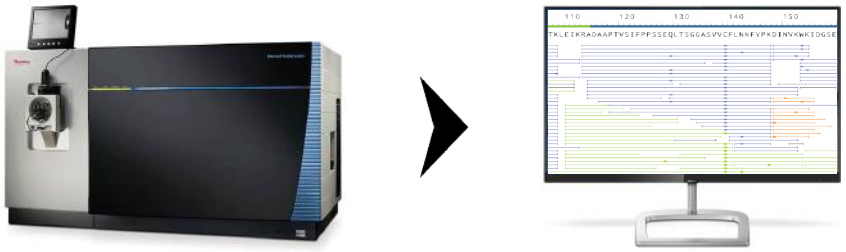
ANTIBODY PROTEIN SEQUENCING

Have you **lost** the hybridoma for your key research antibody?

Has batch-to-batch variability made your research **irreproducible**?

Are you down to the **last 9µg** of your sample?



Mass spectrometry-based protein sequencing can rescue lost antibodies, improve reproducibility & identify glycosylation sites. Due to the sensitivity & resolution of modern mass spectrometers, and the advancement of machine learning-based algorithms, researchers are now able to safeguard their efforts and ensure the legitimacy, accuracy & reproducibility of their research.

REmAb®

- Is the **leading** protein sequencing platform
- Achieves full sequence coverage with the **highest accuracy and throughput**
- Succesfully handles protein contaminants and **oligoclonal** backgrounds
- Safeguards **lifetime reproducibility**

You regularly backup your hard drive,
it's time to start backing up your research.

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OUR PROCESS

de novo PROTEIN SEQUENCING

REmAb®

Our REmAb® platform uses proprietary algorithms incorporating Big Data and machine learning to determine the highest probability sequence.

We ensure you receive not only 100% coverage, but also 100% accuracy.

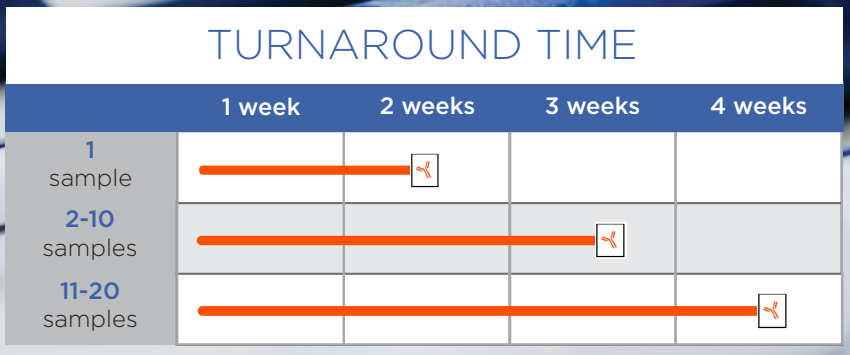
Upon receiving your sample, we perform proprietary protein chemistry and multiple digestions, utilizing a minimum of 5 enzymes. We then analyze your samples using industry leading Orbitrap™ mass spectrometers.

Once the mass spec acquisition is complete, the data is automatically uploaded and analyzed by our REmAb® sequencing platform. Although our sequencing and assembly stages are fully automated, our bioinformatics specialists also manually check the resulting sequence alongside the generated spectra, ensuring we attain not only 100% coverage, but also 100% accuracy.

Results are then delivered electronically (password encrypted) within **1-2 weeks.**

** expedited options are available*

TURNAROUND TIME

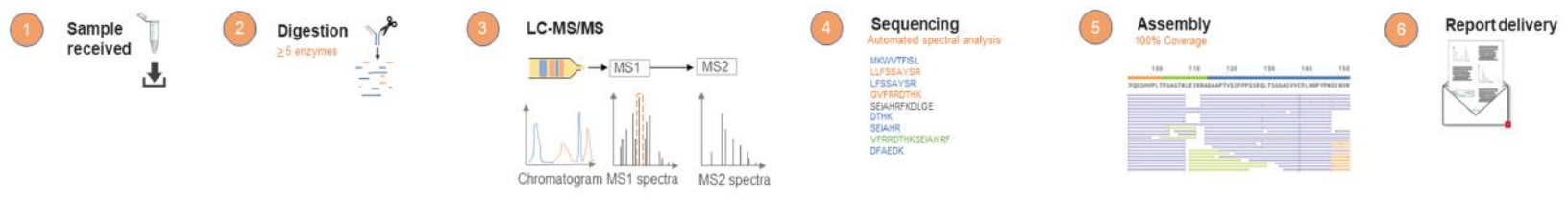


≥ **100** µg of sample

≥ **80%** purity

Any Species. Any Isotype.

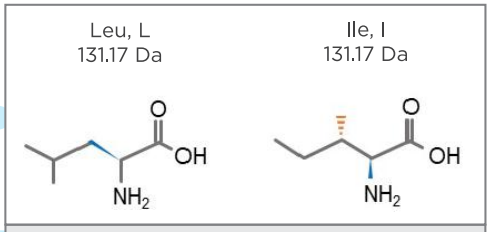
The REmAb® Process



Contact us today

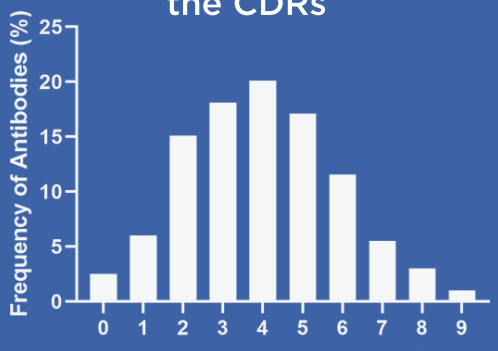
Find out why 9 of the Top 10 Pharmas REmAb® their mAbs

WILD®



Isoleucine (I) and leucine (L) are isobaric amino acids, meaning they have **the same molecular mass**. Using conventional MS techniques, you cannot easily distinguish between the two.

2017 Study of the Prevalence of I/L in the CDRs



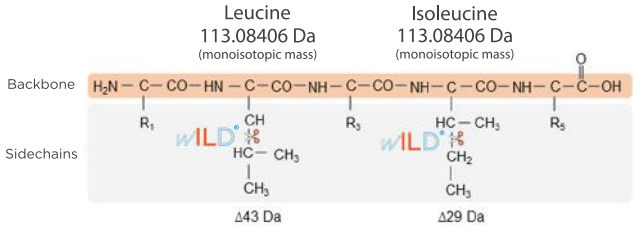
97% mAbs will contain >1 Ile/Leu residue in their CDRs

>50% mAbs contained >4 Ile/Leu residues in their CDRs

~10% of sequenced mAbs contained >7 Ile/Leu residues

WILD® uncovers all Ile and Leu residues **accurately** and with **high throughput**

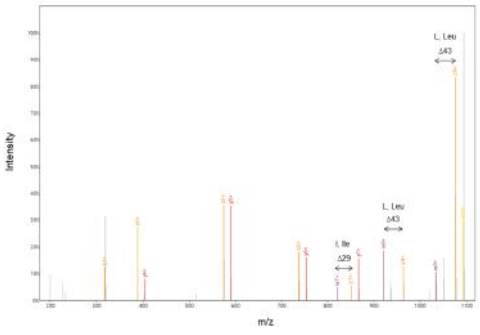
How does WILD® work?



Though I and L are isobaric, their w-ions are not.

To sequence a protein, digested peptides are analyzed in a mass spectrometer, where the peptide backbone undergoes fragmentation into many N- and C-terminal ions, including *z*-ions. C-terminal *z*-ions contain the sidechains of the peptide backbone. Fragmentation of the *z*-ion sidechainds yields *w*-ions.

Rapid Novor employs proprietary protein chemistry & Orbitrap Fusion™ instruments that perform electron-transfer high energy collision dissociation (EThcD). By observing the difference between the mass of *z*- and *w*-ions, we are able to distinguish isoleucine from leucine.



References:

McDonald, Z., et al. (2018) "Large Scale Study of the w-ion Isoleucine and Leucine Determination (WILD™) Method in Antibody De Novo Protein Sequencing," in 66th ASMS. 2018: San Diego.

Le Bihan, T., et al. (2019) "Increased De Novo Protein Sequencing Coverage with Optimal Protease Cocktail," in 67th ASMS. 2019: Atlanta.

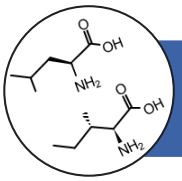
Ma, B. (2015). Novor: real-time peptide de novo sequencing software . J Amer Soc Mass Spec 26(11): 1885-1894

Johnson, R.S., Martin, S.A., and Biemann, K (1987). Novel Fragmentation Process of Peptides by Collision-Induced Decomposition in a Tandem Mass Spectrometer: Differentiation of Leucine and Isoleucine," Anal Chem 59 (21): 2621-2625

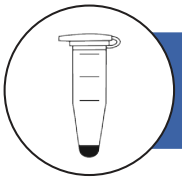
Zhokhov, S. S., Kovalyov, S. V., Samgina, T. Y., and Lebedev, A. T. (2017) "An EThcD-Based Method for Discrimination of Leucine and Isoleucine Residues in Tryptic Peptides," J. Amer Soc Mass Spec 28(8): 1600-1611

RAPID NOVOR
SPEED UP DISCOVERY

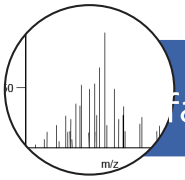
WHY RAPID NOVOR?



We were the first to offer a high-throughput commercial solution to distinguish between isoleucine and leucine



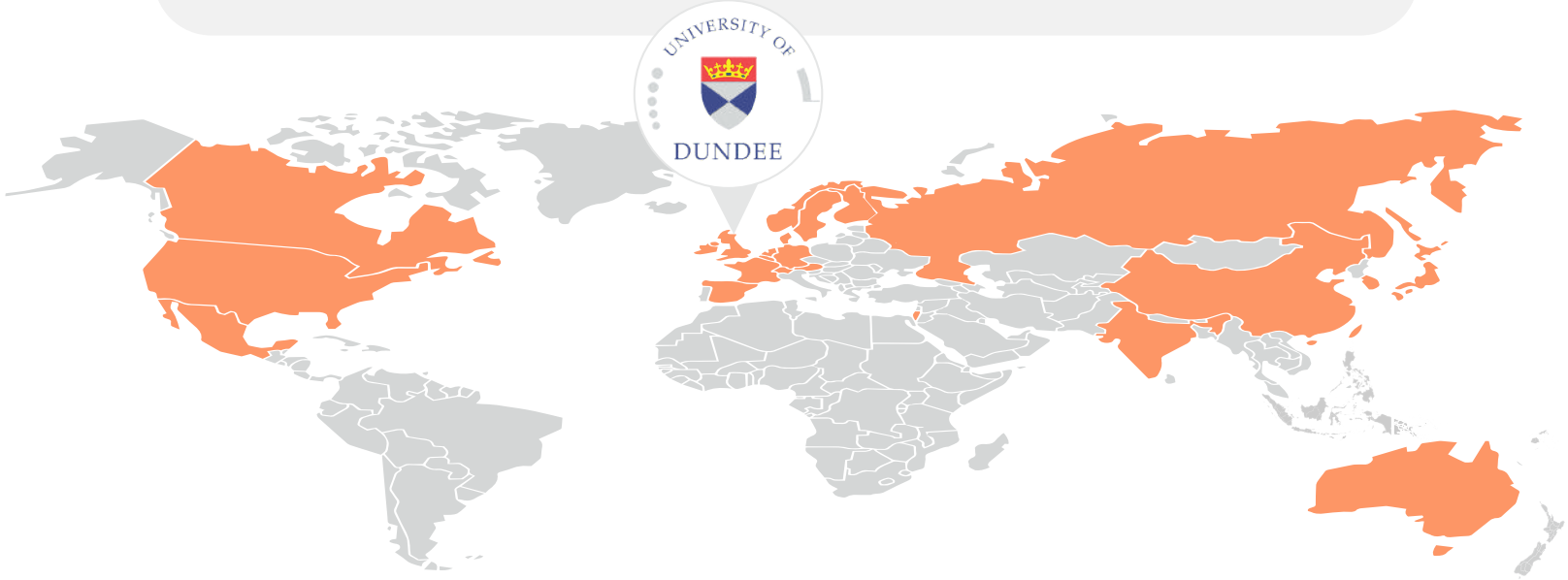
We have successfully delivered a full protein sequence with only 9µg of starting material



We are the largest privately funded mass spec proteomics facility in Canada

We have a proven track record of successfully sequencing oligoclonal projects

> *"We were focused on species isotype switching for our research. As there is high species diversity, there is no hybridoma. Sequencing our antibodies saved us money and time in evaluating targets and characterising them."*



Rapid Novor Inc, has successfully completed **thousands of protein sequencing projects** and has won the trust of more than **230** scientific institutions around the world.

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