

ABSTRACT

Shotgun proteomics is the technology of choice for exploratory, large-scale studies of the proteome. In a typical experiment, the aim is to establish **protein expression profiles** for various biological conditions. However, the **genetic variation is routinely neglected** at the protein level. **Decryptor allows the detection of protein variants** in standard shotgun proteomics data. This **poster shows the required steps** to perform such an analysis of MS/MS spectra.



INSTITUTE OF MOLECULAR AND TRANSLATIONAL MEDICINE



SIGNING UP

Navigate to <http://decryptor.imtm.cz>.

decryptor (1.1.3) analyses data from tandem mass spectrometry of human proteome for presence of point alterations. Subsequently, decryptor deduces DNA/mRNA alterations whenever possible.

See example.
(email: *guest*, password: *guest*).

To use decryptor, you need to [log-in](#). If not registered yet, [sign-up](#).

[Materials](#) | [Release notes](#) | [Changelog](#) | [Acknowledgement](#) | [Contact us](#)

Register.

First Name:

Last Name:

Affiliation:

Email Address:

Password:

Confirm your email address.

Welcome miroslav.hruska@upol.cz!

You can confirm your email through the link below:

[Confirm my account](#)

Log in.

Email Address:

Password:

DATA SEARCHING

Specify search parameters and upload the sample.

Fill-in last configuration | Reset configuration

(?) MS/MS files [.mzML, .mzXML, .mgf; [Spectra convertor](#)] (max: 4 GB)

Browse... SILAC_R2-10_TR-A_...mzML

(?) Fixed modifications: Carbamidomethyl (C +57.02 Da)

(?) Filter modifications: Car

(?) Variable modifications: Carbamidomethyl (D +57.02 Da), Carbamidomethyl (E +57.02 Da), Carbamidomethyl (H +57.02 Da), Carbamidomethyl (K +57.02 Da), Carbamidomethyl (N-term +57.02 Da), CarbamidomethylIDTT (C +20.01 Da), Carbamyl (C +43.01 Da)

(?) Protease: trypsin

(?) Fragmentation: CID

(?) Precursor tolerance: 10 ppm

(?) Fragment tolerance: 0.5 Da

(?) Mail: miroslav.hruska@upol.cz

Choose mzML spectra to search.

Add fixed and variable modifications that correspond to the sample.

Select additional parameters for the search.

Specify email to get informed about the end of the search.

Experiment status

Experiment ID: 2a4980acb9ac301b

Subexperiments

ID	Results	Queued	Running	Log
2a4980acb9ac301b_0000	Open	0	0	mzML Conversion: OK. Reference proteome results: OK. Mutant proteome results: OK. Denovo results: OK. Processed results: OK.

Wait until the results are ready to be opened.

Dear user,

decryptor has just finished processing your results from experiment "SILAC_R2-10_TR-A_". You can access them at http://decryptor.imtm.cz/experiment_view/2a4980acb9ac301b_0000.

DETECTION RESULTS

Browse the results using multiple views, or export them.

[Filter results](#)

[Experimental meta-information](#)

[Export results](#)

Identification

Summary: 1262 proteins, 5421 ref. peptides, 20 alterations

Proteins with sequence alterations

Protein	Spectra / Peptides / Unique peptides	Alterations	Detrimental effect	DNA/mRNA alteration source	Disease relevance
electron-transfer-flavoprotein, alpha polypeptide (ETFA)	22 / 10 / 10	73: T>I 171: I>L	1.52	COSMIC v.68—large_intestine	
small nuclear ribonucleoprotein polypeptide A' (SNRPA1)	20 / 6 / 6	87: P>L	0.76	COSMIC v.68—lung ICGC 15.1—LUSC-US	

I. Protein/Gene information

Protein: small nuclear ribonucleoprotein polypeptide A'

Protein ID: ENSP00000452836

Coverage: 66.23 %, isoform-specific peptides: 1

Synonyms: Lea1

External: MIM:603521, HGNC:HGNC:11152, Ensembl:ENSG00000131876, HPRD:04629, Vega:OTTHUMG00000149871, Entrez:6627

[UniProt summary](#)

[NCBI GeneRif](#)

[Gene Ontology](#)

Peptide view

<< Protein view

Peptide sequence: IGEGLDQALLCTELILTNNLSVELGDLPLASLK

Peptide-spectrum matches

sequence	modifications	charge	MZ	RT	XTandem -Log ₁₀ E-Value	Alteration	Alternative interpretation of alteration
IGEGLDQALLCTELILTNNLSVELGDLPLASLK	11(Carbamidomethyl)	3	1251.01	5978.7263	2.19382	P>L (16.0313 Da)	[9] P-Oxidation or Hydroxylation [10] C-Oxidation or Hydroxylation