4. Next, tumor samples are "spun down" and disaggregated to separate individual cells. Single cell, whole exome and/or RNA sequencing may be utilized at this stage to ensure the tumor sample accurately reflects the genomic characteristics of its tumor type.

5. Individual tumor types may need a different "recipe" for how models are generated in the lab. Since these samples are rare, many times the full list of proper ingredients is not known. As a result, up to 100 experimental conditions involving nutrients and temperature may be tried to attempt to derive a model from a single patient sample.

6. Once a model is generated, genomic sequencing is again utilized to credential the model, ensuring it has retained the proper features of its tumor type.

7. A model continues to grow for 3-12 months. Some models may stop growing during this period. Key information may still be obtained from the results through the growth period, and in some situations, the lab may be able to re-initiate the model process from the start.

8. A successful model is expanded to more vials, which are frozen for further expansion and used in research. Those vials are shared with a public bio repository such as ATCC which broadly distributes research models to the scientific community.

Pattern.org, an initiative of the Rare Cancer Research Foundation, empowers cancer patients to take an active role in advancing research for their disease.