中国科学院生物物理研究所

贝时璋讲座

Distinguishing coding and non-coding transcription across mammalian genomes

报 告 人：Nicholas Proudfoot

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主 持 人：俞洋 研究员

报告人简介

University of Oxford, UK:
Fellow of the Royal Society (2005-present)； Brownlee-Abraham Chair of Molecular Biology (2003-present)；
Royal Society/Wolfson Research Merit Award (2002-2007)； EMBO Member (1982-present)；
Fellow and Tutor in Biochemistry at Brasenose College, Oxford (1982-2003)；
Lecturer then Professor in Chemical Pathology, Sir William Dunn School of Pathology (1981-2003)
California Institute of Technology and Harvard University USA:
Senior Research Fellow with T. Maniatis (1979-1981)
MRC Laboratory of Molecular Biology Cambridge UK:
Junior Research Fellowship, St John's College, Cambridge (1976-1979)； MRC Scientific Staff (1978-1979)；
Junior Beit Memorial Research Fellowship (1975-1978)； MRC Studentship (1973-1975)

【报告摘要】The dramatic achievement of sequencing the whole human genome has been tempered by the subsequent realisation that the human transcriptome is far more complex than initially anticipated; far from any clear understanding of how and why it is made. My lab has focused on the basic mechanism of transcriptional termination and associated RNA 3' end processing by the major RNA polymerase II (Pol II) that is responsible for the synthesis of all pre messenger RNA and most non coding RNAs. We have uncovered a surprising diversity of termination mechanisms using gene specific analyses. We are now applying new native elongating transcription (NET) sequencing strategies to define all Pol II transcription units (especially mammalian NET-seq). Using this technology we are uncovering unanticipated mechanistic cross talk between the basic transcription process and associated pre-mRNA and long non coding RNA processing.

【研究成果】：

1. Schlackow M**, … ,Proudfoot NJ**. **(2017)** Distinctive Patterns of Transcription and RNA Processing for Human lincRNAs. ***Mol Cell***
2. Nojima T**, … ,Proudfoot NJ**. **(2015)** Mammalian NET-seq reveals genome-wide nascent transcription coupled to RNA processing. ***Cell***
3. Dhir A**, … ,Proudfoot NJ, …** . **(2015)** Microprocessor mediates transcriptional termination of long noncoding RNA transcripts hosting microRNAs. ***NSMB***
4. Skourti-Stathaki K**, … , Proudfoot NJ**. **(2014)** *R-loops induce repressive chromatin marks over mammalian gene terminators.* ***Nature***
5. Tan-Wong SM**, … , Proudfoot NJ**. **(2012)** *Gene loops enhance transcriptional directionality.* ***Science***
6. Skourti-Stathaki K**, Proudfoot NJ, …** .**(2011)** *Human senataxin resolves RNA/DNA hybrids formed at transcriptional pause sites to promote Xrn2-dependent termination.* ***Mol Cell***
7. Gullerova M**, Proudfoot NJ**. **(2008)** *Cohesin complex promotes transcriptional termination between convergent genes in S. pombe.* ***Cell***