

## Transfer-RNA deciphered

In April 1953, after a year and a half of thinking and tinkering in laboratories and coffee shops at Cambridge University, James Watson, Francis Crick and Maurice Wilkins announced the structure of DNA (deoxyribonucleic acid), the large and complex molecule in which heredity resides.

Discovery of the double helix thrust molecular biology headlong into the forefront of research which has since produced profound insights into the function of DNA and RNA (ribonucleic acid), the molecule that carries the coded message for protein synthesis from DNA to manufacturing plants in the cell.

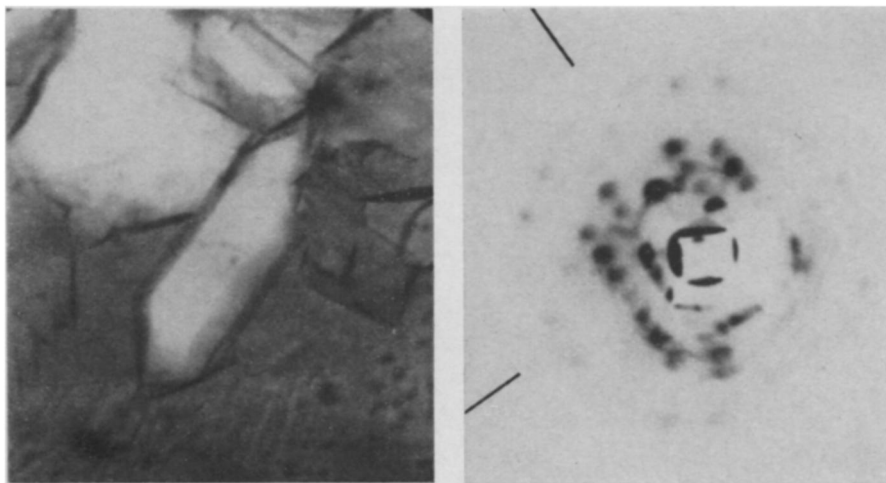
But for all that is known, nucleic acid research is really just beginning. Detailed understanding of the process that begins with DNA and ends with a newly made protein, and, in fact, confirmation of the double helix—postulated by fitting limited evidence to theory—requires atom by atom blueprints of the architecture of nucleic acids.

One of the best methods of deciphering three-dimensional structure—one which has been used successfully with proteins—is X-ray crystallography. Penetrating X-rays bounce off atoms within molecules, producing a scatter pattern that shows just where each atom is positioned. Evidence that DNA is a double helix came from crystallographic work, but because the Cambridge group studied DNA fibers, rather than pure crystals, they got only two dimensional information.

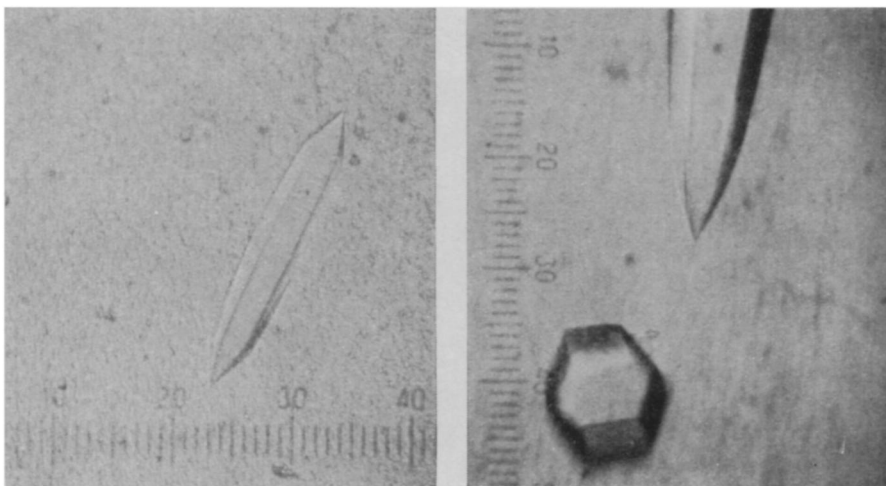
So far, DNA crystals have not been obtained, but researchers in Massachusetts and Wisconsin have produced the first pure crystals of a nucleic acid with crystallization of transfer-RNA. Now, with a minimum of difficulty, X-ray crystallographers will be able to reveal the architecture of this clover leaf molecule, the molecule that picks up protein-making instructions from messenger RNA, retrieves the appropriate protein-building amino acid from the cytoplasm and transfers it to ribosomes—the manufacturing plants. Knowing its crystalline structure is a first step to solid understanding of its function.

“Once we know its structure,” says Dr. Alexander Rich of the Massachusetts Institute of Technology, “we’ll know which of its surfaces are exposed, how they’re constructed and how they fit into the molecules with which they interact.”

While DNA and m-RNA molecules are thought to be in linear arrangements when carrying out their biological functions, t-RNA is thought to maintain its convoluted shape while at work.



*Crystals, X-ray pattern of one form of bacterial tRNA obtained at MIT.*



*Another form of bacterial tRNA, grown at Wisconsin from Escherichia coli.*

Dr. Rich, who with Dr. Sung-Hou Kim reported t-RNA crystallization in the Dec. 20 issue of *SCIENCE*, compares t-RNA to a key that fits into a lock—in this case, ribosomes and molecules known as activating enzymes. “The shape of the key will tell us the shape of the lock. We’ll learn the mechanism for the essential step in protein synthesis, the transfer of genetic information.”

Difficulty in crystallizing a nucleic acid, long an aim of researchers, “may be due to the lack of a systematic approach to crystallization which is still as much an art as a science,” observes Dr. Arnold Hampel who, with associ-

ates at the University of Wisconsin in Madison, also reports t-RNA crystallization in the Dec. 20 *SCIENCE*. Transfer-RNA takes at least 20 different forms, one specific to each type of amino acid. One problem lay in obtaining a single form of t-RNA, another in creating conditions in which it would hold that configuration and crystallize.

In addition to studying the function of t-RNA, the Wisconsin researchers’ long range plans include collaboration with Dr. H. Gobind Khorana, one of this year’s Nobel Prize winners (*SN*: 10/26/68, p. 411) who is working on synthesis of the first artificial gene.

## PULSARS

### The lighthouse effect

Neutron stars, one of the early suggestions as to the identity of pulsars, are now returning to favor, but not in quite the way they were first presented. They now appear as rotating bodies rather than pulsating ones.

New evidence regarding the slowing down of the objects’ rate seems, at least

for the present, to rule out both binary and pulsating sources as explanations.

A month earlier (*SN*: 11/23/68, p. 521) one pulsar that seemed to be slowing down was reported. Now there are four, says Dr. A. G. Lyne of Jodrell Bank Observatory in England. He presented data to the Fourth Texas Sym-