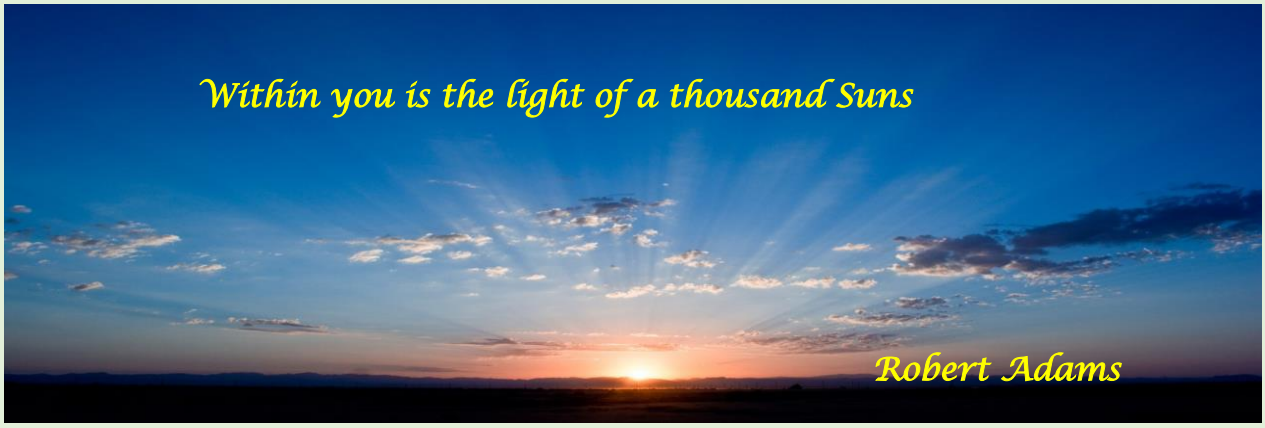
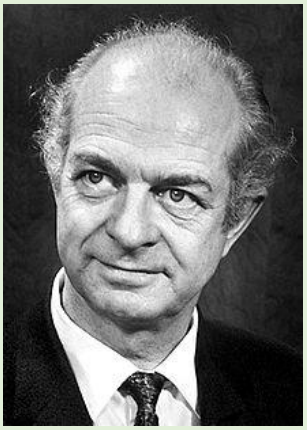
The Biochemistry Chronicles



THE PEACE LOVING BIOCHEMIST-LINUS PAULING

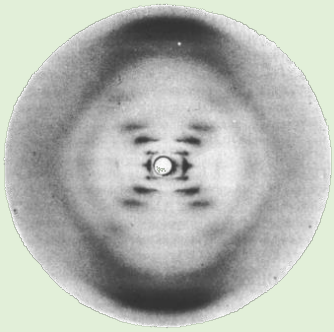


LINUS PAULING

Linus Pauling, also known as Linus Carl Pauling, a multi-skilled American chemist, biochemist, chemical engineer, peace activist, author and educator was born on 28th February 1901. He was one of the four double Nobel laureates and is enlisted in the list of "Twenty Greatest Scientist" of the world. His pioneering works in the nature of chemical bonds, ionic structure of molecules and molecular genetics and nutrition deserves special mention. In the year 1954, Linus Pauling won the Nobel Prize in Chemistry for his research on nature of Chemical Bonds. Linus Pauling worked with Roscoe Dickinson on x-ray crystallography. This technique was first to provide detailed information about alignment of atoms with respect to each other in a crystal.

The tragedy of atomic bombardments of Hiroshima and Nagasaki shivered the entire humanity. This devastating incident was a turning point in Linus Paulings life too. In 1959, Pauling prepared the blueprint of the document issued after the Fifth world Conference against Atom bombs entitled "Hiroshima Appeal". Pauling instigated the Soviet Union and Great Britain for nuclear test ban treaty that was validated on 10th October, 1963. He won his second Nobel Prize in Peace in 1962. He is one of two scientist who have won noble prize in different fields. He was also a recipient of Lenin Peace Prize. Pauling spent his last years directing research at the Linus Pauling Institute. Linus Pauling breathed his last on August 19, 1994.

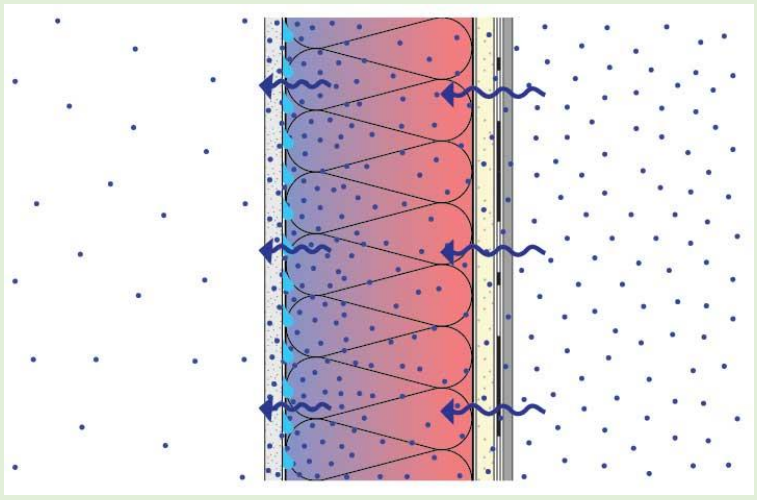
X-RAY CRYSTALLOGRAPHY



This technique is used in identification of three-dimensional structure of biomolecules or biopolymers. Linus Pauling used the technique of X-ray diffraction to understand the detailed information about alignment of atoms with respect to each other in a crystal. This paved the way for John Kendrew in 1960 in describing the 3D structure of Myoglobin. 3-Dimensional model that displays an item in a form that appears to be physically present with a designated structure. The three dimensional structure of protein is determined by the spatial arrangement of atoms of amino acids in the polypeptide chain.

A Crystal, is a solid in which atoms are packed with particular arrangement within unit cell and repeated indefinitely in principle 3 directions in space or 3 dimensional lattice of molecules. A crystal can be prepared from a protein solution when it's homogenous mixture is perturbed by change of PH, temperature, ionic strength or concentration of precipitating agents to produce a state of saturation. The Crystals can be produced by two techniques:

1. **Dialysis:** Desired protein solution is dialysed against a supersaturated solution of precipitant or by gradual change in pH or ionic strength. With the advent of microdialysis technique even < 50 cu.mm of volume of protein will be sufficient.



2. **Vapour Diffusion**: This technique relies on the controlled equilibration through the vapour phase to produce super-saturation in the sample .It can be of two categories: *Hanging drop method or sitting drop method.*

   For resolution of structure of small protein, x-ray with wave lengths in the range of 0.07-0.15 nm must be used. The atoms of crystals act like grating and X-ray gets diffracted producing a pattern, the pattern of image is collected and reconstructed by mathematical technique called ***Fouriers transform***. Conventionally diffractometers and photo graphic film was used. Only the diffraction pattern is not sufficient for the determination of structure. Each diffraction maximum has both an amplitude and phase, but only amplitude is determined by X-ray crystallography. The diffraction data is processed to construct an electron density map using computer graphics to construct a 3D Model. The 3D structure of the protein can be validated using the repertoire of Protein Data bank (https://www.pdb.org/) Lastly, the 3Dimensional structure derived from crystal is flexible like Native protein can be validated by diffusing the substrate in crystalline enzyme and getting the desired product. However, the advent of Nuclear Magnetic Resonance Spectroscopy have revolutionized the technique of 3D structure identification of biopolymers. The basic advantages of NMR

is that in can be done in an aqueous sample whereas Crystal preparation is a pre-requisite for X-ray crystallography. NMR can be performed with a sample having protein concentration in the range 0.1 – 3 millimole/L. In recent times, newer techniques like Cryo Electron Microscopy & Dual Polarisation interferometry has revolutionized the protein structure determination to a newer height.

Contributors:-

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