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Resources

De Novo Antibody
Protein Sequencing with
Mass Spectrometry

**Leucine Isoleucine
Determination**

Review: Antibody
Protein Sequence
Analysis Using Mass
Spectrometry

Coverage View

Moving Towards
Recombinant mAbs

ASMS 2016 Poster

WILD™

Stop **guessing**. Go WILD™.

Ile ? Leu



W ion Ile/Leu Determination

What's WILD™?

W-ion **I**soleucine **L**eucine **D**etermination (WILD™) is the first high-throughput commercial grade service that can distinguish Leucine and Isoleucine with certainty using mass spectrometry.

Why this is important?

Although Leucine and Isoleucine have the same molecular weight, the difference in their structure will cause differences in biological activities. In the context of antibodies, Leucine and Isoleucine in and around the CDR regions may have significant impact on the antibodies' affinity and specificity.

With WILD™, you can stop trying alternative forms during expression. In the past, to increase the chance of success, expression of multiple alternative forms are generally

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preferred. This means somewhere between 2 to 16 forms depending on how many I/L positions one has to try. But the cost associated with this can be prohibitive. In some undesirable situations, we have seen as many as 9 I/L positions in the CDRs, which means one needs to express 512 forms in order to be sure that everything is covered. With the WILD™, we take the guessing out of your sequences.

How can I take advantages of WILD™?

WILD™ is offered as part of our REmAb™ sequencing service. We perform WILD™ on all our sequencing project. With the WILD™, w-ions are used to determine each and every Leucine/Isoleucine position in the variable region of the heavy and light chain sequences.

References

- Johnson, R. S., Martin, S., Biemann, K., Stults, J. T., & Watson, J. T. (1987). Novel fragmentation process of peptides by collision-induced decomposition in a tandem mass spectrometer: differentiation of leucine and isoleucine. *Analytical Chemistry*, 59(21), 2621–2625.
- Xiao, Y., Vecchi, M. M., & Wen, D. (2016). Distinguishing between Leucine and Isoleucine by Integrated LC-MS Analysis using an Orbitrap Fusion Mass Spectrometer. *Analytical Chemistry*, acs.analchem.6b03409. <http://doi.org/10.1021/acs.analchem.6b03409>
- Zhokhov, S.S., Kovalyov, S.V., Samgina, T.Y. et al. An EThcD-Based Method for Discrimination of Leucine and Isoleucine Residues in Tryptic Peptides. *J. Am. Soc. Mass Spectrom.* (2017) 28: 1600.

Further Readings

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