# Writing exercise S10: Abstracts

## Dr. Morgan Feeney, AY 2024-25

### Exercise A.

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

1. Is it well-written?
2. Why (or why not?)
3. How can it be improved?

Example 1.

Bacterial RNA polymerase (RNAP) is a multisubunit enzyme that copies DNA into RNA in a process known as transcription. Bacteria use σ factors to recruit RNAP to promoter regions of genes that need to be transcribed, with 60% bacteria containing at least one specialized σ factor, σ54. σ54 recruits RNAP to promoters of genes associated with stress responses and forms a stable closed complex that does not spontaneously isomerize to the open state where promoter DNA is melted out and competent for transcription. The σ54-mediated open complex formation requires specific AAA+ proteins (ATPases Associated with diverse cellular Activities) known as bacterial enhancer-binding proteins (bEBPs). We have now obtained structures of new intermediate states of bEBP-bound complexes during transcription initiation, which elucidate the mechanism of DNA melting driven by ATPase activity of bEBPs and suggest a mechanistic model that couples the Adenosine triphosphate (ATP) hydrolysis cycle within the bEBP hexamer with σ54 unfolding. Our data reveal that bEBP forms a nonplanar hexamer with the hydrolysis-ready subunit located at the furthest/highest point of the spiral hexamer relative to the RNAP. ATP hydrolysis induces conformational changes in bEBP that drives a vectoral transiting of the regulatory N terminus of σ54 into the bEBP hexamer central pore causing the partial unfolding of σ54, while forming specific bEBP contacts with promoter DNA. Furthermore, our data suggest a mechanism of the bEBP AAA+ protein that is distinct from the hand-over-hand mechanism proposed for many other AAA+ proteins, highlighting the versatile mechanisms utilized by the large protein family.

Example 2.

**Introduction:**The *rpoE-chrR* pair is a regulatory system used by photosynthetic microorganisms to overcome singlet oxygen stress. *rpoE* and *chrR* encode the sigma factor σE and anti-sigma factor ChrR, respectively. Stenotrophomonas maltophilia, an opportunistic pathogen, is a multidrug-resistant gram-negative bacterium. Although it is not a photosynthetic microorganism, a *rpoE-chrR* homolog (*smlt2377-smlt2378*) was found in the *S. maltophilia* genome. In this study, we aimed to assess the significance of σEc-ChrR pair in oxidative stress alleviation and antibiotic susceptibility of *S. maltophilia* KJ.

**Methods:**Reverse transcription-polymerase chain reaction was used to validate the presence of operon. The contribution of *rpoEc-chrR-chrA* operon to oxidative stress alleviation and antibiotic susceptibility was evaluated using mutant constructs and stress-tolerance assays. RNA-seq transcriptome assay of wild-type KJ, KJΔChrR (*chrR* mutant), and KJΔChrRΔRpoEc (*chrR/rpoEc* double mutant) was performed to reveal the σEc regulon.

**Results:**The *rpoEc-chrR* pair and downstream chrA formed an operon. Inactivation of *chrR* upregulated the expression of *rpoEc-chrR-chrA* operon in an σEc- and ChrA-dependent manner. σEc activation contributed to superoxide tolerance and increased β-lactam susceptibility but did not affect the tolerance to singlet oxygen and hydrogen peroxide. Transcriptome analysis revealed that expression of the nine-gene cluster, *smlt2375-smlt2367*, was significantly upregulated in KJΔChrR and reverted to the wild-type level in KJΔChrRΔRpoEc. *smlt2375-smlt2367* cluster was located upstream of the *rpoEc-chrR-chrA* operon and divergently transcribed, seeming to be involved in membrane lipid modification. Deletion of *smlt2375-smlt2367* cluster from the chromosome of KJΔChrR reverted the superoxide tolerance and β-lactam susceptibility to the wild-type level.

**Discussion:**The *rpoEc-chrR* pair of *S. maltophilia* was involved in superoxide tolerance and β-lactam susceptibility. Notably, a novel regulatory circuit involving *rpoEc-chrR-chrA* operon and *smlt2375-smlt2367* cluster was revealed.

Example 3.

In *Xanthomonas axonopodis* pv. *glycines* (*Xag*), *rpoE* (encoding *σ*E) resided within the conserved *rseA*-*mucD* operon but was dually repressed by DSF signaling and the global regulator Clp. Although H2O2 induced *rpoE* transcription, its expression was paradoxically downregulated by H2O2-detoxification genes (*oxyR*, *ahpC*, *ahpF*, *catB*), suggesting a potential feedback loop. Notably, the *rpoE* mutant exhibited attenuated soybean virulence characterized by (1) reduced cell wall-degrading enzymes (CWDEs) production, leading to diminished activation of soybean innate immunity (ROS burst, callose deposition, programmed cell death, and jasmonic acid accumulation); (2) increased H2O2 sensitivity with impaired siderophore-mediated iron acquisition; (3) failure to elicit hypersensitive response (HR) in nonhosts. Significantly, *rpoE* complementation fully restored virulence traits. Collectively, RpoE emerges as a central regulator orchestrating oxidative stress adaptation, stealth pathogenesis via CWDEs-mediated immune suppression, and host-specific virulence/HR elicitation in *Xag* through its unique network, redefining sigma factor functionality in xanthomonads and providing targets for disrupting pathogen-host interactions.

### Exercise 1B.

As you read papers for your literature search/introduction, **pay attention to the quality of the writing**.

Select one paragraph that you think is **particularly well-written,** and one paragraph that you think is **particularly poorly-written**, and submit these to Dr. Feeney via e-mail before our meeting next week.

### References

1. Gao F, Ye F, Buck M, Zhang X. Subunit specialization in AAA+ proteins and substrate unfolding during transcription complex remodeling. *Proc Natl Acad Sci U S A*. 2025;122(17):e2425868122. doi:10.1073/pnas.2425868122
2. Ku RH, Lu HF, Li LH, Yeh TY, Lin YT, Yang TC. Roles of the *rpoEc-chrR-chrA* operon in superoxide tolerance and β-lactam susceptibility of *Stenotrophomonas maltophilia*. *Front Cell Infect Microbiol*. 2025;15:1492008. Published 2025 Feb 4. doi:10.3389/fcimb.2025.1492008
3. Geng H, Su R, Tao Y, et al. RpoE Orchestrates Oxidative Stress Adaptation, Virulence, and Dual Plant Immune Modulation in *Xanthomonas axonopodis* pv. *glycines*. *J Agric Food Chem*. Published online April 28, 2025. doi:10.1021/acs.jafc.5c00235