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Fugugenome rough draft completed

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Fugu rubripes - the Japanese puffer fish - is farmed in Japan for its flesh and is considered a great delicacy. But it is its 365 million base genome that interests scientists of the Fugu Genome Sequencing Consortium.

The [Fugugenome](#) contains similar genes and regulatory sequences to the human genome, but has substantially less 'junk DNA' compared to the 3 billion bases that constitute the human genome. On 26 October 2001, at the [13th International Genome Sequencing and Analysis Conference](#), San Diego, California, [Sydney Brenner](#) and colleagues from the *Fugu* Genome Sequencing Consortium announced the completion of the *Fugu* genome sequencing project.

The consortium employed a whole-genome shotgun strategy to sequence the fish's genome. The DNA was fragmented into pieces small enough to sequence and then reassembled by a new computational algorithm, JAZZ, which had been developed at the US Department of Energy's Joint Genome Institute (JGI) in Walnut Creek, California.

According to Brenner this "will illuminate the human genome sequence and help us to understand it." Trevor Hawkins, Director of the JGI, said, "comparative genomics programs are key to understanding the biology of the human genome."

The Consortium intends to publish an initial analysis of the draft *Fugu* genome early in 2002.

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