

Resource Summary Report

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Frey Lab

RRID:SCR_008859

Type: Tool

Proper Citation

Frey Lab (RRID:SCR_008859)

Resource Information

URL: <http://genes.toronto.edu/>

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Description: The Frey Lab develops techniques that use large scale datasets to derive predictive models of how genes and many other genomic features act in combination to produce genetic messages that control cellular activities. We have most recently focused on how organisms use alternative splicing to generate a tremendous level of biological complexity that cannot be explained by gene expression alone (Nature, 2010). Some of the tools, software and databases provided by the Frey Lab are affinity propagation, splicing prediction, PTMClust - A Post-translational Modification Refinement Algorithm, the "epitome": A new model of patterns, transformation invariant clustering and subspaces, learning flexible sprites from images and videos, phase unwrapping by loopy belief propagation, useful Matlab scripts, bioinformatics links, and SeedSearcher: A motif finder.

Abbreviations: Frey Lab

Synonyms: U of T Frey Lab, University of Toronto - Frey Lab, Frey Lab - Probabilistic and Statistical Inference Group University of Toronto

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

Keywords: gene, genetic message, affinity propagation, alternative splicing prediction, motif, tool, software, database, flobjct analysis, signal processing, graphical model, inference algorithm, computational vision, alternative splicing, transcriptome, genome, gene function prediction, gene function, computational biology, message passing

Resource Name: Frey Lab

Resource ID: SCR_008859

Alternate IDs: nlx_149187

Record Creation Time: 20220129T080249+0000

Record Last Update: 20260801T190731+0000

Ratings and Alerts

No rating or validation information has been found for Frey Lab.

No alerts have been found for Frey Lab.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

Chung C, et al. (2011) Computational refinement of post-translational modifications predicted from tandem mass spectrometry. Bioinformatics (Oxford, England), 27(6), 797.