# **Resource Summary Report**

Generated by dkNET on Apr 27, 2025

# **Noble Research Lab**

RRID:SCR\_007204

Type: Tool

### **Proper Citation**

Noble Research Lab (RRID:SCR\_007204)

#### **Resource Information**

URL: http://noble.gs.washington.edu/

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**Description:** Our research group develops and applies computational techniques for modeling and understanding biological processes at the molecular level. Our research emphasizes the application of statistical and machine learning techniques, such as hidden Markov models and support vector machines. We apply these techniques to various types of biological data, including DNA and protein sequence data, as well as gene expression data from microarray experiments. We are currently developing methods for analyzing shotgun proteomics data, for characterizing protein function, structure and interactions, and for understanding the structure and regulatory influence of chromatin.

Synonyms: Noble Lab

Resource Type: data or information resource, organization portal, laboratory portal, portal

**Funding:** 

Resource Name: Noble Research Lab

Resource ID: SCR\_007204

Alternate IDs: nlx\_45779

**Record Creation Time:** 20220129T080240+0000

**Record Last Update:** 20250426T055920+0000

## Ratings and Alerts

No rating or validation information has been found for Noble Research Lab.

No alerts have been found for Noble Research Lab.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

Schreiber J, et al. (2021) Prioritizing transcriptomic and epigenomic experiments using an optimization strategy that leverages imputed data. Bioinformatics (Oxford, England), 37(4), 439.

Ramachandran S, et al. (2021) FPTMS: Frequency-based approach to identify the peptide from the low-energy collision-induced dissociation tandem mass spectra. Journal of proteomics, 235, 104116.