



## Cosmic Baby, Magnetic Protein—Cosmic Connection to Human : A possibility

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### Abstract

Protein crystal plays an important role in creation of human eyes i.e. high quality protein crystallization ensures the formation of beautiful eyes in human faces as well as ageless appearance in body structure. Cosmic Baby, i.e. the Swift J1818.0 – 1607, provides a possible clues to the scientists in the form of “Triaxiality” for creation of beautiful eyes. This author suggests that the “triaxiality” phase appears at the early stage of birth when human embryo (inside the mother’s womb) faces the effect of change in shape of the gestational sac (that covers the human embryo) from circular shape to ellipsoidal shape. Effect of magnetic field and its magnetization force offer an opportunity to the scientists for understanding the physics of creation of high quality protein crystals. To ensure the exact role of “Triaxiality” towards beautiful eye formation needs a lot of investigations on crystallization of protein in strong magnetic field as well as finding the link of cosmic connection with human beautiful eyes.



### Article History

Received: 02 December 2024  
Accepted: 31 December 2024

### Keywords:

Crystallization;  
Cosmic Baby;  
Human Eye;  
Protein;  
Triaxiality.

### Introduction

The main function of proteins in living organisms including human are: (a) controlling of almost all the biological reactions, and (b) to maintain a deep relationship through their structure and function which are related to the development of life.<sup>1</sup> In one side it is considered that neighboring atom formation<sup>2</sup> are the main structural basis in many biological systems while in other side the attached hydrogen atoms take an active part in playing biological functions, such as mechanism of enzyme production.<sup>3,4</sup> In deep sense, the precise location

of this hydrogen atoms is very much crucial in order to understand the physics of origin or mechanism related to the concerned biological problems by maintaining a relationship with solid state physics.<sup>5,6</sup>

The unknown crystal structure, in general, is resolved through the conventional method, i.e. the X-ray diffraction technique<sup>7,8</sup> but the problem arises due to the interaction of X-rays with the electrons of the atoms located inside the crystal structure. An alternate is to consider heavy atoms having neutrons with its isotropic form or other

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Doi: <https://dx.doi.org/10.13005/OJPS10.01.11>

so that the determination of the crystal structure is possible based on the relative position of a hydrogen atom located with reference to the known presence of relatively heavy atoms.<sup>9,10</sup> Therefore, control of physical parameters are essential for obtaining accurate result. Various methods have been developed in this regard by controlling the physical parameters such as the temperature,<sup>11</sup> hydrodynamic field,<sup>12</sup> electric field,<sup>13</sup> magnetic field<sup>14</sup> and electromagnetic field.<sup>15</sup> Out of these, magnetic field method has a great potential for understanding the protein crystal structure and its growth.

Although it is uncertain yet scientists believe that the knowledge of protein were known during the period in the 19th and early 20<sup>th</sup> Century. In 1938 Berzelius first coined the term "Protein" but remained unpopular under the influence of more popular terms like "proteid", "albuminous", "colloids" on that time. Looking back into the past the available literature indicates that in 1840 Friedrich Ludwig Hünefeld first observed protein crystal serendipitously in a sample of dried menstrual blood stucked between glass plates used for experiments in his laboratory (figure 1B ).<sup>16</sup>

In fact, the word "Protein" is derived from the Greek word 'Proteios' which means primary/primary importance because proteins are the most important chemical substances which are essential for growth,

repair and development of life. These proteins have been found in all living cells implying that they occur in every part of the body and form the fundamental basis of structure and functions of life. For example, in human body skin, hair, haemoglobin, nails, enzymes and cells, etc. all are made of proteins.

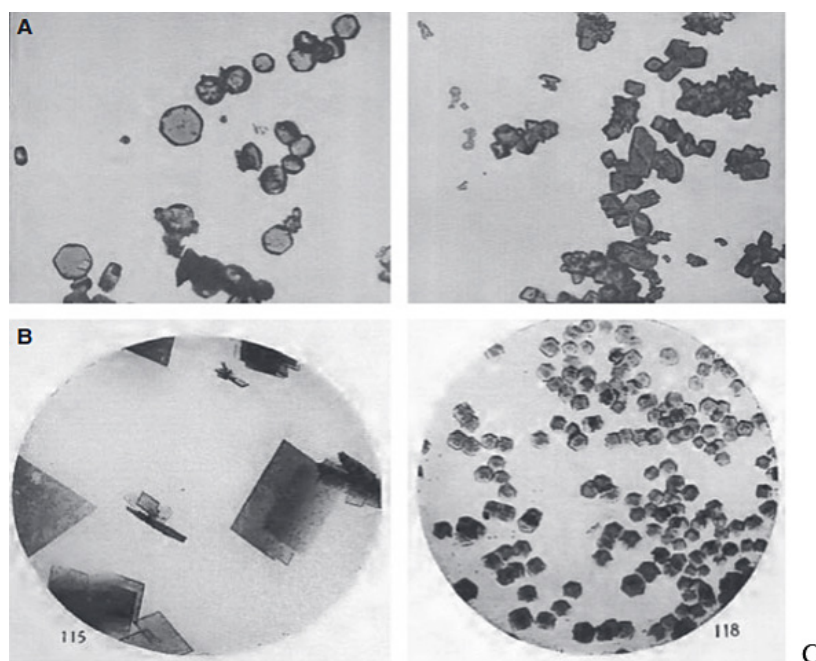
However, through gradual studies protein crystallization area developed a lot and it has become an input part of our life, in particular through which we visualize the objects in the world.

## Materials & Methods

### The Birth of Biocrystallogenesis

Initially, protein crystal was confined its purification and then turned as instrumental tool to demonstrate its catalytic activities in the form of "enzyme" that resides with the protein itself. In the 19<sup>th</sup> Century the most of the crystalline proteins (i.e. haemoglobins and albumins) which were considered as pure substance. Because of their availability in the micro-scale. But in 1934 a breakthrough occurred in this field when John D. Bernal and Dorothy Crowfoot Hodgkin (see the review Parui 2024<sup>19</sup>) described the secret structure / pattern inside the protein first time through X-ray diffraction. This opened a new era in chemistry and physiology as biocrystallogenesis. Below a few landmarks are mentioned in protein crystallization.

Year	Macromolecular Form	Crystallized Entity	Source
1840	Globins	Haemoglobin	Human blood
1855	Phytoglobulins	Excelsin	Brazil Nut
1890	Enzymes	HEW Lysozyme	Pig
1926	Hormones	Insuline	Rabbit
1935	Viruses	Plant virus	TMV
1937	Enzymes	Cotalase	Beef liver
1969	Antibodies	Intact 1g G	Human
1971	Toxins	Erabutoxin	Sea Snake
1975	Sweet testing Proteins	Thaumalin	Thaumato cocus Daniellii
1980	Membrane Protein	Porin	Escheriochia Coli
1980	Ribosomes		Bacillus Stearo thermophiles
1984	Protein DNA Complexes	Nucleosome	Xenopus laevis
1988	DNA fragments	Synthetic DNA duplexes	



**Fig. 1 :** shows photographs of protein crystallization. (A) Crystals of excelsa exelsin from the Brazil nut (left) and of *Avena sativa* avenalin from oat kernels (right) 20; (B) photographs of a-oxyhaemoglobin showing groups of plates in parallel growth (left) and of b-oxyhaemoglobin showing small dodecahedral crystals (right); (C) schematized drawing of the above crystals emphasizing their prismatic (left) and dodecahedral (right) habits ( adopted from Reichert & Brown, *Crystallization of Hemoglobins*, 1909 20 ; COURTESY- Carnegie Institution, Washington, USA).

### Protein Crystallization in Living Cells

Protein crystallization in living cell was observed surprisingly as an evidence of phenomenon for recombinant protein. It means that this micrometer-sized can be used for structural biology. For example, this in *cellulo* crystallization could offer us a new possibilities that do not crystallize under normal conventional approach. In other words, this unknown mode of regulation of native in *cellulo* crystal formation offers a challenge to the scientists. Although the mechanism of how intracellular protein self-assembled is not known yet scientists believed that the hidden regulatory mechanism (different from normal regulatory approach) may have a link to a specific function which is either disease associated or new form of recombinant as a protein crystallization chamber that systematically exploit living cells.

### Protein Storage

In nature, nutrient storage is observed as a normal process in living objects in the form of eggs or seeds in the form of crystallize yolk proteins as a source

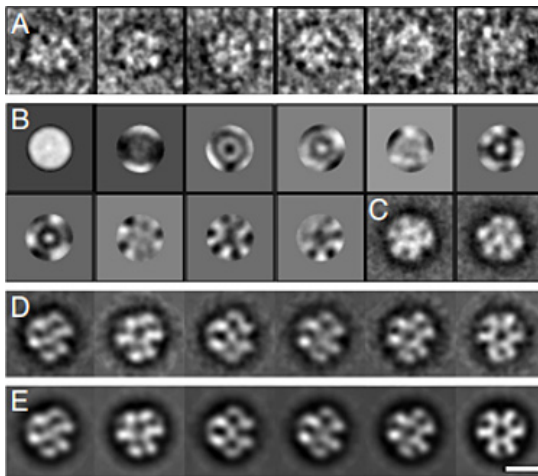
of constant nutrient supply for the offspring. In the case of human eyes it was thought that the only 10 or so crystalline proteins ( like alpha ( $\alpha$ ), beta ( $\beta$ ) and gamma ( $\gamma$ )) are involved in the evolution of eyes. The remaining lens proteins are non-conserved, diverse group used as enzymes elsewhere in the body.

### Sturcture of Eye Lense

Eyes collect light through an aperture and focus it with a lens photoreceptor cells convert photons into neural signals. Lenses are of tightly packed proteins. In the case of human lenses (i.e. vertebrates) these are actually formed from modified epithelial cells containing highly concentrated soluble proteins, so called "crystallins" because of their packing arrangements into an arrays ). As mentioned above that the 10 or so crystalline proteins found in human eyes which are unique to lens tissue but present thought is of the large number of crystallins i.e. alpha ( $\alpha$ ), beta ( $\beta$ ) and gamma ( $\gamma$ ) crystallins that are indeed also specialized lens proteins. In fact, crystallins or transparent proteins are arranged

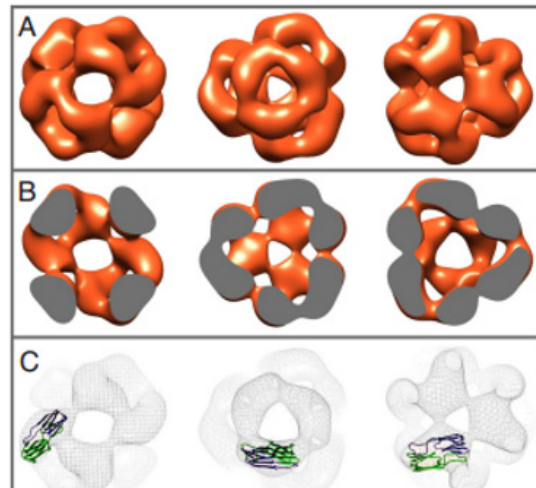
in approximately 20,000 thin concentric layers (i) whose average concentration is about twice than that of other intracellular proteins, and (2) that may play a structural role during the development of eye-lens. It means that in one side the eye lens can be used as a source to study the mechanism of aggregation and deposition of other “mis-folded” proteins that cause cataract while in another side the same eye lens provides a mechanism of aggregation of exogenous proteins whose developing approaches provides a clue how to protect the cells from the accumulation of aggregated proteins. Note that out of the earlier mentioned the 10 or so crystallins proteins alpha ( $\alpha$ ) and beta ( $\beta$ ) crystallins are specialized lens protein that are related to heat shock proteins (in the case of vertebrates) and schistosome egg antigen, respectively. In case of the remaining vertebrates the lens proteins are a non-conserved and diverse group. This implies that one gene coding for a protein have two entirely different functions which is known as “gene sharing” and it may be a prelude a “gene duplication”

As mentioned earlier that in human eye (i.e. vertebrate) the alpha ( $\alpha$ -), beta ( $\beta$ -) and gamma ( $\gamma$ -) crystallins are known abundant vertebrate eye lens protein because of their presence more than 90% of total proteins. Not only that, presence of enzymes in eye lens also act as structural proteins, receptors, connexins, water channel aquaporin and cytoskeletal proteins. Basically, alpha ( $\alpha$ -) crystallin, as a small heat shock protein, interacts with partly folded proteins in a chaperone manner as well as prevents their irreversible aggregation and precipitation, beta ( $\beta$ -) and gamma ( $\gamma$ -) crystallins are primarily composed of antiparallel beta ( $\beta$ -) sheet. Finally, these three i.e. the  $\alpha$ -,  $\beta$ -, and  $\gamma$ -crystallins representing in all vertebrate lineages may have evolved from proteins that support this kind of filament system as well as may shed light on the functions of these proteins in lens and non-lens cells.



**Fig. 2 : Observed image analysis of negatively stained  $\alpha$ B-crystallin oligomers as obtained by Peschek team.<sup>24</sup>**

- (A) Gallery of single  $\alpha$ B-crystallin oligomers
- (B) First 10 eigenimages
- (C) Apparent 3-fold and mirror-symmetries result
- (D) Characteristic final class average
- (E) 2D representation of 3D model of  $\alpha$ B-crystallin



**Fig. 3 : 3D reconstruction of human recombinant  $\alpha$ B-crystallin performed by Peschek team.<sup>24</sup>**

- (A) Surface representation of recombinant  $\alpha$ B-crystallin
- (B) Density cross-section of 3D model of  $\alpha$ B-crystallin
- (C) Superposition of ribbon representation

(Note : for detailed description see ref. 24) (fig.2 & 3 : adopted from Peschek team 24 . PNAS, vol-106 , 2009)

### Eye Lens Chaperon A-Crystallins and Triaxial Shape

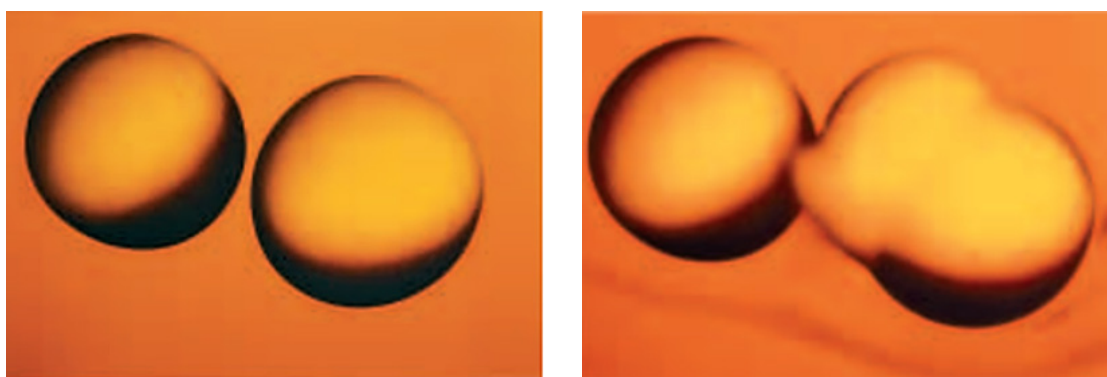
The  $\alpha$ -crystallins are molecular chaperons which belongs to the small heat shock protein family. The cellular function of this  $\alpha$ -crystallins is to bind to partially unfolded polypeptides and nurture them so that they are within a refolding competent state<sup>21,23</sup> such that their acting as molecular traps ultimately protect the cells from the consequences of irreversible protein aggregation.

There are two types  $\alpha$ -crystallin genes, namely,  $\alpha$ A and  $\alpha$ B. In a study of the structures of the recombinant  $\alpha$ -crystallins, in particular  $\alpha$ B-crystallins, by electron microscope<sup>24</sup> it was found human  $\alpha$ A- and  $\alpha$ B- crystallins were recombinantly expressed in "*Escherichia Coli*". Further analysis using selected 2565 single particle images (fig.2A) and *Eigenimages* (i.e. *images representing the most important differences in the data set* (fig. 4B) and preliminary class averages (fig.2C and D) they found human  $\alpha$ B-crystallin oligomer is roughly spherical with a diameter of 13.5 nm (fig. 3A). This *oligomer* also accommodates a large central cavity of  $\approx$  8.5 nm diameter which is surrounded by a symmetrical protein shell ( with a mean thickness varying from 2.5 to 4 nm. (fig.3B). In addition, they also found the protein shell that contains.

openings at the positions of the 2-fold axes ( with diameter of  $\sim$  3.5 nm ) and 3-fold axes (with 3 and 2 nm for the two unequals ). The overall structure of human recombinant  $\alpha$ B-crystallins is nearly circular based on the surface representation of 3D model (fig. 3B) and density cross section through 3D model (fig. 3B).

### Aquaporin (AQP1) Water Transporter

In another investigation<sup>25</sup> for understanding the function of protein (i.e. 28kDa ) as water transporter in human eye-lens it was demonstrated that under the injected controlled *oocyte* with water in *Xenopus laevis* the protein was christened " aquaporin" ( so called "AQP1) such that initially with a circular shape it deformed from its circular shape to deformed triaxial shape in the case of injected with cRNA. A noticeable change in shape they observed 30 seconds later from the time injection i.e. the AQP1 *oocyte* had begun swell as seen in figure 4 ( i.e. shape changes from circular to triaxial) and after 3 minutes the swelled AQP1 *oocyte* had further deformed ( i.e. from triaxial shape to ellipsoidal) and finally exploded. This implies that the AQP1 *oocyte* changes its shape from initial circular to triaxial shape (during the beginning of swelling) and finally exploded when triaxial shape turns into more deformed phase ( which was more unstable resulting which it exploded).



**Fig. 4:** Shows the representation of functional expression of AQP1 water channels in *Xenopus laevis* oocytes observed by Preston group.<sup>25</sup> Description: (Left)- control oocyte was injected with water and (Right) – AQP1 was injected with cRNA. After 3minutes the AQP1 oocyte has exploded (bottom) (Courtesy : reprinted from Science<sup>25</sup> and adopted from Nobel lecture given by Peter Agre on 8<sup>th</sup> December, 2003<sup>26</sup>)

### Results

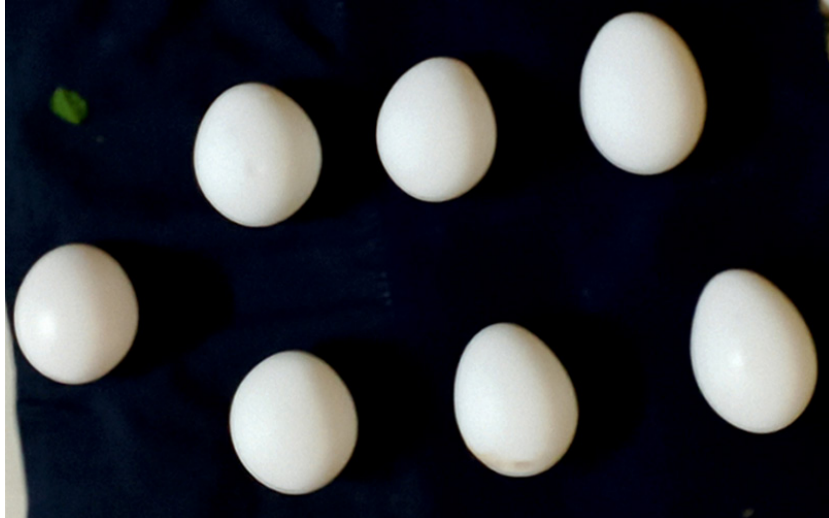
#### Physical Observation of Hen-eggs

Physically observed of hen eggs by this author are shown in figure 5. A variety of egg shapes are

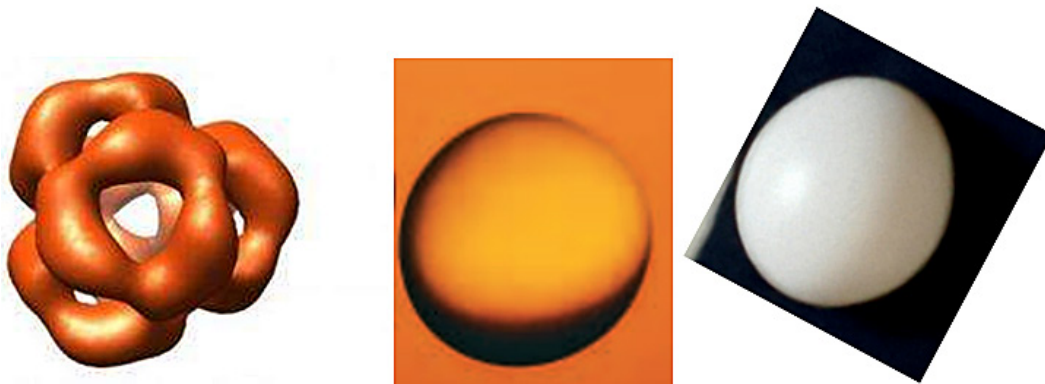
circular (serial no 1), triaxial (sl. No 2,3,7), ellipsoidal (sl. No.4. 5, 6 ). Comparing the observed shape of 3D reconstruction of human recombinant  $\alpha$ B-crystallin with the physically observed shapes of hen's egg it

is revealed that the nearly circular shapes are triaxial shapes. This means that in human eye-lens proteins are associated in "Triaxial Shpes". Of course, this

needs further precise imaging of  $\alpha$ -crystallin to confirm it.



**Fig. 5:** Physically observed hen's egg. Clockwise (top four) — 1<sup>st</sup> is circular shape, 2<sup>nd</sup>, 3<sup>rd</sup> and (below three) 7<sup>th</sup> are in their triaxial shape while 4<sup>th</sup>, 5<sup>th</sup>, and 6<sup>th</sup> are ellipsoidal shape.



**Fig. 6:** Comparison of the structure of protective protein in the human eye lens with the observed AQP1 and hen's egg reveals that triaxial shape is prominent

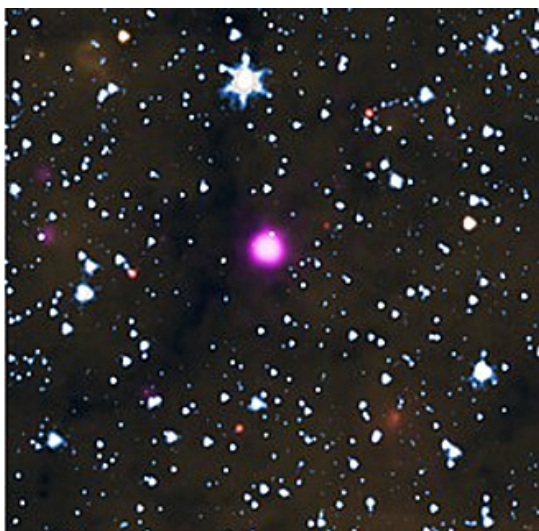
**Discovery of Cosmic Baby**

During the analysis of observed X-ray data (for short burst originated from magnetar) collected by *Swift* X-ray telescope (XRT) Esposito team<sup>30</sup> discovered a typical characteristic of short burst from a magnetar on 12<sup>th</sup> March 2020 at 21:16: 49 UT.<sup>27,28</sup> This newly discovered magnetar was actually an uncataloged X-ray source as *Swift J1818.0 – 1607* and presently known as "Cosmic Baby" (see fig. 7). It is called "baby" ( with age only 240 years) in the sense that

till date all the discovered magnetars are about million years aged. The significant parameters of Cosmic Baby are:

Characteristic age	~ 240 years <sup>29</sup>
Magnetic field strength at Surface	~ 2.7 x 10 <sup>14</sup> G
Magnetic field strength at poles	~ 7 x 10 <sup>14</sup> G
Spin period	= 0.7333920 s
Coherent periodicity of X-ray signal	= 1.36s
Period derivative	~ 9 x 10 <sup>-11</sup> s.s <sup>-130</sup>

Using the initial observed parameters at the time of discovery Parui<sup>31,33</sup> estimated the internal core magnetic field inside the magnetar and its associated ellipticity (a property measuring the deformation) of this Cosmic Baby and found  $8.9424 \times 10^{17}$  G and  $9 \times 10^{-3}$ , respectively. It is seen that the estimated deformation of this object due to super-strong magnetic field turns it into a "Triaxial Star". In fact, as its age is 240 years the estimated value hints that this cosmic baby will exhibit its triaxial nature for the next 760 years. The importance of cosmic baby is that it shows the possible evidence of the existence of a "Triaxial Star" that was predicted by S. Chandrasekhar in 1969 i.e. more than 50 years ago.<sup>34</sup> This implies that physical existence of a "Triaxial Star" is possible.



**Fig.7 : Photographic image of Cosmic Baby i.e. Swift J1818.0 – 1607 (pink colour composited with an infrared photograph of its location in the sky ( CREDIT : Chandra X-ray Observatory, NASA ; Courtesy – Wikipedia)**

Another significant finding arises from the discovery of NANO Grav<sup>35-37</sup> which suggests that characteristics observed in cosmic objects, the same characteristics can also be possible to observe in human. Based on this Parui<sup>38</sup> suggested that triaxiality and other characteristics possibly be observable in human.

#### **Crystallization of Protein in Magnetic field**

Proteins play a significant role in governing almost all biochemical reactions in living things, particularly in human eye-lens from its structure formation to

development. X-ray diffraction analysis shows that a protein single crystal is.

- with length > 0.1 mm ;
- of high quality is indispensable ;
- with main problem is the crystallization that has been a bottleneck.

A possible solution to overcome these difficulties is investigation of the effect of magnetic field on protein crystallization. In an investigation of hen-egg white lysozyme as model protein and its effect on magnetic field<sup>39</sup> it was found that magnetic field effects on protein crystal is really a complex which needs a large quantity of high quality single protein crystal in order to understand the realistic characteristics of protein behavior, particularly on the orientation, crystal habit, growth rate of crystal, convection in aqueous solution, etc. In other words, effects of magnetic field and its magnetization force<sup>40,41</sup> on protein crystal offers an opportunity to the scientists a possible clue of high-resolution structural information that ultimately leads to high quality protein crystals.

#### **Discussion**

Protein crystallization in living cells,<sup>42,43</sup> particularly in human eye-lens plays a crucial role not only for beautiful eyes but also its various side-effects that create constraints via eye-diseases for clear vision. Investigations<sup>44-46</sup> of magnetic field effects on protein crystal growth provide possible clues to the scientists for obtaining high quality protein crystals that is required for clear vision's tenure for a long years. Discovery of Cosmic Baby hints that deformation due to strong magnetic field in the form of "Triaxiality" is applicable for human eyes also. This implies that at the early birth phase of zygote formation the human embryo may turn its shape into "Triaxiality" when the gestational sac follows a shape change from circular to ellipsoidal. Thus, "Triaxiality" arises during the transition from circular to ellipsoidal shape of the gestational sac (that covers the embryo inside the mother's womb) provides an invaluable opportunity to the scientists for investigating the exact role of "Triaxiality" for ensuring formation of beautiful eyes as well as ageless appearance in women's body structure.

#### **Acknowledgement**

The author is greatly indebted to the anonymous reviewers for their invaluable comments and

suggestions. The author wishes to thank Prof. H N K Sarma, Dept. of Physics, Manipur University, B K Ganguly, Mrs. Tapati Parui and specially to Rajarshi Parui for his help in computer works.

#### Funding Sources

The author(s) received no financial support for the research, authorship, and/or publication of this article.

#### Conflict of Interest

The author does not have any conflict of interest.

#### Data Availability Statement

Data sharing is not applicable as no data sets were analyzed.

#### Ethics statement

This research did not involve human participants, animal subjects, or any material that requires ethical approval.

#### Informed Consent Statement

This study did not involve human participants, and therefore, informed consent was not required.

#### Author Contributions

The sole author was responsible for the conceptualization, methodology, data collection, analysis, writing, and final approval of the manuscript.

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