# Writing exercise S07: Figure legends

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A figure legend should allow you to understand the contents of the figure without having to refer to the rest of the text. At the same time, it should be concise (more detailed explanation of the methods and results should be found in the appropriate sections). Writing a good figure legend is an art.

### Exercise A.

Read each sample figure legend and ask yourself 3 questions:

1. Do you understand what the figure is presenting (without having to read any additional text)?
2. Why (or why not?)
3. How can it be improved?

### Example 11.

A close-up of a test

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**Fig 1** A hairpin structure, *galE* hairpin, is responsible for the functioning of the 3′ end of *galE* mRNA as an exo-block. (**A**) Galactose operon (top) and nucleotide sequence (bottom) of the 3′ end of *galE* mRNA (green) in the WT *gal* operon. The *galE* stop codon is highlighted in red, and the *galT* initiator codon and SD sequence are highlighted in green and blue (underlined), respectively. The *galE* hairpin structure is depicted based on base complementarity between positions 1142 and 1161. Numbers indicate the nucleotide residue coordinate of the *gal* operon, which starts from the transcription initiation site of the *galP1* promoter. (**B**) Schematics of *galE*-hMM2 and *galE*-hMM5 mutants. The base changes are in red. The *gal* mutants were generated in the single-copy plasmid, pGal, where the entire *gal* operon is cloned and assayed in MG1655 cells from where the entire *gal* has been removed, MG1655Δ*gal*. (**C**) 3′ RACE assay of *galE* mRNA 3′ ends from MG155 cells harboring the plasmid-borne *galE*-hMM2 and *galE*-hMM5 mutant operons. The *galE* mRNA 3′ ends (1166–1172) are missing in lanes 2 and 3. DNA sequencing ladders that serve as length markers are in lanes marked G, A, T, and C.

### Example 22.

A close-up of a chart

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**Figure 2**. Phylogenetic analysis of six *Kodamaea ohmeri* strains based on core genome SNPs.

### Example 33.

A group of graphs showing different numbers

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**Figure 3**. Antibiotic susceptibility of WT, ∆*rpoN*, and ⸬*rpoN* strains. The vertical axis represents the *OD*600 value, while the horizontal axis represents the concentration of different antibiotics (mg/mL). The blue, red, and green bars indicate the *OD*600 values of WT, Δ*rpoN*, and ⸬*rpoN* strains at different antibiotic concentrations. Compared to WT, the Δ*rpoN* strain exhibited significantly decreased susceptibility to amoxicillin **(A)**, ampicillin **(B)**, metronidazole **(C)**, vancomycin **(D)**, norfloxacin **(E)**, cefotetan **(F)**, and kanamycin **(G)**, whereas the ⸬*rpoN* strain showed partial restoration of susceptibility to these antibiotics compared to WT.

### Exercise B.

Write a legend for the following figure. Compare your legend with the authors’4.

A diagram of a graph

AI-generated content may be incorrect.

### References

1. Jeon HJ, et al. Rho-dependent termination and RNase E-mediated cleavage: dual pathways for RNA 3′ end processing in polycistronic mRNA. Journal of Bacteriology 207, e00437-24 (2025).https://doi.org/10.1128/jb.00437-24
2. Wang, S.-J., Yu, X., Liang, J.-h., Zheng, D.-y. & Cao, C.-W. Emerging pathogens: the underestimated risk of Kodamaea ohmeri infection in hospitals. Frontiers in Microbiology Volume 16 - 2025 (2025). <https://doi.org/10.3389/fmicb.2025.1572747>
3. Yang, Y. et al. The sigma factor σ54 (*rpoN*) functions as a global regulator of antibiotic resistance, motility, metabolism, and virulence in *Clostridioides difficile*. Frontiers in Microbiology Volume 16 - 2025 (2025). <https://doi.org/10.3389/fmicb.2025.1569627>
4. Zhang, J. et al. *Borrelia burgdorferi* loses essential genetic elements and cell proliferative potential during stationary phase in culture but not in the tick vector. Journal of Bacteriology 207, e00457-00424 (2025). https://doi.org/doi:10.1128/jb.00457-24