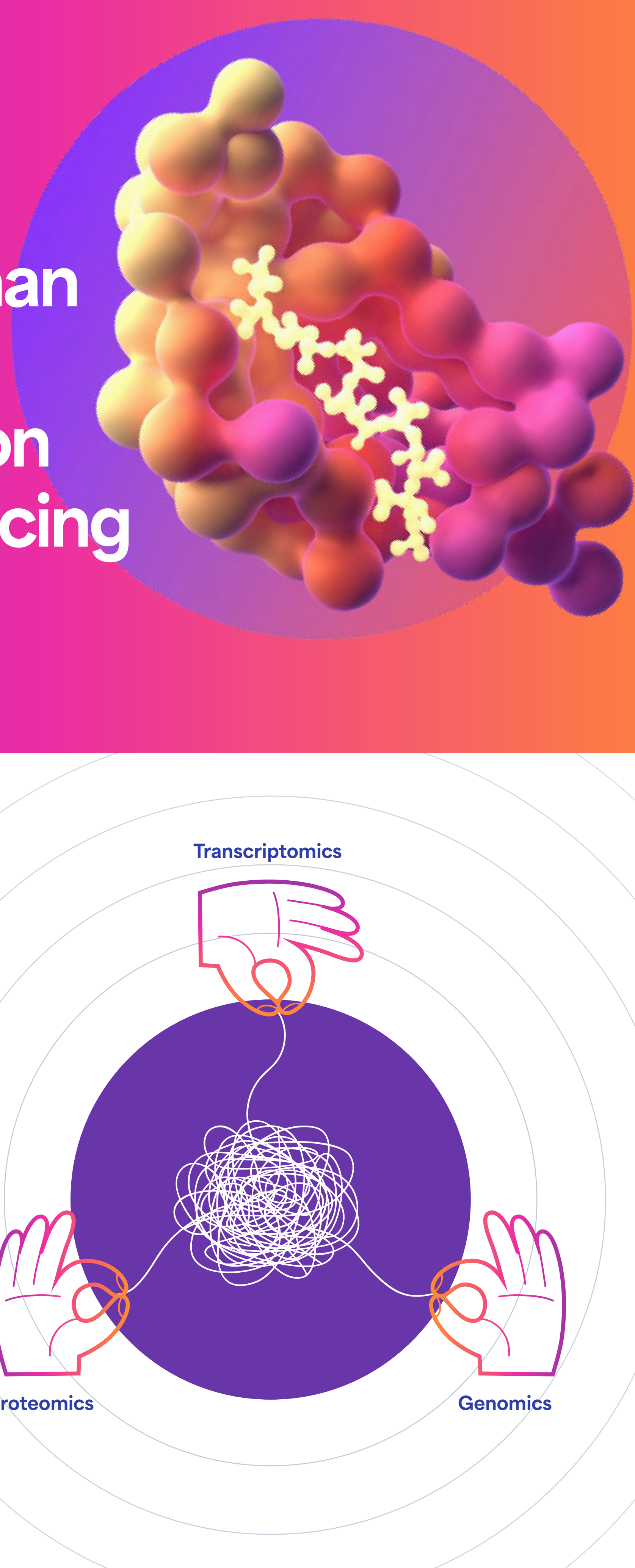
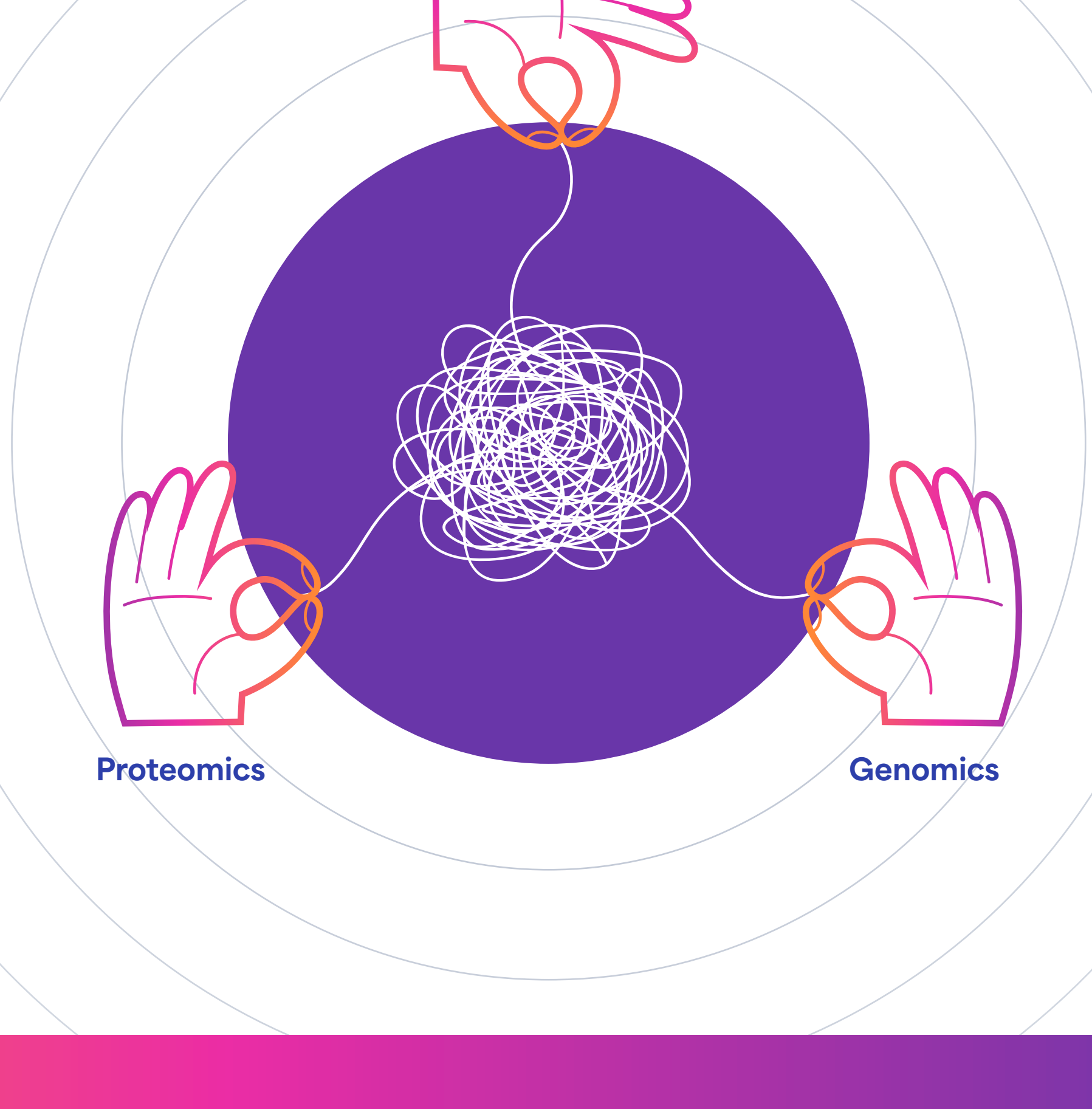


Unravel the Secrets of Human Disease with Next-Generation Protein Sequencing



Protein-level analyses are crucial aspects of human disease research; they unveil the molecular complexities that underpin pathogenesis. However, proteomic insights often lack the accuracy, specificity and depth recorded at the genomic or transcriptomic level.

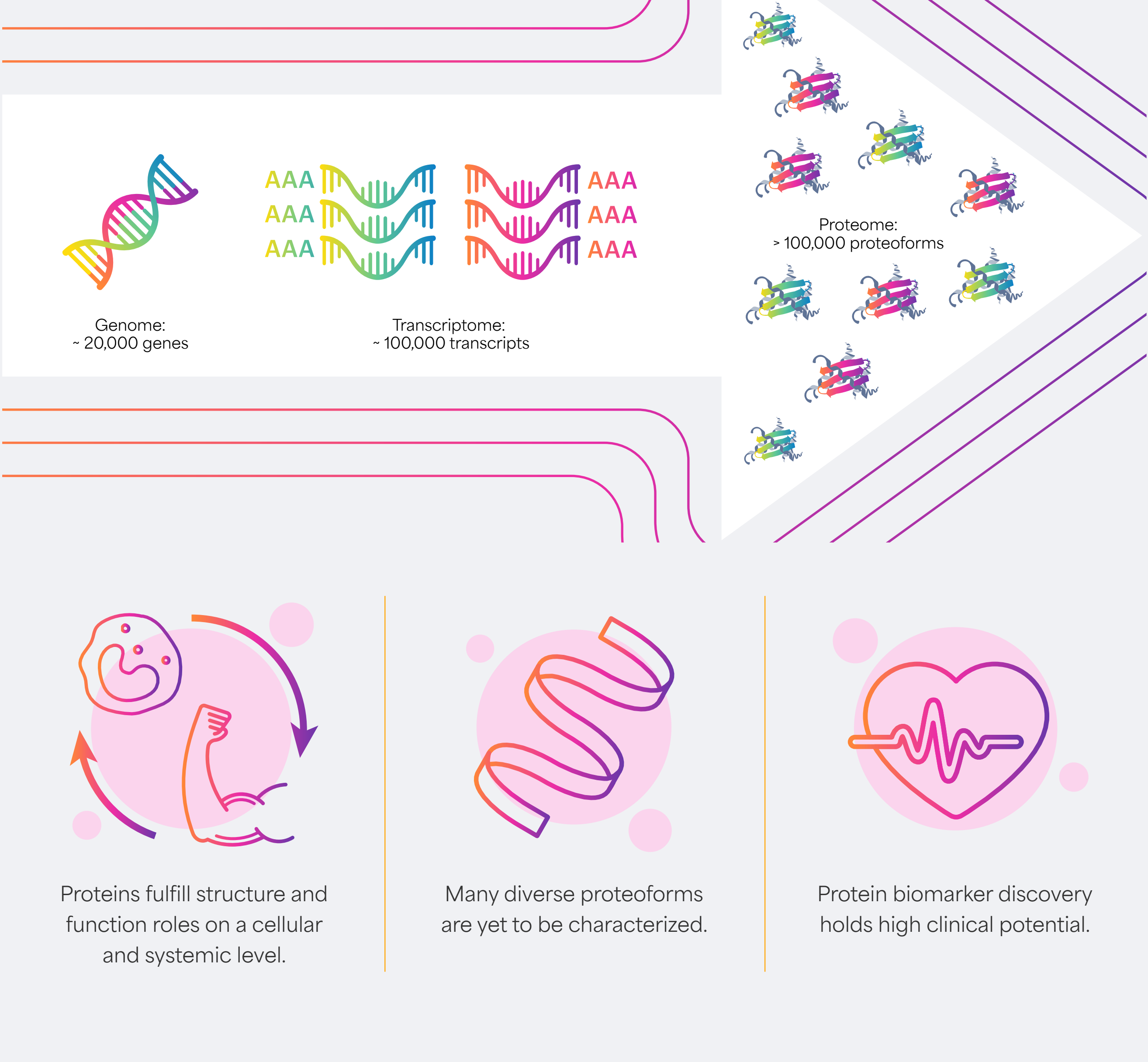
Next-Generation Protein Sequencing™ can complement other omics technologies by delivering unique detail about the human proteome. It provides information-rich insights into the primary structure, interactions and modifications of diverse proteins, supporting an understanding of biological function.



This infographic highlights the role of next-generation protein sequencing in human disease research. It presents the latest single-molecule technologies for sensitive, scalable and accessible approaches to single-molecule proteomic analysis.

The impact of the proteome

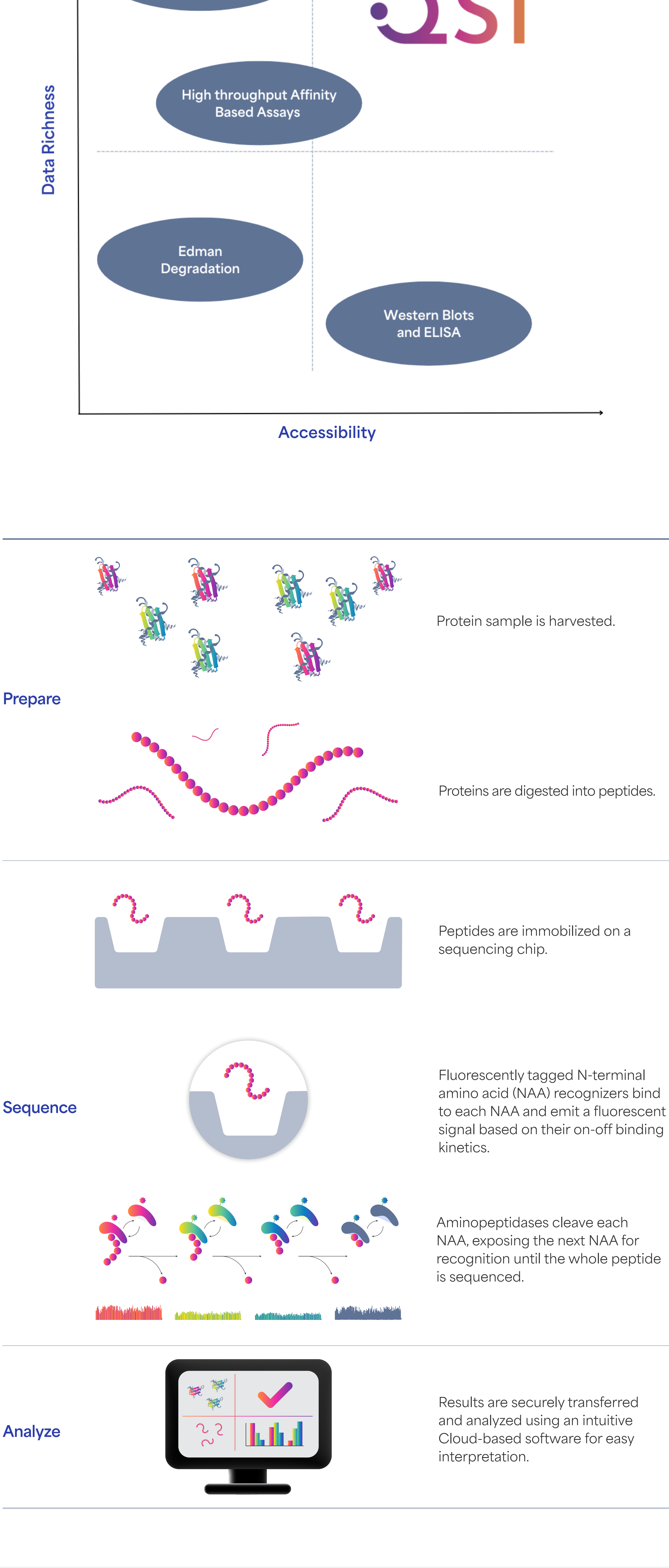
Over 20,000 protein-coding genes exist in the human genome¹. Many of these genes code for multiple protein isoforms, each of which may undergo cleavage, folding and post-translational modification resulting in over a million proteoforms. Hence, the impact of the proteome reflects a variety of biological functions that are difficult to infer from genomic or transcriptomic data alone.



Protein analysis approaches

A variety of protein-level analysis techniques exist that can complement other omics data and hold varying degrees of discovery power. Quantum-Si's sequencer stands out among these techniques by offering both accessibility and comprehensive data. A necessary advancement for protein researchers seeking a versatile solution.

UNLEASHING INSIGHTS AT UNPRECEDENTED ACCESSIBILITY



Choosing the right proteomics approach

Selecting the appropriate proteomics method is crucial to unraveling the secrets of human disease. The choice of method can impact data quality and coverage, and it can enhance discovery power.

I'm a proteomics researcher looking to resolve isoform differences. I need an affordable solution that can differentiate isomers.

Next-generation protein sequencing approaches can accurately differentiate between isomers and identify protein variants and modifications at the amino acid level.²

I'm new to proteomics but know a lot about genomes, and I also know that transcription does not equal translation. I need an easy-to-use solution that can help me correlate gene sequence to protein sequence.

Next-generation protein sequencing probes multiple peptides in real time.³ It works in an information-rich manner, providing context about each amino acid residue in each peptide and aligning each peptide to a protein for simplified protein identification.

I perform a lot of immunoassays, but these methods require highly specific antibodies and they don't provide me with information about protein sequence or variants. Is there a more specific method I could use that does not require specific antibodies for detection?

Next-generation protein sequencing enables deeper discoveries through the interrogation of amino acid residues without the need for highly specific antibodies to perform the analysis.⁴

See beyond the genome

[Platinum® Next-Generation Protein Sequencer™](#) from Quantum-Si is the world's first accessible single-molecule protein sequencing instrument. This scalable sequencing instrument fits on your benchtop and seamlessly integrates into any workflow, making deeper proteomic insights accessible to every lab, everywhere. Its intuitive interface allows experts and novice users to sequence a variety of sample types with the same high-level resolution once limited to genomic data.



Unravel the Secrets of Human Disease with [Platinum](#)

References

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