European Alternative Splicing Network

EURASNET

Alternative splicing increases the coding capacity and the proteome diversity of eukaryotes. Understanding the complex regulation and consequences of alternative splicing and the functions of derived proteins is a major goal for biological and medical research. Defects in the control of alternative splicing frequently cause, or exacerbate, pathological conditions and link to many diseases including various cancers and neurodegenerative conditions.

Leading European laboratories in research on alternative splicing are now united in a European Commission funded Network of Excellence (NoE), EURASNET, the European Alternative Splicing Network. The coordinator of this Network is Reinhard Lührmann, MPI-Göttingen. The original consortium brings together 30 research groups from 25 participating institutions in 13 countries. The partners are involved in alternative splicing research in human, animal, plant and yeast systems. EURASNET has secured ten million Euros in funding for the next five years, within the Framework 6 Program (FP6) of the European Union, for research in alternative splicing.

By integrating wide-ranging expertise of different organisms and functional genomics technologies, the NoE aims to understand the complex regulation of alternative splicing and the consequences, in terms of disease, of any defects or break down in regulation. New knowledge and applications will be generated which will impact human health and well-being.

EURASNET Objectives

The NoE has three important objectives:

1. **Pursue an ambitious research program via a Joint Research Program.**
2. **Integrate young investigators in the field into the Network, via a Young Investigator Program.**
3. **Disseminate awareness of the importance of alternative splicing among medical practitioners, policy makers and the general public.**

The joint program is organized in 22 work packages covering research, integration and dissemination. The NoE will provide a broad-based research programme and portfolio to promote understanding of the complex regulation of alternative splicing in different systems and will establish an active and vibrant network to share and exchange information, methods and material among the network partners. Communication of the importance of RNA biology and alternative splicing to policy makers and the general public and to disseminate the results and outcomes of the EURASNET research to the scientific and medical communities is an essential aspect of the programme.

For further information see:
www.eurasnet.info

The Network

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Human DNA viruses as model systems to decipher basic regulatory mechanism controlling gene expression at the level of RNA biogenesis and RNA processing.

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Development of database and tools for alternative splicing

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Alternative splicing evolution, primate-specific genomic diversity; and the link to genetic disorders and cancer.

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Plant SR proteins and their impact on alternative splicing and plant development.

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Pre-mRNA splicing defects involved in the pathogenesis of human diseases and their possible prevention and treatment through recombinant DNA procedures.

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Pre mRNA splicing in the yeast Saccharomyces cerevisiae.

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Deregulation of alternative splicing in tumor progression and novel mechanisms to control pre-mRNA splicing by redirecting the sub-cellular distribution of splicing factors.

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Regulation of alternative splicing by intronic regulatory elements.

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Computational approaches to the evolution and functional consequences of alternative splicing

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RNA and RNP structure-function analysis and the effect of pre-mRNA structure on alternative splicing.

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Regulation of alternative splicing in plants and the link between splicing and nonsense-mediated decay.

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Trans-acting factors involved in the regulation of alternative splicing and multiple roles of SR proteins in post-transcriptional regulation of expression.

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Dynamics of spliceosome assembly and recruitment of factors to transcription sites

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Activator and repressor proteins in determining splice site choice and the development of methods for a kinetic analysis of spliceosome dynamics.

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Splicing regulation in plants and the connection between proteins involved in RNA metabolism and abiotic stresses.

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Mechanisms of alternative splicing involved in regulation of HIV-1 and medium chain acyl-CoA dehydrogenase (MCAD) mRNA splicing.

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Regulation of alternative pre-mRNA splicing involving coupling of transcription and splicing and co-ordination of alternative splicing events.

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Splicing proteins that function in 3' splice site definition at the onset of spliceosome assembly and the regulation of SF1 activity.

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Functional organisation of the cell nucleus and the mechanism of pre-mRNA splicing in mammalian cells.

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Structure and function of spliceosomal and sub-spliceosomal complexes in pre-mRNA splicing.

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Organisation of pre-mRNA splicing in the cell nucleus and the action of snRNPs in co-transcriptional spliceosome assembly and alternative splicing.

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Manipulation of specific alternative splicing events for gene therapeutic approaches for genetic and acquired diseases.

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Assembly of stable and dynamic protein complexes in splicing regulation and the role of RNA decay pathways in alternative splicing.

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Molecular mechanisms of regulated alternative splicing in model gene systems and the function of splicing regulators.

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Stress-induced transcriptional and post-transcriptional regulation of the acetylcholinesterase (*AChE*) gene and the function of AChE variants.

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Novel regulation of alternative splicing by external stimuli and small RNAs.

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RNA-interacting proteins and the molecular mechanisms of regulation of alternative splicing in humans.

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Tissue-specific and developmentally regulated splice site selection and n and pairing of 5' and 3' splice sites and targeting of splicing factors by small chemical molecules.

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Cis-and trans- nonspliceosomal splicing by the archaeal MJ endonuclease in mouse cells and in mice.

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Molecular mechanisms of alternative splicing regulation and the functions of trans-acting factors and the link to cell differentiation and cancer progression.

Newly joined young investigators :

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Science Advisory Board

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