第74回HiHA Webinar

Hiroshima Research Center for Healthy Aging (HiHA)

主催: 広島大学健康長寿研究拠点

HIROSHIMA UNIVERSITY

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Professor, Specially Appointed
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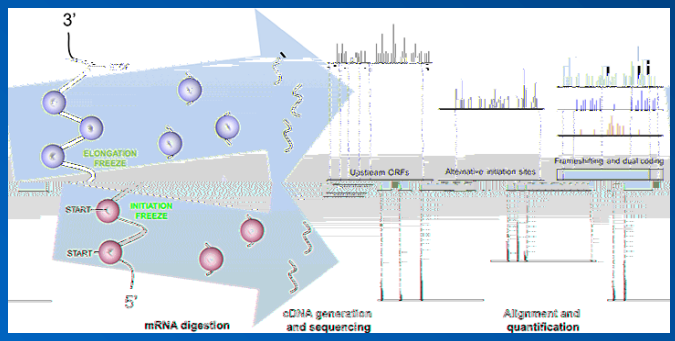
≪Summary≫

Proteins play diverse functions in our cells as enzymes, scaffolds for our cell structure, molecular motors, membrane channels, receptors, etc. Cells spend most of their energy on the biosynthesis of proteins. Therefore, it is important to understand the full repertoire of proteins encoded by the human genome. Recent evidence suggests the existence of numerous proteins and proteoforms encoded outside of currently annotated genomic regions. To help identification of these proteoforms we established several computational tools (GWIPS-viz and Trips-Viz) for the evaluation of processed publicly available high-throughput data (RNA-seq, ribosome profiling, mass spec proteomics, etc). The evaluation of these data in combination with orthogonal approaches for studying expression of individual genes suggests that the plurality of translation initiation sites (enabled by leaky scanning and reinitiation) is the main contributor to the observable decoding diversity together with hitherto poorly characterized heterogeneity of RNA transcripts.



□セミナーは、□合□ー□□□□□セミナーとして、プログラム共同セミナーの□□です

開催日時: 令和4年 6月 28日(火) 16:00-17:00

Zoom　　web
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