Universität Basel

Research Project

RNATRAIN - The European non-coding RNA training network

Third-party funded project

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A surprising outcome from the human genome sequencing project was that the number of protein coding ăgenes only amounts to about 21.000 – a number not dramatically different from that found in much simpler ăeukaryotes. So what can explain and form the molecular basis for the significantly increased complexity

found, for instance, in mammals? Part of the answer resides in one of the most important and unexpected ăbiological findings within the last decade; the realization that the vast majority of the mammalian genome is ăactively transcribed at some stage in development despite a lack of translation to protein. The regions ăencompassing protein coding potential (exons) in humans only amount to approximately 2% of the genome ăand this fraction has been the focus for the majority of scientific studies over the last many decades. New ăhigh-throughput methodologies, such as next generation sequencing (NGS) and tiling arrays have

demonstrated the existence of multiple new classes of non-coding RNA, such as microRNA (miRNA), long ăintergenic ncRNA (lincRNAs) and RNA molecules produced at promoter and enhancer regions, PROMPTs ăand eRNAs, respectively. Although our knowledge on the multitude of transcripts produced by the noncoding

98% of the genome is still very sketchy, pivotal roles have been established for ncRNAs in ăorganismal development and homeostasis, in cellular proliferation, differentiation and apoptosis and in a ăbroad range of human pathologies.

As the field is very new and holds the promise of major leaps in biological understanding and therapeutics ădevelopment, it constitutes an important and very fertile breeding ground for a new generation of scientists.

Importantly, such leaps in understanding can only be brought about using a multidisciplinary and cross-sectorial ăapproach, in which techniques and knowhow from diverse fields like genetics, biochemistry, ăinformatics and commercialization is combined and aligned. Accordingly, we here propose to form a pan-European RNA training network, RNATRAIN. This network will be devoted to educating the next ăgeneration of European researchers focusing on the functions and importance of ncRNAs and ăapplying their skills in multidisciplinary projects in which the ncRNAs are studied in the context of ădevelopment, differentiation and disease.

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Add publication

Published results

3208069, Kanitz, Alexander; Gypas, Foivos; Gruber, Andreas J; Gruber, Andreas R; Martin, Georges; Zavolan, Mihaela, Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data, 1465-6906, Genome biology, Publication: JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

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Add documents

Specify cooperation partners

ID	Kreditinhaber	Kooperationspartner	Institution	Laufzeit - von	Laufzeit - bis
2354617	Zavolan, Mihaela	Lund, Anders H.	University of Copenhagen	01.10.2013	30.09.2017
2354619	Zavolan, Mihaela	Huarte, Maite	University of Navarra (FIMA)	01.10.2013	30.09.2017
2354620	Zavolan, Mihaela	Agami, Reuven	NKI The Netherlands Cancer Institute	01.10.2013	30.09.2017
2354623	Zavolan, Mihaela	Landthaler, Markus	Max-Delbrück-Center for Molecular Medicine (MDC)	01.10.2013	30.09.2017
2354624	Zavolan, Mihaela	Kanduri, Chandrasekhar	Gothenburg University	01.10.2013	30.09.2017
2354626	Zavolan, Mihaela	Svoboda, Petr	Institute of Molecular Genetics of the ASCR	01.10.2013	30.09.2017
2354628	Zavolan, Mihaela	Bozzoni, Irene	Universita Degli Studi di Roma la Sapienza	01.10.2013	30.09.2017
2354630	Zavolan, Mihaela	Meister, Gunter	University of Regensburg	01.10.2013	30.12.2030
2354631	Zavolan, Mihaela	Hannus, Stefan	Intana Bioscience GmbH	01.10.2013	30.09.2017
2354633	Zavolan, Mihaela	Schnack Nielsen, Boye	Bioneer A/S	01.10.2013	30.09.2017