What is Protein ?

- Proteins are large molecules consisting of amino acids which our bodies and the cells in our bodies need to function properly.
- Our body structures, functions, the regulation of the body’s cells, tissues and organs cannot exist without proteins.
- Our muscles, skin, bones and many other parts of the body contain significant amounts of protein.
- Protein accounts for 20% of total body Weight.

Why do we need Protein ?

- Your hair, your nails, and the outer layers of your skin are made of the protein keratin. Keratin is a protein resistant to digestive enzymes. So if you bite your nails, you can’t digest them.
- Bone has plenty of protein. the soft material inside the bone, also contains protein.
- Red blood cells contain hemoglobin, a protein compound that carries oxygen throughout the body.
- Finally, proteins play an important part in the creation of every new cell and every new individual.

- Application or s/w that requires high computing capabilities and they are having large data sets may cause high I/O operations.

- Due to these requirements they are overusing the super computing and cluster computing Infrastructures.
- Protein structure Prediction is a computationally intensive task fundamental for different types research in the life sciences.
- The prediction of the protein structure will help the medical scientists to develop new drugs.
- This task requires the investigation of protein structure at so many number of states and also it is creating a large no of computing calculations for all of these states.
- The computational Power required for this prediction can now be acquired online, without owning it.
- Cloud computing grants the access to such capacity on pay per use basis.
- A project that can analyze the use of cloud Technologies for protein structure prediction is JEEVA PORTAL.
- It is an integrated web portal that enables the scientists to do the prediction task using cloud techniques.
- This prediction Task uses machine learning techniques for explaining the secondary structure of proteins.
- These techniques will convert the problem in a manner so that they can be classified into 3 phases :initialization, classification and a final phase.
- As It is already cleared By it’s name it the first phase of this prediction named “Initialization of protein structure prediction”.
- The actual Prediction starts in the initialization phase .
- In the second phase the execution is get completed concurrently.
- This will reduce the computational time.
- The prediction algorithm is then transformed into a Task graph and that is submitted to Aneka
- Aneka is a platform and a framework for developing distributed applications on the

Cloud. It harnesses the spare CPU cycles of a heterogeneous network of desktop PCs and servers or datacenters on demand.

- Aneka provides developers with a rich set of APIs for transparently exploiting such resources and expressing the business logic of applications by using the preferred programming abstractions.
- System administrators can leverage on a collection of tools to monitor and control the deployed infrastructure. This can be a public cloud available to anyone through the Internet, or a private cloud constituted by a set of nodes with restricted access.

- Jeeva is a computational platform which simplifies the development of new prediction algorithms and improves the efficiency at the same time.
- Jeeva web portal system consists of an interactive web interface and a Grid middleware.
- With the interactive web interface, users can submit prediction requests for protein secondary structures, collect results, and manage the history of prediction data.
- By means of the Grid middleware, researchers can not only deploy their prediction applications in a distributed environment easily, but also monitor and manage the execution in the distributed environment.