batgap protocol

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1. Initially screened studies for secondary full-text screening are marked as N in “exclude\_title” and Y in “include” in the cleaned search edit CSV
2. Study inclusion criteria: estimate(s) of bat coronavirus prevalence or seroprevalence. In many cases, we will have multiple detection estimate records per study.
3. Articles can be rapidly screened by reviewing the Methods and Results for detection estimates, number of sampled and number of positive bats, or supplemental data
4. If relevant data *do not* exist (e.g., authors only report detection of a novel sequence but not the total bats sampled nor number positive), mark N in “include” column
5. If relevant data *do* exist, add the ID and study values from the search AirTable columns into the entry AirTable columns
6. Number of bats and number of positives should be listed as integers
7. Detection estimates should be included as proportions
8. Virus genus should be alphacoronavirus, betacoronavirus, or gammacoronavirus. Some papers may use alternative namings (e.g, group 1, group 2). These are synonyms for the viral genus (group 1 = alpha, group 2 = beta, group 3 = gamma).
9. If possible, include the subgenus. For betacoronavirus, these include Embecovirus (lineage A), Sarbecovirus (lineage B), Merbecovirus (lineage C), Nobecovirus (lineage D), Hibecovirus. More subgenera are available for alphacoronavirus (Wiki)
10. Include the listed species and/or strain name, if provided
11. Study type should be cross-sectional or longitudinal
12. Detection method can be broadly listed as detection of RNA or IHC (antigen), antibody, or live virus
13. Method specific can be the actual assay used. If multiple assays, separate with “;”
14. Tissue should ideally be a single value per row (i.e., prevalence is provided for each tissue type). If prevalence is pooled across tissue, list multiple tissues with “;”
15. Gene targets can be separated with “;” if multiple targets were used
16. State: note the broadest geopolitical division in country (e.g., state in the US/Brazil)
17. Start/end sampling: applicable if authors only report prevalence over some time period greater than a month (e.g., June through September). Use MM/DD/YYYY.
18. Month/season/year: if detection estimates is reported per month, season, or year, provide single values
19. Bat species should ideally be one row per species (Latin names only)