Unlock the Power of Immune Checkpoint Inhibitors

By harnessing the body’s immune system to detect and destroy tumor cells, immune checkpoint inhibitors are rapidly ushering in a new era of precision medicine. Although immune checkpoint inhibitors have demonstrated durable clinical responses across several tumor types, these therapies are costly and may present toxic side effects.

Identify Patients More Likely to Respond to Immune Checkpoint Inhibitors with Biomarker Testing from Caris Molecular Intelligence:

**PD-L1**

*Programmed death ligand-1 (PD-L1)* is among the most important checkpoint proteins that mediate tumor-induced immune suppression through T-cell downregulation\(^1\). PD-L1 expression may indicate response to immune checkpoint inhibitors.

Caris has performed more than 30,000 PD-L1 tests across all lineages.

**MSI**

*Microsatellite instability (MSI)* is caused by failure of the DNA mismatch repair (MMR) system. MSI-High correlates to an increased neoantigen burden, which may respond more favorably to immune checkpoint inhibitors.

MSI testing is included for all colorectal and endometrial cancers.

**TML**

*Total mutational load (TML)* measures the total number of non-synonymous somatic mutations identified per megabase of the genome coding area. Tumors with high TML likely harbor neoantigens and may respond more favorably to immune checkpoint inhibitors.

TML is reported for all solid tumors tested with Next-Generation Sequencing (592 genes).

Comprehensive genomic and proteomic profiling with Caris Molecular Intelligence can help you make more informed therapy decisions when considering immune checkpoint inhibitors.

Total Mutational Load – Immune Checkpoint Inhibitors Response

Caris Molecular Intelligence® tumor profiling includes Total Mutational Load (TML) status. TML is an emerging indicator for predicting response to immune checkpoint inhibitors across a wide spectrum of tumor types, including CRC, melanoma, NSCLC and urothelial carcinomas (bladder, renal, etc.).

High TML Across Caris Molecular Intelligence Cases

Genomic profiling with Caris Molecular Intelligence can help you make more informed therapy decisions when considering immune checkpoint inhibitors.

How It Works

Total mutational load by Next-Generation Sequencing measures the total number of non-synonymous, somatic mutations identified per megabase (Mb) of the genome coding area (a megabase is 1,000,000 DNA basepairs).

- Non-synonymous mutations are changes in DNA that result in amino acid changes in the protein.
- The new protein changes result in new shapes (neo-antigens) that are considered to be foreign to the immune system.
- Immune checkpoint inhibitors are able to stimulate and allow the immune system to detect these neo-antigens and destroy the tumor.
- Germline (inherited) mutations are not included in TML because the immune system has a higher likelihood of recognizing these alterations as normal.

TML: Immune Checkpoint Indication for Response

Tumors with significant numbers of mutations resulting in altered proteins (neo-antigens) may respond more effectively to immunotherapies.

To order or learn more, visit www.CarisMolecularIntelligence.com.

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