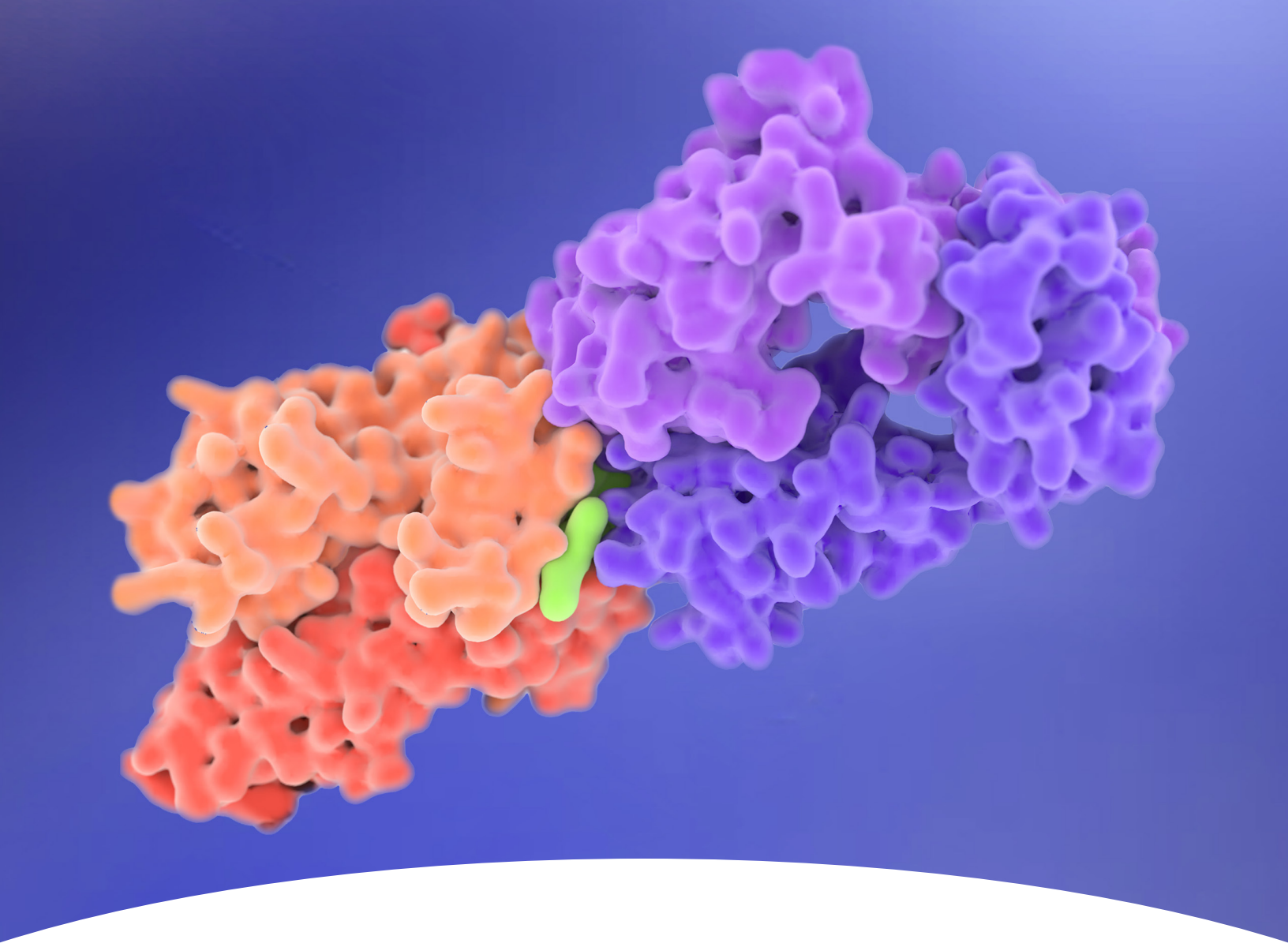


Genomics Solutions for Neoantigen Based Cancer Therapies

High quality, comprehensive genomic data and analytics for personalized cancer therapy development

Personalis®

Precision Genomics for Immuno-Oncology

Enabling Truly Personalized Neoantigen Based Cancer Therapies

The first step of developing personalized cancer therapeutics is the identification of patient-specific neoantigens. With ImmunoID NeXT™, our partners can utilize our proprietary methods for predicting which neoantigens are more likely to elicit an immune response.

ImmunoID NeXT delivers high quality, exome-scale analysis of both DNA and RNA to guide the development of personalized cancer vaccines and personalized adoptive cellular therapies. The entire workflow is optimized to ensure that expedited turnaround timelines are routinely met for personalized cancer therapy development. The added regulatory support and quality assurance processes aid in sample compliance and facilitate the implementation of the platform in all phases of drug development from translational research, clinical trials, and, when applicable, post-approval and beyond.

Accurate Sequencing

ImmunoID NeXT for tumor and germline sequencing includes NeXT Exome™ and NeXT Transcriptome™ powered by Personalis' ACE Platform®

Reliable Delivery

Project tracking, genomic information management, rapid timelines, and seamless data upload via the Cloud

Comprehensive Reporting

ImmunoID NeXT computational solutions produce data-rich outputs including accurate somatic variant calls, germline HLA typing, neoantigen prediction, and related novel biomarkers

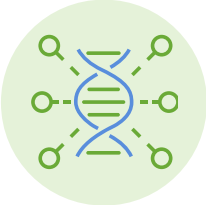
Personalis®

Advanced Genomics Platform for Neoantigen Identification

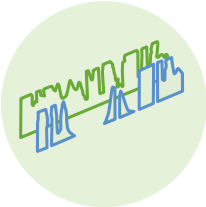
ImmunoID NeXT is a broad immunogenomics solution that combines Personalis' augmented and analytically-validated NeXT Exome and NeXT Transcriptome sequencing assays, with uniquely enhanced features that are key for the development of personalized cancer vaccines and adoptive cell therapies.

Key features of ImmunoID NeXT™:

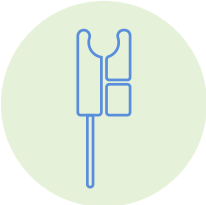
- Optimized dual extraction of both DNA and RNA from the same, precious tumor sample.



- Deep sequencing of tumor DNA at a mean coverage of ~300X, normal DNA at a mean coverage of ~150X, and tumor RNA at 200 Million total reads to provide comprehensive mutational landscape assessment.



- Use of our proprietary ACE Platform® to provide augmented coverage of difficult-to-sequence gene regions across the entire ~20,000-gene footprint.



- High Quality HLA typing of Class I and Class II alleles.
- Increase in the coverage of HLA alleles by targeting alternative reference sequences in the NeXT Exome design.

- Integration of both proprietary and publicly-available advanced analytical algorithms and tools to generate high quality and informative analytical reports.

Advanced Analytics

Detecting tumor-specific neoantigens and predicting those that will be presented is a complex problem. Our ImmunoID NeXT combines highly sensitive exome-scale DNA and RNA sequencing with the NeoantigenID™† analytics engine for a comprehensive survey of putative neoantigens.

The advanced computational pipeline configurations produce data-rich analytics:

- Accurate identification of SNVs, indels and fusions, which are an abundant source of potentially-immunogenic neoantigens
- Robust and accurate HLA typing of Class I and Class II MHC loci
- Comprehensive characterization of each putative neoantigen by combining tumor-specific small variants and fusions with the patient-specific HLA types and predicting neoantigens using our internally developed pan-allelic machine learning algorithm, SHERPA™*
  - SHERPA relies upon a proprietary, high quality and unambiguous training dataset generated by performing immunopeptidomics on ~70 MHC Class I alleles using monoallelic cell lines. The scale and scope of SHERPA was further expanded by using a large, systematically reprocessed and curated repository of publicly available mono- and multi-allelic immunopeptidomics datasets, as well as publicly available binding affinity data. This combined approach resulted in one of the largest training datasets consisting of 180 unique human alleles. Integrating data from diverse cell line and tissue types improved the generalizability of our models, a critically important aspect when applying our models to patient samples.
  - SHERPA incorporates peptide and binding pocket information, expression level of the source protein, proteasomal cleavage, and features representing genes and regions propensities to comprehensively capture all aspects of epitope presentation.
- Additional immunogenomics analytics to capture the full tumor biology and the complexity of the tumor microenvironment

†Please refer to NeoantigenID Analytics brochure for more information.
*Please refer to SHERPA data sheet for detailed information.

ImmunoID NeXT integrates industry-standard algorithms and tools to produce a high quality and comprehensive dataset:

DNA Pipeline	RNA Pipeline
Raw data files and variant calls	Raw data files and variant calls
Somatic variant annotation	Somatic variant annotation
Copy Number Alternations (CNA)	Gene expression
Germline HLA typing by allele	Fusion events
NeoantigenID Analytics	
Tumor mutational burden, Neoantigen burden, and Personalis Composite Neoantigen Presentation Score (NEOPS)	
SHERPA-powered neoantigen characterization, binding and presentation prediction, secondary immunogenicity parameters, expression metrics	
InfiltrateID™ Analytics	
InfiltrateID leverages the augmented gene expression data derived from the NeXT Transcriptome to compute enrichment scores for eight distinct immune cell types from a single tumor specimen, using the single-sample gene set enrichment analysis.	
ImmunogenomicsID™ Analytics	
HLA loss of heterozygosity, Microsatellite instability status, Integrated summary of DNA and RNA data related to key pathways in immuno-oncology	
Oncoviruses	
Detection of the main oncoviruses and their genotypes	
Optional Analytics	
Optional clinical report on the genetic alterations found in 247 cancer-related genes for targeted therapy selection as well as tumor mutational burden (TMB) and microsatellite instability (MSI) status for immunotherapy selection. The clinical report also delivers relevant therapy recommendations and clinical trial matches.	

Reliable Project and Data Delivery

Processes and systems to ensure your project is delivered within the agreed upon timelines:

Single Point of Contact

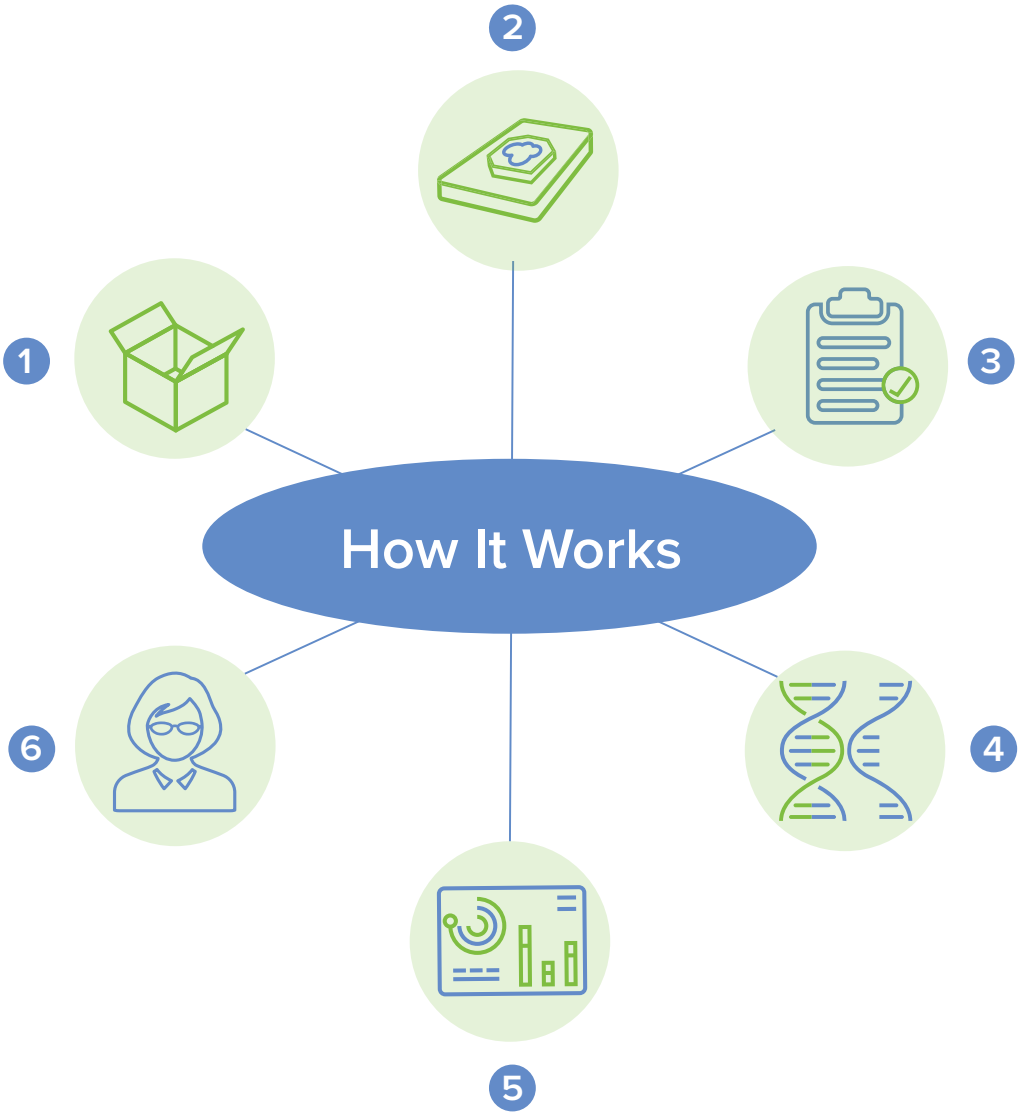
- A project manager (PM) is assigned to the study and will be your point of contact for status updates and ongoing communication
- PMs are PhD-level scientists with deep scientific and laboratory experience

Real-time Project and Sample Status

- Symphony Genomics Management System links LIMS, pipelines, databases, and other internal systems for real-time project status and sample-level tracking with our PM team
- Symphony enables visibility to the process through automated QC alerts for key milestones and delivery of data with an expedited turnaround time

Lock Down of the Platform and Pipeline Versions

- Symphony allows lock down of the platform and analytical pipeline versions for the life of your study
- Customization in reporting to meet the needs of client's downstream process and pipelines



1 Sample Arrival

ImmunoID NeXT requires paired tumor and matched normal analysis. The moment samples arrive at our CAP-accredited, CLIA-certified laboratory, the samples are given a unique sample ID and are tracked in LIMS and Symphony.

2 Sample Sparing Preparation

Our laboratory staff bring a wealth of operational expertise, allowing us to implement our optimized sample-sparing method.

3 Quality Review

Prior to sequencing, samples undergo robust QC assessment. Automated QC alert is provided to customers at key milestones in the process.

4 Sequencing

The NeXT Exome and NeXT Transcriptome assays run simultaneously to streamline processes and save time.

5 Analysis

Data is then processed through our integrated analytical pipelines to produce a comprehensive immuno-genomics dataset.

6 Technical and Scientific Support

Upon data delivery, a Field Application Scientist is available to walk through the data with you, answer questions, and follow up with our scientific team as needed.

Personalis®

Working Together For More Effective Neoantigen Based Cancer Therapeutics

When you work with Personalis for personalized cancer therapy development, you get a team of scientific and operational experts who are focused on your success.

Unlike other genomics providers that require multiple specimens, or the shipping of specimens to additional partner labs, ImmunoID NeXT requires only one tumor sample and one normal sample—simplifying operations and decreasing risks.

ImmunoID NeXT provides enhanced coverage of all coding genes to help you identify neoantigens that would otherwise be missed by standard exome assays. We provide you with raw data and variant calls as well as enhanced computational analysis for deeper insights into tumor biology.

Through our broad platform, advanced analytics, and seamless project management we reliably deliver high quality immunogenomics data to better inform your clinical and translational studies.

Get in touch

To learn more about how we can help with your neoantigen identification needs, contact us at **info@personalis.com.**

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