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## International consortium announces the 1000 Genomes Project

**Hinxton, 22 January 2008** – An international research consortium today announced the 1000 Genomes Project, an ambitious effort to sequence the genomes of at least 1000 people to create the most detailed and medically useful catalogue to date of human genetic variation.

Drawing on the expertise of multi-disciplinary research teams, the map developed by the 1000 Genomes Project will provide a view of biomedically relevant DNA variations at a resolution unmatched by current resources. The European Bioinformatics Institute (EBI), working with long-term collaborator the US National Institute of Biotechnology Information (NCBI), will make the data swiftly available to the worldwide scientific community through freely available public databases. The EBI and NCBI will collect and analyse sequence generated by the Wellcome Trust Sanger Institute, the Beijing

Genomics Institute, Shenzhen, China, and the USA's National Human Genome Research Institute Large-Scale Sequencing Network.

During its two-year production phase, the 1000 Genomes Project will deliver sequence at an average rate of about 8.2 billion bases per day, the equivalent of more than two human genomes every 24 hours. The volume of data – and the interpretation of those data – will pose a major challenge for leading experts in the fields of bioinformatics and statistical genetics.

It's a challenge that Paul Flicek, lead investigator on the EBI's part of the project, is eager to rise to. 'The 1000 Genomes Project represents an important step in relating DNA sequence information to each individual's risk of disease and response to drugs – we're on the cusp of building an important bridge between biology and medicine,' he says. ●

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### Contact:

Louisa Wright PhD, EMBL-EBI Scientific Outreach Officer, Hinxton, UK, Tel: +44 1223 494665, [www.ebi.ac.uk](http://www.ebi.ac.uk), [louisa@ebi.ac.uk](mailto:louisa@ebi.ac.uk)  
Anna-Lynn Wegener, EMBL Press Officer, Heidelberg, Germany, Tel: +49 6221 387 452, [www.embl.org](http://www.embl.org), [wegener@embl.de](mailto:wegener@embl.de)

## Notes for Editors

To learn more about the 1000 Genomes Project as the effort develops, and to read A Workshop to Plan a Deep Catalog of Human Genetic Variation, which summarizes the meeting that laid the groundwork for the project, go to [www.1000genomes.org](http://www.1000genomes.org).

### About EMBL:

The European Molecular Biology Laboratory is a basic research institute funded by public research monies from 19 member states (Austria, Belgium, Croatia, Denmark, Finland, France, Germany, Greece, Iceland, Ireland, Israel, Italy, the Netherlands, Norway, Portugal, Spain, Sweden, Switzerland and the United Kingdom). Research at EMBL is conducted by approximately 80 independent groups covering the spectrum of molecular biology. The Laboratory has five units: the main Laboratory in Heidelberg, and Outstations in Hinxton (the European Bioinformatics Institute), Grenoble, Hamburg, and Monterotondo near Rome. The cornerstones of EMBL's mission are: to perform basic research in molecular biology; to train scientists, students and visitors at all levels; to offer vital services to scientists in the member states; to develop new instruments and methods in the life sciences and to actively engage in technology transfer activities. EMBL's International PhD Programme has a student body of about 170. The Laboratory also sponsors an active Science and Society programme. Visitors from the press and public are welcome.

### About EBI:

The European Bioinformatics Institute (EBI) is part of the European Molecular Biology Laboratory (EMBL) and is located on the Wellcome Trust Genome Campus in Hinxton near Cambridge (UK). The EBI grew out of EMBL's pioneering work in providing public biological databases to the research community. It hosts some of the world's most important collections of biological data, including DNA sequences (EMBL-Bank), protein sequences (UniProt), animal genomes (Ensembl), three-dimensional structures (the Macromolecular Structure Database), data from microarray experiments (ArrayExpress), protein-protein interactions (IntAct) and pathway information (Reactome). The EBI hosts several research groups and its scientists continually develop new tools for the bio-computing community.

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