The NuRNA™ PCR arrays feature encyclopedic gene contents to profile the expression of mRNAs for protein factors and enzymes in the ground-breaking and recent hottest new research areas, such as epitranscriptomics, central metabolism, small RNA biogenesis, and tRNA modification. Taking the advantage of the gold standard real-time PCR quantification method, our specially designed PCR arrays will allow researchers to avoid massive data processing and tedious screening validations. The panels are easy to use, high in performance, accurate in quantification, and rapid for obtaining instant results in these new research frontiers.

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**tRNA Modification**

**NuRNA™ Human tRNA Modification Enzymes PCR Array**

- tRNAs are most heavily decorated with modifications essential for tuning the tRNAs.
- Best array content covering 85 tRNA modification enzymes and proteins that catalyze and dynamically regulate the tRNA modifications. These are compiled and referenced in UniProt and Modomics.
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**Small RNA Biogenesis**

**NuRNA™ Human Small RNA Biogenesis Proteins PCR Array**

- Simultaneous profiling of the biogenesis pathways for 7 small RNA biotypes: miRNA, piRNA, siRNA, snoRNA, snRNA, tRNA, and tRNA-related fragments (tRF).
- 185 proteins and enzymes comprehensively categorized in the Gene Ontology pathways in the small RNA biogenesis.
- Studying the processes, mechanisms, regulation, and disease association of the biogenesis of all major small RNA biotypes.
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NuRNA™ Human Epitranscriptomics PCR Array
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- An exciting new field of epitranscriptomics beyond genomics, epigenomics and transcriptomics.
- 89 enzymes or protein factors validated or predicted to write, read and erase mRNA epitranscriptomic modifications.
- The transcripts of the epitranscriptomic writers, readers, and erasers detected and quantified based on their canonical protein/subunit sequences in Uniprot.

Human Central Metabolism
NuRNA™ Human Central Metabolism PCR Array
Cat No.: AS-NM-004-1/AS-NM-004-1-R

- Central cell metabolism pathways are the foundation of cellular biology and vital links to major human diseases such as obesity, diabetes and cancer.
- 373 transcripts encoding the enzymes or proteins profiled in the core metabolic pathways and metabolite transporter systems, such as glycolysis, TCA cycle, fatty acid biosynthesis, and nucleotide metabolism.
- Each metabolic gene annotated by integrating with genomic/transcriptomic data at subunit levels with UniProt databases.

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