# Writing exercise S10: Abstracts

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You can think of the abstract as a “paper in miniature” – in a few sentences each, it should encapsulate the introduction, methods, results, and discussion/significance. (The methods are sometimes left implicit, or described at a very high level (e.g., “Structural and biochemical analyses” in the example below.)

Overall, the abstract should be extremely concise, precise, and focused. It should give an enticing description of the paper (so that the reader will want to read it to learn more). It should also be pitched at the correct level so that the reader can understand it (this may depend somewhat on the journal/intended audience for the paper, or in your case, whether you are writing a lay or technical abstract.)

(Tip: when it comes to the lay and technical abstracts, many students seem to write their technical abstract, and then edit it to remove anything that they perceive as technical language, to generate their lay abstract. A better approach is to start the lay abstract with a fresh slate: think of what a non-scientist audience needs to know to understand your work, and begin writing/explaining from there.)

Example abstract1: (Annotated to indicate intro, methods, results, and discussion/significance).

The cyclic dinucleotide c-di-GMP is a signaling molecule with diverse functions in cellular physiology. Here, we report that c-di-GMP can assemble into a tetramer that mediates the effective dimerization of a transcription factor, BldD, which controls the progression of multicellular differentiation in sporulating actinomycete bacteria. BldD represses expression of sporulation genes during vegetative growth in a manner that depends on c-di-GMP-mediated dimerization. Structural and biochemical analyses show that tetrameric c-di-GMP links two subunits of BldD through their C-terminal domains, which are otherwise separated by ~10 Å and thus cannot effect dimerization directly. Binding of the c-di-GMP tetramer by BldD is selective and requires a bipartite RXD-X8-RXXD signature. The findings indicate a unique mechanism of protein dimerization and the ability of nucleotide signaling molecules to assume alternative oligomeric states to effect different functions.

### Exercise A.

Read through each of the following abstracts. For each, ask yourself:

1. Can you identify which parts of the abstract describe introduction, methods, results, and discussion/significance?
2. Is the level of detail appropriate and helpful for the reader?
3. How could the abstract be improved?

Example 12.

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 23.

**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 34.

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 B.

Draft your own abstract. Think carefully about the level of detail required to describe each section, and the information that a reader needs to know about your thesis.

Then, edit your draft. Look for opportunities to make it more concise (omit unneeded words). Ask a friend or colleague for feedback on whether your abstract effectively summarises your project.

### References

1. Tschowri N, Schumacher MA, Schlimpert S, et al. Tetrameric c-di-GMP mediates effective transcription factor dimerization to control Streptomyces development. *Cell*. 2014;158(5):1136-1147. doi:10.1016/j.cell.2014.07.022
2. 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
3. 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
4. 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