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Abstract:

Hutchinson-Gilford progeria syndrome (HGPS) is a rare human genetic disease that leads to premature ageing and ageing-associated phenotype. HGPS is caused by mutation in the lamin A (LMNA) gene that leads, in affected young individuals, to the generation of progerin, a splicing mutant of lamin A. A bioinformatics analysis of the LMNA gene network of interactions is presented. Lamin A seems to be involved in epigenetic regulation of transcription, chromatin remodelling, DNA repair, with key roles in stemness regulation, normal ageing and telomere functions. The study suggests particular relevance of chromatin remodellers and histones covalent modifiers in the LMNA network. Specifically, HTATIP histone acetylase seems to be of particular relevance in the network.

Keywords (Optional):

Hutchinson-Gilford progeria syndrome

Lamin A

HTATIP

Chromatin Remodellers

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SENS Research Themes:

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Ending Aging:

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