Use cases

This use cases apply to the following biological types: “protein”, “protein annotation” and “protein structure”

1. **Findability**: As a user, I would like to find as many proteins resources as possible when looking by protein entity/gene name or protein entity/gene identifier (we cannot really measure this one, it is up to search engine implementations --that will come later)
2. **Summarization**: As a user, whenever I look for a protein entity (or a gene), I would like to see a quick summary with information regarding protein entities. Such summary should contain at least the datasources, ids, names and organisms for the protein entity. Additionally, it could contain gene name, protein entity sequence, citations, protein structure and protein features.
3. **Accessibility**: As a user, I want to be able to distinguish what is a protein, what is a structure, what is a protein feature/domain. I also want to be able to gather structured information from all protein resources; this would be useful, for instance, to create visualization tools or to enrich other pages/databases.