

Protein synthesis: From the whole translome to individual codons and back.

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Rapid developments in information technologies combined with increasing power of high-throughput biochemical techniques are changing how we conduct and communicate research. Vast amount of data have been produced recently, whose potential is far greater than that of the specific goals for which they were generated. This potential can be unleashed via processing and organising the data into public resources that provide instant access, analytical tools and intuitive visualisations. This concept can be illustrated with RiboSeq.Org, an internet portal that we developed for computational resources dedicated to the analysis and visualisation of ribosome profiling data (Ribo-Seq). Ribosome profiling allows transcriptome-wide capturing of ribosome positioning on mRNA with a near single nucleotide resolution. Its application allowed us to characterize stress-induced perturbations in protein synthesis in mammals; discover an evolutionary conserved mechanism of memory formation in mRNA; as well as unusual genetic codes in ciliates - one with frameshifting as a default feature and another with all 64 codons specifying sense codons.