

Gregory (2005). Synergy between sequence and size in large-scale genomics. *Nature Reviews Genetics* 6: 699-.

1. What are the main components of a eukaryotic genome?
2. What is an intron?
3. What are pseudogenes?
4. What are transposable elements?
5. What are the main differences between eukaryotes and prokaryotes?
6. Name some lines of inquiry that have been used over time to investigate the key components of genomes.
7. What are C-values? What was the relevance of seeing constant C-values within individual organisms and species?
8. What is meant by the C-value paradox?
9. Are relatively weak correlations between genome size and gene number also observed in prokaryotes?

10. How can the relatively weak correlation between gene number and genome size in eukaryotes be explained?
11. What is junk DNA? Is junk DNA positively correlated with genome size?
12. Can sequence data be used to study genome size?
13. Are there cautionary notes linked to using sequence data for inferring genome size? Can you give 2 distinct explanations to support your answer?