I. **Copy the sentences which are the main question and results for the following abstracts (5 points each)**

1. Antigenic variation is the main immune escape mechanism for RNA viruses like influenza or SARS-CoV-2. While high mutation rates promote antigenic escape, they also induce large mutational loads and reduced fitness. It remains unclear how this cost-benefit trade-off selects the mutation rate of viruses. Using a traveling wave model for the coevolution of viruses and host immune systems in a finite population, we investigate how immunity affects the evolution of the mutation rate and other nonantigenic traits, such as virulence. We first show that the nature of the wave depends on how cross-reactive immune systems are, reconciling previous approaches. The immune-virus system behaves like a Fisher wave at low cross-reactivities, and like a fitness wave at high cross-reactivities. These regimes predict different outcomes for the evolution of nonantigenic traits. At low cross-reactivities, the evolutionarily stable strategy is to maximize the speed of the wave, implying a higher mutation rate and increased virulence. At large cross-reactivities, where our estimates place H3N2 influenza, the stable strategy is to increase the basic reproductive number, keeping the mutation rate to a minimum and virulence low.
   (a) main question:
   (b) results:

2. Associated microorganisms ("microbiota") are intimately connected to the behavior and physiology of their animal hosts, and defining the mechanisms of these interactions is an urgent imperative. This study focuses on how microorganisms influence the life span of a model host, the fruit fly *Drosophila melanogaster* First, we performed a screen that suggested a strong influence of bacterial methionine metabolism on host life span. Follow-up analyses of gene expression and metabolite abundance identified stronger roles for vitamin B_6 and glucose than methionine metabolism among the tested mutants, possibly suggesting a more limited role for bacterial methionine metabolism genes in host life span effects. In a parallel set of experiments, we created a distinct bacterial strain that expressed life span-extending methionine metabolism genes and showed that this strain can extend fly life span. Therefore, this work identifies specific bacterial genes that influence host life span, including in ways that are consistent with the expectations of methionine restriction.
   (a) main question:
   (b) results:

3. The circadian clock in murine articular cartilage is a critical temporal regulatory mechanism for tissue homeostasis and osteoarthritis. However, translation of these findings into humans has been hampered by the difficulty in obtaining circadian time series human cartilage tissues. As such, a suitable model is needed to understand the initiation and regulation of circadian rhythms in human cartilage. We used a chondrogenic differentiation protocol on human embryonic stem cells (hESCs) as a proxy for early human chondrocyte development. Chondrogenesis was validated using histology and expression of pluripotency and differentiation markers. The molecular circadian clock was tracked in real time by lentiviral transduction of human clock gene luciferase reporters. Differentiation-coupled gene expression was assessed by RNAseq and differential expression analysis. hESCs lacked functional circadian rhythms in clock gene expression. During chondrogenic differentiation, there was an expected reduction of pluripotency markers (e.g., *NANOG* and *OCT4*) and a significant increase of chondrogenic genes (*SOX9*, *COL2A1* and *ACAN*). Histology of the 3D cartilage pellets at day 21 showed a matrix architecture resembling human cartilage, with readily detectable core clock proteins (BMAL1, CLOCK and PER2). Importantly, the circadian clocks in differentiating hESCs were activated between day 11 (end of the 2D stage) and day 21 (10 days after 3D differentiation) in the chondrogenic differentiation protocol. RNA sequencing revealed striking differentiation coupled changes in the expression levels of most clock genes and a range of clock regulators. The circadian clock is gradually activated through a differentiation-coupled mechanism in a human chondrogenesis model. These findings provide a human 3D chondrogenic model to investigate the role of the circadian clock during normal homeostasis and in diseases such as osteoarthritis.

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(a) main question:

(b) results:

4. Lipid transfer proteins (LTPs) maintain the specialized lipid compositions of organellar membranes[1,2]. In humans, many LTPs are implicated in diseases[3], but for the majority, the cargo and auxiliary lipids facilitating transfer remain unknown. We have combined biochemical, lipidomic and computational methods to systematically characterize LTP-lipid complexes[4] and measure how LTP gains of function affect cellular lipidomes. We identified bound lipids for approximately half of the hundred LTPs analyzed, confirming known ligands, while discovering new ones across most LTP families. Gains in LTP function affected the cellular abundance of both their known and newly identified lipid ligands, indicating comparable functional relevance of the two ligand sets. Using structural bioinformatics, we have characterized mechanisms contributing to lipid selectivity, identifying preferences based on head group or acyl chain. We demonstrate some basic principles of how LTPs mobilise their ligands. They commonly interact with several classes of lipids and exhibit broad but selective preference, not only for particular head groups, but also for lipid species with shorter acyl chains containing one or two unsaturations, suggesting that only subsets of lipid species are efficiently mobilized. The datasets represent a resource for further analysis in different cell types and states, such as those associated with pathologies.
   (a) main question:
   (b) result:

II. Reading comprehension: read the following article and answer the questions (10 points each)

The Ancient Spark: Redefining the Neanderthal

For decades, the mastery of fire has been considered the definitive hallmark of human evolution. It was the tool that allowed our ancestors to cook food, ward off predators, and eventually smelt the metals that built civilization. While scientists have long suspected that fire-making was an ancient skill, confirmed evidence of humans actually *starting* fires—rather than just scavenging embers from lightning strikes—only dated back about 50,000 years. However, a groundbreaking study from the site of Barnham in eastern England has shattered that timeline, revealing that Neanderthals were intentionally sparking fires as far back as 400,000 years ago.

The discovery began in 2013 when archaeologist Nick Ashton and his team uncovered flint fragments that had been shattered by intense heat. While intriguing, these stones alone couldn't prove human intent; they could have been the result of a random wildfire. The breakthrough arrived years later when Ashton discovered a two-foot-wide streak of reddened clay in the earth. Lab analysis confirmed this was ancient soil that had been subjected to extreme temperatures. Crucially, the evidence showed that this specific patch of ground had been burned repeatedly over several generations. Because natural wildfires are chaotic and nomadic, the presence of a persistent, localized hearth pointed directly to intentional human activity.

The most compelling evidence, or the "smoking gun," was the discovery of pyrite alongside the heat-shattered flint. When struck against flint, pyrite—often called fool's gold—produces the hot sparks necessary to ignite tinder. This "strike-a-light" technology represents a massive cognitive leap in human history. Perhaps most impressively, pyrite does not occur naturally within forty miles of the Barnham site. This means the Neanderthals didn't just stumble upon these materials; they identified them, understood their value, and transported them over long distances with the specific goal of creating fire on demand.

This find forces a significant rewrite of the Neanderthal narrative. Rather than being the primitive, slow-witted creatures of popular myth, these early humans were capable of forward planning and chemical engineering. By using fire to extract resin from tree bark, they created adhesives to anchor stone spear tips to wooden shafts, a process known as hafting. This level of technical sophistication suggests a species that was highly adapted to its environment and capable of passing complex traditions down through the ages.

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While some researchers argue that this fire-making ability might have been a localized "experiment" limited by the availability of minerals, others believe it was a revolutionary technology that would have spread rapidly through ancient social networks. Regardless of how widespread the practice was, the hearths at Barnham stand as a testament to the ingenuity of our ancient cousins. They prove that the light of technological innovation was flickering in the darkness of prehistory hundreds of thousands of years earlier than we ever imagined.

1. What is the primary discovery discussed in the article, and why is it considered "groundbreaking"?
2. Why was the discovery of "reddened clay" more significant than the discovery of "heat-shattered flint"?
3. How does the absence of natural pyrite within forty miles of the site support the theory of "intentional" fire-making?
4. How does the confirmed date of fire-starting at Barnham compare to previous scientific beliefs?
5. What specific evidence did the researchers use to rule out the possibility that the fires were caused by lightning strikes?

III. Write a 150-word paragraph with a short title on the most exciting biological discovery you have learned about. Briefly explain the discovery and why it has a significant impact on our understanding of life. (10 points)