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Sea Urchin Genome Is a Biology Boon and a Computational Feat

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[摘要] Dec 7 - After identifying 23,300 genes made from 814 million letters of DNA code taken from *Strongylocentrotus purpuratus*, the California purple urchin, an international science team has found that humans share 7,077 genes with urchins. Results from the sequencing project are published in a special six-article section of Science.

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After identifying 23,300 genes made from 814 million letters of DNA code taken from *Strongylocentrotus purpuratus*, the California purple urchin, an international science team has found that humans share 7,077 genes with urchins. Results from the sequencing project are published in a special six-article section of Science. Sorin Istrail, professor of computer science and director of the University

of California Center for Computational Molecular Biology, served as a member of the sea urchin sequencing team. A former research director at Celera Genomics, the private company that sequenced the human genome, Istrail was one of eight scientists in the urchin project who pulled off a complex task. This map, called a transcriptome, represents every experimentally authenticated messenger RNA molecule, or transcript, present in embryonic cells. This information tells scientists which genes are activated, or expressed, during the first two days of development. The group determined whether or about half of all of the animal's genes are

expressed in this critical early stage. "Understanding what genes are active in a cell at any given time is critical to biologists," Istrail said. "This information can tell them what genes do and represents the first step in understanding how they work with other genes during development. While transcriptome maps have been created for other species, none has been completed so quickly. That

was because Istrail and the other scientists on the transcriptome team used a whole-genome tiling array custom-built by NASA. The array allowed them to insert 500,000 bits of DNA into 500,000 cells at a time to see which bits get copied into messenger RNA. The high-resolution transcriptome map helped scientists more rapidly identify and verify genes for the larger sequencing project.

"The sea urchin holds the key to the cis-regulatory code, the blueprint for gene regulatory systems and networks and the functional maps of the control circuitry of the cell," Istrail said. "Now that we have the genome and transcriptome map, we can start to crack this code, which will reveal key insights into human genetic

