

3. In 1969, I joined the Medical Research Council Laboratory of Molecular Biology, Cambridge, where I researched the cellular and genetic structure of the nematode worm, *C. elegans*.

4. It	pecame involved in gen	omics starting in 1	.983, and	played a central	l role in
both the C. el	egans worm and huma	n genome projects	. In 1998	I and my collea	agues

be sequenced.

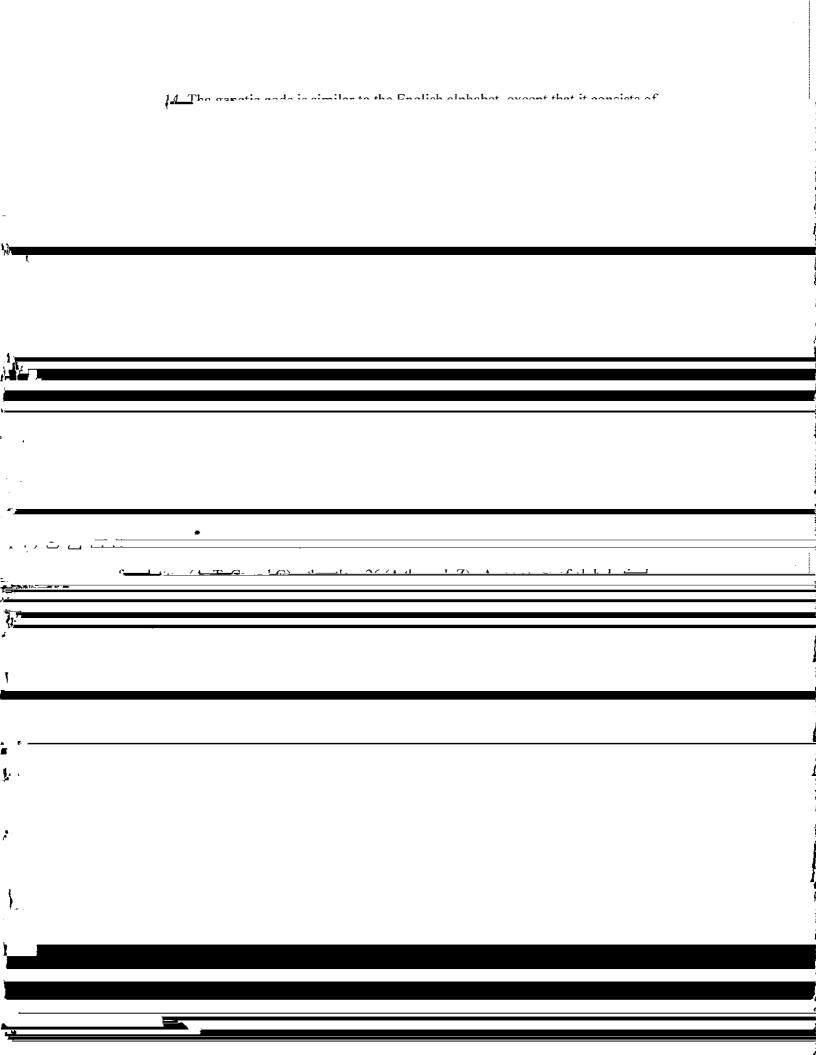
5. From 1992-2000 I served as the first Director of the Wellcome Trust Sanger Institute in Cambridgeshire. During my tenure as Director, the Institute grew from 15

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	human genome, and discusses the importance of ensuring that information contained in	:
	our genome be freely available for the benefit of all.	

9. A full copy of my current curriculum vitae is attached as an Exhibit.

## **Genes and Genetic Sequences**

- 10. Genes and human genetic sequences are not inventions. They are naturally occurring. They are the most fundamental information about humanity, information that is or should be common heritage.
  - 11 Canac are the basic units of heredity in all living organisms. A gene is a



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, co	pyrighted), the informational content of a human gene sequence is fixed. While many
in	ventive steps have been necessary to allow us to extract and read a genetic sequence,
th	e ordering of the 4 letters is determined by nature.
	18. The slight variations that occur among individual genomes are of great
in	terest to some scientists, because they are thought to account for some of the
נט	fferences that we see among us. These "typos" or mutations can be in the form of the

21. Progress in sequencing was slow the first two decades following the discovery of DNA. The first practical method that allowed sequences of many thousands of bases to be read out was invented by Fred Sanger and his colleagues at Cambridge England,

overlapping pieces were produced, and cloning them randomly (the so-called shotgun approach). Each piece was sequenced by an ingenious method involving replication enzymes, radioactive labels and size separation of the resulting complex mixtures in an electric field. The beautiful patterns that emerge look rather like a bar code, and can be

<u> </u>	23. Our ability to sequence genes has been predicated on advances in numerous areas, including chemistry, biochemistry, instrumentation, and computing. Some of these	
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	apply to <i>processes</i> . They do not apply to the data flowing through them.  24. Gene sequencing is used in diagnostic testing. A gene sequence can be examined to determine if it contains any alterations or mutations that have been	
	associated with a particular genetic condition.  25. In order to sequence, or read a gene, we have to remove it from the cell of an	
	organism and place it in a form so that it can be replicated outside of the body. Most	:

commonly, we use a technique called PCR to replicate many times over small segments

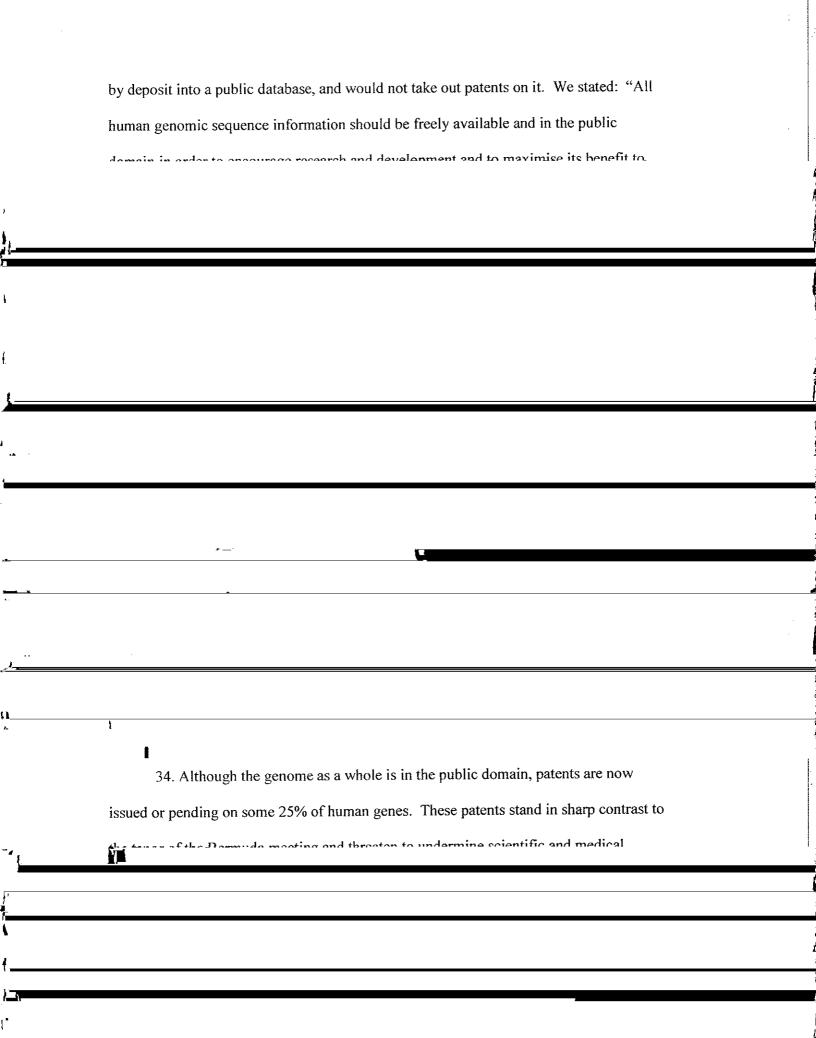
gives a monopoly over this information, regardless of the person from whom the gene is taken or the sequencing process that is used.

## Information Sharing in Genomic Research

- 28. From the point of view of scientific research, human genetic sequences are as basic as you can get in terms of biological information. They are as basic as the elements in the periodic table. Patenting a gene or genetic sequence impedes scientific progress much the same way that patenting a naturally occurring element such as oxygen or gold would impede science.
- 29. From the very beginning of the Human Genome Project, most scientists and even some private companies recognized the importance of keeping the genome freely available to all. In 1994, the pharmaceutical company Merck funded a massive drive to generate genetic sequences and place them into public databases. By doing this Merck not only gave the entire research community, public and private, free access to valuable genomic data; it also made those sequences much more difficult to patent.
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30. In November 1995, a team of researchers at the United Kingdom-based

BRCA2 was sequenced by the Sanger Centre. Over the next two weeks, the ICR team confirmed their results and identified five additional mutations. But the day before their



37. Patents on human genes and genetic sequences are deleterious to the practice of science. Because gene patents tend to cover all uses of that sequence, they are a disincentive to further research on those genes. Patents on genes damage accessibility to 38. Patents on human genes will be deleterious to unraveling their role in medical