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Microsoft

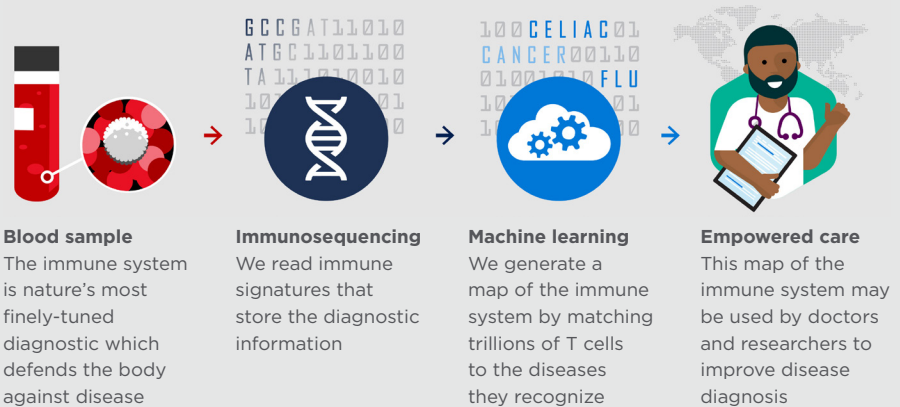
Translating the immune system to help diagnose disease

THE ANTIGEN MAP

Adaptive Biotechnologies' immunoSEQ[®] assay profiles the adaptive immune system using next-generation sequencing of T-cell and B-cell receptors. We are partnering with Microsoft to use its machine learning and computational power with Adaptive's TCR sequencing capabilities to map and decode the human immune system and develop blood-based tests for early-detection, diagnosis and disease monitoring.

A proof-of-concept for this initiative was published in Nature Genetics (Emerson, et al. *Nat Genet.* 2017), demonstrating our ability to identify TCRs capable of diagnosing cytomegalovirus (CMV). Now we are working to expand this effort to develop diagnostic tests for multiple diseases from a single blood test.

LEARNING TO DECODE THE IMMUNE SYSTEM TO HELP DIAGNOSE DISEASE



Apply now to see if your samples meet the criteria for the TCR Antigen Map Project.

adaptivebiotech.com/tcrantigenmap

PARTNER WITH US

We are seeking partnerships for sample sets that can be mined for disease-associated TCRs, on the scale of 100s to 1000s of samples.

HEMATOLOGY/ ONCOLOGY



- Pancreatic Cancer
- Ovarian Cancer

AUTOIMMUNE/ INFLAMMATORY DISEASE



- Type 1 Diabetes
- Celiac Disease

INFECTIOUS DISEASE



- Lyme Disease

Do you study another disease with an unmet need for a blood-based diagnostic? Let us know by submitting a proposal.

Sample Criteria & Benefits

SAMPLES WE'RE LOOKING FOR:

- Blood (2mL or 15µg DNA) or PBMC (-10^6 cells or 5µg DNA), matched tissue where available
- Taken when disease was known to be present but before any treatment that could drastically alter the immune system
- Matched controls (*where available*)
- Sample number: minimum 100 up to 1000s

IN RETURN:

- We'll provide you with the immunoSEQ TCR beta sequences from the samples you contribute to this project
- Your data will be yours to analyze and publish
- We will retain rights to analyze the data in combination with other data sets

**For more information,
contact us:**

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