

Compliant with current HHS screening framework guidance for providers and users of synthetic oligonucleotides, as well as draft updates, Raytheon BBN's FAST-NA Scanner is software designed to integrate seamlessly with your current proprietary workflows to:



Screen nucleic acid sequences with 50 or more base pairs.



Analyze for both nucleic and amino acid matches at <2% false positive rates.



Deliver results at a rate of >10kb/second, approximately 1,000 times faster than BLAST. Unprecedented speed and accuracy for biological threat screening

FAST-NA Scanner signatures cover all threats on the IGSC list, which includes those on the US Commerce Control List and all human, animal, and plant pathogens on the Australia Group Control List.

## Additional Benefits:



Requires low amounts of computational resources: laptop scale vs. server farm scale.



Maintain control of your data: FAST-NA runs on your systems.



Unlimited usage: scan early and often low-cost support for customer prescreening.



Screen any nucleic acid sequence data, including gene or oligo synthesis orders, editing and assembly plans, sequencer reads, design collections, sample libraries, etc.



Support included for backend work-flow system integration and customization.



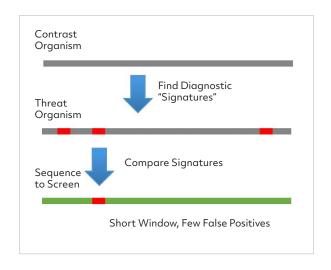
FAST-NA performance is validated against curated National Center for Biotechnology Information (NCBI) datasets for all covered taxa and non-threat sibling taxa (e.g., detection of *B. anthracis* and non-detection of *B. cereus*, *B. thuringiensis*, etc.).

## Included in your subscription:

- 1. FAST-NA Scanner software matcher software and updates.
- 2. Curated precision threat signature collections and updates.
- 3. Customer support and documentation to help you use FAST-NA effectively. A dedicated allotment of hours within your license for customer support, documentation, and integration to help you use FAST-NA effectively.

## Future capabilities in development:

- Combinatorial batch screening for oligos shorter than 50 base pairs.
- Direct screening of amino acid sequences.
- Contact us for additional capability requirements



## Contact us to learn about our customized trials.

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