Table 1 from: Ten Questions for Evolutionary Studies of Disease Vulnerability

Task 1: Define the object of explanation precisely.
Q1. Is the object of explanation a uniform trait in the species, or is the goal to explain variations in a trait among groups or individuals?
Q2. Has the object of explanation been influenced by evolution?
Q3. What kind of trait is the object of explanation?
   a. A fixed human trait, such as the narrow birth canal
   b. A facultative trait, such as the capacity for sweating
   c. Human genes, in the most general sense of the term
   d. Pathogen traits, such as the level of virulence
   e. Pathogen genes, such as those that confer antibiotic resistance
   f. Somatic cell lines, such as those in tumors or the immune system

Task 2: Specify the kind of explanation sought
Q4. Is the goal to explain the evolution of the trait, or its proximate mechanisms?
Q5. Is the goal to explain the trait’s phylogeny, or the evolutionary forces that shaped it?

Task 3: List and consider all viable hypotheses
Q6. Are all viable hypotheses considered and given fair consideration, or are some hypotheses neglected, while others receive favored treatment?
Q7. Could different vulnerabilities cause the disease in different individuals or subgroups?
Q8. What categories of explanation are under consideration?
   a. Mismatch of bodies with environments they did not evolve in
   b. Co-evolution with pathogens that evolve faster than hosts can
   c. Constraints on selection, such as time required, genetic drift, and mutation
   d. Trade-offs, especially costs associated with an apparently superior alternative
   e. Reproductive success at the expense of health
   f. Defenses such as fever and pain that cause harm and suffering, but were shaped by selection because they offer protection in certain situations
Q9. Could multiple explanations be correct?

Task 4: Describe the methods used to test the hypotheses
Q10. What methods are used to test the hypotheses?
   a. Consistency with evolutionary theory
   b. Modeling using quantitative methods
   c. Comparative methods
      i. Comparisons among species
      ii. Comparisons among subgroups of a species
      iii. Comparisons among individuals who vary in a trait
   d. Experimental methods
      i. Extirpation or disruption (e.g. gene knock-out studies or blocking fever)
      ii. Augmentation (e.g. administration of extra testosterone)
      iii. Examining regulation of a facultative trait to see if it behaves as predicted
      iv. Observing evolutionary changes in the lab or the field
   e. Examining the details of fit between observed form and a postulated function