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## Assembling the human genome - for free

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A project that aims to "put the genome on the desk top of biologists worl-wide" has received a major funding boost of more than 8 million pounds over the next five years. The [Ensembl project](#) is operating with an "open philosophy" to make the analysis of data supplied through the Human Genome Project available to biologists free of charge. Using specially developed software, the Ensembl database automatically sorts and identifies genes and other useful features of the data of interest to biologists and medical researchers. "Ensembl is a wonderful way of transmitting genetic information clearly and quickly across the world," according to Dr Michael Dexter, Director of the UK's [Wellcome Trust](#), which is supporting the project, "It is important that information is made available in the most user-friendly and complete way, and made available free of charge." The Ensembl database, located at the [Sanger Centre](#) and the [European Bioinformatics Institute \(EBI\)](#), near Cambridge, UK, is fed with raw DNA sequence taken from the world's DNA data sources. "In the race to complete the genome, researchers increasingly adopted a shotgun approach to blast vast amounts of sequencing data into the central databases," says Russ Hodge from the [European Molecular Biology Laboratory \(EMBL\)](#), which supports the EBI. Putting the DNA jigsaw back together is done using specially developed software that operates within the Ensembl database. Gene-finding software, called Genscan, then predicts the location of gene sequences by identifying DNA regions that may look like genes. These 'candidates' are compared to all known gene sequences in the public databases in order to find supporting evidence for the software's predictions. Users of the Ensembl website can click on an image of the chromosome they are interested in, to examine the markers and details mapped on to the chromosome. To reach the low-level DNA sequence, researchers highlight the section of the chromosome they require in order access the DNA sequence itself and the supporting evidence gathered by the software. "Private companies like Celera have similar tools but are marketing these intensively and are mainly interested in the financial aspects," says Hodge who says that the project will be of special interest to pharmaceutical companies. Because of the way the software is being developed, by multiple users around the world, Hodge suggests that the Ensembl analysis software may even be of a higher standard than those developed by commercial enterprises.

## References

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