1. Saved queries
   1. Purpose: watch an entire category of isolates (e.g., Salmonella) and find any new relevant matches to isolates
   2. Best practices - specific to the purpose and/or species
      1. Make the query specific to the species: taxgroup\_name:”Salmonella enterica”
      2. Minimum distance between isolates: (minsame:0 OR mindiff:0)
      3. Look for new isolates only: new:1
      4. Restrict to only clinical if you want to have fewer results: epi\_type:”clinical”
      5. Restrict to only the US: geo\_loc\_name:”USA”
      6. Look for an AMR geotype with wildcard (for NARMS): AMR\_genotypes:blaKPC\*
   3. Example: [taxgroup\_name:"Vibrio parahaemolyticus" AND new:1 AND (mindiff:1 OR minsame:1)](https://www.ncbi.nlm.nih.gov/pathogens/isolates/#/search/taxgroup_name:"Vibrio parahaemolyticus" AND new:1 AND (mindiff:1 OR minsame:1))
2. Watched clusters
   1. Purpose: watch for matches for an outbreak cluster
   2. Best practices
      1. Find all NCBI SNP clusters that match the outbreak cluster. SNP clusters have NCBI accessions that start with PDS.
      2. For each NCBI SNP cluster, find one or more representatives and click to select them and only them in the Pathogens interface.
      3. Click “Watch” at the top of the screen.
      4. Choose number of SNPs (0 for conservative, 10 for middle-of-the-road, 20+ for casting a wide net)
      5. Give it a name. Usually something like the cluster code.
      6. Wait and see if any email notifications come in the next days or weeks.