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Non-Mendelian inheritance patterns and extreme deviation rates of CGG repeats in autism 1967^{OA}
Dale J. Annear, Geert Vandeweyer, Alba Sanchis-Juan, F. Lucy Raymond, and R. Frank Kooy

Redistribution of lamina-associated domains reshapes binding of pioneer factor FOXA2 in development of nonalcoholic fatty liver disease 1981^{OA}
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Gene essentiality in cancer cell lines is modified by the sex chromosomes 1993^{OA}
Shahar Shohat, Ethel Vol, and Sagiv Shifman

Systematic transcriptome analysis associated with physiological and chronological aging in *Caenorhabditis elegans* 2003
Seokjin Ham, Sieun S. Kim, Sangsoon Park, Eun Ji E. Kim, Sujeong Kwon, Hae-Eun H. Park, Yoonji Jung, and Seung-Jae V. Lee

Genetic exchange with an outcrossing sister species causes severe genome-wide dysregulation in a selfing *Caenorhabditis* nematode 2015^{OA}
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Developmental timing of programmed DNA elimination in *Paramecium tetraurelia* recapitulates germline transposon evolutionary dynamics 2028
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^{OA}Open Access paper



Cover Transposable elements (TEs) have colonized the genome of most living species and represent a major threat to genome integrity. The ciliate *Paramecium* has evolved a mechanism for precise excision of thousands of TE-derived internal eliminated sequences (IESs) at each sexual cycle. IES excision follows a sequential order that reflects their evolutionary age. The most ancient IESs have evolved by optimizing their excision efficiency, acquiring strong sequence determinants and escaping epigenetic control. In this illustration, *Paramecium* cells are trapped in a vortex that depicts evolutionary time, while the timing of IES elimination is represented by the melting clocks inspired by Dali. (Cover artwork by Mickaël Bourge. [For details, see Zangarelli et al., pp. 2028–2042.])