

European Alternative Splicing Network of Excellence

EURASNET

EURASNET, the network of excellence on alternative splicing has been running since January 2006. In addition to the 30 original research groups, 10 young investigators have been added to the network.

EURASNET held its First International Conference on Alternative Splicing in May 2008, in Krakow, Poland. The conference

featured 17 international invited speakers who are experts in the biochemistry, genomics, cell biology and clinical aspects of alternative splicing. Bioinformatics and Media workshops were run during the meeting.

The network has successfully established contacts with the medical community through workshops and training on alternative splicing and disease as well as on genetic diagnostics. The network is also actively building

collaborative research and interactions with exchanges of lab members and students between EURASNET labs.


For further information see:
www.eurasnet.info

The Network




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




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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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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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Modeling proteins important for splicing regulation and new computational tools for structure prediction of RNA and protein-RNA complexes.



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Tissue-specific alternative splicing and mechanisms by which these become subverted in disease.




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




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




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Tissue-specific and developmentally regulated splice site selection and π and ρ splice sites and targeting of splicing factors by small chemical molecules.



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NMR structure determination of RNAs, proteins and protein-RNA complexes associated with post-transcriptional gene regulation.



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Splicing mutations in disease, penetrance and clinical diagnosis: systems for molecular diagnostic testing.



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Regulation of alternative splicing by intronic regulatory elements.



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



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



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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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Protein-RNA interactions and post-translationally modified proteins in protein-RNA complexes.



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Development of database and tools for alternative splicing



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



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Computational approaches to the evolution and functional consequences of alternative splicing.




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Dynamics of spliceosome recruitment of factors to transcription sites.



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



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Organization 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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Molecular mechanisms by which signal transduction pathways modulate alternative splicing.



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



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



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Pre-mRNA splicing in the yeast *Saccharomyces cerevisiae*.



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



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



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



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



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



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Strategies for targeting alternative splicing regulation in tumour cells to produce spliced variants with anti-tumour properties.



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Imaging of intracellular transport of RNA molecules and early steps of mRNA biogenesis.



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



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Bioinformatics of regulation of alternative splicing using comparative genomics and computational methods.




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



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



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Computational methods to study the mechanisms regulating alternative splicing and analyze high-throughput short RNA sequencing data.

Science Advisory Board

The NoE is supported by a scientific advisory board with members:

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