

How to Write a Scientific Abstract

Effective abstracts give readers a snapshot of your work and its importance. Ideally, they will aim not only to describe or summarize your work, but also to position it within existing research questions in your field and clearly explain the contribution your work stands to make towards addressing these questions. More people will read your abstract than will read your paper or attend your talk. For this reason, it is crucial to write a memorable and informative abstract.

Before you begin. Do some research on the journal or conference and read their instructions for submission to determine:

1. The interests or themes of the journal/conference
2. The word count allowed by the conference or journal (typically 250-500)
3. The format of the abstract for the conference or journal (may require specific sections, e.g. “Importance”)
4. The audience (e.g. scientists in your field, scientists outside your field, the community)

Elements of an Abstract. An effective abstract will contain all of the elements of a scientific paper but in one paragraph. This one paragraph should give enough information to stand on its own and entice potential readers or attendees to seek out your paper or talk. For each element, confine yourself to one sentence, maybe two if you have space. Also, keep your audience in mind and adjust the specificity of your abstract accordingly. For example, if you are submitting an abstract to peers within your field, then your introduction can provide a specific topic within your field. If you are attending a conference with a broad audience, then you will want to present a broader topic that is accessible to everyone.

1. **Introduction:** Introduce your topic in one sentence. This sentence should grab your reader’s attention and lead into your key research question.
2. **Key Research Question:** State the key research question that your research addresses.
3. **Gap in the knowledge:** Demonstrate that you are familiar with the current literature in your field and where your work fits in. It is most effective to express what is missing in the current literature, rather than trying to cover everything that has been done (e.g. “Previous work was unable to address...”). Do not cite any studies in your abstract.
4. **Materials and Methods:** Describe how you are going to address the research question from part 2.
5. **Results:** Give a highlight of the experiments that you conducted and of your results, but avoid going into too much detail. If you have space, then this is a good place to expand. Because your abstract is continuously distributed, long after your 15-minute talk, you should avoid being vague about your results (i.e. don’t say “Results will be discussed” for a conference abstract).
6. **Key Impact:** Summarize the key implication of your work. Your work may have many implications, but include only those that are applicable to the journal or conference.
7. **Optional:** If you have the space, you may want to include a sentence about future goals.

Once you have each element written out, make sure each idea smoothly transitions from one to another.

Example. Below is an example abstract published in *Nature*. The parenthesized numbers correspond to the element that each sentence addresses.

Computational design of co-assembling protein–DNA nanowires

(1) Biomolecular self-assemblies are of great interest to nanotechnologists because of their functional versatility and their biocompatibility. (2) Over the past decade, sophisticated single-component nanostructures composed exclusively of nucleic acids, peptides and proteins have been reported, and these nanostructures have been used in a wide range of applications, from drug delivery¹⁶ to molecular computing. (3) Despite these successes, the development of hybrid co-assemblies of nucleic acids and proteins has remained elusive. (4) Here we use computational protein design to create a protein–DNA co-assembling nanomaterial whose assembly is driven via non-covalent interactions. (5) To achieve this, a homodimerization interface is engineered onto the *Drosophila* Engrailed homeodomain (ENH), allowing the dimerized protein complex to bind to two double-stranded DNA (dsDNA) molecules. (5) By varying the arrangement of protein-binding sites on the dsDNA, an irregular bulk nanoparticle or a nanowire with single-molecule width can be spontaneously formed by mixing the protein and dsDNA building blocks. (5) We characterize the protein–DNA nanowire using fluorescence microscopy, atomic force microscopy and X-ray crystallography, confirming that the nanowire is formed via the proposed mechanism. (6) This work lays the foundation for the development of new classes of protein–DNA hybrid materials. (7) Further applications can be explored by incorporating DNA origami, DNA aptamers and/or peptide epitopes into the protein–DNA framework presented here.

Mou, Yun. Yu, Jiun-Tann, Wannier, Timothy M, Guo, Chin-Lin. Mayo, Stephen L. Computational design of co-assembling protein-DNA nanowires. *Nature* 525 (2015) 230