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Looking back at the timely launch of *Nature Structural Biology* in 1994

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Structural biology has continued to advance over the past decades, owing to the development of improved and new technologies. The launch of *Nature Structural Biology*

(NSB) in 1994 provided a much-needed avenue for the dissemination of these advances. This year marks the thirtieth anniversary of the journal, now named *Nature Structural and Molecular Biology*. Although it has expanded far beyond the initial scope, it continues to faithfully serve the structural biology community as a venue to showcase some of their most impactful developments.

In the early 1990s, structural biology relied on protein crystallography as the main experimental technique. Application of this method underpinned the landmark determination of the first protein structure, myoglobin, published in 1958 (ref. 1). Progress in X-ray crystallography, however, experienced a sluggish pace over the subsequent two decades, primarily owing to the lack of availability of instrumentation.

In the late 1980s and early 1990s, there were rapid advances in both methodologies and software for crystallographic structure elucidation. First, the laborious process of X-ray diffraction data collection using silver-based films was replaced by the adoption of wire detectors, then later by the introduction of imaging plate detectors in the early 1990s². The efficacy of imaging plate detectors stemmed from their enabling of complete automation coupled with their versatility to use laboratory sources as well as synchrotron beam lines.

Concurrently, the inauguration of third-generation synchrotrons, exemplified by the European Synchrotron Radiation Facility in Europe and the Advanced Light Source in the USA, both commencing operations in 1993, ushered in a new era. Using

these facilities massively decreased the time needed to collect structural data, which led to the acquisition of substantially larger volumes of diffraction data than previously possible in the same time frame.

One crucial aspect of crystal structure determination was accessibility to computational resources and specialized software. In the mid-1980s, cost-effective medium and small-scale computers became widely available. Around the same time, to fit protein models into crystallographic maps derived from data analysis³, dedicated graphics workstations came onto the market, and the refinement of protein structures became more accessible and user-friendly⁴. The collective advancements in techniques, materials and software led to a huge increase in the throughput of crystal structure determination, as evidenced by the increase in depositions within the Protein Data Bank⁵.

These developments laid the groundwork for structural genomics programs, which emerged in the early 2000s as collaborative initiatives from large consortia. Such efforts led to a surge in the number of solved protein structures. The abundance of structural data generated laid the foundations for a second wave of technical advances in structural biology. These include artificial intelligence software, such as AlphaFold, which is tailored for accurate protein structure prediction⁶. In parallel, cryo-electron microscopy, together with associated software, became robust enough to determine very large structures at atomic resolution without crystallization⁷.

Dissemination through publication is an essential step for researchers. In 1994, the set of journals that published protein structures was limited. Apart from specialized journals in the *Acta Crystallographica* collection, there were no journals dedicated to publishing protein structures. Although papers reporting structural biology are published in specialist biochemistry journals, and selective multidisciplinary publications including *Nature*, *Science* and *Cell*, the number of papers published was small.

The debut of NSB, which was dedicated to the publication of protein structures and complexes and was one of the first sister journals to *Nature*, provided researchers with a platform to publish their work in a high-visibility journal. For many

researchers, the introduction of NSB was very welcome. For example, my research group published a paper in NSB in 1994 (ref. 8), followed by several others in subsequent years. Provision of a dedicated avenue for showcasing structural biology findings was an important step for the growing community of structural biology researchers. Although NSB has evolved into *Nature Structural and Molecular Biology* to expand its scope, it continues to faithfully showcase the field of structural biology and foster and support the broad community of researchers interested in reading about studies that have structural investigation at their heart.

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