# Additional writing exercises (01)

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### Exercise 2A.

Read each sample of scientific writing and ask yourself 3 questions:

1. For each paragraph, can you identify the topic sentence/topic of the paragraph?
2. Do the subsequent sentences logically flow and lead to a sensible, well-supported conclusion?
3. Could the structure/logical order of the paragraph be improved (if so, how?)?

**Sample 1** 1

The method for controlling gall disease involves the use of chemicals such as copper and acids ([Sawalha et al., 2013](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1437536/full" \l "ref41); [Mary Opisa et al., 2020](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1437536/full#ref33)). However, heavy use of these chemicals can contribute to soil pollution, the development of resistant strains, and potential harm to humans. Commercial biocontrol therapies have been available for decades to prevent *R. radiobacter* in some plants. For instance, *A. radiobacter* strain K84 has been shown to produce bacteriocin called agrocin 84 and used to control *A. tumefaciens* in cherry ([Stockwell et al., 1993](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1437536/full#ref45); [Penyalver et al., 2001](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1437536/full" \l "ref38)). While this inhibitory compound is very effective against *R. radiobacter*, the application may adversely affect beneficial microbes that are closely related to other *Rhizobium* species. To date, there is no effective method for curing stem gall disease in highbush blueberry. The best strategy for controlling gall disease is proactive prevention before the onset of the disease.

**Sample 2** 2

Bacteriophages represent an intriguing avenue in the ongoing battle to control bacterial infections. These viruses, which specifically target bacteria, have long been recognized for their potential in combatting bacterial infections (Chang et al., 2022; Sanmukh et al., 2023). Since their discovery in the early 20th century, phages have garnered increasing attention for their unique ability to infect and lyse bacterial cells (Chen et al., 2023). This natural phenomenon has been the driving force behind endeavors to harness phages as potential therapeutic agents against bacterial pathogens (Sharma et al., 2017). The dynamic co-evolution between bacteria and phages has not only shaped the intricate resistance systems of bacteria but has also propelled the adaptation and diversification of phages (Koonjan et al., 2020; Venturini et al., 2022).

**Sample 3** 3

*Klebsiella pneumoniae* is a crucial nosocomial pathogen that causes severe diseases, including bloodstream infections (BSIs). The considerable ability of carbapenem-resistant *K. pneumoniae* (CRKP) to acquire antibiotic resistance is a major health concern [1]. The rapid spread and increased incidence are being observed globally, presenting an enormous challenge in healthcare settings [2, 3]. The dominant clone in China is ST11 CRKP, which produces carbapenem-hydrolyzing *K. pneumoniae* carbapenemase (KPC-2) [4]. Traditionally, CRKP is not considered hypervirulent; nevertheless, in 2016, a fatal outbreak of severe pneumonia caused by ST11 hypervirulent carbapenem-resistant *K. pneumoniae* (hvCRKP) strains occurred in China [5]. The ST11 hvCRKP clone belonged to serotype K47 and harbored a pLVPK-like virulence plasmid carrying the *rmpA2, iucABCD*, and *iutA* virulence genes. Since then, emergence of ST11 hvCRKP infections has become a recent public health crisis [6–8].

**Sample 4** 4

*Borrelia* spirochetes are a group of bacteria that includes pathogens causing the zoonotic diseases Lyme borreliosis ([1](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B1)) and relapsing fever ([2](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B2)). *Borrelia* species feature the most highly segmented genome observed in bacteria to-date, comprised of a linear chromosome and multiple linear and circular extrachromosomal plasmids ([3–6](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B3)). The linear replicons are capped with covalently closed hairpin telomeres, presenting *Borrelia* with the end replication problem associated with linear DNAs ([7–9](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B7)). *Borrelia* species solve the end replication problem by initiating replication of the linear replicons at a bidirectional origin ([10](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B10),[11](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B11)), resulting in a circular dimer of inverted repeats as a DNA replication intermediate (Figure [​(Figure1).1](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/figure/F1/)). The replicated telomeres are recognized by a specialized enzyme, known as telomere resolvase (ResT), which catalyzes a DNA cleavage and rejoining event to resolve the circular dimers and generate hairpin telomere ends on the resulting linear DNA molecules ([9](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B9),[12](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B12),[13](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B13)). Telomere resolvases have also been referred to as protelomerases ([14](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B14)); however several issues exist with the latter nomenclature ([15](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC11317167/#B15)), including the confusion arising from the very different type of activity displayed by eukaryotic telomerases and the fact that a proenzyme is an inactive enzyme precursor.

### References

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3. Chen, T., Wang, Y., Chi, X., Xiong, L., Lu, P., Wang, X., Chen, Y., Luo, Q., Shen, P., & Xiao, Y. (2024). Genetic, virulence, and antimicrobial resistance characteristics associated with distinct morphotypes in ST11 carbapenem-resistant Klebsiella pneumoniae. Virulence, 15(1). <https://doi.org/10.1080/21505594.2024.2349768>
4. Semper, C., Watanabe, N., Karimullina, E., Patel, D. T., Di Leo, R., Castellanos, M., Patel, D. H., Chaconas, G., & Savchenko, A. (2024). Structure analysis of the telomere resolvase from the Lyme disease spirochete Borrelia garinii reveals functional divergence of its C-terminal domain. *Nucleic Acids Research*. https://doi.org/10.1093/nar/gkae580