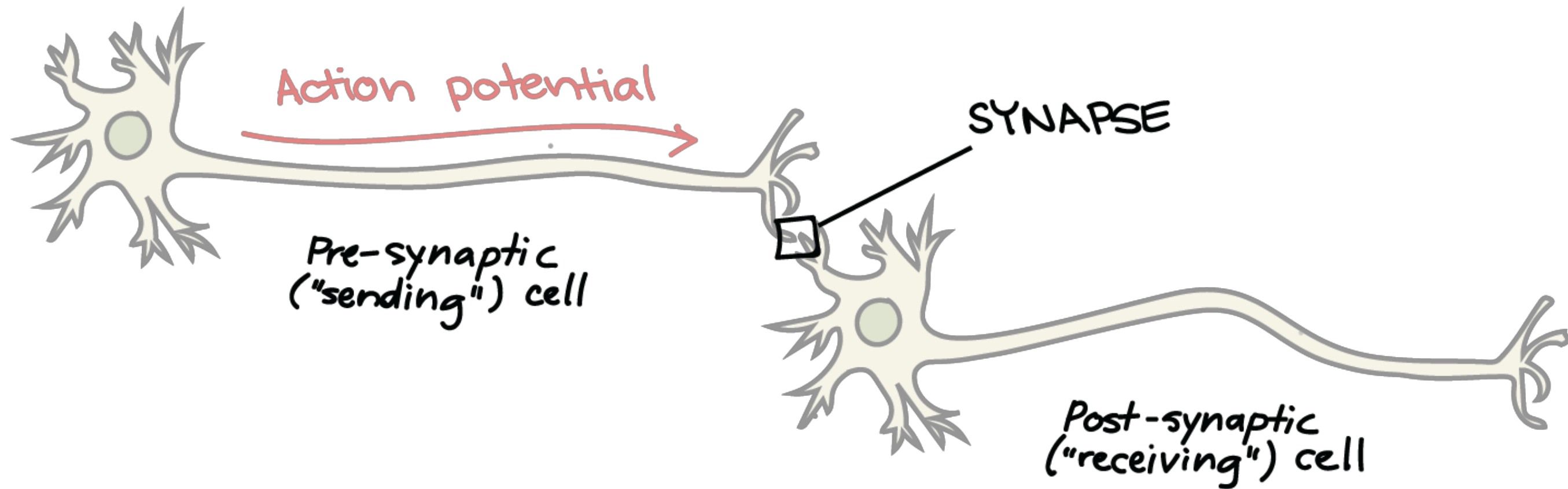
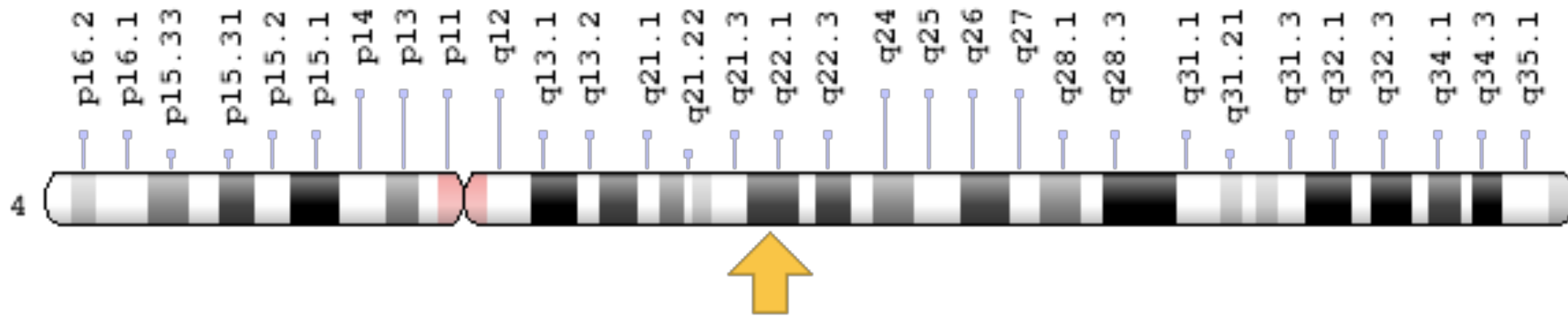


Image 1: <https://ghr.nlm.nih.gov/gene/SNCA#location>

Image 2: <https://www.khanacademy.org/science/biology/human-biology/neuron-nervous-system/a/the-synapse>

# What is SNCA?

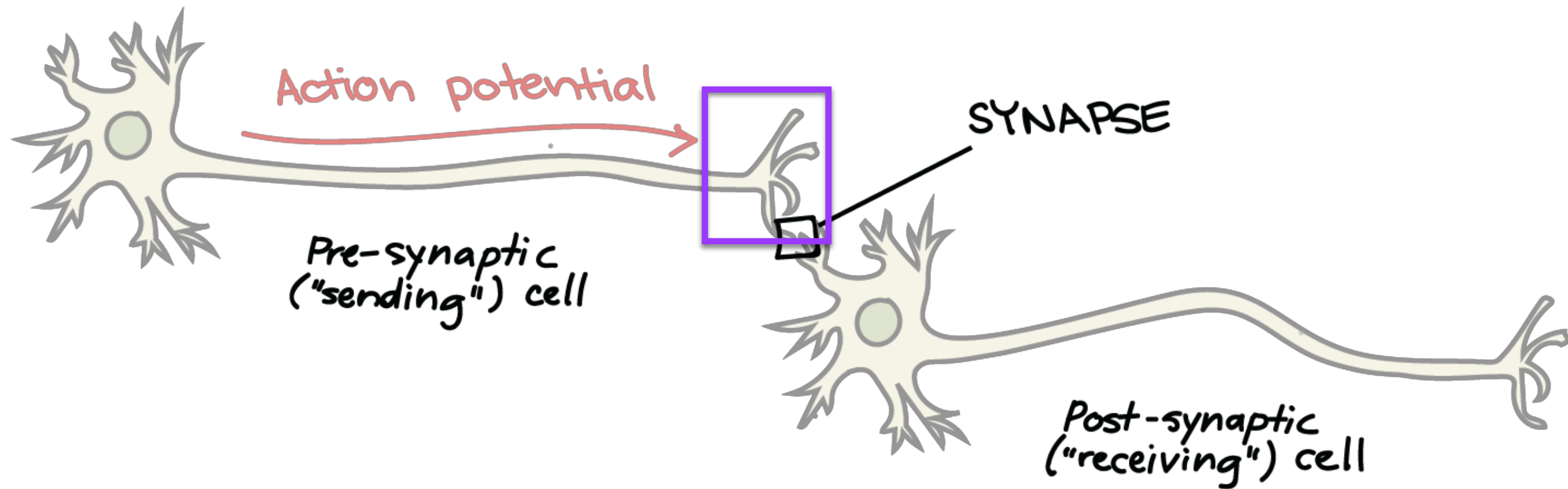
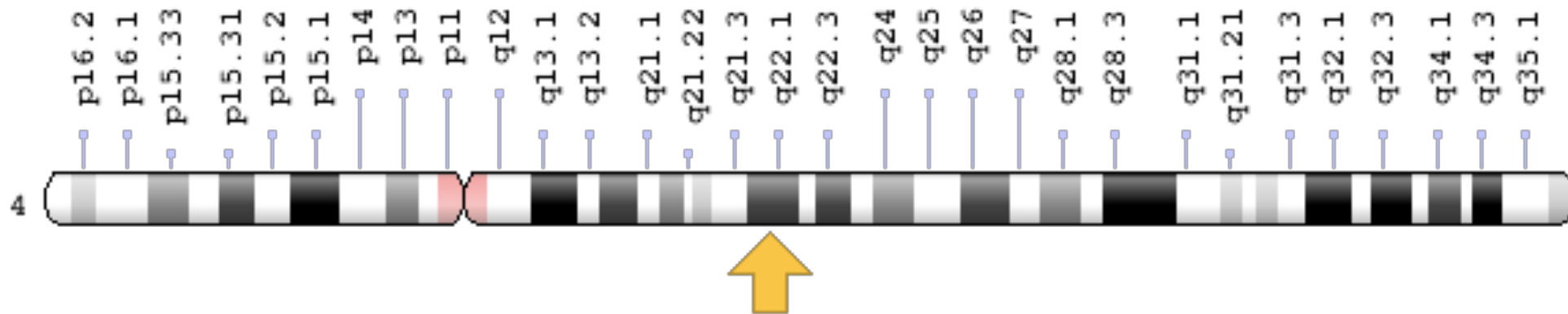
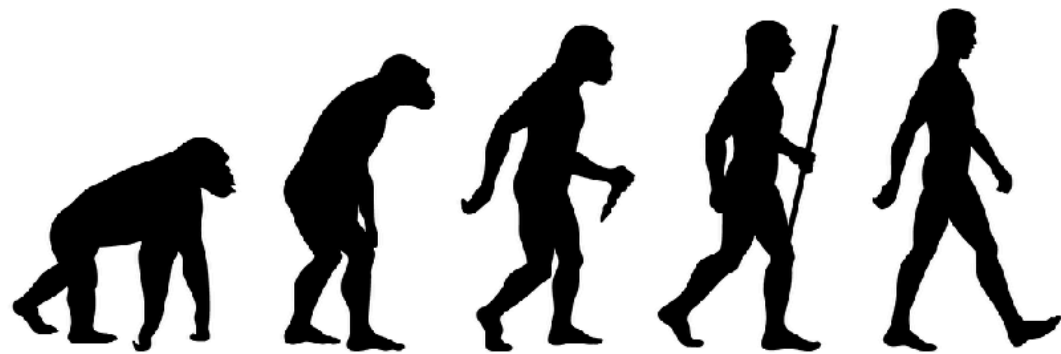


Image 1: <https://ghr.nlm.nih.gov/gene/SNCA#location>

Image 2: <https://www.khanacademy.org/science/biology/human-biology/neuron-nervous-system/a/the-synapse>

# How can studying phylogeny characterize SNCA function?



**Evolutionary Rate**

**+**



**Structural Information**

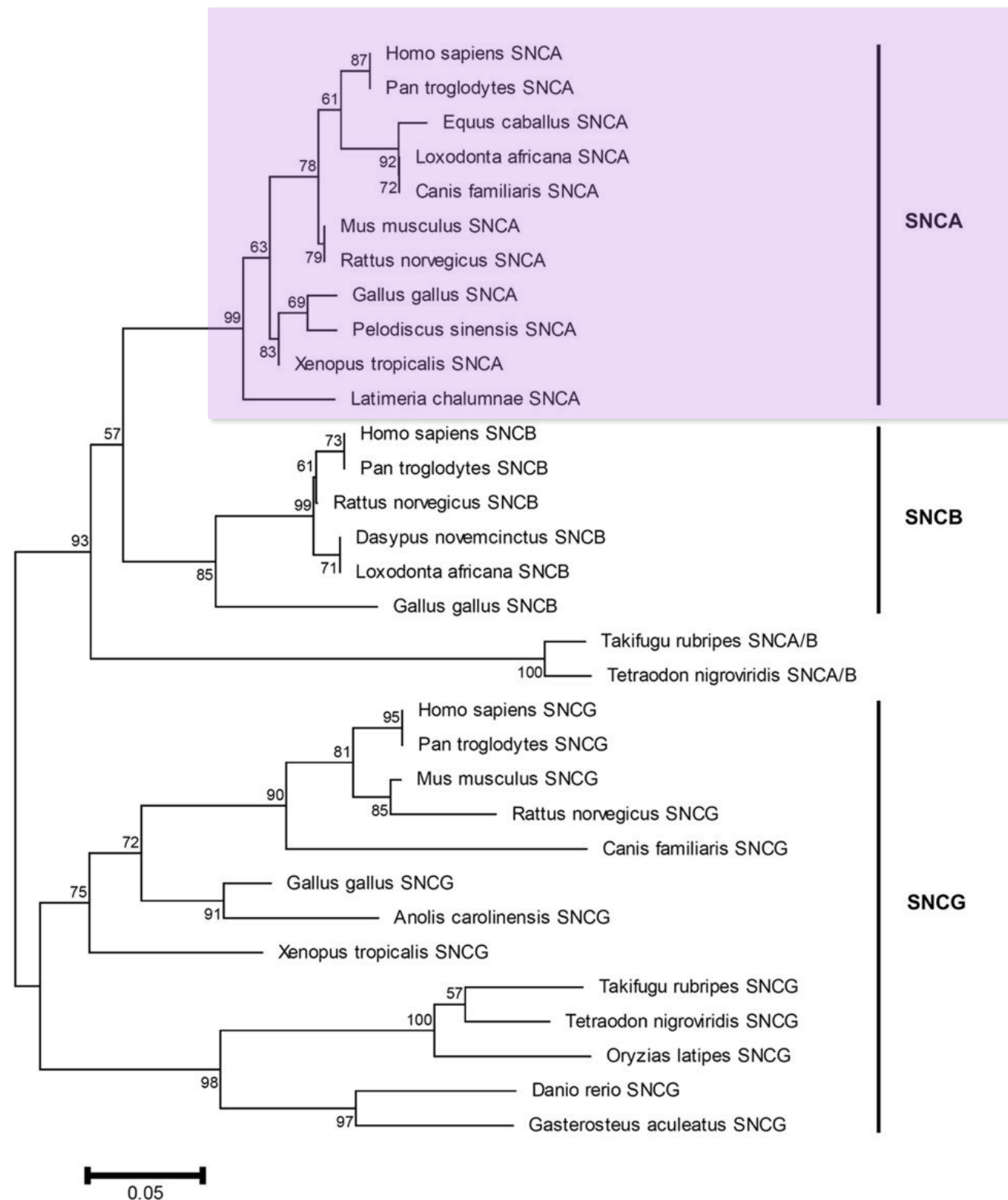
**=**

**Functional Changes**

Image 1: <http://blogs.discovermagazine.com/d-brief/2018/08/09/human-evolution-changes-caused-mental-disorders/>

Image 2: <https://sutherlands.com/d/Building-Materials/2>

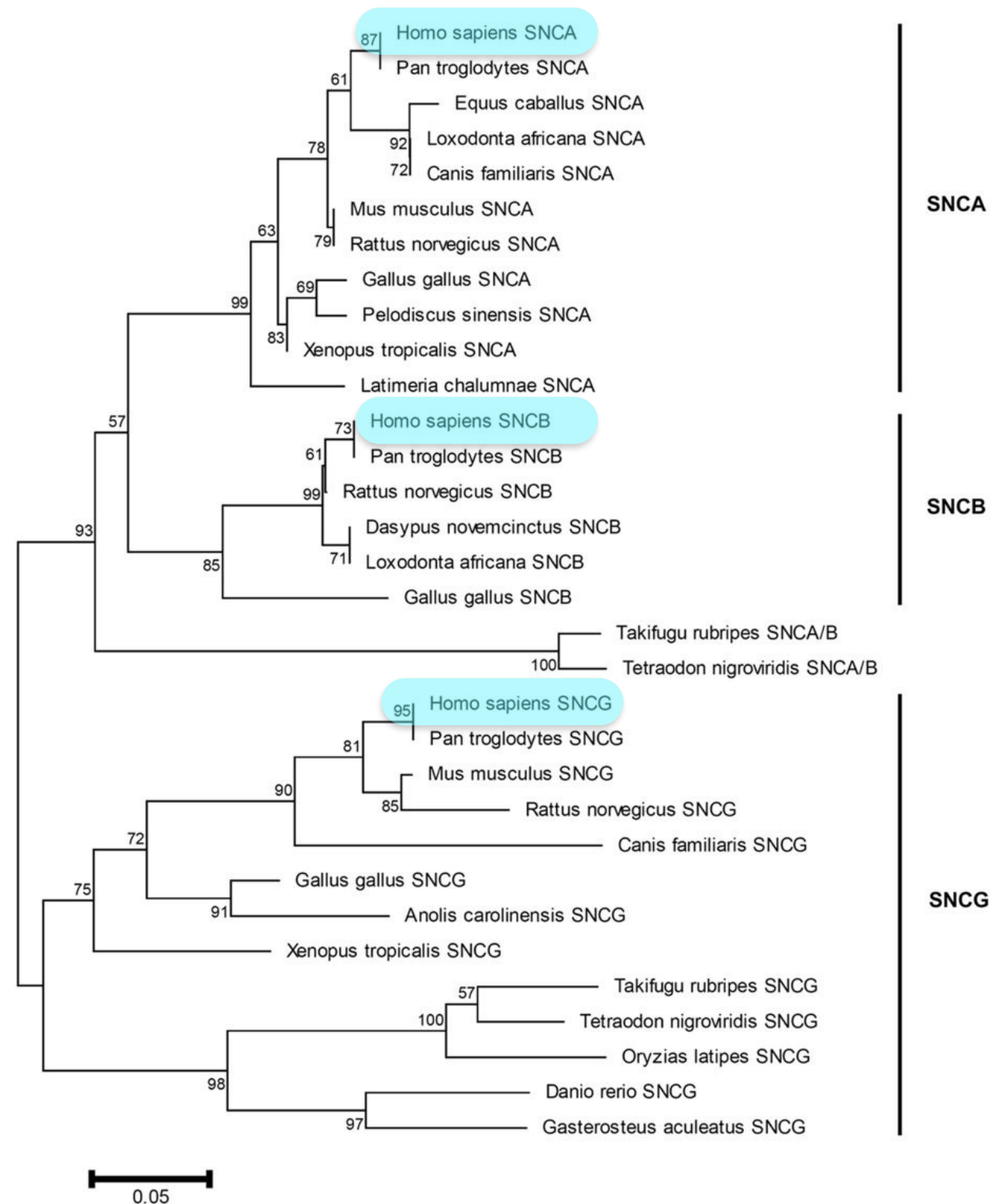
# What are the **orthologs** of SNCA?



Source: Siddiqui IJ, Pervaiz N, Abbasi AA. The Parkinson Disease gene SNCA: Evolutionary and structural insights with pathological implication

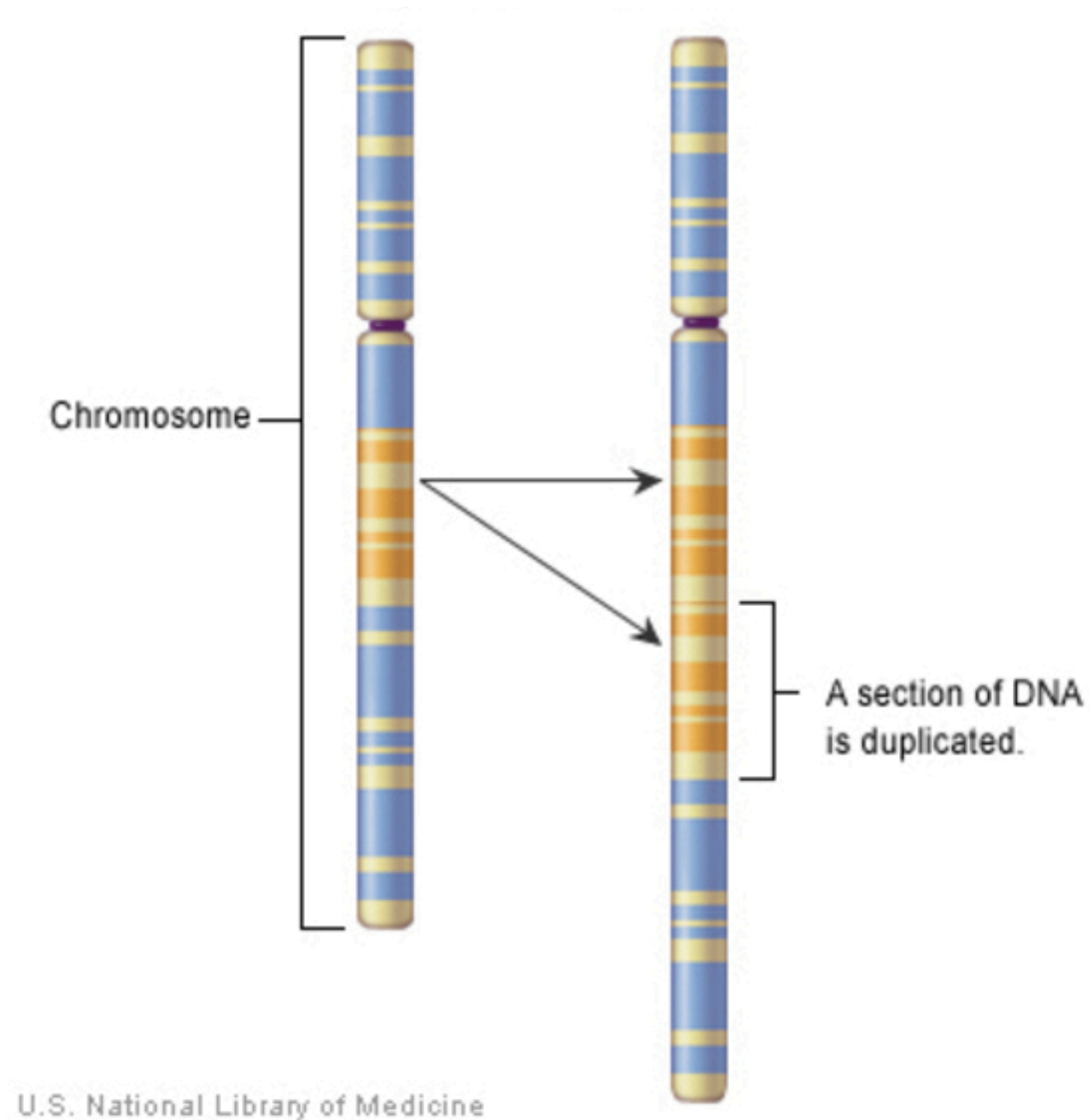


# What are the **paralogs** of SNCA?



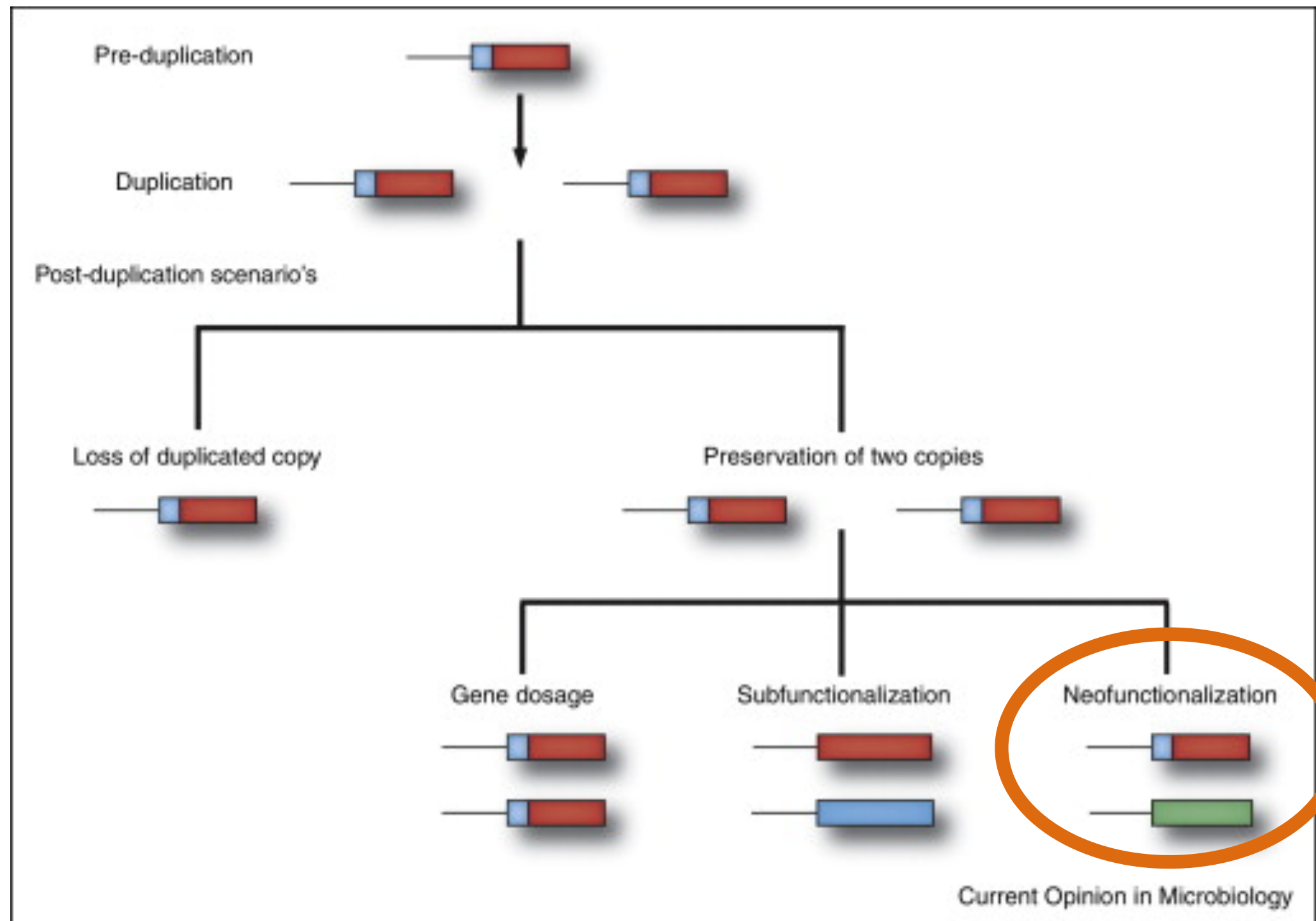
Source: Siddiqui IJ, Pervaiz N, Abbasi AA. The Parkinson Disease gene SNCA: Evolutionary and structural insights with pathological implication

# What is Gene Duplication?



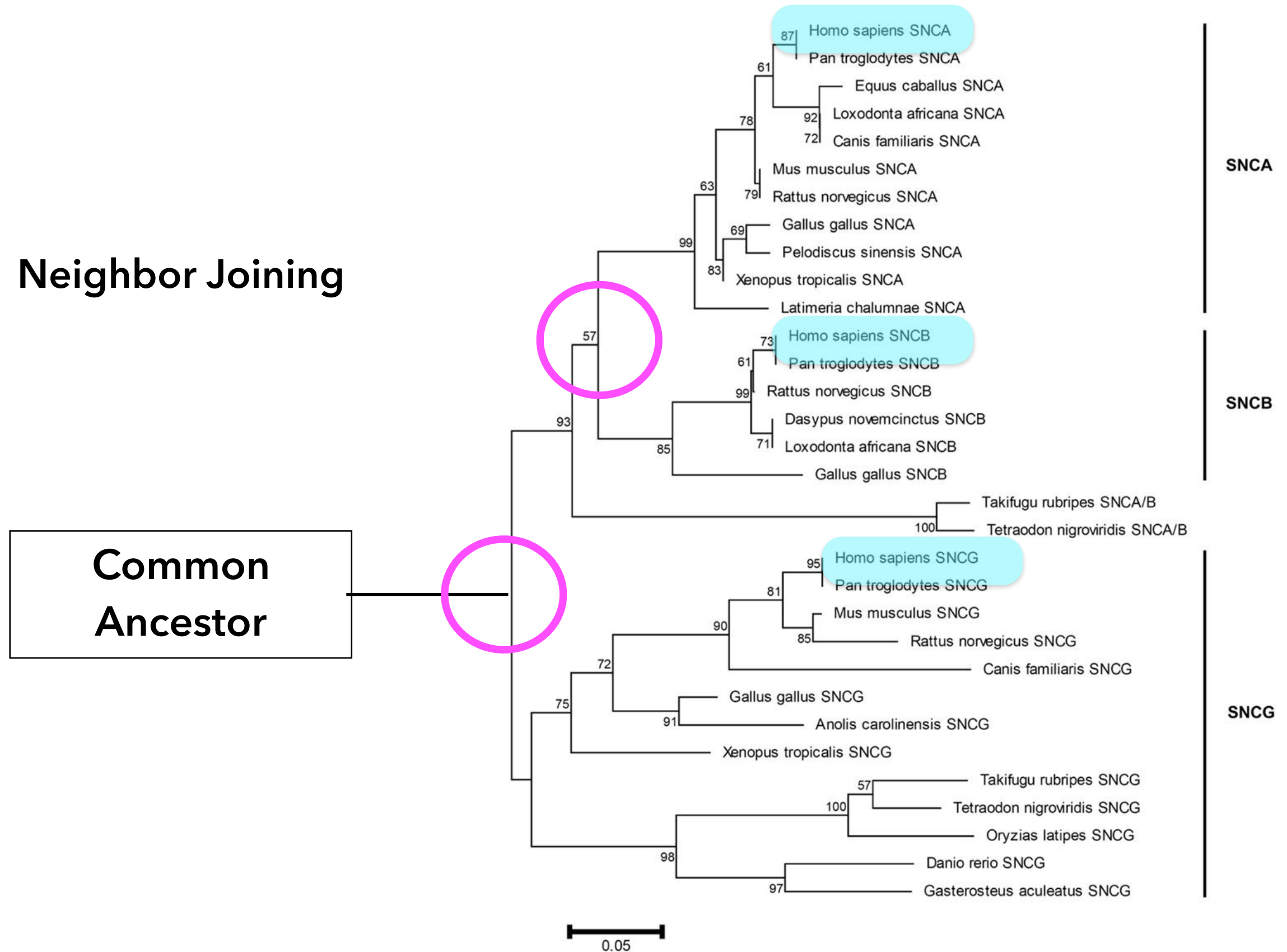
**Gene duplications** are important for genetic diversity and speciation.

# What happens when a gene is duplicated?



# How did gene duplication affect the evolution of SNCA?

Neighbor Joining

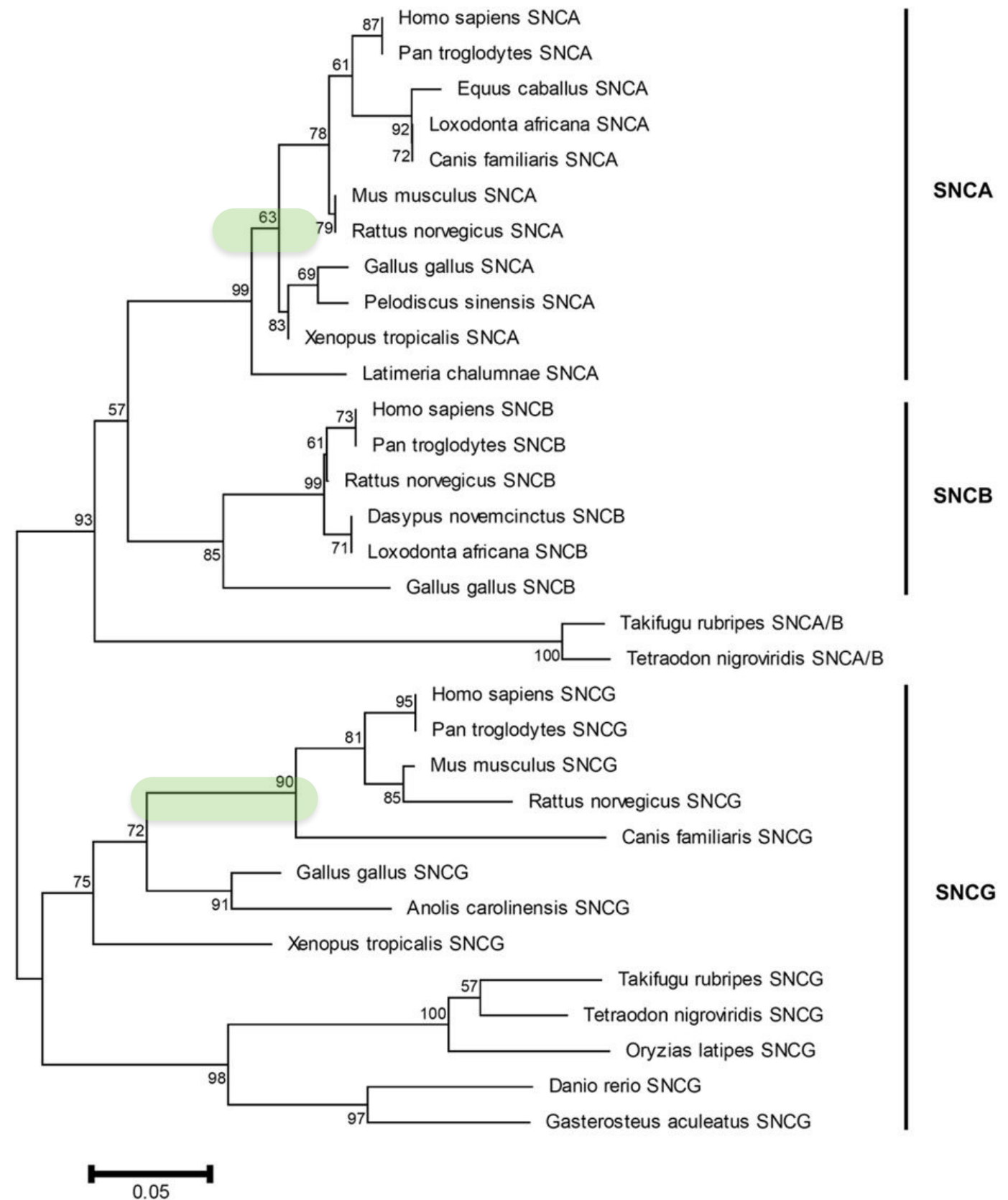




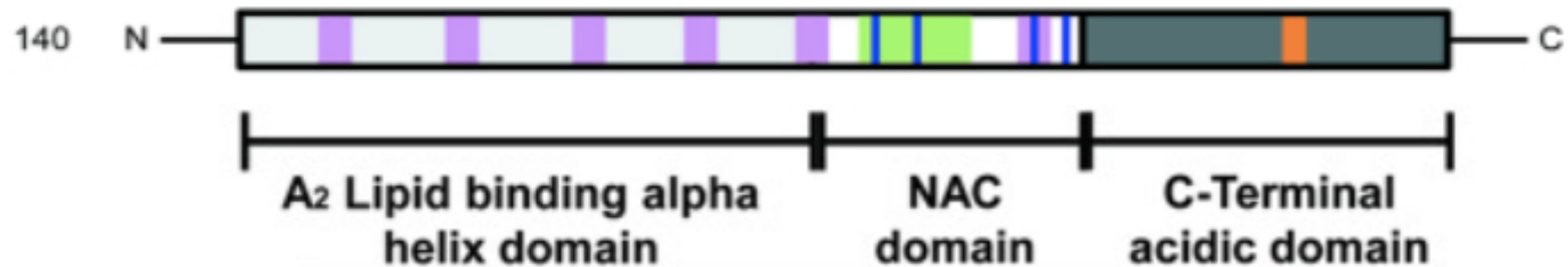
# What else does the phylogenetic tree tell us?

SNCG evolved **fastest**.

Note: Only vertebrates are represented.

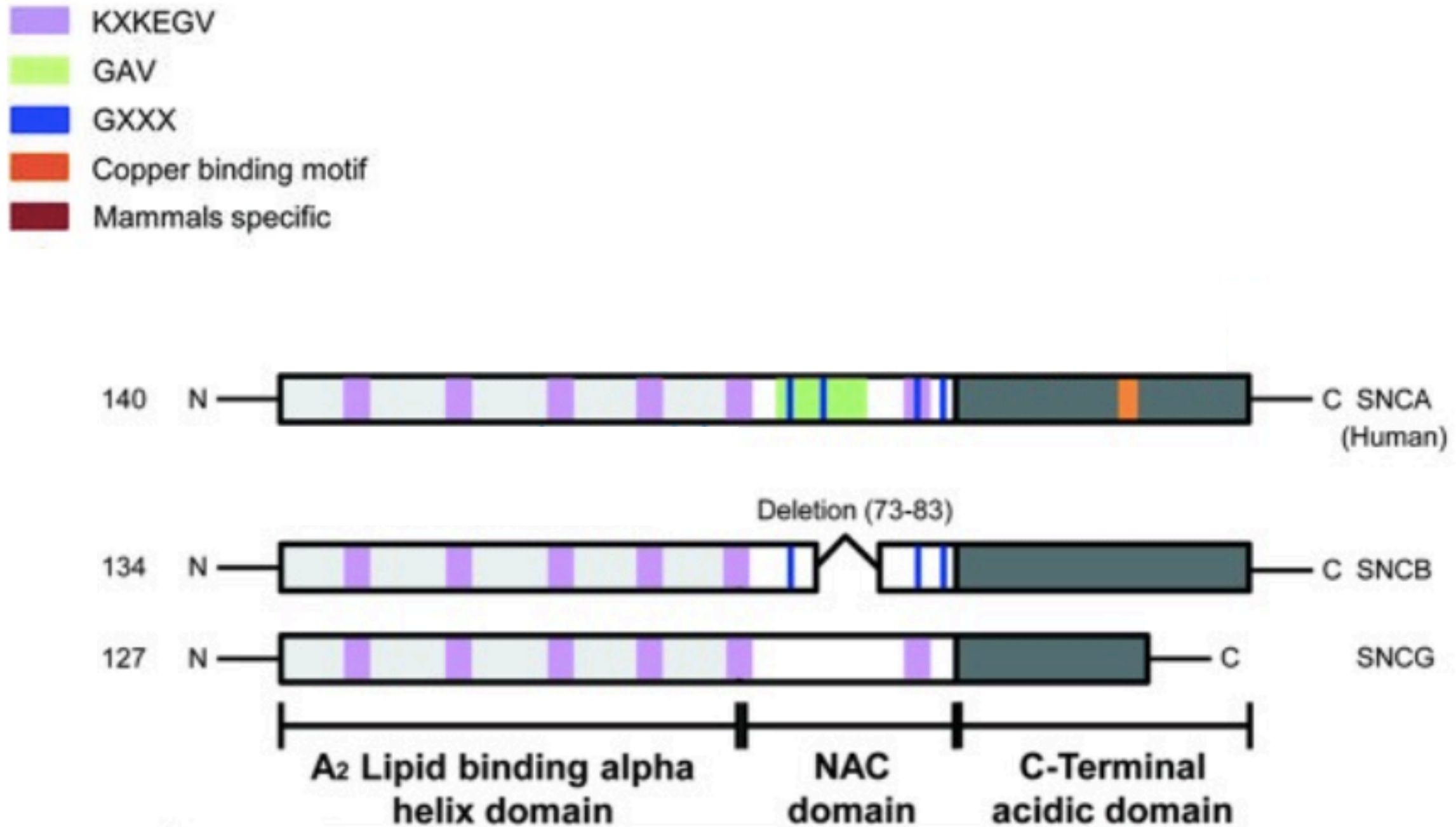


# What does the human SNCA protein look like?

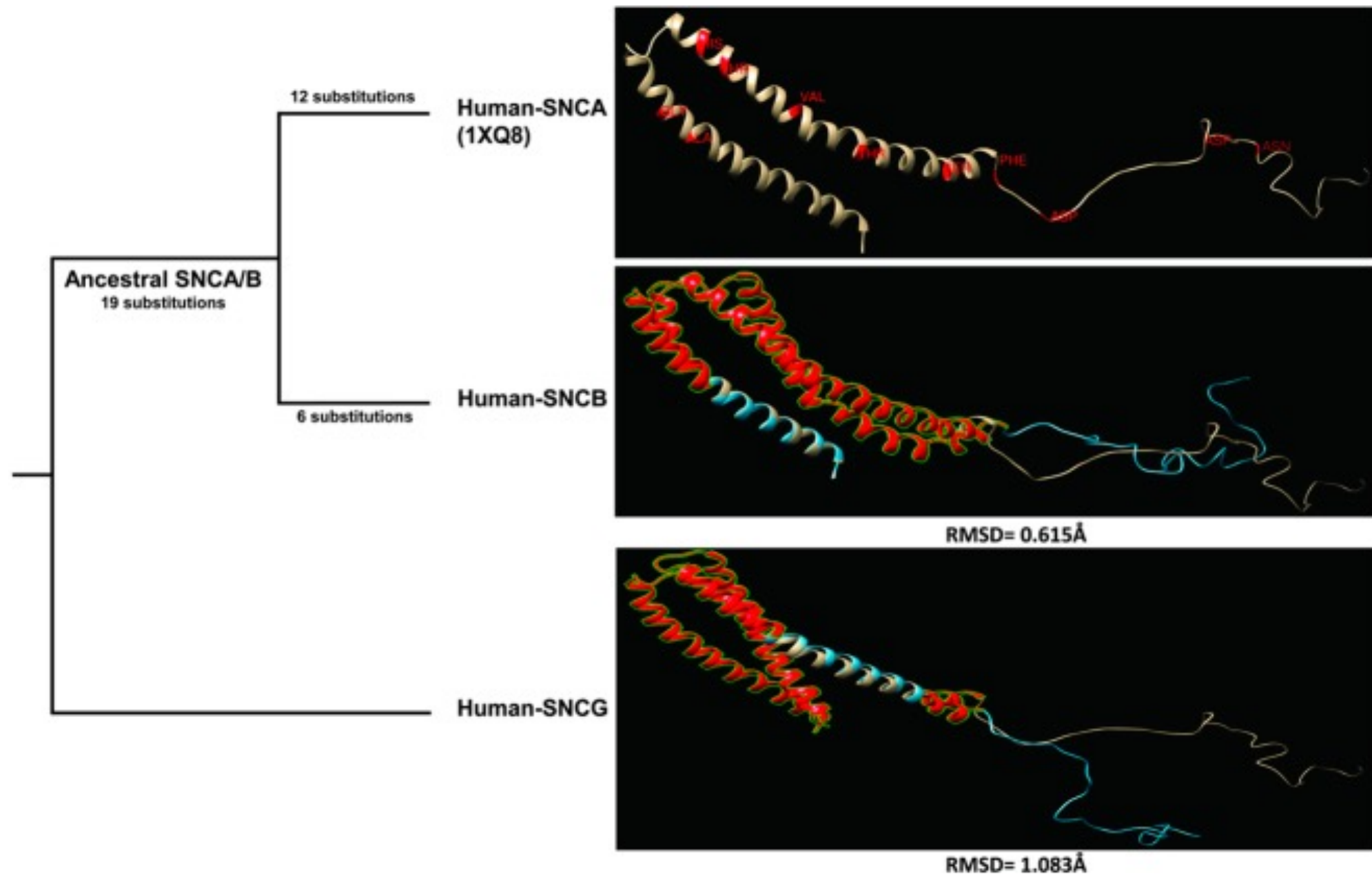


-  KXKEGV - Interaction with Phospholipids
-  GAV - SNCA Aggregation and Fibrillation
-  GXXX
-  Copper binding motif - Accelerates Aggregation and Implicated in Pathology
-  Mammals specific

# What do SNCA paralogs look like?



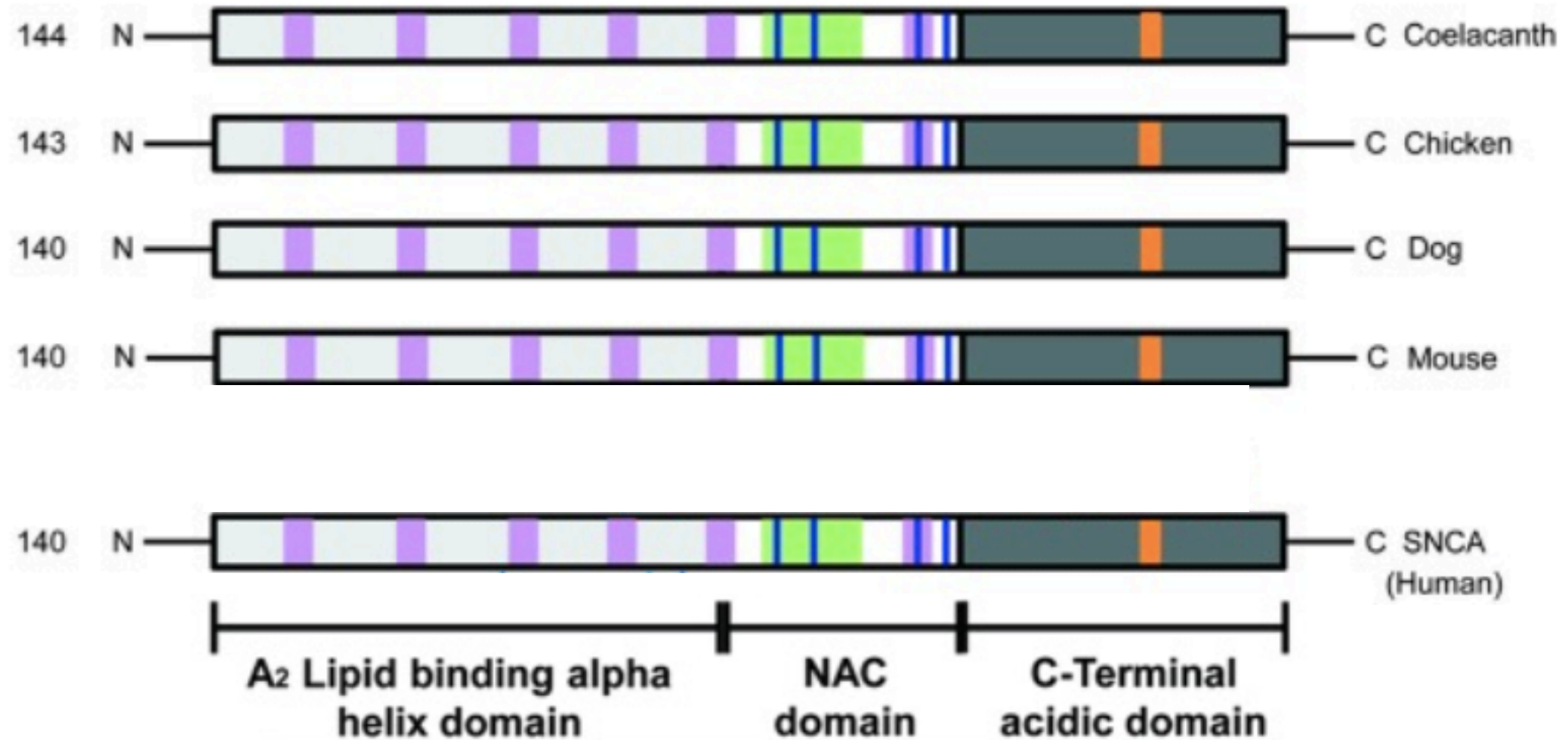
# How do SNCA paralogs compare structurally?



Despite **high sequence homology**, SNCB and SNCG are highly deviant from SNCA in the **lipid binding** and **NAC** domains.



# What do SNCA orthologs look like?



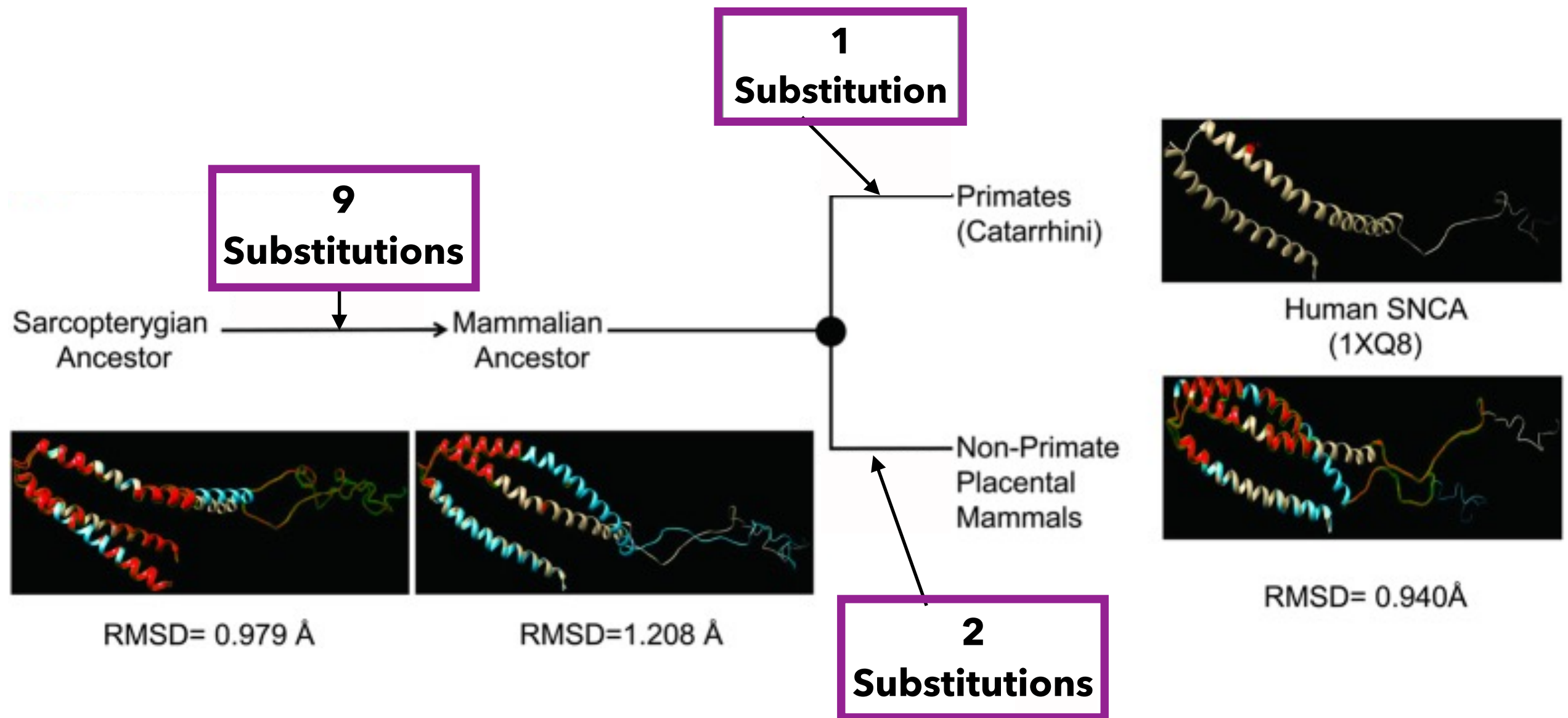
SNCA structure is highly conserved among **orthologs**.

# How are the orthologs different?

Amino Acid Position	Ancestral	Mammal Replacement	Non-Primate Mammal Replacement	Primate Replacement	Preference	Stability Impact
53	T			A	none	-
64	S	T			+	-
68	G		E		-	-
87	N	S			+	-
94	L	F			none	-
95	V		G		-	-
101	A	G			none	-
107	F	A			-	-
112	M	I			+	-
113	M	L			+	-
129	P	S			-	+
132	E	G			-	-

**12** total SNCA amino acid changes have occurred since divergence of SNCA.

# What did the structural evolution of the orthologs look like?



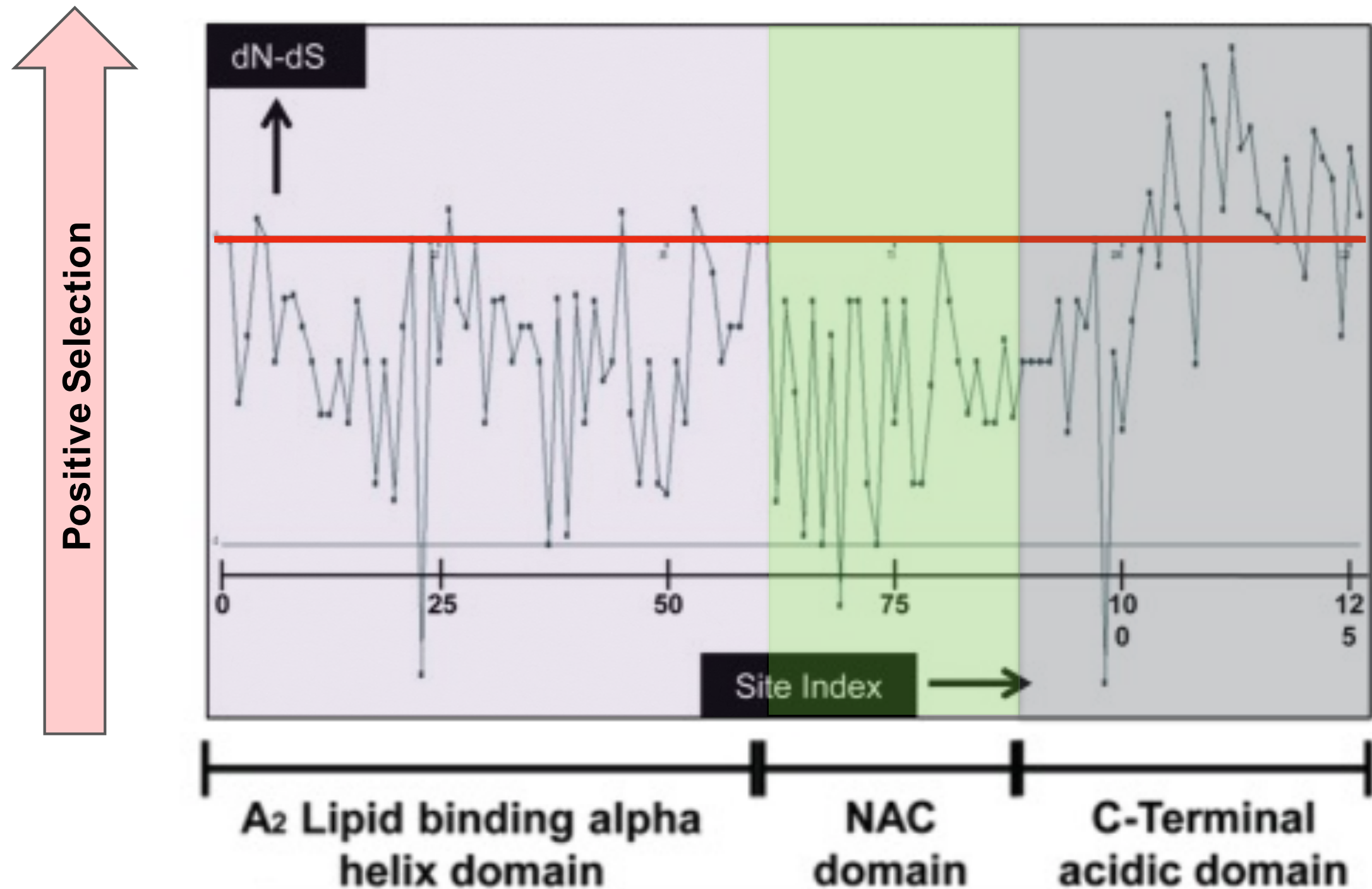
# Are these amino acid changes good or bad?

Amino Acid Position	Ancestral	Mammal Replacement	Non-Primate Mammal Replacement	Primate Replacement	Preference	Stability Impact
53	T			A	none	-
64	S	T			+	-
68	G		E		-	-
87	N	S			+	-
94	L	F			none	-
95	V		G		-	-
101	A	G			none	-
107	F	A			-	-
112	M	I			+	-
113	M	L			+	-
129	P	S			-	+
132	E	G			-	-

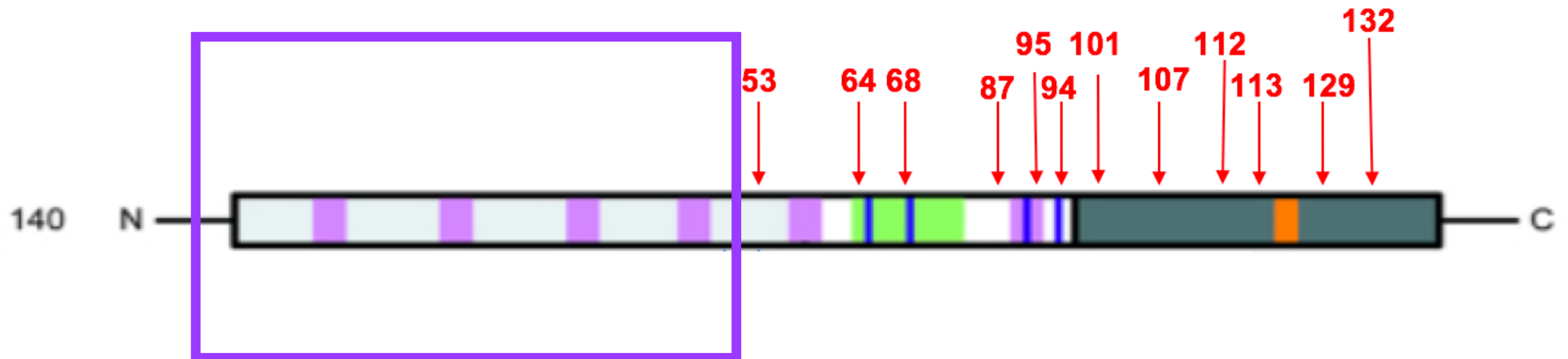
**12** total SNCA amino acid changes have occurred since divergence of SNCA.



# Are the mutations seen in SNCA selected for?



# What do these changes mean for the protein?



# What region of the protein is most important?

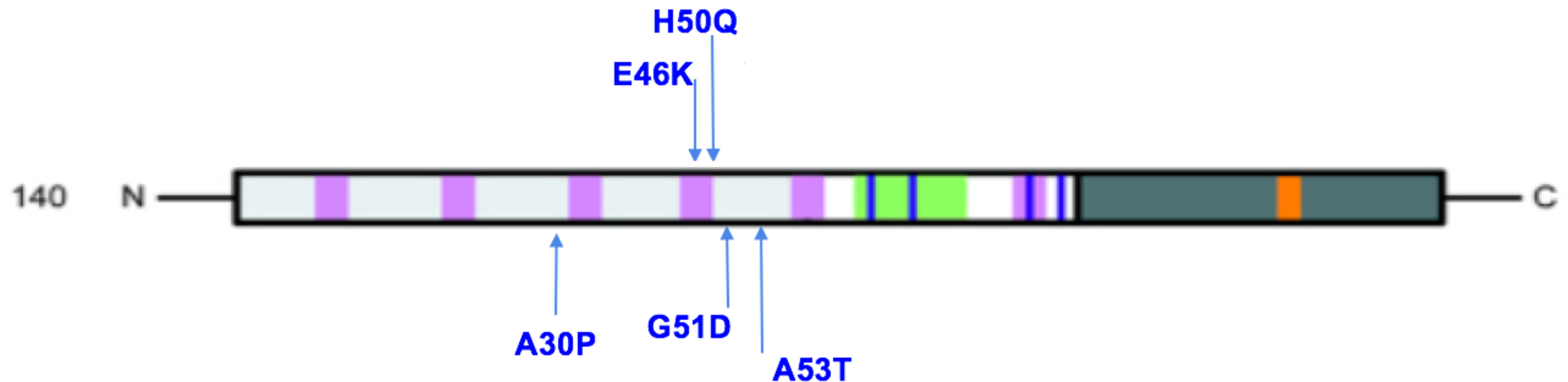
Comparison between lineages	Major change in backbone torsion angles (residue no)	Critical region
Primates ↔ Non Primate Placental Mammals	32–44, 47–58	(32–58) Lipid Binding Domain
	64–74	
	92–113	
Primates ↔ Mammalian Ancestor	37–58	
	70	
Primates ↔ Sarcopterygian Ancestor	8–12, 14, 15, 18, 24, 25, 29–47, 50–55, 58	
	65–77	
	93–107, 109–140	

# What region of the protein is most important?

Comparison between lineages	Major change in backbone torsion angles (residue no)	Critical region
Primates ↔ Non Primate Placental Mammals	32–44, 47–58	(32–58) Lipid Binding Domain
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	92–113	
Primates ↔ Mammalian Ancestor	37–58	
	70	
Primates ↔ Sarcopterygian Ancestor	8–12, 14, 15, 18, 24, 25, 29–47, 50–55, 58	
	65–77	
	93–107, 109–140	

The lipid binding domain undergoes **constant structural evolution** despite high **sequence conservation**.

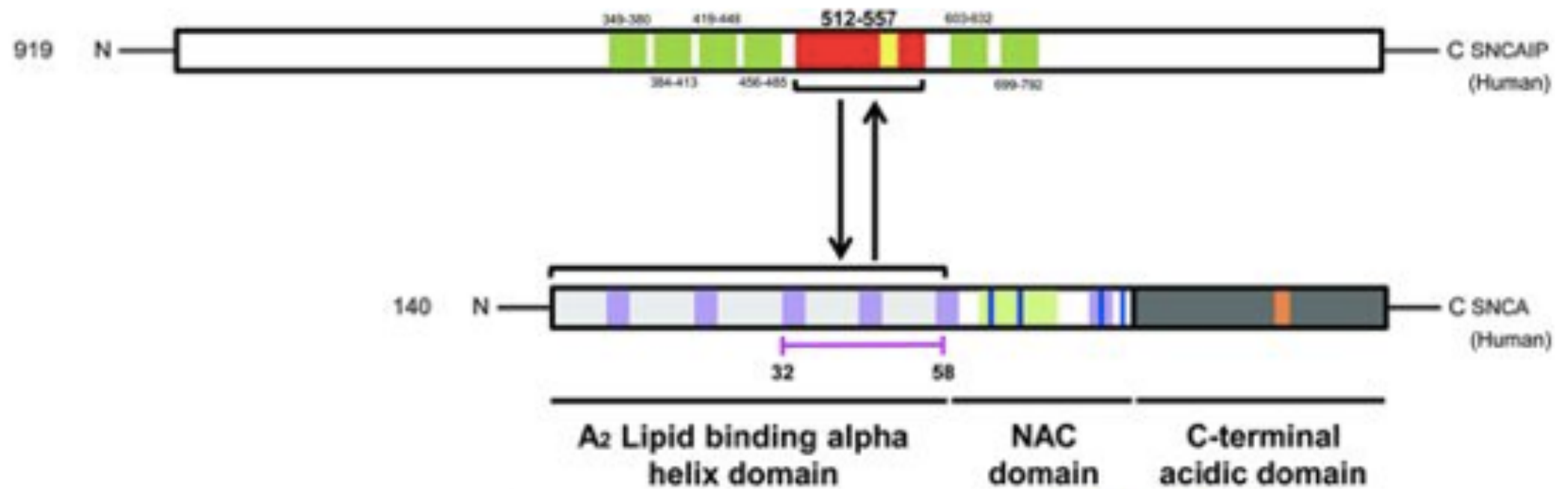
# What does the critical region mean for Parkinson's Disease?



All of the mutations have **different structural effects**, but all cause **high deviance** in the critical region (32-58).



# Why is the critical region so important?

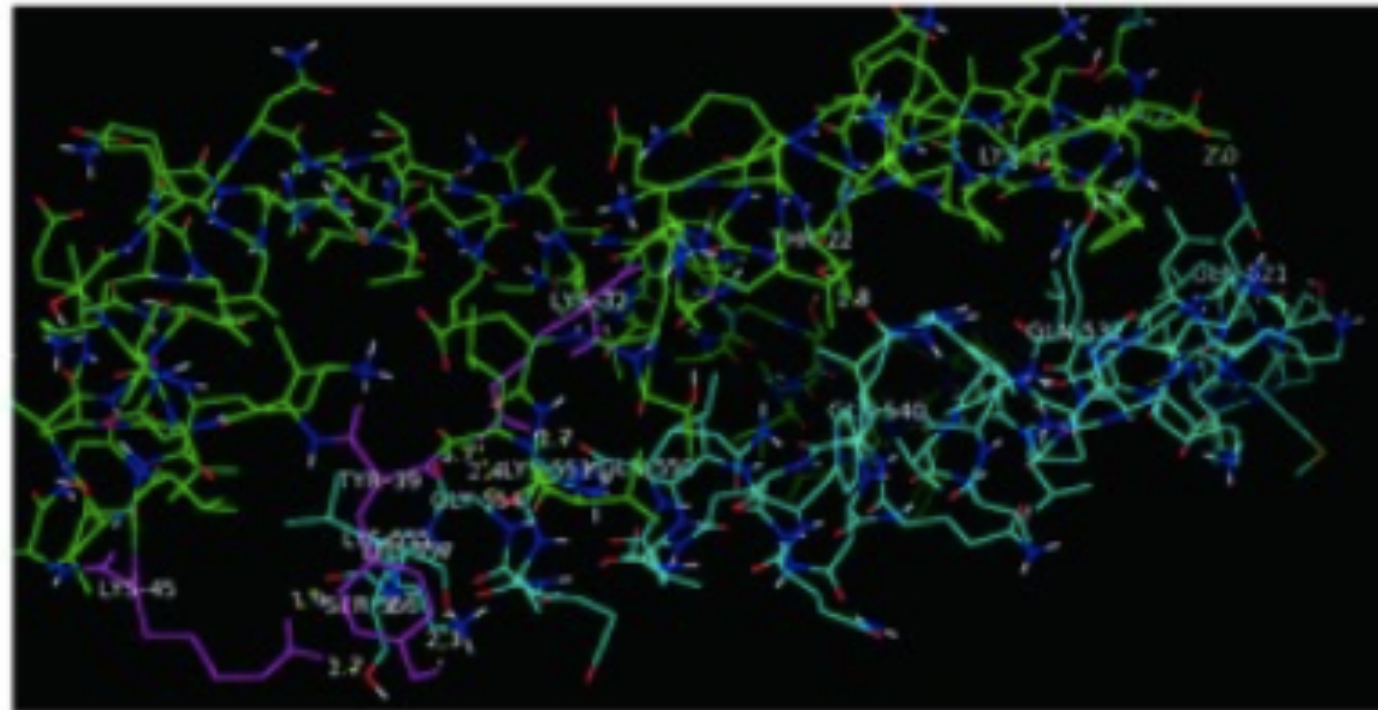


■ Synphilin-1 Coiled-Coil Domain

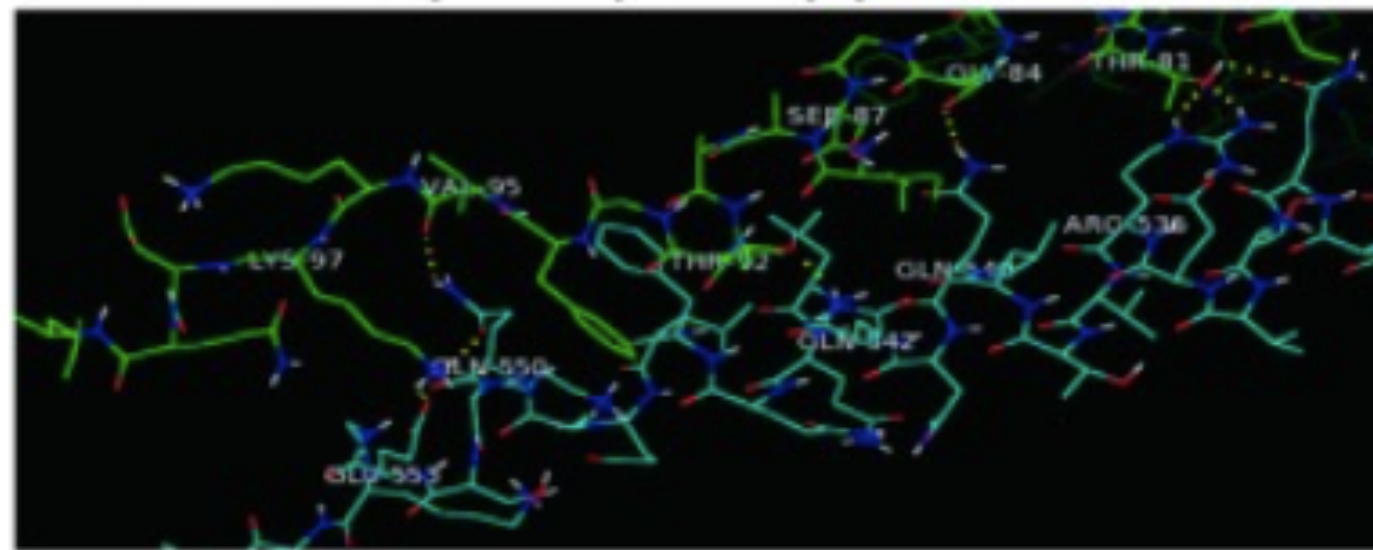
■ Critical Region (32-58)

Synphilin-1 interacts with SNCA at the synapse to facilitate its function.

# How does this interaction differ as a result of mutation?

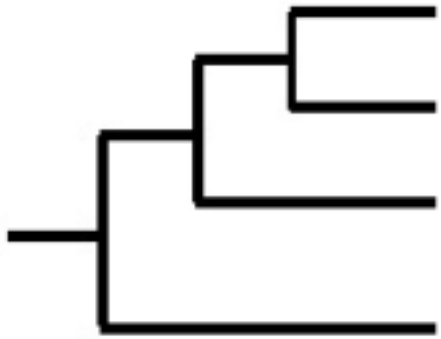


Interaction between primates (catarrhini) specific SNCA and SNCAIP



Interaction between mutant SNCA-A30P and SNCAIP

# Summary



**Phylogenetic analysis indicates the N-terminal sequence of SNCA is highly conserved and changes to the sequence are selected against.**



**Structural analysis identified the lipid binding domain as critical for the maintenance of SNCA's function**



**Interaction analysis identified this critical region as paramount to SNCA synaptic function as well as a promising therapeutic target.**

Image 1:Source: Baum, D. Reading a Phylogenetic Tree:The Meaning of Monophyletic Groups

Image 2: <https://www.shutterstock.com/search/blueprint>

Image 3:[https://www.sciencebuddies.org/science-fair-projects/project-ideas/HumBio\\_p045/human-biology-health/pills](https://www.sciencebuddies.org/science-fair-projects/project-ideas/HumBio_p045/human-biology-health/pills)

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