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Web watch

THE HIGHWAY FROM GENOME TO PROTEOME

- <http://www.peptideatlas.org>

Following the sequencing of the human genome, the next step is the verification and functional annotation of all predicted genes and their protein products. On a proteome scale, protein expression can be analysed by high-throughput proteomics technologies. Before examining the expression of your favourite molecules, navigate the PeptideAtlas database, just in case the data you are generating or looking for are already available.

The PeptideAtlas is “a multi-organism, publicly accessible compendium of peptides identified in a large set of tandem mass spectrometry proteomics experiments.” The goal of the project is “full annotation of eukaryotic genomes through a thorough validation of expressed proteins.”

To ensure a high-quality database, all results of sequence searching have been processed through a robust and accurate statistical approach, PeptideProphet. All peptides have been mapped to Ensembl and can be viewed on the Ensembl Genome Browser.

PeptideAtlas was developed by the Seattle Proteome Center (SPC), a highly interactive, multidisciplinary group that brings together scientific expertise from diverse areas such as biology, chemistry, proteomics, physics, bioinformatics and statistics. The aim of SPC is to enhance and develop innovative proteomics technologies and software tools and apply them to biological questions. Some of their experimental data have already been published, such as the budding yeast and the human plasma PeptideAtlas, but many are still unpublished.

The online database administers data in the public domain, and if you use any data from the PeptideAtlas project in a publication, you are asked to cite the relevant PeptideAtlas papers. You are also encouraged to contribute your own findings.

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