

## Setting a framework to evaluate dangers of antibiotic resistance

We have read with interest the Correspondence on our Opinion article ([What is a resistance gene? Ranking risks in resistomes](#)) by Bengtsson-Palme and Larsson ([Antibiotic resistance genes in the environment: prioritizing risks](#)) and appreciate the observations raised by the authors. As they acknowledge, our article proposes the first framework (termed resistance readiness condition (RESCon)) for evaluating the risks associated with the presence of antibiotic resistance genes in bacterial metagenomes. Here, we wish to clarify and refine some of the arguments that this framework is based on.

The framework we propose relies on two fundamental principles: the likelihood of a known antibiotic resistance gene having a harmful effect on human health (during antibiotic therapy) and whether or not it is likely to transfer to human pathogens (the probability of which increases if it is located on a mobile genetic element). Following this scheme, we consider those resistance genes that are present on mobile elements and for which a role in resistance in human pathogens has been demonstrated to represent the highest risk (defined as RESCon 1).

First, our framework does not only consider environmental ecosystems, as the ranking system also applies to resistance genes in human and animal microbiomes, in which transfer of resistance genes among pathogens and commensals is likely to occur. In the case of genes that are present in the microbiomes of animals, the risk may be quite high as the transfer of genes via mobile genetic elements has been documented between human and animal bacteria.

**The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis. Read full, original post: [Prioritizing risks of antibiotic resistance genes in all metagenomes](#)**