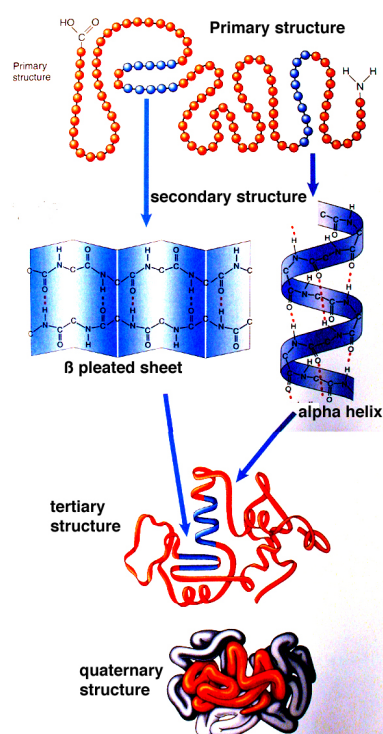


## Structural Proteomics

### Overview:

Traditional proteomic approaches give information on the amino acid composition, or primary structure, of proteins. Advanced structural proteomics gives information on the secondary, tertiary, and quaternary structure of proteins. It can also be used to distinguish between protein isoforms, or proteins with the same amino acid sequence but different structures due to post-translational modifications, mutations, or other factors.



[http://swh.schoolworkhelper.netdna-cdn.com/wp-content/uploads/2010/11/protein\\_structure.jpg?e6ecea](http://swh.schoolworkhelper.netdna-cdn.com/wp-content/uploads/2010/11/protein_structure.jpg?e6ecea)

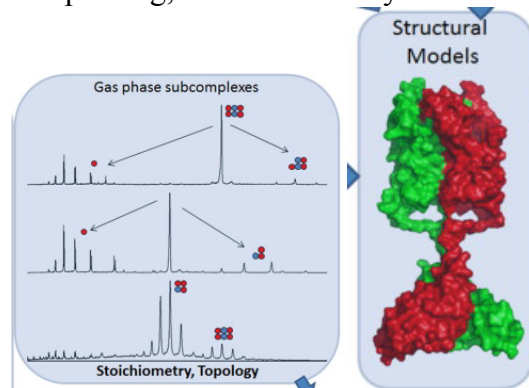
### Importance:

Understanding the more complex structural properties of proteins gives more information on how these proteins function. Structural proteomics can also be used to determine the protein structural changes in response to a stimulus such as introduction of a pathogen or an environmental stress. The structure of proteins can also provide information on binding sites and protein interactions. These techniques are often used in tandem with traditional proteomics

methods. Once the target proteins have been identified, the structures can be determined. Currently, most studies using these rapidly developing approaches are human medical papers and microbiology papers. As the methods are further refined, marine scientists will use them more frequently.

### Techniques:

Structural proteomic methods enable the visualization of the 3D structure of a protein. Differences such as post-translational modifications, mutations, and other distinguishing properties of individual proteins can also be observed. Methods include Native MS, Hydroxyl Radical Footprinting, and Ion Mobility-MS.



Native MS data (left) is used to visualize a 3D protein model (right) (Marcoux and Cianferani, 2015)

### Examples:

- Chen et al. (2010) generated a low-resolution model of the RNA polymerase II protein complex.
- Herzog et al. (2012) analyzed a human protein complex and identified a network of dozens of proteins cross-linked to this complex.
- Housden et al. (2013) showed how protein complexes interact on the surface of *E. coli* when a bacteriocin initiates cell death.

### References:

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